(19) **United States**

(12) **Patent Application Publication**

McLeod et al.

(10) **Pub. No.: US 2020/0283391 A1**

(43) **Pub. Date: Sep. 10, 2020**

(54) **COMPOUNDS AND METHODS FOR TREATING, DETECTING, AND IDENTIFYING COMPOUNDS TO TREAT APICOMPLEXAN PARASITIC DISEASES**

(71) Applicant: **The University Of Chicago**, Chicago, IL (US)

(72) Inventors: **Rima McLeod**, Chicago, IL (US); **Martin McPhillie**, Leeds (GB); **Colin W.G. Fishwick**, Leeds (GB); **Hernan Alejandro Lorenzi**, Rockville, MD (US); **Kai Wang**, Seattle, WA (US); **Taek-Kyun Kim**, Seattle, WA (US); **Yong Zhou**, Seattle, WA (US); **Leroy E. Hood**, Seattle, WA (US); **Ying Zhou**, Chicago, IL (US); **Kamal El Bissati**, Chicago (US); **James Gordon**, Leeds (GB); **Mark Hickman**, Silver Spring, MD (US); **QiGui Li**, Silver Spring, MD (US); **Craig Roberts**, Glasgow (GB)

(21) Appl. No.: **16/063,877**

(22) PCT Filed: **Dec. 20, 2016**

(86) PCT No.: **PCT/US2016/067795**

§ 371 (c)(1),
(2) Date: **Jun. 19, 2018**

Related U.S. Application Data

(60) Provisional application No. 62/270,264, filed on Dec. 21, 2015, provisional application No. 62/306,385, filed on Mar. 10, 2016.

Publication Classification

(51) **Int. Cl.**

C07D 215/233	(2006.01)
C07D 487/04	(2006.01)
C07D 401/12	(2006.01)
C07D 405/12	(2006.01)
A61P 33/06	(2006.01)
C07D 471/04	(2006.01)

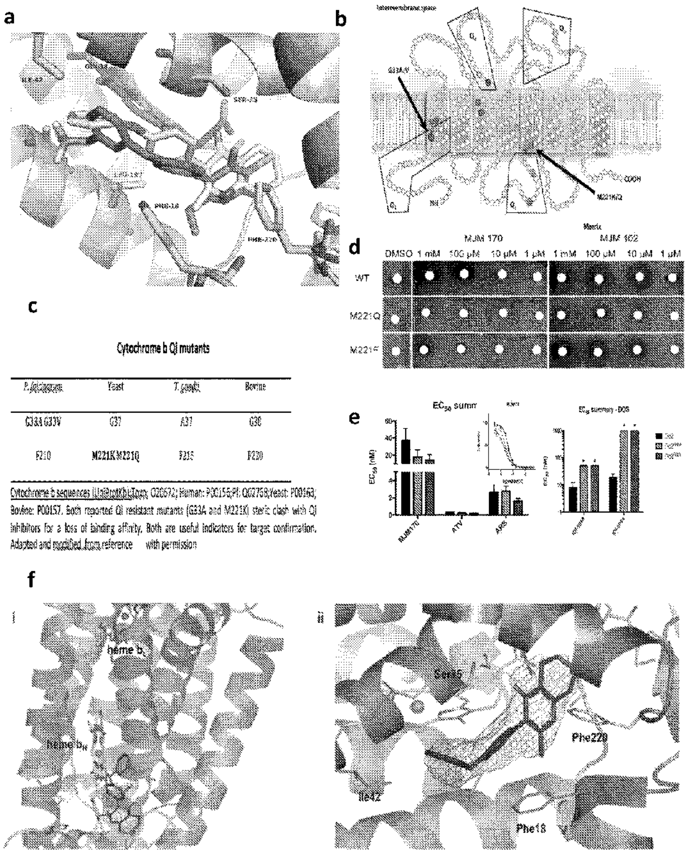
(52) **U.S. Cl.**

CPC ***C07D 215/233*** (2013.01); ***C07D 487/04*** (2013.01); ***C07D 471/04*** (2013.01); ***C07D 405/12*** (2013.01); ***A61P 33/06*** (2018.01); ***C07D 401/12*** (2013.01)

(57) **ABSTRACT**

Disclosed herein; are novel compounds for treating apicomplexan parasite related disorders, methods for their use; cell line and non-human animal models of the dormant parasite phenotype and methods for their use in identifying new drugs to treat apicomplexan parasite related disorders, and biomarkers to identify disease due to the parasite and its response to treatment.

Specification includes a Sequence Listing.



Cytochrome b Qi mutants

P. falciparum	Yeast	T. gondii	Bovine
G33A G33V	G37	A37	G38
F210	M221K M221Q	F215	F220

Cytochrome b sequences (UniProtKB) Toxo: Q20672; Human: P00156; Pf: Q02768; Yeast: P00163; Bovine: P00157. Both reported Qi resistant mutants (G33A and M221K) steric clash with Qi inhibitors for a loss of binding affinity. Both are useful indicators for target confirmation. Adapted and modified from reference with permission

FIGURE 1A

Figure 1: Host transcriptomics data during EGS infections of human HFF, MM6 or NSC cells. Differential gene expression analysis of human fibroblasts infected with T. gondii EGS strain after 2 hs, 18 hs, and 48 hs, monomac 6 cells infected with T. gondii EGS for 18 hs or neuronal stem cells infected with T. gondii EGS strain for 18 hs.

gene_ID	logFC HFF (2h / Uninf)	logFC HFF (18h / Uninf)	logFC HFF (48h / Uninf)	logFC MM6 (18h / Uninf)	logFC NSC (18h / Uninf)	Product Name
ENSG00000004846	-0.15	-4.24	-10.36	#N/A	#N/A	ATP-binding cassette, sub-family B (MDR/TAP), member 5
ENSG00000196616	-0.27	-5.58	-12.98	#N/A	#N/A	alcohol dehydrogenase 1B (class I), beta polypeptide
ENSG00000169607	0.88	4.90	5.69	#N/A	#N/A	cytoskeleton associated protein 2-like
ENSG00000089685	0.19	2.98	3.78	#N/A	#N/A	baculoviral IAP repeat containing 5
ENSG00000131747	0.64	4.07	4.31	#N/A	#N/A	topoisomerase (DNA) II alpha 170kDa
ENSG00000101057	-0.06	3.84	3.04	#N/A	#N/A	v-myb avian myeloblastosis viral oncogene homolog-like 2
ENSG00000148773	0.70	4.04	4.33	#N/A	#N/A	marker of proliferation Ki-67
ENSG00000170458	-0.94	-3.04	-5.04	2.15	#N/A	CD14 molecule
ENSG00000138347	1.33	3.91	3.54	#N/A	#N/A	myopalladin
ENSG00000138180	0.87	3.79	4.54	#N/A	#N/A	centrosomal protein 55kDa
ENSG00000078401	1.16	-2.53	-3.32	#N/A	#N/A	endothelin 1
ENSG00000154839	0.78	4.73	4.72	#N/A	#N/A	spindle and kinetochore associated complex subunit 1
ENSG00000068489	0.81	3.48	4.36	1.68	#N/A	proline rich 11
ENSG00000123358	2.02	-4.40	-4.52	#N/A	#N/A	nuclear receptor subfamily 4, group A, member 1
ENSG00000145386	0.51	4.28	4.94	#N/A	#N/A	cyclin A2
ENSG00000072571	0.67	4.37	4.79	#N/A	#N/A	hyaluronan-mediated motility receptor (RHAMM)
ENSG00000092853	0.39	3.85	3.52	#N/A	#N/A	claspin
ENSG00000093009	0.12	4.32	3.54	#N/A	#N/A	cell division cycle 45
ENSG00000142945	0.27	3.50	4.13	#N/A	#N/A	kinesin family member 2C
ENSG00000169679	0.24	4.10	4.82	#N/A	#N/A	BUB1 mitotic checkpoint serine/threonine kinase
ENSG00000111206	0.25	2.79	3.52	#N/A	#N/A	forkhead box M1
ENSG00000109805	0.10	4.51	4.61	#N/A	#N/A	non-SMC condensin I complex, subunit G
ENSG00000088325	0.04	2.99	3.84	#N/A	#N/A	TPX2, microtubule-associated
ENSG00000117724	0.46	3.94	4.54	#N/A	#N/A	centromere protein F, 350/400kDa
ENSG00000101447	1.24	3.43	4.52	#N/A	#N/A	family with sequence similarity 83, member D
ENSG00000168078	0.72	4.09	4.74	#N/A	#N/A	PDZ binding kinase
ENSG00000161888	-0.25	3.20	3.54	#N/A	#N/A	SPC24, NDC80 kinetochore complex component
ENSG00000237649	0.72	3.39	3.39	#N/A	#N/A	kinesin family member C1
ENSG00000111665	0.23	3.06	3.69	#N/A	#N/A	cell division cycle associated 3
ENSG00000138778	0.68	3.81	3.89	#N/A	#N/A	centromere protein E, 312kDa
ENSG00000196611	0.45	4.45	4.97	#N/A	#N/A	matrix metallopeptidase 1
ENSG00000146670	0.67	3.86	3.37	#N/A	#N/A	cell division cycle associated 5
ENSG00000198901	0.27	2.81	3.41	#N/A	#N/A	protein regulator of cytokinesis 1
ENSG00000186871	-1.06	4.11	4.13	#N/A	#N/A	excision repair cross-complementation group 6-like
ENSG00000090889	0.17	3.53	3.88	#N/A	#N/A	kinesin family member 4A
ENSG00000112742	-0.24	4.17	4.79	#N/A	#N/A	TTK protein kinase
ENSG00000165480	0.58	4.30	4.54	#N/A	#N/A	spindle and kinetochore associated complex subunit 3
ENSG00000164109	0.51	3.73	4.53	#N/A	#N/A	MAD2 mitotic arrest deficient-like 1 (yeast)
ENSG00000076382	-0.05	3.24	3.58	#N/A	#N/A	sperm associated antigen 5
ENSG00000119508	1.48	-3.24	-4.26	#N/A	#N/A	nuclear receptor subfamily 4, group A, member 3

gene_ID	logFC HFF (2h / Uninf)	logFC HFF (18h / Uninf)	logFC HFF (48h / Uninf)	logFC MM6 (18h / Uninf)	logFC NSC (18h / Uninf)	Product Name
ENSG00000100644	#N/A	#N/A	#N/A	1.07	#N/A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
ENSG00000173486	#N/A	#N/A	#N/A	1.07	2.60	FK506 binding protein 2, 13kDa
ENSG00000169926	#N/A	#N/A	#N/A	1.07	#N/A	Kruppel-like factor 13
ENSG00000010404	#N/A	#N/A	#N/A	1.07	#N/A	iduronate 2-sulfatase
ENSG00000153132	#N/A	#N/A	#N/A	1.06	#N/A	calmegin
ENSG00000282230	#N/A	#N/A	#N/A	1.06	#N/A	ADAM metallopeptidase domain 9
ENSG00000079739	#N/A	#N/A	#N/A	1.06	#N/A	phosphoglucomutase 1
ENSG00000143198	#N/A	#N/A	#N/A	1.06	1.23	microsomal glutathione S-transferase 3
ENSG00000143458	#N/A	#N/A	#N/A	1.06	#N/A	GA binding protein transcription factor, beta subunit 2
ENSG00000173221	#N/A	#N/A	#N/A	1.06	2.42	glutaredoxin (thioltransferase)
ENSG00000153048	#N/A	#N/A	#N/A	1.06	#N/A	calcium regulated heat stable protein 1, 24kDa
ENSG00000101363	#N/A	#N/A	#N/A	1.06	1.05	mannosidase, beta A, lysosomal-like
ENSG00000120727	#N/A	#N/A	#N/A	1.06	#N/A	poly(A) binding protein interacting protein 2
ENSG00000103335	#N/A	#N/A	#N/A	1.05	#N/A	piezo-type mechanosensitive ion channel component 1
ENSG00000112773	#N/A	#N/A	#N/A	1.05	#N/A	family with sequence similarity 46, member A
ENSG00000121067	#N/A	#N/A	#N/A	1.05	#N/A	speckle-type POZ protein
ENSG00000142002	#N/A	#N/A	#N/A	1.05	#N/A	dipeptidyl-peptidase 9
ENSG00000178567	#N/A	#N/A	#N/A	1.05	#N/A	EPM2A (laforin) interacting protein 1
ENSG00000103671	#N/A	#N/A	#N/A	1.05	#N/A	thyroid hormone receptor interactor 4
ENSG00000247556	#N/A	#N/A	#N/A	1.05	#N/A	OIP5 antisense RNA 1
ENSG00000256235	#N/A	#N/A	#N/A	1.05	#N/A	small integral membrane protein 3
ENSG00000119844	#N/A	#N/A	#N/A	1.05	#N/A	aftiphilin
ENSG00000119471	#N/A	#N/A	#N/A	1.04	#N/A	hydroxysteroid dehydrogenase like 2
ENSG00000102910	#N/A	#N/A	#N/A	1.04	#N/A	lon peptidase 2, peroxisomal
ENSG00000106261	#N/A	#N/A	#N/A	1.04	#N/A	zinc finger with KRAB and SCAN domains 1
ENSG00000138085	#N/A	#N/A	#N/A	1.04	#N/A	all-trans retinoic acid-induced differentiation factor
ENSG00000102908	#N/A	#N/A	#N/A	1.04	#N/A	nuclear factor of activated T-cells 5, tonicity-responsive
ENSG00000161955	#N/A	#N/A	#N/A	1.04	#N/A	tumor necrosis factor (ligand) superfamily, member 13
ENSG00000189343	#N/A	#N/A	#N/A	1.04	#N/A	ribosomal protein S2 pseudogene 46
ENSG00000148908	#N/A	#N/A	#N/A	1.04	1.21	regulator of G-protein signaling 10
ENSG00000135090	#N/A	#N/A	#N/A	1.04	#N/A	TAO kinase 3
ENSG00000165118	#N/A	#N/A	#N/A	1.04	#N/A	chromosome 9 open reading frame 64
ENSG00000167193	#N/A	#N/A	#N/A	1.03	#N/A	v-crk avian sarcoma virus CT10 oncogene homolog
ENSG00000172830	#N/A	#N/A	#N/A	1.03	#N/A	slingshot protein phosphatase 3
ENSG00000166927	#N/A	#N/A	#N/A	1.03	#N/A	membrane-spanning 4-domains, subfamily A, member 7
ENSG00000123975	#N/A	#N/A	#N/A	1.03	1.87	CDC28 protein kinase regulatory subunit 2
ENSG00000107819	#N/A	#N/A	#N/A	1.03	#N/A	sideroflexin 3
ENSG00000143369	#N/A	#N/A	#N/A	1.03	#N/A	extracellular matrix protein 1
ENSG00000038219	#N/A	#N/A	#N/A	1.02	#N/A	biorientation of chromosomes in cell division 1-like 1
ENSG00000127507	#N/A	#N/A	#N/A	1.02	#N/A	adhesion G protein-coupled receptor E2

FIGURE 1B

ENSG00000143476	0.29	3.85	3.54	#N/A	#N/A	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
ENSG00000107968	1.88	-1.74	-1.01	#N/A	#N/A	mitogen-activated protein kinase kinase kinase 8
ENSG00000198826	0.20	3.21	4.14	#N/A	#N/A	Rho GTPase activating protein 11A
ENSG00000013810	-0.03	3.02	3.08	#N/A	#N/A	transforming, acidic coiled-coil containing protein 3
ENSG00000172548	0.61	-4.93	-4.60	#N/A	#N/A	NIPA-like domain containing 4
ENSG00000137331	2.18	-2.15	-2.31	#N/A	#N/A	immediate early response 3
ENSG00000024526	0.14	4.26	5.66	-1.12	#N/A	DEP domain containing 1
ENSG00000112984	0.64	3.00	4.41	#N/A	#N/A	kinesin family member 20A
ENSG00000166592	1.27	-5.02	-3.14	#N/A	#N/A	Ras-related associated with diabetes
ENSG00000158402	-0.76	3.59	4.21	#N/A	#N/A	cell division cycle 25C
ENSG00000108342	6.25	2.52	8.82	#N/A	#N/A	colony stimulating factor 3 (granulocyte)
ENSG00000171241	0.64	3.95	4.06	#N/A	#N/A	SHC SH2-domain binding protein 1
ENSG00000122952	-0.15	3.44	3.18	#N/A	1.03	ZW10 interacting kinetochore protein
ENSG00000163874	2.83	-2.49	-1.21	#N/A	#N/A	zinc finger CCCH-type containing 12A
ENSG00000131153	0.82	3.78	3.05	#N/A	#N/A	GINS complex subunit 2 (Psf2 homolog)
ENSG00000167900	0.10	2.57	3.19	#N/A	#N/A	thymidine kinase 1, soluble
ENSG00000143228	0.11	4.22	4.72	#N/A	#N/A	NUF2, NDC80 kinetochore complex component
ENSG00000149968	0.49	2.82	3.64	#N/A	#N/A	matrix metallopeptidase 3
ENSG00000241644	-0.77	-3.80	-4.78	#N/A	#N/A	indolethylamine N-methyltransferase
ENSG00000117399	-0.15	3.12	3.85	#N/A	#N/A	cell division cycle 20
ENSG00000175063	1.38	4.46	4.61	#N/A	1.74	ubiquitin-conjugating enzyme E2C
ENSG00000134690	-0.42	3.65	3.73	#N/A	#N/A	cell division cycle associated 8
ENSG00000154027	0.45	3.28	2.92	#N/A	#N/A	adenylate kinase 5
ENSG00000122877	1.33	-6.24	-6.00	#N/A	#N/A	early growth response 2
ENSG00000183856	-0.17	3.03	3.39	#N/A	#N/A	IQ motif containing GTPase activating protein 3
ENSG00000205835	-0.09	-2.62	-7.23	#N/A	#N/A	geminin coiled-coil domain containing
ENSG00000011426	0.40	3.53	4.15	#N/A	#N/A	anillin, actin binding protein
ENSG00000071539	0.62	3.37	3.86	#N/A	#N/A	thyroid hormone receptor interactor 13
ENSG00000080986	-0.06	3.45	3.76	#N/A	#N/A	NDC80 kinetochore complex component
ENSG00000090339	1.49	-2.27	-1.20	1.35	#N/A	intercellular adhesion molecule 1
ENSG00000087494	0.30	-3.14	-5.48	#N/A	#N/A	parathyroid hormone-like hormone
ENSG00000118193	0.70	4.18	5.11	#N/A	#N/A	kinesin family member 14
ENSG00000179388	1.29	-7.45	-6.06	#N/A	#N/A	early growth response 3
ENSG00000137193	1.29	-2.09	-1.63	#N/A	#N/A	Pim-1 proto-oncogene, serine/threonine kinase
ENSG00000163535	0.27	2.63	3.64	#N/A	#N/A	shugoshin-like 2 (S. pombe)
ENSG00000075702	1.30	4.35	4.16	-1.33	#N/A	WD repeat domain 62
ENSG00000151725	0.29	3.71	3.38	#N/A	#N/A	centromere protein U
ENSG00000163808	-0.26	3.65	3.89	#N/A	#N/A	kinesin family member 15
ENSG00000137310	0.62	3.71	3.13	#N/A	#N/A	transcription factor 19
ENSG00000065328	0.49	4.75	4.19	#N/A	#N/A	minichromosome maintenance complex component 10
ENSG00000186185	0.82	4.66	4.16	#N/A	#N/A	kinesin family member 18B
ENSG00000122966	0.01	3.37	3.77	#N/A	#N/A	citron rho-interacting serine/threonine kinase
ENSG00000161800	0.23	3.00	3.46	#N/A	#N/A	Rac GTPase activating protein 1
ENSG00000087586	0.05	3.07	4.40	#N/A	#N/A	aurora kinase A
ENSG00000162063	-0.09	2.39	2.97	#N/A	#N/A	cyclin F
ENSG00000182667	-0.13	4.36	4.03	#N/A	#N/A	neurotrimin

ENSG00000113971	#N/A	#N/A	#N/A	1.02	#N/A	nephronophthisis 3 (adolescent)
ENSG00000182179	#N/A	#N/A	#N/A	1.02	#N/A	ubiquitin-like modifier activating enzyme 7
ENSG00000124357	#N/A	#N/A	#N/A	1.02	1.42	N-acetylglucosamine kinase
ENSG00000114423	#N/A	#N/A	#N/A	1.02	#N/A	Cbl proto-oncogene B, E3 ubiquitin protein ligase
ENSG00000135441	#N/A	#N/A	#N/A	1.02	#N/A	biogenesis of lysosomal organelles complex-1, subunit 1
ENSG00000129292	#N/A	#N/A	#N/A	1.02	#N/A	PHD finger protein 20-like 1
ENSG00000024862	#N/A	#N/A	#N/A	1.02	#N/A	coiled-coil domain containing 28A
ENSG00000102893	#N/A	#N/A	#N/A	1.02	#N/A	phosphorylase kinase, beta
ENSG00000099860	#N/A	#N/A	#N/A	1.02	#N/A	growth arrest and DNA-damage-inducible, beta
ENSG00000124226	#N/A	#N/A	#N/A	1.02	1.05	ring finger protein 114
ENSG00000133639	#N/A	#N/A	#N/A	1.02	#N/A	B-cell translocation gene 1, anti-proliferative
ENSG00000162222	#N/A	#N/A	#N/A	1.02	1.13	tetratricopeptide repeat domain 9C
ENSG00000131408	#N/A	#N/A	#N/A	1.02	#N/A	nuclear receptor subfamily 1, group H, member 2
ENSG00000117407	#N/A	#N/A	#N/A	1.01	#N/A	artemin
ENSG00000282031	#N/A	#N/A	#N/A	1.01	1.59	transmembrane BAX inhibitor motif containing 4
ENSG00000170145	#N/A	#N/A	#N/A	1.01	#N/A	salt-inducible kinase 2
ENSG00000179152	#N/A	#N/A	#N/A	1.01	#N/A	T cell activation inhibitor, mitochondrial
ENSG00000122257	#N/A	#N/A	#N/A	1.01	#N/A	retinoblastoma binding protein 6
ENSG00000107798	#N/A	#N/A	#N/A	1.01	#N/A	lipase A, lysosomal acid, cholesterol esterase
ENSG00000106780	#N/A	#N/A	#N/A	1.01	#N/A	multiple EGF-like-domains 9
ENSG00000104976	#N/A	#N/A	#N/A	1.01	#N/A	small nuclear RNA activating complex, polypeptide 2, 45kDa
ENSG00000175550	#N/A	#N/A	#N/A	1.01	1.44	DR1-associated protein 1 (negative cofactor 2 alpha)
ENSG00000162244	#N/A	#N/A	#N/A	1.01	#N/A	ribosomal protein L29
ENSG00000161202	#N/A	#N/A	#N/A	1.00	#N/A	dishevelled segment polarity protein 3
ENSG00000125629	#N/A	#N/A	#N/A	1.00	#N/A	insulin induced gene 2
ENSG00000008513	#N/A	#N/A	#N/A	1.00	1.09	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
ENSG00000206190	#N/A	#N/A	#N/A	1.00	#N/A	ATPase, class V, type 10A
ENSG00000035141	#N/A	#N/A	#N/A	-1.00	#N/A	family with sequence similarity 136, member A
ENSG00000140403	#N/A	#N/A	#N/A	-1.00	#N/A	DnaJ (Hsp40) homolog, subfamily A, member 4
ENSG00000107104	#N/A	#N/A	#N/A	-1.00	#N/A	KN motif and ankyrin repeat domains 1
ENSG00000114867	#N/A	#N/A	#N/A	-1.00	#N/A	eukaryotic translation initiation factor 4 gamma, 1
ENSG00000108883	#N/A	#N/A	#N/A	-1.00	#N/A	elongation factor Tu GTP binding domain containing 2
ENSG00000102900	#N/A	#N/A	#N/A	-1.00	#N/A	nucleoporin 93kDa
ENSG00000168936	#N/A	#N/A	#N/A	-1.00	#N/A	transmembrane protein 129, E3 ubiquitin protein ligase
ENSG00000163389	#N/A	#N/A	#N/A	-1.00	#N/A	protein O-glucosyltransferase 1
ENSG00000213639	#N/A	#N/A	#N/A	-1.01	#N/A	protein phosphatase 1, catalytic subunit, beta isozyme
ENSG00000057663	#N/A	#N/A	#N/A	-1.01	#N/A	autophagy related 5
ENSG00000109736	#N/A	#N/A	#N/A	-1.01	#N/A	major facilitator superfamily domain containing 10
ENSG00000025156	#N/A	#N/A	#N/A	-1.01	#N/A	heat shock transcription factor 2
ENSG00000138018	#N/A	#N/A	#N/A	-1.01	#N/A	ethanolaminephosphotransferase 1
ENSG00000156557	#N/A	#N/A	#N/A	-1.01	#N/A	transmembrane emp24 protein transport domain containing 3
ENSG00000185344	#N/A	#N/A	#N/A	-1.01	#N/A	ATPase, H+ transporting, lysosomal V0 subunit a2
ENSG00000160803	#N/A	#N/A	#N/A	-1.01	#N/A	ubiquilin 4
ENSG00000087365	#N/A	#N/A	#N/A	-1.01	#N/A	splicing factor 3b, subunit 2, 145kDa
ENSG00000188971	#N/A	#N/A	#N/A	-1.01	#N/A	RP11-427H3.3
ENSG00000258984	#N/A	#N/A	#N/A	-1.01	#N/A	UBE2F-SCLY readthrough (NMD candidate)

FIGURE 1C

ENSG00000171848	0.58	4.37	3.90	#N/A	1.32	ribonucleotide reductase M2
ENSG00000166396	1.78	4.16	6.43	#N/A	#N/A	serpin peptidase inhibitor, clade B (ovalbumin), member 7
ENSG00000136928	0.35	3.84	1.79	#N/A	#N/A	gamma-aminobutyric acid (GABA) B receptor, 2
ENSG00000178999	-0.69	3.44	3.23	#N/A	#N/A	aurora kinase B
ENSG00000126787	1.32	4.22	5.01	#N/A	#N/A	discs, large (Drosophila) homolog-associated protein 5
ENSG00000075218	0.49	3.75	4.04	#N/A	#N/A	G-2 and S-phase expressed 1
ENSG00000100297	-0.09	2.60	2.08	#N/A	#N/A	minichromosome maintenance complex component 5
ENSG00000138182	0.15	2.83	3.53	#N/A	#N/A	kinesin family member 20B
ENSG00000094804	0.36	3.73	2.48	#N/A	1.11	cell division cycle 6
ENSG00000113368	0.13	3.46	3.48	-1.30	#N/A	lamin B1
ENSG00000170312	-0.09	3.99	4.30	#N/A	#N/A	cyclin-dependent kinase 1
ENSG00000184557	1.82	-0.87	-0.62	4.68	1.34	suppressor of cytokine signaling 3
ENSG00000134057	0.66	2.53	3.68	#N/A	#N/A	cyclin B1
ENSG00000104738	-0.02	2.88	2.46	#N/A	#N/A	minichromosome maintenance complex component 4
ENSG00000166825	0.16	1.90	2.26	#N/A	#N/A	alanyl (membrane) aminopeptidase
ENSG00000187955	-0.61	-1.71	-4.96	#N/A	#N/A	collagen, type XIV, alpha 1
ENSG00000119969	0.17	3.62	2.99	#N/A	#N/A	helicase, lymphoid-specific
ENSG00000198554	-0.12	2.80	2.38	#N/A	#N/A	WD repeat and HMG-box DNA binding protein 1
ENSG00000056558	1.63	-2.76	-2.64	2.34	#N/A	TNF receptor-associated factor 1
ENSG00000185215	1.70	-1.55	-0.76	#N/A	#N/A	tumor necrosis factor, alpha-induced protein 2
ENSG00000260549	1.01	4.18	4.77	#N/A	#N/A	metallothionein 1L (gene/pseudogene)
ENSG00000166803	0.16	3.47	3.72	1.69	2.21	KIAA0101
ENSG00000166851	0.23	2.92	3.93	#N/A	#N/A	polo-like kinase 1
ENSG00000163710	-0.97	-2.19	-4.49	#N/A	#N/A	procollagen C-endopeptidase enhancer 2
ENSG00000163507	0.33	2.95	3.63	#N/A	#N/A	KIAA1524
ENSG00000105011	0.41	3.22	2.67	1.06	#N/A	anti-silencing function 1B histone chaperone
ENSG00000137804	0.33	3.32	3.40	#N/A	#N/A	nucleolar and spindle associated protein 1
ENSG00000124875	2.87	4.34	7.68	#N/A	#N/A	chemokine (C-X-C motif) ligand 6
ENSG00000144554	-0.26	2.88	2.71	#N/A	#N/A	Fanconi anemia, complementation group D2
ENSG00000085999	0.07	3.49	2.56	-1.23	#N/A	RAD54-like (S. cerevisiae)
ENSG00000140525	0.02	3.13	3.13	#N/A	#N/A	Fanconi anemia, complementation group I
ENSG00000041982	0.99	4.02	3.66	#N/A	2.22	tenascin C
ENSG00000164611	0.00	2.28	3.42	#N/A	#N/A	pituitary tumor-transforming 1
ENSG00000125740	1.12	-6.58	-5.90	#N/A	#N/A	FBJ murine osteosarcoma viral oncogene homolog B
ENSG00000112312	0.18	2.89	2.87	#N/A	1.56	geminin, DNA replication inhibitor
ENSG00000184661	0.98	4.37	4.56	#N/A	#N/A	cell division cycle associated 2
ENSG00000117650	1.02	4.19	5.34	#N/A	#N/A	NIMA-related kinase 2
ENSG00000157456	0.32	2.54	3.65	#N/A	#N/A	cyclin B2
ENSG00000103489	0.96	2.97	3.00	#N/A	#N/A	xylosyltransferase I
ENSG00000187741	-0.37	2.61	2.16	#N/A	#N/A	Fanconi anemia, complementation group A
ENSG00000123485	-0.04	3.68	3.36	#N/A	#N/A	Holliday junction recognition protein
ENSG00000134222	-0.49	2.04	2.62	#N/A	#N/A	proline/serine-rich coiled-coil 1
ENSG00000242265	0.30	3.02	4.24	#N/A	#N/A	paternally expressed 10
ENSG00000198355	1.28	-2.29	-1.39	#N/A	#N/A	Pim-3 proto-oncogene, serine/threonine kinase
ENSG00000101412	-0.25	2.76	2.08	#N/A	#N/A	E2F transcription factor 1
ENSG00000146918	0.23	2.81	2.91	#N/A	#N/A	non-SMC condensin II complex, subunit G2
ENSG00000113810	0.29	2.03	2.69	1.36	#N/A	structural maintenance of chromosomes 4
ENSG00000166508	-0.12	2.12	2.01	#N/A	#N/A	minichromosome maintenance complex component 7

ENSG00000175467	#N/A	#N/A	#N/A	-1.01	#N/A	squamous cell carcinoma antigen recognized by T cells 1
ENSG00000171497	#N/A	#N/A	#N/A	-1.01	#N/A	peptidylprolyl isomerase D
ENSG00000163444	#N/A	#N/A	#N/A	-1.01	#N/A	transmembrane protein 183A
ENSG00000112249	#N/A	#N/A	#N/A	-1.01	#N/A	activating signal cointegrator 1 complex subunit 3
ENSG00000170854	#N/A	#N/A	#N/A	-1.01	#N/A	MYC induced nuclear antigen
ENSG00000172053	#N/A	#N/A	#N/A	-1.01	#N/A	glutaminyl-tRNA synthetase
ENSG00000204946	#N/A	#N/A	#N/A	-1.01	#N/A	zinc finger family member 783
ENSG00000169045	#N/A	#N/A	#N/A	-1.02	#N/A	heterogeneous nuclear ribonucleoprotein H1 (H)
ENSG00000198799	#N/A	#N/A	#N/A	-1.02	#N/A	leucine-rich repeats and immunoglobulin-like domains 2
ENSG00000105676	#N/A	#N/A	#N/A	-1.02	#N/A	armadillo repeat containing 6
ENSG00000043514	#N/A	#N/A	#N/A	-1.02	#N/A	tRNA isopentenyltransferase 1
ENSG00000169689	#N/A	#N/A	#N/A	-1.02	#N/A	stimulated by retinoic acid 13
ENSG00000230257	#N/A	#N/A	#N/A	-1.02	#N/A	nuclear factor, erythroid 4
ENSG00000134186	#N/A	#N/A	#N/A	-1.02	#N/A	pre-mRNA processing factor 38B
ENSG00000161996	#N/A	#N/A	#N/A	-1.02	#N/A	WD repeat domain 90
ENSG00000132819	#N/A	#N/A	#N/A	-1.02	#N/A	RNA binding motif protein 38
ENSG00000273562	#N/A	#N/A	#N/A	-1.02	#N/A	nucleosome assembly protein 1-like 4
ENSG00000141522	#N/A	#N/A	#N/A	-1.02	#N/A	Rho GDP dissociation inhibitor (GDI) alpha
ENSG00000111144	#N/A	#N/A	#N/A	-1.02	#N/A	leukotriene A4 hydrolase
ENSG00000111667	#N/A	#N/A	#N/A	-1.02	#N/A	ubiquitin specific peptidase 5 (isopeptidase T)
ENSG00000103148	#N/A	#N/A	#N/A	-1.02	#N/A	NPR3-like, GATOR1 complex subunit
ENSG00000086289	#N/A	#N/A	#N/A	-1.02	#N/A	ependymin related 1
ENSG00000160949	#N/A	#N/A	#N/A	-1.02	#N/A	tonsoku-like, DNA repair protein
ENSG00000146463	#N/A	#N/A	#N/A	-1.02	#N/A	zinc finger, MYM-type 4
ENSG00000137288	#N/A	#N/A	#N/A	-1.02	#N/A	ubiquinol-cytochrome c reductase complex assembly factor 2
ENSG00000175634	#N/A	#N/A	#N/A	-1.03	#N/A	ribosomal protein S6 kinase, 70kDa, polypeptide 2
ENSG00000095319	#N/A	#N/A	#N/A	-1.03	#N/A	nucleoporin 188kDa
ENSG00000001497	#N/A	#N/A	#N/A	-1.03	#N/A	LAS1-like, ribosome biogenesis factor
ENSG00000113048	#N/A	#N/A	#N/A	-1.03	#N/A	mitochondrial ribosomal protein S27
ENSG00000106628	#N/A	#N/A	#N/A	-1.03	#N/A	polymerase (DNA directed), delta 2, accessory subunit
ENSG00000165792	#N/A	#N/A	#N/A	-1.03	#N/A	methyltransferase like 17
ENSG00000118900	#N/A	#N/A	#N/A	-1.03	#N/A	ubinuclein 1
ENSG00000008441	#N/A	#N/A	#N/A	-1.03	#N/A	nuclear factor I/X (CCAAT-binding transcription factor)
ENSG00000162613	#N/A	#N/A	#N/A	-1.03	#N/A	far upstream element (FUSE) binding protein 1
ENSG00000128309	#N/A	#N/A	#N/A	-1.03	#N/A	mercaptopyruvate sulfurtransferase
ENSG00000166987	#N/A	#N/A	#N/A	-1.04	#N/A	methyl-CpG binding domain protein 6
ENSG00000168439	#N/A	#N/A	#N/A	-1.04	#N/A	stress-induced phosphoprotein 1
ENSG00000132323	#N/A	#N/A	#N/A	-1.04	#N/A	integrin-linked kinase-associated serine/threonine phosphatase
ENSG00000089280	#N/A	#N/A	#N/A	-1.04	#N/A	FUS RNA binding protein
ENSG00000186501	#N/A	#N/A	#N/A	-1.04	#N/A	transmembrane protein 222
ENSG00000160131	#N/A	#N/A	#N/A	-1.04	#N/A	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)
ENSG00000165688	#N/A	#N/A	#N/A	-1.04	#N/A	peptidase (mitochondrial processing) alpha
ENSG00000163349	#N/A	#N/A	#N/A	-1.04	#N/A	homeodomain interacting protein kinase 1
ENSG00000153574	#N/A	#N/A	#N/A	-1.04	#N/A	ribose 5-phosphate isomerase A
ENSG00000261739	#N/A	#N/A	#N/A	-1.04	#N/A	golgin A8 family, member S
ENSG00000008853	#N/A	#N/A	#N/A	-1.04	#N/A	Rho-related BTB domain containing 2
ENSG00000013306	#N/A	#N/A	#N/A	-1.04	#N/A	solute carrier family 25, member 39
ENSG00000169914	#N/A	#N/A	#N/A	-1.04	#N/A	OTU deubiquitinase 3

FIGURE 1D

ENSG00000164283	1.64	6.40	7.66	#N/A	#N/A	endothelial cell-specific molecule 1
ENSG00000115163	-0.38	3.06	3.71	#N/A	#N/A	centromere protein A
ENSG00000143333	1.02	-2.95	-4.51	1.97	#N/A	regulator of G-protein signaling 16
ENSG00000187479	1.79	-4.03	-4.59	#N/A	#N/A	chromosome 11 open reading frame 96
ENSG00000132510	1.26	-2.92	-2.40	#N/A	#N/A	lysine (K)-specific demethylase 6B
ENSG00000177084	0.02	2.23	2.19	#N/A	#N/A	polymerase (DNA directed), epsilon, catalytic subunit
ENSG00000136982	0.99	4.46	4.19	#N/A	#N/A	DNA replication and sister chromatid cohesion 1
ENSG00000171320	-0.07	4.76	4.58	1.04	#N/A	establishment of sister chromatid cohesion N-acetyltransferase 2
ENSG00000169908	1.18	3.57	5.06	#N/A	#N/A	transmembrane 4 L six family member 1
ENSG00000156970	1.76	5.01	5.31	#N/A	#N/A	BUB1 mitotic checkpoint serine/threonine kinase B
ENSG00000165244	-0.04	2.80	2.23	#N/A	#N/A	zinc finger protein 367
ENSG00000167306	-0.97	-2.67	-4.75	#N/A	#N/A	myosin VB
ENSG00000138160	0.05	3.23	3.66	#N/A	#N/A	kinesin family member 11
ENSG00000189057	-0.19	3.88	3.37	1.31	#N/A	family with sequence similarity 111, member B
ENSG00000135451	-0.09	3.31	3.97	#N/A	#N/A	trophinin associated protein
ENSG00000276043	0.07	2.69	2.23	#N/A	#N/A	ubiquitin-like with PHD and ring finger domains 1
ENSG00000167670	0.01	2.41	2.16	#N/A	#N/A	chromatin assembly factor 1, subunit A (p150)
ENSG00000156802	0.33	3.25	2.89	#N/A	#N/A	ATPase family, AAA domain containing 2
ENSG00000051341	0.53	4.21	4.11	#N/A	#N/A	polymerase (DNA directed), theta
ENSG00000100906	1.67	-0.87	-0.23	#N/A	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
ENSG00000137831	0.00	2.30	1.72	#N/A	#N/A	uveal autoantigen with coiled-coil domains and ankyrin repeats
ENSG00000117632	-0.01	1.81	2.57	#N/A	#N/A	stathmin 1
ENSG00000162772	1.58	-3.01	-3.59	#N/A	1.66	activating transcription factor 3
ENSG00000147883	1.36	-1.47	-2.87	#N/A	#N/A	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
ENSG00000176907	1.20	-1.74	-2.47	#N/A	#N/A	chromosome 8 open reading frame 4
ENSG00000107984	-0.16	2.07	1.52	#N/A	1.69	dickkopf WNT signaling pathway inhibitor 1
ENSG00000110031	-0.32	1.85	3.30	#N/A	#N/A	leupaxin
ENSG00000106462	0.62	3.33	2.81	#N/A	#N/A	enhancer of zeste 2 polycomb repressive complex 2 subunit
ENSG00000165304	-0.38	2.37	2.36	#N/A	#N/A	maternal embryonic leucine zipper kinase
ENSG00000163545	1.42	-1.57	-1.39	#N/A	#N/A	NUAK family, SNF1-like kinase, 2
ENSG00000138166	1.24	-1.95	-2.01	#N/A	#N/A	dual specificity phosphatase 5
ENSG00000139618	-0.03	3.88	3.86	#N/A	#N/A	breast cancer 2, early onset
ENSG00000092470	-0.09	3.01	2.74	#N/A	#N/A	WD repeat domain 76
ENSG00000073111	-0.05	2.29	1.86	#N/A	#N/A	minichromosome maintenance complex component 2
ENSG00000085840	-0.02	4.14	3.64	#N/A	#N/A	origin recognition complex, subunit 1
ENSG00000137033	0.95	4.43	2.76	#N/A	#N/A	interleukin 33
ENSG00000012048	0.13	2.99	2.48	#N/A	#N/A	breast cancer 1, early onset
ENSG00000269289	-0.64	-6.83	-3.25	#N/A	#N/A	CTB-92J24.3
ENSG00000176890	-0.07	2.76	2.67	#N/A	#N/A	thymidylate synthetase
ENSG00000137812	0.01	4.03	4.66	#N/A	#N/A	cancer susceptibility candidate 5
ENSG00000183763	-0.01	3.19	2.94	#N/A	#N/A	TRAF interacting protein
ENSG00000112118	-0.26	2.24	1.67	#N/A	#N/A	minichromosome maintenance complex component 3
ENSG00000171223	1.12	-3.19	-2.49	#N/A	#N/A	jun B proto-oncogene
ENSG00000077152	-0.51	2.30	2.47	1.06	#N/A	ubiquitin-conjugating enzyme E2T
ENSG00000168685	1.73	3.83	4.66	#N/A	#N/A	interleukin 7 receptor

ENSG00000280987	#N/A	#N/A	#N/A	-1.04	#N/A	matrin 3
ENSG00000007080	#N/A	#N/A	#N/A	-1.04	#N/A	coiled-coil domain containing 124
ENSG00000004455	#N/A	#N/A	#N/A	-1.05	#N/A	adenylate kinase 2
ENSG00000241945	#N/A	#N/A	#N/A	-1.05	#N/A	PWP2 periodic tryptophan protein homolog (yeast)
ENSG00000138363	#N/A	#N/A	#N/A	-1.05	#N/A	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
ENSG00000167721	#N/A	#N/A	#N/A	-1.05	#N/A	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
ENSG00000234495	#N/A	#N/A	#N/A	-1.05	#N/A	tripartite motif containing 27
ENSG00000170085	#N/A	#N/A	#N/A	-1.05	#N/A	SUMO-interacting motifs containing 1
ENSG00000178952	#N/A	#N/A	#N/A	-1.05	#N/A	Tu translation elongation factor, mitochondrial
ENSG00000163875	#N/A	#N/A	#N/A	-1.05	#N/A	MYST/Esa1-associated factor 6
ENSG00000146223	#N/A	#N/A	#N/A	-1.05	#N/A	ribosomal protein L7-like 1
ENSG00000134440	#N/A	#N/A	#N/A	-1.05	#N/A	asparaginyl-tRNA synthetase
ENSG00000110721	#N/A	#N/A	#N/A	-1.05	#N/A	choline kinase alpha
ENSG00000096746	#N/A	#N/A	#N/A	-1.05	#N/A	heterogeneous nuclear ribonucleoprotein H3 (2H9)
ENSG00000198301	#N/A	#N/A	#N/A	-1.05	#N/A	SDA1 domain containing 1
ENSG00000171612	#N/A	#N/A	#N/A	-1.05	#N/A	solute carrier family 25 (pyrimidine nucleotide carrier), member 33
ENSG00000164024	#N/A	#N/A	#N/A	-1.05	#N/A	methionyl aminopeptidase 1
ENSG00000261221	#N/A	#N/A	#N/A	-1.05	#N/A	zinc finger protein 865
ENSG00000189306	#N/A	#N/A	#N/A	-1.05	#N/A	ribosomal RNA processing 7 homolog A
ENSG00000196700	#N/A	#N/A	#N/A	-1.05	#N/A	zinc finger protein 512B
ENSG00000118640	#N/A	#N/A	#N/A	-1.06	#N/A	vesicle-associated membrane protein 8
ENSG00000276187	#N/A	#N/A	#N/A	-1.06	#N/A	ER membrane-associated RNA degradation
ENSG00000071626	#N/A	#N/A	#N/A	-1.06	#N/A	DAZ associated protein 1
ENSG00000211460	#N/A	#N/A	#N/A	-1.06	#N/A	translin
ENSG00000025796	#N/A	#N/A	#N/A	-1.06	#N/A	SEC63 homolog (S. cerevisiae)
ENSG00000115306	#N/A	#N/A	#N/A	-1.06	#N/A	spectrin, beta, non-erythrocytic 1
ENSG00000169750	#N/A	#N/A	#N/A	-1.06	#N/A	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
ENSG00000118508	#N/A	#N/A	#N/A	-1.06	#N/A	RAB32, member RAS oncogene family
ENSG00000090376	#N/A	#N/A	#N/A	-1.07	#N/A	interleukin-1 receptor-associated kinase 3
ENSG00000105472	#N/A	#N/A	#N/A	-1.07	#N/A	C-type lectin domain family 11, member A
ENSG00000035115	#N/A	#N/A	#N/A	-1.07	#N/A	SH3 and SYLF domain containing 1
ENSG00000128050	#N/A	#N/A	#N/A	-1.07	#N/A	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
ENSG00000039123	#N/A	#N/A	#N/A	-1.07	#N/A	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
ENSG00000110075	#N/A	#N/A	#N/A	-1.07	#N/A	protein phosphatase 6, regulatory subunit 3
ENSG00000139437	#N/A	#N/A	#N/A	-1.07	#N/A	trichoplein, keratin filament binding
ENSG00000103319	#N/A	#N/A	#N/A	-1.07	#N/A	eukaryotic elongation factor 2 kinase
ENSG00000169660	#N/A	#N/A	#N/A	-1.07	#N/A	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing
ENSG00000086504	#N/A	#N/A	#N/A	-1.07	#N/A	mitochondrial ribosomal protein L28
ENSG00000170606	#N/A	#N/A	#N/A	-1.07	#N/A	heat shock 70kDa protein 4
ENSG00000215440	#N/A	#N/A	#N/A	-1.07	#N/A	aminopeptidase-like 1
ENSG00000163528	#N/A	#N/A	#N/A	-1.07	#N/A	coiled-coil-helix-coiled-coil-helix domain containing 4
ENSG00000136463	#N/A	#N/A	#N/A	-1.07	#N/A	translational activator of mitochondrially encoded cytochrome c oxidase I
ENSG00000230124	#N/A	#N/A	#N/A	-1.07	#N/A	acyl-CoA binding domain containing 6
ENSG00000184428	#N/A	#N/A	#N/A	-1.08	#N/A	topoisomerase (DNA) I, mitochondrial
ENSG00000156261	#N/A	#N/A	#N/A	-1.08	#N/A	chaperonin containing TCP1, subunit 8 (theta)

FIGURE 1E

ENSG00000152253	0.69	3.66	3.56	1.04	#N/A	SPC25, NDC80 kinetochore complex component
ENSG00000137563	0.32	1.70	3.07	#N/A	#N/A	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
ENSG00000110427	0.17	3.55	3.72	#N/A	#N/A	KIAA1549-like
ENSG00000142910	-1.22	-2.85	-4.45	#N/A	#N/A	tubulointerstitial nephritis antigen-like 1
ENSG00000144655	1.26	-2.21	-1.94	#N/A	#N/A	cysteine-serine-rich nuclear protein 1
ENSG00000112029	-0.08	3.25	2.94	#N/A	#N/A	F-box protein 5
ENSG00000128805	-0.08	1.32	2.28	#N/A	#N/A	Rho GTPase activating protein 22
ENSG00000079616	-0.33	1.96	2.04	#N/A	#N/A	kinesin family member 22
ENSG00000100162	-0.41	3.29	3.25	#N/A	#N/A	centromere protein M
ENSG00000163735	2.40	5.85	9.49	#N/A	#N/A	chemokine (C-X-C motif) ligand 5
ENSG00000167513	1.52	3.71	2.81	#N/A	#N/A	chromatin licensing and DNA replication factor 1
ENSG00000175505	1.32	-1.44	-2.26	#N/A	#N/A	cardiotrophin-like cytokine factor 1
ENSG00000121152	-0.49	3.34	3.02	#N/A	#N/A	non-SMC condensin I complex, subunit H
ENSG00000146232	1.13	-1.58	-1.06	#N/A	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
ENSG00000228716	0.45	2.25	2.64	#N/A	#N/A	dihydrofolate reductase
ENSG00000130816	0.13	1.85	1.79	#N/A	#N/A	DNA (cytosine-5-)-methyltransferase 1
ENSG00000109674	0.38	3.66	3.88	#N/A	#N/A	nei endonuclease VIII-like 3 (E. coli)
ENSG00000111247	0.50	3.90	3.50	#N/A	#N/A	RAD51 associated protein 1
ENSG00000120129	1.10	-1.54	-1.58	#N/A	#N/A	dual specificity phosphatase 1
ENSG00000145358	-0.60	2.26	2.59	#N/A	#N/A	DNA-damage-inducible transcript 4-like
ENSG00000106003	0.71	-4.29	-5.56	#N/A	#N/A	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
ENSG00000168389	1.63	-2.35	-1.35	#N/A	#N/A	major facilitator superfamily domain containing 2A
ENSG00000165349	-0.66	-2.65	-4.52	#N/A	#N/A	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
ENSG00000125347	1.54	-0.69	-0.83	1.09	#N/A	interferon regulatory factor 1
ENSG00000168496	-0.02	2.10	1.92	#N/A	#N/A	flap structure-specific endonuclease 1
ENSG00000116717	1.30	-1.09	-1.49	#N/A	1.98	growth arrest and DNA-damage-inducible, alpha
ENSG00000165891	0.23	3.49	3.93	#N/A	#N/A	E2F transcription factor 7
ENSG00000170961	2.39	3.39	6.89	#N/A	#N/A	hyaluronan synthase 2
ENSG00000111602	-0.12	1.96	1.76	#N/A	#N/A	timeless circadian clock
ENSG00000006210	1.06	-3.23	-2.84	#N/A	#N/A	chemokine (C-X3-C motif) ligand 1
ENSG00000139734	0.10	2.06	2.40	#N/A	#N/A	diaphanous-related formin 3
ENSG00000164087	0.58	2.54	2.68	-1.02	#N/A	POC1 centriolar protein A
ENSG00000149503	-0.73	1.66	1.91	#N/A	#N/A	inner centromere protein antigens 135/155kDa
ENSG00000167325	0.03	2.32	2.37	#N/A	#N/A	ribonucleotide reductase M1
ENSG00000102384	0.80	3.28	3.54	#N/A	#N/A	centromere protein I
ENSG00000221829	-0.51	2.01	1.64	#N/A	#N/A	Fanconi anemia, complementation group G
ENSG00000164104	-1.11	1.50	1.59	#N/A	#N/A	high mobility group box 2
ENSG00000105486	-0.02	2.09	1.95	#N/A	#N/A	ligase I, DNA, ATP-dependent
ENSG00000197467	0.33	2.56	2.25	#N/A	#N/A	collagen, type XIII, alpha 1
ENSG00000118503	2.49	-0.89	0.22	#N/A	1.14	tumor necrosis factor, alpha-induced protein 3
ENSG00000164045	1.67	4.63	3.94	-1.24	#N/A	cell division cycle 25A
ENSG00000066279	0.02	3.73	4.53	#N/A	#N/A	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
ENSG00000014138	-0.19	2.10	1.81	#N/A	#N/A	polymerase (DNA directed), alpha 2, accessory subunit
ENSG00000136108	-0.12	2.35	2.88	#N/A	#N/A	cytoskeleton associated protein 2
ENSG00000080839	0.05	2.60	2.52	#N/A	#N/A	retinoblastoma-like 1
ENSG00000241749	0.85	3.93	4.37	#N/A	#N/A	ribosomal protein SA pseudogene 52
ENSG00000162267	-0.18	-3.94	-4.98	#N/A	#N/A	inter-alpha-trypsin inhibitor heavy chain 3

ENSG00000145191	#N/A	#N/A	#N/A	-1.08	#N/A	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
ENSG00000106415	#N/A	#N/A	#N/A	-1.08	#N/A	glucocorticoid induced 1
ENSG00000108773	#N/A	#N/A	#N/A	-1.08	#N/A	K(lysine) acetyltransferase 2A
ENSG00000114030	#N/A	#N/A	#N/A	-1.08	#N/A	karyopherin alpha 1 (importin alpha 5)
ENSG00000175471	#N/A	#N/A	#N/A	-1.08	#N/A	multiple C2 domains, transmembrane 1
ENSG00000198160	#N/A	#N/A	#N/A	-1.08	#N/A	mesoderm induction early response 1, transcriptional regulator
ENSG00000135776	#N/A	#N/A	#N/A	-1.08	#N/A	ATP-binding cassette, sub-family B (MDR/TAP), member 10
ENSG00000160221	#N/A	#N/A	#N/A	-1.08	#N/A	chromosome 21 open reading frame 33
ENSG00000005801	#N/A	#N/A	#N/A	-1.08	#N/A	zinc finger protein 195
ENSG00000104522	#N/A	#N/A	#N/A	-1.08	1.12	tissue specific transplantation antigen P35B
ENSG00000187961	#N/A	#N/A	#N/A	-1.08	#N/A	kelch-like family member 17
ENSG00000152234	#N/A	#N/A	#N/A	-1.08	#N/A	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
ENSG00000184967	#N/A	#N/A	#N/A	-1.08	#N/A	nucleolar complex associated 4 homolog
ENSG00000196756	#N/A	#N/A	#N/A	-1.09	#N/A	small nucleolar RNA host gene 17
ENSG00000154174	#N/A	#N/A	#N/A	-1.09	#N/A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
ENSG00000109689	#N/A	#N/A	#N/A	-1.09	#N/A	stromal interaction molecule 2
ENSG00000101194	#N/A	#N/A	#N/A	-1.09	#N/A	solute carrier family 17 (vesicular nucleotide transporter), member 9
ENSG00000116489	#N/A	#N/A	#N/A	-1.09	#N/A	capping protein (actin filament) muscle Z-line, alpha 1
ENSG00000274523	#N/A	#N/A	#N/A	-1.09	#N/A	Williams-Beuren syndrome chromosome region 16
ENSG00000100220	#N/A	#N/A	#N/A	-1.09	#N/A	RNA 2',3'-cyclic phosphate and 5'-OH ligase
ENSG00000277278	#N/A	#N/A	#N/A	-1.09	#N/A	HECT and RLD domain containing E3 ubiquitin protein ligase 2
ENSG00000120685	#N/A	#N/A	#N/A	-1.09	#N/A	proline and serine rich 1
ENSG00000130731	#N/A	#N/A	#N/A	-1.09	#N/A	chromosome 16 open reading frame 13
ENSG00000130935	#N/A	#N/A	#N/A	-1.09	#N/A	nucleolar protein 11
ENSG00000147813	#N/A	#N/A	#N/A	-1.09	#N/A	nicotinate phosphoribosyltransferase
ENSG00000115419	#N/A	#N/A	#N/A	-1.09	#N/A	glutaminase
ENSG00000165699	#N/A	#N/A	#N/A	-1.09	#N/A	tuberous sclerosis 1
ENSG00000100216	#N/A	#N/A	#N/A	-1.09	#N/A	translocase of outer mitochondrial membrane 22 homolog (yeast)
ENSG00000173638	#N/A	#N/A	#N/A	-1.09	#N/A	solute carrier family 19 (folate transporter), member 1
ENSG00000110080	#N/A	#N/A	#N/A	-1.09	#N/A	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
ENSG00000099804	#N/A	#N/A	#N/A	-1.09	#N/A	cell division cycle 34
ENSG00000275700	#N/A	#N/A	#N/A	-1.09	#N/A	apoptosis antagonizing transcription factor
ENSG00000134697	#N/A	#N/A	#N/A	-1.09	#N/A	guanine nucleotide binding protein-like 2 (nucleolar)
ENSG00000125912	#N/A	#N/A	#N/A	-1.10	#N/A	nicalin
ENSG00000004487	#N/A	#N/A	#N/A	-1.10	#N/A	lysine (K)-specific demethylase 1A
ENSG00000115827	#N/A	#N/A	#N/A	-1.10	#N/A	DDB1 and CUL4 associated factor 17
ENSG00000165733	#N/A	#N/A	#N/A	-1.10	#N/A	BMS1 ribosome biogenesis factor
ENSG00000167969	#N/A	#N/A	#N/A	-1.10	#N/A	enoyl-CoA delta isomerase 1
ENSG00000075240	#N/A	#N/A	#N/A	-1.10	#N/A	GRAM domain containing 4
ENSG00000164654	#N/A	#N/A	#N/A	-1.10	#N/A	missing oocyte, meiosis regulator, homolog (Drosophila)
ENSG00000121210	#N/A	#N/A	#N/A	-1.10	#N/A	KIAA0922
ENSG00000124784	#N/A	#N/A	#N/A	-1.10	#N/A	RIO kinase 1
ENSG00000075856	#N/A	#N/A	#N/A	-1.10	#N/A	squamous cell carcinoma antigen recognized by T cells 3
ENSG00000151849	#N/A	#N/A	#N/A	-1.10	#N/A	centromere protein J
ENSG00000067533	#N/A	#N/A	#N/A	-1.10	#N/A	ribosomal RNA processing 15 homolog
ENSG00000120694	#N/A	#N/A	#N/A	-1.10	#N/A	heat shock 105kDa/110kDa protein 1
ENSG00000136682	#N/A	#N/A	#N/A	-1.10	#N/A	COBW domain containing 2

FIGURE 1F

ENSG00000136492	0.38	3.02	2.87	#N/A	#N/A	BRCA1 interacting protein C-terminal helicase 1
ENSG00000101003	-0.03	2.71	2.38	#N/A	#N/A	GINS complex subunit 1 (Psf1 homolog)
ENSG00000142731	0.53	3.67	3.96	#N/A	#N/A	polo-like kinase 4
ENSG00000181938	-0.35	3.06	2.86	#N/A	#N/A	GINS complex subunit 3 (Psf3 homolog)
ENSG00000214357	0.13	2.76	2.58	#N/A	#N/A	neuralized E3 ubiquitin protein ligase 1B
ENSG00000010292	-0.03	1.62	1.99	#N/A	#N/A	non-SMC condensin I complex, subunit D2
ENSG00000164619	0.94	4.34	3.77	#N/A	#N/A	BMP binding endothelial regulator
ENSG00000125538	1.38	1.67	4.66	#N/A	#N/A	interleukin 1, beta
ENSG00000136244	2.43	-2.45	0.13	#N/A	4.71	interleukin 6
ENSG00000213853	0.15	1.34	2.16	2.06	1.66	epithelial membrane protein 2
ENSG00000138658	-0.80	2.29	1.96	#N/A	#N/A	zinc finger, GRF-type containing 1
ENSG00000091409	-0.12	2.32	3.30	#N/A	#N/A	integrin, alpha 6
ENSG00000184992	-0.19	2.28	1.67	#N/A	#N/A	BRI3 binding protein
ENSG00000117266	-0.57	-4.50	-1.79	#N/A	#N/A	cyclin-dependent kinase 18
ENSG00000104889	0.26	2.12	2.09	#N/A	#N/A	ribonuclease H2, subunit A
ENSG00000171033	0.73	3.21	6.54	#N/A	#N/A	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
ENSG00000095303	-0.01	1.51	2.14	2.10	#N/A	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
ENSG00000133110	0.90	4.32	5.10	#N/A	#N/A	periostin, osteoblast specific factor
ENSG00000109685	-0.27	1.43	1.82	#N/A	#N/A	Wolf-Hirschhorn syndrome candidate 1
ENSG00000166845	-0.56	2.97	3.15	#N/A	#N/A	chromosome 18 open reading frame 54
ENSG00000128342	1.32	-5.64	-4.48	#N/A	#N/A	leukemia inhibitory factor
ENSG00000162607	-0.15	2.03	1.87	-1.09	#N/A	ubiquitin specific peptidase 1
ENSG00000278259	-0.23	1.78	1.40	#N/A	1.16	myosin XIX
ENSG00000114346	-0.30	2.06	2.81	#N/A	#N/A	epithelial cell transforming 2
ENSG00000109881	-0.13	0.98	2.65	3.98	3.78	coiled-coil domain containing 34
ENSG00000000460	-0.74	2.45	2.27	#N/A	#N/A	chromosome 1 open reading frame 112
ENSG00000101868	-0.19	1.98	1.48	#N/A	#N/A	polymerase (DNA directed), alpha 1, catalytic subunit
ENSG00000176619	-0.05	0.91	1.73	#N/A	#N/A	lamin B2
ENSG00000180875	-0.33	1.72	1.27	#N/A	#N/A	gremlin 2, DAN family BMP antagonist
ENSG00000186638	0.42	3.33	2.50	#N/A	#N/A	kinesin family member 24
ENSG00000144354	1.20	2.83	3.70	-1.35	#N/A	cell division cycle associated 7
ENSG00000123473	0.57	2.80	2.79	#N/A	#N/A	SCL/TAL1 interrupting locus
ENSG00000121621	1.08	3.32	4.23	#N/A	#N/A	kinesin family member 18A
ENSG00000121211	0.70	3.50	3.00	#N/A	#N/A	meiotic nuclear divisions 1 homolog (S. cerevisiae)
ENSG00000146263	0.09	2.71	2.21	#N/A	#N/A	MMS22-like, DNA repair protein
ENSG00000171208	0.82	3.06	3.01	#N/A	#N/A	neuropilin (NRP) and tolloid (TLL)-like 2
ENSG00000125885	-0.45	2.30	1.90	#N/A	#N/A	minichromosome maintenance complex component 8
ENSG00000188486	0.30	1.98	1.79	#N/A	1.34	H2A histone family, member X
ENSG00000132436	0.45	2.20	2.28	-1.00	#N/A	fidgetin-like 1
ENSG00000179750	0.33	2.80	2.94	#N/A	#N/A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
ENSG00000127586	-0.53	2.54	2.57	-1.78	#N/A	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)
ENSG00000133392	1.31	-0.80	-2.69	#N/A	#N/A	myosin, heavy chain 11, smooth muscle
ENSG00000144810	0.61	1.79	1.93	#N/A	#N/A	collagen, type VIII, alpha 1
ENSG00000262406	1.10	2.84	2.79	#N/A	#N/A	matrix metallopeptidase 12
ENSG00000185697	0.63	3.47	3.45	#N/A	#N/A	v-myb avian myeloblastosis viral oncogene homolog-like 1

ENSG00000112208	#N/A	#N/A	#N/A	-1.11	#N/A	BCL2-associated athanogene 2
ENSG00000004809	#N/A	#N/A	#N/A	-1.11	#N/A	solute carrier family 22 (organic cation/carnitine transporter), member 16
ENSG00000164933	#N/A	#N/A	#N/A	-1.11	#N/A	solute carrier family 25 (mitochondrial folate carrier), member 32
ENSG00000118308	#N/A	#N/A	#N/A	-1.11	#N/A	lymphoid-restricted membrane protein
ENSG00000071859	#N/A	#N/A	#N/A	-1.11	#N/A	family with sequence similarity 50, member A
ENSG00000116459	#N/A	#N/A	#N/A	-1.11	#N/A	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1
ENSG00000116133	#N/A	#N/A	#N/A	-1.11	#N/A	24-dehydrocholesterol reductase
ENSG00000174579	#N/A	#N/A	#N/A	-1.11	#N/A	male-specific lethal 2 homolog (Drosophila)
ENSG00000128059	#N/A	#N/A	#N/A	-1.11	#N/A	phosphoribosyl pyrophosphate amidotransferase
ENSG00000164050	#N/A	#N/A	#N/A	-1.11	#N/A	plexin B1
ENSG00000138758	#N/A	#N/A	#N/A	-1.11	#N/A	septin 11
ENSG00000197774	#N/A	#N/A	#N/A	-1.11	#N/A	essential meiotic structure-specific endonuclease subunit 2
ENSG00000162384	#N/A	#N/A	#N/A	-1.11	#N/A	chromosome 1 open reading frame 123
ENSG00000103495	#N/A	#N/A	#N/A	-1.11	#N/A	MYC-associated zinc finger protein (purine-binding transcription factor)
ENSG00000077312	#N/A	#N/A	#N/A	-1.12	#N/A	small nuclear ribonucleoprotein polypeptide A
ENSG00000196547	#N/A	#N/A	#N/A	-1.12	#N/A	mannosidase, alpha, class 2A, member 2
ENSG00000099783	#N/A	#N/A	#N/A	-1.12	#N/A	heterogeneous nuclear ribonucleoprotein M
ENSG00000023734	#N/A	#N/A	#N/A	-1.12	#N/A	serine/threonine kinase receptor associated protein
ENSG00000106554	#N/A	#N/A	#N/A	-1.12	#N/A	coiled-coil-helix-coiled-coil-helix domain containing 3
ENSG00000115761	#N/A	#N/A	#N/A	-1.12	#N/A	nucleolar protein 10
ENSG00000164880	#N/A	#N/A	#N/A	-1.12	#N/A	integrator complex subunit 1
ENSG00000123505	#N/A	#N/A	#N/A	-1.12	#N/A	adenosylmethionine decarboxylase 1
ENSG00000130204	#N/A	#N/A	#N/A	-1.12	#N/A	translocase of outer mitochondrial membrane 40 homolog (yeast)
ENSG00000175376	#N/A	#N/A	#N/A	-1.12	#N/A	eukaryotic translation initiation factor 1A domain containing
ENSG00000079134	#N/A	#N/A	#N/A	-1.12	#N/A	THO complex 1
ENSG00000114770	#N/A	#N/A	#N/A	-1.12	#N/A	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
ENSG00000157778	#N/A	#N/A	#N/A	-1.12	#N/A	proteasome (prosome, macropain) assembly chaperone 3
ENSG00000141456	#N/A	#N/A	#N/A	-1.13	#N/A	proline, glutamate and leucine rich protein 1
ENSG00000234032	#N/A	#N/A	#N/A	-1.13	#N/A	valyl-tRNA synthetase 2, mitochondrial
ENSG00000149115	#N/A	#N/A	#N/A	-1.13	#N/A	tankyrase 1 binding protein 1, 182kDa
ENSG00000006652	#N/A	#N/A	#N/A	-1.13	#N/A	interferon-related developmental regulator 1
ENSG00000155850	#N/A	#N/A	#N/A	-1.13	#N/A	solute carrier family 26 (anion exchanger), member 2
ENSG00000100359	#N/A	#N/A	#N/A	-1.13	#N/A	small G protein signaling modulator 3
ENSG00000187051	#N/A	#N/A	#N/A	-1.13	#N/A	ribosomal protein S19 binding protein 1
ENSG00000213465	#N/A	#N/A	#N/A	-1.13	#N/A	ADP-ribosylation factor-like 2
ENSG00000085415	#N/A	#N/A	#N/A	-1.13	#N/A	SEH1-like nucleoporin
ENSG00000168259	#N/A	#N/A	#N/A	-1.13	#N/A	DnaJ (Hsp40) homolog, subfamily C, member 7
ENSG00000148296	#N/A	#N/A	#N/A	-1.13	#N/A	surfeit 6
ENSG00000138698	#N/A	#N/A	#N/A	-1.13	#N/A	RAP1, GTP-GDP dissociation stimulator 1
ENSG00000184164	#N/A	#N/A	#N/A	-1.13	#N/A	cysteine-rich with EGF-like domains 2
ENSG00000176058	#N/A	#N/A	#N/A	-1.13	#N/A	taperin
ENSG00000065060	#N/A	#N/A	#N/A	-1.13	#N/A	UHRF1 binding protein 1
ENSG00000100722	#N/A	#N/A	#N/A	-1.13	#N/A	zinc finger CCCH-type containing 14
ENSG00000163257	#N/A	#N/A	#N/A	-1.13	#N/A	DDB1 and CUL4 associated factor 16
ENSG00000275176	#N/A	#N/A	#N/A	-1.13	#N/A	acetyl-CoA carboxylase alpha

FIGURE 1G

ENSG00000013573	-0.24	2.45	2.13	#N/A	#N/A	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11
ENSG00000137309	0.51	1.53	2.25	-1.64	#N/A	high mobility group AT-hook 1
ENSG00000153044	0.02	1.77	2.61	#N/A	#N/A	centromere protein H
ENSG00000075213	0.37	1.91	0.58	#N/A	#N/A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
ENSG00000173207	-0.66	1.39	1.98	1.24	2.30	CDC28 protein kinase regulatory subunit 1B
ENSG00000130695	-1.34	1.72	1.43	#N/A	#N/A	centrosomal protein 85kDa
ENSG00000176208	1.29	4.01	3.88	#N/A	#N/A	ATPase family, AAA domain containing 5
ENSG00000147536	0.15	2.62	2.49	#N/A	#N/A	GINS complex subunit 4 (Sld5 homolog)
ENSG00000005513	0.21	-5.82	-2.86	#N/A	#N/A	SRY (sex determining region Y)-box 8
ENSG00000132646	-0.03	2.19	1.74	#N/A	1.15	proliferating cell nuclear antigen
ENSG00000128578	-1.00	2.24	2.24	#N/A	#N/A	striatin interacting protein 2
ENSG00000159259	-0.03	2.61	1.83	#N/A	#N/A	chromatin assembly factor 1, subunit B (p60)
ENSG00000213551	-0.54	1.67	1.63	#N/A	1.23	DnaJ (Hsp40) homolog, subfamily C, member 9
ENSG00000129534	0.32	2.28	2.76	#N/A	#N/A	MIS18 binding protein 1
ENSG00000151503	-0.22	1.94	1.80	#N/A	#N/A	non-SMC condensin II complex, subunit D3
ENSG00000183814	-0.47	2.39	2.93	#N/A	#N/A	lin-9 DREAM MuvB core complex component
ENSG00000172061	0.04	1.30	2.10	#N/A	#N/A	leucine rich repeat containing 15
ENSG00000178966	-0.45	2.35	2.26	#N/A	#N/A	RecQ mediated genome instability 1
ENSG00000137807	0.44	2.28	2.42	#N/A	#N/A	kinesin family member 23
ENSG00000136824	-0.01	2.08	2.29	#N/A	#N/A	structural maintenance of chromosomes 2
ENSG00000139354	0.83	3.43	4.41	#N/A	#N/A	growth arrest-specific 2 like 3
ENSG00000120539	0.47	2.29	1.94	#N/A	#N/A	microtubule associated serine/threonine kinase-like
ENSG00000051180	-0.07	2.68	1.99	#N/A	#N/A	RAD51 recombinase
ENSG00000123416	0.44	2.01	1.99	#N/A	#N/A	tubulin, alpha 1b
ENSG00000169213	0.41	1.85	1.53	#N/A	#N/A	RAB3B, member RAS oncogene family
ENSG00000058804	0.03	1.87	2.15	-1.61	#N/A	NDC1 transmembrane nucleoporin
ENSG00000123374	-0.10	1.66	1.50	#N/A	1.09	cyclin-dependent kinase 2
ENSG00000198056	0.56	3.48	3.31	#N/A	#N/A	primase, DNA, polypeptide 1 (49kDa)
ENSG00000111331	-0.20	1.08	1.84	6.19	1.73	2'-5'-oligoadenylate synthetase 3, 100kDa
ENSG00000185361	0.80	0.68	2.86	#N/A	#N/A	tumor necrosis factor, alpha-induced protein 8 like 1
ENSG00000122861	0.92	2.38	2.71	#N/A	#N/A	plasminogen activator, urokinase
ENSG00000131979	1.36	-1.71	-1.31	#N/A	#N/A	GTP cyclohydrolase 1
ENSG00000138395	0.15	2.09	2.15	#N/A	#N/A	cyclin-dependent kinase 15
ENSG00000125148	1.19	2.84	3.25	3.99	#N/A	metallothionein 2A
ENSG00000144802	2.35	-0.28	0.47	1.41	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
ENSG00000152457	0.03	1.46	2.22	3.93	#N/A	DNA cross-link repair 1C
ENSG00000251562	0.54	-0.66	2.93	1.52	#N/A	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
ENSG00000031691	-0.32	2.00	2.16	#N/A	#N/A	centromere protein Q
ENSG00000197299	-0.50	3.27	3.03	-1.16	#N/A	Bloom syndrome, RecQ helicase-like
ENSG00000057019	-0.08	1.90	2.12	#N/A	#N/A	discoidin, CUB and LCCL domain containing 2
ENSG00000062822	-0.14	1.94	1.56	#N/A	#N/A	polymerase (DNA directed), delta 1, catalytic subunit
ENSG00000135476	0.53	2.29	2.01	#N/A	#N/A	extra spindle pole bodies homolog 1 (S. cerevisiae)
ENSG00000163814	0.26	2.79	4.19	#N/A	1.22	CUB domain containing protein 1
ENSG00000101670	1.15	-1.59	-2.77	#N/A	#N/A	lipase, endothelial
ENSG00000138669	0.16	2.16	1.93	#N/A	#N/A	protein kinase, cGMP-dependent, type II
ENSG00000011201	-0.64	3.95	4.88	#N/A	#N/A	anosmin 1
ENSG00000006468	-1.14	1.02	2.50	#N/A	#N/A	ets variant 1

ENSG00000107262	#N/A	#N/A	#N/A	-1.13	#N/A	BCL2-associated athanogene
ENSG00000168906	#N/A	#N/A	#N/A	-1.13	#N/A	methionine adenosyltransferase II, alpha
ENSG00000185104	#N/A	#N/A	#N/A	-1.14	#N/A	Fas (TNFRSF6) associated factor 1
ENSG00000187954	#N/A	#N/A	#N/A	-1.14	#N/A	cysteine/histidine-rich 1
ENSG00000158882	#N/A	#N/A	#N/A	-1.14	#N/A	translocase of outer mitochondrial membrane 40 homolog (yeast)-like
ENSG00000141385	#N/A	#N/A	#N/A	-1.14	#N/A	AFG3-like AAA ATPase 2
ENSG00000168944	#N/A	#N/A	#N/A	-1.14	#N/A	centrosomal protein 120kDa
ENSG00000119929	#N/A	#N/A	#N/A	-1.14	#N/A	cutC copper transporter
ENSG00000132953	#N/A	#N/A	#N/A	-1.14	#N/A	exportin 4
ENSG00000116120	#N/A	#N/A	#N/A	-1.14	#N/A	phenylalanyl-tRNA synthetase, beta subunit
ENSG00000180198	#N/A	#N/A	#N/A	-1.14	#N/A	regulator of chromosome condensation 1
ENSG00000127837	#N/A	#N/A	#N/A	-1.14	#N/A	angio-associated, migratory cell protein
ENSG00000138399	#N/A	#N/A	#N/A	-1.14	#N/A	FAST kinase domains 1
ENSG00000130024	#N/A	#N/A	#N/A	-1.14	#N/A	PHD finger protein 10
ENSG00000087191	#N/A	#N/A	#N/A	-1.14	#N/A	proteasome (prosome, macropain) 26S subunit, ATPase, 5
ENSG00000116791	#N/A	#N/A	#N/A	-1.14	#N/A	crystallin, zeta (quinone reductase)
ENSG00000166986	#N/A	#N/A	#N/A	-1.14	#N/A	methionyl-tRNA synthetase
ENSG00000112640	#N/A	#N/A	#N/A	-1.14	#N/A	protein phosphatase 2, regulatory subunit B', delta
ENSG00000120948	#N/A	#N/A	#N/A	-1.15	#N/A	TAR DNA binding protein
ENSG00000146701	#N/A	#N/A	#N/A	-1.15	#N/A	malate dehydrogenase 2, NAD (mitochondrial)
ENSG00000130810	#N/A	#N/A	#N/A	-1.15	#N/A	peter pan homolog (Drosophila)
ENSG00000173457	#N/A	#N/A	#N/A	-1.15	#N/A	protein phosphatase 1, regulatory (inhibitor) subunit 14B
ENSG00000182162	#N/A	#N/A	#N/A	-1.15	#N/A	purinergic receptor P2Y, G-protein coupled, 8
ENSG00000008838	#N/A	#N/A	#N/A	-1.15	#N/A	mediator complex subunit 24
ENSG00000100029	#N/A	#N/A	#N/A	-1.15	#N/A	pescadillo ribosomal biogenesis factor 1
ENSG00000162852	#N/A	#N/A	#N/A	-1.15	#N/A	consortin, connexin sorting protein
ENSG00000169718	#N/A	#N/A	#N/A	-1.15	#N/A	dihydrouridine synthase 1-like
ENSG00000116898	#N/A	#N/A	#N/A	-1.15	#N/A	mitochondrial ribosomal protein S15
ENSG00000083750	#N/A	#N/A	#N/A	-1.15	#N/A	Ras-related GTP binding B
ENSG00000145907	#N/A	#N/A	#N/A	-1.15	#N/A	GTPase activating protein (SH3 domain) binding protein 1
ENSG00000163539	#N/A	#N/A	#N/A	-1.15	#N/A	cytoplasmic linker associated protein 2
ENSG00000104164	#N/A	#N/A	#N/A	-1.15	#N/A	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin
ENSG00000012983	#N/A	#N/A	#N/A	-1.15	#N/A	mitogen-activated protein kinase kinase kinase kinase 5
ENSG00000166411	#N/A	#N/A	#N/A	-1.15	#N/A	isocitrate dehydrogenase 3 (NAD+) alpha
ENSG00000128191	#N/A	#N/A	#N/A	-1.16	#N/A	DGCR8 microprocessor complex subunit
ENSG00000125247	#N/A	#N/A	#N/A	-1.16	#N/A	transmembrane and tetratricopeptide repeat containing 4
ENSG00000138668	#N/A	#N/A	#N/A	-1.16	#N/A	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
ENSG00000177830	#N/A	#N/A	#N/A	-1.16	#N/A	chitinase domain containing 1
ENSG00000129351	#N/A	#N/A	#N/A	-1.16	#N/A	interleukin enhancer binding factor 3, 90kDa
ENSG00000100410	#N/A	#N/A	#N/A	-1.16	#N/A	PHD finger protein 5A
ENSG00000138442	#N/A	#N/A	#N/A	-1.16	#N/A	WD repeat domain 12
ENSG00000124181	#N/A	#N/A	#N/A	-1.16	#N/A	phospholipase C, gamma 1
ENSG00000105063	#N/A	#N/A	#N/A	-1.16	#N/A	protein phosphatase 6, regulatory subunit 1
ENSG00000084090	#N/A	#N/A	#N/A	-1.16	#N/A	StAR-related lipid transfer (START) domain containing 7
ENSG00000150768	#N/A	#N/A	#N/A	-1.16	#N/A	dihydrolipoamide S-acetyltransferase
ENSG00000182694	#N/A	#N/A	#N/A	-1.16	#N/A	exostosin-like glycosyltransferase 2
ENSG00000037474	#N/A	#N/A	#N/A	-1.16	#N/A	NOP2/Sun RNA methyltransferase family, member 2

FIGURE 1H

ENSG00000184445	0.18	2.29	2.20	#N/A	#N/A	kinetochore associated 1
ENSG00000198576	1.64	-4.85	-3.67	#N/A	#N/A	activity-regulated cytoskeleton-associated protein
ENSG00000119707	0.28	0.07	2.18	-1.07	#N/A	RNA binding motif protein 25
ENSG00000146410	-0.20	2.53	2.86	#N/A	#N/A	mitochondrial fission regulator 2
ENSG00000157601	-0.47	-1.71	1.61	6.39	#N/A	MX dynamin-like GTPase 1
ENSG00000077514	-0.28	1.94	1.10	#N/A	#N/A	polymerase (DNA-directed), delta 3, accessory subunit
ENSG00000049541	0.54	2.03	1.61	#N/A	#N/A	replication factor C (activator 1) 2, 40kDa
ENSG00000158050	2.41	-2.86	-2.01	#N/A	#N/A	dual specificity phosphatase 2
ENSG00000013297	0.15	1.26	1.73	#N/A	#N/A	claudin 11
ENSG00000178878	-0.34	2.06	1.50	1.01	#N/A	apolipoprotein L domain containing 1
ENSG00000100526	-0.12	2.40	3.38	#N/A	#N/A	cyclin-dependent kinase inhibitor 3
ENSG00000159388	1.01	-0.94	-0.93	2.26	#N/A	BTG family, member 2
ENSG00000166250	0.19	1.69	1.24	#N/A	#N/A	CXADR-like membrane protein
ENSG00000115687	-0.57	2.30	1.63	#N/A	#N/A	PAS domain containing serine/threonine kinase
ENSG00000123136	0.46	1.27	1.78	#N/A	1.08	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A
ENSG00000121957	-0.84	0.55	1.70	#N/A	#N/A	G-protein signaling modulator 2
ENSG00000133119	0.08	2.91	2.71	#N/A	#N/A	replication factor C (activator 1) 3, 38kDa
ENSG00000030419	-1.59	1.18	1.54	#N/A	#N/A	IKAROS family zinc finger 2 (Helios)
ENSG00000166004	-0.42	1.76	1.59	#N/A	#N/A	centrosomal protein 295kDa
ENSG00000108691	2.19	-2.42	-0.76	#N/A	1.98	chemokine (C-C motif) ligand 2
ENSG00000176974	-0.45	1.19	1.61	#N/A	#N/A	serine hydroxymethyltransferase 1 (soluble)
ENSG00000149948	0.97	2.68	3.27	#N/A	#N/A	high mobility group AT-hook 2
ENSG00000163739	4.12	0.05	4.15	#N/A	#N/A	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
ENSG00000123496	0.92	4.12	3.29	#N/A	#N/A	interleukin 13 receptor, alpha 2
ENSG00000168393	-0.04	1.34	1.46	#N/A	#N/A	deoxythymidylate kinase (thymidylate kinase)
ENSG00000170779	0.50	2.28	2.05	#N/A	#N/A	cell division cycle associated 4
ENSG00000160957	-0.44	2.00	1.31	-1.45	#N/A	RecQ protein-like 4
ENSG00000072501	-0.16	1.27	1.22	#N/A	#N/A	structural maintenance of chromosomes 1A
ENSG00000105738	0.17	1.25	1.70	#N/A	#N/A	signal-induced proliferation-associated 1 like 3
ENSG00000023171	0.36	2.31	2.23	#N/A	#N/A	GRAM domain containing 1B
ENSG00000079156	0.05	1.74	1.90	#N/A	#N/A	oxysterol binding protein-like 6
ENSG00000100578	-0.27	1.19	1.71	#N/A	#N/A	KIAA0586
ENSG00000151014	2.03	-0.03	-0.27	#N/A	#N/A	CCR4 carbon catabolite repression 4-like (S. cerevisiae)
ENSG00000122483	0.54	1.73	2.17	#N/A	#N/A	coiled-coil domain containing 18
ENSG00000257219	1.21	2.82	2.13	#N/A	#N/A	RP11-54A9.1
ENSG00000097021	0.54	1.73	1.58	#N/A	#N/A	acyl-CoA thioesterase 7
ENSG00000103995	0.05	2.35	1.89	1.58	#N/A	centrosomal protein 152kDa
ENSG00000140534	0.38	2.44	1.72	#N/A	#N/A	TOPBP1-interacting checkpoint and replication regulator
ENSG00000149554	-0.21	1.56	1.66	#N/A	#N/A	checkpoint kinase 1
ENSG00000100714	0.26	1.51	1.34	-1.11	#N/A	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
ENSG00000156113	0.32	1.82	0.73	#N/A	#N/A	potassium channel, calcium activated large conductance subfamily M alpha, member 1
ENSG00000069399	1.07	-1.57	-0.63	2.30	#N/A	B-cell CLL/lymphoma 3

ENSG00000185883	#N/A	#N/A	#N/A	-1.17	#N/A	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
ENSG00000100060	#N/A	#N/A	#N/A	-1.17	#N/A	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
ENSG00000135624	#N/A	#N/A	#N/A	-1.17	#N/A	chaperonin containing TCP1, subunit 7 (eta)
ENSG00000116560	#N/A	#N/A	#N/A	-1.17	#N/A	splicing factor proline/glutamine-rich
ENSG00000196591	#N/A	#N/A	#N/A	-1.17	#N/A	histone deacetylase 2
ENSG00000135372	#N/A	#N/A	#N/A	-1.17	#N/A	N-acetyltransferase 10 (GCN5-related)
ENSG00000169710	#N/A	#N/A	#N/A	-1.17	#N/A	fatty acid synthase
ENSG00000103202	#N/A	#N/A	#N/A	-1.17	#N/A	NME/NM23 nucleoside diphosphate kinase 4
ENSG00000183431	#N/A	#N/A	#N/A	-1.17	#N/A	splicing factor 3a, subunit 3, 60kDa
ENSG00000239285	#N/A	#N/A	#N/A	-1.17	#N/A	lymphocyte antigen 6 complex, locus G5B
ENSG00000084073	#N/A	#N/A	#N/A	-1.17	#N/A	zinc metallopeptidase STE24
ENSG00000152117	#N/A	#N/A	#N/A	-1.17	#N/A	AC093838.4
ENSG00000109586	#N/A	#N/A	#N/A	-1.17	#N/A	polypeptide N-acetylgalactosaminyltransferase 7
ENSG00000138709	#N/A	#N/A	#N/A	-1.18	#N/A	La ribonucleoprotein domain family, member 1B
ENSG00000085998	#N/A	#N/A	#N/A	-1.18	#N/A	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)
ENSG00000084754	#N/A	#N/A	#N/A	-1.18	#N/A	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
ENSG00000110200	#N/A	#N/A	#N/A	-1.18	#N/A	anaphase promoting complex subunit 15
ENSG00000145494	#N/A	#N/A	#N/A	-1.18	#N/A	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
ENSG00000274081	#N/A	#N/A	#N/A	-1.18	#N/A	poly-U binding splicing factor 60KDa
ENSG00000105176	#N/A	#N/A	#N/A	-1.18	#N/A	URI1, prefoldin-like chaperone
ENSG00000115241	#N/A	#N/A	#N/A	-1.18	#N/A	protein phosphatase, Mg2+/Mn2+ dependent, 1G
ENSG00000146731	#N/A	#N/A	#N/A	-1.18	#N/A	chaperonin containing TCP1, subunit 6A (zeta 1)
ENSG00000232045	#N/A	#N/A	#N/A	-1.18	#N/A	euchromatic histone-lysine N-methyltransferase 2
ENSG00000077097	#N/A	#N/A	#N/A	-1.18	#N/A	topoisomerase (DNA) II beta 180kDa
ENSG00000163468	#N/A	#N/A	#N/A	-1.18	#N/A	chaperonin containing TCP1, subunit 3 (gamma)
ENSG00000128626	#N/A	#N/A	#N/A	-1.19	#N/A	mitochondrial ribosomal protein S12
ENSG00000137449	#N/A	#N/A	#N/A	-1.19	#N/A	cytoplasmic polyadenylation element binding protein 2
ENSG00000130764	#N/A	#N/A	#N/A	-1.19	#N/A	leucine rich repeat containing 47
ENSG00000231502	#N/A	#N/A	#N/A	-1.19	#N/A	LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000141577	#N/A	#N/A	#N/A	-1.19	#N/A	centrosomal protein 131kDa
ENSG00000075239	#N/A	#N/A	#N/A	-1.19	#N/A	acetyl-CoA acetyltransferase 1
ENSG00000104903	#N/A	#N/A	#N/A	-1.19	#N/A	lymphoblastic leukemia associated hematopoiesis regulator 1
ENSG00000163597	#N/A	#N/A	#N/A	-1.19	#N/A	small nucleolar RNA host gene 16
ENSG00000108395	#N/A	#N/A	#N/A	-1.19	#N/A	tripartite motif containing 37
ENSG00000276681	#N/A	#N/A	#N/A	-1.19	#N/A	leukocyte receptor cluster (LRC) member 8
ENSG00000092529	#N/A	#N/A	#N/A	-1.19	#N/A	calpain 3
ENSG00000187630	#N/A	#N/A	#N/A	-1.19	#N/A	dehydrogenase/reductase (SDR family) member 4 like 2
ENSG00000011485	#N/A	#N/A	#N/A	-1.20	#N/A	protein phosphatase 5, catalytic subunit
ENSG00000185803	#N/A	#N/A	#N/A	-1.20	#N/A	solute carrier family 52 (riboflavin transporter), member 2
ENSG00000204843	#N/A	#N/A	#N/A	-1.20	#N/A	dynactin 1
ENSG00000152990	#N/A	#N/A	#N/A	-1.20	#N/A	adhesion G protein-coupled receptor A3
ENSG00000107581	#N/A	#N/A	#N/A	-1.20	#N/A	eukaryotic translation initiation factor 3, subunit A

FIGURE 1I

ENSG00000005189	-0.26	1.84	1.82	#N/A	#N/A	Putative RNA exonuclease NEF-sp
ENSG00000157193	0.29	1.84	1.73	-1.04	#N/A	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
ENSG00000181751	0.15	1.78	1.72	#N/A	#N/A	chromosome 5 open reading frame 30
ENSG00000117155	0.05	1.91	1.97	#N/A	#N/A	synovial sarcoma, X breakpoint 2 interacting protein
ENSG00000118655	0.14	2.30	1.83	#N/A	#N/A	DNA cross-link repair 1B
ENSG00000143493	-0.01	1.74	1.50	#N/A	#N/A	integrator complex subunit 7
ENSG00000101911	0.06	1.90	1.50	#N/A	#N/A	phosphoribosyl pyrophosphate synthetase 2
ENSG00000095002	0.28	1.85	1.48	#N/A	#N/A	mutS homolog 2
ENSG00000138376	0.40	2.59	2.69	#N/A	#N/A	BRCA1 associated RING domain 1
ENSG00000205208	-0.77	1.35	1.34	#N/A	#N/A	chromosome 4 open reading frame 46
ENSG00000187173	0.25	2.04	0.77	#N/A	#N/A	late cornified envelope 2A
ENSG00000120802	0.09	1.82	2.28	#N/A	#N/A	thymopoietin
ENSG00000182481	-0.05	1.26	1.65	#N/A	#N/A	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
ENSG00000148848	0.59	1.59	1.54	#N/A	#N/A	ADAM metallopeptidase domain 12
ENSG00000145147	0.39	2.07	2.20	#N/A	#N/A	slit homolog 2 (Drosophila)
ENSG00000187257	-0.10	0.27	1.68	1.99	#N/A	round spermatid basic protein 1-like
ENSG00000120549	0.09	1.94	2.54	#N/A	#N/A	KIAA1217
ENSG00000138092	0.34	2.12	1.70	#N/A	#N/A	centromere protein O
ENSG00000050438	-0.12	1.49	2.19	#N/A	#N/A	solute carrier family 4, sodium bicarbonate cotransporter, member 8
ENSG00000164171	0.60	2.78	2.60	#N/A	2.08	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
ENSG00000095752	1.30	-2.81	-2.40	#N/A	#N/A	interleukin 11
ENSG00000172167	-0.54	2.43	2.57	#N/A	#N/A	MDM2 binding protein
ENSG00000124207	0.06	1.83	1.90	#N/A	#N/A	CSE1 chromosome segregation 1-like (yeast)
ENSG00000177606	1.01	-0.56	-0.58	1.93	1.11	jun proto-oncogene
ENSG00000145779	1.43	-0.15	-0.02	#N/A	#N/A	tumor necrosis factor, alpha-induced protein 8
ENSG00000143401	0.05	0.98	1.62	#N/A	#N/A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
ENSG00000175166	0.15	1.22	1.28	#N/A	#N/A	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
ENSG00000041353	0.38	2.34	2.66	#N/A	#N/A	RAB27B, member RAS oncogene family
ENSG00000171914	-0.17	1.30	0.95	#N/A	#N/A	talin 2
ENSG00000099250	-0.13	1.32	1.21	#N/A	#N/A	neuropilin 1
ENSG00000164985	-0.09	0.95	1.38	#N/A	#N/A	PC4 and SFRS1 interacting protein 1
ENSG00000163781	-0.01	1.51	1.39	#N/A	#N/A	topoisomerase (DNA) II binding protein 1
ENSG00000117748	0.21	1.86	1.16	#N/A	#N/A	replication protein A2, 32kDa
ENSG00000137959	#N/A	#N/A	#N/A	8.67	#N/A	interferon-induced protein 44-like
ENSG00000185885	#N/A	#N/A	#N/A	8.20	#N/A	interferon induced transmembrane protein 1
ENSG00000088827	#N/A	#N/A	#N/A	8.08	#N/A	sialic acid binding Ig-like lectin 1, sialoadhesin
ENSG00000111335	#N/A	#N/A	#N/A	7.66	#N/A	2'-5'-oligoadenylate synthetase 2, 69/71kDa
ENSG00000213626	#N/A	#N/A	#N/A	7.25	1.15	limb bud and heart development
ENSG00000137965	#N/A	#N/A	#N/A	6.74	1.71	interferon-induced protein 44
ENSG00000100453	#N/A	#N/A	#N/A	6.72	#N/A	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
ENSG00000133106	#N/A	#N/A	#N/A	6.54	#N/A	epithelial stromal interaction 1 (breast)
ENSG00000115155	#N/A	#N/A	#N/A	6.51	#N/A	otoferlin
ENSG00000137801	#N/A	#N/A	#N/A	6.42	#N/A	thrombospondin 1
ENSG00000198959	#N/A	#N/A	#N/A	6.36	1.96	transglutaminase 2
ENSG00000133316	#N/A	#N/A	#N/A	6.27	6.33	WD repeat domain 74
ENSG00000089127	#N/A	#N/A	#N/A	6.14	#N/A	2'-5'-oligoadenylate synthetase 1, 40/46kDa

ENSG00000235125	#N/A	#N/A	#N/A	-1.20	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1
ENSG00000239900	#N/A	#N/A	#N/A	-1.20	#N/A	adenylosuccinate lyase
ENSG00000117448	#N/A	#N/A	#N/A	-1.20	#N/A	aldo-keto reductase family 1, member A1 (aldehyde reductase)
ENSG00000224531	#N/A	#N/A	#N/A	-1.21	#N/A	small integral membrane protein 13
ENSG00000091527	#N/A	#N/A	#N/A	-1.21	#N/A	CDV3 homolog (mouse)
ENSG00000196642	#N/A	#N/A	#N/A	-1.21	#N/A	RAB, member RAS oncogene family-like 6
ENSG00000166669	#N/A	#N/A	#N/A	-1.21	#N/A	activating transcription factor 7 interacting protein 2
ENSG00000155189	#N/A	#N/A	#N/A	-1.21	#N/A	1-acylglycerol-3-phosphate O-acyltransferase 5
ENSG00000140474	#N/A	#N/A	#N/A	-1.21	#N/A	unc-51 like kinase 3
ENSG00000086848	#N/A	#N/A	#N/A	-1.21	#N/A	ALG9, alpha-1,2-mannosyltransferase
ENSG00000100448	#N/A	#N/A	#N/A	-1.21	2.60	cathepsin G
ENSG00000184465	#N/A	#N/A	#N/A	-1.21	#N/A	WD repeat domain 27
ENSG00000125445	#N/A	#N/A	#N/A	-1.21	#N/A	mitochondrial ribosomal protein S7
ENSG00000170632	#N/A	#N/A	#N/A	-1.21	#N/A	armadillo repeat containing 10
ENSG00000198888	#N/A	#N/A	#N/A	-1.21	#N/A	mitochondrially encoded NADH dehydrogenase 1
ENSG00000156876	#N/A	#N/A	#N/A	-1.21	#N/A	SAS-6 centriolar assembly protein
ENSG00000205903	#N/A	#N/A	#N/A	-1.22	#N/A	zinc finger protein 316
ENSG00000113360	#N/A	#N/A	#N/A	-1.22	#N/A	drosha, ribonuclease type III
ENSG00000112290	#N/A	#N/A	#N/A	-1.22	#N/A	WAS protein family, member 1
ENSG00000051128	#N/A	#N/A	#N/A	-1.22	#N/A	homer scaffolding protein 3
ENSG00000125630	#N/A	#N/A	#N/A	-1.22	#N/A	polymerase (RNA) I polypeptide B, 128kDa
ENSG00000179304	#N/A	#N/A	#N/A	-1.22	#N/A	family with sequence similarity 156, member B
ENSG00000148840	#N/A	#N/A	#N/A	-1.22	#N/A	peroxisome proliferator-activated receptor gamma, coactivator-related 1
ENSG00000247982	#N/A	#N/A	#N/A	-1.22	#N/A	long intergenic non-protein coding RNA 926
ENSG00000075415	#N/A	#N/A	#N/A	-1.22	#N/A	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
ENSG00000256269	#N/A	#N/A	#N/A	-1.22	#N/A	hydroxymethylbilane synthase
ENSG00000107833	#N/A	#N/A	#N/A	-1.22	1.45	nucleophosmin/nucleoplasmin 3
ENSG00000167136	#N/A	#N/A	#N/A	-1.22	#N/A	endonuclease G
ENSG00000109534	#N/A	#N/A	#N/A	-1.22	1.88	GAR1 homolog, ribonucleoprotein
ENSG00000065809	#N/A	#N/A	#N/A	-1.22	#N/A	family with sequence similarity 107, member B
ENSG00000274811	#N/A	#N/A	#N/A	-1.22	#N/A	CLPTM1-like
ENSG00000163938	#N/A	#N/A	#N/A	-1.22	#N/A	guanine nucleotide binding protein-like 3 (nucleolar)
ENSG00000169682	#N/A	#N/A	#N/A	-1.23	#N/A	spinster homolog 1 (Drosophila)
ENSG00000197451	#N/A	#N/A	#N/A	-1.23	#N/A	heterogeneous nuclear ribonucleoprotein A/B
ENSG00000185420	#N/A	#N/A	#N/A	-1.23	#N/A	SET and MYND domain containing 3
ENSG00000141858	#N/A	#N/A	#N/A	-1.23	#N/A	sterile alpha motif domain containing 1
ENSG00000281184	#N/A	#N/A	#N/A	-1.23	#N/A	proteasome (prosome, macropain) subunit, beta type, 1
ENSG00000108651	#N/A	#N/A	#N/A	-1.23	#N/A	UTP6, small subunit (SSU) processome component, homolog (yeast)
ENSG00000100726	#N/A	#N/A	#N/A	-1.23	#N/A	telomere maintenance 2
ENSG00000164151	#N/A	#N/A	#N/A	-1.23	#N/A	interactor of little elongation complex ELL subunit 1
ENSG00000212907	#N/A	#N/A	#N/A	-1.24	#N/A	mitochondrially encoded NADH dehydrogenase 4L
ENSG00000233369	#N/A	#N/A	#N/A	-1.24	#N/A	general transcription factor IIi, pseudogene 4
ENSG00000182568	#N/A	#N/A	#N/A	-1.24	#N/A	SATB homeobox 1
ENSG00000136950	#N/A	#N/A	#N/A	-1.24	#N/A	actin related protein 2/3 complex, subunit 5-like
ENSG00000168101	#N/A	#N/A	#N/A	-1.24	#N/A	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1
ENSG00000152193	#N/A	#N/A	#N/A	-1.24	#N/A	ring finger protein 219

FIGURE 1J

ENSG00000169871	#N/A	#N/A	#N/A	6.10	3.97	tripartite motif containing 56
ENSG00000135114	#N/A	#N/A	#N/A	5.99	#N/A	2'-5'-oligoadenylate synthetase-like
ENSG00000072694	#N/A	#N/A	#N/A	5.87	#N/A	Fc fragment of IgG, low affinity IIb, receptor (CD32)
ENSG00000196562	#N/A	#N/A	#N/A	5.78	#N/A	sulfatase 2
ENSG00000189221	#N/A	#N/A	#N/A	5.62	#N/A	monoamine oxidase A
ENSG00000269337	#N/A	#N/A	#N/A	5.61	#N/A	AL591479.1
ENSG00000181195	#N/A	#N/A	#N/A	5.60	#N/A	proenkephalin
ENSG00000225614	#N/A	#N/A	#N/A	5.52	#N/A	zinc finger protein 469
ENSG00000134369	#N/A	#N/A	#N/A	5.24	#N/A	neuron navigator 1
ENSG00000152404	#N/A	#N/A	#N/A	5.23	3.59	CWF19-like 2, cell cycle control (S. pombe)
ENSG00000142192	#N/A	#N/A	#N/A	5.11	#N/A	amyloid beta (A4) precursor protein
ENSG00000154153	#N/A	#N/A	#N/A	5.00	#N/A	family with sequence similarity 134, member B
ENSG00000134321	#N/A	#N/A	#N/A	4.99	#N/A	radical S-adenosyl methionine domain containing 2
ENSG00000126709	#N/A	#N/A	#N/A	4.96	3.67	interferon, alpha-inducible protein 6
ENSG00000187608	#N/A	#N/A	#N/A	4.89	2.10	ISG15 ubiquitin-like modifier
ENSG00000136960	#N/A	#N/A	#N/A	4.79	#N/A	ectonucleotide pyrophosphatase/phosphodiesterase 2
ENSG00000196141	#N/A	#N/A	#N/A	4.74	#N/A	spermatogenesis associated, serine-rich 2-like
ENSG00000136235	#N/A	#N/A	#N/A	4.71	2.66	glycoprotein (transmembrane) nmb
ENSG00000115414	#N/A	#N/A	#N/A	4.65	#N/A	fibronectin 1
ENSG00000152104	#N/A	#N/A	#N/A	4.50	#N/A	protein tyrosine phosphatase, non-receptor type 14
ENSG00000115977	#N/A	#N/A	#N/A	4.50	2.36	AP2 associated kinase 1
ENSG00000213918	#N/A	#N/A	#N/A	4.46	#N/A	deoxyribonuclease I
ENSG00000028277	#N/A	#N/A	#N/A	4.45	3.74	POU class 2 homeobox 2
ENSG00000130821	#N/A	#N/A	#N/A	4.44	#N/A	solute carrier family 6 (neurotransmitter transporter), member 8
ENSG00000184979	#N/A	#N/A	#N/A	4.42	#N/A	ubiquitin specific peptidase 18
ENSG00000203812	#N/A	#N/A	#N/A	4.25	2.44	histone cluster 2, H2aa3
ENSG00000130589	#N/A	#N/A	#N/A	4.25	#N/A	helicase with zinc finger 2, transcriptional coactivator
ENSG00000181458	#N/A	#N/A	#N/A	4.21	#N/A	transmembrane protein 45A
ENSG00000247095	#N/A	#N/A	#N/A	4.19	#N/A	MIR210 host gene
ENSG00000135931	#N/A	#N/A	#N/A	4.16	1.76	armadillo repeat containing 9
ENSG00000180509	#N/A	#N/A	#N/A	4.04	#N/A	potassium channel, voltage gated subfamily E regulatory beta subunit 1
ENSG00000038427	#N/A	#N/A	#N/A	4.02	#N/A	versican
ENSG00000114013	#N/A	#N/A	#N/A	3.95	#N/A	CD86 molecule
ENSG00000204642	#N/A	#N/A	#N/A	3.94	#N/A	major histocompatibility complex, class I, F
ENSG00000203710	#N/A	#N/A	#N/A	3.88	#N/A	complement component (3b/4b) receptor 1 (Knops blood group)
ENSG00000244509	#N/A	#N/A	#N/A	3.86	2.18	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
ENSG00000143190	#N/A	#N/A	#N/A	3.85	2.95	POU class 2 homeobox 1
ENSG00000185650	#N/A	#N/A	#N/A	3.85	#N/A	ZFP36 ring finger protein-like 1
ENSG00000179029	#N/A	#N/A	#N/A	3.85	#N/A	transmembrane protein 107
ENSG00000182578	#N/A	#N/A	#N/A	3.85	#N/A	colony stimulating factor 1 receptor
ENSG00000187193	#N/A	#N/A	#N/A	3.85	#N/A	metallothionein 1X
ENSG00000110324	#N/A	#N/A	#N/A	3.83	#N/A	interleukin 10 receptor, alpha
ENSG00000261064	#N/A	#N/A	#N/A	3.83	#N/A	RP11-1000B6.3
ENSG00000166750	#N/A	#N/A	#N/A	3.81	#N/A	schlafen family member 5

ENSG00000270647	#N/A	#N/A	#N/A	-1.24	#N/A	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
ENSG00000140650	#N/A	#N/A	#N/A	-1.24	#N/A	phosphomannomutase 2
ENSG00000106263	#N/A	#N/A	#N/A	-1.24	#N/A	eukaryotic translation initiation factor 3, subunit B
ENSG00000049449	#N/A	#N/A	#N/A	-1.25	#N/A	reticulocalbin 1, EF-hand calcium binding domain
ENSG00000066044	#N/A	#N/A	#N/A	-1.25	#N/A	ELAV like RNA binding protein 1
ENSG00000165684	#N/A	#N/A	#N/A	-1.25	#N/A	small nuclear RNA activating complex, polypeptide 4, 190kDa
ENSG00000111641	#N/A	#N/A	#N/A	-1.25	#N/A	NOP2 nucleolar protein
ENSG00000143952	#N/A	#N/A	#N/A	-1.25	#N/A	vacuolar protein sorting 54 homolog (S. cerevisiae)
ENSG00000058600	#N/A	#N/A	#N/A	-1.25	#N/A	polymerase (RNA) III (DNA directed) polypeptide E (80kD)
ENSG00000167113	#N/A	#N/A	#N/A	-1.25	#N/A	coenzyme Q4
ENSG00000264364	#N/A	#N/A	#N/A	-1.25	#N/A	dynein, light chain, LC8-type 2
ENSG00000104529	#N/A	#N/A	#N/A	-1.25	#N/A	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
ENSG00000165874	#N/A	#N/A	#N/A	-1.25	#N/A	family with sequence similarity 35, member B, pseudogene
ENSG00000165271	#N/A	#N/A	#N/A	-1.26	#N/A	nucleolar protein 6 (RNA-associated)
ENSG00000161618	#N/A	#N/A	#N/A	-1.26	#N/A	aldehyde dehydrogenase 16 family, member A1
ENSG00000134215	#N/A	#N/A	#N/A	-1.26	#N/A	vav 3 guanine nucleotide exchange factor
ENSG00000124571	#N/A	#N/A	#N/A	-1.26	#N/A	exportin 5
ENSG00000104907	#N/A	#N/A	#N/A	-1.26	#N/A	tRNA methyltransferase 1 homolog (S. cerevisiae)
ENSG00000165097	#N/A	#N/A	#N/A	-1.26	#N/A	lysine (K)-specific demethylase 1B
ENSG00000107949	#N/A	#N/A	#N/A	-1.26	#N/A	BRCA2 and CDKN1A interacting protein
ENSG00000116221	#N/A	#N/A	#N/A	-1.26	#N/A	mitochondrial ribosomal protein L37
ENSG00000141759	#N/A	#N/A	#N/A	-1.26	#N/A	thioredoxin-like 4A
ENSG00000090447	#N/A	#N/A	#N/A	-1.26	#N/A	transcription factor AP-4 (activating enhancer binding protein 4)
ENSG00000036549	#N/A	#N/A	#N/A	-1.26	#N/A	zinc finger, ZZ-type containing 3
ENSG00000213593	#N/A	#N/A	#N/A	-1.27	#N/A	thioredoxin-related transmembrane protein 2
ENSG00000204149	#N/A	#N/A	#N/A	-1.27	#N/A	ArfGAP with GTPase domain, ankyrin repeat and PH domain 6
ENSG00000031003	#N/A	#N/A	#N/A	-1.27	#N/A	family with sequence similarity 13, member B
ENSG00000100522	#N/A	#N/A	#N/A	-1.27	#N/A	glucosamine-phosphate N-acetyltransferase 1
ENSG00000167702	#N/A	#N/A	#N/A	-1.27	#N/A	kinesin family member C2
ENSG00000095906	#N/A	#N/A	#N/A	-1.27	#N/A	nucleotide binding protein 2
ENSG00000028310	#N/A	#N/A	#N/A	-1.27	#N/A	bromodomain containing 9
ENSG00000243725	#N/A	#N/A	#N/A	-1.27	#N/A	tetratricopeptide repeat domain 4
ENSG00000156697	#N/A	#N/A	#N/A	-1.27	#N/A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
ENSG00000115232	#N/A	#N/A	#N/A	-1.27	#N/A	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
ENSG00000087087	#N/A	#N/A	#N/A	-1.27	#N/A	serrate, RNA effector molecule
ENSG00000086200	#N/A	#N/A	#N/A	-1.27	#N/A	importin 11
ENSG00000188352	#N/A	#N/A	#N/A	-1.27	#N/A	focadhesin
ENSG00000164818	#N/A	#N/A	#N/A	-1.27	#N/A	dynein, axonemal, assembly factor 5
ENSG00000134748	#N/A	#N/A	#N/A	-1.27	#N/A	pre-mRNA processing factor 38A
ENSG00000138028	#N/A	#N/A	#N/A	-1.27	#N/A	cell growth regulator with EF-hand domain 1
ENSG00000255587	#N/A	#N/A	#N/A	-1.28	#N/A	RAB44, member RAS oncogene family
ENSG00000145725	#N/A	#N/A	#N/A	-1.28	#N/A	diphosphoinositol pentakisphosphate kinase 2
ENSG00000198824	#N/A	#N/A	#N/A	-1.28	#N/A	chromosome alignment maintaining phosphoprotein 1
ENSG00000152520	#N/A	#N/A	#N/A	-1.28	#N/A	PAN3 poly(A) specific ribonuclease subunit

FIGURE 1K

ENSG00000116741	#N/A	#N/A	#N/A	3.79	#N/A	regulator of G-protein signaling 2
ENSG00000020633	#N/A	#N/A	#N/A	3.79	#N/A	runt-related transcription factor 3
ENSG00000125726	#N/A	#N/A	#N/A	3.77	#N/A	CD70 molecule
ENSG00000243004	#N/A	#N/A	#N/A	3.71	2.92	AC005062.2
ENSG00000114268	#N/A	#N/A	#N/A	3.70	#N/A	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
ENSG00000185507	#N/A	#N/A	#N/A	3.67	#N/A	interferon regulatory factor 7
ENSG00000153815	#N/A	#N/A	#N/A	3.63	#N/A	c-Maf inducing protein
ENSG00000204103	#N/A	#N/A	#N/A	3.59	#N/A	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B
ENSG00000163633	#N/A	#N/A	#N/A	3.58	#N/A	chromosome 4 open reading frame 36
ENSG00000102524	#N/A	#N/A	#N/A	3.57	#N/A	tumor necrosis factor (ligand) superfamily, member 13b
ENSG00000196739	#N/A	#N/A	#N/A	3.57	#N/A	collagen, type XXVII, alpha 1
ENSG00000259112	#N/A	#N/A	#N/A	3.56	#N/A	NDUFC2-KCTD14 readthrough
ENSG00000088826	#N/A	#N/A	#N/A	3.55	#N/A	spermine oxidase
ENSG00000188313	#N/A	#N/A	#N/A	3.54	#N/A	phospholipid scramblase 1
ENSG00000134326	#N/A	#N/A	#N/A	3.53	#N/A	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
ENSG00000186918	#N/A	#N/A	#N/A	3.49	1.09	zinc finger protein 395
ENSG00000158769	#N/A	#N/A	#N/A	3.47	#N/A	F11 receptor
ENSG00000124762	#N/A	#N/A	#N/A	3.47	#N/A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
ENSG00000049323	#N/A	#N/A	#N/A	3.47	#N/A	latent transforming growth factor beta binding protein 1
ENSG00000138640	#N/A	#N/A	#N/A	3.46	#N/A	family with sequence similarity 13, member A
ENSG00000275565	#N/A	#N/A	#N/A	3.45	#N/A	arachidonate 5-lipoxygenase
ENSG00000213741	#N/A	#N/A	#N/A	3.42	2.02	ribosomal protein S29
ENSG00000130402	#N/A	#N/A	#N/A	3.42	1.80	actinin, alpha 4
ENSG00000251474	#N/A	#N/A	#N/A	3.39	#N/A	ribosomal protein L32 pseudogene 3
ENSG00000177410	#N/A	#N/A	#N/A	3.37	1.74	ZNFX1 antisense RNA 1
ENSG00000138433	#N/A	#N/A	#N/A	3.32	2.18	corepressor interacting with RBPJ, 1
ENSG00000267855	#N/A	#N/A	#N/A	3.28	2.60	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
ENSG00000115165	#N/A	#N/A	#N/A	3.28	#N/A	cytohesin 1 interacting protein
ENSG00000109107	#N/A	#N/A	#N/A	3.25	#N/A	aldolase C, fructose-bisphosphate
ENSG00000072682	#N/A	#N/A	#N/A	3.21	#N/A	prolyl 4-hydroxylase, alpha polypeptide II
ENSG00000138496	#N/A	#N/A	#N/A	3.19	#N/A	poly (ADP-ribose) polymerase family, member 9
ENSG00000111674	#N/A	#N/A	#N/A	3.17	#N/A	enolase 2 (gamma, neuronal)
ENSG00000165029	#N/A	#N/A	#N/A	3.17	#N/A	ATP-binding cassette, sub-family A (ABC1), member 1
ENSG00000101745	#N/A	#N/A	#N/A	3.17	2.19	ankyrin repeat domain 12
ENSG00000259529	#N/A	#N/A	#N/A	3.15	#N/A	Uncharacterized protein
ENSG00000163823	#N/A	#N/A	#N/A	3.15	#N/A	chemokine (C-C motif) receptor 1
ENSG00000160593	#N/A	#N/A	#N/A	3.13	#N/A	adhesion molecule, interacts with CXADR antigen 1
ENSG00000166012	#N/A	#N/A	#N/A	3.10	2.17	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa
ENSG00000119547	#N/A	#N/A	#N/A	3.06	#N/A	one cut homeobox 2
ENSG00000160932	#N/A	#N/A	#N/A	3.06	#N/A	lymphocyte antigen 6 complex, locus E
ENSG00000187837	#N/A	#N/A	#N/A	3.05	#N/A	histone cluster 1, H1c
ENSG00000186660	#N/A	#N/A	#N/A	3.04	#N/A	ZFP91 zinc finger protein
ENSG00000171858	#N/A	#N/A	#N/A	3.03	1.93	ribosomal protein S21

ENSG00000206053	#N/A	#N/A	#N/A	-1.28	#N/A	hematological and neurological expressed 1-like
ENSG00000007376	#N/A	#N/A	#N/A	-1.28	#N/A	RNA pseudouridylate synthase domain containing 1
ENSG00000150401	#N/A	#N/A	#N/A	-1.28	#N/A	DCN1, defective in cullin neddylation 1, domain containing 2
ENSG00000087495	#N/A	#N/A	#N/A	-1.28	#N/A	phosphatase and actin regulator 3
ENSG00000099899	#N/A	#N/A	#N/A	-1.28	#N/A	tRNA methyltransferase 2 homolog A (S. cerevisiae)
ENSG00000161036	#N/A	#N/A	#N/A	-1.28	#N/A	leucine-rich repeats and WD repeat domain containing 1
ENSG00000197006	#N/A	#N/A	#N/A	-1.28	#N/A	methyltransferase like 9
ENSG00000142864	#N/A	#N/A	#N/A	-1.28	#N/A	SERPINE1 mRNA binding protein 1
ENSG00000187796	#N/A	#N/A	#N/A	-1.29	#N/A	caspase recruitment domain family, member 9
ENSG00000169957	#N/A	#N/A	#N/A	-1.29	#N/A	zinc finger protein 768
ENSG00000198648	#N/A	#N/A	#N/A	-1.29	#N/A	serine threonine kinase 39
ENSG00000167700	#N/A	#N/A	#N/A	-1.29	#N/A	major facilitator superfamily domain containing 3
ENSG00000134684	#N/A	#N/A	#N/A	-1.29	#N/A	tyrosyl-tRNA synthetase
ENSG00000007923	#N/A	#N/A	#N/A	-1.29	#N/A	DnaJ (Hsp40) homolog, subfamily C, member 11
ENSG00000183137	#N/A	#N/A	#N/A	-1.29	#N/A	centrosomal protein 57kDa-like 1
ENSG00000153395	#N/A	#N/A	#N/A	-1.29	#N/A	lysophosphatidylcholine acyltransferase 1
ENSG00000151247	#N/A	#N/A	#N/A	-1.30	#N/A	eukaryotic translation initiation factor 4E
ENSG00000136379	#N/A	#N/A	#N/A	-1.30	#N/A	abhydrolase domain containing 17C
ENSG00000092820	#N/A	#N/A	#N/A	-1.30	#N/A	ezrin
ENSG00000151835	#N/A	#N/A	#N/A	-1.30	#N/A	sacsin molecular chaperone
ENSG00000048162	#N/A	#N/A	#N/A	-1.30	1.07	NOP16 nucleolar protein
ENSG00000162402	#N/A	#N/A	#N/A	-1.30	#N/A	ubiquitin specific peptidase 24
ENSG00000086475	#N/A	#N/A	#N/A	-1.30	#N/A	selenophosphate synthetase 1
ENSG00000188976	#N/A	#N/A	#N/A	-1.30	#N/A	NOC2-like nucleolar associated transcriptional repressor
ENSG00000167792	#N/A	#N/A	#N/A	-1.30	#N/A	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
ENSG00000104884	#N/A	#N/A	#N/A	-1.30	#N/A	excision repair cross-complementation group 2
ENSG00000230903	#N/A	#N/A	#N/A	-1.30	#N/A	RPL9P8
ENSG00000100890	#N/A	#N/A	#N/A	-1.30	#N/A	KIAA0391
ENSG00000188452	#N/A	#N/A	#N/A	-1.31	#N/A	ceramide kinase-like
ENSG00000076248	#N/A	#N/A	#N/A	-1.31	#N/A	uracil DNA glycosylase
ENSG00000165661	#N/A	#N/A	#N/A	-1.31	#N/A	quiescin Q6 sulfhydryl oxidase 2
ENSG00000250067	#N/A	#N/A	#N/A	-1.31	#N/A	YjeF N-terminal domain containing 3
ENSG00000131323	#N/A	#N/A	#N/A	-1.31	#N/A	TNF receptor-associated factor 3
ENSG00000070785	#N/A	#N/A	#N/A	-1.31	#N/A	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa
ENSG00000057757	#N/A	#N/A	#N/A	-1.31	#N/A	PITH (C-terminal proteasome-interacting domain of thioredoxin-like) domain containing 1
ENSG00000135316	#N/A	#N/A	#N/A	-1.31	#N/A	synaptotagmin binding, cytoplasmic RNA interacting protein
ENSG00000122965	#N/A	#N/A	#N/A	-1.31	#N/A	RNA binding motif protein 19
ENSG00000181472	#N/A	#N/A	#N/A	-1.31	#N/A	zinc finger and BTB domain containing 2
ENSG00000125485	#N/A	#N/A	#N/A	-1.31	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31
ENSG00000135596	#N/A	#N/A	#N/A	-1.32	#N/A	microtubule associated monooxygenase, calponin and LIM domain containing 1
ENSG00000135763	#N/A	#N/A	#N/A	-1.32	#N/A	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)
ENSG00000228253	#N/A	#N/A	#N/A	-1.32	1.36	MT-ATP8
ENSG00000139842	#N/A	#N/A	#N/A	-1.32	#N/A	cullin 4A

FIGURE 1L

ENSG00000169715	#N/A	#N/A	#N/A	3.01	1.39	metallothionein 1E
ENSG00000138642	#N/A	#N/A	#N/A	3.01	#N/A	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
ENSG00000197555	#N/A	#N/A	#N/A	3.00	#N/A	signal-induced proliferation-associated 1 like 1
ENSG00000177409	#N/A	#N/A	#N/A	2.97	#N/A	sterile alpha motif domain containing 9-like
ENSG00000178726	#N/A	#N/A	#N/A	2.95	3.11	thrombomodulin
ENSG00000133059	#N/A	#N/A	#N/A	2.95	#N/A	dual serine/threonine and tyrosine protein kinase
ENSG00000095066	#N/A	#N/A	#N/A	2.94	1.30	hook microtubule-tethering protein 2
ENSG00000176171	#N/A	#N/A	#N/A	2.92	#N/A	BCL2/adenovirus E1B 19kDa interacting protein 3
ENSG00000170412	#N/A	#N/A	#N/A	2.92	#N/A	G protein-coupled receptor, class C, group 5, member C
ENSG00000141905	#N/A	#N/A	#N/A	2.92	2.13	nuclear factor I/C (CCAAT-binding transcription factor)
ENSG00000134597	#N/A	#N/A	#N/A	2.91	2.28	RNA binding motif protein, X-linked 2
ENSG00000181690	#N/A	#N/A	#N/A	2.89	#N/A	pleiomorphic adenoma gene 1
ENSG00000147872	#N/A	#N/A	#N/A	2.89	#N/A	perilipin 2
ENSG00000267121	#N/A	#N/A	#N/A	2.87	#N/A	CTD-2020K17.1
ENSG00000134955	#N/A	#N/A	#N/A	2.87	#N/A	solute carrier family 37 (glucose-6-phosphate transporter), member 2
ENSG00000173821	#N/A	#N/A	#N/A	2.86	#N/A	ring finger protein 213
ENSG00000153006	#N/A	#N/A	#N/A	2.85	2.34	SREK1-interacting protein 1
ENSG00000184678	#N/A	#N/A	#N/A	2.85	#N/A	histone cluster 2, H2be
ENSG00000203875	#N/A	#N/A	#N/A	2.84	1.98	small nucleolar RNA host gene 5
ENSG00000131944	#N/A	#N/A	#N/A	2.84	#N/A	Fanconi anemia core complex associated protein 24
ENSG00000122884	#N/A	#N/A	#N/A	2.84	#N/A	prolyl 4-hydroxylase, alpha polypeptide I
ENSG00000055332	#N/A	#N/A	#N/A	2.84	#N/A	eukaryotic translation initiation factor 2-alpha kinase 2
ENSG00000270316	#N/A	#N/A	#N/A	2.82	#N/A	C10orf32-ASMT readthrough (NMD candidate)
ENSG00000197013	#N/A	#N/A	#N/A	2.81	#N/A	zinc finger protein 429
ENSG00000165071	#N/A	#N/A	#N/A	2.79	#N/A	transmembrane protein 71
ENSG00000270882	#N/A	#N/A	#N/A	2.78	#N/A	histone cluster 2, H4a
ENSG00000177954	#N/A	#N/A	#N/A	2.77	1.98	ribosomal protein S27
ENSG00000146192	#N/A	#N/A	#N/A	2.76	#N/A	FYVE, RhoGEF and PH domain containing 2
ENSG00000067082	#N/A	#N/A	#N/A	2.75	1.37	Kruppel-like factor 6
ENSG00000143315	#N/A	#N/A	#N/A	2.74	#N/A	phosphatidylinositol glycan anchor biosynthesis, class M
ENSG00000280755	#N/A	#N/A	#N/A	2.73	#N/A	SP110 nuclear body protein
ENSG00000171766	#N/A	#N/A	#N/A	2.73	#N/A	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
ENSG00000132274	#N/A	#N/A	#N/A	2.73	#N/A	tripartite motif containing 22
ENSG00000118515	#N/A	#N/A	#N/A	2.73	#N/A	serum/glucocorticoid regulated kinase 1
ENSG00000140941	#N/A	#N/A	#N/A	2.72	#N/A	microtubule-associated protein 1 light chain 3 beta
ENSG00000162959	#N/A	#N/A	#N/A	2.70	#N/A	mediator of cell motility 1
ENSG00000169403	#N/A	#N/A	#N/A	2.67	#N/A	platelet-activating factor receptor
ENSG00000205413	#N/A	#N/A	#N/A	2.67	#N/A	sterile alpha motif domain containing 9
ENSG00000008952	#N/A	#N/A	#N/A	2.66	2.15	SEC62 homolog (S. cerevisiae)
ENSG00000088888	#N/A	#N/A	#N/A	2.65	1.19	mitochondrial antiviral signaling protein
ENSG00000139626	#N/A	#N/A	#N/A	2.65	#N/A	integrin, beta 7
ENSG00000100592	#N/A	#N/A	#N/A	2.64	#N/A	dishevelled associated activator of morphogenesis 1
ENSG00000197358	#N/A	#N/A	#N/A	2.62	#N/A	BCL2/adenovirus E1B 19kDa interacting protein 3 pseudogene 1
ENSG00000113140	#N/A	#N/A	#N/A	2.61	#N/A	secreted protein, acidic, cysteine-rich (osteonectin)
ENSG00000104765	#N/A	#N/A	#N/A	2.58	#N/A	BCL2/adenovirus E1B 19kDa interacting protein 3-like
ENSG00000135916	#N/A	#N/A	#N/A	2.55	#N/A	integral membrane protein 2C

ENSG00000033011	#N/A	#N/A	#N/A	-1.32	#N/A	ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase
ENSG00000237550	#N/A	#N/A	#N/A	-1.32	#N/A	RPL9P9
ENSG00000146540	#N/A	#N/A	#N/A	-1.33	#N/A	chromosome 7 open reading frame 50
ENSG00000099901	#N/A	#N/A	#N/A	-1.33	#N/A	RAN binding protein 1
ENSG00000107815	#N/A	#N/A	#N/A	-1.33	#N/A	chromosome 10 open reading frame 2
ENSG00000101220	#N/A	#N/A	#N/A	-1.33	#N/A	chromosome 20 open reading frame 27
ENSG00000112787	#N/A	#N/A	#N/A	-1.33	#N/A	fibrosin-like 1
ENSG00000122566	#N/A	#N/A	#N/A	-1.33	#N/A	heterogeneous nuclear ribonucleoprotein A2/B1
ENSG00000072274	#N/A	#N/A	#N/A	-1.33	#N/A	transferrin receptor
ENSG00000148300	#N/A	#N/A	#N/A	-1.33	#N/A	REX4 homolog, 3'-5' exonuclease
ENSG00000099949	#N/A	#N/A	#N/A	-1.33	#N/A	leucine-zipper-like transcription regulator 1
ENSG00000174744	#N/A	#N/A	#N/A	-1.33	#N/A	breast cancer metastasis suppressor 1
ENSG00000164163	#N/A	#N/A	#N/A	-1.33	#N/A	ATP-binding cassette, sub-family E (OABP), member 1
ENSG00000110042	#N/A	#N/A	#N/A	-1.33	#N/A	deltex 4, E3 ubiquitin ligase
ENSG00000138074	#N/A	#N/A	#N/A	-1.33	#N/A	solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6
ENSG00000165724	#N/A	#N/A	#N/A	-1.34	#N/A	zinc finger, MYND-type containing 19
ENSG00000136718	#N/A	#N/A	#N/A	-1.34	#N/A	IMP4, U3 small nucleolar ribonucleoprotein
ENSG00000197498	#N/A	#N/A	#N/A	-1.34	#N/A	ribosome production factor 2 homolog
ENSG00000154277	#N/A	#N/A	#N/A	-1.34	#N/A	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
ENSG00000172232	#N/A	#N/A	#N/A	-1.34	#N/A	azurocidin 1
ENSG00000177225	#N/A	#N/A	#N/A	-1.34	#N/A	Parkinson disease 7 domain containing 1
ENSG00000125910	#N/A	#N/A	#N/A	-1.34	#N/A	sphingosine-1-phosphate receptor 4
ENSG00000162408	#N/A	#N/A	#N/A	-1.34	#N/A	nucleolar protein 9
ENSG00000117450	#N/A	#N/A	#N/A	-1.34	#N/A	peroxiredoxin 1
ENSG00000033050	#N/A	#N/A	#N/A	-1.34	#N/A	ATP-binding cassette, sub-family F (GCN20), member 2
ENSG00000142875	#N/A	#N/A	#N/A	-1.34	#N/A	protein kinase, cAMP-dependent, catalytic, beta
ENSG00000133422	#N/A	#N/A	#N/A	-1.34	#N/A	MORC family CW-type zinc finger 2
ENSG00000065978	#N/A	#N/A	#N/A	-1.34	#N/A	Y box binding protein 1
ENSG00000168066	#N/A	#N/A	#N/A	-1.34	#N/A	splicing factor 1
ENSG00000048052	#N/A	#N/A	#N/A	-1.34	#N/A	histone deacetylase 9
ENSG00000142409	#N/A	#N/A	#N/A	-1.35	#N/A	zinc finger protein 787
ENSG00000148334	#N/A	#N/A	#N/A	-1.35	#N/A	prostaglandin E synthase 2
ENSG00000163291	#N/A	#N/A	#N/A	-1.35	#N/A	progestin and adipoQ receptor family member III
ENSG00000155393	#N/A	#N/A	#N/A	-1.35	#N/A	HEAT repeat containing 3
ENSG00000108106	#N/A	#N/A	#N/A	-1.35	#N/A	ubiquitin-conjugating enzyme E2S
ENSG00000174547	#N/A	#N/A	#N/A	-1.35	#N/A	mitochondrial ribosomal protein L11
ENSG00000144867	#N/A	#N/A	#N/A	-1.35	#N/A	signal recognition particle receptor, B subunit
ENSG00000184207	#N/A	#N/A	#N/A	-1.35	#N/A	phosphoglycolate phosphatase
ENSG00000130638	#N/A	#N/A	#N/A	-1.35	#N/A	ataxin 10
ENSG00000001084	#N/A	#N/A	#N/A	-1.35	#N/A	glutamate-cysteine ligase, catalytic subunit
ENSG00000228875	#N/A	#N/A	#N/A	-1.35	#N/A	casein kinase 2, beta polypeptide
ENSG00000104341	#N/A	#N/A	#N/A	-1.35	#N/A	lysosomal protein transmembrane 4 beta
ENSG00000117419	#N/A	#N/A	#N/A	-1.35	#N/A	ERI1 exoribonuclease family member 3
ENSG00000184281	#N/A	#N/A	#N/A	-1.35	#N/A	tumor suppressing subtransferable candidate 4
ENSG00000173145	#N/A	#N/A	#N/A	-1.36	#N/A	NOC3-like DNA replication regulator
ENSG00000073060	#N/A	#N/A	#N/A	-1.36	#N/A	scavenger receptor class B, member 1

FIGURE 1M

ENSG00000171475	#N/A	#N/A	#N/A	2.55	#N/A	WAS/WASL interacting protein family, member 2
ENSG00000274233	#N/A	#N/A	#N/A	2.55	#N/A	chemokine (C-C motif) ligand 5
ENSG00000163565	#N/A	#N/A	#N/A	2.54	#N/A	interferon, gamma-inducible protein 16
ENSG00000155926	#N/A	#N/A	#N/A	2.54	#N/A	Src-like-adaptor
ENSG00000138172	#N/A	#N/A	#N/A	2.53	#N/A	calcium homeostasis modulator 2
ENSG00000171724	#N/A	#N/A	#N/A	2.53	#N/A	vesicle amine transport 1-like
ENSG00000197063	#N/A	#N/A	#N/A	2.53	1.54	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog G
ENSG00000171860	#N/A	#N/A	#N/A	2.52	#N/A	complement component 3a receptor 1
ENSG00000108771	#N/A	#N/A	#N/A	2.52	#N/A	DEXH (Asp-Glu-X-His) box polypeptide 58
ENSG00000137815	#N/A	#N/A	#N/A	2.52	1.82	RTF1 homolog, Paf1/RNA polymerase II complex component
ENSG00000103111	#N/A	#N/A	#N/A	2.52	#N/A	MON1 secretory trafficking family member B
ENSG00000217555	#N/A	#N/A	#N/A	2.51	#N/A	chemokine-like factor
ENSG00000189060	#N/A	#N/A	#N/A	2.49	1.05	H1 histone family, member 0
ENSG00000165233	#N/A	#N/A	#N/A	2.48	1.71	chromosome 9 open reading frame 89
ENSG00000278550	#N/A	#N/A	#N/A	2.48	#N/A	solute carrier family 43 (amino acid system L transporter), member 2
ENSG00000076053	#N/A	#N/A	#N/A	2.47	#N/A	RNA binding motif protein 7
ENSG00000138646	#N/A	#N/A	#N/A	2.47	#N/A	HECT and RLD domain containing E3 ubiquitin protein ligase 5
ENSG00000234545	#N/A	#N/A	#N/A	2.44	2.26	family with sequence similarity 133, member B
ENSG00000135318	#N/A	#N/A	#N/A	2.44	#N/A	5'-nucleotidase, ecto (CD73)
ENSG00000141027	#N/A	#N/A	#N/A	2.44	#N/A	nuclear receptor corepressor 1
ENSG00000104081	#N/A	#N/A	#N/A	2.43	#N/A	Bcl2 modifying factor
ENSG00000139289	#N/A	#N/A	#N/A	2.42	#N/A	pleckstrin homology-like domain, family A, member 1
ENSG00000270898	#N/A	#N/A	#N/A	2.42	1.57	GPR75-ASB3 readthrough
ENSG00000138061	#N/A	#N/A	#N/A	2.42	3.33	cytochrome P450, family 1, subfamily B, polypeptide 1
ENSG00000007944	#N/A	#N/A	#N/A	2.41	#N/A	myosin regulatory light chain interacting protein
ENSG00000167851	#N/A	#N/A	#N/A	2.41	#N/A	CD300a molecule
ENSG00000173193	#N/A	#N/A	#N/A	2.41	#N/A	poly (ADP-ribose) polymerase family, member 14
ENSG00000107201	#N/A	#N/A	#N/A	2.40	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
ENSG00000000938	#N/A	#N/A	#N/A	2.39	#N/A	FGR proto-oncogene, Src family tyrosine kinase
ENSG00000125676	#N/A	#N/A	#N/A	2.39	1.80	THO complex 2
ENSG00000123384	#N/A	#N/A	#N/A	2.38	#N/A	low density lipoprotein receptor-related protein 1
ENSG00000132530	#N/A	#N/A	#N/A	2.38	#N/A	XIAP associated factor 1
ENSG00000142089	#N/A	#N/A	#N/A	2.36	#N/A	interferon induced transmembrane protein 3
ENSG00000158373	#N/A	#N/A	#N/A	2.36	#N/A	histone cluster 1, H2bd
ENSG00000111424	#N/A	#N/A	#N/A	2.36	#N/A	vitamin D (1,25- dihydroxyvitamin D3) receptor
ENSG00000188177	#N/A	#N/A	#N/A	2.35	#N/A	zinc finger CCCH-type containing 6
ENSG00000196968	#N/A	#N/A	#N/A	2.34	#N/A	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)
ENSG00000139168	#N/A	#N/A	#N/A	2.33	1.71	zinc finger CCHC-type and RNA binding motif 1
ENSG00000272886	#N/A	#N/A	#N/A	2.33	#N/A	decapping mRNA 1A
ENSG00000258472	#N/A	#N/A	#N/A	2.33	#N/A	Uncharacterized protein
ENSG00000171992	#N/A	#N/A	#N/A	2.33	#N/A	synaptopodin
ENSG00000162599	#N/A	#N/A	#N/A	2.33	#N/A	nuclear factor I/A
ENSG00000143847	#N/A	#N/A	#N/A	2.33	#N/A	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4

ENSG00000156502	#N/A	#N/A	#N/A	-1.36	#N/A	suppressor of var1, 3-like 1 (S. cerevisiae)
ENSG00000272325	#N/A	#N/A	#N/A	-1.36	#N/A	nudix (nucleoside diphosphate linked moiety X)-type motif 3
ENSG00000096384	#N/A	#N/A	#N/A	-1.36	#N/A	heat shock protein 90kDa alpha (cytosolic), class B member 1
ENSG00000269713	#N/A	#N/A	#N/A	-1.36	#N/A	neuroblastoma breakpoint family, member 9
ENSG00000213339	#N/A	#N/A	#N/A	-1.36	#N/A	queuine tRNA-ribosyltransferase 1
ENSG00000145220	#N/A	#N/A	#N/A	-1.37	#N/A	Ly1 antibody reactive
ENSG00000006744	#N/A	#N/A	#N/A	-1.37	#N/A	elaC ribonuclease Z 2
ENSG00000005844	#N/A	#N/A	#N/A	-1.37	#N/A	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
ENSG00000050393	#N/A	#N/A	#N/A	-1.37	#N/A	mitochondrial calcium uniporter regulator 1
ENSG00000165138	#N/A	#N/A	#N/A	-1.37	#N/A	ankyrin repeat and sterile alpha motif domain containing 6
ENSG00000105447	#N/A	#N/A	#N/A	-1.37	#N/A	glutamate-rich WD repeat containing 1
ENSG00000185198	#N/A	#N/A	#N/A	-1.38	#N/A	protease, serine, 57
ENSG00000135002	#N/A	#N/A	#N/A	-1.38	#N/A	riboflavin kinase
ENSG00000068383	#N/A	#N/A	#N/A	-1.38	#N/A	inositol polyphosphate-5-phosphatase, 40kDa
ENSG00000149557	#N/A	#N/A	#N/A	-1.38	#N/A	fasciculation and elongation protein zeta 1 (zygin I)
ENSG00000235569	#N/A	#N/A	#N/A	-1.38	#N/A	mutS homolog 5
ENSG00000124587	#N/A	#N/A	#N/A	-1.38	#N/A	peroxisomal biogenesis factor 6
ENSG00000005379	#N/A	#N/A	#N/A	-1.38	#N/A	benzodiazepine receptor (peripheral) associated protein 1
ENSG00000144381	#N/A	#N/A	#N/A	-1.38	#N/A	heat shock 60kDa protein 1 (chaperonin)
ENSG00000110619	#N/A	#N/A	#N/A	-1.38	#N/A	cysteinyl-tRNA synthetase
ENSG00000146433	#N/A	#N/A	#N/A	-1.39	#N/A	transmembrane protein 181
ENSG00000074071	#N/A	#N/A	#N/A	-1.39	#N/A	mitochondrial ribosomal protein S34
ENSG00000124562	#N/A	#N/A	#N/A	-1.39	#N/A	small nuclear ribonucleoprotein polypeptide C
ENSG00000100401	#N/A	#N/A	#N/A	-1.39	#N/A	Ran GTPase activating protein 1
ENSG00000114767	#N/A	#N/A	#N/A	-1.39	#N/A	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)
ENSG00000155229	#N/A	#N/A	#N/A	-1.39	#N/A	MMS19 homolog, cytosolic iron-sulfur assembly component
ENSG00000228300	#N/A	#N/A	#N/A	-1.39	#N/A	chromosome 19 open reading frame 24
ENSG00000122025	#N/A	#N/A	#N/A	-1.39	#N/A	fms-related tyrosine kinase 3
ENSG00000140750	#N/A	#N/A	#N/A	-1.39	#N/A	Rho GTPase activating protein 17
ENSG00000047188	#N/A	#N/A	#N/A	-1.39	#N/A	YTH domain containing 2
ENSG00000176022	#N/A	#N/A	#N/A	-1.39	#N/A	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6
ENSG00000164164	#N/A	#N/A	#N/A	-1.40	#N/A	OTU deubiquitinase 4
ENSG00000121716	#N/A	#N/A	#N/A	-1.40	#N/A	paired immunoglobin-like type 2 receptor beta
ENSG00000111666	#N/A	#N/A	#N/A	-1.40	#N/A	choline phosphotransferase 1
ENSG00000113013	#N/A	#N/A	#N/A	-1.40	#N/A	heat shock 70kDa protein 9 (mortalin)
ENSG00000136261	#N/A	#N/A	#N/A	-1.40	#N/A	basic leucine zipper and W2 domains 2
ENSG00000106211	#N/A	#N/A	#N/A	-1.40	#N/A	heat shock 27kDa protein 1
ENSG00000160208	#N/A	#N/A	#N/A	-1.40	#N/A	ribosomal RNA processing 1B
ENSG00000204839	#N/A	#N/A	#N/A	-1.40	#N/A	maestro heat-like repeat family member 6
ENSG00000179051	#N/A	#N/A	#N/A	-1.40	#N/A	regulator of chromosome condensation 2
ENSG00000153811	#N/A	#N/A	#N/A	-1.40	#N/A	WD repeat domain 43
ENSG00000077232	#N/A	#N/A	#N/A	-1.40	#N/A	DnaJ (Hsp40) homolog, subfamily C, member 10
ENSG00000163362	#N/A	#N/A	#N/A	-1.41	#N/A	chromosome 1 open reading frame 106

FIGURE 1N

ENSG00000216490	#N/A	#N/A	#N/A	2.32	1.20	interferon, gamma-inducible protein 30
ENSG00000147894	#N/A	#N/A	#N/A	2.32	#N/A	chromosome 9 open reading frame 72
ENSG00000116017	#N/A	#N/A	#N/A	2.31	#N/A	AT rich interactive domain 3A (BRIGHT-like)
ENSG00000146247	#N/A	#N/A	#N/A	2.30	#N/A	pleckstrin homology domain interacting protein
ENSG00000151461	#N/A	#N/A	#N/A	2.30	1.58	UPF2 regulator of nonsense transcripts homolog (yeast)
ENSG00000145012	#N/A	#N/A	#N/A	2.29	#N/A	LIM domain containing preferred translocation partner in lipoma
ENSG00000237727	#N/A	#N/A	#N/A	2.29	#N/A	allograft inflammatory factor 1
ENSG00000180573	#N/A	#N/A	#N/A	2.28	1.48	histone cluster 1, H2ac
ENSG00000188825	#N/A	#N/A	#N/A	2.28	#N/A	long intergenic non-protein coding RNA 910
ENSG00000143546	#N/A	#N/A	#N/A	2.28	#N/A	S100 calcium binding protein A8
ENSG00000101384	#N/A	#N/A	#N/A	2.28	#N/A	jagged 1
ENSG00000271605	#N/A	#N/A	#N/A	2.28	#N/A	mast cell immunoglobulin-like receptor 1
ENSG00000127920	#N/A	#N/A	#N/A	2.27	#N/A	guanine nucleotide binding protein (G protein), gamma 11
ENSG00000183486	#N/A	#N/A	#N/A	2.27	#N/A	MX dynamin-like GTPase 2
ENSG00000135185	#N/A	#N/A	#N/A	2.26	1.53	transmembrane protein 243, mitochondrial
ENSG00000130208	#N/A	#N/A	#N/A	2.26	#N/A	apolipoprotein C-I
ENSG00000172831	#N/A	#N/A	#N/A	2.26	#N/A	carboxylesterase 2
ENSG00000159140	#N/A	#N/A	#N/A	2.25	#N/A	SON DNA binding protein
ENSG00000197323	#N/A	#N/A	#N/A	2.24	1.91	tripartite motif containing 33
ENSG00000183354	#N/A	#N/A	#N/A	2.22	#N/A	KIAA2026
ENSG00000145592	#N/A	#N/A	#N/A	2.22	#N/A	ribosomal protein L37
ENSG00000156603	#N/A	#N/A	#N/A	2.22	1.56	mediator complex subunit 19
ENSG00000169439	#N/A	#N/A	#N/A	2.21	#N/A	syndecan 2
ENSG00000165801	#N/A	#N/A	#N/A	2.21	#N/A	Rho guanine nucleotide exchange factor (GEF) 40
ENSG00000139266	#N/A	#N/A	#N/A	2.20	#N/A	membrane-associated ring finger (C3HC4) 9
ENSG00000182899	#N/A	#N/A	#N/A	2.20	1.64	ribosomal protein L35a
ENSG00000147443	#N/A	#N/A	#N/A	2.20	#N/A	docking protein 2, 56kDa
ENSG00000101966	#N/A	#N/A	#N/A	2.19	1.71	X-linked inhibitor of apoptosis, E3 ubiquitin protein ligase
ENSG00000168209	#N/A	#N/A	#N/A	2.19	#N/A	DNA-damage-inducible transcript 4
ENSG00000126759	#N/A	#N/A	#N/A	2.18	#N/A	complement factor properdin
ENSG00000196199	#N/A	#N/A	#N/A	2.18	1.60	M-phase phosphoprotein 8
ENSG00000164096	#N/A	#N/A	#N/A	2.18	#N/A	chromosome 4 open reading frame 3
ENSG00000165355	#N/A	#N/A	#N/A	2.17	#N/A	F-box protein 33
ENSG00000166482	#N/A	#N/A	#N/A	2.17	#N/A	microfibrillar-associated protein 4
ENSG00000188157	#N/A	#N/A	#N/A	2.16	#N/A	agrin
ENSG00000204130	#N/A	#N/A	#N/A	2.16	#N/A	RUN and FYVE domain containing 2
ENSG00000178951	#N/A	#N/A	#N/A	2.15	1.24	zinc finger and BTB domain containing 7A
ENSG00000058272	#N/A	#N/A	#N/A	2.15	#N/A	protein phosphatase 1, regulatory subunit 12A
ENSG00000275342	#N/A	#N/A	#N/A	2.15	1.14	Tyrosine-protein kinase SgK223
ENSG00000205758	#N/A	#N/A	#N/A	2.14	#N/A	crystallin, zeta (quinone reductase)-like 1
ENSG00000099337	#N/A	#N/A	#N/A	2.14	1.60	potassium channel, two pore domain subfamily K, member 6
ENSG00000160602	#N/A	#N/A	#N/A	2.13	#N/A	NIMA-related kinase 8
ENSG00000174938	#N/A	#N/A	#N/A	2.13	#N/A	seizure related 6 homolog (mouse)-like 2
ENSG00000104419	#N/A	#N/A	#N/A	2.13	#N/A	N-myc downstream regulated 1
ENSG00000229314	#N/A	#N/A	#N/A	2.13	#N/A	orosomucoid 1

ENSG00000184110	#N/A	#N/A	#N/A	-1.41	#N/A	eukaryotic translation initiation factor 3, subunit C
ENSG00000170144	#N/A	#N/A	#N/A	-1.41	#N/A	heterogeneous nuclear ribonucleoprotein A3
ENSG00000169714	#N/A	#N/A	#N/A	-1.41	#N/A	CCHC-type zinc finger, nucleic acid binding protein
ENSG00000169683	#N/A	#N/A	#N/A	-1.41	#N/A	leucine rich repeat containing 45
ENSG00000188807	#N/A	#N/A	#N/A	-1.41	#N/A	transmembrane protein 201
ENSG00000181666	#N/A	#N/A	#N/A	-1.41	#N/A	HKR1, GLI-Kruppel zinc finger family member
ENSG00000105281	#N/A	#N/A	#N/A	-1.41	#N/A	solute carrier family 1 (neutral amino acid transporter), member 5
ENSG00000184220	#N/A	#N/A	#N/A	-1.41	#N/A	cms1 ribosomal small subunit homolog (yeast)
ENSG00000148362	#N/A	#N/A	#N/A	-1.41	#N/A	chromosome 9 open reading frame 142
ENSG00000198786	#N/A	#N/A	#N/A	-1.42	#N/A	mitochondrially encoded NADH dehydrogenase 5
ENSG00000148824	#N/A	#N/A	#N/A	-1.42	#N/A	mitochondrial ribosome-associated GTPase 1
ENSG00000152620	#N/A	#N/A	#N/A	-1.42	#N/A	NAD kinase 2, mitochondrial
ENSG00000175857	#N/A	#N/A	#N/A	-1.42	#N/A	GRB2-binding adaptor protein, transmembrane
ENSG00000131778	#N/A	#N/A	#N/A	-1.42	#N/A	chromodomain helicase DNA binding protein 1-like
ENSG00000158715	#N/A	#N/A	#N/A	-1.43	#N/A	solute carrier family 45, member 3
ENSG00000140691	#N/A	#N/A	#N/A	-1.44	#N/A	armadillo repeat containing 5
ENSG00000068654	#N/A	#N/A	#N/A	-1.44	#N/A	polymerase (RNA) I polypeptide A, 194kDa
ENSG00000181029	#N/A	#N/A	#N/A	-1.44	#N/A	trafficking protein particle complex 5
ENSG00000074582	#N/A	#N/A	#N/A	-1.44	#N/A	BC1 (ubiquinol-cytochrome c reductase) synthesis-like
ENSG00000120053	#N/A	#N/A	#N/A	-1.44	#N/A	glutamic-oxaloacetic transaminase 1, soluble
ENSG00000101255	#N/A	#N/A	#N/A	-1.45	#N/A	tribbles pseudokinase 3
ENSG00000108963	#N/A	#N/A	#N/A	-1.45	#N/A	diphthamide biosynthesis 1
ENSG00000198868	#N/A	#N/A	#N/A	-1.45	#N/A	MT-ND4
ENSG00000101444	#N/A	#N/A	#N/A	-1.45	#N/A	adenosylhomocysteinase
ENSG00000140743	#N/A	#N/A	#N/A	-1.45	#N/A	cerebellar degeneration-related protein 2, 62kDa
ENSG00000142686	#N/A	#N/A	#N/A	-1.45	#N/A	chromosome 1 open reading frame 216
ENSG00000214753	#N/A	#N/A	#N/A	-1.45	#N/A	heterogeneous nuclear ribonucleoprotein U-like 2
ENSG00000104835	#N/A	#N/A	#N/A	-1.45	#N/A	seryl-tRNA synthetase 2, mitochondrial
ENSG00000167685	#N/A	#N/A	#N/A	-1.45	#N/A	zinc finger protein 444
ENSG00000198945	#N/A	#N/A	#N/A	-1.45	#N/A	l(3)mbt-like 3 (Drosophila)
ENSG00000130713	#N/A	#N/A	#N/A	-1.46	#N/A	exosome component 2
ENSG00000009830	#N/A	#N/A	#N/A	-1.46	#N/A	protein-O-mannosyltransferase 2
ENSG00000149150	#N/A	#N/A	#N/A	-1.46	#N/A	solute carrier family 43 (amino acid system L transporter), member 1
ENSG00000084774	#N/A	#N/A	#N/A	-1.46	#N/A	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
ENSG00000270629	#N/A	#N/A	#N/A	-1.46	#N/A	neuroblastoma breakpoint family, member 14
ENSG00000205560	#N/A	#N/A	#N/A	-1.46	#N/A	carnitine palmitoyltransferase 1B (muscle)
ENSG00000148843	#N/A	#N/A	#N/A	-1.46	#N/A	programmed cell death 11
ENSG00000178718	#N/A	#N/A	#N/A	-1.46	#N/A	ribonuclease P/MRP 25kDa subunit
ENSG00000130826	#N/A	#N/A	#N/A	-1.46	#N/A	dyskeratosis congenita 1, dyskerin
ENSG00000132361	#N/A	#N/A	#N/A	-1.46	#N/A	clustered mitochondria (cluA/CLU1) homolog
ENSG00000214160	#N/A	#N/A	#N/A	-1.46	#N/A	ALG3, alpha-1,3- mannosyltransferase
ENSG00000128973	#N/A	#N/A	#N/A	-1.47	#N/A	ceroid-lipofuscinosis, neuronal 6, late infantile, variant
ENSG00000214706	#N/A	#N/A	#N/A	-1.47	#N/A	interferon-related developmental regulator 2
ENSG00000137168	#N/A	#N/A	#N/A	-1.47	#N/A	peptidylprolyl isomerase (cyclophilin)-like 1
ENSG00000125257	#N/A	#N/A	#N/A	-1.47	#N/A	ATP-binding cassette, sub-family C (CFTR/MRP), member 4

FIGURE 1o

ENSG00000059804	#N/A	#N/A	#N/A	2.12	#N/A	solute carrier family 2 (facilitated glucose transporter), member 3
ENSG00000139278	#N/A	#N/A	#N/A	2.11	#N/A	GLI pathogenesis-related 1
ENSG00000157350	#N/A	#N/A	#N/A	2.10	#N/A	ST3 beta-galactoside alpha-2,3-sialyltransferase 2
ENSG00000146278	#N/A	#N/A	#N/A	2.10	#N/A	proline-rich nuclear receptor coactivator 1
ENSG00000119004	#N/A	#N/A	#N/A	2.10	#N/A	cytochrome P450, family 20, subfamily A, polypeptide 1
ENSG00000121281	#N/A	#N/A	#N/A	2.09	#N/A	adenylate cyclase 7
ENSG00000245209	#N/A	#N/A	#N/A	2.08	#N/A	AP001007.1
ENSG00000204054	#N/A	#N/A	#N/A	2.08	3.38	long intergenic non-protein coding RNA 963
ENSG00000166595	#N/A	#N/A	#N/A	2.08	1.08	family with sequence similarity 96, member B
ENSG00000160613	#N/A	#N/A	#N/A	2.07	#N/A	proprotein convertase subtilisin/kexin type 7
ENSG00000103248	#N/A	#N/A	#N/A	2.07	#N/A	methenyltetrahydrofolate synthetase domain containing
ENSG00000162645	#N/A	#N/A	#N/A	2.06	#N/A	guanylate binding protein 2, interferon-inducible
ENSG00000135218	#N/A	#N/A	#N/A	2.05	#N/A	CD36 molecule (thrombospondin receptor)
ENSG00000120688	#N/A	#N/A	#N/A	2.05	2.06	WW domain binding protein 4
ENSG00000059728	#N/A	#N/A	#N/A	2.05	#N/A	MAX dimerization protein 1
ENSG00000196227	#N/A	#N/A	#N/A	2.05	#N/A	family with sequence similarity 217, member B
ENSG00000198863	#N/A	#N/A	#N/A	2.05	#N/A	RUN domain containing 1
ENSG00000136826	#N/A	#N/A	#N/A	2.05	#N/A	Kruppel-like factor 4 (gut)
ENSG00000233927	#N/A	#N/A	#N/A	2.04	#N/A	ribosomal protein S28
ENSG00000179085	#N/A	#N/A	#N/A	2.04	2.39	dolichyl-phosphate mannosyltransferase polypeptide 3
ENSG00000065989	#N/A	#N/A	#N/A	2.04	#N/A	phosphodiesterase 4A, cAMP-specific
ENSG00000129667	#N/A	#N/A	#N/A	2.03	#N/A	rhomboid 5 homolog 2 (Drosophila)
ENSG00000116977	#N/A	#N/A	#N/A	2.03	#N/A	lectin, galactoside-binding, soluble, 8
ENSG00000242711	#N/A	#N/A	#N/A	2.02	#N/A	proteasome (prosome, macropain) subunit, beta type, 9
ENSG00000135637	#N/A	#N/A	#N/A	2.01	2.03	coiled-coil domain containing 142
ENSG00000186162	#N/A	#N/A	#N/A	2.01	#N/A	cell death-inducing DFFA-like effector c pseudogene
ENSG00000197956	#N/A	#N/A	#N/A	2.00	1.50	S100 calcium binding protein A6
ENSG00000273686	#N/A	#N/A	#N/A	2.00	1.53	beta-2-microglobulin
ENSG00000163536	#N/A	#N/A	#N/A	2.00	#N/A	serpin peptidase inhibitor, clade I (neuroserpin), member 1
ENSG00000116667	#N/A	#N/A	#N/A	2.00	#N/A	chromosome 1 open reading frame 21
ENSG00000163221	#N/A	#N/A	#N/A	2.00	#N/A	S100 calcium binding protein A12
ENSG00000235309	#N/A	#N/A	#N/A	1.99	#N/A	major histocompatibility complex, class I, J (pseudogene)
ENSG00000163644	#N/A	#N/A	#N/A	1.99	1.18	protein phosphatase, Mg2+/Mn2+ dependent, 1K
ENSG00000101336	#N/A	#N/A	#N/A	1.98	#N/A	HCK proto-oncogene, Src family tyrosine kinase
ENSG00000130813	#N/A	#N/A	#N/A	1.98	#N/A	chromosome 19 open reading frame 66
ENSG00000110077	#N/A	#N/A	#N/A	1.98	#N/A	membrane-spanning 4-domains, subfamily A, member 6A
ENSG00000140948	#N/A	#N/A	#N/A	1.98	#N/A	zinc finger, CCHC domain containing 14
ENSG00000172809	#N/A	#N/A	#N/A	1.97	1.54	ribosomal protein L38
ENSG00000167207	#N/A	#N/A	#N/A	1.97	#N/A	nucleotide-binding oligomerization domain containing 2
ENSG00000131503	#N/A	#N/A	#N/A	1.97	#N/A	ankyrin repeat and KH domain containing 1
ENSG00000136770	#N/A	#N/A	#N/A	1.97	1.43	DnaJ (Hsp40) homolog, subfamily C, member 1
ENSG00000167604	#N/A	#N/A	#N/A	1.97	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta
ENSG00000170801	#N/A	#N/A	#N/A	1.96	#N/A	HtrA serine peptidase 3
ENSG00000131067	#N/A	#N/A	#N/A	1.96	#N/A	gamma-glutamyltransferase 7
ENSG00000111981	#N/A	#N/A	#N/A	1.95	#N/A	UL16 binding protein 1
ENSG00000196576	#N/A	#N/A	#N/A	1.94	#N/A	plexin B2

ENSG00000082516	#N/A	#N/A	#N/A	-1.47	#N/A	gem (nuclear organelle) associated protein 5
ENSG00000130726	#N/A	#N/A	#N/A	-1.47	#N/A	tripartite motif containing 28
ENSG00000123545	#N/A	#N/A	#N/A	-1.48	#N/A	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4
ENSG00000135521	#N/A	#N/A	#N/A	-1.48	#N/A	LTV1 ribosome biogenesis factor
ENSG00000215041	#N/A	#N/A	#N/A	-1.48	#N/A	neuralized E3 ubiquitin protein ligase 4
ENSG00000065150	#N/A	#N/A	#N/A	-1.48	#N/A	importin 5
ENSG00000143643	#N/A	#N/A	#N/A	-1.48	#N/A	tetratricopeptide repeat domain 13
ENSG00000134905	#N/A	#N/A	#N/A	-1.48	#N/A	cysteinyl-tRNA synthetase 2, mitochondrial (putative)
ENSG00000185504	#N/A	#N/A	#N/A	-1.48	#N/A	Fanconi anemia core complex associated protein 100
ENSG00000110090	#N/A	#N/A	#N/A	-1.49	#N/A	carnitine palmitoyltransferase 1A (liver)
ENSG00000196535	#N/A	#N/A	#N/A	-1.49	#N/A	myosin XVIIIA
ENSG00000144136	#N/A	#N/A	#N/A	-1.49	1.19	solute carrier family 20 (phosphate transporter), member 1
ENSG00000124541	#N/A	#N/A	#N/A	-1.49	#N/A	ribosomal RNA processing 36
ENSG00000075407	#N/A	#N/A	#N/A	-1.49	#N/A	zinc finger protein 37A
ENSG00000241978	#N/A	#N/A	#N/A	-1.49	#N/A	A kinase (PRKA) anchor protein 2
ENSG00000142185	#N/A	#N/A	#N/A	-1.49	#N/A	transient receptor potential cation channel, subfamily M, member 2
ENSG00000273645	#N/A	#N/A	#N/A	-1.50	#N/A	kelch repeat and BTB (POZ) domain containing 11
ENSG00000100219	#N/A	#N/A	#N/A	-1.50	#N/A	X-box binding protein 1
ENSG00000112159	#N/A	#N/A	#N/A	-1.50	#N/A	midasin AAA ATPase 1
ENSG00000178921	#N/A	#N/A	#N/A	-1.50	#N/A	phosphoribosylformylglycinamidine synthase
ENSG00000108179	#N/A	#N/A	#N/A	-1.50	#N/A	peptidylprolyl isomerase F
ENSG00000197150	#N/A	#N/A	#N/A	-1.50	#N/A	ATP-binding cassette, sub-family B (MDR/TAP), member 8
ENSG00000106105	#N/A	#N/A	#N/A	-1.50	#N/A	glycyl-tRNA synthetase
ENSG00000185238	#N/A	#N/A	#N/A	-1.50	#N/A	protein arginine methyltransferase 3
ENSG00000085511	#N/A	#N/A	#N/A	-1.51	#N/A	mitogen-activated protein kinase kinase kinase 4
ENSG00000163393	#N/A	#N/A	#N/A	-1.51	#N/A	solute carrier family 22, member 15
ENSG00000149136	#N/A	#N/A	#N/A	-1.51	#N/A	structure specific recognition protein 1
ENSG00000112578	#N/A	#N/A	#N/A	-1.51	#N/A	bystin-like
ENSG00000274679	#N/A	#N/A	#N/A	-1.52	#N/A	spermatogenesis and centriole associated 1-like
ENSG00000132305	#N/A	#N/A	#N/A	-1.52	#N/A	inner membrane protein, mitochondrial
ENSG00000116922	#N/A	#N/A	#N/A	-1.52	#N/A	chromosome 1 open reading frame 109
ENSG00000164934	#N/A	#N/A	#N/A	-1.52	#N/A	DDB1 and CUL4 associated factor 13
ENSG00000071655	#N/A	#N/A	#N/A	-1.52	#N/A	methyl-CpG binding domain protein 3
ENSG00000165209	#N/A	#N/A	#N/A	-1.52	#N/A	spermatid perinuclear RNA binding protein
ENSG00000166123	#N/A	#N/A	#N/A	-1.52	#N/A	glutamic pyruvate transaminase (alanine aminotransferase) 2
ENSG00000167962	#N/A	#N/A	#N/A	-1.53	#N/A	zinc finger protein 598
ENSG00000179271	#N/A	#N/A	#N/A	-1.53	#N/A	growth arrest and DNA-damage-inducible, gamma interacting protein 1
ENSG00000268006	#N/A	#N/A	#N/A	-1.53	#N/A	PTOV1 antisense RNA 1
ENSG00000185760	#N/A	#N/A	#N/A	-1.54	#N/A	potassium channel, voltage gated KQT-like subfamily Q, member 5
ENSG00000230606	#N/A	#N/A	#N/A	-1.54	#N/A	AC159540.1
ENSG00000247077	#N/A	#N/A	#N/A	-1.54	#N/A	phosphoglycerate mutase family member 5
ENSG00000197728	#N/A	#N/A	#N/A	-1.54	#N/A	ribosomal protein S26
ENSG00000140263	#N/A	#N/A	#N/A	-1.54	#N/A	sorbitol dehydrogenase
ENSG00000171262	#N/A	#N/A	#N/A	-1.55	#N/A	family with sequence similarity 98, member B
ENSG00000277804	#N/A	#N/A	#N/A	-1.55	#N/A	proteinase 3
ENSG00000198727	#N/A	#N/A	#N/A	-1.55	#N/A	mitochondrially encoded cytochrome b

FIGURE 1P

ENSG00000085514	#N/A	#N/A	#N/A	1.93	#N/A	paired immunoglobin-like type 2 receptor alpha
ENSG00000114023	#N/A	#N/A	#N/A	1.93	#N/A	family with sequence similarity 162, member A
ENSG00000197903	#N/A	#N/A	#N/A	1.92	1.45	histone cluster 1, H2bk
ENSG00000053254	#N/A	#N/A	#N/A	1.92	#N/A	forkhead box N3
ENSG00000106479	#N/A	#N/A	#N/A	1.92	#N/A	zinc finger protein 862
ENSG00000131469	#N/A	#N/A	#N/A	1.92	1.75	ribosomal protein L27
ENSG00000148180	#N/A	#N/A	#N/A	1.92	#N/A	gelsolin
ENSG00000176788	#N/A	#N/A	#N/A	1.91	1.39	brain abundant, membrane attached signal protein 1
ENSG00000112343	#N/A	#N/A	#N/A	1.91	#N/A	tripartite motif containing 38
ENSG00000234741	#N/A	#N/A	#N/A	1.91	#N/A	growth arrest-specific 5 (non-protein coding)
ENSG00000125657	#N/A	#N/A	#N/A	1.91	#N/A	tumor necrosis factor (ligand) superfamily, member 9
ENSG00000051523	#N/A	#N/A	#N/A	1.90	#N/A	cytochrome b-245, alpha polypeptide
ENSG00000197879	#N/A	#N/A	#N/A	1.90	#N/A	myosin IC
ENSG00000257529	#N/A	#N/A	#N/A	1.89	#N/A	RPL36A-HNRNPH2 readthrough
ENSG00000110628	#N/A	#N/A	#N/A	1.89	#N/A	solute carrier family 22, member 18
ENSG00000130303	#N/A	#N/A	#N/A	1.89	#N/A	bone marrow stromal cell antigen 2
ENSG00000196369	#N/A	#N/A	#N/A	1.88	#N/A	SLIT-ROBO Rho GTPase activating protein 2B
ENSG00000156482	#N/A	#N/A	#N/A	1.88	1.43	ribosomal protein L30
ENSG00000071082	#N/A	#N/A	#N/A	1.88	#N/A	ribosomal protein L31
ENSG00000089335	#N/A	#N/A	#N/A	1.87	#N/A	zinc finger protein 302
ENSG00000060339	#N/A	#N/A	#N/A	1.87	1.65	cell division cycle and apoptosis regulator 1
ENSG00000115415	#N/A	#N/A	#N/A	1.87	#N/A	signal transducer and activator of transcription 1, 91kDa
ENSG00000122694	#N/A	#N/A	#N/A	1.87	#N/A	GLI pathogenesis-related 2
ENSG00000090863	#N/A	#N/A	#N/A	1.87	#N/A	golgi glycoprotein 1
ENSG00000115267	#N/A	#N/A	#N/A	1.86	#N/A	interferon induced with helicase C domain 1
ENSG00000160445	#N/A	#N/A	#N/A	1.86	#N/A	zyg-11 related, cell cycle regulator
ENSG00000196209	#N/A	#N/A	#N/A	1.86	#N/A	signal-regulatory protein beta 2
ENSG00000073803	#N/A	#N/A	#N/A	1.86	#N/A	mitogen-activated protein kinase kinase kinase 13
ENSG00000125733	#N/A	#N/A	#N/A	1.85	1.21	thyroid hormone receptor interactor 10
ENSG00000166913	#N/A	#N/A	#N/A	1.85	#N/A	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta
ENSG00000204164	#N/A	#N/A	#N/A	1.85	#N/A	BMS1P5
ENSG00000114480	#N/A	#N/A	#N/A	1.85	#N/A	glucan (1,4-alpha-), branching enzyme 1
ENSG00000169925	#N/A	#N/A	#N/A	1.84	#N/A	bromodomain containing 3
ENSG00000152256	#N/A	#N/A	#N/A	1.84	#N/A	pyruvate dehydrogenase kinase, isozyme 1
ENSG00000100918	#N/A	#N/A	#N/A	1.84	#N/A	REC8 meiotic recombination protein
ENSG00000130775	#N/A	#N/A	#N/A	1.84	#N/A	thymocyte selection associated family member 2
ENSG00000106404	#N/A	#N/A	#N/A	1.84	#N/A	claudin 15
ENSG00000168461	#N/A	#N/A	#N/A	1.83	#N/A	RAB31, member RAS oncogene family
ENSG00000141506	#N/A	#N/A	#N/A	1.83	#N/A	phosphoinositide-3-kinase, regulatory subunit 5
ENSG00000034713	#N/A	#N/A	#N/A	1.83	#N/A	GABA(A) receptor-associated protein like 2
ENSG00000002549	#N/A	#N/A	#N/A	1.83	#N/A	leucine aminopeptidase 3
ENSG00000120594	#N/A	#N/A	#N/A	1.83	#N/A	plexin domain containing 2
ENSG00000174720	#N/A	#N/A	#N/A	1.83	1.74	La ribonucleoprotein domain family, member 7
ENSG00000139182	#N/A	#N/A	#N/A	1.82	#N/A	calsyntenin 3
ENSG00000068697	#N/A	#N/A	#N/A	1.82	1.21	lysosomal protein transmembrane 4 alpha
ENSG00000183401	#N/A	#N/A	#N/A	1.82	#N/A	coiled-coil domain containing 159

ENSG00000109917	#N/A	#N/A	#N/A	-1.55	#N/A	ZPR1 zinc finger
ENSG00000007392	#N/A	#N/A	#N/A	-1.56	#N/A	LUC7-like
ENSG00000130725	#N/A	#N/A	#N/A	-1.56	#N/A	ubiquitin-conjugating enzyme E2M
ENSG00000112651	#N/A	#N/A	#N/A	-1.56	#N/A	mitochondrial ribosomal protein L2
ENSG00000166197	#N/A	#N/A	#N/A	-1.56	#N/A	nucleolar and coiled-body phosphoprotein 1
ENSG00000108561	#N/A	#N/A	#N/A	-1.56	#N/A	complement component 1, q subcomponent binding protein
ENSG00000103876	#N/A	#N/A	#N/A	-1.56	#N/A	fumarylacetoacetate hydrolase (fumarylacetoacetase)
ENSG00000178605	#N/A	#N/A	#N/A	-1.56	#N/A	GTP binding protein 6 (putative)
ENSG00000162129	#N/A	#N/A	#N/A	-1.56	#N/A	ClpB homolog, mitochondrial AAA ATPase chaperonin
ENSG00000224078	#N/A	#N/A	#N/A	-1.57	#N/A	small nucleolar RNA host gene 14
ENSG00000204316	#N/A	#N/A	#N/A	-1.57	#N/A	mitochondrial ribosomal protein L38
ENSG00000146830	#N/A	#N/A	#N/A	-1.57	#N/A	GRB10 interacting GYF protein 1
ENSG00000255302	#N/A	#N/A	#N/A	-1.57	#N/A	EP300 interacting inhibitor of differentiation 1
ENSG00000226950	#N/A	#N/A	#N/A	-1.57	#N/A	differentiation antagonizing non-protein coding RNA
ENSG00000145703	#N/A	#N/A	#N/A	-1.58	#N/A	IQ motif containing GTPase activating protein 2
ENSG00000244165	#N/A	#N/A	#N/A	-1.58	#N/A	purinergic receptor P2Y, G-protein coupled, 11
ENSG00000132382	#N/A	#N/A	#N/A	-1.59	#N/A	MYB binding protein (P160) 1a
ENSG00000096063	#N/A	#N/A	#N/A	-1.59	#N/A	SRSF protein kinase 1
ENSG00000161547	#N/A	#N/A	#N/A	-1.59	#N/A	serine/arginine-rich splicing factor 2
ENSG00000131828	#N/A	#N/A	#N/A	-1.59	#N/A	pyruvate dehydrogenase (lipoamide) alpha 1
ENSG00000142102	#N/A	#N/A	#N/A	-1.59	#N/A	ATH1, acid trehalase-like 1 (yeast)
ENSG00000196510	#N/A	#N/A	#N/A	-1.59	#N/A	anaphase promoting complex subunit 7
ENSG00000140006	#N/A	#N/A	#N/A	-1.59	#N/A	WD repeat domain 89
ENSG00000165526	#N/A	#N/A	#N/A	-1.60	#N/A	RNA pseudouridylate synthase domain containing 4
ENSG00000184575	#N/A	#N/A	#N/A	-1.60	#N/A	exportin, tRNA
ENSG00000183010	#N/A	#N/A	#N/A	-1.60	#N/A	pyrroline-5-carboxylate reductase 1
ENSG00000117174	#N/A	#N/A	#N/A	-1.60	#N/A	zinc finger, HIT-type containing 6
ENSG00000143093	#N/A	#N/A	#N/A	-1.61	#N/A	striatin interacting protein 1
ENSG00000155846	#N/A	#N/A	#N/A	-1.62	#N/A	peroxisome proliferator-activated receptor gamma, coactivator 1 beta
ENSG00000138095	#N/A	#N/A	#N/A	-1.62	#N/A	leucine-rich pentatricopeptide repeat containing
ENSG00000133265	#N/A	#N/A	#N/A	-1.62	#N/A	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1
ENSG00000223705	#N/A	#N/A	#N/A	-1.63	#N/A	NOP2/Sun domain family, member 5 pseudogene 1
ENSG00000126602	#N/A	#N/A	#N/A	-1.63	#N/A	TNF receptor-associated protein 1
ENSG00000123064	#N/A	#N/A	#N/A	-1.64	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
ENSG00000070061	#N/A	#N/A	#N/A	-1.64	#N/A	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
ENSG00000197785	#N/A	#N/A	#N/A	-1.64	#N/A	ATPase family, AAA domain containing 3A
ENSG00000106344	#N/A	#N/A	#N/A	-1.65	#N/A	RNA binding motif protein 28
ENSG00000254870	#N/A	#N/A	#N/A	-1.65	#N/A	ATP6V1G2-DDX39B readthrough (NMD candidate)
ENSG00000118513	#N/A	#N/A	#N/A	-1.65	#N/A	v-myb avian myeloblastosis viral oncogene homolog
ENSG00000171163	#N/A	#N/A	#N/A	-1.65	#N/A	zinc finger protein 692
ENSG00000131368	#N/A	#N/A	#N/A	-1.65	#N/A	mitochondrial ribosomal protein S25
ENSG00000184232	#N/A	#N/A	#N/A	-1.66	#N/A	out at first homolog
ENSG00000017483	#N/A	#N/A	#N/A	-1.66	#N/A	solute carrier family 38, member 5
ENSG00000125901	#N/A	#N/A	#N/A	-1.67	#N/A	mitochondrial ribosomal protein S26
ENSG00000140044	#N/A	#N/A	#N/A	-1.67	#N/A	Jun dimerization protein 2
ENSG00000184787	#N/A	#N/A	#N/A	-1.67	#N/A	ubiquitin-conjugating enzyme E2G 2

FIGURE 1Q

ENSG00000069329	#N/A	#N/A	#N/A	1.81	#N/A	VPS35 retromer complex component
ENSG00000121858	#N/A	#N/A	#N/A	1.80	#N/A	tumor necrosis factor (ligand) superfamily, member 10
ENSG00000281490	#N/A	#N/A	#N/A	1.80	#N/A	capicua transcriptional repressor pseudogene 14
ENSG00000066933	#N/A	#N/A	#N/A	1.79	#N/A	myosin IXA
ENSG00000137628	#N/A	#N/A	#N/A	1.79	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
ENSG00000105939	#N/A	#N/A	#N/A	1.79	#N/A	zinc finger CCCH-type, antiviral 1
ENSG00000121310	#N/A	#N/A	#N/A	1.79	#N/A	enoyl CoA hydratase domain containing 2
ENSG00000085117	#N/A	#N/A	#N/A	1.78	#N/A	CD82 molecule
ENSG00000141096	#N/A	#N/A	#N/A	1.78	#N/A	dipeptidase 3
ENSG00000142156	#N/A	#N/A	#N/A	1.78	#N/A	collagen, type VI, alpha 1
ENSG00000197756	#N/A	#N/A	#N/A	1.77	#N/A	ribosomal protein L37a
ENSG00000160352	#N/A	#N/A	#N/A	1.77	#N/A	zinc finger protein 714
ENSG00000204138	#N/A	#N/A	#N/A	1.76	1.16	phosphatase and actin regulator 4
ENSG00000136819	#N/A	#N/A	#N/A	1.76	1.55	chromosome 9 open reading frame 78
ENSG00000153029	#N/A	#N/A	#N/A	1.76	#N/A	major histocompatibility complex, class I-related
ENSG00000149187	#N/A	#N/A	#N/A	1.75	#N/A	CUGBP, Elav-like family member 1
ENSG00000166888	#N/A	#N/A	#N/A	1.74	#N/A	signal transducer and activator of transcription 6, interleukin-4 induced
ENSG00000214176	#N/A	#N/A	#N/A	1.74	#N/A	pleckstrin homology domain containing, family M (with RUN domain) member 1 pseudogene
ENSG00000175061	#N/A	#N/A	#N/A	1.74	#N/A	LRRC75A antisense RNA 1
ENSG00000170525	#N/A	#N/A	#N/A	1.73	#N/A	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
ENSG00000121289	#N/A	#N/A	#N/A	1.73	#N/A	centrosomal protein 89kDa
ENSG00000077380	#N/A	#N/A	#N/A	1.73	#N/A	dynein, cytoplasmic 1, intermediate chain 2
ENSG00000133112	#N/A	#N/A	#N/A	1.73	#N/A	tumor protein, translationally-controlled 1
ENSG00000178695	#N/A	#N/A	#N/A	1.72	#N/A	potassium channel tetramerization domain containing 12
ENSG00000131669	#N/A	#N/A	#N/A	1.72	#N/A	ninjurin 1
ENSG00000143771	#N/A	#N/A	#N/A	1.72	1.96	cornichon family AMPA receptor auxiliary protein 4
ENSG00000158270	#N/A	#N/A	#N/A	1.72	#N/A	collectin sub-family member 12
ENSG00000109390	#N/A	#N/A	#N/A	1.72	1.37	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
ENSG00000276701	#N/A	#N/A	#N/A	1.71	#N/A	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
ENSG00000105639	#N/A	#N/A	#N/A	1.71	#N/A	Janus kinase 3
ENSG00000185432	#N/A	#N/A	#N/A	1.71	#N/A	methyltransferase like 7A
ENSG00000160991	#N/A	#N/A	#N/A	1.70	1.04	ORAI calcium release-activated calcium modulator 2
ENSG00000128524	#N/A	#N/A	#N/A	1.70	1.96	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F
ENSG00000110002	#N/A	#N/A	#N/A	1.70	#N/A	von Willebrand factor A domain containing 5A
ENSG00000163171	#N/A	#N/A	#N/A	1.69	#N/A	CDC42 effector protein (Rho GTPase binding) 3
ENSG00000143891	#N/A	#N/A	#N/A	1.68	#N/A	galactose mutarotase (aldose 1-epimerase)
ENSG00000008988	#N/A	#N/A	#N/A	1.68	1.26	ribosomal protein S20
ENSG00000162735	#N/A	#N/A	#N/A	1.68	#N/A	peroxisomal biogenesis factor 19
ENSG00000102921	#N/A	#N/A	#N/A	1.68	#N/A	NEDD4 binding protein 1
ENSG00000212338	#N/A	#N/A	#N/A	1.68	#N/A	Small nucleolar RNA SNORA67
ENSG00000135046	#N/A	#N/A	#N/A	1.68	#N/A	annexin A1
ENSG00000070190	#N/A	#N/A	#N/A	1.68	#N/A	dual adaptor of phosphotyrosine and 3-phosphoinositides
ENSG00000083444	#N/A	#N/A	#N/A	1.67	#N/A	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1
ENSG00000232388	#N/A	#N/A	#N/A	1.67	1.34	long intergenic non-protein coding RNA 493
ENSG00000103066	#N/A	#N/A	#N/A	1.66	#N/A	phospholipase A2, group XV
ENSG00000112715	#N/A	#N/A	#N/A	1.66	1.02	vascular endothelial growth factor A
ENSG00000101040	#N/A	#N/A	#N/A	1.66	#N/A	zinc finger, MYND-type containing 8

ENSG00000175602	#N/A	#N/A	#N/A	-1.67	#N/A	coiled-coil domain containing 85B
ENSG00000139514	#N/A	#N/A	#N/A	-1.68	#N/A	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
ENSG00000128272	#N/A	#N/A	#N/A	-1.69	#N/A	activating transcription factor 4
ENSG00000272752	#N/A	#N/A	#N/A	-1.70	#N/A	STAG3L5P-PVRIG2P-PILRB readthrough
ENSG00000107937	#N/A	#N/A	#N/A	-1.70	#N/A	GTP binding protein 4
ENSG00000180730	#N/A	#N/A	#N/A	-1.70	#N/A	shisa family member 2
ENSG00000065183	#N/A	#N/A	#N/A	-1.70	#N/A	WD repeat domain 3
ENSG00000177192	#N/A	#N/A	#N/A	-1.70	#N/A	pseudouridylate synthase 1
ENSG00000090273	#N/A	#N/A	#N/A	-1.70	#N/A	nudC nuclear distribution protein
ENSG00000115053	#N/A	#N/A	#N/A	-1.71	#N/A	nucleolin
ENSG00000167635	#N/A	#N/A	#N/A	-1.71	#N/A	zinc finger protein 146
ENSG00000227686	#N/A	#N/A	#N/A	-1.71	#N/A	valyl-tRNA synthetase
ENSG00000115652	#N/A	#N/A	#N/A	-1.72	#N/A	UDP-glucuronate decarboxylase 1
ENSG00000104635	#N/A	#N/A	#N/A	-1.72	#N/A	solute carrier family 39 (zinc transporter), member 14
ENSG00000135972	#N/A	#N/A	#N/A	-1.72	#N/A	mitochondrial ribosomal protein S9
ENSG00000160256	#N/A	#N/A	#N/A	-1.72	#N/A	family with sequence similarity 207, member A
ENSG00000167114	#N/A	#N/A	#N/A	-1.72	#N/A	solute carrier family 27 (fatty acid transporter), member 4
ENSG00000261236	#N/A	#N/A	#N/A	-1.72	#N/A	block of proliferation 1
ENSG00000182168	#N/A	#N/A	#N/A	-1.73	#N/A	unc-5 netrin receptor C
ENSG00000183889	#N/A	#N/A	#N/A	-1.73	#N/A	Protein LOC102724993
ENSG00000171793	#N/A	#N/A	#N/A	-1.73	#N/A	CTP synthase 1
ENSG00000053372	#N/A	#N/A	#N/A	-1.73	#N/A	MRT4 homolog, ribosome maturation factor
ENSG00000140284	#N/A	#N/A	#N/A	-1.73	#N/A	solute carrier family 27 (fatty acid transporter), member 2
ENSG00000080608	#N/A	#N/A	#N/A	-1.73	#N/A	KIAA0020
ENSG00000091127	#N/A	#N/A	#N/A	-1.73	#N/A	pseudouridylate synthase 7 (putative)
ENSG00000136444	#N/A	#N/A	#N/A	-1.74	#N/A	radical S-adenosyl methionine domain containing 1
ENSG00000165689	#N/A	#N/A	#N/A	-1.75	#N/A	serologically defined colon cancer antigen 3
ENSG00000108578	#N/A	#N/A	#N/A	-1.75	#N/A	bleomycin hydrolase
ENSG00000117528	#N/A	#N/A	#N/A	-1.76	#N/A	ATP-binding cassette, sub-family D (ALD), member 3
ENSG00000188933	#N/A	#N/A	#N/A	-1.78	#N/A	ubiquitin specific peptidase 32 pseudogene 1
ENSG00000160214	#N/A	#N/A	#N/A	-1.78	#N/A	ribosomal RNA processing 1
ENSG00000110104	#N/A	#N/A	#N/A	-1.78	#N/A	coiled-coil domain containing 86
ENSG00000007520	#N/A	#N/A	#N/A	-1.78	#N/A	TSR3, 20S rRNA accumulation, homolog (S. cerevisiae)
ENSG00000125459	#N/A	#N/A	#N/A	-1.79	#N/A	misato 1, mitochondrial distribution and morphology regulator
ENSG00000189007	#N/A	#N/A	#N/A	-1.79	#N/A	adenosine deaminase, tRNA-specific 2
ENSG00000063241	#N/A	#N/A	#N/A	-1.79	#N/A	isochorismatase domain containing 2
ENSG00000179041	#N/A	#N/A	#N/A	-1.80	1.20	ribosome biogenesis regulator homolog
ENSG00000169230	#N/A	#N/A	#N/A	-1.80	#N/A	PRELI domain containing 1
ENSG00000180900	#N/A	#N/A	#N/A	-1.82	#N/A	scribbled planar cell polarity protein
ENSG00000213066	#N/A	#N/A	#N/A	-1.82	#N/A	FGFR1 oncogene partner
ENSG00000152642	#N/A	#N/A	#N/A	-1.82	#N/A	glycerol-3-phosphate dehydrogenase 1-like
ENSG00000134987	#N/A	#N/A	#N/A	-1.82	#N/A	WD repeat domain 36
ENSG00000167965	#N/A	#N/A	#N/A	-1.82	#N/A	MTOR associated protein, LST8 homolog
ENSG00000115758	#N/A	#N/A	#N/A	-1.82	#N/A	ornithine decarboxylase 1
ENSG00000071994	#N/A	#N/A	#N/A	-1.82	#N/A	programmed cell death 2
ENSG00000100427	#N/A	#N/A	#N/A	-1.82	#N/A	megalencephalic leukoencephalopathy with subcortical cysts 1
ENSG00000182676	#N/A	#N/A	#N/A	-1.83	#N/A	protein phosphatase 1, regulatory subunit 27

FIGURE 1R

ENSG00000113811	#N/A	#N/A	#N/A	1.66	1.90	selenoprotein K
ENSG00000185068	#N/A	#N/A	#N/A	1.65	2.29	GTF2H5
ENSG00000186468	#N/A	#N/A	#N/A	1.65	#N/A	ribosomal protein S23
ENSG00000164733	#N/A	#N/A	#N/A	1.64	#N/A	cathepsin B
ENSG00000127663	#N/A	#N/A	#N/A	1.64	#N/A	lysine (K)-specific demethylase 4B
ENSG00000223960	#N/A	#N/A	#N/A	1.64	#N/A	AC009948.5
ENSG00000105647	#N/A	#N/A	#N/A	1.64	#N/A	phosphoinositide-3-kinase, regulatory subunit 2 (beta)
ENSG00000162909	#N/A	#N/A	#N/A	1.64	#N/A	calpain 2, (m/II) large subunit
ENSG00000164687	#N/A	#N/A	#N/A	1.63	#N/A	fatty acid binding protein 5 (psoriasis-associated)
ENSG00000254635	#N/A	#N/A	#N/A	1.63	#N/A	WAC antisense RNA 1 (head to head)
ENSG00000198918	#N/A	#N/A	#N/A	1.63	#N/A	ribosomal protein L39
ENSG00000174428	#N/A	#N/A	#N/A	1.63	#N/A	GTF2I repeat domain containing 2B
ENSG00000172530	#N/A	#N/A	#N/A	1.63	#N/A	BTG3 associated nuclear protein
ENSG00000137145	#N/A	#N/A	#N/A	1.63	#N/A	DENN/MADD domain containing 4C
ENSG00000100439	#N/A	#N/A	#N/A	1.63	#N/A	abhydrolase domain containing 4
ENSG00000132256	#N/A	#N/A	#N/A	1.63	#N/A	tripartite motif containing 5
ENSG00000265972	#N/A	#N/A	#N/A	1.62	#N/A	thioredoxin interacting protein
ENSG00000245910	#N/A	#N/A	#N/A	1.62	1.53	small nucleolar RNA host gene 6
ENSG00000067066	#N/A	#N/A	#N/A	1.62	#N/A	SP100 nuclear antigen
ENSG00000166681	#N/A	#N/A	#N/A	1.62	#N/A	nerve growth factor receptor (TNFRSF16) associated protein 1
ENSG00000117475	#N/A	#N/A	#N/A	1.61	#N/A	basic leucine zipper nuclear factor 1
ENSG00000125691	#N/A	#N/A	#N/A	1.61	1.27	ribosomal protein L23
ENSG00000168172	#N/A	#N/A	#N/A	1.61	1.10	hook microtubule-tethering protein 3
ENSG00000010278	#N/A	#N/A	#N/A	1.61	#N/A	CD9 molecule
ENSG00000173214	#N/A	#N/A	#N/A	1.61	#N/A	KIAA1919
ENSG00000126860	#N/A	#N/A	#N/A	1.60	#N/A	ecotropic viral integration site 2A
ENSG00000167419	#N/A	#N/A	#N/A	1.60	#N/A	lactoperoxidase
ENSG00000118263	#N/A	#N/A	#N/A	1.60	#N/A	Kruppel-like factor 7 (ubiquitous)
ENSG00000235823	#N/A	#N/A	#N/A	1.60	#N/A	oligodendrocyte maturation-associated long intergenic non-coding RNA
ENSG00000111859	#N/A	#N/A	#N/A	1.60	#N/A	neural precursor cell expressed, developmentally down-regulated 9
ENSG00000089041	#N/A	#N/A	#N/A	1.60	#N/A	purinergic receptor P2X, ligand gated ion channel, 7
ENSG00000125810	#N/A	#N/A	#N/A	1.60	#N/A	CD93 molecule
ENSG00000113494	#N/A	#N/A	#N/A	1.59	#N/A	prolactin receptor
ENSG00000163993	#N/A	#N/A	#N/A	1.59	#N/A	S100 calcium binding protein P
ENSG00000124831	#N/A	#N/A	#N/A	1.59	#N/A	leucine rich repeat (in FLII) interacting protein 1
ENSG00000170581	#N/A	#N/A	#N/A	1.59	#N/A	signal transducer and activator of transcription 2, 113kDa
ENSG00000056972	#N/A	#N/A	#N/A	1.59	#N/A	TRAF3 interacting protein 2
ENSG00000218739	#N/A	#N/A	#N/A	1.59	3.17	CEBPZ opposite strand
ENSG00000204272	#N/A	#N/A	#N/A	1.58	#N/A	RP11-622K12.1
ENSG00000176845	#N/A	#N/A	#N/A	1.58	#N/A	meteorin, glial cell differentiation regulator-like
ENSG00000185880	#N/A	#N/A	#N/A	1.58	#N/A	tripartite motif containing 69
ENSG00000156587	#N/A	#N/A	#N/A	1.58	#N/A	ubiquitin-conjugating enzyme E2L 6
ENSG00000101347	#N/A	#N/A	#N/A	1.58	#N/A	SAM domain and HD domain 1
ENSG00000159792	#N/A	#N/A	#N/A	1.58	#N/A	protein serine kinase H1

ENSG00000253729	#N/A	#N/A	#N/A	-1.83	#N/A	protein kinase, DNA-activated, catalytic polypeptide
ENSG00000106133	#N/A	#N/A	#N/A	-1.84	#N/A	NOP2/Sun domain family, member 5 pseudogene 2
ENSG00000232169	#N/A	#N/A	#N/A	-1.84	#N/A	ATP-binding cassette, sub-family F (GCN20), member 1
ENSG00000068831	#N/A	#N/A	#N/A	-1.84	#N/A	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
ENSG00000168924	#N/A	#N/A	#N/A	-1.84	#N/A	leucine zipper-EF-hand containing transmembrane protein 1
ENSG00000162676	#N/A	#N/A	#N/A	-1.85	#N/A	growth factor independent 1 transcription repressor
ENSG00000196449	#N/A	#N/A	#N/A	-1.85	#N/A	yrdC N(6)-threonylcarbamoyltransferase domain containing
ENSG00000170571	#N/A	#N/A	#N/A	-1.85	#N/A	embigin
ENSG00000004478	#N/A	#N/A	#N/A	-1.85	#N/A	FK506 binding protein 4, 59kDa
ENSG00000141569	#N/A	#N/A	#N/A	-1.86	#N/A	tripartite motif containing 65
ENSG00000007541	#N/A	#N/A	#N/A	-1.86	#N/A	phosphatidylinositol glycan anchor biosynthesis, class Q
ENSG00000188206	#N/A	#N/A	#N/A	-1.86	#N/A	HNRNPU antisense RNA 1
ENSG00000123213	#N/A	#N/A	#N/A	-1.87	#N/A	neurolysin (metallopeptidase M3 family)
ENSG00000060982	#N/A	#N/A	#N/A	-1.87	#N/A	branched chain amino-acid transaminase 1, cytosolic
ENSG00000120254	#N/A	#N/A	#N/A	-1.87	#N/A	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
ENSG00000196305	#N/A	#N/A	#N/A	-1.89	#N/A	isoleucyl-tRNA synthetase
ENSG00000103253	#N/A	#N/A	#N/A	-1.89	#N/A	hydroxyacylglutathione hydrolase-like
ENSG00000171791	#N/A	#N/A	#N/A	-1.89	#N/A	B-cell CLL/lymphoma 2
ENSG00000105677	#N/A	#N/A	#N/A	-1.90	#N/A	transmembrane protein 147
ENSG00000178105	#N/A	#N/A	#N/A	-1.90	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
ENSG00000132768	#N/A	#N/A	#N/A	-1.91	#N/A	DPH2 homolog
ENSG00000133706	#N/A	#N/A	#N/A	-1.91	#N/A	leucyl-tRNA synthetase
ENSG00000116649	#N/A	#N/A	#N/A	-1.92	#N/A	spermidine synthase
ENSG00000171492	#N/A	#N/A	#N/A	-1.92	#N/A	leucine rich repeat containing 8 family, member D
ENSG00000120438	#N/A	#N/A	#N/A	-1.92	#N/A	t-complex 1
ENSG00000183426	#N/A	#N/A	#N/A	-1.94	#N/A	nuclear pore complex interacting protein family, member A1
ENSG00000172366	#N/A	#N/A	#N/A	-1.95	#N/A	family with sequence similarity 195, member A
ENSG00000183048	#N/A	#N/A	#N/A	-1.96	#N/A	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
ENSG00000144485	#N/A	#N/A	#N/A	-1.97	#N/A	hes family bHLH transcription factor 6
ENSG00000282283	#N/A	#N/A	#N/A	-1.97	#N/A	LPPR3
ENSG00000083097	#N/A	#N/A	#N/A	-1.97	#N/A	dopey family member 1
ENSG00000146457	#N/A	#N/A	#N/A	-1.97	#N/A	Wilms tumor 1 associated protein
ENSG00000132780	#N/A	#N/A	#N/A	-1.98	#N/A	nuclear autoantigenic sperm protein (histone-binding)
ENSG00000198744	#N/A	#N/A	#N/A	-1.98	#N/A	MT-CO3
ENSG00000114631	#N/A	#N/A	#N/A	-1.98	#N/A	podocalyxin-like 2
ENSG00000196497	#N/A	#N/A	#N/A	-1.99	#N/A	importin 4
ENSG00000172179	#N/A	#N/A	#N/A	-2.01	#N/A	prolactin
ENSG00000102241	#N/A	#N/A	#N/A	-2.03	#N/A	HIV-1 Tat specific factor 1
ENSG00000175416	#N/A	#N/A	#N/A	-2.03	#N/A	clathrin, light chain B
ENSG00000070081	#N/A	#N/A	#N/A	-2.03	#N/A	nucleobindin 2
ENSG00000198520	#N/A	#N/A	#N/A	-2.05	#N/A	chromosome 1 open reading frame 228
ENSG00000113575	#N/A	#N/A	#N/A	-2.08	#N/A	protein phosphatase 2, catalytic subunit, alpha isozyme
ENSG00000135069	#N/A	#N/A	#N/A	-2.08	#N/A	phosphoserine aminotransferase 1
ENSG00000124802	#N/A	#N/A	#N/A	-2.09	#N/A	eukaryotic translation elongation factor 1 epsilon 1

FIGURE 1S

ENSG00000226710	#N/A	#N/A	#N/A	1.57	1.67	chromosome 6 open reading frame 48
ENSG00000025708	#N/A	#N/A	#N/A	1.57	#N/A	thymidine phosphorylase
ENSG00000115548	#N/A	#N/A	#N/A	1.57	#N/A	lysine (K)-specific demethylase 3A
ENSG00000070214	#N/A	#N/A	#N/A	1.57	#N/A	solute carrier family 44 (choline transporter), member 1
ENSG00000188243	#N/A	#N/A	#N/A	1.56	#N/A	COMM domain containing 6
ENSG00000132024	#N/A	#N/A	#N/A	1.56	#N/A	coiled-coil and C2 domain containing 1A
ENSG00000168056	#N/A	#N/A	#N/A	1.56	#N/A	latent transforming growth factor beta binding protein 3
ENSG00000125482	#N/A	#N/A	#N/A	1.56	#N/A	transcription termination factor, RNA polymerase I
ENSG00000109099	#N/A	#N/A	#N/A	1.56	2.11	peripheral myelin protein 22
ENSG00000130066	#N/A	#N/A	#N/A	1.55	1.38	spermidine/spermine N1-acetyltransferase 1
ENSG00000171617	#N/A	#N/A	#N/A	1.55	#N/A	ectodermal-neural cortex 1 (with BTB domain)
ENSG00000138814	#N/A	#N/A	#N/A	1.55	1.40	protein phosphatase 3, catalytic subunit, alpha isozyme
ENSG00000148660	#N/A	#N/A	#N/A	1.54	#N/A	calcium/calmodulin-dependent protein kinase II gamma
ENSG00000168528	#N/A	#N/A	#N/A	1.54	#N/A	serine incorporator 2
ENSG00000138398	#N/A	#N/A	#N/A	1.54	1.39	peptidylprolyl isomerase G (cyclophilin G)
ENSG00000111596	#N/A	#N/A	#N/A	1.53	1.45	CCR4-NOT transcription complex, subunit 2
ENSG00000135686	#N/A	#N/A	#N/A	1.53	#N/A	kelch-like family member 36
ENSG00000081189	#N/A	#N/A	#N/A	1.53	#N/A	myocyte enhancer factor 2C
ENSG00000134419	#N/A	#N/A	#N/A	1.53	#N/A	ribosomal protein S15a
ENSG00000089159	#N/A	#N/A	#N/A	1.52	#N/A	paxillin
ENSG00000141012	#N/A	#N/A	#N/A	1.52	#N/A	galactosamine (N-acetyl)-6-sulfatase
ENSG00000104998	#N/A	#N/A	#N/A	1.52	#N/A	interleukin 27 receptor, alpha
ENSG00000164609	#N/A	#N/A	#N/A	1.52	#N/A	SLU7 splicing factor homolog (S. cerevisiae)
ENSG00000243749	#N/A	#N/A	#N/A	1.51	#N/A	ZMYM6 neighbor
ENSG00000187243	#N/A	#N/A	#N/A	1.51	#N/A	melanoma antigen family D4B
ENSG00000146425	#N/A	#N/A	#N/A	1.51	1.56	dynein, light chain, Tctex-type 1
ENSG00000103121	#N/A	#N/A	#N/A	1.51	1.81	C-x(9)-C motif containing 2
ENSG00000134138	#N/A	#N/A	#N/A	1.50	#N/A	Meis homeobox 2
ENSG00000265148	#N/A	#N/A	#N/A	1.50	#N/A	BZRAP1 antisense RNA 1
ENSG00000165030	#N/A	#N/A	#N/A	1.49	#N/A	nuclear factor, interleukin 3 regulated
ENSG00000121060	#N/A	#N/A	#N/A	1.49	#N/A	tripartite motif containing 25
ENSG00000103018	#N/A	#N/A	#N/A	1.49	#N/A	cytochrome b5 type B (outer mitochondrial membrane)
ENSG00000163840	#N/A	#N/A	#N/A	1.49	#N/A	deltex 3 like, E3 ubiquitin ligase
ENSG00000151366	#N/A	#N/A	#N/A	1.49	2.39	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
ENSG00000132432	#N/A	#N/A	#N/A	1.49	2.10	Sec61 gamma subunit
ENSG00000106771	#N/A	#N/A	#N/A	1.49	#N/A	transmembrane protein 245
ENSG00000160691	#N/A	#N/A	#N/A	1.48	#N/A	SHC (Src homology 2 domain containing) transforming protein 1
ENSG00000099977	#N/A	#N/A	#N/A	1.48	1.09	D-dopachrome tautomerase
ENSG00000181523	#N/A	#N/A	#N/A	1.48	#N/A	N-sulfoglucosamine sulfohydrolase
ENSG00000011422	#N/A	#N/A	#N/A	1.48	#N/A	plasminogen activator, urokinase receptor
ENSG00000100055	#N/A	#N/A	#N/A	1.48	#N/A	cytohesin 4
ENSG00000164125	#N/A	#N/A	#N/A	1.48	#N/A	family with sequence similarity 198, member B
ENSG00000039523	#N/A	#N/A	#N/A	1.48	#N/A	family with sequence similarity 65, member A
ENSG00000142534	#N/A	#N/A	#N/A	1.48	#N/A	ribosomal protein S11
ENSG00000188021	#N/A	#N/A	#N/A	1.48	#N/A	ubiquilin 2
ENSG00000131446	#N/A	#N/A	#N/A	1.48	#N/A	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
ENSG00000134825	#N/A	#N/A	#N/A	1.47	2.06	transmembrane protein 258

ENSG00000099624	#N/A	#N/A	#N/A	-2.09	#N/A	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
ENSG00000087269	#N/A	#N/A	#N/A	-2.09	#N/A	NOP14 nucleolar protein
ENSG00000185163	#N/A	#N/A	#N/A	-2.10	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51
ENSG00000221823	#N/A	#N/A	#N/A	-2.10	#N/A	protein phosphatase 3, regulatory subunit B, alpha
ENSG00000155380	#N/A	#N/A	#N/A	-2.11	#N/A	solute carrier family 16 (monocarboxylate transporter), member 1
ENSG00000235173	#N/A	#N/A	#N/A	-2.11	#N/A	HGH1 homolog
ENSG00000198763	#N/A	#N/A	#N/A	-2.11	#N/A	mitochondrially encoded NADH dehydrogenase 2
ENSG00000103266	#N/A	#N/A	#N/A	-2.11	#N/A	STIP1 homology and U-box containing protein 1, E3 ubiquitin protein ligase
ENSG00000282367	#N/A	#N/A	#N/A	-2.12	#N/A	phosphatidylserine synthase 2
ENSG00000116455	#N/A	#N/A	#N/A	-2.12	#N/A	WD repeat domain 77
ENSG00000179862	#N/A	#N/A	#N/A	-2.15	#N/A	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
ENSG00000139675	#N/A	#N/A	#N/A	-2.17	#N/A	heterogeneous nuclear ribonucleoprotein A1-like 2
ENSG00000243716	#N/A	#N/A	#N/A	-2.18	#N/A	nuclear pore complex interacting protein family, member B5
ENSG00000183751	#N/A	#N/A	#N/A	-2.19	#N/A	transducin (beta)-like 3
ENSG00000114446	#N/A	#N/A	#N/A	-2.20	#N/A	intraflagellar transport 57
ENSG00000183605	#N/A	#N/A	#N/A	-2.21	#N/A	sideroflexin 4
ENSG00000103342	#N/A	#N/A	#N/A	-2.26	#N/A	G1 to S phase transition 1
ENSG00000198899	#N/A	#N/A	#N/A	-2.26	#N/A	mitochondrially encoded ATP synthase 6
ENSG00000120738	#N/A	#N/A	#N/A	-2.28	#N/A	early growth response 1
ENSG00000007264	#N/A	#N/A	#N/A	-2.29	#N/A	megakaryocyte-associated tyrosine kinase
ENSG00000226916	#N/A	#N/A	#N/A	-2.33	#N/A	WD repeat domain 46
ENSG00000174669	#N/A	#N/A	#N/A	-2.33	#N/A	solute carrier family 29 (equilibrative nucleoside transporter), member 2
ENSG00000183688	#N/A	#N/A	#N/A	-2.36	#N/A	family with sequence similarity 101, member B
ENSG00000116852	#N/A	#N/A	#N/A	-2.36	#N/A	kinesin family member 21B
ENSG00000074935	#N/A	#N/A	#N/A	-2.39	#N/A	tubulin, epsilon 1
ENSG00000160072	#N/A	#N/A	#N/A	-2.41	#N/A	ATPase family, AAA domain containing 3B
ENSG00000224877	#N/A	#N/A	#N/A	-2.45	#N/A	chromosome 17 open reading frame 89
ENSG00000110660	#N/A	#N/A	#N/A	-2.45	#N/A	solute carrier family 35, member F2
ENSG00000011052	#N/A	#N/A	#N/A	-2.45	#N/A	NME/NM23 nucleoside diphosphate kinase 2
ENSG00000070669	#N/A	#N/A	#N/A	-2.45	#N/A	asparagine synthetase (glutamine-hydrolyzing)
ENSG00000277957	#N/A	#N/A	#N/A	-2.46	#N/A	SENP3-EIF4A1 readthrough (NMD candidate)
ENSG00000106070	#N/A	#N/A	#N/A	-2.46	#N/A	growth factor receptor-bound protein 10
ENSG00000262814	#N/A	#N/A	#N/A	-2.54	#N/A	mitochondrial ribosomal protein L12
ENSG00000175445	#N/A	#N/A	#N/A	-2.60	#N/A	lipoprotein lipase
ENSG00000160818	#N/A	#N/A	#N/A	-2.67	#N/A	G patch domain containing 4
ENSG00000164284	#N/A	#N/A	#N/A	-2.72	#N/A	GrpE-like 2, mitochondrial (E. coli)
ENSG00000052749	#N/A	#N/A	#N/A	-2.74	#N/A	ribosomal RNA processing 12 homolog
ENSG00000106588	#N/A	#N/A	#N/A	-2.77	#N/A	proteasome (prosome, macropain) subunit, alpha type, 2
ENSG00000169246	#N/A	#N/A	#N/A	-3.18	#N/A	nuclear pore complex interacting protein family, member B3
ENSG00000169136	#N/A	#N/A	#N/A	-3.29	#N/A	activating transcription factor 5
ENSG00000176076	#N/A	#N/A	#N/A	-3.41	#N/A	potassium channel, voltage gated subfamily E regulatory beta subunit 5
ENSG00000239672	#N/A	#N/A	#N/A	-4.00	#N/A	NME/NM23 nucleoside diphosphate kinase 1
ENSG00000128965	#N/A	#N/A	#N/A	-4.85	#N/A	ChaC glutathione-specific gamma-glutamylcyclotransferase 1
ENSG00000263006	#N/A	#N/A	#N/A	#N/A	7.14	Rho-associated, coiled-coil containing protein kinase 1 pseudogene 1
ENSG00000240184	#N/A	#N/A	#N/A	#N/A	5.51	protocadherin gamma subfamily C, 3
ENSG00000099139	#N/A	#N/A	#N/A	#N/A	4.94	proprotein convertase subtilisin/kexin type 5
ENSG00000230453	#N/A	#N/A	#N/A	#N/A	4.79	ankyrin repeat domain 18B

FIGURE 1T

ENSG00000106948	#N/A	#N/A	#N/A	1.47	#N/A	AT-hook transcription factor
ENSG00000187098	#N/A	#N/A	#N/A	1.47	#N/A	microphthalmia-associated transcription factor
ENSG00000257923	#N/A	#N/A	#N/A	1.47	#N/A	cut-like homeobox 1
ENSG00000118181	#N/A	#N/A	#N/A	1.47	1.10	ribosomal protein S25
ENSG00000228474	#N/A	#N/A	#N/A	1.47	1.33	oligosaccharyltransferase complex subunit 4 (non-catalytic)
ENSG00000104731	#N/A	#N/A	#N/A	1.47	#N/A	kelch domain containing 4
ENSG00000177981	#N/A	#N/A	#N/A	1.47	#N/A	ankyrin repeat and SOCS box containing 8
ENSG00000067057	#N/A	#N/A	#N/A	1.46	#N/A	phosphofructokinase, platelet
ENSG00000118267	#N/A	#N/A	#N/A	1.46	1.30	ZNF271
ENSG00000143226	#N/A	#N/A	#N/A	1.45	#N/A	Fc fragment of IgG, low affinity IIa, receptor (CD32)
ENSG00000172936	#N/A	#N/A	#N/A	1.45	#N/A	myeloid differentiation primary response 88
ENSG00000069966	#N/A	#N/A	#N/A	1.45	#N/A	guanine nucleotide binding protein (G protein), beta 5
ENSG00000014914	#N/A	#N/A	#N/A	1.45	#N/A	myotubularin related protein 11
ENSG00000078124	#N/A	#N/A	#N/A	1.44	1.52	alkaline ceramidase 3
ENSG00000132823	#N/A	#N/A	#N/A	1.44	#N/A	oxidative stress responsive serine-rich 1
ENSG00000123360	#N/A	#N/A	#N/A	1.44	#N/A	phosphodiesterase 1B, calmodulin-dependent
ENSG00000027697	#N/A	#N/A	#N/A	1.44	#N/A	interferon gamma receptor 1
ENSG00000119801	#N/A	#N/A	#N/A	1.44	#N/A	yippee-like 5
ENSG00000134107	#N/A	#N/A	#N/A	1.44	1.27	basic helix-loop-helix family, member e40
ENSG00000104921	#N/A	#N/A	#N/A	1.44	#N/A	Fc fragment of IgE, low affinity II, receptor for (CD23)
ENSG00000028137	#N/A	#N/A	#N/A	1.43	#N/A	tumor necrosis factor receptor superfamily, member 1B
ENSG00000105355	#N/A	#N/A	#N/A	1.43	#N/A	perilipin 3
ENSG00000109475	#N/A	#N/A	#N/A	1.43	#N/A	ribosomal protein L34
ENSG00000255439	#N/A	#N/A	#N/A	1.43	#N/A	Uncharacterized protein
ENSG00000137575	#N/A	#N/A	#N/A	1.43	#N/A	syndecan binding protein (syntenin)
ENSG00000168273	#N/A	#N/A	#N/A	1.43	#N/A	small integral membrane protein 4
ENSG00000086065	#N/A	#N/A	#N/A	1.43	#N/A	charged multivesicular body protein 5
ENSG00000205542	#N/A	#N/A	#N/A	1.43	#N/A	thymosin beta 4, X-linked
ENSG00000105193	#N/A	#N/A	#N/A	1.42	#N/A	ribosomal protein S16
ENSG00000163220	#N/A	#N/A	#N/A	1.42	#N/A	S100 calcium binding protein A9
ENSG00000168404	#N/A	#N/A	#N/A	1.42	#N/A	mixed lineage kinase domain-like
ENSG00000085719	#N/A	#N/A	#N/A	1.42	#N/A	copine III
ENSG00000157895	#N/A	#N/A	#N/A	1.41	1.14	chromosome 12 open reading frame 43
ENSG00000140199	#N/A	#N/A	#N/A	1.41	#N/A	solute carrier family 12 (potassium/chloride transporter), member 6
ENSG00000137818	#N/A	#N/A	#N/A	1.41	#N/A	ribosomal protein, large, P1
ENSG00000272657	#N/A	#N/A	#N/A	1.41	#N/A	AP000320.7
ENSG00000164587	#N/A	#N/A	#N/A	1.41	#N/A	ribosomal protein S14
ENSG00000131981	#N/A	#N/A	#N/A	1.41	#N/A	lectin, galactoside-binding, soluble, 3
ENSG00000254995	#N/A	#N/A	#N/A	1.41	#N/A	STX16-NPEPL1 readthrough (NMD candidate)
ENSG00000095951	#N/A	#N/A	#N/A	1.41	#N/A	human immunodeficiency virus type I enhancer binding protein 1
ENSG00000133816	#N/A	#N/A	#N/A	1.41	#N/A	microtubule associated monooxygenase, calponin and LIM domain containing 2
ENSG00000270106	#N/A	#N/A	#N/A	1.40	#N/A	TSNAX-DISC1 readthrough (NMD candidate)
ENSG00000196123	#N/A	#N/A	#N/A	1.40	#N/A	KIAA0895-like
ENSG00000115561	#N/A	#N/A	#N/A	1.40	#N/A	charged multivesicular body protein 3
ENSG00000266714	#N/A	#N/A	#N/A	1.40	#N/A	myosin XVB
ENSG00000101132	#N/A	#N/A	#N/A	1.40	1.29	prefoldin subunit 4

ENSG00000159251	#N/A	#N/A	#N/A	#N/A	4.02	actin, alpha, cardiac muscle 1
ENSG00000124212	#N/A	#N/A	#N/A	#N/A	3.55	prostaglandin I2 (prostacyclin) synthase
ENSG00000188483	#N/A	#N/A	#N/A	#N/A	3.43	immediate early response 5-like
ENSG00000100292	#N/A	#N/A	#N/A	#N/A	3.33	heme oxygenase 1
ENSG00000115380	#N/A	#N/A	#N/A	#N/A	3.23	EGF containing fibulin-like extracellular matrix protein 1
ENSG00000069011	#N/A	#N/A	#N/A	#N/A	3.14	paired-like homeodomain 1
ENSG00000130513	#N/A	#N/A	#N/A	#N/A	2.72	growth differentiation factor 15
ENSG00000115541	#N/A	#N/A	#N/A	#N/A	2.68	heat shock 10kDa protein 1
ENSG00000115461	#N/A	#N/A	#N/A	#N/A	2.53	insulin-like growth factor binding protein 5
ENSG00000102802	#N/A	#N/A	#N/A	#N/A	2.53	mesenteric estrogen-dependent adipogenesis
ENSG00000139343	#N/A	#N/A	#N/A	#N/A	2.52	small nuclear ribonucleoprotein polypeptide F
ENSG00000197182	#N/A	#N/A	#N/A	#N/A	2.49	MIRLET7B host gene
ENSG00000104368	#N/A	#N/A	#N/A	#N/A	2.46	plasminogen activator, tissue
ENSG00000239927	#N/A	#N/A	#N/A	#N/A	2.43	ribonuclease P/MRP 21kDa subunit
ENSG00000111057	#N/A	#N/A	#N/A	#N/A	2.38	keratin 18, type I
ENSG00000145708	#N/A	#N/A	#N/A	#N/A	2.36	corticotropin releasing hormone binding protein
ENSG00000081870	#N/A	#N/A	#N/A	#N/A	2.36	heat shock protein family B (small), member 11
ENSG00000175768	#N/A	#N/A	#N/A	#N/A	2.36	translocase of outer mitochondrial membrane 5 homolog (yeast)
ENSG00000182004	#N/A	#N/A	#N/A	#N/A	2.26	small nuclear ribonucleoprotein polypeptide E
ENSG00000148671	#N/A	#N/A	#N/A	#N/A	2.22	adipogenesis regulatory factor
ENSG00000075826	#N/A	#N/A	#N/A	#N/A	2.22	SEC31 homolog B, COPII coating complex component
ENSG00000106591	#N/A	#N/A	#N/A	#N/A	2.13	mitochondrial ribosomal protein L32
ENSG00000143977	#N/A	#N/A	#N/A	#N/A	2.10	small nuclear ribonucleoprotein polypeptide G
ENSG00000164182	#N/A	#N/A	#N/A	#N/A	2.09	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2
ENSG00000008394	#N/A	#N/A	#N/A	#N/A	2.05	microsomal glutathione S-transferase 1
ENSG00000152518	#N/A	#N/A	#N/A	#N/A	2.03	ZFP36 ring finger protein-like 2
ENSG00000262771	#N/A	#N/A	#N/A	#N/A	1.98	single-stranded DNA binding protein 1, mitochondrial
ENSG00000142396	#N/A	#N/A	#N/A	#N/A	1.98	endogenous retrovirus group K3, member 1
ENSG00000162385	#N/A	#N/A	#N/A	#N/A	1.98	mago homolog, exon junction complex core component
ENSG00000235385	#N/A	#N/A	#N/A	#N/A	1.95	GS1-600G8.5
ENSG00000179958	#N/A	#N/A	#N/A	#N/A	1.94	dCTP pyrophosphatase 1
ENSG00000168003	#N/A	#N/A	#N/A	#N/A	1.94	solute carrier family 3 (amino acid transporter heavy chain), member 2
ENSG00000173436	#N/A	#N/A	#N/A	#N/A	1.91	mitochondrial inner membrane organizing system 1
ENSG00000163156	#N/A	#N/A	#N/A	#N/A	1.91	sodium channel modifier 1
ENSG00000143256	#N/A	#N/A	#N/A	#N/A	1.91	prefoldin subunit 2
ENSG00000112769	#N/A	#N/A	#N/A	#N/A	1.91	laminin, alpha 4
ENSG00000082515	#N/A	#N/A	#N/A	#N/A	1.89	mitochondrial ribosomal protein L22
ENSG00000127922	#N/A	#N/A	#N/A	#N/A	1.88	split hand/foot malformation (ectrodactyly) type 1
ENSG00000198211	#N/A	#N/A	#N/A	#N/A	1.88	tubulin, beta 3 class III
ENSG00000090263	#N/A	#N/A	#N/A	#N/A	1.87	mitochondrial ribosomal protein S33
ENSG00000217930	#N/A	#N/A	#N/A	#N/A	1.87	presequence translocase-associated motor 16 homolog (S. cerevisiae)
ENSG00000104825	#N/A	#N/A	#N/A	#N/A	1.86	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta
ENSG00000229833	#N/A	#N/A	#N/A	#N/A	1.86	PET100 homolog
ENSG00000123353	#N/A	#N/A	#N/A	#N/A	1.86	ORMDL sphingolipid biosynthesis regulator 2
ENSG00000167779	#N/A	#N/A	#N/A	#N/A	1.86	insulin-like growth factor binding protein 6
ENSG00000147862	#N/A	#N/A	#N/A	#N/A	1.86	nuclear factor I/B

FIGURE 1U

ENSG00000124370	#N/A	#N/A	#N/A	1.40	#N/A	methylmalonyl CoA epimerase
ENSG00000156052	#N/A	#N/A	#N/A	1.40	#N/A	guanine nucleotide binding protein (G protein), q polypeptide
ENSG00000119950	#N/A	#N/A	#N/A	1.39	#N/A	MAX interactor 1, dimerization protein
ENSG00000163319	#N/A	#N/A	#N/A	1.39	2.47	mitochondrial ribosomal protein S18C
ENSG00000161970	#N/A	#N/A	#N/A	1.39	#N/A	ribosomal protein L26
ENSG00000197747	#N/A	#N/A	#N/A	1.39	#N/A	S100 calcium binding protein A10
ENSG00000186318	#N/A	#N/A	#N/A	1.39	#N/A	beta-site APP-cleaving enzyme 1
ENSG00000204364	#N/A	#N/A	#N/A	1.39	#N/A	complement component 2
ENSG00000158006	#N/A	#N/A	#N/A	1.39	#N/A	platelet-activating factor acetylhydrolase 2, 40kDa
ENSG00000088970	#N/A	#N/A	#N/A	1.39	#N/A	kizuna centrosomal protein
ENSG00000114737	#N/A	#N/A	#N/A	1.38	#N/A	cytokine inducible SH2-containing protein
ENSG00000115738	#N/A	#N/A	#N/A	1.38	#N/A	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
ENSG00000257341	#N/A	#N/A	#N/A	1.38	#N/A	cysteine-rich protein 1 (intestinal)
ENSG00000160710	#N/A	#N/A	#N/A	1.38	#N/A	adenosine deaminase, RNA-specific
ENSG00000142347	#N/A	#N/A	#N/A	1.38	#N/A	myosin IF
ENSG00000121552	#N/A	#N/A	#N/A	1.38	#N/A	cystatin A (stefin A)
ENSG00000198258	#N/A	#N/A	#N/A	1.38	1.92	ubiquitin-like 5
ENSG00000136816	#N/A	#N/A	#N/A	1.38	#N/A	torsin family 1, member B (torsin B)
ENSG00000243147	#N/A	#N/A	#N/A	1.37	2.14	mitochondrial ribosomal protein L33
ENSG00000119720	#N/A	#N/A	#N/A	1.37	#N/A	NRDE-2, necessary for RNA interference, domain containing
ENSG00000115866	#N/A	#N/A	#N/A	1.37	#N/A	aspartyl-tRNA synthetase
ENSG00000276276	#N/A	#N/A	#N/A	1.37	#N/A	ADP-ribosylation factor-like 17B
ENSG00000224152	#N/A	#N/A	#N/A	1.36	#N/A	AC009506.1
ENSG00000143553	#N/A	#N/A	#N/A	1.36	1.15	SNAP-associated protein
ENSG00000124172	#N/A	#N/A	#N/A	1.36	1.47	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
ENSG00000105374	#N/A	#N/A	#N/A	1.36	#N/A	natural killer cell granule protein 7
ENSG00000186174	#N/A	#N/A	#N/A	1.36	#N/A	B-cell CLL/lymphoma 9-like
ENSG00000169860	#N/A	#N/A	#N/A	1.36	#N/A	purinergic receptor P2Y, G-protein coupled, 1
ENSG00000159399	#N/A	#N/A	#N/A	1.36	#N/A	hexokinase 2
ENSG00000122026	#N/A	#N/A	#N/A	1.36	1.09	ribosomal protein L21
ENSG00000189043	#N/A	#N/A	#N/A	1.36	1.46	NDUFA4, mitochondrial complex associated
ENSG00000143382	#N/A	#N/A	#N/A	1.36	#N/A	ADAMTS-like 4
ENSG00000167461	#N/A	#N/A	#N/A	1.36	#N/A	RAB8A, member RAS oncogene family
ENSG00000214022	#N/A	#N/A	#N/A	1.36	1.82	replication initiator 1
ENSG00000185722	#N/A	#N/A	#N/A	1.36	#N/A	ankyrin repeat and FYVE domain containing 1
ENSG00000166147	#N/A	#N/A	#N/A	1.35	#N/A	fibrillin 1
ENSG00000117523	#N/A	#N/A	#N/A	1.35	#N/A	proline-rich coiled-coil 2C
ENSG00000169756	#N/A	#N/A	#N/A	1.35	#N/A	LIM and senescent cell antigen-like domains 1
ENSG00000177917	#N/A	#N/A	#N/A	1.35	#N/A	ADP-ribosylation factor-like 6 interacting protein 6
ENSG00000143545	#N/A	#N/A	#N/A	1.35	#N/A	RAB13, member RAS oncogene family
ENSG00000100097	#N/A	#N/A	#N/A	1.35	#N/A	lectin, galactoside-binding, soluble, 1
ENSG00000237945	#N/A	#N/A	#N/A	1.35	#N/A	long intergenic non-protein coding RNA 649
ENSG00000111640	#N/A	#N/A	#N/A	1.35	#N/A	glyceraldehyde-3-phosphate dehydrogenase
ENSG00000186812	#N/A	#N/A	#N/A	1.34	#N/A	zinc finger protein 397
ENSG00000065518	#N/A	#N/A	#N/A	1.34	1.55	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
ENSG00000168275	#N/A	#N/A	#N/A	1.34	#N/A	cytochrome c oxidase assembly factor 6

ENSG00000177426	#N/A	#N/A	#N/A	#N/A	1.85	TGFB-induced factor homeobox 1
ENSG00000080823	#N/A	#N/A	#N/A	#N/A	1.85	MOK protein kinase
ENSG00000154723	#N/A	#N/A	#N/A	#N/A	1.81	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6
ENSG00000111832	#N/A	#N/A	#N/A	#N/A	1.79	RWD domain containing 1
ENSG00000176731	#N/A	#N/A	#N/A	#N/A	1.78	chromosome 8 open reading frame 59
ENSG00000198498	#N/A	#N/A	#N/A	#N/A	1.78	translation machinery associated 16 homolog (S. cerevisiae)
ENSG00000174917	#N/A	#N/A	#N/A	#N/A	1.75	chromosome 19 open reading frame 70
ENSG00000154582	#N/A	#N/A	#N/A	#N/A	1.74	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
ENSG00000171303	#N/A	#N/A	#N/A	#N/A	1.73	potassium channel, two pore domain subfamily K, member 3
ENSG00000171246	#N/A	#N/A	#N/A	#N/A	1.72	neuronal pentraxin I
ENSG00000105185	#N/A	#N/A	#N/A	#N/A	1.72	programmed cell death 5
ENSG00000148688	#N/A	#N/A	#N/A	#N/A	1.71	ribonuclease P/MRP 30kDa subunit
ENSG00000130770	#N/A	#N/A	#N/A	#N/A	1.71	ATPase inhibitory factor 1
ENSG00000161011	#N/A	#N/A	#N/A	#N/A	1.70	sequestosome 1
ENSG00000146066	#N/A	#N/A	#N/A	#N/A	1.69	HIG1 hypoxia inducible domain family, member 2A
ENSG00000165389	#N/A	#N/A	#N/A	#N/A	1.68	serine palmitoyltransferase, small subunit A
ENSG00000203805	#N/A	#N/A	#N/A	#N/A	1.67	phosphatidic acid phosphatase type 2 domain containing 1A
ENSG00000163827	#N/A	#N/A	#N/A	#N/A	1.66	leucine rich repeat containing 2
ENSG00000133169	#N/A	#N/A	#N/A	#N/A	1.65	brain expressed, X-linked 1
ENSG00000114784	#N/A	#N/A	#N/A	#N/A	1.65	eukaryotic translation initiation factor 1B
ENSG00000196352	#N/A	#N/A	#N/A	#N/A	1.65	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
ENSG00000147669	#N/A	#N/A	#N/A	#N/A	1.64	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
ENSG00000100902	#N/A	#N/A	#N/A	#N/A	1.64	proteasome (prosome, macropain) subunit, alpha type, 6
ENSG00000105825	#N/A	#N/A	#N/A	#N/A	1.63	tissue factor pathway inhibitor 2
ENSG00000185112	#N/A	#N/A	#N/A	#N/A	1.63	family with sequence similarity 43, member A
ENSG00000214046	#N/A	#N/A	#N/A	#N/A	1.62	small integral membrane protein 7
ENSG00000125743	#N/A	#N/A	#N/A	#N/A	1.62	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
ENSG00000119705	#N/A	#N/A	#N/A	#N/A	1.61	SRA stem-loop interacting RNA binding protein
ENSG00000148690	#N/A	#N/A	#N/A	#N/A	1.61	fragile site, folic acid type, rare, fra(10)(q23.3) or fra(10)(q24.2) candidate 1
ENSG00000145354	#N/A	#N/A	#N/A	#N/A	1.61	CDGSH iron sulfur domain 2
ENSG00000104763	#N/A	#N/A	#N/A	#N/A	1.61	N-acylsphingosine amidohydrolase (acid ceramidase) 1
ENSG00000160799	#N/A	#N/A	#N/A	#N/A	1.61	coiled-coil domain containing 12
ENSG00000227051	#N/A	#N/A	#N/A	#N/A	1.61	chromosome 14 open reading frame 132
ENSG00000171453	#N/A	#N/A	#N/A	#N/A	1.61	polymerase (RNA) I polypeptide C, 30kDa
ENSG00000147535	#N/A	#N/A	#N/A	#N/A	1.61	phosphatidic acid phosphatase type 2 domain containing 1B
ENSG00000136897	#N/A	#N/A	#N/A	#N/A	1.60	mitochondrial ribosomal protein L50
ENSG00000130332	#N/A	#N/A	#N/A	#N/A	1.60	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000173113	#N/A	#N/A	#N/A	#N/A	1.60	tRNA methyltransferase 11-2 homolog (S. cerevisiae)
ENSG00000273397	#N/A	#N/A	#N/A	#N/A	1.59	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
ENSG00000143158	#N/A	#N/A	#N/A	#N/A	1.57	mitochondrial pyruvate carrier 2
ENSG00000166347	#N/A	#N/A	#N/A	#N/A	1.57	cytochrome b5 type A (microsomal)
ENSG00000161980	#N/A	#N/A	#N/A	#N/A	1.57	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
ENSG00000167863	#N/A	#N/A	#N/A	#N/A	1.57	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
ENSG00000101361	#N/A	#N/A	#N/A	#N/A	1.57	NOP56 ribonucleoprotein
ENSG00000120963	#N/A	#N/A	#N/A	#N/A	1.56	zinc finger protein 706
ENSG00000060762	#N/A	#N/A	#N/A	#N/A	1.56	mitochondrial pyruvate carrier 1

FIGURE 1V

ENSG00000125977	#N/A	#N/A	#N/A	1.34	1.64	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
ENSG00000144791	#N/A	#N/A	#N/A	1.34	#N/A	LIM domains containing 1
ENSG00000206573	#N/A	#N/A	#N/A	1.34	#N/A	THUMPD3 antisense RNA 1
ENSG00000240344	#N/A	#N/A	#N/A	1.33	#N/A	peptidylprolyl isomerase (cyclophilin)-like 3
ENSG00000188559	#N/A	#N/A	#N/A	1.33	#N/A	Ral GTPase activating protein, alpha subunit 2 (catalytic)
ENSG00000175482	#N/A	#N/A	#N/A	1.33	#N/A	polymerase (DNA-directed), delta 4, accessory subunit
ENSG00000134970	#N/A	#N/A	#N/A	1.33	#N/A	transmembrane emp24 protein transport domain containing 7
ENSG00000131507	#N/A	#N/A	#N/A	1.33	#N/A	Nedd4 family interacting protein 1
ENSG00000231500	#N/A	#N/A	#N/A	1.33	#N/A	ribosomal protein S18
ENSG00000101608	#N/A	#N/A	#N/A	1.33	#N/A	myosin, light chain 12A, regulatory, non-sarcomeric
ENSG00000187210	#N/A	#N/A	#N/A	1.33	#N/A	glucosaminyl (N-acetyl) transferase 1, core 2
ENSG00000180964	#N/A	#N/A	#N/A	1.33	#N/A	transcription elongation factor A (SII)-like 8
ENSG00000118260	#N/A	#N/A	#N/A	1.32	#N/A	cAMP responsive element binding protein 1
ENSG00000105829	#N/A	#N/A	#N/A	1.32	1.29	Bet1 golgi vesicular membrane trafficking protein
ENSG00000163975	#N/A	#N/A	#N/A	1.32	#N/A	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5
ENSG00000169032	#N/A	#N/A	#N/A	1.32	#N/A	mitogen-activated protein kinase kinase 1
ENSG00000196683	#N/A	#N/A	#N/A	1.32	1.15	translocase of outer mitochondrial membrane 7 homolog (yeast)
ENSG00000070814	#N/A	#N/A	#N/A	1.32	2.22	Treacher Collins-Franceschetti syndrome 1
ENSG00000111275	#N/A	#N/A	#N/A	1.32	#N/A	aldehyde dehydrogenase 2 family (mitochondrial)
ENSG00000182534	#N/A	#N/A	#N/A	1.32	#N/A	matrix-remodelling associated 7
ENSG00000214413	#N/A	#N/A	#N/A	1.32	1.69	BBSome interacting protein 1
ENSG00000136448	#N/A	#N/A	#N/A	1.32	#N/A	N-myristoyltransferase 1
ENSG00000150991	#N/A	#N/A	#N/A	1.31	#N/A	ubiquitin C
ENSG00000119878	#N/A	#N/A	#N/A	1.31	1.58	cysteine-rich PDZ-binding protein
ENSG00000197256	#N/A	#N/A	#N/A	1.31	#N/A	KN motif and ankyrin repeat domains 2
ENSG00000280828	#N/A	#N/A	#N/A	1.31	#N/A	RP11-274B21.1
ENSG00000262418	#N/A	#N/A	#N/A	1.31	#N/A	protein tyrosine phosphatase, receptor type, C
ENSG00000120709	#N/A	#N/A	#N/A	1.31	#N/A	family with sequence similarity 53, member C
ENSG00000106560	#N/A	#N/A	#N/A	1.31	#N/A	GTPase, IMAP family member 2
ENSG00000177738	#N/A	#N/A	#N/A	1.31	#N/A	CTD-2201E18.3
ENSG00000155876	#N/A	#N/A	#N/A	1.30	#N/A	Ras-related GTP binding A
ENSG00000119820	#N/A	#N/A	#N/A	1.30	#N/A	Yip1 domain family, member 4
ENSG00000136238	#N/A	#N/A	#N/A	1.30	1.13	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
ENSG00000124201	#N/A	#N/A	#N/A	1.30	#N/A	zinc finger, NFX1-type containing 1
ENSG00000124614	#N/A	#N/A	#N/A	1.30	#N/A	ribosomal protein S10
ENSG00000141526	#N/A	#N/A	#N/A	1.30	#N/A	solute carrier family 16 (monocarboxylate transporter), member 3
ENSG00000198604	#N/A	#N/A	#N/A	1.30	#N/A	bromodomain adjacent to zinc finger domain, 1A
ENSG00000104814	#N/A	#N/A	#N/A	1.30	#N/A	mitogen-activated protein kinase kinase kinase kinase 1
ENSG00000110700	#N/A	#N/A	#N/A	1.30	#N/A	ribosomal protein S13
ENSG00000198682	#N/A	#N/A	#N/A	1.30	#N/A	3'-phosphoadenosine 5'-phosphosulfate synthase 2
ENSG00000167850	#N/A	#N/A	#N/A	1.29	#N/A	CD300c molecule

ENSG00000189403	#N/A	#N/A	#N/A	#N/A	1.55	high mobility group box 1
ENSG00000185043	#N/A	#N/A	#N/A	#N/A	1.55	calcium and integrin binding 1 (calmyrin)
ENSG00000133398	#N/A	#N/A	#N/A	#N/A	1.54	mediator complex subunit 10
ENSG00000104332	#N/A	#N/A	#N/A	#N/A	1.54	secreted frizzled-related protein 1
ENSG00000186577	#N/A	#N/A	#N/A	#N/A	1.54	chromosome 6 open reading frame 1
ENSG00000176953	#N/A	#N/A	#N/A	#N/A	1.54	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein
ENSG00000163170	#N/A	#N/A	#N/A	#N/A	1.53	bolA family member 3
ENSG00000180992	#N/A	#N/A	#N/A	#N/A	1.53	mitochondrial ribosomal protein L14
ENSG00000120875	#N/A	#N/A	#N/A	#N/A	1.52	dual specificity phosphatase 4
ENSG00000116473	#N/A	#N/A	#N/A	#N/A	1.52	RAP1A, member of RAS oncogene family
ENSG00000205981	#N/A	#N/A	#N/A	#N/A	1.52	DnaJ (Hsp40) homolog, subfamily C, member 19
ENSG00000275724	#N/A	#N/A	#N/A	#N/A	1.51	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 3, 9kDa, isoform CRA_e; NDUFA3 protein; cDNA FLJ76508, highly similar to Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa (NDUFA3), mRNA
ENSG00000172336	#N/A	#N/A	#N/A	#N/A	1.51	POP7 homolog, ribonuclease P/MRP subunit
ENSG00000139233	#N/A	#N/A	#N/A	#N/A	1.51	LLP homolog, long-term synaptic facilitation (Aplysia)
ENSG00000164258	#N/A	#N/A	#N/A	#N/A	1.50	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
ENSG00000141837	#N/A	#N/A	#N/A	#N/A	1.50	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
ENSG00000120533	#N/A	#N/A	#N/A	#N/A	1.49	enhancer of yellow 2 homolog (Drosophila)
ENSG00000100142	#N/A	#N/A	#N/A	#N/A	1.48	polymerase (RNA) II (DNA directed) polypeptide F
ENSG00000122641	#N/A	#N/A	#N/A	#N/A	1.48	inhibin, beta A
ENSG00000197070	#N/A	#N/A	#N/A	#N/A	1.48	arrestin domain containing 1
ENSG00000125356	#N/A	#N/A	#N/A	#N/A	1.47	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
ENSG00000255717	#N/A	#N/A	#N/A	#N/A	1.47	small nucleolar RNA host gene 1
ENSG00000225921	#N/A	#N/A	#N/A	#N/A	1.45	nucleolar protein 7, 27kDa
ENSG00000171735	#N/A	#N/A	#N/A	#N/A	1.45	calmodulin binding transcription activator 1
ENSG00000124882	#N/A	#N/A	#N/A	#N/A	1.44	epiregulin
ENSG00000175606	#N/A	#N/A	#N/A	#N/A	1.43	transmembrane protein 70
ENSG00000167772	#N/A	#N/A	#N/A	#N/A	1.43	angiopoietin-like 4
ENSG00000164114	#N/A	#N/A	#N/A	#N/A	1.42	microtubule-associated protein 9
ENSG00000100836	#N/A	#N/A	#N/A	#N/A	1.42	poly(A) binding protein, nuclear 1
ENSG00000055044	#N/A	#N/A	#N/A	#N/A	1.42	NOP58 ribonucleoprotein
ENSG00000235162	#N/A	#N/A	#N/A	#N/A	1.42	chromosome 12 open reading frame 75
ENSG00000163463	#N/A	#N/A	#N/A	#N/A	1.39	keratinocyte associated protein 2
ENSG00000170088	#N/A	#N/A	#N/A	#N/A	1.38	transmembrane protein 192
ENSG00000178127	#N/A	#N/A	#N/A	#N/A	1.38	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
ENSG00000106803	#N/A	#N/A	#N/A	#N/A	1.38	Sec61 beta subunit
ENSG00000178896	#N/A	#N/A	#N/A	#N/A	1.38	exosome component 4
ENSG00000136888	#N/A	#N/A	#N/A	#N/A	1.37	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1
ENSG00000071462	#N/A	#N/A	#N/A	#N/A	1.37	Williams Beuren syndrome chromosome region 22
ENSG00000183726	#N/A	#N/A	#N/A	#N/A	1.37	transmembrane protein 50A
ENSG00000111237	#N/A	#N/A	#N/A	#N/A	1.37	VPS29 retromer complex component
ENSG00000164405	#N/A	#N/A	#N/A	#N/A	1.37	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa

FIGURE 1W

ENSG00000198265	#N/A	#N/A	#N/A	1.29	#N/A	helicase with zinc finger
ENSG00000113108	#N/A	#N/A	#N/A	1.29	#N/A	amyloid beta (A4) precursor protein-binding, family B, member 3
ENSG00000186470	#N/A	#N/A	#N/A	1.28	#N/A	butyrophilin, subfamily 3, member A2
ENSG00000109046	#N/A	#N/A	#N/A	1.28	#N/A	WD repeat and SOCS box containing 1
ENSG00000185808	#N/A	#N/A	#N/A	1.28	#N/A	phosphatidylinositol glycan anchor biosynthesis, class P
ENSG00000159055	#N/A	#N/A	#N/A	1.28	#N/A	MIS18 kinetochore protein A
ENSG00000164054	#N/A	#N/A	#N/A	1.28	#N/A	shisa family member 5
ENSG00000168961	#N/A	#N/A	#N/A	1.28	#N/A	lectin, galactoside-binding, soluble, 9
ENSG00000102265	#N/A	#N/A	#N/A	1.28	#N/A	TIMP metallopeptidase inhibitor 1
ENSG00000198951	#N/A	#N/A	#N/A	1.28	#N/A	N-acetylgalactosaminidase, alpha-
ENSG00000147439	#N/A	#N/A	#N/A	1.27	#N/A	bridging integrator 3
ENSG00000085224	#N/A	#N/A	#N/A	1.27	#N/A	alpha thalassemia/mental retardation syndrome X-linked
ENSG00000124067	#N/A	#N/A	#N/A	1.27	#N/A	solute carrier family 12 (potassium/chloride transporter), member 4
ENSG00000129810	#N/A	#N/A	#N/A	1.27	#N/A	shugoshin-like 1 (S. pombe)
ENSG00000145743	#N/A	#N/A	#N/A	1.27	#N/A	F-box and leucine-rich repeat protein 17
ENSG00000157349	#N/A	#N/A	#N/A	1.27	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19B
ENSG00000281794	#N/A	#N/A	#N/A	1.26	#N/A	long intergenic non-protein coding RNA 969
ENSG00000253230	#N/A	#N/A	#N/A	1.26	#N/A	long intergenic non-protein coding RNA 599
ENSG00000100599	#N/A	#N/A	#N/A	1.26	#N/A	Ras and Rab interactor 3
ENSG00000105372	#N/A	#N/A	#N/A	1.26	#N/A	ribosomal protein S19
ENSG00000068137	#N/A	#N/A	#N/A	1.26	#N/A	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
ENSG00000248092	#N/A	#N/A	#N/A	1.26	#N/A	NNT antisense RNA 1
ENSG00000132963	#N/A	#N/A	#N/A	1.26	2.08	proteasome maturation protein
ENSG00000130164	#N/A	#N/A	#N/A	1.26	#N/A	low density lipoprotein receptor
ENSG00000144034	#N/A	#N/A	#N/A	1.25	2.52	TP53RK binding protein
ENSG00000102977	#N/A	#N/A	#N/A	1.25	#N/A	adrenocortical dysplasia homolog (mouse)
ENSG00000128016	#N/A	#N/A	#N/A	1.25	#N/A	ZFP36 ring finger protein
ENSG00000117394	#N/A	#N/A	#N/A	1.25	#N/A	solute carrier family 2 (facilitated glucose transporter), member 1
ENSG00000163125	#N/A	#N/A	#N/A	1.25	1.52	regulation of nuclear pre-mRNA domain containing 2
ENSG00000229117	#N/A	#N/A	#N/A	1.24	#N/A	ribosomal protein L41
ENSG00000169499	#N/A	#N/A	#N/A	1.24	#N/A	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2
ENSG00000117614	#N/A	#N/A	#N/A	1.24	1.50	SYF2 pre-mRNA-splicing factor
ENSG00000082074	#N/A	#N/A	#N/A	1.24	#N/A	FYN binding protein
ENSG00000090013	#N/A	#N/A	#N/A	1.24	#N/A	biliverdin reductase B
ENSG00000135974	#N/A	#N/A	#N/A	1.24	#N/A	chromosome 2 open reading frame 49
ENSG00000132950	#N/A	#N/A	#N/A	1.24	#N/A	zinc finger, MYM-type 5
ENSG00000205423	#N/A	#N/A	#N/A	1.23	#N/A	CTD nuclear envelope phosphatase 1 regulatory subunit 1
ENSG00000143353	#N/A	#N/A	#N/A	1.23	#N/A	lysophospholipase-like 1
ENSG00000172725	#N/A	#N/A	#N/A	1.23	#N/A	coronin, actin binding protein, 1B
ENSG00000254999	#N/A	#N/A	#N/A	1.23	1.59	BRICK1, SCAR/WAVE actin-nucleating complex subunit
ENSG00000175727	#N/A	#N/A	#N/A	1.23	1.32	MLX interacting protein
ENSG00000221983	#N/A	#N/A	#N/A	1.23	1.41	ubiquitin A-52 residue ribosomal protein fusion product 1
ENSG00000143507	#N/A	#N/A	#N/A	1.22	#N/A	dual specificity phosphatase 10
ENSG00000239382	#N/A	#N/A	#N/A	1.22	#N/A	alkB homolog 6
ENSG00000118985	#N/A	#N/A	#N/A	1.22	#N/A	elongation factor, RNA polymerase II, 2

ENSG00000115363	#N/A	#N/A	#N/A	#N/A	1.37	eva-1 homolog A (C. elegans)
ENSG00000100889	#N/A	#N/A	#N/A	#N/A	1.37	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
ENSG00000104823	#N/A	#N/A	#N/A	#N/A	1.35	enoyl CoA hydratase 1, peroxisomal
ENSG00000100028	#N/A	#N/A	#N/A	#N/A	1.35	small nuclear ribonucleoprotein D3 polypeptide 18kDa
ENSG00000112667	#N/A	#N/A	#N/A	#N/A	1.35	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
ENSG00000146386	#N/A	#N/A	#N/A	#N/A	1.34	ABRA C-terminal like
ENSG00000131586	#N/A	#N/A	#N/A	#N/A	1.34	MRPL20
ENSG00000171813	#N/A	#N/A	#N/A	#N/A	1.34	PWWP domain containing 2B
ENSG00000111231	#N/A	#N/A	#N/A	#N/A	1.33	GPN-loop GTPase 3
ENSG00000136213	#N/A	#N/A	#N/A	#N/A	1.33	carbohydrate (chondroitin 4) sulfotransferase 12
ENSG00000171204	#N/A	#N/A	#N/A	#N/A	1.32	transmembrane protein 126B
ENSG00000138175	#N/A	#N/A	#N/A	#N/A	1.32	ADP-ribosylation factor-like 3
ENSG00000134049	#N/A	#N/A	#N/A	#N/A	1.32	immediate early response 3 interacting protein 1
ENSG00000105518	#N/A	#N/A	#N/A	#N/A	1.31	transmembrane protein 205
ENSG00000172465	#N/A	#N/A	#N/A	#N/A	1.31	transcription elongation factor A (SII)-like 1
ENSG00000108010	#N/A	#N/A	#N/A	#N/A	1.31	glutaredoxin 3
ENSG00000272835	#N/A	#N/A	#N/A	#N/A	1.31	single-pass membrane protein with aspartate-rich tail 1
ENSG00000162520	#N/A	#N/A	#N/A	#N/A	1.31	syncoilin, intermediate filament protein
ENSG00000136810	#N/A	#N/A	#N/A	#N/A	1.31	thioredoxin
ENSG00000206408	#N/A	#N/A	#N/A	#N/A	1.31	G patch domain and ankyrin repeats 1
ENSG00000165502	#N/A	#N/A	#N/A	#N/A	1.30	ribosomal protein L36a-like
ENSG00000111364	#N/A	#N/A	#N/A	#N/A	1.30	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
ENSG00000197019	#N/A	#N/A	#N/A	#N/A	1.30	SERTA domain containing 1
ENSG00000167747	#N/A	#N/A	#N/A	#N/A	1.30	chromosome 19 open reading frame 48
ENSG00000173915	#N/A	#N/A	#N/A	#N/A	1.30	up-regulated during skeletal muscle growth 5 homolog (mouse)
ENSG00000143106	#N/A	#N/A	#N/A	#N/A	1.30	proteasome (prosome, macropain) subunit, alpha type, 5
ENSG00000172977	#N/A	#N/A	#N/A	#N/A	1.29	K(lysine) acetyltransferase 5
ENSG00000108175	#N/A	#N/A	#N/A	#N/A	1.29	zinc finger, MIZ-type containing 1
ENSG00000172586	#N/A	#N/A	#N/A	#N/A	1.29	coiled-coil-helix-coiled-coil-helix domain containing 1
ENSG00000165782	#N/A	#N/A	#N/A	#N/A	1.28	transmembrane protein 55B
ENSG00000070010	#N/A	#N/A	#N/A	#N/A	1.28	ubiquitin fusion degradation 1 like (yeast)
ENSG00000150551	#N/A	#N/A	#N/A	#N/A	1.28	LY6/PLAUR domain containing 1
ENSG00000162300	#N/A	#N/A	#N/A	#N/A	1.28	zinc finger protein-like 1
ENSG00000090266	#N/A	#N/A	#N/A	#N/A	1.28	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
ENSG00000005075	#N/A	#N/A	#N/A	#N/A	1.28	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa
ENSG00000183527	#N/A	#N/A	#N/A	#N/A	1.27	proteasome (prosome, macropain) assembly chaperone 1
ENSG00000168653	#N/A	#N/A	#N/A	#N/A	1.27	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
ENSG00000170791	#N/A	#N/A	#N/A	#N/A	1.27	coiled-coil-helix-coiled-coil-helix domain containing 7
ENSG00000101182	#N/A	#N/A	#N/A	#N/A	1.26	proteasome (prosome, macropain) subunit, alpha type, 7
ENSG00000115350	#N/A	#N/A	#N/A	#N/A	1.26	polymerase (DNA-directed), epsilon 4, accessory subunit
ENSG00000171202	#N/A	#N/A	#N/A	#N/A	1.26	transmembrane protein 126A
ENSG00000148834	#N/A	#N/A	#N/A	#N/A	1.25	glutathione S-transferase omega 1
ENSG00000164032	#N/A	#N/A	#N/A	#N/A	1.25	H2A histone family, member Z
ENSG00000261740	#N/A	#N/A	#N/A	#N/A	1.25	Uncharacterized protein
ENSG00000143387	#N/A	#N/A	#N/A	#N/A	1.25	cathepsin K

FIGURE 1X

ENSG00000178802	#N/A	#N/A	#N/A	1.22	#N/A	mannose phosphate isomerase
ENSG00000135452	#N/A	#N/A	#N/A	1.22	#N/A	tetraspanin 31
ENSG00000227669	#N/A	#N/A	#N/A	1.22	#N/A	major histocompatibility complex, class I, H (pseudogene)
ENSG00000106617	#N/A	#N/A	#N/A	1.22	#N/A	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
ENSG00000117697	#N/A	#N/A	#N/A	1.22	1.25	NSL1, MIS12 kinetochore complex component
ENSG00000168255	#N/A	#N/A	#N/A	1.21	#N/A	polymerase (RNA) II (DNA directed) polypeptide J3
ENSG00000166128	#N/A	#N/A	#N/A	1.21	#N/A	RAB8B, member RAS oncogene family
ENSG00000129696	#N/A	#N/A	#N/A	1.21	#N/A	TELO2 interacting protein 2
ENSG00000141971	#N/A	#N/A	#N/A	1.21	#N/A	multivesicular body subunit 12A
ENSG00000145247	#N/A	#N/A	#N/A	1.21	1.50	OCIA domain containing 2
ENSG00000166341	#N/A	#N/A	#N/A	1.21	#N/A	dachsous cadherin-related 1
ENSG00000186010	#N/A	#N/A	#N/A	1.20	1.82	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
ENSG00000125971	#N/A	#N/A	#N/A	1.20	1.45	dynein, light chain, roadblock-type 1
ENSG00000160223	#N/A	#N/A	#N/A	1.20	#N/A	inducible T-cell co-stimulator ligand
ENSG00000165264	#N/A	#N/A	#N/A	1.20	1.14	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
ENSG00000163131	#N/A	#N/A	#N/A	1.20	#N/A	cathepsin S
ENSG00000158869	#N/A	#N/A	#N/A	1.20	#N/A	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
ENSG00000114439	#N/A	#N/A	#N/A	1.20	#N/A	bobby sox homolog (Drosophila)
ENSG00000114062	#N/A	#N/A	#N/A	1.20	#N/A	ubiquitin protein ligase E3A
ENSG00000162704	#N/A	#N/A	#N/A	1.19	#N/A	actin related protein 2/3 complex, subunit 5, 16kDa
ENSG00000102316	#N/A	#N/A	#N/A	1.19	#N/A	melanoma antigen family D2
ENSG00000005238	#N/A	#N/A	#N/A	1.19	#N/A	family with sequence similarity 214, member B
ENSG00000149257	#N/A	#N/A	#N/A	1.19	#N/A	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
ENSG00000084676	#N/A	#N/A	#N/A	1.18	#N/A	nuclear receptor coactivator 1
ENSG00000124766	#N/A	#N/A	#N/A	1.18	#N/A	SRY (sex determining region Y)-box 4
ENSG00000114391	#N/A	#N/A	#N/A	1.18	#N/A	ribosomal protein L24
ENSG00000159882	#N/A	#N/A	#N/A	1.18	#N/A	zinc finger protein 230
ENSG00000141428	#N/A	#N/A	#N/A	1.18	#N/A	chromosome 18 open reading frame 21
ENSG00000142687	#N/A	#N/A	#N/A	1.18	#N/A	KIAA0319-like
ENSG00000127540	#N/A	#N/A	#N/A	1.18	1.82	ubiquinol-cytochrome c reductase, complex III subunit XI
ENSG00000160753	#N/A	#N/A	#N/A	1.18	#N/A	RUN and SH3 domain containing 1
ENSG00000114796	#N/A	#N/A	#N/A	1.17	#N/A	kelch-like family member 24
ENSG00000196154	#N/A	#N/A	#N/A	1.17	#N/A	S100 calcium binding protein A4
ENSG00000177576	#N/A	#N/A	#N/A	1.17	#N/A	chromosome 18 open reading frame 32
ENSG00000164167	#N/A	#N/A	#N/A	1.17	#N/A	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000278461	#N/A	#N/A	#N/A	1.17	1.50	mitochondrial ribosomal protein S36
ENSG00000096996	#N/A	#N/A	#N/A	1.17	#N/A	interleukin 12 receptor, beta 1
ENSG00000137806	#N/A	#N/A	#N/A	1.16	1.27	NADH dehydrogenase (ubiquinone) complex I, assembly factor 1
ENSG00000175305	#N/A	#N/A	#N/A	1.16	#N/A	cyclin E2
ENSG00000185088	#N/A	#N/A	#N/A	1.16	1.76	ribosomal protein S27-like
ENSG00000104812	#N/A	#N/A	#N/A	1.16	#N/A	glycogen synthase 1 (muscle)
ENSG00000160049	#N/A	#N/A	#N/A	1.16	1.27	DNA fragmentation factor, 45kDa, alpha polypeptide

ENSG00000102007	#N/A	#N/A	#N/A	#N/A	1.24	proteolipid protein 2 (colonic epithelium-enriched)
ENSG00000078668	#N/A	#N/A	#N/A	#N/A	1.23	voltage-dependent anion channel 3
ENSG00000173163	#N/A	#N/A	#N/A	#N/A	1.23	copper metabolism (Murr1) domain containing 1
ENSG00000106355	#N/A	#N/A	#N/A	#N/A	1.23	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000183291	#N/A	#N/A	#N/A	#N/A	1.23	15 kDa selenoprotein
ENSG00000144681	#N/A	#N/A	#N/A	#N/A	1.22	SH3 and cysteine rich domain
ENSG00000135919	#N/A	#N/A	#N/A	#N/A	1.22	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
ENSG00000090581	#N/A	#N/A	#N/A	#N/A	1.22	N-acetylglucosamine-1-phosphate transferase, gamma subunit
ENSG00000135047	#N/A	#N/A	#N/A	#N/A	1.22	cathepsin L
ENSG00000213024	#N/A	#N/A	#N/A	#N/A	1.22	nucleoporin 62kDa
ENSG00000154719	#N/A	#N/A	#N/A	#N/A	1.21	mitochondrial ribosomal protein L39
ENSG00000078140	#N/A	#N/A	#N/A	#N/A	1.21	ubiquitin-conjugating enzyme E2K
ENSG00000150779	#N/A	#N/A	#N/A	#N/A	1.21	translocase of inner mitochondrial membrane 8 homolog B (yeast)
ENSG00000155115	#N/A	#N/A	#N/A	#N/A	1.21	general transcription factor IIIC, polypeptide 6, alpha 35kDa
ENSG00000102103	#N/A	#N/A	#N/A	#N/A	1.21	polyglutamine binding protein 1
ENSG00000206283	#N/A	#N/A	#N/A	#N/A	1.20	prefoldin subunit 6
ENSG00000103496	#N/A	#N/A	#N/A	#N/A	1.20	syntaxin 4
ENSG00000165996	#N/A	#N/A	#N/A	#N/A	1.19	3-hydroxyacyl-CoA dehydratase 1
ENSG00000187514	#N/A	#N/A	#N/A	#N/A	1.19	prothymosin, alpha
ENSG00000104131	#N/A	#N/A	#N/A	#N/A	1.19	eukaryotic translation initiation factor 3, subunit J
ENSG00000133997	#N/A	#N/A	#N/A	#N/A	1.19	mediator complex subunit 6
ENSG00000131876	#N/A	#N/A	#N/A	#N/A	1.19	small nuclear ribonucleoprotein polypeptide A'
ENSG00000256591	#N/A	#N/A	#N/A	#N/A	1.19	Uncharacterized protein
ENSG00000107404	#N/A	#N/A	#N/A	#N/A	1.19	dishevelled segment polarity protein 1
ENSG00000103152	#N/A	#N/A	#N/A	#N/A	1.19	N-methylpurine DNA glycosylase
ENSG00000120656	#N/A	#N/A	#N/A	#N/A	1.19	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
ENSG00000136003	#N/A	#N/A	#N/A	#N/A	1.18	iron-sulfur cluster assembly enzyme
ENSG00000273841	#N/A	#N/A	#N/A	#N/A	1.18	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
ENSG00000111775	#N/A	#N/A	#N/A	#N/A	1.18	cytochrome c oxidase subunit VIa polypeptide 1
ENSG00000182154	#N/A	#N/A	#N/A	#N/A	1.18	mitochondrial ribosomal protein L41
ENSG00000090674	#N/A	#N/A	#N/A	#N/A	1.18	mucolipin 1
ENSG00000147684	#N/A	#N/A	#N/A	#N/A	1.17	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
ENSG00000092020	#N/A	#N/A	#N/A	#N/A	1.17	protein phosphatase 2, regulatory subunit B", gamma
ENSG00000140307	#N/A	#N/A	#N/A	#N/A	1.17	general transcription factor IIA, 2, 12kDa
ENSG00000161281	#N/A	#N/A	#N/A	#N/A	1.17	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
ENSG00000176340	#N/A	#N/A	#N/A	#N/A	1.17	cytochrome c oxidase subunit VIIIA (ubiquitous)
ENSG00000155034	#N/A	#N/A	#N/A	#N/A	1.16	F-box and leucine-rich repeat protein 18
ENSG00000131732	#N/A	#N/A	#N/A	#N/A	1.16	zinc finger, CCHC domain containing 9
ENSG00000131462	#N/A	#N/A	#N/A	#N/A	1.16	tubulin, gamma 1
ENSG00000228907	#N/A	#N/A	#N/A	#N/A	1.15	ring finger protein 5, E3 ubiquitin protein ligase
ENSG00000171621	#N/A	#N/A	#N/A	#N/A	1.15	splA/ryanodine receptor domain and SOCS box containing 1
ENSG00000126653	#N/A	#N/A	#N/A	#N/A	1.15	nuclear speckle splicing regulatory protein 1

FIGURE 1Y

ENSG00000197324	#N/A	#N/A	#N/A	1.16	#N/A	low density lipoprotein receptor-related protein 10
ENSG00000196628	#N/A	#N/A	#N/A	1.16	#N/A	transcription factor 4
ENSG00000269858	#N/A	#N/A	#N/A	1.16	#N/A	egl-9 family hypoxia-inducible factor 2
ENSG00000134248	#N/A	#N/A	#N/A	1.16	1.73	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5
ENSG00000223745	#N/A	#N/A	#N/A	1.16	#N/A	RP4-717I23.3
ENSG00000158417	#N/A	#N/A	#N/A	1.16	2.14	eukaryotic translation initiation factor 5B
ENSG00000185950	#N/A	#N/A	#N/A	1.15	#N/A	insulin receptor substrate 2
ENSG00000007047	#N/A	#N/A	#N/A	1.15	#N/A	MAP/microtubule affinity-regulating kinase 4
ENSG00000105220	#N/A	#N/A	#N/A	1.15	#N/A	glucose-6-phosphate isomerase
ENSG00000153113	#N/A	#N/A	#N/A	1.15	#N/A	calpastatin
ENSG00000135926	#N/A	#N/A	#N/A	1.15	#N/A	transmembrane BAX inhibitor motif containing 1
ENSG00000145050	#N/A	#N/A	#N/A	1.15	1.56	mesencephalic astrocyte-derived neurotrophic factor
ENSG00000183648	#N/A	#N/A	#N/A	1.14	1.45	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
ENSG00000113732	#N/A	#N/A	#N/A	1.14	1.49	ATPase, H+ transporting. lysosomal 9kDa, V0 subunit e1
ENSG00000124006	#N/A	#N/A	#N/A	1.14	#N/A	obscurin-like 1
ENSG00000105856	#N/A	#N/A	#N/A	1.14	#N/A	HMG-box transcription factor 1
ENSG00000196507	#N/A	#N/A	#N/A	1.14	1.28	transcription elongation factor A (SII)-like 3
ENSG00000187118	#N/A	#N/A	#N/A	1.14	#N/A	C-x(9)-C motif containing 1
ENSG00000166928	#N/A	#N/A	#N/A	1.14	#N/A	membrane-spanning 4-domains, subfamily A, member 14
ENSG00000167625	#N/A	#N/A	#N/A	1.14	#N/A	zinc finger protein 526
ENSG00000102144	#N/A	#N/A	#N/A	1.13	#N/A	phosphoglycerate kinase 1
ENSG00000174282	#N/A	#N/A	#N/A	1.13	#N/A	zinc finger and BTB domain containing 4
ENSG00000156535	#N/A	#N/A	#N/A	1.13	#N/A	CD109 molecule
ENSG00000229252	#N/A	#N/A	#N/A	1.13	#N/A	major histocompatibility complex, class I, E
ENSG00000134954	#N/A	#N/A	#N/A	1.13	#N/A	v-ets avian erythroblastosis virus E26 oncogene homolog 1
ENSG00000275199	#N/A	#N/A	#N/A	1.13	#N/A	v-akt murine thymoma viral oncogene homolog 3
ENSG00000076650	#N/A	#N/A	#N/A	1.13	#N/A	G patch domain containing 1
ENSG00000117616	#N/A	#N/A	#N/A	1.13	#N/A	arginine/serine-rich protein 1
ENSG00000114544	#N/A	#N/A	#N/A	1.13	#N/A	solute carrier family 41, member 3
ENSG00000075711	#N/A	#N/A	#N/A	1.13	#N/A	discs, large homolog 1 (Drosophila)
ENSG00000005448	#N/A	#N/A	#N/A	1.13	#N/A	WD repeat domain 54
ENSG00000088854	#N/A	#N/A	#N/A	1.13	#N/A	chromosome 20 open reading frame 194
ENSG00000265681	#N/A	#N/A	#N/A	1.13	#N/A	ribosomal protein L17
ENSG00000168802	#N/A	#N/A	#N/A	1.12	#N/A	chromosome transmission fidelity factor 8
ENSG00000139684	#N/A	#N/A	#N/A	1.12	#N/A	esterase D
ENSG00000008324	#N/A	#N/A	#N/A	1.12	#N/A	synovial sarcoma translocation gene on chromosome 18-like 2
ENSG00000124098	#N/A	#N/A	#N/A	1.12	#N/A	family with sequence similarity 210, member B
ENSG00000170315	#N/A	#N/A	#N/A	1.12	#N/A	ubiquitin B
ENSG00000064393	#N/A	#N/A	#N/A	1.12	#N/A	homeodomain interacting protein kinase 2
ENSG00000177200	#N/A	#N/A	#N/A	1.12	#N/A	chromodomain helicase DNA binding protein 9
ENSG00000105640	#N/A	#N/A	#N/A	1.12	#N/A	ribosomal protein L18a
ENSG00000006534	#N/A	#N/A	#N/A	1.12	#N/A	aldehyde dehydrogenase 3 family, member B1
ENSG00000276879	#N/A	#N/A	#N/A	1.12	#N/A	interferon, alpha-inducible protein 27-like 2
ENSG00000125870	#N/A	#N/A	#N/A	1.11	1.33	small nuclear ribonucleoprotein polypeptide B
ENSG00000164074	#N/A	#N/A	#N/A	1.11	#N/A	chromosome 4 open reading frame 29

ENSG00000177889	#N/A	#N/A	#N/A	#N/A	1.15	ubiquitin-conjugating enzyme E2N
ENSG00000159199	#N/A	#N/A	#N/A	#N/A	1.15	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1 (subunit 9)
ENSG00000128708	#N/A	#N/A	#N/A	#N/A	1.14	histone acetyltransferase 1
ENSG00000162961	#N/A	#N/A	#N/A	#N/A	1.14	dpy-30 histone methyltransferase complex regulatory subunit
ENSG00000169062	#N/A	#N/A	#N/A	#N/A	1.14	UPF3 regulator of nonsense transcripts homolog A (yeast)
ENSG00000105379	#N/A	#N/A	#N/A	#N/A	1.14	electron-transfer-flavoprotein, beta polypeptide
ENSG00000275145	#N/A	#N/A	#N/A	#N/A	1.14	FSHD region gene 1
ENSG00000163281	#N/A	#N/A	#N/A	#N/A	1.14	glucosamine-6-phosphate deaminase 2
ENSG00000143314	#N/A	#N/A	#N/A	#N/A	1.14	mitochondrial ribosomal protein L24
ENSG00000127184	#N/A	#N/A	#N/A	#N/A	1.14	cytochrome c oxidase subunit VIIc
ENSG00000277359	#N/A	#N/A	#N/A	#N/A	1.13	40S ribosomal protein S9; Ribosomal protein S9, isoform CRA_c
ENSG00000105755	#N/A	#N/A	#N/A	#N/A	1.13	ethylmalonic encephalopathy 1
ENSG00000168734	#N/A	#N/A	#N/A	#N/A	1.13	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
ENSG00000105364	#N/A	#N/A	#N/A	#N/A	1.12	mitochondrial ribosomal protein L4
ENSG00000159079	#N/A	#N/A	#N/A	#N/A	1.12	chromosome 21 open reading frame 59
ENSG00000105202	#N/A	#N/A	#N/A	#N/A	1.12	fibrillarin
ENSG00000136942	#N/A	#N/A	#N/A	#N/A	1.12	ribosomal protein L35
ENSG00000125835	#N/A	#N/A	#N/A	#N/A	1.12	small nuclear ribonucleoprotein polypeptides B and B1
ENSG00000198840	#N/A	#N/A	#N/A	#N/A	1.12	mitochondrially encoded NADH dehydrogenase 3
ENSG00000185222	#N/A	#N/A	#N/A	#N/A	1.11	WW domain binding protein 5
ENSG00000147533	#N/A	#N/A	#N/A	#N/A	1.11	golgin A7
ENSG00000100632	#N/A	#N/A	#N/A	#N/A	1.11	enhancer of rudimentary homolog (Drosophila)
ENSG00000104915	#N/A	#N/A	#N/A	#N/A	1.11	syntaxin 10
ENSG00000188643	#N/A	#N/A	#N/A	#N/A	1.11	S100 calcium binding protein A16
ENSG00000130766	#N/A	#N/A	#N/A	#N/A	1.11	sestrin 2
ENSG00000113068	#N/A	#N/A	#N/A	#N/A	1.11	prefoldin subunit 1
ENSG00000173141	#N/A	#N/A	#N/A	#N/A	1.10	mitochondrial ribosomal protein L57
ENSG00000054148	#N/A	#N/A	#N/A	#N/A	1.10	phosphohistidine phosphatase 1
ENSG00000147996	#N/A	#N/A	#N/A	#N/A	1.10	COBW domain containing 5
ENSG00000083457	#N/A	#N/A	#N/A	#N/A	1.10	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
ENSG00000117280	#N/A	#N/A	#N/A	#N/A	1.10	RAB29, member RAS oncogene family
ENSG00000157613	#N/A	#N/A	#N/A	#N/A	1.10	cAMP responsive element binding protein 3-like 1
ENSG00000174021	#N/A	#N/A	#N/A	#N/A	1.10	guanine nucleotide binding protein (G protein), gamma 5
ENSG00000133641	#N/A	#N/A	#N/A	#N/A	1.10	chromosome 12 open reading frame 29
ENSG00000101843	#N/A	#N/A	#N/A	#N/A	1.09	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10
ENSG00000138785	#N/A	#N/A	#N/A	#N/A	1.09	integrator complex subunit 12
ENSG00000175334	#N/A	#N/A	#N/A	#N/A	1.09	barrier to autointegration factor 1
ENSG00000104979	#N/A	#N/A	#N/A	#N/A	1.09	chromosome 19 open reading frame 53
ENSG00000070423	#N/A	#N/A	#N/A	#N/A	1.09	ring finger protein 126
ENSG00000147586	#N/A	#N/A	#N/A	#N/A	1.08	mitochondrial ribosomal protein S28
ENSG00000186283	#N/A	#N/A	#N/A	#N/A	1.08	torsin family 3, member A
ENSG00000162783	#N/A	#N/A	#N/A	#N/A	1.08	immediate early response 5
ENSG00000162407	#N/A	#N/A	#N/A	#N/A	1.08	phosphatidic acid phosphatase type 2B
ENSG00000160201	#N/A	#N/A	#N/A	#N/A	1.08	U2 small nuclear RNA auxiliary factor 1
ENSG00000257727	#N/A	#N/A	#N/A	#N/A	1.08	canopy FGF signaling regulator 2

FIGURE 1Z

ENSG00000163110	#N/A	#N/A	#N/A	1.11	#N/A	PDZ and LIM domain 5
ENSG00000164088	#N/A	#N/A	#N/A	1.11	#N/A	protein phosphatase, Mg2+/Mn2+ dependent, 1M
ENSG00000125354	#N/A	#N/A	#N/A	1.11	#N/A	septin 6
ENSG00000130311	#N/A	#N/A	#N/A	1.10	1.42	DET1 and DDB1 associated 1
ENSG00000206503	#N/A	#N/A	#N/A	1.10	#N/A	major histocompatibility complex, class I, A
ENSG00000141298	#N/A	#N/A	#N/A	1.10	#N/A	slingshot protein phosphatase 2
ENSG00000116205	#N/A	#N/A	#N/A	1.10	#N/A	transcription elongation factor A (SII) N-terminal and central domain containing 2
ENSG00000237765	#N/A	#N/A	#N/A	1.10	1.23	family with sequence similarity 200, member B
ENSG00000107738	#N/A	#N/A	#N/A	1.09	#N/A	chromosome 10 open reading frame 54
ENSG00000038002	#N/A	#N/A	#N/A	1.09	#N/A	aspartylglucosaminidase
ENSG00000153250	#N/A	#N/A	#N/A	1.09	#N/A	RNA binding motif, single stranded interacting protein 1
ENSG00000161203	#N/A	#N/A	#N/A	1.09	#N/A	adaptor-related protein complex 2, mu 1 subunit
ENSG00000132694	#N/A	#N/A	#N/A	1.09	#N/A	Rho guanine nucleotide exchange factor (GEF) 11
ENSG00000184752	#N/A	#N/A	#N/A	1.09	2.00	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
ENSG00000133246	#N/A	#N/A	#N/A	1.09	#N/A	PML-RARA regulated adaptor molecule 1
ENSG00000125037	#N/A	#N/A	#N/A	1.09	#N/A	ER membrane protein complex subunit 3
ENSG00000241343	#N/A	#N/A	#N/A	1.09	1.18	ribosomal protein L36a
ENSG00000163960	#N/A	#N/A	#N/A	1.09	#N/A	UBX domain protein 7
ENSG00000108599	#N/A	#N/A	#N/A	1.09	#N/A	A kinase (PRKA) anchor protein 10
ENSG00000150540	#N/A	#N/A	#N/A	1.09	#N/A	histamine N-methyltransferase
ENSG00000082996	#N/A	#N/A	#N/A	1.08	#N/A	ring finger protein 13
ENSG00000110492	#N/A	#N/A	#N/A	1.08	#N/A	midkine (neurite growth-promoting factor 2)
ENSG00000105849	#N/A	#N/A	#N/A	1.08	1.33	TWIST neighbor
ENSG00000160058	#N/A	#N/A	#N/A	1.08	#N/A	BSD domain containing 1
ENSG00000105223	#N/A	#N/A	#N/A	1.08	#N/A	phospholipase D family, member 3
ENSG00000129636	#N/A	#N/A	#N/A	1.08	#N/A	integrin alpha FG-GAP repeat containing 1
ENSG00000034510	#N/A	#N/A	#N/A	1.08	#N/A	thymosin beta 10
ENSG00000143119	#N/A	#N/A	#N/A	1.08	#N/A	CD53 molecule
ENSG00000132581	#N/A	#N/A	#N/A	1.07	1.11	stromal cell-derived factor 2
ENSG00000105404	#N/A	#N/A	#N/A	1.07	#N/A	Rab acceptor 1 (prenylated)
ENSG00000205220	#N/A	#N/A	#N/A	1.07	#N/A	proteasome (prosome, macropain) subunit, beta type, 10
ENSG00000262349	#N/A	#N/A	#N/A	1.07	#N/A	RP11-620J15.3
ENSG00000143013	#N/A	#N/A	#N/A	1.07	#N/A	LIM domain only 4

ENSG00000136868	#N/A	#N/A	#N/A	#N/A	1.08	solute carrier family 31 (copper transporter), member 1
ENSG00000138495	#N/A	#N/A	#N/A	#N/A	1.08	COX17 cytochrome c oxidase copper chaperone
ENSG00000100442	#N/A	#N/A	#N/A	#N/A	1.07	FK506 binding protein 3, 25kDa
ENSG00000182117	#N/A	#N/A	#N/A	#N/A	1.07	NOP10 ribonucleoprotein
ENSG00000185022	#N/A	#N/A	#N/A	#N/A	1.07	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
ENSG00000156467	#N/A	#N/A	#N/A	#N/A	1.07	ubiquinol-cytochrome c reductase binding protein
ENSG00000115446	#N/A	#N/A	#N/A	#N/A	1.07	unc-50 homolog (C. elegans)
ENSG00000171421	#N/A	#N/A	#N/A	#N/A	1.06	mitochondrial ribosomal protein L36
ENSG00000188612	#N/A	#N/A	#N/A	#N/A	1.06	small ubiquitin-like modifier 2
ENSG00000157881	#N/A	#N/A	#N/A	#N/A	1.06	pantothenate kinase 4
ENSG00000131495	#N/A	#N/A	#N/A	#N/A	1.06	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
ENSG00000152684	#N/A	#N/A	#N/A	#N/A	1.06	pelota homolog (Drosophila)
ENSG00000118363	#N/A	#N/A	#N/A	#N/A	1.06	signal peptidase complex subunit 2
ENSG00000113460	#N/A	#N/A	#N/A	#N/A	1.05	BRX1, biogenesis of ribosomes
ENSG00000167641	#N/A	#N/A	#N/A	#N/A	1.05	protein phosphatase 1, regulatory (inhibitor) subunit 14A
ENSG00000213619	#N/A	#N/A	#N/A	#N/A	1.05	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
ENSG00000128463	#N/A	#N/A	#N/A	#N/A	1.05	ER membrane protein complex subunit 4
ENSG00000010165	#N/A	#N/A	#N/A	#N/A	1.05	methyltransferase like 13
ENSG00000173465	#N/A	#N/A	#N/A	#N/A	1.05	Sjogren syndrome/scleroderma autoantigen 1
ENSG00000117395	#N/A	#N/A	#N/A	#N/A	1.04	EBNA1 binding protein 2
ENSG00000160888	#N/A	#N/A	#N/A	#N/A	1.04	immediate early response 2
ENSG00000141560	#N/A	#N/A	#N/A	#N/A	1.04	fructosamine 3 kinase related protein
ENSG00000185651	#N/A	#N/A	#N/A	#N/A	1.04	ubiquitin-conjugating enzyme E2L 3
ENSG00000115539	#N/A	#N/A	#N/A	#N/A	1.03	phosducin-like 3
ENSG00000128609	#N/A	#N/A	#N/A	#N/A	1.03	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
ENSG00000167283	#N/A	#N/A	#N/A	#N/A	1.02	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G
ENSG00000118292	#N/A	#N/A	#N/A	#N/A	1.02	chromosome 1 open reading frame 54
ENSG00000237403	#N/A	#N/A	#N/A	#N/A	1.02	protein phosphatase 1, regulatory (inhibitor) subunit 11
ENSG00000183520	#N/A	#N/A	#N/A	#N/A	1.02	UTP11-like, U3 small nucleolar ribonucleoprotein (yeast)
ENSG00000116750	#N/A	#N/A	#N/A	#N/A	1.02	ubiquitin carboxyl-terminal hydrolase L5
ENSG00000146574	#N/A	#N/A	#N/A	#N/A	1.02	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated
ENSG00000183011	#N/A	#N/A	#N/A	#N/A	1.01	N(alpha)-acetyltransferase 38, NatC auxiliary subunit
ENSG00000232112	#N/A	#N/A	#N/A	#N/A	1.01	translation machinery associated 7 homolog (S. cerevisiae)
ENSG00000112096	#N/A	#N/A	#N/A	#N/A	1.01	superoxide dismutase 2, mitochondrial

FIGURE 2A

Figure 2: Host miRNA transcriptomics data during EGS infections of MM6 or NSC cells. Differential expression analysis of human miRNA genes from MM6 or NSC cells infected with T. gondii EGS strain for 18 hours.

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
hsa-mir-708-5p	-11.46	-2.19
hsa-mir-708-3p	-10.28	-3.19
hsa-mir-29b-3p	-5.46	-1.23
ENST00000474173	-9.95	-10.14
hsa-mir-32-5p	-5.48	#N/A
hsa-mir-142-3p	-4.62	-3.24
ENST00000500868	-6.60	-8.05
ENST00000500633	-6.57	-9.22
hsa-mir-3656-3p	-9.66	-2.65
hsa-mir-19a-3p	-3.65	-1.59
ENST00000499697	-5.03	-6.24
ENST00000498989	-4.61	-9.27
hsa-mir-101-3p	-3.27	#N/A
ENST00000500011	-5.20	-4.72
hsa-mir-210-5p	-7.79	#N/A
hsa-mir-34c-5p	-7.76	#N/A
hsa-mir-218-5p	-5.28	#N/A
ENST00000501638	-4.61	-6.90
hsa-mir-212-3p	-5.02	#N/A
ENST00000500409	-5.57	-9.86
ENST00000501230	-4.65	#N/A
ENST00000500974	-4.29	-6.16
hsa-mir-132-5p	-4.09	#N/A
hsa-mir-10b-5p	-5.43	-2.77
hsa-mir-455-5p	-3.82	-1.03
hsa-mir-21-3p	-3.49	#N/A
hsa-mir-199a-5p	-4.21	1.41
ENST00000384148	3.83	#N/A
hsa-mir-132-3p	-3.23	#N/A
hsa-mir-142-5p	-3.27	-3.39
ENST00000500340	-4.55	-10.64
ENST00000487032	-4.88	-6.20
hsa-mir-381-3p	-4.26	#N/A
hsa-mir-374a-3p	-3.87	#N/A
hsa-mir-212-5p	-4.29	#N/A
hsa-mir-19b-3p	-2.65	-1.53

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
ENST00000384610	-2.08	#N/A
ENST00000384238	2.17	#N/A
hsa-mir-140-5p	-2.23	1.04
ENST00000500700	1.82	#N/A
ENST00000363657	-2.50	#N/A
hsa-mir-652-5p	-2.45	#N/A
ENST00000364950	2.12	#N/A
ENST00000452327	2.70	#N/A
hsa-mir-331-3p	-2.25	#N/A
ENST00000365663	3.48	#N/A
hsa-mir-4531-3p	-2.94	#N/A
ENST00000408175	2.02	#N/A
ENST00000384483	2.68	#N/A
ENST00000364596	2.10	#N/A
ENST00000365625	2.13	#N/A
hsa-mir-6087-5p	-2.30	#N/A
ENST00000384388	2.78	#N/A
hsa-mir-143-3p	-2.04	#N/A
ENST00000384240	2.13	-2.57
ENST00000384526	2.69	#N/A
ENST00000502243	2.40	#N/A
ENST00000490494	-3.34	#N/A
ENST00000365462	2.09	#N/A
ENST00000411366	2.08	-2.72
ENST00000383919	2.03	#N/A
ENST00000459329	2.14	#N/A
ENST00000408454	1.87	2.15
hsa-mir-1273h-5p	2.08	#N/A
ENST00000364273	-2.23	#N/A
ENST00000363894	2.14	#N/A
hsa-mir-92a-5p	1.99	#N/A
ENST00000501184	-3.02	#N/A
ENST00000365197	2.56	#N/A
ENST00000363640	2.02	#N/A
ENST00000486682	-2.38	-7.19
ENST00000365068	1.99	#N/A

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
ENST00000410312	1.93	#N/A
ENST00000461378	-1.57	#N/A
hsa-mir-1307-3p	1.45	#N/A
ENST00000458797	-1.36	#N/A
ENST00000500188	-1.77	#N/A
ENST00000362765	1.49	-1.54
ENST00000364829	1.74	#N/A
ENST00000492060	#N/A	-4.44
ENST00000461045	#N/A	-3.00
ENST00000501999	#N/A	-5.48
ENST00000501119	#N/A	-5.04
hsa-mir-155-5p	#N/A	3.53
ENST00000501823	#N/A	-5.54
hsa-mir-95-3p	#N/A	-4.08
ENST00000493956	#N/A	-1.90
ENST00000463737	#N/A	-1.84
ENST00000480364	#N/A	-2.93
ENST00000498894	#N/A	-4.31
hsa-mir-7974-3p	#N/A	2.69
ENST00000501120	#N/A	-4.02
ENST00000500692	#N/A	2.78
ENST00000500159	#N/A	-2.59
ENST00000499784	#N/A	-3.99
ENST00000491379	#N/A	-1.85
ENST00000500638	#N/A	-4.24
ENST00000479524	#N/A	-1.51
hsa-mir-486-5p	#N/A	-3.23
ENST00000458546	#N/A	2.69
ENST00000500895	#N/A	2.29
ENST00000468873	#N/A	4.77
ENST00000468972	#N/A	-2.69
ENST00000491707	#N/A	-2.21
hsa-mir-1268a-5p	#N/A	2.87
ENST00000501850	#N/A	-7.62
ENST00000489722	#N/A	-2.07
hsa-mir-181b-5p	#N/A	1.41

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
ENST00000363130	#N/A	-1.04
ENST00000365274	#N/A	-1.11
hsa-mir-410-3p	#N/A	1.07
ENST00000364699	#N/A	-1.12
hsa-mir-7976-5p	#N/A	1.47
ENST00000384335	#N/A	-1.21
ENST00000502222	#N/A	2.25
ENST00000364685	#N/A	-1.18
ENST00000401362	#N/A	1.91
ENST00000385578	#N/A	1.17

FIGURE 2B

hsa-mir-3179-3p	3.39	#N/A
ENST00000363443	-4.61	#N/A
ENST00000499746	-4.64	-9.78
hsa-mir-424-5p	-3.01	#N/A
ENST00000364915	4.86	#N/A
ENST00000410796	-3.51	-4.69
ENST00000471237	1.78	1.28
ENST00000489413	5.42	#N/A
hsa-mir-362-3p	-4.94	#N/A
ENST00000364931	3.72	3.90
ENST00000363549	4.96	#N/A
hsa-mir-4488-5p	-3.98	-3.11
ENST00000500066	-4.75	#N/A
ENST00000500656	3.30	#N/A
hsa-mir-151a-5p	-4.30	-1.88
hsa-mir-30a-5p	-2.87	#N/A
ENST00000500845	-4.48	#N/A
ENST00000499817	-3.61	#N/A
ENST00000363367	2.99	#N/A
hsa-mir-140-3p	-3.07	1.73
ENST00000501386	-4.68	-6.83
ENST00000498132	2.95	#N/A
hsa-mir-374a-5p	-2.73	#N/A
hsa-mir-20a-5p	-1.72	#N/A
hsa-mir-379-5p	-3.92	#N/A
hsa-mir-148a-3p	-2.11	#N/A
ENST00000499637	2.82	#N/A
hsa-mir-3065-5p	-3.45	#N/A
hsa-mir-301a-3p	-3.39	#N/A
hsa-mir-370-3p	-4.31	1.80
hsa-mir-590-3p	-2.63	#N/A
ENST00000458848	2.94	#N/A
ENST00000411281	-4.29	#N/A
hsa-mir-30e-5p	-2.60	#N/A
ENST00000481863	-3.29	#N/A
ENST00000502220	2.83	#N/A
ENST00000480442	-2.58	#N/A
hsa-mir-100-5p	-3.22	#N/A
ENST00000365477	-3.17	#N/A
hsa-mir-184-3p	-3.71	-1.45
ENST00000470561	2.84	1.31
hsa-mir-199b-5p	-2.79	#N/A
ENST00000408139	-2.57	#N/A
ENST00000459424	2.71	#N/A
ENST00000408564	2.78	#N/A

ENST00000362915	3.36	#N/A
ENST00000363651	1.99	#N/A
ENST00000384504	1.94	#N/A
hsa-mir-124-3p	-2.05	#N/A
ENST00000384312	3.77	#N/A
ENST00000474558	-5.43	#N/A
ENST00000498916	3.80	#N/A
ENST00000499645	-2.06	#N/A
ENST00000363674	2.04	-2.38
hsa-mir-152-5p	-2.07	#N/A
hsa-mir-1299-3p	-3.51	#N/A
ENST00000384254	2.62	#N/A
ENST00000499152	1.88	#N/A
ENST00000363985	1.92	-1.32
ENST00000500276	-2.45	#N/A
ENST00000500380	-2.84	#N/A
ENST00000365487	2.30	#N/A
hsa-mir-1273h-3p	1.87	#N/A
ENST00000363248	2.04	#N/A
ENST00000475825	-2.00	-1.77
hsa-mir-183-5p	1.81	-1.77
ENST00000499376	-5.79	#N/A
ENST00000487435	-2.38	#N/A
ENST00000384248	2.25	#N/A
ENST00000383994	2.09	#N/A
ENST00000499568	-2.94	-7.55
hsa-mir-660-5p	-1.94	#N/A
ENST00000384677	1.85	#N/A
ENST00000500705	-2.62	#N/A
ENST00000365046	2.74	#N/A
ENST00000500169	2.74	#N/A
ENST00000362412	2.38	#N/A
ENST00000465104	-1.89	#N/A
hsa-mir-494-3p	-2.78	#N/A
ENST00000384376	2.59	#N/A
ENST00000384762	2.44	#N/A
ENST00000487797	-1.74	#N/A
ENST00000501255	-2.32	#N/A
ENST00000364805	2.04	#N/A
ENST00000362918	2.03	#N/A
ENST00000384686	2.49	#N/A
ENST00000484473	-3.21	#N/A
ENST00000499929	-3.27	#N/A
ENST00000384373	2.13	#N/A
ENST00000384068	2.50	#N/A

ENST00000502135	#N/A	-3.51
hsa-mir-30a-3p	#N/A	1.42
hsa-mir-30c-3p	#N/A	1.70
ENST00000458878	#N/A	-2.06
ENST00000470405	#N/A	-4.22
ENST00000499710	#N/A	-2.31
ENST00000488123	#N/A	-1.31
ENST00000478633	#N/A	-1.91
ENST00000410413	#N/A	1.92
ENST00000501562	#N/A	-3.53
hsa-mir-574-5p	#N/A	1.49
ENST00000498924	#N/A	-7.09
ENST00000364315	#N/A	1.29
ENST00000363473	#N/A	1.25
ENST00000365651	#N/A	1.24
ENST00000362400	#N/A	1.25
ENST00000364485	#N/A	1.24
ENST00000496486	#N/A	-1.53
ENST00000365387	#N/A	1.24
ENST00000501284	#N/A	-4.74
ENST00000365055	#N/A	1.23
ENST00000363500	#N/A	1.24
ENST00000363511	#N/A	1.24
ENST00000362482	#N/A	1.24
ENST00000365656	#N/A	1.25
ENST00000491757	#N/A	-4.79
ENST00000410545	#N/A	1.79
ENST00000363040	#N/A	1.24
ENST00000364718	#N/A	1.24
ENST00000362464	#N/A	1.23
ENST00000363439	#N/A	-1.96
ENST00000363962	#N/A	-2.46
ENST00000410396	#N/A	1.26
ENST00000362526	#N/A	1.22
ENST00000500227	#N/A	-3.53
ENST00000362467	#N/A	1.23
ENST00000363754	#N/A	1.22
ENST00000500354	#N/A	-3.66
hsa-mir-93-5p	#N/A	1.22
hsa-mir-148b-3p	#N/A	1.16
ENST00000468070	#N/A	-3.51
ENST00000385582	#N/A	1.24
ENST00000363194	#N/A	-1.86
ENST00000483476	#N/A	-1.07
hsa-mir-3152-5p	#N/A	3.37

FIGURE 2C

ENST00000500754	-3.39	#N/A
ENST00000473313	-2.37	#N/A
hsa-mir-20a-3p	-2.55	#N/A
ENST00000489202	-2.70	-2.04
hsa-mir-30b-5p	-2.76	#N/A
hsa-mir-1307-5p	-2.59	#N/A
hsa-mir-29c-3p	-3.22	#N/A
ENST00000365574	2.88	2.02
ENST00000384314	2.96	#N/A
ENST00000500611	-3.82	-3.52
ENST00000364572	3.27	#N/A
ENST00000485443	-2.74	-1.38
hsa-mir-34a-5p	-3.03	#N/A
ENST00000384273	3.21	#N/A
ENST00000391230	-3.72	-5.34
hsa-mir-493-3p	-3.70	#N/A
ENST00000501131	5.23	#N/A
ENST00000499694	-3.29	#N/A
ENST00000499716	-3.34	#N/A
hsa-mir-1304-5p	2.62	#N/A
ENST00000500755	-3.42	-2.84
ENST00000365467	2.57	#N/A
ENST00000463508	1.59	1.35
ENST00000384084	2.72	#N/A
ENST00000364784	2.55	#N/A
ENST00000384106	3.24	#N/A
ENST00000493557	-2.78	#N/A
ENST00000362808	3.01	#N/A
ENST00000362881	3.14	#N/A
ENST00000363299	2.58	2.16
ENST00000383873	2.84	#N/A
ENST00000363250	3.36	#N/A
ENST00000384741	2.98	#N/A
ENST00000384743	2.92	#N/A
ENST00000364542	2.73	#N/A
hsa-mir-4301-5p	3.54	#N/A
hsa-mir-29c-5p	-3.39	#N/A
ENST00000365439	2.70	#N/A
ENST00000384650	2.72	#N/A
ENST00000384547	3.00	1.63
hsa-mir-134-5p	-4.20	#N/A
ENST00000501210	-2.79	#N/A
ENST00000362507	2.88	5.45
ENST00000384413	2.70	1.18
ENST00000491051	-2.69	#N/A

ENST00000364407	2.02	#N/A
ENST00000458898	2.05	#N/A
ENST00000500772	-2.10	#N/A
ENST00000470693	1.94	#N/A
ENST00000390872	1.95	#N/A
ENST00000501958	-2.27	#N/A
ENST00000363389	1.84	#N/A
ENST00000490522	-1.70	#N/A
ENST00000363880	1.92	#N/A
ENST00000501780	-2.66	#N/A
ENST00000499816	-3.21	-3.40
ENST00000502117	-1.94	#N/A
hsa-mir-191-3p	1.68	#N/A
ENST00000384627	2.16	#N/A
ENST00000410868	1.82	#N/A
hsa-mir-20b-5p	-1.72	#N/A
ENST00000384268	1.96	-1.66
ENST00000501629	-1.82	#N/A
ENST00000362512	2.63	#N/A
ENST00000410494	1.79	#N/A
ENST00000384753	1.94	#N/A
ENST00000501143	-3.31	#N/A
ENST00000384087	1.79	#N/A
ENST00000472430	-2.56	-2.83
ENST00000476501	-2.56	#N/A
ENST00000499786	-2.27	#N/A
ENST00000363963	1.78	#N/A
ENST00000384708	1.86	#N/A
ENST00000483314	3.27	#N/A
ENST00000384398	3.11	#N/A
ENST00000365370	2.73	#N/A
ENST00000363100	-5.71	#N/A
ENST00000362692	1.94	#N/A
ENST00000461728	3.29	#N/A
ENST00000458930	1.80	#N/A
ENST00000384586	2.64	#N/A
ENST00000363872	1.98	#N/A
ENST00000408082	1.82	#N/A
ENST00000499877	-1.87	#N/A
ENST00000364018	1.83	#N/A
ENST00000458932	1.93	#N/A
ENST00000363840	-1.60	#N/A
ENST00000390904	3.45	#N/A
ENST00000431050	-5.33	#N/A
ENST00000501637	-5.33	#N/A

hsa-mir-4485-3p	#N/A	-2.69
hsa-mir-222-3p	#N/A	1.16
ENST00000489326	#N/A	-1.66
ENST00000364768	#N/A	-1.78
ENST00000410569	#N/A	-6.76
ENST00000365559	#N/A	-6.80
ENST00000500404	#N/A	1.85
hsa-mir-15b-3p	#N/A	1.95
ENST00000363792	#N/A	-1.81
hsa-mir-1246-5p	#N/A	-1.38
ENST00000499345	#N/A	-3.03
ENST00000362455	#N/A	-6.76
ENST00000363450	#N/A	1.61
hsa-mir-99b-3p	#N/A	1.46
hsa-mir-548o-3p	#N/A	1.54
ENST00000493731	#N/A	-1.64
ENST00000481041	#N/A	-2.54
ENST00000465317	#N/A	2.21
ENST00000500146	#N/A	-2.62
ENST00000499533	#N/A	-3.94
ENST00000362704	#N/A	1.62
ENST00000365659	#N/A	1.55
ENST00000494556	#N/A	-1.85
ENST00000463081	#N/A	-1.15
ENST00000410731	#N/A	-6.71
ENST00000364361	#N/A	-6.71
ENST00000486381	#N/A	-4.22
ENST00000498581	#N/A	-1.11
ENST00000362344	#N/A	-1.81
ENST00000364588	#N/A	-4.02
ENST00000500497	#N/A	-3.11
ENST00000492114	#N/A	-1.69
ENST00000482200	#N/A	-1.75
hsa-mir-30b-3p	#N/A	3.48
ENST00000365328	#N/A	1.44
hsa-mir-345-5p	#N/A	1.46
hsa-mir-484-5p	#N/A	1.16
ENST00000410216	#N/A	-1.80
ENST00000498986	#N/A	-4.29
ENST00000481141	#N/A	1.58
ENST00000501686	#N/A	-3.37
ENST00000495906	#N/A	-1.98
ENST00000501339	#N/A	-3.39
ENST00000362928	#N/A	-1.68
ENST00000498933	#N/A	-3.58

FIGURE 2D

hsa-mir-493-5p	-3.37	1.10
hsa-mir-942-5p	2.48	2.00
ENST00000470848	-2.71	#N/A
ENST00000410183	-2.52	#N/A
ENST00000362423	2.25	#N/A
hsa-mir-33a-3p	-4.35	#N/A
ENST00000490401	-3.11	#N/A
ENST00000499204	-6.41	#N/A
hsa-mir-21-5p	-1.46	#N/A
ENST00000500894	2.54	#N/A
ENST00000499768	-6.36	#N/A
ENST00000499304	-2.84	#N/A
ENST00000384172	2.79	#N/A
ENST00000476850	3.02	#N/A
ENST00000501145	-2.90	#N/A
ENST00000364310	6.40	#N/A
hsa-mir-106b-5p	-2.59	#N/A
ENST00000501334	-3.08	#N/A
ENST00000362477	2.74	2.10
ENST00000384585	3.45	#N/A
ENST00000500576	-6.69	#N/A
ENST00000458981	3.08	#N/A
ENST00000408749	2.41	3.03
ENST00000384007	2.81	#N/A
ENST00000387943	2.38	2.74
ENST00000495608	-2.64	#N/A
ENST00000364234	2.39	#N/A
hsa-mir-124-5p	-2.48	#N/A
ENST00000365537	3.18	#N/A
hsa-mir-193a-3p	-3.42	#N/A
ENST00000363696	2.36	#N/A
ENST00000458922	-3.37	#N/A
ENST00000502038	-3.15	#N/A
hsa-mir-654-3p	-3.05	#N/A
ENST00000365037	-6.31	#N/A
ENST00000479561	-2.60	-5.15
ENST00000365606	3.07	#N/A
ENST00000365312	3.38	#N/A
ENST00000384637	2.86	#N/A
ENST00000365666	3.03	#N/A
ENST00000384178	2.34	#N/A
ENST00000485528	2.82	#N/A
ENST00000362698	2.30	1.92
ENST00000384245	2.57	#N/A
ENST00000363444	2.65	1.52

hsa-mir-224-5p	-5.43	#N/A
hsa-mir-4284-5p	-5.43	#N/A
ENST00000364632	-5.43	#N/A
hsa-mir-338-3p	-5.43	#N/A
ENST00000499616	-3.40	#N/A
ENST00000384416	1.69	#N/A
ENST00000478115	-1.97	-3.57
ENST00000363836	2.07	#N/A
hsa-mir-4791-5p	-1.94	#N/A
ENST00000363171	1.93	#N/A
ENST00000384078	1.98	#N/A
ENST00000384737	2.39	#N/A
ENST00000484776	2.17	#N/A
ENST00000468731	2.40	#N/A
ENST00000391033	1.73	#N/A
ENST00000471029	2.01	#N/A
ENST00000384297	1.86	#N/A
ENST00000501443	-2.80	#N/A
ENST00000364879	1.71	#N/A
ENST00000487144	-1.82	#N/A
ENST00000384653	1.89	#N/A
ENST00000362452	2.16	#N/A
ENST00000383874	2.41	#N/A
ENST00000365399	-1.88	#N/A
ENST00000363331	2.14	-1.85
hsa-mir-1537-3p	-5.77	#N/A
ENST00000384749	2.15	#N/A
ENST00000480363	2.28	#N/A
ENST00000501540	-2.26	#N/A
ENST00000384067	1.68	1.25
ENST00000501105	-1.93	#N/A
ENST00000384090	2.03	#N/A
hsa-mir-659-5p	-2.55	#N/A
ENST00000362721	2.02	#N/A
ENST00000363810	-2.17	#N/A
hsa-mir-6747-3p	1.66	#N/A
ENST00000461956	-3.20	#N/A
ENST00000384097	1.88	#N/A
ENST00000384136	1.75	#N/A
ENST00000383990	1.88	-1.81
ENST00000411192	1.82	#N/A
ENST00000383978	1.88	#N/A
ENST00000458975	1.80	#N/A
ENST00000410344	1.96	#N/A
ENST00000501171	-2.60	#N/A

ENST00000501370	#N/A	-2.90
hsa-mir-151b-3p	#N/A	-1.88
ENST00000472187	#N/A	-1.14
ENST00000476122	#N/A	-1.43
ENST00000498896	#N/A	-2.46
ENST00000363251	#N/A	-1.61
ENST00000499098	#N/A	-4.38
hsa-mir-618-5p	#N/A	1.42
ENST00000364533	#N/A	1.47
ENST00000410801	#N/A	-1.67
ENST00000500582	#N/A	-6.05
ENST00000410597	#N/A	-1.70
ENST00000363766	#N/A	-3.05
ENST00000500818	#N/A	-6.37
ENST00000410533	#N/A	1.42
ENST00000491227	#N/A	-1.54
hsa-mir-503-5p	#N/A	1.64
ENST00000502035	#N/A	-3.55
ENST00000364447	#N/A	-3.20
hsa-mir-1301-3p	#N/A	1.42
hsa-mir-541-5p	#N/A	3.11
ENST00000364774	#N/A	-1.53
ENST00000486026	#N/A	-3.74
ENST00000469345	#N/A	2.06
ENST00000478479	#N/A	-1.50
ENST00000364469	#N/A	-1.48
hsa-mir-23a-5p	#N/A	1.71
ENST00000499059	#N/A	1.73
hsa-mir-1468-5p	#N/A	1.63
hsa-mir-584-5p	#N/A	1.70
ENST00000500977	#N/A	-2.52
ENST00000499115	#N/A	-2.06
hsa-mir-324-3p	#N/A	1.36
hsa-mir-485-5p	#N/A	-1.27
ENST00000364009	#N/A	1.50
ENST00000463796	#N/A	1.03
ENST00000363301	#N/A	-1.39
ENST00000488256	#N/A	-1.63
ENST00000478663	#N/A	1.39
ENST00000459543	#N/A	2.60
ENST00000385575	#N/A	1.29
ENST00000471568	#N/A	-1.60
ENST00000410292	#N/A	-5.91
ENST00000502160	#N/A	-5.91
hsa-mir-193b-5p	#N/A	-1.67

FIGURE 2E

ENST00000363462	2.66	#N/A
ENST00000499246	-3.20	-4.41
ENST00000502018	-2.65	#N/A
hsa-mir-210-3p	-2.49	#N/A
ENST00000384205	2.59	#N/A
ENST00000501900	-2.87	-3.69
ENST00000463853	-3.34	#N/A
ENST00000499762	2.79	#N/A
ENST00000459194	2.52	#N/A
ENST00000383948	2.63	#N/A
ENST00000364628	2.67	#N/A
ENST00000384604	2.89	#N/A
ENST00000384302	2.97	#N/A
ENST00000491230	-2.55	#N/A
ENST00000364358	2.72	#N/A
ENST00000501607	-2.39	#N/A
hsa-mir-153-3p	-2.95	#N/A
ENST00000365484	2.58	#N/A
ENST00000501173	2.59	#N/A
hsa-mir-99a-3p	-3.27	#N/A
ENST00000384619	2.32	1.50
hsa-mir-19b-5p	-2.71	#N/A
hsa-mir-502-5p	-3.99	#N/A
ENST00000469579	-2.23	#N/A
ENST00000384530	3.09	#N/A
ENST00000481391	2.67	#N/A
ENST00000363977	3.09	#N/A
ENST00000501074	5.20	#N/A
ENST00000365153	-3.03	#N/A
ENST00000488304	-3.18	#N/A
ENST00000501998	3.08	#N/A
ENST00000365599	2.93	#N/A
ENST00000475810	3.68	#N/A
ENST00000466170	-2.19	#N/A
hsa-mir-3173-5p	2.67	#N/A
hsa-mir-190a-5p	-3.62	#N/A
ENST00000384026	2.70	#N/A
ENST00000384385	2.46	#N/A
ENST00000411404	2.64	#N/A
ENST00000364696	3.17	#N/A
ENST00000482377	-3.21	#N/A
hsa-mir-151a-3p	-2.41	#N/A
hsa-mir-146b-5p	2.01	#N/A
ENST00000500516	-2.63	#N/A
ENST00000384577	2.97	#N/A

ENST00000384210	2.41	#N/A
ENST00000500508	-2.50	#N/A
ENST00000476674	-1.80	-1.76
ENST00000474075	-1.97	-2.96
hsa-mir-369-3p	-2.71	#N/A
hsa-mir-548f-5p	-2.11	#N/A
ENST00000491516	-1.66	-1.97
ENST00000363750	2.33	#N/A
ENST00000384419	1.95	#N/A
ENST00000384656	1.84	#N/A
ENST00000384187	1.86	#N/A
hsa-mir-152-3p	-1.93	#N/A
ENST00000475628	1.83	#N/A
ENST00000419895	2.06	#N/A
ENST00000365571	1.36	#N/A
hsa-mir-27b-5p	-1.96	#N/A
ENST00000499014	-1.85	#N/A
ENST00000499438	-2.64	#N/A
ENST00000501856	-2.32	#N/A
ENST00000459135	-2.00	#N/A
ENST00000462879	-3.34	-5.22
ENST00000363548	1.86	#N/A
ENST00000363094	1.85	#N/A
ENST00000502161	-3.50	-4.95
ENST00000499095	-2.16	#N/A
hsa-mir-27a-3p	-1.49	#N/A
ENST00000500893	-2.21	-5.22
ENST00000363925	2.23	-1.34
ENST00000364208	-5.71	#N/A
ENST00000384119	1.82	-1.68
ENST00000384600	2.15	#N/A
ENST00000391196	1.71	#N/A
ENST00000501934	-2.08	#N/A
ENST00000501587	-2.08	#N/A
ENST00000500518	-1.76	#N/A
ENST00000365672	1.53	#N/A
ENST00000364916	1.68	-1.61
ENST00000493125	1.83	#N/A
ENST00000502192	1.72	#N/A
ENST00000364535	1.75	#N/A
ENST00000363660	1.56	#N/A
ENST00000363068	1.56	#N/A
ENST00000501338	2.54	#N/A
ENST00000365063	1.63	#N/A
ENST00000384344	2.21	#N/A

hsa-mir-4473-3p	#N/A	1.28
hsa-mir-887-3p	#N/A	3.11
ENST00000408376	#N/A	1.81
ENST00000502206	#N/A	-2.96
ENST00000362487	#N/A	-1.56
ENST00000362779	#N/A	1.38
hsa-mir-197-3p	#N/A	-1.31
ENST00000364393	#N/A	-1.81
ENST00000390997	#N/A	1.75
ENST00000408563	#N/A	-1.34
hsa-mir-3662-3p	#N/A	2.73
ENST00000501149	#N/A	-2.63
ENST00000468500	#N/A	-1.26
ENST00000500970	#N/A	2.56
ENST00000363046	#N/A	1.00
ENST00000363220	#N/A	-1.35
ENST00000499220	#N/A	3.74
ENST00000363257	#N/A	-1.42
ENST00000499917	#N/A	1.52
ENST00000365617	#N/A	-1.38
hsa-mir-375-3p	#N/A	1.58
ENST00000472473	#N/A	-3.52
hsa-mir-3182-5p	#N/A	-1.55
ENST00000467798	#N/A	-1.41
ENST00000499978	#N/A	-2.19
ENST00000500358	#N/A	-2.52
ENST00000487309	#N/A	1.92
ENST00000473668	#N/A	1.87
ENST00000363120	#N/A	1.26
ENST00000501042	#N/A	1.61
ENST00000411347	#N/A	-4.04
ENST00000410669	#N/A	-1.34
ENST00000465779	#N/A	-2.16
ENST00000365172	#N/A	1.21
ENST00000364377	#N/A	-1.54
ENST00000485927	#N/A	-1.23
hsa-mir-3613-5p	#N/A	-1.55
ENST00000365254	#N/A	-2.94
ENST00000363593	#N/A	1.31
ENST00000462216	#N/A	-1.95
ENST00000363849	#N/A	-5.65
ENST00000501275	#N/A	-2.99
ENST00000461333	#N/A	-1.47
ENST00000501646	#N/A	-2.42
ENST00000408481	#N/A	1.73

FIGURE 2F

ENST00000363723	-3.62	#N/A
ENST00000469253	-2.32	#N/A
hsa-mir-409-3p	-3.50	#N/A
hsa-mir-1254-5p	2.22	#N/A
hsa-mir-15a-5p	-2.13	#N/A
ENST00000410462	2.41	#N/A
ENST00000384161	2.31	#N/A
ENST00000492745	-2.14	#N/A
ENST00000383898	2.46	#N/A
ENST00000363435	2.44	#N/A
ENST00000500207	-2.96	-4.36
ENST00000363286	2.14	1.02
ENST00000501174	-2.70	#N/A
ENST00000482497	3.89	-1.08
ENST00000365604	2.82	2.51
ENST00000362591	2.21	#N/A
hsa-mir-651-5p	-2.18	#N/A
hsa-mir-31-5p	-6.76	#N/A
ENST00000471133	6.06	#N/A
ENST00000501075	-3.27	-2.95
ENST00000383895	5.35	#N/A
ENST00000365341	2.54	#N/A
hsa-mir-17-3p	-2.36	#N/A
ENST00000365532	2.51	#N/A
ENST00000387069	2.28	2.88
ENST00000499572	-2.57	-6.22
ENST00000410793	-2.41	#N/A
ENST00000362352	2.27	#N/A
hsa-mir-411-5p	-3.16	#N/A
ENST00000364102	2.41	1.38
ENST00000384606	3.07	#N/A
ENST00000471114	-2.28	-2.95
ENST00000384633	2.71	#N/A
ENST00000384630	2.71	#N/A
hsa-mir-455-3p	-2.29	#N/A
ENST00000500702	-2.46	-1.88
hsa-mir-127-3p	-2.61	#N/A
ENST00000384563	2.65	#N/A
ENST00000499656	-3.07	#N/A
ENST00000363636	2.17	#N/A
ENST00000362353	2.17	#N/A
ENST00000362562	2.16	#N/A
ENST00000487060	2.35	#N/A
ENST00000363624	2.11	#N/A
ENST00000384323	2.02	2.16

ENST00000499426	-5.21	#N/A
ENST00000501219	-5.21	#N/A
hsa-mir-889-3p	-5.21	#N/A
hsa-mir-6847-5p	3.41	#N/A
ENST00000470833	5.42	#N/A
hsa-mir-505-5p	5.42	#N/A
ENST00000365030	1.56	#N/A
ENST00000384567	1.61	#N/A
ENST00000459367	1.83	#N/A
ENST00000362695	2.27	#N/A
ENST00000364251	1.62	#N/A
ENST00000410290	1.57	#N/A
ENST00000384010	1.57	1.14
ENST00000491152	2.35	#N/A
ENST00000452527	-3.06	#N/A
ENST00000410694	1.88	#N/A
ENST00000384782	1.57	1.16
ENST00000383886	2.28	#N/A
ENST00000383861	1.56	1.13
ENST00000458811	1.82	1.67
ENST00000383925	1.57	1.13
ENST00000364228	1.40	#N/A
ENST00000485447	-2.38	#N/A
ENST00000501894	-1.70	#N/A
ENST00000483592	1.84	#N/A
hsa-mir-548aj-5p	-2.13	#N/A
ENST00000365208	1.66	#N/A
ENST00000384278	1.56	1.16
ENST00000501814	-1.82	-4.77
ENST00000362421	1.72	#N/A
ENST00000390910	1.79	#N/A
ENST00000363421	1.60	#N/A
ENST00000364558	-1.76	#N/A
ENST00000383869	1.55	1.15
ENST00000363271	1.68	#N/A
ENST00000410557	1.60	#N/A
ENST00000384659	1.55	1.11
ENST00000384135	1.62	#N/A
ENST00000499695	-1.69	-4.65
ENST00000411009	2.42	#N/A
ENST00000364348	1.67	#N/A
ENST00000459508	1.72	#N/A
ENST00000410794	1.78	#N/A
ENST00000383860	2.04	#N/A
ENST00000500662	-2.64	-4.95

ENST00000364948	#N/A	-1.08
ENST00000501116	#N/A	-2.39
ENST00000475601	#N/A	-1.47
hsa-mir-511-5p	#N/A	-2.75
ENST00000489070	#N/A	1.21
ENST00000363915	#N/A	-1.49
hsa-mir-107-3p	#N/A	1.17
ENST00000501853	#N/A	-3.57
hsa-mir-431-3p	#N/A	1.35
ENST00000362607	#N/A	1.25
ENST00000475473	#N/A	2.54
hsa-mir-215-5p	#N/A	-1.84
ENST00000499222	#N/A	-2.06
ENST00000363044	#N/A	-1.49
ENST00000501427	#N/A	-2.29
ENST00000401297	#N/A	1.69
ENST00000459083	#N/A	1.26
hsa-mir-1185-3p	#N/A	1.29
ENST00000434673	#N/A	-2.16
ENST00000501348	#N/A	-2.74
hsa-mir-5701-5p	#N/A	-1.19
hsa-mir-664a-3p	#N/A	-1.47
ENST00000499712	#N/A	-2.29
ENST00000364259	#N/A	1.67
ENST00000478832	#N/A	-1.23
ENST00000364819	#N/A	-1.28
ENST00000390833	#N/A	1.16
ENST00000485828	#N/A	-1.51
ENST00000466944	#N/A	-1.94
hsa-mir-451a-5p	#N/A	-2.74
ENST00000486576	#N/A	-2.65
ENST00000473410	#N/A	-1.18
ENST00000385607	#N/A	1.24
hsa-mir-16-3p	#N/A	1.08
ENST00000500979	#N/A	-2.22
hsa-mir-485-3p	#N/A	-1.15
ENST00000365138	#N/A	-1.59
ENST00000410482	#N/A	1.07
ENST00000408061	#N/A	1.10
hsa-mir-3620-5p	#N/A	5.55
ENST00000499775	#N/A	-5.34
ENST00000501399	#N/A	-5.34
hsa-mir-30d-3p	#N/A	2.00
hsa-mir-3591-3p	#N/A	-2.26
ENST00000501304	#N/A	-3.13

FIGURE 2G

ENST00000411187	2.82	#N/A
ENST00000499932	-3.00	#N/A
ENST00000493141	-3.03	-2.58
ENST00000384589	2.61	#N/A
ENST00000365085	2.20	#N/A
ENST00000364164	2.44	#N/A
hsa-mir-146b-3p	2.32	#N/A
ENST00000384781	2.80	#N/A
ENST00000501615	-2.78	#N/A
ENST00000500663	-2.61	-6.37
ENST00000363190	2.86	#N/A
ENST00000384744	2.04	#N/A
ENST00000384776	2.49	#N/A
hsa-mir-301b-3p	-2.98	#N/A
ENST00000391154	2.11	#N/A
ENST00000491579	-2.31	#N/A
ENST00000362862	2.23	#N/A
ENST00000500553	-2.39	#N/A
ENST00000391172	2.23	#N/A
ENST00000383975	-2.28	#N/A
ENST00000365160	2.64	1.80
ENST00000459189	2.04	#N/A
ENST00000497848	1.92	#N/A
ENST00000384527	2.48	#N/A
ENST00000499508	1.98	1.12
ENST00000499850	-2.34	#N/A
ENST00000496399	1.70	#N/A
hsa-mir-33a-5p	-3.67	#N/A
ENST00000362912	-2.49	#N/A
ENST00000498971	-3.72	#N/A
ENST00000501356	-6.07	#N/A
hsa-mir-4690-3p	-6.07	#N/A
ENST00000384281	2.15	#N/A
ENST00000499378	-2.69	-5.46
hsa-mir-27b-3p	-1.84	#N/A
ENST00000364641	2.38	#N/A
hsa-mir-582-5p	-2.75	#N/A
ENST00000384727	3.50	#N/A
ENST00000384534	2.34	#N/A
hsa-mir-582-3p	-2.27	#N/A
ENST00000501902	-2.25	-4.80
hsa-mir-382-5p	-3.50	#N/A
ENST00000383934	2.58	#N/A
ENST00000489347	-2.53	#N/A
ENST00000362710	2.40	-1.20

ENST00000363858	2.61	#N/A
ENST00000362931	1.55	#N/A
ENST00000501144	2.90	#N/A
ENST00000391084	2.07	#N/A
ENST00000364308	1.47	#N/A
ENST00000363552	1.87	#N/A
ENST00000384436	1.56	#N/A
ENST00000364113	1.50	#N/A
ENST00000390895	1.57	#N/A
ENST00000383890	1.49	#N/A
ENST00000502138	-2.01	#N/A
ENST00000408209	1.94	#N/A
ENST00000485481	1.54	#N/A
ENST00000384138	1.73	-1.65
hsa-mir-4746-5p	1.54	#N/A
ENST00000365096	-1.67	-1.24
ENST00000384462	-1.63	#N/A
ENST00000384541	1.49	#N/A
ENST00000363358	-2.69	#N/A
ENST00000424643	-2.29	#N/A
ENST00000365099	-2.29	#N/A
hsa-mir-543-3p	-2.20	#N/A
hsa-mir-145-5p	-1.67	#N/A
ENST00000362963	-2.01	#N/A
hsa-mir-744-5p	1.46	1.08
hsa-mir-3912-3p	-1.60	#N/A
ENST00000364128	1.69	#N/A
ENST00000384626	1.82	#N/A
ENST00000500637	-1.66	#N/A
ENST00000411315	1.62	1.36
ENST00000481967	1.56	#N/A
ENST00000364960	2.96	#N/A
ENST00000474109	2.44	#N/A
hsa-mir-130a-3p	-5.53	#N/A
ENST00000499796	-5.53	#N/A
hsa-mir-590-5p	-5.53	#N/A
ENST00000495498	1.74	#N/A
ENST00000444141	1.56	#N/A
hsa-mir-29a-3p	-1.49	#N/A
hsa-mir-323a-3p	-5.53	#N/A
ENST00000502175	-5.53	#N/A
hsa-mir-182-5p	1.53	#N/A
hsa-mir-449c-5p	-2.55	#N/A
ENST00000362680	1.62	#N/A
hsa-mir-16-5p	-1.48	#N/A

hsa-mir-425-3p	#N/A	1.05
ENST00000410856	#N/A	1.27
ENST00000500809	#N/A	-2.58
ENST00000499055	#N/A	1.24
hsa-mir-625-3p	#N/A	-1.39
hsa-mir-874-3p	#N/A	1.03
ENST00000384110	#N/A	-1.35
ENST00000362911	#N/A	-1.24
ENST00000411012	#N/A	1.10
ENST00000363091	#N/A	-1.23
ENST00000496134	#N/A	1.70
hsa-mir-1287-5p	#N/A	1.22
ENST00000500202	#N/A	-2.26
ENST00000496828	#N/A	-1.78
ENST00000458893	#N/A	1.13
ENST00000463779	#N/A	-2.71
hsa-mir-431-5p	#N/A	1.24
hsa-mir-1255a-5p	#N/A	1.62
ENST00000363656	#N/A	-1.12
ENST00000365668	#N/A	-1.55
ENST00000365202	#N/A	-1.09
ENST00000410717	#N/A	-1.22
ENST00000499483	#N/A	1.45
ENST00000500023	#N/A	-2.53
ENST00000480526	#N/A	1.41
hsa-mir-584-3p	#N/A	2.78
ENST00000486970	#N/A	-3.04
ENST00000366303	#N/A	2.23
hsa-mir-671-3p	#N/A	-1.01
ENST00000386847	#N/A	1.06
ENST00000460738	#N/A	1.51
ENST00000500043	#N/A	-2.87
ENST00000365598	#N/A	-5.22
ENST00000408548	#N/A	2.03
ENST00000363341	#N/A	-1.06
ENST00000363964	#N/A	-1.37
ENST00000364648	#N/A	-2.11
ENST00000478019	#N/A	-1.20
ENST00000363738	#N/A	-1.20
ENST00000401270	#N/A	1.40
hsa-mir-7704-5p	#N/A	-1.27
hsa-mir-671-5p	#N/A	1.11
ENST00000500738	#N/A	-2.64
ENST00000362645	#N/A	-1.08
ENST00000364914	#N/A	1.25

FIGURE 2H

ENST00000363455	2.11	#N/A
ENST00000384793	2.24	2.07
ENST00000467195	-2.39	-3.18
ENST00000459096	-2.15	#N/A
ENST00000501034	-2.70	#N/A
ENST00000501134	-2.43	#N/A
ENST00000363899	2.14	#N/A
ENST00000383924	1.91	#N/A
ENST00000362354	2.22	-3.09
ENST00000365075	2.18	#N/A
ENST00000499473	-2.86	#N/A
ENST00000364654	-2.86	#N/A
ENST00000384001	2.22	#N/A
ENST00000499305	-2.34	#N/A
ENST00000384127	2.63	#N/A
ENST00000410624	2.16	#N/A
ENST00000364337	2.57	#N/A
ENST00000411164	2.03	#N/A
ENST00000384716	2.18	#N/A
ENST00000383913	2.74	#N/A
ENST00000364432	3.07	#N/A
ENST00000459107	2.22	#N/A
hsa-mir-548x-5p	-2.59	#N/A
ENST00000500112	2.04	#N/A
hsa-mir-6516-3p	-2.92	#N/A
ENST00000384341	2.05	#N/A
ENST00000363372	2.21	#N/A
ENST00000471506	2.17	#N/A
hsa-mir-194-5p	-1.93	#N/A
ENST00000364937	3.92	#N/A
ENST00000501249	-2.33	#N/A
ENST00000362697	2.12	#N/A
ENST00000499758	-2.13	-2.44
ENST00000476606	-2.33	-3.13
hsa-mir-4521-5p	2.09	#N/A
ENST00000499909	-2.32	#N/A
ENST00000499925	-2.37	#N/A
ENST00000384750	2.11	#N/A
ENST00000486830	2.68	#N/A
ENST00000384378	3.29	#N/A
hsa-mir-4420-3p	1.97	#N/A
ENST00000365498	2.16	-1.88
hsa-mir-450b-5p	-2.32	#N/A
ENST00000501091	-2.24	#N/A
ENST00000363141	3.52	#N/A

ENST00000362667	-1.91	#N/A
ENST00000500049	-1.60	#N/A
ENST00000501843	-1.78	#N/A
ENST00000497631	1.71	#N/A
ENST00000363186	1.60	#N/A
ENST00000459124	1.41	#N/A
ENST00000499566	2.03	#N/A
ENST00000498910	-1.47	#N/A
hsa-mir-296-3p	1.40	2.08
ENST00000499061	-1.59	#N/A
ENST00000410129	1.49	#N/A
ENST00000364419	-1.64	#N/A
ENST00000496990	1.63	2.17
ENST00000386062	1.62	#N/A
hsa-mir-33b-3p	1.49	#N/A
hsa-mir-542-3p	-2.13	#N/A
ENST00000362540	1.50	-1.41
ENST00000459577	1.55	2.83
ENST00000459229	1.61	#N/A
ENST00000498878	1.50	#N/A
ENST00000500846	-1.66	#N/A
ENST00000364938	1.52	#N/A
ENST00000487367	2.35	#N/A
ENST00000502133	-2.91	#N/A
ENST00000447991	-2.91	#N/A
ENST00000501462	-2.99	#N/A
ENST00000500114	-2.99	#N/A
hsa-mir-450a-5p	-1.86	#N/A
ENST00000459041	1.54	#N/A
ENST00000501043	2.98	#N/A
ENST00000496481	-1.50	#N/A
ENST00000501125	-1.74	#N/A
ENST00000500444	-2.24	#N/A
ENST00000499480	-2.31	#N/A
ENST00000501658	-1.69	#N/A
ENST00000484771	1.90	#N/A
ENST00000501592	-2.99	#N/A
ENST00000499665	-1.84	#N/A
ENST00000502181	-1.71	#N/A
ENST00000475606	-5.09	#N/A
ENST00000480177	-5.09	#N/A
ENST00000499640	-5.09	#N/A
ENST00000410205	1.59	#N/A
ENST00000462564	-1.61	1.38
ENST00000362438	2.17	#N/A

ENST00000362750	#N/A	1.22
hsa-mir-1262-5p	#N/A	1.29
ENST00000484912	#N/A	-1.01
ENST00000499698	#N/A	2.70
ENST00000410980	#N/A	-2.34
hsa-mir-130b-3p	#N/A	1.16
ENST00000499543	#N/A	-1.44
ENST00000500134	#N/A	-1.93
hsa-mir-1268b-5p	#N/A	2.61
ENST00000384033	#N/A	1.48
ENST00000501159	#N/A	-2.84
ENST00000501903	#N/A	-2.84
ENST00000410818	#N/A	-2.95
ENST00000498954	#N/A	-2.95
ENST00000501206	#N/A	-1.79
ENST00000466665	#N/A	-1.06
ENST00000363788	#N/A	-2.10
hsa-mir-219a-3p	#N/A	1.68
hsa-mir-1180-3p	#N/A	1.06
hsa-mir-214-5p	#N/A	1.06
ENST00000481252	#N/A	-1.04
hsa-mir-548j-5p	#N/A	1.40
ENST00000410798	#N/A	-1.07
ENST00000502153	#N/A	5.20
hsa-mir-6720-5p	#N/A	5.20
ENST00000499262	#N/A	-5.08
ENST00000499793	#N/A	-5.08
ENST00000364448	#N/A	-1.53
hsa-mir-410-5p	#N/A	1.92
ENST00000499894	#N/A	-1.03
hsa-mir-3687-3p	#N/A	1.66
hsa-mir-3129-5p	#N/A	1.64
hsa-mir-937-3p	#N/A	-2.27
ENST00000408778	#N/A	2.00
ENST00000499388	#N/A	1.18
ENST00000501058	#N/A	-2.26
ENST00000499580	#N/A	1.87
ENST00000487740	#N/A	-1.47
ENST00000501092	#N/A	-1.63
hsa-mir-454-5p	#N/A	1.22
hsa-mir-489-3p	#N/A	-2.86
ENST00000444772	#N/A	-2.18
hsa-mir-122-5p	#N/A	-1.15
ENST00000384274	#N/A	-1.28
ENST00000410718	#N/A	-1.02

FIGURE 3A

Figure 3: EGS transcriptomics data during MM6 infections. Differencial expression analysis of T. gondii genes from MM6 cells infected with T. gondii EGS strain for 18 hours compared to T. gondii gene expression from MM6 cells infected with GT1, ME49 or VEG strains for 18 hours.

gene ID	logFC (EGS/GT1)	logFC (EGS/ME49)	logFC (EGS/VEG)	Product Name
TGME49_232955	8.01	8.68	6.65	hypothetical protein
TGME49_323400	7.44	8.28	8.19	cytochrome c oxidase subunit iii subfamily protein
TGME49_322200	7.72	8.34	8.72	apocytochrome b, putative
TGME49_206550	4.89	2.98	6.27	hypothetical protein
TGME49_330000	8.23	9.02	7.63	cytochrome b
TGME49_237130	8.00	8.26	7.60	cytochrome b, putative
TGME49_255060	6.97	7.47	7.02	cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_252065	3.93	4.28	3.49	KRUF family protein
TGME49_305460	2.60	2.65	1.90	methionine aminopeptidase 2, putative
TGME49_301222	2.58	2.86	2.73	DNA repair protein Rad4 domain-containing protein
TGME49_252220	2.24	#N/A	1.54	tetratricopeptide repeat domain containing protein
TGME49_250670	3.64	#N/A	1.06	hypothetical protein
TGME49_302055	8.07	10.62	8.51	ribosomal protein RPS12
TGME49_279340	2.25	2.37	1.48	hypothetical protein
TGME49_252070	3.61	3.75	6.63	KRUF family protein
TGME49_225555	1.93	1.82	1.58	hypothetical protein
TGME49_275860	2.23	2.29	2.17	hypothetical protein
TGME49_217530	3.58	3.78	2.37	hypothetical protein
TGME49_254030	1.93	2.07	2.13	zinc finger CDGSH-type domain-containing protein
TGME49_253790	2.72	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_249230	3.23	#N/A	#N/A	hypothetical protein
TGME49_260250	-2.90	-2.61	-1.90	cyclin domain protein, cyclin H family protein
TGME49_294400	-3.34	-2.54	-3.73	hypothetical protein
TGME49_226310	-2.88	-3.64	-2.13	zinc finger (CCCH type) motif-containing protein
TGME49_233925	10.75	10.32	10.59	hypothetical protein
TGME49_319860	-1.01	#N/A	#N/A	DNA polymerase family B protein
TGME49_216750	-1.10	-1.10	#N/A	Paf1/RNA polymerase II complex component LEO1
TGME49_202510	1.65	#N/A	#N/A	multi-pass transmembrane protein
TGME49_261720	-0.98	-1.16	-0.99	metal cation transporter, ZIP family protein
TGME49_262860	-1.51	-1.63	-2.20	ADP-ribosylation factor family protein 1, putative
TGME49_207990	0.97	#N/A	#N/A	ribosomal RNA large subunit methyltransferase J protein
TGME49_320650	-1.52	-1.43	#N/A	ankyrin repeat-containing protein
TGME49_221160	1.68	#N/A	#N/A	acetyltransferase, GNAT family protein
TGME49_309090	-1.20	-1.08	#N/A	hypothetical protein
TGME49_237550	1.76	1.49	#N/A	hypothetical protein
TGME49_244680	1.39	#N/A	#N/A	hypothetical protein
TGME49_231870	-1.74	-1.89	-1.86	tetratricopeptide repeat-containing protein
TGME49_308020	-0.87	#N/A	#N/A	SAG-related sequence SRS57
TGME49_251470	-1.01	#N/A	#N/A	hypothetical protein
TGME49_253960	1.10	2.02	1.85	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_232750	0.95	#N/A	#N/A	23S rRNA (adenine(1618)-N(6))-methyltransferase, putative
TGME49_254000	0.92	1.26	1.63	hypothetical protein
TGME49_237190	1.43	#N/A	#N/A	hypothetical protein
TGME49_269730	-0.92	#N/A	#N/A	myosin-light-chain kinase
TGME49_202430	-1.36	#N/A	-1.38	hypothetical protein
TGME49_225080	1.55	#N/A	1.56	ribosomal protein RPS18
TGME49_231200	1.47	#N/A	#N/A	hypothetical protein
TGME49_262690	2.92	#N/A	3.11	ribosomal protein RPL27
TGME49_272910	0.85	#N/A	#N/A	T-complex protein 1 delta subunit
TGME49_311625	-1.37	-1.42	-1.49	WD domain, G-beta repeat-containing protein

FIGURE 3B

TGME49_223660	1.91	2.65	2.39	50S ribosomal protein L4, putative
TGME49_235630	1.82	1.28	1.89	hypothetical protein
TGME49_286928	-3.71	-3.10	-3.90	hypothetical protein
TGME49_294980	4.14	1.48	#N/A	hypothetical protein
TGME49_273870	-2.06	-1.83	-1.97	SWI2/SNF2 ISWI-like (AT hook)
TGME49_260430	3.50	2.69	4.09	hypothetical protein
TGME49_251180	2.60	3.13	2.36	KRUF family protein
TGME49_301250	7.47	8.53	8.01	hypothetical protein
TGME49_299030	1.91	2.12	1.79	RNA recognition motif 2 protein
TGME49_285710	2.51	1.31	1.39	hypothetical protein
TGME49_290150	-2.45	-2.18	-1.42	hypothetical protein
TGME49_260480	2.83	2.05	#N/A	leucine rich repeat-containing protein
TGME49_277270	2.73	3.04	1.95	NTPase II
TGME49_322000	-2.57	-2.38	-3.55	myosin-light-chain kinase
TGME49_258390	2.65	1.39	#N/A	DnaJ protein, putative
TGME49_266740	3.44	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_300010	-4.97	-4.45	-4.50	hypothetical protein
TGME49_242240	-3.22	-2.54	-3.68	rhoptry kinase family protein ROP19A
TGME49_207430	-2.44	-1.84	-2.11	ATP-dependent RNA helicase DDX1, putative
TGME49_253900	2.85	1.57	1.38	parasite porphobilinogen synthase PBGS
TGME49_212940	-8.20	-10.97	-7.44	hypothetical protein
TGME49_315885	5.95	5.94	6.02	glycosyltransferase, putative
TGME49_251170	2.42	2.24	1.98	KRUF family protein
TGME49_234460	2.14	2.80	#N/A	hypothetical protein
TGME49_259950	2.03	0.86	#N/A	carbonate dehydratase, eukaryotic-type domain-containing protein
TGME49_213067	1.80	1.98	#N/A	hypothetical protein
TGME49_221320	2.55	2.37	1.65	acetyl-CoA carboxylase ACC1
TGME49_257350	1.55	1.40	1.05	eukaryotic translation initiation factor, putative
TGME49_313100	-3.03	-2.51	-2.94	signal recognition particle SRP54 protein
TGME49_241155	3.09	1.88	#N/A	hypothetical protein
TGME49_215430	4.78	4.60	4.46	hypothetical protein
TGME49_200310	1.68	1.64	1.55	hypothetical protein
TGME49_236270	-3.59	-3.34	-2.80	hypothetical protein

TGME49_231180	-2.31	-2.97	-3.51	hypothetical protein
TGME49_259570	-1.51	#N/A	#N/A	CMP/dCMP deaminase, zinc-binding, putative
TGME49_212310	0.98	1.04	0.97	vacuolar ATP synthetase
TGME49_237280	-0.92	#N/A	#N/A	TLD protein
TGME49_276220	0.97	1.35	#N/A	hypothetical protein
TGME49_268680	0.90	#N/A	#N/A	hypothetical protein
TGME49_275420	-1.14	-1.19	#N/A	histone lysine-specific demethylase LSD1/BHC110/KDMA1A
TGME49_235140	-0.88	#N/A	-0.86	hypothetical protein
TGME49_219750	0.84	#N/A	#N/A	cytochrome c, putative
TGME49_227830	-1.02	#N/A	#N/A	mitochondrial inner membrane translocase TIM44, putative
TGME49_318650	0.85	0.90	1.08	transhydrogenase
TGME49_291620	-0.92	#N/A	#N/A	hypothetical protein
TGME49_227570	0.90	1.08	#N/A	transmembrane amino acid transporter protein
TGME49_316660	-1.10	#N/A	-1.20	cullin family protein
TGME49_207665	-2.56	#N/A	#N/A	kinesin motor domain-containing protein
TGME49_207120	-1.46	#N/A	#N/A	Sad1/UNC family protein
TGME49_273595	1.50	#N/A	#N/A	hypothetical protein
TGME49_210360	1.17	1.08	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 family protein
TGME49_311160	-0.88	#N/A	#N/A	PWI domain-containing protein
TGME49_286580	0.92	#N/A	#N/A	hypothetical protein
TGME49_280770	1.02	#N/A	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_217820	-0.96	-0.93	#N/A	PCI domain-containing protein
TGME49_226020	0.95	1.25	#N/A	transporter, major facilitator family protein
TGME49_216230	-0.92	#N/A	#N/A	hypothetical protein
TGME49_253410	0.98	#N/A	#N/A	hypothetical protein
TGME49_255660	-1.12	-1.26	#N/A	EF hand domain-containing protein
TGME49_270120	-1.15	#N/A	#N/A	thioredoxin-like protein TLP1
TGME49_205130	-0.83	#N/A	#N/A	hypothetical protein
TGME49_249410	1.07	#N/A	#N/A	hypothetical protein
TGME49_209090	-1.16	-1.32	-1.65	proteasome maturation factor ump1 protein
TGME49_277760	-0.91	#N/A	#N/A	adenylosuccinate lyase, putative
TGME49_211630	-0.80	#N/A	#N/A	hypothetical protein
TGME49_310950	-0.80	#N/A	#N/A	AP2 domain transcription factor AP2XI-3

FIGURE 3C

TGME49_275640	1.79	1.61	1.67	hypothetical protein
TGME49_299080	1.66	1.84	1.66	VTC domain-containing protein
TGME49_232600	2.23	1.57	#N/A	phospholipase, patatin family protein
TGME49_312140	-4.04	-4.67	#N/A	hypothetical protein
TGME49_215930	-8.19	-7.79	-6.94	mediator complex subunit MED21
TGME49_299000	2.45	#N/A	#N/A	hypothetical protein
TGME49_254710	1.72	1.44	1.05	serine esterase (DUF676) protein
TGME49_247410	1.50	1.28	1.36	hypothetical protein
TGME49_233130	3.15	2.06	#N/A	nucleoside transporter protein
TGME49_267020	-2.38	-4.42	#N/A	hypothetical protein
TGME49_253750	1.73	1.65	1.53	PLU-1 family protein
TGME49_227810	1.57	1.65	#N/A	rhoptry kinase family protein ROP11 (incomplete catalytic triad)
TGME49_207960	-2.40	-2.30	-2.73	hypothetical protein
TGME49_272410	3.57	3.54	3.71	phosphogluconate dehydrogenase (decarboxylating), NAD binding domain-containing protein
TGME49_215940	-2.46	-2.34	-1.97	Acetyl-coenzyme A transporter, putative
TGME49_233870	1.95	1.82	0.98	hypothetical protein
TGME49_254690	1.57	1.25	#N/A	phospholipase/carboxylesterase
TGME49_217555	1.35	1.38	0.89	hypothetical protein
TGME49_240700	-2.10	-1.71	-1.63	ubiquitin family protein
TGME49_260310	2.97	1.84	1.52	ATP-binding cassette transporter ABC.B1
TGME49_258720	1.64	1.93	1.99	Ubiquitin family protein, putative
TGME49_301280	-3.03	-2.29	#N/A	hypothetical protein
TGME49_254660	1.60	1.43	1.25	ankyrin repeat-containing protein
TGME49_247930	-3.26	-2.87	-2.90	SNARE domain-containing protein
TGME49_268225	-8.90	-9.99	-9.10	hypothetical protein
TGME49_206695	3.11	1.95	#N/A	hypothetical protein
TGME49_231370	2.43	1.26	#N/A	phospholipase, patatin family protein
TGME49_214380	-2.49	-1.99	#N/A	hypothetical protein
TGME49_259010	-1.97	-1.82	-1.66	vacuolar ATP synthase subunit d, putative
TGME49_306020	2.01	1.21	1.32	hypothetical protein
TGME49_254080	1.47	1.48	1.13	metal cation transporter, ZIP family protein
TGME49_240250	-1.53	-1.40	-1.39	macro domain-containing protein
TGME49_283790	3.32	#N/A	#N/A	protein kinase, putative
TGME49_293820	-1.59	-1.22	-1.01	calpain family cysteine protease domain-containing protein

TGME49_225240	0.91	1.15	#N/A	50S ribosomal protein L13, putative
TGME49_213010	-1.19	-2.88	#N/A	hypothetical protein
TGME49_204060	-1.35	-1.44	#N/A	SNARE domain-containing protein
TGME49_227780	1.46	1.55	#N/A	hypothetical protein
TGME49_238230	0.96	0.85	#N/A	Ser/Thr phosphatase family protein
TGME49_211030	-0.85	-1.10	#N/A	hypothetical protein
TGME49_228330	-1.61	#N/A	#N/A	NLI interacting factor family phosphatase
TGME49_310802	-1.21	#N/A	#N/A	CRAL/TRIO domain-containing protein
TGME49_219590	-1.13	#N/A	#N/A	RuvB family 1 protein
TGME49_319600	-1.15	#N/A	#N/A	alpha-tubulin N-acetyltransferase, putative
TGME49_280410	-0.91	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_301170	-6.07	-9.48	-7.08	SAG-related sequence SRS19D
TGME49_235560	1.73	#N/A	#N/A	hypothetical protein
TGME49_280750	-0.98	#N/A	#N/A	rudimentary enhancer, putative
TGME49_254380	-1.33	#N/A	#N/A	ribosomal protein L11, putative
TGME49_252280	1.08	#N/A	1.54	hypothetical protein
TGME49_230850	-0.86	#N/A	#N/A	hypothetical protein
TGME49_248690	-1.36	-1.32	#N/A	hypothetical protein
TGME49_278205	-0.80	#N/A	#N/A	hypothetical protein
TGME49_215640	-0.99	-1.04	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_202390	-0.93	#N/A	#N/A	S15 sporozoite-expressed protein
TGME49_257685	0.90	#N/A	#N/A	hypothetical protein
TGME49_228010	-1.60	-1.70	#N/A	hypothetical protein
TGME49_278060	-1.66	-3.05	-1.76	Mre11 DNA-binding domain-containing protein
TGME49_313200	-1.67	-1.66	-2.23	leucine rich repeat-containing protein
TGME49_257300	-0.97	#N/A	#N/A	hypothetical protein
TGME49_219190	-1.06	#N/A	#N/A	nuclear movement protein domain containing protein
TGME49_246178	-1.17	#N/A	#N/A	hypothetical protein
TGME49_248870	-0.98	#N/A	#N/A	SNARE associated Golgi protein
TGME49_213930	-1.48	#N/A	#N/A	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_287515	-1.69	#N/A	#N/A	hypothetical protein
TGME49_297720	-1.02	-1.24	-1.14	trehalose-phosphatase
TGME49_251730	-1.16	-1.40	#N/A	hypothetical protein
TGME49_205200	0.92	1.04	1.15	hypothetical protein

FIGURE 3D

TGME49_258790	-1.72	-2.03	-1.35	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_220240	1.59	2.02	1.45	hypothetical protein
TGME49_295935	1.50	1.37	1.08	KRUF family protein
TGME49_246490	-1.55	-1.02	-0.91	hypothetical protein
TGME49_225930	1.29	1.14	0.78	triose-phosphate isomerase TPI-I
TGME49_297495	-7.98	-9.14	#N/A	hypothetical protein
TGME49_240510	2.77	1.44	#N/A	hypothetical protein
TGME49_299210	1.86	1.80	#N/A	CTP synthase
TGME49_306895	1.69	1.61	1.38	hypothetical protein
TGME49_321540	-1.74	-1.49	-1.18	hypothetical protein
TGME49_254770	1.45	1.66	1.67	Ser/Thr phosphatase family protein
TGME49_290580	-2.49	-3.63	-2.61	ATP-binding cassette G family transporter ABCG89
TGME49_234640	-1.84	-1.52	-1.24	hypothetical protein
TGME49_208440	1.33	1.46	1.59	hypothetical protein
TGME49_252310	1.63	#N/A	1.02	hypothetical protein
TGME49_252360	1.57	1.05	1.78	rhoptry kinase family protein ROP24 (incomplete catalytic triad)
TGME49_254620	1.89	1.10	1.56	ribosomal protein RPL39
TGME49_243410	-2.01	-1.79	-1.36	tetratricopeptide repeat-containing protein
TGME49_279350	2.28	2.79	1.20	hypothetical protein
TGME49_293280	2.37	#N/A	#N/A	cyclin protein
TGME49_224220	-1.94	-1.73	-1.35	serine/threonine-protein phosphatase PP2A catalytic subunit
TGME49_253470	1.39	1.48	1.02	alveolin domain containing intermediate filament IMC13
TGME49_239270	-1.71	-2.30	-1.67	hypothetical protein
TGME49_203540	1.80	1.51	#N/A	RNA binding protein, putative
TGME49_293430	1.38	1.33	1.13	hypothetical protein
TGME49_244370	6.17	6.57	6.32	TDC1, putative
TGME49_219520	-1.51	-1.34	-1.38	histone arginine methyltransferase PRMT1
TGME49_261750	-1.75	-1.87	-1.64	rhoptry neck protein RON10
TGME49_242340	1.66	#N/A	0.96	ribosomal protein RPS29
TGME49_285190	-1.73	-1.76	-1.68	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_319540	-2.36	-2.49	-1.62	hypothetical protein
TGME49_278050	-1.45	-1.03	#N/A	proteasome subunit alpha type 1, putative

TGME49_213388	-1.46	-1.41	#N/A	hypothetical protein
TGME49_254480	1.45	#N/A	1.42	WD domain, G-beta repeat-containing protein
TGME49_238180	-0.95	#N/A	#N/A	26s proteasome regulatory complex subunit, putative
TGME49_220470	-1.04	#N/A	#N/A	hypothetical protein
TGME49_218740	1.54	#N/A	#N/A	membrane protein, putative
TGME49_222110	-1.24	#N/A	#N/A	PUB domain-containing protein
TGME49_236250	-1.28	#N/A	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_310230	-1.14	-1.13	#N/A	hypothetical protein
TGME49_256060	-1.00	-1.24	#N/A	nucleosome assembly protein (nap) protein
TGME49_205250	0.96	1.32	7.91	rhoptry protein ROP18
TGME49_240570	1.00	#N/A	#N/A	hypothetical protein
TGME49_312160	0.89	1.26	#N/A	hypothetical protein
TGME49_315280	-1.30	-1.86	#N/A	hypothetical protein
TGME49_256760	-0.93	#N/A	#N/A	pyruvate kinase PyK1
TGME49_217400	1.51	-1.37	-1.32	hypothetical protein
TGME49_254470	0.87	1.02	0.95	hypothetical protein
TGME49_217770	0.82	1.14	#N/A	hypothetical protein
TGME49_252210	1.25	#N/A	#N/A	pentatricopeptide repeat domain-containing protein
TGME49_306610	-1.56	-1.45	#N/A	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_308093	0.79	#N/A	1.75	rhoptry kinase family protein (incomplete catalytic triad)
TGME49_261460	-1.01	-1.01	#N/A	transcriptional elongation factor FACT80
TGME49_240910	-1.09	#N/A	-1.21	hypothetical protein
TGME49_294180	-1.26	#N/A	#N/A	tRNA -methyltransferase family protein
TGME49_234900	-0.85	-0.99	#N/A	PHD-finger domain-containing protein
TGME49_214470	-1.19	#N/A	#N/A	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_224070	-1.28	-1.32	#N/A	hypothetical protein
TGME49_221670	-0.81	#N/A	#N/A	transcriptional elongation factor FACT140
TGME49_242010	1.26	#N/A	#N/A	glucose inhibited division protein A subfamily protein
TGME49_254090	1.09	0.96	#N/A	hypothetical protein
TGME49_216910	-1.01	#N/A	#N/A	hypothetical protein
TGME49_269438	1.09	#N/A	#N/A	hypothetical protein
TGME49_279430	1.00	#N/A	#N/A	cwf18 pre-mRNA splicing factor protein

FIGURE 3E

TGME49_247340	2.08	#N/A	4.66	hypothetical protein
TGME49_320005	-2.72	-2.78	-2.39	hypothetical protein
TGME49_305160	3.60	3.04	2.59	histone H2Ba
TGME49_289050	2.13	1.75	#N/A	FIKK kinase, putative
TGME49_252290	1.69	#N/A	1.16	importin alpha, putative
TGME49_262010	1.74	1.18	#N/A	calmodulin CAM2
TGME49_249770	2.68	1.95	#N/A	Nmda1 protein
TGME49_228750	2.50	#N/A	#N/A	TGME49_228750 CAM kinase, RAD family
TGME49_277700	2.31	1.39	#N/A	ribosomal protein S14 precursor, putative
TGME49_233500	1.50	#N/A	0.89	triose-phosphate isomerase TPI-II
TGME49_311440	1.65	1.24	1.31	SAG-related sequence SRS50
TGME49_308840	1.66	#N/A	1.87	SAG-related sequence SRS51
TGME49_277710	-1.81	-1.81	-1.61	hypothetical protein
TGME49_215390	2.51	1.69	2.46	TIM10 family protein, putative
TGME49_215895	1.71	0.96	0.98	AP2 domain-containing protein
TGME49_260520	1.96	1.94	#N/A	hypothetical protein
TGME49_278510	-1.51	-1.43	-1.62	protein phosphatase 2C domain-containing protein
TGME49_252390	1.30	0.73	1.81	hypothetical protein
TGME49_312310	-2.52	-2.41	-2.24	ATPase, AAA family protein
TGME49_254050	1.39	1.59	1.30	optic atrophy 3 protein (opa3) protein
TGME49_213280	1.45	2.31	1.97	SAG-related sequence SRS25
TGME49_260210	-2.94	-2.82	-2.52	DnaJ domain-containing protein
TGME49_246978	-2.87	-2.84	-2.90	hypothetical protein
TGME49_279450	-7.76	-8.01	-7.66	adenylosuccinate synthetase, putative
TGME49_233030	-1.36	-1.03	-1.20	gliding-associated protein GAP70
TGME49_270530	-1.63	-1.14	-1.26	ubiquitin fusion degradation protein UFD1CY
TGME49_308090	2.51	#N/A	2.58	rhoptry protein ROP5
TGME49_205680	1.65	1.88	1.48	hypothetical protein
TGME49_268570	-1.42	-1.14	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_263270	-1.53	#N/A	#N/A	glycerophosphodiester phosphodiesterase family protein
TGME49_262910	2.83	1.44	#N/A	NADH-cytochrome b5 reductase 1, putative
TGME49_219832	-2.70	-2.64	-2.42	cyclin-dependent kinase regulatory subunit protein
TGME49_217010	-1.86	-1.53	-1.33	hypothetical protein
TGME49_312600	1.17	1.81	1.23	heat shock protein HSP21

TGME49_275650	1.13	#N/A	1.27	hypothetical protein
TGME49_225170	-1.22	#N/A	#N/A	hypothetical protein
TGME49_286790	-1.12	-1.22	#N/A	nuclear factor NF2
TGME49_295960	-1.27	#N/A	#N/A	hypothetical protein
TGME49_233430	1.41	#N/A	#N/A	hypothetical protein
TGME49_253070	1.36	#N/A	#N/A	hydrolase, TatD family protein
TGME49_249900	1.17	#N/A	#N/A	adenine nucleotide translocator, putative
TGME49_273140	-1.37	-1.45	#N/A	radical SAM methylthiotransferase, MiaB/RimO family protein
TGME49_231480	0.94	#N/A	#N/A	GCN1, putative
TGME49_321650	-0.82	-0.79	#N/A	hypothetical protein
TGME49_319740	-1.41	-1.51	#N/A	transporter, major facilitator family protein
TGME49_201880	0.73	0.72	0.87	hypothetical protein
TGME49_204040	1.61	#N/A	#N/A	hypothetical protein
TGME49_266750	0.85	#N/A	#N/A	transporter/permease protein, putative
TGME49_227150	0.87	#N/A	1.22	glutaredoxin, putative
TGME49_291120	-1.11	-1.11	#N/A	trafficking protein mon1 subfamily protein
TGME49_285950	-1.50	#N/A	#N/A	hypothetical protein
TGME49_239680	0.97	#N/A	#N/A	hypothetical protein
TGME49_213790	-1.09	-1.09	-1.10	hypothetical protein
TGME49_318690	1.29	1.35	1.49	RNA recognition motif-containing protein
TGME49_254290	1.08	1.01	#N/A	hypothetical protein
TGME49_280570	#N/A	5.19	5.07	SAG-related sequence SRS35A
TGME49_291040	#N/A	5.96	4.68	lactate dehydrogenase LDH2
TGME49_259020	#N/A	5.33	6.15	bradyzoite antigen BAG1
TGME49_216140	#N/A	3.66	1.19	tetratricopeptide repeat-containing protein
TGME49_299010	#N/A	4.46	#N/A	hypothetical protein
TGME49_202970	#N/A	-5.95	#N/A	hypothetical protein
TGME49_264240	#N/A	-10.43	-6.12	hypothetical protein
TGME49_312905	#N/A	-3.09	#N/A	hypothetical protein
TGME49_244700	#N/A	-2.91	#N/A	NAD(+)/NADH kinase domain-containing protein
TGME49_280400	#N/A	-3.11	#N/A	hypothetical protein
TGME49_233000	#N/A	-2.52	#N/A	KOW motif domain-containing protein
TGME49_266950	#N/A	-2.61	#N/A	protein kinase, putative
TGME49_203720	#N/A	2.05	1.19	vitamin k epoxide reductase family protein

FIGURE 3F

TGME49_249860	-1.63	-1.42	-1.57	hypothetical protein
TGME49_223040	1.52	1.48	0.97	hypothetical protein
TGME49_275320	-1.56	-1.34	-1.50	penicillin amidase
TGME49_255650	-1.54	#N/A	-1.18	DHHC zinc finger domain-containing protein
TGME49_242110	-2.88	#N/A	-3.56	rhoptry kinase family protein ROP38
TGME49_254520	1.33	1.57	1.45	mediator complex subunit MED11
TGME49_266100	1.48	1.33	1.51	rhoptry kinase family protein ROP41
TGME49_247770	1.21	1.09	#N/A	hypothetical protein
TGME49_215540	-8.74	-8.70	#N/A	hypothetical protein
TGME49_254910	2.11	#N/A	#N/A	hypothetical protein
TGME49_287470	2.41	2.95	#N/A	hypothetical protein
TGME49_252250	2.15	#N/A	1.30	ATPase, AAA family protein
TGME49_240520	2.21	#N/A	#N/A	hypothetical protein
TGME49_220400	2.00	1.70	1.45	actin depolymerizing factor ADF
TGME49_262500	-1.75	-1.50	-1.13	hypothetical protein
TGME49_207630	-3.63	-3.31	-3.45	peptidyl-tRNA hydrolase domain-containing protein
TGME49_210430	-1.34	-1.23	-0.93	DnaJ domain-containing protein
TGME49_290600	6.12	6.38	6.31	succinyl-CoA-synthetase alpha SCSA
TGME49_211220	-1.89	-1.98	#N/A	hypothetical protein
TGME49_286140	-1.99	-1.63	-1.40	hypothetical protein
TGME49_268730	2.02	1.22	#N/A	glutaredoxin-related protein
TGME49_311210	-1.66	-1.38	-1.53	hypothetical protein
TGME49_284190	1.69	#N/A	#N/A	pyruvate carboxylase
TGME49_200595	-9.05	-7.22	#N/A	hypothetical protein
TGME49_271935	1.72	2.09	2.02	hypothetical protein
TGME49_261000	-1.86	-1.73	#N/A	MutS domain V domain-containing protein
TGME49_280518	-1.51	-1.09	#N/A	hypothetical protein
TGME49_320110	2.87	2.51	3.01	proliferating cell nuclear antigen PCNA2
TGME49_209755	-1.64	3.95	3.84	hypothetical protein
TGME49_286720	1.48	0.86	#N/A	heat shock protein HSP28
TGME49_321360	1.18	1.69	1.55	clustered-asparagine-rich protein
TGME49_202540	-1.37	-0.98	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_230490	-1.72	-1.20	-1.58	phosphatidylinositol-4-phosphate 5-kinase
TGME49_297420	-2.07	-1.75	-1.64	beta-tubulin cofactor D, putative
TGME49_253290	1.20	1.29	1.10	valyl-tRNA synthetase
TGME49_217951	-1.96	-2.00	4.96	hypothetical protein

TGME49_235680	#N/A	-2.63	#N/A	peptidase M16 inactive domain-containing protein
TGME49_289350	#N/A	-3.12	#N/A	ATP-binding cassette G family transporter ABCG84
TGME49_307770	#N/A	-2.38	#N/A	fumble protein
TGME49_207210	#N/A	3.26	4.66	hypothetical protein
TGME49_311460	#N/A	-2.95	#N/A	hypothetical protein
TGME49_209940	#N/A	-2.26	#N/A	transporter/permease protein
TGME49_283540	#N/A	1.98	1.10	hypothetical protein
TGME49_210210	#N/A	-9.04	#N/A	hypothetical protein
TGME49_213255	#N/A	-2.66	#N/A	hypothetical protein
TGME49_264260	#N/A	-4.82	#N/A	hypothetical protein
TGME49_280490	#N/A	-1.99	#N/A	U-box domain-containing protein
TGME49_221840	#N/A	3.66	4.30	hypothetical protein
TGME49_306688	#N/A	-3.91	#N/A	hypothetical protein
TGME49_238140	#N/A	-2.18	-1.15	hypothetical protein
TGME49_263820	#N/A	-2.10	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_240220	#N/A	-2.27	#N/A	hypothetical protein
TGME49_216680	#N/A	-2.19	#N/A	ankyrin repeat-containing protein
TGME49_214410	#N/A	1.67	1.11	hypothetical protein
TGME49_253690	#N/A	1.66	1.79	hypothetical protein
TGME49_306338	#N/A	-2.76	#N/A	dynein gamma chain, flagellar outer arm, putative
TGME49_297840	#N/A	-1.92	#N/A	DNA primase, large subunit
TGME49_204050	#N/A	2.64	#N/A	subtilisin SUB1
TGME49_298060	#N/A	-2.83	#N/A	Toxoplasma gondii family C protein
TGME49_202020	#N/A	2.74	2.69	DnAK-TPR
TGME49_275460	#N/A	2.53	1.38	hypothetical protein
TGME49_240880	#N/A	-2.58	#N/A	hypothetical protein
TGME49_205210	#N/A	-5.32	#N/A	hypothetical protein
TGME49_251540	#N/A	1.64	#N/A	dense granule protein GRA9
TGME49_236670	#N/A	2.12	2.81	hypothetical protein
TGME49_316470	#N/A	-2.66	#N/A	hypothetical protein
TGME49_217020	#N/A	-2.26	#N/A	ATPase, AFG1 family protein
TGME49_218750	#N/A	-2.82	#N/A	hypothetical protein
TGME49_312520	#N/A	-2.75	#N/A	tRNA dimethylallyltransferase
TGME49_234530	#N/A	1.69	1.33	hypothetical protein
TGME49_316250	#N/A	1.44	1.00	hypothetical protein
TGME49_315130	#N/A	1.51	0.93	L-isoaspartyl protein carboxyl methyltransferase family protein

FIGURE 3G

TGME49_259530	-1.67	-1.62	-1.69	GalNac
TGME49_268620	-3.08	-2.80	-2.80	blood stage antigen 41-3 precursor, putative
TGME49_223150	-2.63	-2.38	-2.36	START domain-containing protein
TGME49_223840	1.73	#N/A	#N/A	ATP-citrate lyase, putative
TGME49_201790	-1.60	-1.12	#N/A	FHA domain-containing protein
TGME49_237195	-2.18	-1.66	#N/A	hypothetical protein
TGME49_252270	1.93	#N/A	#N/A	L1P family of ribosomal protein
TGME49_253990	1.44	1.02	0.91	hypothetical protein
TGME49_293550	-1.38	-1.09	#N/A	hypothetical protein
TGME49_254610	1.75	1.37	#N/A	Tim10/DDP family zinc finger superfamily protein
TGME49_254900	1.33	0.89	#N/A	proteasome subunit beta type 2, putative
TGME49_306730	-3.20	#N/A	-2.45	hypothetical protein
TGME49_248630	-1.60	-1.11	#N/A	actin-related protein ARP1
TGME49_252500	1.20	1.38	1.53	polo kinase
TGME49_238073	-2.22	#N/A	#N/A	hypothetical protein
TGME49_227330	1.71	1.13	#N/A	hypothetical protein
TGME49_222900	1.37	#N/A	#N/A	phosphoserine phosphatase
TGME49_205510	-1.20	#N/A	#N/A	nucleolar protein 5, putative
TGME49_255635	-4.70	-3.83	-5.53	hypothetical protein
TGME49_204110	-2.91	-2.23	#N/A	eIF2 kinase IF2K-C
TGME49_259115	-2.00	-5.11	-1.48	ABC1 family protein
TGME49_321550	1.54	1.11	#N/A	hypothetical protein
TGME49_213800	-1.29	-0.89	#N/A	protein phosphatase 2b regulatory subunit, putative
TGME49_258030	-2.43	-2.70	#N/A	DNA polymerase
TGME49_252190	2.13	2.25	1.41	KRUF family protein
TGME49_292200	-1.23	-0.93	#N/A	RNA recognition motif-containing protein
TGME49_247530	1.25	1.99	1.67	hypothetical protein
TGME49_298990	1.50	0.89	#N/A	ferredoxin NADP+ oxidoreductase FNR
TGME49_229440	-1.85	-1.88	-2.19	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_293480	1.93	#N/A	2.09	MoeA N-terminal region (domain I and II) domain-containing protein
TGME49_239410	-1.36	-1.12	#N/A	hypothetical protein
TGME49_237410	-1.64	-1.14	-1.13	protein phosphatase 2C domain-containing protein
TGME49_257180	-1.98	-2.08	-1.89	RecF/RecN/SMC N terminal domain-containing protein
TGME49_217350	-2.50	-2.31	-2.26	methyltransferase MTA70, putative

TGME49_240650	#N/A	-1.59	-1.13	coatomer protein complex, subunit alpha, putative
TGME49_297910	#N/A	-3.38	#N/A	hypothetical protein
TGME49_262050	#N/A	2.31	1.98	rhoptry kinase family protein ROP39
TGME49_239250	#N/A	-1.47	#N/A	diacylglycerol kinase, putative
TGME49_268860	#N/A	4.31	4.11	enolase 1
TGME49_240840	#N/A	-2.01	#N/A	histone lysine demethylase JmjC NO66
TGME49_202780	#N/A	1.32	1.04	rhoptry kinase family protein ROP25
TGME49_262590	#N/A	-3.61	#N/A	hypothetical protein
TGME49_312330	#N/A	1.73	#N/A	hypothetical protein
TGME49_301160	#N/A	-3.93	#N/A	SAG-related sequence SRS19C
TGME49_293740	#N/A	1.33	0.99	hypothetical protein
TGME49_244120	#N/A	-2.11	-1.84	hypothetical protein
TGME49_288860	#N/A	-1.61	#N/A	RuvB family 2 protein
TGME49_292975	#N/A	-1.81	#N/A	hypothetical protein
TGME49_253180	#N/A	2.53	2.00	hypothetical protein
TGME49_297492	#N/A	-4.59	-3.43	hypothetical protein
TGME49_277510	#N/A	-1.70	-1.09	cytoplasmic dynein intermediate chain
TGME49_246200	#N/A	-2.81	-2.46	zinc finger (CCCH type) motif-containing protein
TGME49_258230	#N/A	2.52	#N/A	rhoptry kinase family protein ROP20
TGME49_217420	#N/A	-2.47	-1.59	hypothetical protein
TGME49_215700	#N/A	-1.84	#N/A	phosphatidylinositol 3- and 4-kinase
TGME49_225290	#N/A	2.97	#N/A	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_307650	#N/A	-1.81	#N/A	uracil-DNA glycosylase
TGME49_263730	#N/A	-1.66	#N/A	FAD-dependent glycerol-3-phosphate dehydrogenase
TGME49_263100	#N/A	-2.14	#N/A	hypothetical protein
TGME49_248990	#N/A	1.22	#N/A	hypothetical protein
TGME49_269690	#N/A	1.16	#N/A	hypothetical protein
TGME49_310970	#N/A	-1.43	#N/A	hypothetical protein
TGME49_323100	#N/A	1.64	#N/A	hypothetical protein
TGME49_316710	#N/A	1.24	#N/A	hypothetical protein
TGME49_290700	#N/A	1.27	#N/A	hypothetical protein
TGME49_239810	#N/A	1.60	#N/A	hypothetical protein
TGME49_269180	#N/A	-1.20	-1.22	MIF4G domain-containing protein
TGME49_285870	#N/A	1.32	#N/A	SAG-related sequence SRS20A

FIGURE 3H

TGME49_230140	2.10	#N/A	#N/A	vacuolar sorting protein 9 (vps9) domain-containing protein
TGME49_319580	-2.55	-2.72	-2.59	hypothetical protein
TGME49_281450	-1.99	-1.50	#N/A	cell-cycle-associated protein kinase, putative
TGME49_203390	-1.39	-1.16	#N/A	CRAL/TRIO domain-containing protein
TGME49_295950	1.65	2.39	1.36	KRUF family protein
TGME49_270580	2.21	#N/A	3.82	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_243465	3.08	#N/A	#N/A	hypothetical protein
TGME49_253860	1.32	1.25	1.04	Tyrosine kinase-like (TKL) protein
TGME49_251460	-1.84	-1.36	-1.56	hypothetical protein
TGME49_253100	1.15	1.26	1.15	hypothetical protein
TGME49_222040	-2.70	-2.83	-3.28	Ran-interacting Mog1 protein
TGME49_289310	-1.53	-1.26	-1.11	cullin family protein
TGME49_228360	1.39	0.88	1.31	peptidyl-prolyl isomerase FKBP12, putative
TGME49_201260	-1.25	-1.14	-1.27	sugar transporter ST3
TGME49_228630	-1.29	-1.09	#N/A	hypothetical protein
TGME49_232960	-1.48	-1.21	-1.32	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_262825	2.05	1.47	#N/A	peptidase family c50 protein
TGME49_263060	1.64	1.13	#N/A	Proteasome/cyclosome repeat-containing protein
TGME49_240950	-3.19	-3.14	-2.61	hypothetical protein
TGME49_240440	1.45	1.19	1.01	hypothetical protein
TGME49_316270	1.43	1.40	1.61	Rab geranylgeranyl transferase type II beta subunit, putative
TGME49_289720	-1.72	-1.60	#N/A	hypothetical protein
TGME49_273400	-2.22	-1.55	#N/A	hypothetical protein
TGME49_288580	2.50	1.40	#N/A	RNA methylase, putative
TGME49_287160	-1.25	-1.19	#N/A	internal kinesin motor domain protein
TGME49_213635	2.50	2.45	#N/A	hypothetical protein
TGME49_298610	-1.15	-1.02	#N/A	GYF domain-containing protein
TGME49_203730	-2.06	-2.40	-2.44	hypothetical protein
TGME49_313230	2.39	2.44	2.45	eukaryotic initiation factor-2, alpha subunit
TGME49_226755	1.53	1.60	1.13	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_253600	1.77	2.31	1.45	hypothetical protein
TGME49_254630	1.34	1.08	#N/A	CMGC kinase

TGME49_289540	#N/A	1.20	#N/A	hypothetical protein
TGME49_246130	#N/A	1.27	#N/A	serpin (serine proteinase inhibitor) superfamily protein
TGME49_263740	#N/A	-1.88	#N/A	ABC transporter transmembrane region domain-containing protein
TGME49_260190	#N/A	-1.57	#N/A	microneme protein MIC13
TGME49_276920	#N/A	-1.63	-1.73	protein phosphatase 2C domain-containing protein
TGME49_253700	#N/A	1.05	#N/A	transporter, major facilitator family protein
TGME49_254150	#N/A	1.91	1.62	hypothetical protein
TGME49_237015	#N/A	1.37	0.96	hypothetical protein
TGME49_264870	#N/A	1.39	1.20	Sodium:neurotransmitter symporter family protein
TGME49_226580	#N/A	1.12	#N/A	hypothetical protein
TGME49_202620	#N/A	1.18	#N/A	hypothetical protein
TGME49_213680	#N/A	-2.26	-2.37	MmgE/PrpD family protein
TGME49_245530	#N/A	3.38	#N/A	hypothetical protein
TGME49_296015	#N/A	1.22	1.16	hypothetical protein
TGME49_272600	#N/A	-1.29	#N/A	adaptin c-terminal domain-containing protein
TGME49_285830	#N/A	-1.60	-1.21	hypothetical protein
TGME49_226260	#N/A	1.23	#N/A	hypothetical protein
TGME49_310210	#N/A	1.73	#N/A	hypothetical protein
TGME49_255960	#N/A	-1.75	-1.38	hypothetical protein
TGME49_240580	#N/A	-1.94	#N/A	hypothetical protein
TGME49_297180	#N/A	-1.25	#N/A	hypothetical protein
TGME49_311660	#N/A	-1.65	#N/A	histone lysine methyltransferase, SET, putative
TGME49_253490	#N/A	1.38	1.22	hypothetical protein
TGME49_257910	#N/A	4.40	#N/A	hypothetical protein
TGME49_269930	#N/A	-2.18	#N/A	calcium binding egf domain-containing protein
TGME49_201380	#N/A	1.04	#N/A	chorismate synthase, putative
TGME49_253170	#N/A	1.97	1.79	zinc carboxypeptidase, putative
TGME49_307570	#N/A	-1.64	-1.35	glycerol-3-phosphate dehydrogenase (gpdh), putative
TGME49_310100	#N/A	-2.01	#N/A	mannosyltransferase (pig-m) protein
TGME49_299060	#N/A	1.37	#N/A	sodium/hydrogen exchanger NHE2
TGME49_203290	#N/A	1.61	#N/A	hypothetical protein
TGME49_247250	#N/A	-1.28	#N/A	RbAp46

FIGURE 3i

TGME49_309070	-2.16	-1.93	-1.67	hypothetical protein
TGME49_233680	-2.80	-2.92	-2.65	nuclear movement family protein
TGME49_229470	-1.47	-1.06	-1.37	hypothetical protein
TGME49_207180	2.21	#N/A	#N/A	indole-3-glycerol phosphate synthase domain-containing protein
TGME49_290740	-2.43	-2.09	#N/A	hypothetical protein
TGME49_230430	-2.22	-1.88	-2.06	vesicle-associated membrane protein, putative
TGME49_294060	1.52	0.97	#N/A	hypothetical protein
TGME49_300980	2.31	#N/A	#N/A	hypothetical protein
TGME49_286510	1.70	1.27	1.10	hypothetical protein
TGME49_248130	-2.53	-2.03	-2.01	hypothetical protein
TGME49_285470	2.15	1.63	#N/A	patched family protein
TGME49_283550	1.34	1.04	0.97	hypothetical protein
TGME49_300055	-1.16	#N/A	#N/A	hypothetical protein
TGME49_297780	-1.71	-2.60	-1.53	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_293040	-1.91	-1.63	#N/A	hypothetical protein
TGME49_258590	-2.37	-2.06	-2.53	hypothetical protein
TGME49_215785	2.21	1.79	#N/A	rhoptry protein ROP2A
TGME49_214400	1.75	1.71	1.40	hypothetical protein
TGME49_237290	-1.50	-1.34	-1.25	hypothetical protein
TGME49_268810	-1.75	-1.47	-1.52	ck2 beta subunit
TGME49_237830	-1.92	-1.66	-1.95	DNA polymerase I domain-containing protein
TGME49_226380	1.18	1.80	1.34	hypothetical protein
TGME49_227335	2.40	1.44	#N/A	hypothetical protein
TGME49_274070	-2.79	-3.35	-2.85	ThiF family protein
TGME49_215400	-2.20	-1.61	-1.74	RNA recognition motif-containing protein
TGME49_241300	1.80	#N/A	#N/A	hypothetical protein
TGME49_253140	1.54	1.52	1.47	hypothetical protein
TGME49_305990	3.44	2.44	#N/A	hypothetical protein
TGME49_288400	-1.71	-1.81	-1.67	LETM1 family protein
TGME49_273530	-2.31	-1.77	#N/A	flagellar associated protein
TGME49_277540	2.13	1.89	#N/A	hypothetical protein
TGME49_220500	-1.33	#N/A	#N/A	UBX domain-containing protein
TGME49_225440	-4.18	-4.09	-3.61	hypothetical protein
TGME49_293840	1.98	#N/A	#N/A	hypothetical protein
TGME49_212090	1.14	1.15	1.15	hypothetical protein
TGME49_264780	#N/A	-1.66	#N/A	UTP-glucose-1-phosphate uridylyltransferase subfamily protein
TGME49_268790	#N/A	1.04	#N/A	hypothetical protein
TGME49_259700	#N/A	1.16	0.83	hypothetical protein
TGME49_205150	#N/A	-1.81	#N/A	ACR, YagE family COG1723 domain-containing protein
TGME49_248830	#N/A	-1.43	#N/A	phosphoinositide phospholipase PIPLC
TGME49_254580	#N/A	1.29	#N/A	UDP-galactose transporter family protein
TGME49_278270	#N/A	-2.06	-1.58	nucleolar protein, structural component of H/ACA snoRNPs, putative
TGME49_264660	#N/A	1.41	#N/A	SAG-related sequence SRS44
TGME49_229650	#N/A	-1.58	-1.29	josephin protein
TGME49_214540	#N/A	1.16	1.33	hypothetical protein
TGME49_273030	#N/A	-1.68	#N/A	phosphoglycerate mutase family protein
TGME49_311780	#N/A	-1.47	#N/A	Zn-containing alcohol dehydrogenase
TGME49_215360	#N/A	1.53	#N/A	hypothetical protein
TGME49_262970	#N/A	1.54	#N/A	hypothetical protein
TGME49_241140	#N/A	-1.88	-1.55	DEAD/DEAH box helicase domain-containing protein
TGME49_219610	#N/A	1.77	1.62	hypothetical protein
TGME49_277260	#N/A	2.11	2.43	hypothetical protein
TGME49_315910	#N/A	1.44	#N/A	hypothetical protein
TGME49_240430	#N/A	-2.18	-2.23	glyoxalase family protein
TGME49_275755	#N/A	2.33	3.42	hypothetical protein
TGME49_307580	#N/A	-1.23	#N/A	CBS domain-containing protein
TGME49_257360	#N/A	1.87	#N/A	hypothetical protein
TGME49_202830	#N/A	1.10	#N/A	Elicitor-responsive protein, putative
TGME49_258940	#N/A	1.50	#N/A	acylphosphatase family protein
TGME49_279100	#N/A	1.08	1.35	hypothetical protein
TGME49_254880	#N/A	1.03	#N/A	Alpha-galactosidase
TGME49_271430	#N/A	-2.03	-1.77	hypothetical protein
TGME49_257290	#N/A	-1.92	#N/A	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_253710	#N/A	1.14	#N/A	hypothetical protein
TGME49_245980	#N/A	2.76	#N/A	hypothetical protein
TGME49_227390	#N/A	-1.67	#N/A	hypothetical protein
TGME49_272650	#N/A	-1.50	-1.17	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_290970	#N/A	2.67	#N/A	8-amino-7-oxononanoate synthase
TGME49_227430	#N/A	-1.65	2.88	transmembrane amino acid transporter protein
TGME49_258670	#N/A	-1.66	#N/A	hypothetical protein

FIGURE 3J

TGME49_244230	-2.07	-1.85	#N/A	hypothetical protein
TGME49_258410	1.26	1.07	1.02	photosensitized INA-labeled protein PHIL1
TGME49_248160	-2.51	-2.29	-2.51	hypothetical protein
TGME49_261660	1.96	1.38	#N/A	hypothetical protein
TGME49_241610	1.80	#N/A	#N/A	hypothetical protein
TGME49_249390	-1.14	#N/A	#N/A	glutamate/leucine/phenylalanine/valine dehydrogenase family protein
TGME49_205330	1.10	1.39	1.01	hypothetical protein
TGME49_214970	-1.38	-1.28	-1.23	DNA replication licensing factor, putative
TGME49_291930	3.85	3.68	3.85	RNA recognition motif-containing protein
TGME49_309990	1.26	1.37	1.54	hypothetical protein
TGME49_210380	-1.30	-1.26	-1.15	hypothetical protein
TGME49_213570	4.50	4.95	4.84	hypothetical protein
TGME49_221675	1.12	1.51	#N/A	hypothetical protein
TGME49_246530	2.25	1.85	#N/A	phospholipase D active site domain-containing protein
TGME49_289620	1.19	0.81	#N/A	cathepsin CPC1
TGME49_294890	-1.47	-1.25	#N/A	hypothetical protein
TGME49_202580	2.00	1.59	#N/A	ATPase, AAA family protein
TGME49_266860	1.40	#N/A	#N/A	BTB/POZ domain-containing protein
TGME49_312270	1.16	1.48	1.37	rhoptry protein ROP13
TGME49_266280	-1.44	-1.16	#N/A	HEAT repeat-containing protein
TGME49_218960	1.65	#N/A	#N/A	AP2 domain transcription factor AP2XII-1
TGME49_263860	-2.07	-1.85	#N/A	hypothetical protein
TGME49_310130	-1.62	-1.52	-1.58	Spc97 / Spc98 family protein
TGME49_316255	1.05	1.20	#N/A	hypothetical protein
TGME49_254720	1.69	2.04	1.44	dense granule protein GRA8
TGME49_271930	-1.06	-1.06	-0.99	hypothetical protein
TGME49_225130	-2.67	-3.12	-3.05	hypothetical protein
TGME49_301130	-2.25	-1.69	#N/A	hypothetical protein
TGME49_248400	1.31	1.09	#N/A	glyoxalase I, putative
TGME49_270830	1.20	1.18	#N/A	small nuclear ribonucleoprotein
TGME49_221330	-1.48	-1.02	-1.17	DNA gyrase/topoisomerase IV, A subunit domain-containing protein
TGME49_255510	-1.22	-1.31	-1.43	ankyrin repeat-containing protein
TGME49_253780	1.32	1.16	#N/A	GTP cyclohydrolase I, putative
TGME49_238240	4.88	5.33	5.25	bystin protein
TGME49_208910	-1.58	-1.60	-1.53	hypothetical protein
TGME49_225470	1.44	0.98	#N/A	peptide methionine sulfoxide reductase

TGME49_208010	#N/A	1.18	#N/A	hypothetical protein
TGME49_224830	#N/A	-2.46	#N/A	hypothetical protein
TGME49_293500	#N/A	-2.44	-2.99	hypothetical protein
TGME49_217640	#N/A	1.39	#N/A	hypothetical protein
TGME49_295400	#N/A	-2.03	-1.87	hypothetical protein
TGME49_267590	#N/A	-1.55	-1.36	hypothetical protein
TGME49_289340	#N/A	1.81	#N/A	hypothetical protein
TGME49_323110	#N/A	1.76	1.47	hypothetical protein
TGME49_280580	#N/A	1.79	3.89	SAG-related sequence SRS35B
TGME49_251520	#N/A	1.15	#N/A	hypothetical protein
TGME49_247360	#N/A	0.99	1.07	PAP2 superfamily protein
TGME49_244040	#N/A	-1.83	-1.68	HEAT repeat-containing protein
TGME49_295472	#N/A	-1.50	-1.45	C2 domain-containing protein
TGME49_318480	#N/A	-1.61	#N/A	SWI2/SNF2-containing protein RAD5
TGME49_224540	#N/A	-1.65	-1.52	hypothetical protein
TGME49_200320	#N/A	-1.13	-1.28	hypoxanthine-xanthine-guanine phosphoribosyl transferase HXGPRT
TGME49_300030	#N/A	-1.19	#N/A	hypothetical protein
TGME49_203790	#N/A	1.02	0.81	hypothetical protein
TGME49_206610	#N/A	-1.41	#N/A	pyruvate dehydrogenase complex subunit PDH-E2
TGME49_209050	#N/A	-1.38	-1.37	Tyrosine kinase-like (TKL) protein
TGME49_236890	#N/A	1.02	0.88	hypothetical protein
TGME49_313910	#N/A	1.57	#N/A	RNA recognition motif 2 protein
TGME49_254390	#N/A	1.58	#N/A	CRAL/TRIO domain-containing protein
TGME49_277490	#N/A	1.05	#N/A	hypothetical protein
TGME49_261022	#N/A	-2.98	#N/A	dynein heavy chain family protein
TGME49_273950	#N/A	-1.88	-1.68	replication factor C subunit 5, putative
TGME49_242570	#N/A	-1.04	#N/A	hypothetical protein
TGME49_207830	#N/A	1.05	#N/A	MORN repeat-containing protein
TGME49_212100	#N/A	-1.56	#N/A	ThiF family protein
TGME49_253940	#N/A	1.04	#N/A	CAM Kinase family, incomplete catalytic triad
TGME49_224170	#N/A	1.76	2.34	SAG-related sequence SRS60A
TGME49_220910	#N/A	-1.47	-1.62	HEAT repeat-containing protein
TGME49_249990	#N/A	1.43	#N/A	hypothetical protein
TGME49_224020	#N/A	1.06	1.06	hypothetical protein
TGME49_293470	#N/A	-1.12	-0.93	hypothetical protein
TGME49_208040	#N/A	-1.50	#N/A	aldo-keto reductase

FIGURE 3K

TGME49_310390	1.86	1.34	#N/A	hypothetical protein
TGME49_279410	1.27	0.99	#N/A	hypothetical protein
TGME49_270550	1.65	#N/A	#N/A	gamma-glutamyl phosphate reductase, putative
TGME49_247590	1.92	#N/A	#N/A	methyltransferase domain-containing protein
TGME49_262880	1.76	#N/A	#N/A	hypothetical protein
TGME49_293380	-2.19	-2.21	-1.76	histone lysine acetyltransferase HAT1
TGME49_224520	-1.10	-0.76	#N/A	alveolin domain containing intermediate filament IMC8
TGME49_259240	4.14	3.87	4.06	ribosomal protein RPS21
TGME49_319530	-1.18	-0.93	#N/A	splicing factor SF2
TGME49_312105	-2.30	-1.90	#N/A	hypothetical protein
TGME49_289940	1.77	#N/A	#N/A	uroporphyrinogen decarboxylase
TGME49_226240	1.50	1.06	1.60	bud site selection protein, putative
TGME49_244380	2.38	2.30	2.19	cactin
TGME49_283820	-2.80	-2.68	-2.83	glycine cleavage T-protein (aminomethyl transferase) domain-containing protein
TGME49_241305	1.59	#N/A	#N/A	hypothetical protein
TGME49_296121	1.39	1.48	#N/A	hypothetical protein
TGME49_288890	1.67	#N/A	#N/A	hypothetical protein
TGME49_299240	1.61	1.62	1.64	hypothetical protein
TGME49_255410	-1.45	-1.21	#N/A	hypothetical protein
TGME49_288000	1.31	#N/A	#N/A	hypothetical protein
TGME49_216020	-1.98	-1.83	-1.87	peptidase family c78 protein
TGME49_220640	-1.66	#N/A	#N/A	hypothetical protein
TGME49_320050	7.35	7.07	7.08	ribosomal protein RPL5
TGME49_278800	-1.23	-1.21	#N/A	zinc finger protein 36 family 3 protein
TGME49_298830	2.52	2.69	#N/A	hypothetical protein
TGME49_253330	1.55	3.85	1.57	Rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_265840	-1.35	-1.01	#N/A	hypothetical protein
TGME49_297730	-1.93	-1.75	-1.86	transcription elongation factor 1, putative
TGME49_239490	1.17	1.04	#N/A	dehydrogenase E1 component family protein
TGME49_226680	-1.19	-1.23	#N/A	hypothetical protein
TGME49_260790	-1.74	-1.54	#N/A	RAP domain-containing protein
TGME49_283710	-1.48	-1.50	-1.20	Longevity-assurance protein (LAG1) domain-containing protein
TGME49_266450	1.70	#N/A	#N/A	lysine decarboxylase family protein
TGME49_306890	2.64	#N/A	#N/A	hypothetical protein

TGME49_212300	#N/A	0.96	#N/A	hypothetical protein
TGME49_286180	#N/A	-2.39	#N/A	tRNA ligases class I (M) protein
TGME49_299015	#N/A	1.90	#N/A	hypothetical protein
TGME49_237860	#N/A	-2.24	#N/A	protein kinase domain-containing protein
TGME49_213730	#N/A	0.99	#N/A	lanthionine synthetase C family protein
TGME49_244670	#N/A	0.95	1.34	hypothetical protein
TGME49_225480	#N/A	-1.79	#N/A	hypothetical protein
TGME49_264970	#N/A	-1.82	-1.84	hypothetical protein
TGME49_253360	#N/A	0.97	0.86	hypothetical protein
TGME49_232780	#N/A	-1.39	#N/A	hypothetical protein
TGME49_220610	#N/A	-1.34	#N/A	protein phosphatase 2C domain-containing protein
TGME49_320610	#N/A	-1.67	-1.49	hypothetical protein
TGME49_208370	#N/A	1.17	#N/A	myosin heavy chain, putative
TGME49_234180	#N/A	1.08	1.00	hypothetical protein
TGME49_262600	#N/A	-2.01	#N/A	hypothetical protein
TGME49_207160	#N/A	1.90	2.16	SAG-related sequence SRS49D
TGME49_206640	#N/A	-1.11	#N/A	hypothetical protein
TGME49_214220	#N/A	1.16	#N/A	hypothetical protein
TGME49_286440	#N/A	1.01	0.97	malic enzyme
TGME49_294200	#N/A	1.35	#N/A	glucose-6-phosphate 1-dehydrogenase
TGME49_320430	#N/A	-1.26	#N/A	cell-cycle-control protein (translation regulation), putative
TGME49_284010	#N/A	-1.68	#N/A	5'-3' exonuclease, N-terminal resolvase family domain-containing protein
TGME49_293330	#N/A	1.37	#N/A	hypothetical protein
TGME49_243430	#N/A	1.04	#N/A	OTU family cysteine protease
TGME49_241130	#N/A	-2.00	#N/A	hypothetical protein
TGME49_261400	#N/A	-0.97	#N/A	hypothetical protein
TGME49_224210	#N/A	-1.35	#N/A	hypothetical protein
TGME49_209970	#N/A	-1.38	-1.33	Spc97 / Spc98 family protein
TGME49_213300	#N/A	-1.59	#N/A	hypothetical protein
TGME49_297940	#N/A	-1.28	#N/A	single-strand binding protein
TGME49_311770	#N/A	-1.18	#N/A	hypothetical protein
TGME49_318760	#N/A	1.10	#N/A	hypothetical protein
TGME49_245475	#N/A	1.52	#N/A	hypothetical protein
TGME49_260620	#N/A	0.84	#N/A	hypothetical protein

FIGURE 3L

TGME49_250100	1.44	1.23	1.71	hypothetical protein
TGME49_263710	-1.52	-1.68	-1.45	acyl-CoA:cholesterol acyltransferase alpha ACAT1-alpha
TGME49_236050	-3.84	-2.92	#N/A	fructose-bisphosphate aldolase, putative
TGME49_225250	1.27	0.88	1.03	LSU ribosomal protein L14P, putative
TGME49_311920	-1.24	-1.12	-1.17	GRAM domain-containing protein
TGME49_300240	-1.77	#N/A	-1.37	syntaxin 6, n-terminal protein
TGME49_203180	1.79	#N/A	#N/A	leucine rich repeat-containing protein
TGME49_267460	2.01	2.48	#N/A	AP2 domain transcription factor AP2IX-1
TGME49_209985	1.74	#N/A	2.85	cAMP-dependent protein kinase
TGME49_295990	1.16	1.11	1.00	ubiquitin conjugating enzyme E2, putative
TGME49_252630	1.14	1.10	0.91	hypothetical protein
TGME49_209440	1.71	#N/A	#N/A	hypothetical protein
TGME49_228160	1.14	1.73	1.84	acid phosphatase
TGME49_221410	-1.40	-1.15	-1.09	actin-like protein ALP4
TGME49_214270	2.82	2.72	2.98	translation initiation factor IF-2, putative
TGME49_280700	-1.43	#N/A	-1.78	arginine decarboxylase
TGME49_204055	-2.14	-1.67	#N/A	hypothetical protein
TGME49_290670	1.08	0.99	#N/A	leucyl aminopeptidase LAP
TGME49_315620	-1.29	-1.14	-1.02	vacuolar ATP synthase subunit C, putative
TGME49_271270	1.10	0.92	#N/A	hypothetical protein
TGME49_316230	-1.61	-1.42	-1.65	SAC1 phosphoinositide phosphatase, putative
TGME49_252430	1.05	1.30	1.46	hypothetical protein
TGME49_308010	-1.98	-1.86	#N/A	hypothetical protein
TGME49_295030	-1.06	#N/A	#N/A	hypothetical protein
TGME49_289650	1.03	0.98	0.97	PEP-carboxykinase I
TGME49_233160	-1.12	#N/A	#N/A	hypothetical protein
TGME49_208730	0.96	1.76	1.05	microneme protein, putative
TGME49_321410	2.80	2.79	2.86	hypothetical protein
TGME49_315300	-1.40	#N/A	-1.20	transcription factor IIB, putative
TGME49_262120	-1.16	-0.97	#N/A	IQ calmodulin-binding motif domain-containing protein
TGME49_289910	1.02	0.80	#N/A	hypothetical protein
TGME49_231960	-1.88	-3.35	-1.88	omega secalin, putative
TGME49_212210	1.36	#N/A	#N/A	hypothetical protein
TGME49_214100	-1.36	#N/A	#N/A	hypothetical protein
TGME49_314790	-1.76	-1.48	#N/A	small nuclear ribonucleoprotein G, putative
TGME49_293260	1.75	1.38	#N/A	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein

TGME49_270510	#N/A	-1.37	-1.76	asparaginyl-tRNA synthetase (NOB+tRNA synthase)
TGME49_239740	#N/A	1.16	#N/A	dense granule protein GRA14
TGME49_308950	#N/A	1.04	1.08	histidine acid phosphatase superfamily protein
TGME49_254270	#N/A	1.10	1.33	hypothetical protein
TGME49_306190	#N/A	0.96	#N/A	hypothetical protein
TGME49_225990	#N/A	-1.34	#N/A	acyl transferase domain-containing protein
TGME49_247485	#N/A	-1.40	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_225790	#N/A	1.61	#N/A	PDI family protein
TGME49_226520	#N/A	1.14	#N/A	hypothetical protein
TGME49_304750	#N/A	-1.89	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_295015	#N/A	1.45	#N/A	patched family protein
TGME49_201840	#N/A	1.27	#N/A	aspartyl protease ASP1
TGME49_272380	#N/A	0.85	#N/A	hypothetical protein
TGME49_210370	#N/A	0.86	0.74	hypothetical protein
TGME49_222100	#N/A	1.01	#N/A	hypothetical protein
TGME49_291150	#N/A	-1.79	#N/A	hypothetical protein
TGME49_315600	#N/A	-1.37	#N/A	MCM2/3/5 family protein
TGME49_214600	#N/A	-1.21	#N/A	hypothetical protein
TGME49_205265	#N/A	1.64	#N/A	transporter, cation channel family protein
TGME49_218920	#N/A	0.86	0.76	proteasome subunit beta type, putative
TGME49_201780	#N/A	1.52	#N/A	microneme protein MIC2
TGME49_254070	#N/A	0.92	0.93	hypothetical protein
TGME49_273815	#N/A	-1.49	#N/A	hypothetical protein
TGME49_212270	#N/A	1.15	#N/A	hypothetical protein
TGME49_253640	#N/A	0.95	#N/A	hypothetical protein
TGME49_316260	#N/A	0.99	0.98	hypothetical protein
TGME49_316430	#N/A	-1.74	-1.77	target of rapamycin (TOR), putative
TGME49_217520	#N/A	0.98	0.87	hypothetical protein
TGME49_258050	#N/A	-1.98	#N/A	actin like protein ALP2a
TGME49_315580	#N/A	-0.97	#N/A	hypothetical protein
TGME49_320190	#N/A	-1.69	7.35	SAG-related sequence SRS16B
TGME49_257800	#N/A	-1.81	-1.66	polynucleotide adenylyltransferase
TGME49_295658	#N/A	-1.27	#N/A	zinc finger in N-recognin protein
TGME49_220950	#N/A	1.49	1.44	hypothetical protein
TGME49_254510	#N/A	1.21	1.11	ankyrin repeat-containing protein
TGME49_242030	#N/A	-1.58	-1.71	hypothetical protein

FIGURE 3M

TGME49_269710	-1.40	-1.47	-1.49	hypothetical protein
TGME49_211440	-1.48	-1.86	-1.34	hypothetical protein
TGME49_251500	-1.24	-1.28	-1.23	eukaryotic initiation factor-3, subunit 3, putative
TGME49_254365	1.08	1.40	1.07	phosphatidate cytidylyltransferase
TGME49_246330	-1.24	-1.15	-1.14	CRAL/TRIO domain-containing protein
TGME49_214090	1.76	1.81	#N/A	signal peptidase
TGME49_288040	-1.30	-1.13	-1.09	hypothetical protein
TGME49_262935	2.22	#N/A	#N/A	hypothetical protein
TGME49_239710	-1.71	-1.61	#N/A	phosphomannomutase
TGME49_267420	0.99	1.43	0.95	mago nashi family protein 2, putative
TGME49_304520	-1.27	-0.94	#N/A	hypothetical protein
TGME49_202770	-1.12	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_226710	0.97	#N/A	#N/A	hypothetical protein
TGME49_321630	-1.29	#N/A	-1.02	RNA recognition motif-containing protein
TGME49_207060	-1.46	#N/A	#N/A	ribonucleoside-diphosphate reductase small subunit
TGME49_300285	-1.55	#N/A	#N/A	hypothetical protein
TGME49_235740	-1.65	-1.69	-1.50	hypothetical protein
TGME49_249180	0.99	1.05	#N/A	bifunctional dihydrofolate reductase-thymidylate synthase
TGME49_258490	-1.76	-1.42	#N/A	hypothetical protein
TGME49_222952	2.17	#N/A	#N/A	phosphohistidine phosphatase
TGME49_285230	-1.63	-1.43	#N/A	PRP38 family protein
TGME49_290310	-2.41	#N/A	#N/A	hypothetical protein
TGME49_223600	-1.87	-1.69	#N/A	hypothetical protein
TGME49_213820	1.24	0.89	1.35	hypothetical protein
TGME49_204270	-1.57	-1.92	-1.63	hypothetical protein
TGME49_225050	1.08	#N/A	0.85	adenosylhomocysteinase, putative
TGME49_263480	1.83	#N/A	#N/A	sodium/hydrogen exchanger 3 protein
TGME49_265450	1.53	#N/A	#N/A	hexokinase
TGME49_275630	1.12	#N/A	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_237160	-1.53	-1.22	#N/A	hypothetical protein
TGME49_262780	-1.49	-1.80	-1.60	FHA domain-containing protein
TGME49_244130	1.91	#N/A	#N/A	hypothetical protein
TGME49_265650	-1.60	-1.18	#N/A	protein phosphatase 2C domain-containing protein

TGME49_312420	#N/A	0.88	#N/A	hypothetical protein
TGME49_208420	#N/A	1.49	#N/A	Sodium:neurotransmitter symporter family protein
TGME49_313970	#N/A	-2.25	-2.61	Phytanoyl-CoA dioxygenase (PhyH) superfamily protein
TGME49_203050	#N/A	1.29	#N/A	AP2 domain transcription factor AP2VIIa-6
TGME49_298070	#N/A	-2.10	#N/A	hypothetical protein
TGME49_216510	#N/A	-1.35	-1.55	thioredoxin, putative
TGME49_258826	#N/A	-1.97	#N/A	hypothetical protein
TGME49_290160	#N/A	-1.03	-1.13	sortilin, putative
TGME49_250220	#N/A	1.23	#N/A	hypothetical protein
TGME49_270330	#N/A	1.36	#N/A	cell-cycle-associated protein kinase, putative
TGME49_304955	#N/A	0.93	#N/A	serine/threonine specific protein phosphatase
TGME49_236870	#N/A	1.69	#N/A	hypothetical protein
TGME49_301290	#N/A	-1.43	#N/A	hypothetical protein
TGME49_266690	#N/A	-0.95	#N/A	hypothetical protein
TGME49_213480	#N/A	2.09	#N/A	hypothetical protein
TGME49_272370	#N/A	1.06	#N/A	hypothetical protein
TGME49_214980	#N/A	0.80	0.77	hypothetical protein
TGME49_279420	#N/A	1.17	#N/A	hypothetical protein
TGME49_255400	#N/A	1.35	#N/A	hypothetical protein
TGME49_318290	#N/A	-1.31	#N/A	hypothetical protein
TGME49_259990	#N/A	-1.01	#N/A	SAC3/GANP family protein
TGME49_220230	#N/A	-1.27	#N/A	leucine rich repeat-containing protein
TGME49_201710	#N/A	1.23	1.59	WD domain, G-beta repeat-containing protein
TGME49_310530	#N/A	-1.33	#N/A	SNF2 family N-terminal domain-containing protein
TGME49_285290	#N/A	1.07	#N/A	hypothetical protein
TGME49_232550	#N/A	0.93	#N/A	hypothetical protein
TGME49_278530	#N/A	0.76	#N/A	multiprotein bridging factor type 1 family transcriptional co-activator, putative
TGME49_210682	#N/A	1.85	#N/A	hypothetical protein
TGME49_218930	#N/A	3.26	#N/A	BTB/POZ domain-containing protein
TGME49_247330	#N/A	-0.87	#N/A	hypothetical protein
TGME49_299070	#N/A	0.88	#N/A	pyruvate kinase PyKII
TGME49_206680	#N/A	1.12	#N/A	hypothetical protein
TGME49_240590	#N/A	0.94	#N/A	DNA-directed RNA polymerase II RPB5

FIGURE 3N

TGME49_242640	1.08	1.10	#N/A	hypothetical protein
TGME49_208590	-1.26	-1.04	-1.08	vacuolar ATP synthase subunit 54kD, putative
TGME49_305340	-1.03	-0.97	-1.17	corepressor complex CRC230
TGME49_217780	1.70	1.47	#N/A	Sec20 protein
TGME49_299250	1.42	1.19	1.06	hypothetical protein
TGME49_314070	1.15	1.29	1.14	hypothetical protein
TGME49_258740	-1.51	-1.35	-1.35	eukaryotic initiation factor-2A, putative
TGME49_269425	-1.35	#N/A	#N/A	hypothetical protein
TGME49_231140	3.19	2.39	3.09	ribosomal protein RPS25
TGME49_305950	1.63	1.09	#N/A	tetratricopeptide repeat-containing protein
TGME49_285170	-3.11	-2.94	-2.95	methyltransferase small, putative
TGME49_245460	4.21	3.64	4.06	ribosomal protein RPS8
TGME49_320620	1.73	#N/A	#N/A	queuine tRNA ribosyl transferase
TGME49_309580	-1.39	-1.05	#N/A	transporter, major facilitator family protein
TGME49_254950	1.60	1.38	#N/A	RNA cap guanine-N2 methyltransferase
TGME49_305080	2.30	#N/A	#N/A	hypothetical protein
TGME49_275990	1.24	1.29	1.26	hypothetical protein
TGME49_268380	2.64	2.05	#N/A	RNA recognition motif-containing protein
TGME49_300060	1.24	1.00	1.01	signal peptidase subunit protein
TGME49_246080	-1.16	-0.95	#N/A	NAD dependent epimerase/dehydratase family protein
TGME49_275430	-1.69	-2.15	-1.69	hypothetical protein
TGME49_231100	1.16	0.90	#N/A	hypothetical protein
TGME49_237110	-1.34	-1.22	-1.16	replication factor C subunit 2, putative
TGME49_289680	1.16	0.82	#N/A	Ras-related protein Rab11
TGME49_249350	-1.19	#N/A	#N/A	esterase/lipase/thioesterase domain-containing protein
TGME49_248900	-1.98	-2.04	-1.61	hypothetical protein
TGME49_253950	1.35	1.22	#N/A	protein fam50a, putative
TGME49_224060	0.99	0.94	#N/A	thioredoxin, putative
TGME49_216375	-2.42	-2.35	#N/A	hypothetical protein
TGME49_318370	2.04	#N/A	#N/A	hypothetical protein
TGME49_218830	-2.05	-2.05	-1.83	hypothetical protein
TGME49_215010	-1.06	#N/A	#N/A	hypothetical protein
TGME49_217360	-1.96	-2.15	-2.11	hypothetical protein
TGME49_310360	-1.15	-1.20	-1.10	hypothetical protein

TGME49_214810	#N/A	1.18	1.24	hypothetical protein
TGME49_200450	#N/A	-1.67	-1.73	hypothetical protein
TGME49_253130	#N/A	0.85	#N/A	transporter, major facilitator family protein
TGME49_249670	#N/A	0.96	#N/A	cathepsin B
TGME49_229930	#N/A	0.93	#N/A	p25-alpha family protein
TGME49_231120	#N/A	1.02	1.05	ribosomal protein S11, putative
TGME49_221190	#N/A	1.32	#N/A	mrna cleavage factor family protein, putative
TGME49_273380	#N/A	1.10	#N/A	ion channel protein
TGME49_218610	#N/A	-1.45	#N/A	ATPase (DUF699) protein
TGME49_244570	#N/A	-1.74	#N/A	hypothetical protein
TGME49_221590	#N/A	0.87	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_233380	#N/A	1.13	#N/A	hypothetical protein
TGME49_319570	#N/A	-0.96	#N/A	WD domain, G-beta repeat-containing protein
TGME49_269940	#N/A	-1.72	#N/A	zinc finger motif, C2HC5-type protein
TGME49_289600	#N/A	0.79	#N/A	heat shock protein HSP29
TGME49_221440	#N/A	-1.36	#N/A	RPGR, putative
TGME49_242380	#N/A	-0.94	#N/A	fatty acid elongase
TGME49_250690	#N/A	-0.83	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_244530	#N/A	1.03	#N/A	hypothetical protein
TGME49_315720	#N/A	-1.23	#N/A	Smg-4/UPF3 family protein
TGME49_313385	#N/A	1.23	1.64	hypothetical protein
TGME49_293900	#N/A	1.04	#N/A	sporozoite protein with an altered thrombospondin repeat SPATR
TGME49_247370	#N/A	-1.52	-1.54	hypothetical protein
TGME49_216490	#N/A	-1.65	#N/A	hypothetical protein
TGME49_308580	#N/A	-1.44	-1.64	Lon protease family protein
TGME49_246140	#N/A	-1.42	#N/A	hypothetical protein
TGME49_268220	#N/A	4.47	5.79	hypothetical protein
TGME49_316700	#N/A	1.40	#N/A	uridine kinase
TGME49_277840	#N/A	0.86	#N/A	Ras family protein
TGME49_214490	#N/A	-1.37	#N/A	peptidase M16 inactive domain-containing protein
TGME49_233450	#N/A	1.51	#N/A	SAG-related sequence SRS29A
TGME49_227580	#N/A	-1.02	-1.25	transmembrane amino acid transporter protein
TGME49_253320	#N/A	1.18	#N/A	hypothetical protein
TGME49_265790	#N/A	0.83	0.83	hypothetical protein

FIGURE 3o

TGME49_218730	-1.39	#N/A	#N/A	hypothetical protein
TGME49_209945	2.28	#N/A	#N/A	hypothetical protein
TGME49_272010	-1.63	-1.23	#N/A	Gar1 protein RNA binding region protein
TGME49_308060	1.48	1.36	#N/A	hypothetical protein
TGME49_260580	1.56	#N/A	#N/A	hypothetical protein
TGME49_265440	-1.26	-1.16	#N/A	hypothetical protein
TGME49_235980	-1.64	-1.58	#N/A	ARIADNE family protein
TGME49_214170	-1.70	-2.00	-1.82	hypothetical protein
TGME49_309400	-1.56	#N/A	#N/A	RecF/RecN/SMC N terminal domain-containing protein
TGME49_270140	-1.57	-1.27	#N/A	splicing factor DIM1, putative
TGME49_211250	-1.10	#N/A	#N/A	hypothetical protein
TGME49_312260	-1.42	-1.13	#N/A	hypothetical protein
TGME49_321560	-1.35	-1.47	-1.29	zinc knuckle domain-containing protein
TGME49_321640	-1.69	-2.03	#N/A	cell division protein CDC48AP
TGME49_268170	-1.89	-1.58	#N/A	hypothetical protein
TGME49_254915	3.02	2.78	2.20	hypothetical protein
TGME49_255290	-2.99	-3.89	-2.61	hypothetical protein
TGME49_222370	1.40	#N/A	#N/A	SAG-related sequence SRS13
TGME49_215347	-2.65	#N/A	#N/A	hypothetical protein
TGME49_286480	2.29	2.55	#N/A	hypothetical protein
TGME49_217220	-1.22	#N/A	-1.57	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_240060	1.23	2.18	0.98	hypothetical protein
TGME49_268200	1.63	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_272640	-1.40	-1.31	#N/A	eukaryotic initiation factor-2B, epsilon subunit, putative
TGME49_321570	1.11	#N/A	#N/A	beta-hydroxyacyl-acyl carrier protein dehydratase (FABZ)
TGME49_216040	-2.01	-2.16	#N/A	30S ribosomal protein S15, putative
TGME49_232050	-1.13	-0.93	#N/A	DnaJ domain-containing protein
TGME49_228150	1.93	#N/A	#N/A	hypothetical protein
TGME49_250955	1.98	1.57	1.59	KRUF family protein
TGME49_228320	-3.53	-3.92	-4.10	hypothetical protein
TGME49_264820	1.40	#N/A	#N/A	RbAp48
TGME49_232130	-1.00	-0.77	-0.98	hypothetical protein
TGME49_290300	1.03	1.44	1.15	hypothetical protein
TGME49_255340	-1.52	-1.77	-1.29	tetratricopeptide repeat-containing protein

TGME49_246120	#N/A	0.98	#N/A	tetratricopeptide repeat-containing protein
TGME49_218570	#N/A	0.92	#N/A	Nin one binding (NOB1) Zn-ribbon family protein
TGME49_318525	#N/A	-1.15	-1.59	hypothetical protein
TGME49_319900	#N/A	-1.12	#N/A	hypothetical protein
TGME49_281910	#N/A	1.21	#N/A	hypothetical protein
TGME49_297230	#N/A	-1.25	-1.67	Vps53 family, N-terminal protein
TGME49_278815	#N/A	-0.92	#N/A	hypothetical protein
TGME49_306310	#N/A	-0.96	#N/A	RecF/RecN/SMC N terminal domain-containing protein
TGME49_255900	#N/A	0.75	#N/A	Bax inhibitor-1, putative
TGME49_218600	#N/A	-1.24	#N/A	RNA recognition motif-containing protein
TGME49_309380	#N/A	-1.21	#N/A	Nuf2
TGME49_200430	#N/A	-1.64	#N/A	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_216435	#N/A	-1.06	#N/A	hypothetical protein
TGME49_301380	#N/A	-1.44	#N/A	elongation factor Tu GTP binding domain-containing protein
TGME49_213900	#N/A	-0.88	#N/A	regulator of chromosome condensation RCC1
TGME49_308075	#N/A	-0.99	#N/A	hypothetical protein
TGME49_268210	#N/A	-1.35	#N/A	AGC kinase
TGME49_268980	#N/A	0.81	0.80	hypothetical protein
TGME49_223540	#N/A	-1.08	#N/A	importin-beta N-terminal domain-containing protein
TGME49_228980	#N/A	-1.55	-1.68	hypothetical protein
TGME49_235398	#N/A	-1.20	#N/A	hypothetical protein
TGME49_209930	#N/A	-1.40	#N/A	hypothetical protein
TGME49_236010	#N/A	0.76	#N/A	prenylcysteine oxidase
TGME49_236630	#N/A	0.79	#N/A	hypothetical protein
TGME49_218520	#N/A	1.39	#N/A	microneme protein MIC6
TGME49_275610	#N/A	-1.03	#N/A	protein kinase, other
TGME49_278450	#N/A	0.78	#N/A	hypothetical protein
TGME49_222120	#N/A	-1.52	-1.66	hypothetical protein
TGME49_235880	#N/A	0.82	#N/A	brain protein 44 family protein
TGME49_213460	#N/A	-1.05	#N/A	hypothetical protein
TGME49_253300	#N/A	1.61	#N/A	hypothetical protein
TGME49_250950	#N/A	1.30	#N/A	KRUF family protein
TGME49_313480	#N/A	-2.19	-2.71	hypothetical protein
TGME49_285840	#N/A	-1.13	#N/A	RAP domain-containing protein

FIGURE 3P

TGME49_207230	1.10	1.16	0.90	hypothetical protein
TGME49_240740	-1.49	-1.43	#N/A	Sec1 family protein
TGME49_228300	-1.88	-1.74	-1.69	CCDC25 protein
TGME49_215040	-1.26	-1.33	#N/A	HEAT repeat-containing protein
TGME49_313590	-1.70	-1.47	-1.54	hypothetical protein
TGME49_294690	-1.04	#N/A	#N/A	rhomboid protease ROM5
TGME49_254730	1.74	#N/A	#N/A	POPLD (NUC188) domain-containing protein
TGME49_289150	-1.30	#N/A	#N/A	hypothetical protein
TGME49_300048	1.09	1.65	0.86	hypothetical protein
TGME49_281570	-1.64	-1.42	#N/A	hypothetical protein
TGME49_290840	-1.24	#N/A	#N/A	serine protease
TGME49_313180	-0.96	-0.87	-1.05	cell-cycle-associated protein kinase PRP4, putative
TGME49_289320	-1.06	#N/A	#N/A	casein kinase I, putative
TGME49_294730	-1.44	-1.42	-1.37	hypothetical protein
TGME49_251640	-1.48	-1.13	-1.29	ubiquitin-conjugating enzyme subfamily protein
TGME49_266990	-1.05	-1.22	-1.18	beta-COP
TGME49_288360	1.42	1.28	-1.24	tryptophanyl-tRNA synthetase (TrpRS2)
TGME49_263610	-1.62	-1.39	-1.84	hypothetical protein
TGME49_280560	-1.19	-1.50	-1.12	selenide, water dikinase
TGME49_251790	1.23	#N/A	#N/A	hypothetical protein
TGME49_318360	-1.34	#N/A	#N/A	hypothetical protein
TGME49_266900	1.15	1.04	1.65	cyclin, N-terminal domain-containing protein
TGME49_225800	1.18	0.91	#N/A	iron-sulfur assembly ATPase
TGME49_261850	2.02	#N/A	#N/A	helicase, putative
TGME49_288840	1.13	1.26	#N/A	hypothetical protein
TGME49_253000	1.04	1.22	1.28	ELMO/CED-12 family protein
TGME49_318320	-1.94	-2.05	-1.92	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP domain-containing protein
TGME49_201200	-2.28	-1.97	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_288700	-1.75	-1.76	-2.16	RecF/RecN/SMC N terminal domain-containing protein
TGME49_262430	1.49	#N/A	#N/A	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
TGME49_244260	-2.77	-3.96	#N/A	hypothetical protein
TGME49_254930	0.99	1.37	1.20	hypothetical protein
TGME49_214210	-1.23	#N/A	#N/A	rRNA pseudouridine synthase
TGME49_223950	1.07	#N/A	0.97	hypothetical protein
TGME49_202250	1.21	1.03	#N/A	hypothetical protein

TGME49_257530	#N/A	1.55	#N/A	transporter, major facilitator family protein
TGME49_232630	#N/A	0.73	#N/A	hypothetical protein
TGME49_285510	#N/A	0.78	#N/A	hypothetical protein
TGME49_269410	#N/A	1.18	#N/A	hypothetical protein
TGME49_231950	#N/A	0.82	#N/A	hypothetical protein
TGME49_205670	#N/A	0.79	#N/A	SF-assemblin/beta giardin protein
TGME49_248570	#N/A	-1.51	-1.74	hypothetical protein
TGME49_221580	#N/A	-0.96	-1.20	ribosomal RNA large subunit methyltransferase J protein
TGME49_249010	#N/A	0.83	#N/A	hypothetical protein
TGME49_237840	#N/A	-1.28	#N/A	hypothetical protein
TGME49_239087	#N/A	-1.40	#N/A	hypothetical protein
TGME49_253740	#N/A	-1.12	-1.22	hypothetical protein
TGME49_211330	#N/A	-1.87	#N/A	methionine aminopeptidase
TGME49_233838	#N/A	-1.99	#N/A	PET112 family, C terminal region domain-containing protein
TGME49_237500	#N/A	0.84	#N/A	protein phosphatase 2C domain-containing protein
TGME49_299270	#N/A	1.01	#N/A	hypothetical protein
TGME49_229340	#N/A	-1.63	#N/A	hypothetical protein
TGME49_258180	#N/A	-1.49	#N/A	hypothetical protein
TGME49_244220	#N/A	-1.97	#N/A	hypothetical protein
TGME49_276170	#N/A	0.73	#N/A	phosphatidylinositol 3- and 4-kinase
TGME49_202420	#N/A	1.43	#N/A	hypothetical protein
TGME49_208030	#N/A	1.24	#N/A	microneme protein MIC4
TGME49_312500	#N/A	-0.98	#N/A	hypothetical protein
TGME49_273770	#N/A	0.86	#N/A	hypothetical protein
TGME49_242260	#N/A	-1.23	-2.03	hypothetical protein
TGME49_245428	#N/A	1.44	2.67	hypothetical protein
TGME49_311250	#N/A	-1.11	-1.39	hypothetical protein
TGME49_318580	#N/A	-0.96	#N/A	glucosephosphate-mutase GPM2
TGME49_219070	#N/A	-0.99	#N/A	cyclic nucleotide-binding domain-containing protein
TGME49_213600	#N/A	1.73	#N/A	hypothetical protein
TGME49_206600	#N/A	-1.24	#N/A	sigma-70, region 3 protein
TGME49_266850	#N/A	1.02	1.27	3-demethylubiquinone-9 3-O-methyltransferase
TGME49_239600	#N/A	1.33	1.75	rhoptry kinase family protein ROP23 (incomplete catalytic triad)
TGME49_211410	#N/A	-1.26	#N/A	translation initiation factor sui1 protein
TGME49_219820	#N/A	1.02	#N/A	polyubiquitin UbC, putative

FIGURE 3Q

TGME49_270650	1.57	#N/A	2.02	deoxyribose-phosphate aldolase
TGME49_260610	-2.51	-2.50	-2.15	methyltransferase
TGME49_215710	-1.39	-1.38	-1.14	hypothetical protein
TGME49_318570	2.26	1.98	#N/A	SFT2 family protein
TGME49_202650	-1.59	-1.66	#N/A	hypothetical protein
TGME49_226830	-1.17	-0.98	#N/A	DnaK family protein
TGME49_312380	-1.95	-1.92	-2.37	tetratricopeptide repeat-containing protein
TGME49_218200	-2.13	-2.16	-2.74	UDP-sugar pyrophospharylase
TGME49_260390	-1.48	#N/A	#N/A	hypothetical protein
TGME49_267450	-1.51	-1.25	-1.26	alpha-tubulin suppressor protein
TGME49_319930	-1.46	-1.27	#N/A	hypothetical protein
TGME49_253370	1.14	1.27	#N/A	hypothetical protein
TGME49_298840	1.20	1.36	1.64	hypothetical protein
TGME49_235490	-1.11	-0.90	-0.97	hypothetical protein
TGME49_300290	-1.47	#N/A	#N/A	SNARE domain-containing protein
TGME49_311310	-1.09	-1.08	#N/A	protein phosphatase 2B catalytic subunit, calcineurin family phosphatse superfamily protein
TGME49_225560	-1.13	-1.03	-1.11	hypothetical protein
TGME49_269430	-1.63	-1.43	#N/A	polyprenyl synthetase superfamily protein
TGME49_267620	1.08	#N/A	#N/A	multi-pass transmembrane protein
TGME49_268580	-1.25	-1.03	#N/A	hypothetical protein
TGME49_253560	1.29	0.99	#N/A	hypothetical protein
TGME49_319308	-1.95	#N/A	-3.01	hypothetical protein
TGME49_252230	1.47	#N/A	#N/A	hypothetical protein
TGME49_282170	1.22	#N/A	#N/A	hypothetical protein
TGME49_294820	1.18	#N/A	#N/A	type I fatty acid synthase, putative
TGME49_265390	-1.40	-1.28	#N/A	hypothetical protein
TGME49_233760	-1.53	-2.58	#N/A	hypothetical protein
TGME49_309280	-1.70	#N/A	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_229250	1.53	#N/A	1.42	ribosomal protein RPL28
TGME49_313830	-1.30	-1.28	#N/A	AARP2CN (NUC121) domain-containing protein
TGME49_235020	-0.99	-0.87	-0.85	COPI protein, putative
TGME49_269420	2.18	2.15	#N/A	hypothetical protein
TGME49_211020	-1.69	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_252260	1.73	#N/A	1.92	hypothetical protein
TGME49_254110	1.55	#N/A	#N/A	tryptophanyl-tRNA synthetase (TrpRS1)

TGME49_216760	#N/A	-1.38	-1.52	RNA pseudouridine synthase superfamily protein
TGME49_221200	#N/A	0.86	#N/A	CW-type Zinc Finger protein
TGME49_206415	#N/A	-0.99	#N/A	myosin K
TGME49_232640	#N/A	1.17	1.87	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_243340	#N/A	-1.43	#N/A	atypical MEK-related kinase (incomplete catalytic triad)
TGME49_270450	#N/A	-1.71	#N/A	MCM2/3/5 family protein
TGME49_236240	#N/A	-0.96	#N/A	Tyrosine kinase-like (TKL) protein
TGME49_247680	#N/A	-1.68	-2.26	hypothetical protein
TGME49_313760	#N/A	0.81	#N/A	hypothetical protein
TGME49_262740	#N/A	-1.64	#N/A	hypothetical protein
TGME49_298970	#N/A	0.88	1.21	LSM3, U6 small nuclear RNA associated isoform 2 family protein
TGME49_313120	#N/A	-1.89	#N/A	DNA-directed RNA polymerase, alpha subunit
TGME49_229490	#N/A	-0.97	#N/A	tetratricopeptide repeat-containing protein
TGME49_219170	#N/A	-0.87	#N/A	hypothetical protein
TGME49_246090	#N/A	-1.11	#N/A	hypothetical protein
TGME49_278540	#N/A	0.93	#N/A	hypothetical protein
TGME49_307610	#N/A	-0.87	#N/A	elongation factor TS, putative
TGME49_249810	#N/A	-1.68	-1.84	activating signal cointegrator 1 complex subunit 3, putative
TGME49_299980	#N/A	0.75	#N/A	hypothetical protein
TGME49_223590	#N/A	0.69	#N/A	proteasome subunit
TGME49_277770	#N/A	-1.42	#N/A	hypothetical protein
TGME49_215530	#N/A	0.97	#N/A	hypothetical protein
TGME49_230410	#N/A	-1.11	#N/A	peroxiredoxin PRX3
TGME49_229620	#N/A	-1.21	#N/A	hypothetical protein
TGME49_315820	#N/A	-1.15	#N/A	hypothetical protein
TGME49_209020	#N/A	-1.85	-2.11	hypothetical protein
TGME49_216650	#N/A	0.72	#N/A	S15 sporozoite-expressed protein
TGME49_207420	#N/A	0.81	#N/A	hypothetical protein
TGME49_305120	#N/A	1.05	#N/A	transporter, solute:sodium symporter (SSS) family protein
TGME49_235920	#N/A	-1.00	-1.14	dynein, axonemal, heavy chain 2 family protein
TGME49_220330	#N/A	-1.48	#N/A	hypothetical protein
TGME49_259630	#N/A	0.85	#N/A	hypothetical protein
TGME49_227060	#N/A	-1.03	#N/A	hypothetical protein
TGME49_223410	#N/A	0.85	#N/A	eukaryotic initiation factor-4E, putative
TGME49_298050	#N/A	-1.10	#N/A	hypothetical protein

FIGURE 3R

TGME49_264840	-2.19	-2.86	#N/A	ATP-dependent DNA helicase, RecQ family protein
TGME49_263085	-1.79	#N/A	#N/A	hypothetical protein
TGME49_204420	-1.23	#N/A	#N/A	oocyst wall protein OWP1
TGME49_214180	-0.96	#N/A	#N/A	ENTH domain-containing protein
TGME49_222920	1.22	1.08	1.31	mbp-1 interacting protein-2a family protein
TGME49_212130	-1.33	-1.06	-1.20	phospholipase, patatin family protein
TGME49_316140	-1.10	#N/A	#N/A	hypothetical protein
TGME49_278770	-1.28	-1.27	-1.20	hypothetical protein
TGME49_270930	-1.14	-1.08	-0.99	hypothetical protein
TGME49_220940	1.41	1.51	1.84	ribosomal RNA methyltransferase (FtsJ) family protein
TGME49_253730	1.23	0.96	1.16	importin-beta N-terminal domain-containing protein
TGME49_225060	-1.19	-0.95	#N/A	nucleoredoxin family protein
TGME49_234360	-1.04	#N/A	#N/A	DNA topoisomerase I, putative
TGME49_249950	-1.55	#N/A	#N/A	Mak16 protein
TGME49_214530	-1.85	-2.24	#N/A	DnaJ domain-containing protein
TGME49_267580	2.00	1.62	#N/A	cyclin2 related protein
TGME49_204880	1.39	#N/A	#N/A	hypothetical protein
TGME49_311510	0.88	#N/A	#N/A	eIF2 kinase IF2K-B
TGME49_216920	-1.58	-1.49	-1.69	mediator complex subunit MED8
TGME49_310910	1.39	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_231210	-1.13	#N/A	#N/A	sarcalumenin/eps15 family protein
TGME49_314660	-1.21	-0.96	-1.09	TPRX1 protein
TGME49_224730	-1.53	#N/A	#N/A	hypothetical protein
TGME49_301216	-2.44	-2.44	-2.21	endonuclease/exonuclease/phosphatase family protein
TGME49_244600	-1.52	-1.44	#N/A	hypothetical protein
TGME49_212220	0.94	#N/A	#N/A	hypothetical protein
TGME49_292110	1.45	1.84	#N/A	formate/nitrite transporter protein
TGME49_249620	-1.31	-1.53	#N/A	histone deacetylase HDAC2
TGME49_207680	-1.13	#N/A	#N/A	suppressor of kinetochore protein 1, putative
TGME49_289710	1.56	#N/A	#N/A	AP2 domain transcription factor AP2IX-5
TGME49_312050	-0.96	#N/A	#N/A	small GTPase Rab2, putative
TGME49_220290	-1.77	-1.84	#N/A	hypothetical protein
TGME49_313350	-1.35	-1.21	-1.19	hypothetical protein
TGME49_261540	1.31	#N/A	#N/A	DNA-directed RNA polymerase I RPAC2
TGME49_262980	-1.74	-1.73	-1.55	hypothetical protein

TGME49_220510	#N/A	1.22	#N/A	hypothetical protein
TGME49_233830	#N/A	-1.85	#N/A	hypothetical protein
TGME49_310470	#N/A	0.80	#N/A	cytochrome C oxidase subunit IIb, putative
TGME49_233480	#N/A	1.85	#N/A	SAG-related sequence SRS29C
TGME49_312670	#N/A	-1.43	#N/A	hypothetical protein
TGME49_258480	#N/A	-0.96	#N/A	hypothetical protein
TGME49_212200	#N/A	-1.40	#N/A	hypothetical protein
TGME49_214840	#N/A	0.81	#N/A	AP2 domain transcription factor AP2X-7
TGME49_214150	#N/A	-1.32	#N/A	mitochondrial inner membrane translocase subunit TIM17, putative
TGME49_207800	#N/A	0.92	#N/A	hypothetical protein
TGME49_203700	#N/A	0.94	#N/A	SFT2 family protein
TGME49_209570	#N/A	0.97	#N/A	suppressor of mitotic defects protein
TGME49_225160	#N/A	0.81	0.88	hypothetical protein
TGME49_293760	#N/A	0.71	#N/A	EF hand domain-containing protein
TGME49_270770	#N/A	-0.99	#N/A	PWI domain-containing protein
TGME49_268280	#N/A	-0.76	#N/A	'chromo' (CHRromatin Organization MOdifier) domain-containing protein
TGME49_310870	#N/A	-1.03	#N/A	integral membrane protein, putative
TGME49_320480	#N/A	-0.83	#N/A	Rab11b
TGME49_241150	#N/A	-1.02	#N/A	hypothetical protein
TGME49_218260	#N/A	1.31	#N/A	histone H3.3
TGME49_240500	#N/A	0.99	#N/A	hypothetical protein
TGME49_295410	#N/A	-0.98	#N/A	transcription initiation factor TFIID complex subunit TAF6
TGME49_315660	#N/A	-1.25	#N/A	hypothetical protein
TGME49_290330	#N/A	-1.39	#N/A	chloride transporter, chloride channel (ClC) family protein
TGME49_269130	#N/A	-1.63	#N/A	hypothetical protein
TGME49_310730	#N/A	-0.94	-1.22	hypothetical protein
TGME49_293180	#N/A	0.77	#N/A	NADP-specific glutamate dehydrogenase
TGME49_297710	#N/A	-1.42	#N/A	hypothetical protein
TGME49_272400	#N/A	-1.45	-1.58	casein kinase ii regulatory subunit protein
TGME49_232390	#N/A	-1.67	#N/A	18S rRNA biogenesis protein RCL1 protein
TGME49_267680	#N/A	-1.03	-1.21	microneme protein MIC12
TGME49_249560	#N/A	-1.17	#N/A	DNA-directed RNA polymerase alpha chain rpoA
TGME49_253540	#N/A	1.00	#N/A	hypothetical protein
TGME49_220460	#N/A	-1.73	-2.59	SNF7 family protein
TGME49_216460	#N/A	0.89	#N/A	hypothetical protein

FIGURE 3S

TGME49_229350	-1.31	#N/A	#N/A	HEAT repeat-containing protein
TGME49_299780	1.00	#N/A	0.89	hypothetical protein
TGME49_268900	-1.44	-1.22	#N/A	dense granular protein GRA10
TGME49_280710	-1.25	-1.05	#N/A	20S proteasome subunit beta 7, putative
TGME49_237260	-1.08	#N/A	#N/A	Coiled-coil domain containing 124 family protein
TGME49_263595	-1.57	-1.37	#N/A	RNA-binding protein
TGME49_246800	-1.24	-1.04	-1.47	acylaminoacyl-peptidase, putative
TGME49_205700	1.48	1.33	1.58	cyclophilin precursor
TGME49_268230	-2.84	-3.64	-3.86	hypothetical protein
TGME49_212800	-1.49	-1.48	#N/A	hypothetical protein
TGME49_273320	-0.86	#N/A	#N/A	hypothetical protein
TGME49_231230	-2.42	#N/A	#N/A	hypothetical protein
TGME49_214580	-3.68	-5.07	#N/A	tetratricopeptide repeat-containing protein
TGME49_209095	-1.13	#N/A	#N/A	hypothetical protein
TGME49_259600	1.52	#N/A	#N/A	hypothetical protein
TGME49_208820	1.15	1.40	#N/A	1-deoxy-D-xylulose-5-phosphate synthase
TGME49_224980	-1.23	#N/A	#N/A	hypothetical protein
TGME49_235610	-1.70	-1.73	#N/A	ATPase, AAA family protein
TGME49_294790	0.91	0.85	0.93	hypothetical protein
TGME49_248610	1.33	#N/A	#N/A	hypothetical protein
TGME49_292610	1.36	1.62	#N/A	Toxoplasma gondii family C protein
TGME49_253310	1.22	1.17	1.20	hypothetical protein
TGME49_275870	1.41	1.90	2.70	tubulin/FtsZ family, GTPase domain-containing protein
TGME49_292950	1.10	0.99	#N/A	hypothetical protein
TGME49_315100	2.60	5.72	#N/A	hypothetical protein
TGME49_200360	1.25	1.62	1.64	hypothetical protein
TGME49_207900	-1.23	-1.09	#N/A	transcription initiation factor TFIIIB
TGME49_314695	-1.50	#N/A	#N/A	hypothetical protein
TGME49_230705	1.26	1.20	1.07	hypothetical protein
TGME49_297510	-1.70	-1.54	-1.52	hypothetical protein
TGME49_228720	-1.65	#N/A	#N/A	hypothetical protein
TGME49_226100	-2.58	-3.82	#N/A	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_270160	-1.39	#N/A	#N/A	hypothetical protein

TGME49_235500	#N/A	-1.48	#N/A	hypothetical protein
TGME49_294220	#N/A	0.93	#N/A	hypothetical protein
TGME49_209080	#N/A	2.34	#N/A	transport protein particle (trapp) component, bet3 protein
TGME49_209200	#N/A	0.83	#N/A	hypothetical protein
TGME49_312950	#N/A	0.82	#N/A	hypothetical protein
TGME49_295125	#N/A	1.05	#N/A	rhoptry protein ROP4
TGME49_220350	#N/A	-1.05	#N/A	tRNA ligases class II (D, K and N) domain-containing protein
TGME49_289780	#N/A	0.98	#N/A	ATP-dependent hsl protease ATP-binding subunit hslU, putative
TGME49_289110	#N/A	-1.75	#N/A	hypothetical protein
TGME49_223530	#N/A	1.04	#N/A	hypothetical protein
TGME49_263130	#N/A	0.88	#N/A	citrate synthase, putative
TGME49_295050	#N/A	-0.97	#N/A	tRNA ligase class II core domain (G, H, P, S and T) domain-containing protein
TGME49_224350	#N/A	-0.82	#N/A	aminopeptidase N, putative
TGME49_230220	#N/A	-0.92	#N/A	hypothetical protein
TGME49_231750	#N/A	-1.19	#N/A	hypothetical protein
TGME49_291630	#N/A	-1.59	#N/A	hypothetical protein
TGME49_270690	#N/A	-0.96	-1.09	arginyl-tRNA synthetase
TGME49_282000	#N/A	1.40	#N/A	hypothetical protein
TGME49_236030	#N/A	-1.72	#N/A	hypothetical protein
TGME49_247960	#N/A	1.49	#N/A	hypothetical protein
TGME49_260670	#N/A	-1.26	#N/A	centrin, putative
TGME49_283860	#N/A	-1.48	-1.72	leucine rich repeat-containing protein
TGME49_301340	#N/A	-0.84	#N/A	DnaJ domain-containing protein
TGME49_254280	#N/A	1.24	#N/A	DNA-directed RNA polymerase III RPC9
TGME49_214080	#N/A	#N/A	7.75	toxofilin
TGME49_313440	#N/A	#N/A	4.65	hypothetical protein
TGME49_245432	#N/A	#N/A	2.70	hypothetical protein
TGME49_315802	#N/A	#N/A	-9.71	hypothetical protein
TGME49_320180	#N/A	#N/A	4.38	SAG-related sequence SRS16C
TGME49_254840	#N/A	#N/A	-2.21	tetratricopeptide repeat-containing protein
TGME49_241880	#N/A	#N/A	-1.64	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_221220	#N/A	#N/A	3.98	hypothetical protein
TGME49_218192	#N/A	#N/A	-2.95	hypothetical protein

FIGURE 3T

TGME49_278830	-0.99	-1.44	-1.19	glucose-6-phosphate 1-dehydrogenase
TGME49_249550	-1.45	-1.52	-1.70	hypothetical protein
TGME49_271030	1.84	1.47	#N/A	AP2 domain transcription factor AP2VIII-6
TGME49_246050	-2.03	-2.18	#N/A	hypothetical protein
TGME49_314700	1.42	#N/A	#N/A	hypothetical protein
TGME49_254800	1.27	2.05	1.68	hypothetical protein
TGME49_207065	1.19	1.20	1.08	hypothetical protein
TGME49_208740	1.29	2.17	#N/A	microneme protein, putative
TGME49_253820	0.94	1.05	1.08	hypothetical protein
TGME49_267660	-1.04	#N/A	#N/A	hypothetical protein
TGME49_267750	-1.15	-1.38	-1.06	hypothetical protein
TGME49_224310	-1.28	-1.12	#N/A	DHHC zinc finger domain-containing protein
TGME49_223910	-1.14	-1.53	#N/A	acyltransferase domain-containing protein
TGME49_258980	-1.74	#N/A	-1.61	hypothetical protein
TGME49_309010	-1.67	#N/A	#N/A	elongation factor P, putative
TGME49_238170	1.47	1.16	#N/A	hypothetical protein
TGME49_275450	0.85	1.04	1.16	hypothetical protein
TGME49_253650	0.84	1.02	1.12	DnaJ C terminal region domain-containing protein
TGME49_315250	1.10	1.11	#N/A	GAMM1 protein, putative
TGME49_221230	-1.20	#N/A	-1.10	hypothetical protein
TGME49_304670	-1.33	#N/A	-1.51	leucine rich repeat-containing protein
TGME49_284660	1.30	1.58	1.34	mitochondrial ribosomal protein s6-2, putative
TGME49_249380	-1.03	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_311905	-2.42	-2.49	-2.69	hypothetical protein
TGME49_263840	-1.19	-1.10	#N/A	hypothetical protein
TGME49_263785	-2.30	-3.00	-2.59	phosphatidate cytidylyltransferase
TGME49_272030	-1.20	-1.05	#N/A	kelch repeat-containing protein
TGME49_268690	1.67	#N/A	#N/A	hypothetical protein
TGME49_244870	-1.26	-1.10	#N/A	quinone oxidoreductase, putative
TGME49_214320	1.13	1.16	#N/A	facilitative glucose transporter GT1
TGME49_229140	1.35	#N/A	#N/A	MaoC family domain-containing protein
TGME49_255240	-1.71	-1.95	-2.42	hypothetical protein
TGME49_247690	-1.07	#N/A	-1.05	phospholipid-translocating P-type ATPase, flippase subfamily protein

TGME49_297647	#N/A	#N/A	3.99	hypothetical protein
TGME49_257750	#N/A	#N/A	-2.35	homocysteine s-methyltransferase domain-containing protein
TGME49_212250	#N/A	#N/A	1.38	XPG N-terminal domain-containing protein
TGME49_319350	#N/A	#N/A	-1.82	SAG-related sequence SRS17B
TGME49_243298	#N/A	#N/A	-2.67	ICE family protease (caspase) p20 domain-containing protein
TGME49_223480	#N/A	#N/A	-2.62	sushi domain (scr repeat) domain-containing protein
TGME49_310060	#N/A	#N/A	1.91	small nuclease
TGME49_313870	#N/A	#N/A	-1.40	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_236990	#N/A	#N/A	2.33	beta-ketoacyl synthase, N-terminal domain-containing protein
TGME49_223020	#N/A	#N/A	-1.62	coproporphyrinogen III oxidase
TGME49_323320	#N/A	#N/A	-2.94	hypothetical protein
TGME49_229640	#N/A	#N/A	-1.65	hypothetical protein
TGME49_230830	#N/A	#N/A	2.06	ATPase family associated with various cellular activities (AAA) domain-containing protein
TGME49_267070	#N/A	#N/A	1.12	aquaporin 2
TGME49_314250	#N/A	#N/A	2.07	bradyzoite rhoptry protein BRP1
TGME49_214575	#N/A	#N/A	1.71	hypothetical protein
TGME49_230080	#N/A	#N/A	-1.72	DEAD/DEAH box helicase domain-containing protein
TGME49_319312	#N/A	#N/A	-2.01	hypothetical protein
TGME49_207880	#N/A	#N/A	-1.59	hypothetical protein
TGME49_232060	#N/A	#N/A	1.73	hypothetical protein
TGME49_282190	#N/A	#N/A	-1.15	hydrolase, NUDIX family protein
TGME49_232270	#N/A	#N/A	-1.53	histidine acid phosphatase superfamily protein
TGME49_233300	#N/A	#N/A	-1.71	RhoGAP domain-containing protein
TGME49_242118	#N/A	#N/A	-3.74	myosin-light-chain kinase
TGME49_206430	#N/A	#N/A	-1.19	formin FRM1
TGME49_249730	#N/A	#N/A	-1.78	hypothetical protein
TGME49_243580	#N/A	#N/A	-1.07	Hit family protein involved in cell-cycle regulation, putative
TGME49_257340	#N/A	#N/A	-2.29	Ras family protein
TGME49_270595	#N/A	#N/A	2.39	UBA/TS-N domain-containing protein
TGME49_312560	#N/A	#N/A	-1.26	hypothetical protein
TGME49_277920	#N/A	#N/A	1.19	hypothetical protein
TGME49_315750	#N/A	#N/A	-1.33	hypothetical protein
TGME49_257120	#N/A	#N/A	-1.63	sugar transporter ST1

FIGURE 3U

TGME49_214750	-1.02	#N/A	-0.97	hypothetical protein
TGME49_263510	-1.86	-3.66	-2.31	Spc97 / Spc98 family protein
TGME49_308050	-1.10	#N/A	#N/A	thioredoxin domain-containing protein
TGME49_321170	1.39	1.06	1.75	Toxoplasma gondii family C protein
TGME49_222245	-1.08	#N/A	#N/A	hypothetical protein
TGME49_258070	-1.18	-1.50	-1.42	hypothetical protein
TGME49_289140	0.96	0.87	1.06	ribosomal protein l22/l43, putative
TGME49_247460	0.85	#N/A	#N/A	proliferating cell nuclear antigen PCNA1
TGME49_251530	2.11	2.18	#N/A	hypothetical protein
TGME49_226270	1.09	0.91	#N/A	hypothetical protein
TGME49_204350	2.00	#N/A	#N/A	hypothetical protein
TGME49_228070	1.56	#N/A	#N/A	hypothetical protein
TGME49_280375	2.33	2.90	#N/A	hypothetical protein
TGME49_203080	1.05	1.07	#N/A	RNA recognition motif-containing protein
TGME49_301890	-1.68	-3.19	#N/A	Toxoplasma gondii family B protein
TGME49_235540	1.00	0.92	#N/A	eukaryotic initiation factor-2 beta, putative
TGME49_306260	1.02	1.17	#N/A	hypothetical protein
TGME49_299180	-1.97	#N/A	#N/A	prenylated protein, putative
TGME49_294310	1.42	#N/A	#N/A	hypothetical protein
TGME49_261670	1.33	#N/A	#N/A	ribonuclease H1/H2 small subunit protein
TGME49_208830	1.17	#N/A	1.16	hypothetical protein
TGME49_245540	-1.08	#N/A	#N/A	hypothetical protein
TGME49_216880	3.06	#N/A	2.88	guanine nucleotide-binding protein
TGME49_253615	1.30	1.46	#N/A	hypothetical protein
TGME49_295070	1.17	#N/A	#N/A	helicase associated domain (ha2) protein
TGME49_228110	-1.31	-1.12	#N/A	hypothetical protein
TGME49_285490	-1.46	-1.37	#N/A	helix-hairpin-helix motif domain-containing protein
TGME49_276930	0.90	1.44	1.04	hypothetical protein
TGME49_214780	-1.54	-1.33	#N/A	hydrolase, NUDIX family protein
TGME49_224480	-1.12	-1.03	#N/A	cell-cycle-associated protein kinase CLK, putative
TGME49_202280	-1.90	-3.15	-2.17	WD domain, G-beta repeat-containing protein
TGME49_210255	0.92	0.81	0.99	hypothetical protein
TGME49_265410	1.53	1.20	#N/A	G-protein beta WD-40 repeat containing protein

TGME49_262630	#N/A	#N/A	2.15	hypothetical protein
TGME49_221170	#N/A	#N/A	-1.28	CAAX metallo endopeptidase
TGME49_269290	#N/A	#N/A	-1.82	hypothetical protein
TGME49_213050	#N/A	#N/A	1.31	hypothetical protein
TGME49_229690	#N/A	#N/A	-1.13	autophagy-related protein 7 atg7, putative
TGME49_318750	#N/A	#N/A	1.30	deoxyribose-phosphate aldolase
TGME49_310460	#N/A	#N/A	-1.11	Rab6
TGME49_288245	#N/A	#N/A	1.31	hypothetical protein
TGME49_240710	#N/A	#N/A	-1.19	RNA recognition motif-containing protein
TGME49_314970	#N/A	#N/A	-1.05	root hair defective 3 gtp-binding protein (rhd3) protein
TGME49_204400	#N/A	#N/A	-0.97	ATPase synthase subunit alpha, putative
TGME49_243730	#N/A	#N/A	1.29	rhoptry protein ROP9
TGME49_298030	#N/A	#N/A	-1.96	Ubiquinol-cytochrome c chaperone, putative
TGME49_216810	#N/A	#N/A	1.13	5'-nucleotidase, C-terminal domain-containing protein
TGME49_238040	#N/A	#N/A	-1.31	protein disulfide-isomerase domain-containing protein
TGME49_314780	#N/A	#N/A	-1.05	myosin G
TGME49_306350	#N/A	#N/A	1.14	variable surface lipoprotein
TGME49_258090	#N/A	#N/A	-1.11	hypothetical protein
TGME49_240450	#N/A	#N/A	1.47	Maf family protein
TGME49_242870	#N/A	#N/A	-1.50	histone lysine methyltransferase, SET, putative
TGME49_298980	#N/A	#N/A	1.08	RNA pseudouridine synthase superfamily protein
TGME49_297320	#N/A	#N/A	-1.30	hypothetical protein
TGME49_310300	#N/A	#N/A	-1.53	hypothetical protein
TGME49_274160	#N/A	#N/A	-1.05	hypothetical protein
TGME49_290040	#N/A	#N/A	0.97	macrophage migration inhibitory factor, putative
TGME49_329800	#N/A	#N/A	-1.24	hypothetical protein
TGME49_218530	#N/A	#N/A	-1.09	proteasome-interacting thioredoxin domain-containing protein
TGME49_255215	#N/A	#N/A	1.78	hypothetical protein
TGME49_203600	#N/A	#N/A	-1.16	hypothetical protein
TGME49_270010	#N/A	#N/A	-1.50	hypothetical protein
TGME49_264760	#N/A	#N/A	-1.12	Oxysterol-binding protein
TGME49_297880	#N/A	#N/A	-1.54	dense granule protein DG32
TGME49_262070	#N/A	#N/A	-0.99	ribosomal rna assembly protein mis3, putative

FIGURE 3V

TGME49_245500	1.22	#N/A	#N/A	dipeptidyl peptidase iv (dpp iv) n-terminal region domain-containing protein
TGME49_245480	2.22	2.41	#N/A	hypothetical protein
TGME49_202980	-1.12	-1.34	-1.02	hypothetical protein
TGME49_209210	-1.10	-1.25	#N/A	hypothetical protein
TGME49_319710	-1.31	-1.20	#N/A	kinesin motor domain-containing protein
TGME49_220160	2.33	#N/A	#N/A	WD domain-containing protein
TGME49_263080	0.90	1.10	1.04	hypothetical protein
TGME49_306470	-1.14	-1.34	-1.10	isoprenylcysteine carboxyl methyltransferase (icmt) family protein
TGME49_313277	-2.03	#N/A	#N/A	hypothetical protein
TGME49_285540	-1.59	#N/A	#N/A	DNA-directed DNA polymerase
TGME49_201220	-1.50	-1.39	#N/A	zinc finger protein
TGME49_293190	-1.01	-0.97	-1.18	endonuclease/exonuclease/phosphatase family protein
TGME49_319500	-1.04	#N/A	#N/A	hypothetical protein
TGME49_238110	-1.50	-1.61	#N/A	replication factor a protein 3 protein
TGME49_246760	-2.21	-2.02	#N/A	hypothetical protein
TGME49_313600	-1.33	-1.36	-1.30	DDHD domain-containing protein
TGME49_265520	-0.89	#N/A	#N/A	hypothetical protein
TGME49_203350	1.48	#N/A	#N/A	hypothetical protein
TGME49_215060	-1.03	#N/A	#N/A	small GTP-binding protein sar1, putative
TGME49_211860	1.10	#N/A	1.16	hypothetical protein
TGME49_312940	0.97	#N/A	#N/A	hypothetical protein
TGME49_246970	-1.45	-1.31	#N/A	3'-5' exonuclease domain-containing protein
TGME49_320000	-1.41	-1.35	#N/A	SCY kinase (incomplete catalytic triad)
TGME49_294930	-1.08	-1.37	#N/A	leucine rich repeat-containing protein
TGME49_219720	1.24	#N/A	#N/A	Ras-related protein Rab-5C, putative
TGME49_254460	1.01	1.12	1.22	hypothetical protein
TGME49_266070	1.33	1.28	1.31	ribosomal protein RPL31
TGME49_305140	1.08	#N/A	#N/A	phospholipase, patatin family protein
TGME49_293790	1.08	5.43	4.52	hypothetical protein
TGME49_257595	-1.23	#N/A	#N/A	hypothetical protein
TGME49_254120	0.96	1.77	1.66	autophagy-related protein 8 atg8, putative
TGME49_221390	-1.24	-1.37	#N/A	hypothetical protein
TGME49_293220	1.44	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_311890	-0.94	-0.98	-0.86	hypothetical protein

TGME49_271760	#N/A	#N/A	-1.67	seryl-tRNA synthetase (SerRS2)
TGME49_216770	#N/A	#N/A	2.12	hypothetical protein
TGME49_235515	#N/A	#N/A	1.91	MORN repeat-containing protein
TGME49_306440	#N/A	#N/A	-1.34	hypothetical protein
TGME49_306280	#N/A	#N/A	0.99	mediator complex subunit MED7
TGME49_259860	#N/A	#N/A	-1.24	hypothetical protein
TGME49_224810	#N/A	#N/A	-1.98	hypothetical protein
TGME49_251620	#N/A	#N/A	-1.24	flap structure-specific endonuclease 1, putative
TGME49_262710	#N/A	#N/A	0.96	Ctr copper transporter family protein
TGME49_216730	#N/A	#N/A	-0.88	MCM2/3/5 family protein
TGME49_291940	#N/A	#N/A	-1.03	hypothetical protein
TGME49_248750	#N/A	#N/A	-1.52	hypothetical protein
TGME49_229790	#N/A	#N/A	-1.43	hypothetical protein
TGME49_239010	#N/A	#N/A	1.54	hypothetical protein
TGME49_223690	#N/A	#N/A	1.13	hypothetical protein
TGME49_222400	#N/A	#N/A	-0.85	hypothetical protein
TGME49_222380	#N/A	#N/A	-0.86	importin-beta N-terminal domain-containing protein
TGME49_247760	#N/A	#N/A	-1.29	AMP-binding enzyme domain-containing protein
TGME49_203170	#N/A	#N/A	-1.11	OB-fold nucleic acid binding domain-containing protein
TGME49_318430	#N/A	#N/A	-0.91	malate dehydrogenase MDH
TGME49_271300	#N/A	#N/A	1.38	DNA-directed RNA polymerase II RPB7
TGME49_274150	#N/A	#N/A	-1.72	hypothetical protein
TGME49_223490	#N/A	#N/A	1.15	hypothetical protein
TGME49_271960	#N/A	#N/A	0.83	hypothetical protein
TGME49_232450	#N/A	#N/A	-1.21	SWI2/SNF2-containing protein RAD54
TGME49_239560	#N/A	#N/A	-1.46	myosin E
TGME49_259190	#N/A	#N/A	-1.93	hypothetical protein
TGME49_217600	#N/A	#N/A	-0.98	calcium-dependent protein kinase CDPK9
TGME49_217670	#N/A	#N/A	-1.35	ribosomal protein RPS6
TGME49_250880	#N/A	#N/A	-0.81	kinase, pfkB family protein
TGME49_305900	#N/A	#N/A	1.13	hypothetical protein
TGME49_213030	#N/A	#N/A	0.78	hypothetical protein
TGME49_290940	#N/A	#N/A	-0.95	EMP/nonaspanin domain family protein
TGME49_240890	#N/A	#N/A	-0.94	6-phosphofructokinase

FIGURE 3W

TGME49_278740	-1.25	#N/A	#N/A	diaminopimelate decarboxylase
TGME49_253880	0.81	0.86	0.81	GNS1/SUR4 family protein
TGME49_213910	-1.27	-1.12	#N/A	hypothetical protein
TGME49_304680	-1.43	-1.82	-1.73	ubiquitin family protein
TGME49_275810	1.45	#N/A	1.36	ribosomal protein RPS10
TGME49_221510	-1.15	#N/A	#N/A	hypothetical protein
TGME49_228370	-1.26	-1.53	-1.57	hypothetical protein
TGME49_315590	-1.38	-1.24	-1.80	macro domain-containing protein
TGME49_263290	1.46	#N/A	#N/A	rhomboid protease ROM2
TGME49_290270	-1.20	#N/A	#N/A	SPRY domain-containing protein
TGME49_202240	-2.36	-2.25	-2.68	RAP domain-containing protein
TGME49_248370	1.41	#N/A	#N/A	prefoldin subunit 6, putative
TGME49_290720	-0.83	#N/A	#N/A	vacuolar proton translocating ATPase subunit, putative
TGME49_263660	-2.33	-2.43	-2.37	hypothetical protein
TGME49_213710	-1.28	-1.86	-1.50	WD domain, G-beta repeat-containing protein
TGME49_283585	-1.30	#N/A	#N/A	hypothetical protein
TGME49_237480	-1.55	#N/A	#N/A	BRCA1 C Terminus (BRCT) domain-containing protein
TGME49_220530	-1.64	-1.91	-1.67	AP2 domain transcription factor AP2V-1
TGME49_263720	-1.87	-2.18	-2.27	HMG (high mobility group) box domain-containing protein
TGME49_249240	1.13	1.22	1.10	calmodulin, putative
TGME49_225680	-1.74	-2.00	-1.74	hypothetical protein
TGME49_201400	-1.41	-2.11	-2.01	Sin3-associated polypeptide SAP18
TGME49_306410	-1.76	-2.03	-2.16	hypothetical protein
TGME49_249480	1.07	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_216260	-0.98	#N/A	#N/A	eukaryotic initiation factor-2B, gamma subunit, putative
TGME49_289180	-1.21	-1.13	#N/A	thioredoxin family redox-active protein, putative
TGME49_252640	1.57	5.22	5.49	P-type ATPase PMA1
TGME49_290950	-0.86	#N/A	#N/A	clathrin heavy chain, putative
TGME49_262700	-1.61	-1.71	-1.59	tetratricopeptide repeat-containing protein
TGME49_269075	1.68	#N/A	#N/A	hypothetical protein
TGME49_253380	0.83	#N/A	0.81	AP2 domain transcription factor AP2III-2
TGME49_258105	-2.15	-1.98	#N/A	hypothetical protein
TGME49_237230	1.11	1.49	1.16	hypothetical protein
TGME49_202300	-1.29	-1.24	-1.23	inosine triphosphate pyrophosphatase, putative
TGME49_215990	-1.57	-1.45	#N/A	helicase, putative

TGME49_297220	#N/A	#N/A	-1.93	AMP-binding enzyme domain-containing protein
TGME49_207400	#N/A	#N/A	0.91	hypothetical protein
TGME49_314460	#N/A	#N/A	-1.55	hypothetical protein
TGME49_216630	#N/A	#N/A	-1.53	trigger factor protein, putative
TGME49_297150	#N/A	#N/A	-1.26	MORN repeat-containing protein
TGME49_281480	#N/A	#N/A	1.05	WD domain, G-beta repeat-containing protein
TGME49_215370	#N/A	#N/A	1.03	hypothetical protein
TGME49_293780	#N/A	#N/A	1.38	hypothetical protein
TGME49_309752	#N/A	#N/A	0.75	succinate-Coenzyme A ligase, beta subunit, putative
TGME49_248950	#N/A	#N/A	-1.47	carrier superfamily protein
TGME49_209610	#N/A	#N/A	1.07	oocyst wall protein OWP2
TGME49_310560	#N/A	#N/A	-1.83	hypothetical protein
TGME49_274010	#N/A	#N/A	-1.62	hypothetical protein
TGME49_221630	#N/A	#N/A	-1.23	hypothetical protein
TGME49_300130	#N/A	#N/A	1.58	apical membrane antigen 1 domain-containing protein
TGME49_243690	#N/A	#N/A	0.80	hypothetical protein
TGME49_268000	#N/A	#N/A	-1.45	hypothetical protein
TGME49_319590	#N/A	#N/A	1.20	hypothetical protein
TGME49_267350	#N/A	#N/A	0.91	LSM domain-containing protein
TGME49_220140	#N/A	#N/A	1.47	EF hand domain-containing protein
TGME49_235905	#N/A	#N/A	-1.99	ribonuclease z, putative
TGME49_249300	#N/A	#N/A	-0.75	hypothetical protein
TGME49_314540	#N/A	#N/A	-1.32	hypothetical protein
TGME49_313410	#N/A	#N/A	-0.90	proteasome 26S regulatory subunit
TGME49_306460	#N/A	#N/A	-1.21	bromodomain-containing protein
TGME49_311140	#N/A	#N/A	-1.58	hypothetical protein
TGME49_237010	#N/A	#N/A	-0.94	hypothetical protein
TGME49_221470	#N/A	#N/A	-0.79	hypothetical protein
TGME49_307605	#N/A	#N/A	1.08	hypothetical protein
TGME49_254606	#N/A	#N/A	1.31	hypothetical protein
TGME49_307830	#N/A	#N/A	-0.80	hypothetical protein
TGME49_245710	#N/A	#N/A	-0.95	phosphatidylinositol-4-phosphate 5-kinase, putative
TGME49_306330	#N/A	#N/A	-1.00	phospholipase
TGME49_228690	#N/A	#N/A	-1.37	phosphatidylinositol 3- and 4-kinase
TGME49_235700	#N/A	#N/A	1.00	sedoheptulose-1,7-bisphosphatase

FIGURE 3X

TGME49_314840	-1.19	#N/A	#N/A	ubiquitin carboxyl-terminal hydrolase
TGME49_253440	0.81	1.17	1.15	cell-cycle-associated protein kinase SRPK, putative
TGME49_213950	-1.11	#N/A	#N/A	hypothetical protein
TGME49_308040	-1.22	#N/A	#N/A	ZPR1 zinc finger domain-containing protein
TGME49_207970	-3.06	#N/A	#N/A	HEAT repeat-containing protein
TGME49_208850	1.56	#N/A	2.52	SAG-related sequence SRS11
TGME49_210408	1.42	1.67	#N/A	HMG (high mobility group) box domain-containing protein
TGME49_254820	0.97	#N/A	#N/A	hypothetical protein
TGME49_293680	-1.30	-1.47	#N/A	hypothetical protein
TGME49_291690	-1.33	-1.27	#N/A	hypothetical protein
TGME49_260830	-2.20	-2.72	#N/A	hypothetical protein
TGME49_295420	-0.94	#N/A	#N/A	hypothetical protein
TGME49_226320	-1.05	-1.07	#N/A	hypothetical protein
TGME49_245730	2.35	#N/A	#N/A	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_262730	0.88	1.38	1.45	rhoptry protein ROP16
TGME49_312210	1.76	1.89	#N/A	hypothetical protein
TGME49_240600	0.97	#N/A	#N/A	chaperonin cpn60, putative
TGME49_301460	1.63	#N/A	#N/A	hypothetical protein
TGME49_297650	-1.02	#N/A	#N/A	Ser/Thr phosphatase family protein
TGME49_259720	-1.19	-1.18	#N/A	hypothetical protein
TGME49_305860	-0.87	-1.42	#N/A	calcium-dependent protein kinase CDPK3
TGME49_208580	-1.19	-1.26	-1.58	DNA ligase 1, putative
TGME49_291350	-1.66	#N/A	#N/A	hypothetical protein
TGME49_226080	-1.60	#N/A	#N/A	polyA polymerase
TGME49_215250	-1.94	-1.94	-2.07	thiamin pyrophosphokinase, catalytic domain-containing protein

TGME49_318510	#N/A	#N/A	-1.07	N-ethylmaleimide-sensitive fusion protein, putative
TGME49_297980	#N/A	#N/A	-1.38	hypothetical protein
TGME49_222960	#N/A	#N/A	-1.28	SCY kinase-related protein (incomplete catalytic triad)
TGME49_219860	#N/A	#N/A	-0.82	replication licensing factor, putative
TGME49_239480	#N/A	#N/A	-1.11	RNB family domain-containing protein
TGME49_273060	#N/A	#N/A	1.06	ribosomal protein S17, putative
TGME49_289640	#N/A	#N/A	1.30	hypothetical protein
TGME49_276120	#N/A	#N/A	1.32	histone lysine methyltransferase, SET, putative
TGME49_259550	#N/A	#N/A	-0.82	dihydropteroate synthase
TGME49_209270	#N/A	#N/A	-1.44	hypothetical protein
TGME49_249740	#N/A	#N/A	1.12	translation machinery associated tma7 protein
TGME49_232320	#N/A	#N/A	-1.70	hypothetical protein
TGME49_238880	#N/A	#N/A	1.11	hypothetical protein
TGME49_313160	#N/A	#N/A	-1.11	hypothetical protein
TGME49_310930	#N/A	#N/A	-0.95	hypothetical protein
TGME49_320588	#N/A	#N/A	-1.36	glycosyl hydrolases family 35 protein
TGME49_255330	#N/A	#N/A	-1.84	hypothetical protein
TGME49_297360	#N/A	#N/A	-1.00	hypothetical protein
TGME49_218910	#N/A	#N/A	1.76	hypothetical protein
TGME49_209070	#N/A	#N/A	0.99	hypothetical protein
TGME49_233220	#N/A	#N/A	-0.83	hypothetical protein
TGME49_267670	#N/A	#N/A	-2.57	hypothetical protein
TGME49_312360	#N/A	#N/A	-1.69	hypothetical protein
TGME49_249840	#N/A	#N/A	-1.64	dynein heavy chain 2, putative

FIGURE 4A

Figure 4: EGS expression during NSC infections. Differencial expression analysis of T. gondii genes from neuronal stem cells infected with T. gondii EGS strain for 18 hours compared to T. gondii gene expression from neuronal stem cells infected with either GT1, ME49 or VEG strain for 18 hours.

Gene ID	LogFC(EGS/GT1)	LogFC(EGS/ME49)	LogFC(EGS/VEG)	Gene Name
TGME49_233925	6.94	7.05	9.00	hypothetical protein
TGME49_237130	7.84	8.63	10.14	cytochrome b, putative
TGME49_320050	4.19	4.45	4.35	ribosomal protein RPL5
TGME49_322200	12.41	10.27	12.41	apocytochrome b, putative
TGME49_330000	8.50	9.84	10.97	cytochrome b
TGME49_290600	3.14	3.32	2.50	succinyl-CoA-synthetase alpha SCSA
TGME49_323400	7.83	10.51	10.92	cytochrome c oxidase subunit iii subfamily protein
TGME49_322800	12.26	12.26	12.26	hypothetical protein
TGME49_301250	7.82	8.17	8.14	hypothetical protein
TGME49_255060	7.95	8.34	10.42	cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_321360	3.31	3.10	2.94	clustered-asparagine-rich protein
TGME49_232955	11.47	11.71	13.87	hypothetical protein
TGME49_302055	11.93	11.93	11.93	ribosomal protein RPS12
TGME49_251180	4.23	3.68	2.68	KRUF family protein
TGME49_262690	1.96	1.87	1.88	ribosomal protein RPL27
TGME49_261240	7.55	8.23	5.94	histone H3
TGME49_238240	2.08	2.80	2.64	bystin protein
TGME49_250710	2.10	1.75	1.13	microneme protein MIC10
TGME49_244370	3.57	3.61	3.44	TDC1, putative
TGME49_213280	2.15	2.05	1.16	SAG-related sequence SRS25
TGME49_218520	1.84	1.97	1.22	microneme protein MIC6
TGME49_217530	4.13	4.39	4.18	hypothetical protein
TGME49_211695	4.77	3.87	3.16	hypothetical protein
TGME49_287040	3.80	2.26	1.45	hypothetical protein
TGME49_277230	3.85	4.50	3.76	hypothetical protein
TGME49_311230	1.78	1.55	1.23	hypothetical protein
TGME49_237230	1.90	1.74	1.26	hypothetical protein
TGME49_223660	3.08	2.72	3.20	50S ribosomal protein L4, putative
TGME49_293790	4.56	6.17	8.48	hypothetical protein

Gene ID	LogFC(EGS/GT1)	LogFC(EGS/ME49)	LogFC(EGS/VEG)	Gene Name
TGME49_219850	-1.44	-1.03	-1.48	prolyl-tRNA synthetase (ProRS)
TGME49_281910	1.12	1.57	1.35	hypothetical protein
TGME49_226540	1.29	#N/A	#N/A	protein kinase
TGME49_233310	-3.35	-3.28	-3.41	peptidase D, putative
TGME49_268280	-1.09	-1.00	#N/A	'chromo' (CHRromatin Organization MOdifier) domain-containing protein
TGME49_231200	-2.31	-2.78	-2.96	hypothetical protein
TGME49_253020	-2.34	-2.98	-2.14	hypothetical protein
TGME49_297140	-2.67	-2.97	-2.91	U6 snRNA-associated sm family protein Lsm2, putative
TGME49_318300	-2.67	-2.49	-2.54	hypothetical protein
TGME49_309050	-8.03	-8.05	-8.38	hypothetical protein
TGME49_264030	-1.62	-1.66	-1.99	aminotransferase, putative
TGME49_203620	-3.35	-3.25	-3.12	hypothetical protein
TGME49_222840	1.50	1.67	1.21	Ser/Thr phosphatase family protein
TGME49_236780	-3.35	-3.23	-3.31	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_228230	1.08	1.22	1.30	hypothetical protein
TGME49_243410	-3.35	-3.39	-4.05	tetratricopeptide repeat-containing protein
TGME49_219300	1.39	1.38	1.11	ran binding protein
TGME49_313160	-2.67	-2.33	-3.20	hypothetical protein
TGME49_270150	-2.67	-2.79	-2.98	hypothetical protein
TGME49_253490	1.69	1.80	2.08	hypothetical protein
TGME49_300280	-2.36	-1.96	-2.41	LSM domain-containing protein
TGME49_206605	1.58	1.20	2.24	hypothetical protein
TGME49_204060	-2.67	-2.77	-2.62	SNARE domain-containing protein
TGME49_295850	-1.16	-1.35	-1.01	cyclic nucleotide-binding domain-containing protein
TGME49_278550	-1.98	-1.78	-1.52	elongation factor Tu GTP binding domain-containing protein
TGME49_215490	-1.27	#N/A	#N/A	transporter, major facilitator family protein
TGME49_200330	-1.65	-1.47	-1.42	hypothetical protein
TGME49_239320	-7.99	-7.58	-8.28	BolA family protein
TGME49_275780	-7.99	-8.35	-7.94	hypothetical protein

FIGURE 4B

TGME49_293170	-5.98	-5.85	-5.65	hypothetical protein
TGME49_205680	3.65	2.99	2.15	hypothetical protein
TGME49_271935	2.89	2.66	1.85	hypothetical protein
TGME49_254710	2.29	2.02	1.52	serine esterase (DUF676) protein
TGME49_275860	2.82	2.43	2.23	hypothetical protein
TGME49_253690	1.70	1.87	1.24	hypothetical protein
TGME49_221840	4.60	4.42	6.21	hypothetical protein
TGME49_251400	3.32	2.83	3.02	hypothetical protein
TGME49_240060	2.01	1.66	#N/A	hypothetical protein
TGME49_224760	6.80	3.36	3.19	SAG-related sequence SRS40E
TGME49_236910	-4.99	-4.53	-4.60	U2 snRNP auxiliary factor, putative
TGME49_243615	4.37	3.28	3.29	hypothetical protein
TGME49_225790	2.95	1.70	#N/A	PDI family protein
TGME49_277080	1.51	#N/A	#N/A	microneme protein MIC5
TGME49_211030	-3.57	-3.84	-3.41	hypothetical protein
TGME49_259260	-2.69	-2.40	-2.61	membrane protein FtsH1
TGME49_261720	-5.75	-5.72	-6.53	metal cation transporter, ZIP family protein
TGME49_229010	-2.20	-2.17	-2.37	rhoptry neck protein RON4
TGME49_273320	2.17	2.45	1.83	hypothetical protein
TGME49_233450	1.96	1.48	1.37	SAG-related sequence SRS29A
TGME49_239790	-10.72	-10.48	-10.51	BRCA1 C Terminus (BRCT) domain-containing protein
TGME49_275640	2.47	2.00	2.21	hypothetical protein
TGME49_290020	2.52	2.52	2.27	cyclin dependent kinase binding protein
TGME49_287170	-10.73	-10.57	-10.29	hypothetical protein
TGME49_269330	-10.62	-10.42	-10.60	hypothetical protein
TGME49_208370	1.60	1.75	1.58	myosin heavy chain, putative
TGME49_275870	4.13	2.54	4.24	tubulin/FtsZ family, GTPase domain-containing protein
TGME49_260430	5.02	3.90	4.88	hypothetical protein
TGME49_270700	2.17	1.73	1.62	hypothetical protein
TGME49_312140	-3.17	-3.53	#N/A	hypothetical protein
TGME49_228160	1.95	2.03	2.44	acid phosphatase
TGME49_214980	1.71	1.82	1.39	hypothetical protein
TGME49_201170	-2.54	-2.61	-2.77	hypothetical protein
TGME49_301222	3.12	3.03	3.48	DNA repair protein Rad4 domain-containing protein
TGME49_252430	1.96	1.68	2.15	hypothetical protein

TGME49_202080	-7.99	-8.07	-8.15	hypothetical protein
TGME49_203010	-1.15	-1.01	#N/A	aurora kinase
TGME49_216240	-1.77	-1.76	-1.96	hypothetical protein
TGME49_315590	-2.07	-1.95	-2.04	macro domain-containing protein
TGME49_228030	1.87	1.56	2.04	hypothetical protein
TGME49_297760	-7.99	-8.05	-8.91	hypothetical protein
TGME49_255160	-7.99	-8.88	-8.87	hypothetical protein
TGME49_260420	-1.77	-1.62	-1.69	HEC/Ndc80p family protein
TGME49_235420	-1.16	-1.30	-1.03	hypothetical protein
TGME49_268910	1.28	1.34	1.66	signal peptidase I protein
TGME49_215070	1.03	#N/A	1.23	ferodoxin FD
TGME49_228980	-8.00	-8.20	-8.67	hypothetical protein
TGME49_268750	-3.35	-3.38	-3.47	peptidyl-prolyl cis-trans isomerase E, putative
TGME49_224810	-3.54	-3.46	-3.76	hypothetical protein
TGME49_264420	4.88	2.95	3.44	lipoprotein, putative
TGME49_232960	-1.60	-1.60	-1.86	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_218370	-2.06	-2.02	-2.20	hypothetical protein
TGME49_294020	-7.99	-8.74	-8.71	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_321550	1.09	1.04	#N/A	hypothetical protein
TGME49_249020	-2.07	-2.21	-2.17	kinesin motor domain-containing protein
TGME49_250500	-3.37	-3.58	-3.24	hypothetical protein
TGME49_226090	-3.34	-3.35	-2.55	DEAD/DEAH box helicase domain-containing protein
TGME49_234300	1.28	#N/A	1.07	hypothetical protein
TGME49_218800	-8.01	-8.20	-7.86	hypothetical protein
TGME49_305920	-3.30	-3.50	-3.62	endonuclease III family 1 protein
TGME49_211470	1.56	2.49	2.32	Fcf2 pre-rRNA processing protein
TGME49_299015	-8.24	-6.90	-8.68	hypothetical protein
TGME49_213445	-1.70	-1.43	#N/A	hypothetical protein
TGME49_265380	-2.07	-1.96	-1.86	tetratricopeptide repeat (TPR)-/ U-box domain-containing protein
TGME49_319570	-1.68	-1.66	-1.90	WD domain, G-beta repeat-containing protein
TGME49_213590	-1.24	#N/A	-1.33	hypothetical protein
TGME49_289910	-1.33	-1.02	#N/A	hypothetical protein
TGME49_215520	-1.24	#N/A	#N/A	hypothetical protein
TGME49_257170	-3.30	-3.23	-2.95	hypothetical protein
TGME49_228630	-1.22	-1.14	-1.36	hypothetical protein

FIGURE 4C

TGME49_290700	2.40	2.22	1.76	hypothetical protein
TGME49_226310	-4.12	-4.25	-3.47	zinc finger (CCCH type) motif-containing protein
TGME49_251540	1.84	2.03	1.30	dense granule protein GRA9
TGME49_293570	-3.09	-3.03	-3.13	translocation protein sec62, putative
TGME49_290200	-2.13	-1.63	-2.00	NAD/NADP octopine/nopaline dehydrogenase, alpha-helical domain-containing protein
TGME49_261520	-5.37	-5.22	-5.14	nucleolar GTP-binding protein 1, putative
TGME49_306670	-3.53	-3.50	-3.72	hypothetical protein
TGME49_249990	2.26	2.33	1.69	hypothetical protein
TGME49_208450	1.90	1.40	#N/A	protease inhibitor PI2
TGME49_214220	1.64	1.87	1.37	hypothetical protein
TGME49_315885	2.12	2.57	2.61	glycosyltransferase, putative
TGME49_254620	1.38	#N/A	1.17	ribosomal protein RPL39
TGME49_219520	-2.77	-2.28	-2.64	histone arginine methyltransferase PRMT1
TGME49_269310	4.41	3.54	5.30	hypothetical protein
TGME49_239440	-10.43	-10.30	-10.36	protein kinase (incomplete catalytic triad)
TGME49_254120	2.06	2.28	1.94	autophagy-related protein 8 atg8, putative
TGME49_214350	-3.27	-2.91	-2.94	GTP-binding protein, putative
TGME49_206550	5.36	3.26	7.43	hypothetical protein
TGME49_245980	4.18	2.90	3.58	hypothetical protein
TGME49_222380	-2.54	-2.55	-2.57	importin-beta N-terminal domain-containing protein
TGME49_314500	-2.83	-3.17	-3.32	subtilisin SUB2
TGME49_266050	1.90	2.21	2.37	hypothetical protein
TGME49_223930	1.66	1.62	1.70	RNA recognition motif-containing protein
TGME49_319500	-10.40	-10.71	-10.47	hypothetical protein
TGME49_217820	-2.95	-2.54	-3.27	PCI domain-containing protein
TGME49_298620	-5.25	-5.08	-4.77	hypothetical protein
TGME49_265190	-4.42	-4.49	-4.37	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_245460	1.32	1.09	1.16	ribosomal protein RPS8
TGME49_315620	-5.25	-5.11	-5.42	vacuolar ATP synthase subunit C, putative
TGME49_282070	-2.08	-2.02	-1.87	hypothetical protein
TGME49_300220	-3.34	-3.20	-3.26	hypothetical protein

TGME49_290640	-1.34	-1.52	-1.13	DNA mismatch repair protein MSH6-1, putative
TGME49_238410	-2.63	-2.83	-3.02	hypothetical protein
TGME49_215060	-1.26	-1.16	-1.54	small GTP-binding protein sar1, putative
TGME49_320460	-3.30	-3.51	-3.20	ABC transporter transmembrane region domain-containing protein
TGME49_254200	-7.98	-8.32	-7.85	anticodon binding domain-containing protein
TGME49_203160	1.32	1.09	1.08	hypothetical protein
TGME49_247680	1.68	#N/A	#N/A	hypothetical protein
TGME49_282130	-2.28	-2.12	-2.19	hypothetical protein
TGME49_311150	-3.31	-3.61	-3.92	hypothetical protein
TGME49_222910	-1.50	-1.34	-1.38	phosphoglycerate mutase
TGME49_285272	-7.99	-8.13	-7.86	hypothetical protein
TGME49_281900	-1.14	-1.27	#N/A	SET domain containing lysine methyltransferase KMTox
TGME49_288330	-3.30	-3.47	-3.41	histone lysine methyltransferase, SET, putative
TGME49_247930	-7.98	-7.69	-8.15	SNARE domain-containing protein
TGME49_226280	1.72	2.12	1.85	ribosomal protein L28, putative
TGME49_216750	1.04	#N/A	#N/A	Paf1/RNA polymerase II complex component LEO1
TGME49_271930	-1.16	-1.34	-1.52	hypothetical protein
TGME49_209210	-1.63	-2.20	-1.97	hypothetical protein
TGME49_301400	1.16	1.14	1.69	hypothetical protein
TGME49_312520	-3.33	-4.02	-2.69	tRNA dimethylallyltransferase
TGME49_305870	-2.64	-2.29	-2.08	DAD family protein
TGME49_226270	-2.66	-2.89	-3.07	hypothetical protein
TGME49_278230	-3.30	-3.04	-3.05	prenyltransferase and squalene oxidase repeat-containing protein
TGME49_243200	-1.25	-1.43	-1.33	hypothetical protein
TGME49_289720	-1.65	-1.42	-1.57	hypothetical protein
TGME49_222240	-1.28	-1.20	-1.27	hypothetical protein
TGME49_294250	-1.87	-1.84	-2.11	WD domain, G-beta repeat-containing protein
TGME49_311625	-2.04	-2.07	-1.97	WD domain, G-beta repeat-containing protein
TGME49_323110	1.18	1.44	1.42	hypothetical protein
TGME49_278160	-3.34	-3.38	-3.39	vesicle transport v-snare protein
TGME49_305540	-1.56	-1.62	-1.64	hypothetical protein

FIGURE 4D

TGME49_240650	-2.32	-2.36	-2.44	coatomer protein complex, subunit alpha, putative
TGME49_292920	-2.40	-1.88	-2.22	heat shock protein 75, putative
TGME49_260500	-2.03	-1.98	-2.19	COPI associated protein, putative
TGME49_277000	-4.45	-4.39	-4.77	transport protein Sec24, putative
TGME49_305160	3.42	3.64	2.96	histone H2Ba
TGME49_278870	-1.83	-1.62	-1.81	myosin F
TGME49_212880	-2.79	-2.89	-2.83	surface antigen repeat-containing protein
TGME49_220930	-3.07	-2.68	-2.83	hypothetical protein
TGME49_250340	-2.65	-2.25	-2.60	centrin 2
TGME49_287460	3.46	3.42	3.08	hypothetical protein
TGME49_209050	-10.21	-10.26	-10.25	Tyrosine kinase-like (TKL) protein
TGME49_261022	-2.70	-2.86	#N/A	dynein heavy chain family protein
TGME49_253170	1.86	1.61	2.14	zinc carboxypeptidase, putative
TGME49_238895	-3.36	-3.03	-2.84	hypothetical protein
TGME49_259240	1.55	1.36	1.03	ribosomal protein RPS21
TGME49_200300	6.27	6.44	3.36	hypothetical protein
TGME49_239260	6.69	3.42	3.08	histone H4
TGME49_228690	-5.20	-5.43	-5.44	phosphatidylinositol 3- and 4-kinase
TGME49_321530	1.55	1.44	#N/A	cathepsin CPL
TGME49_244280	-1.60	-1.19	-2.12	hypothetical protein
TGME49_247530	3.32	3.16	2.40	hypothetical protein
TGME49_263870	-5.18	-5.03	-5.22	glutamate-tRNA ligase
TGME49_270360	-5.16	-5.18	-5.33	hypothetical protein
TGME49_257910	4.73	4.29	#N/A	hypothetical protein
TGME49_251740	-3.48	-3.84	-3.65	AP2 domain transcription factor AP2XII-9
TGME49_240280	-2.57	-2.24	-2.45	S1/P1nuclease
TGME49_210300	-5.16	-5.29	-5.07	hypothetical protein
TGME49_249350	-10.14	-10.09	-10.39	esterase/lipase/thioesterase domain-containing protein
TGME49_242290	-2.55	-2.37	-2.68	proteasome subunit alpha1, putative
TGME49_286120	-2.44	-2.26	-2.35	prolyl endopeptidase
TGME49_244880	-4.25	-4.05	-4.08	DNA-directed RNA polymerase I RPA1
TGME49_294820	2.77	#N/A	#N/A	type I fatty acid synthase, putative
TGME49_289710	-2.76	-2.62	-2.53	AP2 domain transcription factor AP2IX-5
TGME49_261070	-4.20	-3.67	-3.15	apicoplast triosephosphate translocator APT1
TGME49_294640	-1.70	-1.47	-1.55	ribonucleoside-diphosphate reductase large chain

TGME49_236630	-1.03	#N/A	-1.36	hypothetical protein
TGME49_285810	-7.92	-8.37	-7.85	MYND finger domain-containing protein
TGME49_290310	-2.04	-2.05	-1.79	hypothetical protein
TGME49_232680	1.24	#N/A	1.15	hypothetical protein
TGME49_291590	-7.92	-8.34	-8.12	hypothetical protein
TGME49_295040	-1.04	#N/A	-1.24	HEAT repeat-containing protein
TGME49_251710	1.67	2.12	1.15	hypothetical protein
TGME49_278250	1.78	1.24	1.10	hypothetical protein
TGME49_270190	-2.73	-2.74	-2.57	protein phosphatase 2C domain-containing protein
TGME49_246130	1.18	1.26	#N/A	serpin (serine proteinase inhibitor) superfamily protein
TGME49_211230	-1.40	-1.40	-1.32	eukaryotic initiation factor-2B, alpha subunit, putative
TGME49_258450	-1.18	#N/A	#N/A	hypothetical protein
TGME49_249890	1.63	1.64	1.71	hypothetical protein
TGME49_211640	1.08	#N/A	1.34	hypothetical protein
TGME49_284540	-1.11	-1.03	-1.31	ATP synthase F1, delta subunit protein
TGME49_232750	-1.19	#N/A	#N/A	23S rRNA (adenine(1618)-N(6))-methyltransferase, putative
TGME49_254660	1.09	1.21	1.48	ankyrin repeat-containing protein
TGME49_311220	-1.93	-2.25	-1.94	hypothetical protein
TGME49_216510	-3.26	-3.95	-4.30	thioredoxin, putative
TGME49_212940	-7.92	-10.38	-7.86	hypothetical protein
TGME49_201150	-1.56	-2.17	-1.77	heavy metal translocating P-type ATPase subfamily protein
TGME49_263440	-2.25	-1.71	-1.58	hypothetical protein
TGME49_260830	-2.63	-3.12	#N/A	hypothetical protein
TGME49_255960	-1.46	-1.45	-1.25	hypothetical protein
TGME49_210778	-1.73	-1.95	-1.97	hemimethylated DNA binding domain-containing protein
TGME49_313960	-3.31	-2.93	-3.09	ribosomal protein L19 protein
TGME49_208440	1.08	1.14	1.13	hypothetical protein
TGME49_267530	1.84	1.93	1.83	hypothetical protein
TGME49_246990	-2.60	-2.22	-2.24	hypothetical protein
TGME49_214380	1.51	1.31	1.30	hypothetical protein
TGME49_312660	-2.01	-1.51	-2.08	hypothetical protein
TGME49_269320	-7.92	-8.53	-8.43	hypothetical protein
TGME49_232000	1.02	1.15	#N/A	hypothetical protein
TGME49_232970	-3.26	-3.14	-2.94	hypothetical protein
TGME49_281980	-1.28	-1.49	-1.12	phosphatidate cytidylyltransferase

FIGURE 4E

TGME49_290270	1.95	2.38	2.17	SPRY domain-containing protein
TGME49_202980	-2.87	-2.59	-2.28	hypothetical protein
TGME49_259010	-5.04	-4.48	-5.10	vacuolar ATP synthase subunit d, putative
TGME49_237210	-5.01	-4.90	-4.79	Tyrosine kinase-like (TKL) protein
TGME49_228280	2.80	2.37	2.53	hypothetical protein
TGME49_259550	-2.88	-2.93	-3.33	dihydropteroate synthase
TGME49_231410	-2.46	-2.14	-2.50	hypothetical protein
TGME49_272370	1.86	#N/A	1.71	hypothetical protein
TGME49_294610	-1.60	-1.61	-1.38	histone lysine methyltransferase, SET, putative
TGME49_241830	2.46	2.13	2.35	peptidyl-prolyl cis-trans isomerase
TGME49_260800	2.39	1.71	1.69	hypothetical protein
TGME49_232650	2.05	2.25	2.06	hypothetical protein
TGME49_202420	2.21	2.25	1.97	hypothetical protein
TGME49_316280	-5.04	-5.04	-5.19	transporter, major facilitator family protein
TGME49_214410	2.79	2.96	3.26	hypothetical protein
TGME49_232560	-3.04	-2.22	-2.40	hypothetical protein
TGME49_253750	2.24	1.94	2.28	PLU-1 family protein
TGME49_214970	-1.94	-1.69	-1.90	DNA replication licensing factor, putative
TGME49_301270	1.53	1.26	1.33	Tyrosine kinase-like (TKL) protein
TGME49_274060	-2.24	-1.82	-2.10	2-oxoglutarate/malate translocase OMT
TGME49_291890	1.28	1.33	#N/A	microneme protein MIC1
TGME49_293480	2.74	#N/A	3.17	MoeA N-terminal region (domain I and II) domain-containing protein
TGME49_246330	-5.04	-5.33	-5.17	CRAL/TRIO domain-containing protein
TGME49_208530	-3.18	-3.01	-3.36	nicotinate phosphoribosyltransferase
TGME49_313870	2.00	1.67	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_255650	-10.23	-10.24	-10.91	DHHC zinc finger domain-containing protein
TGME49_262380	-3.40	-3.08	-3.11	elongation factor Tu, putative
TGME49_207460	1.59	2.16	1.67	Rab5B protein
TGME49_221470	-2.08	-2.20	-2.15	hypothetical protein
TGME49_254080	1.41	1.64	1.59	metal cation transporter, ZIP family protein
TGME49_321650	-2.67	-2.84	-2.55	hypothetical protein
TGME49_267670	4.04	#N/A	1.90	hypothetical protein
TGME49_260440	1.42	1.37	1.21	nuclear factor NF3

TGME49_227050	-3.26	-3.36	-2.81	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_320005	-3.26	-3.18	-3.28	hypothetical protein
TGME49_297230	-1.72	-1.95	-2.06	Vps53 family, N-terminal protein
TGME49_243790	-1.85	-1.82	-1.57	SAG-related sequence SRS33
TGME49_269720	1.99	1.63	#N/A	hypothetical protein
TGME49_207230	-1.74	#N/A	#N/A	hypothetical protein
TGME49_239700	-2.60	-3.30	-2.87	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_219170	-1.55	-1.93	-1.51	hypothetical protein
TGME49_228170	1.28	1.04	#N/A	inner membrane complex protein IMC2A
TGME49_266810	-1.31	-1.25	-1.62	hypothetical protein
TGME49_305020	1.21	#N/A	#N/A	hypothetical protein
TGME49_309770	1.00	#N/A	#N/A	hypothetical protein
TGME49_271800	-1.50	#N/A	#N/A	serine esterase (DUF676) protein
TGME49_316240	-1.72	-1.51	-1.32	hypothetical protein
TGME49_202430	1.31	1.19	1.22	hypothetical protein
TGME49_214280	-7.97	-8.13	-7.97	phosphoadenosine phosphosulfate reductase family protein
TGME49_289640	1.47	1.86	2.07	hypothetical protein
TGME49_288900	1.61	1.26	1.82	Yos1 family protein
TGME49_270595	-1.69	-3.32	#N/A	UBA/TS-N domain-containing protein
TGME49_203290	1.35	1.50	1.89	hypothetical protein
TGME49_283800	-1.89	-1.99	-2.23	hypothetical protein
TGME49_248550	-3.34	-3.55	-3.59	SPX domain-containing protein
TGME49_228060	-3.35	-3.21	-2.94	hypothetical protein
TGME49_205050	2.54	#N/A	#N/A	hypothetical protein
TGME49_211680	-1.20	-1.12	-1.71	protein disulfide isomerase
TGME49_275750	-1.65	-1.31	-1.76	small nuclear ribonucleoprotein E, putative
TGME49_208050	-2.27	-2.54	-2.66	ABC transporter, putative
TGME49_240900	1.01	#N/A	1.11	AP2 domain transcription factor AP2VI-2
TGME49_204550	-2.60	-2.70	-2.74	hypothetical protein
TGME49_288620	1.02	1.03	#N/A	Erv1 / Alr family protein
TGME49_209880	-1.09	-1.19	#N/A	glutamic acid-rcih protein, putative
TGME49_204410	-1.86	-2.01	-1.68	endonuclease/exonuclease/phosphatase family protein
TGME49_254900	-1.23	#N/A	-1.09	proteasome subunit beta type 2, putative

FIGURE 4F

TGME49_294770	-4.96	-4.97	-5.13	Armadillo/beta-catenin family repeat-containing protein
TGME49_218530	-9.93	-9.55	-10.01	proteasome-interacting thioredoxin domain-containing protein
TGME49_254720	1.30	1.02	#N/A	dense granule protein GRA8
TGME49_316600	1.58	1.38	#N/A	hypothetical protein
TGME49_219700	-1.98	-1.55	-1.94	DNA replication licensing factor MCM4, putative
TGME49_305590	-4.08	-4.24	-4.21	ABC transporter transmembrane region domain-containing protein
TGME49_213410	-2.26	-2.18	-1.97	small nuclear ribonucleoprotein f (snrnp-f), putative
TGME49_323310	4.18	2.03	#N/A	hypothetical protein
TGME49_250820	-2.77	-2.93	-2.94	hypothetical protein
TGME49_297530	-9.90	-9.43	-9.68	DNA-directed RNA polymerase I RPA2
TGME49_299780	1.88	1.64	1.14	hypothetical protein
TGME49_226960	-1.42	-1.13	-1.58	phosphofructokinase PFKII
TGME49_228190	-2.01	-1.56	-1.90	eukaryotic initiation factor-3, subunit 5, putative
TGME49_207680	-4.07	-3.93	-4.57	suppressor of kinetochore protein 1, putative
TGME49_310750	-2.08	-1.99	-2.52	emp24/gp25L/p24 family protein
TGME49_218880	-2.55	-2.02	-2.54	SF-assemblin, putative
TGME49_253570	2.47	2.76	2.19	hypothetical protein
TGME49_235130	-3.68	-4.32	-3.97	transmembrane protein
TGME49_220250	1.74	1.86	1.84	Nucleotide-sensitive chloride conductance regulator (ICln) protein
TGME49_243430	2.37	2.08	1.86	OTU family cysteine protease
TGME49_217700	-9.90	-9.79	-9.87	AP2 domain transcription factor AP2XII-2
TGME49_254470	1.47	1.48	1.10	hypothetical protein
TGME49_211150	-4.87	-5.27	-4.82	hypothetical protein
TGME49_203300	2.63	2.78	2.96	hypothetical protein
TGME49_268980	1.73	1.49	1.13	hypothetical protein
TGME49_278510	-2.53	-2.72	-2.92	protein phosphatase 2C domain-containing protein
TGME49_227650	-3.07	-2.52	-2.35	microtubule-associated protein RP/EB family, putative
TGME49_318310	-2.15	-1.89	-2.07	transketolase
TGME49_239420	1.07	1.11	#N/A	protein kinase
TGME49_232500	-9.85	-9.78	-9.93	hypothetical protein
TGME49_273050	2.18	1.75	1.84	hypothetical protein
TGME49_228660	-3.57	-3.59	-3.53	Sec7 domain-containing protein

TGME49_219550	-1.08	#N/A	-1.13	dihydrolipoyllysine-residue succinyltransferase component of oxoglutarate dehydrogenase
TGME49_233000	-1.28	-1.97	-1.07	KOW motif domain-containing protein
TGME49_202640	-7.85	-8.13	-8.04	RNA pseudouridine synthase superfamily protein
TGME49_220208	-7.86	-8.29	-7.90	hypothetical protein
TGME49_306950	-7.97	-7.84	-8.04	RAP domain-containing protein
TGME49_309390	-7.85	-7.64	-8.27	hypothetical protein
TGME49_277550	-7.86	-8.26	-8.19	UvrD/REP helicase domain-containing protein
TGME49_246780	-7.85	-8.42	-7.65	hypothetical protein
TGME49_299150	-7.85	-8.50	-8.75	AP2 domain transcription factor AP2III-3
TGME49_321640	-1.74	-1.84	#N/A	cell division protein CDC48AP
TGME49_298050	-1.82	-1.36	#N/A	hypothetical protein
TGME49_286740	2.43	2.15	3.41	microneme-like protein
TGME49_276990	-3.21	-3.32	-3.93	cytochrome b5 family heme/steroid binding domain-containing protein
TGME49_232320	-7.85	-8.04	-8.59	hypothetical protein
TGME49_216530	-7.86	-7.84	-8.54	ribosome recycling factor protein
TGME49_288210	1.38	1.11	1.19	PUL domain-containing protein
TGME49_215380	-3.24	-3.38	-3.25	hypothetical protein
TGME49_281675	1.77	1.68	1.83	protein kinase, putative
TGME49_209740	1.57	1.31	1.69	hypothetical protein
TGME49_243910	1.61	1.05	#N/A	Cof family hydrolase subfamily protein
TGME49_239250	1.05	#N/A	#N/A	diacylglycerol kinase, putative
TGME49_235402	-7.86	-8.39	-7.51	CorA family Mg2+ transporter protein
TGME49_269710	-1.12	#N/A	#N/A	hypothetical protein
TGME49_290960	-1.31	-1.20	-1.21	pyruvate phosphate dikinase, pep/pyruvate binding domain-containing protein
TGME49_247610	1.57	2.01	1.39	small nuclear ribonucleoprotein E, putative
TGME49_228000	1.14	#N/A	#N/A	splicing factor 3A subunit 2, putative
TGME49_321170	2.39	2.26	2.76	Toxoplasma gondii family C protein
TGME49_214190	1.61	#N/A	1.70	SAG-related sequence SRS46
TGME49_310730	-1.38	-1.10	-1.36	hypothetical protein
TGME49_323100	1.22	1.12	#N/A	hypothetical protein
TGME49_288045	-3.25	-3.53	-3.28	hypothetical protein
TGME49_224620	1.22	1.54	#N/A	hypothetical protein

FIGURE 4G

TGME49_250030	2.80	2.66	2.94	hypothetical protein
TGME49_239410	-2.31	-2.63	-2.59	hypothetical protein
TGME49_228100	-2.62	-1.89	-1.98	hypothetical protein
TGME49_204530	1.26	1.30	#N/A	microneme protein MIC11
TGME49_206610	-3.63	-3.26	-3.18	pyruvate dehydrogenase complex subunit PDH-E2
TGME49_306060	-1.39	-1.32	-1.59	rhoptry neck protein RON8
TGME49_231430	-9.83	-9.75	-9.84	oligosaccharyl transferase stt3 protein, putative
TGME49_201860	1.08	1.09	#N/A	hypothetical protein
TGME49_223050	-1.44	-1.25	-1.58	ribosomal protein RPS20
TGME49_216730	-1.68	-1.23	-1.60	MCM2/3/5 family protein
TGME49_216820	1.42	1.54	#N/A	transporter, major facilitator family protein
TGME49_249540	1.55	1.86	1.71	hypothetical protein
TGME49_305180	-9.79	-9.86	-9.93	Na+/H+ exchanger NHE3
TGME49_200360	2.53	2.31	1.90	hypothetical protein
TGME49_255410	-4.81	-4.73	-4.79	hypothetical protein
TGME49_316660	-9.79	-9.87	-10.13	cullin family protein
TGME49_210682	5.42	2.68	3.05	hypothetical protein
TGME49_286450	1.08	1.00	#N/A	dense granule protein GRA5
TGME49_227810	1.36	1.34	#N/A	rhoptry kinase family protein ROP11 (incomplete catalytic triad)
TGME49_278800	-2.27	-2.53	-1.89	zinc finger protein 36 family 3 protein
TGME49_268225	-5.13	-4.79	-5.03	hypothetical protein
TGME49_205580	1.68	1.39	1.37	nuclear factor NF4
TGME49_247460	-1.69	-1.50	-1.81	proliferating cell nuclear antigen PCNA1
TGME49_255180	-9.77	-10.08	-9.46	ubiquitin carboxyl-terminal hydrolase
TGME49_296010	-1.92	-1.76	-1.93	phosphatidylinositol 3- and 4-kinase
TGME49_293660	-3.96	-3.66	-3.81	hypothetical protein
TGME49_239540	-9.77	-9.86	-9.89	LEM3 (ligand-effect modulator 3) family / CDC50 family protein
TGME49_294630	-2.17	-2.14	-2.37	hypothetical protein
TGME49_207640	-2.14	-1.63	-2.13	isoleucyl-tRNA synthetase family protein
TGME49_318770	-4.78	-4.68	-4.35	aurora kinase(incomplete catalytic triad)
TGME49_314410	-2.66	-2.52	-2.67	aquarius, putative
TGME49_257360	2.37	1.80	1.01	hypothetical protein
TGME49_250840	-9.73	-9.60	-9.48	hypothetical protein

TGME49_297360	-1.55	-1.34	-1.42	hypothetical protein
TGME49_280590	-3.28	-2.85	#N/A	hypothetical protein
TGME49_242110	-7.85	-6.77	-8.92	rhoptry kinase family protein ROP38
TGME49_268000	-2.56	-2.24	-2.63	hypothetical protein
TGME49_263130	1.16	1.21	#N/A	citrate synthase, putative
TGME49_284050	-1.53	-1.75	-1.41	DEAD/DEAH box helicase domain-containing protein
TGME49_275568	-1.53	-1.39	-1.11	GPI transamidase subunit PIG-U protein
TGME49_203390	-1.21	-1.15	-1.41	CRAL/TRIO domain-containing protein
TGME49_260310	1.50	1.61	1.21	ATP-binding cassette transporter ABC.B1
TGME49_244130	-1.50	-1.54	-1.39	hypothetical protein
TGME49_286640	-3.20	-2.84	-2.49	GTPase
TGME49_218960	-1.52	-1.28	-1.07	AP2 domain transcription factor AP2XII-1
TGME49_273500	-2.28	-1.78	#N/A	O-linked N-acetylglucosamine transferase
TGME49_210380	-1.33	-1.18	-1.26	hypothetical protein
TGME49_266110	1.48	1.30	1.44	DEAD/DEAH box helicase domain-containing protein
TGME49_235700	-1.43	-1.43	-1.05	sedoheptulose-1,7-bisphosphatase
TGME49_204400	-1.08	#N/A	-1.50	ATPase synthase subunit alpha, putative
TGME49_298020	-1.25	-1.19	-1.33	DEAD-family helicase
TGME49_262120	-1.20	-1.20	-1.51	IQ calmodulin-binding motif domain-containing protein
TGME49_310802	1.17	1.67	1.52	CRAL/TRIO domain-containing protein
TGME49_233680	-7.78	-8.49	-8.47	nuclear movement family protein
TGME49_223125	-1.80	-2.03	-1.82	ubiquitin family protein
TGME49_241840	1.44	1.36	#N/A	hypothetical protein
TGME49_269250	-1.11	#N/A	-1.29	Mov34/MPN/PAD-1 family protein
TGME49_211410	-3.17	-4.13	-3.86	translation initiation factor sui1 protein
TGME49_301300	-7.78	-8.35	-7.66	hypothetical protein
TGME49_314460	-7.78	-7.58	-8.49	hypothetical protein
TGME49_278770	-1.17	#N/A	-1.25	hypothetical protein
TGME49_307800	1.62	1.81	1.30	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_218280	-1.01	#N/A	-1.18	eukaryotic porin, putative
TGME49_259000	-7.78	-8.10	-8.11	hypothetical protein
TGME49_237110	-1.57	-1.68	-1.56	replication factor C subunit 2, putative
TGME49_261940	-7.78	-8.35	-8.16	hydrolase, alpha/beta fold family protein

FIGURE 4H

TGME49_293190	-2.94	-2.84	-3.24	endonuclease/exonuclease/phosphatase family protein
TGME49_253860	1.48	1.41	1.66	Tyrosine kinase-like (TKL) protein
TGME49_278050	-2.35	-2.32	-2.22	proteasome subunit alpha type 1, putative
TGME49_280490	-2.79	-3.83	-2.50	U-box domain-containing protein
TGME49_246580	-3.90	-3.68	-4.08	hypothetical protein
TGME49_232280	-9.84	-9.83	-9.89	hypothetical protein
TGME49_266070	1.16	1.25	#N/A	ribosomal protein RPL31
TGME49_271820	-9.72	-9.52	-8.87	lipoyltransferase and lipoate-protein ligase subfamily protein
TGME49_321690	-3.97	-3.66	-3.95	hypothetical protein
TGME49_227952	-2.77	-2.43	-2.49	14-3-3 superfamily protein
TGME49_293410	2.50	2.96	2.64	hypothetical protein
TGME49_212900	1.48	1.59	1.72	hypothetical protein
TGME49_313230	2.03	2.54	2.07	eukaryotic initiation factor-2, alpha subunit
TGME49_250330	-9.69	-9.74	-9.57	hypothetical protein
TGME49_294870	1.07	1.00	#N/A	universal stress family protein
TGME49_315530	-4.70	-4.61	-4.61	hypothetical protein
TGME49_267500	1.21	1.01	1.02	hypothetical protein
TGME49_205010	-2.30	-2.22	-2.55	U2 small nuclear ribonucleoprotein family protein, putative
TGME49_229020	-9.67	-9.96	-9.88	cell-cycle-associated protein kinase CDK, putative
TGME49_206690	-2.61	-2.42	-2.30	glideosome-associated protein with multiple-membrane spans GAPM2B
TGME49_268230	-9.94	-9.74	-10.16	hypothetical protein
TGME49_319370	-9.68	-9.43	-9.43	hypothetical protein
TGME49_293710	-2.10	-1.88	-1.65	Zn-finger in Ran binding protein and others domain-containing protein
TGME49_294690	1.74	1.96	1.64	rhomboid protease ROM5
TGME49_245510	-2.43	-2.58	-2.73	phospholipid-translocating P-type ATPase, flippase subfamily protein
TGME49_265390	-9.66	-9.76	-9.23	hypothetical protein
TGME49_213920	-3.43	-3.63	-3.03	hypothetical protein
TGME49_247360	2.42	2.39	2.19	PAP2 superfamily protein
TGME49_264830	-4.67	-4.61	-4.67	hypothetical protein
TGME49_202310	2.07	2.33	1.71	O-sialoglycoprotein endopeptidase
TGME49_234510	1.59	1.90	2.08	ankyrin repeat-containing protein
TGME49_290170	-2.49	-2.60	-2.51	kelch repeat domain containing/Serine/threonine protein phosphatase protein
TGME49_278940	1.78	1.80	1.40	HECT-domain (ubiquitin-transferase) domain-containing protein

TGME49_263230	-1.19	-1.17	#N/A	hypothetical protein
TGME49_223560	-2.58	-2.75	#N/A	hypothetical protein
TGME49_263210	-7.78	-8.59	-8.42	ubiquitin interaction motif domain-containing protein
TGME49_259650	-3.21	-2.79	#N/A	hypothetical protein
TGME49_252490	-1.96	-1.77	-2.36	vacuolar protein sorting 29, putative
TGME49_261780	1.11	1.08	#N/A	microneme protein MIC7
TGME49_254650	1.46	#N/A	#N/A	zinc finger protein
TGME49_256090	-7.77	-7.95	-8.16	glycerophosphodiester phosphodiesterase family protein
TGME49_228460	-1.69	-1.67	-1.50	hypothetical protein
TGME49_300130	1.76	1.92	3.11	apical membrane antigen 1 domain-containing protein
TGME49_271430	-3.16	-3.83	-3.18	hypothetical protein
TGME49_253800	-3.20	-3.15	-2.89	ribosomal protein L15, putative
TGME49_230150	1.31	#N/A	#N/A	ChAPs (Chs5p-Arf1p-binding proteins) protein
TGME49_277870	-1.80	-1.69	-2.06	hypothetical protein
TGME49_288930	-1.97	-2.41	-2.33	hypothetical protein
TGME49_222410	-1.36	-1.35	-1.18	hypothetical protein
TGME49_210960	-1.52	-1.20	-1.36	replication factor C subunit 4, putative
TGME49_225300	-1.58	-1.82	-1.76	hypothetical protein
TGME49_207160	-1.95	#N/A	4.41	SAG-related sequence SRS49D
TGME49_248445	-1.12	#N/A	#N/A	hypothetical protein
TGME49_236140	1.78	1.10	1.53	hypothetical protein
TGME49_290840	-1.41	-1.37	-1.05	serine protease
TGME49_230860	-1.96	-2.24	-2.33	hypothetical protein
TGME49_230050	1.49	1.74	1.85	50S ribosomal protein L3, putative
TGME49_248400	-1.77	-1.92	-1.92	glyoxalase I, putative
TGME49_254940	1.01	#N/A	#N/A	MIF4G domain-containing protein
TGME49_269800	-2.16	-1.93	-2.08	glutamine-dependent NAD(+) synthetase protein, putative
TGME49_205720	-7.77	-8.02	-7.98	Adenosine/AMP deaminase domain-containing protein
TGME49_221905	-1.03	#N/A	#N/A	hypothetical protein
TGME49_311380	-3.43	-3.97	#N/A	hypothetical protein
TGME49_218955	1.43	1.39	1.82	hypothetical protein
TGME49_225910	1.16	1.30	1.48	hypothetical protein
TGME49_283830	1.91	1.73	2.46	type I inorganic pyrophosphatase PPase

FIGURE 4i

TGME49_277720	-2.34	-2.24	-2.27	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_265110	-9.66	-9.30	-9.30	ribosome biogenesis protein, putative
TGME49_310030	-2.04	-2.08	-1.89	cyclase-associated protein, putative
TGME49_315100	4.95	3.08	#N/A	hypothetical protein
TGME49_254520	1.40	1.63	1.24	mediator complex subunit MED11
TGME49_212170	-9.63	-9.28	-9.18	GIY-YIG catalytic domain-containing protein
TGME49_265870	-3.46	-3.49	-3.80	pantoate-beta-alanine ligase
TGME49_213010	-4.86	-6.45	-4.64	hypothetical protein
TGME49_286460	3.16	2.96	5.01	hypothetical protein
TGME49_254410	1.95	1.74	1.12	protein phosphatase 2C, putative
TGME49_230410	-1.96	-2.13	-2.03	peroxiredoxin PRX3
TGME49_208020	2.18	3.67	4.25	AP2 domain transcription factor AP2Ib-1
TGME49_313290	1.71	1.62	1.19	MORN repeat-containing protein
TGME49_309990	4.23	2.22	3.23	hypothetical protein
TGME49_315780	-3.14	-3.15	-3.31	myosin regulatory light chain, putative
TGME49_289370	1.70	#N/A	#N/A	hypothetical protein
TGME49_224880	-3.47	-4.06	-3.34	kinesin motor domain-containing protein
TGME49_240870	-2.71	-2.54	-2.88	beta adaptin protein, putative
TGME49_277940	-3.85	-4.02	-4.03	hypothetical protein
TGME49_252880	-2.57	-2.76	-2.78	hypothetical protein
TGME49_254050	1.64	1.81	1.82	optic atrophy 3 protein (opa3) protein
TGME49_239590	-4.66	-4.32	-4.54	WD domain, G-beta repeat-containing protein
TGME49_237550	2.81	2.61	2.49	hypothetical protein
TGME49_258150	-1.92	-1.69	-2.22	proteasome subunit alpha type 7, putative
TGME49_297745	-4.27	-4.28	-4.07	hypothetical protein
TGME49_239270	-2.16	-1.73	-1.16	hypothetical protein
TGME49_281400	-3.21	-2.67	-2.25	phosphofructokinase domain-containing protein
TGME49_318660	1.26	1.66	1.29	PP2C, putative
TGME49_305060	1.48	1.38	#N/A	CAP-Gly domain-containing protein
TGME49_262970	1.65	#N/A	#N/A	hypothetical protein
TGME49_229690	-9.57	-9.70	-10.43	autophagy-related protein 7 atg7, putative
TGME49_214575	2.05	1.73	2.55	hypothetical protein
TGME49_229470	-4.65	-4.34	-4.47	hypothetical protein
TGME49_251440	-9.71	-9.06	-8.69	troponin c, isotype gamma, putative
TGME49_226705	-9.69	-9.73	-10.02	hypothetical protein

TGME49_213370	1.08	1.00	1.33	formin FRM3
TGME49_202230	-1.55	#N/A	-1.18	histone deacetylase HDAC5
TGME49_217560	1.08	1.18	#N/A	DNA-directed RNA polymerase II RPB10
TGME49_257755	1.96	2.33	#N/A	hypothetical protein
TGME49_266320	1.01	#N/A	#N/A	hypothetical protein
TGME49_309070	1.76	1.63	1.55	hypothetical protein
TGME49_234470	-1.77	-1.36	-1.48	hypothetical protein
TGME49_258380	-2.16	-2.01	-1.84	elongation factor p (ef-p) kow family domain-containing protein
TGME49_289510	1.23	1.20	1.58	hypothetical protein
TGME49_202350	-1.77	-1.53	-1.39	50S ribosomal protein L21, putative
TGME49_253540	1.43	1.51	1.31	hypothetical protein
TGME49_215030	-1.93	-2.16	-1.70	hypothetical protein
TGME49_212800	-1.42	-1.35	-1.48	hypothetical protein
TGME49_248630	-1.49	-1.39	-1.79	actin-related protein ARP1
TGME49_264450	-1.93	-1.93	-2.01	DNA topoisomerase III beta-1, putative
TGME49_217450	1.47	1.95	2.11	general transcription factor IIH polypeptide 5 GTF2H5
TGME49_213890	-7.79	-8.58	-8.36	Myb family DNA-binding domain-containing protein
TGME49_293060	-1.68	-1.75	-1.81	SPRY domain-containing protein
TGME49_276190	-2.20	-1.91	-2.20	hypothetical protein
TGME49_286180	-7.70	-8.73	-7.84	tRNA ligases class I (M) protein
TGME49_239300	-1.55	-1.58	-1.69	hypothetical protein
TGME49_273595	-1.66	-1.64	#N/A	hypothetical protein
TGME49_278170	-2.17	-1.69	-1.90	hypothetical protein
TGME49_294360	-1.32	#N/A	-1.28	ubiquitin specific protease 39 isoform 2, putative
TGME49_309920	-3.12	-3.37	-3.29	hypothetical protein
TGME49_311740	-2.16	-1.98	-1.75	hypothetical protein
TGME49_288710	1.43	1.75	1.81	hypothetical protein
TGME49_230830	1.48	#N/A	4.39	ATPase family associated with various cellular activities (AAA) domain-containing protein
TGME49_265070	-2.50	-2.53	-2.87	hypothetical protein
TGME49_227860	-7.70	-8.26	-8.00	hypothetical protein
TGME49_248110	1.24	1.41	#N/A	hypothetical protein
TGME49_297690	1.18	1.33	#N/A	hypothetical protein
TGME49_209950	-1.12	#N/A	-1.25	thioredoxin, putative
TGME49_244570	-7.71	-8.31	-8.04	hypothetical protein
TGME49_270760	-7.72	-8.29	-7.99	asparagine synthase

FIGURE 4J

TGME49_246490	-2.25	-2.01	-2.68	hypothetical protein
TGME49_220880	1.93	2.15	1.87	hypothetical protein
TGME49_225580	-9.55	-9.25	-9.25	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9, putative
TGME49_209060	-3.78	-3.86	-3.82	thrombospondin type 1 domain-containing protein
TGME49_265790	1.15	1.22	#N/A	hypothetical protein
TGME49_215590	-1.91	-1.78	-2.03	flavoprotein subunit of succinate dehydrogenase
TGME49_247960	2.06	2.01	1.46	hypothetical protein
TGME49_214140	1.26	1.33	1.35	hypothetical protein
TGME49_218560	-1.88	-1.73	-2.00	acetyl-coA carboxylase ACC2
TGME49_214230	1.64	1.80	1.24	Dopey, N-terminal domain-containing protein
TGME49_254370	-1.66	-1.59	-1.54	guanylyl cyclase
TGME49_260180	-1.99	-2.09	-2.13	hypothetical protein
TGME49_203830	-3.79	-3.78	-2.97	FHA domain-containing protein
TGME49_265500	-9.53	-9.38	-9.34	chloride transporter, chloride channel (ClC) family protein
TGME49_219730	1.55	1.51	1.33	hypothetical protein
TGME49_272010	-4.60	-3.93	-4.20	Gar1 protein RNA binding region protein
TGME49_254220	2.33	2.34	2.22	hypothetical protein
TGME49_237890	-4.58	-4.49	-3.76	calcium-dependent protein kinase CDPK4
TGME49_218362	-2.67	-2.55	-2.30	zinc finger protein ZFP1
TGME49_209440	-2.15	-2.34	-1.70	hypothetical protein
TGME49_232710	-1.08	#N/A	-1.01	ribosomal protein RPS3A
TGME49_222860	-1.58	-1.30	-1.33	eukaryotic translation initiation factor, putative
TGME49_274190	-4.63	-4.60	-4.96	eukaryotic initiation factor 2B epsilon subunit, putative
TGME49_248260	2.20	2.78	1.66	hypothetical protein
TGME49_254030	2.15	2.17	1.86	zinc finger CDGSH-type domain-containing protein
TGME49_295080	-9.53	-9.17	-8.87	hypothetical protein
TGME49_267620	-3.12	-2.52	-2.90	multi-pass transmembrane protein
TGME49_246570	2.72	2.11	1.56	hypothetical protein
TGME49_231150	2.64	3.03	2.83	hypothetical protein
TGME49_211250	-3.07	-2.84	-3.09	hypothetical protein
TGME49_231950	1.86	1.71	#N/A	hypothetical protein
TGME49_289300	-2.17	-1.85	-2.10	methionyl-tRNA synthetase
TGME49_205360	-2.51	-2.34	-2.57	hypothetical protein
TGME49_251170	2.93	2.39	2.43	KRUF family protein

TGME49_209120	1.31	1.35	#N/A	hypothetical protein
TGME49_309880	-1.33	-1.14	-1.04	hypothetical protein
TGME49_265460	1.09	1.37	1.18	hypothetical protein
TGME49_263505	-3.14	-3.18	-3.14	hypothetical protein
TGME49_294060	-1.05	-1.03	#N/A	hypothetical protein
TGME49_249870	-1.27	#N/A	#N/A	hypothetical protein
TGME49_271240	-2.48	-2.26	-1.91	hypothetical protein
TGME49_271990	1.28	#N/A	1.10	hypothetical protein
TGME49_242810	-3.14	-3.25	-3.27	hypothetical protein
TGME49_280450	-7.69	-8.54	-7.80	hypothetical protein
TGME49_288860	-2.73	-5.22	-2.93	RuvB family 2 protein
TGME49_214990	-1.75	-1.36	#N/A	hypothetical protein
TGME49_221390	-1.75	-1.78	-1.59	hypothetical protein
TGME49_305800	-1.75	-1.54	-1.83	6-pyruvoyl tetrahydrobiopterin synthase
TGME49_294730	-1.50	-1.46	-1.19	hypothetical protein
TGME49_263480	-1.46	#N/A	#N/A	sodium/hydrogen exchanger 3 protein
TGME49_201800	-1.16	-1.08	-1.91	hypothetical protein
TGME49_269770	-2.48	-2.73	-2.69	WD domain, G-beta repeat-containing protein
TGME49_213040	-1.54	-1.55	-1.45	hypothetical protein
TGME49_308090	1.09	#N/A	1.26	rhoptry protein ROP5
TGME49_235880	1.02	1.06	#N/A	brain protein 44 family protein
TGME49_258970	1.01	#N/A	#N/A	hypothetical protein
TGME49_286270	-1.54	-2.25	-1.67	hypothetical protein
TGME49_263190	-3.12	-2.61	-2.46	adenylosuccinate lyase, putative
TGME49_227300	1.82	#N/A	1.91	hypothetical protein
TGME49_304750	-2.13	-2.09	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_232630	-1.10	#N/A	#N/A	hypothetical protein
TGME49_301170	-7.68	-10.53	-7.53	SAG-related sequence SRS19D
TGME49_220440	-1.93	-2.04	-2.07	cyclin-dependent kinase regulatory subunit protein
TGME49_265650	-3.11	-3.43	-3.16	protein phosphatase 2C domain-containing protein
TGME49_234420	-1.37	#N/A	#N/A	ATPase, AAA family protein
TGME49_214400	-2.45	-2.07	-1.96	hypothetical protein
TGME49_272730	1.81	#N/A	3.75	hypothetical protein
TGME49_245710	-1.15	#N/A	-1.51	phosphatidylinositol-4-phosphate 5-kinase, putative

FIGURE 4K

TGME49_276970	-3.33	-3.38	-3.19	hypothetical protein
TGME49_269660	-2.64	-2.22	-2.16	TFIIH basal transcription factor complex helicase XPB subunit
TGME49_252390	1.43	#N/A	1.12	hypothetical protein
TGME49_266750	-1.78	-1.29	-1.53	transporter/permease protein, putative
TGME49_221675	1.34	1.45	1.46	hypothetical protein
TGME49_266990	-1.79	-1.44	-1.94	beta-COP
TGME49_312110	-2.50	-2.43	-2.32	apicoplast-associated thioredoxin family protein Atrx1
TGME49_268176	-2.82	-2.90	-3.25	hypothetical protein
TGME49_237170	-3.09	#N/A	-1.72	hypothetical protein
TGME49_238100	-2.33	-2.04	-2.61	transmembrane protein
TGME49_254730	1.89	2.31	2.50	POPLD (NUC188) domain-containing protein
TGME49_235020	-1.87	-1.55	-1.75	COPI protein, putative
TGME49_262150	-9.48	-9.22	-9.42	kelch repeat and K+ channel tetramerisation domain containing protein
TGME49_295990	1.50	1.76	1.59	ubiquitin conjugating enzyme E2, putative
TGME49_249530	-1.80	-1.59	-1.77	exportin 1, putative
TGME49_319880	-4.52	-4.75	-4.00	MORN repeat-containing protein
TGME49_283540	1.64	2.10	1.14	hypothetical protein
TGME49_229420	-9.48	-9.23	-9.54	cytochrome c, putative
TGME49_310460	-2.85	-2.51	-3.13	Rab6
TGME49_204520	2.74	2.76	3.39	hypothetical protein
TGME49_222710	-2.82	-2.47	-2.64	IMP-specific 5'-nucleotidase 1, putative
TGME49_213660	-1.51	-1.12	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_202470	-9.48	-9.34	-8.80	rRNA metabolism protein, SBDS family protein
TGME49_290980	-2.82	-2.49	-2.32	glycine C-acetyltransferase, putative
TGME49_263550	1.66	1.82	1.76	39S ribosomal protein L47, mitochondrial precursor, putative
TGME49_219080	-9.48	-9.43	-9.29	edge expressed protein, putative
TGME49_293740	1.80	1.93	1.56	hypothetical protein
TGME49_263490	2.11	2.29	2.10	ubiquitin conjugating enzyme E2, putative
TGME49_219810	1.87	1.50	1.25	hypothetical protein
TGME49_205040	-1.79	-1.55	-1.73	PGAP1 family protein
TGME49_270770	-4.56	-4.45	-4.53	PWI domain-containing protein

TGME49_208722	-3.11	-3.32	-3.48	hypothetical protein
TGME49_217760	1.21	1.31	#N/A	GTP-binding protein
TGME49_231930	-3.15	-2.67	-2.46	hypothetical protein
TGME49_214530	-1.60	-2.02	#N/A	DnaJ domain-containing protein
TGME49_225110	1.03	1.07	#N/A	AP2 domain transcription factor AP2X-2
TGME49_216580	-1.64	-1.43	-1.57	hypothetical protein
TGME49_248370	1.14	1.74	1.12	prefoldin subunit 6, putative
TGME49_259600	-1.75	-1.56	#N/A	hypothetical protein
TGME49_254610	1.77	1.73	1.59	Tim10/DDP family zinc finger superfamily protein
TGME49_223480	-7.62	-8.02	-10.14	sushi domain (scr repeat) domain-containing protein
TGME49_319720	-3.13	-3.43	-2.96	hypothetical protein
TGME49_258930	-2.46	#N/A	#N/A	peptidylprolyl isomerase
TGME49_316520	-1.37	-1.13	-1.32	1,4-alpha-glucan-branching enzyme
TGME49_209170	-1.18	#N/A	-1.29	hypothetical protein
TGME49_329800	-1.37	-1.74	-2.18	hypothetical protein
TGME49_270370	-2.18	-2.01	-2.15	clathrin assembly protein AP19, putative
TGME49_218230	-1.72	#N/A	-1.33	histone lysine methyltransferase, SET, putative
TGME49_220330	-3.14	-4.05	-2.44	hypothetical protein
TGME49_212930	1.81	2.47	1.87	NifU family domain-containing protein
TGME49_291690	-3.07	-3.21	-3.09	hypothetical protein
TGME49_200430	-7.63	-8.32	-8.30	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_208070	-1.14	#N/A	#N/A	inositol polyphosphate kinase
TGME49_301310	1.75	#N/A	#N/A	hypothetical protein
TGME49_266800	-1.61	-1.65	-1.94	integral membrane protein, putative
TGME49_224670	-1.87	-2.14	-1.89	DnaJ domain-containing protein
TGME49_245650	1.82	2.51	2.08	hypothetical protein
TGME49_294190	-3.07	-3.66	-2.87	enoyl-CoA hydratase/isomerase family protein
TGME49_225920	-2.09	-2.52	-2.30	hypothetical protein
TGME49_232210	-7.62	-8.23	-8.74	hypothetical protein
TGME49_247670	-2.15	#N/A	-2.02	ribulose-phosphate 3 epimerase family protein
TGME49_263730	-1.72	-2.70	-1.92	FAD-dependent glycerol-3-phosphate dehydrogenase

FIGURE 4L

TGME49_213067	1.34	1.18	#N/A	hypothetical protein
TGME49_237015	1.45	1.75	1.50	hypothetical protein
TGME49_280730	-9.46	-9.23	-8.90	cytosolic fe-s cluster assembling factor nbp35, putative
TGME49_227420	-9.48	-9.15	-9.24	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
TGME49_310220	-4.57	-4.80	-4.55	hypothetical protein
TGME49_318400	-2.00	-1.56	-1.30	hypothetical protein
TGME49_257520	1.53	1.64	1.11	synaptobrevin protein
TGME49_226220	-2.77	-2.58	-2.89	alveolin domain containing intermediate filament IMC9
TGME49_244910	-3.71	-4.10	-4.11	MIZ/SP-RING zinc finger domain-containing protein
TGME49_309380	-3.25	-3.07	-3.21	Nuf2
TGME49_274110	-9.43	-8.93	-8.80	glycoprotease family protein
TGME49_225250	2.04	1.74	1.93	LSU ribosomal protein L14P, putative
TGME49_223010	-3.26	-2.84	-3.05	hypothetical protein
TGME49_278720	-9.47	-9.16	-8.84	hypothetical protein
TGME49_320130	1.97	1.91	2.02	hypothetical protein
TGME49_267690	-4.49	-4.44	-3.85	hypothetical protein
TGME49_222930	-2.77	-2.69	-2.32	hypothetical protein
TGME49_297800	-3.02	-2.72	-2.56	RecF/RecN/SMC N terminal domain-containing protein
TGME49_203730	-9.41	-9.21	-9.23	hypothetical protein
TGME49_226910	-4.49	-4.89	-4.34	Amylo-alpha-1,6-glucosidase
TGME49_266410	1.84	1.99	1.53	hypothetical protein
TGME49_292130	-1.14	-1.30	-1.31	ribosomal protein RPL13A
TGME49_289730	-2.34	-2.12	-2.27	Pep3/Vps18/deep orange family protein
TGME49_201870	-2.79	-2.12	-2.21	tetratricopeptide repeat-containing protein
TGME49_216020	-9.41	-9.29	-9.61	peptidase family c78 protein
TGME49_313445	2.13	1.67	2.08	hypothetical protein
TGME49_225990	-3.24	-2.75	-2.62	acyl transferase domain-containing protein
TGME49_240860	-3.69	-3.68	-3.67	acyltransferase domain-containing protein
TGME49_285140	-9.42	-10.00	-9.49	hypothetical protein
TGME49_319580	-9.39	-9.39	-9.35	hypothetical protein
TGME49_247580	-9.41	-9.25	-9.15	glutaredoxin domain-containing protein
TGME49_253470	1.68	1.71	1.58	alveolin domain containing intermediate filament IMC13
TGME49_246100	-2.64	-2.24	-2.29	phosducin, putative

TGME49_232270	-7.62	-9.16	-9.76	histidine acid phosphatase superfamily protein
TGME49_315670	-1.18	#N/A	-1.26	HEAT repeat-containing protein
TGME49_262000	-3.11	-2.84	#N/A	AP2 domain transcription factor AP2VIIb-2
TGME49_273550	-3.06	-3.34	-3.42	hypothetical protein
TGME49_249600	-7.61	-7.86	-8.35	hypothetical protein
TGME49_232530	-2.09	-2.03	-1.66	hypothetical protein
TGME49_309780	-1.87	-1.66	#N/A	hypothetical protein
TGME49_286010	1.27	1.40	#N/A	hypothetical protein
TGME49_218830	1.45	#N/A	1.57	hypothetical protein
TGME49_281450	-2.45	-2.60	-2.46	cell-cycle-associated protein kinase, putative
TGME49_222160	-3.06	-3.52	#N/A	aldehyde dehydrogenase
TGME49_233540	-3.16	-3.25	-3.17	transporter, major facilitator family protein
TGME49_252400	2.27	2.06	2.94	HIT zinc finger protein
TGME49_221170	-1.08	#N/A	-1.40	CAAX metallo endopeptidase
TGME49_238940	1.86	2.31	1.18	GDP mannose 4,6-dehydratase, putative
TGME49_224490	-3.09	-3.25	-2.80	polyprenyl synthetase superfamily protein
TGME49_287980	-1.59	-1.59	-1.58	FHA domain-containing protein
TGME49_251920	1.40	1.67	2.09	hypothetical protein
TGME49_211650	-1.30	#N/A	#N/A	hypothetical protein
TGME49_251620	1.03	#N/A	#N/A	flap structure-specific endonuclease 1, putative
TGME49_221922	-3.06	-3.47	-3.32	NifU family domain-containing protein
TGME49_272550	-1.17	-1.18	#N/A	hypothetical protein
TGME49_271440	-2.41	-2.42	-2.60	NPL4 family protein
TGME49_272710	1.08	#N/A	#N/A	AP2 domain transcription factor AP2VIII-4
TGME49_297330	1.28	1.06	1.08	hypothetical protein
TGME49_288460	-1.07	-1.02	#N/A	hypothetical protein
TGME49_293310	1.04	1.21	#N/A	ribosomal protein L20, putative
TGME49_258650	-2.41	-2.21	-1.90	protoheme ferro-lyase, putative
TGME49_252270	1.74	#N/A	1.90	L1P family of ribosomal protein
TGME49_314030	1.88	1.86	1.50	hypothetical protein
TGME49_206300	-2.41	-2.18	-1.99	hypothetical protein
TGME49_315360	-1.30	-1.25	-1.35	hypothetical protein
TGME49_258990	-2.40	-2.65	-2.61	bromodomain-containing protein

FIGURE 4M

TGME49_270930	-3.02	-3.19	-3.08	hypothetical protein
TGME49_241240	1.03	#N/A	#N/A	hypothetical protein
TGME49_294940	1.69	1.57	1.46	hypothetical protein
TGME49_226500	-4.54	-4.91	-4.82	hypothetical protein
TGME49_226430	-1.44	-1.36	-1.31	reticulon protein
TGME49_299250	2.72	2.76	2.79	hypothetical protein
TGME49_288820	1.59	1.34	1.67	hypothetical protein
TGME49_247760	-2.95	-2.70	-3.35	AMP-binding enzyme domain-containing protein
TGME49_311720	-1.01	#N/A	-1.30	chaperonin protein BiP
TGME49_306660	1.31	1.30	1.73	RNA pseudouridine synthase superfamily protein
TGME49_254000	1.44	1.26	1.37	hypothetical protein
TGME49_233140	-2.54	-2.06	-2.48	deoxyuridine 5'-triphosphate nucleotidohydrolase, putative
TGME49_280400	-9.41	-12.29	-9.61	hypothetical protein
TGME49_290160	-1.66	-1.61	-1.68	sortilin, putative
TGME49_271470	-4.41	-4.36	-3.99	hypothetical protein
TGME49_214960	1.60	1.61	1.13	AP2 domain transcription factor AP2X-8
TGME49_202920	-9.36	-9.54	-9.53	p-aminobenzoic acid synthase
TGME49_309590	1.01	#N/A	#N/A	rhoptry protein ROP1
TGME49_270270	-3.68	-3.76	-4.08	hypothetical protein
TGME49_271810	-1.62	-1.16	-1.39	lanp, putative
TGME49_286260	-9.33	-9.40	-8.89	tetratricopeptide repeat-containing protein
TGME49_216770	-4.44	-4.35	-3.45	hypothetical protein
TGME49_205750	-2.90	-2.41	-2.43	histone deacetylase complex subunit Sin3
TGME49_201400	-4.43	-4.23	-4.47	Sin3-associated polypeptide SAP18
TGME49_273905	-4.39	-3.86	-4.37	hypothetical protein
TGME49_249360	-2.40	-2.22	-2.24	RED family protein
TGME49_310450	-2.42	-2.75	-2.34	myosin heavy chain, putative
TGME49_248860	2.36	1.77	1.86	hypothetical protein
TGME49_222400	1.21	1.64	1.08	hypothetical protein
TGME49_313880	-9.36	-8.94	-9.55	nuclear protein-like family protein
TGME49_247220	1.32	1.11	#N/A	nudix -type motif 9 isoform a family protein
TGME49_246930	-2.21	-2.30	-2.33	calmodulin CAM1
TGME49_259710	-2.95	-3.08	-3.61	protein kinase
TGME49_313380	-1.15	-1.15	-1.25	hypothetical protein

TGME49_249380	1.18	1.58	1.41	DHHC zinc finger domain-containing protein
TGME49_257990	-1.24	-1.50	-1.53	heat shock protein 101, putative
TGME49_269075	-7.64	-8.96	-8.49	hypothetical protein
TGME49_202730	-2.08	-1.96	-1.71	hypothetical protein
TGME49_246978	-3.01	-3.26	-2.93	hypothetical protein
TGME49_312220	-3.02	-3.23	-3.50	mitochondrial inner membrane translocase subunit TIM17, putative
TGME49_250090	1.08	#N/A	1.00	hypothetical protein
TGME49_221460	-1.18	#N/A	-1.54	phosphoglycerate mutase family protein
TGME49_243390	-2.40	-2.76	-2.56	hypothetical protein
TGME49_272720	-1.85	-1.84	#N/A	methyltransferase domain-containing protein
TGME49_288010	1.77	3.19	2.59	hypothetical protein
TGME49_246040	-1.56	-1.69	-1.87	MIF4G domain-containing protein
TGME49_240710	-1.49	-1.70	-1.71	RNA recognition motif-containing protein
TGME49_274000	-2.06	-2.41	-2.90	hypothetical protein
TGME49_240800	-1.41	-2.11	-2.22	MORN repeat-containing protein
TGME49_264820	1.31	#N/A	1.45	RbAp48
TGME49_243350	1.47	#N/A	#N/A	gamma-glutamyl hydrolase
TGME49_276130	1.13	#N/A	#N/A	cathepsin CPC2
TGME49_246690	-2.05	-1.83	-1.66	alpha amylase, catalytic domain-containing protein
TGME49_308940	-7.53	-8.29	-8.39	hypothetical protein
TGME49_209140	-1.16	-1.15	-1.18	anti-silencing protein, ASF1 family protein
TGME49_313300	1.14	1.35	1.28	YL1 nuclear protein C-terminal domain-containing protein
TGME49_263150	-7.53	-8.28	-8.57	tetratricopeptide repeat-containing protein
TGME49_227640	-1.39	#N/A	#N/A	hypothetical protein
TGME49_231940	-1.43	-1.13	-1.63	ThiF family protein
TGME49_300010	-7.54	-8.20	-8.38	hypothetical protein
TGME49_249850	-1.57	-1.52	-1.83	GAP40 protein
TGME49_266930	1.35	1.45	1.09	general transcription factor IIH polypeptide 3 GTF2H3
TGME49_253820	1.02	1.03	#N/A	hypothetical protein
TGME49_229720	-2.36	-3.02	#N/A	hypothetical protein
TGME49_270330	1.28	1.56	1.39	cell-cycle-associated protein kinase, putative
TGME49_312360	-3.00	-2.81	-2.92	hypothetical protein
TGME49_311260	-1.07	#N/A	#N/A	myosin light chain MLC1, putative
TGME49_277090	2.01	2.17	2.09	carrier superfamily protein

FIGURE 4N

TGME49_214200	-9.38	-9.55	-9.04	WD domain, G-beta repeat-containing protein
TGME49_243930	1.38	1.31	#N/A	hypothetical protein
TGME49_215420	-9.31	-8.88	-9.16	SNARE protein
TGME49_311680	-1.89	-1.73	-1.45	FUN14 family protein
TGME49_259200	-4.39	-4.23	-3.90	Na+/H+ exchanger NHE1
TGME49_268580	-4.42	-3.87	-4.26	hypothetical protein
TGME49_269450	2.62	1.94	2.15	hypothetical protein
TGME49_266450	1.76	1.31	1.34	lysine decarboxylase family protein
TGME49_288360	-1.46	-1.31	-3.81	tryptophanyl-tRNA synthetase (TrpRS2)
TGME49_261480	1.77	1.95	1.76	phosphatidyl serine synthase
TGME49_210245	-9.40	-9.73	#N/A	hypothetical protein
TGME49_288400	-9.31	-9.50	-9.50	LETM1 family protein
TGME49_226810	-3.20	-3.51	-3.47	histone lysine methyltransferase SET1
TGME49_239800	-2.88	-3.25	-3.12	hypothetical protein
TGME49_270550	-9.37	-9.05	-9.15	gamma-glutamyl phosphate reductase, putative
TGME49_249250	1.28	1.13	1.14	ribosomal protein RPL35A
TGME49_207880	-9.44	-9.56	-10.92	hypothetical protein
TGME49_269920	-1.46	-1.18	-1.47	phosphatidylserine decarboxylase
TGME49_278815	-3.62	-3.98	-3.71	hypothetical protein
TGME49_207690	-4.37	-4.30	-4.73	programmed cell death 5 protein
TGME49_203720	2.55	3.14	1.89	vitamin k epoxide reductase family protein
TGME49_237500	1.34	1.01	#N/A	protein phosphatase 2C domain-containing protein
TGME49_320090	-3.11	-2.61	-2.20	hypothetical protein
TGME49_286630	-1.68	-1.41	-1.63	redoxin domain-containing protein
TGME49_257380	1.16	1.09	#N/A	hypothetical protein
TGME49_225050	-1.78	-1.53	-1.56	adenosylhomocysteinase, putative
TGME49_305980	-2.30	-2.23	-2.14	pyruvate dehydrogenase complex subunit PDH-E3I
TGME49_289600	1.41	#N/A	#N/A	heat shock protein HSP29
TGME49_223760	-9.25	-9.33	-9.63	hypothetical protein
TGME49_289050	1.24	1.02	#N/A	FIKK kinase, putative
TGME49_213060	1.66	1.34	1.91	WD domain, G-beta repeat-containing protein
TGME49_269690	1.26	1.49	#N/A	hypothetical protein

TGME49_277010	-7.53	-8.00	-8.62	Fe-S metabolism associated domain-containing protein
TGME49_260840	-3.00	-3.08	-2.63	hypothetical protein
TGME49_236580	-1.27	#N/A	-1.15	Prp31-15.5k-U4 Snrna Complex family protein
TGME49_256920	1.51	1.22	#N/A	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_241170	-1.12	-1.21	#N/A	hypothetical protein
TGME49_248200	1.30	1.03	#N/A	ribosomal RNA (adenine(1779)-N(6)/adenine(1780)-N(6))-dimethyltransferase, putative
TGME49_226420	-1.21	-1.59	-1.98	peptidase family M3 protein
TGME49_221870	1.26	1.23	#N/A	hypothetical protein
TGME49_202480	-2.96	-3.07	-3.28	hypothetical protein
TGME49_228380	3.13	2.35	2.83	hypothetical protein
TGME49_305190	1.02	#N/A	#N/A	CorA family Mg2+ transporter protein
TGME49_213870	-1.14	-1.13	-1.72	UBA/TS-N domain-containing protein
TGME49_311750	1.96	#N/A	1.92	mago binding protein
TGME49_220160	-2.96	-3.23	-2.94	WD domain-containing protein
TGME49_235610	-2.96	-3.11	-3.19	ATPase, AAA family protein
TGME49_280522	-1.16	-1.27	-1.47	hypothetical protein
TGME49_244860	1.40	1.46	1.42	hypothetical protein
TGME49_315640	1.32	1.67	1.35	lipoyl(octanoyl) transferase
TGME49_294860	-1.54	-1.71	-1.68	hypothetical protein
TGME49_215480	-1.81	-1.74	-1.40	Adenosine/AMP deaminase domain-containing protein
TGME49_285880	1.58	1.31	#N/A	hypothetical protein
TGME49_260150	1.60	#N/A	1.15	tetratricopeptide repeat-containing protein
TGME49_314530	-3.00	-3.48	-2.77	RPAP1 family, C-terminal protein
TGME49_277820	-2.36	-2.43	-2.05	hypothetical protein
TGME49_310660	-2.96	-3.08	-3.40	Dullard family phosphatase domain-containing protein
TGME49_250060	1.45	1.17	#N/A	DNA-directed RNA polymerase I RPA12
TGME49_306020	-1.44	-1.68	-1.31	hypothetical protein
TGME49_319710	-1.38	-1.36	-1.07	kinesin motor domain-containing protein
TGME49_205240	-1.13	-1.20	#N/A	cleft lip and palate transmembrane protein 1 (clptm1) protein
TGME49_203710	-1.14	-1.16	#N/A	AP2 domain transcription factor AP2VIIa-4
TGME49_285700	-2.99	-2.83	#N/A	ubiquitin fusion degradation protein UFD1AP
TGME49_306510	1.91	1.82	3.54	hypothetical protein

FIGURE 4o

TGME49_228750	-3.59	-3.68	-3.53	TGME49_228750 CAM kinase, RAD family
TGME49_315250	-4.35	-3.92	-4.09	GAMM1 protein, putative
TGME49_320490	1.85	1.62	2.04	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D family protein
TGME49_312300	-1.87	-1.75	-1.71	Sec7 domain-containing protein
TGME49_260670	-9.26	-9.06	-9.55	centrin, putative
TGME49_273815	-9.34	-8.57	-8.62	hypothetical protein
TGME49_299200	1.77	1.45	1.21	Bet3 transport protein, putative
TGME49_236250	2.11	1.47	2.02	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_204310	-1.40	-1.36	-1.56	hypothetical protein
TGME49_292160	1.77	1.89	1.97	hypothetical protein
TGME49_234980	1.96	1.83	1.94	hypothetical protein
TGME49_215390	2.45	2.61	3.43	TIM10 family protein, putative
TGME49_291940	-4.30	-4.60	-4.65	hypothetical protein
TGME49_234390	-9.29	-8.59	-8.45	hypothetical protein
TGME49_289580	-9.23	-9.72	-9.34	strictosidine synthase subfamily protein
TGME49_205510	-1.74	-1.43	-1.74	nucleolar protein 5, putative
TGME49_224540	-9.38	-9.79	-9.10	hypothetical protein
TGME49_284190	-3.70	-4.12	-3.49	pyruvate carboxylase
TGME49_227060	-9.25	-9.07	-9.03	hypothetical protein
TGME49_221720	-4.62	-4.67	-4.40	hypothetical protein
TGME49_238200	1.96	#N/A	#N/A	alpha/beta hydrolase fold domain-containing protein
TGME49_304460	-1.70	-1.44	-1.05	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_205540	-9.24	-9.08	-8.65	DEAD/DEAH box helicase domain-containing protein
TGME49_269650	-1.97	-1.61	-1.46	FFD and TFG box motifs protein
TGME49_320588	-9.23	-10.06	-9.75	glycosyl hydrolases family 35 protein
TGME49_320640	-9.26	-9.58	-9.58	peptidylprolyl isomerase domain-containing protein
TGME49_265010	-9.20	-8.94	-8.88	glutamate 5-kinase domain-containing protein
TGME49_314540	-9.20	-8.99	-9.02	hypothetical protein
TGME49_204420	3.59	3.11	2.28	oocyst wall protein OWP1
TGME49_263630	1.20	1.32	1.13	hypothetical protein
TGME49_288945	-2.45	-1.50	-1.45	hypothetical protein

TGME49_204100	-1.27	#N/A	-1.49	eIF2 kinase IF2K-C
TGME49_271170	-2.95	-3.53	-3.28	dolichol kinase
TGME49_244140	-3.04	-3.04	#N/A	hypothetical protein
TGME49_319930	-1.25	-1.28	#N/A	hypothetical protein
TGME49_277490	1.04	1.26	#N/A	hypothetical protein
TGME49_219750	1.10	#N/A	#N/A	cytochrome c, putative
TGME49_315190	-1.06	-1.13	#N/A	CAM kinase, SNF1 family
TGME49_226060	1.15	1.40	1.29	transmembrane amino acid transporter protein
TGME49_311390	1.35	2.33	2.33	tRNA (guanine(9)-N(1))-methyltransferase
TGME49_235905	-2.32	-2.10	-2.00	ribonuclease z, putative
TGME49_319320	-1.38	-1.77	-1.36	hypothetical protein
TGME49_270670	1.17	2.08	3.19	hypothetical protein
TGME49_240430	1.18	1.11	1.39	glyoxalase family protein
TGME49_315920	-2.01	#N/A	-1.75	DNA-directed RNA polymerase II RPB11A
TGME49_310210	1.03	#N/A	1.01	hypothetical protein
TGME49_203050	1.92	1.88	1.66	AP2 domain transcription factor AP2VIIa-6
TGME49_237195	1.68	#N/A	#N/A	hypothetical protein
TGME49_320690	-1.64	-1.29	-1.59	gamma-soluble NSF attachment protein, putative
TGME49_309940	-1.54	-1.30	-1.26	phospholipase D active site domain-containing protein
TGME49_246178	-1.78	-2.02	-1.91	hypothetical protein
TGME49_212100	-7.44	-9.12	-7.23	ThiF family protein
TGME49_203480	-2.97	-3.25	-3.09	hypothetical protein
TGME49_295460	1.07	#N/A	#N/A	Got1 family protein
TGME49_291350	-2.95	-3.01	-3.06	hypothetical protein
TGME49_240090	1.51	1.67	#N/A	rhoptry kinase family protein ROP34, putative
TGME49_257960	-2.32	-2.82	-3.03	GDP-D-mannose pyrophosphorylase
TGME49_315910	1.03	1.65	1.00	hypothetical protein
TGME49_221518	-1.84	#N/A	#N/A	hypothetical protein
TGME49_242320	-1.23	-1.15	-1.31	B-box zinc finger domain-containing protein
TGME49_295980	-1.65	-1.62	-1.93	hypothetical protein
TGME49_215940	-1.29	-1.15	-1.37	Acetyl-coenzyme A transporter, putative

FIGURE 4P

TGME49_240570	-2.67	-2.74	-2.61	hypothetical protein
TGME49_249590	-1.74	-1.64	-1.85	proteasome subunit alpha type 5-2, putative
TGME49_216430	-1.75	-1.88	-1.58	TBC domain-containing protein
TGME49_282000	1.79	1.99	1.43	hypothetical protein
TGME49_242055	-9.20	-9.26	-8.91	DEAD/DEAH box helicase domain-containing protein
TGME49_318210	-9.22	-8.87	-8.65	hypothetical protein
TGME49_246970	-9.20	-8.84	-8.71	3'-5' exonuclease domain-containing protein
TGME49_280770	-1.52	-1.02	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_319910	1.82	1.73	1.90	WD domain, G-beta repeat-containing protein
TGME49_222960	-9.20	-9.40	-9.37	SCY kinase-related protein (incomplete catalytic triad)
TGME49_239740	1.01	#N/A	#N/A	dense granule protein GRA14
TGME49_310930	-3.09	-2.79	-3.22	hypothetical protein
TGME49_278630	-9.17	-9.11	-8.95	tetratricopeptide repeat-containing protein
TGME49_220950	1.20	1.59	1.57	hypothetical protein
TGME49_225745	-9.20	-9.66	-9.21	hypothetical protein
TGME49_207100	-9.17	-9.35	-8.99	hypothetical protein
TGME49_271460	2.14	1.54	2.34	protein c14orf29, putative
TGME49_239752	-1.50	-1.15	-1.35	hypothetical protein
TGME49_297870	-2.35	-2.13	-2.31	hypothetical protein
TGME49_226590	1.50	1.73	1.17	cytochrome C oxidase subunit IIa, putative
TGME49_236890	1.44	1.05	1.14	hypothetical protein
TGME49_241890	-9.17	-8.91	-9.04	hypothetical protein
TGME49_228770	-4.30	-3.81	-4.13	hypothetical protein
TGME49_222210	-9.17	-8.50	-8.80	SPFH domain / Band 7 family protein
TGME49_271060	-4.26	-4.00	-3.68	Sec1 family protein
TGME49_253180	2.52	1.98	1.95	hypothetical protein
TGME49_203740	-2.48	-1.93	-2.36	hypothetical protein
TGME49_205280	1.30	1.20	#N/A	hypothetical protein
TGME49_313400	-2.19	-1.86	-2.09	DnaJ domain-containing protein
TGME49_201680	-1.13	#N/A	-1.14	eukaryotic initiation factor-3 subunit 10, putative
TGME49_311070	-3.53	-3.69	-3.50	hypothetical protein

TGME49_249270	-1.19	#N/A	-1.22	protein disulfide isomerase-related protein (provisional), putative
TGME49_266280	-1.08	#N/A	#N/A	HEAT repeat-containing protein
TGME49_252065	1.65	2.13	1.94	KRUF family protein
TGME49_271010	1.80	#N/A	3.30	hypothetical protein
TGME49_226400	-1.41	-1.48	-1.44	lipoic acid synthase LIPA
TGME49_314890	-2.90	-3.63	-3.65	ThiF family protein
TGME49_222120	-2.90	-3.23	-3.12	hypothetical protein
TGME49_294750	-2.90	-2.84	-2.55	hypothetical protein
TGME49_251510	1.45	1.46	1.29	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_313690	-1.22	-1.22	-1.69	Sel1 repeat-containing protein
TGME49_267700	-2.92	-3.35	-2.87	hypothetical protein
TGME49_248340	-1.04	#N/A	#N/A	GTP-binding nuclear protein ran/tc4
TGME49_227260	-2.31	-2.26	-2.49	RIO1 family protein
TGME49_255300	-1.33	-1.61	-1.56	hypothetical protein
TGME49_259080	1.89	1.81	#N/A	hypothetical protein
TGME49_229030	-1.17	-1.13	-1.68	hypothetical protein
TGME49_233120	-1.37	-1.16	#N/A	AP2 domain transcription factor AP2VIII-2
TGME49_298980	-1.21	#N/A	#N/A	RNA pseudouridine synthase superfamily protein
TGME49_275770	-1.32	-1.31	-1.15	hypothetical protein
TGME49_267400	-1.04	-1.40	-1.28	ribosomal protein RPL32
TGME49_286130	1.59	#N/A	1.11	hypothetical protein
TGME49_316480	1.69	#N/A	#N/A	XRN 5'-3' exonuclease N-terminus protein
TGME49_208390	1.29	1.44	1.32	hypothetical protein
TGME49_259720	1.14	#N/A	#N/A	hypothetical protein
TGME49_225420	-2.28	-2.02	-2.04	histidine triad domain-containing protein
TGME49_281420	-2.28	-2.28	#N/A	histone deacetylase HDAC1
TGME49_270530	-2.02	-2.36	-2.87	ubiquitin fusion degradation protein UFD1CY
TGME49_246630	-1.49	#N/A	-1.70	DNA-directed RNA polymerase I RPA43
TGME49_253960	1.52	1.92	1.17	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_274150	-2.90	-3.51	-3.79	hypothetical protein
TGME49_246010	2.82	#N/A	2.37	hypothetical protein

FIGURE 4Q

TGME49_205200	1.37	1.28	1.97	hypothetical protein
TGME49_250670	1.80	1.04	2.24	hypothetical protein
TGME49_212270	2.01	1.79	1.53	hypothetical protein
TGME49_219860	-1.38	#N/A	-1.53	replication licensing factor, putative
TGME49_248490	2.15	1.75	#N/A	hypothetical protein
TGME49_245730	-9.14	-9.31	-8.95	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_203560	-9.21	-9.37	-9.40	hypothetical protein
TGME49_282150	-9.14	-9.14	-9.37	hypothetical protein
TGME49_239020	-9.22	-10.28	-8.90	ABC transporter transmembrane region domain-containing protein
TGME49_306440	-9.14	-9.17	-9.84	hypothetical protein
TGME49_305860	-1.98	-2.23	-2.36	calcium-dependent protein kinase CDPK3
TGME49_216070	-9.14	-9.09	-9.10	hypothetical protein
TGME49_209730	-9.14	-9.22	-9.53	hypothetical protein
TGME49_259090	1.54	1.29	#N/A	ubiquitin-conjugating enzyme subfamily protein
TGME49_209280	-4.24	-4.39	-4.06	hypothetical protein
TGME49_248530	-9.14	-9.02	-9.31	FATC domain-containing protein
TGME49_258470	1.18	1.46	#N/A	hypothetical protein
TGME49_249650	-9.14	-9.09	-9.59	apolipoprotein A-I binding protein, putative
TGME49_278975	-2.28	-2.23	-2.23	ICE family protease (caspase) p20 domain-containing protein
TGME49_204360	2.57	#N/A	#N/A	subtilisin SUB4
TGME49_202572	-9.14	-8.93	-8.95	ribophorin i protein
TGME49_210230	-9.18	-9.59	-9.02	hypothetical protein
TGME49_262040	-2.58	-2.27	-2.75	SAC3/GANP family protein
TGME49_223855	2.71	2.76	2.84	RNA recognition motif-containing protein
TGME49_240520	-9.14	-9.00	-8.80	hypothetical protein
TGME49_221350	-4.21	-3.63	-3.51	Ctr copper transporter family protein
TGME49_278700	-3.46	-3.04	-2.60	hypothetical protein
TGME49_280390	-2.58	-2.94	-2.68	HEAT repeat-containing protein
TGME49_294270	-9.11	-9.02	-8.83	histone arginine methyltransferase PRMT4/CARM1
TGME49_249470	-9.11	-8.94	-9.34	rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_225800	-3.47	-3.24	-3.04	iron-sulfur assembly ATPase
TGME49_282220	1.49	1.53	1.93	AP2 domain transcription factor AP2VIIa-9

TGME49_297170	1.44	1.43	#N/A	50S ribosomal protein L17, putative
TGME49_290225	-2.90	-3.16	-3.01	hypothetical protein
TGME49_279390	-1.25	-1.07	-1.24	proliferation-associated protein 2G4, putative
TGME49_231040	-2.91	-2.69	-2.71	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_263470	-1.17	#N/A	#N/A	ubiquitin carboxyl-terminal hydrolase UCHL3
TGME49_242625	-1.29	-1.28	#N/A	ATPase family associated with various cellular activities (AAA) subfamily protein
TGME49_267040	-2.28	-2.37	-2.52	hypothetical protein
TGME49_254606	1.64	2.48	2.32	hypothetical protein
TGME49_270975	-1.68	#N/A	-1.36	hypothetical protein
TGME49_284598	-7.35	-9.64	#N/A	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_269705	1.40	2.18	2.25	hypothetical protein
TGME49_299030	1.22	1.06	1.19	RNA recognition motif 2 protein
TGME49_206415	-1.19	-1.34	-1.42	myosin K
TGME49_237840	-1.61	-1.42	#N/A	hypothetical protein
TGME49_307260	1.81	2.82	#N/A	Toxoplasma gondii family C protein
TGME49_226040	-1.13	-1.12	#N/A	EF hand domain-containing protein
TGME49_286190	-1.20	#N/A	#N/A	hypothetical protein
TGME49_222870	-1.34	-1.16	-1.41	hypothetical protein
TGME49_277540	-7.34	-8.33	-8.37	hypothetical protein
TGME49_254510	1.59	1.19	#N/A	ankyrin repeat-containing protein
TGME49_245770	2.70	#N/A	#N/A	hypothetical protein
TGME49_305820	-1.48	-1.53	#N/A	SGS domain-containing protein
TGME49_305620	-1.52	-1.42	-1.31	hypothetical protein
TGME49_278890	-1.97	-1.95	-1.74	hypothetical protein
TGME49_246050	-7.42	-7.93	-8.34	hypothetical protein
TGME49_260270	-1.44	-1.44	-1.34	HEAT repeat-containing protein
TGME49_213020	1.58	1.30	1.68	hypothetical protein
TGME49_220530	1.68	1.37	1.44	AP2 domain transcription factor AP2V-1
TGME49_209190	-1.16	#N/A	-1.05	ABC transporter transmembrane region domain-containing protein
TGME49_277850	-1.88	#N/A	-1.63	trypsin domain-containing protein
TGME49_294350	-1.06	#N/A	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_202520	1.16	1.23	1.22	hypothetical protein

FIGURE 4R

TGME49_264600	-2.40	-2.43	-2.67	hypothetical protein
TGME49_297400	1.36	1.14	#N/A	hypothetical protein
TGME49_224960	1.35	1.34	1.40	hypothetical protein
TGME49_251410	-2.32	-1.71	-1.96	tetratricopeptide repeat-containing protein
TGME49_254870	1.36	1.24	1.70	hypothetical protein
TGME49_200320	-2.28	-2.54	-3.25	hypoxanthine-xanthine-guanine phosphoribosyl transferase HXGPRT
TGME49_294550	-1.62	-1.96	-2.09	dynein heavy chain
TGME49_318880	2.77	2.22	2.26	hypothetical protein
TGME49_305240	-3.04	-3.22	-3.24	XPA binding protein 2 family protein
TGME49_223800	-4.23	-4.26	-3.73	hypothetical protein
TGME49_286790	-4.19	-4.13	-4.49	nuclear factor NF2
TGME49_316200	1.65	1.42	1.12	phosphoglycerate mutase family protein
TGME49_266730	-9.08	-9.20	-8.85	leucyl-tRNA synthetase (LeuRS2)
TGME49_257700	2.48	3.12	3.22	hypothetical protein
TGME49_234460	1.47	2.22	#N/A	hypothetical protein
TGME49_236670	1.93	2.50	3.04	hypothetical protein
TGME49_270140	-9.11	-8.77	-8.70	splicing factor DIM1, putative
TGME49_268760	-1.32	#N/A	-1.21	hypothetical protein
TGME49_306960	-2.52	-2.15	-2.56	phenylalanine--tRNA ligase, beta subunit protein
TGME49_272770	-4.19	-3.81	-3.67	hypothetical protein
TGME49_314920	2.44	2.19	2.18	hypothetical protein
TGME49_251500	-1.41	-1.11	-1.61	eukaryotic initiation factor-3, subunit 3, putative
TGME49_244500	-1.77	-2.01	-1.75	Tubulin-tyrosine ligase family protein
TGME49_295658	-3.40	-3.61	-3.34	zinc finger in N-recognin protein
TGME49_294990	-9.08	-9.90	-9.75	hypothetical protein
TGME49_249460	-9.08	-8.57	-8.46	WD domain, G-beta repeat-containing protein
TGME49_314700	1.38	#N/A	1.31	hypothetical protein
TGME49_236860	-4.25	-4.69	-3.69	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_291020	-2.13	-1.63	-2.06	myosin head (motor domain) domain-containing protein
TGME49_289700	-3.00	-2.49	-2.82	hypothetical protein
TGME49_200350	2.37	3.12	3.55	subtilisin SUB3
TGME49_257350	1.19	1.35	1.50	eukaryotic translation initiation factor, putative
TGME49_301380	-4.21	-4.18	-3.92	elongation factor Tu GTP binding domain-containing protein
TGME49_310140	-9.05	-8.97	-9.32	hypothetical protein

TGME49_277710	-1.12	-1.08	-1.23	hypothetical protein
TGME49_206700	-2.89	-2.96	-2.69	hypothetical protein
TGME49_238070	-2.84	-2.73	-3.39	glutaredoxin domain-containing protein
TGME49_242830	-1.39	-1.55	-1.77	XRN 5'-3' exonuclease N-terminus protein
TGME49_217780	1.28	#N/A	#N/A	Sec20 protein
TGME49_306195	2.13	2.36	2.44	hypothetical protein
TGME49_221410	-1.07	#N/A	-1.11	actin-like protein ALP4
TGME49_310330	-1.95	-2.05	-1.81	hypothetical protein
TGME49_244630	1.49	1.48	1.36	hypothetical protein
TGME49_215450	2.17	1.99	1.91	aquaporin 1
TGME49_261430	-1.58	-2.17	-1.36	hypothetical protein
TGME49_232090	-1.71	-1.63	-2.06	3-hydroxyacyl-CoA dehydrogenase, NAD binding domain-containing protein
TGME49_204080	-1.18	-1.55	-1.68	histidine acid phosphatase superfamily protein
TGME49_299060	-1.06	-1.08	-1.02	sodium/hydrogen exchanger NHE2
TGME49_312210	-2.23	-2.28	-2.95	hypothetical protein
TGME49_228070	1.21	#N/A	1.00	hypothetical protein
TGME49_229160	-2.87	-3.02	-2.82	DHHC zinc finger domain-containing protein
TGME49_318690	1.15	2.02	2.72	RNA recognition motif-containing protein
TGME49_301010	-1.14	-1.13	#N/A	serine/threonine protein phosphatase, putative
TGME49_263710	-1.18	-1.06	#N/A	acyl-CoA:cholesterol acyltransferase alpha ACAT1-alpha
TGME49_212735	-2.27	-2.65	-1.98	hypothetical protein
TGME49_221850	1.41	#N/A	#N/A	prohibitin family protein, putative
TGME49_307860	1.05	1.18	1.15	hypothetical protein
TGME49_227900	1.49	#N/A	1.54	AP2 domain transcription factor AP2X-1
TGME49_285930	-1.79	-1.89	-1.73	hypothetical protein
TGME49_268730	1.15	1.39	1.12	glutaredoxin-related protein
TGME49_229790	-1.71	-1.61	-1.96	hypothetical protein
TGME49_244010	-1.91	-2.04	-1.83	hypothetical protein
TGME49_272000	-1.91	-2.08	-1.96	hypothetical protein
TGME49_201770	1.67	#N/A	1.42	cullin 3, putative
TGME49_228780	1.20	1.11	1.08	Toxoplasma gondii family C protein
TGME49_309400	-1.94	-2.52	-2.53	RecF/RecN/SMC N terminal domain-containing protein
TGME49_320210	-1.21	#N/A	#N/A	WD domain, G-beta repeat domain containing protein
TGME49_292110	1.19	#N/A	#N/A	formate/nitrite transporter protein

FIGURE 4S

TGME49_213325	-9.08	-9.41	-9.45	TBC domain-containing protein
TGME49_221270	-1.90	-1.11	-1.47	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_227030	-2.15	-1.78	-2.14	hypothetical protein
TGME49_215040	-2.38	-2.23	-2.05	HEAT repeat-containing protein
TGME49_299970	-1.47	-1.03	#N/A	tetratricopeptide repeat-containing protein
TGME49_274010	-4.16	-4.10	-4.26	hypothetical protein
TGME49_305470	-9.05	-9.47	-8.93	hypothetical protein
TGME49_231910	-1.73	-1.42	-1.74	ATP synthase F1 gamma subunit
TGME49_313830	-2.96	-2.78	-2.96	AARP2CN (NUC121) domain-containing protein
TGME49_228730	-9.05	-8.79	-8.45	hypothetical protein
TGME49_257050	-9.02	-8.85	-9.48	3-methyl-2-oxobutanoate hydroxymethyltransferase
TGME49_220430	-9.02	-9.22	-8.87	hypothetical protein
TGME49_240880	2.26	#N/A	3.30	hypothetical protein
TGME49_291680	-1.53	-1.47	-2.05	Sec23/Sec24 trunk domain-containing protein
TGME49_235398	-9.02	-9.26	-9.07	hypothetical protein
TGME49_271270	-1.73	-1.54	-1.79	hypothetical protein
TGME49_248450	-2.96	-2.70	-2.80	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_225480	-4.14	-4.30	-3.93	hypothetical protein
TGME49_287270	-2.97	-2.62	-2.49	hypothetical protein
TGME49_215570	-3.39	-3.51	-3.01	AP2 domain transcription factor AP2X-11
TGME49_279340	1.67	1.85	#N/A	hypothetical protein
TGME49_257490	-3.40	-3.88	-3.98	prefoldin subunit superfamily protein
TGME49_260390	-9.02	-8.88	-8.85	hypothetical protein
TGME49_272410	1.37	1.54	1.63	phosphogluconate dehydrogenase (decarboxylating), NAD binding domain-containing protein
TGME49_210760	-9.02	-8.72	-8.72	glutamine amidotransferase-related, putative
TGME49_264080	-1.51	-1.65	-1.60	acyl carrier protein ACP
TGME49_269970	1.29	1.73	1.32	hypothetical protein
TGME49_264130	1.98	1.68	1.50	hypothetical protein
TGME49_313780	-1.63	-1.52	-1.69	hypothetical protein
TGME49_214750	1.30	1.14	#N/A	hypothetical protein
TGME49_253090	1.71	2.14	2.21	DEAD/DEAH box helicase domain-containing protein
TGME49_306460	-9.02	-8.92	-9.19	bromodomain-containing protein
TGME49_313020	-3.36	-3.63	-4.21	STAS domain-containing protein

TGME49_234900	-1.02	-1.30	-1.13	PHD-finger domain-containing protein
TGME49_313660	1.36	1.32	3.66	hypothetical protein
TGME49_299190	1.15	#N/A	1.52	B-box zinc finger domain-containing protein
TGME49_258080	-1.59	-1.64	-1.75	hypothetical protein
TGME49_258100	-2.85	-2.95	-2.78	TPR repeat region protein
TGME49_315420	1.07	1.37	1.08	hypothetical protein
TGME49_213690	-1.55	-1.28	-1.36	ring box protein 1 family protein
TGME49_204350	-1.55	-1.93	-1.51	hypothetical protein
TGME49_272290	-1.21	-1.07	-1.01	pyruvate dehydrogenase complex subunit PD-HE1Beta
TGME49_245475	1.21	1.46	1.32	hypothetical protein
TGME49_268680	-1.07	#N/A	#N/A	hypothetical protein
TGME49_219530	-2.84	-2.83	-3.40	hypothetical protein
TGME49_240910	-1.36	-1.50	-1.84	hypothetical protein
TGME49_232380	-1.49	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_226390	2.45	2.08	2.47	hypothetical protein
TGME49_225190	2.72	2.20	2.25	hypothetical protein
TGME49_298010	-1.23	-1.28	-1.13	hypothetical protein
TGME49_230230	1.31	1.08	#N/A	hypothetical protein
TGME49_202030	-1.05	-1.49	-1.60	hypothetical protein
TGME49_259700	-1.20	#N/A	-1.57	hypothetical protein
TGME49_217000	-1.43	-1.21	-1.36	hypothetical protein
TGME49_243590	-1.72	#N/A	-1.45	endonuclease/exonuclease/phosphatase family protein
TGME49_223040	1.07	1.49	1.13	hypothetical protein
TGME49_208040	-1.68	-1.85	-2.08	aldo-keto reductase
TGME49_297840	-1.11	-2.00	#N/A	DNA primase, large subunit
TGME49_255340	-1.12	-1.09	-1.08	tetratricopeptide repeat-containing protein
TGME49_314550	-2.19	#N/A	-2.38	hypothetical protein
TGME49_263840	-1.68	#N/A	-2.06	hypothetical protein
TGME49_316180	-1.68	#N/A	-2.10	hypothetical protein
TGME49_313280	1.19	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_242845	-2.79	-3.08	-3.56	hypothetical protein
TGME49_200440	1.38	#N/A	1.32	hypothetical protein
TGME49_249702	-1.82	#N/A	-2.29	MC family transporter, putative

FIGURE 4T

TGME49_218740	3.24	1.73	1.68	membrane protein, putative
TGME49_291050	-1.84	-1.74	-1.43	histone kinase SNF1, putative
TGME49_219270	-1.01	#N/A	-1.21	multi-pass transmembrane protein
TGME49_310530	-4.14	-4.38	-4.26	SNF2 family N-terminal domain-containing protein
TGME49_227948	-1.31	-1.07	-1.37	peptidase M16 inactive domain-containing protein
TGME49_306520	1.91	1.87	1.58	tRNA pseudouridine synthase B, putative
TGME49_282040	-4.17	-4.28	-3.95	hypothetical protein
TGME49_225770	-8.99	-9.28	-8.97	Tyrosine kinase-like (TKL) protein
TGME49_205460	-8.99	-8.74	-8.77	AN1 family Zinc finger domain-containing protein
TGME49_214580	-4.14	-4.05	#N/A	tetratricopeptide repeat-containing protein
TGME49_268890	-1.88	-1.69	-1.90	citrate synthase I
TGME49_253600	2.37	1.71	1.18	hypothetical protein
TGME49_289750	-1.06	-1.04	-1.30	ribosomal-ubiquitin protein RPL40
TGME49_306310	-2.51	-2.68	-2.25	RecF/RecN/SMC N terminal domain-containing protein
TGME49_290970	-1.58	#N/A	2.51	8-amino-7-oxononanoate synthase
TGME49_320450	-3.41	-3.24	-3.22	ribosome biogenesis regulatory protein (rrs1) protein
TGME49_243210	1.30	1.03	#N/A	DUF862 domain-containing protein
TGME49_243250	-1.48	-1.35	-1.70	myosin H
TGME49_264220	-8.99	-8.61	-8.96	hypothetical protein
TGME49_234490	-2.94	-2.81	-2.36	kelch repeat-containing protein
TGME49_213400	-2.70	-2.62	-2.32	zinc finger (CCCH type) motif-containing protein
TGME49_273370	-3.09	-2.91	-2.82	coatomer gamma 2-subunit protein, putative
TGME49_205000	-8.99	-8.94	-8.94	phosphoglycerate mutase family protein
TGME49_215430	1.95	1.89	1.72	hypothetical protein
TGME49_306600	-8.99	-9.05	-9.22	RNA recognition motif-containing protein
TGME49_216380	-2.76	-2.49	-2.22	phospholipid-translocating P-type ATPase, flippase subfamily protein
TGME49_213600	-8.99	-8.29	-8.28	hypothetical protein
TGME49_203350	-9.03	-9.01	-9.18	hypothetical protein
TGME49_312622	-2.19	-2.27	-2.72	DUF803 domain-containing protein
TGME49_261750	-2.50	-2.87	-2.65	rhoptry neck protein RON10
TGME49_307820	1.88	1.95	1.77	hypothetical protein

TGME49_221450	1.22	#N/A	#N/A	SPRY domain-containing protein
TGME49_251480	1.55	1.95	1.76	DEAD/DEAH box helicase domain-containing protein
TGME49_263360	-1.68	-1.96	-1.63	WD domain, G-beta repeat-containing protein
TGME49_238870	1.12	#N/A	#N/A	hypothetical protein
TGME49_214470	-1.87	-2.20	-2.19	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_310770	-1.24	-1.15	-1.46	hypothetical protein
TGME49_264890	-2.19	-2.35	-2.25	hypothetical protein
TGME49_224890	1.01	#N/A	#N/A	hypothetical protein
TGME49_255195	1.40	1.92	1.10	hypothetical protein
TGME49_218200	-2.18	-2.17	-2.66	UDP-sugar pyrophospharylase
TGME49_288990	-2.23	-2.21	-2.26	hypothetical protein
TGME49_205730	-2.18	-2.76	-2.44	hypothetical protein
TGME49_214500	1.19	1.12	1.38	ankyrin repeat-containing protein
TGME49_243240	1.56	1.37	1.26	WD domain, G-beta repeat-containing protein
TGME49_259230	-2.18	-2.42	-2.45	site-specific recombinase, phage integrase family protein
TGME49_267480	1.00	#N/A	1.07	tRNA (guanine(26)-N(2))-dimethyltransferase, putative
TGME49_320610	-2.21	-2.18	-1.92	hypothetical protein
TGME49_235450	1.19	#N/A	1.02	ubiquitin-conjugating enzyme subfamily protein
TGME49_255440	1.22	1.26	1.29	hypothetical protein
TGME49_207950	-1.54	-1.42	-1.58	hypothetical protein
TGME49_219832	-1.70	#N/A	#N/A	cyclin-dependent kinase regulatory subunit protein
TGME49_295590	1.30	1.36	1.89	hypothetical protein
TGME49_308930	-1.40	-1.24	-1.52	50S ribosomal protein L33, putative
TGME49_226620	-1.66	-1.65	#N/A	hypothetical protein
TGME49_202020	1.11	2.49	4.47	DnAK-TPR
TGME49_286510	-1.72	-1.62	#N/A	hypothetical protein
TGME49_319740	-1.53	#N/A	#N/A	transporter, major facilitator family protein
TGME49_304720	-1.57	-1.79	-1.72	hypothetical protein
TGME49_209090	-1.19	-1.13	-1.90	proteasome maturation factor ump1 protein
TGME49_203280	-2.18	-1.98	-2.28	hypothetical protein
TGME49_313570	-1.16	-1.31	-1.33	regulator of chromosome condensation (RCC1) repeat-containing protein

FIGURE 4U

TGME49_215460	-1.44	-1.16	-1.56	ribosomal protein RPS24
TGME49_221500	-8.98	-8.62	-8.71	dual specificity phosphatase, catalytic domain-containing protein
TGME49_319900	-2.01	-2.15	-1.86	hypothetical protein
TGME49_206600	-8.95	-8.94	-8.37	sigma-70, region 3 protein
TGME49_213635	4.91	2.19	-1.02	hypothetical protein
TGME49_294400	-2.02	-2.37	-2.42	hypothetical protein
TGME49_262060	-3.32	-2.90	-3.03	hypothetical protein
TGME49_306895	1.23	#N/A	1.09	hypothetical protein
TGME49_245670	-1.30	-1.06	#N/A	pyruvate dehydrogenase complex subunit PDH-E1Alpha
TGME49_214370	-8.95	-8.68	-8.91	hypothetical protein
TGME49_316350	-8.98	-8.75	-8.71	hypothetical protein
TGME49_297790	-2.45	-1.46	-2.08	hypothetical protein
TGME49_213620	2.19	1.68	3.04	ABC1 family protein
TGME49_277685	-9.05	-8.69	-7.38	hypothetical protein
TGME49_217740	-2.10	-1.89	-1.92	3-ketoacyl-(acyl-carrier-protein) reductase
TGME49_288290	2.38	1.85	#N/A	hypothetical protein
TGME49_280800	-1.79	-1.86	-1.91	SWI2/SNF2 SRCAP/Ino80
TGME49_306620	2.54	2.00	3.84	AP2 domain transcription factor AP2IX-9
TGME49_278850	-1.35	-1.38	-1.26	DHHC zinc finger domain-containing protein
TGME49_292235	-8.95	-9.04	-8.85	hypothetical protein
TGME49_271780	-2.90	-3.11	-2.75	Filamin/ABP280 repeat-containing protein
TGME49_309110	1.53	1.29	1.83	tRNA methyl transferase
TGME49_219485	1.57	1.26	2.11	hypothetical protein
TGME49_299000	1.46	1.03	#N/A	hypothetical protein
TGME49_267330	-2.42	-2.03	-2.30	fumarate hydratase
TGME49_284660	-8.95	-8.32	-8.53	mitochondrial ribosomal protein s6-2, putative
TGME49_205340	1.16	1.26	#N/A	ribosomal protein RPS12
TGME49_266470	-8.92	-8.81	-9.09	hypothetical protein
TGME49_227450	1.21	1.05	1.27	hydrolase, NUDIX family protein
TGME49_286650	-8.92	-9.00	-9.01	hypothetical protein
TGME49_290720	-1.63	-1.86	-1.87	vacuolar proton translocating ATPase subunit, putative
TGME49_278950	2.09	1.84	1.74	LSM domain-containing protein
TGME49_239340	-8.92	-8.79	-9.25	hypothetical protein
TGME49_262930	-8.92	-9.04	-9.47	hypothetical protein

TGME49_301120	-1.24	#N/A	-1.62	acetyl-CoA acetyltransferase
TGME49_311160	-1.15	-1.32	-1.53	PWI domain-containing protein
TGME49_238040	-1.13	-1.07	-1.90	protein disulfide-isomerase domain-containing protein
TGME49_262450	-1.10	-1.06	-1.15	hypothetical protein
TGME49_290630	1.03	#N/A	1.17	AP2 domain transcription factor AP2IX-7
TGME49_221630	-2.14	-3.28	-3.23	hypothetical protein
TGME49_215360	1.25	1.97	1.59	hypothetical protein
TGME49_273540	-1.52	#N/A	#N/A	phosphatidylserine synthase, putative
TGME49_207720	-1.30	-1.26	-1.20	hypothetical protein
TGME49_207960	-1.51	#N/A	-1.98	hypothetical protein
TGME49_288370	1.17	#N/A	1.28	hypothetical protein
TGME49_219710	1.08	#N/A	#N/A	hypothetical protein
TGME49_200375	-2.17	#N/A	-2.41	hypothetical protein
TGME49_292610	-7.12	-7.13	-8.91	Toxoplasma gondii family C protein
TGME49_224980	-1.09	#N/A	-1.23	hypothetical protein
TGME49_249690	-2.78	-2.89	-3.64	hypothetical protein
TGME49_273970	-2.72	-3.20	-3.09	CorA family Mg2+ transporter protein
TGME49_265470	1.29	#N/A	#N/A	hypothetical protein
TGME49_240730	-2.72	-2.99	-3.44	hypothetical protein
TGME49_293220	1.96	#N/A	1.85	DHHC zinc finger domain-containing protein
TGME49_305260	-2.72	-2.57	-2.89	hypothetical protein
TGME49_202800	-7.14	-8.37	-8.15	cytochrome c oxidase assembly protein COX11, putative
TGME49_266680	-1.66	#N/A	#N/A	hypothetical protein
TGME49_245530	2.61	2.09	#N/A	hypothetical protein
TGME49_278080	1.37	2.04	7.20	Toxoplasma gondii family A protein
TGME49_208430	1.29	1.13	#N/A	serine proteinase inhibitor PI-2, putative
TGME49_307575	-2.73	-3.79	-2.70	hypothetical protein
TGME49_320670	-1.11	-1.24	-1.24	vacuolar protein sorting 16, putative
TGME49_270350	-1.10	#N/A	-1.13	hypothetical protein
TGME49_255670	-2.72	-2.82	-3.09	methyltransferase domain-containing protein
TGME49_266380	-7.12	-7.15	-9.53	hypothetical protein
TGME49_213000	2.03	2.22	#N/A	replication factor C, subunit 5, putative
TGME49_240080	1.26	#N/A	#N/A	hypothetical protein
TGME49_244100	-1.12	#N/A	-1.43	snoRNA binding domain-containing protein

FIGURE 4V

TGME49_239780	-3.35	-3.53	-3.58	hypothetical protein
TGME49_309950	-8.92	-8.54	-8.45	NLE (NUC135) domain-containing protein
TGME49_285180	-1.64	-1.87	#N/A	hypothetical protein
TGME49_255250	-8.92	-8.70	-8.73	tRNA (cytosine(34)-C(5))-methyltransferase, putative
TGME49_250100	2.61	2.16	3.11	hypothetical protein
TGME49_231120	1.56	1.93	1.68	ribosomal protein S11, putative
TGME49_235630	1.16	1.36	1.72	hypothetical protein
TGME49_235740	-4.04	-3.29	-3.95	hypothetical protein
TGME49_222192	-8.92	-8.69	-8.27	hypothetical protein
TGME49_256880	-8.92	-8.93	-8.89	protein kinase domain-containing protein
TGME49_257720	2.71	#N/A	#N/A	proton ATPase, putative
TGME49_245580	2.05	1.12	1.03	hypothetical protein
TGME49_233500	1.39	1.19	1.23	triose-phosphate isomerase TPI-II
TGME49_214820	1.55	1.64	1.43	G-patch domain-containing protein
TGME49_288340	-8.89	-8.91	-9.30	UBX domain-containing protein
TGME49_254230	2.06	1.91	1.89	hypothetical protein
TGME49_285970	-8.88	-9.02	-8.90	30S ribosomal protein S5, putative
TGME49_222020	-2.64	-2.53	-2.29	phosphoglycerate kinase PGKII
TGME49_267340	2.10	1.75	2.16	hypothetical protein
TGME49_293440	-1.65	-1.84	-1.64	hypothetical protein
TGME49_266890	-1.81	-1.47	-1.43	hypothetical protein
TGME49_263540	2.06	2.32	2.39	hypothetical protein
TGME49_217688	-8.88	-8.98	-9.21	hypothetical protein
TGME49_293860	-8.88	-8.93	-9.03	hypothetical protein
TGME49_229380	-8.88	-8.60	-8.73	hypothetical protein
TGME49_265220	-4.07	-4.04	-3.83	co-chaperone GrpE protein
TGME49_209860	-8.89	-8.20	-8.38	SRP40, C-terminal domain-containing protein
TGME49_204280	1.22	1.27	1.28	cell-cycle-associated protein kinase DYRK, putative
TGME49_216335	2.20	1.13	3.61	hypothetical protein
TGME49_316680	1.23	1.10	#N/A	RNA pseudouridine synthase superfamily protein
TGME49_251680	-1.35	-1.19	-1.49	histamine-releasing factor, putative
TGME49_306930	-1.41	#N/A	-1.60	proteasome subunit beta type 7 precursor, putative
TGME49_266400	-8.92	-9.03	-8.79	hypothetical protein

TGME49_272570	1.42	1.57	2.02	dihydrouridine synthase (dus) protein
TGME49_247590	-1.83	-1.75	-1.86	methyltransferase domain-containing protein
TGME49_293050	-2.14	-2.81	-2.64	sybindin family protein
TGME49_214130	-1.12	#N/A	#N/A	hypothetical protein
TGME49_248750	2.15	#N/A	#N/A	hypothetical protein
TGME49_316750	-2.72	-2.93	-2.99	DEAD/DEAH box helicase domain-containing protein
TGME49_276100	-1.66	#N/A	-1.58	hypothetical protein
TGME49_227820	-1.22	-1.10	-1.19	hypothetical protein
TGME49_295430	-1.65	#N/A	#N/A	hypothetical protein
TGME49_232060	-1.54	#N/A	#N/A	hypothetical protein
TGME49_266860	1.15	#N/A	#N/A	BTB/POZ domain-containing protein
TGME49_258625	-7.11	-7.88	-8.44	peptidyl-prolyl cis-trans isomerase, FKBP type domain-containing protein
TGME49_276910	-1.07	-1.45	-1.02	endoplasmic reticulum lumen protein retaining receptor (ERD2) family protein
TGME49_223900	1.30	2.09	1.89	hypothetical protein
TGME49_244040	-1.40	#N/A	#N/A	HEAT repeat-containing protein
TGME49_216220	-1.06	-1.21	#N/A	AP2 domain transcription factor AP2XI-5
TGME49_248660	-1.64	#N/A	#N/A	hypothetical protein
TGME49_292960	1.35	#N/A	#N/A	hypothetical protein
TGME49_211480	-1.61	#N/A	-1.47	GTP-binding protein engA, putative
TGME49_207065	-1.61	-1.48	-1.77	hypothetical protein
TGME49_321600	-1.04	-1.13	#N/A	hypothetical protein
TGME49_203362	-2.71	-3.02	-3.06	hypothetical protein
TGME49_293700	-1.29	-1.37	-1.14	WD domain, G-beta repeat-containing protein
TGME49_218580	-1.61	-1.63	#N/A	RNA methyltransferase, TrmH family protein
TGME49_202190	1.08	1.29	1.15	hypothetical protein
TGME49_213388	1.10	#N/A	1.25	hypothetical protein
TGME49_263510	-1.16	-1.51	#N/A	Spc97 / Spc98 family protein
TGME49_314720	1.09	#N/A	#N/A	Sedlin, N-terminal region protein, putative
TGME49_219540	-1.52	#N/A	#N/A	cytosolic tRNA-Ala synthetase
TGME49_269700	1.37	1.67	1.75	NLI interacting factor family phosphatase
TGME49_322000	-1.27	#N/A	-2.58	myosin-light-chain kinase
TGME49_216055	-1.16	#N/A	#N/A	hypothetical protein
TGME49_257980	2.55	2.23	2.38	ribosome recycling factor protein

FIGURE 4W

TGME49_246460	-4.03	-4.13	-3.97	hypothetical protein
TGME49_290900	-8.89	-9.25	-9.44	hydrolase, NUDIX family protein
TGME49_221180	1.10	1.04	#N/A	hypothetical protein
TGME49_270620	2.33	2.77	2.90	DEAD/DEAH box helicase domain-containing protein
TGME49_320740	-1.78	-2.10	-1.72	hypothetical protein
TGME49_202580	1.81	2.05	#N/A	ATPase, AAA family protein
TGME49_260620	1.67	1.87	1.54	hypothetical protein
TGME49_226600	-2.24	-1.86	-1.80	syntaxin 5, putative
TGME49_304700	-3.99	-4.04	-3.83	hypothetical protein
TGME49_310860	-2.59	-2.48	-2.48	U5 snRNP-specific protein
TGME49_221590	1.01	1.58	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_217730	2.08	1.06	1.00	hypothetical protein
TGME49_268170	-8.95	-8.41	-8.46	hypothetical protein
TGME49_213900	1.20	#N/A	1.12	regulator of chromosome condensation RCC1
TGME49_230580	-8.85	-8.56	-8.23	hypothetical protein
TGME49_304710	-1.30	#N/A	-1.16	eukaryotic peptide chain release factor, putative
TGME49_253000	1.29	1.21	1.17	ELMO/CED-12 family protein
TGME49_223450	-1.94	-1.97	-1.66	ubiquitin carboxyl-terminal hydrolase
TGME49_291980	-1.59	-1.53	-1.26	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_212960	-8.89	-8.41	-8.61	hypothetical protein
TGME49_253100	1.20	#N/A	1.03	hypothetical protein
TGME49_264730	-8.85	-8.77	-8.53	hypothetical protein
TGME49_244530	1.01	1.56	#N/A	hypothetical protein
TGME49_231980	-8.85	-9.12	-9.49	hypothetical protein
TGME49_215260	-1.63	-1.22	-1.52	carbamoylphosphate synthetase
TGME49_253640	1.34	1.24	1.08	hypothetical protein
TGME49_268880	-3.23	-3.50	-2.91	hypothetical protein
TGME49_292375	3.37	#N/A	#N/A	KRUF family protein
TGME49_311870	-2.39	-2.50	-2.45	WD domain, G-beta repeat-containing protein
TGME49_253360	1.27	1.32	#N/A	hypothetical protein
TGME49_289150	1.52	1.83	1.12	hypothetical protein
TGME49_267600	-2.83	-3.08	-2.73	FHA domain-containing protein
TGME49_207665	-8.89	-7.99	-8.04	kinesin motor domain-containing protein
TGME49_308880	-8.85	-8.48	-8.45	ImpB/MucB/SamB family protein

TGME49_224090	-1.61	-1.72	-1.96	enoyl-CoA hydratase/isomerase family protein
TGME49_305030	-1.46	-1.51	-2.10	kinase, pfkB family protein
TGME49_307605	-1.00	-1.52	#N/A	hypothetical protein
TGME49_315710	1.43	#N/A	#N/A	hypothetical protein
TGME49_239310	-2.12	-2.79	-2.12	ribulose 5-phosphate isomerase
TGME49_215250	-1.79	-1.77	-1.72	thiamin pyrophosphokinase, catalytic domain-containing protein
TGME49_237160	-1.32	-1.25	#N/A	hypothetical protein
TGME49_218810	-1.29	#N/A	#N/A	histidyl-tRNA synthetase
TGME49_216960	1.10	1.04	#N/A	elongation factor Tu GTP binding domain-containing protein
TGME49_238080	1.27	#N/A	1.21	hypothetical protein
TGME49_293600	1.05	#N/A	#N/A	ribosomal protein RPL27
TGME49_289615	1.86	#N/A	#N/A	hypothetical protein
TGME49_267650	-1.48	-1.36	#N/A	hypothetical protein
TGME49_297270	-2.08	-2.35	-2.48	hypothetical protein
TGME49_239087	-1.78	#N/A	#N/A	hypothetical protein
TGME49_246730	1.03	1.38	#N/A	hypothetical protein
TGME49_243600	-1.04	-1.26	-1.08	acetyltransferase, GNAT family protein
TGME49_293680	-1.28	-1.52	-1.29	hypothetical protein
TGME49_264210	1.02	1.37	1.09	hypothetical protein
TGME49_249300	-1.63	#N/A	-1.97	hypothetical protein
TGME49_249310	-2.65	-2.82	-3.77	hypothetical protein
TGME49_210478	2.28	-1.44	5.25	hypothetical protein
TGME49_267855	-1.02	#N/A	-1.04	hypothetical protein
TGME49_255430	-1.48	#N/A	#N/A	Rad9 protein
TGME49_234280	-1.08	#N/A	#N/A	AMP deaminase
TGME49_238140	-1.15	-1.89	-1.19	hypothetical protein
TGME49_203750	-1.78	-1.89	-1.83	hypothetical protein
TGME49_246182	-1.29	#N/A	#N/A	hypothetical protein
TGME49_254480	1.43	#N/A	1.36	WD domain, G-beta repeat-containing protein
TGME49_262990	-2.67	-3.05	-3.00	hypothetical protein
TGME49_269417	-2.65	-2.99	#N/A	hypothetical protein
TGME49_258010	-1.62	-1.52	-1.64	calcium signaling protein kinase RAD53, putative
TGME49_211330	-2.18	#N/A	#N/A	methionine aminopeptidase
TGME49_219510	1.51	1.85	1.66	GTP binding protein 7 isoform 2 family protein, putative

FIGURE 4X

TGME49_263500	-4.01	-3.88	-4.19	vacuolar protein sorting-associated protein 26, putative
TGME49_219770	-8.91	-8.87	-8.54	30S ribosomal protein S12, putative
TGME49_310100	-8.85	-8.73	-8.67	mannosyltransferase (pig-m) protein
TGME49_211040	-1.31	-1.22	-1.61	Sec61beta family protein
TGME49_214830	-3.98	-3.85	-3.30	hypothetical protein
TGME49_285210	-8.90	-8.51	-8.47	hypothetical protein
TGME49_313330	-8.99	-9.05	-9.34	rhoptry kinase family protein ROP27
TGME49_271760	-8.81	-8.98	-9.37	seryl-tRNA synthetase (SerRS2)
TGME49_309870	-8.81	-9.03	-9.48	hypothetical protein
TGME49_207480	-2.36	-2.40	-1.95	GCC2 and GCC3 domain-containing protein
TGME49_294290	-2.03	-1.98	-2.21	Der1ER1
TGME49_313760	1.01	#N/A	#N/A	hypothetical protein
TGME49_264690	-8.81	-8.55	-8.84	cyclin 4, putative
TGME49_272390	-8.82	-8.67	-7.80	hypothetical protein
TGME49_230190	-1.99	-1.94	-2.17	hypothetical protein
TGME49_209700	-3.96	-3.97	-4.13	hypothetical protein
TGME49_242800	-1.99	-1.79	-1.67	ribosome biogenesis protein NSA2, putative
TGME49_252380	1.97	1.24	1.82	hypothetical protein
TGME49_249610	-2.36	-2.58	-2.92	hypothetical protein
TGME49_257480	-2.96	-2.42	-2.41	NADP-dependent succinate-semialdehyde dehydrogenase
TGME49_259950	2.29	1.96	2.05	carbonate dehydratase, eukaryotic-type domain-containing protein
TGME49_250950	2.30	2.04	#N/A	KRUF family protein
TGME49_305090	1.60	1.86	2.15	kinase binding protein cgi-121 protein
TGME49_264780	-8.81	-9.08	-8.72	UTP-glucose-1-phosphate uridylyltransferase subfamily protein
TGME49_231030	-3.96	-3.65	-3.52	hypothetical protein
TGME49_221600	-8.81	-8.86	-8.12	hypothetical protein
TGME49_221200	1.50	1.24	1.15	CW-type Zinc Finger protein
TGME49_310130	-8.78	-9.44	-9.82	Spc97 / Spc98 family protein
TGME49_271200	-1.77	-1.34	-1.43	AP2 domain transcription factor AP2VIII-5
TGME49_217770	1.40	1.55	1.34	hypothetical protein
TGME49_202120	-1.56	-1.54	-1.59	hypothetical protein
TGME49_289100	-2.15	-1.72	-1.59	hypothetical protein
TGME49_261400	-1.51	-2.00	-1.02	hypothetical protein
TGME49_320550	-2.12	-1.90	-1.82	hypothetical protein
TGME49_231215	-8.78	-8.68	-8.75	hypothetical protein
TGME49_205380	-1.48	-1.55	-2.23	fructose-bisphospatase I

TGME49_288560	-1.21	-1.61	-1.87	hypothetical protein
TGME49_248800	2.35	#N/A	#N/A	hypothetical protein
TGME49_289950	-1.08	-1.16	-1.01	hypothetical protein
TGME49_316150	-1.32	-1.76	#N/A	ULK kinase
TGME49_218192	-6.99	-7.38	-9.70	hypothetical protein
TGME49_232520	-1.24	#N/A	#N/A	brix domain-containing protein
TGME49_237100	1.27	#N/A	1.06	RAP domain-containing protein
TGME49_235660	-1.32	-1.29	#N/A	hypothetical protein
TGME49_311040	-1.12	#N/A	#N/A	hypothetical protein
TGME49_283900	-1.45	#N/A	-1.47	ATPase, AAA family protein
TGME49_226520	-1.12	#N/A	#N/A	hypothetical protein
TGME49_297980	1.38	#N/A	#N/A	hypothetical protein
TGME49_287480	1.04	#N/A	1.55	hypothetical protein
TGME49_204150	1.32	#N/A	#N/A	hypothetical protein
TGME49_264752	-2.63	-3.41	-3.52	HEAT repeat-containing protein
TGME49_203950	-1.04	#N/A	#N/A	Myb family DNA-binding domain-containing protein
TGME49_220150	-1.74	-1.79	-1.72	50S ribosomal protein L16, putative
TGME49_258050	-2.03	-2.05	-2.35	actin like protein ALP2a
TGME49_273885	-2.04	#N/A	-2.34	hypothetical protein
TGME49_246000	1.33	#N/A	1.66	large subunit ribosomal protein IMG2
TGME49_210310	-1.74	#N/A	-1.63	hypothetical protein
TGME49_312820	-1.43	#N/A	-1.86	hypothetical protein
TGME49_240480	-2.70	-2.92	#N/A	cpw-wpc domain-containing protein
TGME49_295090	1.07	1.32	#N/A	hypothetical protein
TGME49_255310	-1.27	-1.51	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_257070	-2.03	-2.02	-2.10	hypothetical protein
TGME49_293490	1.72	1.78	1.85	hypothetical protein
TGME49_251590	1.17	1.31	1.10	hypothetical protein
TGME49_273380	1.42	#N/A	#N/A	ion channel protein
TGME49_309960	-1.03	#N/A	#N/A	hypothetical protein
TGME49_262933	-1.61	-1.56	#N/A	hypothetical protein
TGME49_209530	1.26	#N/A	1.41	hypothetical protein
TGME49_262420	1.18	#N/A	#N/A	AP2 domain transcription factor APVIIb-1/ADA2-B
TGME49_271370	-1.82	#N/A	#N/A	hypothetical protein
TGME49_268640	2.40	#N/A	#N/A	BING4CT (NUC141) domain-containing protein
TGME49_212290	-1.10	#N/A	-1.20	ribosomal protein RPS19

FIGURE 4Y

TGME49_220100	-2.45	-2.35	-2.84	phosphoribosylpyrophosphate synthetase
TGME49_250690	-1.08	-1.30	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_318330	-8.77	-9.40	-9.40	histone lysine acetyltransferase MYST-A
TGME49_227930	1.20	1.43	1.31	hypothetical protein
TGME49_321440	-1.30	-1.15	-1.18	SWI2/SNF2 ISWI-like SANT
TGME49_202950	-1.45	-1.27	-1.07	hypothetical protein
TGME49_300290	-8.80	-8.49	-8.98	SNARE domain-containing protein
TGME49_249030	1.25	#N/A	#N/A	endonuclease/exonuclease/phosphatase family protein
TGME49_280380	1.22	#N/A	#N/A	poly(ADP-ribose) glycohydrolase
TGME49_311460	-2.88	-3.71	#N/A	hypothetical protein
TGME49_261620	1.56	2.13	1.94	hypothetical protein
TGME49_219070	1.18	#N/A	1.38	cyclic nucleotide-binding domain-containing protein
TGME49_310010	-1.27	-1.42	-1.26	rhoptry neck protein RON1
TGME49_237830	-8.77	-9.23	-9.48	DNA polymerase I domain-containing protein
TGME49_251800	1.68	2.31	2.19	hypothetical protein
TGME49_213790	-2.78	-3.06	-2.78	hypothetical protein
TGME49_219310	-1.41	-1.29	-1.31	DnaK family protein
TGME49_240300	-8.80	-8.47	-8.36	zinc finger domain, LSD1 subclass domain-containing protein
TGME49_298830	1.64	2.37	1.81	hypothetical protein
TGME49_236570	-1.26	-1.19	-1.58	lysine decarboxylase family protein
TGME49_289570	1.04	1.27	#N/A	phosphatidylinositol transfer protein
TGME49_266970	-3.21	-2.77	-3.02	hypothetical protein
TGME49_231130	-8.74	-9.12	-9.23	hypothetical protein
TGME49_252340	1.57	#N/A	1.23	hypothetical protein
TGME49_240540	-2.36	-2.20	-2.03	hypothetical protein
TGME49_209820	-8.77	-8.54	-8.59	syntaxin protein
TGME49_318410	-1.38	-1.14	-1.37	TCP-1 chaperonin, putative
TGME49_246800	-1.79	-1.35	-1.73	acylaminoacyl-peptidase, putative
TGME49_319640	1.06	1.11	1.26	hypothetical protein
TGME49_263040	-1.10	#N/A	-1.12	ribosomal protein RPS16
TGME49_297420	-3.92	-4.00	-3.85	beta-tubulin cofactor D, putative
TGME49_264840	-8.74	-9.06	-8.15	ATP-dependent DNA helicase, RecQ family protein
TGME49_237000	-3.90	-4.10	-4.26	polyphosphoinositide binding protein, putative
TGME49_237530	-8.74	-8.94	-8.75	hypothetical protein

TGME49_260640	-1.54	-2.13	-1.78	autophagy protein apg9 protein
TGME49_306890	-1.30	-1.42	#N/A	hypothetical protein
TGME49_233770	2.55	#N/A	-2.20	calcium-translocating P-type ATPase, PMCA-type protein
TGME49_310500	-1.12	#N/A	-1.17	hypothetical protein
TGME49_313090	-1.74	#N/A	-1.77	hypothetical protein
TGME49_278020	-2.58	-3.17	-2.94	hypothetical protein
TGME49_254420	2.12	#N/A	#N/A	phospholipase, patatin family protein
TGME49_292035	1.30	1.40	#N/A	hypothetical protein
TGME49_219130	-1.39	-1.87	-1.55	NADPH-glutathione reductase
TGME49_261960	1.21	1.52	1.20	hypothetical protein
TGME49_262880	-1.15	-1.50	-1.55	hypothetical protein
TGME49_288245	-1.00	#N/A	#N/A	hypothetical protein
TGME49_219100	-1.39	-1.60	-1.28	cyclin-dependent kinase regulatory subunit protein
TGME49_240700	-1.29	-1.21	-1.67	ubiquitin family protein
TGME49_316770	-1.39	-1.34	-1.37	undecaprenyl diphosphate synthase
TGME49_226350	1.16	#N/A	1.01	hypothetical protein
TGME49_289790	-2.58	-3.16	-2.92	hypothetical protein
TGME49_213752	-1.54	#N/A	-1.67	herpesviridae ul52/ul70 dna primase
TGME49_220460	-6.86	-8.40	-8.72	SNF7 family protein
TGME49_247280	-1.70	-2.16	-2.26	hypothetical protein
TGME49_278030	1.09	#N/A	#N/A	hypothetical protein
TGME49_211020	-1.39	-1.46	-1.86	RNA recognition motif-containing protein
TGME49_255270	1.98	#N/A	#N/A	hypothetical protein
TGME49_226080	1.13	#N/A	#N/A	polyA polymerase
TGME49_313630	2.69	#N/A	#N/A	hypothetical protein
TGME49_229200	-1.40	-1.32	#N/A	hypothetical protein
TGME49_242880	-1.70	-1.61	-1.76	flavoprotein
TGME49_286610	1.41	#N/A	#N/A	ribosomal protein RPS14, putative
TGME49_285660	-1.55	-2.12	-1.93	DEAD/DEAH box helicase domain-containing protein
TGME49_263560	1.13	1.29	#N/A	hypothetical protein
TGME49_257060	-1.70	-1.93	-2.12	translation initiation factor sui1 protein
TGME49_277260	#N/A	2.05	1.81	hypothetical protein
TGME49_202970	#N/A	-12.46	#N/A	hypothetical protein
TGME49_213570	#N/A	1.61	1.39	hypothetical protein

FIGURE 4Z

TGME49_280410	-1.95	-1.82	-1.69	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_290940	-1.57	-1.28	-1.48	EMP/nonaspanin domain family protein
TGME49_250115	1.14	#N/A	#N/A	hypothetical protein
TGME49_286750	-1.46	-1.50	-1.34	MA3 domain-containing protein
TGME49_270800	-3.97	-4.18	-4.23	GAF domain-containing protein
TGME49_223690	-8.74	-8.28	-8.14	hypothetical protein
TGME49_253320	-8.74	-8.05	-8.09	hypothetical protein
TGME49_217020	-3.37	-4.05	-2.23	ATPase, AFG1 family protein
TGME49_306470	-2.49	-2.47	-2.66	isoprenylcysteine carboxyl methyltransferase (icmt) family protein
TGME49_314280	2.69	2.21	2.47	AAR2 protein
TGME49_225690	-1.29	-1.43	-1.09	hypothetical protein
TGME49_292950	-1.21	#N/A	#N/A	hypothetical protein
TGME49_236550	-1.37	-1.20	-1.54	hypothetical protein
TGME49_226260	1.11	1.38	#N/A	hypothetical protein
TGME49_224600	-3.90	-3.70	-3.49	GTP binding protein
TGME49_216410	-8.82	-8.77	-8.55	hypothetical protein
TGME49_224310	-8.76	-8.90	-9.06	DHHC zinc finger domain-containing protein
TGME49_275755	2.14	3.25	3.34	hypothetical protein
TGME49_312330	-1.16	#N/A	#N/A	hypothetical protein
TGME49_219820	-1.23	#N/A	-1.03	polyubiquitin UbC, putative
TGME49_231180	1.62	#N/A	1.22	hypothetical protein
TGME49_261970	1.26	1.55	1.71	hypothetical protein
TGME49_212140	-4.01	-4.43	-4.21	hypothetical protein
TGME49_314730	-3.90	-3.97	-3.97	ALG6, ALG8 glycosyltransferase family protein
TGME49_297810	-1.39	-1.31	-1.71	hypothetical protein
TGME49_238950	-1.54	-1.75	-2.83	fatty acyl-CoA desaturase, putative
TGME49_294980	2.12	1.48	1.58	hypothetical protein
TGME49_292975	-3.16	-3.56	-2.70	hypothetical protein
TGME49_312860	-3.18	-2.92	-3.01	hypothetical protein
TGME49_268600	-3.13	-2.76	-2.96	DNA polymerase epsilon subunit B protein
TGME49_264860	-3.88	-3.77	-3.63	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_270900	-3.25	-3.24	-3.05	ATPase, AAA family protein
TGME49_269670	-3.14	-3.25	-2.67	hypothetical protein

TGME49_208740	#N/A	1.73	1.85	microneme protein, putative
TGME49_253430	#N/A	1.25	#N/A	asparagine synthetase, putative
TGME49_301890	#N/A	-3.97	#N/A	Toxoplasma gondii family B protein
TGME49_236040	#N/A	1.22	#N/A	fructose-1,6-bisphosphate aldolase
TGME49_267020	#N/A	-4.00	#N/A	hypothetical protein
TGME49_216140	#N/A	2.28	2.32	tetratricopeptide repeat-containing protein
TGME49_295440	#N/A	2.62	1.48	hypothetical protein
TGME49_210408	#N/A	1.13	#N/A	HMG (high mobility group) box domain-containing protein
TGME49_213255	#N/A	-5.17	#N/A	hypothetical protein
TGME49_286470	#N/A	1.35	1.18	AGC kinase
TGME49_269840	#N/A	1.41	#N/A	proteasome regulatory subunit
TGME49_242090	#N/A	1.04	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_205265	#N/A	2.34	#N/A	transporter, cation channel family protein
TGME49_217520	#N/A	1.29	1.16	hypothetical protein
TGME49_201390	#N/A	1.07	#N/A	hypothetical protein
TGME49_201785	#N/A	1.34	#N/A	hypothetical protein
TGME49_297940	#N/A	-2.13	#N/A	single-strand binding protein
TGME49_205170	#N/A	2.05	1.23	hypothetical protein
TGME49_217420	#N/A	-4.93	-4.14	hypothetical protein
TGME49_275610	#N/A	-1.70	#N/A	protein kinase, other
TGME49_295360	#N/A	1.14	#N/A	hypothetical protein
TGME49_275630	#N/A	-2.31	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_259115	#N/A	-3.62	#N/A	ABC1 family protein
TGME49_316470	#N/A	-3.66	#N/A	hypothetical protein
TGME49_297910	#N/A	-4.84	-2.63	hypothetical protein
TGME49_217400	#N/A	-3.18	-2.97	hypothetical protein
TGME49_213730	#N/A	1.28	#N/A	lanthionine synthetase C family protein
TGME49_306338	#N/A	-2.72	#N/A	dynein gamma chain, flagellar outer arm, putative
TGME49_291040	#N/A	4.27	8.36	lactate dehydrogenase LDH2
TGME49_249230	#N/A	-4.63	-4.83	hypothetical protein
TGME49_304740	#N/A	1.11	1.38	rhoptry kinase family protein ROP35
TGME49_289540	#N/A	1.20	#N/A	hypothetical protein
TGME49_217550	#N/A	1.24	#N/A	hypothetical protein

FIGURE 4AA

TGME49_219800	-1.19	-1.05	-1.29	vacuolar ATP synthase subunit b, putative
TGME49_235490	-1.71	-1.64	-1.85	hypothetical protein
TGME49_312650	2.16	1.35	1.34	hypothetical protein
TGME49_244720	-3.87	-3.24	-3.58	hypothetical protein
TGME49_233410	1.71	2.08	1.48	Sof1 family domain-containing protein
TGME49_208200	-3.90	-3.86	-3.87	PHD-finger domain-containing protein
TGME49_205558	-1.08	#N/A	#N/A	NAC domain-containing protein
TGME49_256770	-1.33	-1.30	-1.47	eukaryotic translation initiation factor 4A, isoform 3, putative
TGME49_225160	1.17	#N/A	#N/A	hypothetical protein
TGME49_216120	-2.30	-2.20	-2.18	hypothetical protein
TGME49_272270	-8.70	-7.90	-7.71	radical SAM domain-containing protein
TGME49_264140	-1.79	-2.24	-1.45	hypothetical protein
TGME49_207770	-1.45	-1.29	-1.66	PCI domain-containing protein
TGME49_202280	-3.93	-4.40	-2.99	WD domain, G-beta repeat-containing protein
TGME49_310850	-8.75	-8.54	-8.68	MYND finger domain-containing protein
TGME49_223780	-1.90	-1.60	-1.76	hypothetical protein
TGME49_275350	-2.29	-1.94	-1.73	TBC domain-containing protein
TGME49_270580	-8.69	-10.08	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_253850	2.01	1.84	2.47	hypothetical protein
TGME49_252310	-2.02	-1.80	-1.27	hypothetical protein
TGME49_289310	-2.17	-2.16	-2.38	cullin family protein
TGME49_222060	-2.57	#N/A	-2.32	hypothetical protein
TGME49_310230	-8.70	-9.18	-9.01	hypothetical protein
TGME49_306530	-8.70	-8.20	-8.15	hypothetical protein
TGME49_276930	1.21	1.54	#N/A	hypothetical protein
TGME49_259520	-8.69	-8.72	-9.00	hypothetical protein
TGME49_210390	-8.74	-8.25	-8.60	WD domain, G-beta repeat-containing protein
TGME49_246230	-8.73	-8.45	-8.49	hypothetical protein
TGME49_307010	2.11	1.66	1.54	histone lysine demethylase JMJC1/KDM5D/JARID1D
TGME49_258670	-8.78	-9.80	-7.67	hypothetical protein
TGME49_294830	-2.83	-3.42	-2.72	methyltransferase domain-containing protein
TGME49_315600	-8.73	-9.28	-8.42	MCM2/3/5 family protein

TGME49_248820	#N/A	-9.38	#N/A	hypothetical protein
TGME49_244700	#N/A	-2.01	1.43	NAD(+)/NADH kinase domain-containing protein
TGME49_311100	#N/A	1.22	1.01	zinc finger (CCCH type) motif-containing protein
TGME49_218750	#N/A	-3.67	#N/A	hypothetical protein
TGME49_236540	#N/A	1.04	#N/A	RNA recognition motif-containing protein
TGME49_253930	#N/A	-2.02	-1.03	GCC2 and GCC3 domain-containing protein
TGME49_307770	#N/A	-2.20	#N/A	fumble protein
TGME49_254690	#N/A	1.06	#N/A	phospholipase/carboxylesterase
TGME49_294970	#N/A	1.33	#N/A	hypothetical protein
TGME49_245560	#N/A	1.10	1.35	hypothetical protein
TGME49_293900	#N/A	1.09	#N/A	sporozoite protein with an altered thrombospondin repeat SPATR
TGME49_318650	#N/A	1.15	#N/A	transhydrogenase
TGME49_239890	#N/A	1.15	#N/A	SCP family extracellular subfamily protein
TGME49_217410	#N/A	-9.14	-6.96	hypothetical protein
TGME49_269930	#N/A	-1.97	2.31	calcium binding egf domain-containing protein
TGME49_285870	#N/A	1.51	#N/A	SAG-related sequence SRS20A
TGME49_226580	#N/A	1.19	#N/A	hypothetical protein
TGME49_209940	#N/A	-2.39	#N/A	transporter/permease protein
TGME49_280500	#N/A	-4.11	#N/A	inorganic anion transporter, sulfate permease (SulP) family protein
TGME49_209985	#N/A	-2.18	1.72	cAMP-dependent protein kinase
TGME49_201780	#N/A	1.32	#N/A	microneme protein MIC2
TGME49_214100	#N/A	1.37	#N/A	hypothetical protein
TGME49_293760	#N/A	1.11	#N/A	EF hand domain-containing protein
TGME49_298070	#N/A	-9.23	-7.52	hypothetical protein
TGME49_269010	#N/A	1.25	1.36	AP2 domain transcription factor AP2VIII-7
TGME49_252500	#N/A	1.20	1.13	polo kinase
TGME49_299210	#N/A	1.03	#N/A	CTP synthase
TGME49_307570	#N/A	-1.29	#N/A	glycerol-3-phosphate dehydrogenase (gpdh), putative
TGME49_259020	#N/A	5.30	6.07	bradyzoite antigen BAG1
TGME49_301160	#N/A	-4.31	#N/A	SAG-related sequence SRS19C
TGME49_280370	#N/A	1.17	#N/A	hypothetical protein
TGME49_288530	#N/A	1.42	1.62	NOL1/NOP2/sun family protein

FIGURE 4BB

TGME49_315860	-2.13	-2.27	-2.21	EF hand domain-containing protein
TGME49_260320	-2.72	-2.93	-2.79	Noc2p family protein
TGME49_214770	-1.22	#N/A	-1.16	small GTP binding protein rab1a, putative
TGME49_294705	-8.71	-7.95	-8.35	hypothetical protein
TGME49_211630	1.02	1.20	#N/A	hypothetical protein
TGME49_255890	-3.11	-2.68	-2.76	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_292140	1.08	1.16	1.46	NIMA-related protein kinase NIMA1
TGME49_202620	1.02	1.00	#N/A	hypothetical protein
TGME49_290580	-3.84	-4.58	-3.90	ATP-binding cassette G family transporter ABCG89
TGME49_223150	-8.66	-8.53	-8.29	START domain-containing protein
TGME49_319312	2.20	2.19	#N/A	hypothetical protein
TGME49_243580	-2.65	-2.99	-4.10	Hit family protein involved in cell-cycle regulation, putative
TGME49_201900	-3.84	-3.84	-3.75	hypothetical protein
TGME49_243960	-1.04	#N/A	-1.09	nuclear transport factor 2 (ntf2) domain-containing protein
TGME49_255700	-1.94	-2.36	-2.42	hypothetical protein
TGME49_207180	-8.69	-8.79	-8.43	indole-3-glycerol phosphate synthase domain-containing protein
TGME49_292330	1.20	#N/A	1.16	hypothetical protein
TGME49_208970	-1.83	-1.94	-1.95	RNA recognition motif-containing protein
TGME49_264090	-3.12	-3.49	-3.20	hypothetical protein
TGME49_224020	1.43	1.50	1.43	hypothetical protein
TGME49_293380	-8.69	-8.48	-8.83	histone lysine acetyltransferase HAT1
TGME49_216390	-3.08	-3.12	-2.81	RNA methyltransferase, TrmH family protein
TGME49_249410	-2.51	-2.13	-1.73	hypothetical protein
TGME49_258230	-3.05	#N/A	-2.70	rhoptry kinase family protein ROP20
TGME49_229370	-3.81	-4.00	-4.19	AP2 domain transcription factor AP2VIII-1
TGME49_278440	-1.90	-2.00	-2.07	SWI2/SNF2 Brahma-like putative
TGME49_278930	-2.03	-1.48	-1.65	Tubulin-tyrosine ligase family protein
TGME49_313270	-1.48	-1.51	-1.44	hypothetical protein
TGME49_203358	-3.84	-3.26	-3.49	hypothetical protein
TGME49_252190	2.27	1.94	1.56	KRUF family protein
TGME49_291140	-1.15	-1.02	-1.02	CCR4-Not complex component, Not1 protein

TGME49_305120	#N/A	1.18	#N/A	transporter, solute:sodium symporter (SSS) family protein
TGME49_264240	#N/A	-9.04	-7.39	hypothetical protein
TGME49_205700	#N/A	1.01	#N/A	cyclophilin precursor
TGME49_229630	#N/A	1.02	1.10	eIF2 kinase IF2K-A (incomplete catalytic triad)
TGME49_278830	#N/A	-1.14	-1.79	glucose-6-phosphate 1-dehydrogenase
TGME49_207210	#N/A	2.74	6.79	hypothetical protein
TGME49_295960	#N/A	1.65	1.15	hypothetical protein
TGME49_301440	#N/A	-1.05	-1.17	calcium-dependent protein kinase CDPK1
TGME49_225000	#N/A	-1.48	#N/A	hypothetical protein
TGME49_295030	#N/A	1.07	#N/A	hypothetical protein
TGME49_260190	#N/A	-1.70	#N/A	microneme protein MIC13
TGME49_262050	#N/A	1.21	#N/A	rhoptry kinase family protein ROP39
TGME49_307610	#N/A	-2.05	-1.42	elongation factor TS, putative
TGME49_264740	#N/A	1.01	#N/A	hypothetical protein
TGME49_267420	#N/A	1.12	#N/A	mago nashi family protein 2, putative
TGME49_263750	#N/A	-2.21	-1.31	hypothetical protein
TGME49_298840	#N/A	1.42	1.11	hypothetical protein
TGME49_314070	#N/A	1.40	1.30	hypothetical protein
TGME49_247250	#N/A	-1.57	#N/A	RbAp46
TGME49_306300	#N/A	-1.64	#N/A	hypothetical protein
TGME49_300055	#N/A	1.21	#N/A	hypothetical protein
TGME49_228200	#N/A	1.13	1.16	vacuolar (h+)-atpase g subunit protein
TGME49_263100	#N/A	-2.77	#N/A	hypothetical protein
TGME49_218910	#N/A	2.04	3.84	hypothetical protein
TGME49_215775	#N/A	-1.20	-1.13	rhoptry protein ROP8
TGME49_230350	#N/A	-1.13	-1.27	hypothetical protein
TGME49_257945	#N/A	2.51	4.42	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_233760	#N/A	-2.63	-2.10	hypothetical protein
TGME49_219738	#N/A	-1.76	-1.15	hypothetical protein
TGME49_312530	#N/A	1.09	1.08	splicing factor, CC1 family protein
TGME49_223570	#N/A	1.23	#N/A	hypothetical protein

FIGURE 4CC

TGME49_251885	-8.67	-7.96	-8.45	hypothetical protein
TGME49_296015	1.63	1.78	1.78	hypothetical protein
TGME49_310910	-8.67	-9.25	-8.88	WD domain, G-beta repeat-containing protein
TGME49_249790	-3.81	-3.89	-4.15	hypothetical protein
TGME49_269150	-8.65	-8.38	-8.45	DHHC zinc finger domain-containing protein
TGME49_300250	1.02	#N/A	#N/A	MtN3/saliva family protein
TGME49_216630	-8.62	-8.21	-9.05	trigger factor protein, putative
TGME49_207800	-8.62	-8.11	-8.93	hypothetical protein
TGME49_218240	-1.16	#N/A	#N/A	hypothetical protein
TGME49_227320	-8.71	-8.68	-8.94	hypothetical protein
TGME49_222290	-3.81	-3.78	-4.11	LSM domain-containing protein
TGME49_225060	-2.43	-2.45	-2.83	nucleoredoxin family protein
TGME49_221295	-3.81	-4.08	-4.16	hypothetical protein
TGME49_285950	-8.68	-8.19	-8.09	hypothetical protein
TGME49_245590	2.04	1.89	1.27	rhomboid protease ROM6
TGME49_228130	1.71	1.67	1.68	hypothetical protein
TGME49_251850	-1.68	-1.52	-1.73	serine/threonine protein phosphatase
TGME49_215660	-8.62	-8.35	-8.11	hypothetical protein
TGME49_216170	-3.96	-3.81	-3.66	SufS subfamily cysteine desulfurase
TGME49_229490	-2.69	-2.71	-2.83	tetratricopeptide repeat-containing protein
TGME49_268900	-8.61	-8.63	-8.21	dense granular protein GRA10
TGME49_308060	-2.51	-2.21	-3.13	hypothetical protein
TGME49_305930	2.60	1.51	1.10	hypothetical protein
TGME49_293500	2.16	#N/A	1.06	hypothetical protein
TGME49_310270	-3.88	-4.08	-3.99	hypothetical protein
TGME49_277910	1.20	1.02	1.46	thrombospondin type 1 domain-containing protein
TGME49_289670	2.63	1.85	2.35	DNA repair metallo-beta-lactamase
TGME49_229500	-3.78	-3.82	-3.75	hypothetical protein
TGME49_212840	-8.67	-8.68	-8.08	HIT zinc finger protein
TGME49_294812	-3.81	-2.65	-3.12	RNA recognition motif-containing protein
TGME49_227010	-8.72	-8.64	-8.41	rhoptry kinase family protein ROP30
TGME49_310670	-1.23	-1.17	-1.38	glycogen phosphorylase 1, putative
TGME49_231480	-1.54	-1.68	-1.60	GCN1, putative
TGME49_230950	-8.61	-9.15	-9.09	hypothetical protein

TGME49_225290	#N/A	2.09	3.12	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_315470	#N/A	-1.22	#N/A	hypothetical protein
TGME49_286090	#N/A	1.21	1.08	translation initiation factor SUI1, putative
TGME49_284780	#N/A	-1.22	-1.33	hypothetical protein
TGME49_308810	#N/A	-1.22	-1.91	rhoptry neck protein RON9
TGME49_264190	#N/A	-2.85	-2.55	hypothetical protein
TGME49_219260	#N/A	-1.30	-1.05	cation-transporting ATPase, putative
TGME49_293780	#N/A	1.19	3.35	hypothetical protein
TGME49_280570	#N/A	2.08	6.96	SAG-related sequence SRS35A
TGME49_261570	#N/A	-1.05	-1.13	ribosomal protein RPL7A
TGME49_206320	#N/A	-1.23	#N/A	hypothetical protein
TGME49_255400	#N/A	1.34	1.27	hypothetical protein
TGME49_252640	#N/A	3.47	5.57	P-type ATPase PMA1
TGME49_315720	#N/A	-2.06	#N/A	Smg-4/UPF3 family protein
TGME49_289140	#N/A	1.35	1.10	ribosomal protein l22/l43, putative
TGME49_320750	#N/A	1.34	1.40	hypothetical protein
TGME49_232640	#N/A	1.84	2.93	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_307650	#N/A	-1.55	#N/A	uracil-DNA glycosylase
TGME49_299010	#N/A	2.76	#N/A	hypothetical protein
TGME49_252280	#N/A	-1.75	#N/A	hypothetical protein
TGME49_240220	#N/A	-1.35	#N/A	hypothetical protein
TGME49_211720	#N/A	-1.07	#N/A	AP2 domain transcription factor AP2IV-5
TGME49_253615	#N/A	1.10	1.20	hypothetical protein
TGME49_246020	#N/A	-1.71	-1.58	SprT domain-containing protein
TGME49_253330	#N/A	2.26	#N/A	Rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_214900	#N/A	1.01	1.39	hypothetical protein
TGME49_248830	#N/A	-1.37	#N/A	phosphoinositide phospholipase PIPLC
TGME49_205690	#N/A	1.01	1.07	hypothetical protein
TGME49_318170	#N/A	1.25	1.50	hypothetical protein
TGME49_284645	#N/A	-2.12	-1.55	hypothetical protein
TGME49_218790	#N/A	-3.40	-3.03	elongation factor G C-terminus domain-containing protein
TGME49_293770	#N/A	1.29	#N/A	chitinase-like protein CLP1
TGME49_214520	#N/A	1.30	1.79	general transcription factor IIH polypeptide 4 GTF2H4
TGME49_263820	#N/A	-1.71	#N/A	DEAD/DEAH box helicase domain-containing protein

FIGURE 4DD

TGME49_243298	-8.61	-8.97	-8.88	ICE family protease (caspase) p20 domain-containing protein
TGME49_234190	-1.19	-1.10	-1.51	serine hydroxymethyltransferase 2, putative
TGME49_203060	1.16	1.09	#N/A	hypothetical protein
TGME49_295420	1.41	1.47	1.39	hypothetical protein
TGME49_233340	-2.45	-2.04	-2.23	hypothetical protein
TGME49_210980	1.49	1.58	1.67	alternative splicing type 3 and, putative
TGME49_270050	1.87	1.81	#N/A	hypothetical protein
TGME49_226900	1.66	1.23	1.11	hypothetical protein
TGME49_293730	-1.72	-1.95	-2.04	DHHC zinc finger domain-containing protein
TGME49_270090	-3.06	-3.16	-3.26	hypothetical protein
TGME49_318575	-8.61	-8.32	-8.69	hypothetical protein
TGME49_222940	3.27	1.75	4.65	hypothetical protein
TGME49_316900	-1.89	-1.47	-1.67	Sas10 C-terminal domain-containing protein
TGME49_239720	-8.57	-9.11	-8.71	50S ribosomal protein l24, putative
TGME49_299900	-8.57	-8.72	-8.45	hypothetical protein
TGME49_204380	-1.66	-1.72	-1.45	hypothetical protein
TGME49_263270	-1.32	#N/A	#N/A	glycerophosphodiester phosphodiesterase family protein
TGME49_290890	-2.41	-2.29	-2.85	carbonyl reductase 1, putative
TGME49_310570	-8.66	-8.60	-9.12	hypothetical protein
TGME49_217870	1.24	1.03	#N/A	DHHC zinc finger domain-containing protein
TGME49_306910	-2.21	-1.84	-2.37	hypothetical protein
TGME49_290740	-8.60	-8.14	-8.14	hypothetical protein
TGME49_309100	2.42	2.16	1.77	hypothetical protein
TGME49_223640	-8.67	-8.89	-7.99	hypothetical protein
TGME49_310300	-3.06	-2.61	-2.62	hypothetical protein
TGME49_291030	-3.82	-3.57	-3.67	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_244510	-8.57	-8.46	-7.58	AP2 domain transcription factor AP2VI-3
TGME49_310590	1.88	1.36	1.85	hypothetical protein
TGME49_262980	-8.57	-8.46	-8.65	hypothetical protein
TGME49_249950	-3.06	-2.20	-2.28	Mak16 protein
TGME49_219250	1.08	#N/A	1.12	acetyltransferase, GNAT family protein
TGME49_275310	-3.06	-3.07	-3.07	hypothetical protein
TGME49_285780	-8.61	-8.75	-8.59	hypothetical protein
TGME49_268430	-3.80	-3.45	-3.47	hypothetical protein

TGME49_306390	#N/A	-1.05	-1.62	hypothetical protein
TGME49_277220	#N/A	1.44	1.36	hypothetical protein
TGME49_239600	#N/A	-2.30	#N/A	rhoptry kinase family protein ROP23 (incomplete catalytic triad)
TGME49_311080	#N/A	-1.92	-1.63	transporter, cation channel family protein
TGME49_271770	#N/A	-2.65	-2.03	hypothetical protein
TGME49_221260	#N/A	1.13	1.36	Class-II DAHP synthetase family protein
TGME49_209610	#N/A	1.15	#N/A	oocyst wall protein OWP2
TGME49_311780	#N/A	-1.84	#N/A	Zn-containing alcohol dehydrogenase
TGME49_269885	#N/A	-1.06	-1.18	rhoptry metalloprotease toxolysin TLN1
TGME49_230080	#N/A	-2.25	-2.14	DEAD/DEAH box helicase domain-containing protein
TGME49_320480	#N/A	-1.14	#N/A	Rab11b
TGME49_315760	#N/A	-1.17	#N/A	AP2 domain transcription factor AP2XI-4
TGME49_231380	#N/A	1.20	#N/A	DNA-directed RNA polymerase II RPB4
TGME49_295610	#N/A	-1.14	-1.06	histone lysine methyltransferase, SET, putative
TGME49_222100	#N/A	-1.23	#N/A	hypothetical protein
TGME49_207830	#N/A	1.11	#N/A	MORN repeat-containing protein
TGME49_214940	#N/A	1.07	#N/A	MIC2-associated protein M2AP
TGME49_232980	#N/A	1.64	1.16	hypothetical protein
TGME49_240890	#N/A	-1.06	-1.27	6-phosphofructokinase
TGME49_225310	#N/A	-1.18	-1.30	ARF1-directed GTPase-activating protein, putative
TGME49_320100	#N/A	-1.06	#N/A	RNA recognition motif-containing protein
TGME49_262390	#N/A	-1.58	-1.70	TLD protein
TGME49_202410	#N/A	-1.62	-1.34	hypothetical protein
TGME49_281650	#N/A	-1.66	-1.49	hypothetical protein
TGME49_258350	#N/A	1.36	1.50	hypothetical protein
TGME49_311890	#N/A	-1.06	-1.36	hypothetical protein
TGME49_306540	#N/A	1.22	1.19	phosphotransferase enzyme family protein
TGME49_309190	#N/A	1.05	#N/A	hypothetical protein
TGME49_260520	#N/A	1.24	1.26	hypothetical protein
TGME49_223668	#N/A	1.55	1.96	LYAR-type C2HC zinc finger protein
TGME49_236510	#N/A	1.02	1.16	hypothetical protein
TGME49_241180	#N/A	-1.11	-1.49	hypothetical protein
TGME49_236070	#N/A	1.16	#N/A	pyrroline-5-carboxylate reductase
TGME49_306250	#N/A	1.53	1.16	hypothetical protein

FIGURE 4EE

TGME49_300020	-3.75	-3.85	-3.92	ATP-dependent metallopeptidase HflB subfamily protein
TGME49_313350	-3.75	-3.88	-3.92	hypothetical protein
TGME49_229290	-8.59	-7.86	-7.57	kelch repeat-containing protein
TGME49_258480	-1.88	-2.15	-1.89	hypothetical protein
TGME49_310710	-3.75	-3.67	-3.72	small ribosomal subunit Rsm22 protein
TGME49_230000	1.49	#N/A	#N/A	hypothetical protein
TGME49_295015	1.87	1.43	#N/A	patched family protein
TGME49_272640	-2.08	-1.99	-1.55	eukaryotic initiation factor-2B, epsilon subunit, putative
TGME49_208820	-3.81	-3.36	-4.32	1-deoxy-D-xylulose-5-phosphate synthase
TGME49_222920	-2.21	-1.66	-1.76	mbp-1 interacting protein-2a family protein
TGME49_232160	1.18	1.17	1.33	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_245485	1.89	2.07	2.12	microneme protein MIC9
TGME49_243490	-8.57	-8.38	-8.22	BCS1 family isoform 9, putative
TGME49_249560	-8.58	-8.94	-8.49	DNA-directed RNA polymerase alpha chain rpoA
TGME49_289290	-1.79	-1.62	-1.92	hypothetical protein
TGME49_244000	-8.57	-8.89	-8.53	DEAD/DEAH box helicase domain-containing protein
TGME49_285990	-3.82	-3.59	-3.77	Filamin/ABP280 repeat-containing protein
TGME49_260580	-2.07	-2.25	-2.15	hypothetical protein
TGME49_296340	3.34	4.60	3.29	hypothetical protein
TGME49_256030	-1.17	-1.04	#N/A	hypothetical protein
TGME49_263410	6.14	5.23	4.20	scavenger receptor cysteine-rich domain-containing protein
TGME49_249698	-8.60	-8.18	-8.20	hypothetical protein
TGME49_255740	-3.07	-2.80	-2.80	hypothetical protein
TGME49_235960	-8.56	-7.45	-8.01	hypothetical protein
TGME49_248570	-3.80	-3.88	-3.77	hypothetical protein
TGME49_268220	9.62	#N/A	6.66	hypothetical protein
TGME49_221440	-8.58	-9.14	-8.53	RPGR, putative
TGME49_259850	-8.53	-8.28	-8.38	hypothetical protein
TGME49_240370	6.91	8.07	8.58	Toxoplasma gondii family E protein
TGME49_248150	-3.75	-3.61	-3.97	hypothetical protein
TGME49_243340	-8.53	-8.47	-8.35	atypical MEK-related kinase (incomplete catalytic triad)
TGME49_209130	-8.53	-9.11	-9.35	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_239830	-1.38	#N/A	#N/A	TBC domain-containing protein
TGME49_221585	-8.57	-8.19	-8.53	hypothetical protein

TGME49_212920	#N/A	1.27	1.53	hypothetical protein
TGME49_229450	#N/A	-1.79	-1.76	hypothetical protein
TGME49_301410	#N/A	-1.28	#N/A	hypothetical protein
TGME49_227270	#N/A	2.27	1.71	hypothetical protein
TGME49_308070	#N/A	-1.96	-2.16	hypothetical protein
TGME49_209070	#N/A	1.13	1.56	hypothetical protein
TGME49_255290	#N/A	-2.21	#N/A	hypothetical protein
TGME49_262170	#N/A	-2.13	-1.76	hypothetical protein
TGME49_240580	#N/A	-1.63	#N/A	hypothetical protein
TGME49_251790	#N/A	1.04	1.27	hypothetical protein
TGME49_242790	#N/A	-1.35	-1.81	trichohyalin, putative
TGME49_312480	#N/A	1.13	1.19	uracil phosphoribosyltransferase FUR1, putative
TGME49_226320	#N/A	1.14	1.17	hypothetical protein
TGME49_223130	#N/A	1.41	1.81	hypothetical protein
TGME49_272520	#N/A	-1.18	-1.36	hypothetical protein
TGME49_290000	#N/A	-7.76	-8.91	hypothetical protein
TGME49_264970	#N/A	-1.26	#N/A	hypothetical protein
TGME49_244290	#N/A	-1.20	#N/A	adapter-related protein
TGME49_273580	#N/A	-2.08	-1.81	hypothetical protein
TGME49_244250	#N/A	-1.02	-1.08	hypothetical protein
TGME49_265410	#N/A	1.14	#N/A	G-protein beta WD-40 repeat containing protein
TGME49_304490	#N/A	1.05	#N/A	hypothetical protein
TGME49_209755	#N/A	2.88	6.35	hypothetical protein
TGME49_316760	#N/A	1.37	1.08	hypothetical protein
TGME49_318730	#N/A	-1.21	-1.30	glycosyl transferase
TGME49_258700	#N/A	-1.09	-1.25	transporter, major facilitator family protein
TGME49_280580	#N/A	1.19	4.14	SAG-related sequence SRS35B
TGME49_267590	#N/A	-1.24	-1.10	hypothetical protein
TGME49_266690	#N/A	-1.12	-1.12	hypothetical protein
TGME49_233520	#N/A	-1.13	-1.09	ATP-dependent RNA helicase
TGME49_309610	#N/A	-3.07	-3.05	hypothetical protein
TGME49_237870	#N/A	-3.04	-3.13	FYVE zinc finger domain-containing protein
TGME49_244412	#N/A	-2.38	-1.85	hypothetical protein
TGME49_254915	#N/A	-2.51	#N/A	hypothetical protein

FIGURE 4FF

TGME49_242870	-8.53	-8.42	-9.02	histone lysine methyltransferase, SET, putative
TGME49_227115	-8.53	-8.32	-8.38	hypothetical protein
TGME49_304900	-1.22	#N/A	#N/A	hypothetical protein
TGME49_269130	-8.53	-7.92	-7.97	hypothetical protein
TGME49_228490	-2.63	-2.73	-2.64	hypothetical protein
TGME49_261650	-1.52	-1.11	#N/A	hypothetical protein
TGME49_304470	-3.00	-2.98	-2.80	oxidoreductase, putative
TGME49_283790	-1.57	-1.79	-1.31	protein kinase, putative
TGME49_280720	-8.53	-7.98	-8.46	hypothetical protein
TGME49_212860	1.22	1.11	1.90	hypothetical protein
TGME49_240460	-3.00	-2.50	-2.70	AP2 domain transcription factor AP2VI-1
TGME49_279430	-2.66	-2.90	-2.75	cwf18 pre-mRNA splicing factor protein
TGME49_281510	-3.01	-3.35	-3.11	ribonuclease H1 large subunit, putative
TGME49_213460	2.47	#N/A	#N/A	hypothetical protein
TGME49_239560	-8.60	-8.57	-8.96	myosin E
TGME49_285260	2.21	2.73	2.87	hypothetical protein
TGME49_313360	1.44	1.10	1.20	hypothetical protein
TGME49_247300	1.01	1.39	#N/A	hypothetical protein
TGME49_256840	-3.72	-3.89	-4.47	hypothetical protein
TGME49_259530	-3.72	-3.93	-4.38	GalNac
TGME49_311500	-8.58	-8.99	-8.88	ThiF family protein
TGME49_251840	1.29	1.40	1.67	hypothetical protein
TGME49_250220	2.17	2.42	2.46	hypothetical protein
TGME49_216130	-1.94	-1.93	-2.29	ubiquitin conjugating enzyme E2, putative
TGME49_278130	-2.14	-1.77	-2.05	hypothetical protein
TGME49_293460	-3.75	-3.13	-2.94	ATP-dependent DNA ligase domain-containing protein
TGME49_308990	-3.72	-3.37	-2.98	transporter, solute:sodium symporter (SSS) family protein
TGME49_248790	2.18	2.11	1.96	hypothetical protein
TGME49_227140	2.65	2.29	3.00	hypothetical protein
TGME49_250830	-1.53	-1.24	-1.69	SAC3/GANP family protein
TGME49_305560	-3.72	-3.83	-4.05	Vps51/Vps67 protein
TGME49_300048	1.07	1.38	#N/A	hypothetical protein
TGME49_263290	2.97	2.59	2.69	rhomboid protease ROM2
TGME49_286560	-8.57	-8.68	-8.93	U6 snRNA-associated Sm family protein
TGME49_276900	-3.75	-3.60	-3.11	hypothetical protein

TGME49_300180	#N/A	-3.00	-2.69	hypothetical protein
TGME49_280750	#N/A	1.06	#N/A	rudimentary enhancer, putative
TGME49_222245	#N/A	1.08	#N/A	hypothetical protein
TGME49_293350	#N/A	-1.37	-1.06	mitochondrial carrier superfamily protein
TGME49_261990	#N/A	-1.08	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_278260	#N/A	-2.99	-2.82	polynucleotide adenylyltransferase
TGME49_231100	#N/A	-1.07	-1.00	hypothetical protein
TGME49_225330	#N/A	-1.14	-1.38	hypothetical protein
TGME49_220300	#N/A	-1.53	#N/A	ribosomal protein L15 protein
TGME49_232760	#N/A	1.05	#N/A	protein phosphatase inhibitor IPP2
TGME49_309010	#N/A	1.77	#N/A	elongation factor P, putative
TGME49_295950	#N/A	1.48	1.42	KRUF family protein
TGME49_267760	#N/A	-1.67	-1.87	hypothetical protein
TGME49_249320	#N/A	-1.99	-1.97	flavodoxin domain-containing protein
TGME49_313790	#N/A	1.11	#N/A	hypothetical protein
TGME49_261490	#N/A	-1.03	#N/A	hypothetical protein
TGME49_275420	#N/A	-1.37	-1.12	histone lysine-specific demethylase LSD1/BHC110/KDMA1A
TGME49_262860	#N/A	-2.30	-2.77	ADP-ribosylation factor family protein 1, putative
TGME49_221990	#N/A	-1.01	#N/A	hypothetical protein
TGME49_223600	#N/A	-1.99	-2.00	hypothetical protein
TGME49_262130	#N/A	-1.41	-1.55	hypothetical protein
TGME49_204880	#N/A	-1.82	#N/A	hypothetical protein
TGME49_320720	#N/A	-2.34	-2.05	hypothetical protein
TGME49_223270	#N/A	1.19	1.19	hypothetical protein
TGME49_236840	#N/A	-1.11	-1.26	zinc finger (C-x8-C-x5-C-x3-H)-2, putative
TGME49_240950	#N/A	-3.00	-2.50	hypothetical protein
TGME49_279370	#N/A	-1.05	#N/A	SNARE associated Golgi protein
TGME49_247640	#N/A	1.04	#N/A	hypothetical protein
TGME49_276120	#N/A	-2.46	#N/A	histone lysine methyltransferase, SET, putative
TGME49_231920	#N/A	1.38	1.51	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_200250	#N/A	-1.00	#N/A	microneme protein MIC17A
TGME49_278780	#N/A	-1.37	-1.56	hypothetical protein
TGME49_285830	#N/A	-1.04	#N/A	hypothetical protein
TGME49_264460	#N/A	-2.02	#N/A	DNA-directed RNA polymerase III RPC5
TGME49_305230	#N/A	-2.30	#N/A	hypothetical protein

FIGURE 4GG

TGME49_286800	-8.52	-8.40	-8.64	hypothetical protein
TGME49_274130	-8.48	-8.65	-8.63	TBC domain-containing protein
TGME49_206695	1.84	2.04	2.63	hypothetical protein
TGME49_227350	-3.09	-3.12	-2.22	hypothetical protein
TGME49_209270	-8.57	-8.33	-8.29	hypothetical protein
TGME49_221710	-2.60	-2.51	-2.21	TBC domain-containing protein
TGME49_202750	-8.48	-8.29	-8.29	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_320440	-2.35	-2.81	-1.56	hypothetical protein
TGME49_262550	-6.48	-6.21	-7.88	hypothetical protein
TGME49_268960	-2.98	-3.24	-3.38	5'-AMP-activated protein kinase subunit beta-1 family protein, putative
TGME49_218358	-8.52	-8.28	-8.17	zinc knuckle domain-containing protein
TGME49_262650	-3.77	-3.55	-3.54	WD domain, G-beta repeat-containing protein
TGME49_202010	-2.51	-3.08	-2.20	hypothetical protein
TGME49_319308	-2.63	-1.88	-4.12	hypothetical protein
TGME49_273920	-2.61	-2.42	-2.55	aldose reductase, putative
TGME49_249740	1.50	1.72	1.51	translation machinery associated tma7 protein
TGME49_309130	-8.48	-8.47	-8.17	hypothetical protein
TGME49_297900	1.40	1.69	1.37	hypothetical protein
TGME49_312960	1.26	1.72	1.67	hypothetical protein
TGME49_278240	-8.75	-8.54	#N/A	Zn-finger in Ran binding protein and others domain-containing protein
TGME49_295060	-8.49	-8.17	-7.75	exonuclease
TGME49_248870	1.36	1.25	#N/A	SNARE associated Golgi protein
TGME49_266390	-8.48	-8.00	-8.07	DNA mismatch repair protein, C-terminal domain-containing protein
TGME49_248140	3.21	#N/A	#N/A	hypothetical protein
TGME49_270230	-8.48	-8.80	-8.58	hypothetical protein
TGME49_248160	-8.48	-8.80	-9.03	hypothetical protein
TGME49_219660	3.07	#N/A	3.10	hypothetical protein
TGME49_279540	-8.54	-7.14	-8.72	hypothetical protein
TGME49_221280	-1.56	-1.31	-1.03	hypothetical protein
TGME49_318260	-3.69	-3.49	-3.67	transcription initiation factor TFIID subunit TAF5
TGME49_247700	1.31	1.14	1.32	AP2 domain transcription factor AP2XII-4
TGME49_253410	2.32	1.99	2.32	hypothetical protein
TGME49_250680	-2.58	-2.11	-2.09	TBC domain-containing kinase (incomplete catalytic triad)
TGME49_254390	1.06	#N/A	#N/A	CRAL/TRIO domain-containing protein

TGME49_208990	#N/A	1.21	1.48	hypothetical protein
TGME49_285680	#N/A	1.13	#N/A	dihydrolipoamide acyltransferase, putative
TGME49_214120	#N/A	-2.91	-2.85	hypothetical protein
TGME49_249450	#N/A	-2.89	-2.70	hypothetical protein
TGME49_255245	#N/A	1.40	#N/A	hypothetical protein
TGME49_252250	#N/A	-1.61	#N/A	ATPase, AAA family protein
TGME49_230920	#N/A	-2.86	-2.89	adaptor complexes medium subunit family protein
TGME49_214630	#N/A	-1.37	#N/A	hypothetical protein
TGME49_231815	#N/A	-1.98	#N/A	hypothetical protein
TGME49_315980	#N/A	-1.92	-2.11	EREBP-4 family protein
TGME49_287970	#N/A	-1.02	#N/A	hypothetical protein
TGME49_214170	#N/A	-1.58	-1.46	hypothetical protein
TGME49_270170	#N/A	-1.56	-1.44	hypothetical protein
TGME49_244150	#N/A	-1.93	#N/A	glycerate kinase
TGME49_201380	#N/A	1.15	#N/A	chorismate synthase, putative
TGME49_208360	#N/A	1.14	1.48	hypothetical protein
TGME49_285720	#N/A	-2.21	-1.90	ATP binding protein, putative
TGME49_249160	#N/A	-2.22	#N/A	UAA transporter family protein
TGME49_267440	#N/A	1.14	#N/A	RING zinc finger protein
TGME49_260480	#N/A	-2.84	-3.42	leucine rich repeat-containing protein
TGME49_227440	#N/A	1.02	1.14	WD domain, G-beta repeat-containing protein
TGME49_286030	#N/A	-1.08	#N/A	hypothetical protein
TGME49_278110	#N/A	-1.59	#N/A	1,3-beta-glucan synthase component protein
TGME49_305010	#N/A	-1.73	-1.71	pre-mRNA branch site protein p14, putative
TGME49_230890	#N/A	-1.40	#N/A	PHD-finger domain-containing protein
TGME49_252230	#N/A	-1.16	#N/A	hypothetical protein
TGME49_222300	#N/A	-1.18	#N/A	hypothetical protein
TGME49_234560	#N/A	-1.19	-1.08	hypothetical protein
TGME49_258940	#N/A	1.34	1.21	acylphosphatase family protein
TGME49_239690	#N/A	1.21	#N/A	hypothetical protein
TGME49_225120	#N/A	1.05	#N/A	hypothetical protein
TGME49_314710	#N/A	-1.22	-1.20	carrier superfamily protein
TGME49_209870	#N/A	-1.84	#N/A	HAD hydrolase, family IIA protein
TGME49_278060	#N/A	-1.62	#N/A	Mre11 DNA-binding domain-containing protein

FIGURE 4HH

TGME49_220175	2.95	2.52	2.87	hypothetical protein
TGME49_227910	-1.23	-1.06	-1.72	hypothetical protein
TGME49_203760	1.36	1.63	1.68	hypothetical protein
TGME49_297245	-1.46	-1.42	-1.09	transporter, major facilitator family protein
TGME49_271625	-8.49	-8.19	-8.07	serine--tRNA ligase
TGME49_205300	1.32	1.24	#N/A	hypothetical protein
TGME49_226030	-1.07	#N/A	-1.35	AGC kinase
TGME49_309890	-3.00	-3.19	-2.78	hypothetical protein
TGME49_260510	-2.95	-2.70	-2.86	ubiquitin thioesterase otubain-like family protein
TGME49_300285	-8.57	-8.51	-8.56	hypothetical protein
TGME49_229930	1.35	#N/A	#N/A	p25-alpha family protein
TGME49_248990	1.18	1.70	1.29	hypothetical protein
TGME49_209240	1.56	1.50	1.25	RNA methyltransferase
TGME49_289890	-3.06	-2.45	-2.64	hypothetical protein
TGME49_235478	-3.79	-4.09	-4.14	pantothenate kinase
TGME49_277840	1.13	#N/A	#N/A	Ras family protein
TGME49_270940	-8.50	-8.13	-8.10	hypothetical protein
TGME49_224580	-1.86	-1.73	-1.95	RNA recognition motif-containing protein
TGME49_242118	-8.44	-8.65	-9.98	myosin-light-chain kinase
TGME49_253510	2.42	2.70	2.46	transporter/permease protein
TGME49_220450	-8.43	-8.51	-7.24	ribonuclease HI protein
TGME49_262030	-8.43	-8.59	-7.63	ALG6, ALG8 glycosyltransferase family protein
TGME49_208500	-2.35	-2.69	-2.68	protein phosphatase 2C domain-containing protein
TGME49_243530	-8.44	-8.23	-7.39	pentatricopeptide repeat domain-containing protein
TGME49_316300	-8.44	-8.83	-8.15	ATP-dependent DNA helicase, RecQ family protein
TGME49_227310	-3.69	-3.45	-3.61	hypothetical protein
TGME49_230590	-8.44	-8.41	-8.73	chitobiosyldiphosphodolichol beta-mannosyltransferase
TGME49_309580	-2.95	-2.79	-2.64	transporter, major facilitator family protein
TGME49_213420	-8.43	-7.88	-7.90	RAP domain-containing protein
TGME49_270720	-8.55	-8.74	-8.70	hypothetical protein
TGME49_264870	1.73	1.57	1.55	Sodium:neurotransmitter symporter family protein

TGME49_275740	#N/A	-2.83	-2.66	hypothetical protein
TGME49_304650	#N/A	-1.23	#N/A	histidine acid phosphatase superfamily protein
TGME49_284040	#N/A	-1.33	-1.16	hypothetical protein
TGME49_313970	#N/A	-1.87	-2.25	Phytanoyl-CoA dioxygenase (PhyH) superfamily protein
TGME49_298060	#N/A	-2.00	#N/A	Toxoplasma gondii family C protein
TGME49_249190	#N/A	1.34	1.62	AP2 domain transcription factor AP2XII-6
TGME49_277895	#N/A	-1.39	#N/A	ubiquitin carboxyl-terminal hydrolase
TGME49_236130	#N/A	1.74	1.59	signal recognition particle (SRP9) domain-containing protein
TGME49_273310	#N/A	-1.30	-1.66	hypothetical protein
TGME49_211610	#N/A	1.00	#N/A	hypothetical protein
TGME49_215080	#N/A	-1.29	#N/A	hypothetical protein
TGME49_318320	#N/A	-2.16	-1.88	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP domain-containing protein
TGME49_203030	#N/A	1.10	#N/A	N-methyl-D-aspartate receptor-associated protein
TGME49_234370	#N/A	-2.22	-2.11	SAG-related sequence SRS42
TGME49_240490	#N/A	-2.20	#N/A	hypothetical protein
TGME49_230990	#N/A	1.32	1.09	hypothetical protein
TGME49_204040	#N/A	-2.11	-2.00	hypothetical protein
TGME49_268010	#N/A	-1.26	-1.15	hypothetical protein
TGME49_308030	#N/A	-1.38	-1.36	hypothetical protein
TGME49_263580	#N/A	1.49	1.27	bromodomain-containing protein
TGME49_226980	#N/A	1.29	#N/A	hypothetical protein
TGME49_268560	#N/A	-1.60	#N/A	XPG N-terminal domain-containing protein
TGME49_218610	#N/A	-1.64	-1.51	ATPase (DUF699) protein
TGME49_265080	#N/A	-1.01	#N/A	Tubulin-tyrosine ligase family protein
TGME49_301450	#N/A	-1.00	#N/A	FG-GAP repeat-containing protein
TGME49_233300	#N/A	-2.07	-2.85	RhoGAP domain-containing protein
TGME49_318720	#N/A	1.15	#N/A	pyridoxal phosphate enzyme, YggS family protein
TGME49_320470	#N/A	1.90	1.79	hypothetical protein
TGME49_289010	#N/A	-1.78	#N/A	RNA recognition motif-containing protein
TGME49_225108	#N/A	-1.44	#N/A	SNF7 family protein
TGME49_257780	#N/A	-1.44	-1.56	hypothetical protein

FIGURE 4ii

TGME49_268210	-8.89	-9.53	-8.82	AGC kinase
TGME49_202180	-1.70	-1.32	#N/A	hypothetical protein
TGME49_318525	-1.80	-2.33	-1.61	hypothetical protein
TGME49_260160	3.22	2.71	2.93	hypothetical protein
TGME49_233220	1.38	1.04	#N/A	hypothetical protein
TGME49_285490	-8.43	-9.04	-9.07	helix-hairpin-helix motif domain-containing protein
TGME49_268590	1.07	1.10	#N/A	rhomboid protease ROM4
TGME49_259210	-8.43	-8.66	-8.38	jmjC domain-containing protein C2orf60
TGME49_215210	2.40	2.39	2.76	hypothetical protein
TGME49_234670	1.96	1.80	1.81	actin-like family protein
TGME49_263000	1.16	1.31	1.31	Beige/BEACH domain-containing protein
TGME49_229780	-3.65	-3.83	-4.23	GHMP kinase, N-terminal domain-containing protein
TGME49_316250	1.68	2.06	1.34	hypothetical protein
TGME49_261510	3.43	3.26	3.07	hypothetical protein
TGME49_289180	-8.44	-8.64	-8.35	thioredoxin family redox-active protein, putative
TGME49_213240	-8.45	-8.83	-8.59	hypothetical protein
TGME49_278470	-3.77	-3.38	-3.72	hypothetical protein
TGME49_254910	-2.58	-2.81	-2.61	hypothetical protein
TGME49_309250	-1.73	-1.54	-1.53	hypothetical protein
TGME49_278920	-2.97	-2.72	-3.20	hypothetical protein
TGME49_224660	1.13	1.12	1.20	transcription factor s-ii (tfiis), central domain-containing protein
TGME49_254090	-1.68	-1.39	#N/A	hypothetical protein
TGME49_285650	-1.50	-1.41	#N/A	hypothetical protein
TGME49_285840	1.67	1.36	1.80	RAP domain-containing protein
TGME49_206480	1.17	1.40	#N/A	hypothetical protein
TGME49_232020	-1.94	-1.93	-1.92	hypothetical protein
TGME49_271870	-8.39	-8.47	-8.96	zinc carboxypeptidase superfamily protein
TGME49_317705	-2.02	-1.73	-1.59	enoyl-CoA hydratase/isomerase family protein
TGME49_271350	-8.39	-8.50	-9.10	bifunctional protein FolC subfamily protein
TGME49_204050	1.54	3.19	#N/A	subtilisin SUB1
TGME49_231600	-2.33	-1.91	-2.49	HEAT repeat-containing protein
TGME49_203450	-2.15	-2.25	-2.19	DUF3228 domain-containing protein

TGME49_232730	#N/A	1.04	#N/A	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme
TGME49_300330	#N/A	1.01	1.06	hypothetical protein
TGME49_294902	#N/A	-1.58	#N/A	hypothetical protein
TGME49_264200	#N/A	-1.76	#N/A	hypothetical protein
TGME49_245435	#N/A	1.27	#N/A	hypothetical protein
TGME49_301460	#N/A	1.13	1.27	hypothetical protein
TGME49_206500	#N/A	-2.71	-2.88	hypothetical protein
TGME49_240450	#N/A	1.35	1.81	Maf family protein
TGME49_239580	#N/A	-7.04	-9.11	hypothetical protein
TGME49_217500	#N/A	2.01	#N/A	HMG (high mobility group) box domain-containing protein
TGME49_257500	#N/A	1.30	1.33	hypothetical protein
TGME49_288640	#N/A	1.19	1.49	radical SAM domain-containing protein
TGME49_220260	#N/A	1.22	#N/A	hypothetical protein
TGME49_247240	#N/A	-1.21	-1.96	ubiquitin carboxyl-terminal hydrolase, family 1 protein
TGME49_242240	#N/A	-1.15	-1.32	rhoptry kinase family protein ROP19A
TGME49_227920	#N/A	-1.40	-1.66	hypothetical protein
TGME49_256910	#N/A	1.28	#N/A	hypothetical protein
TGME49_238130	#N/A	-1.23	-1.24	hypothetical protein
TGME49_243310	#N/A	1.37	#N/A	hypothetical protein
TGME49_258550	#N/A	-1.36	#N/A	SAG-related sequence SRS28
TGME49_247370	#N/A	-1.40	#N/A	hypothetical protein
TGME49_295680	#N/A	-1.29	-1.29	periodic tryptophan protein PWP2, putative
TGME49_269760	#N/A	1.16	1.29	'chromo' (CHRromatin Organization MOdifier) domain-containing protein
TGME49_289130	#N/A	-2.02	-1.94	hypothetical protein
TGME49_255320	#N/A	1.18	#N/A	mRNA turnover 4 (MRT4) family protein
TGME49_231625	#N/A	-1.76	#N/A	hypothetical protein
TGME49_206470	#N/A	1.11	#N/A	pyruvate dehydrogenase complex subunit PDH-E3II
TGME49_228010	#N/A	-1.53	#N/A	hypothetical protein
TGME49_256820	#N/A	-1.52	-1.65	zinc finger (CCCH type) motif-containing protein
TGME49_269630	#N/A	1.13	1.47	hypothetical protein
TGME49_243750	#N/A	2.11	2.44	tetratricopeptide repeat-containing protein
TGME49_236990	#N/A	1.16	4.01	beta-ketoacyl synthase, N-terminal domain-containing protein

FIGURE 4JJ

TGME49_272680	-8.39	-8.53	-8.28	hypothetical protein
TGME49_224150	-8.39	-7.83	-8.15	hypothetical protein
TGME49_223510	-8.39	-8.72	-8.57	hypothetical protein
TGME49_311110	-3.62	-3.95	-4.24	Ubiquitin-fold modifier 1 precursor family protein, putative
TGME49_226970	1.16	1.03	#N/A	ribosomal protein RPS11
TGME49_264660	-1.28	#N/A	#N/A	SAG-related sequence SRS44
TGME49_263330	-8.48	-8.17	-8.20	Adaptin ear-binding coat-associated protein 2 (NECAP-2) isoform 2 family protein
TGME49_254290	1.41	1.44	1.66	hypothetical protein
TGME49_267560	2.04	1.64	1.89	folate-binding protein YgfZ protein
TGME49_228320	-8.39	-7.69	-7.90	hypothetical protein
TGME49_246060	-8.46	-8.09	-8.64	DNA-dependent RNA polymerase
TGME49_284010	-3.62	-3.91	-3.01	5'-3' exonuclease, N-terminal resolvase family domain-containing protein
TGME49_270750	-2.18	-2.27	-1.69	hypothetical protein
TGME49_283850	-1.69	-1.75	-1.94	peptidyl-prolyl cis-trans isomerase
TGME49_209460	-8.39	-8.00	-7.97	hypothetical protein
TGME49_240960	2.32	2.00	1.75	AIG2 family protein
TGME49_234520	-2.31	-1.54	-2.17	U2 snRNP auxilliary factor, large subunit, splicing factor subfamily protein
TGME49_216850	-8.38	-7.64	-8.06	hypothetical protein
TGME49_261000	-1.53	-1.56	-1.53	MutS domain V domain-containing protein
TGME49_284170	-8.39	-8.22	-8.25	DHHC zinc finger domain-containing protein
TGME49_293840	1.34	1.05	#N/A	hypothetical protein
TGME49_221370	-3.61	-3.47	-3.01	hypothetical protein
TGME49_228340	-8.39	-8.49	-8.07	hypothetical protein
TGME49_275670	-1.17	-1.25	#N/A	alveolin domain containing intermediate filament IMC15
TGME49_318480	-2.29	-2.48	-2.01	SWI2/SNF2-containing protein RAD5
TGME49_246030	-8.38	-8.35	-8.28	mediator complex subunit MED17
TGME49_268870	-1.28	-1.11	-1.08	tetratricopeptide repeat-containing protein
TGME49_281990	1.60	1.70	1.70	Nicotinamidase
TGME49_264880	-2.29	-2.19	-2.05	NEDD8-activating enzyme E1 catalytic subunit
TGME49_288800	3.01	3.24	2.81	endonuclease/exonuclease/phosphatase family protein
TGME49_246190	-2.53	-2.68	-2.48	hypothetical protein
TGME49_312500	-1.52	-1.57	-1.71	hypothetical protein

TGME49_218000	#N/A	-1.71	-1.61	hypothetical protein
TGME49_305460	#N/A	1.60	#N/A	methionine aminopeptidase 2, putative
TGME49_217951	#N/A	-1.28	8.04	hypothetical protein
TGME49_267970	#N/A	-1.22	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_215100	#N/A	-1.38	#N/A	PP-loop family protein
TGME49_219218	#N/A	-1.31	#N/A	hypothetical protein
TGME49_216440	#N/A	2.43	#N/A	OTU family cysteine protease
TGME49_238510	#N/A	-1.71	-2.21	hypothetical protein
TGME49_275840	#N/A	-1.96	#N/A	protein phosphatase 2C domain-containing protein
TGME49_267460	#N/A	-1.97	-2.04	AP2 domain transcription factor AP2IX-1
TGME49_222430	#N/A	-1.27	-1.21	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_211730	#N/A	-1.55	#N/A	histone lysine methyltransferase SET8
TGME49_214740	#N/A	-1.09	#N/A	hypothetical protein
TGME49_253070	#N/A	-2.03	#N/A	hydrolase, TatD family protein
TGME49_289340	#N/A	1.80	#N/A	hypothetical protein
TGME49_233245	#N/A	-1.96	-2.09	hypothetical protein
TGME49_220480	#N/A	-2.53	-2.94	hypothetical protein
TGME49_297080	#N/A	-1.48	#N/A	pyridoxal kinase
TGME49_288700	#N/A	-1.11	-1.33	RecF/RecN/SMC N terminal domain-containing protein
TGME49_271610	#N/A	-1.05	#N/A	pyrroline-5-carboxylate reductase
TGME49_226240	#N/A	1.13	#N/A	bud site selection protein, putative
TGME49_231280	#N/A	1.09	#N/A	WD domain, G-beta repeat-containing protein
TGME49_267450	#N/A	-1.01	-1.07	alpha-tubulin suppressor protein
TGME49_268240	#N/A	1.24	1.64	hypothetical protein
TGME49_228110	#N/A	-1.24	#N/A	hypothetical protein
TGME49_226068	#N/A	-1.02	#N/A	DnaJ domain-containing protein
TGME49_217900	#N/A	-1.14	-1.50	hypothetical protein
TGME49_257390	#N/A	-1.97	#N/A	ribosome biogenesis GTP-binding protein YsxC protein
TGME49_248770	#N/A	-1.51	#N/A	hypothetical protein
TGME49_216700	#N/A	-2.50	-3.00	hypothetical protein
TGME49_273130	#N/A	1.43	1.66	SAG-related sequence SRS30A
TGME49_273720	#N/A	-1.15	#N/A	hypothetical protein

FIGURE 4KK

TGME49_208340	-1.20	#N/A	#N/A	hypothetical protein
TGME49_262950	1.01	1.23	1.05	hypothetical protein
TGME49_220870	1.62	1.88	1.59	hypothetical protein
TGME49_221610	-2.13	-2.20	-1.91	ubiquitin carboxyl-terminal hydrolase
TGME49_211600	-2.28	-2.40	-2.09	hypothetical protein
TGME49_268720	-2.91	-2.96	-2.88	Hrf1 family protein
TGME49_312190	-1.68	-1.66	-2.11	hypothetical protein
TGME49_300270	1.12	1.23	#N/A	hypothetical protein
TGME49_248740	1.35	1.20	#N/A	hypothetical protein
TGME49_275990	1.20	1.31	1.41	hypothetical protein
TGME49_217050	1.16	1.06	#N/A	ADA2-A transcriptional co-activator SAGA component
TGME49_221690	-3.61	-3.74	-3.80	hypothetical protein
TGME49_224950	-1.17	#N/A	#N/A	calcium-dependent protein kinase CDPK5
TGME49_321590	-1.34	#N/A	-1.41	hypothetical protein
TGME49_316230	-2.26	-2.08	-2.47	SAC1 phosphoinositide phosphatase, putative
TGME49_248640	-1.33	-1.23	-1.50	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_243290	-2.10	-1.78	-2.13	hypothetical protein
TGME49_225470	1.25	1.29	1.35	peptide methionine sulfoxide reductase
TGME49_275980	-3.58	-3.59	-3.79	coenzyme q (ubiquinone) biosynthesis protein coq4 protein
TGME49_286140	-2.10	-1.35	-1.68	hypothetical protein
TGME49_294390	-8.33	-8.18	-8.48	myosin light chain MLC4, putative
TGME49_237480	-3.58	-3.84	-3.95	BRCA1 C Terminus (BRCT) domain-containing protein
TGME49_310520	-3.61	-3.49	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_244670	-1.56	-1.63	-1.41	hypothetical protein
TGME49_233860	-8.40	-8.46	-7.90	DALR anticodon binding domain-containing protein
TGME49_307020	-1.89	-1.40	-1.40	hypothetical protein
TGME49_239620	-3.58	-3.81	-4.01	5'-nucleotidase, C-terminal domain-containing protein
TGME49_310360	-1.39	-1.33	-1.82	hypothetical protein
TGME49_278960	-1.75	-1.71	-1.55	hypothetical protein
TGME49_312340	-8.33	-8.15	-8.46	hypothetical protein
TGME49_209960	-1.70	-1.69	-2.20	glycosyltransferase
TGME49_310380	-8.34	-8.38	-8.50	brix domain containing protein
TGME49_318590	-8.37	-7.96	-8.02	MRP family domain-containing protein

TGME49_231220	#N/A	-1.93	-2.14	hypothetical protein
TGME49_218840	#N/A	-1.23	#N/A	mutS domain protein
TGME49_283585	#N/A	1.23	#N/A	hypothetical protein
TGME49_249770	#N/A	1.47	#N/A	Nmda1 protein
TGME49_229350	#N/A	-1.24	-1.98	HEAT repeat-containing protein
TGME49_291120	#N/A	-1.23	-1.24	trafficking protein mon1 subfamily protein
TGME49_239070	#N/A	-1.47	-1.63	hypothetical protein
TGME49_287220	#N/A	1.78	1.87	hypothetical protein
TGME49_258826	#N/A	-1.74	#N/A	hypothetical protein
TGME49_268290	#N/A	-2.00	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_219230	#N/A	-1.11	-1.11	AMP-binding enzyme domain-containing protein
TGME49_255660	#N/A	-1.14	-1.64	EF hand domain-containing protein
TGME49_232310	#N/A	-1.63	-1.73	endonuclease/exonuclease/phosphatase family protein
TGME49_277680	#N/A	-1.13	-1.63	hypothetical protein
TGME49_270070	#N/A	2.20	#N/A	synaptobrevin family protein
TGME49_210440	#N/A	1.04	1.04	polynucleotide adenylyltransferase
TGME49_270300	#N/A	1.54	#N/A	hypothetical protein
TGME49_232590	#N/A	1.28	1.37	glutamate-cysteine ligase, catalytic subunit domain-containing protein
TGME49_230140	#N/A	-1.13	#N/A	vacuolar sorting protein 9 (vps9) domain-containing protein
TGME49_294420	#N/A	-1.89	-1.86	programmed cell death protein 2, c-terminal domain-containing protein
TGME49_249550	#N/A	-1.14	#N/A	hypothetical protein
TGME49_319600	#N/A	-1.17	#N/A	alpha-tubulin N-acetyltransferase, putative
TGME49_262700	#N/A	1.19	1.22	tetratricopeptide repeat-containing protein
TGME49_306590	#N/A	1.35	1.47	hypothetical protein
TGME49_205550	#N/A	-1.43	-1.54	AGC kinase
TGME49_217340	#N/A	-1.15	-1.32	hypothetical protein
TGME49_200460	#N/A	1.18	1.17	hypothetical protein
TGME49_264670	#N/A	-1.01	-1.16	DNA polymerase family B protein
TGME49_316490	#N/A	1.24	#N/A	hypothetical protein
TGME49_313530	#N/A	-1.06	-1.22	transmembrane protein 167, putative
TGME49_231870	#N/A	-1.60	-1.59	tetratricopeptide repeat-containing protein
TGME49_208850	#N/A	-1.13	#N/A	SAG-related sequence SRS11
TGME49_314390	#N/A	-1.19	-1.37	hypothetical protein

FIGURE 4LL

TGME49_201120	-1.68	-1.57	-1.34	ELMO/CED-12 family protein
TGME49_203840	1.45	1.53	1.84	DEAD/DEAH box helicase domain-containing protein
TGME49_264960	-8.34	-8.46	-8.59	hypothetical protein
TGME49_218820	-1.40	-1.39	-1.92	alba 2
TGME49_239080	-8.34	-8.07	-7.62	carrier superfamily protein
TGME49_239710	-8.33	-8.40	-8.73	phosphomannomutase
TGME49_244110	-1.27	-1.41	-1.59	nucleosome assembly protein (nap) protein
TGME49_258680	-2.07	-1.83	-2.11	TATA-box binding protein TBP2
TGME49_227390	-2.88	-2.55	-2.14	hypothetical protein
TGME49_240660	-8.35	-8.19	-8.05	hypothetical protein
TGME49_290340	-2.30	-1.97	-2.42	HEAT repeat-containing protein
TGME49_259830	1.56	1.66	1.49	diacylglycerol kinase catalytic domain-containing protein
TGME49_261600	1.04	1.15	1.08	creatinase domain-containing protein
TGME49_306330	-1.93	-2.15	-2.75	phospholipase
TGME49_224900	-1.16	#N/A	-1.32	adenylate kinase, putative
TGME49_246530	-3.69	-3.12	-3.15	phospholipase D active site domain-containing protein
TGME49_230010	-1.93	-1.43	-1.88	hypothetical protein
TGME49_203970	-2.86	-2.59	-2.35	dolichyl-diphosphooligosaccharide--protein glycosyltransferase
TGME49_283810	-3.59	-3.03	-3.72	hypothetical protein
TGME49_297890	1.20	1.72	1.19	hypothetical protein
TGME49_300260	-1.04	#N/A	-1.11	threonyl-tRNA synthetase family protein
TGME49_255940	1.68	1.79	2.44	hypothetical protein
TGME49_294720	-2.56	-2.34	-2.11	hypothetical protein
TGME49_260650	-3.58	-3.62	-3.12	glycosyltransferase, group 2 family protein
TGME49_257290	-8.36	-10.23	-8.16	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_316570	1.04	1.05	#N/A	hypothetical protein
TGME49_238170	1.36	1.05	1.11	hypothetical protein
TGME49_224235	-8.28	-8.78	-8.25	translation initiation factor IF-3 protein
TGME49_224230	2.04	1.50	1.97	AP2 domain transcription factor AP2X-3
TGME49_242260	1.48	1.15	#N/A	hypothetical protein
TGME49_299050	1.17	1.05	#N/A	ribosomal protein RPL17
TGME49_315500	-1.60	-1.24	-1.57	hypothetical protein
TGME49_206390	-8.28	-8.38	-8.25	hypothetical protein

TGME49_205250	#N/A	#N/A	11.29	rhoptry protein ROP18
TGME49_214080	#N/A	#N/A	6.66	toxofilin
TGME49_319350	#N/A	#N/A	-1.78	SAG-related sequence SRS17B
TGME49_226100	#N/A	#N/A	6.20	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_320190	#N/A	#N/A	8.02	SAG-related sequence SRS16B
TGME49_270510	#N/A	#N/A	-1.78	asparaginyl-tRNA synthetase (NOB+tRNA synthase)
TGME49_245432	#N/A	#N/A	2.68	hypothetical protein
TGME49_289170	#N/A	#N/A	4.85	adenylate and guanylate cyclase catalytic domain-containing protein
TGME49_212250	#N/A	#N/A	2.42	XPG N-terminal domain-containing protein
TGME49_255210	#N/A	#N/A	3.10	ATPase, AAA family protein
TGME49_315320	#N/A	#N/A	-1.69	SAG-related sequence SRS52A
TGME49_253790	#N/A	#N/A	1.73	zinc finger (CCCH type) motif-containing protein
TGME49_320180	#N/A	#N/A	5.44	SAG-related sequence SRS16C
TGME49_279100	#N/A	#N/A	1.23	hypothetical protein
TGME49_203600	#N/A	#N/A	-1.53	hypothetical protein
TGME49_257530	#N/A	#N/A	-2.22	transporter, major facilitator family protein
TGME49_297880	#N/A	#N/A	-2.17	dense granule protein DG32
TGME49_217890	#N/A	#N/A	-1.40	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen, putative
TGME49_237560	#N/A	#N/A	-1.20	iron-sulfur cluster protein ISCU
TGME49_307830	#N/A	#N/A	-1.52	hypothetical protein
TGME49_213050	#N/A	#N/A	2.16	hypothetical protein
TGME49_308950	#N/A	#N/A	1.10	histidine acid phosphatase superfamily protein
TGME49_224460	#N/A	#N/A	-2.12	aminopeptidase n, putative
TGME49_313440	#N/A	#N/A	4.64	hypothetical protein
TGME49_254840	#N/A	#N/A	-3.32	tetratricopeptide repeat-containing protein
TGME49_320630	#N/A	#N/A	-1.44	phosphotransferase enzyme family protein
TGME49_262630	#N/A	#N/A	3.44	hypothetical protein
TGME49_257750	#N/A	#N/A	-2.12	homocysteine s-methyltransferase domain-containing protein
TGME49_323320	#N/A	#N/A	-3.55	hypothetical protein
TGME49_315750	#N/A	#N/A	-1.69	hypothetical protein
TGME49_258580	#N/A	#N/A	-1.04	rhoptry protein ROP17
TGME49_253880	#N/A	#N/A	1.18	GNS1/SUR4 family protein
TGME49_227380	#N/A	#N/A	1.17	hypothetical protein

FIGURE 4MM

TGME49_248880	-1.20	#N/A	-1.41	GTPase RAB7
TGME49_261710	-1.64	-1.46	-1.75	ankyrin repeat-containing protein
TGME49_294430	-3.54	-3.16	-3.04	hypothetical protein
TGME49_252070	1.65	2.10	10.19	KRUF family protein
TGME49_230500	-3.54	-3.42	-3.30	hypothetical protein
TGME49_293330	-8.28	-8.34	-8.42	hypothetical protein
TGME49_217350	-8.29	-8.53	-9.07	methyltransferase MTA70, putative
TGME49_216500	-3.54	-3.88	-4.05	tRNA synthetase, putative
TGME49_212725	-2.49	-2.24	-1.90	hypothetical protein
TGME49_238000	-3.58	-3.00	-3.04	peptidyl-prolyl isomerase
TGME49_236800	-8.29	-8.28	-8.45	hypothetical protein
TGME49_215550	-2.55	-1.97	-2.32	hypothetical protein
TGME49_294050	1.60	1.76	1.52	hypothetical protein
TGME49_258180	-8.34	-8.18	-7.91	hypothetical protein
TGME49_246160	2.25	2.31	2.70	hypothetical protein
TGME49_288260	-1.61	-1.37	-1.70	hypothetical protein
TGME49_254380	-8.29	-8.44	-8.45	ribosomal protein L11, putative
TGME49_221950	-1.47	-1.13	-1.25	splicesome-associated protein, putative
TGME49_257370	2.21	1.96	2.16	hypothetical protein
TGME49_205160	1.94	1.40	1.90	hypothetical protein
TGME49_307980	2.27	1.51	1.94	GTP-binding protein lepA, putative
TGME49_216870	-2.22	-1.78	-1.78	DNA excision repair helicase
TGME49_235140	1.74	#N/A	#N/A	hypothetical protein
TGME49_216930	-1.60	-1.62	-1.54	cholinephosphate cytidylyltransferase
TGME49_313385	1.96	1.47	1.79	hypothetical protein
TGME49_264650	-8.32	-8.61	-7.56	phosphoacetylglucosamine mutase
TGME49_232780	-2.50	-3.16	-2.87	hypothetical protein
TGME49_297150	-1.30	-1.07	-1.20	MORN repeat-containing protein
TGME49_306030	-1.53	-1.69	-1.89	glutathione s-transferase, n-terminal domain containing protein
TGME49_216920	-2.52	-1.80	-1.94	mediator complex subunit MED8
TGME49_313418	-8.32	-8.06	-8.87	hypothetical protein
TGME49_226330	-8.28	-8.33	-7.92	hypothetical protein
TGME49_233890	-2.25	-1.95	-2.17	hypothetical protein
TGME49_312905	1.94	-1.52	2.29	hypothetical protein
TGME49_294380	-2.83	-2.19	-2.32	PP-loop domain-containing protein

TGME49_207370	#N/A	#N/A	1.01	hypothetical protein
TGME49_201820	#N/A	#N/A	1.51	hypothetical protein
TGME49_229480	#N/A	#N/A	-1.02	calcium binding protein precursor, putative
TGME49_231160	#N/A	#N/A	-1.01	hypothetical protein
TGME49_269980	#N/A	#N/A	-1.07	preprotein translocase Sec61, putative
TGME49_207620	#N/A	#N/A	-1.28	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_241880	#N/A	#N/A	-1.35	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_269420	#N/A	#N/A	1.21	hypothetical protein
TGME49_262640	#N/A	#N/A	-1.53	Cg8 family protein
TGME49_253440	#N/A	#N/A	1.08	cell-cycle-associated protein kinase SRPK, putative
TGME49_238970	#N/A	#N/A	-9.70	hypothetical protein
TGME49_282190	#N/A	#N/A	-1.51	hydrolase, NUDIX family protein
TGME49_290660	#N/A	#N/A	-1.01	RNA recognition motif-containing protein
TGME49_227580	#N/A	#N/A	-1.59	transmembrane amino acid transporter protein
TGME49_285510	#N/A	#N/A	-1.44	hypothetical protein
TGME49_249180	#N/A	#N/A	-1.22	bifunctional dihydrofolate reductase-thymidylate synthase
TGME49_268790	#N/A	#N/A	1.03	hypothetical protein
TGME49_309930	#N/A	#N/A	1.37	melibiase subfamily protein
TGME49_308010	#N/A	#N/A	1.53	hypothetical protein
TGME49_314400	#N/A	#N/A	-1.11	pyruvate dehydrogenase E1 component, beta subunit, putative
TGME49_286928	#N/A	#N/A	-2.53	hypothetical protein
TGME49_260260	#N/A	#N/A	-1.04	ribosomal protein RPP1
TGME49_214290	#N/A	#N/A	-1.17	DJ-1 family protein
TGME49_313180	#N/A	#N/A	-1.09	cell-cycle-associated protein kinase PRP4, putative
TGME49_308020	#N/A	#N/A	-1.24	SAG-related sequence SRS57
TGME49_233030	#N/A	#N/A	-1.11	gliding-associated protein GAP70
TGME49_216620	#N/A	#N/A	-1.15	EF hand domain-containing protein
TGME49_209260	#N/A	#N/A	-1.17	cytochrome c oxidase subunit, putative
TGME49_267070	#N/A	#N/A	1.24	aquaporin 2
TGME49_267680	#N/A	#N/A	-1.27	microneme protein MIC12
TGME49_271790	#N/A	#N/A	1.67	hypothetical protein
TGME49_247550	#N/A	#N/A	-1.04	heat shock protein HSP60
TGME49_215610	#N/A	#N/A	-1.93	hypothetical protein
TGME49_254160	#N/A	#N/A	-3.79	hypothetical protein
TGME49_278660	#N/A	#N/A	-1.24	P-type ATPase4, putative

FIGURE 4NN

TGME49_273030	-2.83	-3.34	-2.31	phosphoglycerate mutase family protein
TGME49_311090	-1.28	-1.25	-1.64	ubiquitin carboxyl-terminal hydrolase
TGME49_285980	1.02	1.15	#N/A	glucosephosphate-mutase GPM1
TGME49_271110	-3.54	-3.33	-2.96	hypothetical protein
TGME49_309800	-1.53	-1.21	-1.60	RNA recognition motif-containing protein
TGME49_264720	-3.51	-3.91	-3.61	hypothetical protein
TGME49_312430	1.36	1.71	1.25	hypothetical protein
TGME49_277070	1.47	1.30	1.37	SWI2/SNF2-containing protein
TGME49_271860	-8.31	-8.37	-7.92	tRNA (Uracil-5-)-methyltransferase
TGME49_226740	1.27	1.36	1.06	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_281570	-3.51	-3.93	-3.77	hypothetical protein
TGME49_203180	-3.51	-4.41	-3.69	leucine rich repeat-containing protein
TGME49_306410	-3.51	-3.96	-4.00	hypothetical protein
TGME49_221580	-1.28	-1.57	-1.50	ribosomal RNA large subunit methyltransferase J protein
TGME49_294740	-1.91	-2.10	-2.06	hypothetical protein
TGME49_257340	-8.23	-8.55	-8.65	Ras family protein
TGME49_305850	-1.04	#N/A	-1.10	RNA recognition motif-containing protein
TGME49_211090	-1.51	#N/A	-1.06	aminotransferase, class V superfamily protein
TGME49_266100	1.08	1.05	1.28	rhoptry kinase family protein ROP41
TGME49_306560	-2.91	-2.99	-3.30	hypothetical protein
TGME49_217750	-3.51	-3.64	-3.69	hypothetical protein
TGME49_301130	-8.23	-8.11	-8.47	hypothetical protein
TGME49_226560	-3.51	-3.45	-3.67	zinc finger (CCCH type) motif-containing protein
TGME49_306210	-8.34	-8.28	-8.50	RNA polymerase II accessory factor CDC73
TGME49_202630	-1.21	-1.16	-1.38	ATP-dependent metallopeptidase HflB subfamily protein
TGME49_289190	-8.23	-8.32	-7.82	tetratricopeptide repeat-containing protein
TGME49_313140	1.42	1.34	#N/A	isocitrate dehydrogenase
TGME49_213115	-8.23	-7.52	-8.68	hypothetical protein
TGME49_282140	1.28	#N/A	#N/A	cwf21 protein
TGME49_264040	-1.11	#N/A	-1.19	hypothetical protein
TGME49_208780	-2.45	-2.72	-3.00	ubiquitin-conjugating enzyme subfamily protein
TGME49_272670	-8.23	-8.33	-8.28	peptidase family M3 protein
TGME49_238180	-1.10	#N/A	-1.04	26s proteasome regulatory complex subunit, putative

TGME49_253160	#N/A	#N/A	1.30	hypothetical protein
TGME49_236210	#N/A	#N/A	-1.08	peptidase M16 family potein, putative
TGME49_235150	#N/A	#N/A	-1.01	transporter, major facilitator family protein
TGME49_310490	#N/A	#N/A	-1.20	ribosomal protein RPL27A
TGME49_266900	#N/A	#N/A	1.49	cyclin, N-terminal domain-containing protein
TGME49_305330	#N/A	#N/A	-1.02	cyclin, N-terminal domain-containing protein
TGME49_222370	#N/A	#N/A	1.49	SAG-related sequence SRS13
TGME49_209030	#N/A	#N/A	-1.03	actin ACT1
TGME49_226072	#N/A	#N/A	-1.13	Ser/Thr phosphatase family protein
TGME49_224935	#N/A	#N/A	1.43	hypothetical protein
TGME49_269390	#N/A	#N/A	1.20	CRAL/TRIO domain-containing protein
TGME49_311470	#N/A	#N/A	-1.07	rhoptry neck protein RON5
TGME49_289680	#N/A	#N/A	-1.06	Ras-related protein Rab11
TGME49_211340	#N/A	#N/A	1.29	hypothetical protein
TGME49_321410	#N/A	#N/A	1.14	hypothetical protein
TGME49_256000	#N/A	#N/A	-1.01	endoplasmic reticulum retention receptor
TGME49_224110	#N/A	#N/A	-1.33	adhesion regulating molecule region protein, putative
TGME49_308093	#N/A	#N/A	1.13	rhoptry kinase family protein (incomplete catalytic triad)
TGME49_314660	#N/A	#N/A	-1.38	TPRX1 protein
TGME49_213480	#N/A	#N/A	-2.18	hypothetical protein
TGME49_208710	#N/A	#N/A	1.64	DNA/RNA non-specific endonuclease
TGME49_250880	#N/A	#N/A	-1.64	kinase, pfkB family protein
TGME49_231640	#N/A	#N/A	-1.24	alveolin domain containing intermediate filament IMC1
TGME49_233130	#N/A	#N/A	1.32	nucleoside transporter protein
TGME49_306430	#N/A	#N/A	-1.32	hypothetical protein
TGME49_248700	#N/A	#N/A	-1.40	alveolin domain containing intermediate filament IMC12
TGME49_277760	#N/A	#N/A	-1.28	adenylosuccinate lyase, putative
TGME49_255635	#N/A	#N/A	-3.63	hypothetical protein
TGME49_289920	#N/A	#N/A	1.18	hypothetical protein
TGME49_209160	#N/A	#N/A	-1.05	myristoyl CoA:protein N-myristoyltransferase
TGME49_306350	#N/A	#N/A	1.06	variable surface lipoprotein
TGME49_260400	#N/A	#N/A	1.33	hypothetical protein
TGME49_249780	#N/A	#N/A	-1.23	hypothetical protein

FIGURE 4oo

TGME49_233490	-8.29	-8.54	-8.38	hypothetical protein
TGME49_233790	-8.22	-8.60	-8.77	serine/threonine protein kinase AktR, putative
TGME49_293280	1.31	#N/A	2.97	cyclin protein
TGME49_286230	1.29	#N/A	#N/A	hypothetical protein
TGME49_310320	-3.51	-3.68	-3.88	calreticulin family protein
TGME49_252870	1.95	1.89	2.35	hypothetical protein
TGME49_237290	-1.40	-1.58	-1.30	hypothetical protein
TGME49_268620	-8.23	-8.00	-7.69	blood stage antigen 41-3 precursor, putative
TGME49_221640	2.25	1.86	1.56	hypothetical protein
TGME49_213880	2.50	2.67	2.68	hypothetical protein
TGME49_309160	-2.03	-1.94	-2.28	IgA-specific metalloendopeptidase
TGME49_260450	-8.23	-8.80	-8.14	DEAD/DEAH box helicase domain-containing protein
TGME49_248850	-8.24	-8.35	-8.91	methionine aminopeptidase
TGME49_254800	1.72	1.78	1.43	hypothetical protein
TGME49_300380	-2.80	-2.99	-2.52	endoplasmic reticulum oxidoreductin, putative
TGME49_276170	1.39	1.53	1.24	phosphatidylinositol 3- and 4-kinase
TGME49_307040	-1.48	-1.31	-1.59	shikimate dehydrogenase substrate binding domain-containing protein
TGME49_265850	1.90	1.76	1.78	hypothetical protein
TGME49_269290	-2.43	-2.87	-3.04	hypothetical protein
TGME49_318610	1.60	1.10	3.56	AP2 domain transcription factor AP2IV-3
TGME49_235460	1.27	1.27	1.19	hypothetical protein
TGME49_311250	-2.87	-3.38	-3.17	hypothetical protein
TGME49_202680	-1.26	-1.16	-1.56	peptidase M16, alpha subunit, putative
TGME49_234220	-1.87	-2.06	-1.77	hypothetical protein
TGME49_215920	1.79	1.80	1.30	hypothetical protein
TGME49_244470	-1.14	-1.10	#N/A	hypothetical protein
TGME49_244660	-3.51	-3.10	-3.40	hypothetical protein
TGME49_252320	-8.22	-8.67	-7.92	Sas10/Utp3/C1D family protein
TGME49_270060	-2.22	-1.85	-1.61	hypothetical protein
TGME49_262500	-1.42	-1.33	-1.65	hypothetical protein
TGME49_315700	-2.80	-2.75	-3.13	hypothetical protein
TGME49_316540	-1.15	#N/A	#N/A	IMC sub-compartment protein ISP3
TGME49_214870	1.67	1.93	1.97	ribosomal protein L9, N-terminal domain-containing protein

TGME49_258060	#N/A	#N/A	-1.13	myosin heavy chain, putative
TGME49_240810	#N/A	#N/A	-1.07	hypothetical protein
TGME49_234410	#N/A	#N/A	-1.04	transporter, small conductance mechanosensitive ion channel (MscS) family protein
TGME49_212970	#N/A	#N/A	3.81	protein kinase (incomplete catalytic triad)
TGME49_320260	#N/A	#N/A	1.68	hypothetical protein
TGME49_315930	#N/A	#N/A	-1.08	integral membrane protein, DUF56 family protein, putative
TGME49_295340	#N/A	#N/A	-1.12	UV excision repair protein Rad23 protein
TGME49_201220	#N/A	#N/A	-1.90	zinc finger protein
TGME49_224170	#N/A	#N/A	1.95	SAG-related sequence SRS60A
TGME49_281500	#N/A	#N/A	1.89	hypothetical protein
TGME49_235970	#N/A	#N/A	-1.02	eukaryotic initiation factor-2 gamma, putative
TGME49_206640	#N/A	#N/A	1.11	hypothetical protein
TGME49_304670	#N/A	#N/A	-1.33	leucine rich repeat-containing protein
TGME49_258980	#N/A	#N/A	-2.00	hypothetical protein
TGME49_288720	#N/A	#N/A	-1.43	ribosomal protein RPL10
TGME49_209150	#N/A	#N/A	-1.16	non-proton pumping type-II NADH dehydrogenase I
TGME49_283820	#N/A	#N/A	1.31	glycine cleavage T-protein (aminomethyl transferase) domain-containing protein
TGME49_216910	#N/A	#N/A	1.30	hypothetical protein
TGME49_286480	#N/A	#N/A	1.10	hypothetical protein
TGME49_244440	#N/A	#N/A	-1.06	nucleoside transporter protein
TGME49_293650	#N/A	#N/A	1.82	hypothetical protein
TGME49_314295	#N/A	#N/A	-3.23	ribosomal l25 family protein
TGME49_235730	#N/A	#N/A	1.57	hypothetical protein
TGME49_281630	#N/A	#N/A	-1.30	hydroxyacylglutathione hydrolase
TGME49_290990	#N/A	#N/A	1.02	HEAT repeat-containing protein
TGME49_212200	#N/A	#N/A	1.28	hypothetical protein
TGME49_275470	#N/A	#N/A	1.49	dense granule protein GRA15
TGME49_254890	#N/A	#N/A	1.60	hypothetical protein
TGME49_226790	#N/A	#N/A	1.95	ABC transporter, ATP-binding domain-containing protein
TGME49_201670	#N/A	#N/A	1.33	DnaJ domain-containing protein
TGME49_210840	#N/A	#N/A	-1.09	arginyl-tRNA synthetase family protein
TGME49_220520	#N/A	#N/A	1.04	hypothetical protein
TGME49_281920	#N/A	#N/A	-1.32	V-type ATPase, D subunit protein

FIGURE 4PP

TGME49_258030	-1.82	-1.31	#N/A	DNA polymerase
TGME49_253700	1.04	1.05	#N/A	transporter, major facilitator family protein
TGME49_251670	-3.47	-3.69	-3.72	wemer helicase interacting protein 1, putative
TGME49_313860	1.80	1.64	1.64	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_249840	-8.17	-8.94	-8.71	dynein heavy chain 2, putative
TGME49_272320	1.53	1.24	1.74	DHHC zinc finger domain-containing protein
TGME49_218270	-1.01	#N/A	#N/A	hypothetical protein
TGME49_263610	-1.59	-1.78	-1.78	hypothetical protein
TGME49_202460	-1.77	-1.92	-1.69	diacylglycerol kinase accessory domain (presumed) domain-containing protein
TGME49_271000	-2.27	-2.15	-1.88	hypothetical protein
TGME49_321300	-3.47	-3.61	-3.13	autophagy-related 12 variant 1, putative
TGME49_234950	1.64	2.07	1.59	protein kinase (incomplete catalytic triad)
TGME49_220920	-8.17	-8.04	-8.01	hypothetical protein
TGME49_235560	-8.18	-9.20	-8.05	hypothetical protein
TGME49_257595	-2.88	-2.54	-2.65	hypothetical protein
TGME49_305600	-8.17	-8.06	-8.12	hypothetical protein
TGME49_223672	1.66	#N/A	1.31	3'(2'),5'-bisphosphate nucleotidase
TGME49_229340	-8.17	-7.92	-8.33	hypothetical protein
TGME49_247380	-8.17	-8.91	-8.78	hypothetical protein
TGME49_239610	-3.47	-3.57	-3.56	hypothetical protein
TGME49_273850	-2.77	-2.77	-2.95	hypothetical protein
TGME49_312380	-8.17	-8.28	-8.34	tetratricopeptide repeat-containing protein
TGME49_230710	-3.53	-3.17	-2.93	cell division protein CDC48
TGME49_316360	-3.53	-3.41	-3.48	hypothetical protein
TGME49_229940	-2.40	-2.15	-2.14	cyclophilin, putative
TGME49_242850	-2.40	-2.07	-2.81	hypothetical protein
TGME49_216680	-2.15	-4.00	-2.46	ankyrin repeat-containing protein
TGME49_289000	-2.77	-3.04	-2.86	hypothetical protein
TGME49_228720	-8.17	-7.93	-7.96	hypothetical protein
TGME49_252360	1.02	#N/A	#N/A	rhoptry kinase family protein ROP24 (incomplete catalytic triad)
TGME49_312618	-1.89	#N/A	#N/A	hypothetical protein
TGME49_321610	-8.17	-8.43	-7.86	hypothetical protein
TGME49_235750	-8.17	-8.31	-8.43	ULK kinase

TGME49_218950	#N/A	#N/A	1.33	hypothetical protein
TGME49_310630	#N/A	#N/A	-1.27	hypothetical protein
TGME49_226000	#N/A	#N/A	-1.08	ATP synthase, putative
TGME49_216260	#N/A	#N/A	-1.03	eukaryotic initiation factor-2B, gamma subunit, putative
TGME49_287470	#N/A	#N/A	-1.60	hypothetical protein
TGME49_319920	#N/A	#N/A	-1.01	2-oxo acid dehydrogenases acyltransferase (catalytic domain) domain-containing protein
TGME49_254365	#N/A	#N/A	-1.17	phosphatidate cytidylyltransferase
TGME49_255930	#N/A	#N/A	1.41	hypothetical protein
TGME49_261030	#N/A	#N/A	-3.23	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_224740	#N/A	#N/A	1.13	hypothetical protein
TGME49_217610	#N/A	#N/A	-1.83	hypothetical protein
TGME49_239050	#N/A	#N/A	1.05	hypothetical protein
TGME49_280790	#N/A	#N/A	1.23	phosphatidylinositol n-acetylglucosaminyltransferase
TGME49_231590	#N/A	#N/A	-1.57	SGS domain-containing protein
TGME49_230210	#N/A	#N/A	-1.10	alveolin domain containing intermediate filament IMC10
TGME49_208350	#N/A	#N/A	1.00	hypothetical protein
TGME49_216800	#N/A	#N/A	2.12	flagellar/basal body protein
TGME49_318430	#N/A	#N/A	-1.22	malate dehydrogenase MDH
TGME49_289120	#N/A	#N/A	1.08	hypothetical protein
TGME49_223020	#N/A	#N/A	-1.11	coproporphyrinogen III oxidase
TGME49_277970	#N/A	#N/A	1.14	dolichol-phosphate-mannose synthase family protein
TGME49_240050	#N/A	#N/A	1.14	hypothetical protein
TGME49_321540	#N/A	#N/A	-1.00	hypothetical protein
TGME49_243780	#N/A	#N/A	1.03	hypothetical protein
TGME49_207450	#N/A	#N/A	-1.41	DNA segment, Chr 10, Wayne State University 52, expressed family protein
TGME49_232035	#N/A	#N/A	-1.99	hypothetical protein
TGME49_288510	#N/A	#N/A	2.14	ubiquitin carboxyl-terminal hydrolase
TGME49_255215	#N/A	#N/A	2.48	hypothetical protein
TGME49_311320	#N/A	#N/A	-2.37	hypothetical protein
TGME49_207120	#N/A	#N/A	1.11	Sad1/UNC family protein
TGME49_221480	#N/A	#N/A	-1.20	hypothetical protein
TGME49_216190	#N/A	#N/A	1.35	hypothetical protein
TGME49_227630	#N/A	#N/A	2.27	hypothetical protein

FIGURE 4QQ

TGME49_216970	-1.15	-1.17	-1.81	coronin, putative
TGME49_260370	-1.99	-2.21	-1.97	AtPH1 family protein
TGME49_315690	-3.47	-3.51	-3.70	DnaJ domain-containing protein
TGME49_270610	1.55	1.83	1.83	hypothetical protein
TGME49_238110	-2.21	-2.31	-2.69	replication factor a protein 3 protein
TGME49_248890	-2.40	-2.11	-2.93	actin-like protein ALP3b
TGME49_235680	-1.67	-2.96	-1.51	peptidase M16 inactive domain-containing protein
TGME49_319940	-8.17	-8.19	-8.17	hypothetical protein
TGME49_312310	-2.81	-2.15	-2.50	ATPase, AAA family protein
TGME49_239630	-3.49	-3.10	-3.39	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_272475	-8.17	-8.78	-8.57	protein kinase domain-containing protein
TGME49_212090	1.11	#N/A	1.09	hypothetical protein
TGME49_275330	-3.46	-4.05	-3.59	ribosomal protein RPL29
TGME49_201230	-2.76	-2.62	-2.70	kinesin motor domain-containing protein
TGME49_252220	-1.36	-2.92	-1.20	tetratricopeptide repeat domain containing protein
TGME49_207940	-3.47	-3.27	-3.35	ribosomal protein S9, putative
TGME49_318460	-1.58	-1.48	-1.35	P-type ATPase of unknown pump specificity (type V) protein
TGME49_204270	-2.21	-2.35	-1.92	hypothetical protein
TGME49_263590	-2.42	-1.94	-2.38	hypothetical protein
TGME49_309220	-1.37	-1.77	-1.98	GTPase activating protein for Arf protein
TGME49_210360	1.75	1.72	1.47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 family protein
TGME49_310350	-1.78	-1.49	-1.75	PGAP1 family protein
TGME49_300990	1.85	#N/A	1.11	Toxoplasma gondii family C protein
TGME49_263530	-1.60	-1.22	-1.36	chaperonin , putative
TGME49_265400	-1.62	-1.73	-1.46	hypothetical protein
TGME49_213670	-1.46	-1.10	-1.45	hypothetical protein
TGME49_238230	-2.77	-2.62	-3.04	Ser/Thr phosphatase family protein
TGME49_267390	-1.57	-1.02	-1.31	DNA-directed RNA polymerase I RPAC1
TGME49_300060	-1.10	#N/A	#N/A	signal peptidase subunit protein
TGME49_208590	-1.53	-1.79	-2.13	vacuolar ATP synthase subunit 54kD, putative
TGME49_232360	-1.60	-1.87	-1.82	exonuclease
TGME49_288570	-2.74	-2.66	-3.23	hypothetical protein
TGME49_239130	1.45	1.07	1.43	Tyrosine kinase-like (TKL) protein

TGME49_258780	#N/A	#N/A	1.03	OTU family cysteine protease
TGME49_249425	#N/A	#N/A	-1.13	hypothetical protein
TGME49_263070	#N/A	#N/A	-1.00	CMGC kinase, CK2 family
TGME49_257120	#N/A	#N/A	-1.20	sugar transporter ST1
TGME49_224470	#N/A	#N/A	1.05	hypothetical protein
TGME49_222270	#N/A	#N/A	-1.25	hypothetical protein
TGME49_265780	#N/A	#N/A	-1.16	flagellar/basal body protein
TGME49_223420	#N/A	#N/A	1.31	DnaJ domain-containing protein
TGME49_320620	#N/A	#N/A	-1.94	queuine tRNA ribosyl transferase
TGME49_286050	#N/A	#N/A	1.09	hypothetical protein
TGME49_258462	#N/A	#N/A	-1.26	hypothetical protein
TGME49_264980	#N/A	#N/A	1.18	hypothetical protein
TGME49_219290	#N/A	#N/A	1.07	F-actin-capping protein subunit beta, putative
TGME49_260790	#N/A	#N/A	-1.90	RAP domain-containing protein
TGME49_310620	#N/A	#N/A	-1.02	starch binding domain-containing protein
TGME49_309370	#N/A	#N/A	-1.09	adaptin n terminal region domain-containing protein
TGME49_312700	#N/A	#N/A	1.71	hypothetical protein
TGME49_309730	#N/A	#N/A	-1.23	thioredoxin reductase
TGME49_289780	#N/A	#N/A	-1.42	ATP-dependent hsl protease ATP-binding subunit hslU, putative
TGME49_245540	#N/A	#N/A	-1.11	hypothetical protein
TGME49_250040	#N/A	#N/A	-1.57	hypothetical protein
TGME49_263240	#N/A	#N/A	-1.31	hypothetical protein
TGME49_272210	#N/A	#N/A	-2.18	hypothetical protein
TGME49_255980	#N/A	#N/A	-1.31	hypothetical protein
TGME49_305510	#N/A	#N/A	-1.13	hypothetical protein
TGME49_251560	#N/A	#N/A	-1.03	hypothetical protein
TGME49_291820	#N/A	#N/A	1.27	RNA helicase (UPF2 interacting domain) protein
TGME49_270520	#N/A	#N/A	-1.26	hypothetical protein
TGME49_240500	#N/A	#N/A	-1.31	hypothetical protein
TGME49_311140	#N/A	#N/A	-2.15	hypothetical protein
TGME49_259860	#N/A	#N/A	-1.21	hypothetical protein
TGME49_314800	#N/A	#N/A	-1.12	hypothetical protein
TGME49_223710	#N/A	#N/A	-1.04	tetratricopeptide repeat-containing protein

FIGURE 4RR

TGME49_318750	1.28	1.70	2.56	deoxyribose-phosphate aldolase
TGME49_226660	-1.30	-1.22	-1.34	hypothetical protein
TGME49_247330	-1.75	-2.74	-2.07	hypothetical protein
TGME49_269140	-1.79	-1.56	-1.49	transport protein particle component, Bet3 domain-containing protein
TGME49_219460	-2.74	-2.98	-2.53	hypothetical protein
TGME49_270160	-8.11	-8.21	-7.88	hypothetical protein
TGME49_311280	-8.12	-7.86	-7.97	hypothetical protein
TGME49_234610	-1.55	-1.14	-1.31	WD-40 repeat protein
TGME49_310810	-1.83	-1.85	-2.03	apyrase
TGME49_214800	-8.11	-8.10	-7.90	hypothetical protein
TGME49_301180	2.01	#N/A	3.30	SAG-related sequence SRS19F
TGME49_234440	-3.44	-4.26	#N/A	aminotransferase, putative
TGME49_240830	-8.11	-8.19	-7.68	hydrolase, alpha/beta fold family protein
TGME49_236280	2.04	1.77	1.75	hypothetical protein
TGME49_252510	1.49	1.41	#N/A	hypothetical protein
TGME49_297510	-8.12	-8.90	-8.74	hypothetical protein
TGME49_270650	1.77	1.20	2.01	deoxyribose-phosphate aldolase
TGME49_224330	-1.28	-1.03	#N/A	proteasome activator pa28 beta subunit protein
TGME49_310560	-3.42	-3.68	-3.74	hypothetical protein
TGME49_297720	-1.07	-1.26	-1.12	trehalose-phosphatase
TGME49_307810	-1.21	#N/A	-1.22	hypothetical protein
TGME49_258920	-8.13	-7.87	-8.20	hypothetical protein
TGME49_205570	-2.73	-2.75	-2.49	hypothetical protein
TGME49_255170	-3.43	-3.19	-2.43	hypothetical protein
TGME49_255690	-2.74	-2.81	-2.46	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase domain-containing protein
TGME49_227430	-1.72	-1.89	2.34	transmembrane amino acid transporter protein
TGME49_257150	-2.73	-2.37	-2.60	NOT2 / NOT3 / NOT5 family protein
TGME49_226840	-2.74	-2.20	-2.45	hypothetical protein
TGME49_267120	-2.74	-2.41	-2.50	hypothetical protein
TGME49_248130	-8.13	-8.09	-7.87	hypothetical protein
TGME49_253300	2.29	1.79	2.25	hypothetical protein
TGME49_306290	-1.87	-1.91	-2.04	DNA-directed RNA polymerase III RPC1
TGME49_297460	-8.12	-8.18	-8.51	hypothetical protein
TGME49_204140	-8.17	-8.24	-7.74	PHD-finger domain-containing protein
TGME49_209080	1.29	#N/A	#N/A	transport protein particle (trapp) component, bet3 protein

TGME49_318360	#N/A	#N/A	-1.64	hypothetical protein
TGME49_285480	#N/A	#N/A	1.45	hypothetical protein
TGME49_226690	#N/A	#N/A	-1.20	hypothetical protein
TGME49_267280	#N/A	#N/A	1.34	hypothetical protein
TGME49_309280	#N/A	#N/A	-2.10	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_307270	#N/A	#N/A	-1.37	hypothetical protein
TGME49_224160	#N/A	#N/A	1.03	hypothetical protein
TGME49_322010	#N/A	#N/A	-1.61	myosin-light-chain kinase
TGME49_233260	#N/A	#N/A	-1.52	GTP-binding protein, putative
TGME49_263785	#N/A	#N/A	1.23	phosphatidate cytidylyltransferase
TGME49_206710	#N/A	#N/A	2.02	hypothetical protein
TGME49_261370	#N/A	#N/A	1.03	hypothetical protein
TGME49_283730	#N/A	#N/A	-1.10	endomembrane protein 70 subfamily protein
TGME49_320070	#N/A	#N/A	-1.11	CDK-activating kinase assembly factor MAT1 protein
TGME49_262590	#N/A	#N/A	1.57	hypothetical protein
TGME49_267550	#N/A	#N/A	-1.06	leucine-rich repeat protein LRR1
TGME49_206490	#N/A	#N/A	-1.12	ICE family protease (caspase) p20 domain-containing protein
TGME49_225710	#N/A	#N/A	-2.09	mitochondrial inner membrane translocase subunit TIM17, putative
TGME49_289110	#N/A	#N/A	1.52	hypothetical protein
TGME49_221700	#N/A	#N/A	-1.11	hypothetical protein
TGME49_288730	#N/A	#N/A	1.41	hypothetical protein
TGME49_201810	#N/A	#N/A	1.07	hypothetical protein
TGME49_248180	#N/A	#N/A	2.57	hypothetical protein
TGME49_269050	#N/A	#N/A	-1.21	hypothetical protein
TGME49_257560	#N/A	#N/A	1.25	WD domain, G-beta repeat-containing protein
TGME49_300980	#N/A	#N/A	-1.20	hypothetical protein
TGME49_268250	#N/A	#N/A	-1.39	WD domain, G-beta repeat-containing protein
TGME49_219620	#N/A	#N/A	1.14	hypothetical protein
TGME49_305040	#N/A	#N/A	-1.59	HEAT repeat-containing protein
TGME49_213930	#N/A	#N/A	-1.72	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_214310	#N/A	#N/A	1.60	hypothetical protein
TGME49_223725	#N/A	#N/A	2.08	hypothetical protein
TGME49_295000	#N/A	#N/A	-1.23	hypothetical protein
TGME49_246610	#N/A	#N/A	-2.04	hypothetical protein
TGME49_297060	#N/A	#N/A	-1.30	phosphoglycerate mutase PGMII

FIGURE 4SS

TGME49_273840	-2.40	-1.75	-2.09	brix domain-containing protein
TGME49_209930	-8.12	-9.20	-8.28	hypothetical protein
TGME49_308580	-2.37	-2.50	-2.51	Lon protease family protein
TGME49_313240	-2.78	-2.92	-3.07	ethylene-responsive RNA helicase, putative
TGME49_264440	-1.83	-1.58	-1.69	signal recognition particle receptor beta subunit protein
TGME49_231890	-1.86	-1.41	-1.25	beta-ketoacyl-acyl carrier protein synthase III, putative
TGME49_215290	-3.39	-3.84	-4.16	saccharopine dehydrogenase domain-containing protein
TGME49_299110	-1.95	-1.81	-2.10	cleft lip and palate transmembrane protein 1 (clptm1) protein
TGME49_223060	-1.76	-1.63	#N/A	MORN repeat-containing protein
TGME49_314840	-1.63	-1.71	-1.49	ubiquitin carboxyl-terminal hydrolase
TGME49_311510	-1.44	-1.14	-1.21	eIF2 kinase IF2K-B
TGME49_304760	1.05	#N/A	1.04	RNA recognition motif-containing protein
TGME49_221490	-2.70	-2.37	-2.34	cell cycle regulator protein
TGME49_297780	-2.34	-2.98	-2.36	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_257710	-3.39	-3.55	-3.82	actin-like protein ALP 5
TGME49_225680	-2.70	-2.84	-2.74	hypothetical protein
TGME49_227600	-1.12	-1.49	-1.37	ribosomal protein RPL34
TGME49_224350	-1.37	-1.10	-1.28	aminopeptidase N, putative
TGME49_233820	-8.05	-7.82	-8.59	DNA polymerase epsilon subunit B protein
TGME49_255390	-3.39	-3.61	-3.38	HEAT repeat-containing protein
TGME49_217360	-2.70	-2.95	-3.36	hypothetical protein
TGME49_273350	1.51	1.74	2.12	molybdopterin converting factor, subunit 2 protein
TGME49_230430	-8.05	-8.37	-9.16	vesicle-associated membrane protein, putative
TGME49_244230	-8.06	-8.91	-8.73	hypothetical protein
TGME49_242435	-3.39	-3.54	-3.49	hypothetical protein
TGME49_312280	-1.39	-1.31	-1.54	pre-mRNA-splicing factor ATP-dependent RNA helicase, putative
TGME49_295450	-1.22	#N/A	-1.26	sjoegren syndrome nuclear autoantigen 1 family protein
TGME49_212150	-8.06	-8.74	-8.79	hypothetical protein
TGME49_251890	-3.39	-4.36	-3.22	hypothetical protein
TGME49_318290	-8.05	-8.76	-8.23	hypothetical protein
TGME49_233090	-8.06	-8.10	-8.51	XPG N-terminal domain-containing protein

TGME49_216040	#N/A	#N/A	-1.19	30S ribosomal protein S15, putative
TGME49_203860	#N/A	#N/A	1.40	hypothetical protein
TGME49_263740	#N/A	#N/A	1.97	ABC transporter transmembrane region domain-containing protein
TGME49_309420	#N/A	#N/A	-1.37	ferlin family protein
TGME49_299040	#N/A	#N/A	-1.13	phosphatidylinositol n-acetylglucosaminyltransferase
TGME49_254810	#N/A	#N/A	1.22	hypothetical protein
TGME49_209290	#N/A	#N/A	-1.03	ribosomal protein RPS28
TGME49_290240	#N/A	#N/A	1.41	hypothetical protein
TGME49_313470	#N/A	#N/A	1.15	helix-hairpin-helix motif domain-containing protein
TGME49_201240	#N/A	#N/A	1.15	hypothetical protein
TGME49_205100	#N/A	#N/A	-1.46	hypothetical protein
TGME49_248840	#N/A	#N/A	-1.42	transporter, major facilitator family protein
TGME49_211300	#N/A	#N/A	-1.66	DUF74 family protein, putative
TGME49_308590	#N/A	#N/A	-1.13	Mov34/MPN/PAD-1 family protein
TGME49_249710	#N/A	#N/A	-1.46	Parkinson disease 7 domain containing 1 family protein
TGME49_210750	#N/A	#N/A	1.78	Ferredoxin-fold anticodon binding domain-containing protein
TGME49_320700	#N/A	#N/A	1.09	AP2 domain transcription factor AP2IV-1
TGME49_249490	#N/A	#N/A	-1.08	hypothetical protein
TGME49_277500	#N/A	#N/A	-1.47	26S proteasome regulatory subunit 7, putative
TGME49_270130	#N/A	#N/A	1.08	hypothetical protein
TGME49_298610	#N/A	#N/A	-1.04	GYF domain-containing protein
TGME49_250955	#N/A	#N/A	1.38	KRUF family protein
TGME49_258800	#N/A	#N/A	1.07	rhoptry kinase family protein ROP31
TGME49_313070	#N/A	#N/A	-1.21	hypothetical protein
TGME49_265510	#N/A	#N/A	-1.01	hypothetical protein
TGME49_320680	#N/A	#N/A	1.44	AP2 domain transcription factor AP2IV-2
TGME49_269430	#N/A	#N/A	1.14	polyprenyl synthetase superfamily protein
TGME49_202220	#N/A	#N/A	1.47	hypothetical protein
TGME49_238190	#N/A	#N/A	-1.01	DNA-directed RNA polymerase II RPB3
TGME49_262460	#N/A	#N/A	-1.19	hypothetical protein
TGME49_239748	#N/A	#N/A	-1.39	hypothetical protein

FIGURE 4TT

TGME49_320015	-8.05	-8.10	-7.73	hypothetical protein
TGME49_218250	-2.13	-2.10	-2.35	TAP42 family protein
TGME49_203420	1.97	1.65	1.62	4'-phosphopantetheinyl transferase domain-containing protein
TGME49_221360	-2.13	-1.98	-1.89	hypothetical protein
TGME49_219140	-1.48	-1.50	-1.77	EF-1 guanine nucleotide exchange domain-containing protein
TGME49_312840	-1.82	-1.83	-2.14	hypothetical protein
TGME49_221830	1.87	3.37	3.34	subtilisin SUB12
TGME49_285470	1.99	1.28	1.85	patched family protein
TGME49_270450	-8.05	-8.04	-7.98	MCM2/3/5 family protein
TGME49_224190	-1.56	-1.33	-1.15	cation-transporting atpase family protein
TGME49_223070	-1.12	-1.16	-1.18	hypothetical protein
TGME49_313150	2.10	1.58	#N/A	DUF89/Fructose bisphosphatase
TGME49_226940	-3.41	-3.11	-2.78	ubiquitin carboxyl-terminal hydrolase
TGME49_291090	-8.07	-8.87	-8.45	SWI2/SNF2-containing protein
TGME49_297210	1.08	#N/A	#N/A	hypothetical protein
TGME49_217880	-8.05	-8.37	-7.75	RNA-binding protein Nova-1, putative
TGME49_290180	2.38	2.52	2.30	AP2 domain transcription factor AP2IX-6
TGME49_267140	-8.08	-7.60	-8.43	SAG-related sequence SRS38B
TGME49_230520	-1.22	-1.04	#N/A	cyclophilin 1, putative
TGME49_291010	2.02	1.83	2.29	hypothetical protein
TGME49_301350	-8.10	-8.70	-7.79	SNARE associated protein
TGME49_285520	-3.38	-3.05	-3.31	RNA cap guanine-N2 methyltransferase
TGME49_249820	-2.67	-2.97	-3.04	ATP-binding cassette sub-family B member 5
TGME49_208730	-1.15	#N/A	1.55	microneme protein, putative
TGME49_314000	1.22	1.47	#N/A	peptide methionine sulfoxide reductase msrB, putative
TGME49_216760	-8.06	-7.92	-8.19	RNA pseudouridine synthase superfamily protein
TGME49_314970	-1.21	-1.13	-1.54	root hair defective 3 gtp-binding protein (rhd3) protein
TGME49_258850	-8.04	-8.13	-8.11	hypothetical protein
TGME49_220110	1.72	1.56	2.05	hypothetical protein
TGME49_321660	-3.42	-3.15	#N/A	mannosyltransferase, putative
TGME49_319950	-1.79	#N/A	#N/A	rRNA-processing protein FCF1, putative
TGME49_244610	-3.34	-3.73	-3.43	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_288840	1.74	1.59	1.69	hypothetical protein
TGME49_205625	-3.38	-3.24	-2.80	hypothetical protein

TGME49_262760	#N/A	#N/A	-1.21	poly(ADP-ribose) glycohydrolase
TGME49_288240	#N/A	#N/A	1.21	hypothetical protein
TGME49_300320	#N/A	#N/A	2.19	dimethyladenosine transferase
TGME49_212770	#N/A	#N/A	-1.33	hypothetical protein
TGME49_269000	#N/A	#N/A	-1.62	ABC transporter family protein
TGME49_219682	#N/A	#N/A	-1.11	pyruvate dehydrogenase kinase, putative
TGME49_285670	#N/A	#N/A	1.81	hypothetical protein
TGME49_313710	#N/A	#N/A	-1.22	hypothetical protein

FIGURE 5A

Figure 5: EGS transcriptomics data during HFF infections. Differencial T. gondii gene expressin analysis of human HFF cells infected with T. gondii EGS strain for 2 hs, 18 hs or 48 hs compared to the average T. gondii gene expression of human MM6 and neuronal stem cells infected with either GT1, ME49 or VEG strains of T. gondii for 18 hours.

gene ID	logFC 2hs	logFC 18hs	logFC 48hs	Product name
TGME49_462910	1.31	12.08	11.89	large subunit ribosomal RNA
TGME49_457990	1.31	17.05	14.29	28S ribosomal RNA
TGME49_200010	11.50	9.86	10.81	hypothetical protein
TGME49_208370	4.76	1.14	#N/A	myosin heavy chain, putative
TGME49_280570	1.98	5.30	6.48	SAG-related sequence SRS35A
TGME49_251180	1.08	#N/A	1.09	KRUF family protein
TGME49_275860	1.98	1.13	1.07	hypothetical protein
TGME49_252430	1.08	#N/A	#N/A	hypothetical protein
TGME49_290700	1.98	1.34	1.15	hypothetical protein
TGME49_205250	11.50	3.92	4.15	rhoptry protein ROP18
TGME49_321480	1.31	5.25	4.55	SAG-related sequence SRS12B
TGME49_316250	1.31	#N/A	#N/A	hypothetical protein
TGME49_206550	4.76	4.04	3.33	hypothetical protein
TGME49_293790	1.98	4.41	3.95	hypothetical protein
TGME49_204050	11.50	#N/A	#N/A	subtilisin SUB1
TGME49_226380	1.56	#N/A	#N/A	hypothetical protein
TGME49_214980	2.42	#N/A	#N/A	hypothetical protein
TGME49_275460	1.98	#N/A	#N/A	hypothetical protein
TGME49_212300	2.42	#N/A	#N/A	hypothetical protein
TGME49_311100	1.31	1.01	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_214080	2.42	4.01	3.46	toxofilin
TGME49_289920	1.98	#N/A	#N/A	hypothetical protein
TGME49_312420	1.31	#N/A	#N/A	hypothetical protein
TGME49_270700	1.98	#N/A	#N/A	hypothetical protein
TGME49_215960	2.42	#N/A	1.03	hypothetical protein
TGME49_249990	1.08	#N/A	#N/A	hypothetical protein
TGME49_205680	11.50	#N/A	#N/A	hypothetical protein
TGME49_288475	1.98	3.36	3.34	hypothetical protein
TGME49_287040	1.98	1.24	1.15	hypothetical protein
TGME49_301250	1.31	3.87	3.67	hypothetical protein
TGME49_240060	1.08	#N/A	#N/A	hypothetical protein
TGME49_208450	4.76	#N/A	#N/A	protease inhibitor PI2
TGME49_233450	1.56	1.33	#N/A	SAG-related sequence SRS29A

gene ID	logFC 2hs	logFC 18hs	logFC 48hs	Product name
TGME49_270800	1.98	#N/A	1.35	GAF domain-containing protein
TGME49_220360	2.42	#N/A	#N/A	FAD binding domain-containing protein
TGME49_315310	1.31	#N/A	#N/A	hypothetical protein
TGME49_254220	1.08	#N/A	#N/A	hypothetical protein
TGME49_280375	1.98	#N/A	#N/A	hypothetical protein
TGME49_202620	11.50	#N/A	#N/A	hypothetical protein
TGME49_216770	2.42	#N/A	#N/A	hypothetical protein
TGME49_218910	2.42	#N/A	#N/A	hypothetical protein
TGME49_220470	2.42	#N/A	#N/A	hypothetical protein
TGME49_300020	1.31	#N/A	#N/A	ATP-dependent metallopeptidase HflB subfamily protein
TGME49_278030	1.98	#N/A	#N/A	hypothetical protein
TGME49_206460	11.50	#N/A	#N/A	hypothetical protein
TGME49_255250	-4.38	#N/A	#N/A	tRNA (cytosine(34)-C(5))-methyltransferase, putative
TGME49_251840	1.08	#N/A	#N/A	hypothetical protein
TGME49_306630	1.31	#N/A	#N/A	tRNA methyltransferase complex GCD14 subunit protein
TGME49_246610	1.08	#N/A	#N/A	hypothetical protein
TGME49_282140	1.98	#N/A	#N/A	cwf21 protein
TGME49_300052	1.31	#N/A	#N/A	hypothetical protein
TGME49_234350	1.56	#N/A	#N/A	hypothetical protein
TGME49_281440	1.98	#N/A	#N/A	hypothetical protein
TGME49_222070	1.56	#N/A	#N/A	elongation factor Tu GTP binding domain-containing protein
TGME49_233080	1.56	#N/A	#N/A	G-patch domain-containing protein
TGME49_202025	11.50	3.76	2.76	hypothetical protein
TGME49_269075	1.98	#N/A	#N/A	hypothetical protein
TGME49_232590	1.56	#N/A	#N/A	glutamate-cysteine ligase, catalytic subunit domain-containing protein
TGME49_288670	1.98	#N/A	#N/A	hypothetical protein
TGME49_275750	1.98	1.29	1.80	small nuclear ribonucleoprotein E, putative
TGME49_300990	1.31	#N/A	1.84	Toxoplasma gondii family C protein
TGME49_257755	2.35	#N/A	#N/A	hypothetical protein
TGME49_320640	1.31	#N/A	#N/A	peptidylprolyl isomerase domain-containing protein
TGME49_248660	1.08	1.70	#N/A	hypothetical protein
TGME49_236000	1.56	#N/A	#N/A	ferredoxin, putative
TGME49_208540	4.76	#N/A	#N/A	DEAD/DEAH box helicase domain-containing protein

FIGURE 5B

TGME49_213280	2.42	#N/A	#N/A	SAG-related sequence SRS25
TGME49_230830	1.56	1.42	#N/A	ATPase family associated with various cellular activities (AAA) domain-containing protein
TGME49_308020	1.31	#N/A	1.10	SAG-related sequence SRS57
TGME49_207400	4.76	#N/A	#N/A	hypothetical protein
TGME49_220380	2.42	#N/A	#N/A	hypothetical protein
TGME49_272370	1.98	1.03	#N/A	hypothetical protein
TGME49_320490	1.31	#N/A	#N/A	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D family protein
TGME49_207210	4.76	4.66	4.91	hypothetical protein
TGME49_249030	1.08	#N/A	#N/A	endonuclease/exonuclease/phosphatase family protein
TGME49_275870	1.98	2.37	1.43	tubulin/FtsZ family, GTPase domain-containing protein
TGME49_289050	1.98	#N/A	#N/A	FIKK kinase, putative
TGME49_214410	2.42	#N/A	#N/A	hypothetical protein
TGME49_289600	1.98	#N/A	#N/A	heat shock protein HSP29
TGME49_237230	1.08	#N/A	#N/A	hypothetical protein
TGME49_313440	1.31	1.91	1.66	hypothetical protein
TGME49_226540	1.56	#N/A	#N/A	protein kinase
TGME49_289630	1.98	#N/A	#N/A	microneme protein MIC16
TGME49_206510	11.50	#N/A	#N/A	toxolysin TLN4
TGME49_260310	2.35	1.66	3.09	ATP-binding cassette transporter ABC.B1
TGME49_294200	1.98	#N/A	#N/A	glucose-6-phosphate 1-dehydrogenase
TGME49_216820	2.42	#N/A	#N/A	transporter, major facilitator family protein
TGME49_321530	1.31	#N/A	#N/A	cathepsin CPL
TGME49_252390	1.08	#N/A	#N/A	hypothetical protein
TGME49_254460	1.08	1.68	1.98	hypothetical protein
TGME49_220950	2.42	#N/A	#N/A	hypothetical protein
TGME49_217680	2.42	#N/A	#N/A	hypothetical protein
TGME49_201785	11.50	#N/A	#N/A	hypothetical protein
TGME49_214575	2.42	#N/A	1.31	hypothetical protein
TGME49_283540	1.98	#N/A	#N/A	hypothetical protein
TGME49_323110	1.31	1.23	#N/A	hypothetical protein
TGME49_250115	1.08	#N/A	#N/A	hypothetical protein
TGME49_243930	1.08	#N/A	#N/A	hypothetical protein
TGME49_314970	1.31	#N/A	#N/A	root hair defective 3 gtp-binding protein (rhd3) protein
TGME49_218520	2.42	#N/A	#N/A	microneme protein MIC6

TGME49_299000	1.31	#N/A	#N/A	hypothetical protein
TGME49_246010	1.08	#N/A	#N/A	hypothetical protein
TGME49_224160	1.56	#N/A	#N/A	hypothetical protein
TGME49_289170	1.98	#N/A	#N/A	adenylate and guanylate cyclase catalytic domain-containing protein
TGME49_221220	2.42	2.68	2.66	hypothetical protein
TGME49_273500	1.98	#N/A	#N/A	O-linked N-acetylglucosamine transferase
TGME49_313495	1.31	#N/A	#N/A	hypothetical protein
TGME49_217610	2.42	#N/A	#N/A	hypothetical protein
TGME49_217640	2.42	#N/A	#N/A	hypothetical protein
TGME49_293580	1.98	#N/A	#N/A	prefoldin subunit protein
TGME49_269705	1.98	#N/A	#N/A	hypothetical protein
TGME49_281910	1.98	#N/A	#N/A	hypothetical protein
TGME49_245730	1.08	#N/A	#N/A	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_305090	1.31	#N/A	#N/A	kinase binding protein cgi-121 protein
TGME49_232640	1.56	1.73	1.57	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_211695	4.76	-7.00	#N/A	hypothetical protein
TGME49_217010	2.42	#N/A	#N/A	hypothetical protein
TGME49_258720	2.35	#N/A	#N/A	Ubiquitin family protein, putative
TGME49_262060	2.35	#N/A	#N/A	hypothetical protein
TGME49_268320	1.47	#N/A	#N/A	hypothetical protein
TGME49_306520	1.31	#N/A	#N/A	tRNA pseudouridine synthase B, putative
TGME49_252510	1.08	#N/A	#N/A	hypothetical protein
TGME49_262970	2.35	#N/A	#N/A	hypothetical protein
TGME49_219250	2.42	#N/A	#N/A	acetyltransferase, GNAT family protein
TGME49_313060	1.31	#N/A	#N/A	eukaryotic translation initiation factor 2B, putative
TGME49_314070	1.31	#N/A	#N/A	hypothetical protein
TGME49_255270	2.35	#N/A	#N/A	hypothetical protein
TGME49_206500	11.50	#N/A	#N/A	hypothetical protein
TGME49_271320	1.98	2.97	3.07	hypothetical protein
TGME49_212090	4.76	#N/A	#N/A	hypothetical protein
TGME49_294750	1.98	#N/A	#N/A	hypothetical protein
TGME49_228780	1.56	#N/A	#N/A	Toxoplasma gondii family C protein
TGME49_202780	11.50	#N/A	#N/A	rhoptry kinase family protein ROP25
TGME49_222245	1.56	#N/A	#N/A	hypothetical protein

FIGURE 5C

TGME49_257380	2.35	#N/A	#N/A	hypothetical protein
TGME49_251170	1.08	#N/A	#N/A	KRUF family protein
TGME49_276170	1.98	#N/A	#N/A	phosphatidylinositol 3- and 4-kinase
TGME49_219120	2.42	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_236890	1.08	#N/A	#N/A	hypothetical protein
TGME49_277080	1.98	#N/A	#N/A	microneme protein MIC5
TGME49_228170	1.56	#N/A	#N/A	inner membrane complex protein IMC2A
TGME49_225540	1.56	#N/A	#N/A	hypothetical protein
TGME49_233140	1.56	#N/A	#N/A	deoxyuridine 5'-triphosphate nucleotidohydrolase, putative
TGME49_259950	2.35	#N/A	#N/A	carbonate dehydratase, eukaryotic-type domain-containing protein
TGME49_214940	2.42	#N/A	#N/A	MIC2-associated protein M2AP
TGME49_305980	1.31	#N/A	#N/A	pyruvate dehydrogenase complex subunit PDH-E3I
TGME49_243730	1.08	#N/A	#N/A	rhoptry protein ROP9
TGME49_286470	1.98	#N/A	#N/A	AGC kinase
TGME49_202020	11.50	3.09	3.30	DnAK-TPR
TGME49_222130	1.56	#N/A	1.02	hypothetical protein
TGME49_321360	1.31	#N/A	#N/A	clustered-asparagine-rich protein
TGME49_206610	4.76	#N/A	#N/A	pyruvate dehydrogenase complex subunit PDH-E2
TGME49_226020	1.56	#N/A	#N/A	transporter, major facilitator family protein
TGME49_212900	2.42	#N/A	#N/A	hypothetical protein
TGME49_298980	1.31	#N/A	1.58	RNA pseudouridine synthase superfamily protein
TGME49_307820	1.31	#N/A	1.33	hypothetical protein
TGME49_270320	1.98	#N/A	1.34	protein phosphatase 2C domain-containing protein
TGME49_252190	1.08	#N/A	1.56	KRUF family protein
TGME49_246550	1.08	#N/A	#N/A	aspartyl protease ASP3
TGME49_289540	1.98	#N/A	#N/A	hypothetical protein
TGME49_268860	1.98	3.33	5.65	enolase 1
TGME49_217740	2.42	-9.88	#N/A	3-ketoacyl-(acyl-carrier-protein) reductase
TGME49_293260	1.98	1.17	#N/A	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_227100	1.56	3.51	#N/A	hypothetical protein
TGME49_209060	4.76	#N/A	#N/A	thrombospondin type 1 domain-containing protein
TGME49_221320	2.42	#N/A	#N/A	acetyl-CoA carboxylase ACC1
TGME49_313910	1.31	#N/A	#N/A	RNA recognition motif 2 protein
TGME49_252070	1.08	3.55	4.63	KRUF family protein
TGME49_203310	11.50	#N/A	#N/A	dense granule protein GRA7
TGME49_232670	1.56	#N/A	#N/A	hypothetical protein
TGME49_200360	11.50	#N/A	#N/A	hypothetical protein

TGME49_277150	1.98	#N/A	#N/A	XPG N-terminal domain-containing protein
TGME49_232955	1.56	#N/A	-5.63	hypothetical protein
TGME49_217510	2.42	#N/A	#N/A	hypothetical protein
TGME49_313360	1.31	#N/A	#N/A	hypothetical protein
TGME49_234490	1.56	#N/A	#N/A	kelch repeat-containing protein
TGME49_202510	11.50	#N/A	#N/A	multi-pass transmembrane protein
TGME49_219240	2.42	#N/A	#N/A	Peptidyl-tRNA hydrolase PTH2 domain-containing protein
TGME49_229500	1.56	#N/A	1.54	hypothetical protein
TGME49_259830	2.35	#N/A	#N/A	diacylglycerol kinase catalytic domain-containing protein
TGME49_266940	2.35	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_202450	11.50	#N/A	#N/A	hypothetical protein
TGME49_300320	1.31	#N/A	#N/A	dimethyladenosine transferase
TGME49_215440	2.42	#N/A	#N/A	WWE domain-containing protein
TGME49_313110	1.31	#N/A	#N/A	hypothetical protein
TGME49_264650	2.35	#N/A	#N/A	phosphoacetylglucosamine mutase
TGME49_204320	11.50	#N/A	#N/A	hypothetical protein
TGME49_211480	4.76	#N/A	#N/A	GTP-binding protein engA, putative
TGME49_264030	2.35	#N/A	#N/A	aminotransferase, putative
TGME49_208570	4.76	#N/A	#N/A	ubiquitin conjugating enzyme E2, putative
TGME49_231020	1.56	#N/A	#N/A	hypothetical protein
TGME49_215540	2.42	#N/A	-6.53	hypothetical protein
TGME49_295950	1.31	#N/A	#N/A	KRUF family protein
TGME49_262680	2.35	-6.86	#N/A	hypothetical protein
TGME49_224990	1.56	#N/A	#N/A	hypothetical protein
TGME49_299780	1.31	#N/A	#N/A	hypothetical protein
TGME49_275755	1.98	2.12	1.72	hypothetical protein
TGME49_248540	1.08	#N/A	#N/A	hypothetical protein
TGME49_239795	1.08	#N/A	#N/A	hypothetical protein
TGME49_271935	1.98	#N/A	#N/A	hypothetical protein
TGME49_209680	4.76	#N/A	#N/A	hypothetical protein
TGME49_318880	1.31	-7.09	#N/A	hypothetical protein
TGME49_246160	1.08	#N/A	#N/A	hypothetical protein
TGME49_241175	1.08	1.89	#N/A	hypothetical protein
TGME49_316360	1.31	#N/A	#N/A	hypothetical protein
TGME49_209490	4.76	1.17	#N/A	hypothetical protein
TGME49_270805	1.98	#N/A	#N/A	hypothetical protein
TGME49_213020	2.42	#N/A	#N/A	hypothetical protein

FIGURE 5D

TGME49_221590	1.92	#N/A	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_277230	1.98	#N/A	#N/A	hypothetical protein
TGME49_212270	4.76	#N/A	#N/A	hypothetical protein
TGME49_254470	1.08	#N/A	#N/A	hypothetical protein
TGME49_232000	1.56	#N/A	#N/A	hypothetical protein
TGME49_296340	1.31	2.61	2.84	hypothetical protein
TGME49_225170	1.56	#N/A	#N/A	hypothetical protein
TGME49_297400	1.31	#N/A	#N/A	hypothetical protein
TGME49_277260	1.98	1.36	1.08	hypothetical protein
TGME49_304500	1.31	#N/A	#N/A	hypothetical protein
TGME49_215360	2.42	#N/A	#N/A	hypothetical protein
TGME49_259020	2.35	4.75	5.87	bradyzoite antigen BAG1
TGME49_252640	1.08	6.04	5.81	P-type ATPase PMA1
TGME49_269690	1.98	#N/A	#N/A	hypothetical protein
TGME49_253690	1.08	1.30	#N/A	hypothetical protein
TGME49_247220	1.08	#N/A	#N/A	nudix -type motif 9 isoform a family protein
TGME49_247360	1.08	#N/A	#N/A	PAP2 superfamily protein
TGME49_262400	2.35	#N/A	#N/A	lipase
TGME49_254120	1.08	#N/A	#N/A	autophagy-related protein 8 atg8, putative
TGME49_280380	1.98	#N/A	#N/A	poly(ADP-ribose) glycohydrolase
TGME49_323400	1.31	3.56	4.59	cytochrome c oxidase subunit iii subfamily protein
TGME49_263550	2.35	1.57	#N/A	39S ribosomal protein L47, mitochondrial precursor, putative
TGME49_287460	1.98	2.09	3.13	hypothetical protein
TGME49_246130	1.08	#N/A	#N/A	serpin (serine proteinase inhibitor) superfamily protein
TGME49_264870	2.35	#N/A	#N/A	Sodium:neurotransmitter symporter family protein
TGME49_209100	4.76	#N/A	#N/A	PUB domain-containing protein
TGME49_240090	1.08	#N/A	#N/A	rhoptry kinase family protein ROP34, putative
TGME49_304740	1.31	#N/A	#N/A	rhoptry kinase family protein ROP35
TGME49_204520	11.50	2.00	1.45	hypothetical protein
TGME49_201780	11.50	#N/A	#N/A	microneme protein MIC2
TGME49_213050	2.42	#N/A	#N/A	hypothetical protein
TGME49_208020	4.76	#N/A	#N/A	AP2 domain transcription factor AP2Ib-1
TGME49_319640	1.31	#N/A	#N/A	hypothetical protein
TGME49_250710	1.08	#N/A	#N/A	microneme protein MIC10

TGME49_260220	2.35	#N/A	#N/A	folate/biopterin transporter subfamily protein
TGME49_295020	1.62	-7.23	#N/A	Sterol-sensing domain of SREBP cleavage-activation domain-containing protein
TGME49_248830	1.08	#N/A	#N/A	phosphoinositide phospholipase PIPLC
TGME49_258850	2.35	#N/A	#N/A	hypothetical protein
TGME49_262600	2.35	#N/A	#N/A	hypothetical protein
TGME49_264730	2.35	#N/A	#N/A	hypothetical protein
TGME49_260470	2.35	#N/A	#N/A	heat shock protein DNAJ pfj4, putative
TGME49_222940	1.56	3.09	#N/A	hypothetical protein
TGME49_221640	1.56	#N/A	#N/A	hypothetical protein
TGME49_224090	1.56	#N/A	#N/A	enoyl-CoA hydratase/isomerase family protein
TGME49_316200	1.31	#N/A	#N/A	phosphoglycerate mutase family protein
TGME49_215380	2.42	#N/A	#N/A	hypothetical protein
TGME49_282170	1.98	#N/A	#N/A	hypothetical protein
TGME49_263220	2.35	#N/A	#N/A	rhoptry kinase family protein ROP21
TGME49_254090	1.08	#N/A	1.06	hypothetical protein
TGME49_256090	2.35	#N/A	#N/A	glycerophosphodiester phosphodiesterase family protein
TGME49_309410	1.31	#N/A	#N/A	AP2 domain transcription factor AP2XI-1
TGME49_219660	2.42	#N/A	2.21	hypothetical protein
TGME49_251450	1.08	#N/A	1.06	hypothetical protein
TGME49_310390	1.31	#N/A	#N/A	hypothetical protein
TGME49_301350	1.31	#N/A	#N/A	SNARE associated protein
TGME49_205200	11.50	#N/A	#N/A	hypothetical protein
TGME49_254950	1.08	#N/A	#N/A	RNA cap guanine-N2 methyltransferase
TGME49_206340	11.50	#N/A	#N/A	hypothetical protein
TGME49_286430	1.98	#N/A	#N/A	hypothetical protein
TGME49_243680	1.08	#N/A	#N/A	dihydrodipicolinate reductase
TGME49_250955	1.08	#N/A	#N/A	KRUF family protein
TGME49_251920	1.08	#N/A	#N/A	hypothetical protein
TGME49_277070	1.98	#N/A	#N/A	SWI2/SNF2-containing protein
TGME49_280470	1.98	#N/A	#N/A	AP2 domain transcription factor AP2VIIa-1
TGME49_254890	1.08	#N/A	1.83	hypothetical protein
TGME49_238970	1.08	#N/A	#N/A	hypothetical protein
TGME49_254280	1.08	2.32	#N/A	DNA-directed RNA polymerase III RPC9
TGME49_224890	1.56	#N/A	#N/A	hypothetical protein

FIGURE 5E

TGME49_232410	1.56	1.17	1.14	PDI family protein
TGME49_253440	1.08	#N/A	#N/A	cell-cycle-associated protein kinase SRPK, putative
TGME49_214440	2.42	#N/A	#N/A	4'-phosphopantetheinyl transferase superfamily protein
TGME49_313760	1.31	#N/A	#N/A	hypothetical protein
TGME49_314430	1.31	#N/A	#N/A	serine/threonine specific protein phosphatase
TGME49_291940	1.98	#N/A	#N/A	hypothetical protein
TGME49_260620	2.35	#N/A	#N/A	hypothetical protein
TGME49_297650	1.31	#N/A	#N/A	Ser/Thr phosphatase family protein
TGME49_225790	1.56	#N/A	#N/A	PDI family protein
TGME49_293252	1.98	3.40	4.86	hypothetical protein
TGME49_231430	1.56	#N/A	#N/A	oligosaccharyl transferase stt3 protein, putative
TGME49_233380	1.56	#N/A	#N/A	hypothetical protein
TGME49_314700	1.31	#N/A	#N/A	hypothetical protein
TGME49_310130	1.31	#N/A	#N/A	Spc97 / Spc98 family protein
TGME49_291040	1.98	4.24	5.12	lactate dehydrogenase LDH2
TGME49_315910	1.31	#N/A	#N/A	hypothetical protein
TGME49_310520	1.31	#N/A	1.52	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_209140	4.76	#N/A	#N/A	anti-silencing protein, ASF1 family protein
TGME49_220240	2.42	#N/A	#N/A	hypothetical protein
TGME49_215895	2.42	#N/A	#N/A	AP2 domain-containing protein
TGME49_216680	2.42	#N/A	#N/A	ankyrin repeat-containing protein
TGME49_244530	1.08	#N/A	#N/A	hypothetical protein
TGME49_254390	1.08	1.48	1.21	CRAL/TRIO domain-containing protein
TGME49_286460	1.98	#N/A	#N/A	hypothetical protein
TGME49_253560	1.08	#N/A	#N/A	hypothetical protein
TGME49_228160	1.56	#N/A	#N/A	acid phosphatase
TGME49_294980	1.98	#N/A	1.32	hypothetical protein
TGME49_222020	1.56	#N/A	#N/A	phosphoglycerate kinase PGKII
TGME49_225160	1.56	#N/A	#N/A	hypothetical protein
TGME49_276930	1.98	#N/A	#N/A	hypothetical protein
TGME49_209985	4.76	2.97	1.97	cAMP-dependent protein kinase
TGME49_229930	1.56	#N/A	#N/A	p25-alpha family protein
TGME49_247530	1.08	#N/A	#N/A	hypothetical protein
TGME49_218540	2.42	#N/A	#N/A	peptidase S15, putative

TGME49_218610	2.42	#N/A	#N/A	ATPase (DUF699) protein
TGME49_214960	2.42	#N/A	#N/A	AP2 domain transcription factor AP2X-8
TGME49_228150	1.56	#N/A	#N/A	hypothetical protein
TGME49_242730	1.08	#N/A	#N/A	guanylate kinase family protein
TGME49_233770	1.56	#N/A	#N/A	calcium-translocating P-type ATPase, PMCA-type protein
TGME49_215750	2.42	#N/A	2.18	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_255350	2.35	2.40	#N/A	ATPase, putative
TGME49_320700	1.31	1.63	#N/A	AP2 domain transcription factor AP2IV-1
TGME49_225230	1.56	#N/A	#N/A	hypothetical protein
TGME49_278080	1.98	4.04	4.54	Toxoplasma gondii family A protein
TGME49_249410	1.08	#N/A	#N/A	hypothetical protein
TGME49_211610	4.76	#N/A	#N/A	hypothetical protein
TGME49_308965	1.31	#N/A	#N/A	hypothetical protein
TGME49_270595	1.98	#N/A	#N/A	UBA/TS-N domain-containing protein
TGME49_220250	2.42	#N/A	#N/A	Nucleotide-sensitive chloride conductance regulator (ICln) protein
TGME49_218740	2.42	-8.05	#N/A	membrane protein, putative
TGME49_277090	1.98	#N/A	#N/A	carrier superfamily protein
TGME49_273640	1.98	#N/A	#N/A	hypothetical protein
TGME49_225470	1.56	#N/A	1.32	peptide methionine sulfoxide reductase
TGME49_288370	1.98	#N/A	#N/A	hypothetical protein
TGME49_268840	1.98	-8.64	#N/A	N6-adenosine-methyltransferase, putative
TGME49_270890	1.98	#N/A	#N/A	hypothetical protein
TGME49_200385	11.50	#N/A	#N/A	Myb family DNA-binding domain-containing protein
TGME49_253510	1.08	1.81	#N/A	transporter/permease protein
TGME49_289550	1.98	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_297730	1.31	1.62	#N/A	transcription elongation factor 1, putative
TGME49_232960	1.56	#N/A	#N/A	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_250940	1.08	#N/A	#N/A	hypothetical protein
TGME49_266880	2.35	#N/A	#N/A	dihydrouridine synthase, putative
TGME49_217560	2.42	#N/A	#N/A	DNA-directed RNA polymerase II RPB10
TGME49_226640	1.56	2.46	#N/A	zinc binding protein, putative
TGME49_319090	1.31	#N/A	#N/A	IgA-specific serine endopeptidase
TGME49_304490	1.31	#N/A	#N/A	hypothetical protein
TGME49_261590	2.35	#N/A	#N/A	ankyrin, putative

FIGURE 5F

TGME49_309580	1.31	#N/A	#N/A	transporter, major facilitator family protein
TGME49_266310	2.35	#N/A	#N/A	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
TGME49_293770	1.98	#N/A	#N/A	chitinase-like protein CLP1
TGME49_275640	1.98	1.46	#N/A	hypothetical protein
TGME49_239420	1.08	#N/A	#N/A	protein kinase
TGME49_254000	1.08	#N/A	1.21	hypothetical protein
TGME49_305460	1.31	2.07	2.50	methionine aminopeptidase 2, putative
TGME49_250220	1.08	1.94	1.36	hypothetical protein
TGME49_323100	1.31	#N/A	#N/A	hypothetical protein
TGME49_263560	2.35	#N/A	#N/A	hypothetical protein
TGME49_266760	2.35	#N/A	#N/A	isocitrate dehydrogenase
TGME49_210682	4.76	#N/A	#N/A	hypothetical protein
TGME49_312160	1.31	2.15	1.57	hypothetical protein
TGME49_255260	2.35	#N/A	#N/A	apical membrane antigen AMA1
TGME49_227390	1.56	#N/A	#N/A	hypothetical protein
TGME49_286000	1.98	#N/A	#N/A	hypothetical protein
TGME49_316710	1.31	#N/A	#N/A	hypothetical protein
TGME49_208590	4.76	#N/A	1.30	vacuolar ATP synthase subunit 54kD, putative
TGME49_288210	1.98	#N/A	#N/A	PUL domain-containing protein
TGME49_306620	1.31	1.44	#N/A	AP2 domain transcription factor AP2IX-9
TGME49_275420	1.98	#N/A	#N/A	histone lysine-specific demethylase LSD1/BHC110/KDMA1A
TGME49_209900	4.76	#N/A	#N/A	hypothetical protein
TGME49_253470	1.08	1.07	1.44	alveolin domain containing intermediate filament IMC13
TGME49_288650	1.98	#N/A	#N/A	dense granule protein GRA12
TGME49_300055	1.31	#N/A	#N/A	hypothetical protein
TGME49_217530	2.42	#N/A	#N/A	hypothetical protein
TGME49_255180	1.08	#N/A	#N/A	ubiquitin carboxyl-terminal hydrolase
TGME49_226310	1.56	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_259880	2.35	#N/A	#N/A	hypothetical protein
TGME49_212250	4.76	1.34	#N/A	XPG N-terminal domain-containing protein
TGME49_215550	2.42	#N/A	1.25	hypothetical protein
TGME49_213635	2.42	2.41	#N/A	hypothetical protein
TGME49_288840	1.98	#N/A	#N/A	hypothetical protein
TGME49_222948	1.56	-8.96	#N/A	hypothetical protein
TGME49_232750	1.56	#N/A	#N/A	23S rRNA (adenine(1618)-N(6))-methyltransferase, putative

TGME49_237015	1.08	#N/A	#N/A	hypothetical protein
TGME49_277870	1.98	#N/A	#N/A	hypothetical protein
TGME49_252880	1.08	#N/A	1.68	hypothetical protein
TGME49_250500	1.08	-7.08	#N/A	hypothetical protein
TGME49_222970	1.56	#N/A	#N/A	inositol(myo)-1(or 4)-monophosphatase 2, putative
TGME49_202310	11.50	#N/A	#N/A	O-sialoglycoprotein endopeptidase
TGME49_250670	1.08	#N/A	#N/A	hypothetical protein
TGME49_305080	1.31	#N/A	#N/A	hypothetical protein
TGME49_217430	2.42	#N/A	#N/A	protease inhibitor PI1
TGME49_225410	1.56	1.74	#N/A	histone H3 centromeric CENH3
TGME49_227860	1.56	#N/A	#N/A	hypothetical protein
TGME49_261220	2.35	#N/A	#N/A	transcription elongation factor SPT4
TGME49_270300	1.98	#N/A	#N/A	hypothetical protein
TGME49_270610	1.98	#N/A	#N/A	hypothetical protein
TGME49_252870	1.08	#N/A	1.32	hypothetical protein
TGME49_319620	1.31	#N/A	#N/A	hypothetical protein
TGME49_301180	1.31	#N/A	#N/A	SAG-related sequence SRS19F
TGME49_268980	1.98	#N/A	#N/A	hypothetical protein
TGME49_218950	2.42	#N/A	#N/A	hypothetical protein
TGME49_267970	2.35	-8.22	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_285470	1.98	#N/A	1.70	patched family protein
TGME49_240300	1.08	#N/A	#N/A	zinc finger domain, LSD1 subclass domain-containing protein
TGME49_289250	1.98	#N/A	#N/A	cyclophilin, putative
TGME49_220208	2.42	#N/A	#N/A	hypothetical protein
TGME49_257020	2.35	#N/A	#N/A	hypothetical protein
TGME49_230150	1.56	#N/A	#N/A	ChAPs (Chs5p-Arf1p-binding proteins) protein
TGME49_294990	1.98	#N/A	#N/A	hypothetical protein
TGME49_236670	-4.91	#N/A	#N/A	hypothetical protein
TGME49_309190	1.31	#N/A	#N/A	hypothetical protein
TGME49_312280	1.31	#N/A	#N/A	pre-mRNA-splicing factor ATP-dependent RNA helicase, putative
TGME49_208722	4.76	#N/A	#N/A	hypothetical protein
TGME49_256880	2.35	-8.61	#N/A	protein kinase domain-containing protein
TGME49_222850	1.56	#N/A	#N/A	stress responsive a/b barrel domain-containing protein
TGME49_219150	2.42	#N/A	#N/A	zinc finger, zz type domain-containing protein
TGME49_216030	2.42	#N/A	#N/A	hypothetical protein

FIGURE 5G

TGME49_270260	1.98	#N/A	2.03	hypothetical protein
TGME49_253750	1.08	#N/A	#N/A	PLU-1 family protein
TGME49_295420	1.31	#N/A	#N/A	hypothetical protein
TGME49_315680	1.31	#N/A	#N/A	vacuolar protein sorting-associated protein vps4, putative
TGME49_321630	1.31	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_284010	1.98	#N/A	#N/A	5'-3' exonuclease, N-terminal resolvase family domain-containing protein
TGME49_269310	1.98	#N/A	#N/A	hypothetical protein
TGME49_222240	1.56	#N/A	#N/A	hypothetical protein
TGME49_217750	2.42	#N/A	-4.62	hypothetical protein
TGME49_288000	1.98	#N/A	#N/A	hypothetical protein
TGME49_251540	1.08	#N/A	#N/A	dense granule protein GRA9
TGME49_209755	4.76	4.10	5.58	hypothetical protein
TGME49_219590	2.42	#N/A	#N/A	RuvB family 1 protein
TGME49_290190	1.98	#N/A	#N/A	hypothetical protein
TGME49_220440	2.42	#N/A	#N/A	cyclin-dependent kinase regulatory subunit protein
TGME49_260540	2.35	#N/A	#N/A	alveolin domain containing intermediate filament IMC14
TGME49_220890	2.42	#N/A	#N/A	hypothetical protein
TGME49_232160	1.56	1.08	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_216500	2.42	#N/A	#N/A	tRNA synthetase, putative
TGME49_261790	2.35	#N/A	#N/A	hypothetical protein
TGME49_245490	1.08	#N/A	#N/A	microneme protein MIC8
TGME49_202580	11.50	#N/A	1.20	ATPase, AAA family protein
TGME49_243470	1.08	4.58	4.67	hypothetical protein
TGME49_244450	1.08	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_249230	1.08	#N/A	#N/A	hypothetical protein
TGME49_268010	2.35	#N/A	#N/A	hypothetical protein
TGME49_299030	1.31	1.42	1.73	RNA recognition motif 2 protein
TGME49_265400	2.35	#N/A	#N/A	hypothetical protein
TGME49_226520	1.56	#N/A	#N/A	hypothetical protein
TGME49_293280	1.98	#N/A	#N/A	cyclin protein
TGME49_312105	1.31	-8.91	-5.44	hypothetical protein
TGME49_222050	1.56	#N/A	#N/A	hypothetical protein
TGME49_274150	1.98	#N/A	#N/A	hypothetical protein
TGME49_254710	1.08	#N/A	#N/A	serine esterase (DUF676) protein
TGME49_215210	2.42	#N/A	#N/A	hypothetical protein
TGME49_221350	2.42	#N/A	#N/A	Ctr copper transporter family protein

TGME49_222180	1.56	#N/A	#N/A	hypothetical protein
TGME49_227430	1.56	#N/A	2.76	transmembrane amino acid transporter protein
TGME49_221500	2.42	#N/A	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_220260	2.42	#N/A	#N/A	hypothetical protein
TGME49_310970	1.31	-4.58	#N/A	hypothetical protein
TGME49_239530	1.08	-6.09	#N/A	alanine-glyoxylate aminotransferase
TGME49_207160	4.76	3.72	4.66	SAG-related sequence SRS49D
TGME49_244700	1.08	-4.99	#N/A	NAD(+)/NADH kinase domain-containing protein
TGME49_253330	1.08	2.37	2.64	Rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_249260	1.08	-9.86	#N/A	cell-cycle-associated protein kinase CDK, putative
TGME49_313270	1.31	-4.80	#N/A	hypothetical protein
TGME49_208730	4.76	1.74	1.06	microneme protein, putative
TGME49_290970	1.98	2.59	2.50	8-amino-7-oxononanoate synthase
TGME49_312660	1.31	-9.00	#N/A	hypothetical protein
TGME49_209970	4.76	-9.27	#N/A	Spc97 / Spc98 family protein
TGME49_243210	1.08	-10.07	#N/A	DUF862 domain-containing protein
TGME49_319730	1.31	-8.83	#N/A	YOU2 family C2C2 zinc finger protein
TGME49_310530	1.31	-9.05	#N/A	SNF2 family N-terminal domain-containing protein
TGME49_299990	1.31	1.99	1.46	archease family protein
TGME49_208740	4.76	1.28	#N/A	microneme protein, putative
TGME49_291810	1.98	-4.40	#N/A	thioredoxin domain-containing protein
TGME49_269438	1.98	-9.21	#N/A	hypothetical protein
TGME49_241305	1.08	-8.92	#N/A	hypothetical protein
TGME49_312430	1.31	-8.70	#N/A	hypothetical protein
TGME49_209070	4.76	-9.94	#N/A	hypothetical protein
TGME49_228180	1.56	-8.92	#N/A	cytochrome C oxidase assembly factor COX15, putative
TGME49_286928	1.98	-8.89	#N/A	hypothetical protein
TGME49_318575	1.31	-8.67	#N/A	hypothetical protein
TGME49_264670	2.35	-8.85	#N/A	DNA polymerase family B protein
TGME49_229200	1.56	-8.72	#N/A	hypothetical protein
TGME49_273840	1.98	-8.66	#N/A	brix domain-containing protein
TGME49_298990	1.31	1.79	#N/A	ferredoxin NADP+ oxidoreductase FNR
TGME49_312140	1.31	-4.37	#N/A	hypothetical protein
TGME49_224600	1.56	-8.73	#N/A	GTP binding protein
TGME49_216930	2.42	1.78	#N/A	cholinephosphate cytidylyltransferase
TGME49_220370	2.42	-5.05	#N/A	hypothetical protein

FIGURE 5H

TGME49_221840	1.56	4.17	4.38	hypothetical protein
TGME49_268225	2.35	-9.66	-7.05	hypothetical protein
TGME49_265460	2.35	#N/A	#N/A	hypothetical protein
TGME49_249540	1.08	#N/A	#N/A	hypothetical protein
TGME49_266920	2.35	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_268230	2.35	-9.26	-9.26	hypothetical protein
TGME49_226580	1.56	#N/A	#N/A	hypothetical protein
TGME49_234530	1.56	#N/A	#N/A	hypothetical protein
TGME49_248110	1.08	#N/A	#N/A	hypothetical protein
TGME49_202572	11.50	#N/A	#N/A	ribophorin i protein
TGME49_220390	2.42	#N/A	#N/A	hypothetical protein
TGME49_315440	1.31	#N/A	#N/A	hypothetical protein
TGME49_223750	1.56	#N/A	#N/A	hypothetical protein
TGME49_244300	1.08	#N/A	#N/A	hypothetical protein
TGME49_258710	2.35	#N/A	#N/A	T-complex protein 10 C-terminus protein
TGME49_202770	11.50	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_232035	1.56	-8.62	-4.53	hypothetical protein
TGME49_254690	1.08	1.06	1.20	phospholipase/carboxylesterase
TGME49_280370	1.98	#N/A	#N/A	hypothetical protein
TGME49_242845	1.08	-8.83	#N/A	hypothetical protein
TGME49_226990	1.56	#N/A	#N/A	hypothetical protein
TGME49_207100	4.76	#N/A	#N/A	hypothetical protein
TGME49_219810	2.42	#N/A	#N/A	hypothetical protein
TGME49_280522	1.98	#N/A	#N/A	hypothetical protein
TGME49_315950	1.31	#N/A	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_212940	2.42	-8.65	#N/A	hypothetical protein
TGME49_203060	11.50	#N/A	#N/A	hypothetical protein
TGME49_269130	1.98	#N/A	#N/A	hypothetical protein
TGME49_258030	2.35	#N/A	#N/A	DNA polymerase
TGME49_224970	1.56	#N/A	#N/A	nucleolar protein,nop52 protein
TGME49_221180	2.42	#N/A	#N/A	hypothetical protein
TGME49_311230	1.31	#N/A	1.03	hypothetical protein
TGME49_247300	1.08	#N/A	#N/A	hypothetical protein
TGME49_319590	1.31	#N/A	#N/A	hypothetical protein
TGME49_240780	1.08	#N/A	#N/A	hypothetical protein
TGME49_208310	4.76	#N/A	#N/A	hypothetical protein
TGME49_254920	1.08	2.59	2.48	hypothetical protein

TGME49_272000	1.98	-8.53	#N/A	hypothetical protein
TGME49_232550	1.56	1.62	1.18	hypothetical protein
TGME49_245580	1.08	-8.59	#N/A	hypothetical protein
TGME49_278500	1.98	-8.69	#N/A	ribosomal RNA large subunit methyltransferase J protein
TGME49_309950	1.31	-8.44	#N/A	NLE (NUC135) domain-containing protein
TGME49_221900	1.56	-8.31	#N/A	hypothetical protein
TGME49_249560	1.08	-8.51	#N/A	DNA-directed RNA polymerase alpha chain rpoA
TGME49_264660	2.35	1.56	1.29	SAG-related sequence SRS44
TGME49_238020	1.08	-8.56	#N/A	hypothetical protein
TGME49_240970	1.08	-8.94	#N/A	hypothetical protein
TGME49_301430	1.31	-8.67	#N/A	septum formation protein maf, putative
TGME49_214340	2.42	-4.76	#N/A	hypothetical protein
TGME49_230000	1.56	-8.74	#N/A	hypothetical protein
TGME49_246060	1.08	-8.27	#N/A	DNA-dependent RNA polymerase
TGME49_263710	2.35	-5.14	#N/A	acyl-CoA:cholesterol acyltransferase alpha ACAT1-alpha
TGME49_261740	2.35	1.22	1.29	hypothetical protein
TGME49_305050	1.31	1.88	#N/A	calmodulin, putative
TGME49_246590	1.08	-8.29	#N/A	hypothetical protein
TGME49_235460	1.56	-8.56	#N/A	hypothetical protein
TGME49_266950	2.35	-9.24	#N/A	protein kinase, putative
TGME49_219290	2.42	-8.61	#N/A	F-actin-capping protein subunit beta, putative
TGME49_203760	11.50	-8.87	#N/A	hypothetical protein
TGME49_246200	1.08	-8.46	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_313960	1.31	-8.02	#N/A	ribosomal protein L19 protein
TGME49_249480	1.08	1.62	1.21	tetratricopeptide repeat-containing protein
TGME49_254080	1.08	1.09	1.41	metal cation transporter, ZIP family protein
TGME49_230110	1.56	-8.60	#N/A	hypothetical protein
TGME49_268770	1.98	-8.36	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_240660	1.08	-8.25	#N/A	hypothetical protein
TGME49_244160	1.08	-8.35	#N/A	transcription initiation factor TFIID complex subunit TAF12
TGME49_271145	1.98	-8.12	#N/A	hypothetical protein
TGME49_319940	1.31	-8.14	#N/A	hypothetical protein
TGME49_243298	1.08	-8.28	#N/A	ICE family protease (caspase) p20 domain-containing protein
TGME49_297320	1.31	-9.10	#N/A	hypothetical protein
TGME49_268170	2.35	-8.39	-4.39	hypothetical protein
TGME49_221585	2.42	-8.87	#N/A	hypothetical protein
TGME49_270620	1.98	-8.01	#N/A	DEAD/DEAH box helicase domain-containing protein

FIGURE 5i

TGME49_221480	2.42	#N/A	#N/A	hypothetical protein
TGME49_204530	11.50	#N/A	#N/A	microneme protein MIC11
TGME49_213730	2.42	#N/A	#N/A	lanthionine synthetase C family protein
TGME49_293270	1.98	#N/A	#N/A	hypothetical protein
TGME49_304880	1.31	#N/A	#N/A	hypothetical protein
TGME49_252420	1.08	2.16	#N/A	histone arginine methyltransferase PRMT3
TGME49_265790	2.35	#N/A	#N/A	hypothetical protein
TGME49_270865	1.98	#N/A	#N/A	adenylate cyclase, putative
TGME49_269950	1.98	#N/A	#N/A	hypothetical protein
TGME49_245630	1.08	#N/A	#N/A	hypothetical protein
TGME49_220330	2.42	#N/A	#N/A	hypothetical protein
TGME49_215160	2.42	#N/A	#N/A	hypothetical protein
TGME49_231890	1.56	#N/A	#N/A	beta-ketoacyl-acyl carrier protein synthase III, putative
TGME49_310210	1.31	#N/A	#N/A	hypothetical protein
TGME49_225680	1.56	-8.69	#N/A	hypothetical protein
TGME49_242640	1.08	#N/A	#N/A	hypothetical protein
TGME49_255690	2.35	#N/A	#N/A	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase domain-containing protein
TGME49_253640	1.08	#N/A	#N/A	hypothetical protein
TGME49_237500	1.08	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_308040	1.31	#N/A	#N/A	ZPR1 zinc finger domain-containing protein
TGME49_211460	4.76	#N/A	#N/A	hypothetical protein
TGME49_300048	1.31	#N/A	#N/A	hypothetical protein
TGME49_250730	1.08	#N/A	#N/A	60S ribosomal protein L7-B, putative
TGME49_306040	1.31	#N/A	#N/A	CHY zinc finger protein
TGME49_315100	1.31	3.51	3.91	hypothetical protein
TGME49_250950	1.08	#N/A	#N/A	KRUF family protein
TGME49_202520	11.50	#N/A	#N/A	hypothetical protein
TGME49_257080	2.35	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_205180	11.50	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_266450	2.35	#N/A	#N/A	lysine decarboxylase family protein
TGME49_315280	1.31	-8.97	#N/A	hypothetical protein

TGME49_278270	1.98	-8.09	#N/A	nucleolar protein, structural component of H/ACA snoRNPs, putative
TGME49_254630	1.08	1.35	1.64	CMGC kinase
TGME49_298060	1.31	-8.32	#N/A	Toxoplasma gondii family C protein
TGME49_297510	1.31	-8.78	#N/A	hypothetical protein
TGME49_285850	1.98	-8.30	#N/A	peptidyl-prolyl cis-trans isomerase, FKBP-type domain-containing protein
TGME49_313480	1.31	-8.44	#N/A	hypothetical protein
TGME49_257290	2.35	-8.13	#N/A	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_313200	1.31	-8.34	#N/A	leucine rich repeat-containing protein
TGME49_252440	1.08	2.33	2.11	peptidase c13 family protein
TGME49_254365	1.08	1.24	1.44	phosphatidate cytidylyltransferase
TGME49_238190	1.08	1.55	#N/A	DNA-directed RNA polymerase II RPB3
TGME49_267340	2.35	1.84	#N/A	hypothetical protein
TGME49_262050	2.35	1.14	1.18	rhoptry kinase family protein ROP39
TGME49_204490	11.50	-7.99	#N/A	hypothetical protein
TGME49_232510	1.56	-8.65	#N/A	hypothetical protein
TGME49_283585	1.98	-8.28	#N/A	hypothetical protein
TGME49_247610	1.08	-8.03	#N/A	small nuclear ribonucleoprotein E, putative
TGME49_240480	1.08	-8.00	#N/A	cpw-wpc domain-containing protein
TGME49_244200	1.08	1.00	#N/A	2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor, putative
TGME49_258940	2.35	-7.94	#N/A	acylphosphatase family protein
TGME49_317705	1.31	-5.13	#N/A	enoyl-CoA hydratase/isomerase family protein
TGME49_280580	1.98	1.89	2.66	SAG-related sequence SRS35B
TGME49_293500	1.98	-8.17	#N/A	hypothetical protein
TGME49_227115	1.56	-8.32	#N/A	hypothetical protein
TGME49_316090	1.31	-7.84	#N/A	RNAse P Rpr2/Rpp21 subunit domain-containing protein
TGME49_253790	1.08	1.16	1.53	zinc finger (CCCH type) motif-containing protein
TGME49_258780	2.35	-8.93	#N/A	OTU family cysteine protease
TGME49_275780	1.98	-7.96	#N/A	hypothetical protein
TGME49_220230	2.42	-4.57	#N/A	leucine rich repeat-containing protein
TGME49_255215	1.08	-8.40	#N/A	hypothetical protein
TGME49_205010	11.50	1.08	#N/A	U2 small nuclear ribonucleoprotein family protein, putative

FIGURE 5J

TGME49_330000	1.31	3.95	4.62	cytochrome b
TGME49_207065	4.76	#N/A	#N/A	hypothetical protein
TGME49_209095	4.76	#N/A	#N/A	hypothetical protein
TGME49_238510	1.08	#N/A	#N/A	hypothetical protein
TGME49_232340	1.56	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_250100	1.08	#N/A	#N/A	hypothetical protein
TGME49_228980	1.56	-8.09	-4.97	hypothetical protein
TGME49_321450	1.31	#N/A	#N/A	Myb family DNA-binding domain-containing protein
TGME49_260410	2.35	#N/A	#N/A	hypothetical protein
TGME49_225990	1.56	#N/A	#N/A	acyl transferase domain-containing protein
TGME49_205490	11.50	#N/A	#N/A	integral membrane protein, putative
TGME49_236800	1.08	#N/A	#N/A	hypothetical protein
TGME49_257350	2.35	#N/A	1.09	eukaryotic translation initiation factor, putative
TGME49_223660	1.56	#N/A	#N/A	50S ribosomal protein L4, putative
TGME49_306890	1.31	#N/A	#N/A	hypothetical protein
TGME49_230180	1.56	#N/A	#N/A	hypothetical protein
TGME49_203280	11.50	#N/A	#N/A	hypothetical protein
TGME49_268680	1.98	#N/A	#N/A	hypothetical protein
TGME49_223390	1.56	#N/A	#N/A	activating signal cointegrator 1 complex subunit 3 family 1 ASCC3L1, putative
TGME49_206450	11.50	#N/A	#N/A	autophagy-related cysteine peptidase atg4, putative
TGME49_273970	1.98	#N/A	#N/A	CorA family Mg2+ transporter protein
TGME49_277270	1.98	#N/A	#N/A	NTPase II
TGME49_263420	2.35	#N/A	#N/A	ubiquitin-specific protease USP4
TGME49_239710	1.08	-8.73	#N/A	phosphomannomutase
TGME49_286480	1.98	#N/A	#N/A	hypothetical protein
TGME49_278230	1.98	#N/A	#N/A	prenyltransferase and squalene oxidase repeat-containing protein
TGME49_207930	4.76	#N/A	#N/A	phosphatidylethanolamine-binding protein
TGME49_219820	2.42	#N/A	#N/A	polyubiquitin UbC, putative
TGME49_258870	2.35	#N/A	#N/A	hypothetical protein
TGME49_243430	1.08	#N/A	#N/A	OTU family cysteine protease
TGME49_215910	2.42	#N/A	#N/A	hypothetical protein
TGME49_259200	2.35	#N/A	#N/A	Na+/H+ exchanger NHE1
TGME49_225900	1.56	#N/A	#N/A	hypothetical protein
TGME49_251400	1.08	#N/A	1.27	hypothetical protein

TGME49_279540	1.98	-8.17	#N/A	hypothetical protein
TGME49_244645	1.08	-7.70	1.38	hypothetical protein
TGME49_250900	1.08	-7.59	#N/A	hypothetical protein
TGME49_301310	1.31	-4.46	#N/A	hypothetical protein
TGME49_248670	1.08	1.02	#N/A	V-type H(+)-translocating pyrophosphatase VP1
TGME49_223150	1.56	-8.54	#N/A	START domain-containing protein
TGME49_230080	1.56	-8.52	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_226700	1.56	-7.84	#N/A	nuclease, putative
TGME49_235478	1.56	-4.89	#N/A	pantothenate kinase
TGME49_248440	1.08	-8.41	#N/A	hypothetical protein
TGME49_255930	2.35	-8.12	#N/A	hypothetical protein
TGME49_226280	1.56	-7.80	#N/A	ribosomal protein L28, putative
TGME49_221370	2.42	-8.41	#N/A	hypothetical protein
TGME49_310290	1.31	-7.56	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_264752	2.35	-7.90	#N/A	HEAT repeat-containing protein
TGME49_309390	1.31	2.01	#N/A	hypothetical protein
TGME49_314790	1.31	-5.50	#N/A	small nuclear ribonucleoprotein G, putative
TGME49_309080	1.31	-7.56	#N/A	hypothetical protein
TGME49_239087	1.08	-8.18	#N/A	hypothetical protein
TGME49_269430	1.98	-8.29	#N/A	polyprenyl synthetase superfamily protein
TGME49_289000	1.98	-8.54	#N/A	hypothetical protein
TGME49_217450	2.42	-8.05	#N/A	general transcription factor IIH polypeptide 5 GTF2H5
TGME49_277700	1.98	-7.85	#N/A	ribosomal protein S14 precursor, putative
TGME49_281950	1.98	-8.54	#N/A	membrane protein, putative
TGME49_209930	4.76	-8.42	#N/A	hypothetical protein
TGME49_316470	1.31	-8.45	#N/A	hypothetical protein
TGME49_323010	1.31	-7.77	#N/A	hypothetical protein
TGME49_289010	1.98	-8.16	#N/A	RNA recognition motif-containing protein
TGME49_243760	1.08	-8.49	#N/A	hypothetical protein
TGME49_263215	2.35	-7.63	-4.51	hypothetical protein
TGME49_306338	1.31	-8.39	#N/A	dynein gamma chain, flagellar outer arm, putative
TGME49_254930	1.08	1.13	#N/A	hypothetical protein
TGME49_293860	1.98	-4.63	#N/A	hypothetical protein
TGME49_236990	1.08	1.82	1.74	beta-ketoacyl synthase, N-terminal domain-containing protein

FIGURE 5K

TGME49_200450	11.50	#N/A	#N/A	hypothetical protein
TGME49_242810	1.08	#N/A	#N/A	hypothetical protein
TGME49_302055	1.31	#N/A	#N/A	ribosomal protein RPS12
TGME49_259040	2.35	#N/A	#N/A	hypothetical protein
TGME49_314500	1.31	#N/A	#N/A	subtilisin SUB2
TGME49_295430	1.31	#N/A	#N/A	hypothetical protein
TGME49_250870	1.08	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_287515	1.98	-7.54	#N/A	hypothetical protein
TGME49_260430	2.35	3.55	2.41	hypothetical protein
TGME49_279350	1.98	#N/A	#N/A	hypothetical protein
TGME49_248850	1.08	#N/A	#N/A	methionine aminopeptidase
TGME49_285700	1.98	#N/A	#N/A	ubiquitin fusion degradation protein UFD1AP
TGME49_253950	1.08	#N/A	#N/A	protein fam50a, putative
TGME49_318440	1.31	#N/A	#N/A	helicase associated domain (ha2) protein
TGME49_200430	11.50	#N/A	#N/A	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_283702	1.98	#N/A	#N/A	FATC domain-containing protein
TGME49_262080	2.35	#N/A	#N/A	hypothetical protein
TGME49_293000	1.98	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_261480	2.35	#N/A	#N/A	phosphatidyl serine synthase
TGME49_204360	11.50	#N/A	#N/A	subtilisin SUB4
TGME49_318170	1.31	#N/A	#N/A	hypothetical protein
TGME49_224620	1.56	#N/A	#N/A	hypothetical protein
TGME49_301170	1.31	-7.88	#N/A	SAG-related sequence SRS19D
TGME49_225550	1.56	#N/A	#N/A	phosphatidylserine decarboxylase
TGME49_213460	2.42	1.08	1.36	hypothetical protein
TGME49_201710	11.50	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_291890	1.98	#N/A	#N/A	microneme protein MIC1
TGME49_253700	1.08	#N/A	#N/A	transporter, major facilitator family protein
TGME49_252065	1.08	#N/A	1.68	KRUF family protein
TGME49_278940	1.98	#N/A	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_209770	4.76	#N/A	#N/A	helicase, putative
TGME49_285950	1.98	#N/A	#N/A	hypothetical protein
TGME49_217160	2.42	#N/A	2.35	Der1 family protein
TGME49_286010	1.98	#N/A	#N/A	hypothetical protein
TGME49_286050	1.98	#N/A	#N/A	hypothetical protein

TGME49_220150	2.42	-8.31	#N/A	50S ribosomal protein L16, putative
TGME49_236130	1.56	-8.58	#N/A	signal recognition particle (SRP9) domain-containing protein
TGME49_284170	1.98	-7.74	#N/A	DHHC zinc finger domain-containing protein
TGME49_321170	1.31	1.91	2.39	Toxoplasma gondii family C protein
TGME49_218790	2.42	-7.73	#N/A	elongation factor G C-terminus domain-containing protein
TGME49_310200	1.31	-8.08	#N/A	hypothetical protein
TGME49_290240	1.98	-8.41	#N/A	hypothetical protein
TGME49_288290	1.98	-8.19	#N/A	hypothetical protein
TGME49_244680	1.08	-7.56	#N/A	hypothetical protein
TGME49_242118	1.08	-8.30	-4.57	myosin-light-chain kinase
TGME49_224200	1.56	-7.93	#N/A	tRNA pseudouridine synthase
TGME49_220480	2.42	-7.77	#N/A	hypothetical protein
TGME49_229290	1.56	-7.60	#N/A	kelch repeat-containing protein
TGME49_295320	1.31	-8.26	#N/A	embryo sac development arrest EDA7, putative
TGME49_243265	1.08	-7.82	#N/A	protamine P1 protein
TGME49_229720	1.56	-8.10	#N/A	hypothetical protein
TGME49_220530	2.42	-8.48	#N/A	AP2 domain transcription factor AP2V-1
TGME49_226090	1.56	-7.82	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_270050	1.98	1.95	#N/A	hypothetical protein
TGME49_270960	1.98	-8.11	#N/A	hypothetical protein
TGME49_269830	1.98	2.93	#N/A	RAP domain-containing protein
TGME49_288845	1.98	-8.19	#N/A	hypothetical protein
TGME49_257160	2.35	1.16	1.02	hypothetical protein
TGME49_243615	1.08	-7.78	#N/A	hypothetical protein
TGME49_297460	1.31	-8.44	#N/A	hypothetical protein
TGME49_254200	1.08	1.84	#N/A	anticodon binding domain-containing protein
TGME49_248800	1.08	-7.78	#N/A	hypothetical protein
TGME49_205050	11.50	-8.15	-5.06	hypothetical protein
TGME49_254135	1.08	-7.46	#N/A	hypothetical protein
TGME49_311790	1.31	1.99	#N/A	hypothetical protein
TGME49_233838	1.56	-7.66	#N/A	PET112 family, C terminal region domain-containing protein
TGME49_227270	1.56	-8.24	#N/A	hypothetical protein
TGME49_254840	1.08	-7.96	#N/A	tetratricopeptide repeat-containing protein
TGME49_288240	1.98	-7.71	#N/A	hypothetical protein
TGME49_242110	1.08	-7.95	#N/A	rhoptry kinase family protein ROP38

FIGURE 5L

TGME49_269010	1.98	#N/A	#N/A	AP2 domain transcription factor AP2VIII-7
TGME49_248990	1.08	#N/A	#N/A	hypothetical protein
TGME49_217410	2.42	#N/A	#N/A	hypothetical protein
TGME49_253180	1.08	#N/A	1.08	hypothetical protein
TGME49_232360	1.56	#N/A	#N/A	exonuclease
TGME49_301400	1.31	#N/A	#N/A	hypothetical protein
TGME49_211330	4.76	#N/A	#N/A	methionine aminopeptidase
TGME49_205265	11.50	#N/A	#N/A	transporter, cation channel family protein
TGME49_277490	1.98	#N/A	#N/A	hypothetical protein
TGME49_279100	1.98	#N/A	#N/A	hypothetical protein
TGME49_216140	2.42	2.20	2.49	tetratricopeptide repeat-containing protein
TGME49_263190	2.35	#N/A	#N/A	adenylosuccinate lyase, putative
TGME49_230820	1.56	#N/A	#N/A	hypothetical protein
TGME49_239748	1.08	#N/A	#N/A	hypothetical protein
TGME49_293650	1.98	#N/A	#N/A	hypothetical protein
TGME49_256840	2.35	#N/A	#N/A	hypothetical protein
TGME49_305990	1.31	1.86	1.67	hypothetical protein
TGME49_251770	1.08	#N/A	1.01	hypothetical protein
TGME49_305930	1.31	#N/A	#N/A	hypothetical protein
TGME49_264220	2.35	#N/A	#N/A	hypothetical protein
TGME49_217790	2.42	#N/A	#N/A	S1 RNA binding domain-containing protein
TGME49_310410	1.31	-7.42	#N/A	WD domain, G-beta repeat-containing protein
TGME49_266480	2.35	#N/A	#N/A	hypothetical protein
TGME49_247030	1.08	#N/A	#N/A	hypothetical protein
TGME49_216810	2.42	#N/A	#N/A	5'-nucleotidase, C-terminal domain-containing protein
TGME49_312600	1.31	#N/A	1.07	heat shock protein HSP21
TGME49_254150	1.08	#N/A	#N/A	hypothetical protein
TGME49_202730	11.50	#N/A	#N/A	hypothetical protein
TGME49_319580	1.31	#N/A	#N/A	hypothetical protein
TGME49_255980	2.35	#N/A	#N/A	hypothetical protein
TGME49_213300	2.42	#N/A	#N/A	hypothetical protein
TGME49_242870	1.08	#N/A	#N/A	histone lysine methyltransferase, SET, putative
TGME49_270720	1.98	#N/A	#N/A	hypothetical protein
TGME49_274130	1.98	#N/A	#N/A	TBC domain-containing protein
TGME49_293900	1.98	#N/A	#N/A	sporozoite protein with an altered thrombospondin repeat SPATR

TGME49_285510	1.98	1.03	1.03	hypothetical protein
TGME49_204140	11.50	-7.83	#N/A	PHD-finger domain-containing protein
TGME49_269940	1.98	-7.77	#N/A	zinc finger motif, C2HC5-type protein
TGME49_300130	1.31	2.35	#N/A	apical membrane antigen 1 domain-containing protein
TGME49_201180	11.50	-8.19	#N/A	hypothetical protein
TGME49_226670	1.56	-7.51	#N/A	hypothetical protein
TGME49_316480	1.31	-7.54	#N/A	XRN 5'-3' exonuclease N-terminus protein
TGME49_314530	1.31	-7.84	#N/A	RPAP1 family, C-terminal protein
TGME49_300360	1.31	-8.03	#N/A	ADP/ATP translocase
TGME49_215400	2.42	-8.32	#N/A	RNA recognition motif-containing protein
TGME49_210310	4.76	-7.90	#N/A	hypothetical protein
TGME49_238070	1.08	-8.06	#N/A	glutaredoxin domain-containing protein
TGME49_209460	4.76	-7.93	#N/A	hypothetical protein
TGME49_202240	11.50	-7.95	#N/A	RAP domain-containing protein
TGME49_301280	1.31	-7.38	#N/A	hypothetical protein
TGME49_207180	4.76	-7.87	#N/A	indole-3-glycerol phosphate synthase domain-containing protein
TGME49_224150	1.56	-7.63	#N/A	hypothetical protein
TGME49_268740	1.98	-7.62	#N/A	hypothetical protein
TGME49_216370	2.42	-7.59	#N/A	hypothetical protein
TGME49_246930	1.08	1.17	1.29	calmodulin CAM1
TGME49_222210	1.56	-4.48	#N/A	SPFH domain / Band 7 family protein
TGME49_309610	1.31	-7.99	#N/A	hypothetical protein
TGME49_251590	1.08	-4.36	#N/A	hypothetical protein
TGME49_316490	1.31	-7.84	#N/A	hypothetical protein
TGME49_221980	1.56	-7.78	#N/A	U1 zinc finger protein
TGME49_223530	1.56	1.30	#N/A	hypothetical protein
TGME49_318380	1.31	-8.30	#N/A	hypothetical protein
TGME49_246690	1.08	-7.90	#N/A	alpha amylase, catalytic domain-containing protein
TGME49_247290	1.08	-8.11	#N/A	hypothetical protein
TGME49_262000	2.35	-7.73	#N/A	AP2 domain transcription factor AP2VIIb-2
TGME49_277770	1.98	-8.16	#N/A	hypothetical protein
TGME49_285540	1.98	-7.78	#N/A	DNA-directed DNA polymerase
TGME49_232220	1.56	-7.38	#N/A	SWIB/MDM2 domain-containing protein
TGME49_258826	2.35	-8.03	#N/A	hypothetical protein
TGME49_228040	1.56	-7.48	#N/A	PPIC-type PPIASE domain-containing protein

FIGURE 5M

TGME49_211470	4.76	#N/A	#N/A	Fcf2 pre-rRNA processing protein
TGME49_301300	1.31	-8.04	#N/A	hypothetical protein
TGME49_291600	1.98	#N/A	#N/A	gamma interferon inducible lysosomal thiol reductase (GILT) protein
TGME49_272380	1.98	#N/A	#N/A	hypothetical protein
TGME49_242670	1.08	-7.47	#N/A	hypothetical protein
TGME49_207040	4.76	#N/A	#N/A	hypothetical protein
TGME49_313340	1.31	#N/A	#N/A	hypothetical protein
TGME49_236620	2.44	#N/A	#N/A	protein kinase (incomplete catalytic triad)
TGME49_262590	2.35	-7.98	-5.38	hypothetical protein
TGME49_226060	1.56	#N/A	#N/A	transmembrane amino acid transporter protein
TGME49_273050	1.98	#N/A	#N/A	hypothetical protein
TGME49_308590	1.31	#N/A	#N/A	Mov34/MPN/PAD-1 family protein
TGME49_313418	1.31	#N/A	#N/A	hypothetical protein
TGME49_200590	11.50	#N/A	#N/A	Toxoplasma gondii family C protein
TGME49_237130	1.08	4.00	4.35	cytochrome b, putative
TGME49_273280	1.98	#N/A	#N/A	hypothetical protein
TGME49_269700	1.98	#N/A	#N/A	NLI interacting factor family phosphatase
TGME49_312380	1.31	-8.23	#N/A	tetratricopeptide repeat-containing protein
TGME49_297900	1.31	#N/A	#N/A	hypothetical protein
TGME49_213480	2.42	#N/A	#N/A	hypothetical protein
TGME49_237530	1.08	#N/A	#N/A	hypothetical protein
TGME49_200350	11.50	#N/A	#N/A	subtilisin SUB3
TGME49_254380	1.08	#N/A	1.62	ribosomal protein L11, putative
TGME49_202610	11.50	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_240240	1.08	#N/A	#N/A	subtilisin SUB5
TGME49_255060	1.08	3.16	3.30	cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_309600	1.31	#N/A	#N/A	hypothetical protein
TGME49_271840	1.98	#N/A	#N/A	hypothetical protein
TGME49_320620	1.31	#N/A	#N/A	queuine tRNA ribosyl transferase
TGME49_289620	1.98	#N/A	#N/A	cathepsin CPC1
TGME49_226260	1.56	#N/A	#N/A	hypothetical protein
TGME49_255190	1.08	#N/A	#N/A	myosin C
TGME49_218850	2.42	-7.60	#N/A	ribosomal protein RPS9
TGME49_277560	1.98	-8.40	#N/A	hypothetical protein
TGME49_254555	1.08	#N/A	#N/A	histone lysine acetyltransferase GCN5-A
TGME49_225510	1.56	#N/A	#N/A	RAP domain-containing protein

TGME49_311060	1.31	-7.75	#N/A	metal-dependent phosphohydrolase HD domain-containing protein
TGME49_210478	4.76	2.80	#N/A	hypothetical protein
TGME49_309000	1.31	-7.64	#N/A	hypothetical protein
TGME49_305610	1.31	-7.34	#N/A	hypothetical protein
TGME49_273530	1.98	-7.78	#N/A	flagellar associated protein
TGME49_246560	1.08	1.01	#N/A	vacuolar ATP synthase subunit g, putative
TGME49_249450	1.08	-7.65	#N/A	hypothetical protein
TGME49_258820	2.35	1.08	1.48	hypothetical protein
TGME49_310910	1.31	1.39	#N/A	WD domain, G-beta repeat-containing protein
TGME49_264070	2.35	-7.41	#N/A	F5/8 type C domain-containing protein
TGME49_310250	1.31	-7.69	#N/A	hypothetical protein
TGME49_217470	2.42	-7.70	#N/A	hypothetical protein
TGME49_224170	1.56	2.43	2.22	SAG-related sequence SRS60A
TGME49_219640	2.42	-7.67	#N/A	hypothetical protein
TGME49_271280	1.98	-7.40	#N/A	60S ribosome subunit biogenesis protein NIP7, putative
TGME49_262810	2.35	-7.54	#N/A	iron donor protein CyaY protein
TGME49_305455	1.31	-7.11	#N/A	hypothetical protein
TGME49_241860	1.08	-7.70	#N/A	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein PigA, family GT4 protein
TGME49_270940	1.98	-7.74	#N/A	hypothetical protein
TGME49_232240	1.56	-7.27	#N/A	hypothetical protein
TGME49_304640	1.31	-7.64	#N/A	hypothetical protein
TGME49_255160	1.08	-7.75	#N/A	hypothetical protein
TGME49_299270	1.31	1.55	#N/A	hypothetical protein
TGME49_273550	1.98	-8.07	#N/A	hypothetical protein
TGME49_251530	1.08	-7.49	#N/A	hypothetical protein
TGME49_299070	1.31	1.18	1.47	pyruvate kinase PyKII
TGME49_205625	11.50	-7.77	#N/A	hypothetical protein
TGME49_283740	1.98	-7.60	#N/A	RNA recognition motif-containing protein
TGME49_262630	2.35	-7.33	#N/A	hypothetical protein
TGME49_268350	1.98	-7.61	#N/A	hypothetical protein
TGME49_218192	2.42	-7.59	#N/A	hypothetical protein
TGME49_297925	1.31	-7.46	#N/A	HesB-like domain-containing protein
TGME49_221880	1.56	-8.02	#N/A	hypothetical protein
TGME49_215347	2.42	-7.36	#N/A	hypothetical protein
TGME49_246140	1.08	-8.20	#N/A	hypothetical protein
TGME49_318490	1.31	-7.78	#N/A	hypothetical protein

FIGURE 5N

TGME49_229020	1.56	#N/A	#N/A	cell-cycle-associated protein kinase CDK, putative
TGME49_221490	2.42	#N/A	#N/A	cell cycle regulator protein
TGME49_253960	1.08	#N/A	1.29	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_260520	2.35	#N/A	1.01	hypothetical protein
TGME49_288800	1.98	#N/A	#N/A	endonuclease/exonuclease/phosphatase family protein
TGME49_222370	1.56	1.35	1.97	SAG-related sequence SRS13
TGME49_313160	1.31	#N/A	#N/A	hypothetical protein
TGME49_299980	1.31	#N/A	1.08	hypothetical protein
TGME49_216335	2.42	2.91	1.84	hypothetical protein
TGME49_288820	1.98	#N/A	1.04	hypothetical protein
TGME49_244540	1.08	#N/A	#N/A	mitochondrial carrier superfamily protein
TGME49_310310	1.31	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_227780	1.56	#N/A	#N/A	hypothetical protein
TGME49_234670	1.56	#N/A	#N/A	actin-like family protein
TGME49_299240	1.31	#N/A	#N/A	hypothetical protein
TGME49_244510	1.08	-7.66	#N/A	AP2 domain transcription factor AP2VI-3
TGME49_253570	1.08	#N/A	#N/A	hypothetical protein
TGME49_225500	1.56	#N/A	#N/A	hypothetical protein
TGME49_249698	1.08	#N/A	#N/A	hypothetical protein
TGME49_239290	1.08	#N/A	#N/A	hypothetical protein
TGME49_240960	1.08	#N/A	#N/A	AIG2 family protein
TGME49_275980	1.98	#N/A	#N/A	coenzyme q (ubiquinone) biosynthesis protein coq4 protein
TGME49_233220	1.56	#N/A	#N/A	hypothetical protein
TGME49_259650	2.35	#N/A	#N/A	hypothetical protein
TGME49_209820	4.76	#N/A	#N/A	syntaxin protein
TGME49_206700	4.76	#N/A	#N/A	hypothetical protein
TGME49_286740	1.98	#N/A	#N/A	microneme-like protein
TGME49_263580	2.35	#N/A	#N/A	bromodomain-containing protein
TGME49_273310	1.98	#N/A	#N/A	hypothetical protein
TGME49_205190	11.50	#N/A	#N/A	hypothetical protein
TGME49_204130	11.50	#N/A	#N/A	perforin-like protein PLP1
TGME49_203050	11.50	#N/A	#N/A	AP2 domain transcription factor AP2VIIa-6
TGME49_313680	1.31	#N/A	#N/A	hypothetical protein
TGME49_201390	11.50	#N/A	#N/A	hypothetical protein
TGME49_223480	1.56	#N/A	#N/A	sushi domain (scr repeat) domain-containing protein

TGME49_241310	1.08	-7.57	#N/A	hypothetical protein
TGME49_230920	1.56	-7.70	#N/A	adaptor complexes medium subunit family protein
TGME49_242580	1.08	-7.80	#N/A	iron only hydrogenase large subunit, c-terminal domain-containing protein
TGME49_253530	1.08	-7.47	#N/A	hypothetical protein
TGME49_314680	1.31	-7.00	#N/A	hypothetical protein
TGME49_235640	1.56	-7.65	#N/A	formyl transferase domain-containing protein
TGME49_244140	1.08	-7.17	#N/A	hypothetical protein
TGME49_243610	1.08	-7.67	#N/A	C-5 cytosine-specific DNA methylase superfamily protein
TGME49_209530	4.76	-7.62	#N/A	hypothetical protein
TGME49_269750	1.98	-7.63	#N/A	CrcB family protein
TGME49_211400	4.76	-7.61	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_222160	1.56	1.75	#N/A	aldehyde dehydrogenase
TGME49_314295	1.31	2.11	#N/A	ribosomal l25 family protein
TGME49_268340	1.98	2.13	#N/A	glycosyltransferase family 28 C-terminal domain-containing protein
TGME49_314920	1.31	-7.87	#N/A	hypothetical protein
TGME49_266870	2.35	-7.38	#N/A	transporter, major facilitator family protein
TGME49_313273	1.31	-7.84	#N/A	hypothetical protein
TGME49_277050	1.98	-7.26	#N/A	hypothetical protein
TGME49_291010	1.98	-7.55	#N/A	hypothetical protein
TGME49_204055	11.50	-7.60	#N/A	hypothetical protein
TGME49_297495	1.31	-6.99	#N/A	hypothetical protein
TGME49_262510	2.35	-7.33	#N/A	GTP-binding protein engB, putative
TGME49_223580	1.56	-7.81	#N/A	mediator complex subunit MED4
TGME49_249930	1.08	-7.03	#N/A	hypothetical protein
TGME49_286550	1.98	1.37	#N/A	hypothetical protein
TGME49_261410	2.35	-7.58	#N/A	protein-tyrosine-phosphatase
TGME49_301160	1.31	-7.44	#N/A	SAG-related sequence SRS19C
TGME49_261030	2.35	-7.65	#N/A	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_274120	1.98	1.07	#N/A	hypothetical protein
TGME49_323320	1.31	-7.24	#N/A	hypothetical protein
TGME49_216840	2.42	-7.25	#N/A	hypothetical protein
TGME49_257980	2.35	-7.57	#N/A	ribosome recycling factor protein
TGME49_271190	1.98	-7.37	#N/A	bicoid-interacting protein BIN3
TGME49_291330	1.98	1.08	#N/A	RNA recognition motif-containing protein
TGME49_258420	2.35	-4.66	#N/A	hypothetical protein

FIGURE 5o

TGME49_245428	1.08	#N/A	#N/A	hypothetical protein
TGME49_265260	2.35	#N/A	#N/A	hypothetical protein
TGME49_316220	1.31	#N/A	#N/A	mediator complex subunit MED6
TGME49_263390	2.35	#N/A	1.37	hypothetical protein
TGME49_313710	1.31	#N/A	#N/A	hypothetical protein
TGME49_237550	1.08	#N/A	#N/A	hypothetical protein
TGME49_285710	1.98	1.37	1.72	hypothetical protein
TGME49_208550	4.76	#N/A	#N/A	hypothetical protein
TGME49_233830	1.56	-7.61	#N/A	hypothetical protein
TGME49_260150	2.35	-7.18	1.72	tetratricopeptide repeat-containing protein
TGME49_231800	1.56	#N/A	#N/A	helicase, putative
TGME49_269420	1.98	#N/A	1.15	hypothetical protein
TGME49_262900	2.35	#N/A	#N/A	hypothetical protein
TGME49_207980	4.76	#N/A	#N/A	PIG-P protein
TGME49_253600	1.08	#N/A	#N/A	hypothetical protein
TGME49_249680	1.08	#N/A	#N/A	RNA polymerase II associated Paf1 complex component PAF1
TGME49_212735	2.42	#N/A	#N/A	hypothetical protein
TGME49_217692	2.42	-7.66	#N/A	hypothetical protein
TGME49_253940	1.08	#N/A	1.02	CAM Kinase family, incomplete catalytic triad
TGME49_221190	2.42	#N/A	#N/A	mma cleavage factor family protein, putative
TGME49_257700	2.35	#N/A	#N/A	hypothetical protein
TGME49_218720	2.42	#N/A	#N/A	calcium-dependent protein kinase CDPK6
TGME49_249840	1.08	#N/A	#N/A	dynein heavy chain 2, putative
TGME49_318610	1.31	#N/A	#N/A	AP2 domain transcription factor AP2IV-3
TGME49_235360	1.56	#N/A	#N/A	hypothetical protein
TGME49_267775	2.35	-7.80	#N/A	hypothetical protein
TGME49_233540	1.56	#N/A	#N/A	transporter, major facilitator family protein
TGME49_291590	1.98	-7.62	#N/A	hypothetical protein
TGME49_286240	1.98	#N/A	#N/A	kelch repeat protein, putative
TGME49_266930	2.35	#N/A	#N/A	general transcription factor IIH polypeptide 3 GTF2H3
TGME49_236870	1.08	#N/A	#N/A	hypothetical protein
TGME49_234230	1.56	#N/A	#N/A	hypothetical protein
TGME49_225490	1.56	#N/A	#N/A	calcium-dependent protein kinase CDPK2
TGME49_280410	1.98	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_258100	2.35	-7.80	#N/A	TPR repeat region protein
TGME49_276210	1.98	#N/A	1.17	phosphoglycerate mutase family protein

TGME49_270630	1.98	-7.29	#N/A	hypothetical protein
TGME49_219720	2.42	1.15	#N/A	Ras-related protein Rab-5C, putative
TGME49_308930	1.31	1.34	1.46	50S ribosomal protein L33, putative
TGME49_329100	1.31	-7.28	#N/A	Toxoplasma gondii family C protein
TGME49_244580	1.08	-7.43	#N/A	L1P family of ribosomal protein
TGME49_255870	2.35	-7.37	#N/A	WD domain, G-beta repeat-containing protein
TGME49_216190	2.42	-7.43	#N/A	hypothetical protein
TGME49_254140	1.08	-6.57	#N/A	DNA-directed RNA polymerase II RPABC4
TGME49_313090	1.31	-7.45	#N/A	hypothetical protein
TGME49_210770	4.76	-7.39	#N/A	hypothetical protein
TGME49_271290	1.98	-7.33	#N/A	hypothetical protein
TGME49_273540	1.98	-7.60	#N/A	phosphatidylserine synthase, putative
TGME49_320580	1.31	-7.38	#N/A	hypothetical protein
TGME49_268985	1.98	-7.07	#N/A	hypothetical protein
TGME49_262430	2.35	1.19	1.17	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
TGME49_239310	1.08	1.33	#N/A	ribulose 5-phosphate isomerase
TGME49_253680	1.08	-7.15	#N/A	hypothetical protein
TGME49_225360	1.56	-7.78	#N/A	hypothetical protein
TGME49_244430	1.08	-7.77	#N/A	pseudouridylate synthase, putative
TGME49_263323	2.35	-7.32	#N/A	tetratricopeptide repeat protein 11, putative
TGME49_264420	2.35	-7.53	#N/A	lipoprotein, putative
TGME49_275470	1.98	-7.33	#N/A	dense granule protein GRA15
TGME49_220212	2.42	-7.25	#N/A	pseudouridine synthase
TGME49_263430	2.35	-7.50	#N/A	3-hydroxyisobutyrate dehydrogenase
TGME49_207970	4.76	-7.09	-5.26	HEAT repeat-containing protein
TGME49_254260	1.08	1.66	#N/A	COX19 cytochrome c oxidase assembly family protein
TGME49_289900	1.98	-7.04	#N/A	n-acetyltransferase family protein
TGME49_316610	1.31	-7.62	#N/A	hypothetical protein
TGME49_271250	1.98	-7.50	#N/A	hypothetical protein
TGME49_201840	11.50	1.04	#N/A	aspartyl protease ASP1
TGME49_312680	1.31	1.54	#N/A	60S ribosomal protein L27, putative
TGME49_233930	1.56	-7.30	#N/A	CAF1 family ribonuclease
TGME49_306455	1.31	2.46	#N/A	hypothetical protein
TGME49_223725	1.56	-7.40	#N/A	hypothetical protein
TGME49_258900	2.35	1.36	#N/A	hypothetical protein
TGME49_222155	1.56	-6.92	#N/A	hypothetical protein

FIGURE 5P

TGME49_253100	1.08	1.49	1.81	hypothetical protein
TGME49_234510	1.56	1.01	#N/A	ankyrin repeat-containing protein
TGME49_294690	1.98	#N/A	#N/A	rhomboid protease ROM5
TGME49_285480	1.98	#N/A	#N/A	hypothetical protein
TGME49_227560	1.56	#N/A	#N/A	IWS1 transcription factor, putative
TGME49_234980	1.56	-4.80	#N/A	hypothetical protein
TGME49_255330	2.35	#N/A	#N/A	hypothetical protein
TGME49_285170	1.98	-7.62	#N/A	methyltransferase small, putative
TGME49_232760	1.56	#N/A	#N/A	protein phosphatase inhibitor IPP2
TGME49_232630	1.56	#N/A	#N/A	hypothetical protein
TGME49_216700	2.42	#N/A	#N/A	hypothetical protein
TGME49_314250	1.31	3.09	2.65	bradyzoite rhoptry protein BRP1
TGME49_283550	1.98	#N/A	#N/A	hypothetical protein
TGME49_267580	2.35	1.04	#N/A	cyclin2 related protein
TGME49_203160	11.50	#N/A	#N/A	hypothetical protein
TGME49_263490	2.35	#N/A	#N/A	ubiquitin conjugating enzyme E2, putative
TGME49_293780	1.98	1.77	1.90	hypothetical protein
TGME49_299250	1.31	#N/A	#N/A	hypothetical protein
TGME49_261075	2.35	#N/A	1.60	hypothetical protein
TGME49_306510	1.31	#N/A	#N/A	hypothetical protein
TGME49_234460	1.56	1.01	#N/A	hypothetical protein
TGME49_254770	1.08	1.21	#N/A	Ser/Thr phosphatase family protein
TGME49_297647	1.31	#N/A	#N/A	hypothetical protein
TGME49_237425	1.08	#N/A	#N/A	AP2 domain transcription factor AP2X-6
TGME49_207665	4.76	#N/A	#N/A	kinesin motor domain-containing protein
TGME49_205110	11.50	-7.19	#N/A	hypothetical protein
TGME49_246120	1.08	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_245432	1.08	#N/A	#N/A	hypothetical protein
TGME49_268560	1.98	#N/A	#N/A	XPG N-terminal domain-containing protein
TGME49_311450	1.31	#N/A	#N/A	zinc finger, c2h2 type domain-containing protein
TGME49_268000	2.35	#N/A	#N/A	hypothetical protein
TGME49_305950	1.31	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_265170	2.35	#N/A	#N/A	hypothetical protein
TGME49_220510	2.42	#N/A	#N/A	hypothetical protein
TGME49_246990	1.08	#N/A	#N/A	hypothetical protein
TGME49_310560	1.31	#N/A	#N/A	hypothetical protein

TGME49_290630	1.98	1.29	#N/A	AP2 domain transcription factor AP2IX-7
TGME49_269417	1.98	-7.03	#N/A	hypothetical protein
TGME49_207470	4.76	-7.26	#N/A	hypothetical protein
TGME49_210800	4.76	1.23	#N/A	activator of hsp90 ATPase, putative
TGME49_233130	1.56	1.30	1.18	nucleoside transporter protein
TGME49_207070	4.76	2.47	#N/A	glycosyl transferase, putative
TGME49_257740	2.35	1.11	#N/A	UMP-CMP kinase
TGME49_263410	2.35	2.78	#N/A	scavenger receptor cysteine-rich domain-containing protein
TGME49_244260	1.08	-7.47	#N/A	hypothetical protein
TGME49_254520	1.08	#N/A	1.88	mediator complex subunit MED11
TGME49_253880	1.08	#N/A	1.45	GNS1/SUR4 family protein
TGME49_276940	1.98	#N/A	1.41	ribosome associated membrane protein RAMP4, putative
TGME49_293840	1.98	#N/A	2.10	hypothetical protein
TGME49_248740	1.08	#N/A	1.82	hypothetical protein
TGME49_313900	1.31	#N/A	2.08	non-specific serine/threonine protein kinase
TGME49_229990	1.56	#N/A	1.15	T-complex protein 1 subunit alpha, putative
TGME49_315220	1.31	#N/A	1.15	rhoptry protein ROP14
TGME49_310060	1.31	#N/A	1.98	small nuclease
TGME49_264240	2.35	#N/A	-4.81	hypothetical protein
TGME49_299200	1.31	#N/A	1.55	Bet3 transport protein, putative
TGME49_247770	1.08	#N/A	1.08	hypothetical protein
TGME49_223900	1.56	#N/A	2.97	hypothetical protein
TGME49_276140	1.98	#N/A	1.13	ADP ribosylation factor ARF1
TGME49_207830	4.76	#N/A	1.54	MORN repeat-containing protein
TGME49_315250	1.31	#N/A	1.54	GAMM1 protein, putative
TGME49_254400	1.08	#N/A	2.00	LSU ribosomal protein L2P, putative
TGME49_239500	1.08	#N/A	1.30	proteasome subunit alpha type, putative
TGME49_319550	1.31	#N/A	1.10	membrane protein C17G8.08c, putative
TGME49_253000	1.08	#N/A	1.20	ELMO/CED-12 family protein
TGME49_260870	2.35	#N/A	2.09	zinc finger cdgsh type protein
TGME49_226755	1.56	#N/A	1.30	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_218270	2.42	#N/A	1.22	hypothetical protein
TGME49_239490	1.08	#N/A	1.14	dehydrogenase E1 component family protein
TGME49_209850	4.76	#N/A	1.51	RNA recognition motif-containing protein
TGME49_249780	1.08	#N/A	1.09	hypothetical protein
TGME49_254570	1.08	#N/A	1.21	hypothetical protein

FIGURE 5Q

TGME49_297770	1.31	#N/A	#N/A	hypothetical protein
TGME49_206540	11.50	#N/A	#N/A	hypothetical protein
TGME49_236140	1.56	-7.22	#N/A	hypothetical protein
TGME49_279330	1.98	#N/A	1.31	DEAD/DEAH box helicase family protein
TGME49_254730	1.08	#N/A	#N/A	POPLD (NUC188) domain-containing protein
TGME49_319360	1.31	#N/A	#N/A	SAG-related sequence SRS17A
TGME49_319720	1.31	#N/A	#N/A	hypothetical protein
TGME49_243510	1.08	#N/A	#N/A	OTU family cysteine protease
TGME49_226850	1.56	#N/A	#N/A	TBC domain-containing protein
TGME49_298830	1.31	#N/A	#N/A	hypothetical protein
TGME49_271800	1.98	#N/A	#N/A	serine esterase (DUF676) protein
TGME49_264120	2.35	-7.79	#N/A	Myb family DNA-binding domain-containing protein
TGME49_320680	1.31	-7.24	#N/A	AP2 domain transcription factor AP2IV-2
TGME49_207900	4.76	#N/A	#N/A	transcription initiation factor TFIIB
TGME49_270580	1.98	-7.35	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_266740	2.35	2.00	1.93	RNA recognition motif-containing protein
TGME49_239810	1.08	#N/A	#N/A	hypothetical protein
TGME49_253490	1.08	#N/A	#N/A	hypothetical protein
TGME49_255245	1.08	#N/A	#N/A	hypothetical protein
TGME49_230170	1.56	#N/A	#N/A	hypothetical protein
TGME49_311280	1.31	#N/A	#N/A	hypothetical protein
TGME49_288860	1.98	#N/A	#N/A	RuvB family 2 protein
TGME49_239910	1.08	#N/A	#N/A	cyclin-dependent kinase
TGME49_231215	1.56	#N/A	#N/A	hypothetical protein
TGME49_292055	1.98	#N/A	#N/A	calcium dependent protein kinase CDPK8
TGME49_226100	1.56	-7.32	-7.32	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_310500	1.31	#N/A	#N/A	hypothetical protein
TGME49_237020	1.08	#N/A	#N/A	exonuclease
TGME49_205540	11.50	#N/A	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_296121	1.31	#N/A	#N/A	hypothetical protein
TGME49_293480	1.98	#N/A	#N/A	MoeA N-terminal region (domain I and II) domain-containing protein
TGME49_213060	2.42	-4.64	#N/A	WD domain, G-beta repeat-containing protein
TGME49_254720	1.08	#N/A	#N/A	dense granule protein GRA8
TGME49_219230	2.42	#N/A	#N/A	AMP-binding enzyme domain-containing protein
TGME49_280700	1.98	#N/A	#N/A	arginine decarboxylase
TGME49_214580	2.42	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_289140	1.98	#N/A	#N/A	ribosomal protein l22/l43, putative

TGME49_208850	4.76	#N/A	2.67	SAG-related sequence SRS11
TGME49_211010	4.76	#N/A	1.79	hypothetical protein
TGME49_278020	1.98	#N/A	1.86	hypothetical protein
TGME49_225050	1.56	#N/A	1.06	adenosylhomocysteinase, putative
TGME49_283790	1.98	#N/A	1.50	protein kinase, putative
TGME49_292260	1.98	#N/A	3.28	SAG-related sequence SRS36B
TGME49_254410	1.08	#N/A	1.30	protein phosphatase 2C, putative
TGME49_276220	1.98	#N/A	1.53	hypothetical protein
TGME49_320515	1.31	#N/A	1.15	hypothetical protein
TGME49_290678	1.98	#N/A	1.70	hypothetical protein
TGME49_213820	2.42	#N/A	1.16	hypothetical protein
TGME49_258550	2.35	#N/A	1.79	SAG-related sequence SRS28
TGME49_259700	2.35	#N/A	1.14	hypothetical protein
TGME49_288880	1.98	#N/A	2.14	hypothetical protein
TGME49_260480	2.35	#N/A	1.80	leucine rich repeat-containing protein
TGME49_311490	1.31	#N/A	2.49	hypothetical protein
TGME49_285720	1.98	#N/A	1.70	ATP binding protein, putative
TGME49_288870	1.98	#N/A	1.95	hypothetical protein
TGME49_289090	1.98	#N/A	2.52	hypothetical protein
TGME49_253970	1.08	#N/A	1.91	hypothetical protein
TGME49_223095	1.56	#N/A	2.42	hypothetical protein
TGME49_245475	1.08	#N/A	1.73	hypothetical protein
TGME49_270560	1.98	#N/A	1.90	peptidyl-prolyl cis-trans isomerase family 1
TGME49_257685	2.35	#N/A	1.16	hypothetical protein
TGME49_275770	1.98	#N/A	1.18	hypothetical protein
TGME49_315260	1.31	#N/A	-4.45	alanine dehydrogenase
TGME49_298970	1.31	#N/A	1.05	LSM3, U6 small nuclear RNA associated isoform 2 family protein
TGME49_309130	1.31	#N/A	2.10	hypothetical protein
TGME49_306640	1.31	#N/A	1.55	hypothetical protein
TGME49_252290	1.08	#N/A	1.33	importin alpha, putative
TGME49_286560	1.98	#N/A	1.58	U6 snRNA-associated Sm family protein
TGME49_226068	1.56	#N/A	1.08	DnaJ domain-containing protein
TGME49_233695	1.56	#N/A	1.09	hypothetical protein
TGME49_230100	1.56	#N/A	1.63	membrane protein, putative
TGME49_231000	1.56	#N/A	1.28	START domain-containing protein
TGME49_223610	1.56	#N/A	1.63	hypothetical protein
TGME49_218810	2.42	#N/A	1.22	histidyl-tRNA synthetase

FIGURE 5R

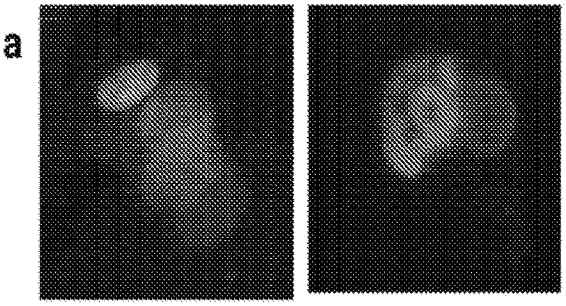
TGME49_219630	2.42	#N/A	#N/A	flavodoxin domain-containing protein
TGME49_278250	1.98	#N/A	#N/A	hypothetical protein
TGME49_257370	2.35	#N/A	#N/A	hypothetical protein
TGME49_295960	1.31	#N/A	#N/A	hypothetical protein
TGME49_278720	1.98	#N/A	#N/A	hypothetical protein
TGME49_224270	1.56	#N/A	#N/A	hypothetical protein
TGME49_284590	1.98	#N/A	#N/A	hypothetical protein
TGME49_267670	2.35	-7.58	#N/A	hypothetical protein
TGME49_245980	1.08	-8.63	#N/A	hypothetical protein
TGME49_275310	1.98	#N/A	#N/A	hypothetical protein
TGME49_250090	1.08	#N/A	#N/A	hypothetical protein
TGME49_210360	4.76	#N/A	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 family protein
TGME49_226560	1.56	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_262480	2.35	#N/A	1.16	dynein light chain roadblock-type 2, putative
TGME49_229390	1.56	#N/A	#N/A	hypothetical protein
TGME49_268650	1.98	#N/A	#N/A	chaperone clpB protein, putative
TGME49_287430	1.98	#N/A	#N/A	hypothetical protein
TGME49_242270	1.08	#N/A	#N/A	hypothetical protein
TGME49_284598	1.98	#N/A	#N/A	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_312210	1.31	1.63	1.28	hypothetical protein
TGME49_268730	1.98	#N/A	1.94	glutaredoxin-related protein
TGME49_224470	1.56	#N/A	#N/A	hypothetical protein
TGME49_225290	1.56	2.64	3.06	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_273660	1.98	#N/A	#N/A	AP2 domain transcription factor AP2VIII-3
TGME49_305120	1.31	1.15	#N/A	transporter, solute:sodium symporter (SSS) family protein
TGME49_266890	2.35	#N/A	#N/A	hypothetical protein
TGME49_269200	1.98	#N/A	#N/A	crooked neck family 1 protein isoform 2, putative
TGME49_309990	1.31	#N/A	#N/A	hypothetical protein
TGME49_220880	2.42	#N/A	#N/A	hypothetical protein
TGME49_271600	1.98	#N/A	#N/A	hypothetical protein
TGME49_248450	1.08	#N/A	1.22	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_267370	2.35	#N/A	#N/A	kinesin motor domain-containing protein
TGME49_220870	2.42	#N/A	#N/A	hypothetical protein
TGME49_216800	2.42	#N/A	#N/A	flagellar/basal body protein

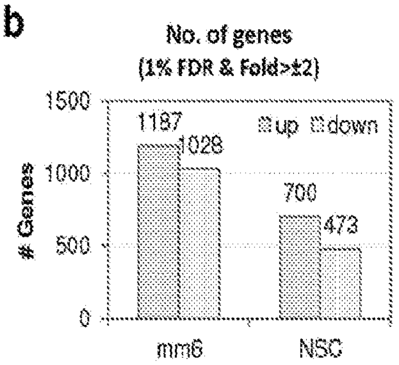
TGME49_276130	1.98	#N/A	1.13	cathepsin CPC2
TGME49_271090	1.98	#N/A	1.87	hypothetical protein
TGME49_249890	1.08	#N/A	1.73	hypothetical protein
TGME49_243980	1.08	#N/A	1.48	hypothetical protein
TGME49_238420	1.08	#N/A	1.45	hypothetical protein
TGME49_313040	1.31	#N/A	1.23	hypothetical protein
TGME49_294040	1.98	#N/A	1.03	KDEL endoplasmic reticulum proteinretention receptor 2 (KDELR2), putative
TGME49_212960	2.42	#N/A	1.39	hypothetical protein
TGME49_233100	1.56	#N/A	1.21	SPFH domain / Band 7 family protein
TGME49_310070	1.31	#N/A	1.00	methyltransferase, putative
TGME49_238880	1.08	#N/A	1.82	hypothetical protein
TGME49_309380	1.31	#N/A	1.09	Nuf2
TGME49_213746	2.42	#N/A	1.98	hypothetical protein
TGME49_308090	1.31	#N/A	1.04	rhoptry protein ROP5
TGME49_258490	2.35	#N/A	1.73	hypothetical protein
TGME49_299080	1.31	#N/A	1.04	VTC domain-containing protein
TGME49_239610	1.08	#N/A	1.28	hypothetical protein
TGME49_253730	1.08	#N/A	1.12	importin-beta N-terminal domain-containing protein
TGME49_310220	1.31	#N/A	1.17	hypothetical protein
TGME49_243480	1.08	#N/A	1.88	50S ribosomal protein L3, putative
TGME49_253900	1.08	#N/A	1.26	parasite porphobilinogen synthase PBGS
TGME49_204060	11.50	#N/A	1.41	SNARE domain-containing protein
TGME49_217400	2.42	#N/A	1.19	hypothetical protein
TGME49_260660	2.35	#N/A	1.25	50S ribosomal protein L23, putative
TGME49_252630	1.08	#N/A	1.05	hypothetical protein
TGME49_211860	4.76	#N/A	1.05	hypothetical protein
TGME49_301222	1.31	#N/A	1.27	DNA repair protein Rad4 domain-containing protein
TGME49_228710	1.56	#N/A	1.91	hypothetical protein
TGME49_271240	1.98	#N/A	1.25	hypothetical protein
TGME49_218530	2.42	#N/A	1.09	proteasome-interacting thioredoxin domain-containing protein
TGME49_256100	2.35	#N/A	1.60	tetratricopeptide repeat-containing protein
TGME49_262910	2.35	#N/A	1.72	NADH-cytochrome b5 reductase 1, putative
TGME49_255890	2.35	#N/A	1.19	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_231940	1.56	#N/A	1.10	ThiF family protein

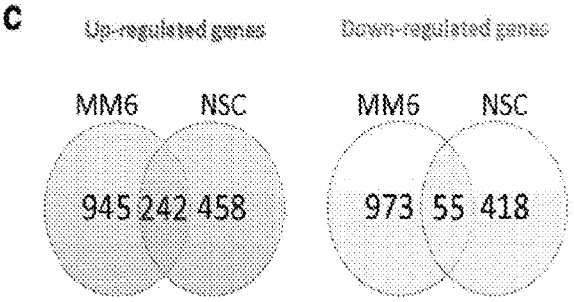
FIGURE 5S

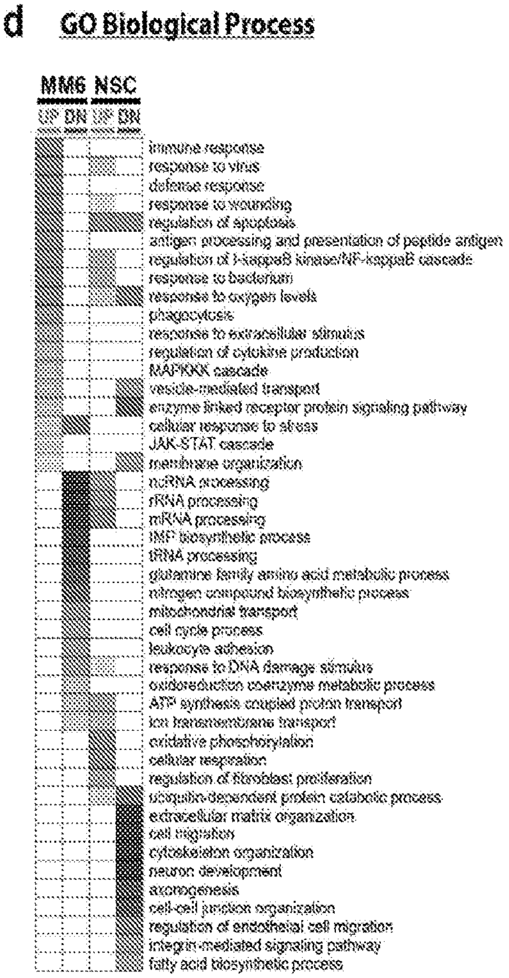
TGME49_258010	2.35	#N/A	#N/A	calcium signaling protein kinase RAD53, putative
TGME49_202568	11.50	#N/A	#N/A	hypothetical protein
TGME49_257560	2.35	-7.70	#N/A	WD domain, G-beta repeat-containing protein
TGME49_247340	1.08	2.56	#N/A	hypothetical protein
TGME49_258458	2.35	#N/A	#N/A	hypothetical protein
TGME49_236790	-4.71	#N/A	#N/A	hypothetical protein

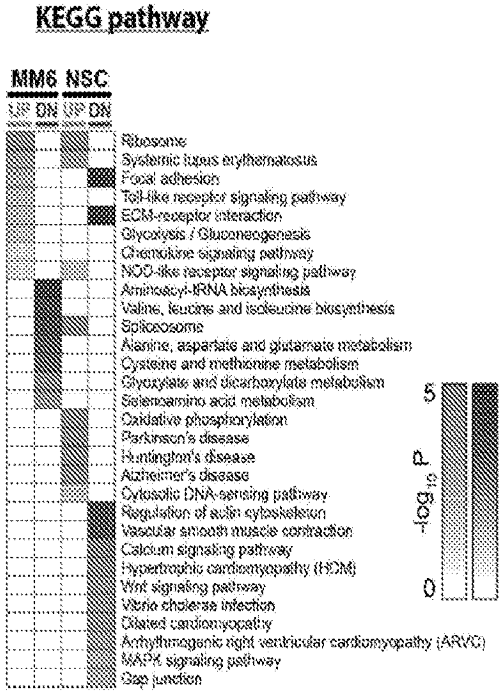
TGME49_251570	1.08	#N/A	2.16	CAAX amino terminal protease family protein
TGME49_310840	1.31	#N/A	1.42	hypothetical protein
TGME49_313700	1.31	#N/A	1.58	hypothetical protein
TGME49_262040	2.35	#N/A	1.01	SAC3/GANP family protein
TGME49_234300	1.56	#N/A	1.29	hypothetical protein
TGME49_285810	1.98	#N/A	1.46	MYND finger domain-containing protein











e MIRs most altered

MIR	logFC (cont)	Log cpm	P value	FDR
hsa-mir-708	-11.46	5.67	6.11E-22	2.54E-18
hsa-mir-29b	-5.46	5.99	1.85E-15	2.56E-12
ENST00000474173	-9.95	4.25	7.09E-15	7.34E-12
hsa-mir-32	-5.48	7.42	8.85E-15	7.34E-12
hsa-mir-142	-4.62	10.48	1.77E-13	1.23E-10
hsa-mir-3655	-9.66	4.01	2.28E-11	1.05E-08

Figure 6

FIGURE 7

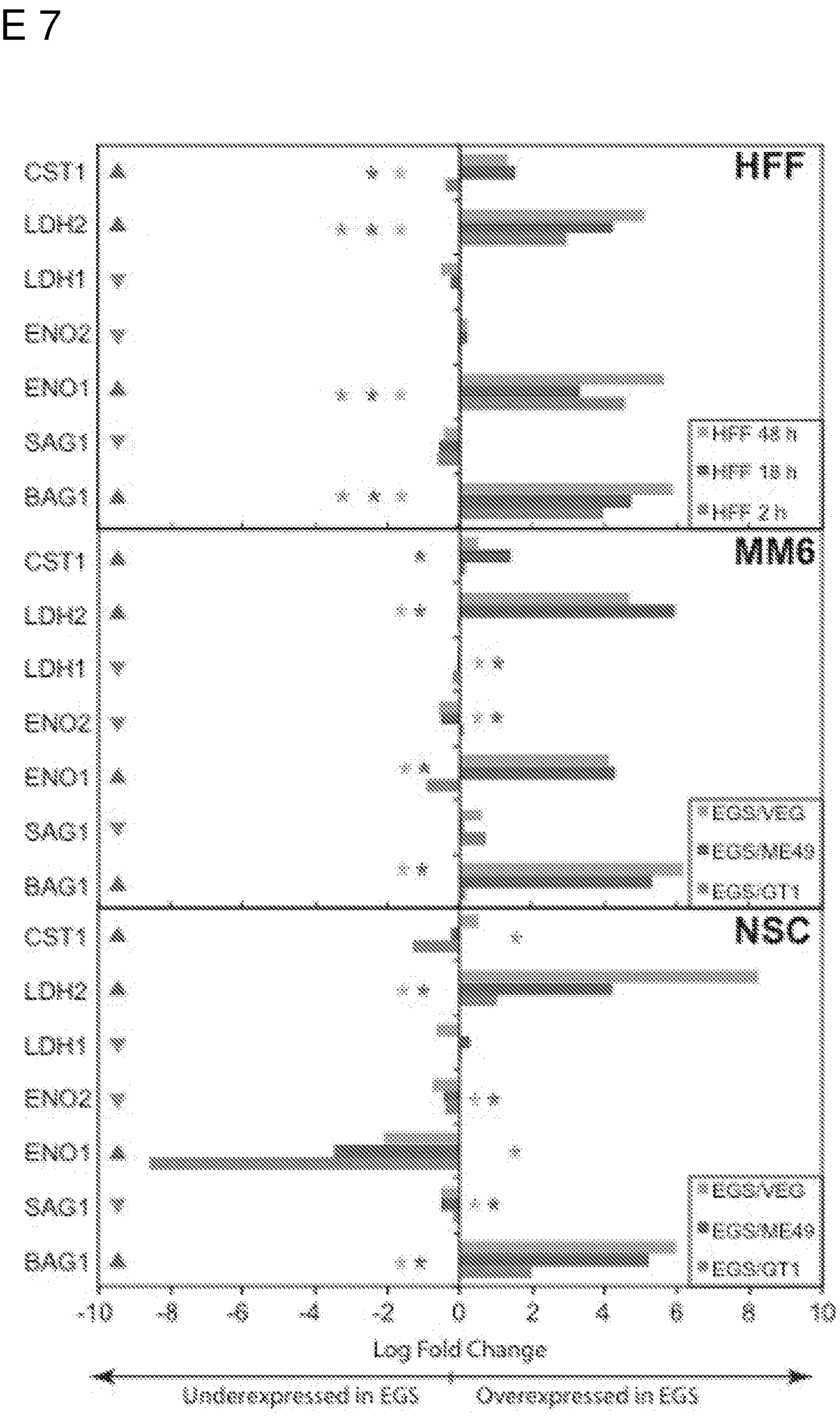

a
HFF
MM6
NSC
CST1
LDH2
LDH1
ENO2
ENO1
SAG1
BAG1
HFF 48 h
HFF 18 h
HFF 2 h
EGS/VEG
EGS/ME49
EGS/GT1
-10
-8
-6
-4
-2
0
2
4
6
8
10
Log Fold Change
Underexpressed in EGS
Overexpressed in EGS

FIGURE 7

b

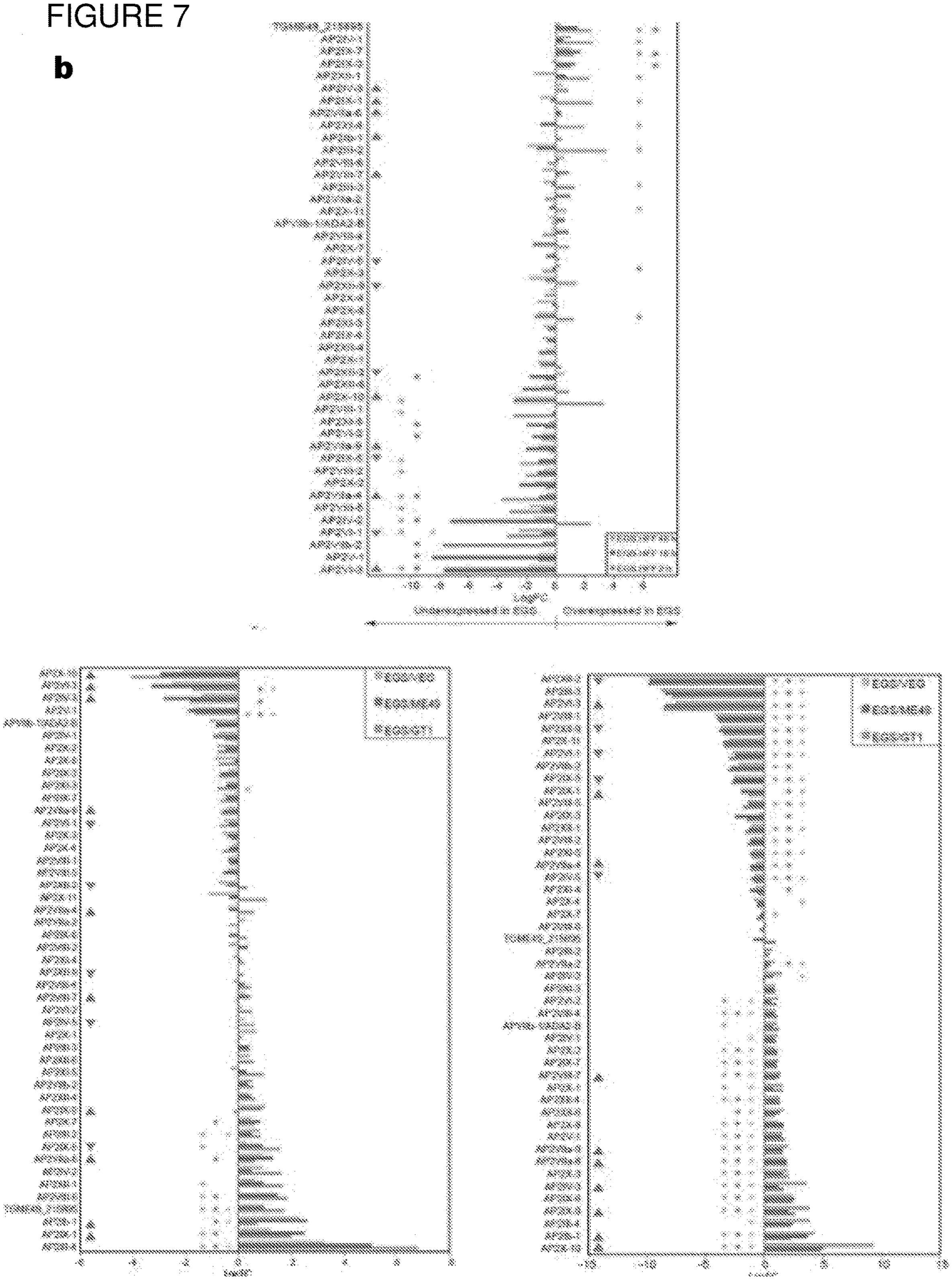

-10
-8
-6
-4
-2
0
2
4
6
LogFC
Underexpressed in EGS
Overexpressed in EGS
EGS/VEG
EGS/ME49
EGS/GT1

FIGURE 7

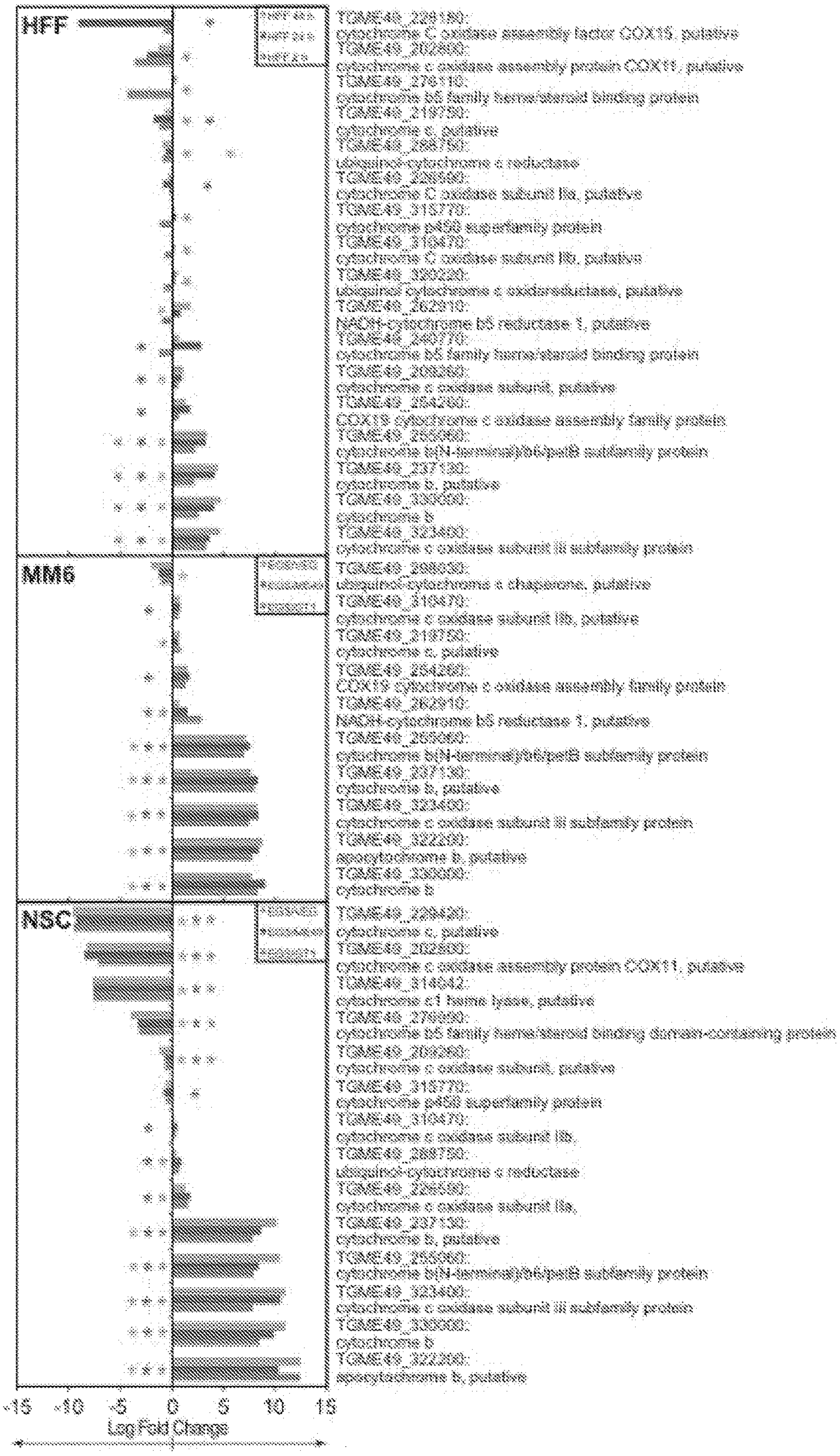
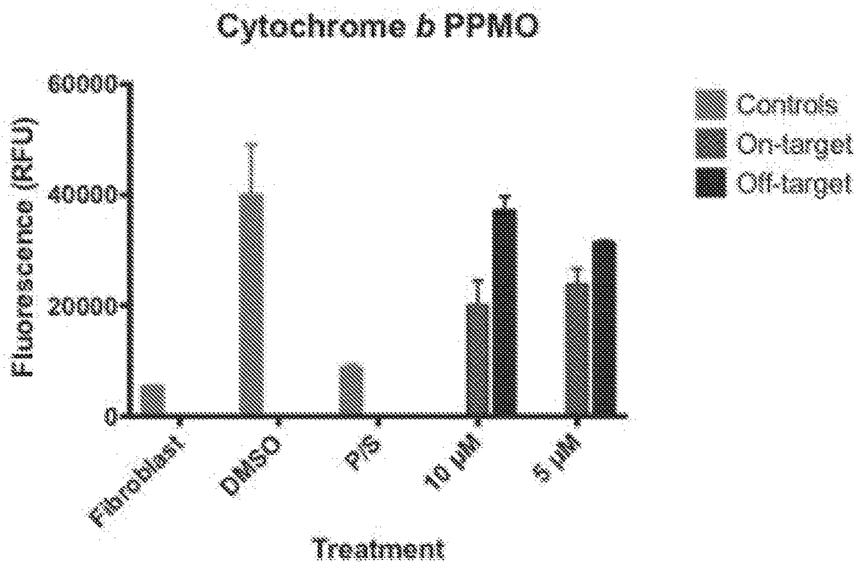
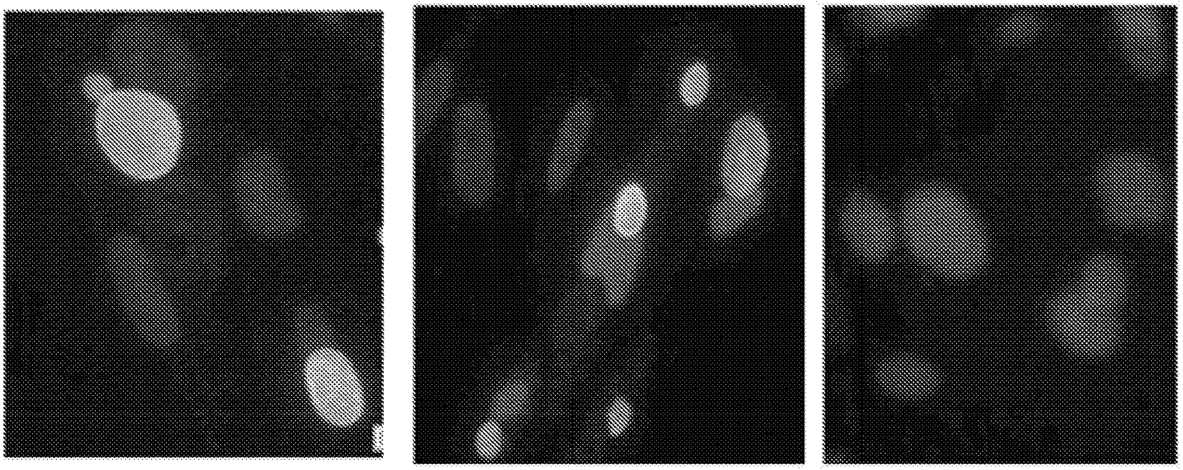

HFF
TGME49_228180:
cytochrome C oxidase assembly factor COX15, putative
TGME49_202800:
cytochrome c oxidase assembly protein COX11, putative
TGME49_276110:
cytochrome b5 family heme/steroid binding protein
TGME49_219750:
cytochrome c, putative
TGME49_288750:
ubiquinol-cytochrome c reductase
TGME49_226590:
cytochrome C oxidase subunit IIa, putative
TGME49_315770:
cytochrome p450 superfamily protein
TGME49_310470:
cytochrome C oxidase subunit IIb, putative
TGME49_320220:
ubiquinol cytochrome c oxidoreductase, putative
TGME49_262910:
NADH-cytochrome b5 reductase 1, putative
TGME49_240770:
cytochrome b5 family heme/steroid binding protein
TGME49_209260:
cytochrome c oxidase subunit, putative
TGME49_254260:
COX19 cytochrome c oxidase assembly family protein
TGME49_255060:
cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_237130:
cytochrome b, putative
TGME49_330000:
cytochrome b
TGME49_323400:
cytochrome c oxidase subunit iii subfamily protein
MM6
TGME49_298030:
ubiquinol-cytochrome c chaperone, putative
TGME49_310470:
cytochrome c oxidase subunit IIb, putative
TGME49_219750:
cytochrome c, putative
TGME49_254260:
COX19 cytochrome c oxidase assembly family protein
TGME49_262910:
NADH-cytochrome b5 reductase 1, putative
TGME49_255060:
cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_237130:
cytochrome b, putative
TGME49_323400:
cytochrome c oxidase subunit iii subfamily protein
TGME49_322200:
apocytochrome b, putative
TGME49_330000:
cytochrome b
NSC
TGME49_229420:
cytochrome c, putative
TGME49_202800:
cytochrome c oxidase assembly protein COX11, putative
TGME49_314042:
cytochrome c1 heme lyase, putative
TGME49_276090:
cytochrome b5 family heme/steroid binding domain-containing protein
TGME49_209260:
cytochrome c oxidase subunit, putative
TGME49_315770:
cytochrome p450 superfamily protein
TGME49_310470:
cytochrome c oxidase subunit IIb,
TGME49_288750:
ubiquinol-cytochrome c reductase
TGME49_226590:
cytochrome c oxidase subunit IIa,
TGME49_237130:
cytochrome b, putative
TGME49_255060:
cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_323400:
cytochrome c oxidase subunit iii subfamily protein
TGME49_330000:
cytochrome b
TGME49_322200:
apocytochrome b, putative
-15
-10
-5
0
5
10
15
Log Fold Change

FIGURE 7

d


Cytochrome *b* PPMO
60000
40000
20000
0
Fluorescence (RFU)
Controls
On-target
Off-target
Fibroblast
DMSO
P/S
10 μM
5 μM
Treatment



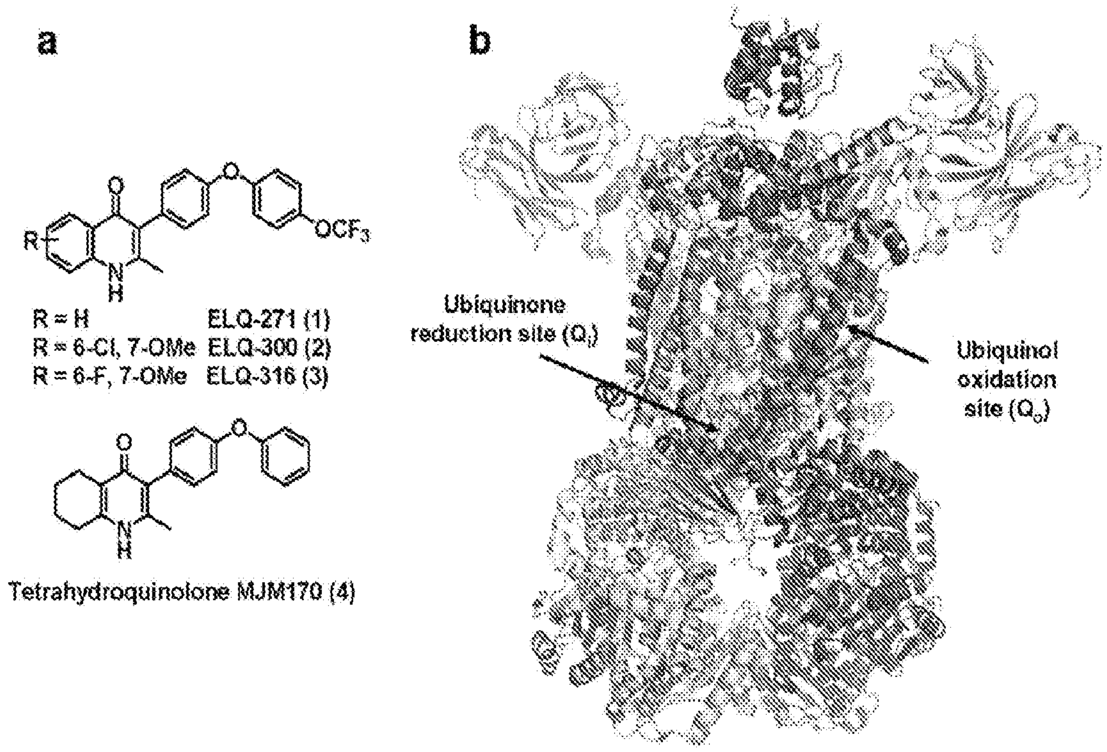

a
b
R
O
O
OCF$_3$
N
H
R = H ELQ-271 (1)
R = 6-Cl, 7-OMe ELQ-300 (2)
R = 6-F, 7-OMe ELQ-316 (3)
O
O
N
H
Tetrahydroquinolone MJM170 (4)
Ubiquinone reduction site (Q$_i$)
Ubiquinol oxidation site (Q$_o$)

Figure 8

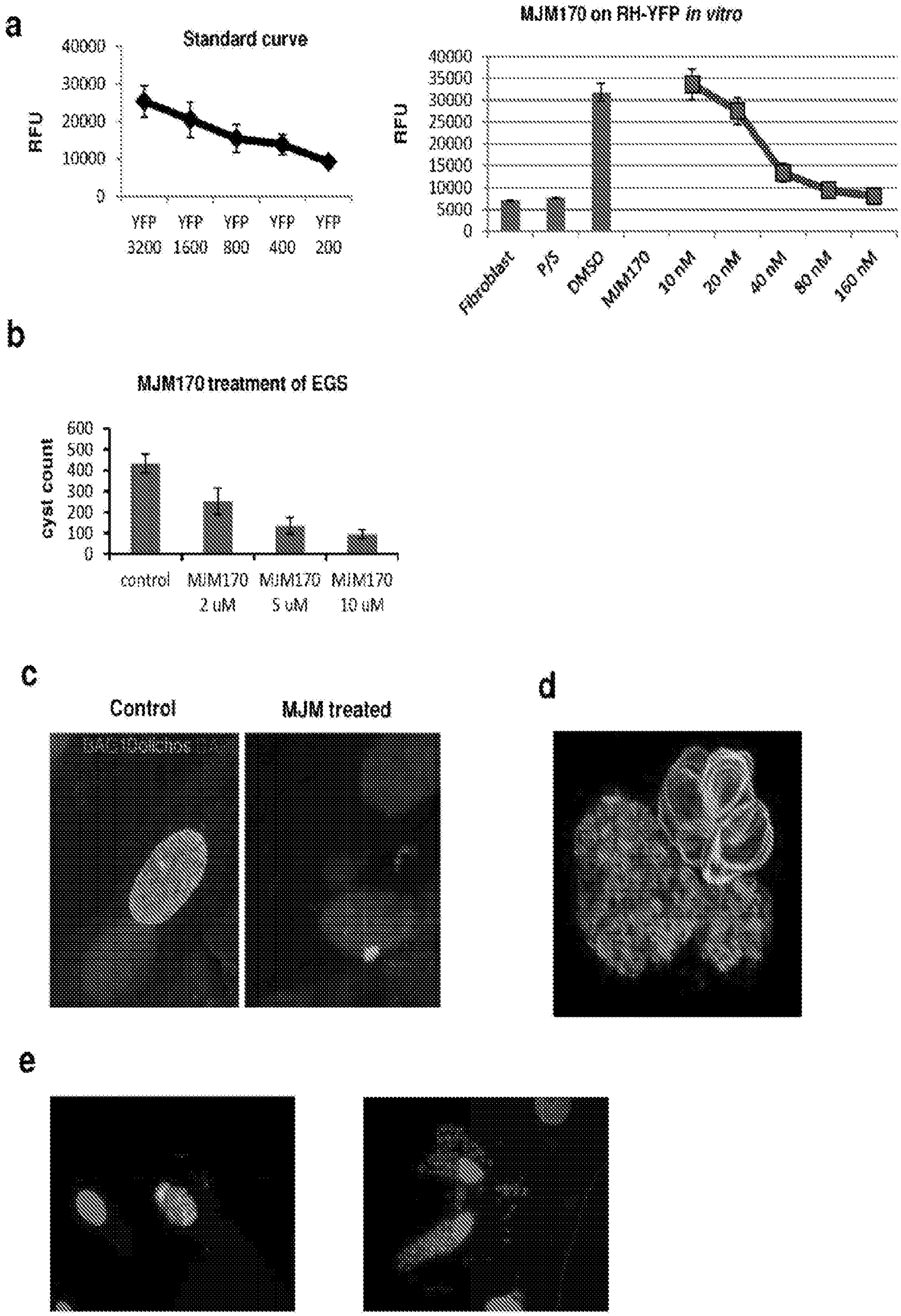

a
Standard curve
RFU
40000
30000
20000
10000
0
YFP 3200
YFP 1600
YFP 800
YFP 400
YFP 200
MJM170 on RH-YFP in vitro
RFU
40000
35000
30000
25000
20000
15000
10000
5000
0
Fibroblast
P/S
DMSO
MJM170
10 nM
20 nM
40 nM
80 nM
160 nM
b
MJM170 treatment of EGS
cyst count
600
500
400
300
200
100
0
control
MJM170 2 uM
MJM170 5 uM
MJM170 10 uM
c
Control
MJM treated
d
e

Figure 9

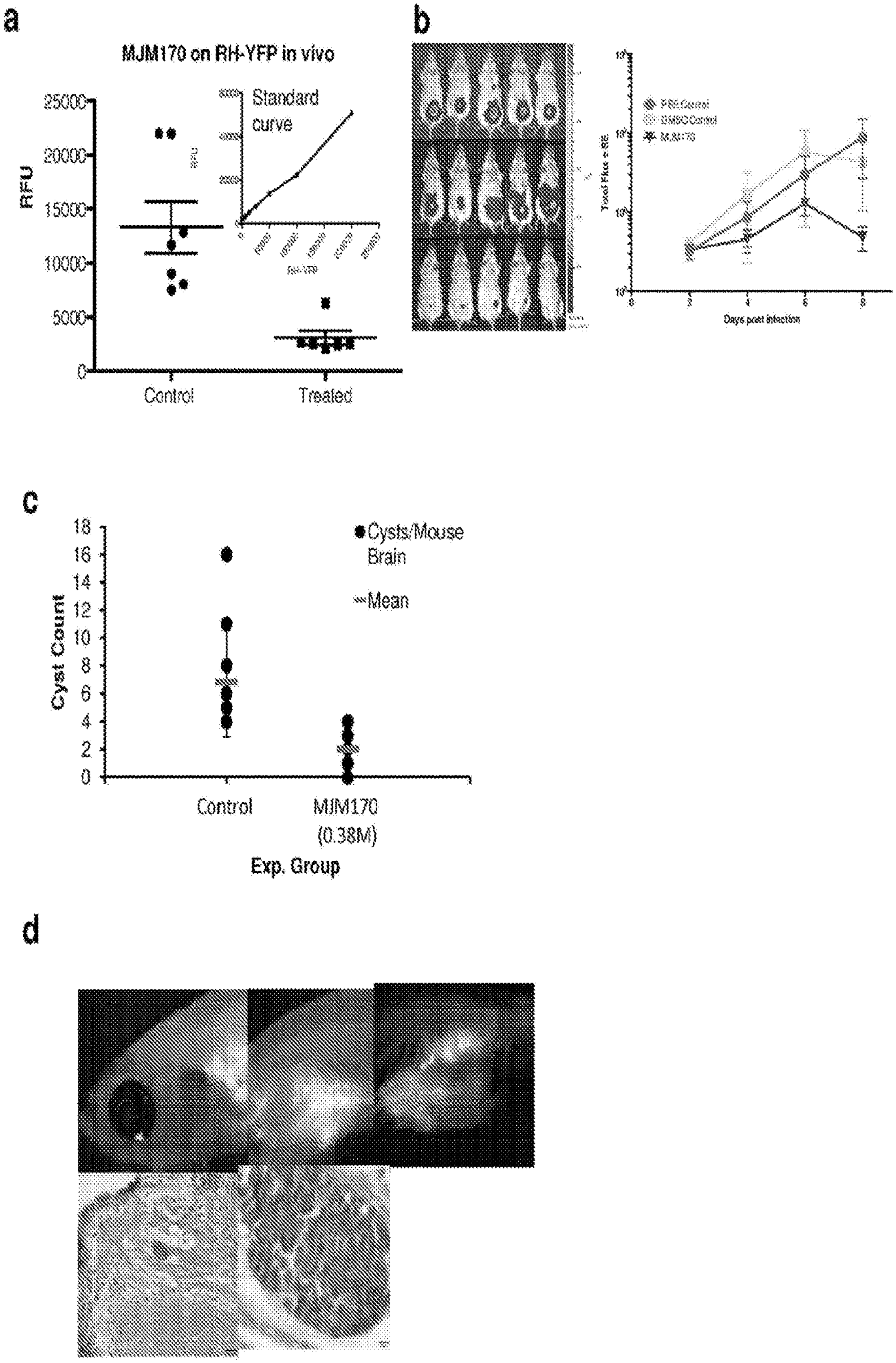
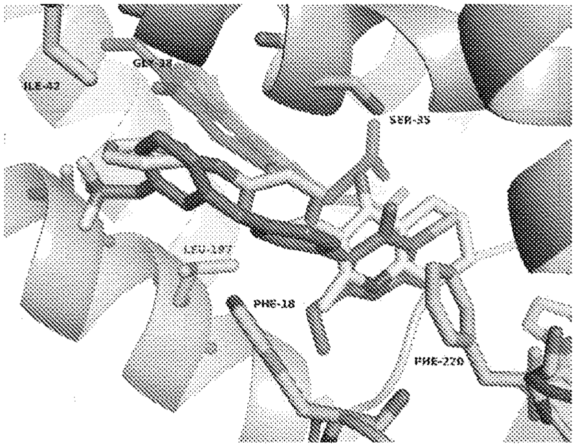

a
MJM170 on RH-YFP in vivo
RFU
25000
20000
15000
10000
5000
0
Control
Treated
Standard curve
RFU
RH-YFP
b
PBS Control
DMSO Control
MJM170
Total Flux ± SE
0
2
4
6
8
Days post infection
c
Cyst Count
18
16
14
12
10
8
6
4
2
0
Cysts/Mouse Brain
Mean
Control
MJM170 (0.38M)
Exp. Group
d

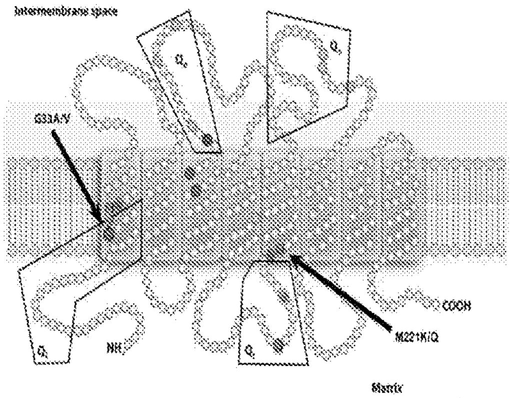
Figure 10

Figure 11

a



b



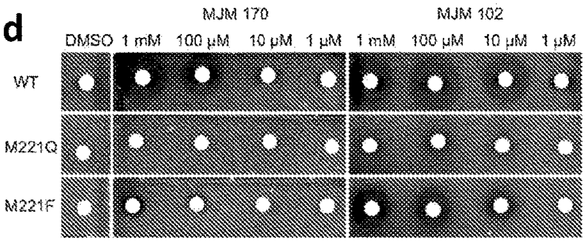
c

Cytochrome b Qi mutants

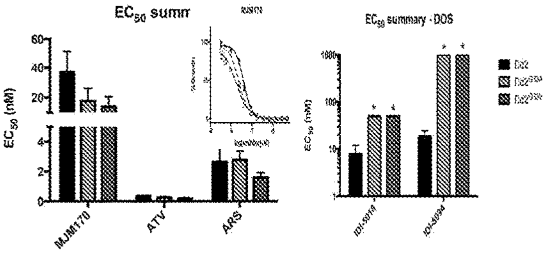
P. falciparum	Yeast	*T. gondii*	Bovine
G33A G33V	G37	A37	G38
F210	M221K M221Q	F215	F220

Cytochrome b sequences (UniProtKb):Toxo: O20672; Human: P00156;Pf: Q02758;Yeast: P00163; Bovine: P00157. Both reported Qi resistant mutants (G33A and M221K) steric clash with QI inhibitors for a loss of binding affinity. Both are useful indicators for target confirmation. Adapted and modified from reference ___ with permission

d



e



f

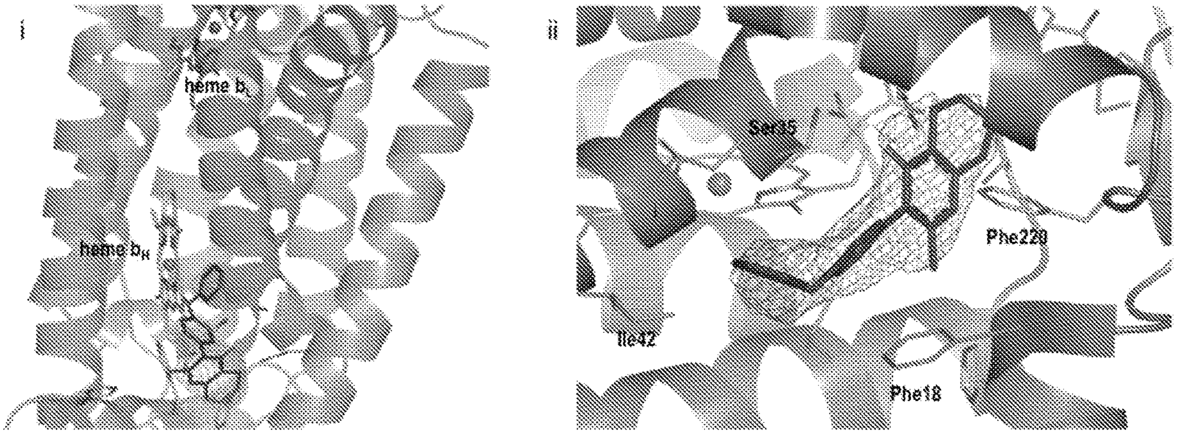
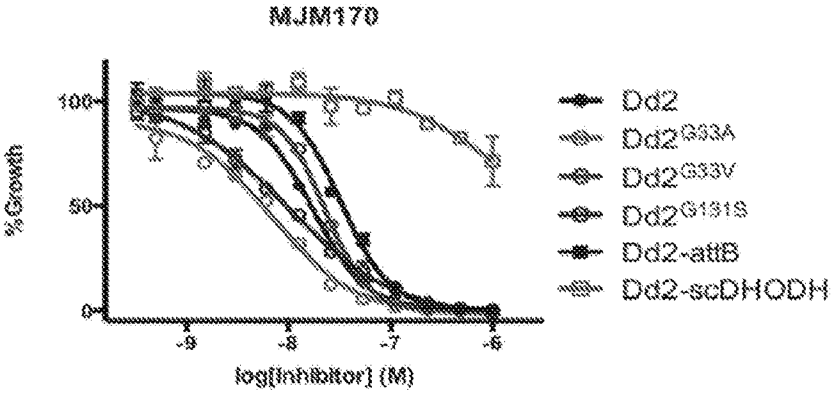


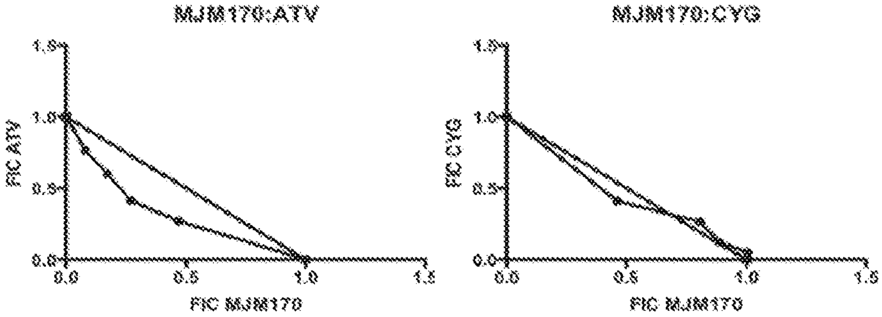
Figure 12

a



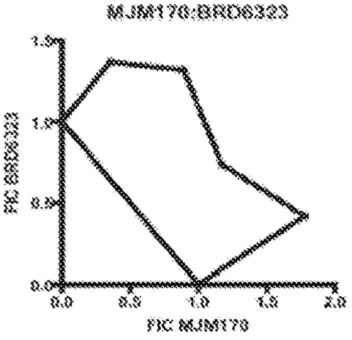
	Dd2	Dd2: G33A	Dd2: G33V	Dd2: G131S	Dd2-attB	Dd2-scDHODH
MJM170	29.5 ± 9.9	16.4 ± 9	14.3 ± 11	12.4 ± 3.8	35.5 ± 9.9	> 1,000
IDI-5918	9.24 ± 2.6	171 ± 73	> 1,000	5.85 ± 3	15.4 ± 3.2	> 1,000
BRD6323	35.6 ± 13	> 1,000	> 1,000	36.9 ± 13	81.8 ± 18	> 1,000
IDI-0020	49.0 ± 31	37.8 ± 24	21.7 ± 24	> 1,000	69.0 ± 56	> 1,000
Artesunate	2.95 ± 0.94	2.53 ± 0.69	2.08 ± 1.4	3.38 ± 0.48	4.40 ± 2.3	3.97 ± 2.3
Atovaquone	0.461 ± 0.14	0.365 ± 0.053	3.85 ± 7.1	0.479 ± 0.17	1.11 ± 0.27	> 50

b



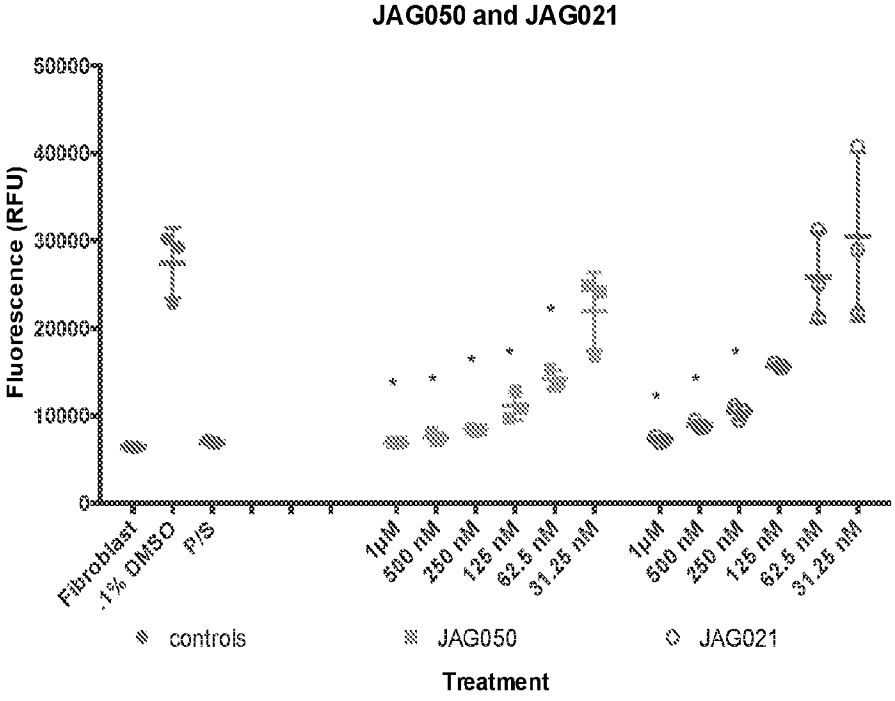
Ratio MJM170:ATV or CYG	MJM170 + ATV			MJM170 + CYG		
	FIC MJM170	FIC ATV	Σ FIC	FIC MJM170	FIC CYG	Σ FIC
8:2	0.47 ± 0.08	0.35 ± 0.06	0.82	0.65 ± 0.2	0.41 ± 0.003	1.1
6:4	0.27 ± 0.03	0.53 ± 0.1	0.79	0.83 ± 0.04	0.2 ± 0.05	1.0
4:6	0.16 ± 0.02	0.72 ± 0.1	0.89	0.83 ± 0.05	0.089 ± 0.03	0.92
2:8	0.069 ± 0.01	0.82 ± 0.05	0.89	0.89 ± 0.1	0.036 ± 0.01	0.93

c



Ratio MJM170:BRD6323	MJM170 + BRD6323		
	FIC MJM170	FIC BRD6323	Σ FIC
8:2	1.6 ± 0.4	0.39 ± 0.1	2
6:4	0.85 ± 0.3	0.55 ± 0.2	1.4
4:6	0.60 ± 0.3	0.91 ± 0.4	1.5
2:8	0.30 ± 0.08	1.2 ± 0.4	1.5

Figure 13



* denotes p-value <0.05

Figure 14

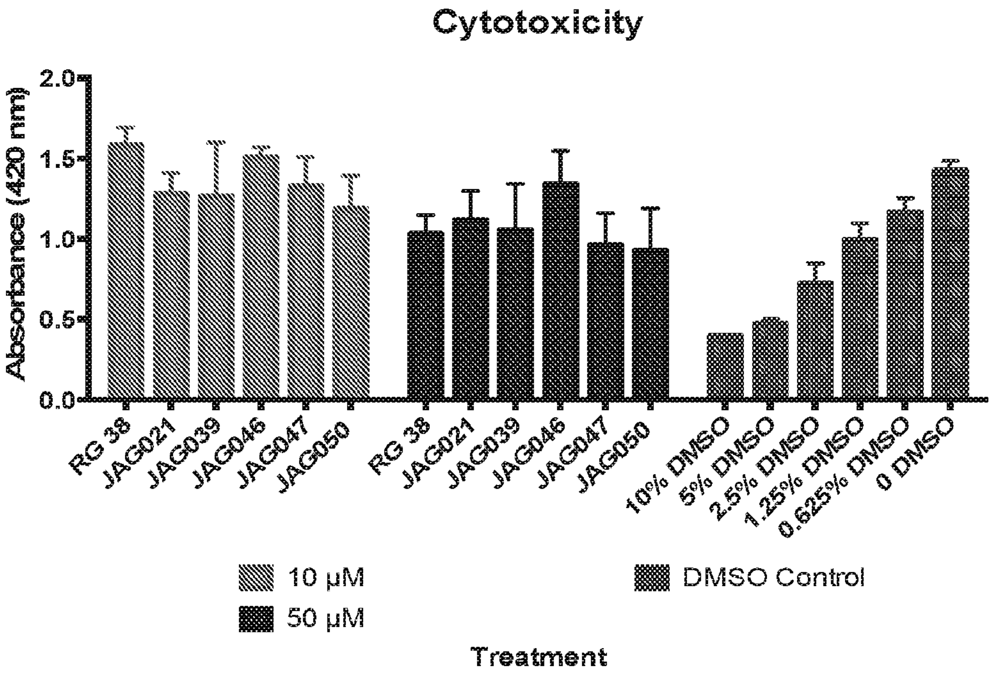

Cytotoxicity
Absorbance (420 nm)
2.0
1.5
1.0
0.5
0.0
RG 38
JAG021
JAG039
JAG046
JAG047
JAG050
RG 38
JAG021
JAG039
JAG046
JAG047
JAG050
10% DMSO
5% DMSO
2.5% DMSO
1.25% DMSO
0.625% DMSO
0 DMSO
10 µM
50 µM
DMSO Control
Treatment

Figure 15

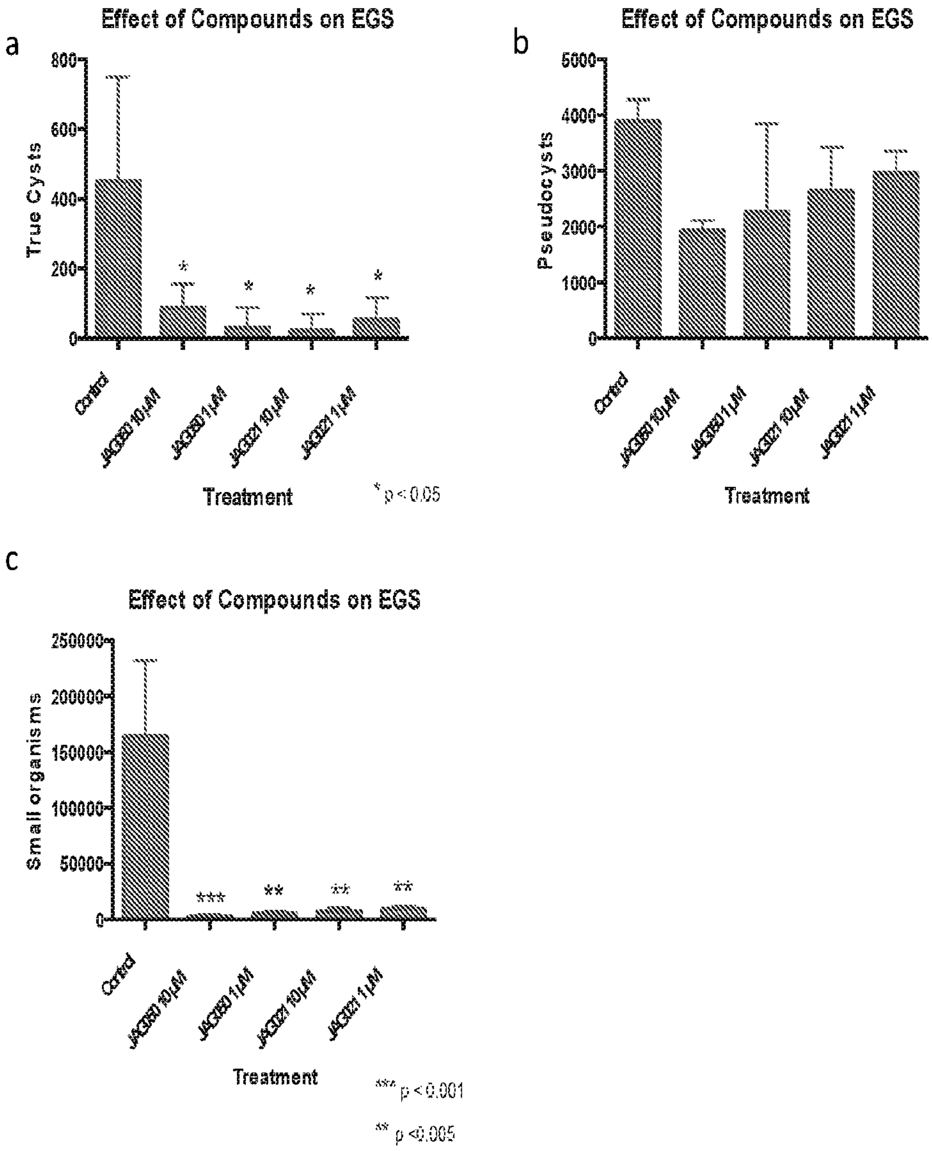
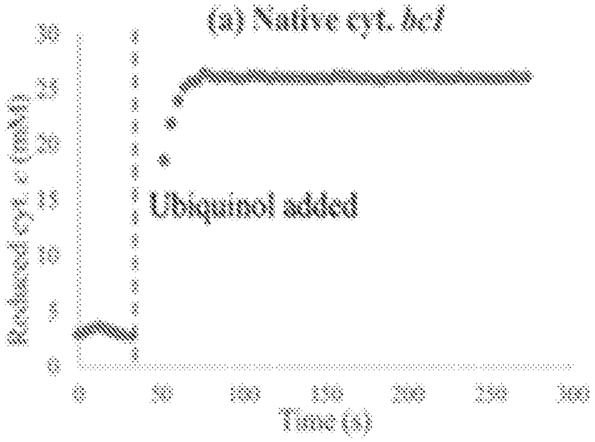

a
Effect of Compounds on EGS
True Cysts
800
600
400
200
0
*
*
*
*
Control
JAG350 10μM
JAG350 1μM
JAG021 10μM
JAG021 1μM
Treatment
* p < 0.05
b
Effect of Compounds on EGS
Pseudocysts
5000
4000
3000
2000
1000
0
Control
JAG350 10μM
JAG350 1μM
JAG021 10μM
JAG021 1μM
Treatment
c
Effect of Compounds on EGS
Small organisms
250000
200000
150000
100000
50000
0
***
**
**
**
Control
JAG350 10μM
JAG350 1μM
JAG021 10μM
JAG021 1μM
Treatment
*** p < 0.001
** p <0.005

Figure 16. Binding assays of JAG 21 to bovine cytochrome bc (Kansa Sveta



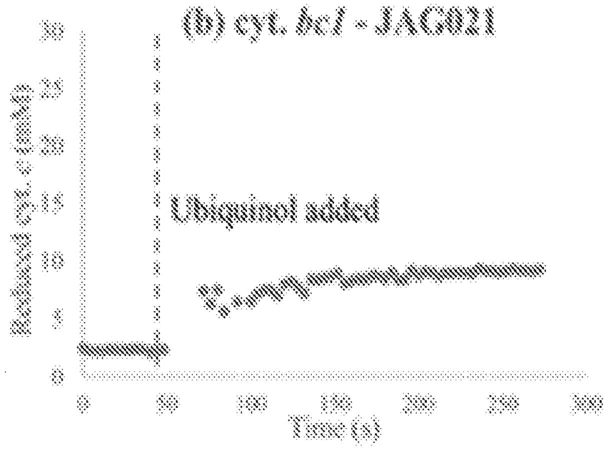


Figure 17.

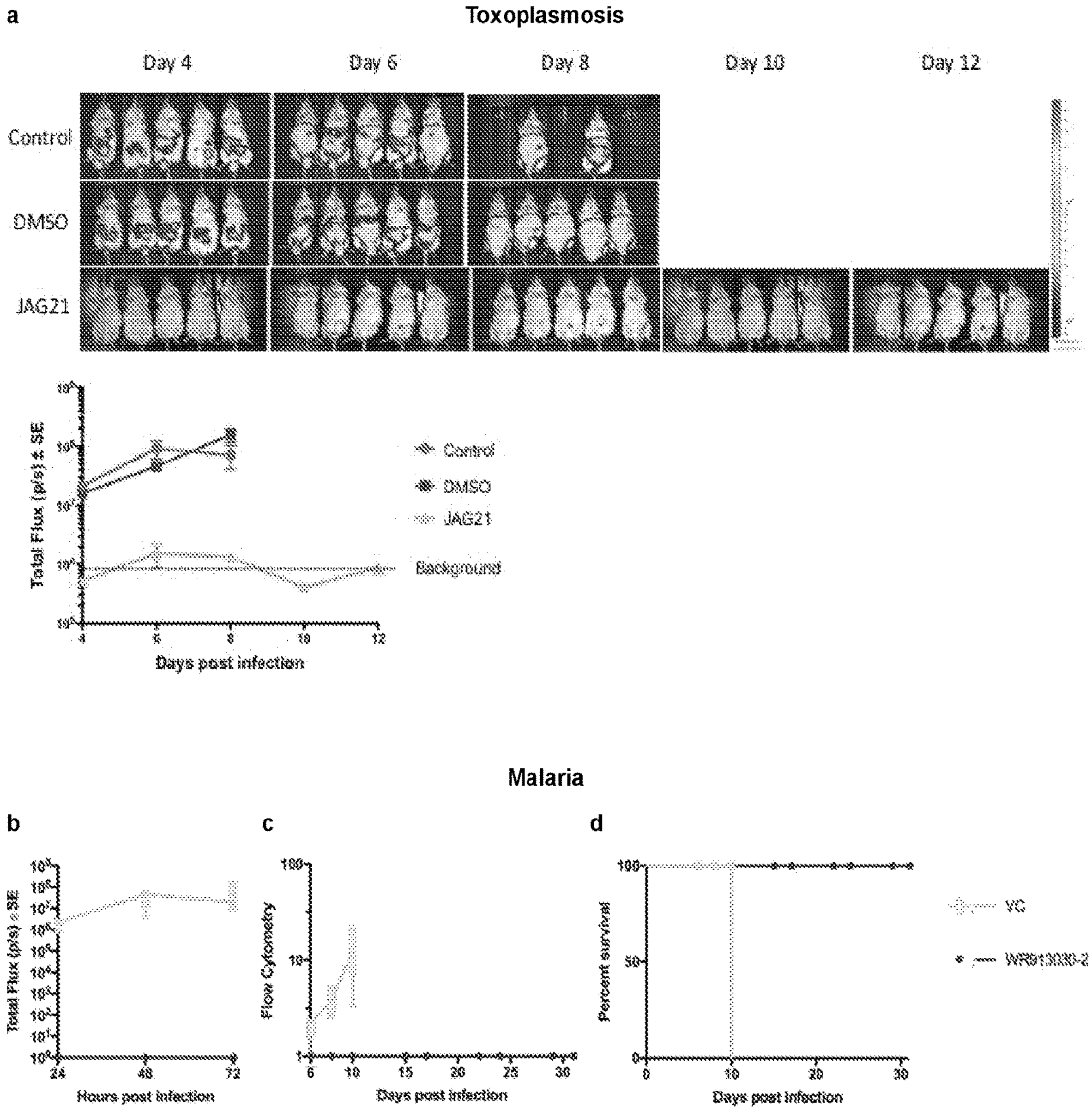
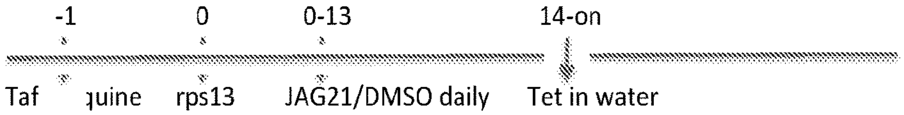

a
Toxoplasmosis
Day 4
Day 6
Day 8
Day 10
Day 12
Control
DMSO
JAG21
Total Flux (p/s) ± SE
Days post infection
4
6
8
10
12
Control
DMSO
JAG21
Background
Malaria
b
c
d
Total Flux (p/s) ± SE
Hours post infection
24
48
72
Flow Cytometry
100
10
1
Days post infection
6
10
15
20
25
30
Percent survival
100
50
0
Days post infection
0
10
20
30
VC
WR913030-2

Figure 18.

Goal: To test if JAG21 and/or Tafenoquine be able to kill the dormant stage of T. gondii: rps13

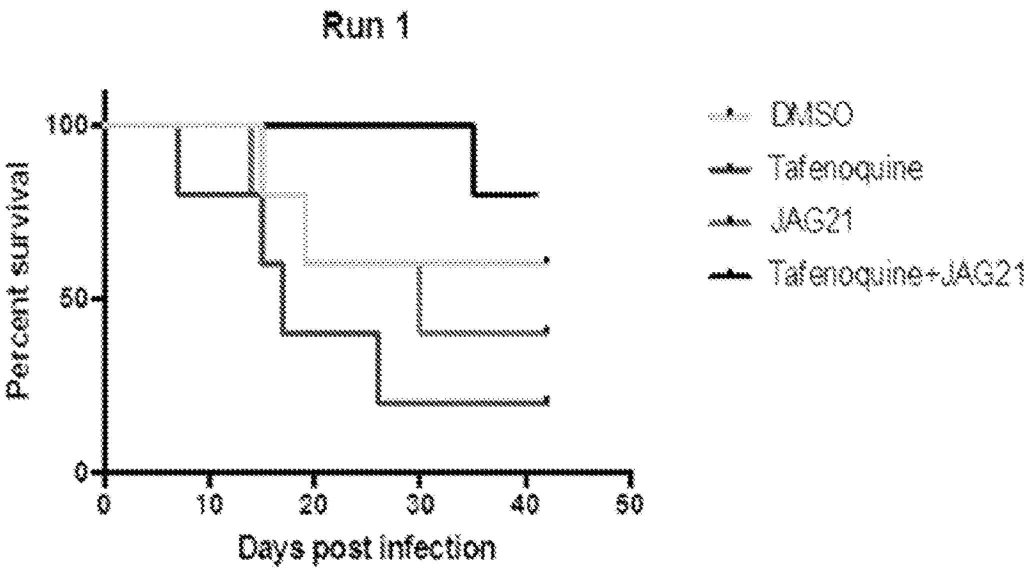
Experiment design:



4 groups: 5/group	D-1: Inject Tafenoquine	D0 Inject rps13	D0-D13 daily Inject JAG21	D0-D13 daily Inject DMSO
Control		x		x
Tafenoquine	x	x		x
JAG21		x	x	
T+J	x	x	x	

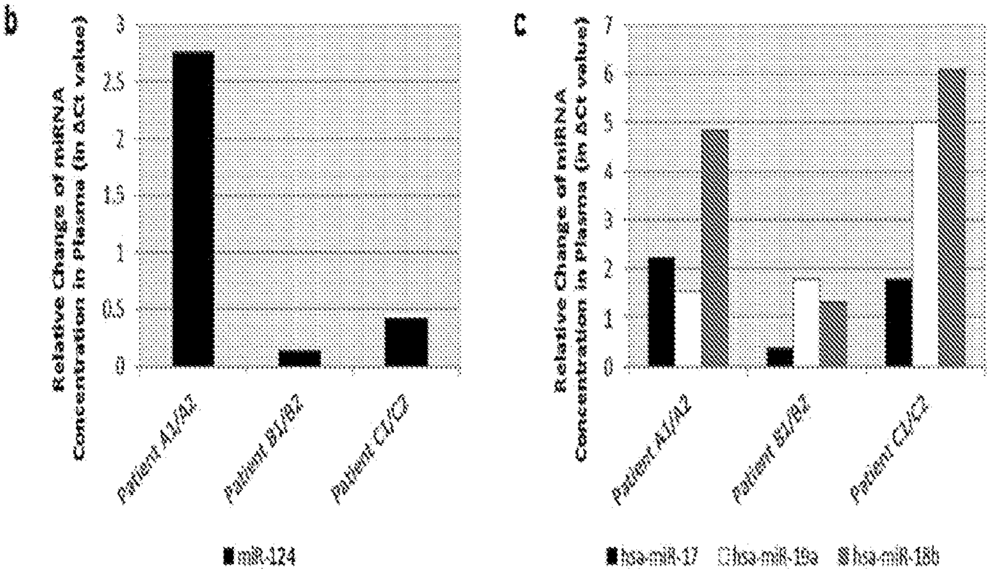
4 groups: 5/group	D14 Give tet water
Control	x
Tafenoquine	x
JAG21	x
T+J	x

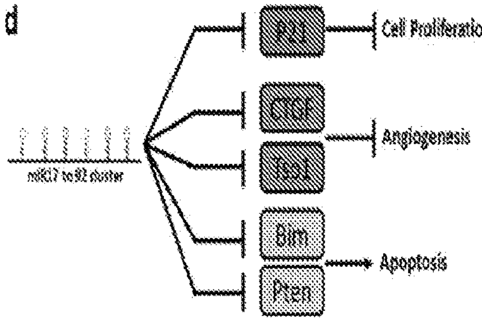
Monitor the mice
Take out the spleen once the
mouse is really sick for histopath



a

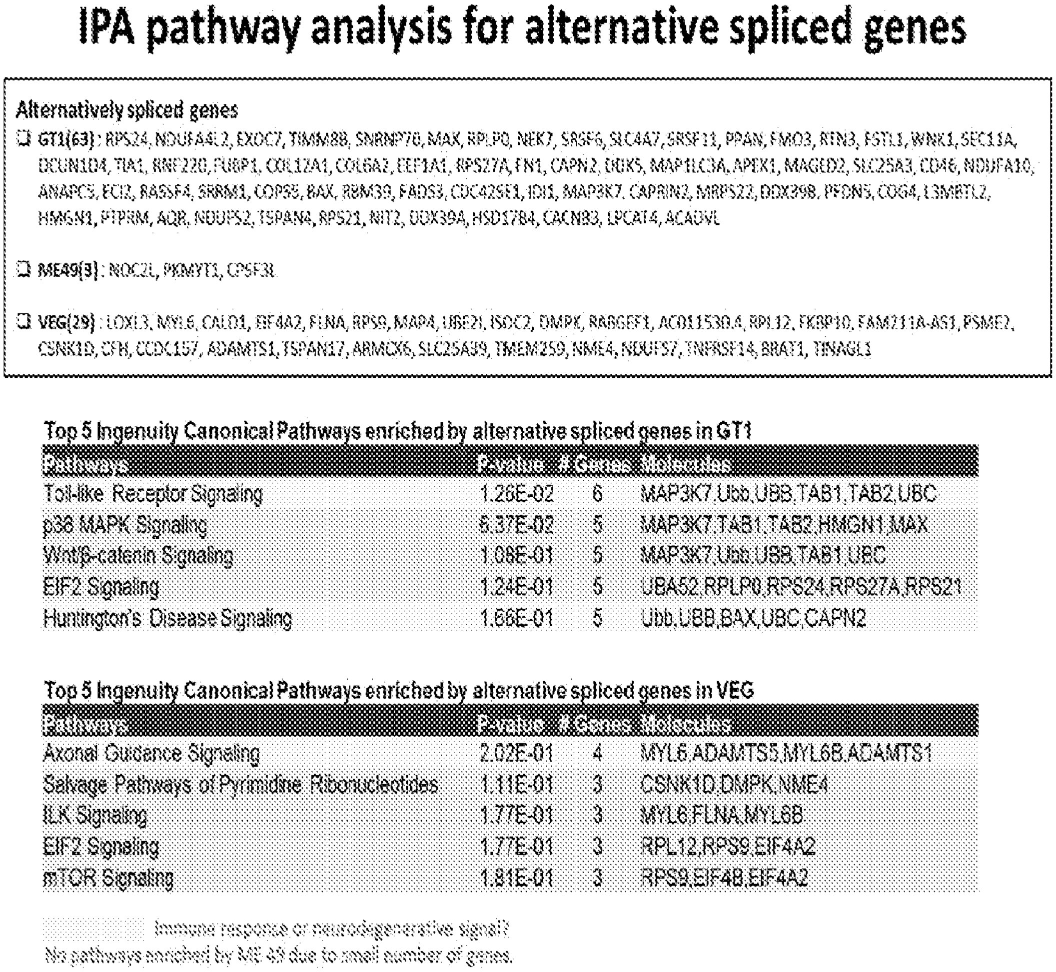
Pt	Ethnicity	New Seizure	Macular Disease	Increase Dye Test	Elevated CSF Protein
1a	Caucasian	Yes (myoclonic)	Yes	Yes	Yes
1b	Caucasian	No	No	ND	ND
2a	Filipino/Caucasian	Yes (myoclonic)	Yes	Yes	Yes
2b	Filipino/Caucasian	No	No	ND	ND
3a	Hispanic	Yes (hypsarrhythmia)	Yes	ND	ND
3b	Hispanic	No	No	ND	ND





Protein Name	Protein Description	Organ	Endogenous Peptide abundances (Ratio to 100fmol of Spiked in Heavy peptide)					
			Patient A1	Patient A2	Patient B1	Patient B2	Patient C1	Patient C2
APCS	Serum Amyloid P-Component	Liver	22.264	18.772	18.723	9.468	32.580	23.006
GC	Vitamin D-Binding Protein Precursor	Liver	36.239	15.782	31.835	14.418	32.795	17.156
APCS	Serum Amyloid P-Component	Liver	12.985	7.802	12.680	7.363	20.619	12.146
APCS	Serum Amyloid P-Component	Liver	8.034	4.470	8.229	4.580	14.184	7.808
OXT	Oxytocin-Neurophysin 1	Brain	3.606	1.305	7.806	1.667	5.928	2.087
CLU	Clusterin	Brain	12.508	3.859	5.743	4.917	5.485	4.565
C4BPB	Component 4 Binding Protein, Beta	Liver	0.417	0.341	0.823	0.244	0.502	0.081
APOA1	Apolipoprotein A-I	Liver	0.798	2.594	3.888	1.361	0.423	0.786
PGLYRP2	N-Acetylmuramoyl-L-Alanine Amidase	Brain	3.980	5.382	4.676	3.964	2.800	4.280
SERPINA4	Kallistatin	Liver	6.807	8.867	4.802	4.588	2.530	4.926
APOA4	Apolipoprotein A-Iv	Liver	8.798	15.984	11.276	23.713	3.799	8.938
HPX	Hemopexin	Liver	157.608	167.909	124.487	102.803	28.478	101.113

Figure 19



IPA pathway analysis for alternative spliced genes

Alternatively spliced genes

- ☐ **GT1(63)**: RPS24, NDUFA4L2, EXOC7, TIMM8B, SNRNP70, MAX, RPLP0, NEK7, SRSF6, SLC4A7, SRSF11, PPAN, FMO3, RTN3, FSTL1, WNK1, SEC11A, DCUN1D4, TIA1, RNF220, FUBP1, COL12A1, COL6A2, EEF1A1, RPS27A, FN1, CAPN2, DDX5, MAP1LC3A, APEX1, MAGED2, SLC25A3, CD46, NDUFA10, ANAPC5, ECI2, RASSF4, SRRM1, COPS5, BAX, RBM39, FADS3, CDC42SE1, IDI1, MAP3K7, CAPRIN2, MRPS22, DDX39B, PFDN5, COG4, L3MBTL2, HMGN1, PTPRM, AQR, NDUFS2, TSPAN4, RPS21, NIT2, DDX39A, HSD17B4, CACNB3, LPCAT4, ACADVL

- ☐ **ME49(3)**: NOC2L, PKMYT1, CPSF3L

- ☐ **VEG(29)**: LOXL3, MYL6, CALD1, EIF4A2, FLNA, RPS9, MAP4, UBE2I, ISOC2, DMPK, RABGEF1, AC011530.4, RPL12, FKBP10, FAM211A-AS1, PSME2, CSNK1D, CFH, CCDC157, ADAMTS1, TSPAN17, ARMCX6, SLC25A39, TMEM259, NME4, NDUFS7, TNFRSF14, BRAT1, TINAGL1

Top 5 Ingenuity Canonical Pathways enriched by alternative spliced genes in GT1

Pathways	P-value	# Genes	Molecules
Toll-like Receptor Signaling	1.26E-02	6	MAP3K7,Ubb,UBB,TAB1,TAB2,UBC
p38 MAPK Signaling	6.37E-02	5	MAP3K7,TAB1,TAB2,HMGN1,MAX
Wnt/β-catenin Signaling	1.08E-01	5	MAP3K7,Ubb,UBB,TAB1,UBC
EIF2 Signaling	1.24E-01	5	UBA52,RPLP0,RPS24,RPS27A,RPS21
Huntington's Disease Signaling	1.66E-01	5	Ubb,UBB,BAX,UBC,CAPN2

Top 5 Ingenuity Canonical Pathways enriched by alternative spliced genes in VEG

Pathways	P-value	# Genes	Molecules
Axonal Guidance Signaling	2.02E-01	4	MYL6,ADAMTS5,MYL6B,ADAMTS1
Salvage Pathways of Pyrimidine Ribonucleotides	1.11E-01	3	CSNK1D,DMPK,NME4
ILK Signaling	1.77E-01	3	MYL6,FLNA,MYL6B
EIF2 Signaling	1.77E-01	3	RPL12,RPS9,EIF4A2
mTOR Signaling	1.81E-01	3	RPS9,EIF4B,EIF4A2

▨ Immune response or neurodegenerative signal?

No pathways enriched by ME 49 due to small number of genes.

Figure 19E

FIGURE 20A

GOBP

GO id	GO term	mm6_up	mm6_down	NSC_up	NSC_down
GO:0006955	immune response	CD8A, IL27RA, BNIP3, TNFSF13, IFI44L, APOBEC3G, B2M, CFP, NOD2, MYD88, NFIL3, APLN, ICAM1, HLA-H, SP100, HLA-J, BST2, NCF2, LY96, HLA-A, COLEC12, CTSS, HLA-E, HLA-F, OSM, DCLRE1C, CD86, TNFSF13B, ULBP1, VEGFA, CD300LF, ICOSLG, PTAFR, GBP2, HLA-DRA, MAVS, PSMB10, GPR183, IFIH1, CCL2, HLA-DRB1, ENPP2, IFITM3, CCR1, OAS3, GPR65, RSAD2, HFE, OAS1, CD70, OAS2, CCL5, MIF, SLC11A1, TMED7, TNFRSF18, POU2F2, FCER1G, BCL3, MR1, C2, THBS1, DHX58, FYB, PTPRC, CR1, IL8, SAMHD1, MYO1F, CD300C, TNFSF9, TRIM22, AIM2, PSMB9, DDX58, TRAF3IP2, CYBA, GPI, TNFSF10, OASL, CBLB, FCGR2B, CD300A, ETS1, BNIP3L, POMP, TGFBR3, CD14, IFI6	None	None	None
GO:0009615	response to virus	MAVS, IFIH1, FGR, ZC3HAV1, RSAD2, BNIP3, RPS15A, APOBEC3G, CCL5, TRIM5, ISG15, BCL3, MX1, MX2, IFNGR1, PTPRC, BST2, SAMHD1, IFI44, IFI16, STAT1, TRIM22, STAT2, DDX58, IRF9, PLSCR1, IRF7, BNIP3L, EIF2AK2	None	MAVS, PLSCR1, IL6, BST2, ISG15, IRF7, IFI44, MX1, CCL5, BANF1	None
GO:0006952	defense response	S100A8, IL27RA, AIF1, S100A9, BNIP3, APOBEC3G, MMP25, CFP, NLRC4, NOD2, MYD88, HIST1H2BK, HMOX1, AOAH, HIST1H2BJ, HCP5, MX1, MX2, NFKB2, SP100, NCF2, LY96, F8, COLEC12, NLRP1, SIGLEC1, HIF1A, HIST2H2BE, ICOSLG, PTAFR, HLA-DRA, ACVR1, MAVS, C3AR1, IFIH1, CCL2, NFKBID, FGR, CCR1, RSAD2, CCL5, MIF, TMED7, SLC11A1, TNFRSF1B, LGALS3BP, MEFV, RAC1, BCL3, C2, THBS1, DHX58, SPP1, FN1, PTPRC, HIST1H2BC, CR1, LIPA, IL8, HCK, ANXA1, SAMHD1, MYO1F, CD300C, TP73, S100A12, DDX58, ORM1, CYBA, P2RX7, NUPR1, PENK, IRF7, BNIP3L, ALOX5, IGFBP4, CD14	None	None	None
GO:0009611	response to wounding	PPARA, S100A8, AIF1, S100A9, MMP25, CFP, NLRC4, MYD88, GSN, HMOX1, AOAH, SERPINE1, NFKBIZ, GATM, LY96, F8, STXBP1, PLAUR, SIGLEC1, CD36, THBD, HIF1A, GNAQ, VCAN, CTSB, PROS1, PTAFR, ACVR1, C3AR1, CCL2, NFKBID, CCR1, COL3A1, NINJ1, CCL5, MDK, TPM1, MIF, CD9, TMED7, SLC11A1, TNFRSF1B, MEFV, P2RY1, RAC1, C2, THBS1, PAPSS2, SPP1, FN1, KLF6, CR1, LIPA, MAP2K1, IL8, ANXA1, TP73, S100A12, ORM1, CYBA, PLSCR1, P2RX7, NUPR1, CD59, IRF7, ALOX5, IGFBP4, CD14	None	CCL2, TNC, C1R, CCL5, CASP6, S1PR3, HMCN1, HMOX1, RAC1, TFPI2, RAB27A, SCG2, PLAT, KLF6, IL6, LY96, LYZ, ITGA2, SOD2, PLSCR1, CD55, THBD, EREG, F3, IRF7, NGF	None
GO:0042981	regulation of apoptosis	MEF2C, PTGS2, MITF, BNIP3, TNFSF13, RPS27L, CRADD, ZFP91, NLRC4, PCGF2, APP, NOD2, MYD88, HMOX1, TPT1, NGFRAP1, MX1, MAP2K6, ADAM9, NOL3, RARG, ACTN4, DFFA, SOCS3, NDUFA13, IFI16, PRKCE, NLRP1, ARHGEF11, BTG2, TNFSF13B, BTG1, JUN, HIPK2, VEGFA, UBC, UBB, CTSB, UBA52, ACVR1, TRAF1, FGD2, ING4, IFIH1, CCL2, XIAP, PAFAH2, ADAMTSL4, SOX4, CD70, MIF, VDR, DDX19B, RAC1, TGM2, BCL3, BCL6, THBS1, PHLDA3, BMF, RUNX3, PHLDA1, TXNIP, PTPRC, LGALS1, CREB1, ANXA1, YWHAB, STAT1, BIRC3, TP73, TRADD, CDKN1A, SON, TNFSF10, P2RX7, PRLR, NUPR1, ETS1, BNIP3L, NLRP12, MAPK8IP1, IFI6	None	RPS27L, PMAIP1, GDNF, ZFP91, CASP6, PTGIS, HTRA2, HMOX1, NDUFS3, MX1, RAB27A, AIFM2, ACTN4, SOCS3, DFFA, NDUFA13, DDIT3, INHBA, KRT18, JUN, F3, VEGFA, TNFAIP3, UBA52, NGF, HMGB1, CCL2, XIAP, SOX4, NFKBIA, BCL2L2, DPF1, UTP11L, SQSTM1, RAC1, TGM2, TAF9, HSPE1, SCG2, ANGPTL4, IL6, TBX3, NR4A2, BIRC3, SOD2, SFRP1, NUP62, ROCK1P1, PDCD5, IFI6, CACNA1A	WFS1, PPP3R1, PRKDC, TGFB2, MAGED1, IGF1R, RB1CC1, PPP2CA, PIK3CA, HSPA5, DYRK2, THBS1, ERCC2, FGD4, APC, DHCR24, ZFP91-CNTF, TXNIP, PRKCA, HTT, NF1, ITGA1, BIRC6, ARHGEF17, PDE3A, STAT1, ARHGEF12, NME2, UACA, CUL4A, BNIP3L, SORT1, MYO18A, KALRN
GO:0048002	antigen processing and presentation of peptide antigen	HLA-H, SLC11A1, HLA-A, IFI30, HFE, FCER1G, MR1, HLA-E, HLA-DRA, B2M, HLA-F	None	None	None
GO:0043122	regulation of I-kappaB kinase/NF-kappaB cascade	MAVS, BST2, C9ORF89, LGALS1, NDFIP1, ECM1, LGALS9, TRADD, TRAF3IP2, TRIM38, TMED7, C18ORF32, TNFSF10, NOD2, MYD88, HMOX1, SHISA5, NLRP12, TGM2, OTUD7B, CC2D1A	None	MAVS, UBE2N, TRAF3IP2, BST2, NUP62, SLC20A1, SQSTM1, C9ORF89, HMOX1, TGM2, TNFAIP3	None
GO:0009617	response to bacterium	MAVS, CCL2, FGR, IL27RA, PTGS2, CCL5, B2M, CFP, SLC11A1, NOD2, NLRC4, MYD88, HIST1H2BK, HIST1H2BJ, BCL3, HIST1H2BC, LY96, SOCS3, HCK, MYO1F, STAT1, S100A12, P2RX7, THBD, HIST2H2BE, JUN, CD14, PTAFR	None	MAVS, IL6, HIST1H2BC, CCL2, SOCS3, LY96, LYZ, NFKBIA, CCL5, B2M, THBD, HIST1H2BK, JUN, MGST1, CTSG, NGF	None
GO:0070482	response to oxygen levels	PPARA, CAV1, SLC8A1, CCL2, FLT1, NOL3, ACTN4, SOCS3, ALDOC, APOLD1, EGLN2, BNIP3, CAPN2, DDIT4, CDKN1A, HIF1A, PLOD1, CAS, PLOD2, HMOX1, VEGFA, ALDH2, THBS1	None	PLAT, CCL2, ACTN4, SOCS3, HMOX1, VEGFA, NR4A2, ITGA2, DPP4, SOD2, ANGPTL4	EDNRA, SLC8A1, ALDOC, NF1, EDN1, PDE5A, PDGFRA, ABAT, THBS1, ITPR2, TGFB2
GO:0006909	phagocytosis	SLC11A1, P2RX7, CD36, LRP1, CD93, HCK, FCER1G, COLEC12, ABCA1, THBS1, CD14	None	None	None
GO:0009991	response to extracellular stimulus	PPARA, CAV1, CCL2, PTGS2, IL6ST, HFE, VDR, RASGRP4, GSN, HMOX1, SPP1, SLC8A1, SP100, RARG, GATM, SOCS3, AXL, STAT1, CDKN1A, P2RX7, RPS19, JUN, COL1A1, ALOX5, KLF4	None	None	None
GO:0001817	regulation of cytokine production	MAVS, IL27RA, IL6ST, CREB1, NDFIP1, DDX58, TMED7, SLC11A1, NOD2, CD86, P2RX7, MYD88, HIF1A, HMOX1, NLRP12, IRF1, BCL3, FCER1G, BCL6, THBS1, CD14	None	None	None
GO:0000165	MAPKKK cascade	PTPRC, FGFR1, CAV1, FLT1, MAP2K1, TAOK3, DUSP10, MAP4K1, PDE6G, DUSP4, SH2D3C, P2RX7, GAB1, SHC1, MAPK8IP1, MAPK7, THBS1, GADD45B, MAP3K13, MAP2K6, ADAM9	None	None	None
GO:0016192	vesicle-mediated transport	LDLR, CHMP5, C16ORF70, HOOK3, HOOK2, BLZF1, APP, CD93, GSN, KDELR3, STXBP1, COLEC12, CD36, LRP10, RIN2, RAB13, CUX1, VAMP1, ERC1, RIN3, CAV1, BET1, HFE, ABCA1, CCL5, SLC11A1, PLIN3, RAC1, BLOC1S1, FCER1G, VPS35, STX11, TRIP10, THBS1, SNAP25, AP2M1, GABARAPL2, RAB8A, HCK, LIN7B, MYO1F, SNAPIN, WIPI1, P2RX7, ARL17B, LRP1, NEDD4, CPNE3, MAPK8IP1, CD14	None	None	AP4E1, AP1G1, CLTC, DAB2, DOCK1, GSN, DNAJC6, SCARB1, DOPEY1, THBS1, RHOBTB3, HTT, ATP6V1H, LIN7A, COG4, NME2, CD36, RABEP1, LRP6, OPHN1, SORT1, CPNE3, SYTL2, UNC13A, MYH10, KALRN
GO:0007167	enzyme linked receptor protein signaling pathway	FGFR1, CCL2, CD8A, LTBP3, IL6ST, COL3A1, PXN, PHIP, RASGRP4, GAB1, SHC1, AGRN, SIK2, ADAM9, CSF1R, TXNIP, IRS2, FLT1, BAIAP2, ARID5B, CREB1, AXL, DOK2, PRLR, JUN, CSRNP1, HIPK2, VEGFA, COL1A2, TGFBR3, JAK3, ACVR1	None	None	TXNIP, PTPRJ, NDN, NIN, USP9Y, ARID5B, USP9X, RHOQ, FSTL1, KIT, DDR2, TGFB2, IGF1R, EPS8, CTGF, NTRK2, PDGFRA, SORT1, SPTBN1, PDGFRB, FGFI
GO:0033554	cellular response to stress	ING4, CAV1, XIAP, FAM175A, DUSP10, HFE, MAP4K1, RPS27L, TPM1, PXN, ACD, INSIG2, HMOX1, GAB1, FBXO6, BCL3, BCL6, THBS1, PHLDA3, C19ORF40, MAP2K6, LPO, SP100, TAOK3, IFI16, GTF2H5, EPPD1, FOXN3, ESCO2, TP73, ATRX, DCLRE1C, SH2D3C, POLD4, CDKN1A, HIF1A, NUPR1, BTG2, NEDD4, JUN, IRF7, HIPK2, FBXO31, VCAN, MAPK8IP1, EIF2AK2, MAP3K13	MMS19, TNF, BLM, C17ORF70, UNG, CLPB, PRKDC, BCCIP, ASNS, PRDX1, ERCC8, MAP3K4, GTF2H2C, CHD1L, ATG5, BCL2, AATF, DYRK2, NTHL1, ETV5, EIF2B3, ATRIP, EIF2B5, ERCC2, RECQL4, MRPS26, SSRP1, USP1, MSH5, EME2, TREX2, WRN, PPP1CB, RAD54L, PYCR1, MAP4K5, ATF4, HDAC2, CUL4A, MRPS9, HIPK1, SFPQ, POLD2, MPO, RBM38	None	None
GO:0007259	JAK-STAT cascade	OSM, CCL2, PRLR, SOCS3, IL6ST, STAT1, STAT2	None	None	None
GO:0016044	membrane organization	CAV1, LDLR, HFE, BNIP3, ABCA1, HOOK2, SLC11A1, CD9, APP, CD93, BLOC1S1, RAC1, FCER1G, AGRN, THBS1, TRIP10, STX11, RAB8A, HCK, STXBP1, COLEC12, PLSCR1, P2RX7, CD36, LRP1, LRP10, NEDD4, OTOF, RIN2, CD14, RIN3	None	None	OPA1, HTT, AP1G1, ATP6V1H, CLTC, DAB2, NME2, CD36, DOCK1, RABEP1, LRP6, OPHN1, SORT1, DNAJC6, SCARB1, PAFAH1B1, THBS1, MYH10, DHCR24
GO:0034470	ncRNA processing	None	ELAC2, PUS1, GAR1, PUSL1, UTP6, INTS1, TRMT1, QTRT1, BOP1, PUS7, DCAF13, SRRT, WDR36, RRP1B, DKC1, DGCR8, ADAT2, NPM3, WDR12, DUS1L, IMP4, NSUN2, RPP25, TBL3, PDCD11, RRP1, EXOSC2, RRP9, TRMT61A, NOP14, NOP2, NOLC1, TRMT12, POP1, WDR3, PES1, UTP14A, TRIT1, DDX51	RPL35A, EXOSC8, RPP21, GAR1, LSM6, EXOSC4, INTS12, PIN4, NOP10, FBL, UTP11L, FRG1, RPP30, NOP58, NPM3, NOP56, POP7	None
GO:0006364	rRNA processing	None	PDCD11, TBL3, RRP1, GAR1, UTP6, EXOSC2, BOP1, RRP9, NOP14, DCAF13, WDR36, NOP2, RRP1B, DKC1, NOLC1, NPM3, WDR12, WDR3, PES1, UTP14A, IMP4, DDX51	RPL35A, EXOSC8, GAR1, LSM6, EXOSC4, PIN4, NOP10, FBL, UTP11L, FRG1, NOP58, NPM3, NOP56	None
GO:0006397	mRNA processing	None	HNRNPA1L2, FUS, STRAP, PPIL1, SYNCRIP, SKIV2L2, WTAP, SART1, YBX1, SF3B2, HNRNPA3, HNRNPM, TARDBP, WDR77, HNRNPD, LSM2, RBM28, RBM25, GEMIN5, EFTUD2, HNRNPA2B1, SF1, SRPK1, SF3A3, HNRNPH3, SFPQ, LSM11, SNRPA, RBM38, SNRPC, PHF5A, HNRNPH1, PRPF38B, PUF60, TXNL4A, THOC1, PRPF38A	RPL36A, POLR2F, POLR2K, LSM6, SNRPD3, POLR2J, SNRPB2, LSM7, ZCRB1, SNRPD2, WBP4, CIR1, FRG1, U2AF1, LSM5, MAGOHB, SCNM1, CCAR1, PABPN1, SNRPA1, MAGOH, PPIH, UPF3B, SNRPB, SYF2, CPSF4, THOC2, SNRPF, SNRPE, SNRPG	None
GO:0006188	IMP biosynthetic process	None	ATIC, ADSL, PAICS, PPAT, PFAS	None	None
GO:0008033	tRNA processing	None	RPP25, ELAC2, PUS1, PUSL1, TRMT1, QTRT1, TRMT61A, PUS7, ADAT2, TRMT12, POP1, NSUN2, DUS1L, TRIT1	None	None
GO:0009064	glutamine family amino acid metabolic process	None	PYCR1, GCLC, GOT1, ALDH5A1, GLS, ASRGL1, CAD, ASNS, PPAT, PFAS, FAH	None	None
GO:0044271	nitrogen compound biosynthetic process	None	ATP5D, BCAT1, SRM, CAD, ASNS, RSAD1, QTRT1, PPAT, PFAS, MTHFD1, ATP6V0C, GOT1, FXN, ATIC, AMD1, NAPRT1, ODC1, MAT2A, HMBS, ATP5F1, NME4, PYCR1, NME2, CTH, ATP6V0E2, NME1, RFK, ADSL, ATP5A1, PSAT1, PAICS, ATP6V0A2	None	None
GO:0006839	mitochondrial transport	None	SLC25A30, PPIF, ATP5D, CPT1B, GRPEL2, KIAA1279, TOMM70A, BCL2, TOMM40, TOMM22	None	None
GO:0022402	cell cycle process	None	BCAT1, CEP120, BLM, CDC34, RCC1, SART1, CGREF1, PSMB1, SAC3D1, SEH1L, TARDBP, BCL2, TUBE1, RANBP1, CLASP2, GFI1, NUDC, DHCR24, MSH5, SF1, TREX2, ILF3, CENPJ, PPP1CB, RAD54L, CDC25A, DCTN1, PPM1G, SASS6, PSMC5, NOLC1, GSPT1, RCC2, CUL4A, SGSM3, CENPV, RRS1, ANAPC7, PES1, TXNL4A, PPP5C, DSCC1	None	None
GO:0007159	leukocyte adhesion	None	ITGAL, EZR, TNF, GMDS, TSTA3, ITGA4	None	None
GO:0006974	response to DNA damage stimulus	None	MMS19, C17ORF70, BLM, UNG, PRKDC, BCCIP, ERCC8, GTF2H2C, CHD1L, AATF, DYRK2, ATRIP, NTHL1, ERCC2, RECQL4, SSRP1, MRPS26, USP1, MSH5, EME2, TREX2, WRN, RAD54L, PPP1CB, HIPK1, MRPS9, CUL4A, SFPQ, POLD2, RBM38	CLSPN, HMGB1, XIAP, SHFM1, RPS27L, GTF2H5, KAT5, DDIT3, SOD2, UBE2N, DCLRE1C, MPG, HMOX1, IRF7, PCNA, NSMCE2, H2AFX, ALKBH2, GADD45A, CIB1	None
GO:0006733	oxidoreduction coenzyme metabolic process	None	COQ4, COQ3, RPIA, PDSS1, IDH3A, MDH2, NAPRT1	None	None
GO:0015986	ATP synthesis coupled proton transport	None	ATP5D, ATP6V0C, ATP6V0E2, ATP5F1, ATP5A1, ATP6V0A2	ATP5E, ATP6V0E1, ATP5L, ATP5G1, ATP5H, ATP6V1F, ATP5J	None
GO:0034220	ion transmembrane transport	None	ATP5D, ATP6V0C, ATP6V0E2, ATP5F1, ATP5A1, ATP6V0A2	ATP5E, ATP6V0E1, ATP5L, ATP5G1, ATP5H, ATP6V1F, ATP5J	None
GO:0006119	oxidative phosphorylation	None	None	ATP5E, NDUFB4, ATP6V0E1, NDUFB6, NDUFB9, ATP5G1, NDUFAF1, NDUFB1, NDUFB2, NDUFS5, NDUFS4, ATP5L, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, NDUFA6, NDUFC2, NDUFC1, NDUFA1, ATP6V1F, NDUFV2, UQCRB	None

FIGURE 20B

GO:0045333	cellular respiration	None	None	NDUFA4, NDUFB4, NDUFA5, NDUFA2, NDUFA3, NDUFB6, NDUFB9, NDUFA6, NDUFC2, NDUFC1, NDUFAF1, NDUFA1, NDUFB1, SOD2, NDUFB2, NDUFS5, NDUFS4, NDUFV2, NDUFS3, UQCRB	None
GO:0048145	regulation of fibroblast proliferation	None	None	S100A6, NDUFS4, EREG, ZMIZ1, IFI30, TGIF1, SOD2	None
GO:0006511	ubiquitin-dependent protein catabolic process	None	None	UFD1L, UBE2C, CDC26, PSMA7, UBE2L3, USP18, SEC61B, PSMA6, SQSTM1, UBE2K, PSMA5, PSMD10, UCHL5, TCEB1, UBA52	TBL1XR1, UBE4A, USP9Y, USP9X, UBR3, UBR2, UBR1, EDEM1, CYLD, CUL4A, UBR5, USP46, USP22, AMFR, CUL4B, USP34
GO:0030198	extracellular matrix organization	None	None	None	None
GO:0016477	cell migration	None	None	None	None
GO:0007010	cytoskeleton organization	None	None	None	None
GO:0048666	neuron development	None	None	None	None
GO:0007409	axonogenesis	None	None	None	None
GO:0045216	cell-cell junction organization	None	None	None	None
GO:0010594	regulation of endothelial cell migration	None	None	None	HDAC5, NF1, EDN1, SCARB1, THBS1
GO:0007229	integrin-mediated signaling pathway	None	None	None	DOCK1, CTGF, ITGA7, ITGA1, ADAMTS1, ITGA4, MYH9
GO:0006633	fatty acid biosynthetic process	None	None	None	GGT5, TPI1, SCD, EDN1, ACACA, FASN, FADS2

KEGG

KEGG id	KEGG pathway	mm6_up	mm6_down	NSC_up	NSC_down
hsa03010	Ribosome	RPL17, RPL36A, RPS15A, RPL37, RPS27L, RPL38, RPL39, RPS25, RPS27, RPL30, RPS28, RPS29, RPL31, RPL34, RPLP1, RPS20, RPS21, RPS23, RPL35A, RPL26, RPL27, RPL24, RPL29, RPS18, RPS19, RPS16, RPL41, RPL18A, RPL23, RPL21, RPS13, RPL37A, RPS10, RPS11, UBA52	None	RPL35A, RPL36A, RPL35, RPS9, RPL27, RPS27L, RPL38, RPS25, RPS27, RPL30, RPL23, RPS29, RPL21, RPS20, RPS21, UBA52, RPL36AL	None
hsa05322	Systemic lupus erythematosus	HIST1H2AC, HIST2H2AA3, HIST1H2BC, HIST1H2BD, ACTN4, HLA-DRB1, HIST1H2AG, HIST2H4A, CD86, FCGR2B, HIST1H2BK, HIST2H2BE, HIST2H2AC, HIST1H2BJ, HIST3H2A, FCGR2A, C2, HIST1H4J, HIST1H4H, HLA-DRA	None	HIST2H2AA3, HIST1H2AC, HIST1H2BC, ACTN4, SNRPD3, ELANE, C1R, HIST1H2BK, H2AFZ, SNRPB, H2AFX, CTSG, HIST1H4H	None
hsa04510	Focal adhesion	CAV1, XIAP, COL3A1, ITGB5, PXN, ITGB7, RAC1, PPP1R12A, COL6A1, PIK3R5, SHC1, THBS1, AKT3, FN1, SPP1, COL4A1, FLT1, ACTN4, MAP2K1, MYL12A, BIRC3, CAPN2, JUN, VEGFA, COL1A2, COL1A1, CRK	None	None	PRKCA, ACTB, TLN1, COL4A2, COL4A1, ROCK2, ITGA1, ITGA4, COL5A3, COL5A2, ACTG1, IGF1R, DOCK1, ITGA7, PDGFRA, PDGFRB, PIK3CA, RELN, LAMC1, THBS1, COL11A1, MYLK, AKT3
hsa04620	Toll-like receptor signaling pathway	IL8, MAP2K1, LY96, STAT1, CCL5, TMED7, CD86, MYD88, JUN, IRF7, RAC1, PIK3R5, MAP2K6, AKT3, CD14, SPP1	None	None	None
hsa04512	ECM-receptor interaction	COL4A1, COL3A1, HSPG2, ITGB5, SDC2, CD36, ITGB7, COL1A2, COL6A1, COL1A1, AGRN, THBS1, FN1, SPP1	None	None	COL4A2, COL4A1, ITGA1, ITGA4, COL5A3, COL5A2, SDC2, CD36, ITGA7, RELN, LAMC1, THBS1, COL11A1
hsa00010	Glycolysis / Gluconeogenesis	GPI, GALM, ALDOC, PGM1, HK2, ENO2, PFKP, ALDH2, PGK1, GAPDH, ALDH3B1	None	None	None
hsa04062	Chemokine signaling pathway	CCL2, MAP2K1, FGR, IL8, ADCY7, HCK, CCR1, ADCY6, GNG11, CCL5, STAT1, PXN, STAT2, CCR10, RAC1, GNB5, PIK3R5, SHC1, JAK3, CRK, AKT3	None	None	None
hsa04621	NOD-like receptor signaling pathway	NLRC4, NOD2, CCL2, MEFV, IL8, XIAP, BIRC3, CCL5, NLRP1	None	IL6, CCL2, XIAP, NFKBIB, NFKBIA, TNFAIP3, BIRC3, CCL5	None
hsa00970	Aminoacyl-tRNA biosynthesis	None	CARS, YARS, VARS2, NARS, GARS, QARS, VARS, SARS2, IARS, LARS, FARSB, CARS2, TARSL2, MARS	None	None
hsa00290	Valine, leucine and isoleucine biosynthesis	None	IARS, BCAT1, VARS2, LARS, PDHA1, VARS	None	None
hsa03040	Spliceosome	None	HNRNPA1L2, EFTUD2, PPIL1, SART1, SF3A3, SF3B2, HNRNPA3, HNRNPM, SNRPA, SNRPC, LSM2, PHF5A, PRPF38B, PUF60, RBM25, PRPF38A, THOC1, TXNL4A	SNRPA1, CCDC12, MAGOH, SNRPD3, LSM6, LSM7, SNRPB2, SNRPD2, PPIH, SNRPB, PQBP1, SYF2, LSM5, U2AF1, MAGOHB, THOC2, SNRPF, SNRPE, SNRPG	None
hsa00250	Alanine, aspartate and glutamate metabolism	None	GOT1, ALDH5A1, GLS, ADSL, CAD, ASNS, GPT2, PPAT	None	None
hsa00270	Cysteine and methionine metabolism	None	CTH, AHCY, GOT1, SRM, MAT2A, MTAP, AMD1, MPST	None	None
hsa00630	Glyoxylate and dicarboxylate metabolism	None	MTHFD1, PGP, MTHFD1L, MDH2, HYI	None	None
hsa00450	Selenoamino acid metabolism	None	LCMT1, CTH, SEPHS1, AHCY, MAT2A, MARS	None	None
hsa00190	Oxidative phosphorylation	None	None	ATP5E, NDUFB4, ATP6V0E1, NDUFB6, NDUFB9, COX7C, ATP6V1G1, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, ATP5L, NDUFS3, COX17, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, NDUFA1, ATP6V1F, NDUFV2, COX6A1, UQCRB	None
hsa05012	Parkinson's disease	None	None	ATP5E, NDUFB4, NDUFB6, NDUFB9, COX7C, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, HTRA2, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, UBE2L3, NDUFA1, VDAC3, NDUFV2, COX6A1, UQCRB	None
hsa05016	Huntington's disease	None	None	ATP5E, NDUFB4, POLR2F, NDUFB6, POLR2K, NDUFB9, POLR2J, COX7C, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, TGM2, CREB3L1, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, NDUFA1, VDAC3, SOD2, NDUFV2, COX6A1, UQCRB	None
hsa05010	Alzheimer's disease	None	None	ATP5E, NDUFB4, NDUFB6, NDUFB9, COX7C, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, PPP3CA, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, ITPR3, NDUFA1, NDUFV2, COX6A1, UQCRB	None
hsa04623	Cytosolic DNA-sensing pathway	None	None	MAVS, IL6, POLR3K, NFKBIB, IRF7, NFKBIA, POLR1C, CCL5	None
hsa04810	Regulation of actin cytoskeleton	None	None	None	ACTB, ROCK2, ITGA1, FGF11, ITGA4, MYH9, ARHGEF12, ACTG1, DOCK1, GSN, ITGA7, PDGFRA, CYFIP2, PDGFRB, PIK3CA, FGF1, MYLK, MYH10, APC
hsa04270	Vascular smooth muscle contraction	None	None	None	PRKCA, ACTA2, ROCK2, CALD1, PPP1R12B, MRV 1, PRKCH, PRKG1, ARHGEF12, ITPR2, EDNRA, PLCB4, MYLK
hsa04020	Calcium signaling pathway	None	None	None	PRKCA, SLC8A1, PHKB, PPP3R1, ITPR2, EDNRA, PLCB4, PDE1C, TBXA2R, PPP3CB, PDGFRA, PDGFRB, CACNA1H, MYLK
hsa05410	Hypertrophic cardiomyopathy (HCM)	None	None	None	ACTG1, ACTB, SLC8A1, CACNA2D1, DMD, ITGA7, ITGA1, ITGA4, TGFB2
hsa04310	Wnt signaling pathway	None	None	None	PRKCA, TBL1XR1, PLCB4, ROCK2, PPP2CA, PPP2R5D, NFATS, PPP3CB, LRP6, PPP3R1, DAAM2, APC
hsa05110	Vibrio cholerae infection	None	None	None	PRKCA, ACTG1, ACTB, ATP6V1A, TJP1, ATP6V1H, SEC61A1
hsa05414	Dilated cardiomyopathy	None	None	None	ACTG1, ACTB, SLC8A1, CACNA2D1, DMD, ITGA7, ITGA1, ITGA4, TGFB2
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	None	None	None	ACTG1, ACTB, SLC8A1, CACNA2D1, DMD, ITGA7, ITGA1, ITGA4
hsa04010	MAPK signaling pathway	None	None	None	PRKCA, CACNA2D1, MAP2K3, NF1, MAP2K4, PPP3R1, FGF11, TGFB2, DUSP5, NTRK2, PPP3CB, PDGFRA, CACNA1H, PDGFRB, FGF1, AKT3
hsa04540	Gap junction	None	None	None	PRKCA, TJP1, PLCB4, PDGFRA, PDGFRB, PRKG1, TUBA1A, ITPR2

FIGURE 21A

List of candidate genes as targets for the developments of antiparasitic compounds that inhibit bradyzoite development and/or survival in the host.

Gene ID	Product Name	Protein sequence	Chromosome location in reference assembly ME49
TGME49_215895	AP2 domain-containing protein	MLSRRCKRSSAEDSGANEVGANADQSKRLRHSLDSIIEKGGDPVNHDSAMLLDCAPTQTGRAFAFLSMPAPIEPSGNEESAPAVHRDSGVGGIDYPRPVASISVESSSGVVAPRDENPSASYQRRGDSPPSLRNGGDRQERKRTAVAP EANEPQDNETKNEEWLQLARLKPKVEGVCFDRFFRRWAKRAGLKKVYFPVVKYGFDRAYELAVATRRGLENDAAAGIRAVGALRPRISEAAGCTSSPGMLSEDACPEKPPVPVQPPRTLSTRATAAQAEVKSGDSAESTKNDSEGAN VLEGAELQTPERSTSNTICWATAAEGSISKTDGFQNRSSPSGFGHGSRNKPELSQQKVETTSRGIRSASASCNREKDQGGSACSVLSIASFSLSQIDEELEGINDEAYEAERLQADEDRSHAPAASHGEGGTSAGESTAASTTGSEDSG PLRAATSPLMFPQGSEGSASSASTEMVLDDESMQQALVTASAETLNKLRSTLPAGVHFDFASKRWFAVYSSHESPEATQRDPVRPKERVRIFDPTQYEGSMLKAFHACRSFCGSVEAGASDWDSVPQLVPEQRKQGECQDTSGSSD QGANRLSPTETENPPTADHPRSLSATTRPEGSLEQTQHPQRNRGILGIQPGETEGLQVPSNGHGVNAGDIETNLLDAEFGSETRARTTALPHLRRSQRRADPARSVHSNTFAGQELHQSPKPGNQTSRGESGRSSLRRKNQVSTNEKG LPGEGGCRTDEKSKQVSYVSFSEPITVRYQQVPTESASTRGCSQRRPQNAEELEDRRSPLTRQEERTESDPRTTAGLCQENPHPSYRFLRQQSRELAVRCLLVIFGNLADVCTPALFRLFPQDRCRRVRAVLQHRDLLQSGKHTSVLLS AYFQLFWPLLETRTLPQHYSADYIRRLLNGMHNVAAMHKSLFPEYPLRGELDNREGPYAFLCDTAAEGINFFETDFDEP (SEQ ID NO: 7)	TGME49_chrXI:6,550,702..6,563,171(+)
TGME49_320700	AP2 domain transcription factor AP2IV-1	MAYQRRRAAACTIEVSPDLFSPERNLHDNFSSLAITMAFRTVSKVLPTLSHCFPGPLSVAASSSLPGHSKGEESVPCRVHRSFRLSPVADHEAEALSGSGNDTSGCSQRDRFCAGNGSDCKARRTSDGNGSPPTNARMSEKLSLFKNH AYSCLECRACPASNRNLGDTAACPLSAFCRSLVRRTPSRLWLPPQCSLLSGCSARSCPPKISVRATNGASEQASWQDFHPALGRAVVPLSLSGRGTAGTHLVRKFGTQRVVQKRRHQMRILHPAQTAYVPVEQRPPPIPHSLTASSTV KRLLNNNTVAAKEAAKRNWGAYISHQRGVRWHPQGAWRVQFSRRNHERNFFVRCECYFRVGTYGFQMAKDLAIRYRQRLEKEWEELQEQWTKLDILEAECRAKYKEKREEHLLLGAGEEPELHSRRSK (SEQ ID NO: 8)	TGME49_chrIV:130,940..133,193(-)
TGME49_290630	AP2 domain transcription factor AP2IX-7	MDGSGESSGHLFKPGHGEARVSVHRGSLTDSGSLPAASRCHSQDNKLSLPCAGSMLPASSGRFSCDSALFGGPVDSACSSDWTPVVSPSRDLSADGTDSSSVSGSRGSSLPFGSPTSALLRPSSEASANFPRLHKSVHALDDKMRG LDAQLYVRPHQTLPLQPRLRETDLCRNGEDGRPGKFDSPHLGSSAGPYGHSFLANPQLTPFVPQHLSSSPPQPVLSPPGEEGRNSAAFGKTVSRLNTGGGERQDSSEDQVGGTGRQSDQATKANSGSTFAGCAQTAGLLTDVQSSG TNVEHGREHFSTPQKPADGSARTCGFRETRVSPSNSSLPRTACRSRLDAFLPQKSVSPDHEHVRGTGGARAFVGGDSPFPEKPDTLPATVTAELATEAPPASRDPPVEEFPGAHELESLPPPHVNSGRPPIGEKDGAAASPGVSRLPS QERVHTLLYPNEKDASSLSRQCPSSMQPPPAGPRQEEARSFSVSAASAPGAPPGIVYQASACASPATVASFATPLTTPVGASAQSEPAALHAHSRSRTCAHPEALPPGVPGVTSQLGRGARGDRETLAGGARPGQDGVCERRGDVAR GRLGGVSYAGDEAAEGTSHKAALEGAYVQDGCSPQPLNPHAPSGISAPTNGSSELASSAIPASTCHDAFVRSPVSGSDCMSVANPGGPPGALGGLPPSPRGPSGPRPTPHPAQMAFAFVGQQPVFPGFDASQPAGSTPQYPPIRGAV SGVSPPPPMHPSSFAQPVVSPTSVPSSSVSSSVSSSGVSSSAPPPLAVGPQNPCPWRPTAPRDRSEGGAGSPGVSCGSAPPAPTHPTGKGGAAGRAGKQLGQATRFLSSVSGVVYDKGGEKWIARWSENGKPFKKTFAVGKHGFD AARKMAEDCRLQALYAKRWNSASGLPASFSKSNSLGRSTPGDRGKTESTNSAKCKRDTSGESGCTDTGLRSLHMGGAGDLSSLGHPGTPPRDQEGAPASFLLEGTGVVRSSQVQTPFRLYDSVPSPLRSGDALGAQRGLVPQLLNN ALVGVPFAPPPGASHSGCSAALPPGPGAPVQVSSPHTGFVAPADVDAPPRDGLEGLGGAAEVSPQIAVQDGSKKGEGLLGSASLSVRRRRKREPDEKFSPGESNAAVKKTPRPGSFHPHSCPGSEGFRSHDGPGDSTEARCAGLPA FQHATAPSSVCWPSTASLFSLDKAGQRAEHAGPSAFSSFSSVQQSPGSVETWRPEGDGGPASFARDAGRRGAESEERETGELAGPFAGVSASAGSASRKGQQKQLTRQIQRQQQLYRQQEALLQNQEELFSRLLRRRSRQERSDV RRRMQRDVSSLRRLPAMLLSPLRDTLVASAARLPLATRGTKRESQKERRDQGAGIGGETASEKKEMAEPVRVHRRDRGGARDEEKPSTEGVRQADPKGRKAEGFPTKVIPPNEELKAAQVLRALRVQRRAAAREGKLLESLLVHRGE GEGTFSEETEGNTGIEDAGTESDATVTQETAEKVVENVQKMEELESKVEKENERRREAEDETPKQSSEEAPGVQQSPHKLSTNNENDASPQKLTKSVRFAESVAGSSSAVQTAGAADEEPLATETLEGRRVGDIPVPATSSPAPVFPCT AAQLGDLCMDTLYALGTVRPQWRRQDHRRAFGWHLSQIKFDLILPSLHASRVLRRLSPRPSNAVEFPREELAAASSAAGLVYGEGLSSHHTLRSYVDAFRPLFSSPSSPPLEFLHLSSGDLLMSLWQLEEGGRAAVIDNVLLALDALYER HTGRRLRGTAPPPFAVSSPSSAPSSLFALAHLQGGATSTTPLPATALPSPPFPRVSSAPDSPVFAPDASHGPSQRRQVSPHVTFETPFTHPRDRDSETSVERNASPEASPQAATLAAPAPCDGDREENFVLAYNPEAKALRQVNFLAVG VRVFLHLEVVEEMLHLQAKMQRTPGRQDRATASSGPSVDDGSGLMTSLPSTCSGVSGKKDPMHWSALFVTVPAPSVSTAASKPLFVVAEMVDRRLQVPCGEQLLFRPLPLSPAAPSALLAFAPARVCQLLRAGAMCLTRFTEKEGGKR FRGSAQRCSAASSFFYSPPPLDLSHLASFAPAASTLTPPSSPASSPSASASQTGPGRAKSRGTSPVGPESPEAASTTSDGLAVPGSASAVSTPGVPAGASGASLGAPAPSPMASPGGSPGRPPKPVCCPAAPGIETAWRCKCSHRRH ELQLEIKQKLRQDKKRCLAIREYPQLSLLVGAPPATPREKETGAKRQAPEGRRTATPSGSGTLTAKGGDLQGSTPSGAGLLSLARTSQLEMLAYLVEVDPWKYAKNRQDAPKPEEIPGLLAKYKAAVRTAEYGRMLQKWPAGQSREDE GRGGADGRKEGDGLLSPTASPPSRRKQGKDSSPNSASSQASGPAPSPSLSPGAGAAAVLEAEKPEPGSPQESPCPLEPAAGGEPRATSSALPAQSPPWALPLVPPGGSPRASVSPSVLEELLRIQTAMSQLAIGTAICVRVKALLGLPA GAEQHRQVVTRNALKFPWEKPAAPQVQAAGPSVGASRTSPSRRLSGGVLPGDEAGERREKGGARRGVAEGDTEKKEDEGTALCAGSRETEADGAGYLTLSLNNRKEEFILSFREVQCLVAQDDLRLVRTRARQWVSSFGPQPSADR KGEREEEKETGGRTRKFVVDEDF (SEQ ID NO: 9)	TGME49_chrIX:3,784,225..3,794,690(+)
TGME49_218960	AP2 domain transcription factor AP2XII-1	MDSGRDVKDGTAGSRPKDGGDGVGETRASGRESEERSLQLEANECPGAVMSRREDEAEPQSSPSSSPPREEGPQNVDDADTANGSGEAGLQRPPQKPRLEQGLEAEAGVGSSRVEEVEAVQRKRPAFSGVADAFLERPVTLKNSS EEDAARLSGDDAAGASLLSVRSAGALTQDPPSSSSRLPAMLSGARGENAEESVRDAHTPAQDSRDSALASFAPTLAPGQESEYTRAKLWSIEKAFDAFLADQKANGRRQGSRSMREPSHAHPGLSAERETSSGASAATSDLSREDVEE LFRQHGVSPRELVRMLSGRRDGPGTSPEELRAAVAWARQLFPAAPRSPSELRMYLQRAVLDRCKRLRERWGAEANPCGDASVYGDEKLREHLSDLSAFMPHLDAGREVYMQWQRSRGRRDFDAFVRPPGLTPFRDSSSRQGDFAA SPLYSFSSRTPWASACKEASTPPAAKQGAPPPSLWNLPNRFQPYTLADVQEAMEGPEGVLRVARPLTGFGEDAESLSFASLPKGAETLFVSSGRGLYFLRHLERTKAGEHDVVGEAGVWVAASEEEFGGRIHRKFSVAKFGFERAKM LACRWYNDRGEARRGQHALPHREKPKGMSSDRPLSREAAPEASRFSASRAGELSGKAQEAPKSTGGTAAEHPRASQKCRVMDTTCPVPGVRYDSRDRAWLATWHQGVRQYKRCFSIKKYGFAKAKECAIRMKMSLVGQPGVSGS GRQAPPPVRPPTSRACSPLQDFFREGDRRVAASSFSLLPSGRGEPRGSLGSSQGADDERSKPQSCRGLVEQLLARFQDSEGFTRGLPGDDENRGKRLSKQAQDDFQSWRPPPGARFGSAAQASRHSTDEVGGFAGFPGFAASHGG EKPGGEGPSFLQKSGFVQENAFSPPSERFETGVHRRVPSLSSELANPQVTEEVEEFLFSLSTRARQSLLASLRRGAEDSRRSAWPGASRDCHTGAGTPGGTDVADPRATRETRRDREGEESTSEDGTVRRETDAGAVSPDEVSRANA EERAAGEKTRSSERKWTGEGERSAGDRDDKGEGEGGGGVVEGRTEKGGDDDKKPGEEESAEREEELKNDAYAYFTHLTNREWDLLDYLDTLDFETVDLDAVMPFINQVPKYRGVCFDRKGLYWISQWHSQKKHREWFGVKRLGF RKAWALAVCVRRDAEKVEDEPVDYPKLPDYEEVLGVTYARFASGRYWVAHYMRPAAPSSGCLGSVGRKLFPVSESSFEEARSQAVAVATAFPLPLAFPVDPERRATSAFESARAENLQGDKQVLLSKNCLFNVFTWLNGGASWTNVR RWAHAKRMQLAEDDWPQQFFSLPSPAKGDSFAEAEKERAEERTGGEEVKANSASRAAAKSEWPVASTTSPAEDLASSGSPRDLQKLSPLLADSSLTKELLGGDRELGNAMDGARGPRGLDTAKGRAKDEERLTAKDAESRQATLPG GRAAHGGGVGGSLGTACEEELDEPLSPLDIESIVADAYESFSDEDAEGEGDGGKPGKRIRLPKIGGVYYKRDGNYKAWAASWHIQGKRTRRYFTVKKHGFRNAYLKAVRARREAERHEGISVKHRHHALVPGHPGNMLGASKVCAESH EVSGFPHGDEDSRLTRGGASHAAVAPGRVNRERSVALVDRATKDDEDDERDLQREKTGAGGGEACSGESVKVALGTRHDSFSDGSCRTLDKLSTGFEQKPRGGAGEEAEHPTRKQGQETGGVDEPLSRAASIVGGREVRLTSGVSV HLTPLERVAKAVDVDLKELTDRVSRAAFRGGDSRLFHRTVDNCEGEADEVAQGLDTHREDVDVTRNLEFAMARETLDVLLSDLYSVVAKLSGAGRWTSLVSPTAAEAEPLVSAWDRSAREERREKFEDTNAASDEPGVPTSSAQIHVAI QLVVKHYLATVRTANPVEQIAPLLALFEPCIKQGMLPHECALPRLRWLYCQLCRASLPWLDESDVLTDALLYRHLEELVETEEAEAPQEGVPPGGQIVFSAGFAEGNSTVASPNVFTGESRVAGGFRTDSEKESGIDDRDEASLAALICLP GKGKKLREEADVEKDDTSASLNCESGKKTEAESQHSRSPTEVAASSVSGSEGKDGSSDNERSGDADDATEGSEKCEKTRGGDQRRAAPRTSSASTASGETPEKSKNRGSDALKGKNEGGATGTSGEQRDDEDRDLENVEISKDTRA GSGGRRRTGERRGQRFCASGGELRVSEESPDRAKTEKSKGEPVRDSLSPDASSRLPSRCGTPPPAAATGSCATVESDVPA (SEQ ID NO: 10)	TGME49_chrXII:1,176,841..1,187,769(-)
TGME49_315760	AP2 domain transcription factor AP2XI-4	MTTVSPAHASRSRRKSRDEDSEGSSLPAVGIHETQSPVFSREGHEGDRAAQPEDVVAAESHSNPQWFTPLDTGFDKGAPPLGCSRSEELRSPPMASGSFHGSGTGGDGGCLLSLEAHAVSKDSERQVNSGLPGGGDEISGRLSPSC ASLPLVAAALSPVEDTRLERDSSIPVLKPSLSIPNLLVTSPSLTSVSVYVCEADRSAEGKAPSMDALPPSHSAAPESGLWRECDERGKNSFFSSGLPAHFEGNGERAGEGQDPRSGDFETFEEAAFSVQRLQESEELFLLSGCAREDRGG ESDAAFKTMTRSEGAFSREPAHRHAFAKPGNGGESEFFMSIDEERAASPSASGPSSYAFLSFEETSAGSRRSPDAQSPPLSGHLSDGDRTQRKAGERFLEDPRGNLKRSRSPLIARDCNRSLGTCDSSLTTRGPVASDTSPRRGYTDQ WHSHRKAQSPGRFRRTNTEGNATPVDSQSSPFSKKRCCLAERFAFERRRGPPVPLPSVASAVAAALAQFPPGACTAAVERADQVPPEGSGNGVLPGGEVSDLSLSDRKSGASPRQTLDTFLPAKGASAALKQEGSSSEIGEGCPASD DAAVAATLSGWKRGRGPRSGCVSGSSRASSLEHAGARPRSGVERKRREKRKAALATAAVVSASVRRLALVAAPCLVENTLRQWWRLQEQVGDELDNGGVSEEQTTGRSGRRTGKNPIVGGRVKEGEQSVRLEIERSGDSPRNTAKT EPGDQGAAQGQGGPEQIAENESGTERMETSQTKQEAQDLPLHREAASASATPPIPEGRTQERDSYLRYTLFAASQVLNSGQFRQAIRMFPGADSPRGDQRSRCVVRVYKQSLRKRRLSGDRNRRVGEDGNLVSVSLRDLLANSGED WEPSSPSAATRPLPLAPSALSAHQARSSFGSFSRRSAEGVPGPSPWGGDCSPTAARSPLPLSTSHDLRRRRVCPPRRRYSPSESVHSSDGRGGACAIAAKKPKGRRSRGREEQTREEVSESRCSTFRSCSSVRYAVSDGSPASSRA HLGRPQDEGDERMTGGQRTPRGTPGEGEDSDFLPAGMSGLRGGTLPLDQLGERSRSAERWMPAPSVAVVPFAPNILAKKHAEDVENQLDGGKMSLDGVGGKECGLVETGDTGEQEAAVAASEKRRPLEAQTPGRHGTTVLMKGEG LLAGRTSEVDGDRTGEKTTQISPFSEATGICILRRSPPRVQSNSSEASRTAVRSTEGLETSDKLGVDVGTTNKEADSFSASCDSPRDSLERNYGEIVAIWARARDAKQGGRIRRRVWLFPGMATHGGHEGNEQNNEAICGGGATPMMK TERAMEEGRGDAKTHPVGGTYAETEKKVVDEMKAWWSKLTCASVEAVPVQTLTLDDFARAFSTVANRAVDLLCLAFRARGAGPVFRPVLSSSPKQQGNSPQPESEDVETRIETYRQQVRRLYRRRQQLHEATGNSPFSSSRVGGALQ RRIGELQRLREAHGRVDIPNEGPRREEDSEKCPASLWDVPLRQRKQGRKRVSPWYSVGVRWLADFSAFEYFVVKNYRKEDLGATVSLSNRGEASCTTWSVDGTGSQRAPVPCLSRAGTPRTVSPSPPSADAMNLWAQAYAPSLNQP RGMSPATTPPLSESATPRGNVSPPFSEASSSGQRGKKVAPGPSADEKKDEDYQSAGSLRWEVDGGQRRQYQVRSRLLLHELLQPPSLDATGLRTALVLIVLRLQRFLRLKEGGVNNRGRGQRSERKRKCRAMPPIFIFRDDSNAFQEA LLAKKLDIRLDSDSPHTDVPSRRSLDGEVGDERRRLRSVKPTNSNDLSDERGPPPPSTMSPHSLGSGPCDTQEGVQNLQQDASLFSPALAQQQAHAHTQAVPGARHQDVLPRSPRFPVVDAGPEETPRPEVESMLDSESGDFTGLGQ ASRRRWRGRGSRTSVQRTVSTCLNEDHSGDKTPREETFGGDAASLLRVASSVPPSTCSSPQSSSGGPRERGRRGVRGRRGRGRLISQQGSSLLGQTVSAGALSSGDTAGAISTSGENRRNAVRPGALEHSDEDKEDLSASSPPSDD GISQRSSGSGGDSSSSGGPSSEACRKTTSHVAAKADSASPRALHPSARPQPRGTASWTPGGEPAVSGVQHPSALTPSPSRGRFSEDNVASRVSRVSSVGALLRSRCVVGEEQKETQNSCSLWVVEKGALEPFYWRTASAVGCVSA GRRDHSDKDANRLRLADKEAGTGPLQDFVLPDFSGSAREIHGDERGSDSDASCKSAALSTTSDSSGISEVSLDLESTVQEVALGTILSSALSALHGKTGDGDTQESDAEREANADDGSATGVNEKDLRGESRPELPSPIPGKDELGSQE EGKTASSLPSVKAEQGGSERGGADEIVKKATSVLRACKQFDEATSTSLVPEGEDENDACGALEPDSLVSVSALGESSEELFTEVPQNEKELKKTLQHVDPRLCQQMLHGGLCFIRTYVDLETKKESLQAGPFAAKRRRVAQLLRGLQGL FDALESVREREGDDLSGEHEGDSASGGLFTAEQEKEGADKVSGDRENAGERGQKTAAETGDQKASIEDAVAAAFCRRVGAAIATETCGSIQTVFPEIGEAYDVEDSVARLGAPPRAPVRTRRECTGTGFTSTAALPEPRGEDGRKQET SEPLGVEAADKTDKQGEYAQESEHTWTQEMGRKASLFLSGTLELAQLKEEQQVEELQGEGDPLTSFLLPSDQSDSTKKANEECMGGRTARELYAERSEDVKTLGRRREAQTESRARGPHVDSSAEAASVAQGDEGGEEARKRKKQEK REKRSGNAFLDALLEPALREDVGRAFLTDFGSQAPQNSTDAGKPIRLSPCVFGVRGGARWKKLGLFNDEAQREGTESSPWRNDCSDPMSYRADAPHTWRRHEGLLWGSSRHAASALRHHGRKSPAFLSPQWEDDERLSLSSSADE RGYTSSGSERFLSIPTRRKYGLRFQRRSTKTGRAPSPTAGRSSVNRSQWRETLRPSSGFSGEETPRSLSSRRRRGGLGGSSPTAFRPPMTRAATGKAAACVRHGDGDECAEPDSQFGAFGSADLGLSDRRGEAGEADTREEKAGGS ARHGKRGSGVRSGGAREAGSDAGTDTLWVAPGSSPNTCRSGRKSPAAAALSSLPTGVYFDASRKLWRCQWRENGRFKTKGFSLNVYKTLKEARRACVVYRCLMSGWEVDPRWLGPDDDEQDNSGGADEVGRPVPSDGISDVVGE ARRKGEY (SEQ ID NO: 11)	TGME49_chrXI:4,949,378..4,965,499(+)

FIGURE 21B

TGME49_253390	AP2 domain transcription factor AP2III-2	MINLHQLFRVFSRVSSSASDFSASNPSPASLVSVPALQTLSFPALQQQDLLASLAAASLFGPDSVTMSSSFTSVLNSGFCSLPSSRKPAALPFPATSPKTPHLSDSFPASAISGPSSPGLQELLASPELAAAALASLQKQQLRLALGTERGGCGARGDEHLHSLLQHKATSENAMRWSWHAGRDGAQELDTVPETFDLPLSLSSFLGVAPQQFSSLPRGSLLPPTDFSLTDGTLRVSSSMLPALATGSESGSSRGLNSAQASPSFSSLRGPFVSVPEEEVSGSLEGSPGPFSSGHFPAAPSHPCSTVSGADTQEAEPPLLTLVAVNTPDAQDPAVDGASLCASKEGMRTSSADLGDSLLAPPGHGSAAPLPGRHLGSDATRTTTTTGSGAPESPSLPLARGDCEGAERGLALLEAPVNGFNLAASGSVLGGFAADTRGEAGEKGIAPQSRKARKPGTAVETAGAPEAVRRGRAACNGEAETTGLETAPQQVSTSEETAKSGRELACARAGMDEEEDAAFPSHVVSEFRGPPEISNVFNDLDCSSAVERPQGQLQHAAVQPFLPAVAPEVRPSATTAGRTPMGLWSEAGRVSSLETDTAEIGRRLDGESSGSPDRWGDARLSSPDSVPSSADVPVFSRPQCQEQVPQVDPDSSHPLFASCSAGSSSTAGSASALAGLASPFPPPKSPKTGANDPRMTPSEGEMRAVSGAPPSLHMSPPIPPLALQDSFGECTASSLAGVDAPEATAGGLAEGVATGGGSDSVGEGRLPGAASLEVPSSFSALLSGAPASLLLLLRNGQSGAAALVAAMQQHQALSGDAEEALEAVLAGGSNVGDMANSSRGLETVGDGTRGSAHTTHAAHSSGRNAVGACPAPDREGETVAVPTSVLTMNPASTSKTMPSVYSTPASAGLSLTSSSTPPVLPTPNPGAGMPPLASAHAASPAVPGDANLQSLFFWAPQACPLQPGALAVDASASSCGGVGSCNGGPAPPGPSPVAELLDASGSGPFGAAGSGAQLAAGPFGAATPASATFQQQLLLLSAAFDQIGSSSFPVVGGENFIGYSALSAARPDASDLSASGGPPASLPVLLAAANAGVGPGAAGVGDQPDFLALLGGGSASREGARDPVGGELGGAGNSATSMKGVKRQFVQNGHGTASQTHPEENTQGPGRSAAVVGRATKKQRRGPPHSGAAVSSGAPSGVLAVPGCLGPPSVAKGPGSDEFNLQQLQQSRDSRHSADNASGIPNWPPVFSNGNHTLGVGTRSPSPSVCSISHDAGFFGASGSNHAGSLSTPVCLPQLFGAASASEGPCEAQQTPPGSIPEATTLGGLSAASGNPNSTFSVSAGGGVAPAILNLSSASRTSSGTSPCCPTAPGSLLSGGSGPALFFAGPPSPLQKAPVYAGGSGSVCASSGDAIAAAALLHLRTLQQLQELQRHFGRPGSLPPAVTPACLPSGVAGCSPAGLGASTPGTHSVVCNSSASPVPGASRVPRRPDGRGTGGAGGDFGPSKRGSVSVSPSAQQFVLLQLKQQQPGSHGNALSLGTQGNSSNPAPAGGAGAPQQHHPGVCYSPPKDVWRARITVDGRQHEQQFSVKRHGFEEARLLAVQWRAHMENLRLGGAAKGKGKASASSASAATATSQGSSQSSHQPPLGSLMVSGNSGMSGPGAGPLANRGL (SEQ ID NO: 12)	TGME49_chrIII:904,923..917,480(+)
TGME49_298150	AP2 domain transcription factor AP2III-3	MSDYAPSRFASPPGNAHPKSPLFARPHSCREMETRASYGTSRGSRQPLCLRGSPHGCLSPQKGQDRLPSFSPLRTQPTLLSPFFPSKGCFSSCLPSSQAFTSHRARGPSPEVHAVSADASTSSSPISPASRSASEQQPRREMCSPPGASSDSTSPTGSSSCSAEQDDVLCFRQRFHLPPLLHLSTSRKRLREEDASASACISSLGNLPLDVDTKRRRQEYDRLSTASLSSFRSPKTPRLPSCLARRDPEESHADLSESRTFLQRLEAAGQSRKGDTSRETIEADEKKVLSTHSTDTSVQRSPSESAERRSFGKRSDPNNGLPMAHSPTPFTSKRTDLGHALDNALSMRAASRCGFPGPAEATVAPAASGASRTASPLPFTVPVVLAASPPTMPSACSPDLGRASTSPLSCAGVSSLDAPQAVGRRSEVAACVSPAASEETVGDTREHADLSSPVAWPVACLASSPGVAKKPLDLQIDFEQPRGNDKLVEPEFFGGTAAVSESAPVAGADAPRLCDYGLSEAGVLPASGPWLRKPNPMLTFQTEWAAPSSQEDRACTQKETSAARLAPNLLYRQADAAADNVTKGHEDDSQFPLRSGSFTSSAVACPSPPDVQADSEAACTWGTPGNGDTCESTGGWRGATNVEAHTCLTGEDGSRYGLQGPLSQDSPFQPPLPSMRPVHFGGFEAWGGNSEASQGDAQGLQFPRVERFSSRRTEHGSEGGFCGQLAGELLPTSTSGCPHSQHVADLESHTGAVFASCDPAMHAHASLYGYPGAFYNSFGTASSIFDLTQPPQAFLYGGTYGNNGPDDYCVHRTNSTSCQGFTAPDNISTGTLNTADAQQEWTTPAPVSDAAVGHWETSDFGPQHLNGRASSSVPDHGGGLPFGGNGNSWGTSGNGDAWGTPGNGDTCESTGGWRGTTNVEGHTCLTGEDGSRYGLQAPLSQDSPYQPPLPPMQPVHFANFYSACFPPLPPPPVFFGIGCVSASYPDILLPQARFLSQSCPGPPSVLRCPPPAALLRGSSPLDQWSLPALPSLPRIPSDFASDPASVPLPAAVQNLPEDSPRLRLPCQGASTRQQSPLQYEGNFGGSDEVLRPQVEVAENRGTPNFLAASYSLLGAFSCEGQNRDNEYETQLWQQLNESGELGVSGLPQPYSVEEGRRQELQSPYPAPYENIPYSTPSYNSVSYTAASKDRLVGDNTAYNGAAYCPFYGGSGMVETPQRSEENSLYSADPQVHFSESEKTGSSDSFPVSFFSLGTPALYPGGSLQTGAHLEEVPGSGDAEGSAWSPSLESRRLRGRTRSPHAQSPNSNRSRGAAWTFSPASLPFEVPAAAKASGRKRRAPGSLPAQTDRGHKDFLLELLASRLEPVKGVHMQRLRKTWVASWLVGKRRITRIFSFQKFGFFGAREQAIRHRREALLNPELDNSERREALANVERATDDELQQAADALPFVVGVTYHRASRCWVANHRKPMGKIVQRKKFAVAELGFLEARYHAAVMMFCWNKQGRTQEFEDYDGGATEAFNSRQVPQRPGDDRAFEFSHPTCSENEPLYTLKALDSGTCDDAMVLLAFICGSPWRKICRGQQCGDDPTLLEAASTIGTEKSLWRTRVKSAADEVREGPQRRLEGTDAGDSGAFPRGQSPEKGRPRRRRKTATLREQEDVTEDKTEDGREDKTEDGGEDKTEDGGEDGREDEGEDEGEDPGHGWGERRRCRKSDRENAGEAERGQKREKRQQSEGRCVVAEVDLRDAKDTVVRRNRVARREGLETQFGKKNAKSGAESCLSQTPALGFSSPPFPVSFKKRRKSSSREADLRQSRPHRHRNDTEEARSICEDSPSSEVAPTPASSSFSPAASLSSDGSRLSSHNNDLTDSGRSASVSRGRSTDFSMFAGLPYLKSLESNTRFVPPSRPGESGLPNVYASYNSGLAFEANRPCPLAFCSRADPTGWPHTFPHPAEAYGSGIASWTPNANGFFESLAYTGNLEELRDLCGRTPDARDSSDHWQEAAAAASSRLPLRPPAVHSWQDAPCAKDPAPCVELARDECLAGGDRQTCRFHSAFDSADAGDYKFNTDARCLRGPTPNPHSNAVATLRREQEAARGASGQTPSFFFPRLVPVAQTDWEADPGRGSGDSLSAPHEAGEAVGVSEGSEGAPCEWNFERDAHPVILPTSNCSHGHERLASSNAFTEAKCRNALRCTPQETVGGVNENGSPLFSTHRDAPEAMSALTEVSDRETQRGPAVLQGGNTEALLQDSTSNSAGPTQRRAHGLDPEPDESKARGERSKEEDRETLRTEAPSKGRKQILSPPTERNSMYGEAMSIDPQVSALPTLLSHGTAFP (SEQ ID NO: 13)	TGME49_chrIII:2,145,570..2,154,749(-)
TGME49_320680	AP2 domain transcription factor AP2IV-2	MAAASPPAQPLGATSPCTFSPPCSFSPSDTCSVFFATPSRAVSAVPELPATSSAQLPERTRLRNRSIQSASTTEASPFVDSASLFPESLSEAPKAVSVDGESRRTRERRRKSRSLLAAAEETPEATAASPNGSSSEISDEASTFVLTPATASLAPAALPPFMTERSDPTEKKYEAQNMQVTAVEPVGLAPRSASRSELGDAESLSAGKSGLQGESAAPTAALEADAGETRLETGLAGEFVNSSSEGVGYGGDEGTVAGETREPGTAEEKLGDLKPEVRPRFHAVAEQDVCAWATSMLARKELRKLKAAAVKLEGDRMPRSDVVGLYFKKHRPCWSVDYHTRQGKRKTVEFFVPDLSRETIELVLVHAISCRKYMPRRFDQAPAFVPEPQDTTSGMPYRYGARLLSPKVLAWIVENTNGSGRTSQHGHGQSRRLEGDKVGEGDAGAQLLSGPAGIDAFGSRSPRAGFARGRDNNSRRQGKASGCRPGADLATSSEEKATREGETELPGQSAGPGSVPAGTAYGDYARQLPSEGYQTPPTMEGRMTPAGLLSGQEFGHGGGMQGAGVMWRDDPRQALQAMPQPLNLAPHATPFMSRAGGLYDQREASVEPGRDVYPVHYPTPYAYGPGIPADAGAFSAGPGPYPHQFPSGGAGYVVNGRVPDSADHEAHSPRSPESYWGPQAGSQGAEDKDCQVVGCMLPNGSEMAMRRMESYVGDRDNLRGSAAFAGDGRTQAEGLSPQCEPNAKRRRLQAGGDGSNGGLEASGPERPFPGSQMLQPSDEWARNGQRAFAVQPGTGGRTFMNGGFRQPGPEDARQPLLLSSAPYSPPSVFPAAPPHLSHAVRLPPGSSDAAHRTPMSGAAGCASPVASAFRKEAEASEWPSNEVYGSPQAFPDKANAFAKGVTLPRRQSFAFSDAGLPTPTTSPHHGSYCASTIASSSPKSASPVSQSGCFPCDFYPATAHYSGPGVETPSDVSSFVPAPAETAEQQIHGAGQAAVKTPESGLHMPSSGWPQQASVPGAHGAEFYASRAFANGAHAPSLSLRPSWRYPGGERSEGQLTTGEQNAPAGASPSSPWSGNTGVCTTEGCGWLENRQAAGSVEGAADPGVQGSACMQGKPQEGGRCSPEPALGVRRPAEFAGAPVGACRAVEDRTMTGERGAWGNEARRETVTGDQECCGDQARDPMVFSHMGSRAELSQFDDGSELPPASPLNECMHPLQKPGSRIFPEFGAWPGSPPHEGSFVQEFDIFKENGEGAAGAVDDANALWPNGGAFGQRTDPLAHEEEKEGELWKGQPTPFCSSPALWCVCPVEHTREFDVMDMVTLPDLSHTAGPVSRPLPNAPLCGGCVVAGVGEAQAGDGESKQGAKLAPDSQHLHGGAANPGAVGKLVTDETAQTSGREQHPGEGDSTEQRLSGLAARATPQRETKRPGPSRRTEGEL (SEQ ID NO: 14)	TGME49_chrV:137,960..147,192(+)
TGME49_214960	AP2 domain transcription factor AP2X-8	MDFERGESPGDSRGSVAFLHHTSKLERLFGTGETTIRGMSFTPPYICMERPPRANCSALRLKSPPENRAFSSRSESPSFTPFARECASLGLVWGDEGTRAGLLRTRLFTPPDHTPHLLAETGASCLEDLFFGTVPQLLSHLPSPPPVPGVARASRSSSPLAGGSSLACASPWPRSATPFFAANMPALLPGRGPMRVTKWLDGQVSDPQSDSCLRGGASRVERAAALLQGRSEEEQERERSVDERRLRKAIGVTDEDESERERETEGGVHERLSRCAAATAADRANNLLGLGVERGPEVAGGRLGGYWTTESEVYPQRIGELEGEGLGSPDPVAASALVTAVQDSRENLNCLTGVLTTLRLSSRDSEGDFDLPLFVQSRKWRAKYNRRSLDLKGTVARSKALGYPAGLQIPETYRDLKNCMQRPPSIDAADSRAWRSAEAPRAAKKVFSEGRRATDRDEQVAFVEDEYTEQLLFNANAAVEGTTLYNNLLCKYGLETRCFSTSSAPGNTAFESRLARSDAGPTASSQSASALSHAAVSPSLASALPVSSLLLEDAADAVGDRSELETGSQAEAAPTSEASCMPREKHVGEESRADKGAFLRSASDSTHAEEDGLSGGKDASSREGGSEEREEAAHEAADSLWSLVLNRNIAALPGFMTVGRYECDLLPKRSAFSRKQLAGLVAGSRPLPVLPSSSDTPGSASTELLAERVACALTLDEGEAWNPSDASDLDDFLESSCAPNALRRGRGAVVPVRGARRRRGADLGLSPPPSSPAVRCRSLVRWSQQRPFFSNVSACAGAADSRREEWKDAGKVAKPGSESALTSRDLHASTGLVNAALDSSEQKSGERESSLSPQERILTGVKKELEDERVREKQTIRDKDSEKGQGGESNHHMPGTANGQRTPNEGEAPMETEEAPTLEPSNGMHRDGQDAGARMHSSSTRALEGAVEDEPKVTLPDKDEPHASALCGEREKQRQSFFSSVSSREDAQDEDSRWCVAGGMYNGWKGTYDVWIYRRVSAALREGKGEEEKRREGEKRKTGKGKQSVHTASLGAGGAQGLSPGETQASGLAPGSTPLGSAGTLSAGRNGEETRESTGSPAGAFASSSSLAAKGQNGHASVEDLKTQKEESLGCVLSASALPLNPHSGETREDSAGRDEEKGEERERDENEPPLYEWRVKRFSALIHGHEKASRLACKYCVYLERFGRIRGRLSICSTCCRDACSGCMPSKKRAAGADFSPHCRNGRDAGVGGAGRAPKRRVCAKKGAAGAAGVCGDRARKGKGEDEPERDGLDRREEGGTPSSKQTAERRGAKKEGREEDDRVDGKGTSLSLENNSFESSCPAMRSSLRASFEVKGPLSPSSADDRPNEGAAGRGAPPGSEGPSRDLALRSHSFSSASSSRKSAKNAAESLRRIAGPLFRSSGDLTASQLGAETEESDVLQDVFELYSEAGEAWETCTTPVSFSPSLSVASRDTLVVLGGSQTTAVARLDSGKMSEAVRRSSNALSAAASSFPKGKGFGGASKKTDSVTLSFLARVCRNLRMFLLLCQHNTVAGGLPGDSKCVCRAQSGPGGAGLAGADGRAPGDLGDSKGTAIARGPGGAAGRAHGSEPWASPNYTGGPFFPPAGSAPSGWPPVAQANSRPEVLSAIQGAQGQGPHVAHSLRLAASLSPAQTTSESFLAPESFAAGVRPLLEGSLSVLIPEEPQVGLGPSAGQQLASSSLSPGVSVKAEPSSYFQSAQGTCRDVSAGARTAMPSSFLEQGRPGAAPGHAPSGVGRCPPQGRDASPGCPGPRTPPAGFDGPSSSGAGYSLSPYGYPGTEISFHLAPFFPEPYRRFRESRGGPAWIHSPGSVDVPSSSLQSPFTGFHATSGSSPPRLGPSEGASFAEASPRALAGDLGPAGFLGASAGAPAAEGRGPLFDPSAEGEGKFAPQAGALGTVEGPADCRTQGETGRTADEDEKKAKKAKKHGRITDIEERLAREEPYDVVEEGQDPEPTRQLGLEATEKEQDVPRSGDSKSPDQDSPGQPADIMHGYFKARVRNRRVKDGLLLRMTAVLVGKGFYDLETVEPGAPRRRGGWGESGEEEEESETKYLFSNPASQKPCDFILYFDTRENRDASVALNCALPAPPPRLPPKNGESQARRTLRQLYDHFLEFKCQCLEDKTLKVKHGVINLLGFPRLYVKLNCSMSWDERLSLFSSFLHWLCREDDSQPPPWSSPELHPELLAYLVDLGRKGFASGSAATTAVVNAPDLPLDDSALSKKNAALIRAYMQQDTGASGPSGSVGATSSDPEAPRKDEEAEEGEKDDSNAALVEGPAPETSGDSTGAAQPQGKGREEREAGDKRGPGNEGCGKGDGFGSPVAVAGTTAAPGETESVSCPSSTSGGGASSALSSGPSDSAAAPDGCESSPVALESASLLSFSPSAARAEVLTVPGVGLVNFSLPDGVKFDKSKLAFRCYWREGHAGVVTVGAGAAVSPSSGAGTFVPSRPTVCTAQNKSRTFSCRKYGLYQSRVLALQARLLSELLWPQPPSPARLRVSAMAAVVYGLIAAPMPFTDPWQAVCGYSVAEDALRQRREVWKNLLDPRGRPAPAPISQLSLPPYSGPPHASSATQELPNRPGTPWPGQETVCGARGPAPGLASAWATYGNPGDRDAAEPQSTYVGRGPAGAEGPGGGIAVHREWARNSGSEAAQPQGFGRAVERPVPGPQSSLGPGGDNRGDHMAYDQSPAGPASNAPGPTPPFVGPFSPGLVLRHGPPAFSQDPSLHRPPFAAGTGPAGQRLASDSPYPLKNEASPQLAMAHAPGFENSDGFQGEQPLAKGRKIEGASDRPVPDEGQVLGTISHGKSFAARPVDGDFAPDGRSPLFSGDASGVGGGRPSGVGGQLAAGGKGHFATAPFGSGTLPTTRGFSQPGGDGLSHRSGTEPAAAYSSPAGAAYPSASNASPIYGAAPKREGDSPFGPAPPSGYCRPGSPAVDPKLPGSVPSSGNLDSVNYGSFFPGQQAPQGDGRIAPWGSGHVGAPRGEARGSERVGHAGASRGLTGHELEEGQGGPGEEGAGREREQRKRRKSAMSMSSQGENTPLFAPTSLFPVPFASGDSLADGSGSDFGQQLGPPFSHGSHAPFFPEANAVGSQHFTADNLETPGLPAELGGGDGRRQSGSTHEEVSGPRAGGEKGEFSLEGAPQAAAQQLSAETLTFLLGTNVVWEENEKRWRVQVRPPSFRGCDGEGADGKLGGEKKKRKRQGFSAGGERRRSSTGNEPDDQHKAGTLEWVSMAQLHQAQKLQNQLVGKMERGKGEGGDEERLGGDGRGNIFFDANGSDENAKKAALLKARRWLRRRIVQGQLVTGLSRDGLFSSRPDEPERSSSVSTGAFTGSSPNDKPTDLNAAVPPLSPFFSPIPFGATTAPHRPSPGFYPPAPAHPTEDGCRPPMPAPVPMHAPQGPVDSRTYRGARPVYPGSDVTPQTCHGVRPESMQEEGRAALLAEQGSAFFVSGDGKGDNRGATVGQIRQGTVRVMQSCTASQSLDQGFDLPHPPAPGPAYRGVPYGHGPSGPYYLNGGCVAQRPYATFSNLAGPVQGSFPPLEFSNGGLPTTALGRRGSDSGPQGAGRNASQMQPGFASRPHGPERLGRESAPQSGAPPGFSPHAHGRGERDRPSFSGATTMPLASLTAFSHPAAGPMFVGTEGRGQQGDIHPNLCGVAPVGGPRGPAHAPMPAYGPGGAAGPPRDDRRAEGGAPGVSHSDIFLANDRRLHPEMCLHSAPSWGPAGTFASPDNRQNAEPWPAAHASSNNFFDYTGVNMPAAGPPIQLDWSKVRGAGG (SEQ ID NO: 15)	TGME49_chrX:6,617,595..6,633,783(+)
TGME49_290180	AP2 domain transcription factor AP2IX-6	MDRAGLLFLRGAAGPGPLKCFGPRVEAFSGSISLLSLDSRGPTPFRTPFHTTSALSKSRQPPKESPESAAACTFSPLFPSPVRASPHRNLLGARVSVPCKPLACVGAPKRRHGETSDGFSSRAAVAAEALPPWPSDFLQSEEIAVDSPQKPTGFSRFSNARVSPAPNAWEAAAVFRRLHAFDSGLRGDASGAFAASATCGCLAAASRRNPCLFAYQLSWNLLQARMFGGRAGGLKRRKPRRDPGRVIQSGMGRRQEFFWPEKARRTRVPLYQNSRPKLVYDQRFRRRFMCMWYANGVQVFRPFSCRGRRGGRGKEGLPDGLGIGRGSGTWERARAKAVVLLKQLQRQGHLDRLAKPDVTRSGVRGVYFDTEEKLWVATWNEHGLRRFKAFPTMEMGFDAAYQAAVAVRRQKLRENYIFSMQRNRKKSGRPPPK (SEQ ID NO: 16)	TGME49_chrIX:3,630,931..3,633,002(-)

FIGURE 21C

TGME49_224230	AP2 domain transcription factor AP2X-3	MELPDQAAYGRQLAKRRRLSASEEEATLASKNDGKEGLQEPAGATAGHLLPAEEPGQYTPEHTEGRREFRRHPVVLPGGGRKAASYGLIAVGGGDSLRASRRTRSSASIETSAEEKETYTSPELGPGASWSVSTVKGSKGRSDEEGRAGKRAGACAARDSAAGSRTLAQAHRGADEERMFPHSPARDGSHQVCWDSDALPSPYDLGLSEADDEEVSFQKEALAEKNGLVLFAEGSLQGVGLATLTVFSGATSSKGAFSAGSPFLPGSGTTASPRSPVPRGDKSLGDGSVGSDDVSAKASPHAHHNVTAGADASQSSEDAFFPAAPPGGVPGTLTVEDLLTMPERRQDPEAEKAAKTDFDCLAALIQDALGEAGGAAGRVAPKRRCRTLGAGFNPTHSARPGSGSVAGLEAPGALGRELDALVAGGSPEESRADLEPDGQAAGASWQESLHLQYDTRNGGTYEEDLDSASLSFLLGHSEGSEKGPALSASAGASTAASVSSFFPSEAACGVYAPGQHGRPTQSQDPAKERQRRLARDRETLNLSAQIAARFKSCRTEDVMRLFRRYLAVSSRQVRDPATLERVVAACCYISSRQAMDGLSLSDICHEMDASNGQDLFAAGCEARGKKLADGEGMGRGESDRERAGGANASMRCKSLGKWVRICRKLQLQALPDKDDQPEERANRVLARVKQLLIAKMEEEEQRRPQLVNAFVRATQSAVEKQRLKAEGDRSEADSLASLESLLGDEAFRADARADAEARRQTPAEAQLGDFLDGHQGGEKTGRVSSARINGRAAEASPAPPAPQGSTAPADSTPAAGSEERQALNAIEELLAQVTGGSNLDCFGSATLAAVDSDLASGTSHVDRESCARLRRLDKSGRDAFAADADGPERPTENEVEFEARPGAAGVLAEDVDEASMALTPNPDDRSSSASGDAAEPVASIRLEQREEKNGDASGLSLDICPSLFDPVDMPALSASSEGDSGDSSPFSPILTSLLSASLPPSETLAQAKDMQPAARLQLQRFTWLQKMRAEALEKLKKEKEAVFRGLVLLQRILQLFYDVKQGESDGEREDGEDGEGKKRCKGWTEEDPLDKRWRARGRCDAVSLASLIIVFKWMQPIPQRIALDALHVDRKSVYKRRLEQMHILKTLFGHLRGMVEKKDGSSSSALAEELKASLPPHLASLLGQVVGNPATMQRLLALADEEEELGNFISSQSLGSDGESGKASAGLGGVPPPAAAASPTPVKTSQASFHFQAPAASSPESSAPSVAVEPSQDAASSSFLAAILAEVAAEREVGAVKTRGPGDAERTAAELGFQTRKKRRVSELNAQRSPDNGLGSQLYDEDREASSAVPVASPLANLCSSLSSSSHRNPSEMAAVASVAPSPRAARHPRAPDEMTLQGLAVGKDAGTPRQAGGYAGTFLPGDGDRVGEGEDGRSERVRAPFLAERGSMDASSSFALGFSLAEALLRHGFCLPSPSDPPAGLADAQFATGDLLRDGGSSSGERALRMQPEGFSATRGSRPAVAPGPAGFGIQAEAEHEGRGDVNSTDVIFSNRATRDIIASFLASASTEGHPGTASLTGRGLEDGRSPRLRGPLAAVPKAVSQADRGPGRFNRGASGSCRQPSSRSPPLPVSPYRGPTGDSSRQRPLSPSSLFAAAASMAGVLPGPLPSSRSAGSSALSPGVERSPRERVAAQALEATRRGDVDDRSLHPSSSVSAVRSLLPAEPALGGASPFASSALAMGLPEAGASQAGADAPLASPSIALATVAHLKAAEKALLDSVFDSARVVSLQFERTGQRWVCKWQRHKPAGAPANRKEPWHRRCFSVIKYGYEGAHALAAAVAKKLRDGRRALLQKQRRLEEEGLAEAEEAPRDEEEVGDAECEEPLGAAEEAEETVSPRVDAGGDRSASGSAEAGKQ (SEQ ID NO: 17)	TGME49_chrX:3,204,000..3,213,157(+)
TGME49_220530	AP2 domain transcription factor AP2V-1	MCVKKEGGDGKRGNEKNQVNDKGVKRTGRDVESRHAPSVPHLEKLVDMAMVYSSCLPPCDSSQGGDGERVKRNAGAKRKQGQGESQDRLKALHDSHPLQCYWYLESSPATNITLPSESGSLKSPSSPSKRASPDRVMEVSASLCKEEQKRREGPREGGQWCCSWSFPRGRPTGTKFSVKLFGYEEAKRLALYTALYAYSPEERCDVLQELIDEVLATASSASLSASHLPNPERFPAILELQPQPLSLSSSLSPSLCVRLDACAFPSPVLSGSPLCSSPGLSSRGRNGSKAARETLSIDRGIRLSSQSSASSNAMPSQFPQRWQATEVRMSLLCRSSFRASRRREGGNHGEAEAEAKRAGQTREKTGRRDKGNHPHDLSVNNRKEPNKLEKSHSSCSPRRSLFSSIQVQQDERSGGRLLHGFRGDMEEGKRASRANKHVEAKKGEVTGRRKGVCGGALFGCFPARRGRERGEDEGEREKAGQVNAQH (SEQ ID NO: 18)	TGME49_chrV:441,898..444,991(+)
TGME49_247700	AP2 domain transcription factor AP2XII-4	MAFAPRTSPRLSAGAGGPSEASRGGTAAGAPLGPVETPTGREPSSPFLRSASAKRVTRARAGFLASSPDNQSRSTSPLRPADALRISEASSASAPGVRRSLRASNARFPVSASRGLMGKAGEEGEGASGGGRPGGARRTSGGGEDVCASPRDISYRDKGAGGDATASSNSQSPSSVDAAVSSSYSVASSVSSPPASSLSSALSSSFSSSTLSRSGSSVCPRATSAVSATLQQGERSQESSLLAGERETDRDANRPQRETDEGQGAKSETDRAPEDDRGRSRRGSASPVQGPFSPRGFFSNAVTKENSAYPATSGQSGQEVGCRPNSTLSSVSVQSLSSRPPSTLASDQLLSVPNGDASTVSTSSPSLSCSCSSFSSSSSSLSSSSLLSSSPLSSTPSSFFSSSSSSSSSASVAPPGEGKGRPPVRSGRGACPRKPAGPPPRLCVPYQCQFNVEKREWPARYLFRGQKKMRVFSLARYSFEVAVSLAELFLTFLADNDGIPRSEVIAYWAETLARGPYTATTGTNPKGGNLLGPGASEEETVGGEGGEDAESRAAEKEREEEGKASSSSGSSDQNITRVESSEAKEDGEENSASSKPPGAASAATEPAGGDADGRPGRAASGPGDACRSYTSTETEAAVAVAPEAKGGPSSDVSCTLDKSRESRGNGVAGKRENPAWAVSPSSFAAFVETAKARQWVTEASRLQAASLPPLAPAERPARPPILPTLASSRARRCTSHSLISGLSAREGSQRTVSQGDSLSPASGLAGEPGAVREAEGREAIAVDDETGGEHRDFPHSQGPAGRGRLAGARPSSSDMRGEKRGRRALREGESKRPQRRREDLKSEEGQRERRRRDTAWPAGRREASKGRQDSRVKEETPAPDAGAALALDGRAAAARDRPQKAPSPFGTPEALSSSLTGSGLHPDGRNPHGHPALRVKLAAGRGNGLLAASPASPSSASHASSLASPSASWHAAQGEAEIPGASTGFVDSPCSANGSLDDSGLGGPAAALQKSWRDRKRNRKKLSKSMHRKSLASLGMRAPPQNACLADPSDVGLGVQMPSDAGTVFGSPPSFGASEQKASSSALGLAFRASSSFSPKNGDVEPAGRNPPQFLPTASVQRADPPGTGAPPSQQVVSSASPCSFSALAATASPGACRGGASRNGDPQGERFSFPASPTSQYRWYAHFQGGATGPSCCRQHVGGSGGGGWPVVWLKQLEMAYNGPPKFCSYVEAVDKHLRLGGLRRPVAFLPLASRPASPTGLGGGLGAPGPALRQASEKALAAEGRQGQNEEKQVGWKSATGSKAGMFQGDSGETTSERGAEEAEGTGGGRRGILGKEEEDRNGGEGEKAATPTMGGASPAASDDALSPMKADRPAEALGTGGSAPTHADSRRAPGMPEGEKMTGPSKEQEMAEAGERDRCERSLERNAELVLKENVSMTSASDVSEAAEEKGAPKKLASSPHSVESPQGRTAEKTGTLNTSEKGENTRTAEGDDFGTTIVKEEFPLLPAPETFVTVTAQDLLSPTVYTPRWQATVGKSLELGSLNCEKSCERGHWADASACDLETKDLRLFEDNKSEELKKETGMFLGVEGEQVEESAKSSKEAFSPEERERSEQKESSKAAGGGDSCRTPRQQEATPRASEECQPESRIDMKVSPNTEMMVEKLEETRVQNTEEPEKVEEKEGGSVCRDVSVASPLESPNSRLSEKGDQSETPAGVAPPSSSALEARAGRDSALLSASLPLSPRASCPPTQSASPASRDPTPASLRVSSVASGDRNGPTGILFRPLSSFHKRVSFCLRGGAEPPGRPLSEAVPYPLNARLQEIVSRFRLLQGVSAARVSSHGKGETSSQATPKAVQGEATVKEKATVTPTESAKSLAGGQAETEKGESPSGAEAATQKADEKEKTPDTDATQSRSTSSGFETQEAKTAPASILPASSLPSSDRPSASCSDTHASRDAVPLASSPSSSSSPALRRCSVRGKDLVSAPVDSFSEGDSSDARPPVSVRDLAVKLYRWLEQGEGLPAAAGEPQGADGVGAKAQAREALRIQTVPFISRWRQMLERSLSIASDLRKLDLQVVHLVELTEALHIAVYICGQLRRRLREGAAPDAGAAEDLAPVDVDDPRGCSCQSGDTRDSSSPATPGGRLAGGAGGAATSPKGGAFAPRGGEGEIKPQETGNSGDSKAEGKEASGDANTSEGKRLSGEVDKTAEVETAGSEDINVERGVPGAQAETARTEMNGGVVKGQETSGDILSVGSSQVLSLSSPSLSHLASSSGKGPLKPTSSPSSSLYALSPSSSAASPFSAQLASPSSHAPLSLSFRSSSSPTSLSSPLASYPFPQTLQQTSASPSSSASARFSCASVKPLREAGDLVRAAARAALEQAQVFGVGGKLSDATHQLAARVTVAVRAAMLAKGEGGLTRGDVDLLVEETERFVREARFKAQETAAETTALPDGVAEVVSSEAGLGLQTTNHAPVSFAAAPSAGGAFAGLTEAVEVEARQLPEASERVGRVSSPRGSLGFEAMDLAGELHLVKVLNAFHRHTECLMNERERLIQATNEDLSFLLHAMELALPSGLDTPLLSILEGDVDILPPLFPPNVEALIYLHAVSLAQADASASPSSPSAVAPCLLSPSARLLLAHFAGASPTAGGLGGDSAKGRTMSSFPGRPGEERHRADERKGSVLPVRRGRPPSSARLNALRRLHAVGEPAADAGLDTVNGRFRSKRLRAMSQEEEARRAATHASPTIPYPLSRYLHRPPRLLSFTDAGHFASSYSSPLSHPLSKGSSLTSPKRQRRSVCSEAPEHERKNLRSLFKSPSAQREEAPRSLTRPFGPLKGEGFSPASLGTLGSRRQSELGIRRRDALVAFFPAGMPCHPASPGRRLERPRVDGADMDGERRRRTRCAGDRLEERPRPLGPVYIPTKVRDPATGRVAVCACDTERGERVRKVQLFEKPHVGAFWCARYGPNDEFVRCFSIEKVGSLKALVSAVRFRQYVTGHSLGYGVGNCVPVETIRSAGRRDRNGDVAPDRPLKDAAASPPPAGVAGALGRGEVGQAQDESGETRDAVEEEGRGQEPLGSGEGASGVAAKEGHGSSRGEGEGAEGRTDSAAGSTAGDRSTEDSSRLLSEGRDAKHGSSFAGGSEALAPGGEHALAEGSEKVGRAQETEARKEDLRTSQNETHSGEDVSSLNEKALDSPRSSAPQGKSDQGREPIALRIRSTLPPSEVDKQEAAGQGGSASELAFPTGVSLASPVSPFSALARSPISARASSVSPGACDRPDVSRRHSGSSDEASEALWDLGEDLGFAGDDANFPFLDSENSALLFAPPRHLMSPGSASPTGGGLGIHYDKTKHRWKATWTTLDGQRASTSFSVKVLGMERARELALEARQRALAGLDPREVRDEMVAGGAAARDRERERGRQDGRREGSERRVGFEASAEGTEAASERLRRRGEREDGDEERRRKKTRGDELRGAEGDREERELRRRKTSEERRKGKNEAAKNEAAKNEAAKNEGGKGETWKVREGGKTPLGVKSHRAKVVGQTVERRGEERRRDLRGSRREEGKTVWGQEQDAEHQVFEGVKEDDNERGRRRERRRFEERDSLRGSHGATPSDEQRQMRRQTILGSPEVDGKPLSFQDTHRVDAQLGIQNEVAPPGPQGVGGAGNSLQFGREGERFASSSPVAFLRTKEEDEEIVEVFLTPEGSGSERDKASSVSASSAPRQSRPASPRLRASRLRESARLQRRLEEAEVHDRGSRPLRPEERRVAKRHYAEENVDATFSAGAGGTNKIRPHSSHDFSAEGLSKFQELLTWDCEVEIDGTDAHVWRAVAALFGPRPRPRYV (SEQ ID NO: 19)	TGME49_chrXII:3,507,570..3,519,428(-)
TGME49_227900	AP2 domain transcription factor AP2X-1	MCQERKPRELSLRNNSRARERRGSKLEPGVSCLSLSACPSVAPNDRGGVTTPRSLHAWTREVSACRLFRQQVSRPLPRRSLSRPRSEPDASPVKGPGQRVEASAVEGGPSASSAERLQVDCGLAAMRKTKKGKGEEGGEETERWATQAVEQQGTLKPAGEETAVPGASERSASPQQAMEGSCGVETPETFFGVSTGNGQGSPSPESVAGEEARPERENAEKSATGGSASKAKKPSRESARRPDTALIDRHLIAASPSPSGARRSSTCSPSPHSREGEDKPGSGAPPASSPSANAGALEPAEKGTLGSPPQDVLPALPASSSSPSTGGGSPLSPPPGQAPRAESGAPGSGALSLRRSLRHRQPVRPAAIAVSPLGGPGSSLSSRSASPTRRGGVSPCGPATAVGKGAGAASGAAALPGVGAKAPPSATPLAGLSGRSLLASVSPSAAALGPGAPGKKAGQVQGAAKARGAPPFVLAEYWPGVTLDEMEKGELSWARAAAGLPLPASPHKVPGGPAPPVGGPPARDEDSVAACAGEKGKEKAFLGSGRSQAAQGLPGIDAVAAACWGGAGVDSRVLAFAEGEASGAFGPGGEKKKVHASSDSSGGSRAALGGRASVQGKARKPAGWEEERGRRDDRSRGRRDETDGPRFDVTWFVDDSPLAHTRKRTRWDSLWWRPASPVRVVGDSAPEESPERREGGGRAPDLQASMAKRRTADSGLEEEAQVERGFSSSDSDDCDWHLPTRTVSSSLAPFAASKAHLVPRCCYCLLPRRLPGRHTEAGGPFRDLLGWSTSVESEETRGRYLQLYCACTKRPFGESVLQGAAGRRGLLLPVATNALLYSVRRVALDGAASEQKSEALPTSAVSRPSSAVRARSSCASSGCDDGRAEVAPGAPAETIYRWRDPCTLQTFSSSLDRIQGSLAATAAVAAAAESAGKPVAFLPRLYWDSQADCYIASCLRWEEEAQPTPAAERGEKRNGVERPAEARERGRDEKKPEDPSVPGLRRRSLKLLQKKFSVAFLGDAKAHFYASEWLKWQHKGQRMMDEEDRRGEVARQMLLVSPLLAGRKAFAKAPGGCSKKASSLSAAQLALASGRPLTFEEEAELKRQLENKERQKKQKLLRQQWRRQGAREAKLRLREAEAAAAAAAAAGAPSAPGTTGASQTRSPQSQQKSESLPVLRSKTEVLQPSPGASFAPASSRSTLPAGESGAAPCEGVGTRRSAASATSVAPEKVTGRKSETARDAASASLEAAKSTMVTRGGGRGSSVVAVTPSTSSPSGRAASVASSTLGGFGAR (SEQ ID NO: 20)	TGME49_chrX:744,093..750,892(-)
TGME49_318470	AP2 domain transcription factor AP2IV-4	MAAPAPSAEARPAKRRCFPLPRETPVSSEDETRKTLQHDTLGCLPRSSSGQPELAAASAASQVGHLSSAALLQLVQTQSAGGVPQAVLRNLFSSIHRNPKPLPANALAATPNSSLYASLTSLSSAAALPGAGPAYSQAPSPASADLLQSEQFRSAAKNPSPNEASPILALLQEAARAATTPRTVPALSAVQPAASSGVSLPPASDTLALAQSSLSSSTGCASDVKASRPEEHPAFASGTANRQSLLQALLLSTAPLAFSGPSLSSASTTLPASSGAVSSRNAGAYQFERLLQAEAAKVKALLPNTTSKSMSQSSVPQRDLTRKTSLFPQPRGLSADDASRRYNTRGANSGGAGLRRQTGVHATTEQSGALDAGERTRPFGAGEDESAQGKPDSRGRQRPGALDASNILGLLAAFQPSQAPAIRDLSAPSHLSAAATGALPLTASFTASALASSQCLPAGTPASSSASPPFSEVLSTTEESSTTKETDASASTLLAFLQKYSAVSGLGGASDFLGQLQGKTSLPPLSLAEPSSALPSSFLGGSDGGTIDTRNGNGEKTTPPIHLFQSAFRMPSPSQQNLLDALLASSCTTATSRSDGSGNLGCPVVDERNAKLAGPAHPLPCSFPQISSSSGEPGRKTGGRVHRQGTSQSGGRVRSGKNGGSAAPPRQSSSDNVPSTPTVSSHEAPHRAGFPSQTPYELSASPSHQLDLLRLGAFLGGAGKQDASVHSDETGTLSGEPSHRSGSLSRGLTQESVLQLSDTTSTSREGEPNEPSQGCVNVAASLPAFGFQPSSGAAKAREGRRGAGGAGAAPPVPLRADVTLGGNRPHYHVAKQEWRVRYYMNGKRKMRTYSAKFYGYETAHTMAEDFAHYVDKHEALPDSMMMTAMMLQAQANSAASSGQTVPLARGIRASSASTGAGGHVSKSATKGSVAASSEGSTSMGSDATRSQEGEAAELCPLAAGLSRPLASMHSAAGNAVAQGGRQESKEEAPGGQAWFGEPGKFRASSEAALCGSGSSAEGRDGHESEVLWATLGKVHDASQGKKIKPEKPLTVARGRLALGAEDKSGNLGVDLVDSGEAQGLPGVRQPRQMKNSEECSLRDSDKGMALSKRFGFLPSQTPSCDSMTLPFPGGFDALSLSSALSSCASLPVAHEGNNFQKGHTQDIVALASQSGTQRPASVVLSRDANVSGSSPSHPTWQREGAAVSGRADEPSSLSVTPSTYPLSSFTMEDIKGEKGDPSRRFALVGESMKNVSAPEVQALFFTSSIANAELLPVDFLHSNSCSADKLESSIPRGLAGNNPSMTATAVAATAVSHQIFDTITLFGEFLREFAKEKVNEFHEYGLEASPLTVEASSEYSLFGKATFGRQPVAGGSTPAGISKMSGETLSGLSASELSLVSARTNTTTGEEQFALARGLFPGDSEGDRDEKKPQLSQQELLVLSHALVNLTSSTYVLMHTLKASLSKSTEAVQLHQPLLEAASEAKATDEAKTREEQESSECDHEYPPRSSLEATTGALPFRLSPALSASSKDLPSLSASASLESVTPFAGLPLEEGTLSASVGLASSDDEHDTSLLFKTEAAKKRSLFSTAADGDESRTYNDGLGQPMEEEIRSCVSTSCGEAVATTTLSAIGPGTGASGALLDSESRESLGEKPGAALRAGAHTPAPSRAPTPSRTFSFTSSSTATSAALLCDSNVVHEKLRAQGKDSEAGERKGQSEKEEEVEMWKEEDEEVQRCTGSAETDSTEATRGEEAWRRGKQSEKKPSVITTALNLLETHRHLALTISQLKRPVAQQLRFILPIAAPQLLPCILPPASFQGPGESGDGKAEAEAKGSSSLGQVLETALGHGTRLAPSASAMVFPRKDEAASAVPEAKTFTGLANAGVMREAASRTLEAEQVSRKRSREEVVDSETAGDEGDMENVPETLDATTSPGSRQYDKSPSNGGTKPPATAKSRVIRQQAALERLLLAPPQCTPTCSCTDRPCPCDRQQVADMIYLFYAVPARQCAESSKEGSTQRLQFAARDTNERKDARTQEETQGGETEAKEVIRDPEERGVCEGSSSQNAHTQFDAETASSSMSSDPRADKESNAQDAHMADKTSFVSDLPQPSGEFAPSLLSETSLDVAMADSRGTTSEHGFFTRSDEQKRASFSSSSLLAAGHAVASFSSSLAGVVSGAGERRECAGPSLGDLSTIGLLSLSYPAMLAFILPLQSLLHMVSGMLTLHKKLIHRFICAHLRLVLDDDMRRPAGGALKSRGAHGDTEAAEAQVERRRREHEREETTNLAIGYREGNAEAGNTFPLVDTVSSLLSPGSLRQENSEVERRDNDEERLELITGIARESPKFSEKDSVSPFLSTAPCPGTEAESSDCSAGSACSGTPTEGTEGGETGDIASFLSPSGDVKQTIMLA (SEQ ID NO: 21)	TGME49_chrIV:1,300,392..1,309,960(+)

FIGURE 21D

TGME49_225490	calcium-dependent protein kinase CDPK2	MPLKTSWHCSCNATFPGDLLMVVANHDRVGNWNPQNSVVLSTDASSFPTWRSGEVCFDEQQPVRLEYKLIIRRASGEIYWEPIPTNRVVTLTANTSSVIENVWGSLATCSITFFPLQPIPSPSFYKHAERTKKEASSVHLHSASISDDSGSDTGTCSQVDESRTQRNVRGQPASVGTGKATAAERGGKGYVMPHHQCSTSQRRHSISTQAADEAAGGGNRVSFKRSAFILANTGPITNYYTVSKTIGRGTWGEVKLVIDNGTGARRAAKKIPKCYVEDADRFRQEIEIMKSLDHPNIVRLYETFEDMTDFYLVMEYCTGGELFDRLVHQGVFTEALACRIMRQILAAVAYCHAHRVAHRDLKPENFLFLHDNPESPIKLIDFGLAARFKSGQPMRTRAGTPYYVSPQVLEGRYGPECDVWSAGVMMYILLCGYPPFNAPSDRAIMNKVRAGHYTFPDSEWSRVSLQAKDLISRLLDRHPRTRISAEQALRHAWFAMHAPGDHFEFLGLDILSKFRRFQGLSRLKKLALTVIACHLEDSEIEGLKNLFTQLDTEGDGVLTVEEIRKGIERSGVHLPPDMVLEDVLREVDTAGTGSIDYTEFIAACLHQSHYIREEACRAAFRVLDINGDGLVSAQELRQVFHMAGDLETDAAASLLEADADGDGHITFDEFCGLMRKVPSLALYTEHTVSMMRRTCSRTNISEASLTPRATG (SEQ ID NO: 22)	TGME49_chrX:2,207,266..2,214,584(+)
TGME49_330000	cytochrome b	MVSRTLSLSMSLFRAHLVFYRCALNLNSSYNFGFLVAMTFVLQIITGITLAFRYTSEASCAFASVQHLVREVAAGWEFRMLHATTASFVFLCILHMTRGLYNWSYSYLTTAWMSGLVLYLLTIATAFLGYVLPWGQMSFWGATVITNLLSPIPYLVPWLLGGYYVSDVTLKRFFVLHFILPFIGCIIVLHIFYLHLNGSSNPAGIDTALKVAFYPHMLMTDAKCLSYLIGLIFLQAAFGLMELSHPDNSIPVNRFVTPLHIVPEWYFLAYYAVLKVIPSKTGGLLVFMSSLINLGLLSEIRALNTRMLIRQQFMTRNVVSGWVIWVYSMIFLIIIGSAIPQATYILYGRLATILVLTTGLVLCLY (SEQ ID NO: 23)	KE139166:213..1,319(-)
TGME49_322200	apocytochrome b, putative	KLCKYHHFLCSLTSQLSYLIGLIFLQAAFGLMELSHPDNSIPVNRFVTPLHIVPEWYFLAYYAVLKVIPSKTGGLLVFMSSTCQ (SEQ ID NO: 24)	KE138872:1..386(+)
TGME49_323400	cytochrome c oxidase subunit III subfamily protein	MIAVHHHPTGLLKTAKSVGFQYPTTLRLFHIGYVLGVIYGLLLSLVLTARENYYSDASMISTIVLGVIISETGLFISFFVIGVYTTSWTIGLDLEGLCLPDPSSIVLFMTIMLSALSIVVSSVYLKNQHLYTSCTNIMIFTLVVSFLMLVCTEYLGLSIYINDNGFGNGLFILTGIHFSHVIVGAILGFFNQGMYSSLVTYLPVNCITLSKCKGTLCKIFSEPFTILYLHFVEAVWIMIHVTFVL (SEQ ID NO: 25)	KE139158:359..1,245(+)
TGME49_237130	cytochrome b, putative	MSLFRAHLVFYRCALNLNSSYNFGFLVAMTFVLQIITGITLAFRYTSEASCAFASVQHLVREVAAGWEFRMLHATTASFVFLCILIHMTRGLYNWSYSYLTTAWMSGLVLYLLTIATAFLGYATSNYTTLCQEGSQITLIIFVILIHGVQLVLFLQ (SEQ ID NO: 26)	TGME49_chrX:5,732,558..5,734,754(+)
TGME49_256060	cytochrome b(N-terminal)/b6/petB subfamily protein	WAHHMMTVGLEVDTRAYFSAMTIMIAIFTGTKIFNWLGTYMASHNTTRTIDLWAALCFLLFTLGGTTGVVMGNAGMDIALNDTYYIVAHFHFVLSLGAILATICGFVFYSKDMFGDTLNLFHVNTGSSPYLNIWFVVFLASIMLIFLPMHILGFNVMPRRIPDYPDYLCYINTWCSIVQLVVYTPQKKLINNPYSEMITPSTMVLIILASEYYSYLTTAWMSGLVLYLLTIATAFLGYVLPWGQMSFWGATVITNLLSPIPYLVPWLLGGYYVSDVTLKRFFVLHFILPFIGCIIVLHIFYLHLNGSSNPAGIDTALKVAFYPHMLMTDAKCLSYLIGLIFLQAAFGLMELSHPDNSIPVNRFVTPLHIVPEWYFLAYYAVLKVIPSKTGGLLVFMSSTCQ (SEQ ID NO: 27)	KE139167:91..1,594(-)

COMPOUNDS AND METHODS FOR TREATING, DETECTING, AND IDENTIFYING COMPOUNDS TO TREAT APICOMPLEXAN PARASITIC DISEASES

CROSS REFERENCE

[0001] This application claims priority to U.S. Provisional Patent Applications 62/270,264 filed Dec. 21, 2015, and 62/306,385 filed Mar. 10, 2016, each incorporated by reference herein in their entirety.

STATEMENT OF GOVERNMENT RIGHTS

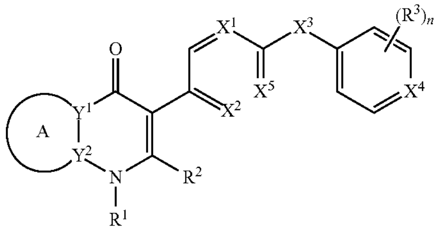
[0002] This invention was made with government support under National Institutes of Health (NIH) contract number HHNS272200900007C, NIH, National Institute of Allergy and Infectious Diseases of the National Institutes of Health (NIAID) award numbers R01AI071319(NIAID) and R01AI027530 (NIAID); NIAID contract Number HHNS272200900007C; NIAID award number U19AI110819: NIAID award numbers U01 AI077887(NIAID) and U01AI082180(NIAID); National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) Grant #5T35DK062719-28: Defense Threat Reduction Agency award number 13-C-0055, and Department of Defense award numbers W911NF-09-D0001 and W911SR-07-C0101. The government has certain rights in the invention.

BACKGROUND

[0003] Apicomplexan parasitic infections, such as *Toxoplasma gondii* infections, can cause systemic symptoms, damage and destroy tissues, especially eye and brain and cause fatalities. Primary infections may be asymptomatic, or cause fever, headache, malaise, lymphadenopathy, and rarely meningoencephalitis, myocarditis, or pericarditis. Retinochoroiditis and retinal scars develop in up to 30% of infected persons, and epilepsy may occur. In immune-compromised and congenitally infected persons, active infection frequently is harmful. Recrudescence arises from incurable, dormant cysts throughout life. Current treatments against active *T. gondii* tachyzoites can have side effects such as hypersensitivity, kidney stones, and bone marrow suppression, limiting their use. Latent bradyzoites are not significantly affected by any medicines. Atovaquone partially, and transiently, limits cyst burden in mice, but resistance develops with clinical use. Thus, *T. gondii* infection is incurable with recrudescence from latent parasites posing a continual threat. Estimates of costs for available, suboptimal medicines to treat active, primary ocular, gestational and congenital infections, in just the U.S. and Brazil, exceed $5 billion per year. Improved medicines are needed urgently. Molecular targets shared by *T. gondii* and *Plasmodia* make re-purposing compounds a productive strategy.

SUMMARY OF THE INVENTION

[0004] In one aspect, the invention provides compounds of the structure of Formula (I), pharmaceutical compositions thereof, and methods for their use in treating apicomplexan parasite related disorders):



(I)

[0005] or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

[0006] ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

[0007] wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

[0008] Y^1 is C or N;

[0009] Y^2 is C or N;

[0010] X^1 is $C(R^{x1})$ or N,

[0011] wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0012] X^2 is $C(R^{x2})$ or N,

[0013] wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0014] X^3 is O, N(R), S or C_{1-3}alkyl;

[0015] X^4 is C or N;

[0016] X^5 is C or N;

[0017] R^1 is hydrogen or ${}_{1-3}$alkyl;

[0018] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

[0019] n is 0, 1, 2, 3 or 4;

[0020] each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl. —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0021] or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

[0022] each R is independently hydrogen or C_{1-3}alkyl.

[0023] In another aspect, the invention provides cell lines infected with an apicomplexan parasite, wherein the apicomplexan parasite genome comprises a gene encoding an Apetela 2 IV-4 protein with an M=>I modification at residue 570 ("AP2 IV-4 M570I") compared to its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470), non-human animal models comprising cell lines of the invention, and methods for use of each in identifying compounds for treating an apicomplexan parasitic infection.

[0024] In another aspect, the invention provides methods for treating an apicomplexan parasite infection (such as a *T. gondii* infection), comprising administering to a subject in need thereof an amount effective to treat the infection of an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of 1 or more of the up-regulated genes listed in FIG. **1** or FIG. **2**.

[0025] In a further aspect, the invention provides methods for identifying test compounds for apicomplexan parasite therapy, comprising identifying test compounds that reduce expression (for up-regulated genes), or increase expression (for down-regulated genes) of 1 or more of the apicomplexan parasite genes in FIGS. **3-5**.

[0026] In one aspect, the invention provides a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIGS. **3-5**, complements thereof, or their expression products, or functional equivalents thereof wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in the EGS strain of *T. gondii* after infection of human fibroblasts, neuronal stem cells or monocytic lineage cells.

[0027] In another aspect, the invention provides a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIG. **1-2**, complements thereof, or their expression products, or functional equivalents thereof, wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in human fibroblasts, neuronal stem cells or monocytic lineage cells after infection with *T. gondii*, including but not limited to infection with the EGS strain of *T. gondii.*

[0028] In another aspect, the invention provides methods for monitoring *T. gondii* infection in a subject, comprising monitoring levels in a blood sample from the subject of one or more markers selected from the group consisting of clusterin, oxytocin, PGLYRP2 (N-acetylmuramoyl-L-alanine amidase), Apolipoprotein A1 (apoA1), miR-17-92, and miR-124, wherein a change in levels of the one or more circulating markers compared to control correlates with *T. gondii* infection in the subject.

[0029] In another aspect, the invention provides methods for treating a *T. gondii* infection, comprising administering to a subject with a *T. gondii* infection an amount effective to treat the infection of ApoA1.

DESCRIPTION OF THE FIGURES

[0030] FIG. **1**. Host transcriptomics data during EGS infections of human HFF, MM6 or NSC cells. Differential gene expression analysis of human fibroblasts infected with *T. gondii* EGS strain after 2 hs, 18 hs, and 48 hs, monomac 6 cells infected with *T. gondii* EGS for 18 hs or neuronal stem cells infected with *T. gondii* EGS strain for 18 hours.

[0031] FIG. **2**. Host miRNA transcriptomics data during EGS infections of MM6 or NSC cells. Differential expression analysis of human miRNA genes from MM6 or NSC cells infected with *T. gondii* EGS strain for 18 hours.

[0032] FIG. **3**. EGS transcriptomics data during MM6 infections. Differential expression analysis of *T. gondii* genes from MM6 cells infected with *T. gondii* EGS strain for 18 hours compared to *T. gondii* gene expression from MM6 cells infected with GT1, ME49 or VEG strains for 18 hours

[0033] FIG. **4**. EGS expression during NSC infections. Differential expression analysis of *T. gondii* genes from neuronal stem cells infected with *T. gondii* EGS strain for 18 hours compared to *T. gondii* gene expression from neuronal stem cells infected with either GT1, ME49 or VEG strain for 18 hours.

[0034] FIG. **5**. EGS transcriptomics data during HFF infections. Differential *T. gondii* gene expressing analysis of human HFF cells infected with *T. gondii* EGS strain for 2 hs, 18 hs or 48 hs compared to the average *T. gondii* gene expression of human MM6 and neuronal stem cells infected with either GT1, ME49 or VEG strains of *T. gondii* for 18 hours

[0035] FIG. **6**. EGS morphology and effect on host cell transcriptomes a. EGS in human MM6 cells and NSC form cysts. Left NSC with EGS. Right MM6 with EGS. Note green dolichos cyst walls and BAG1(red) in NSC. DAPI stained nuclei(blue). b, c, d. Effects of EGS infection on MM6 and NSC transcriptomes: EGS transcripts in MM6 compared with NSC shows overlap of, as well as unique patterns of, transcripts. Differentially expressed genes in MM6 and NSC cells infected with EGS parasite were identified based on criteria of 1% FDR and absolute fold-change ≥2. Number of DEGs in each cell line are presented with bar graph (b) and Venn diagram are used to show general comparison of DEGs identified between the two cell lines (c). There is both communality, overlap in genes modulated and independence in others between cell types indicating cell type also influences cell type. Red and green colors were used to represent up- and down-regulated genes, cell line used is indicated on bottom (b-d). Functional enrichment analysis was performed for gene ontology (GO) biological process and KEGG pathways (d). P-values derived from analysis were –log 10 transformed and presented as a heat map. Pink and blue colors indicate GO terms or KEGG pathways enriched by up- and down-regulated genes, respectively. Enriched pathways or biological processes are listed on right of panels and cell lines are indicated on top. e. Host cell miR-seq analysis reveals that EGS regulates host cell miRNAs critical in pathogenesis and latency. An especially interesting down-modulated miRNA is hsa-miR-708-5p which is expressed particularly in brain and retina cells causing apoptosis[65]. When *T. gondii* down-modulates this as an encysted bradyzoite in neuronal cells, it would prevent hosts from initiating apoptosis to eliminate chronically infected neurons. f Parasite genetics and human host cell type have a profound influence on *T. gondii* gene expression. MDS plot comparing *T. gondii* gene expression profiles from MM6 and NSC cells infected with EGS, GT1, ME49 and VEG strains for 18 hours and HFF cell cultures infected with EGS strain for 2, 18 and 48 hours.

[0036] FIG. **7**. Differential Gene Expression (DGE) analyses and effects of inhibition of cytochrome bc1. a. DGE analysis of bradyzoite- and tachyzoite-specific markers during EGS infections of HFF cultures at 2, 18 and 48 hours (top panel), MM6 cells at 18 hours (middle panel) or NSC cultures at 18 hours (bottom panel) versus infections of same host cells with canonical strains GT1, ME49 or VEG at 18 hours (averaged across the three canonical strains for HFF infections). Genes reported as being over- or under-expressed during bradyzoite differentiation is indicated with red or green arrows respectively. "*", q-value≤0.05; Log FC, logarithm of the fold change in gene expression. CST1, SAG-related sequence SRS44[s114]; LDH2, lactate dehydrogenase 2[S115]; LDH1, lactate dehydrogenase 1[S115]; ENO2, enolase 2; ENO1, enolase 1[S116]; SAG1, SAG-related sequence SRS29B; BAG1, bradyzoite antigen BAG1[S115]. b. DGE analysis of genes encoding AP2 family of transcription factor during the same infection experiments as described in (m). Red and green arrows denote AP2 genes found to be over- or under-expressed during bradyzoite development[S117]. "*", q-value≤0.05. c. *T. gondii* cytochrome family genes differentially expressed during same experimental infections as described in (m). "*", q-value≤0.05. d. Effect of known cytochrome b inhibitors on EGS. Morpholino conjugated to a Vivoporter (called PPMO) designed to knock down cytochrome b compared with off target control has a significant effect in reducing replication of YFP RH strain tachyzoites at 5 and 10 μM ($p<0.05$) but only a very small effect on size and number of EGS cysts in HFF. As a poorly soluble inhibitor of cytochrome b, ELQ271 was reported to partially reduce cyst numbers in mice[27] and is shown herein also to reduce the EGS cysts in vitro at 10 μM in this novel model. This demonstrates the utility of this novel in vitro model by indicating that inhibition of cytochrome b Qi is associated with reduction of cysts in vivo in a mouse model, even when there are serious limitations caused by insolubility of this inhibitory compound. This poor solubility significantly limits ELQ271 as a candidate for progression to a medicine. Increasing selectivity for the parasite enzyme with our new scaffold is another critical challenge.

[0037] FIG. **8**. a. Structures of the ELQ class (1-3) and the tetrahydroquinolone scaffold (4).[27,45,49,53]. Low solubility of the ELQs has been a serious concern going into preclinical evaluation for treatment of malaria.[27] b. *Saccharomyces cerevisiae* cytochrome bc_1 X-ray structure (PDB ID: 1KB9)[5] The complex contains 11 subunits and 3 respiratory subunits (cytochrome b, cytochrome c1 and Rieske protein). The cytochrome b subunit provides both quinone binding sites (Q_o and Q_i) highlighted as grey and pink surfaces respectively.

[0038] FIG. **9**. ELQ inhibitors provide a new scaffold and approach yielding compounds that are potent inhibitors of tachyzoites and cysts in vitro. a-e. Study of Inhibitors in vitro is summarized in Table 2 and led to selection of MJM170 as a promising novel scaffold for both tachyzoites and bradyzoites. a. MJM170 markedly reduces RH YFP tachyzoites in tissue culture robustly at low nanoM levels. (Standard curve left and effect on RH YFP, right panel). b,c. MJM170 markedly reduces EGS bradyzoites in cysts in vitro. Inhibition of cytochrome b Qi eliminates cysts in HFF infected with EGS. Without inhibitory compound in HFF (note, oval cyst with green border staining dolichos) and adjacent panel with inhibitory MJM170 compound (note absence of cysts with small amount of amorphous residual dolichos). MJM170 eliminated tachyzoites followed to 10 days of culture and bradyzoites in cysts in vitro. Summary comparison of each of the compounds tested in vitro and their ADMET is in Table 2. Note improvement in solubility, properties amenable for compounds to cross blood brain barrier with new scaffold. d. EGS transfected with stage specific reporters for fluors, red tachyzoite SAG1, Green bradyzoite LDH2.

[0039] FIG. **10**. MJM170 is also effective against RH and Prugneaud tachyzoites and Me49 bradyzoites, in vivo with translucent zebrafish providing a novel model with potential for scalable in vivo assays in which tachyzoites with fluorescent reporters and bradyzoites in cysts can be visualized efficiently. a: 25 mg/kg daily MJM170 administered intraperitoneally eliminates active infection due to RH tachyzoites stably transfected with YFP in mice (RFU control vs rx with MJM 170, $p<0.004$). For the standard curve in the inset, RFU increase with increasing concentrations of fluorescent tachyzoites ($R^2=0.99$). b. MJM 170 25 mg/kg daily reduces Type 2 parasites. c. MJM 170 reduces cysts in mice infected 2.5 months earlier and treated for 17 days with 12.5 mg/kg daily then without compound for 3 days:cyst count of wet prep of brain homogenate. d. Zebra fish can be used to visualize fluorescent tachyzoites and cysts in more chronic infections.

[0040] FIG. **11**. MJM170 targets apicomplexan cytochrome bc_1 Qi: modelling, yeast surrogate assays, target validation, co-crystallography and nanoM inhibition of *P. falciparum* and *T. gondii* a. Modeling: MJM170 (yellow) modelled within cytochrome b Q_i site (grey) highlighting residues (green) involved in binding. b. Mutations for yeast, *P. falciparum*, predicted for *T. gondii* and bovine enzyme. Relevant mutations are indicated by colored dots in Q_i domains on the bottom of the image of mitochondrion membrane for *S. cerevesiae* and *P. falciparum*, and where those amino acids are in *T. gondii*, human and bovine enzymes. Red dot marks G33A/V in Q_i domain of *P. falciparum*. c. Cytochrome b mutants and sequence accession numbers. d. MJM 170 inhibits wild-type but not mutant yeast. Compounds MJM 170 and ELQ 271 with wild type and mutant yeast validate predictions that M221 K/Q would create a steric clash and resistance. e. MJM170 is a potent low nM inhibitor of *Plasmodium falciparum*. In Table 2, wild type *P. falciparum* also are tested and is inhibited at <50 nM by this scaffold. D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. Mutant G33V did not confirm prediction of a steric clash. f. MJM170 binds within Q_i site of bovine cytochrome bc_1 as shown by X-ray crystallography. f(i). An omit Fo-Fc electron density map (green) at 5σ allows unambiguous positioning of MJM170 (magenta) within the Q_i site with the tetrahydroquinolone group near heme b_H (white) and diphenyl ether directed out of the channel. f(ii)-MJM 170 molecule is included into the structure, the 2Fo-Fc electron density map at 1σ (grey) allows placement of the planar head between heme b_H and Phe220 with the carbonyl group positioned in a polar region surrounded by Ser35 and Asp228. g. A stereo picture of the 2Fo-Fc electron density map. Electron density at 1σ level around cytochrome b α-helixes 118-128 and 183-199 close to MJM180 compound in X-ray structure of cytochromebc1. Inset: Crystal of mammalian cytochrome bc1 complex.

[0041] FIG. **12**. MJM170 potently inhibits *P. falciparum* mitochondrial electron transport important for synthesis of pyrimidines, is modestly synergistic with atovaquone, additive with cycloguanil and antagonistic with Q_i inhibitor. a. MJM170 is highly potent (Dd2, black curve, $EC_{50}=29.5$ nM) without cross-resistance in previously reported cytochrome b drug-resistant mutant parasite lines including ubiquinone reduction site mutants ($Dd2^{G33A}$ and $Dd2^{G33V}$, light blue and dark blue curves, respectively). Dose-response curve from representative assay. MJM170 cannot inhibit a parasite supplemented with a yeast cytosolic DHODH (scDHODH, green curve) demonstrating that its primary activity in *P. falciparum* is to inhibit electron transport necessary for pyrimidine biosynthesis. Inset Table. Dose-response phenotypes of a panel of *P. falciparum* cytochrome b mutant parasite lines. EC_{50} values were calculated using whole-cell SYBR Green assay and listed as mean±standard deviation of three biological replicates, each with triplicate measurements. b., c. Isobolograms with MJM170 plus atovaquone or cycloguanil or Qi inhibitor BRD6323: b. Combinations were with atovaquone (ATV) or cycloguanil (CYG) at multiple fixed volumetric ratios (10:0, 8:2, 6:4, 4:6, 2:8, and 0:10) in Dd2 parasites. Slight synergy observed with combinations of MJM170 and atovaquone while MJM170 and cycloguanil dosed in combination showed additive effect. Fractional inhibitory concentrations (FIC) for each drug were calculated and plotted. Shown is a representative isobologram for each combination of compounds. Table below lists FICs for each compound and ratio tested (values are mean from three independent assays±standard deviation). Synergy was defined as a combined FIC<1.0, addivity as FIC=1.0, and antagonism as FIC>1.0. c. Isobologram Figure: MJM170 was tested in combination with previously reported reduction site inhibitor BRD6323 at multiple fixed volumetric ratios (10:0, 8:2, 6:4, 4:6, 2:8, and 0:10) in Dd2 parasites. Antagonism was observed with combinations of MJM170 and BRD6323, another bulky inhibitor of cytochrome bc, as opposed to synergy observed with oxidation site inhibitor atovaquone. Fractional inhibitory concentrations (FIC) for each drug were calculated and plotted. Representative isobologram of three independent assays is shown. Table below lists FICs for each compound and ratio tested (values are means from three independent assays±standard deviation). Definitions as in b.

[0042] FIG. **13**. Effects of compounds against RH-YFP. Graph is a representative example of an experiment testing two of the compounds against tachyzoites (RH-YFP). On the vertical axis is fluorescence in relative fluorescence units, where decrease in fluorescence compared to the DMSO control indicates parasite inhibition. On the horizontal axis are the different treatment conditions.

[0043] FIG. **14**. The results of a cytotoxicity assay. 10 μM solution of compound was compared to the DMSO control closest to 0.1% DMSO (0% DMSO) and the 50 μM solution was compared to the DMSO control closest to 0.5% DMSO (0.625% DMSO). The differences were not found to be statistically significant.

[0044] FIG. **15**. Effects of compounds against EGS. a-c) Graphs comparing the effects of JAG050 and JAG021 on EGS. Images from scanned slides. Three different forms were observed: cysts, pseudocysts, and small organisms, pictured in (d), untreated control, magnified. e) untreated control f) JAG050 10 μM and g) JAG021 1 μM. Cells were stained with DAPI (blue) to stain nuclei, BAG1 (red), a bradyzoite antigen, and dolichos (green), which stains cyst walls. White arrow marks cyst.

[0045] FIG. **16**. Binding assays show selectivity with binding to the bovine enzyme which is not as robust as has been seen with other cytbc inhibitors

[0046] FIG. **17**. JAG21 is a mature lead that protects against *Toxoplasma gondii* tachyzoites and cures *Plasmodium bergheii* sprorozoites, blood and liver stages with oral administration of single dose 2.5 mg/kg and 3 doses protect at 0.5 mg/kg. Single dose causal prophylaxis in 5 C57BL/6 albino mice at 2.5 mpk dosed on day 0, 1 hour after intravenous administration of 10,000 *P. berghei* sporozoites. 3 dose causal prophylaxis treatment in 5 C57BL/6 albino mice at 0.6 mpk dosed on days −1, 0, and +1. A representative figure for higher dose (5 mg/kg) is shown, but all experiments with the amounts mentioned above had efficacy measured as cure measured as survival, luminesence and parasitemia quantitated by flow cytometry are similar to these.

[0047] FIG. **18**. Tafenoquine and JAG21 are both needed to contain RPS 13Δ. One additional mouse in the tafenoquine and JAG21 died outside the time on this graph others remained healthy.

[0048] FIG. **19**. Serum biomarkers from boys with active brain disease due to *Toxoplasma* reflect infection and neurodegeneration. a. Tabular clinical summary: Three pairs of children, matched demographically; one in each pair had severe disease and one mild or no manifestations. One pair dizygotic, discordant twins. Each ill child had new myoclonic or hypsarrythmic seizures. Two children had T2 weighted abnormalities on brain MRIs similar to active inflammatory and parasitic disease in murine model[8] b-e. Protein and miR serum biomarkers: Panel of nanoproteomics and miR sequencing performed on serum obtained at time of new illness. MiRNA concentration measured and difference in concentration graphed. Abundance of peptides measured. Note: Presence of markers of neurodegeneration, inflammation, and protein misfolding include clusterin, diminished ApoJ, serum amyloid, and oxytocin in ill children compared with their healthy controls.

[0049] FIG. **20**. List of up-regulated or down-regulated genes involved in specific host cell pathways or indications.

[0050] FIG. **21**. List of exemplary proteins important for apicomplexan parasite bradyzoite development and/or survival in the host.

DETAILED DESCRIPTION OF THE INVENTION

[0051] All references cited are herein incorporated by reference in their entirety. Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, Calif.), "Guide to Protein Purification" in *Methods in Enzymology* (M. P. Deutshcer, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, Calif.), *Culture of Animal Cells: A Manual of Basic Technique*, 2^{nd} Ed. (R. I. Freshney. 1987. Liss, Inc. New York, N.Y.), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E. J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, Tex.).

[0052] As used herein, the singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise. "And" as used herein is interchangeably used with "or" unless expressly stated otherwise.

[0053] As used herein, the amino acid residues are abbreviated as follows: alanine (Ala; A), asparagine (Asn; N), aspartic acid (Asp; D), arginine (Arg; R), cysteine (Cys; C), glutamic acid (Glu; E), glutamine (Gln; Q), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

[0054] All embodiments of any aspect of the invention can be used in combination, unless the context clearly dictates otherwise.

[0055] In one aspect, the invention provides cell lines infected with an apicomplexan parasite, wherein the apicomplexan parasite genome comprises a gene encoding an Apetela 2 IV-4 protein with an M=>I modification at residue 570 ("AP2 IV-4 M570I") compared to its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470). As described in the examples that follow, Apetela

2(AP2) IV-iv is known to be a bradyzoite gene expression repressor[56], and the AP2 IV-4 M570I mutant results in an apicomplexan parasite that remains as a bradyzoite in tissue cultures passaged extensively, capable of producing oocysts when administered to cats definitively proving its true bradyzoite phenotype.

[0056] As further described in the examples that follow, critical flaws and limitations of available methods and models for developing medicines to cure apicomplexan infections, such as *T. gondii* infections, include lack of in vitro culture systems for cysts and scalable, easy to use animal models for screening compounds. The cell lines of this aspect of the invention unexpectedly possess a true, dormant parasite phenotype in tissue culture and can be used, for example, to screen for drugs that can be used to treat apicomplexan parasitic infections, as well as a research tool for studying apicomplexan parasites in the dormant phenotype. The cell lines can be used, for example, as a model of bradyzoite infection. A generalized apicomplexan life cycle comprises a rapidly growing tachyzoite and slow-growing, latent bradyzoite that forms tissue cysts (i.e.: dormant phenotype). Such dormant parasites are present in the brains of 2 billion persons worldwide across their lifetimes and are incurable. Quite remarkably, the inventors have discovered that in human cells this encysted parasite turns on host cell pathways important for altering ribosomal function, mis-splicing of transcripts, oxidative pathways, and, those pathways found to be altered in Alzheimer's and Parkinson's diseases. Extensive details on the model are described in the examples that follow.

[0057] In one embodiment, the apicomplexan parasite genome comprises a gene encoding AP2 IV-4 M570I that further differs from its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470) in encoding the amino acid sequence GGNRPHYHVAKQEWRVRYYMNGKRKMRTYSAKFYGYETAHTMAEDFAHYVDKH E (SEQ ID NO: 1) beginning at residue 821. In a further embodiment, the gene encoding AP2 IV-4 M570I encodes the following amino acid sequence, or functional equivalents thereof:

(SEQ ID NO: 2)

MAAPAPSAEARPAKRRCFPLPRETPVSSEDETRKTLQHDTLGCLPRSS

SGQPELAAASAASQVGHLSSAALLQLVQTQSAGGVPQAVLRNLFSSIH

RNPKPLPANALAATPNSSLYASLTSLSSAAALPGAGPAYSQAPSPASA

DLLQSEQFGSAAKNPSPNEASPILALLGEAARAATTPRTVPALSAVCP

AASSGVSLPSASDTLALAQSSLSSSTGCASDVKASRPEEHPAFASGTA

NRQSLLQALLLSTAPLAFSGPSLSSASTTLPASSGAVSSRNAGAYQFE

RLLQAEAAKVKALLPNATSKSMSQSSVPQRDLTRKTSLFPDPRGLSAD

DASRRYNTRGANSGGAGLRRGTGVHATTEQSGALDAGERTRPFGAGED

ESAQGKPDSRGRQRPGALDASNILGLLAAFQPSQAPAIRDLSAPSHLS

AAATGALPLTASFTASALASSQCLPAGTPASSSASPPFSEVLSTTEES

STTKETDASASTLLAFLQKYSAVSGLGGASDFLGQLQGKSSLPPLSLA

EPSSALPSSFLGGSDGGTIDTRNGNGEKTTPPIHLFQSAFR**I**PSPSQQ

NLLDALLASSCTTATSRSDGSGNLGCPVVDERNAKLAGPAHPLPCSFP

-continued

QISSSSGEPGRKTGGRVHRQGTSQSGGRVRSGKNGGSAAPPRQSSSEN

VPSTPTVSSHEAPHRAGFPSQTPYELSASPSHQLDLLRLGAFLGGAGK

QDASVHSDETGTLSGEPSHRSCSLSRGLTQESVLQLSDTTSTSREGEP

NEPSQGCVNVAASLPAFGPQPSSGAAKAREGRRGAGGAGAAPPVPLRA

DVTL**GGNRPHYHVAKQEWRVRYYMNGKRKMRTYSAKFYGYETAHTMAE**

DFAHYVDKHEALPDSMMMTAMMLQAQANSAASSGQTVPLARGIRASSA

SAGAGGHVSKSATKGSVAASSEGSTSMGSDATRSQEGEAAELCPLAAG

LSRPLASMHSAAGNAVAQGRQESKEEAPGGQAWFGEPGKFRASSEAAL

CGSGSSAEGRDGHESEVLWATLGKVHDASQGKKIKPEKPLTVARGRLA

LGAEDKSQNLGVDLGDSGGAQGLPGVRQPRQMKNSEECSLRDSDKGMA

LSKRFGFLPSQTPSCDSMTLPFPGGFDALSLSSALSSCASLPVAHEGN

NFQKGHTGDIVALASQSGTQRPASVVLSRDANVSGSSPSHPTWQREGA

AVSGRADEFSSLSVTPSTVPLSSFTMEDIKGEEGDPSRRFALVGESMK

NVSAPEVQALFPTSSIANAELLPVDFLHSNSCSADKLESSIPRGLAGN

NPSMTATAVAATAVSHQIFDTITLFGEFLREFAKEKVNEFHEYGLEAS

PLTVEASPEVSLFGKATFGRCPVAGGSTPAGISKMSGETLSGLSASEL

SLVSARTNTTTGEEQFALARGLFPGDSEGDRDEKKPQLSQQELLVLSH

ALVNLTSSTYVLMHTLKASLSKSTEAVQLHQPLLEAASEAKATDEAKT

REEQESSECDHEYPPGSSLEATTGALPFRLSPALSASSKDLPSLSASA

SLESVTPFAGLPLEEGTLSASVGLASSDDEHDTSLLFKTEAAKKRSLF

STAADGDESRTYNDGLGQPMEEEIRSCVSTSCGEAVATTTLSAIGPGT

GASGALLDSESRESLGEKPGAALRAGAHTPAPSRAPTPSRTFSFTSSS

TATSAALLCDSNVVHEKLSAQGKDSEAGERKGDSEKEEEVEMWKEEDE

EVQRCTGSAETDSTEATRGEEAWRRGKQSEKKPSVITTALNLLETHRH

LALTISQLKRPVAQQLRFILPIAAPQLLPCILPPASFQGTGESGDGKA

EAEAKGSSSLGQVLETALGHGTRLAPSASAMVPPRKDEAASAVPEAKT

LTGLANAGVTREAASRTLEAEQVSRKRSREEVVDSETAGDEGDMENVP

ETRDGTTRPGSRQYDTSPSNDGTKPPATAKSRVIRDQAALERLLLAPF

QDTPTCSCTDRPCPCDRQQVADMIYLFYAVPARQQAESSKEGSTQRLQ

FAARDTNERKDARTGEETQGGETEAKEVIRDPEERGVCEGSSSQNAHT

QFDAETASSSMSSDPRADKESNAQDAHMADKTSFVSDLPQPSGEFAPS

LLSETSLDVAMADSRGTPSEIHGFFTRSDEQKRASFSSSSLLAAGHAV

ASFSSSLAGVVSGAGERRECAGPSLGDLSTIGLLSLSYPAMLAFILPL

QSLLHTVSGMILTLHKKLIHRFICAHLRLVLDDDMRRPAGGALKSRGA

HGDTEAAEAQVERRRREHEREETTNLAIGYREGNAEAANTFPLVDTVS

SLLSPGSLRQENSEVERRDNDEERLELITGIARESPKPSEKDSVSPFL

STAPCPGTEAESSDCSASSACSGTPTEGTEGGETGDIASFLSPSGEVK

QTIMLA

[0058] The mutations at residue 570 and beginning at residue 821 compared to the Apetela 2 IV-4 orthologous protein encoded by the reference *T. gondii* ME49 strain (gene ID: TGME49_318470) are presented in bold font and underlining in the above sequence. A "functional equivalent" is a gene encoding an Apetela 2 IV-4 protein that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence provided above, includes the noted mutations at residue 570 and beginning residues 821-874, and that does not represses bradyzoite gene expression in a tachyzoite in an apicomplexan parasite.

[0059] As used here, "apicomplexan parasites" are a phylum of the kingdom Protista (formerly a division of protozoa called *Sporozoa*); named for a complex of cell organelles (apical microtubule complex) at the apex of the sporozoite form that can penetrate host cells. It includes, but is not limited to, the medically important genera *Plasmodium, Toxoplasma, Cryptosporidium*, and *Isospora*. Thus, in one embodiment, the apicomplexan parasite is selected from the group consisting of *Plasmodium, Toxoplasma, Cryptosporidium*, and *Isospora*. In a specific embodiment, the apicomplexan is a wild type, mutant, or recombinant *Toxoplasma gondii* strain. In various further embodiments, the apicomplexan parasite is *Toxoplasma gondii* of clade B.

[0060] In another embodiment, the apicomplexan parasite is a G0 arrested parasite, including but not limited to s *Toxoplasma gondii* strain RPS 13 delta (Hutson et al., PLoS One. Nov. 22, 2010; dx.doi.org/10.1371/journal.pone.0014057). This cell line can be used, for example, to identify companion compounds for THQ that eliminate the G0 arrested stage of *T. gondii* along with the active and the slowly growing bradyzoite stage.

[0061] In another embodiment, the apicomplexan parasite is *Toxoplasma gondii* strain EGS (ATCC® Number:PRA-396™). As described in the examples that follow, the EGS strain was extensively characterized in vitro to show that true cysts develop, making the EGS strain especially useful for drug development.

[0062] In all embodiments of this aspect of the invention, the cell line can be any suitable cell line capable of supporting apicomplexan parasitic infection, including but not limited to mammalian cells (mouse, rat, human, etc.), zebrafish cells, etc. In one specific embodiment, the cell line is a human cell line; exemplary human cell lines for use in this aspect of the invention include, but are not limited to fibroblasts, stem cells, neurons, monocytes, and ocular cells 9including primary human cells). As described in the examples that follow, the apicomplexan parasites form cysts in the host cell lines that enlarge over time and then destroy host cell monolayers as single cell organisms. As such, the cell lines of the invention are extremely useful as in vitro models of apicomplexan parasite infection. Such models can be used, for example, to test for candidate compounds that inhibit cyst formation and/or destruction of host cell monolayers; such candidate compounds would be useful in treating apicomplexan parasite infection.

[0063] In another embodiment, the apicomplexan parasite genome is recombinantly engineered to express a reporter polypeptide, including but not limited to fluorescent or luminescent proteins. This embodiment permits ready visualization of the parasite and facilitates automated quantitative analysis. In one embodiment, the reporter polypeptide is operatively linked to a promoter that is activated in the bradyzoite stage or a promoter that is activated in the merozoite stage. Any suitable promoter that is activated in the bradyzoite stage or merozoite stage may be used. In one embodiment the promoter that is activated in the bradyzoite stage is the *T. gondii* BAG1 encoding gene promoter or a functional equivalent thereof. The BAG1 promoter sequence can be obtained as disclosed in Bohne et al., Molecular and Biochemical Parasitology 85 (1997) 89-98. In one embodiment, the BAG promoter comprises SEQ ID NO:3, or functional equivalent thereof, from the *T. gondii* VEG strain.

[0064] A "functional equivalent" of the BAG1 promoter is a promoter from any strain of *T. gondii* that promotes expression of BAG1 in the VEG strain, as well as an promoter nucleic acid sequence that is 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:3 and drives expression of a BAG1 gene in a *T. gondii* strain.

[0065] As described in the examples that follow, the cell lines of the invention can be administered to/ingested by non-human animal models to provide an in vivo model of apicomplexan parasitic infection that develop the classic, gold standard bradyzoite phenotype of producing oocysts. This, in another aspect, the invention provides non-human animal models of apicomplexan parasitic infection, comprising a non-human animal that has ingested or otherwise comprises the cell line of any embodiment or combination of embodiments of the invention. In one embodiment, the non-human animal produces oocysts. Any suitable non-human animal model that produces oocysts can be used, including but not limited to cats.

[0066] In another aspect, the invention provides non-human animal models of apicomplexan parasitic infection, comprising a non-human animal that has ingested or otherwise comprises oocysts produced by the non-human animal model that has ingested or otherwise comprises the cell line of any embodiment or combination of embodiments of the invention. As described in detail in the examples that follow, oocysts given to non-human animal models such as mice created an illness and histopathology phenotypically characteristic for typical, virulent parasites causing dose related proliferation of the parasite (exemplified by *T. gondii*) with necrosis in terminal ileum, pneumonia at 9-10 days, with brain parasites by 17 days and dose-related mortality. Thus, the non-human animal models of this aspect of the invention are particularly useful in screening for drugs to treat the effects of apicomplexan parasite infection.

[0067] As will be understood by those of skill in the art, the oocysts do not need to be isolated prior to ingestion; they may be present, for example, in tissue (including but not limited to brain tissue) taken from the non-human animals that have ingested or otherwise comprise the cell lines of the invention, which then produce oocysts. Any suitable non-human animal model can be used, including but not limited to mice, rats, cats, zebrafish, non-human primates, cattle, sheep, and pigs. In one specific embodiment, the non-human animal is a mouse.

[0068] In another aspect the present invention provides methods of identifying compounds for treating an apicomplexan parasitic infection, comprising contacting one or more test compounds to the cell line of any embodiment or combination of embodiments of the invention, wherein those positive test compounds that reduce bradyzoite cyst amounts in the cell line are candidates to treat an apicomplexan parasitic infection. As disclosed above, the cell lines of the invention unexpectedly possess a true, dormant parasite phenotype in tissue culture and can be used to screen for drugs that can be used to treat apicomplexan parasitic infections. Any reduction in bradyzoite cyst amounts in the cell line indicates that the test compound may be useful for treating an apicomplexan parasitic infection. In various embodiments, positive test compounds are those that reduce bradyzoite cyst amounts by at least 5%, 10%, 15%, 20%, 25%, 50%, 75%, 90%, or more.

[0069] In another aspect the present invention provides methods of identifying compounds for treating an apicomplexan parasitic infection, comprising administering one or more test compounds to the animal model of any aspect or embodiment of the invention, wherein those positive test compounds that reduce one or more symptoms of the infection and/or reduce parasitic titer in the animal model are candidates to treat an apicomplexan parasitic infection. In one embodiment, those positive test compounds that reduce oocyst production and/or reduce bradyzoite cyst amounts in the animal model are candidates to treat an apicomplexan parasitic infection. Any reduction in oocysts production and/or bradyzoite cyst amounts indicate that the test compound may be useful for treating an apicomplexan parasitic infection. In various embodiments, positive test compounds are those that reduce oocysts production and/or bradyzoite cyst amounts by at least 5%, 10%, 15%, 20%, 25%, 50%, 75%, 90%, or more.

[0070] In one embodiment of any of the methods of identifying compounds for treating an apicomplexan parasitic infection of the invention, positive test compounds are candidates for treating *Toxoplasma gondii* or *Plasmodium falciparum*: infection, including drug resistant strains and or other plasmodial infections. The methods can be used to test any suitable type of candidate compound, including but not limited to polypeptides, antibodies, nucleic acids, organic compounds, etc. Treatment effects of the test compounds may be assessed relative to a suitable control, such as the cell lines or non-human animal models of the invention that are not treated with the test compound. It is well within the level of those of skill in the art to determine a suitable control in light of the teachings herein.

[0071] In one specific embodiment, the cell line, or non-human animal model that has ingested or otherwise comprises the cell line, comprises a G0 arrested parasite (such as RPS 13 delta) and is used to identify companion compounds for tetrahydroquinolones (THQ) that eliminate the G0 arrested stage of an apicomplexan parasite, such as *T. gondii*, along with the active and the slowly growing bradyzoite stage.

[0072] RPS 13 Δ is a genetically engineered conditional knockout parasite that has a unique transcriptome documenting its G0 state, G1 arrest in the absence of tetracycline but grows normally in the presence of tetracycline which removes the repressor from the promoter. The method may utilize, for example, a system that when there is no anhydrotetracycline to remove the engineered tetracycline responsive repressor from the 4 tetracycline response elements engineered in tandem in the promoter; these parasites persist in tissue culture for long times (months). This embodiment is based on the observation that this conditional knockout RPS13 delta parasite when it is in its arrested in G1 state is not susceptible to the effect of any inhibitors that effect processes essential to the tachyzoite or bradyzoite form including those tested in vitro so far. In this embodiment the conditional knockout RPS13 delta parasite is amenable to testing inhibitors of hypnozoite like organisms by culturing them without tetracycline in the presence of the compound and determining whether any parasites can be rescued by adding tetracycline to determine whether they are still capable of persisting and becoming tachyzoites that grow rapidly in the presence of tetracycline. Furthermore, the methods may comprise testing RPS13 delta in mice, and involves the observations that when RPS13 delta is administered to wild type mice without tetracycline the RPS13 delta parasite induces a protective immune response as a vaccine dependent on interferon gamma and has no adverse effect on the mice, nor can it be rescued with tetracycline or inhibitors of iNOS (intracellular nitrogen oxide synthase) such as LNAME (L-N^G-Nitroarginine methyl ester) which abrogate effects of interferon gamma after 7 days. For example, that in interferon gamma knock out mice or mice treated with antibody to interferon, RPS13 delta is lethal for the mice, where the attenuated organism persists, can be observed, until mice succumb slowly. Another example may be a SCID mouse or a steroid treated mouse that is more susceptible due to immune compromise.

[0073] In another embodiment, RPS13 delta can be used to test compounds in vitro against this G0 truly dormant stage, and against compounds that can target the hypnozoite state but that must be metabolized in the liver to produce toxic electron containing compounds in vivo.

[0074] In all these embodiments, the methods can be used to determine if compounds have parasiticidal effects on hypnozoite forms and be used in conjunction with THQ compounds, such as tafenoquine, known in primate models and in humans as the only compound besides primaquine which has a lethal effect on the malaria hypnozoite in primates or in humans. However, tafenoquine is not active against actively proliferating organisms and requires a compound that is effective against more rapidly and slowly growing forms to produce radical cure of malaria.

[0075] In another embodiment, the THQ compound may be primaquine, a compound that has a similar effect when metabolized and is ineffective against *T. gondii* tachyzoites in tissue culture and can therefore be utilized in the same manner as tafenoquine to inhibit the hypnozoite form of apicomplexan parasites to produce radical cure.

[0076] Compounds identified using the methods of these various embodiment of the invention can be used together the THQ compound(s) to treat/cure the active tachyzoite, the slowly growing bradyzoite, and the G0 arrested hypnozoite-like phase of the apicomplexan infections the active tachyzoite, the slowly growing bradyzoite, and the G0 arrested hypnozoite-like phase of the apicomplexan infections

[0077] As described in detail in the examples that follow, the inventors carried out transcriptome analysis of both the apicomplexan parasite and the host cells after parasite infection of the host cells. The resulting transcriptomes provide a signature for apicomplexan parasites (such as *T. gondii* strains EGS), which helps in identification of targets for drug development, as well as a signature for infected host cells (such as human foreskin fibroblasts (HFF) human monocytic cells (ex: MM6), and human primary neuronal stem cells (NSC)), which helps in identification of targets for treating apicomplexan infection. As shown in the examples, EGS transcription was influenced by host cell type (FIG. **6**). Transcriptomics using host mRNA and miR profiling of EGS cultures in MM6, and NSC cells for 18 hours demonstrated that this parasite modulates host transcripts involved in protein misfolding, neurodegeneration, endoplasmic reticulum stress, spliceosome alteration, ribosome biogenesis, cell cycle, epilepsy, and brain cancer among others (FIG. **6**). The number of genes significantly up or down regulated in MM6 and NSC cells compared to uninfected controls are depicted in FIG. **6**. Overexpressed genes differ from those of GT1, ME49 and VEG tachyzoite-infected human NSC cells, but modify the same or connected pathways. Hsa-miR-708-5p was the most affected miRNA (down-modulated) by EGS (FIG. **6***e*. miR-708-5p is a regulator that promotes apoptosis in neuronal and retinal cells, which could maintain a niche for EGS-like encysted bradyzoites to persist.

[0078] The genes identified in the host transcriptome study are thus targets for anti-parasite therapy, as well as markers of apicomplexan parasite infection (such as *T. gondii* infection). In various embodiments, the invention may thus comprise methods for treating an apicomplexan parasite infection (such as a *T. gondii* infection), comprising administering to a subject in need thereof an amount effective to treat the infection of an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of 1 or more (i.e.: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) of the up-regulated genes listed in FIG. **1** (protein encoding genes) or FIG. **2** (miRNA). In various non-limiting embodiments, the inhibitor is selected from the group consisting of a target-specific inhibitory antibody, aptamer, siRNA, shRNA, antisense oligonucleotide, or small molecule.

[0079] In one embodiment, the target is miR-708-5p. In various further embodiments the targets are one or more of the genes listed in Table 1 below, or from FIGS. **20-21**, which provide a more complete list of up-regulated or down-regulated genes involved in specific host cell pathways or indications. The table shows up-regulated or down-regulated genes involved in specific host cell pathways or indications ("KEGG pathway"), such as systemic lupus erythematosus, (SLE), Parkinson's disease, etc. In an exemplary embodiment, the methods comprise administering to the subject in need thereof an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of one or more (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or all 13) of genes HIST2H2AA3, HIST1H2AC, HIST1H2BC, ACTN4, SNRPD3, ELANE, C1R, HIST1H2BK, H2AFZ, SNRPB, H2AFX, CTSG, and HIST1H4H, to treat apicomplexan parasite infection-associated SLE. One of skill in the art will understand from the table that the methods may be used to treat apicomplexan parasite infection-associated Parkinson's, Huntington's disease, Alzheimer's disease, etc. using an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) against 1 or more (i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or more, such as all) of the target genes listed for the specific indication. Similarly, one of skill in the art will understand from the table that the methods may be used to treat apicomplexan parasite infection-associated disorders relating to ribosomal assembly, spliceosome assembly, oxidative phosphorylation, etc. using an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) against 1 or more (i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or more, such as all) of the target genes listed for the specific indication.

TABLE 1

KEGG id	KEGG pathway	P-value	Genes
hsa03010	Ribosome	4.6E−07	RPL35A, RPL36A, RPL35, RPS9, RPL27, RPS27L, RPL38, RPS25, RPS27, RPL30, RPL23, RPS29, RPL21, RPS20, RPS21, UBA52, RPL36AL
hsa05322	Systemic lupus erythematosus	0.00082	HIST2H2AA3, HIST1H2AC, HIST1H2BC, ACTN4, SNRPD3, ELANE, C1R, HIST1H2BK, H2AFZ, SNRPB, H2AFX, CTSG, HIST1H4H
hsa04621	NOD-like receptor signalling pathway	0.01458	IL6, CCL2, XIAP, NFKBIB, NFKBIA, TNFAIP3, BIRC3, CCL5
hsa03040	Spliceosome	4.1E−06	SNRPA1, CCDC12, MAGOH, SNRPD3, LSM6, LSM7, SNRPB2, SNRPD2, PPIH, SNRPB, PQBP1, SYF2, LSM5, U2AF1, MAGOHB, THOC2, SNRPF, SNRPE, SNRPG
hsa00190	Oxidative phosphorylation	6.4E−16	ATP5E, NDUFB4, ATP6V0E1, NDUFB6, NDUFB9, COX7C, ATP6V1G1, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, ATP5L, NDUFS3, COX17, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, NDUFA1, ATP6V1F, NDUFV2, COX6A1, UQCRB
hsa05012	Parkinson's disease	2.4E−14	ATP5E, NDUFB4, NDUFB6, NDUFB9, COX7C, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, HTRA2, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, UBE2L3, NDUFA1, VDAC3, NDUFV2, COX6A1, UQCRB
hsa05016	Huntington's disease	2.2E−13	ATP5E, NDUFB4, POLR2F, NDUFB6, POLR2K, NDUFB9, POLR2J, COX7C, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, TGM2, CREB3L1, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6,

TABLE 1-continued

KEGG id	KEGG pathway	P-value	Genes
			COX8A, NDUFC2, NDUFC1, NDUFA1, VDAC3, SOD2, NDUFV2, COX6A1, UQCRB
hsa05010	Alzheimer's disease	9E−11	ATP5E, NDUFB4, NDUFB6, NDUFB9, COX7C, ATP5G1, UQCRQ, NDUFB1, NDUFB2, NDUFS5, NDUFS4, PPP3CA, NDUFS3, ATP5H, ATP5J, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A1, NDUFA6, COX8A, NDUFC2, NDUFC1, ITPR3, NDUFA1, NDUFV2, COX6A1, UQCRB
hsa04623	Cytosolic DNA-sensing pathway	0.0077	MAVS, IL6, POLR3K, NFKBIB, IRF7, NFKBIA, POLR1C, CCL5

[0080] In one embodiment, the invention provides methods for treating an apicomplexan parasite infection, comprising treating a subject with an apicomplexan parasite infection an amount effective to inhibit activity or expression from the apicomplexan parasite of one or more proteins listed in FIG. **21**.

[0081] In another embodiment, the invention provides methods for identifying a compound to treat an apicomplexan infection, comprising identifying a compound that inhibits activity or expression of one or more proteins listed in FIG. **21** from an apicomplexan parasite present in an infected host cell.

[0082] The proteins listed in FIG. **21** are believed to be particularly important for apicomplexan parasite bradyzoite development and/or survival in the host. Thus, targeting expression and/or activity of these proteins from the apicomplexan parasite will be effective to inhibit bradyzoite development and/or survival in the host.

[0083] EGS transcripts in HHF, MM6, and NSC cells were enriched for genes transcribed in bradyzoites, including known bradyzoite transcripts, certain Apetela 2s and cytochrome b and other cytochromes (FIG. **7***b-c*). Among transcripts with the most increased fold change in EGS across all three cell lines were: cytochrome b; cytochrome c oxidase subunit III subfamily protein; apocytochrome b; cytochrome b, putative; and cytochrome b (N-terminal)/b6/petB subfamily protein. Other over-expressed genes include bradyzoite transcription factor AP2IX-9 and plant-like heat-shock protein BAG1 (FIG. **7** *a-c*). The up- or down-regulated genes identified in the parasite transcriptome study are thus targets against which to identify drugs for anti-apicomplexan parasite (such as *T. gondii*) therapy, by identifying test compounds that reduce expression of over-expressed genes, or promote expression of down-regulated genes. In various embodiments, positive test compounds are those that reduce expression (for up-regulated genes), or decrease expression (for down-regulated genes) of 1 or more (i.e.: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 50, 100, or more) of the up-regulated apicomplexan parasite genes in FIGS. **3-5** after host cell infection by at least 5%, 10%, 15%, 20%, 25%, 50%, 75%, 90%, or more. The drug screening assays may employ the cell lines and non-human animal models of the present invention. In one embodiment, the methods comprise identifying test compounds that reduce expression from the apicomplexan parasite after cell infection of 1 or more of cytochrome b; cytochrome c oxidase subunit III subfamily protein; apocytochrome b, cytochrome b, putative, cytochrome b (N-terminal)/b6/petB subfamily protein, bradyzoite transcription factor AP2IX-9 and plant-like heat-shock protein BAG1.

[0084] In another aspect, the invention provides compositions comprising a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIGS. **3-5**, complements thereof, or their expression products, or functional equivalents thereof wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in the EGS strain of *T. gondii* after infection of human fibroblasts, neuronal stem cells or monocytic lineage cells.

[0085] Functional equivalents are allelic variants of the recited marker from other *T. gondii* strains. In one embodiment, the markers include two or more of apetela 2 transcription factors, cytochrome b, cytochrome oxidase, or functional equivalents thereof. The markers may further comprise one or more of enolase 1, lactate dehydrogenase 2, bradyzoite antigen 1 and cyst wall protein, or functional equivalents thereof. In another embodiment,

[0086] In a further aspect, the invention provides a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIG. **1-2**, complements thereof, or their expression products, or functional equivalents thereof, wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in human fibroblasts, neuronal stem cells or monocytic lineage cells after infection with *T. gondii*, including but not limited to infection with the EGS strain of *T. gondii.*

[0087] In one embodiment of each of these aspects, the plurality of isolated probes comprises polynucleotide probes. In another embodiment, the plurality of isolated probes comprises antibody probes. In all of the above embodiments, the isolated probes can be labelled with a detectable label. Methods for detecting the label include, but are not limited to spectroscopic, photochemical, biochemical, immunochemical, physical or chemical techniques. Any suitable detectable label can be used.

[0088] The compositions can be stored frozen, in lyophilized form, or as a solution. In one embodiment, the compositions can be placed on a solid support, such as in a microarray or microplate format; this embodiment facilitates use of the compositions in various detection assays.

[0089] The compositions of the invention can be used, for example, to test patient samples for up-regulation or down-regulation of the one or more markers disclosed in the figures, to assist in diagnosing a subject as having an apicomplexan parasite infection (such as *T. gondii*) or to monitor treatment of a subject receiving therapy for an apicomplexan-associated disorder. In one embodiment, such methods comprise testing the patient samples for increased expression of at least 1, 2, 3, 4, 5, 6, or all 7 of apetela 2 transcription factors, cytochrome b, cytochrome oxidase, enolase 1, lactate dehydrogenase 2, bradyzoite antigen 1 and cyst wall protein, or functional equivalents thereof.

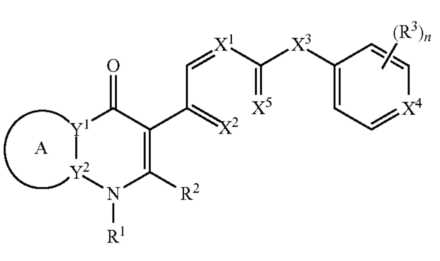
[0090] In one embodiment, the transcriptome provides the signature of cytochrome b as an important part of the bradyzoite transcriptional pathways and a signature that demonstrates effective inhibition of cytochrome b with abrogation of the signature when treatment is with an inhibitor of cytochrome b, which when used early after infection can confirm selectivity of compound. Cytochrome b functions for pyrimidine synthesis in *Plasmodium falciparum* so that it will be synergistic or additive in effect with inhibitors of DHODH.

[0091] The invention thus also provides pathway to improved inhibitors of cytochrome b through co-crystallography that defines the chemical space and pi stacking which facilitates design of improved medicines and their delivery into tachyzoites and bradyzoites using molecular transporters such as octaargine, or carbonate, and also improves their solubility and access to encysted bradyzoites.

[0092] In various embodiments, the methods for monitoring treatment of an apicomplexan parasitic infection (such as a *T. gondii* infection), comprising monitoring expression, protein in serum or plasma, and/or activity of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or all of the markers listed in FIGS. **1-5** (such as a human subject) being treated for an apicomplexan parasitic infection, wherein a decrease or increase in expression and/or presence and/or activity of the one or more markers indicates that the treatment is effective. In one exemplary embodiment, infection is in the subject's brain or other neurologic tissue.

[0093] In another aspect, the present disclosure provides compounds having the structure of Formula (I):

(I)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

[0094] wherein

[0095] ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

[0096] wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

[0097] Y^1 is C or N;

[0098] Y^2 is C or N;

[0099] X^1 is $C(R^{x1})$ or N,

[0100] wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0101] X^2 is $C(R^{x2})$ or N,

[0102] wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0103] X^3 is O, N(R), S or C_{1-3}alkyl;

[0104] X^4 is C or N;

[0105] X^5 is C or N;

[0106] R^1 is hydrogen or $_{1-3}$alkyl;

[0107] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

[0108] n is 0, 1, 2, 3 or 4;

[0109] each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

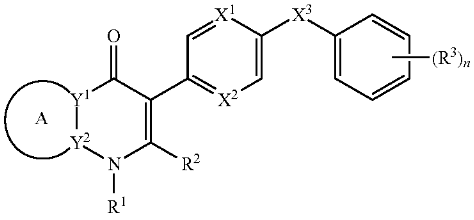
[0110] or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

[0111] each R is independently hydrogen or C_{1-3}alkyl.

[0112] The compounds of the invention have been demonstrated in the examples herein as useful, for example, in treating diseases associated with apicomplexan parasite infection.

[0113] In some embodiments, the compounds are of Formula (Ia):

(Ia)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

[0114] wherein

[0115] ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

[0116] wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3} haloalkyl, —C(O)OR, cyano or phenyl;

[0117] Y^1 is C or N;

[0118] Y^2 is C or N;

[0119] X^1 is $C(R^{x1})$ or N,

[0120] wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0121] X^2 is $C(R^{x2})$ or N,

[0122] wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0123] X^3 is O, N(R), S or C_{1-3}alkyl;

[0124] R^1 is hydrogen or C_{1-3}alkyl;

[0125] R^2 is hydrogen, C_{1-3}alkyl or —C(O)OR;

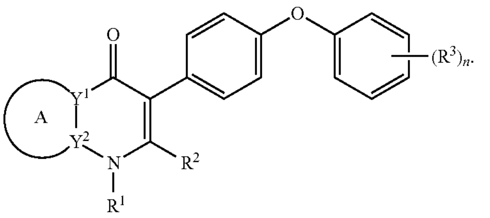
[0126] n is 0, 1, 2, 3 or 4;

[0127] each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5; and

[0128] each R is independently hydrogen or C_{1-3}alkyl.

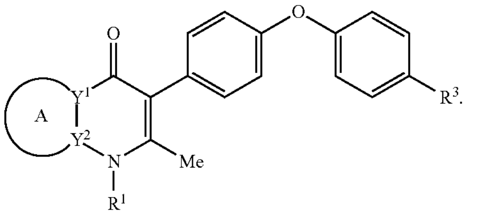
[0129] In some embodiments, the compounds are of Formula (Ib):

(Ib)



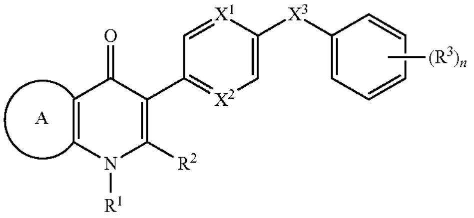
[0130] In some embodiments, the compounds are of Formula (Ic):

(Ic)



[0131] In some embodiments, the compounds are of Formula (II):

(II)

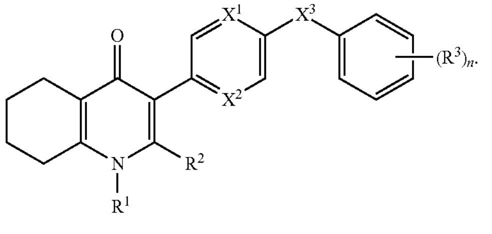


wherein

[0132] ring A combines with the carbon atoms with which it is attached to form a C_{3-7}cycloalkenyl.

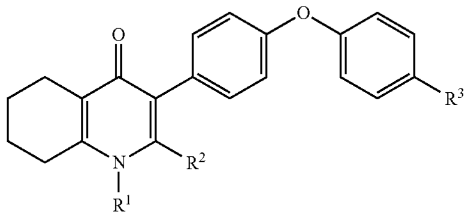
[0133] In some embodiments, the compounds are of Formula (IIa):

(IIa)



[0134] In some embodiments, the compounds are of Formula (IIa-1):

(IIa-1)

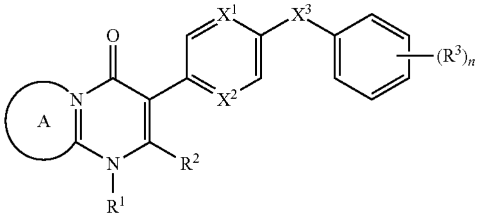


wherein

[0135] R^3 is hydrogen, halogen, C_{1-3}alkyl or C_{1-3}haloalkyl.

[0136] In some embodiments, the compounds are of Formula (III):

(III)

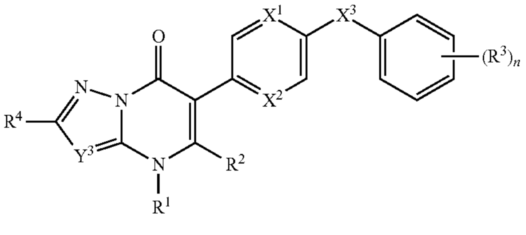


wherein

[0137] ring A combines with the nitrogen atom and carbon atom with which it is attached to form a heteroaryl ring.

[0138] In some embodiments, the compounds are of Formula (IIIa):

(IIIa)



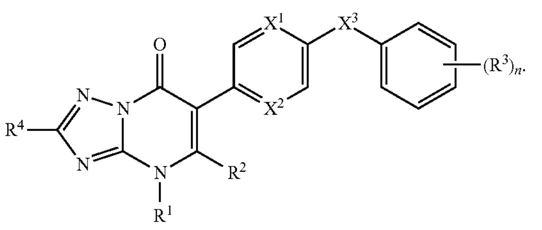
wherein

[0139] Y^3 is $C(R^5)$ or N; and

[0140] R^4 and R^5 are independently hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl.

[0141] In some embodiments, the compounds are of Formula (IIIb):

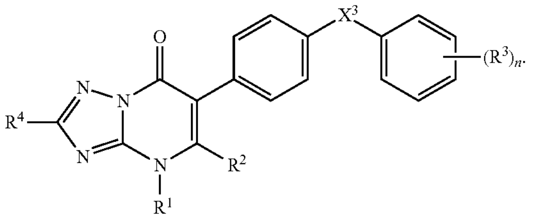
(IIIb)



[0142] In some embodiments, the compounds are of R^4 is hydrogen or C_{1-3}alkyl.

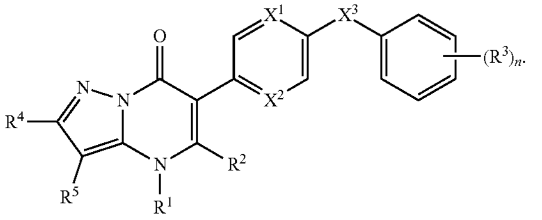
[0143] In some embodiments, the compounds are of Formula (IIIb-1):

(IIIb-1)



[0144] In some embodiments, the compounds are of Formula (IIIc):

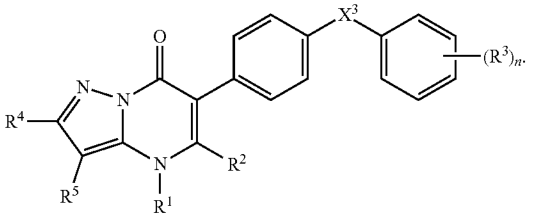
(IIIc)



[0145] In some embodiments,
R^4 is hydrogen or C_{1-3}alkylor phenyl; and
R^5 is hydrogen or cyano.

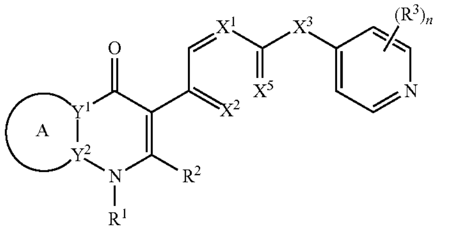
[0146] In some embodiments, the compounds are of Formula (IIIc-1):

(IIIc-1)



[0147] In some embodiments, the compounds are of Formula (IV):

(IV)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

[0148] wherein

[0149] ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

[0150] wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3} haloalkyl, —C(O)OR, cyano or phenyl;

[0151] Y^1 is C or N;

[0152] Y^2 is C or N;

[0153] X^1 is $C(R^{x1})$ or N,

[0154] wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0155] X^2 is $C(R^{x2})$ or N,

[0156] wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

[0157] X^3 is O, N(R), S or C_{1-3}alkyl;

[0158] X^5 is C or N;

[0159] R^1 is hydrogen or C_{1-3}alkyl;

[0160] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

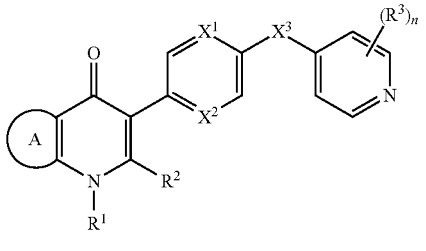
[0161] n is 0, 1, 2, 3 or 4;

[0162] each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5; and

[0163] each R is independently hydrogen or C_{1-3}alkyl.

[0164] In some embodiments, the compounds are of Formula (IVa):

(IVa)

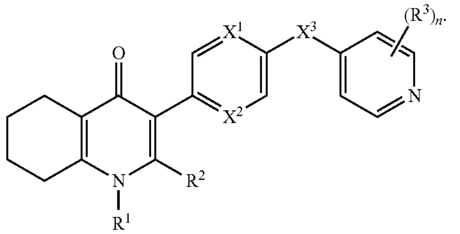


wherein

[0165] ring A combines with the carbon atoms with which it is attached to form a C_{3-7}cycloalkenyl.

[0166] In some embodiments, the compounds are of Formula (IVb):

(IVb)



[0167] In some embodiments, Y^1 is C. In other embodiments, Y^1 is N.

[0168] In some embodiments, Y^2 is C. In other embodiments, Y^2 is N.

[0169] In some embodiments, Y^1 is C. In other embodiments, Y^1 is N.

[0170] In some embodiments, X^1 is $C(R^{x1})$ wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl. In other embodiments, X^1 is N.

[0171] In some embodiments, X^1 is $C(R^{x1})$ wherein R^{x1} is selected from any of groups (1a)-(1x):

[0172] (1a) hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;
[0173] (1b) halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;
[0174] (1c) hydrogen;
[0175] (1d) halogen or C_{1-3}haloalkyl;
[0176] (1e) halogen or C_{1-3}alkyl;
[0177] (1f) C_{1-3}alkyl;
[0178] (1g) hydrogen, methyl or ethyl;
[0179] (1h) methyl or ethyl;
[0180] (1i) methyl;
[0181] (1j) ethyl;
[0182] (1k) propyl;
[0183] (1l) hydrogen, methyl or propyl;
[0184] (1m) methyl or propyl;
[0185] (1n) hydrogen, ethyl or propyl;
[0186] (1o) ethyl or propyl;
[0187] (1p) C_{1-3}haloalkyl;
[0188] (1q) C_{1-3}fluoralkyl;
[0189] (1r) fluoromethyl
[0190] (1s) difluoromethyl
[0191] (1t) trifluoromethyl
[0192] (1u) fluoromethyl
[0193] (1v) fluoropropyl
[0194] (1w) —CH_2OH;
[0195] (1x) —CH_2OR;

[0196] In some embodiments, X^2 is $C(R^{x2})$ wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl. In other embodiments, X^2 is N.

[0197] In some embodiments, X^2 is $C(R^{x2})$ wherein R^{x2} is selected from any of groups (2a)-(2x):

[0198] (2a) hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;
[0199] (2b) halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;
[0200] (2c) hydrogen;
[0201] (2d) halogen or C_{1-3}haloalkyl;
[0202] (2e) halogen or C_{1-3}alkyl;
[0203] (2f) C_{1-3}alkyl;
[0204] (2g) hydrogen, methyl or ethyl;
[0205] (2h) methyl or ethyl;
[0206] (2i) methyl;
[0207] (2j) ethyl;
[0208] (2k) propyl;
[0209] (2l) hydrogen, methyl or propyl;
[0210] (2m) methyl or propyl;
[0211] (2n) hydrogen, ethyl or propyl;
[0212] (2o) ethyl or propyl;
[0213] (2p) C_{1-3}haloalkyl;
[0214] (2q) C_{1-3}fluoralkyl;
[0215] (2r) fluoromethyl
[0216] (2s) difluoromethyl
[0217] (2t) trifluoromethyl
[0218] (2u) fluoromethyl
[0219] (2v) fluoropropyl
[0220] (2w) —CH_2OH;
[0221] (2x) —CH_2OR;

[0222] In some embodiments, X^3 is selected from any of groups (3a)-(3p):

[0223] (3a) O, N(R), S or C_{1-3}alkyl;
[0224] (3b) O, N(R) or S;
[0225] (3c) O or N(R);
[0226] (3d) 0;
[0227] (3e) N(R);
[0228] (3f) S or C_{1-3}alkyl;
[0229] (3g) O, N(R), or C_{1-3}alkyl;
[0230] (3h) O or C_{1-3}alkyl;
[0231] (3i) N(R), S or C_{1-3}alkyl;
[0232] (3j) N(R) or C_{1-3}alkyl;
[0233] (3k) O or C_{1-3}alkyl;
[0234] (3l) C_{1-3}alkyl;
[0235] (3m) methylene
[0236] (3n) ethylene;
[0237] (3o) propylene;
[0238] (3p) NH.

[0239] In some embodiments, X^4 is C. In other embodiments, X^4 is N.

[0240] In some embodiments, X^5 is C. In other embodiments, X^5 is N.

[0241] In some embodiments, R^1 is selected from any of groups (4a)-(4l):

[0242] (4a) hydrogen or C_{1-3}alkyl;
[0243] (4b) hydrogen;
[0244] (4c) C_{1-3}alkyl;
[0245] (4d) hydrogen, methyl or ethyl;
[0246] (4e) methyl or ethyl;
[0247] (4f) methyl;
[0248] (4g) ethyl;
[0249] (4h) propyl;
[0250] (4i) hydrogen, methyl or propyl;
[0251] (4j) methyl or propyl;
[0252] (4k) hydrogen, ethyl or propyl;
[0253] (4l) ethyl or propyl;

[0254] In some embodiments, R^2 is selected from any of groups (5a)-(5gg):

[0255] (5a) hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;
[0256] (5b) C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;
[0257] (5c) hydrogen, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;
[0258] (5d) hydrogen, C_{1-3}alkyl, —CH_2OH, —CH_2OR or —C(O)OR;
[0259] (5e) hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OR or —C(O)OR;

[0260] (5f) hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, or —C(O)OR;

[0261] (5g) hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, or —CH_2OR;

[0262] (5h) hydrogen or C_{1-3}alkyl;

[0263] (5i) hydrogen;

[0264] (5j) C_{1-3}alkyl;

[0265] (5k) hydrogen, methyl or ethyl;

[0266] (5l) methyl or ethyl;

[0267] (5m) methyl;

[0268] (5n) ethyl;

[0269] (5o) propyl;

[0270] (5p) hydrogen, methyl or propyl;

[0271] (5q) methyl or propyl;

[0272] (5r) hydrogen, ethyl or propyl;

[0273] (5s) ethyl or propyl;

[0274] (5t) C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

[0275] (5u) C_{1-3}haloalkyl;

[0276] (5v) C_{1-3}fluoralkyl;

[0277] (5w) fluoromethyl

[0278] (5x) difluoromethyl

[0279] (5y) trifluoromethyl

[0280] (5z) fluoromethyl

[0281] (5aa) fluoropropyl

[0282] (5bb) —CH_2OH;

[0283] (5cc) —CH_2OR;

[0284] (5dd) —C(O)OR;

[0285] (5ee) —C(O)OH;

[0286] (5ff) —C(O)OMe;

[0287] (5gg) —C(O)OEt

[0288] In some embodiments, n is selected from any of groups (6a)-(6k):

[0289] (6a) n is 1, 2, 3, or 4.

[0290] (6b) n is 0, 1, 2, or 3.

[0291] (6c) n is 0, 1, or 2.

[0292] (6d) n is 0 or 1.

[0293] (6e) n is 1 or 2.

[0294] (6f) n is 2 or 3.

[0295] (6g) n is 1.

[0296] (6h) n is 2.

[0297] (6i) n is 3.

[0298] (6j) n is 4.

[0299] (6k) n is 0.

[0300] In some embodiments, R^3 is selected from any of groups (7a)-(7cc):

[0301] (7a) each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, SF_5, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0302] (7b) each R^3 is independently C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3} haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0303] (7c) each R^3 is independently halogen, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0304] (7d) each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0305] (7e) each R^3 is independently halogen, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0306] (7f) each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0307] (7g) each R^3 is independently C_{1-3}alkyl, C_{1-3}alkoxy, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0308] (7h) each R^3 is independently —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0309] (7i) each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3} haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

[0310] (7j) each R^3 is independently halogen, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —C(O)OR, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0311] (7k) each R^3 is independently halogen, C_1haloalkyl, —O—C_1haloalkyl, —C(O)OR, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0312] (7l) each R^3 is independently fluoro, chloro, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —C(O)OR, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0313] (7m) each R^3 is independently fluoro, chloro, trifluoromethyl, —O—C_{1-3}haloalkyl, —C(O)OR, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0314] (7n) each R^3 is independently fluoro, chloro, trifluoromethyl, —OCF_3, —C(O)OR, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0315] (7o) each R^3 is independently fluoro, chloro, trifluoromethyl, —OCF_3, —C(O)OH, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0316] (7p) each R^3 is independently trifluoromethyl, —OCF_3, —C(O)OH, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0317] (7q) each R^3 is independently fluoro, chloro, —OCF_3, —C(O)OH, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0318] (7r) each R^3 is independently fluoro, chloro, trifluoromethyl, —OCF_3, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0319] (7s) each R^3 is independently fluoro, chloro, trifluoromethyl or —OCF_3;

[0320] (7t) each R^3 is independently fluoro, chloro, trifluoromethyl, —OCF_3 or —C(O)OH;

[0321] (7u) each R^3 is independently fluoro, chloro, trifluoromethyl or —OCF_3;

[0322] (7v) each R^3 is independently fluoro, chloro or trifluoromethyl;

[0323] (7w) each R^3 is independently fluoro or chloro;

[0324] (7x) each R^3 is independently fluoro;

[0325] (7y) each R^3 is independently chloro;

[0326] (7z) each R^3 is trifluoromethyl;

[0327] (7aa) each R^3 is —OCF_3;

[0328] (7bb) each R^3 is —C(O)OH;

[0329] (7cc) two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

[0330] In some embodiments, R is selected from any of groups (8a)-(8l):

- **[0331]** (8a) hydrogen or C_{1-3}alkyl;
- **[0332]** (8b) hydrogen;
- **[0333]** (8c) C_{1-3}alkyl;
- **[0334]** (8d) hydrogen, methyl or ethyl;
- **[0335]** (8e) methyl or ethyl;
- **[0336]** (8f) methyl;
- **[0337]** (8g) ethyl;
- **[0338]** (8h) propyl;
- **[0339]** (8i) hydrogen, methyl or propyl;
- **[0340]** (8j) methyl or propyl;
- **[0341]** (8k) hydrogen, ethyl or propyl;
- **[0342]** (8l) ethyl or propyl;

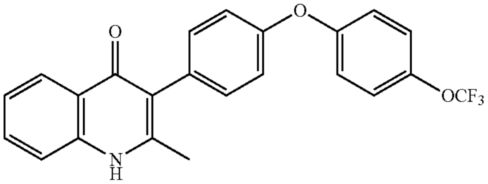
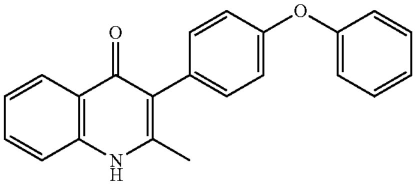
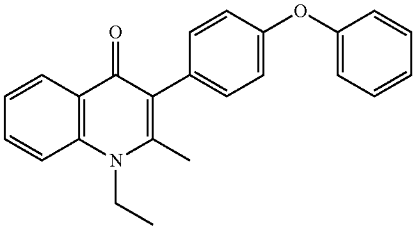
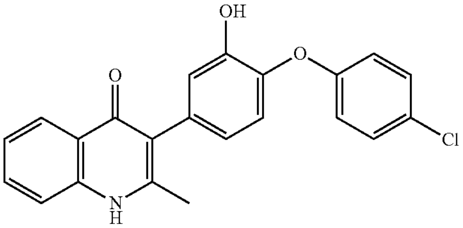
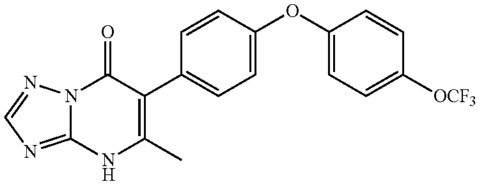
[0343] In some embodiments, the compound is of Formula (I), (Ia), (Ib) or (Ic), and X^1, X^2, X^3, R^1, R^2, R^3 and n are selected from any combination of groups (1a)-(8l).

[0344] In some embodiments, the compound is of Formula (II), (IIa) or (IIa-1), and X^1, X^2, X^3, R^1, R^2, R^3 and n are selected from any combination of groups (1a)-(8l).

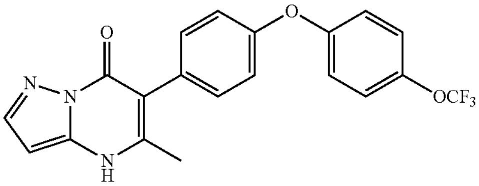
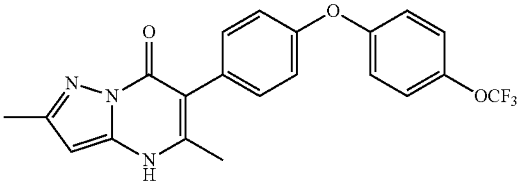
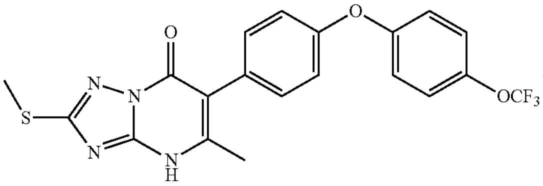
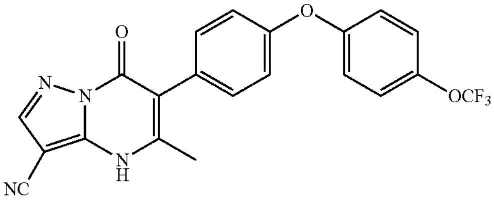
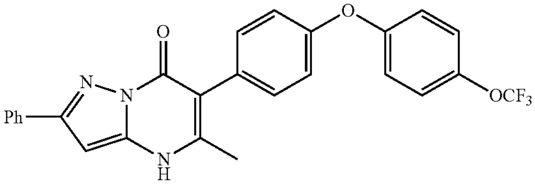
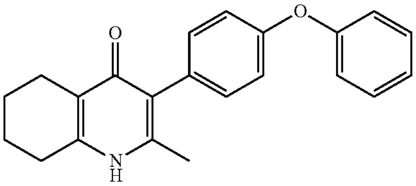
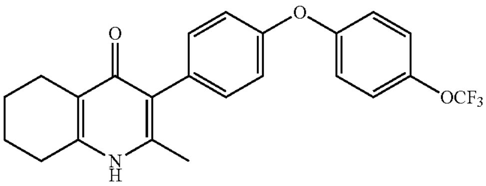
[0345] In some embodiments, the compound is of Formula (III), (IIIa), (IIIb), (IIIb-1), (IIIc) or (IIIc-1), and X^1, X^2, X^3, R^1, R^2, R^3 and n are selected from any combination of groups (1a)-(8l).

[0346] In some embodiments, the compound is of Formula (IV), (IVa) or (IVb) and X^1, X^2. X^3, R^1, R^2, R^3 and n are selected from any combination of groups (1a)-(8l).

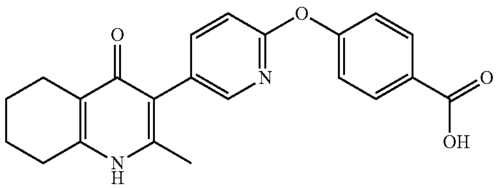
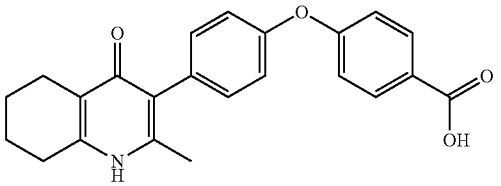
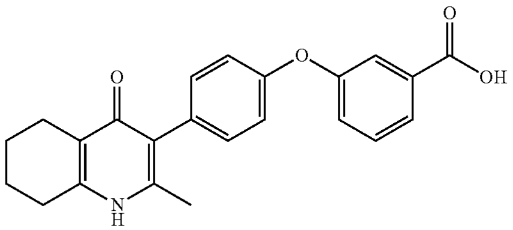
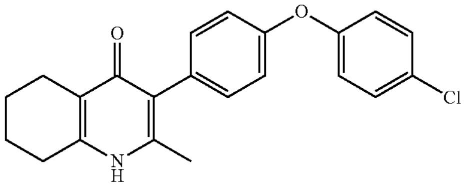
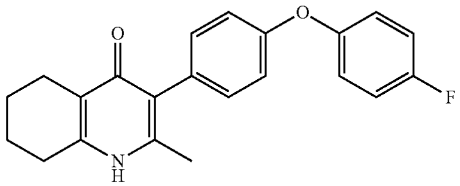
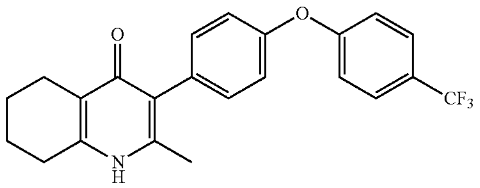
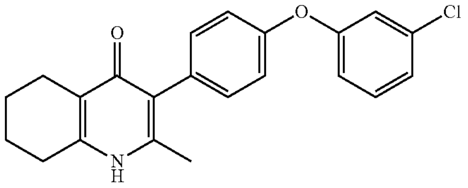
[0347] In some embodiments, the compound is:

No.	ID	Structure	Name
		ELQ-type systems	
PA1	MJM102/ MJM113 (ELQ- 271)		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl) quinolin-4(1H)-one
PA2	MJM 129		2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one
PA3	JM10		1-ethyl-2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one
PA4	RG38		3-(4-(4-chlorophenoxy)-3-hydroxyphenyl)-2-methylquinolin-4(1H)-one
		5,6-fused pyridone systems	
1	MJM136		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one

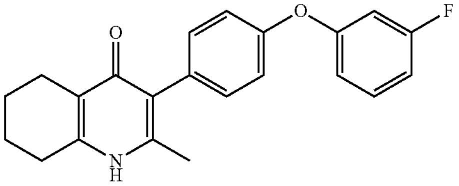
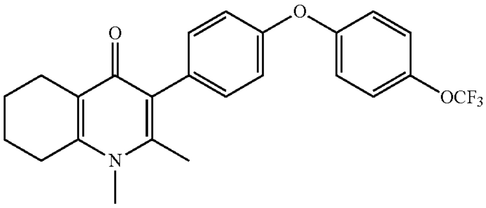
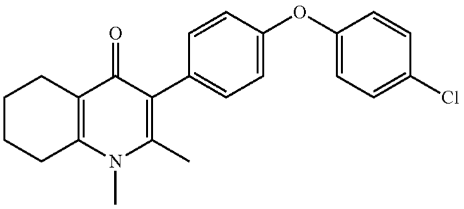
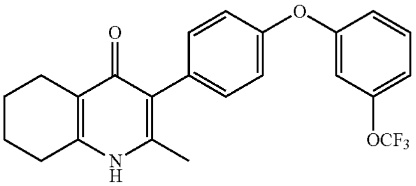
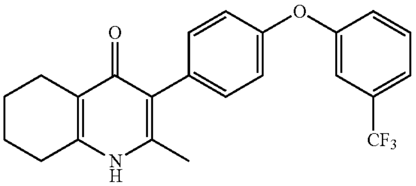
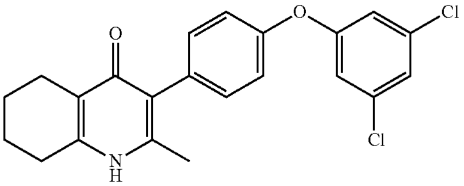
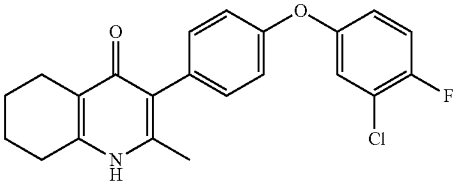
-continued

No.	ID	Structure	Name
2	MJM141		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
3	JAG006		2,5-dimethyl-6-(4 (4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
4	JAG013		5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
5	JAG014		5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile
6	JAG015		5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
		Tetrahydroquinolones (THQ)	
7	MJM170		2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquino1in-4(1H)-one
8	JAG21		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

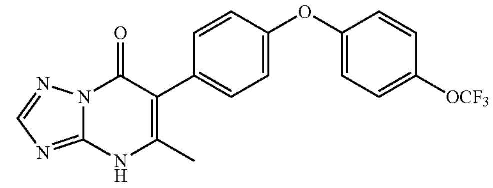
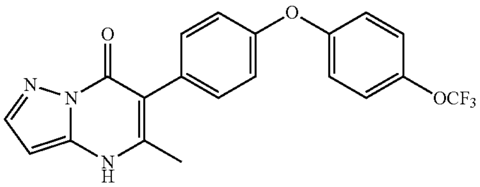
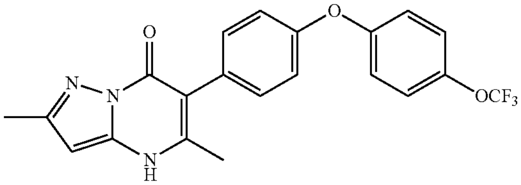
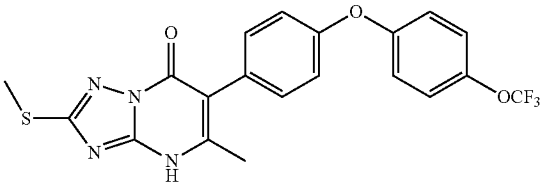
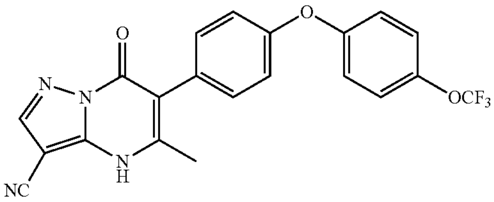
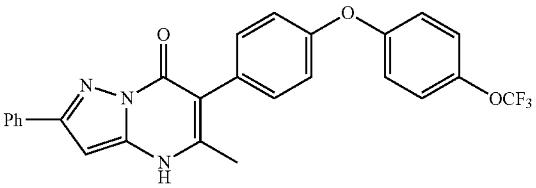
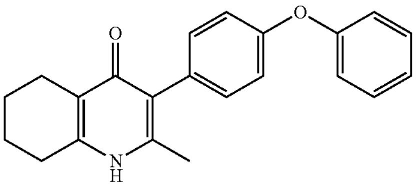
No.	ID	Structure	Name
9	JAG039		4-((5-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)pyridin-2-yl)oxy)benzoic acid
10	JAG046		4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
11	JAG047		3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
12	JAG50		3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
13	JAG58		3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
14	JAG63		2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
15	JAG062		3-(4-(3-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

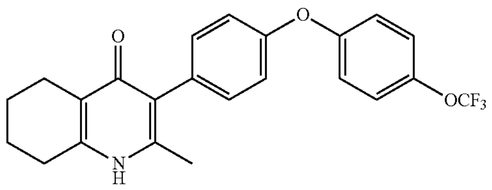
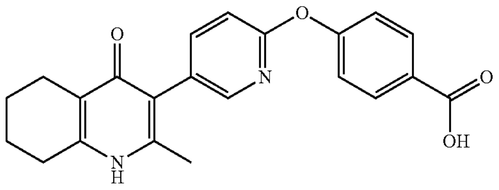
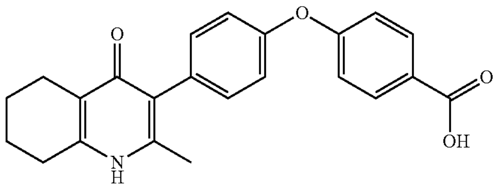
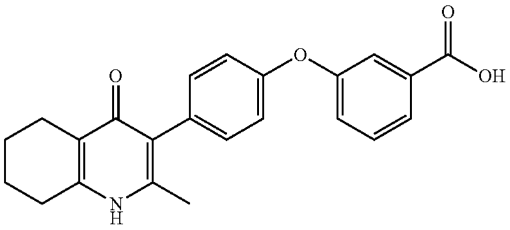
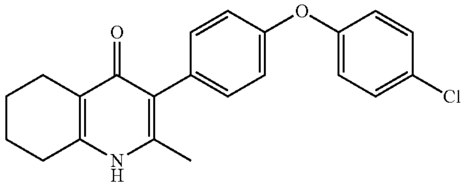
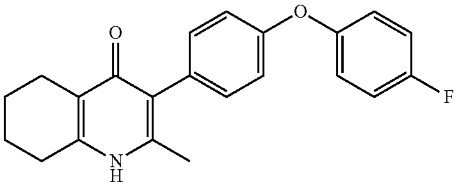
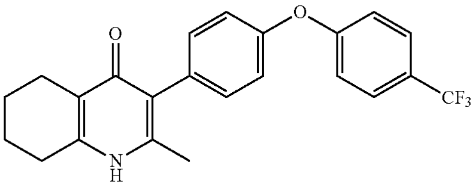
No.	ID	Structure	Name
16	JAG067		3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
17	JAG023		1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
18	JAG077		3-(4-(4-chlorophenoxy)phenyl)-1,2-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
19	AS006		2-methyl-3-(4 (3-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
20	AS0012		2-methyl-3-(4-(3-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
21	AS021		3-(4-(3,5-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
22	AS022		3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof.

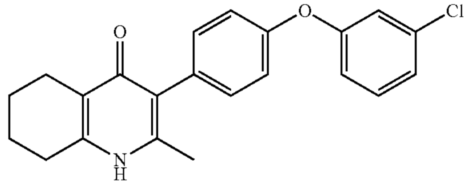
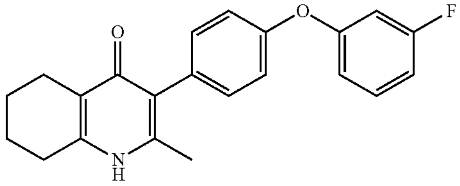
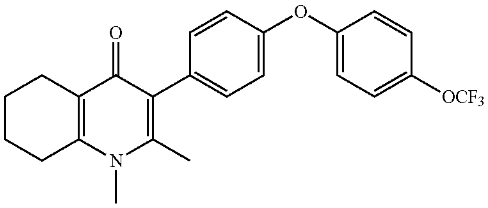
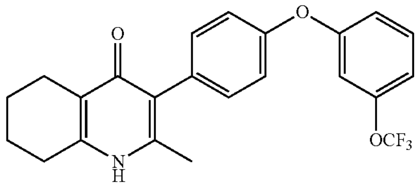
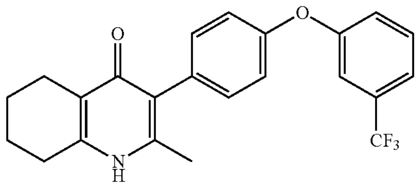
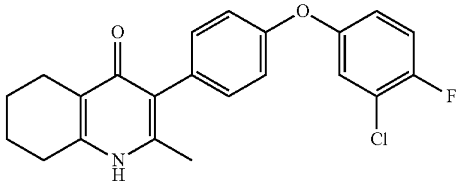
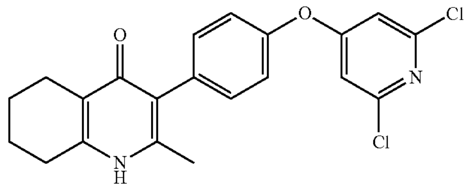
[0348] In some embodiments, the compound is:

ID	Structure	Name
MJM136		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
MJM141		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
JAG006		2,5-dimethyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazool[1,5-a]pyrimidin-7(4H)-one
JAG013		5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo [1,5-a]pyrimidin-7(4H)-one
JAG014		5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile.
JAG015		5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one.
MJM170		2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

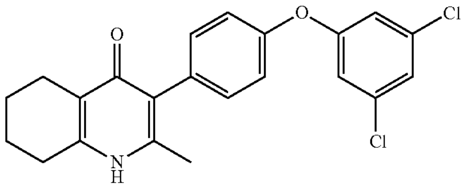
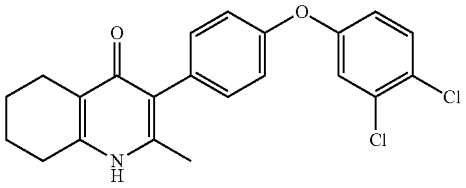
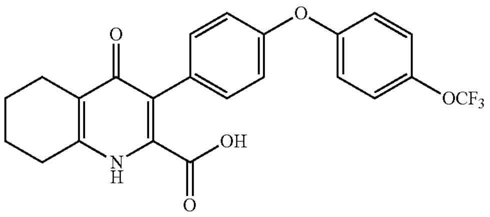
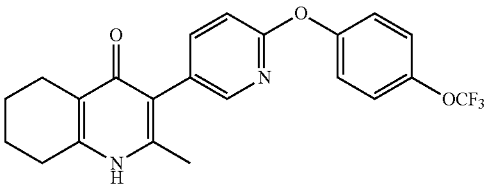
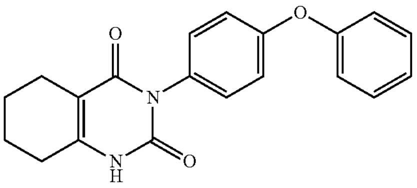
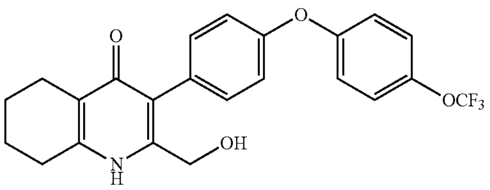
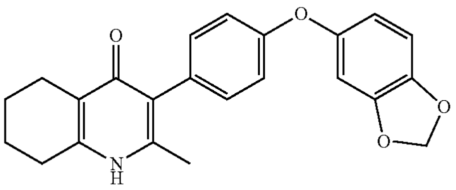
-continued

ID	Structure	Name
JAG21		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG039		methyl 3-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate
JAG046		4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
JAG047		3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
JAG50		3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG58		3-(4-(4-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG63		2-Methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

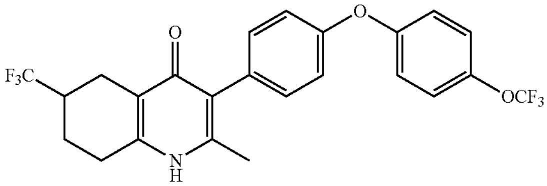
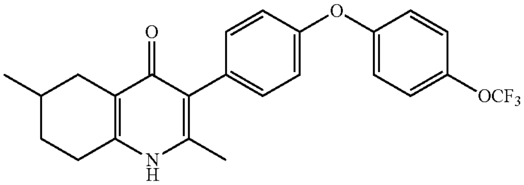
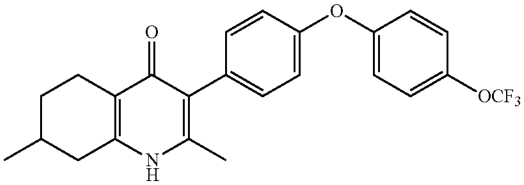
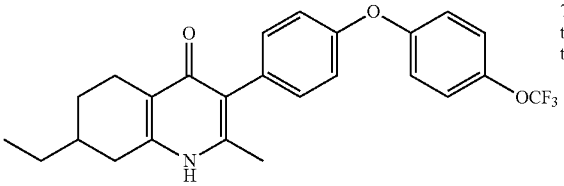
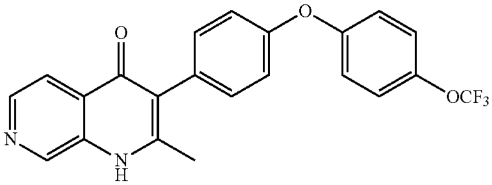
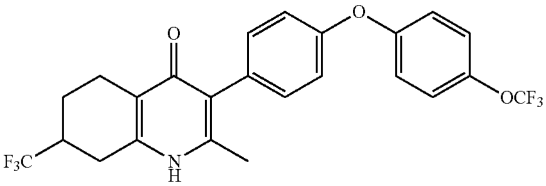
-continued

ID	Structure	Name
JAG062		3-(4-(3-Chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG069		3-(4-(3-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG023		1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4-one
AS006/ JAG143		3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
AS012/ JAG144		3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
AS021/ JAG145		3-[4-(3-chloro-4-fluorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
AS034/ JAG148		3-{4-[(2,6-dichloropyridin-4-yl)oxy]phenyl}-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

-continued

ID	Structure	Name
AS022		3-[4-(3,5-dichlorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4(1H)-one
JAG084		3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG091		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG092		3-(6-(4-Trifluoromethoxyphenoxy)pyrdin-3-yl) -2-methyl-5,6,7,8-tetrahydroquinolin-(4)-one
JAG095		3-(4-Phenonxyphenyl)-1,2,3,4,5,6,7,8-octahydroquinazoline-2,4,dione
JAG099		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(methylhydroxy)-5,6,7,8-tetrahydroquinolin-4(1H)-one
AS032		3-[4-(2H-1,3-benzodioxo1-5-yloxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

-continued

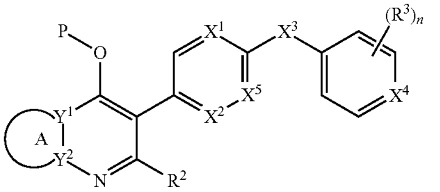
ID	Structure	Name
JAG100		6-Ethyl-3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG106		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG107		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG121		7-Ethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JA129		3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-napthyrid-4(1H)-one
JAG162		7-Trifluromethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

[0349] or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof.

[0350] In another aspect, the invention provides prodrugs of a compound of Formula (I). The term “prodrug” is intended to represent covalently bonded carriers, which are capable of releasing the active ingredient when the prodrug is administered to a mammalian subject. Release of the active ingredient occurs in vivo. Prodrugs can be prepared by techniques known to one skilled in the art. These techniques generally modify appropriate functional groups in a given compound. These modified functional groups however regenerate original functional groups by routine manipulation or in vivo. Prodrugs of compounds of the invention include compounds wherein an amino, hydroxy, carboxylic or a similar group is modified. Examples of prodrugs include, but are not limited to esters (e.g., acetate, formate, and benzoate), carbamates (e.g., N,N-dimethylaminocarbonyl), amides (e.g., trifluoroacetylamino, acetylamino, and the like), and the like. A complete discussion of prodrugs is found in Huttunen, K. M. and Rautio *J. Current Topics in Medicinal Chemistry,* 2011, 11, 2265-2287 and Stella, V. J. et al. (2007). *Prodrugs: Challenges and Awards Part* 1. New York: Springer. The disclosure of both references is herein incorporated by reference in its entirety.

[0351] In some embodiments, the prodrug of a compound of Formula (I) has the structure of Formula (I-p):

(I-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

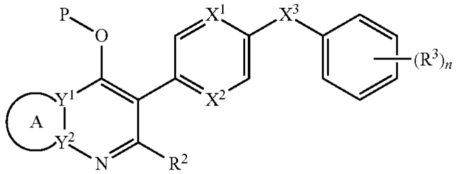
[0352] ring A, Y^1, Y^2, X^1, X^2, X^3, X^4, X^5, R, R^3 and n are as described above;

[0353] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0354] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0355] In some embodiments, the prodrug is a compound of Formula (Ia-p):

(Ia-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

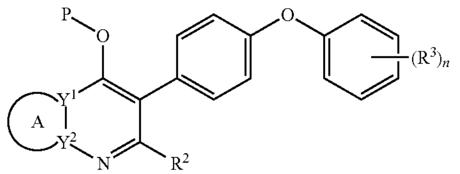
[0356] ring A, Y^1, Y^2, X^1, X^2, X^3, R, R^2, R^3 and n are as described above;

[0357] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0358] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0359] In some embodiments, the prodrug is a compound of Formula (Ib-p):

(Ib-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

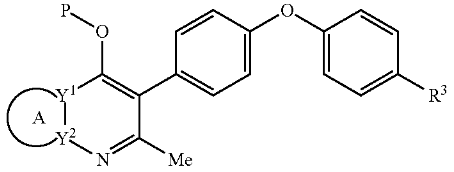
[0360] ring A, Y^1, Y^2, R, R^2, R^3 and n are as described above;

[0361] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0362] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0363] In some embodiments, the prodrug is a compound of Formula (Ic-p):

(Ic-p)



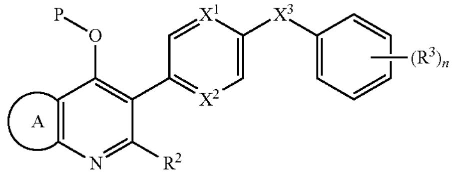
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

[0364] ring A, Y^1, Y^2, R and R^3 are as described above; and

[0365] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0366] In some embodiments, the prodrug is a compound of Formula (II-p):

(II-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

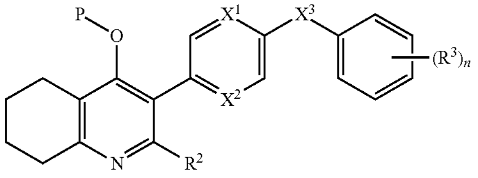
[0367] ring A, X^1, X^2, X^3, R, R^2, R^3 and n are as described above;

[0368] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0369] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0370] In some embodiments, the prodrug is a compound of Formula (IIa-p):

(IIa-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

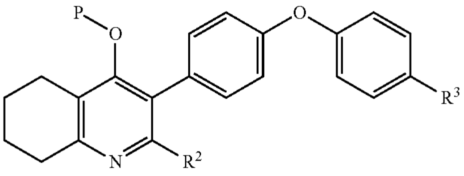
[0371] X^1, X^2, X^3, R, R^2, R^3 and n are as described above;

[0372] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0373] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0374] In some embodiments, the prodrug is a compound of Formula (IIa-1-p):

(IIa-1-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

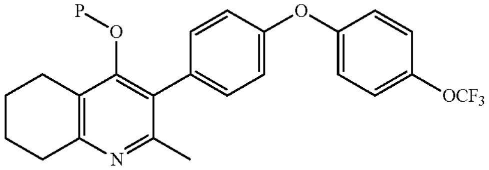
[0375] R, R^2, R^3 and n are as described above;

[0376] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0377] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0378] In some embodiments, the prodrug is a compound of Formula (IIa-2-p):

(IIa-2-p)

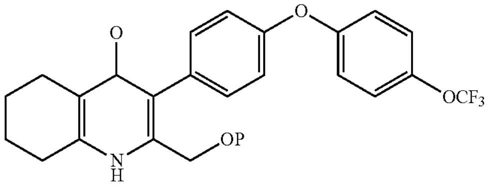


or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

[0379] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0380] In some embodiments, the prodrug is a compound of Formula (IIa-3-p):

(IIa-3-p)

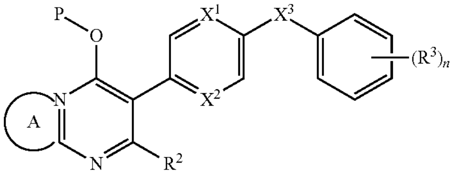


or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

[0381] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0382] In some embodiments, the prodrug is a compound of Formula (III-p):

(III-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

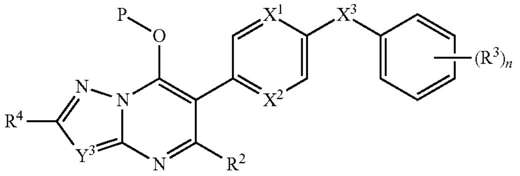
[0383] ring A, X^1, X^2, X^3, R, R^2, R^3 and n are as described above;

[0384] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0385] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0386] In some embodiments, the prodrug is a compound of Formula (IIIa-p):

(IIIa-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

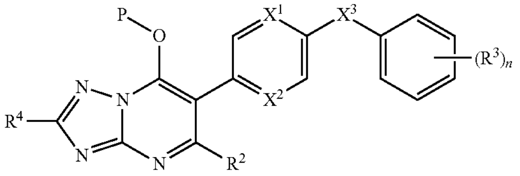
[0387] Y^3, X^1, X^2, X^3, R, R^2, R^3, R^4 and n are as described above;

[0388] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0389] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0390] In some embodiments, the prodrug is a compound of Formula (IIIb-p):

(IIIb-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

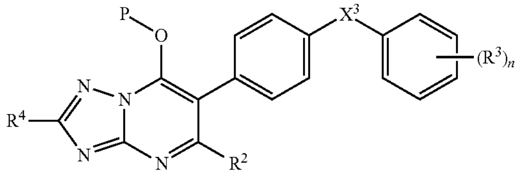
[0391] X^1, X^2, X^3, R, R^2, R^3, R^4 and n are as described above;

[0392] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0393] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C$_{1-3}$alkyl.

[0394] In some embodiments, the prodrug is a compound of Formula (IIIb-1-p):

(IIIb-1-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

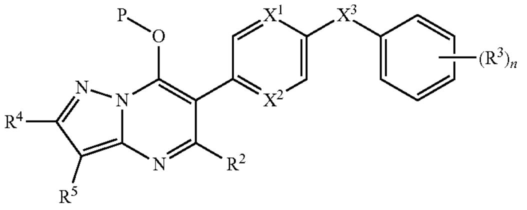
[0395] X^3, R, R^2, R^3, R^4 and n are as described above;

[0396] R^2 is hydrogen, C$_{1-3}$alkyl, C$_{1-3}$haloalkyl, —CH$_2$OR, —C(O)OR or —CH$_2$OP; and

[0397] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C$_{1-3}$alkyl.

[0398] In some embodiments, the prodrug is a compound of Formula (IIIc-p):

(IIIc-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

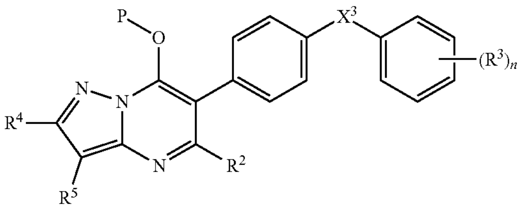
[0399] X^1, X^2, X^3, R, R^2, R^3, R^4, R^5 and n are as described above;

[0400] R^2 is hydrogen, C$_{1-3}$alkyl, C$_{1-3}$haloalkyl, —CH$_2$OH, —CH$_2$OR, —C(O)OR or —CH$_2$OP; and

[0401] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C$_{1-3}$alkyl.

[0402] In some embodiments, the prodrug is a compound of Formula (IIIc-1-p):

(IIIc-1-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

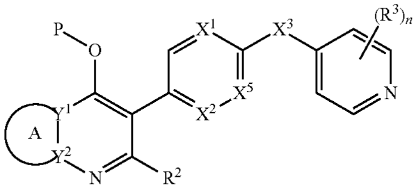
[0403] X^3, R, R^2, R3, R^4, R^5 and n are as described above;

[0404] R^2 is hydrogen, C$_{1-3}$alkyl, C$_{1-3}$haloalkyl, —CH$_2$OH, —CH$_2$OR, —C(O)OR or —CH$_2$OP; and

[0405] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C$_{1-3}$alkyl.

[0406] In some embodiments, the prodrug is a compound of Formula (IV-p):

(IV-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

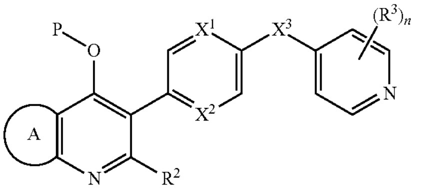
[0407] ring A, Y^1, Y^2, X^1, X^2, X^3, X^5, R, R^2, R^3 and n are as described above;

[0408] R^2 is hydrogen, C$_{1-3}$alkyl, C$_{1-3}$haloalkyl, —CH$_2$OH, —CH$_2$OR, —C(O)OR or —CH$_2$OP; and

[0409] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C$_{1-3}$alkyl.

[0410] In some embodiments, the prodrug is a compound of Formula (IVa-p):

(IVa-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

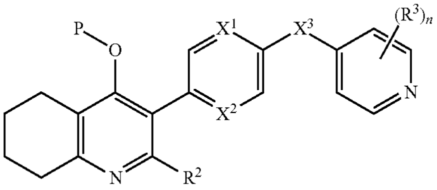
[0411] ring A, X^1, X^2, R, R^2, R^3 and n are as described above;

[0412] R^2 is hydrogen, C$_{1-3}$alkyl, C$_{1-3}$haloalkyl, —CH$_2$OH, —CH$_2$OR, —C(O)OR or —CH$_2$OP; and

[0413] P is —C(O)OR', —C(O)R', —C(O)NR'$_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C$_{1-3}$alkyl.

[0414] In some embodiments, the prodrug is a compound of Formula (IVb-p):

(IVb-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

[0415] X^1, X^2, X^3, R, R^2, R^3 and n are as described above;

[0416] R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP; and

[0417] P is —C(O)OR', —C(O)R', —$C(O)NR'_2$ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl.

[0418] In some embodiments, the compound is of any of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-p), (IIa-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIa-p), (IIIb-p), (IIIb-1-p), (IIIc-p), (IIIc-1-p), (IV-p), (Iva-p) or (IVb-p), and X^1, X^2, X^3, R^1, R^2, R^3 and n are selected from any combination of groups (1a)-(81).

[0419] In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-p), (IIa-1-p). (IIa-2-p), (IIa-3-p), (III-p), (IIIa-p), (IIIb-p), (IIIb-1-p), (IIIc-p), (IIIc-1-p), (IV-p), (Iva-p) or (IVb-p), X^1, X^2, X^3, R^1, R^2, R^3 and n are selected from any combination of groups (1a)-(81), and P is —$C(O)_2R'$.

[0420] In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-p), (IIa-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIa-p), (IIIb-p), (IIIb-1-p), (IIIc-p), (IIIc-1-p), (IV-p), (Iva-p) or (IVb-p), X^1, X^2, X^3, R, R^2, R^3 and n are selected from any combination of groups (1a)-(81), and P is —C(O)R'.

[0421] In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p). (Ic-p), (II-p), (Ia-p), (IIa-1-p). (IIa-2-p), (IIa-3-p), (III-p), (IIIa-p), (IIIb-p), (IIIb-1-p), (IIIc-p), (IIIc-1-p), (IV-p), (Iva-p) or (IVb-p), X^1, X^2, X^3, R, R^2, R^3 and n are selected from any combination of groups (1a)-(81), and P is —$C(O)NR'_2$.

[0422] In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-p), (IIa-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIa-p), (IIIb-p), (IIIb-1-p), (IIIc-p), (IIIc-1-p), (IV-p), (Iva-p) or (IVb-p), X^1, X^2, X^3, R, R^2, R^3 and n are selected from any combination of groups (1a)-(81), and P is —OP(O)(OR')OR'.

[0423] In another aspect, the invention provides a pharmaceutical composition comprising a compound of Formula (I-p) and a pharmaceutically acceptable diluent, excipient, or carrier.

[0424] In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I), an 8-Aminoquinoline drug and a pharmaceutically acceptable diluent, excipient, or carrier.

[0425] In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I), tafenoquine and a pharmaceutically acceptable diluent, excipient, or carrier.

[0426] In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I-p), an 8-Aminoquinoline drug and a pharmaceutically acceptable diluent, excipient, or carrier.

[0427] In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I-p), tafenoquine and a pharmaceutically acceptable diluent, excipient, or carrier.

[0428] In another aspect, the invention provides a pharmaceutical composition comprising a compound of claim Formula (I) and a pharmaceutically acceptable diluent, excipient, or carrier. In another aspect, the invention provides a method for treating an apicomplexan parasitic infection, comprising administering to a subject (such as a human subject) in need thereof an amount effective to treat the infection of the compound of Formula (I) or a pharmaceutical composition comprising a compound of Formula (I). In some embodiments of the method, the infection comprises a *Toxoplasma gondii* infection and/or a *Plasmodium falciparum* infection. In some embodiments of the method, the infection comprises an infection in the subject's brain and/or the subject's eye. In some embodiments of the method, the compound is a prodrug of Formula (I-p).

[0429] In another aspect, the invention provides a method for treating an apicomplexan parasitic infection, comprising administering to a subject (such as a human subject) in need thereof an amount effective to treat the infection of a combination comprising a compound of Formula (I) and a 8-Aminoquinoline drug or a pharmaceutical composition comprising a compound of Formula (I) and a 8-Aminoquinoline drug. In some embodiments of the method, the infection comprises a *Toxoplasma gondii* infection and/or a *Plasmodium falciparum* infection. In some embodiments of the method, the infection comprises an infection in the subject's brain and/or the subject's eye. In some embodiments of the method, the compound is a prodrug of Formula (I-p). In some embodiments of the method, the 8-Aminoquinoline drug is tafenoquine.

[0430] In some embodiments of the method, the subject is immune compromised. In some embodiments of the method, the subject is immune compromised due to cancer/cancer treatment, autoimmune disease, and/or AIDS. In some embodiments of the method, the subject has malaria, and the treating comprises reducing severity of one or more symptoms of malaria, and/or reducing recurrence of symptoms of malaria. In some embodiments of the method, the subject has toxoplasmosis, and the treating comprises reducing severity of one or more symptoms of toxoplasmosis, and/or reducing recurrence of symptoms of toxoplasmosis. In some embodiments of the method, the treating comprises reducing parasitic load in the subject. In some embodiments of the method, the treating comprises reducing the bradyzoite form and/or the tachyzoite form of the parasite in the subject. In some embodiments of the method, the method further comprises administering to the subject one or more additional compounds in an amount effective to treat the infection. In some embodiments of the method, the one or more additional compounds are selected from the group consisting of pyrimethamine, sulfadiazine, cycloguanil, inhibitors of kcalcium kinases or dense granules or vacuolar atpases, atovoquone, and bulky cytochrome Qi inhibitors, itraconazole and other inhibitors of *T. gondii.*

[0431] In another aspect, the invention provides a method for monitoring treatment of an apicomplexan parasitic infection (including but not limited to any of the treatments of claims **23-33**), comprising monitoring expression, protein in serum or plasma, and/or activity of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or all of the markers listed in Table and figures in Example 8/FIG. **8** in the Appendix in a subject (such as a human subject) being treated for an apicomplexan parasitic infection, wherein a decrease or increase in expression and/or presence and/or activity of the one or more markers indicates that the treatment is effective.

[0432] In some embodiments of the method, the infection is a *T. gondii* infection. In some embodiments of the method, the infection is in the subject's brain or other neurologic tissue.

Definitions

[0433] Terms used herein may be preceded and/or followed by a single dash, "—", or a double dash, "=", to indicate the bond order of the bond between the named substituent and its parent moiety; a single dash indicates a single bond and a double dash indicates a double bond or a pair of single bonds in the case of a spiro-substituent. In the absence of a single or double dash it is understood that a single bond is formed between the substituent and its parent moiety; further, substituents are intended to be read "left to right" unless a dash indicates otherwise. For example, alkyl, alkyl-, and -alkyl indicate the same functionality.

[0434] Further, certain terms herein may be used as both monovalent and divalent linking radicals as would be familiar to those skilled in the art, and by their presentation linking between two other moieties. For example, an alkyl group can be both a monovalent radical or divalent radical; in the latter case, it would be apparent to one skilled in the art that an additional hydrogen atom is removed from a monovalent alkyl radical to provide a suitable divalent moiety.

[0435] The term "alkoxy" as used herein, means an alkyl group, as defined herein, appended to the parent molecular moiety through an oxygen atom. Representative examples of alkoxy include, but are not limited to, methoxy, ethoxy, propoxy, 2-propoxy, butoxy, tert-butoxy, pentyloxy, and hexyloxy.

[0436] The term "alkyl" as used herein, means a straight or branched chain hydrocarbon containing from 1 to 10 carbon atoms, unless otherwise specified. Representative examples of alkyl include, but are not limited to, methyl, ethyl, n-propyl, iso-propyl, n-butyl, sec-butyl, iso-butyl, tert-butyl, n-pentyl, isopentyl, neopentyl, n-hexyl, 3-methylhexyl, 2,2-dimethylpentyl, 2,3-dimethylpentyl, n-heptyl, n-octyl, n-nonyl, and n-decyl. When an "alkyl" group is a linking group between two other moieties, then it may also be a straight or branched chain; examples include, but are not limited to $—CH_2—$, $—CH_2CH_2—$, $—CH_2CH_2CHC(CH_3)—$, $—CH_2CH(CH_2CH_3)CH_2—$.

The terms "cyano" and "nitrile" as used herein, mean a —CN group.

[0437] "Cycloalkenyl" as used herein refers to a monocyclic or a bicyclic cycloalkenyl ring system. Monocyclic ring systems are cyclic hydrocarbon groups containing from 3 to 8 carbon atoms, where such groups are unsaturated (i.e., containing at least one annular carbon-carbon double bond), but not aromatic. Examples of monocyclic ring systems include cyclopentenyl and cyclohexenyl. Bicyclic cycloalkenyl rings are bridged monocyclic rings or a fused bicyclic rings. Bridged monocyclic rings contain a monocyclic cycloalkenyl ring where two non-adjacent carbon atoms of the monocyclic ring are linked by an alkylene bridge of between one and three additional carbon atoms (i.e., a bridging group of the form $—(CH_2)_w—$, where w is 1, 2, or 3). Representative examples of bicyclic cycloalkenyls include, but are not limited to, norbomenyl and bicyclo[2.2.2]oct-2-enyl. Fused bicyclic cycloalkenyl ring systems contain a monocyclic cycloalkenyl ring fused to either a phenyl, a monocyclic cycloalkyl, a monocyclic cycloalkenyl, a monocyclic heterocyclyl, or a monocyclic heteroaryl. The bridged or fused bicyclic cycloalkenyl is attached to the parent molecular moiety through any carbon atom contained within the monocyclic cycloalkenyl ring. Cycloalkenyl groups are optionally substituted with one or two groups which are independently oxo or thia.

[0438] The term "halo" or "halogen" as used herein, means —Cl, —Br, —I or –F.

[0439] The term "haloalkyl" as used herein, means at least one halogen, as defined herein, appended to the parent molecular moiety through an alkyl group, as defined herein. Representative examples of haloalkyl include, but are not limited to, chloromethyl, 2-fluoroethyl, trifluoromethyl, pentafluoroethyl, and 2-chloro-3-fluoropentyl.

[0440] The term "heteroaryl," as used herein, means a monocyclic heteroaryl or a bicyclic ring system containing at least one heteroaromatic ring. The monocyclic heteroaryl can be a 5 or 6 membered ring. The 5 membered ring consists of two double bonds and one, two, three or four nitrogen atoms and optionally one oxygen or sulfur atom. The 6 membered ring consists of three double bonds and one, two, three or four nitrogen atoms. The 5 or 6 membered heteroaryl is connected to the parent molecular moiety through any carbon atom or any nitrogen atom contained within the heteroaryl. Representative examples of monocyclic heteroaryl include, but are not limited to, furyl, imidazolyl, isoxazolyl, isothiazolyl, oxadiazolyl, oxazolyl, pyridinyl, pyridazinyl, pyrimidinyl, pyrazinyl, pyrazolyl, pyrrolyl, tetrazolyl, thiadiazolyl, thiazolyl, thienyl, triazolyl, and triazinyl. The bicyclic heteroaryl consists of a monocyclic heteroaryl fused to a phenyl, a monocyclic cycloalkyl, a monocyclic cycloalkenyl, a monocyclic heterocyclyl, or a monocyclic heteroaryl. The fused cycloalkyl or heterocyclyl portion of the bicyclic heteroaryl group is optionally substituted with one or two groups which are independently oxo or thia. When the bicyclic heteroaryl contains a fused cycloalkyl, cycloalkenyl, or heterocyclyl ring, then the bicyclic heteroaryl group is connected to the parent molecular moiety through any carbon or nitrogen atom contained within the monocyclic heteroaryl portion of the bicyclic ring system. When the bicyclic heteroaryl is a monocyclic heteroaryl fused to a phenyl ring or a monocyclic heteroaryl, then the bicyclic heteroaryl group is connected to the parent molecular moiety through any carbon atom or nitrogen atom within the bicyclic ring system. Representative examples of bicyclic heteroaryl include, but are not limited to, benzimidazolyl, benzofuranyl, benzothienyl, benzoxadiazolyl, benzoxathiadiazolyl, benzothiazolyl, cinnolinyl, 5,6-dihydroquinolin-2-yl, 5,6-dihydroisoquinolin-1-yl, furopyridinyl, indazolyl, indolyl, isoquinolinyl, naphthyridinyl, quinolinyl, purinyl, 5,6,7,8-tetrahydroquinolin-2-yl, 5,6,7,8-tetrahydroquinolin-3-yl, 5,6,7,8-tetrahydroquinolin-4-yl, 5,6,7,8-tetrahydroisoquinolin-1-yl, thienopyridinyl, 4,5,6,7-tetrahydrobenzo[c] [1,2,5]oxadiazolyl, and 6,7-dihydrobenzo[c][1,2,5]oxadiazol-4(5H)-onyl. In certain embodiments, the fused bicyclic heteroaryl is a 5 or 6 membered monocyclic heteroaryl ring fused to either a phenyl ring, a 5 or 6 membered monocyclic cycloalkyl, a 5 or 6 membered monocyclic cycloalkenyl, a 5 or 6 membered monocyclic heterocyclyl, or a 5 or 6 membered monocyclic heteroaryl, wherein the fused cycloalkyl, cycloalkenyl, and heterocyclyl groups are optionally substituted with one or two groups which are independently oxo or thia.

[0441] The term "hydroxy" as used herein, means an —OH group.

[0442] The term "nitro" as used herein, means a $—NO_2$ group.

[0443] The term "oxo" as used herein means a =O group.

[0444] The term "saturated" as used herein means the referenced chemical structure does not contain any multiple carbon-carbon bonds. For example, a saturated cycloalkyl group as defined herein includes cyclohexyl, cyclopropyl, and the like.

[0445] The term "thia" as used herein means a =S group.

[0446] The term "unsaturated" as used herein means the referenced chemical structure contains at least one multiple carbon-carbon bond, but is not aromatic. For example, a unsaturated cycloalkyl group as defined herein includes cyclohexenyl, cyclopentenyl, cyclohexadienyl, and the like.

[0447] As used herein, the term "cell" is meant to refer to a cell that is in vitro, ex vivo or in vivo. In some embodiments, an ex vivo cell can be part of a tissue sample excised from an organism such as a mammal. In some embodiments, an in vitro cell can be a cell in a cell culture. In some embodiments, an in vivo cell is a cell living in an organism such as a mammal.

As used herein, the term "contacting" refers to the bringing together of indicated moieties in an in vitro system or an in vivo system. For example, "contacting" a parasite with a compound includes the administration of a compound described herein to an individual or patient, such as a human, infected with the parasite, as well as, for example, introducing a compound into a sample containing a cellular or purified preparation containing the parasite.

[0448] In another aspect, the invention provides methods for monitoring *T. gondii* infection in a subject, comprising monitoring levels in a blood sample from the subject of one or more markers selected from the group consisting of clusterin, oxytocin, PGLYRP2 (N-acetylmuramoyl-L-alanine amidase), Apolipoprotein A1 (apoA1), miR-17-92, and miR-124, wherein a change in levels of the one or more circulating markers compared to control correlates with *T. gondii* infection in the subject. The inventors have discovered these specific markers of active *T. gondii* infection, as described in the examples that follow.

[0449] The blood sample can be whole blood, serum, blood plasma, or any other suitable blood sample in which circulating IgG from a person with toxoplasmosis may be present. For example, the blood sample may be a plasma sample. As used herein, a "plasma sample" means blood plasma, the liquid component of blood, and is prepared, for example, by centrifugation of whole blood to remove blood cells. As used herein, a plasma sample also includes a blood serum sample, in which blood clotting factors have been removed.

[0450] Any suitable control can be used, including but not limited to a reference value obtained from one or more subjects that either do not have a *T. gondii* infection, or that are known to have a *T. gondii* infection, a previous blood sample obtained from the same subject, or any other suitable control. It is well within the level of those of skill in the art to determine an appropriate control for an intended use in light of the teachings herein. The change in level from control that correlates with *T. gondii* infection in the subject may be a difference of 10%, 25%, 50%, 100%, or more. In one embodiment, the difference is a statistically significant increase as judged by standard statistical analysis.

[0451] The level (e.g., quantity or amount) of a particular biomarker can be measured in the blood sample using a variety of methods known to those of skill in the art. Such methods include, but are not limited to, flow cytometry, ELISA using red blood cell, platelet, or white blood cell lysates (e.g., lymphocyte lysates), and radioimmunoassay.

[0452] In one embodiment, the method is used to monitor effect on the subject of a therapy for *T. gondii* infection. In this embodiment, the subject is receiving therapy for a *T. gondii* infection, and the methods permit attending medical personnel to assess efficacy of the therapy. In this embodiment, the blood sample test may, for example, be carried out periodically over time during the course of therapy. In another embodiment, the method is used to diagnose whether the subject is suffering from a *T. gondii* infection. In this embodiment, the subject is suspected of suffering from a *T. gondii* infection based on the presence of one or more symptoms, and the methods can be used to assist in providing a more definitive diagnostic, along with all other factors to be considered by an attending physician.

[0453] In various embodiments of these methods:

(a) an increase in level of one or more of clusterin, oxytocin, miR-17-92, or miR-124 compared to control correlates with active *T. gondii* infection; and/or

(b) a decrease in level of one or more of PGLYRP2 or ApoA1 compared to control correlates with active *T. gondii* infection.

[0454] In further embodiments of these methods:

[0455] (a) a decrease in level of one or more of clusterin, oxytocin, miR-17-92, or miR-124 compared to a level of the one or more markers in a serum sample obtained from the subject at an earlier time point correlates with a positive effect of the therapy in treating active *T. gondii* infection; and/or

[0456] (b) an increase in level of one or more of PGLYRP2 or ApoA1 compared to a level of the one or more markers in a serum sample obtained from the subject at an earlier time point correlates with a positive effect of the therapy in treating correlates with active *T. gondii* infection.

[0457] In one embodiment, the *T. gondii* infection involves neuronal damage and/or retinal damage in the subject. For example, the *T. gondii* infection may involve neuronal damage selected from the group consisting of neurodegeneration and/or seizures.

[0458] In another aspect, the invention provides methods for treating a *T. gondii* infection, comprising administering to a subject with a *T. gondii* infection an amount effective to treat the infection of ApoA1. As shown in the examples that follow, a reduction in apoA1 closely correlates with active *T. gondii* infection. The apoA1 may be administered as a protein therapeutic, or may be administered in an expression construct (such as a recombinant viral vector, etc.) that expresses apoA1 (i.e.: gene therapy).

[0459] In one embodiment, the subject to be treated has a decreased level of serum ApoA1 compared to control.

```
UniProtKB-P02647 (APOA1_HUMAN)
                                        (SEQ ID NO: 4)
MKAAVLTLAV LFLTGSQARH FWQQDEPPQS PWDRVKDLAT

VYVDVLKDSG RDYVSQFEGS ALGKQLNLKL LDNWDSVTST

FSKLREQLGP VTQEFWDNLE KETEGLRQEM SKDLEEVKAK

VQPYLDDFQK KWQEEMELYR QKVEPLRAEL QEGARQKLHE

LQEKLSPLGE EMRDRARAHV DALRTHLAPY SDELRQRLAA
```

```
                -continued
RLEALKENGG ARLAEYHAKA TEHLSTLSEK AKPALEDLRQ

GLLPVLESFK VSFLSALEEY TKKLNTQ.
```

[0460] As used herein, the term “individual” or “patient,” or “subject” used interchangeably, refers to any animal, including mammals, preferably mice, rats, other rodents, rabbits, dogs, cats, swine, cattle, sheep, horses, or primates, and most preferably humans.

[0461] As used herein, the phrase “amount effective”, “therapeutically effective amount” or “effective to treat” refers to the amount of active compound or pharmaceutical agent that elicits the biological or medicinal response that is being sought in a tissue, system, animal, individual or human by a researcher, veterinarian, medical doctor or other clinician.

[0462] In certain embodiments, a therapeutically effective amount can be an amount suitable for (1) preventing the disease; for example, preventing a disease, condition or disorder in an individual who may be predisposed to the disease, condition or disorder but does not yet experience or display the pathology or symptomatology of the disease;

(2) inhibiting the disease; for example, inhibiting a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder; or

(3) ameliorating the disease; for example, ameliorating a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder (i.e., reversing the pathology and/or symptomatology) such as decreasing the severity of disease.

[0463] As used here, the terms “treatment” and “treating” means (i) ameliorating the referenced disease state, for example, ameliorating a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder (i.e., reversing or improving the pathology and/or symptomatology) such as decreasing the severity of disease; or (ii) eliciting the referenced biological effect (e.g., reducing parasitic loador adverse effects the parasite is causing in the human it infects).

[0464] As used herein, the phrase “pharmaceutically acceptable salt” refers to both pharmaceutically acceptable acid and base addition salts and solvates. Such pharmaceutically acceptable salts include salts of acids such as hydrochloric, phosphoric, hydrobromic, sulfuric, sulfinic, formic, toluenesulfonic, methanesulfonic, nitric, benzoic, citric, tartaric, maleic, hydroiodic, alkanoic such as acetic, HOOC—$(CH_2)_n$—COOH where n is 0-4, and the like. Non-toxic pharmaceutical base addition salts include salts of bases such as sodium, potassium, calcium, ammonium, and the like. Those skilled in the art will recognize a wide variety of non-toxic pharmaceutically acceptable addition salts.

Example 1. New Paradigms for Understanding and Step Changes in Treating Active and Chronic, Persistent Apicomplexan Infections

Abstract

[0465] *Toxoplasma gondii*, the most common parasitic infection of human brain and eye, persists across lifetimes, can progressively damage sight, and is currently incurable. New, curative medicines are needed urgently. Herein, we develop novel models to facilitate drug development: EGS strain *T. gondii* forms cysts in vitro that induce oocysts in cats, the gold standard criterion for cysts. These cysts highly express cytochrome b. Using these models, we envisioned, and then created, novel 4-(1H)-quinolone scaffolds that target the cytochrome bc$_1$ complex Q$_i$ site, of which, a substituted 5,6,7,8-tetrahydroquinolin-4-one inhibits active infection (IC$_{50}$, 30 nM) and cysts (IC$_{50}$, 4 μM) in vitro, and in vivo (25 mg/kg), and drug resistant *Plasmodium falciparum* (IC$_{50}$, <30 nM), with clinically relevant synergy. Mutant yeast and co-crystallographic studies demonstrate binding to the bc$_1$ complex Q$_i$ site. Our results have direct impact on improving outcomes for those with toxoplasmosis, malaria, and ~2 billion persons chronically infected with encysted bradyzoites.

[0466] *Toxoplasma gondii* infections can cause systemic symptoms, damage and destroy tissues [1-10], especially eye and brain [1-10] and cause fatalities [S1-20]. Primary infections may be asymptomatic, or cause fever, headache, malaise, lymphadenopathy, and rarely meningoencephalitis, myocarditis, or pericarditis [9,11,12]. Retinochoroiditis and retinal scars develop in up to 30% of infected persons [1,7,13], and epilepsy may occur [6,14]. In immune-compromised and congenitally infected persons, active infection frequently is harmful [1-10] Recrudescence arises from incurable, dormant cysts throughout life [6,7,9,10]. In rodents, chronic infection alters fear, smell, reward pathways, neurotransmitters such as GABA and dopamine, and causes abnormal neurologic functions [15]. Although this parasite is present in the brains of 2-3 billion persons worldwide, consequences are unknown. Neurobehavioral abnormalities and differences in serum cytokines, chemokines, and growth factors were associated with seropositivity in humans [16, 17].

[0467] Current treatments against active *T. gondii* tachyzoites can have side effects such as hypersensitivity, kidney stones, and bone marrow suppression, limiting their use[10]. Latent bradyzoites are not significantly affected by any medicines[6]. Atovaquone partially, and transiently, limits cyst burden in mice[18], but resistance develops with clinical use[19-24.] Thus, *T. gondii* infection is incurable with recrudescence from latent parasites posing a continual threat. Estimates of costs for available, suboptimal medicines to treat active, primary ocular, gestational and congenital infections, in just the U.S. and Brazil, exceed $5 billion per year. Improved medicines are needed urgently. Molecular targets shared by *T. gondii* and *Plasmodia* make re-purposing compounds a productive strategy.

[0468] Critical flaws and limitations of available methods and models for developing medicines to cure *T. gondii* infections include lack of in vitro culture systems for cysts and scalable, easy to use animal models for screening compounds. To address these challenges, we characterized the EGS parasite, isolated in 1994 from amniotic fluid of a congenitally infected Brazilian fetus[24a], that form cyst-like structures in vitro[25]. In our characterization of EGS in vitro, herein, we discovered that true cysts develop, making EGS especially useful for drug development. EGS parasites can infect zebrafish, and we have characterized this, as well as a fluorescent tachyzoite and cyst assay in this new model[26]. Further, cytochrome bc$_1$ expression is markedly increased in encysted EGS bradyzoites suggesting cytochrome bc$_1$ might be a viable drug target for this life stage. This mitochondrial membrane bound protein complex cytochome bc$_1$, part of the electron transport chain responsible for generating ubiquinone for pyrimidine biosynthesis in *Plasmodium*, is the molecular target of the naphthoquinone, atovaquone[27-52]. Partial efficacy, rapid emergence of drug resistance in malaria and toxoplasmosis limit clinical usefulness of atovaquone. We present new 4-(1H)-quinolone scaffolds that target the Q_i site of cytochrome bc1 in apicomplexan parasites. Our lead 5,6,7,8-tetrahydroquinolin-4-one compound, MJM170, is highly effective against apicomplexan parasites and has substantially enhanced solubility compared with other reported quinolones due to its' new scaffold. Direct visualisation in the crystallographic structure opens the way to design a new generation of compounds for both parasites.

Results

Characterization of EGS Strain Develops Novel In Vitro Models to Test Compounds.

[0469] Genotyping and Phylogenetic Analysis of EGS:

[0470] We isolated and sequenced genomic DNA from the EGS[25] (25) parasite, which formed cysts when grown in human foreskin fibroblasts (HFF) in culture. Phylogenetic analysis based on 796,168 SNPs across 62 *T. gondii* genomes revealed that EGS is closely related to other Brazilian strains including TgCatBr1, TgCatBr18 and TgCatBr25 and ancient South American MAS. All these grouped to clade B, haplogroup 4 and 8. Full genome sequence analysis of EGS compared with canonical and geographically closely related parasite genomic sequences reveal a non-synonymous mutation and disordered c terminal sequence in Apetela 2(AP2) IV-iv, a bradyzoite repressor. EGS differs from other isolates by non-synonymous SNPs in Apetela 2 IV-iv, M=>I (570) and a disordered area beginning at 821, GGNRPHYHVAKQEWRVRYYMNG-KRKMRTYSAKFY GYETAHTMAEDFAHYVDKHE (SEQ ID NO: 1). AP2 IV-iv is a member of the plant-like transcription factor family unique to apicomplexan parasites. This AP2 represses tachyzoite to bradyyzoite conversion,[56] among other differences. Because AP2 IV-iv is a bradyzoite gene expression repressor[56], a mutation could create a parasite like EGS that remains as an encysted bradyzoite.

Phenotypes of EGS in Human Cells In Vitro, and in Cats and Mice:

[0471] EGS in Human Foreskin Fibroblasts (HFF).

[0472] In vitro, these EGS parasites form cysts that enlarge over ~48-96 hours and then destroy monolayers as single cell organisms. This created novel, useful in vitro models. Cyst walls are thick in electron micrographs (data not shown). Cyst-like structures' perimeters demonstrate dolichos, with bradyzoites within them staining with BAG1 and nuclei with Dapi. Kinetic analysis of EGS in HFF cultures, 2, 18, and 72 hours after infection, RNA-seq and MiR-seq results demonstrated varied expression signatures over time in culture (FIG. **5**) with expression of bradyzoite markers by 18 hours and Apetela 2 signatures by 2 hours.

[0473] Cats Fed EGS in HFF Cultures or Mouse Brain Produce Oocysts.

[0474] When HFF tissue cultures with these cyst structures were fed to cats, they developed the classic, gold standard bradyzoite phenotype of producing oocysts in two replicate experiments. All other *T. gondii* strains cultured for more than 30 passages, as EGS was since the 1990s, lose the ability to produce oocysts when fed to cats (JP Dubey, personal observations,). This experiment established that these were true bradyzoites in cysts formed in vitro under standard culture conditions. Oocysts also formed 10 days after feeding cats mouse brains infected with EGS stably transfected with tachyzoite SAG1 promoter-driven mcherry, and bradyzoite BAG1 promoter-driven green fluorescent protein (GFP), and merozoite promoter-driven blue fluorescent protein, engineered to facilitate creation of automated, scalable in vitro and in vivo assays. In vitro, these promoters did not provide a fluorescence signal robust enough to detect differences between 2×10^5 and 650 parasites useful in scalable assays (data not shown).

[0475] EGS is Virulent in Mice.

[0476] When these EGS oocysts were fed to mice they produced disease indistinguishable from other virulent Brazilian strains. Oocysts given to mice per-orally created an illness and histopathology phenotypically characteristic for typical, virulent parasites causing dose related proliferation of *T. gondii* with necrosis in terminal ileum, pneumonia at 9-10 days, with brain parasites by 17 days and dose-related mortality.

[0477] EGS has a Bradyzoite/Cyst Morphology and Alters the Transcriptomes of the Biologically Relevant Human Monocytic Cell Line MM6 and Human Primary Neuronal Stem Cells (NSC).

[0478] Human cells particularly relevant to human toxoplasmosis were infected with different strains of *T. gondii* to better characterize EGS parasites. Immunofluorescence staining of EGS-infected MM6 and NSC cultures revealed the development of cysts (FIG. **6***a*) and accordingly, EGS gene expression resembled that of bradyzoites when compared to equivalent infections done with GT1, ME49 or VEG strains. Interestingly, EGS transcription was influenced by host cell type (FIG. **6**). Transcriptomics using host mRNA and miR profiling of EGS cultures in MM6, and NSC cells for 18 hours demonstrated that this parasite modulates host transcripts involved in protein misfolding, neurodegeneration, endoplasmic reticulum stress, spliceosome alteration, ribosome biogenesis, cell cycle, epilepsy, and brain cancer among others (FIG. **6**). The number of genes significantly up or down regulated in MM6 and NSC cells compared to uninfected controls are depicted in FIG. **6**. Overexpressed genes differ from those of GT1, ME49 and VEG tachyzoite-infected human NSC cells (FIG. **7***a*), but modify the same or connected pathways (McLeod et al, unpublished observations). Hsa-miR-708-5p was the most affected miRNA (down-modulated) by EGS (FIG. **6***e*; FIG. **2**). miR-708-5p is a regulator that promotes apoptosis in neuronal and retinal cells, which could maintain a niche for EGS-like encysted bradyzoites to persist.

[0479] EGS Transcripts Demonstrate Importance of Cytochromes and Key Apetela 2 Transcription Factors in this Life Cycle Stage.

[0480] EGS transcripts in HHF, MM6, and NSC cells were enriched for genes transcribed in bradyzoites, including known bradyzoite transcripts, certain Apetela 2s and cytochrome b and other cytochromes (FIG. **7***b-c*). Among transcripts with the most increased fold change in EGS across all three cell lines were: cytochrome b; cytochrome c oxidase subunit III subfamily protein; apocytochrome b; cytochrome b, putative; and cytochrome b (N-terminal)/b6/petB subfamily protein. Other over-expressed genes include bradyzoite transcription factor AP2IX-9 and plant-like heat-shock protein BAG1 (FIG. **7** *a-c*).

Identifying Novel and Efficacious Compounds Against *T. gondii* Cytochrome bc_1.

[0481] Increased expression of cytochromes in EGS (FIG. 7*c*) made it pertinent to synthesize and test an endochin-like quinolone (ELQ) 271, which was previously reported to inhibit *T. gondii* cytochrome bc_1 Q_i site and reduce, but not eliminate, brain cyst numbers in mice[27]. ELQ271 also inhibited EGS in vitro (FIG. 7*d* bottom) demonstrating that our in vitro model correlates with previously reported partial activity of ELQ271 against bradyzoites in cysts in mouse brain. Vivoporter-PMOs inhibiting cytochrome bc_1 had a modest effect on tachyzoite replication and a small effect on size and number of EGS cysts (FIG. 7*d* top). Minimal effect might be related to limited entry of vivoporter into cysts or mitochondria.

[0482] ELQs have been a focus for drug development for malaria (ELQ 300) and toxoplasmosis (ELQ 271 and 316) as they were reported to be potent and selective (versus human cytochrome bc_1) inhibitors of *P. falciparum* cytochrome bc_1 at nanomolar concentrations[27]. ELQs are part of the 4-(1H)-quinolone class of cytochrome bc_1 inhibitor [36,42,40,45,49,52,53,54,56-62] and (Dogget et al, 13th International Toxoplasmosis Meeting Abstract. Gettysburg Pa., June 2015), a scaffold that suffers from limited aqueous solubility. Another aspect of inhibitor design for this system is minimizing the inhibition of mammalian cytochrome bc1, which shares ~40% sequence identity to the *T. gondii* ortholog within the Q substrate sites. Thus, we set out to design potent and selective inhibitors of *T. gondii* cytochrome bc_1 with improved solubility (FIG. **8**) compared to known quinolone-based inhibitors. Noting the previous work of GSK on the preclinical development of Clopidol derivatives which led to terminating studies secondary to toxicity in the rat models, as another serious deficiency[63] and the incorporation of the diphenyl ether group onto the central 4-(1H)-quinolone core as reported by Riscoe et al.[27], we focused on the central core ring system. Doggett, Riscoe et al's[27] ELQ 271 (FIG. **8**) was reported to be ineffective against yeast with a mutation in the Q_i site. Nonetheless, it recently was shown that ELQs can bind both Q_i and Q_o depending on subtle chemical changes [61-3]. As a result of our initial efforts, a 5,6,7,8-tetrahydroquinolone (MJM170, 2) displayed promising results. (FIG. **8**; Table 2). We chose ELQ271 for comparison because it had the greatest activity at the lowest dose (5 mg/kg) in the mouse model of Doggett despite the higher cytotoxicity toward human fibroblasts in the in vitro toxicity studies. [27]

[0483] MJM170 is a potent inhibitor of *T. gondii* tachyzoites (RH-YFP strain, IC_{50} 0.03 μM) and bradyzoites (EGS strain, IC_{50} 4 μM), equipotent to ELQ271 (Table 2, FIG. **9**). MJM170 showed 10-fold improved aqueous kinetic solubility (pH 7.4) over ELQ 271 (Table 2), 3-fold improved FaSSIF/FeSSIF (pH 6.5) solubility, with similar human microsomal stability profiles (146 vs 172 minutes). A different method from that in reference [49] was used. MJM170 has a significantly decreased mouse microsomal stability compared to ELQ 271 (20 vs >200 minutes). MJM170 was further evaluated with MDCK-MDR1 cells (a measure of blood-brain barrier permeability) and results suggest that MJM170 could cross the blood brain barrier and not suffer from P-glycoprotein efflux These data highlight the potential of the 5,6,7,8-tetrahydroquinolin-4-one scaffold for further hit-to-lead development.

TABLE 2

Comparison of ELQ 271 and MJM170 in our biological assays: inhibition of apicomplexan parasites and ADME/Tox. ELQ 271 was synthesised in-house.

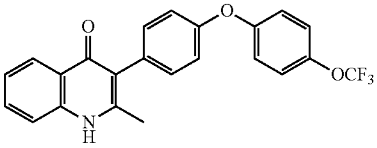
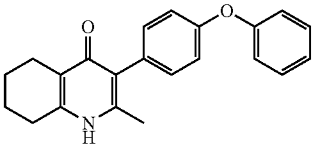
Compound	ELQ 271	MJM170
Structure		
Mol. Wt.	411.4	331.4
T. gondii Tachyzoite IC_{50} μM	0.03	0.03
T. gondii Bradyzoite IC_{50} μM	1	4
P. falciparum IC_{50} μM[a]	0.03 (D6) 0.09 (TM91C235) 0.10 (W2) 0.13 (C2B)	0.01 (D6) 0.03 (TM91C235) 0.03 (W2) 0.01 (C2B)
HFF Toxicity CC_{50} μM	20	20
Kinetic Solubility PBS pH 7.4 μM[b]	0.15	1.97
FaSSIF Solubility pH 6.5 μM[b]	3.4	9.8
Human microsomal stability $T_{1/2}$ mins[b]	171.9	146.3
Mouse microsomal stability $T_{1/2}$ mins[b]	>200	21.0

TABLE 2-continued

Comparison of ELQ 271 and MJM170 in our biological assays: inhibition of apicomplexan parasites and ADME/Tox. ELQ 271 was synthesised in-house.

MDCK-MDR1 P_{app}A-B × 10^6 cm/s^b	N.D.	32.1
MDCK-MDR1 Efflux Ratio^b	N. D.	1.23

[a] The D6 strain (Sierra Leone) is drug sensitive, the TM91C235 (Thailand) is multi-drug resistant, the W2 strain (Thailand) is chloroquine resistant, and the C2B strain is multi-drug resistant with pronounced resistance to atovaquone.

[b] ADME carried out by ChemPartner Shanghai Ltd. N.D. not determined. Human and mouse microsomal stability differs as is known to occur for other compounds such as TMP/SMX.

[0484] MJM 170 is Effective In Vivo Against Tachyzoites, and Modestly Against Bradyzoites in Cysts of Mice, and Development of a Scalable Zebrafish Assay.

[0485] MJM170 was highly efficacious against RH (FIG. **10***a*) and Prugniaud (FIG. **10***b*) strain tachyzoites in mice at 25 mg/kg without toxicity for 5 days ($p<0.00$), and modestly reduced numbers of Me49 strain cysts established >2months earlier when treated with 12.5-25 mg mg/kg for 17 days ($p<0.002$) (FIG. **10***c*). In analysis of parallel histopathology, there was a similar trend (data not shown). Translucent zebra fish can be infected with EGS, other *T. gondii* that make cysts, and RH YFP preparing for a novel model for scalable screening (FIG. **10***d*).

[0486] Cytochrome bc_1 Q_i is the Binding Site of MJM170 which is Potent Against *Plasmodium falciparum* and Yeast. Tetrahydroquinolone Binds to the Q_i Site of Cytochrome bc_1:

[0487] Studies to determine whether cytochrome bc_1 Q_i is the molecular target of MJM170 initially included studies of resistance of yeast and *P. falciparum* with known cytochrome b Q_i mutations predicted to cause a steric clash with MJM170 (FIG. **11**). Recently, we reported co-crystal structures of GSK's cytochrome bc_1 inhibitors bound to bovine cytochrome bc_1 at the Q_i site[52] demonstrating that these pyridone inhibitors and other structurally related inhibitors bind to an alternative site to atovaquone on cytochrome bc_1. This structure allowed us to model MJM170 within the Q_i site using the Maestro Suite from Schrödinger. This molecular modelling predicted steric clashes in mutant yeast and *P. falciparum* cytochrome bc_1 with MJM170 (FIG. **11***a*).

[0488] Co-Crystallization of MJM170 with Bovine Cytochrome bc_1 and Modelling of the *T. gondii* Enzyme Confirm the Target.

[0489] Co-crystallization validates predictions made with modelling and confirmed using assays with *S. cerevesiae* mutants (FIG. **11***d*). There was no steric clash for *P. falciparum*-model based upon this crystal structure, consistent with in vitro assays (FIGS. **11** *e,f*). MJM170 was co-crystallized with bovine cytochrome bc_1 and the resulting good quality electron density maps allowed for unambiguous placement of MJM170 within the Q_i site (FIG. **11***f*). The planar region of the quinolone group is held between heme b_H and Phe220 and the additional ring further extends into the hydrophobic cavity at the apex of the binding site towards Pro24 and Ile27. The carbonyl group of the compound is surrounded by Ser35, Asp228 and the carbonyl of Trp31, while its amine moiety lies between His201 and Ser205. The diphenyl ether group extends outwards towards the hydrophobic residues Ile39 and Ile42 and forms a stacking interaction with Phe18 (FIG. **11***f*). An example of a stereo electron density involving Ile118-Met129 and Phe183-Phe199 is shown in FIG. **11***g*).

[0490] Surrogate Assays Demonstrate Efficacy of Compounds, Providing Target Validation and Added Value as MJM170 is Effective Against Wild Type but not M221Q(F) Mutant Yeast.

[0491] Mutants of *S. cerevesiae* were used to further confirm the molecular target of MJM170 (FIG. **11***d*), and documented that the Q_i domain in cytochrome b is essential for its efficacy. This approach provided insight into binding of compounds to the enzyme. Crystallographic structure of bovine cytochrome bc_1 with GSK932121 [52] indicates that certain amino acids are critical in tetrahydroquinolone binding and explains why there is inhibition by certain compounds. Previous studies reported that no cross-resistance is observed between ELQs and atovaquone in *P. falciparum*. This is rationalised as atovaquone binds the Q_o site on cytochrome bc_1. A yeast M221Q substitution within the Q_i site displayed resistance to ELQ inhibition further confirming that this to be the target site[27]. MJM170 and ELQ271 were effective against *S. cerevisiae* wild type parental AD1-9 strain at ImM, 100, 5 and 1 μM when grown on non-fermentable, glycerol medium forcing reliance on ATP production for respiration. Yeast strains with point mutations in the cytochrome b gene that substitute methionine by glutamine (M221Q) or phenylalanine (M221F) at position 221 in the Q_i site predicted to yield a steric clash upon inhibitor binding were resistant to MJM170 (FIG. **11***d*).

[0492] Tetrahydroquinolones are Potent Against Wild Type *P. falciparum*, and *P. falciparum* G33A/V and Other Drug Resistant Mutants but not DHODH Mutant.

[0493] MJM170 is highly effective against *P. falciparum* (Table 2) including multiple strains resistant to available antimicrobials and a cytochrome bc_1 Q_i mutant (FIG. **12**). Resistance against transgenic *P. falciparum* yeast DHODH mutant strain indicates MJM170 affects mitochondria suggesting that the mode of action against *P. falciparum* is through inhibition of electron transport (FIG. **12***a*).

[0494] Potentially Clinically Useful Combinations with Tetrahydroquinolone Demonstrated in Synergy Studies.

[0495] To determine whether there might be clinically relevant synergies and additive effects, combinations of MJM170 with other clinically available and useful compounds also were tested. Earlier, we had found cycloguanil and related biguanide triazines[64] were active against *T. gondii* tachyzoites and *P. falciparum* making it relevant to test them in combination with MJM170. We observed modest synergy in vitro for atovaquone, additive effect with cycloguanil, and antagonism with BRD6323, a Q_i inhibitor for *P. falciparum* (FIG. **12***b*). Combining atovaquone with proguanil (active component cycloguanil) as Malarone^R for malaria provides an approach to reduce selection of drug resistant *plasmodium* mutants.

Discussion

[0496] The results presented here offer a molecular understanding and therapeutic strategies for one of the most common parasitic infections of human brain and eye, and that persists across lifetimes in around 2 billion people worldwide. We have developed new models to facilitate discovery of curative treatments for toxoplasmosis. We have characterized the Brazilian *T. gondii* isolate called EGS that was known to be morphologically similar to encysted bradyzoites in tissue culture. We further validate the cystic nature of these EGS infected cultures, since they are able to induce the intra-intestinal life cycle when fed to cats ultimately resulting in oocyst secretion. This is the first such description of this phenotype and provides definitive proof that this unique parasite has a true cyst phenotype when maintained in vitro. Our data also provide a number of other major conceptual advances on EGS by demonstrating the following: (i) Genome sequencing of this EGS isolate demonstrates that EGS has a typical Brazilian virulent genotype and phylogeny, (ii) EGS is a haplogroup 4 *T. gondii*. Consistent with a genotype that is known to be pathogenic and virulent for mice, we demonstrate that EGS oocyst induced infection is similar to that of other virulent Brazilian parasites. For example, mice fed EGS oocysts demonstrated ileal parasites causing necrosis, as well as pneumonitis, encephalitis and systemic infection leading to death. This indicates that the ability to form cysts in culture does not alter the pathogenicity of EGS in mice. However, potentially relevant to its in vitro bradyzoite phenotype, full genome sequencing revealed that it has nonsynonymous single nucleotide repeat sequence differences from other Brazilian and canonical U.S. and European parasites which do not share its in vitro bradyzoite phenotype. EGS has a nonsynonymous mutation in a bradyzoite repressor, Apetela 2(AP2) IV-iv, plant like transcription factor. AP2s interact with HATs and HDACs to modulate transcriptional signatures in apicomplexan parasites[55]. This Apetela 2, plant-like transcription factor gene, AP2IV-4, represses bradyzoite genes during the tachyzoite cell cycle, thereby preventing commitment to the bradyzoite developmental pathway[56]. If the observed substitution or disordered N terminus results in a defective or non-functional molecule, this could provide an explanation for the observed bradyzoite phenotype of EGS parasites. This is consistent with our findings that EGS in HFF forms cysts by 24 hours, characterized by BAG1, and Dolichos staining at 24, 48, and 96 hours after infection. These cysts gradually enlarge until 48-96 hrs in culture, when single *T. gondii* begin to destroy HFF monolayers. These are the cultures of bradyzoites in cysts that when fed to cats ~48 hours after infection form oocysts which are virulent in mice, providing definitive proof of an in vitro bradyzoite phenotype for the EGS strain of *T. gondii.*

[0497] The transcriptomic studies with this EGS isolate have provided critical insights into host cell mechanisms that are a prominent part of the ability of the encysted parasite to persist in this untreatable life cycle stage, and biologic consequences of such persistent infection. RNAseq and miR seq of EGS infected human host cells included human fibroblasts, monocytic and neuronal stem cells with this encysted EGS strain parasite. These provide an understanding of the types of perturbations of biologically relevant host cells this bradyzoite life cycle stage can cause, providing insights into unique aspects of pathogenesis of this infection with untreatable cysts and its consequences. We found that EGS modifies critical host cell pathways. For example we find in vitro modulations of host cell pathways in human, primary neuronal stem cells are the same as those associated with modulation of host cell replication as seen with malignancies, and in neurodegenerative diseases. Further, it is noteworthy that the level of a microRNA that specifies apoptosis in eye and brain cells is markedly down modulated by this EGS bradyzoite which would inhibit host protective apoptotic mechanisms allowing parasites to persist in brain and eye without a critical protective mechanism. EGS, as an encysted bradyzoite, clearly alters biologic processes including cell cycle, cell death, alternative splicing, protein synthesis, protein folding and ubiquitination and down regulates hsa-miR-708-5p that specifies apoptosis in neuronal and retinal cells[65].

[0498] RNA and MiR sequencing and transcriptomic analyses of the EGS parasites also identified molecular targets that are critical for the bradyzoite life cycle stage in the parasite as well. These molecular targets include cytochrome b, as critically increased in dormant, encysted parasites. Cytochrome b was increased along with known cyst constituents like enolase 1, Cyst wall protein, Lactate dehydrogenase 2, bradyzoite antigen 1, Apetela 2 plant like transcription factors not present in animals, such as AP2 IX-ix, and cytochrome oxidase. Our work provides a new means to identify stage specific molecular targets, and emphasizes that cytochrome bc 1 complex is a critical target. The transcriptome of EGS parasites in HFF over time are similar to those of in vivo bradyzoites in terms of known critical genes modified. Finally, EGS presents a much-needed assay for identifying novel molecular targets present in bradyzoites in vitro. EGS was also useful to evaluate the effect of inhibitors on encysted bradyzoites in vitro.

[0499] Recent crystallographic studies with the bovine cytochrome bc_1 complex allowed us to rationally design a novel compound to target the Q_i site of cytochrome b. Our novel compound was designed to address issues with poor solubility of existing quinolone/pyridone Q_i inhibitors. One of these compounds MJM170, a substituted 5,6,7,8-tetrahydroquinolin-4-one inhibits active infection (IC_{50} 30 nM) and cysts (IC_{50} 4 μM) in vitro, and in vivo (25 mg/kg). It is predicted to cross the blood brain barrier with no efflux as demonstrated in an in vitro MDR1-MDCK permeability assay (Table 2), indicating this class of compounds have promise for treatment of central nervous system infections. When we tested MJM170 against wild type and multi-drug resistant *P. falciparum*, we found it was also potent (IC_{50}<30 nM against all strains). In combination studies, MJM170 was identified as additive with cycloguanil and modestly synergistic with atovoquone. Studies of yeast and malaria mutants, as surrogate assays, and co-crystallography studies with bovine cytochrome bc_1 confirm the mechanism of action/target for MJM170. The co-crystal structure of MJM170 in complex with bovine cytochrome bc_1 reveals a clear binding mode within the Q_i site. Using homology models of the apicomplexan Qi sites, there are clear differences between the binding sites of the apicomplexan and mammalian orthologs which can be used to fine-tune the selectivity of our scaffold towards apicomplexan bc_1. The larger binding pocket of the apicomplexan versus the mammalian bc_1 may provide a way forward to increase selectivity. Our work provides a conceptual and a practical step change forward that provides a foundation for further testing and improvements to efficacy, toxicity, solubility, oral absorption, large animal toxicology that will be needed to reach the clinic. Our work reported herein not only provides new and important insights into the biology of *T. gondii*, especially the bradyzoite life cycle stage and the remarkable effects of this parasite on its human host's cells, but also provides critical molecular targets and new methods to identify others. Armed with this information, a novel scaffold with intrinsically higher solubility than the equivalent quinolone has been designed with holds promise towards developing a much-needed curative medicine for those with toxoplasmosis, malaria, and ~2 billion persons chronically infected with presently incurable, encysted bradyzoites which persist and can recrudesce lifelong.

Methods

[0500] All methods were carried out in accordance with approved guidelines set at the University of Leeds by the Education & Training Resources office and all experimental protocols were approved by the IRB committees; University of Chicago Institutional Animal Care and Use Committee (IACUC) and all experimental protocols were approved by the IRB committee; United States Department of Agriculture IACUC and all experimental protocols were approved by the IRB committees; J Craig Venter Institute Research ethics committee; University of Liverpool UK Office for Research Integrity (UKRIO) and all experimental protocols were approved by the IRB committees; Harvard School of Public Health HMS IACUC and all experimental protocols were approved by the IRB committees; The Broad Institute IACUC and all experimental protocols were approved by the IRB committees; Walter Reed Army Institute of Research Division of Human Subjects Protection (DHSP) and all experimental protocols were approved by the IRB committees; Oregon State University IACUC and all experimental protocols were approved by the IRB committees; Institute for Systems Biology ethics committee; Albert Einstein College of Medicine IACUC and all experimental protocols were approved by the IRB committees; Strathclyde University Ethics Committee (UEC) and all experimental protocols were approved by the IRB committees; Institute for Integrative Biology of the Cell IACUC and all experimental protocols were approved by the IRB committees, and the Centre national de la recherche scientifique IACUC and all experimental protocols were approved by the IRB committees.

Cells and Parasites for Work with *T. gondii*

[0501] Cells:

[0502] The cells utilized for *T. gondii* assays included human foreskin fibroblasts (HFF), Human MonoMac 6 cells (MM6), and Neuronal Stem cells (NSC) from a temporal lobe biopsy.

[0503] *Toxoplasma gondii.*

[0504] The strains of *T. gondii* utilized in this work were: RH-YFP Tachyzoites of the RH-YFP strain were passaged in human foreskin fibroblasts (HFF cells); EGS-Bradyzoite assays use the EGS strain, isolated from amniotic fluid of human with congenital toxoplasmosis; Other strains used are: Me49; Prugniaud; Beverly; Veg; GT1. All other than EGS are *T. gondii* tachyzoites. These parasites are passaged in HFF.

[0505] Isolation of DNA and RNA.

[0506] EGS single celled organisms were grown in Human Foreskin Fibroblasts, filtered free of host cells. gDNA was isolated and processed for sequencing as described. For isolation of RNA RIN scores were >8.

Gene Sequencing, Genomics, RNA and MiR Sequencing, Systems Analysis, Metabolomics

[0507] Genome Sequencing of *T. gondii* EGS Strain.

[0508] A single Illumina paired-end barcoded library was prepared from tachyzoite gDNA with Illumina TrueSeq library preparation kit. The library was then sequenced using 100 bp pared-end reads in one ninth of a lane of an Illumina HiSeq 2000 machine to generate ~2 Gbp of genome sequence.

[0509] Single Nucleotide Polymorphism (SNP) Identification and Annotation.

[0510] Illumina genome sequencing reads from EGS or downloaded from GenBank SRA database for GT1 (SRR516419), VEG (SRR516406) and TgCatBr1 (SRR350737) were aligned to the *T. gondii* ME49 reference genome assembly (ABPA02000000, ToxoDB release 13.0) with Bowtie2 and realigned around gaps using the GATK toolkit. SNP calls were done simultaneously across all four strains with samtools utility mpileup, requiring a minimum SNP coverage of 5 reads and an alternative allele frequency of 0.8 or higher, given the haploid nature of these genomes. Thereafter, SnpEff and a gff3 file containing the annotation of *T. gondii* ME49 downloaded from ToxoDB v13.0 were used to classify the different types of mutations identified in each strain. Allelic variants that were different between EGS and the rest of the strain were considered EGS-specific.

[0511] Phylogenetic Network Analysis.

[0512] A total of 790,168 single nucleotide polymorphisms spanning the entire *T. gondii* genome from 62 different strains representing all major haplogroups were downloaded from ToxoDB, combined with SNP data from the same sites from the EGS strain and directly incorporated as a FASTA file into SplitsTree v4.13.1 to generate unrooted phylogenetic networks using a neighbor-net method.

[0513] Differential Gene Expression (DGE) Analysis.

[0514] Total RNA extracted from human cell cultures infected (or not) with a number of *T. gondii* strains for 2 h, 18 h or 48 h was treated with miRNeasy Mini Kit columns (Qiagen) following manufacturer instructions to separate mRNA and miRNA fractions. Afterwards, Illumina barcoded sequencing libraries were constructed with TruSeq RNA Sample Preparation Kits v2 (Illumina) for mRNA and miRNA TruSeq Small RNA Library Preparation Kit (Illumina) for miRNA. Libraries were sequenced as 100 bp single reads with Illumina HiSeq 2000 apparatus in pulls of 6 or 9 samples per lane for mRNA (yield ~3 Gbp per sample) and miRNA (yield ~2 Gbp per sample) libraries respectively. For protein coding genes, reads were mapped to the human (release GRCh38) and *T. gondii* ME49 strain (ToxoDB release 13.0) reference genome assemblies and annotations with CLC Genomic Workbench software (CLC Bio-Qiagen, Aarhus, Denmark) and raw read counts per gene were then analyzed with the R package EdgeR using a generalized linear model likelihood ratio test to identify genes that are differentially expressed among samples.

[0515] For miRNA DGE analysis, reads were depleted of adaptor and primer sequences and mapped to the human reference genome assembly (GRCh38) and the miRNA annotation from miRBase v21 (see the mirbase web site) with CLC Genomic Workbench software. Identification of human miRNA genes that are differentially expressed across treatments was carried out with EdgeR from raw read counts per miRNA gene using a generalized linear model likelihood ratio test.

[0516] For both mRNA and miRNA DGE analyses p-values were adjusted for multiple hypotheses testing using the False Discovery Rate method. MDS plots and heat maps were generated with the plotMDS tool from EdgeR and the R tool heatmap. Differentially expressed genes (DEGs) in MM6 and NSC cell lines infected with EGS parasites were identified under the criteria of 1% FDR and absolute log 2-fold-change >1.5 (i.e. fold-change >2 and <0.5 for up- and down-regulated genes, respectively).

[0517] Functional Enrichment Analysis

[0518] GO enrichment analyses were performed for up- or down-regulated genes, by using the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7. GO slim enrichment analysis was performed for genes carrying potential change-of-function mutations in EGS that were absent in strains ME49, VAND or TgCatBr1. GO slim database was downloaded from QuickGO provided by EMBL-EBI. Using taxonomy id "508771" for the ME49 strain, relevant GO slim terms were retrieved. GO slim enrichment analysis was performed with Fisher's exact test based on the GO slim terms.

[0519] Assay for Oocyst Development in Cats.

[0520] Oocysts were collected from feces of *Toxoplasma*-free cats 3-14 days after feeding infected cell cultures or infected mouse brains. Oocysts were separated from feces by sugar floatation, sporulated in 2% sulfuric acid by aeration at room temperature for 1 week. After removing sulfuric acid oocysts were inoculated orally in to Swiss Webster albino mice. All tissues of mice that died or euthanized were studied histologically after staining with hematoxylin and eosin and by BAG1 antibodies to *T. gondii* as described. (Dubey J P, Ferreira L R, Martins J, McLeod R. Oral oocyst-induced mouse model of toxoplasmosis: effect of infection with *Toxoplasma gondii* strains of different genotypes, dose, and mouse strains (transgenic, out-bred, inbred) on pathogenesis and mortality. Parasitology 139:1-13, Epub 2011. PMID: 22078010; also referred t herein as S39)

[0521] Chemical Synthesis.

[0522] Final compounds had >95% purity determined by high performance liquid chromatography (HPLC) and 300 and/or 500 MHz NMR spectrometers. Liquid chromatography-mass spectrometry (LC-MS) and high resolution mass spectrometers (HRMS) analytical systems were used to determine integrity and purity of all intermediates and final compounds.

Synthesis of 2-methyl-5,6,7,8-tetrahydroquinolin-4-one (6)

[0523] Platinum oxide (100 mg, 10 mol %) was added to a solution of 4-hydroxy-2-methylquinoline (5, 1.00 g, 6.28 mmol, 1.00 eq) in glacial acetic acid (10.0 ml). The heterogeneous mixture was catalytically hydrogenated under a balloon of hydrogen. After 22 hrs, TLC (10% MeOH-DCM) confirmed complete reaction. The mixture was filtered through celite under vacuum, washing thoroughly with EtOAc. The filtrate was concentrated and the resulting residue purified by column chromatography (10% MeOH-DCM) to give the desired product as a pale yellow oil (917 mg, 5.65 mmol, 89%); R_f 0.14 (10% MeOH-DCM); δ_H (300 MHz, $CDCl_3$) 1.74-1.76 (4H, m, CH_2), 2.29 (3H, s, Me), 2.49-2.52 (2H, m, CH_2), 2.67-2.70 (2H, m, CH_2), 6.16 (1H, s, Ar-H); δ_C (125 MHz, $CDCl_3$) 19.0 (Me), 21.8 (CH_2), 22.1 (CH_2), 27.1 (CH_2), 112.5 (CH), 122.4 (Cq), 146.4 (Cq), 147.0 (Cq), 178.3 (Cq); Spectroscopic data consistent with literature values (JMC, 1993, 36, 1245-54).

Synthesis of 2-methyl-3-iodo-5,6,7,8-tetrahydroquinolin-4-one (7)

[0524] Butylamine (6.20 ml, 62.8 mmol, 10.0 eq) was added to a suspension of 2-methyl-5,6,7,8-tetrahydroquinolin-4-one (6, 1.02 g, 6.28 mmol, 1.00 eq) in DMF (10.0 ml). To this heterogeneous mixture was added I_2 (1.60 g, 6.28 mmol, 1.00 eq) in a saturated solution of KI (6.00 ml). After 20 hrs stirring at R.T., a precipitate formed in the orange solution, Excess iodine was quenched with 0.1 M sodium thiosulfate solution. The precipitate was filtered by vacuum filtration, washed with distilled H_2O and dried (Na_2SO_4) to give the desired product as a colourless solid (1.76 g, 6.09 mmol, quantative yield); δ_H (300 MHz, DMSO-d_6) 1.61-1.70 (4H, m, CH_2), 2.29 (2H, t, J 6.0, CH_2), 2.43 (2H, s, CH_2), CH_3 under DMSO peak.

Synthesis of 2-methyl-3-iodo-4-ethoxy-5,6,7,8-tetrahydroquinoline (8)

[0525] Potassium carbonate (1.53 g, 11.1 mmol, 2.00 eq) was added to a heterogeneous mixture of 2-methyl-3-iodo-5,6,7,8-tetrahydroquinolin-4-one (7, 1.60 g, 5.56 mmol, 1.00 eq) in DMF (15.0 ml), and the reaction heated to 50° C. for 30 mins. The R.B. flask was removed from the heating mantle and ethyl iodide was added dropwise. The reaction was then heated at 50° C. for 18 hrs. The reaction was cooled to R.T., quenched with water (40 ml). The resulting emulsion formed which was extracted with EtOAc (50 ml). EtOAc layer were washed with water (3×30 ml), brine (3×30 ml), dried (Na_2SO_4) and concentrated to give a pale yellow oil (1.09 g, 3.44 mmol, 61%); R_f 0.88 (1:1 Pet-EtOAc); HPLC (RT=1.67 mins); LCMS (Method A), (RT=1.6 min, m/z (ES) Found MH^+318.0); δ_H (500 MHz, $CDCl_3$) 1.49 (3H, t, J7.0, ethoxy CH_3), 1.73-1.78 (2H, m, CH_2) 1.84-1.88 (2H, m, CH_2), 2.78-2.69 (511H, m, CH_2 & CH_3), 2.84 (2H, t, J6.5, CH_2), 3.97 (2H, q, J 7.0, OCH_2); δ_C (125 MHz, $CDCl_3$) 15.6 (CH_3), 22.3 (CH_2), 22.8 (CH_2), 23.6 (CH_2), 29.3 (CH_3), 32.0 (CH_2), 68.4 (OCH_2), 90.9 (Cq), 124.5 (Cq), 158.3 (Cq), 158.9 (Cq), 163.9 (Cq).

Synthesis of 2-methyl-3-(4-phenoxyphenyl)-4-ethoxy-5,6,7,8-tetrahydroquinoline (10)

[0526] 2-Methyl-3-iodo-4-ethoxy-5,6,7,8-tetrahydroquinoline (8, 0.266 g, 0.839 mmol, 1.00 eq), $Pd(PPh_3)_4$(0.048 mg, 0.0419 mmol, 5 mol %) and 4-phenoxyphenylboronic acid (9, 0.270 mg, 1.26 mmol, 1.50 eq) were charged to a R.B. flask under N_2(g)[49]. Degassed DMF (10.0 ml) was added to the flask followed by 2M K_2CO_3 (1.60 ml). The flask was heated to 85° C. under N_2(g). After 15 mins, TLC (4:1 Pet-EtOAc) confirmed reaction was complete. The reaction was cooled and diluted with EtOAc (15 ml), filtered through celite and partitioned between EtOAc (10 ml) and

H_2O (25 ml). Combined organics were washed with H_2O (3×30 ml), then brine (3×30 ml), dried (Na_2SO_4) and concentrated to give a red oil which was purified by column chromatography (3:1 Pet-EtOAc), to give the desired product as a pale yellow oil (0.235 mg, 0.655 mmol, 78%); R_f 0.31 (3:1 Pet-EtOAc); HPLC (RT=3.08 mins); δ_H (300 MHz, $CDCl_3$) 1.04 (3H, t, J 7.0, ethoxy CH_3), 1.76-1.93 (4H, m, 2×CH_2), 2.32 (3H, s, CH_3) 2.72 (2H, t, J6.0, CH_2), 2.91 (2H, t, J6.5, CH_2), 3.50 (2H, q, J 7.0, OCH_2), 7.05-7.16 (5H, m, Ar-H), 7.20-7.29 (2H, m, Ar-H), 7.31-7.43 (2H, m, Ar-H); δ_C (125 MHz, $CDCl_3$) 15.7 (CH_3), 22.5 (CH_2), 23.0 (CH_3), 23.3 (CH_2), 23.4 (CH_2), 32.7 (CH_2), 68.2 (OCH_2), 118.6 (CH), 118.9 (CH), 123.4 (CH), 126.8 (Cq), 129.8 (CH), 131.5 (CH), 154.9 (Cq), 156.5 (Cq), 157.1 (Cq), 157.3 (Cq); m/z (ES) (Found: MH^+, 360.1973. $C_{24}H_{26}NO_2$ requires MH, 360.1964).

Synthesis of 2-methyl-3-(4-phenoxyphenyl)-4-ethoxy-5,6,7,8-tetrahydroquinoline (MJM170, 4)[49]

[0527] Aqueous hydrobromic acid (>48%) (1.00 ml) was added to a solution of 2-methyl-3-(4-phenoxyphenyl)-4-ethoxy-5,6,7,8-tetrahydroquinoline (10, 0.226 mg, 0.630 mmol, 1.00 eq) in glacial acetic acid (2 ml). The reaction was stirred at 90° C. for 5 days, monitoring by LMCS. The reaction was cooled to R.T. and the pH adjusted to pH5 with 2M NaOH. The precipitate was collected by vacuum filtration and recrystallized from MeOH:H_2O to give the desired product as an off-white solid (0.155 g, 0.467 mmol, 74%); HPLC (RT=2.56 mins); δ_H (500 MHz, DMSO-d_6) 1.66-1.72 (4H, m, 2×CH_2), 2.08 (3H, s, CH_3) 2.31 (2H, t, J 6.0, CH_2), 2.56 (2H, t, J 6.0, CH_2), 6.99 (2H, d, J 8.5, Ar-H), 7.06 (2H, d, J7.5, Ar-H), 7.14-7.18 (3H, m, Ar-H), 7.40-7.43 (2H, m, Ar-H), 11.0 (1H, s, NH); δ_C (125 MHz, DMSO-d_6) 17.7 (CH_3), 21.5 (CH_2), 21.8 (CH_2), 21.9 (CH_2), 26.2 (CH_2), 117.8 (CH), 118.6 (CH), 121.2 (Cq), 123.3 (CH), 123.7 (Cq), 130.0 (CH), 131.4 (Cq), 132.3 (CH), 142.3 (Cq), 143.2 (Cq), 155.0 (Cq), 156.8 (Cq), 175.4 (Cq); m/z (ES) (Found: MH^+, 332.1654. $C_{22}H_{22}NO_2$ requires MH, 332.1645).

[0528] ADME Studies of Inhibitors:

[0529] Compounds that were highly effective in vitro (IC_{50}<1 μM) were tested for ADME profiling[S43-58] by Shanghai ChemPartner Ltd. Initial studies focused on aqueous kinetic solubility pH 7.4, microsomal metabolic stability (human and mouse) and Blood-Brain Barrier (BBB) permeability (performed with MDCK-MDR1 cells as described).

In Vitro Assays

Cytotoxicity Assay

[0530] Toxicity Analysis.

[0531] Lack of toxicity for mammalian host cells was demonstrated first by visual inspection of monolayers following giemsa staining, in separate methods by incorporation of a mitochondrial cell death reagent called WST we used successfully for this purpose and in separate experiments.

[0532] Toxicity assays were conducted using WST-1 cell proliferation reagent (Roche). HFF were grown on a flat, clear-bottomed, black 96-well plate. Confluent HFF were treated with inhibitory compounds at concentrations equal to those being tested in challenge assays. Compounds were diluted in IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. A gradient of 2 fold-decreasing concentrations of DMSO in clear IMDM-C was used as a control. The plate was incubated for 72 hours at 37° C. 10 μl of WST-1 reagent (Roche) were added to each well and the cells were incubated for 30 to 60 minutes. Absorbance was read using a fluorometer at 420 nm. A higher degree of color change (and absorbance) indicated mitochondrial activity and cell viability.

[0533] In Vitro Cellular Assays for Effects on *T. gondii*

[0534] Vivo PMO:

[0535] Vivo-PMO (Vivo porter linked to morpholinos) to knock down cytochrome b and an off-target PPMO (Vivo porter) were utilized at concentrations of 5 and 10 μM as previously described with both cultures of RH-YFP tachyzoites and EGS. Morpholino sequence for cytochrome b/c knockdown is 5' AGTGTTCTCGAAACCATGCTAACAC 3' (SEQ ID NO: 5), and for unrelated sequence, off target, is 5' CCTCTTACCTCAGTTACAATTTATA 3' (SEQ ID NO: 6).

[0536] Tetrahydroquinolone Compounds:

[0537] Compounds synthesized at the University of Leeds were initially prepared in 10 mM Stock solutions made with 100% Dimethyl Sulfoxide (DMSO) [Sigma Aldrich], and working concentrations were made with IMDM-C(1×, [+]glutamine, [+] 25 mM HEPES, [−] Phenol red, 10% FBS) [Gibco, Denmark]).

[0538] Tachyzoite Assays:

[0539] Type 1 Parasites.

[0540] Human foreskin fibroblasts (HFF) were cultured on a flat, clear-bottomed, black 96-well plate to 90% to 100% confluence. IMDM (1×, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS [gibco, Denmark]) was removed from each well and replaced with IMDM-C(1×, [+] glutamine, [+] 25 mM HEPES, [−] Phenol red, 10% FBS)[Gibco, Denmark]). Type I RH parasites expressing Yellow Fluorescent Protein (RH-YFP) were lysed from host cells by double passage through a 27-gauge needle. Parasites were counted and diluted to 32,000/mL in IMDM-C. Fibroblast cultures were infected with 3200 tachyzoites of the Type I RH-YFP strain and returned to incubator at 37° C. for 1-2 hours to allow for infection. Diluted solutions of the compounds were made using IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. Controls included pyrimethamine/sulfadiazine (current standard of treatment), DMSO only, fibroblast only, and an untreated YFP gradient with 2 fold dilutions of the parasite. Cells were incubated at 37° C. for 72 hours. The plates were read using a fluorimeter (Synergy H4 Hybrid Reader, BioTek) To ascertain the amount of yellow fluorescent protein, in relative fluorescence units (RFU), as a measure of parasite burden after treatment. Compounds were not considered effective or pursued for further analysis if there were no signs of inhibition at 1 μM. Data was collected using Gen5 software and analyzed with Excel.

[0541] Type II Parasites.

[0542] To test type II parasites, *T. gondii* ME49 and Prugneaud parasites expressing luciferase or GFP. We tested them in vitro and in vivo as we have described.

[0543] EGS Strain Bradyzoite Assay.

[0544] HFF cells were grown in IMDM (1×, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS, [Gibco, Denmark]) on removable, sterile glass disks in the bottom of a clear, flat-bottomed 24-well plate. Cultures were infected with 3×10^4 parasites (EGS strain) per well, in 0.5 mL media and plate was returned to incubator at 37° C. overnight. The following day, the media was removed and clear IMDM and compounds were added to making various concentrations of the drug, to a total volume of 0.5 mL. Two wells were filled with media only, as a control. Plates were returned to the 37° C. incubator for 72 hours.

[0545] Efficacy was determined following fixation. Staining was used to determine the numbers of cysts in cultures without and with treatment with the test compounds. Cells were fixed using 4% paraformaldehyde and stained with Fluorescein-labeled Dolichos Biflorus Agglutinin, DAPI, and anti-BAG1, and anti-SAG1. Disks were removed and mounted onto glass slides and visualized using microscopy (Nikon TI7). Slides were also scanned using a CRi Pannoramic Scan Whole Slide Scanner and viewed using Panoramic Viewer Software.

[0546] When cysts that had dolichos in their cyst wall were eliminated or markedly reduced in size and number, a compound was considered efficacious against bradyzoites in cysts.

[0547] Statistical Analyses.

[0548] Significance of differences were determined using Student's t-test. $P<0.05$ was considered significant. Every experiment was replicated at least twice. A Pearson test was used to confirm a correlation between increasing dose and increasing inhibition. An ANOVA and subsequent pair wise comparison with Dunnett correction was used to determine whether or not inhibition or toxicity at a given concentration was statistically significant. Stata/SE 12.1 was used for this analysis. This study was approved by the University of Chicago IRB, IBC, and IACUC.

In Vivo Analysis (Mice and Zebra Fish):

[0549] Initial Screening with Tachyzoites Using IVIS, Fluorescence, and Histopathology:

[0550] Ability of compounds to abrogate tachyzoites multiplication was assessed using an in vivo imaging system (IVIS). To facilitate this we have *T. gondii* strains from each of the 3 major lineages expressing the luciferase gene. In these studies mice are injected intraperitoneally with tachyzoites and parasite proliferation followed up to 30 days post infection. Removal of brains at 30 days allows parasite quantitation by bioluminescence ex vivo using the IVIS. As an alternative method to improve screening efficiency and scalability it is possible for initial screening to use zebrafish with histopathology and visualization as shown in FIG. **6**. Quantitation also was performed using QT PCR as described for mice or in translucent Casper zebrafish with parasites with fluors or luciferase to screen rapidly. Tachyzoites and bradyzoites in cysts were used for IP infection and compounds given intraperitoneally.

[0551] Type II Parasites.

[0552] To test type II parasites, we used *T. gondii* Me49 and Prugneaud parasites[S39].

[0553] Encephalitis:

[0554] The ability of compounds to reduce cyst burden and prevent encephalitis induced by the Type II strain of *T. gondii* were tested. Encephalitis was assessed by histological analyses and parasite burdens evaluated by quantitation of cysts.

[0555] Oocyst Induced Disease:

[0556] The oocyst challenge model is ideal for this study because oocysts can be diluted at one time and stored at 4° C. for 12 months without loss of infectivity titer. For treatment of chronic infection there were 5 to 10 mice per group treated 2 months after infection was established by compound in DMSO for parenteral administration administered once per day. Treatment was for 17 days.

[0557] Zebrafish

[0558] Zebrafish were acclimatized to 37 degrees a degree a day and then infected with tachyzoites or cysts of RH YFP, Me49, Veg *T. gondii* as described. The use of RH YFP was performed for the first time herein in order to develop a rapidly scalable assay for drug development. This is the initial demonstration of cyst formation by 10 days in Zebrafish.

[0559] Tissue Processing and Histopathology:

[0560] All organs including eyes and brains were fixed in 0.1M phosphate buffer (pH 7.4) containing 4% formaldehyde. Sections were cut from paraffin-embedded tissues and stained with Hematoxylin and Eosin (H&E) or immunoperoxidase stained. All sections were examined and assessed without knowledge of the group from which they originated[S39].

Testing of Cytochrome b Qi Mutant Yeast

[0561] Target Validation with Mutant *S. cerevisiae* (Growth Inhibition):

[0562] Three *S. cerevisiae* strains were used: M221Q and M221F cytochrome b mutants and wild type. They share the same nuclear genetic background deriving from AD1-9 (kindly given by M.Ghislain, UCL, Belgium). AD1-9 harbors multiple deletions in the ABC transporter genes that render the strain more sensitive to drugs than standard yeast strains[S65].

[0563] Cytochrome b mutant M221F was generated by mitochondrial transformation as described. M221 Q was selected as suppressor from a respiratory deficient mutant. Analysis of revertants from respiratory deficient mutants within the center N of cytochrome b in *Saccharomyces cerevisiae.*

[0564] Protocol: Yeast strains were grown over 48 hours at 33° C. in liquid YPG medium [1% yeast extract, 2% (wt/vol) peptone, and 3% (vol/vol) glycerol). Cultures were diluted to an OD_{600} of 0.05 and grown for 2 hrs. Cultures were then combined with YPG containing 6% melted agar for a total volume of 15-20 mL and poured onto OmniTray single-well rectangular plates that measured 86 mm by 128 mm (ThermoScientific). Filter paper disks (7 mm diameter, 3 um thick) were placed onto the cooled agar plates. Compounds were dissolved in DMSO in diluted concentrations (1 mM, 500 μM, 100 μM, and 10 μM) and 10 microliters were applied to a disk. A single disk with DMSO on each plate was used as a control. Plates were incubated at 33° C. Images were obtained after 4 days using GelDoc XR Imaging System (BioRad) and Quantity One software. Drug effect was assessed by the presence and size of a zone of inhibition around the disks.

[0565] Testing of *P. falciparum*: D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone.

Testing of *P. falciparum* Cytochrome b Qi and DHODH Mutants and Drug Combinations for *P. falciparum*

[0566] Parasite Strains and Culture Maintenance.

[0567] We used the following parasite line from the MR4 repository of the American Type Culture Collection (ATCC): Dd2 (MRA-156). Mutant Dd2 parasites harboring a G33A or G33V substitution in cytochrome b were as reported. Dd2 parasites with a G131 S mutation in cytochrome b and transgenic lines expressing a chromosomally integrated copy of the *S. cerevisiae* DHODH were utilized as previously described. Parasites were cultured by standard methods in RPMI media supplemented with 5% human O^+ serum and 0.25% AlbuMAX® II (Life Technologies 11021-045).

In Vitro Drug Sensitivity and EC_{50} Determinations

[0568] Drug susceptibility was measured using the SYBR Green method. Twelve point curves based on 2-fold dilutions of the test compound were carried out in triplicate each day and replicated on at least three different days. EC_{50} values were calculated using a nonlinear regression curve fit in Prism 6.0 for Mac (GraphPad Software, Inc.).

[0569] Studies of Compound, Drug Combinations In Vitro.

[0570] Isobologram experiments were performed in similar fashion utilizing the modified fixed ratio methodology. Briefly, MJM170 and either atovaquone or cycloguanil or BRD6323 were mixed at multiple fixed volumetric ratios (10:0, 8:2, 6:4, 4:6, 2:8, and 0:10) and then serially diluted in 12-point 2-fold dilutions and dispensed in triplicate to 384-well assay plates and replicated on three different days. EC_{50} values were calculated as above, and FICs were calculated for each drug combination as described [S76]. Synergy was defined as an FIC<1.0, additivity as FIC=1.0, and antagonism as FIC>1.0.

[0571] Molecular Modelling/Chemogenomics.

[0572] X-ray structures of the cytochrome bc_1 complex are available from the Protein DataBanks[S80]. An Homology model of the *T. gondii* cytochrome bc_1 complex was generated using the Phyre webserver. Molecular modelling and docking was performed on high performance Linux clusters at the University of Leeds, using specialist software: SPROUT[S82]& eHiTs[S83] (SymBioSis), Maestro & Glides[S84] (Schrodinger), AutoDock (Scripps Institute), ROCS/EON [S85] & VIDA [S86] (OpenEye) and the Marvin/JChem suites (ChemAxon).

[0573] X-Ray Crystallography:

[0574] Cytochrome bc_1 was purified usig standard techniques. Crude bovine mitochondria were isolated from fresh cow heart and solubilised in DDM. The solution was clarified by ultracentrifugation at 200,000 g for 1 hour at 4° C. and the supernatant applied to a DEAE CL-6B sepharose column ca. 50 ml pre-equilibrated in 50 mM KPi (pH 7.5), 250 mM NaCl, 3 mM NaN_3, 0.1 g/L DDM, washed with two CV and eluted along a gradient from 250 mM to 500 mM NaCl. Cyt. bc_1 containing fractions were pooled and concentrated before loading on a Sepharose S300 column ca. 120 ml equilibrated with 20 mM KMOPS (pH 7.2), 100 mM NaCl, 0.5 mM EDTA, 0.1 g/L DDM at 0.5 ml/min. 10 mM MJM170 stock in DMSO was added to the eluted protein in a two-fold molar excess and allowed to incubate at 4° C. for 1 hour. Increasing amounts of PEG4000 were then added to precipitate cyt. bc_1 and separate remaining contaminants. The cyt. bc_1 was then resuspended before buffer exchange into a final buffer (25 mM KPi (pH 7.5), 3 mM NaN_3, 0.015% DDM) and concentrated to 40 mg/ml. 1.6% HECAMEG was added to the protein solution prior tp crystals growing by the hanging drop vapour diffusion method against a reservoir of 50 mM KPi (pH 6.8), 100 mM NaCl, 3 mM NaN_3, 9% PEG4000, 0.16% HECMAEG. Crystals were flash frozen in 23% glycerol in reservoir solution as a cryoprotectant. Multiple wedges of data were collected at 100K from different points on the same crystal at 124 Diamond Light Source using 0.9686 ÅX-rays with a Pilatus3 6M detector.

[0575] Datasets were processed in iMosflm and combined using Blend to produce a complete merged dataset. Refinement was carried out with Refmac using Prosmart to generate secondary structure restraints to assist in the low-resolution refinement. The ligand MJM170 was produced using JLigand[S92] and modelled in the Q_i site of cyt. bc_1 using Coot. Cycles of alternating Refmac5 and manual modelling resulted in a completed model. Data collection and refinement statistics are summarised In table 1A. For 3715 residues 95.2% are Ramachandran favored, 4.6% allowed and 0.3% outliers.

Interpretation of Data and Statistical Analyses

[0576] (1) Sample Size and Number of Experiments.

[0577] There were 3 replicate samples per group for in vitro experiments. All experiments were performed with sufficient sample sizes to have an 80% power to detect differences at the 5% level of significance.

[0578] (2) Statistics.

[0579] Groups included untreated or mock treated controls. Results were compared using students T test, Chi square analysis or Fisher's exact test as appropriate for the data set. When there were more than two groups, pairwise comparisons were made only when F-test for the ANOVA was significant at the 5% levels using protected least significant difference (LSD) test approach.

REFERENCES FOR EXAMPLE 1

[0580] 1. Arevalo, J. F., Belfort, R. Jr., Muccioli, C. & Espinoza, J. V. Ocular toxoplasmosis in the developing world. Int Ophthalmol Clin. 50, 57-69 (2010).

[0581] 2. Mulanovich, V. E. et al. Toxoplasmosis in allo-SCT patients: Risk factors and outcomes at a transplantation center with a low incidence. *Bone Marrow Transplant.* 46, 273-277 (2011).

[0582] 3. Porter, S. B. & Sande, M. A. Toxoplasmosis of the central nervous system in the acquired immunodeficiency syndrome. *N Engl J Med.* 327, 1643-1648 (1992). 4. McLeod, R. et al. Toxoplasmosis presenting as brain abscesses: Diagnosis by computerized tomography and cytology of aspirated purulent material. *Am. J. Med.* 67, 711-714 (1979).

[0583] 5. McLeod, R. et al. Levels of pyrimethamine in sera and cerebrospinal and ventricular fluids from infants treated for congenital toxoplasmosis: Toxoplasmosis Study Group. *Antimicrob Agents Chemother.* 36, 1040-1048 (1992).

[0584] 6. McAuley, J. et al. Early and longitudinal evaluations of treated infants and children and untreated historical patients with congenital toxoplasmosis: the Chicago Collaborative Treatment Trial. *Clin Infect Dis.* 18, 38-72 (1994).

[0585] 7. Delair, E. et al. Clinical Manifestations of Ocular Toxoplasmosis. *Ocul Immunol Inflamm.* 2, 91-102 (2011).

[0586] 8. Boyer, K. et al. Unrecognized ingestion of *Toxoplasma gondii* oocysts leads to congenital toxoplasmosis and causes epidemics in North America. *Clin Infect Dis.* 53, 1081-1089 (2011).

[0587] 9. McLeod, R. et al. Prematurity & Severity Associate with *T. gondii* Alleles (NCCCTS, 1981-2009). *Clin Infect Dis.* 54, 1595-1605 (2012).

[0588] 10. McLeod, R. et al. Severe sulfadiazine hypersensitivity in a child with reactivated congenital toxoplasmic chorioretinitis. *Pediatr. Infect. Dis. J.* 25, 270-272 (2006).

[0589] 11. Demar, M. et al. Acute toxoplasmosis in immunocompetent patients hospitalized in an intensive care unit in French Guiana. *Clinical Microbiology and Infection.* 18(7), E221-231 (July 2012).

[0590] 12. Townsend, J. J., Wolinsky, J. S., Baringer, J. R. & Johnson, P. C. Acquired toxoplasmosis: A neglected cause of treatable nervous system disease. *Arch Neurol.* 32(5), 335-343 (May 1975).

[0591] 13. Dubey, J. P., Lago, E. G., Gennari, S. M., Su, C. & Jones, J. L. Toxoplasmosis in humans and animals in Brazil: high prevalence, high burden of disease, and epidemiology. *Parasitology.* 139, 1375-1424 (September 2012).

[0592] 14. Stommel, E. W. et al. Cryptogenic Epilepsy: An Infectious Etiology? *Epilepsia.* 42, 436-438 (March 2001).

[0593] 15. Hermes, G. et al. Neurological and behavioral abnormalities, ventricular dilatation, altered cellular functions, inflammation, and neuronal injury in brains of mice due to common, persistent, parasitic infection. *J Neuroinflammation.* 5, 48 (2008).

[0594] 16. Gajewski, P. D., Falkenstein, M., Hengstler, J. G. & Golka, K. *Toxoplasma gondii* impairs memory in infected seniors. *Brain, Behavior, and Immunity.* 36, 193-199 (February 2014).

[0595] 17. Pernas, L., Ramirez, R., Holmes, T. H., Montoya, J. & Boothroyd, J. C. Immune Profiling of Pregnant *Toxoplasma*-Infected US and Colombia Patients Reveals Surprising Impacts of Infection on Peripheral Blood Cytokines. *JID.* 210, 923-931 (2014).

[0596] 18. Araujo, F. G., Huskinson-Mark, J., Gutteridge, W. E. & Remington, J. S. In vitro and in vivo activities of the hydroxynaphthoquinone 566C80 against the cyst form of *Toxoplasma gondii. Antimicrob Agents Chemother.* 36, 326-330 (1992).

[0597] 19. Torres, R. A. et al. Atovaquone/Toxoplasmic Encephalitis Study Group Atovaquone for salvage treatment and suppression of toxoplasmic encephalitis in patients with AIDS. *Clin infect Dis.* 24, 422-429 (1997).

[0598] 20. Chirgwin, K. et al. Randomized phase II trial of atovaquone with pyrimethamine or sulfadiazine for treatment of toxoplasmic encephalitis in patients with acquired immunodeficiency syndrome: ACTG 237/ANRS 039 Study. AIDS Clinical Trials Group 23. *Clin Infect Dis.* 34, 1243-1250 (2002).

[0599] 21. Winterhalter, S. et al. Does atovaquone prolong the disease-free interval of toxoplasmic retinochoroiditis? *Graefes Arch Clin Exp Ophthalmol.* 248, 1187-1192 (2010).

[0600] 22. Djurković-Djaković, O., Milenković, V., Nikolić, A., Bobić, B. & Grujić, J. Efficacy of atovaquone combined with clindamycin against murine infection with a cystogenic (Me49) strain of *Toxoplasma gondii. J Antimicrob Chemother.* 50, 981-987 (2002).

[0601] 23. Meneceur, P. et al. In vitro susceptibility of various genotypic strains of *Toxoplasma gondii* to pyrimethamine, sulfadiazine, and atovaquone. *Antimicrob Agents Chemother.* 52, 1269-1277 (2008).

[0602] 24. McFadden, D. C., Seeber, F. & Boothroyd, J. C. Use of *Toxoplasma gondii* expressing beta-galactosidase for colorimetric assessment of drug activity in vitro. *Antimicrob Agents Chemother.* 41, 1849-1853 (1997).

[0603] 24a. (CASTRO F. C. Correlacáo do diagnóstico pósnatal da toxoplasmose congenita com a reacao em cadeia da polime-rase no líquido amniótico, inoculaqáo em camundongo e achados anatomopatológicos da placenta. Thesis, Belo Horizonte, Brazil, 1999,)

[0604] 25. Paredes-Santos, T. C. et al. Spontaneous cystogenesis in vitro of a Brazilian strain of *Toxoplasma gondii. Parasitol Int.* 62(2), 181-188 (April 2013).

[0605] 26. Sanders, J. et al. The zebrafish, *Danio rerio*, as a model for *Toxoplasma gondii*: an initial description of infection in fish. *J Fish Dis.* 38(7), 675-679 (July 2015).

[0606] 27. Doggett, J. S. et al. Endochin-like quinolones are highly efficacious against acute and latent experimental toxoplasmosis. *Proc Natl Acad Sci USA.* 109(39) 15936-15941 (September 2012).

[0607] 28. Salzer, W., Timmler, H. & Andersag, I. A new type of compound active against avian malaria. *Chem Ber.* 81, 12-19 (1948).

[0608] 29. Gingrich, W. D. & Darrow, E. M. The effect of endochin on experimental toxoplasmosis. *Am J Trop Med Hyg.* 31, 12-17 (1951).

[0609] 30. Kikuth, W. & Mudrow-Reichenow, L. Ueber kausalprophylaktisch bei Vogelmalaria wirksame Substanzen. *Z Hyg Infektionskr.* 127(1-2), 151-165 (1947).

[0610] 31. Fieser, L. & Richardson, A. P. Naphthoquinone antimalarials; correlation of structure and activity against *P. lophurae* in ducks. *J Am Chem Soc.* 70(10), 3156-3165 (1948).

[0611] 32. Looareesuwan, S. et al. Clinical studies of atovaquone, alone or in combination with other antimalarial drugs, for treatment of acute uncomplicated malaria in Thailand. Am. J. *Trop. Med. Hyg.* 54, 62-66 (1996).

[0612] 33. Pudney, M., Yeates, C., Pearce, J., Jones, L. & Fry, M. New 4-pyridone antimalarials which potentiate the activity of atovaquone (566C80). *Proceedings of the XIIIth International Congress for Tropical Medicine and Malaria, Jomtien, Pattaya, Thailand.* Abstract 149 (Nov. 29-Dec. 4, 1992)

[0613] 34. Vercesi, A. E., Rodrigues, C. O., Uyemura, S. A, Zhong, L. & Moreno, S. N. Respiration and oxidative phosphorylation in the apicomplexan parasite *Toxoplasma gondii. J Biol Chem.* 273, 31040-31047 (1992).

[0614] 35. Winter, R. W. et al. Evaluation and lead optimization of anti-malarial acridones. *Exp Parasitol.* 114, 47-56 (2006).

[0615] 36. Winter, R. W. et al. Antimalarial quinolones: synthesis, potency, and mechanistic studies. *Exp Parasitol.* 118, 487-497 (2008).

[0616] 37. Yeates, C. L. et al. Synthesis and structure-activity relationships of 4-pyridones as potential antimalarials. *J. Med. Chem.* 51, 2845-2852 (2008).

[0617] 38. Mphahlele, M. J. & Mtshemla, V. 2-Aryl-4-chloro-3-iodoquinolines as substrates for the synthesis of 2,3-diaryl-4-methoxyquinolines. *J. Chem. Res.* 2008(8). 437-440 (2008).

[0618] 39. Bajohr, L. L. et al. In vitro and in vivo activities of I-hydroxy-2-alkyl-4(1H)quinolone derivatives against *Toxopasma gondii. Antimicrob Agents Chemother.* 54, 517-521 (2010).

[0619] 40. Cross, R. M. et al. Endochin optimization: structure-activity and structure-property relationship studies of 3-substituted 2-methyl-4(1H)-quinolones with antimalarial activity. *J Med Chem.* 53, 7076-7094 (2010).

[0620] 41. Korsinczky, M. et al. Mutations in *Plasmodium falciparum* cytochrome b that are associated with atovaquone resistance are located at a putative drug-binding site. *Antimicrob Agents Chemother.* 44(8), 2100-2108 (2000).

[0621] 42. Winter, R. et al. Optimization of endochin-like quinolones for antimalarial activity. *Exp Parasitol.* 127, 545-551 (2011).

[0622] 43. Cross, R. M. et al. Optimization of 1,2,3,4-tetrahydroacridin-9(10H)-ones as antimalarials utilizing structure-activity and structure-property relationships. *J Med Chem.* 54 4399 (2011).

[0623] 44. Fry, M. & Pudney, M. Site of action of the antimalarial hydroxynaphthoquinone, 2-[trans-4-(4'-chlorophenyl) cyclohexyl]-3-hydroxy-1,4-naphthoquinone (566C80). *Biochem Pharmacol.* 43, 1545 (1992).

[0624] 45. Riscoe, M. K. et al., inventors; Oregon Health & Science University, assignee. Compounds having anti-parasitic or anti-infectious activity. International patent WO 2010/065905 A2. 2010 Jun. 10.

[0625] 46. Vallieres, C. et al. HDQ, A potent inhibitor of *Plasmodium falciparum* proliferation binds to the Qi site of the bc1 complex. *Antimicrob Agents Chemother.* 56, 3739-3747 (2012).

[0626] 47. Biagini, G. A. et al. Generation of quinolone antimalarials targeting the *Plasmodium falciparum* mitochondrial respiratory chain for the treatment and prophylaxis of malaria. *Proc Natl Acad Sci USA.* 109, 8298 (2012).

[0627] 48. LaCrue, A. N. et al. 4(1H)-Quinolones with Liver Stage Activity against *Plasmodium berghei. Antimicrob Agents Chemother.* 57, 417 (2013).

[0628] 49. Nilsen, A. et al. Discovery, Synthesis, and Optimization of Antimalarial 4(1H)-Quinolone-3-Diarylethers. *J Med Chem.* 57(9), 3818-3834 (2014).

[0629] 50. Lukens, A. et al. Diversity-Oriented Synthesis Probe Targets *Plasmodium falciparum* Cytochrome b Ubiquinone Reduction Site and Synergizes With Oxidation Site Inhibitors. *J Infect Dis.* 211(7),1097-1103 (2015).

[0630] 51. Boyom, F. F. et al. Repurposing the Open Access Malaria Box To Discover Potent Inhibitors of *Toxoplasma gondii* and *Entamoeba histolytica. Antimicrob Agents Chemother.* 58(10), 5848-5854 (2014).

[0631] 52. Capper, M. J. et al. Antimalarial 4(1H)-pyridones bind to the Qi site of cytochrome bc1. *Proc. Natl. Acad Sci. USA.* 112(3), 755-760 (2015).

[0632] 53. Nilsen, A. et al. Quinolone-3-diarylethers: a new class of antimalarial drug. *Sci Transl Med.* 5(177) 177ra37 (2013).

[0633] 54, Brasseur, G. & Brivet-Chevillotte, P. Characterization of mutations in the mitochondrial cytochrome b gene of *Saccharomyces cerevisiae* affecting the quinone reductase site (Q_N). *Eur J Biochem.* 230, 1118-1124 (1995).

[0634] 55. Hutson, S. L. et al. *T. gondii* RP promoters & knockdown reveal molecular pathways associated with proliferation and cell-cycle arrest. *PLoS One.* 5(11), e14057 (2010).

[0635] 56. Smilkstein, M. J. et al. A drug-selected *Plasmodium falciparum* lacking the need for conventional electron transport. *Mol Biochem Parasitol.* 159(1), 64-68 (2008).

[0636] 57. Ke, H. et al. Variation among *Plasmodium falciparum* strains in their reliance on mitochondrial electron transport chain function. *Eukaryot Cell.* 10(8), 1053-1061 (2011).

[0637] 58. Trumpower, B. L. & Edwards, C. A. Purification of a reconstitutively active iron-sulfur protein (oxidation factor) from succinate cytochrome c reductase complex of bovine heart mitochondria. *J. Biol. Chem.* 254, 8697-8706 (1979).

[0638] 59. White, N. J. et al. Malaria. *Lancet.* 383, 723-735 (2014).

[0639] 60. Burrows, J. N. et al. Antimalarial drug discovery—the path towards eradication. *Parasitology.* 141, 128-139 (2014).

[0640] 61. Stickles, A. M. et al. Inhibition of cytochrome bc1 as a strategy for single-dose, multi-stage antimalarial therapy. *Am J Trop Med Hyg.* 92(6), 1195-1201 (2015).

[0641] 62. Stickles, A. M. et al. Subtle changes in endochin-like quinolone structure alter the site of inhibition within the cytochrome bc1 complex of *Plasmodium falciparum. Antimicrob Agents Chemother.* 59(4), 1977-1982 (2015).

[0642] 63. Bueno, J. M. et al. Exploration of 4(1H)-pyridones as a novel family of potent antimalarial inhibitors of the plasmodial cytochrome bc1. *Future Medicinal Chemistry.* 4(18), 2311-2323(2012) (doi: 10.4155/fmc.12.177).

[0643] 64. Mui, E. et al. Novel triazine JPC-2067-B inhibits *Toxoplasma gondii* in vitro and in in vivo. *PLoS Negl Trop Dis.* 2(3):e190 (2008).

[0644] 65 Saini, S. et al. MicroRNA-708 induces apoptosis and suppresses tumorigenicity in renal cancer cells. *Cancer Res.* 71, 6208-6219 (2011).

[0645] 66. Radke, J. B., Transcriptional control of *Toxoplasma* development. PhD dissertation, University of South Florida (2014).

Example 2. Potent Anti-Apicomplexan Tetrahydroquinolone

[0646] Summary:

[0647] Apicomplexan infections cause substantial morbidity and mortality. Herein, we created a next generation tetrahydroquinolone that we found to be an anti-apicomplexan, mature, lead compound. We utilized sphere-like 3D space and predicted flexibility conferred by eliminating double bonds in this lead compound. This was to optimize ADMET and create a compound, JAG21, that is potent against *Toxoplasma gondii* tachyzoites (IC 90<125 nM) and bradyzoites (IC 90 500 nM), and drug resistant *Plasmodium falciparum* in vitro (IC 90<50 nM), not toxic to human HepG cells (>17 μM). Further, we demonstrate metabolic stability with assays for human and mouse liver microsomal activity and logs improved aqueous solubility at pH 7.4. This compound displays a balanced set of physicochemical and pharmacologic properties, including clean hERG, CYP profile, and a long (days in humans), predicted half-life and predicted ability to cross blood brain barrier. This allowed progression towards in vivo studies. In vivo *Toxoplasma* tachyzoites were cleared from mice at a dose of 5 mg/kg/day (IP). JAG21 acted in conjunction with tafenoquine (3 mg/kg single dose) to protect against a G0 arrested parasite that could persist in interferon Y knockout mice similar to the effect of tafenoquine for malaria hypnozoites. There was cure with oral dosing, 0.625 mg/kg, 3 oral doses of JAG21, and cure with a single dose of 2.5 mg/kg, of *P. berghei* sporozoite, blood and liver stages in mice. There was no parasitemia and 100% survival at 30 days. This mature lead compound has improved solubility and diminished toxicity relative to other cytochrome b Qi inhibitors, without formulation as a pro-drug. Selectivity for apicomplexan enzyme relative to mammalian enzymes was demonstrated with co-crystallography, binding and enzyme assays. This compound has real promise as a mature, lead compound.

[0648] Malaria results in death of one child every eleven seconds and 1 million children a year, with drug resistance eliminating usefulness of successive generations of new medicines each decade. The related apicomplexan parasite, *Toxoplasma gondii*, is the most frequent parasitic infection of humans, in the world. It is the second most frequent, single cause of food born associated death in the United States; It is the most frequent infectious cause of destruction of the back of the human eye; It is a cause of death and illness from recrudescent disease from its latent form in those who are immune compromised or immunologically immature; It has been estimated that in a ten year period, there are 1.9 million new cases of this congenital infection globally, causing 12 million disability adjusted life years from damage to the fetal brain and eye. This is neglected, rarely diagnosed, and thus often untreated or mistreated disease. There are approximately 2 billion people throughout the world who have this parasite in their brain lifelong. No medicine eliminates this chronic encysted form of the parasite which causes epilepsy and may contribute to neurodegenerative disease. Certainly, new and improved medicines are greatly needed for both these diseases. These two apicomplexan parasites, *Plasmodia* and *Toxoplasma*, often share molecular targets inhibited by the same inhibitory compounds.

[0649] Herein we identify a mature lead compound that is highly efficacious against *T. gondii* tachyzoites and bradyzoites in vitro, tachyzoites in vivo, likely to be active against cysts in vivo with experiments ongoing, all drug resistant forms of *Plasmodium falciparum, Plasmodium berghei* in mouse model in single or three doses at low amounts against the sporozoite, blood and liver stages of *plasmodium* when administered orally at 2.5 mg/kg and at 1.25 mg kg for 100% of mice with three doses. It was found to add to protection in conjunction with tafenoquine in immune compromised mice infected with a G0/tachyzoite form of *T. gondii* which resembles the malaria hypnozoite when treated with tafenoquine in conjunction with anti-blood stage parasite compounds. The data which follow present the creation and characterization of this broad spectrum anti-apicomplexan lead compound.

Materials and Methods

[0650] *Toxoplasma gondii*

[0651] Tachyzoites of the RH-YFP strain were passaged in human foreskin fibroblasts (HFF cells)(15). Bradyzoite assays use the EGS strain, isolated from a human with congenital toxoplasmosis (16,17). These parasites are also passaged in human foreskin fibroblasts. RPS13 delta was prepared and utilized as described (Hutson, McLeod et al 2010)

Tetrahydroquinolone (THQ) Compounds

[0652] The THQ compounds were synthesized at the University of Leeds as described in Example 3. 10 mM stock solutions were made with 100% Dimethyl Sulfoxide (DMSO) [Sigma Aldrich] and working concentrations were made with IMDM-C(1×, [+] glutamine, [+] 25 mM HEPES, [−] Phenol red, 10% FBS)[Gibco, Denmark]). Compounds are shown herein.

In Vitro Challenge Assay for *Toxoplasma* Tachyzoites

[0653] Protocol adapted from Fomovska, et. al. (18,19). Human foreskin fibroblasts (HFF) were cultured on a flat, clear-bottomed, black 96-well plate to 90% to 100% confluence. IMDM (1×, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS [gibco, Denmark]) was removed from each well and replaced with IMDM-C(1×, [+] glutamine, [+] 25 mM HEPES, [−] Phenol red, 10% FBS)[gibco, Denmark]). Type I RH parasites expressing Yellow Fluorescent Protein (RH-YFP) were lysed from host cells by double passage through a 27-gauge needle. Parasites were counted and diluted to 32,000/mL in IMDM-C. Fibroblast cultures were infected with 3200 tachyzoites of the Type I RH strain expressing Yellow Fluorescent Protein (RH-YFP) and returned to incubator at 37° C. for 1-2 hours to allow for infection(15). Various concentrations of the compounds were made using IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. Controls included pyrimethamine/sulfadiazine (current standard of treatment), 0.1% DMSO only, fibroblast only, and an untreated YFP gradient with 2 fold dilutions of the parasite. Cells were incubated at 37° C. for 72 hours. Plates were read using a fluorimeter (Synergy H4 Hybrid Reader, BioTek) to ascertain the amount of yellow fluorescent protein, in relative fluorescence units (RFU), as a measure of parasite burden after treatment. Data was collected using Gen5 software. IC_{50} was calculated by graphical analysis in Excel.

[0654] An initial screening assay of 10 μM, 1 μM, 100 nM, and 10 nM was performed. Compounds were not considered effective or pursued for further analysis if there were no signs of inhibition of tachyzoites at 1 μM. If compounds did appear to be effective at 1 μM, another experiment was conducted to assess effect at 1 μM, 500 nM, 250 nM, 125 nM, 62.5 nM, and 31.25 nM.

Cytotoxicity Assay

[0655] Toxicity assays were conducted using WST-1 cell proliferation reagent (Roche) as described in Fomovska, et. al. (18,19). HFF were grown on a flat, clear-bottomed, black 96-well plate. Confluent HFF were treated with inhibitory compounds at concentrations of 10 μM and 50 μM. Compounds were diluted in IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. A gradient of 2 fold-decreasing concentrations of DMSO from 10% to 0% in clear IMDM-C was used as a control. The plate was incubated for 72 hours at 37° C. 10 μl of WST-1 reagent (Roche) were added to each well and the cells were incubated for 30 to 60 minutes. Absorbance was read using a fluorimeter at 420 nm. A higher degree of color change (and absorbance) indicated mitochondrial activity and cell viability.

In Vitro Challenge Assay for Bradyzoites

[0656] HFF cells were grown in IMDM (1×, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS, [gibco, Denmark]) on removable, sterile glass disks in the bottom of a clear, flat-bottomed 24-well plate. Cultures were infected with 3×10^4 parasites (EGS strain) per well, in 0.5 mL media and plate was returned to incubator at 37° C. overnight. The following day, the media was removed and clear IMDM and compounds were added to making various concentrations of the drug, to a total volume of 0.5 mL. 2 wells were filled with media only, as a control. Plates were returned to the 37° C. incubator for 72 hours, and checked once every 24 hours. If tachyzoites were visible in the control before 72 hours, the cells were fixed and stained.

[0657] Cells were fixed using 4% paraformaldehyde and stained with Fluorescein-labeled Dolichos Biflorus Agglutinin, DAPI, and BAG1. Disks were removed and mounted onto glass slides and visualized using microscopy (Nikon TI7). Slides were scanned using a CRi Pannoramic Scan Whole Slide Scanner and viewed using Panoramic Viewer Software. Effects of the compounds were quantified by counting cysts in the controls and treated cells. Cysts and persisting organisms were counted in a representative field of view and then multiplied by a factor determined by the total area of the disk in order to estimate the number of cysts and organisms in each condition.

Assessment of Compound Degradation and Microbicidal Effect on *Toxoplasma*

[0658] HFF were cultured in a 96-well plate and infected with RH-YFP as described above on Day 0, 20 μL of compound was added to 9 wells for each compound and concentration (3 conditions, 3 wells per condition). In condition I, media was removed and replaced with fresh media on Day 3. In condition II, media was removed and replaced with fresh media and more compound on Day 3. In condition III, media was not replaced on Day 3, nor was the compound refreshed. On Day 6, media was removed and replaced with clean media in all wells. On Day 3, 6, and 9 plate was read in the fluorimeter and analyzed graphically in Prism (GraphPad Software).

Toxoplasma In Vivo

[0659] IVIS. Mice were infected intraperitoneally with 20×10^3 *Toxoplasma gondii* (Pru strain expressing luciferase) tachyzoites. Treatment commenced 2 hours later with JAG21 (5 mg/kg) which was dissolved in DMSO and administered intraperitoneally in a total volume of 0.05 ml. Mice were imaged every second day starting on day 4 post infection using a IVIS Spectrum (Caliper Life Sciences) for a 1 minute exposures, with medium binning, 20 minutes post injection with 150 mg/kg of D-luciferin potassium salt solution.

[0660] Brain cysts: Mice were infected intraperitoneally with 20×10^3. Treatment commenced 2 hours later with JAG21 (5 mg/kg) which was dissolved in DMSO and administered intraperitoneally in a total volume of 0.05 ml. After 30 days, treatment with JAG21 was begun each day for 14 days intraperitoneally. In experiments when tafenoquine was administered alone or with JAG21 in some groups 3 mg/kg tafenoquine was administered once on day −1. Cysts in brain were quantitated after concluding treatment

[0661] RPS13 Δ. This G0 arrested parasite persists in tissue culture for prolonged times in the absence of tetracycline. The design of this experiment is shown in FIG. **18**. The parasite (x) was used to infect interferon gamma knockout mice. For the first y days no tetracycline was administered. After that time tetracycline was administered. Mice were observed and at the time they appeared ill or at the termination of the experiment they were euthanized and tissues fixed in formalin and stained with hematoxylin and eosin or immunoperoxidase stained and parasite burden was assessed.

Malaria Assays

[0662] Methods for enzyme assays[21-3]: Professor Giancarlo A. Biagini, Dr Richard S. Priestley, Department of Parasitology, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool, L3 5QA, UK.

Materials

[0663] *Plasmodium falciparum:* 3D7 strain was obtained from the Liverpool School of Tropical Medicine. Protease cocktail inhibitor was obtained from Roche. Bradford protein assay dye reagent was obtained from Bio-Rad. All other reagents were obtained from Sigma-Aldrich. Decylubiquinol was produced as per Fisher et al. (Fisher et al. 2004)[21]. In brief, 25 mg of decylubiquinone were dissolved in 400 μl of nitrogen-saturated hexane. An equal volume of aqueous 1 M sodium dithionite was added, and the mixture vortexed until colorless. The organic phase containing the decylubiquinol was collected, the solvent was evaporated under N_2 and the decylubiquinol finally dissolved in 100 μl of 96% ethanol (acidified with 10 mM HCl). Concentrations of decylubiquinol was determined spectrophotometrically on a Cary 300 Bio UV/visible spectrophotometer (Varian, UK) from absolute spectra, using $\varepsilon_{288-320}=8.1\ \text{mM-1}\cdot\text{cm}^{-1}$. Decylubiquinol was stored at −80° C. and used within two weeks.

Plasmodium falciparum: Culture and Extract Preparation

[0664] *Plasmodium falciparum*: strain 3D7 blood-stage cultures were maintained by the method of Trager and Jensen (Trager & Jensen 2005)[23]. Cultures contained a 2% suspension of O+ human erythrocytes in RPMI 1640 medium containing L-glutamine and sodium carbonate, and supplemented with 10% pooled human AB+ serum, 25 mM HEPES (pH 7.4) and 20 μM gentamicin sulphate. Cultures were grown under a gaseous headspace of 4% 02 and 3% CO_2 in N_2 at 37° C. Cultures were grown to a parasitaemia of 5% before use.

[0665] The protocol for the preparation of parasite extract was adapted from Fisher et al. (Fisher et al. 2009)[22]. Free parasites were prepared from infected erythrocytes pooled from five T75 flasks, by adding 5 volumes of 0.15% (w/v) saponin in phosphate-buffered saline (137 mM NaCl, 2.7 mM KCl, 1.76 mM K_2HPO_4, 8.0 mM Na_2HPO_4, 5.5 mM D-glucose, pH 7.4) for 5 min, followed by three washes by centrifugation in RPMI containing HEPES (25 mM), and a final resuspension in potassium phosphate buffer (50 mM K_2HPO_4, 50 mM KH_2PO_4, 2 mM EDTA, pH7.4) containing a protease inhibitor cocktail (Complete Mini; Roche). Parasite extract was then prepared by disruption with a sonicating probe for 5 s, followed by a 1 min rest period on ice to prevent the sample overheating. This process was performed three times. The parasite extract was used immediately. The protein concentration of the parasite extract was determined by Bradford protein assay (Bio-Rad).

[0666] Pfbc$_1$ Native Assay

[0667] *Plasmodium falciparum* bc$_1$ complex cytochrome c reductase (Pfbc$_1$) activity was measured by monitoring cytochrome c reduction at 550 versus 542 nm using a Cary 300 Bio UV-Visible Spectrophotometer (Varian, UK), using a protocol adapted from Fisher et al. (Fisher et al. 2009)[21-23]. The assay was performed in potassium phosphate buffer in a quartz cuvette and in a final volume of 700 μL. Potassium cyanide (10 μM), oxidised cytochrome c (30 μM), parasite extract (100 μg protein) and compound/DMSO were added sequentially to the cuvette, with mixing between each addition. Test compounds were added to a final concentration of 1 μM. DMSO (0.1% v/v) and atovaquone (1 μM), a known malarial cytochrome bc$_1$ complex inhibitor, were used as negative and positive controls respectively. The reaction was initiated by the addition of 50 μM decylubiquinol and allowed to proceed for 3 min.

Data Analysis

[0668] Malaria

In Vitro Studies:

[0669] D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. These assays were performed as described.

Compound Activity Against *Plasmodium falciparum:*

[0670] Compound activity against *P. falciparum*, a causative agent of malaria, was tested using the Malaria SYBR Green I—Based Fluorescence (MSF) Assay. This; microtiter plate drug sensitivity assay uses the presence of malarial DNA as a measure of parasitic proliferation in the presence of antimalarial drugs or experimental compounds based on modifications of previously described methods by Plouffe et al (20) and Johnson et al. As the intercalation of SYBR Green I dye and its resulting fluorescence is relative to parasite growth, a test compound that inhibits the growth of the parasite will result in a lower fluorescence.

[0671] Selected compounds were examined for activity against four strains of *P. falciparum*: D6 (CDC/Sierra Leone), a drug-sensitive strain readily killed by chloroquine, TM91-C235, a multi-drug resistant strain resistant to chloroquine, W2, a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone.

P. berghei Model Sporozoite, Blood Stage, and Liver Stage Model.

[0672] *P. berghei* sporozoites. The methods that follow are taken directly from [24,25]: From laboratory-reared female *Anopheles stephensi*, isolation, inoculation and viability check *Plasmodium berghei* sporozoites (luciferase expressing) were obtained and maintained at 18° C. for 17 to 22 days after feeding on malaria-infected Swiss CD-1/ICR mice. From malaria-infected mosquitoes, salivary glands were extracted and sporozoites obtained. Briefly, mosquitoes were separated into head/thorax and abdomen. Thoraxes and heads were triturated with a mortar and pestle and suspended in medium RPMI 1640 containing 1% C57BL/6 mouse serum (Rockland Co, Gilbertsville, Pa., USA). 50-80 heads with glands total were placed into a 0.5 ml Osaki tube on top of glass wool with enough dissection media to cover the heads. Until all mosquitoes had been dissected, the Osaki tube was kept on ice. Sporozoites that were isolated from the same batch of mosquitoes were inoculated into C57BL/6, 2D knock-out and 2D knock-out/2D6 knock-in C57BL/6 mice on the same day to control for biological variability in sporozoite preparations. On day 0, each mouse was inoculated intravenously in the tail vein with approximately 10,000 sporozoites suspended in 0.1 ml volume. They were stained with a vital dye containing fluorescein diacetate (50 mg/ml in acetone) and ethidium bromide (20 μg/ml in phosphate buffered saline; Sigma Chemical Co, St. Louis, Mo., USA) and counted in a haemocytometer to ensure that inoculated sporozoites were viable following the isolation procedure. Viability of the sporozoites ranged from 90 to 100%.

Animals

[0673] The mice used in these experiments were Swiss Webster females. The animals were acclimated for seven days (quarantine) on arrival. The animals were housed in a cage maintained in a room with 34-68% relative humidity, a temperature range of 64-79° F., and a 12-hr light/dark cycles. Water and food were provided during quarantine and throughout the study. The mice were fed a standard rodent maintenance diet. All animal studies were performed under protocols that are IACUC-approved. All animal care, handling, and use was performed in accordance with the current Guide for the Care and Use of Laboratory Animals (1996).

Test Compounds and Administration

[0674] At the time of preparation of the suspension solution, compounds tested in these experiments were dosed based on the body weight. The suspension solution of oral agents, using homogenizer (PRO Scientific Inc, Monroe, Conn., USA) with 10 mm open-slotted generator to homogenize drug powder mixture at 20,000-22,000 rpm for 5 min in ice bath, were prepared in 0.5% (w/v) hydroxyethyl cellulose and 0.2% (0.5% HECT, v/v) Tween-80 in distilled water.

[0675] A three consecutive day-treatment regimen (−1, 0, 1 day) or a once-a-day, one dose on day 0 was used in assessments. Drug suspensions were transferred to a 20-ml bottle, drawn into a 1-ml syringe, and delivered to the designated recipient via intragastric feeder (18 gauge).

[0676] 1 hour after intravenous administration of 10,000 *P. berghei* sporozoites, single dose causal prophylaxis in 5 C57BL/6 albino mice at 2.5 mpk dosed on day 0. In 5 C57BL/6 albino mice, 3 dose causal prophylaxis treatment at 0.6 mpk dosed on days −1, 0, and +1.

In Vivo Imaging System Spectrum

[0677] All of the in vivo imaging system (IVIS) methods utilized have been described previously [6]. Briefly TQ and NPC-1161B were administered orally on days −1, 0 and 1 with respect to sporozoite inoculation. All inoculated mice were tested using the Xenogen IVIS-200 Spectrum (Caliper Life Sciences, Hopkinton, Mass., USA) IVIS instrument at 24, 48 and 72 hr post-sporozoite infection. Additionally, using a flow cytometry system (FC500 MPL, Beckman

Coulter, Miami, Fla., USA), blood-stage infections were measured. For the IVIS calibration in each test, positive and negative controls were used. D-Luciferin potassium salt, (Xenogen, California and Goldbio, St Louis, Mo., USA), the luciferase substrate, was inoculated intraperitoneally into mice at a concentration of 200 mg/kg 15 min before luminescence analysis. Three min post-luciferin administration the mice were anesthetized using isoflurane. The mice, in the IVIS on the 37° C. platform, were then positioned ventral side up. Through nose cone delivery, the mice continued to receive isoflurane. The exposure time of the camera was 5 min for the 24, 48 and 72 hr time points with f-stop=1 and large binning setting. Using Living Image® 3.0 software, photons emitted from specific regions were quantified.

[0678] Parasitemia was measured after days of IVIS imaging. During a total of 30 days, mice were observed and parasitemia level determined using FACs analysis. (Pybus et al. Malaria Journal 2013, 12:212; Marcsisin et al. Malaria Journal 2014, 13:2).

Bovine Cytochrome bc1 Purification Protocol

[0679] Preparation of Crude Mitochondria:

[0680] Whole bovine heart was collected directly from slaughter and transported on ice to the cold room. All work was carried out at 4° C. Fat and other tissues were removed leaving only lean muscle that was then cut into small cubes. The cubes were then transferred to a waring blender and homogenisation buffer (250 mM sucrose; 20 mM K_2HPO_4; 2 mM succinic acid; 0.5 mM EDTA) was added at a ration of 2.6 L buffer per 1 L of muscle tissue. The solution was then homogenised. The resulting homogenate was adjustered to pH 7.8 using 2 M Tris and PMSF was added to a concentration of 0.1 mM. The homogenate was then centrifuged in a Sorvall GS-3 rotor at 3000 rpm for 20 mins. The resulting supernatant was then transferred to a Sorvall GSA rotor and centrifuged at 12,000 rpm for 20 mins. The pellet was then re-suspended and washed in buffer 1 (50 mM KPi (pH 7.5); 0.1 mM PMSF) before centrifugation under the same conditions again. The pellet was collected and frozen at −80° C. for use later.

[0681] Solubilisation of Membrane Proteins:

[0682] The frozen mitochondria were thawed and re-suspended in buffer 2 (50 mM KPi (pH 7.5); 150 mM NaCl; 3 mM NaN_3; 0.1 mM PMSF) and a sample taken for a BCA assay. The remaining sample was centrifuged at 42,000 rpm in a Beckman Ti70 rotor for 60 mins. The pellet was re-suspended in the same wash buffer to a volume of 70 ml with the addition 0.1 mg DDM per 1 mg of protein and centrifuged at 42,000 rpm in a Beckman Ti70 rotor for 60 mins. The pellet was then re-suspended in the same wash buffer to a final volume of 215 ml with the addition of 0.9 mg DDM per 1 mg of protein and centrifuged for a final time at 42,000 rpm in a Beckman Ti70 rotor for 60 mins. The supernatant was collected.

[0683] Purification of Cytochrome bc1:

[0684] Whilst being purified, the presence of protein was determined using 280 nm absorbance and the presence of haem was determined using 415 nm soret band peak and 462 nm absorbance. The solubilised protein solution was first applied to a DEAE-Sepharose CL-6B column (ca. 50 ml) pre-equilibrated in buffer A (50 mM KPi (pH 7.5); 150 mM NaCl; 0.03% DDM; 3 mM NaN_3) washed with 2 CV buffer A and eluted along a gradient with buffer B (50 mM KPi (pH 7.5); 350 mM NaCl; 0.03% DDM; 3 mM NaN_3). The collected protein was pooled and diluted twofold with buffer C (50 mM KPi (pH 7.5); 0.03% DDM; 3 mM NaN_3) before application to a hydroxyapatite column (ca. 15 ml) pre-equilibrated with buffer C. The column was washed with 10 CV of buffer C before elution along a gradient with Buffer C* (1000 mM KPi (pH 7.5); 0.03% DDM; 3 mM NaN_3). Fractions containing cytochrome bc_1, as identified by 415 nm absorbance, were then collected, pooled and concentrated to 1.5 ml using an Amicon Ultra-15 (Amicon, MWCO 100,000). The sample was then applied to a Sephacryl-S300 column (ca. 120 ml) pre-equilibrated in buffer D (25 mM KPi (pH 7.5); 100 mM NaCl; 0.015% DDM; 3 mM NaN_3) and ran at a flow rate of 0.5 ml/min. Purified cytochrome bc_1 fractions were then collected and concentrated to 30 mg/m.

[0685] Bovine Enzyme Crystallography:

[0686] Compounds designed using structure-based analyses of cytochrome b co-crystalized with JAG21 as described in Example 1 [26]. This was done to optimize medicine-like properties using structure activity principles and analyses. Compounds synthesized as above were used in these assays as follows: 10 mM stock solutions were made with 100% Dimethyl Sulfoxide (DMSO) [Sigma Aldrich] and working concentrations were made with IMDM-C(1×, [+] glutamine, [+] 25 mM HEPES, [−] Phenol red, 10% FBS)[gibco, Denmark]).

[0687] Statistical Analysis:

[0688] A Pearson test was used to confirm a correlation between increasing dose and increasing inhibition. An ANOVA and subsequent pairwise comparison with Dunnett correction was used to determine whether or not inhibition or toxicity at a given concentration was statistically significant. Stata/SE 12.1 was used for this analysis.

Results

Tetrahydroquinolone Compounds:

[0689] In Vitro Challenge Assay for Tachyzoites:

[0690] Seven compounds (Table 1) were tested and each compound was tested at least twice. JAG021 and JAG050 demonstrated effect below 1 μM, and were tested at lower concentrations. A representative graph of this data is shown in FIG. **13**. JAG050 and JAG021 were identified as lead compounds because the IC_{50} values were 55 and 188 nM respectively. Correlation between concentration of compound and inhibition of parasite growth and activity (as measured by fluorescence) was observed for all compounds except JAG046.

[0691] Cytotoxicity Assay Using HFF and WST-1 and IC50 with HEP G Cells:

[0692] Because *T. gondii* grows inside cells, if a compound was toxic to host Human Foreskin Fibroblast Cells (HFF), then it would make the compound appear to be spuriously effective; in actuality only toxicity for the host cell would be measured. Cytotoxicity to human foreskin fibroblasts was therefore assessed for all compounds at 10 μM and 50 μM. Results of this experiment are in FIG. **14** and Table 3. A two-way ANOVA and subsequent pairwise comparison found none of the differences in absorbance, compared to the controls, to be statistically significant ($p>0.05$). This suggests that these compounds are not toxic at 10 μM or 50 μM and that toxicity to cells is attributed to DMSO in the solution, not the compound. IC50 with HEP G cells was performed as described and toxicity was: HEP G2 IC50 17.70 microM ($r^2=0.97$) JAG 21; JAG 50 7.1 microM $r^2=0.98$.

TABLE 3

Cytotoxicity to human foreskin fibroblasts was therefore assessed for all compounds at 10 μM and 50 μM. Graph is representative of replicate experiment.

Observation	Control	JAG050 10 μM	JAG050 1 μM	JAG021 10 μM	JAG021 1 μM
		a			
True Cysts	4.67 ± 3.06 [2-8]	1 ± 0.82 [0-2]	0.25 ± 0.5 [0-1]	0.25 ± 0.5 [0-1]	0.5 ± 0.6 [0-1]
Pseudocysts	40.3 ± 11.4 [31-53]	20.5 ± 2.9 [17-24]	23.25 ± 10.31 [14-38]	25.5 ± 5.1 [19-30]	29 ± 6 [21-34]
Small organisms	1600 ± 436 [1100-1900]	31 ± 16 [8-43]	58 ± 24 [27-85]	73.25 ± 30.9 [30-101]	90.5 ± 33.5 [63-137]
		b			
True Cysts	452	88	29	22	54
Pseudocysts	3884	1921	2269	2638	2955
Small organisms	16404	3018	5086	7309	9734

In Vitro Challenge Assay for Bradyzoites

[0693] Lead compounds JAG050 and JAG021 were tested against EGS because of their effects on tachyzoites (RH-YFP). Under immunofluorescence microscopy, the following forms were observed: "true cysts" with a dolichos-staining wall, "pseudocysts" or tight clusters of parasites, and small organisms (FIG. **15***d*). If there were fewer than four parasites visible in a cluster, the organisms were counted individually (as "small organisms"). A statistically significant reduction in the number of true cysts and small organisms was observed at 1 μM and 10 μM for both compounds ($p<0.05$, $p<0.005$, FIG. **15***a-c*).

[0694] ADME properties of THQs.

[0695] In vitro ADME analyse of the THQ compounds were outsourced to ChemPartner Shanghai Ltd. ELQ-271 was tested as a comparison. THQs which were potent inhibitors of *T. gondii* tachyzoites were assessed for their kinetic solubility, metabolic stability in human and mouse liver microsomes, and their ability to permeate across MDCK-MDK1 cell membranes (in vitro measure of blood-brain barrier (BBB) permeability). Solubility, half-life and BBB permeability/efflux results are shown in Table 4. The kinetic solubility (PBS, pH 7.4) of compounds JAG021 and JAG050, 7 and 16 μM respectively, were higher than MJM170 (2 μM) and ELQ-271 (0.2 μM). JAG021 was the most metabolically stable compound in human liver microsomes (>99% remaining after 45 mins) compared with other THQs and ELQ-271, although it displayed a much shorter half-life of 101 mins in mouse liver microsomes. All THQs tested in the MDK1(MJM170, JAG021 and JAG050) MDCK-MDK1 system exhibit high permeability ($P_{app}>10\times10^{6}$ cm/s) and low efflux (efflux ratio <1.5).

TABLE 4

Chart compares properties of solubility and half-life of JAG050 and JAG021 to parent compounds ELQ 271 and MJM170. The test system was 100 mM Phosphate Buffer (pH 7.4).: <10 μM is low solubility, 10-80 μM is moderate solubility and >80 μM is high solubility. A $T_{1/2}$ < 30 minutes indicates susceptibility to metabolism, between 30 and 120 minutes indicates moderate metabolism and >120 minutes indicates stability in the liver.

Compound	Solubility (pH 7.4)*	Human liver microsomes$^{\#}$	Mouse liver microsomes$^{\#}$
ELQ271	0.15 μM	171.93 min	448.13 min
MJM170	1.97 μM	146.33 min	20.97 min
JAG021	7.07 μM	∞	101.09 min
JAG050	16.41 μM	99.04 min	68.55 min

TABLE 4-continued

Chart compares properties of solubility and half-life of JAG050 and JAG021 to parent compounds ELQ 271 and MJM170. The test system was 100 mM Phosphate Buffer (pH 7.4).: <10 μM is low solubility, 10-80 μM is moderate solubility and >80 μM is high solubility. A $T_{1/2}$ < 30 minutes indicates susceptibility to metabolism, between 30 and 120 minutes indicates moderate metabolism and >120 minutes indicates stability in the liver.

[0696] Enzyme Assays:

[0697] Enzyme reduction of cytochrome c by the parasite extract is mediated by *P. falciparum* bc_1 complex cytochrome c reductase ($Pfbc_1$). All three compounds (1 μM) significantly inhibited the reduction of cytochrome c by the parasite extract, (JAG021=86.4±3.2; JAG099=81.3±6.0; MJM170=69.7±11.3% atovaquone response). This clearly demonstrates the compounds are inhibitors of $Pfbc_1$. Additional data demonstrating effect on bovine and *Plasmodium falciparum* enzyme are shown in Table 5. There is selectivity for the malaria enzyme.

TABLE 5

Inhibition of $Pfbc_1$ by compounds.

Compound (1 μM)	Inhibition of cytochrome c reduction (% atovaquone response)
JAG021	86.4 ± 3.2
JAG099	81.3 ± 6.0
MJM170	69.7 ± 11.3

Data shown are mean ± s.e.m. of 4 independent experiments performed in triplicate.

[0698] Binding Assays and Co Crystallography.

[0699] JAG021 has lower binding affinity to bovine cytochrome bc in comparison with previous compounds that we have tested. JAG 21 ‘inhibits’ Cytbc1 but not fully, indicating that it will be less toxic for bovine/human cyt bc (FIG. **16**)

[0700] Assessment of Compound Degradation and Microbicidal Effect on *Toxoplasma gondii*

[0701] Compounds JAG050 and JAG021 were observed for degradation and microbicidal effect. Neither compound was found to be microbicidal; when media was replaced with clean media, the parasites appeared to resume activity and replication. In comparing the 6-day exposure with no addition of compound to the 6-day exposure with the addition of compound, it did not appear that the compound was being degraded over time. In condition II, in which the compound is refreshed, there appears to be a rise in fluorescence on day 6 in the 1 μM treatment group for both compounds. However, these differences were not found to be statistically significant ($p>0.05$).

[0702] Effective of JAG21 on *Toxoplasma gondii.*

[0703] JAG21 at 5 mg/kg eliminates *T. gondii* tachyzoites seen in luminescence studies (FIG. **17**).

[0704] JAG21 Against G0 Arrested and Normal (No Tet Repressor) *Toxoplasma* RPS13 Delta in Interferon Gamma Knockout Mice Plus and Minus Tetracycline.

[0705] Our data show that the combination of JAG21 and tafenoquine treatment is superior to either alone against RPS 13Δ minus tetracycline (FIG. **18**). The data indicates that this appears to be a dormant parasite that is less susceptible to JAG21 than either the slowly growing EGS bradyzoites or the rapidly proliferating tachyzoites.

Malaria:

[0706] In Vitro.

[0707] Results are shown in Table 6. JAG 21 is a 40-65 nM inhibitor of *Plasmodium falciparum* including effect against all drug resistant strains. The effects of the other compounds are also shown in this table and are in the range of 50-200 nM.

Discussion

[0710] JAG050 and JAG021 were identified as lead compounds, demonstrating potent inhibition of tachyzoites and bradyzoites and no toxicity to human foreskin fibroblasts in our in vitro model. While compounds inhibited parasite replication and activity, there did not appear to be a microbicidal effect.

[0711] Toxoplasmosis is highly prevalent and the impact of this disease can be devastatingly severe. Current treatments have toxic side effects and are not curative. JAG050 and JAG021 are lead compounds in the search for a new curative medicine because they demonstrate effect on both life stages and were not toxic to the human cells in our in vitro model.

[0712] Experiments testing the compounds against the EGS strain had some surprising findings. While true cysts in vitro appeared to be completely eliminated by treatment, or their number significantly reduced, parasites did persist in tight, clustered, cyst-like structures, or pseudo-cysts, and small punctate life forms that resemble tachyzoites. One possible explanation is that the dolichos-staining organisms that remain 48 hours after treatment are in a separate, hypnozoite-like life stage that is not affected by the compounds.

[0713] JAG050 and JAG021 do not appear to have a microbicidal effect on the RH-YFP parasites. However, in comparing the two conditions in which cells and parasites were exposed to the drug for 6 days, it does not appear that the parasites or host cells are degrading the compounds. In order to cure toxoplasmosis, a companion drug that can work synergistically with the compounds of the present invention may be helpful. Primaquine and tafenoquine, which are the only medicines that can treat the hypnozoite stage of *Plasmodium vivax* and *P. ovale*, may be potential candidates. We had demonstrated synergy with an earlier generation compound with atovaquone and additive effect with cycloguanil.[26]

TABLE 6

Inhibition of *P falciparum* in vitro including drug resistant isolates

Compound ID	SYBR Green D6 IC50 (uM)	SYBR D6 R^2	SYBR Green C235 IC50 (uM)	SYBR TM91C235 R^2	SYBR Green W2 IC50 (uM)	SYBR W2 R^2	SYBR Green C2B IC50 (uM)	SYBR C2B R^2
JAG006	0.29	0.90	0.88	0.92	2.46	0.92	1.66	0.94
JAG021	0.01435	0.9572	0.06164	0.9706	0.05518	0.9727	0.04042	0.9847
JAG050	0.04664	0.9138	0.06913	0.9562	0.03136	0.9693	0.03635	0.9427
JAG047	3.746	0.9738	12.56	0.9218	9.072	0.9358	7.781	0.9575
JAG039	9.595	0.9532	>20	N/A	>20	N/A	>20	N/A
JAG046	6.716	0.9844	>20	N/A	>20	N/A	>20	N/A
RG38	2.84	0.8936	13.66	0.8338	9.245	0.7954	>20	N/A

[0708] In Vivo.

[0709] Single dose causal prophylaxis in 5 C57BL/6 albino mice at 2.5 mpk dosed on day 0, 1 hour after intravenous administration of 10,000 *P. berghei* sporozoites. 3 dose causal prophylaxis treatment in 5 C57BL/6 albino mice at 0.6 mpk dosed on days −1, 0, and +1. A representative figure for higher dose (5 mg/kg) is shown, but all experiments with the amounts mentioned above had efficacy measured as cure measured as survival, luminesence and parasitemia quantitated by flow cytometry are similar to these. (FIG. **17**)

[0714] JAG21 demonstrated high efficacy against Toxoplasma tachyzoites in our vitro and in vivo models, low nanoM efficacy against drug resistant *P. falciparum*, and single dose causal prophylaxis in a mouse model of *P. berghei* sporozoites infection

References for Example 2

[0715] 1. CDC—Toxoplasmosis [Internet]. [cited 2015 Jul. 1].

[0716] 2. Montoya J, Liesenfeld O. Toxoplasmosis. The Lancet [Internet]. 2004 Jun. 12 [cited 2015 Jul. 1];363 (9425):1965-76.

[0717] 3. McLeod R, Vantubbergen C, Boyer K. Toxoplasmosis (*Toxoplasma gondii*). In: Nelson Textbook of Pediatrics. 20th ed. Elsevier; 2015.

[0718] 4. Jones J L, Holland G N. Annual Burden of Ocular Toxoplasmosis in the United States. Am J Trop Med Hyg [Internet]. 2010 March [cited 2015 Jul. 1];82 (3):464-5.

[0719] 5. Wallon M, Garweg J G, Abrahamowicz M, Comu C, Vinault S, Quantin C, et al. Ophthalmic outcomes of congenital toxoplasmosis followed until adolescence. Pediatrics. 2014 March; 133(3):e601-8.

[0720] 6. Roberts F, McLeod R. Pathogenesis of toxoplasmic retinochoroiditis. Parasitol Today Pers Ed. 1999 February;15(2):51-7.

[0721] 7. McLeod R, Khan A R, Noble G A, Latkany P, Jalbrzikowski J, Boyer K. SEVERE SULFADIAZINE HYPERSENSITIVITY IN A CHILD WITH REACTIVATED CONGENITAL TOXOPLASMIC CHORIORETINITIS: Pediatr Infect Dis J [Internet]. 2006 March [cited 2015 Jun. 16];25(3):270-2.

[0722] 8. Waxman S, Herbert V. Mechanism of pyrimethamine-induced megaloblastosis in human bone marrow. N Engl J Med. 1969 Jun. 12;280(24):1316-9.

[0723] 9. Caumes E, Bocquet H, Guermonprez G, Rogeaux O, Bricaire F, Katlama C, et al. Adverse cutaneous reactions to pyrimethamine/sulfadiazine and pyrimethamine/clindamycin in patients with AIDS and toxoplasmic encephalitis. Clin Infect Dis Off Publ Infect Dis Soc Am. 1995 September; 21(3):656-8.

[0724] 10. Phan L, Kasza K, Jalbrzikowski J, Noble A G, Latkany P, Kuo A, et al. Longitudinal study of new eye lesions in children with toxoplasmosis who were not treated during the first year of life. Am J Ophthalmol. 2008 September; 146(3).

[0725] 11. Vercesi A E, Rodrigues C O, Uyemura S A, Zhong L, Moreno S N J. Respiration and Oxidative Phosphorylation in the Apicomplexan Parasite *Toxoplasma gondii*. J Biol Chem [Internet]. 1998 Nov. 20 [cited 2015 Jun. 16];273(47):31040-7.

[0726] 12. Khan A A, Nasr M, Araujo F G. Two 2-hydroxy-3-alkyl-1,4-naphthoquinones with in vitro and in vivo activities against *Toxoplasma gondii*. Antimicrob Agents Chemother. 1998 September; 42(9):2284-9.

[0727] 13. Doggett J S, Nilsen A, Forquer I, Wegmann K W, Jones-Brando L, Yolken R H, et al. Endochin-like quinolones are highly efficacious against acute and latent experimental toxoplasmosis. Proc Natl Acad Sci USA. 2012 Sep. 25;109(39):15936-41.

[0728] 14. Capper M J, O'Neill P M, Fisher N, Strange R W, Moss D, Ward S A, et al. Antimalarial 4(1H)-pyridones bind to the Qi site of cytochrome bc1. Proc Natl Acad Sci USA. 2015 Jan. 20;112(3):755-60.

[0729] 15. Gubbels M-J, Li C, Striepen B. High-Throughput Growth Assay for *Toxoplasma gondii* Using Yellow Fluorescent Protein. Antimicrob Agents Chemother [Internet]. 2003 January [cited 2015 Jul. 8];47(1):309-16.

[0730] 16. Vidigal P V T, Santos D V V, Castro F C, Couto J C de F, Vitor R W de A, Brasileiro Filho G. Prenatal toxoplasmosis diagnosis from amniotic fluid by PCR. Rev Soc Bras Med Trop [Internet]. 2002 February [cited 2015 Jul. 8];35(1):1-6.

[0731] 17. Silva L A, Brandão GP, Pinheiro B V, Vitor R W A. Immunosuppression with cyclophosphamide favors reinfection with recombinant *Toxoplasma gondii* strains. Parasite J Société Fr Parasitol [Internet]. 2012 August [cited 2015 Jul. 8];19(3):249-57.

[0732] 18. Fomovska A, Huang Q, El Bissati K, Mui E J, Witola W H, Cheng G, et al. Novel N-Benzoyl-2-Hydroxybenzamide Disrupts Unique Parasite Secretory Pathway. Antimicrob Agents Chemother [Internet]. 2012 May [cited 2015 Jul. 8];56(5):2666-82.

[0733] 19. Fomovska A, Wood R D, Mui E, Dubey J P, Ferreira L R, Hickman M R, et al. Salicylanilide inhibitors of *Toxoplasma gondii*. J Med Chem. 2012 Oct. 11;55(19): 8375-91.

[0734] 20. Galen P. Miley, Sovitj Pou, Rolf Winter, Aaron Nilsen, Yuexin Li, Jane X. Kelly, Allison M. Stickles, Michael W. Mather, c Isaac P. Forquer, a April M. Pershing, Karen White, David Shackleford, Jessica Saunders, Gong Chen, Li-Min Ting, Kami Kim, N. Zakharov, Cristina Donini, Jeremy N. Burrows, Akhil B. Vaidya Susan A. Charman, Michael K. Risco, ELQ-300 Prodrugs for Enhanced Delivery and Single-Dose Cure of Malaria 2015 AAC 59: 5555-556

[0735] 21. Fisher, N. et al., 2009. Chapter 17 Type II NADH: Quinone Oxidoreductases of *Plasmodium Falciparum* and *Mycobacterium Tuberculosis*: Kinetic and High-Throughput Assays. In B. T.-M. in Enzymology, ed. *Mitochondrial Function, Part A: Mitochondrial Electron Transport Complexes and Reactive Oxygen Species*. Academic Press, pp. 303-320.

[0736] 22. Fisher, N. et al., 2004. Human disease-related mutations in cytochrome b studied in yeast. *The Journal of biological chemistry,* 279(13), pp. 12951-12958.

[0737] 23. Trager, W. & Jensen, J. B., 2005. Human malaria parasites in continuous culture. 1976. *The Journal of parasitology,* 91(3), pp. 484-486.

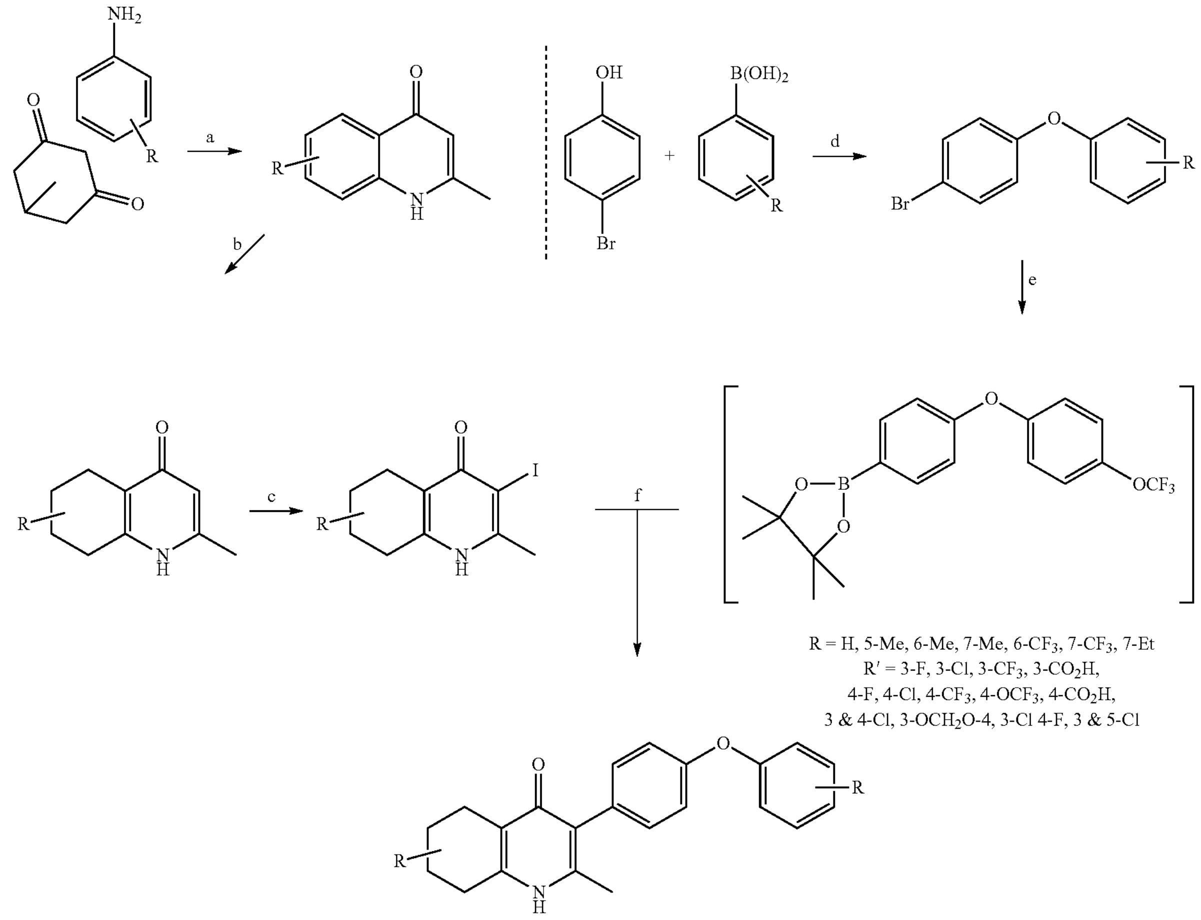
[0738] 24. Pybus et al. Malaria Journal 2013, 12:212.

[0739] 25. Marcsisin et al. Malaria Journal 2014, 13:2.

[0740] 26. McPhillie M SREP(Nature) Jume 2016

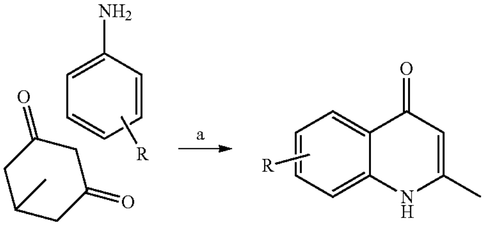
Example 3: Synthesis and Activity of Compounds

[0741] All reagents and solvents were purchased from commercial sources. All commercial reagents and solvents were used as received without further purification. The reactions were monitored using analytical thin layer chromatography (TLC) with 0.25 mm EM Science silica gel plates (60F-254). The developed TLC plates were visualized by short wave UV light (254 nm) or immersion in potassium permanganate solution followed by heating on a hot plate. Flash chromatography was performed with Selecto Scientific silica gel, 32-63 m particle sizes. All reactions were performed in flame or oven-dried glassware under a nitrogen atmosphere. All reactions were stirred magnetically at ambient temperature unless otherwise indicated. ^{1}H NMR spectra were obtained with a Bruker DRX400, Varian VXR400 or VXR300. ^{1}H NMR spectra were reported in parts per million (6) relative to TMS (0.0), DMSO-d6 (2.50) or CD_3OD (4.80) as an internal reference. All ^{1}H NMR spectra were taken in $CDCl_3$ unless otherwise indicated.



R = H, 5-Me, 6-Me, 7-Me, 6-CF_3, 7-CF_3, 7-Et
R′ = 3-F, 3-Cl, 3-CF_3, 3-CO_2H,
4-F, 4-Cl, 4-CF_3, 4-OCF_3, 4-CO_2H,
3 & 4-Cl, 3-OCH_2O-4, 3-Cl 4-F, 3 & 5-Cl

a) i) Meldrums acid, triethylorthoacetate, 110° C., ii) Aniline, 110° C., iii) Dowtherm A, 250° C., b) PtO_2, H_2, AcOH, c) NIS, Acetonitrile, 80° C., d) $Cu(OAc)_2$, Pyridine, TEA, DCM, e) $Pd(dppf)Cl_2$, Bispincolatodiborane, KOAc, DMF, 80° C. f) $Pd(dppf)Cl_2$, Na_2CO_3, DMF, 80° C.



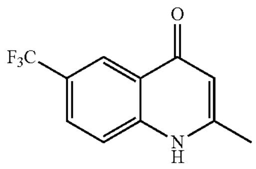
a) i) Meldrums acid, triethylorthoacetate, 110° C., ii) Aniline, 110° C., iii) Dowtherm A, 250° C.

General Method A

[0742] 2,2-Dimethyl-1,3-dioxane-4,6-dione (1.5 equiv.) was dissolved in trimethylorthoacetate (2 equiv.) and heated to 115° C. for 2 hrs. The reaction was cooled to allow the addition of the aniline (1 equiv.) before being heated to 115° C. for a further 2 hrs. The reaction mixture was then allowed to cool and was concentrated in vacuo, remaining solvent was washed off with cold methanol. The precipitate was then dissolved in minimum volume of Dowtherm A and refluxed at 250° C. for 1.5 hours. The reaction mixture was allowed to cool and the precipitate filtered followed by washing with hexane to afford the title compound.

2-Methyl-6-(trifluoromethyl)quinolin-4(1H)-one

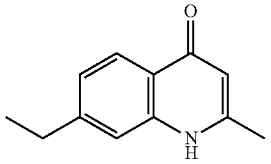
[0743]



[0744] The title compound was synthesised by general method A using 4-trifluoromethyl aniline (2.00 g, 12. 4 mmol) to yield the title compound as a white amorphous solid (466 mg, 2.05 mmol, 17%). ^{1}H NMR (300 MHz, MeOD) δ 8.42 (s, 1H,), 7.81 (dd, J=8.8 Hz, 2.1 Hz, 1H), 7.60 (d, J=8.8 Hz, 1H), 6.16 (s, 1H), 2.40 (s, 3H); M/Z (ESI+); 228.06 (Found MH$^+$228.0634, $C_{11}H_8F_3NO$ requires 228. 0630).

7-ethyl-2-methylquinolin-4(1H)-one

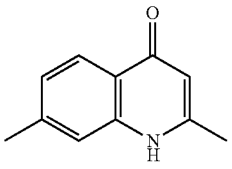
[0745]



[0746] The title compound was synthesised following general procedure A from 3-ethylaniline (1.4 mL, 11.1 mmol). The title compound was isolated as a colourless solid (210 mg, 1.12 mmol, 10%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 9.72 (s, 1H), 8.17 (d, J=8.3 Hz, 1H), 7.16 (s, 1H), 7.10 (d, J=8.3 Hz, 1H), 6.07 (s, 1H), 2.66 (q, J=7.6 Hz, 2H), 2.33 (s, 3H), 1.18 (t, J=7.6 Hz, 3H);

2,7-Dimethylquinolin-4(1H)-one

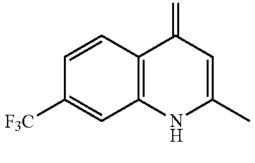
[0747]



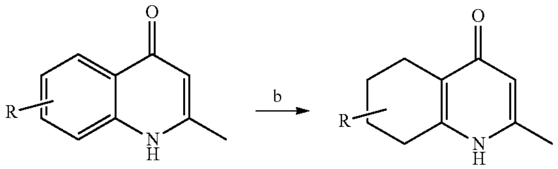
[0748] The title compound was synthesised following general procedure A from 3-methylaniline (7.5 mL, 42 mmol). The title compound was isolated as a colourless solid (370 mg, 2.13 mmol, 5%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 9.58 (s, 1H), 8.24 (d, J=8.3 Hz, 1H), 7.22 (s, 1H), 7.16 (d, J=8.3 Hz, 1H), 6.15 (s, 1H), 2.46 (s, 3H), 2.41 (s, 3H).

7-trifluormethyl-2-methylquinolin-4(1H)-one

[0749]



[0750] The title compound was synthesised following general procedure A from 3-trifluoromethyl-aniline (3 mL, 24 mmol). The title compound was isolated with its regiomer and seperation was not achieved and so was carried forwards as a mixture (1.5 g).



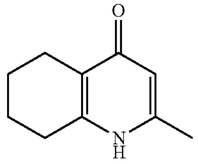
b) PtO_2, H_2, AcOH

General Method B

[0751] The 4-hydroxylquinolone (1 equiv.) was dissolved in acetic acid (10.0 mL) under inert conditions. platinum dioxide (5% weight equiv.) was added and a hydrogen balloon was attached. The reaction was left to proceed for 12 hours. The resulting suspension was filtered through a pad of Celite and washed with ethyl acetate (10.0 mL). The filtrate was concentrated in vacuo to afford a yellow/brown oil. Purification by column chromatography (10% methanol in chloroform) afforded the title compound.

2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

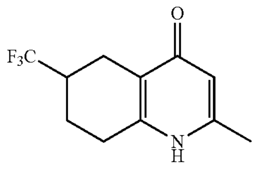
[0752]



[0753] A solution of 4-hydroxyl 2-methyl-quinilone (1.00 g, 6.28 mmol) in acetic acid (10.0 mL) was catalytically hydrogenated over platinum dioxide (0.10 g, 0.44 mmol) for 12 hours. The resulting suspension was filtered through a pad of Celite and washed with ethyl acetate (10.0 mL). The filtrate was concentrated in vacuo to afford a yellow/brown oil. Purification by column chromatography (10% methanol in chloroform) afforded the title compound as a colourless amorphous solid. (1.02 g, 6.25 mmol, 99%). δ H NMR; (500 MHz, Chloroform-d); δ 6.29 (s, 1H), 2.71 (t, J=6.1 Hz, 2H), 2.48 (t, J=6.1 Hz, 2H), 2.32 (s, 3H), 1.78-1.69 (m, 4H); M/Z (ESI+); 164.1122 (Found MH+, 164.11 $C_{10}H_{13}NO$ requires 164.1075).

2-Methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

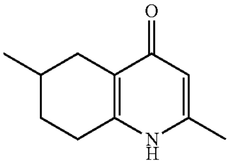
[0754]



[0755] The title compound was synthesised following general procedure B from 2-methyl-6-(trifluoromethyl)quinolin-4(1H)-one (466 mg, 2.0 mmol), The title compound was isolated as colourless solid (230 mg, 0.99 mmol, 49%). ^{1}H NMR (500 MHz, MeOD) δ 6.32 (s, 1H), 2.94 (dd, J=16.7, 5.1 Hz, 1H), 2.86 (dd, J=8.4, 4.1 Hz, 2H), 2.65-2.52 (m, 1H), 2.41 (dd, J=22.8, 11.5 Hz, 1H), 2.36 (s, 3H), 2.28-2.15 (m, 1H), 1.75 (tt, J=12.8, 9.1 Hz); M/Z (ESI+); 232.10 (Found MH$^+$; 232.0955, $C_{11}H_{12}F_3NO$ requires 232.0949).

2,6-Dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

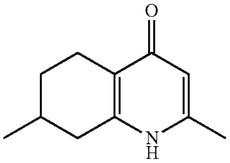
[0756]



[0757] The title compound was synthesised following general procedure B from 2,6-dimethyl-quinolin-4(1H)-one (1.0 g, 5.78 mmol), The title compound was isolated as a colourless solid (780 mg, 4.30 mmol, 76%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 12.26 (s, 1H), 6.09 (s, 1H), 2.88-2.64 (m, 3H), 2.30 (s, 3H), 1.98 (dd, J=16.9, 10.1 Hz, 1H), 1.87 (d, J=12.4 Hz, 1H), 1.77 (m, 1H), 1.39 (ddd, J=23.9, 11.1, 6.0 Hz, 1H), 1.08 (d, J=6.5 Hz, 3H); M/Z (ESI+); 178.13 (Found MH$^+$; 178.1280, $C_{11}H_{15}NO$ requires 177.1154).

2,7-Dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

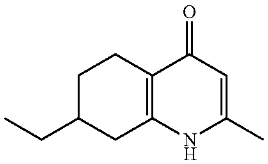
[0758]



[0759] The title compound was synthesised following general procedure B from 2,7-Dimethyl-quinolin-4(1H)-one (350 mg, 2.0 mmol). The title compound was isolated as a colourless solid (311 mg, 1.75 mmol, 88%). ^{1}H NMR (500 MHz, MeOD) δ 6.31 (s, 1H), 2.78 (dd, J=17.0, 5.1 Hz), 2.73 (ddd, J=17.7, 5.2, 2.7 Hz), 2.45-2.31 (m, 2H), 2.00-1.87 (m, 2H), 2.37 (s, Me), 1.37 (m, 2H), 1.13 (d, J=6.6 Hz, 3H); M/Z (ESI+); 178.13 (Found MH$^+$; 178.1278, $C_{11}H_{15}NO$ requires 177.1154).

7-ethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

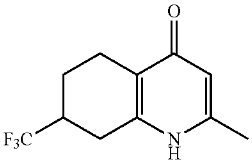
[0760]



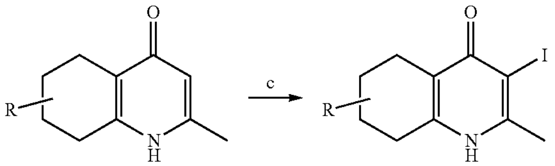
[0761] The title compound was synthesised following general procedure B from 7-ethyl-2-methylquinolin-4(1H)-one (420 mg, 1.78 mmol). The title compound was isolated as a colourless solid (360 mg, 1.5 mmol, 84%). H NMR (400 MHz, $CDCl_3$) δ 12.20 (s, 1H), 6.09 (s, 1H), 2.88-2.66 (m, 2H), 2.46-2.19 (m, 5H, 2-Me), 1.95 (d, J=13.0 Hz, 1H), 1.63 (s, 1H), 1.38 (td, J=13.9, 6.9 Hz, 2H), 1.33-1.22 (m, 1H) 0.94 (t, J=7.4, 3H); M/Z (ESI+); 192.14 (Found MH$^+$; 192.1378 $C_{12}H_{17}NO$ requires 192.1383).

7-trifluormethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

[0762]



[0763] The title compound was synthesised following general procedure B from a mixture of 7-trifluormethyl-2-methylquinolin-4(1H)-one & 5-trifluormethyl-2-methylquinolin-4(1H)-one (1.5 g). The title compound was isolated as a colourless solid (495 mg, 2.14 mmol). ^{1}H NMR (500 MHz, $CDCl_3$/MeOD, 1:1) δ 5.99 (s, 1H), 2.73-2.60 (m, 2H), 2.53 (dd, J=16.3, 12.0 Hz, 1H), 2.35 (s, 1H), 2.20 (ddd, J=17.7, 11.4, 5.9 Hz, 1H), 2.11 (s, 3H), 2.09-2.01 (m, 1H), 1.42 (ddd, J=25.0, 12.1, 5.7 Hz, 1H); M/Z (ESI+); 232.10 (Found MH$^+$; 232.0953, $C_{11}H_{12}F_3NO$ requires 232.0949).



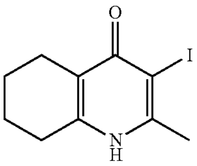
c) NIS, Acetonitrile, 80° C.

General Method C

[0764] Potassium iodide solution (sat aq, 5.60 mL mmol^{-1}) and n-butylamine (10 equiv.) were added to a solution of the tetrahydroquinolin-4(1H)-one (1 equiv.) and iodine (1 equiv.) in DMF (10.0 mL). The reaction mixture was stirred at room temperature for 16 hours. Observed colour change from dark purple to orange. Sodium thiosulphate (250 mg in 10.0 mL water) was then added causing precipitation of a colourless solid. Filtration (washed 2×10 mL water) afforded the title compound.

4(1H), 3-iodo-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

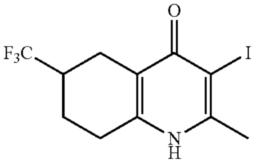
[0765]



[0766] Saturated potassium iodide solution (sat aq, 5.60 mL) and n-butylamine (5.80 mL, 58.3 mmol) was added to a solution of 2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (0.95 g, 5.83 mmol) and iodine (1.48 g, 5.83 mmol) in DMF (10.0 mL). The reaction mixture was stirred at room temperature for 16 hours. Observed colour change from dark purple to orange. Sodium thiosulphate (250 mg in 10.0 mL water) was then added followed by filtration (washed 2×10 mL water) to afford the title compound (39) as colourless microcrystals (1.45 g, 5.02 mmol, 86%). ^{1}H NMR (500 MHz, methanol-d4); δ 2.53 (t, J=6.1 Hz, 2H), 2.44 (s, 3H), 2.30 (t, J=6.1 Hz, 2H), 1.73-1.67 (m, 2H), 1.67-1.61 (m, 2H); M/Z (ESI+); 290.00 (Found MH$^+$, 290.0037 $C_{10}H_{12}INO$ requires 290.0036).

3-Iodo-2-methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

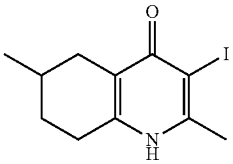
[0767]



[0768] The title compound was synthesised following general procedure C from 2-methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one (230 mg, 1.0 mmol). The title compound was isolated as colourless solid (300 mg, 0.84 mmol, 84%). ^{1}H NMR (400 MHz, DMSO) δ 11.58 (s, 1H), 2.75 (d, J=5.6 Hz, 1H), 2.72-2.67 (m, 2H), 2.62 (dd, J=7.4, 5.8 Hz, 1H), 2.46 (s, 3H), 2.31 (d, J=22.7 Hz, 1H), 2.15 (dd, J=16.4, 11.1 Hz, 1H), 2.07 (dd, J=6.6, 5.4 Hz, 1H), 1.68-1.51 (m, 1H); M/Z (ESI+); 357.99 (Found MH$^+$; 357.9914, $C_{11}H_{11}F_3INO$ requires 357.9910).

3-Iodo-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

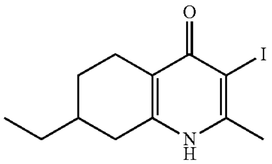
[0769]



[0770] The title compound was synthesised following general procedure C from 2,6-dimethyl-5,6,7,8-tetrahydro quinolin-4(1H)-one (750 mg, 4.24 mmol). The title compound was isolated as colourless solid (740 mg, 2.44 mmol, 58%). ^{1}H NMR (500 MHz, $CDCl_3$/MeOD) δ 2.36 (dd, J=17.3, 4.8 Hz), 2.25 (d, J=4.8 Hz, 2H), 2.15 (s, 3H), 1.57 (dd, J=17.3, 10.4 Hz, 1H), 1.51 (d, J=10.9 Hz, 1H), 1.36 (s, 1H), 1.09-0.94 (m, 1H), 0.69 (d, J=6.6 Hz, 3H); M/Z (ESI+); 304.02 (Found MH$^+$; 304.0190, $C_{11}H_{14}INO$ requires 304.0193).

3-Iodo-7-ethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

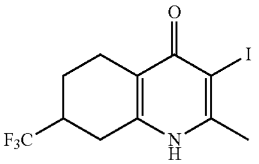
[0771]



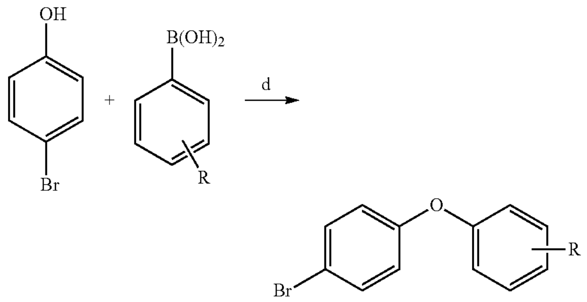
[0772] The title compound was synthesised following general procedure C from 7-ethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (110 mg, 0.57 mmol). The title compound was isolated as colourless solid (180 mg, 0.57 mmol, 99%). ^{1}H NMR (400 MHz, MeOD) δ 2.62 (dd, J=17.2, 4.4 Hz, 2H), 2.47 (s, 3H), 2.34-2.22 (m, 1H), 2.18 (dd, J=17.8, 9.6 Hz, 1H), 1.92-1.81 (m, 1H), 1.64-1.50 (m, 1H), 1.34 (dtd, J=14.1, 7.2, 2.2 Hz, 2H), 1.21 (ddd, J=24.1, 10.9, 5.6 Hz, 1H), 0.91 (t, J=7.4 Hz, 3H); M/Z (ESI+); 318.03 (Found MH$^+$; 318.0261, C12H16INO requires 318.0349).

3-Iodo-7-trifluormethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

[0773]



[0774] The title compound was synthesised following general procedure C from 7-trifluormethyl-2-methylquinolin-4(1H)-one (480 mg, 2.10 mmol). The title compound was isolated as a colourless solid (688 mg, 1.92 mmol, 91%). ^{1}H NMR (500 MHz, $CDCl_3$/MeOD, 1:1) δ 2.40 (dd, J=16.0, 4.9 Hz, 2H), 2.24 (dd, J=17.9, 8.3 Hz, 1H), 2.20-2.12 (m, 1H), 2.12 (s, 2H), 2.00-1.86 (m, 1H), 1.94 (s, 1H), 1.75 (s, 1H), 1.74 (dd, J=13.5, 5.9 Hz, 1H), 1.13 (ddd, J=19.4, 12.1, 5.8 Hz, 1H). M/Z (ESI+); 357.99 (Found MH$^+$; 357.9915, $C_{11}H_{11}F_3INO$ requires 357.9910).



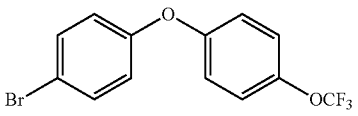
d) Cu(OAc)$_2$, Pyridine, TEA, DCM,

General Procedure d

[0775] Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol^{-1}) over heat-activated 4 A molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol^{-1}) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol^{-1}). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

1-Bromo-4-(4-(trifluoromethoxy)phenoxy)benzene

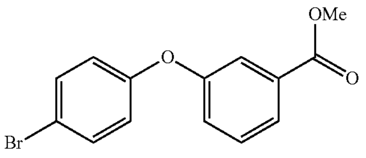
[0776]



[0777] The title compound was synthesised, from 4-bromophenol (0.42 g, 2.43 mmol) and 4-trifluoromethoxy benzene boronic acid (1.00 g, 4.68 mmol), according to general procedure d as a colourless oil (70%, 0.53 g, 1.63 mmol). δ H NMR (500 MHz, Chloroform-d) δ 7.37 (d, J=9.0 Hz, 2H), 7.10 (d, J=9.1 Hz, 2H), 6.91 (d, J=9.1 Hz, 2H), 6.80 (d, J=9.0 Hz, 2H);

Methyl 3-(4-bromophenoxy)benzoate

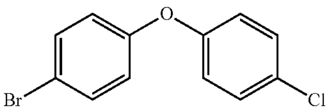
[0778]



[0779] The title compound was synthesised, from 4-bromo-pehonl (0.42 g, 2.43 mmol) and 3-methoxycarbonyl phenyl boronic acid (0.43 g, 2.43 mmol), according to general procedure D. The title compound (43) was isolated as colourless glassy solid (0.21 g, 0.69 mmol, 28%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.73 (dt, J=7.7, 1.2 Hz, 1H), 7.59-7.53 (m, 1H), 7.38 (d, J=9.0 Hz, 2H), 7.34 (t, J=8.4 Hz, 2H), 7.13 (ddd, J=8.4, 2.5, 0.9 Hz, 1H), 6.82 (d, J=9.0 Hz, 2H), 3.83 (s, 3H); M/Z (ESI+); 307.00 (Found MH$^+$, 306.9962 $C_{14}H_{11}BrO_3$ requires; 306.9964).

1-bromo-4-(4-chlorophenoxy)benzene

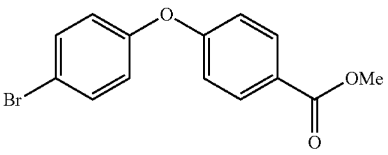
[0780]



[0781] The title compound was synthesised, from 4-bromophenol (0.5 g, 2.80 mmol) and 4-trifluoromethoxy benzene boronic acid (0.6 g, 4.20 mmol), according to general procedure D. The title compound was isolated as a colourless needles (160 mg, 0.56 mmol, 20%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.43 (d, J=9.0 Hz, 2H), 7.30 (d, J=9.0 Hz, 2H), 6.93 (d, J=9.0 Hz, 2H), 6.86 (d, J=9.0 Hz, 2H).

Methyl 4-(4-bromophenoxy)benzoate

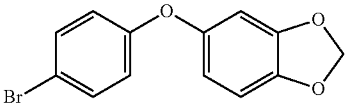
[0782]



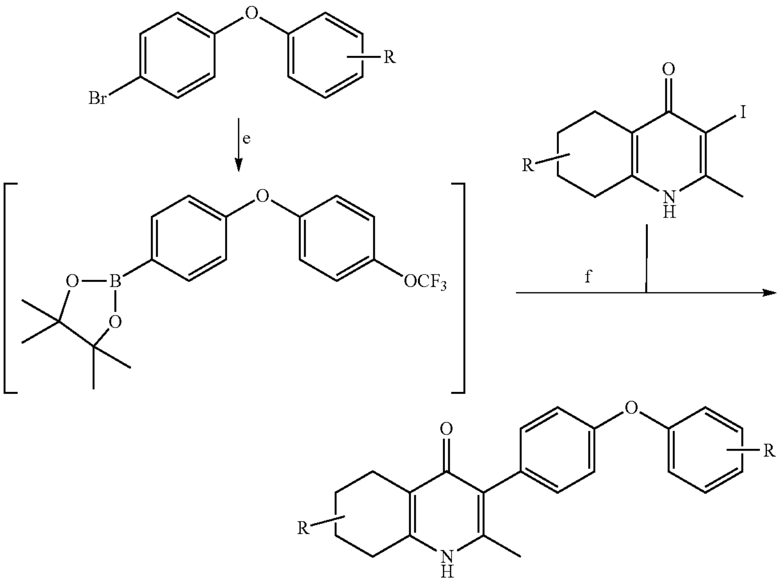
The title compound was synthesised, from 4-bromo-pehonl (0.42 g, 2.43 mmol) and 4-methoxycarbonyl phenyl boronic acid (0.43 g, 2.43 mmol), according to general procedure D. The title compound was isolated as colourless plate crystals (0.25 g, 0.81 mmol, 33%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.94 (d, J=8.9 Hz, 2H), 7.41 (d, J=8.9 Hz, 2H), 6.91 (d, J=8.8 Hz, 2H, 6.87 (d, J=8.9 Hz, 2H), 3.83 (s, 3H); M/Z (ESI+); 307.00 (Found MH$^+$, 306.9961 $C_{14}H_{11}BrO_3$ requires 306.9964).

5-(4-bromophenoxy)-2H-1,3-benzodioxole

[0783]



[0784] The title compound was synthesised, from 4-bromo-pehonl (500 mg, 2.89 mmol) and 3,4-methyleneoxy-phenylboronic acid (719 mg, 4.34 mmol according to general procedure D. The title compound was isolated as a pale yellow oil (196 mg, 0.67 mmol, 23%). δ ^{1}H NMR (500 MHz, Chloroform-d) δ 7.43 (d, J 8.5 Hz, 2H), 6.86 (d, J 8.5 Hz, 2H), 6.79 (d, J 8.5 Hz, 1H), 6.59 (d, J 2.5 Hz, 1H,), 6.51 (dd, J 8.5 & 2.5 Hz, 1H), 6.00 (s, 2H);



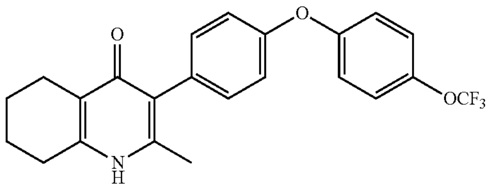
e) Pd(dppf)Cl_2, Bispinocolatodiborane, KOAc, DMF, 80° C. f) Pd(dppf)Cl_2, Na_2CO_3, DMF, 80° C.

1.1 General Method E &F

[0785] A flask charged with the 4-bromo-diarylether (1 equiv.), bispinocolatodiborane (1.1 equiv.), KOAc (3 equiv.) and Pd(dppf)Cl_2 (3 mol %) was flushed with nitrogen. DMF (2.00 mL) was added and the reaction was stirred at 80° C. for 18 hours. After cooling the solution to room temperature, 3-iodotetrahydroquinoline (2 equiv.), $PdCl_2$(dppf) (3 mol %) and Na_2CO_3 (2M, 5 equiv.) were added and the mixture was stirred at 80° C. under nitrogen for a further 24 hours. The solution was cooled to room temperature, the product was extracted with Et_2O (15.0 mL). The organic layers were combined and washed with H_2O (15.0 mL), brine and dried over $MgSO_4$ and concentrated in vacuo. This was followed by purification by silica gel chromatography (ethyl acetate/petroleum ether).

2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

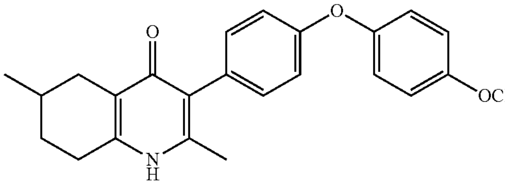
[0786]



[0787] The title compound was synthesised following general procedure E&F from 3-iodo-5,6,7,8-tetrahydroquinolin-4(1H)-one (260 mg, 0.9 mmol) and 4-bromo(4-trifluromethoxyphenoxy)phenyl (200 mg, 0.6 mmol). The title compound was isolated as colourless solid (38 mg, 0.09 mmol, 15%). ^{1}H NMR (500 MHz, DMSO) δ 11.07 (s, 1H), 7.40 (d, J=8.5 Hz, 2H), 7.19 (d, J=8.6 Hz, 2H), 7.13 (d, J=9.0 Hz, 2H), 7.02 (d, J=8.5 Hz, 2H), 2.54 (t, J=6.0 Hz, 2H, H-8), 2.28 (t, J=5.9 Hz, 2H), 2.07 (s, 3H), 1.71 (m, 2H), 1.65 (m, 2H); M/Z (ESI+); 416.15 (Found MH^+, 416.1492 $C_{23}H_{20}F_3NO_3$ requires 416.1473).

3(4-(4-trifluoromethoxyphenoxy)phenyl)-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

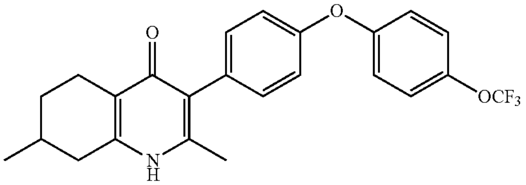
[0788]



[0789] The title compound was synthesised following general procedure E&F from 3-iodo-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (270 mg, 0.9 mmol) and 4-bromo(4-trifluromethoxyphenoxy)phenyl (200 mg, 0.6 mmol). The title compound was isolated as colourless solid (40 mg, 0.09 mmol, 15%). 1'H NMR (500 MHz, $CDCl_3$/MeOD) δ 6.86 (d, J=8.3 Hz, 4H), 6.79-6.64 (m, 4H), 2.43 (dd, J=17.5, 4.9 Hz, 1H), 2.37 (s, 2H), 1.81 (s, 3H), 1.70-1.54 (m, 2H,), 1.45 (m, 1H), 1.09 (dt, J=20.7, 10.5 Hz, 1H), 0.76 (d, J=6.6 Hz, 3H); M/Z (ESI+); 452.14 (Found MNa^+; 452.1446 $C_{24}H_{22}F_3NO_3$ requires 452.1444).

3(4-(4-trifluoromethoxyphenoxy)phenyl)-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

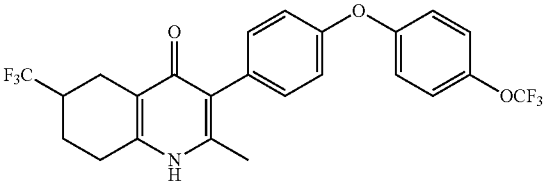
[0790]



[0791] The title compound was synthesised following general procedure E&F from 3-iodo-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (120 mg, 0.4 mmol) and 4-bromo(4-trifluromethoxyphenoxy)phenyl (87 mg, 0.27 mmol). The title compound was isolated as colourless solid (30 mg, 0.07 mmol, 26%). ^{1}H NMR (400 MHz, DMSO) δ 10.90 (s, 1H), 7.41 (d, J=8.5 Hz, 2H), 7.20 (d, J=7.9 Hz, 2H), 7.14 (d, J=8.5 Hz, 2H), 7.03 (d, J=7.9 Hz, 2H), 2.61 (m, 2H), 2.20 (dd, J=16.4, 9.6 Hz, 2H), 2.08 (s, 3H), 1.81 (m, 2H), 1.24 (s, 1H), 1.04 (d, J=5.9 Hz, 3H); M/Z (ESI+); 452.14 (Found MNa$^+$; 452.1446 $C_{24}H_{22}F_3NO_3$ requires 452.1444).

6-Ethyl-3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

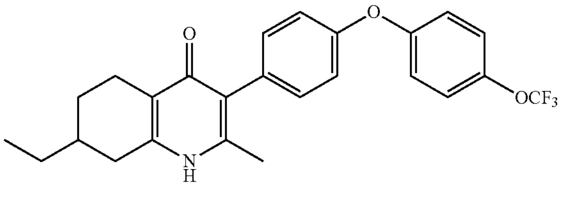
[0792]



[0793] The title compound was synthesised following general procedure E&F from 3-iodo-2-methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one (300 mg, 0.84 mmol) and 4-bromo-(4-trifluromethoxyphenoxy)phenyl (185 mg, 0.56 mmol). The title compound was afforded as a colourless solid. (20 mg, 0.04 mmol, 7%). ^{1}H NMR (500 MHz, TFA) δ 7.39 (d, J=7.7 Hz, 4H), 7.34 (d, J=7.1 Hz, 2H), 7.24 (d, J=8.5 Hz, 2H), 3.32 (d, J=14.9 Hz, 2H), 3.21 (dd, J=13.8, 5.6 Hz, 1H), 2.89 (dd, J=18.0, 9.6 Hz, 1H), 2.73 (dd, J=15.3, 6.9 Hz, 1H), 2.57 (s, 3H), 2.52 (d, J=13.5 Hz, 1H), 2.07 (d, J=16.0 Hz, 1H, H-7b); M/Z (ESI+); 484.14 (Found MH$^+$484.1358, $C_{24}H_{19}F_6NO_3$ requires 484.1342).

7-Ethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

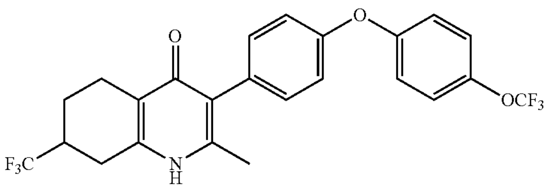
[0794]



[0795] The title compound was synthesised following general procedure E&F from 7-ethyl-2-methylquinolin-4(1H)-one (170 mg, 0.54 mmol) and 4-bromo-(4-trifluromethoxyphenoxy)phenyl (120 mg, 0.36 mmol). The title compound was isolated as a colourless solid (17 mg, 0.04 mmol, 11%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 11.50 (s, 1H), 7.16 (dd, J=15.3, 8.2 Hz, 4H), 6.94 (dd, J=16.6, 8.3 Hz, 4H), 2.78 (d, J=16.1 Hz, 1H), 2.60 (d, J=21.4 Hz, 1H), 2.39 (s, 1H), 2.13 (dd, J=15.8, 10.8 Hz, 1H), 1.96 (s, 3H), 1.59 (s, 1H), 1.43-1.32 (m, 2H), 1.32-1.18 (m, 2H), 0.94 (t, J=7.2 Hz, 3H).; M/Z (ESI+); 444.18 (Found MH$^+$; 444.1784, $C_{25}H_{24}F_3NO_3$ requires 444.1781).

7-trifluromethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

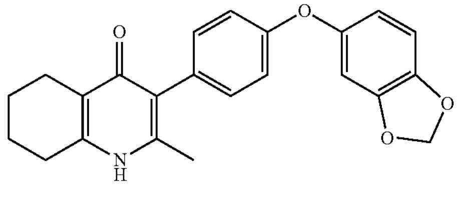
[0796]



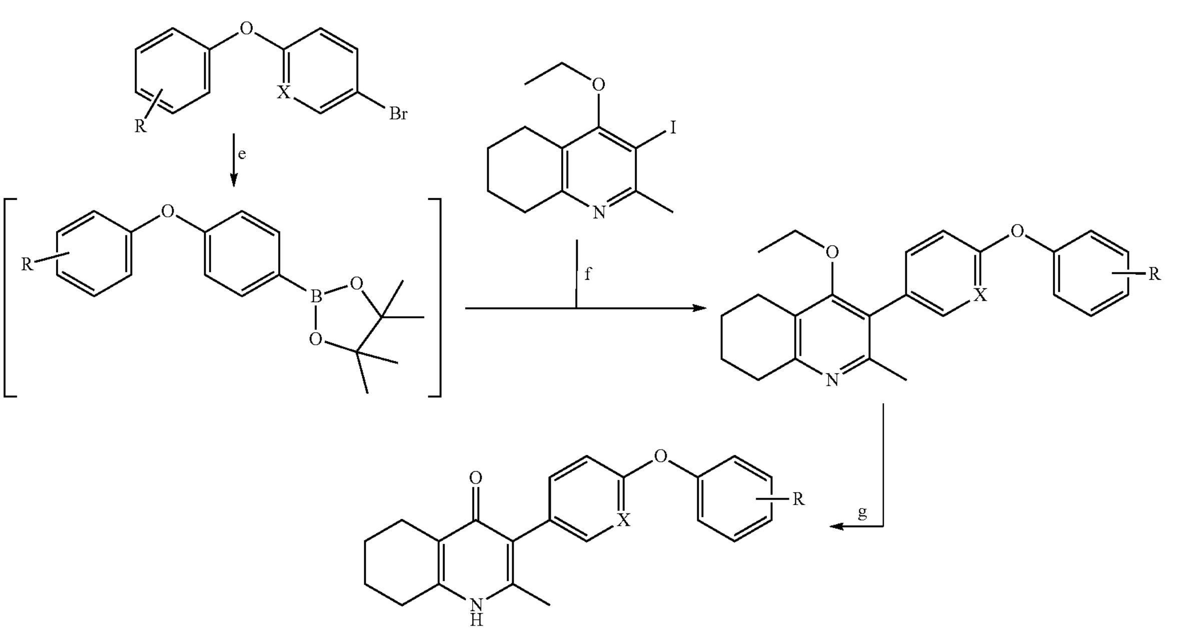
[0797] The title compound was synthesised following general procedure x from 7-trifluormethyl-2-methylquinolin-4(1H)-one (360 mg, 0.99 mmol) and 4-bromo-(4-trifluromethoxyphenoxy)phenyl (220 mg, 0.66 mmol). The title compound was isolated as a colourless solid (95 mg, 0.20 mmol, 30%). M/Z (ESI+); 484.14 (Found MH$^+$484.1358, $C_{24}H_{19}F_6NO_3$ requires 484.1342).

3-[4-(2H-1,3-benzodioxol-5-yloxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

[0798]



[0799] The title compound was synthesised from 5-(4-bromophenoxy)-2H-1,3-benzodioxole (200 mg, 0.68 mmol) and 3-iodo-5,6,7,8-tetrahydroquinolin-4(1H)-one (288 mg, 1.02 mmol). The title compound was isolated as a pale grey solid (40 mg, 0.11 mmol, 16%). HPLC; 3.28 min (86%); δ ^{1}H NMR (500 MHz, TFA) δ 7.35 (d, J 8.5 Hz, 2H), 7.31-7.29 (m, 3H), 6.98 (s, 1H), 6.79 (s, 1H), 6.10 (s, 2H), 3.09 (t, J 5.0 Hz, 2H), 2.90 (t, J 5.0 Hz, 2H), 2.52 (s, 3H), 2.11-2.05 (m, 4H); M/Z (ESI); 375.1563, ($C_{23}H_{21}NO_4$ requires 375.1471).



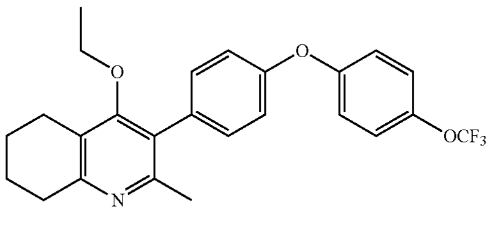
e) Pd(dppf)Cl$_2$, Bispinocolatodiborane, KOAc, DMF, 80° C. f) Pd(dppf)Cl$_2$, Na$_2$CO$_3$, DMF, 80° C., g) HBr, AcOH 120° C.

1.2 General Method E &F

[0800] A flask charged with the 4-bromo-diarylether (1 equiv.), bispinocolatodiborane (1.1 equiv.), KOAc (3 equiv.) and Pd(dppf)Cl$_2$ (3 mol %) was flushed with nitrogen. DMF (2.00 mL) was added and the reaction was stirred at 80° C. for 18 hours. After cooling the solution to room temperature, 3-iodotetrahydroquinoline (2 equiv.), PdCl$_2$(dppf) (3 mol %) and Na$_2$CO$_3$ (2M, 5 equiv.) were added and the mixture was stirred at 80° C. under nitrogen for a further 24 hours. The solution was cooled to room temperature, the product was extracted with Et$_2$O (15.0 mL). The organic layers were combined and washed with H$_2$O (15.0 mL), brine and dried over MgSO$_4$ and concentrated in vacuo. This was followed by purification by silica gel chromatography (ethyl acetate/petroleum ether).

4-ethoxy-2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydro quinoline

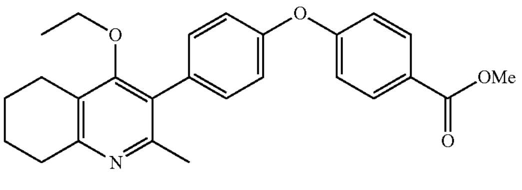
[0801]



[0802] The title compound was synthesised from 1-Bromo-4-(4-(trifluoromethoxy)phenoxy)benzene (100 mg, 0.30 mmol) according to general procedure E&F, to afford the title compound as a colourless gum/viscous oil (30 mg, 0.07 mmol, 23%). ^{1}H NMR (500 MHz, Acetone) δ 7.28 (d, J=8.7 Hz, 2H), 7.26 (d, J=9.1 Hz, 2H), 7.09 (d, J=9.1 Hz, 2H11), 7.07 (d, J=8.7, 2H), 3.52 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.5 Hz, 2H), 2.78 (t, J=6.2 Hz, 2H). 2.26 (s, 3H), 1.89-1.81 (m, 2H), 1.81-1.72 (m, 2H), 0.93 (t, J=7.0 Hz, 3H); M/Z (ESI+); 444.18 (Found MH$^+$, 444.1792 $C_{25}H_{24}F_3NO_3$ requires 444.1781).

Methyl 4-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenoxy)benzoate

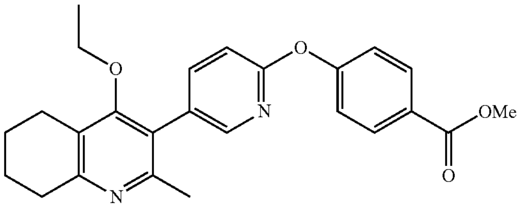
[0803]



[0804] The title compound was synthesised from methyl 4-(4-bromophenoxy)benzoate (150 mg, 0.49 mmol) according to general procedure E&F. The title compound was isolated as colourless microcrystals (56 mg, 0.13 mmol, 27%). ^{1}H NMR (500 MHz, CDCl$_3$) δ 8.03 (d, J=8.7 Hz, 2H), 7.29 (d, J=8.4 Hz, 2H), 7.11 (d, J=8.4 Hz, 2H), 7.03 (d, J=8.7 Hz, 2H), 3.90 (s, 3H), 3.51 (q, J=7.0 Hz, 2H), 2.91 (t, J=6.2 Hz, 2H), 2.72 (t, J=6.0 Hz, 2H). 2.32 (s, 3H), 1.91-1.84 (m, 2H), 1.83-1.76 (m, 2H), 1.04 (t, J=7.0 Hz, 3H); M/Z; 418.20 (ESI+); 418.20 (Found MH$^+$, 418.2037 $C_{26}H_{27}NO_4$ requires 418.2018).

Methyl 4-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate

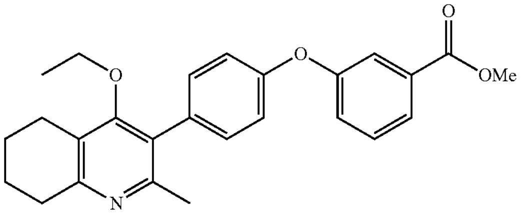
[0805]



[0806] The title compound was synthesised from methyl 3-((5-bromopyridin-2-yl)oxy)benzoate (100 mg, 0.33 mmol) according to general procedure E&F. The title compound was isolated as a colourless gum/semisolid (30 mg, 0.07 mmol, 21%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.13 (d, J=2.3 Hz, 1H, H-6'), 8.10 (d, J=8.7 Hz, 2H), 7.67 (dd, J=8.4, 2.4 Hz, 1H, H-4'), 7.24 (d, J=8.7 Hz, 2H), 7.05 (d, J=8.4 Hz, 1H), 3.91 (s, 3H), 3.53 (q, J=7.0 Hz, 2H), 2.92 (t, J=6.3 Hz, 2H), 2.71 (t, J=6.2 Hz, 2H), 1.06 (t, J=7.0 Hz, 3H); M/Z (ESI+); 419.20 (Found MH^+, 419.1993 $C_{25}H_{26}N_2O_4$ requires 419.1970).

Methyl 3-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenoxy)benzoate

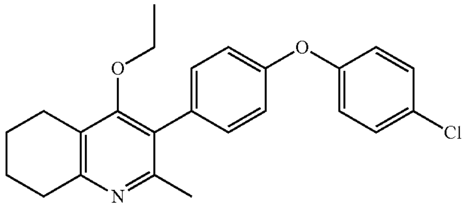
[0807]



[0808] The title compound was synthesised from methyl 3-(4-bromophenoxy)benzoate (150 mg, 0.49 mmol) according to general procedure E&F. The title compound was isolated as colourless crystals (50 mg, 0.12 mmol, 25%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.73 (d, J=7.7 Hz, 1H,), 7.65-7.60 (m, 1H), 7.37 (t, J=7.9 Hz, 1H), 7.19 (m, 3H), 7.00 (d, J=8.6 Hz, 2H), 3.83 (s, J=, 3H), 3.45 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.3 Hz, 2H), 2.65 (t, J=6.2 Hz, 2H), 2.26 (s, 3H), 1.88-1.78 (m, 2H), 1.76-1.67 (m, 2H), 0.99 (t, J=7.0 Hz, 3H); M/Z (ESI+); 418.20 (Found MH^+418.2030, $C_{26}H_{27}NO_4$ requires 418.2018).

Formation of: 3-(4-(4-chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline

[0809]



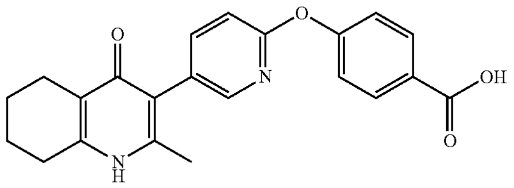
[0810] The title compound was synthesised from 1-bromo-4-(4-chlorophenoxy)benzene (70 mg, 0.24 mmol) according to general procedure E&F. The title compound was isolated as colourless oil (20 mg, 0.05 mmol, 27%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.25 (d, J=8.9 Hz, 2H), 7.17 (d, J=8.7 Hz, 2H), 6.98 (d, J=8.7 Hz, 2H), 6.93 (d, J=8.9 Hz, 2H), 3.45 (q, J=7.0 Hz, 2H), 2.89 (t, J=6.3 Hz, 2H), 2.65 (t, J=6.1 Hz, 2H), 2.28 (s, 3H), 1.90-1.61 (m, 4H), 0.98 (t, J=7.0 Hz, 3H); M/Z (ESI+); 394.16 (Found MH^+394.1575, $C_{24}H_{24}ClNO_2$ requires 394.1568).

1.3 General Method G

[0811] To a solution of the 4-ethoxy-3-(diaryl ether)-hydroxyquinolone (1 equiv.) in acetic acid (2 mL $mmol^{-1}$) was added hydrogen bromide (>48% w/v (aq)) (1 mL $mmol^{-1}$). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound and purified.

Methyl 3-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate

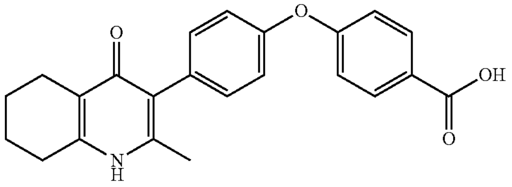
[0812]



[0813] The title compound was synthesised from methyl 4-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl) pyridin-2-yl)oxy) benzoate (30 mg, 0.07 mmol) according to general procedure G. The title compound was isolated as colourless semi solid (13 mg, 0.03 mmol, 45%). ^{1}H NMR (500 MHz, DMSO) δ 12.83 (s, 1H, NH), 11.03 (s, 1H, CO_2H), 8.00 (d, J=8.7 Hz, 2H), 7.99 (s, 1H) 7.73 (dd, J=8.4, 2.4 Hz, 1H), 7.24 (d, J=8.7 Hz, 2H), 7.12 (d, J=8.4 Hz, 1H), 2.56 (t, J=5.8 Hz, 2H), 2.30 (t, J=5.8 Hz, 2H), 2.11 (s, 3H), 1.82-1.51 (m, 4H); M/Z (ESI+); 377.15 (Found MH^+, 377.1497 $C_{22}H_{20}N_2O_4$ requires 377.1496).

4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic Acid

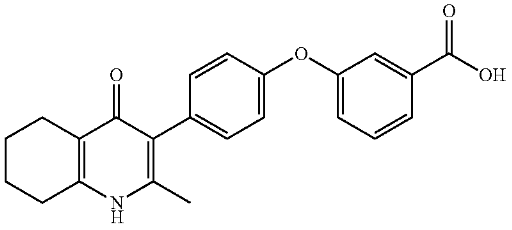
[0814]



[0815] The title compound was synthesised from methyl 4-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl) phenoxy)benzoate (50 mg, 0.17 mmol) according to general procedure G. The title compound was isolated as colourless crystals (33 mg, 0.09 mmol, 48%). ^{1}H NMR (500 MHz, DMSO) δ 13.79 (s, 1H), 12.80 (s (b), 1H), 7.99 (d, J=8.8 Hz, 2H), 7.36 (d, J=8.7 Hz, 2H), 7.24 (d, J=8.7 Hz, 2H), 7.14 (d, J=8.8 Hz, 2H), 2.92 (t, J=5.1 Hz, 2H), 2.62 (t, J=5.0 Hz, 2H), 2.31 (s, 3H), 1.90-1.76 (m, 4H); M/Z (ESI+); 376.16 (Found MH^+, 376.1550, $C_{23}H_{21}NO_4$ requires 376.1543).

3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid

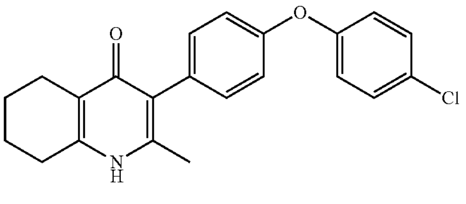
[0816]



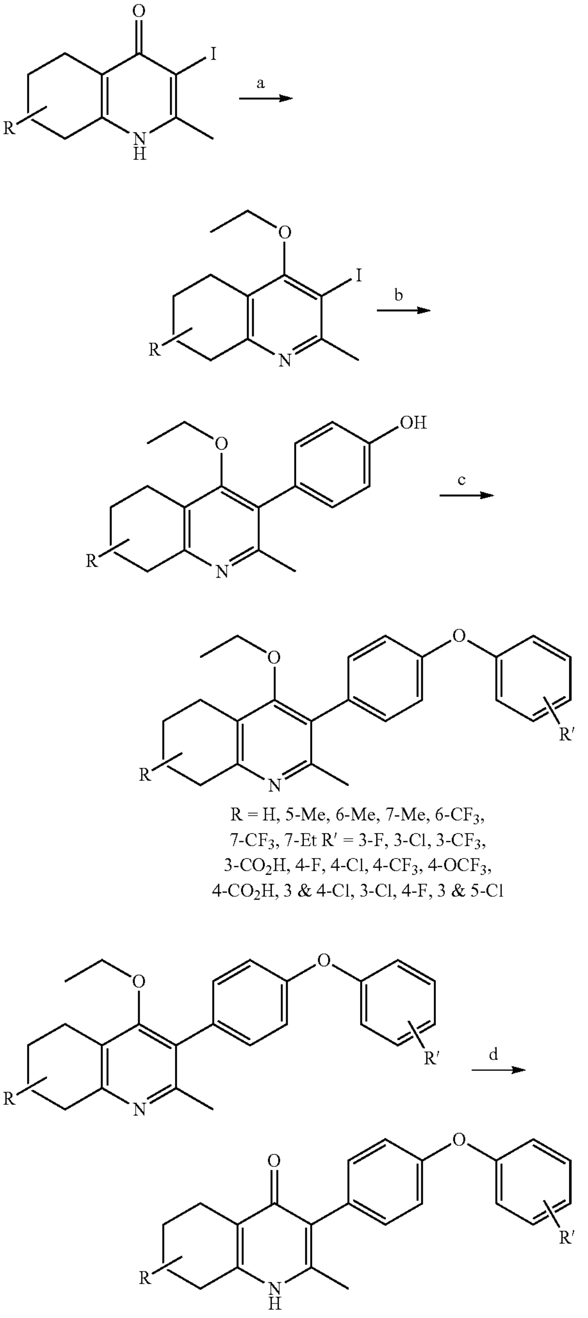
[0817] The title compound was synthesised from 3 methyl 3-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl) phenoxy)benzoate (50 mg, 0.17 mmol) according to general procedure G. The title compound was isolated as colourless crystals (7 mg, 0.02 mmol, 12%). ^{1}H NMR (500 MHz, DMSO) δ 13.00 (s, 1H), 11.31 (s, 1H), 7.70 (d, J=7.9 Hz, 1H), 7.52 (t, J=7.9 Hz, 1H), 7.48 (dd, J=2.2, 1.6 Hz, 1H), 7.31 (dd, J=7.9, 1.6 Hz, 1H), 7.21 (d, J=8.6 Hz, 2H), 7.04 (d, J=8.6 Hz, 2H), 2.58 (t, J=5.8 Hz, 2H), 2.32 (t, J=5.8 Hz, 2H), 2.09 (s, 3H), 1.76-1.59 (m, 4H); M/Z (ESI+); 376.15 (Found MH^+376.1547, $C_{23}H_{21}NO_4$ requires 376.1543).

3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

[0818]

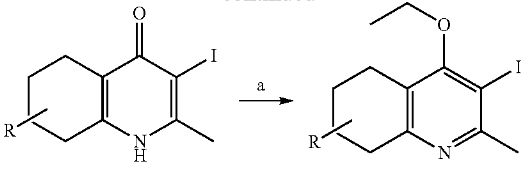


[0819] The title compound was synthesised from 3-(4-(4-chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline (20 mg, 0.5 mmol) according to general procedure G. The title compound was isolated as colourless solid (18 mg, 0.05 mmol, 95%). ^{1}H NMR (500 MHz, DMSO) δ 10.99 (s, 1H), 7.44 (d, J=8.9 Hz, 2H), 7.18 (d, J=8.6 Hz, 2H), 7.05 (d, J=8.9 Hz, 2H), 7.04 (d, J=8.6 Hz, 2H), 2.56 (t, J=5.3 Hz, 2H), 2.29 (t, J=5.3 Hz, 2H), 2.07 (s, 3H), 1.78-1.55 (m, 4H); M/Z (ESI+); 366.13 (Found MH^+366.1262, $C_{22}H_{21}ClNO_2$ requires 366.1253).



R = H, 5-Me, 6-Me, 7-Me, 6-CF_3, 7-CF_3, 7-Et R' = 3-F, 3-Cl, 3-CF_3, 3-CO_2H, 4-F, 4-Cl, 4-CF_3, 4-OCF_3, 4-CO_2H, 3 & 4-Cl, 3-Cl, 4-F, 3 & 5-Cl

-continued

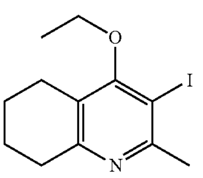


a) EtI, K_2CO_3, DMF, 80° C.

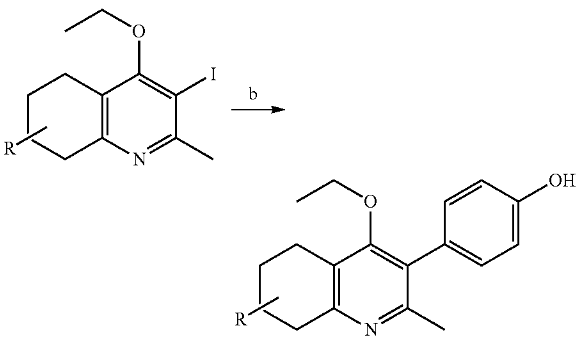
a) EtI, K_2CO_3, DMF, 80° C., b) 4-Hydroxyphenyl boronic acid, $Pd(PPH_3)_4$, Na_2CO_3, DMF, 80° C., c) Phenyl boronic acid, $Cu(OAc)_2$, Pyridine, TEA, DCM, d) HBr (40% aq), Acetic acid, 120° C.

4-ethoxy-3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline

[0820]



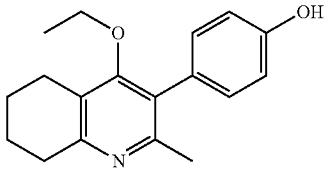
[0821] A suspension of 4(1H), 3-iodo-2-methyl, 5,6,7,8-tetrahydro-quinolinone (2.20 g, 7.61 mmol) and Potassium carbonate (2.10 g, 15.2 mmol) in DMF (20.0 mL) was heated to 50° C. and stirred for 45 minutes. The reaction mixture was removed from the heat and ethyl iodide (0.89 mL, 11.4 mmol) was added dropwise. The reaction mixture was then heated to 50° C. and stirred for a further 18 hours. Formation of a yellow emulsion was observed. The reaction mixture was then quenched with water (40.0 mL). The organic phase was extracted using the polar extraction technique (ethyl acetate, 3×40.0 mL), and the resulting organic layers were combined and dried over $MgSO_4$ and concentrated in vacuo to afford the title compound as an orange oil. (2.00 g, 6.32 mmol, 83%). δ H NMR (500 MHz, Chloroform-d); δ 3.96 (q, J=7.0 Hz, 2H), 2.84 (t, J=6.3 Hz, 2H), 2.74 (t, J=6.3 Hz, 2H), 2.71 (s, 3H), 1.89-1.82 (m, 2H), 1.78-1.72 (m, 2H), 1.49 (t, J=7.0 Hz, 3H); M/Z (ESI+); 318.04 (Found MH^+, 318.0350, $C_{12}H_{17}INO$ requires 318.0349).



b) 4-Hydroxyphenyl boronic acid, $Pd(PPH_3)_4$, Na_2CO_3, DMF, 80° C.,

4-(4-Ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol

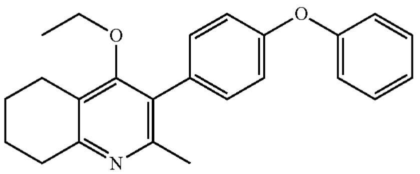
[0822]



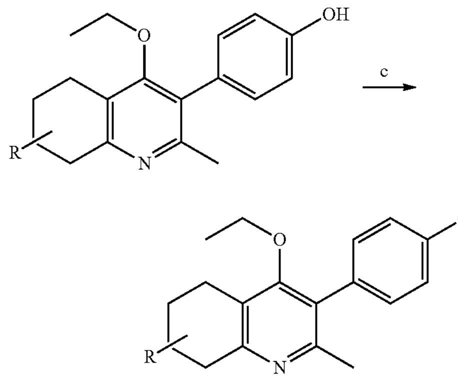
[0823] To a nitrogen flushed flask charged with 4-ethoxy-3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline (400 mg, 1.26 mmol), 4 hydroxybenzene boronic acid (260 mg, 1.89 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (aq) (3 mL, 2 M) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and $MgSO_4$, before concentration in vacuo. The resulting redish brown solid was then recrystallized in ethyl acetate. To yield the title compound as a colourless solid (220 mg, 0.78 mmol, 61%). ^1H NMR (500 MHz, MeOD) δ 7.07 (d, J=8.6 Hz, 2H), 6.86 (d, J=8.6 Hz, 2H), 3.51 (q, J=7.0 Hz, 2H), 2.83 (t, J=6.3 Hz, 2H), 2.72 (t, J=6.1 Hz, 2H), 2.23 (s, 3H), 1.95-1.72 (m, 4H), 1.00 (t, J=7.0 Hz, 3H); M/Z (ESI+); 284.17 (Found MH^+284.1664, $C_{18}H_{21}NO_2$ requires 284.1651).

4-ethoxy-2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinoline

[0824]



[0825] A solution of 4-ethoxy, 3-iodo, 2-methyl, 5,6,7,8-tetrahydro, quinolone (1.00 g, 3.16 mmol), 4-phenoxy phenyl boronic acid (1.01 g, 4.73 mmol), Palladium (II) tetra (tri-phenyl-phosphine) (0.18 g, 0.16 mmol) and dipotassium carbonate (2.00 M, 6.40 mL) dissolved in degassed DMF (20.0 mL) was heated to 85° C. and stirred for 12 hours. Observed colour change from yellow to black. The reaction mixture was allowed to cool to room temperature before dilution with ethyl acetate (15.0 mL). The organic layer was extracted using polar extraction technique, before being collected and dried over $MgSO_4$. The solution was then concentration in vacuo to afford the title compound as colourless fine needles (0.45 g, 1.25 mmol, 40%). δ H NMR (126 MHz, Chloroform-d); δ 7.35 (t, J=7.6 Hz, 2H), 7.23 (d, J=8.5 Hz, 2H), 7.11 (t, J=7.6 Hz, 1H), 7.05 (d, 4H) 3.42 (q, J=7.0 Hz, 2H), 2.82 (t, J=6.4 Hz, 2H), 2.62 (t, J=6.3 Hz, 2H), 2.23 (s, 3H), 1.80-1.74 (m, 2H), 1.73-1.67 (m, 2H), 1.49 (t, J=7.0 Hz, 3H); M/Z (ESI+); 360.20 (Found MH^+, 360.1963, $C_{24}H_{26}NO_2$ requires 360.1958).



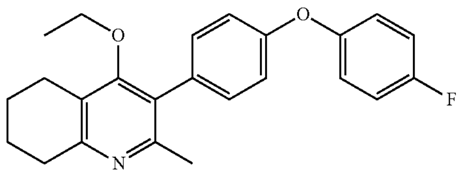
c) Phenyl boronic acid, $Cu(OAc)_2$, Pyridine, TEA, DCM

General Method C

[0826] Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL $mmol^{-1}$) over heat-activated 4 Å molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL $mmol^{-1}$) and filtered through a pad of Celite, followed by repeated washing with water (10 mL $mmol^{-1}$). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

4-Ethoxy-3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline

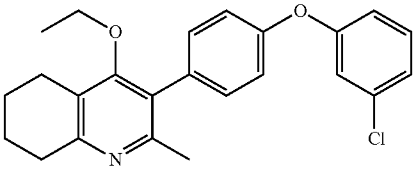
[0827]



[0828] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (60 mg, 0.21 mmol) and 4-fluorobenzene boronic acid (45 mg, 0.31 mmol), according to general procedure C as pink micro crystals (70%, 55 mg, 0.15 mmol). ^1H NMR (500 MHz, Chloroform-d) δ 7.14 (d, J=8.6 Hz, 2H), 6.97 (m, 6H), 3.44 (q, J=7.0 Hz, 2H), 2.87 (t, J=6.2 Hz, 2H), 2.64 (t, J=6.1 Hz, 2H), 2.26 (s, 3H), 1.78 (m, 4H), 0.97 (t, J=7.0 Hz, 3H); M/Z (ESI+); 378.19 (Found MH^+378.1877, $C_{24}H_{24}FNO_2$ requires).

3-(4-(3-Chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline

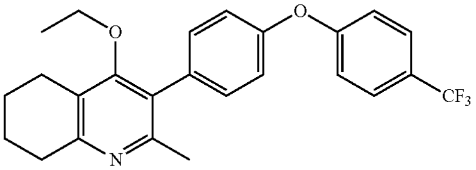
[0829]



[0830] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3-chlorobenzene boronic acid (205 mg, 1.32 mmol), according to general procedure C as a viscous orange oil (78%, 270 mg, 0.68 mmol). ^1H NMR (500 MHz, $CDCl_3$) δ 7.28-7.22 (m, 1H), 7.20 (d, J=8.3 Hz, 2H), 7.02 (d, J=8.3 Hz, 2H), 6.81-6.72 (m, 2H), 6.67 (dd, J=10.2, 2.1 Hz, 1H), 3.44 (q, J=7.0 Hz, 2H), 2.86 (t, J=6.2 Hz, 2H), 2.65 (t, J=6.1 Hz, 2H), 2.26 (s, 3H), 1.82 (m, 2H), 1.77-1.69 (m, 2H), 0.98 (t, J=7.0 Hz, 3H); M/Z (ESI+); 394.16 (Found MH^+; 394.1588, $C_{24}H_{24}ClNO_2$ requires 394.1574).

4-Ethoxy-2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinoline

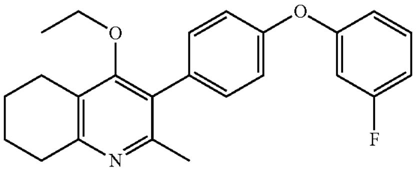
[0831]



[0832] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (60 mg, 0.21 mmol) and 4-trifluoromethylbenzene boronic acid (62 mg, 0.29 mmol), according to general procedure C as a viscous orange oil (55%, 47 mg, 0.11 mmol). ^1H NMR (500 MHz, $CDCl_3$) δ 7.61 (d, J=8.7 Hz, 2H), 7.28 (d, J=8.5 Hz, 2H), 7.15-7.06 (m, 5H), 3.54 (q, J=7.0 Hz, 2H), 2.98 (t, J=6.3 Hz, 2H), 2.72 (t, J=6.2 Hz, 2H), 2.37 (s, 3H), 1.94-1.85 (m, 2H), 1.84-1.77 (m, 2H), 1.06 (t, J=7.0 Hz, 3H), M/Z (ESI+); 428.18 (Found MH^+ 428.1842, $C_{25}H_{24}F_3NO_2$ requires 428.1832).

4-Ethoxy-3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline

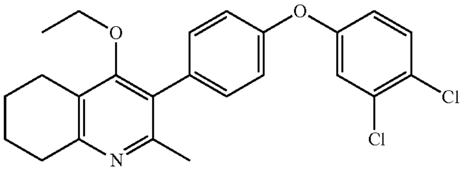
[0833]



[0834] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3-fluorobenzene boronic acid (184 mg, 1.32 mmol), according to general procedure G as a yellow oil (57%, 190 mg, 0.50 mmol). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.25 (dd, J=15.0, 8.2 Hz, 1H), 7.18 (d, J=8.6 Hz, 2H), 7.04 (d, J=8.6 Hz, 2H), 6.81-6.75 (m, 2H), 6.69 (dt, J=10.1, 2.3 Hz, 1H), 3.49 (q, J=7.0 Hz, 2H), 3.04 (m, 2H), 2.65 (t, J=6.2 Hz, 2H), 2.39 (s, 3H), 1.87-1.79 (m, 2H), 1.79-1.70 (m, 2H), 1.02 (t, J=7.0 Hz, 3H); M/Z (ESI+); 378.19 (Found MH^+378.1877, $C_{24}H_{24}FNO_2$ requires).

4-Ethoxy-3-(4-(3,4-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline

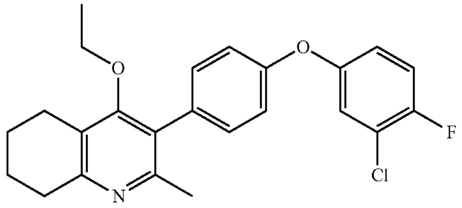
[0835]



[0836] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (100 mg, 0.34 mmol) and 3,4-dichlorobenzene boronic acid (93 mg, 0.51 mmol), according to general procedure C as an orange oil (49%, 70 mg, 0.16 mmol). ^{1}H NMR (300 MHz, $CDCl_3$) δ 7.34 (d, J=8.8 Hz, 1H), 7.20 (dd, J=7.1, 1.6 Hz, 2H), 7.06 (d, J=2.8 Hz, 1H), 7.03-6.97 (m, 2H), 6.85 (dd, J=8.8, 2.8 Hz, 1H), 3.46 (q, J=7.0 Hz, 2H), 2.91 (t, J=6.2 Hz, 2H), 2.65 (t, J=6.1 Hz, 2H), 2.29 (s, 3H), 1.90-1.62 (m, 4H), 0.99 (t, J=7.0 Hz, 3H); M/Z (ESI+); 428.12 (Found MH^+; 428.1202, $C_{24}H_{23}Cl_2NO_2$ requires 428.1184).

4-Ethoxy-3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline

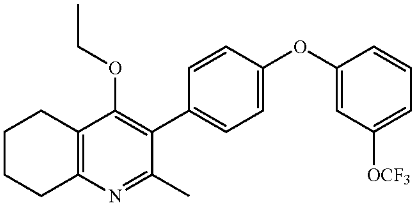
[0837]



[0838] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3-chloro-4-fluorophenylboronic acid (230 mg, 1.32 mmol), according to general procedure C. The title compound was collected as a pale orange solid (104 mg, 0.25 mmol, 29%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 7.26 (d, J=8.2 Hz, 2H), 7.17-7.11 (t, J=8.7 Hz, 1H), 7.09 (dd, J=6.1, 2.9 Hz, 1H), 7.04 (d, J=8.3 Hz, 2H), 6.97-6.91 (m, 1H), 3.50 (dd, J=14.0, 7.0 Hz, 1H), 2.91 (t, J=6.2 Hz, 2H), 2.72 (t, J=5.9 Hz, 2H), 2.31 (s, 3H), 1.95-1.84 (m, 2H), 1.81 (m, 2H), 1.04 (t, J=7.0 Hz, 3H); M/Z (ESI); 412.1489, $C_{24}H_{23}ClFNO_2$ requires 411.1401.

4-Ethoxy-3-(4-(3-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline

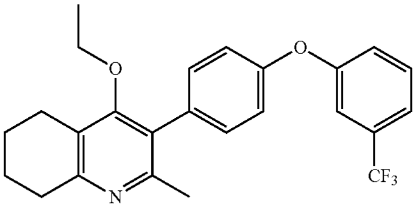
[0839]



[0840] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (200 mg, 0.71 mmol) and 3-trifluoromethoxyphenylboronic acid (218 mg, 1.06 mmol) according to general procedure C. The title compound was collected as a purple/brown oil (132 mg, 0.32 mmol, 42%); ^{1}H NMR (400 MHz, $CDCl_3$) δ 7.29 (t, J=8.3 Hz, 1H), 7.21 (d, J=8.3 Hz, 2H), 7.03 (d, J=8.2 Hz, 2H), 6.90 (d, J=8.2 Hz, 2H), 6.81 (s, 1H), 3.44 (dd, J=14.0, 7.0 Hz, 2H), 2.84 (t, J=6.2 Hz, 2H), 2.65 (t, J=6.0 Hz, 2H), 2.25 (s, 3H), 1.86-1.78 (m, 2H), 1.74 (dd, J=10.2, 4.6 Hz, 2H), 0.97 (t, J=7.0 Hz, 3H); M/Z (ESI); 444.1786, $C_{25}H_{25}F_3NO_3$ requires 444.1781.

4-Ethoxy-3-(4-(3-trifluoromethylphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline

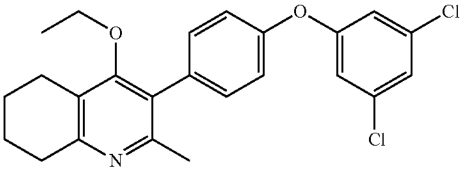
[0841]



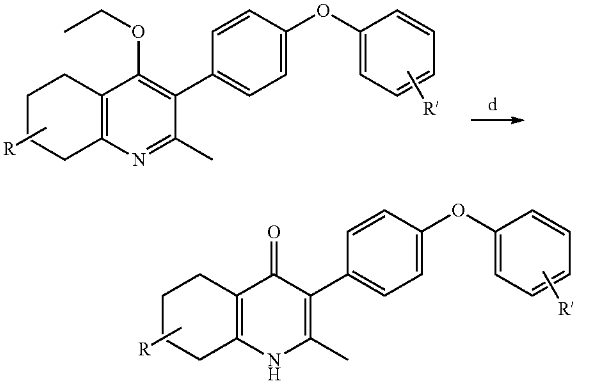
[0842] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (300 mg, 1.06 mmol) and 3-trifluoromethylphenyl boronic acid (302 mg, 1.59 mmol) according to general procedure C. The title compound was collected as a yellow oil (198 mg, 0.46 mmol, 44%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 7.44-7.38 (m, 1H), 7.32 (d, J=7.8 Hz, 1H), 7.17 (s, 2H), 7.12 (d, J=8.3 Hz, 2H), 7.01 (d, J=8.4 Hz, 2H), 3.45 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.0 Hz, 2H), 2.62 (t, J=5.7 Hz, 2H), 2.25 (s, 3H), 1.73 (m, 4H), 1.00 (t, J=7.0 Hz, 3H); M/Z (ESI); 427.1852, $C_{25}H_{24}F_3NO_2$ requires 427.1759.

3-[4-(3,5-dichlorophenoxy)phenyl]-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline

[0843]



[0844] The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3,5-dichlorophenylboronic acid (278 mg, 1.32 mmol according to general procedure C. The title compound was collected as a yellow solid (50 mg, 0.12 mmol, 13%). δ ^{1}H NMR (500 MHz, Chloroform-d) δ 7.34-7.32 (m, 2H), 7.13-7.11 (m, 3H), 6.93 (d, J=1.8 Hz, 2H), 3.54 (q, J=7.0 Hz, 2H), 2.94 (t, J=6.1 Hz, 2H), 2.75 (t, J=6.3 Hz), 2.39 (s, 3H), 1.95-1.81 (m, 4H), 1.08 (t, J=7.0 Hz, 3H); M/Z (ESI); 428.1194, $C_{24}H_{24}Cl_2NO_2$ requires 428.1179.



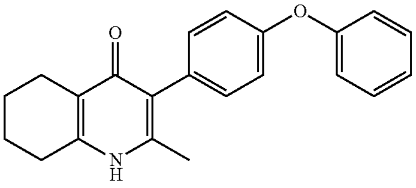
d) HBr (40% aq), Acetic acid, 120° C.

1.4 General Method D

[0845] To a solution of the 4-ethoxy-3-(diaryl ether)-hydroxyquinolone (1 equiv.) in acetic acid (2 mL mmol^{-1}) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol^{-1}). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound and purified.

Formation of: 2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

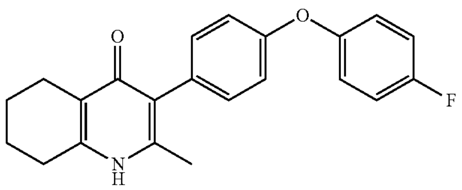
[0846]



[0847] The title compound was synthesised from 4-ethoxy,3-(4-phenoxy, benzene),2-methy,5,6,7,8-hydroquinolone (0.43 g, 1.20 mmol) following general procedure D to afford the title compound as colourless microcrystals (0.39 g, 1.20 mmol, 99%). ^{1}H NMR (500 MHz, DMSO-d$_6$); δ 7.38 (t, J=7.9 Hz, 2H, H-3" & 5"), 7.17 (d, J=8.5 Hz, 2H), 7.14 (t, J=7.4 Hz, 1H), 7.05 (d, J=7.9 Hz, 2H,), 6.98 (d, J=8.5 Hz, 2H), 2.56 (t, J=5.9 Hz, 2H), 2.30 (t, J=6.1 Hz, 2H), 2.08 (s, 3H), 1.75-1.68 (m, 2H,), 1.68-1.62 (m, 2HM/Z (ESI+); 332.17 (Found MH$^+$, 332.1673, $C_{22}H_{21}NO_2$ requires 332.1650).

3-(4-(4-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

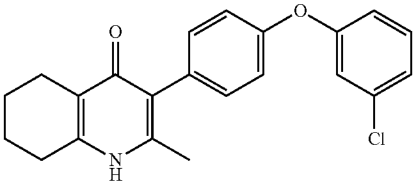
[0848]



[0849] The title compound was synthesised from 4-ethoxy-3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (45 mg, 0.12 mmol) according to general procedure D. The title compound was isolated as colourless solid (25 mg, 0.07 mmol, 60%). ^{1}H NMR (500 MHz, DMSO) δ 7.25 (t, J=8.7 Hz, 2H), 7.17 (d, J=8.5 Hz, 2H), 7.11 (dd, J=8.9, 4.5 Hz, 2H), 6.96 (d, J=8.5 Hz, 2H), 2.59-2.53 (m, 2H), 2.30 (t, J=5.2 Hz, 2H), 2.08 (s, 3H), 1.72 (m, 2H), 1.66 (m, 2H); M/Z (ESI+); 350.16 (Found MH$^+$350.1562, $C_{22}H_{20}FNO_2$ requires 350.1550).

3-(4-(3-Chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

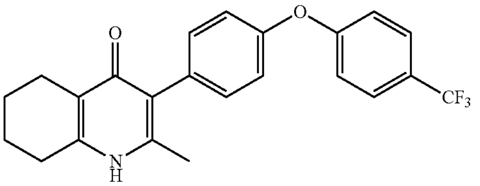
[0850]



[0851] The title compound was synthesised from 3-(4-(3-chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline (200 mg, 0.51 mmol) according to general procedure D. The title compound was isolated as colourless solid (120 mg, 0.33 mmol, 66%). ^{1}H NMR (500 MHz, DMSO) δ 11.71 (s, 1H), 7.44 (t, J=8.2 Hz, 1H), 7.25 (d, J=8.6 Hz, 2H), 7.22 (ddd, J=8.0, 1.9, 0.8 Hz, 1H), 7.10 (t, J=2.0 Hz, 1H), 7.09 (d, J=8.6 Hz, 2H), 7.03 (ddd, J=8.2, 2.3, 0.6, 1H), 2.65 (t, J=5.9 Hz, 2H), 2.39 (t, J=5.2 Hz, 2H), 2.14 (s, 3H), 1.84-1.59 (m, 4H); M/Z (ESI+); 366.13 (Found MH$^+$366.1262, $C_{22}H_{20}ClNO_2$requires 366.1255).

2-Methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

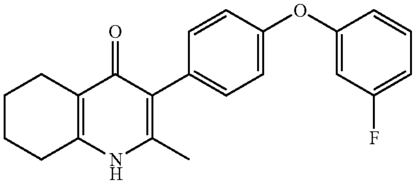
[0852]



[0853] The title compound was synthesised from 4-ethoxy-2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinoline (47 mg, 0.12 mmol) according to general procedure D. The title compound was isolated as colourless solid (25 mg, 0.07 mmol, 60%). ^{1}H NMR (500 MHz, DMSO) δ 11.14 (s, 1H), 7.77 (d, J=8.6 Hz, 2H), 7.26 (d, J=8.6 Hz, 2H), 7.19 (d, J=8.6 Hz, 2H), 7.12 (d, J=8.6 Hz, 2H), 2.59 (t, J=5.8 Hz, 2H), 2.33 (t, J=6.4 Hz, 2H), 2.12 (s, 3H), 1.73 (m, 2H), 1.70-1.64 (m, 2H); M/Z (ESI+); 400.15 (Found MH$^+$; 400.1528, $C_{23}H_{20}F_3NO_2$ requires 400.1519).

3-(4-(3-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

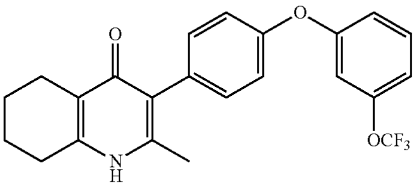
[0854]



[0855] The title compound was synthesised from 4-ethoxy-3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (170 mg, 0.45 mmol) according to general procedure D. The title compound was isolated as colourless solid (110 mg, 0.31 mmol, 70%). ^{1}H NMR (500 MHz, DMSO) δ 7.47 (dt, J=8.6, 7.1 Hz, 1H), 7.31 (d, J=8.7 Hz, 2H), 7.17 (d, J=8.7 Hz, 2H), 7.02 (tdd, J=8.5, 2.3, 0.7 Hz, 1H), 6.97-6.88 (m, 2H), 2.83 (t, J=6.1 Hz, 2H), 2.54 (t, J=5.8 Hz, 2H), 2.25 (s, 3H), 1.87-1.69 (m, 4H); M/Z (ESI+); 350.16 (Found MH$^+$; 350.1569, $C_{22}H_{21}FNO_2$ requires 350.1556).

3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

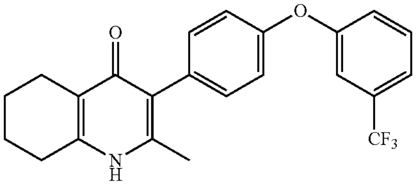
[0856]



[0857] The title compound was synthesised from 4-Ethoxy-3-(4-(3-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (100 mg, 0.23 mmol) according to general procedure D. The title compound was isolated as colourless solid (72 mg, 0.16 mmol, 76%). ^{1}H NMR (501 MHz, DMSO) δ 11.27 (s, 1H, NH), 7.51 (t, J=8.3 Hz, 1H), 7.22 (d, J=8.5 Hz, 2H), 7.12 (d, J=7.6 Hz, 1H), 7.07 (d, J=8.5 Hz, 2H), 7.03 (dd, J=8.6, 1.7 Hz, 1H), 7.00 (s, 1H), 2.58 (t, J=5.2 Hz, 2H), 2.32 (t, J=6.2 Hz, 2H), 2.09 (s, 3H), 1.76-1.69 (m, 2H), 1.69-1.61 (m, 2H); M/Z (ESI+); 416.15 (Found MH$^+$; 416.1469, $C_{23}H_{21}F_3NO_3$ requires 416.1468).

3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

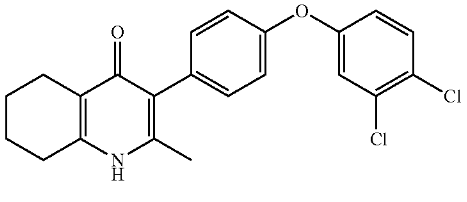
[0858]



[0859] The title compound was synthesised from 4-Ethoxy-3-(4-(3-trifluoromethylphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (193 mg, 0.45 mmol) according to general procedure D. The title compound was isolated as colourless solid (174 mg, 0.44 mmol, 96%). ^{1}H NMR (501 MHz, DMSO) δ 11.15 (s, 1H), 7.63 (t, J=8.6 Hz, 1H), 7.48 (d, J=8.2 Hz, 1H), 7.30 (s, 2H), 7.22 (d, J=8.4 Hz, 2H), 7.07 (d, J=8.4 Hz, 2H), 2.56 (t, J=3.3 Hz, 2H), 2.30 (t, J=5.3 Hz, 2H), 2.08 (s, 3H), 1.71 (dd, J=6.0, 4.6 Hz, 2H), 1.68-1.60 (m, 2H); M/Z (ESI+); 400.15 (Found MH$^+$; 400.1519 requires $C_{23}H_{21}F_3NO_2$ requires 400.1519).

3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

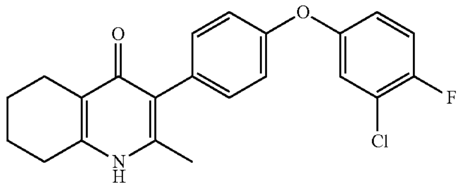
[0860]



[0861] The title compound was synthesised from 4-ethoxy-3-(4-(3,4-dichloro phenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (60 mg, 0.15 mmol) according to general procedure D. The title compound was isolated as colourless solid (35 mg, 0.08 mmol, 59%). ^{1}H NMR (500 MHz, DMSO) δ 10.95 (s, 1H), 7.66 (d, J=8.5 Hz, 1H), 7.31 (s, 1H), 7.23 (d, J=8.2 Hz, 2H), 7.08 (d, J=7.6 Hz, 2H), 7.04 (d, J=8.9 Hz, 1H), 2.55 (m, 2H), 2.30 (m, Hz, 2H), 2.09 (s, 3H), 1.72 (m, 2H), 1.66 (m, 2H); M/Z (ESI+); 400.09 (Found MH$^+$; 400.0881, $C_{22}H_{20}Cl_2NO_2$ requires 400.0866).

3-[4-(3-chloro-4-fluorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

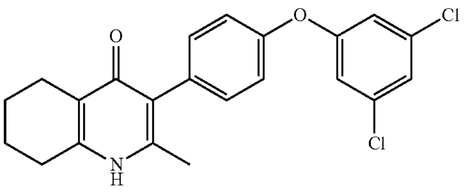
[0862]



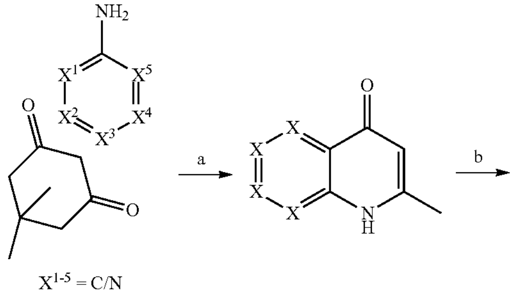
[0863] The title compound was synthesised from 4-Ethoxy-3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (90 mg, 2.18 mmol) The title compound was isolated as a pale grey precipitate (55 mg, 0.14 mmol, 66%). ^{1}H NMR (500 MHz, TFA) δ 7.39 (d, J 8.6 Hz, 2H), 7.32 (d, J 8.5 Hz, 2H), 7.27-7.24 (m, 2H), 7.12-7.09 (m, 1H), 3.10 (t, J 5.8 Hz, 2H), 2.91 (t, J 5.9 Hz, 2H), 2.54 (s, 3H), 2.15-2.03 (m, 4H); M/Z (ESI); 384.1167, ($C_{22}H_{20}ClFNO_2$ requires 384.1161).

3-[4-(3,5-dichlorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4(1H)-one

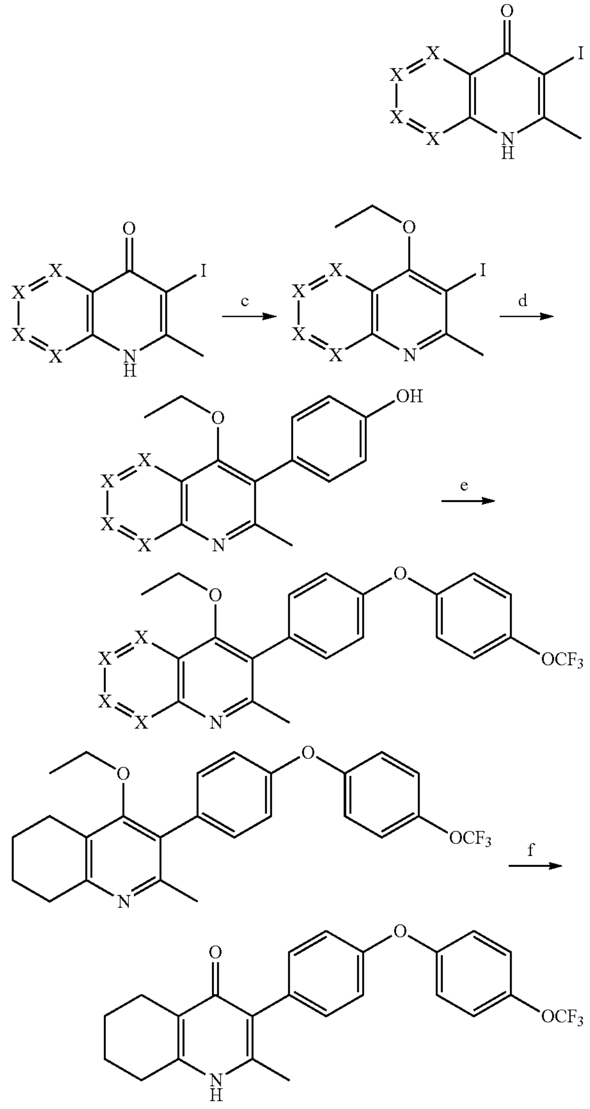
[0864]



[0865] The title compound was synthesised from 3-[4-(3,5-dichlorophenoxy)phenyl]-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline (40 mg, 0.93 mmol) according to general procedure D. The title compound was isolated as colourless solid (31 mg, 0.08 mmol, 83%). δ ^{1}H NMR (500 MHz, TFA) δ 7.44 (d, J=8.5 Hz, 2H), 7.39 (d, J=8.0 Hz, 2H), 7.30 (s, 1H), 7.10 (s, 2H), 3.12 (t, J=5.5 Hz, 2H), 2.93 (t, J=5.5 Hz, 2H), 2.57 (s, 3H), 2.09-2.00 (m, 4H); M/Z (ESI); 400.0874, $C_{22}H_{20}Cl_2NO_2$ requires 400.0866.



-continued



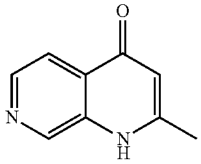
a) i) Meldrums acid, triethylorthoacetate, 110° C., ii) Aniline, 110° C., iii) Dowtherm A, 250° C., b) NIS, Acetonitrile, 80° C., c) EtI, K_2CO_3, DMF, 80° C., d) 4-Hydroxyphenyl boronic acid, $Pd(PPH_3)_4$, Na_2CO_3, DMF, 80° C., e) Phenyl boronic acid, $Cu(OAc)_2$, Pyridine, TEA, DCM, f) HBr (40% aq), Acetic acid, 120° C.

General Method A

[0866] 2,2-Dimethyl-1,3-dioxane-4,6-dione (1.5 equiv.) was dissolved in trimethylorthoacetate (2 equiv.) and heated to 115° C. for 2 hrs. The reaction was cooled to allow the addition of the aniline (1 equiv.) before being heated to 115° C. for a further 2 hrs. The reaction mixture was then allowed to cool and was concentrated in vacuo, remaining solvent was washed off with cold methanol. The precipitate was then dissolved in minimum volume of Dowtherm A and refluxed at 250° C. for 1.5 hours. The reaction mixture was allowed to cool and the precipitate filtered followed by washing with hexane to afford the title compound.

2-Methyl-1,7-napthyrid-4(1H)-one

[0867]



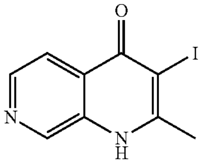
[0868] The title compound was synthesised using 3-amino pyridine (3.0 g, 32 mmol) following general procedure A. To give the title compound as colourless solid (489 mg, 3.1 mmol, 10%). ^{1}H NMR (500 MHz, $CDCl_3$) 8.52 (s, 1H, H-8), 7.72 (d, J=8.0 Hz, J=8.0 Hz, 1H, H-5), 7.59-7.31 (m, 1H, H-6), 6.18 (s, 1H, H-3), 2.28 (s, 3H, Me). M/Z (ESI+); (Found MH$^+$; requires).

General Method B

[0869] 2-Methyl-napthyrid-4(1H)-one (1 equiv.) and N-Iodosuccinamide (1.2 equiv.) were dissolved in acetonitrile (5 mL mmol^{-1}) and stirred and heated at 80° C. for 3 hours. The reaction mixture was then allowed to cool and the mixture filtered, the precipitate was then washed with water (15 mL) to afford the title compound as a colourless solid.

3-Iodo-2-methyl-1,7-napthyrid-4(1H)-one

[0870]



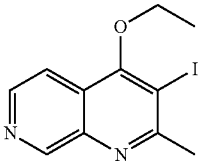
[0871] The title compound was synthesised using 2-Methyl-1,7-napthyrid-4(1H)-one (480 mg, 3.0 mmol) following general procedure B. To give the title compound as colourless solid (740 mg, 2.6 mmol, 86%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.36-7.91 (m, 1H), 7.49 (dd, J=8.4, 1.1 Hz, 1H), 7.18 (dd, J=8.6, 4.2 Hz, 1H), 2.27 (s, 3H). M/Z (ESI+); (Found MH$^+$; requires).

General Method C

[0872] A suspension of the 4(1H), 3-Iodo-2-methyl-napthyrid-4(1H)-one (1 equiv.) and potassium carbonate (2 equiv.) in DMF (20.0 mL) was heated to 50° C. and stirred for 45 minutes. The reaction mixture was removed from the heat and ethyl iodide (1.5 equiv.) was added dropwise. The reaction mixture was then heated and kept at 50° C. with stirring for a further 18 hrs. Formation of a yellow emulsion was observed. The reaction mixture was then quenched with water (40.0 mL). The organic phase was extracted using the polar extraction technique (ethyl acetate, 3×40.0 mL), and the resulting organic layers were combined and dried over $MgSO_4$ and concentrated in vacuo to afford the title compound.

4-Ethoxy-3-iodo-2-methyl-1,7-napthyridine

[0873]



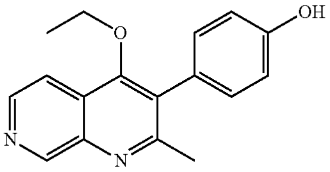
[0874] The title compound was synthesised using, 3-Iodo-2-methyl-napthyrid-4(1H)-one (720 mg, 2.5 mmol) following general procedure C. To give the title compound as brown gum (244 mg, 0.8 mmol, 33%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.87 (dd, J=4.0, 1.5 Hz, 1H), 8.31 (dd, J=8.5, 1.6 Hz, 1H), 7.63 (dd, J=8.5, 4.1 Hz, 1H), 4.84 (q, J=7.0 Hz, 2H), 3.00 (s, 3H), 1.59 (t, J=7.0 Hz, 3); M/Z (ESI+); (Found MH$^+$; requires).

General Method F

[0875] To a nitrogen flushed flask charged with the 4-Ethoxy-3-iodo-2-methyl-napthyridine (400 mg, 1.26 mmol), 4-hydroxybenzene boronic acid (260 mg, 1.89 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (3 mL, 2 $M_{(aq)}$) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and $MgSO_4$, before concentration in vacuo. The resulting solid was then recrystallized in ethyl acetate to afford the title compound.

4-Ethoxy-3-phenol-2-methyl-1,7-napthyridine

[0876]



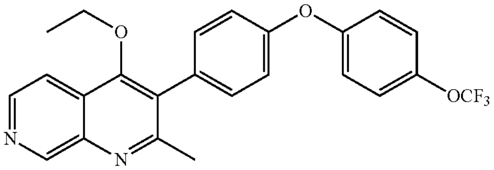
[0877] The title compound was synthesised using, 4-Ethoxy-3-iodo-2-methyl-1,7-napthyridine (230 mg, 0.73 mmol) following general procedure F. To give the title compound an orange powder (80 mg, 0.8 mmol, 28%). ^{1}H NMR (400 MHz, MeOD) δ 8.78 (dd, J=4.1, 1.4 Hz, 1H), 8.24 (dd, J=8.6, 1.4 Hz, 1H), 7.64 (dd, J=8.6, 4.2 Hz, 1H), 7.08 (d, J=8.5 Hz, 2H), 6.84 (d, J=8.5 Hz, 2H), 4.12 (q, J=7.0 Hz, 2H), 2.39 (s, 3H), 1.05 (t, J=7.0 Hz, 3H); M/Z (ESI+); (Found MH$^+$; requires).

General Method G

[0878] Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol^{-1}) over heat-activated 4 A molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol^{-1}) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol^{-1}). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

4-Ethyl-3 (4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-napthyridone

[0879]



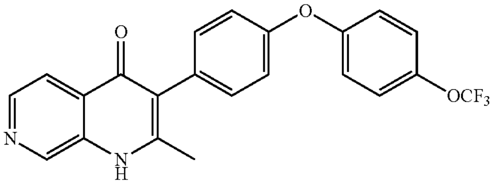
[0880] The title compound was synthesised using 4-Ethoxy-3-iodo-2-methyl-1,7-napthyridine (70 mg, 0.25 mmol) and 4-trifluoromethoxybenzenboronic acid (79 mg, 0.38 mmol) following general procedure G. To give the title compound as a red crystalline solid (34 mg, 0.08 mmol, 20%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 8.90 (dd, J=4.0, 1.3 Hz, 1H), 8.33 (dd, J=8.5, 1.3 Hz, 1H), 7.61 (dd, J=8.5, 4.1 Hz, 1H), 7.31 (d, J=8.5 Hz, 2H), 7.24 (d, J=8.7 Hz, 2H), 7.13 (d, J=8.7 Hz, 2H), 7.10 (d, J=9.1 Hz, 2H), 4.43 (q, J=7.0 Hz, 2H), 2.54 (s, 3H), 1.19 (t, J=7.0 Hz, 3H); M/Z (ESI+); (Found MH$^+$; requires).

General Method J

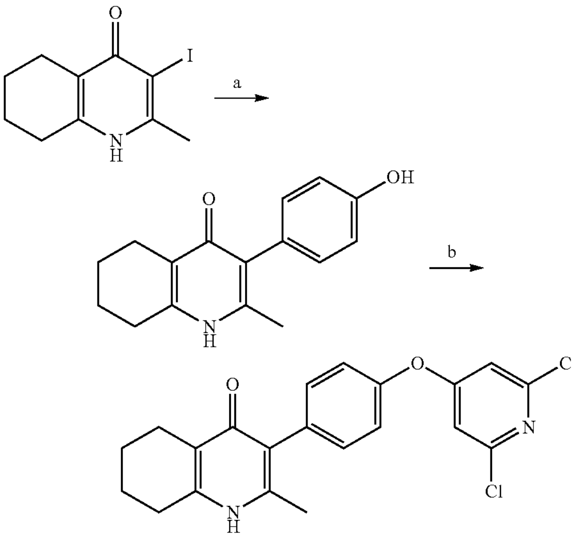
[0881] To a solution of the 4-Ethyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methylnapthyridone (1 equiv.) in acetic acid (2 mL mmol^{-1}) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol^{-1}). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound.

3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-napthyrid-4(1H)-one

[0882]



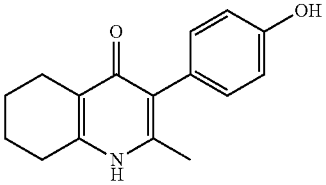
[0883] The title compound was synthesised from 4-Ethyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-napthyridone (31 mg, 0.07 mmol). To give the title compound as a colouress solid (13 mg, 0.03 mmol, 45%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 8.44 (d, J=3.6 Hz, 1H), 7.75 (d, J=8.2 Hz, 1H), 7.36 (dd, J=8.3, 4.1 Hz, 1H), 7.02 (d, J=8.6 Hz, 2H), 6.96 (d, J=8.5 Hz, 2H), 6.83 (d, J=9.2 Hz, 4H), 2.09 (s, 3H); M/Z (ESI+); 413.11 (Found MH$^+$; 413.1104 $C_{22}H_{15}F_3N_2O_3$ requires 413.1107).



a) 4-Hydroxybenzene boronic acid, $Pd(PPH_3)_4$, Na_2CO_3 (aq), DMF 80° C., b) 2,4,6 trichloropyridine, K_2CO_3, DMF, 100° C.

3-phenol-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

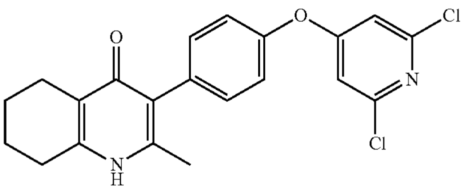
[0884]



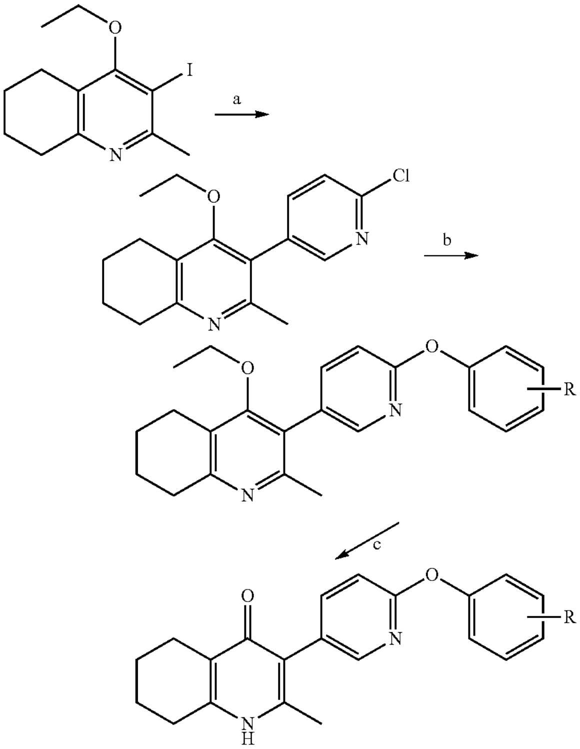
[0885] The title compound was synthesised from 4(1H)-3-iodo-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (500 mg, 1.73 mmol) and 4-hydroxyphenylboronic acid (318 mg, 2.30 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (aq) (3 mL, 2 M) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). Organics were extracted with ethyl acetate (3×10 mL). The aqueous layer was neutralised using hydrochloric acid (2 M), causing the title compound, a grey precipitate to crash out which was collected by vacuum filtration (150 mg, 0.58 mmol, 44%). ^{1}H NMR (400 MHz, MeOD) δ 6.91 (d, J=8.6 Hz, 2H), 6.71 (d, J=8.6 Hz, 2H), 2.57 (t, J=6.0 Hz), 2.39 (t, J=5.6 Hz, 2H), 2.03 (s, 3H), 1.77-1.61 (m, 4H); M/Z (ESI); 255.1341 ($C_{16}H_{17}NO_2$ requires 255.1259).

3-{4-[(2,6-dichloropyridin-4-yl)oxy]phenyl}-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

[0886]



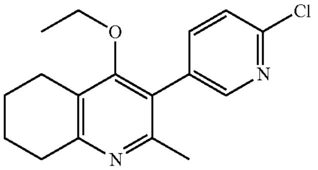
[0887] 3-phenol-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (120 mg, 0.47 mmol) and potassium carbonate (78 mg, 0.56 mmol) were dissolved in DMF (3 mL) and the reaction mixture was stirred for 15 mins. Following this, 2,4,6-Trichloropyridine (86 mg, 0.47 mmol) was added and the mixture was heated to 100° C. and stirred for 18 hours under an inert atmosphere. The reaction mixture was allowed to cool to room temperature and was diluted with water (5 ml). The resulting pale grey precipitate was collected by vacuum filtration, washed with water (5 ml) and dried (118 mg, 0.29 mmol, 63%). δ ^{1}H NMR (500 MHz, TFA) δ 7.66 (d, J 8.5 Hz, 2H), 7.56 (d, J 8.5 Hz, 2H), 7.44 (s, 2H), 3.10 (t, J 5.0 Hz, 2H), 2.90 (t, J 5.0 Hz, 2H), 2.55 (s, 3H), 2.10-2.08 (m, 4H); M/Z (ESI); 400.0826, ($C_{21}H_{18}Cl_2N_2O_2$ requires 400.0745).



a) 2-Chlorpyridine-5-boronic acid, Pd(PPH$_3$)$_4$, Na$_2$CO$_3$ (aq), DMF 80° C., b) Phenol, K$_2$CO$_3$, DMF, 100° C.

4-Ethoxy-3-(6-chloropyrdin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline

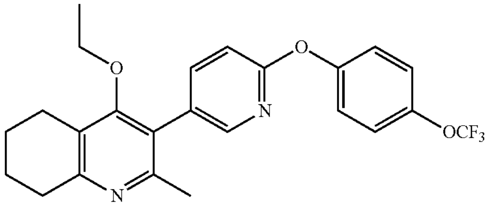
[0888]



[0889] To a nitrogen flushed flask charged with 4-ethoxy-3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline (1.5 g, 4.7 mmol), 2-chloropyridine-5-boronic acid (1.12 g, 7.1 mmol) and palladium tetra(triphenylphosphine) (271 mg, 0.24 mmol) was added degassed DMF (20 mL). Potassium carbonate (3 mL, 2 $M_{(aq)}$) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and $MgSO_4$, before concentration in vacuo. The resulting residue was purified by column chromatography (Pet:EtOAc), to yield the title compound as a yellow platelets (330 mg, 1.09 mmol, 23%). HPLC; 2.17 min (100% ref area); ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.33 (d, J=2.4 Hz, 1H), 7.60 (dd, J=8.2, 2.4 Hz, 1H), 7.44-7.42 (d, J=8.2, 1H), 3.53 (q, J=7.0 Hz, 2H), 2.98 (t, J=6.2 Hz, 2H). 2.72 (t. J=6.2 Hz, 2H), 2.35 (s, 3H), 1.93-1.85 (m, 2H), 1.84-1.76 (m, 2H), 1.06 (t, J=7.0 Hz, 3H); M/Z (ESI+); 303.13 (Found MH$^+$; 303.1266, C17$H_{19}ClN_2O$ requires 303.1259).

4-Ethoxy-3-(6-(4-trifluoromethoxyphenoxy)pyrdin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline

[0890]

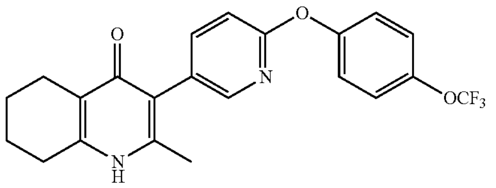


[0891] 4-Ethoxy-3-(6-chloropyrdin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline (250 mg, 0.82 mmol), 4-trifluoromethoxyphenol (178 mg, 1.0 mmol)and potassium carbonate (276 mg, 1.7 mmol) were dissolved in DMF and refluxed at 110° C. for 24 hrs. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and $MgSO_4$, before concentration in vacuo. The resulting residue was purified by reverse phase column chromatography (H_2O: acetonitrile), to yield the title compound as a yellow oil (75 mg, 0.17 mmol, 20%). ^{1}H NMR (400 MHz,

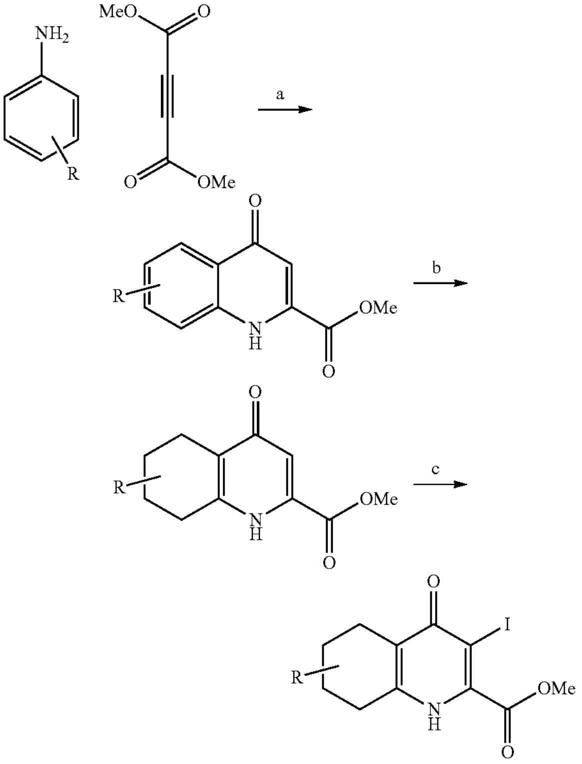
$CDCl_3$) δ 8.03 (d, J=2.2 Hz, 1H), 7.58 (dd, J=8.4, 2.2 Hz, 1H), 7.29-7.07 (m, 4H), 6.95 (d, J=8.4 Hz, 1H), 3.46 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.3 Hz, 2H), 2.64 (t, J=6.1 Hz, 2H), 2.25 (s, 3H), 1.81 (dt, J=12.2, 6.3 Hz, 2H), 1.77-1.68 (m, 2H), 0.99 (t, J=7.0 Hz, 3H); M/Z (ESI+); 445.18 (Found MH^+; 445.1759, $C_{24}H_{23}F_3N_2O_3$ requires 445.1739).

3-(6-(4-Trifluoromethoxyphenoxy)pyrdin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinolin-(4)-one

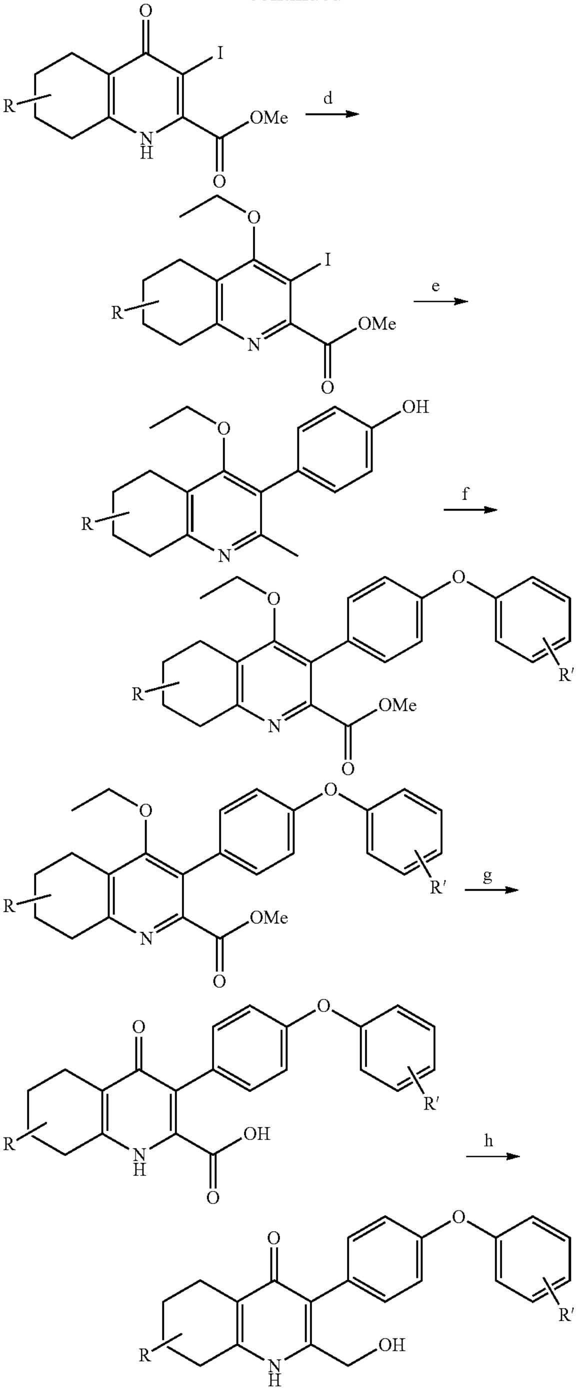
[0892]



[0893] The title compound was synthesised from 4-ethoxy-3-(6-(4-trifluoromethoxyphenoxy)pyrdin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline (70 mg, 0.15 mmol) according to general procedure J. The title compound was isolated as colourless solid (13 mg, 0.03 mmol, 20%). ^1H NMR (400 MHz, DMSO) δ 11.07 (s, 1H), 7.94 (d, J=2.2 Hz, 1H), 7.70 (dd, J=8.4, 2.4 Hz, 1H), 7.43 (d, J=8.7 Hz, 2H), 7.29 (d, J=9.0 Hz, 2H), 7.09 (d, J=8.4 Hz, 1H), 2.56 (t, J=5.1 Hz, 2H), 2.30 (t, J=5.9 Hz, H), 2.10 (s, 3H), 1.79-1.57 (m, 4H); M/Z (ESI+); 417.14 (Found MH^+; 417.1432, $C_{22}H_{19}F_3N_2O_3$ requires 417.1421).



-continued



R = 7-Me 7-CF₃, 7-Et, 7-CH₂OH

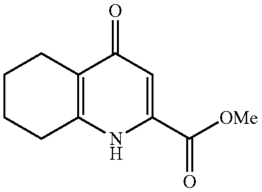
a) i) Ethanol, ii) Dowtherm A, 250° C., b) PtO_2, H_2, AcOH, c) NIS, Acetonitrile, 80° C., D) EtI, K_2CO_3, DMF, 80° C., e) 4-Hydroxyphenyl boronic acid, $Pd(PPH_3)_4$, DMF, 80° C., f) Phenyl boronic acid, $Cu(OAc)_2$, Pyridine, TEA, DCM, g) HBr (40% aq), Acetic acid, 120° C., h) i) MeOH, ii) DiBAl.

General Method B

[0894] The 4-hydroxylquinolone (1 equiv.) was dissolved in acetic acid (10.0 mL) under inert conditions. platinum dioxide (5% weight equiv.) was added and a hydrogen balloon was attached. The reaction was left to proceed for 12 hours. The resulting suspension was filtered through a pad of Celite and washed with ethyl acetate (10.0 mL). The filtrate was concentrated in vacuo to afford a yellow/brown oil. Purification by column chromatography (10% methanol in chloroform) afforded the title compound.

2-(Methoxycarboxylate)-5,6,7,8-tetrahydro quinolin-4(1H)-one

[0895]



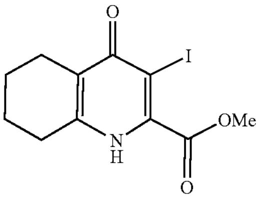
[0896] The title compound was synthesised following general procedure B from 2-(methoxycarboxylate)quinolin-4(1H)-one (500 mg, 2.5 mmol). The title compound was isolated as colourless solid (470 mg, 2.4 mmol, %). ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.89 (s, 1H), 7.07 (s, 1H), 3.95 (s, 3H), 2.74 (t, J=6.1 Hz, 2H), 2.56 (t, J=6.2 Hz, 2H). 1.82 (dt, J=8.0, 6.1 Hz, 1H), 1.79-1.69 (m, 1H); M/Z (ESI+); 208.10 (Found MH^+; 208.0977, $C_{11}H_{13}NO_3$ requires 208.0974).

1.5 General Method C

[0897] The tetrahydroquinolin-4(1H)-one (1 equiv.) and N-Iodosuccinamide (1.2 equiv.) were dissolved in acetonitrile (5 mL $mmol^{-1}$) and stirred and heated at 80° C. for 3 hours. The reaction mixture was then allowed to cool and the mixture filtered, the precipitate was then washed with water (15 mL) to afford the title compound as a colourless solid

3-Iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydro quinolin-4(1H)-one

[0898]



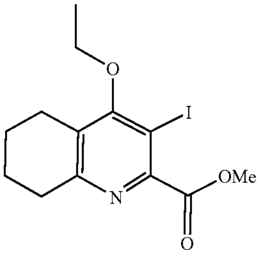
[0899] The title compound was synthesised following general procedure C from 2-(methoxycarboxylate)-5,6,7,8-tetrahydro quinolin-4(1H)-one (450 mg, 2.20 mmol). The title compound was isolated as colourless solid (612 mg, 1.8 mmol, 84%). ^{1}H NMR (400 MHz, DMSO) δ 11.93 (s, 1H), 3.91 (s, 3H), 2.58 (s, 2H), 2.34 (t, 2H), 1.90-1.45 (m, 4H); M/Z (ESI+); 333.99 (Found MH^+; 333.9935, $C_{11}H_{12}INO_3$ requires; 333.9935).

General Method D

[0900] A suspension of the 4(1H), 3-iodo-tetrahydroquinolinone (1 equiv.) and potassium carbonate (2 equiv.) in DMF (20.0 mL) was heated to 50° C. and stirred for 45 minutes. The reaction mixture was removed from the heat and ethyl iodide (1.5 equiv.) was added dropwise. The reaction mixture was then heated and kept at 50° C. with stirring for a further 18 hrs. Formation of a yellow emulsion was observed. The reaction mixture was then quenched with water (40.0 mL). The organic phase was extracted using the polar extraction technique (ethyl acetate, 3x40.0 mL), and the resulting organic layers were combined and dried over $MgSO_4$ and concentrated in vacuo to afford the title compound.

4-Ethoxy-3-iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline

[0901]



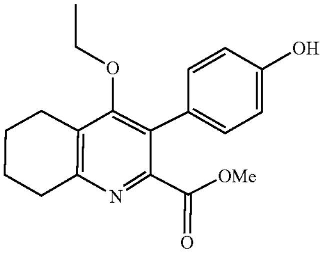
[0902] The title compound was synthesised following general procedure D from 3-iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydro quinolin-4(1H)-one (500 mg, 1.5 mmol). The title compound was isolated as colourless crystals (450 mg, 1.25 mmol, 83%). ^{1}H NMR (300 MHz, $CDCl_3$) δ 3.94 (q, J=7.0 Hz, 2H), 3.90 (s, 3H), 2.84 (t, J=6.4 Hz, 2H), 2.73 (t, J=6.2 Hz, 2H), 1.87-1.64 (m, 4H), 1.43 (t, J=7.0 Hz, 3H); M/Z (ESI+); 362.03 (Found MH^+; 362.0256, $C_{13}H_{16}INO_3$ requires 362.0248).

1.6 General Method E

[0903] To a nitrogen flushed flask charged with the 4-ethoxy-3-iodo-tetrahydroquinoline (400 mg, 1.26 mmol), 4-hydroxybenzene boronic acid (260 mg, 1.89 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (3 mL, 2 $M_{(aq)}$) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3x20 mL). The organic phases were combined and washed with water (3x20 mL) and then dried with brine (1x10 mL) and $MgSO_4$, before concentration in vacuo. The resulting solid was then recrystallized in ethyl acetate to afford the title compound.

4-(4-Ethoxy-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-3-yl)phenol

[0904]



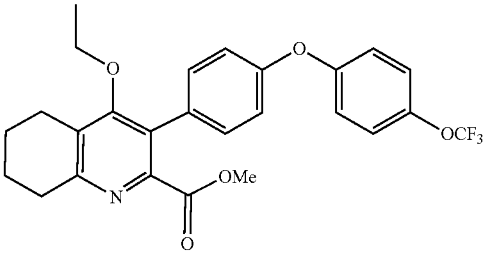
[0905] The title compound was synthesised following general procedure E from 4-ethoxy-3-iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydro quinoline (400 mg, 1.11 mmol). The title compound was isolated as a solid (200 mg, 0.61 mmol, 55%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.11 (d, J=8.6 Hz, 2H), 6.77 (d, J=8.6 Hz, 2H), 3.60 (s, 3H), 3.43 (q, J=7.0 Hz, 2H), 2.91 (t, J=6.4 Hz, 2H), 2.71 (t, J=6.3 Hz, 2H), 1.82 (m, 2H), 1.78-1.69 (m, 2H), 0.98 (t, J=7.0 Hz, 3H); M/Z (ESI+); 328.16 (Found MH$^+$; 328.1551, $C_{19}H_{21}NO_4$ requires; 328.1543).

General Method F

[0906] Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol^{-1}) over heat-activated 4 A molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol^{-1}) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol^{-1}). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

4-Ethoxy-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline

[0907]



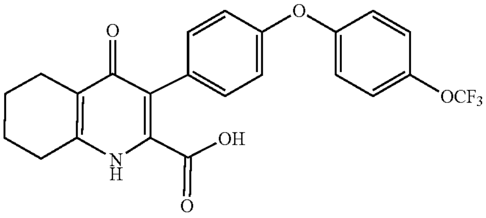
[0908] The title compound was synthesised following general procedure F from 4-(4-ethoxy-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-3-yl)phenol (180 mg, 0.55 mmol). The title compound was isolated as a yellow oil (210 mg, 0.43 mmol, 78%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 7.32 (d, J=8.6 Hz, 2H), 7.22 (d, J=8.6 Hz, 2H), 7.05 (dd, J=8.8, 3.0 Hz, 4H), 3.73 (s, 3H), 3.55 (q, J=7.0 Hz, 2H), 3.05 (t, J=4.7 Hz, 2H), 2.80 (t, J=6.2 Hz, 2H), 1.99-1.88 (m, 2H), 1.88-1.79 (m, 2H), 1.09 (t, J=7.0 Hz, 3H).

General Method G

[0909] To a solution of the 4-ethoxy-3-(diaryl ether)-hydroxyquinolone (1 equiv.) in acetic acid (2 mL mmol^{-1}) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol^{-1}). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound.

3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one

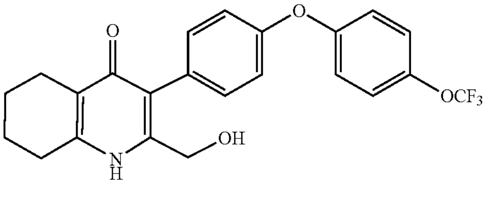
[0910]



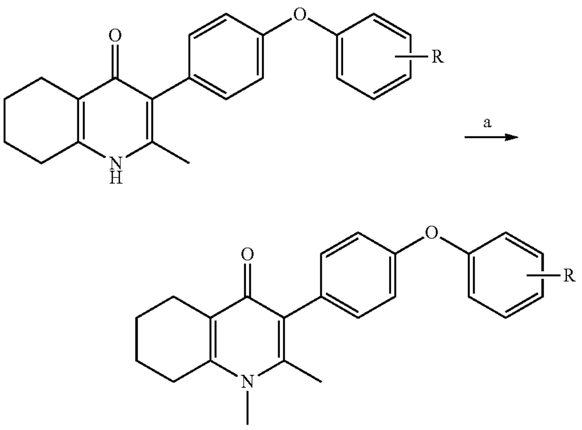
[0911] The title compound was synthesised following general procedure G from 4-ethoxy-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline (200 mg, 0.42 mmol). The title compound was isolated as a colourless solid (80 mg, 0.18 mmol, 43%). ^{1}H NMR (400 MHz, DMSO) δ 7.41 (d, J=8.8 Hz, 2H), 7.21 (d, J=8.3 Hz, 2H), 7.12 (d, J=8.8 Hz, 2H), 7.01 (d, J=8.3 Hz, 2H), 2.64 (t, J=5.6 Hz, 2H), 2.35 (t, J=5.6 Hz, 2H), 1.94-1.33 (m, 4H); M/Z (ESI+); 446.12 (Found MH$^+$; 446.1207, $C_{23}H_{18}F_3NO_5$ requires 446.1210).

3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(methylhydroxy)-5,6,7,8-tetrahydroquinolin-4(1H)-one

[0912]



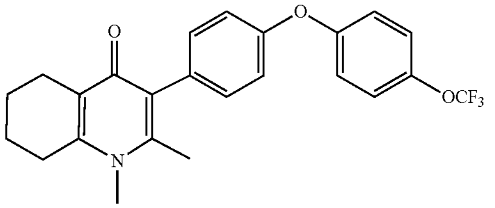
[0913] 3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one (80 mg, 0.17 mmol) was dissolved in methanol (5 mL) with the addition of HCl (1 mL, conc.) heated to 80° C. for 24 hours. The reaction mixture was diluted with water (10 mL) and the organics extracted with EtOAc (3×10 mL) before being dried and concentrated in vacuo. The crude material was then dissolved in dry THF under inert atmosphere and cooled to 0° C. Diisobutylaluminium hydride was then added slowly with stirring. After two hours the reaction pH was lowered to 3 through addition of HCl (2M). Dilution of the solution with water caused precipitation. The title compound was isolated as via filtration as a pale yellow solid (38 mg, 0.09 mmol, 55%). ^{1}H NMR (400 MHz, DMSO) δ 11.06 (s, 1H), 7.41 (d, J=8.8 Hz, 2H), 7.25 (d, J=8.6 Hz, 2H), 7.15 (d, J=9.1 Hz, 2H), 7.05 (d, J=8.6 Hz, 2H), 5.53 (s, 1H), 4.25 (s, 2H), 2.67 (t, J=5.6 Hz, 2H), 2.35 (t, J=6.2 Hz, 2H), 1.82-1.56 (m, 4H); M/Z (ESI+); 432.14 (Found MH+; 432.1445, $C_{23}H_{20}F_3NO_4$ requires 432.1423).



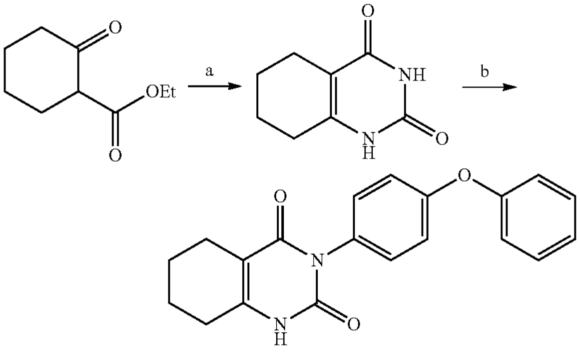
a) MeI, NaH, DMF, 90° C.

1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4-one

[0914]



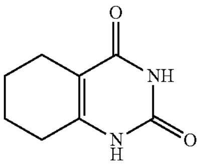
[0915] 2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one (60 mg, 0.14 mmol) was dissolved in DMF (0.1 mL) under Nitrogen. Sodium Hydride (4 mg, 0.17 mmol) was added and the reaction heated to 90° C. for 30 minutes. Methyl iodide (80 mg, 0.56 mmol) was added and the reaction continued for a further 2 hours. Reaction mixture was allowed to cool and organics extracted with ethyl acetate, followed by drying with brine and magnesium sulphate. Organics were concentrated in vacuo and purified by column chromatography (DCM). To give the title compound as a colourless solid (20 mg, 0.04 mmol, 35%). ^{1}H NMR (400 MHz, DMSO) δ 7.41 (d, J=8.6 Hz, 2H), 7.19-7.08 (m, 4H), 7.06 (d, J=8.5 Hz, 2H), 3.53 (s, 3H), 2.71 (t, J=6.2 Hz, 2H), 2.38 (t, J=6.0 Hz, 2H), 2.19 (s, 3H), 1.75 (d, J=5.7 Hz, 2H), 1.66-1.56 (m, 2H).



a) Urea, NaOME, Ethanol, 80° C., b) 4-phenoxyphenyl boronic acid, $CuOAc_2$, Pyridine, triethylamine, Ethanol

1,2,3,4,5,6,7,8-Octahydroquinazoline-2,4,dione

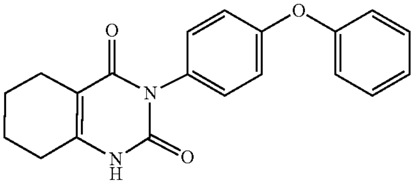
[0916]



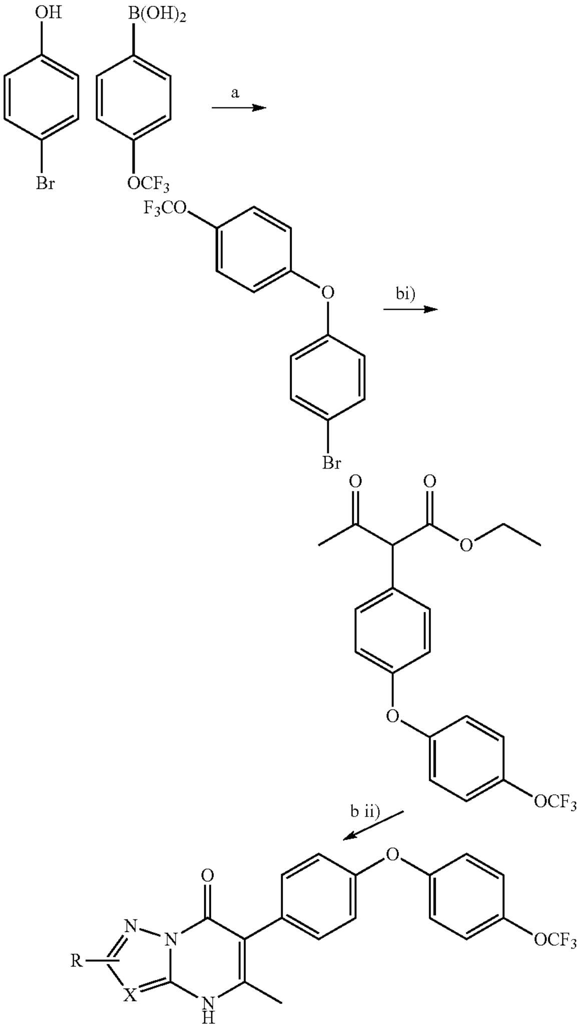
[0917] Urea (0.48 g, 8.0 mmol) and ethyl-2-oxocyclohexancarbonylate (1.0 g. 6.0 mmol) were dissolved in ethanol (10 mL). Sodium methoxide (3 mL, 12.0 mmol) was added and the reaction mixture refluxed at 80° C. for 15 hours. The reaction mixture was allowed to cool and the resulting precipitate was washed with diethyl ether (2×10 mL) to afford the title compound as a white solid. (526 mg 3.17 mmol, 53%). ^{1}H NMR (501 MHz, DMSO) δ 10.72 (s, 1H), 8.50 (s, 1H), 2.28 (t, J=6.2 Hz, 2H), 2.12 (t, J=6.2 Hz, 2H), 1.69-1.60 (m, 2H), 1.59-1.51 (m, 2H); M/Z (ESI+); 167.08 (Found MH$^+$; 167.0815, $C_8H_{10}N_2O_2$ requires 167.0815).

3-(4-Phenonxyphenyl)-1,2,3,4,5,6,7,8-octahydroquinazoline-2,4,dione

[0918]



[0919] 1,2,3,4,5,6,7,8-Octahydroquinazoline-2,4,dione (300 mg, 1.8 mmol), 4phenoxyphenyl boronic acid (600 mg, 2.7 mmol) and copper acetate (330 mg, 1.8 mmol) were dissolved in ethanol (20 mL). Triethylamine (1.2 mL, 9.0 mmol), and pyridine (0.66 mL, 9.0 mmol) were added immediately and the reaction stirred overnight. The reaction was filtered through celite neutralised with HCl (0.5 M, 60 mL) to give crude solid, this was then recrystallized in DCM to afford product as colourless needles (60 mg, 0.18 mmol, 10%). ^{1}H NMR (500 MHz, DMSO) δ 11.04 (s, 1H), 7.45 (t, J=7.1 Hz, 2H), 7.20 (d, J=7.5 Hz, 3H), 7.09 (d, J=7.8 Hz, 2H), 7.04 (d, J=7.9 Hz, 2H), 2.39 (s, 2H), 2.22 (s, 2H), 1.68 (m, 4H); M/Z (ESI+); 335.14 (Found MH$^+$; 335.1394, $C_{20}H_{18}N_2O_3$ requires 335.1390).



R = SMe, Me, CN, Ph
X = C/N

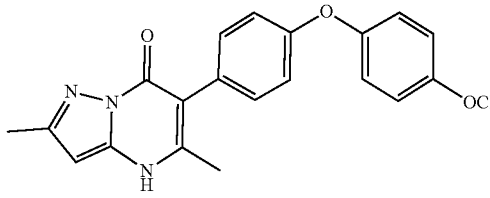
a) $Cu(OAc)_2$, Pyridine, TEA, DCM, b)i) Ethylacetoacetate, $PdOAc_2$, JohnPhos, K_3PO_4, Tol, 90° C., b)ii) pyrazole/triazole, AcOH, 120° C.

General Procedure B

[0920] Toluene (2.00 mL) was added to a flask flushed with nitrogen and charged with 1-Bromo-4-(4-trifluoromethoxy)phenoxy)benzene (0.30 g, 0.90 mmol), ethyl acetoacetate (0.252 mL, 0.99 mmol), palladium acetate (10.1 mg, 0.045 mmol), (2-Biphenyl)di-tert-butylphosphine (26.8 mg, 0.09 mmol) and potassium phosphate (0.252 g, 1.2 mmol). The reaction mixture was then heated to 90° C. for 16 hours. The reaction mixture was cooled to room temperature followed by dilution in DCM (15.0 mL) and filtration through a pad of Celite. The reaction mixture was then concentrated in vacuo and passed through a silica plug. The resulting oil containing crude ethyl 3-oxo-2-4-(4-(trifluoromethoxy)phenoxy)phenyl)butanoate (1 equiv.) was dissolved in acetic acid (2.00 ml). 3-amino-tria-/pyrazole (1 equiv.) was added to the solution. The solution was heated to 120° C. and refluxed for 16 hours. The reaction mixture was then allowed to cool to room temperature. Addition of H_2O (2.00 ml) caused precipitation of a white solid. Precipitate was filtered and washed with H_2O (2×10.0 mL). The solid was then recrystallized in appropriate solvent to give the title compound.

2,5-dimethyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

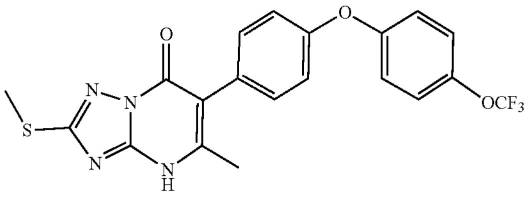
[0921]



[0922] The title compound was synthesised from 3-amino-5 methyl-pyrazole (30.0 mg, 0.31 mmol) according to general procedure B (recrystallized in EtOAc) to afford the title compound as colourless platelets (47.0 mg, 0.11 mmol, 36%). δ H NMR (500 MHz, Chloroform-d); δ 7.27 (d, J=8.6 Hz, 2H), 7.16 (d, J=8.7 Hz, 2H), 6.99 (d, J=8.9 Hz, 2H), 6.95 (d, J=8.6 Hz, 2H), 5.80 (s, 1H), 2.34 (s, 3H,), 2.21 (s, 3H) M/Z (ESI); 419.12 (Found MH$^+$416.1221, $C_{21}H_{16}F_3N_3O_3$ requires 416.1217).

5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo [1,5-a] pyrimidin-7 (4H)-one

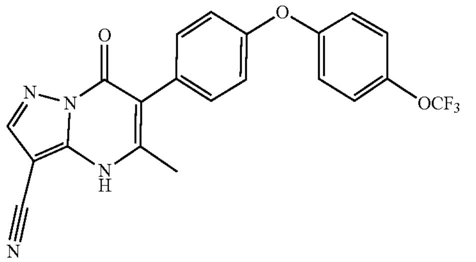
[0923]



[0924] The title compound was synthesised from 3-amino-5-methio-1,2,4triazole (30.0 mg, 0.31 mmol) according to general procedure B to afford the title compound as colourless flake crystals (recrystallized EtOAc) (54.0 mg, 0.12 mmol, 39%). δ H NMR (500 MHz, Chloroform-d); δ 7.30 (d, J=8.6 Hz, 2H), 7.22 (d, J=8.7 Hz, 2H), 7.09 (d, J=8.7 Hz, 2H), 7.07 (d, J=8.6 Hz, 2H), 2.74 (s, 3H), 2.49 (s, 2H); M/Z (ESI); 449.09 (Found MH$^+$449.0893, $C_{20}H_{15}F_3N_4O_3S$ requires 449.0893).

5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile

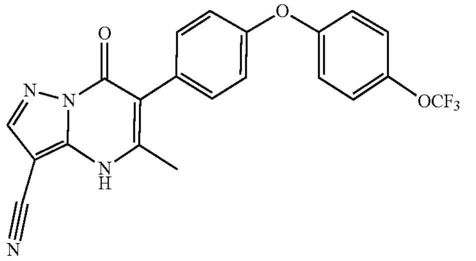
[0925]



[0926] The title compound was synthesised from 3-amino-4-carbonitrile-1,2,pyrazole (45 mg, 0.42 mmol) according to general procedure B to afford the title compound as white flake crystals (recrystallized EtOAc), (43 mg, 0.10 mmol, 23%); ^{1}H NMR (500 MHz, DMSO) δ 8.49 (s, 1H), 7.51 (d, J=8.9 Hz, 2H), 7.44 (d, J=8.6 Hz, 2H), 7.28 (d, J=8.9, Hz, 2H), 7.20 (d, J=8.6 Hz, 2H), 2.32 (s, 3H). M/Z (ESI+); 427.10 (Found MH$^+$427.1018, $C_{21}H_{13}F_3N_4O_3$ requires 427.1012).

5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

[0927]



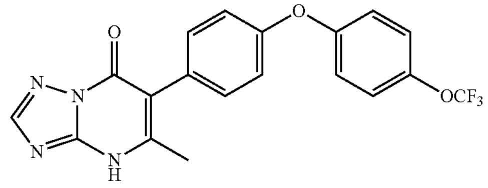
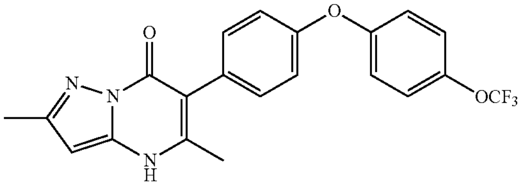
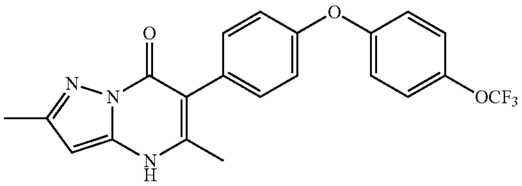
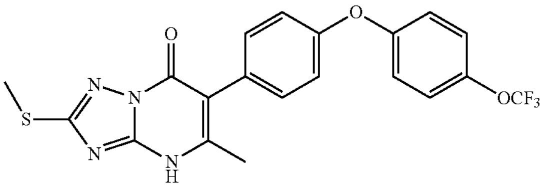
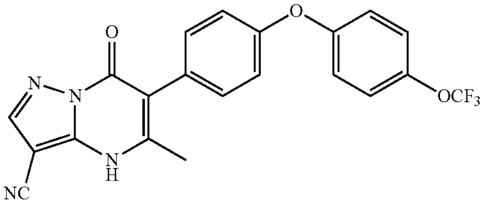
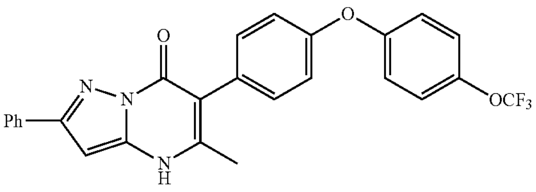
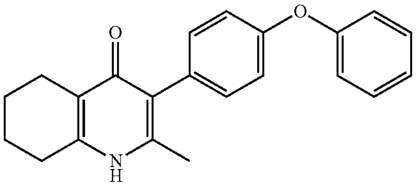
[0928] The title compound was synthesised from 3-amino-4-carbonitrile-1,2,pyrazole (0.067 g, 0.42 mmol) according to general procedure B (recrystallized in DMSO) to afford the title compound as a grey micro crystals (0.15 g, 0.31 mmol, 74%). ^{1}H NMR (500 MHz, DMSO) δ 12.47 (s, 1H, NH), 8.01 (d, J=6.8 Hz, 2H, H-2* & 6*), 7.53-7.40 (m, 5H, H-3*, 4*, 5*,2' & 6'), 7.38 (d, J=8.7 Hz, 2H, H-2" & 6"), 7.20 (d, J=9.1 Hz, 2H, H-3' & 5'), 7.11 (d, J=8.7 Hz, 2H, H-3" & 5"), 6.62 (s, 1H, H-3), 2.22 (s, 3H, Me); M/Z (ESI+); 478.1378 (Found MH+, $C_{26}H_{18}F_3N_3O_3$ requires 478.1373).

In Vitro Challenge Assay for *Toxoplasma* Tachyzoites

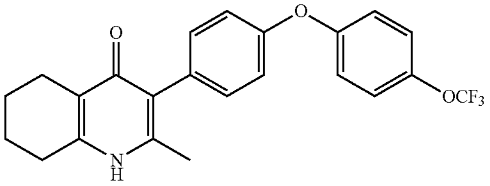
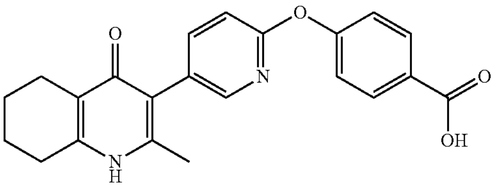
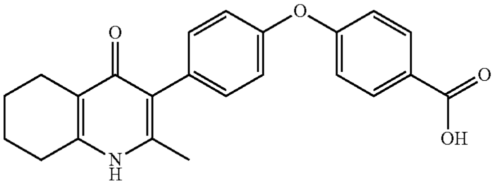
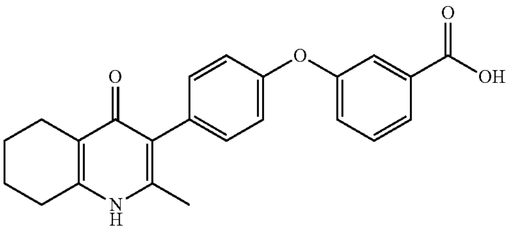
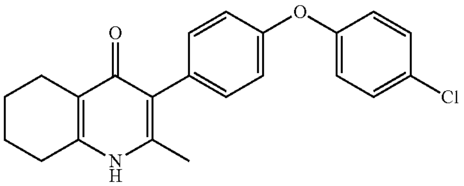
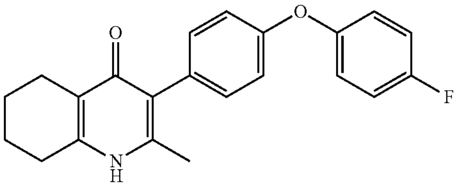
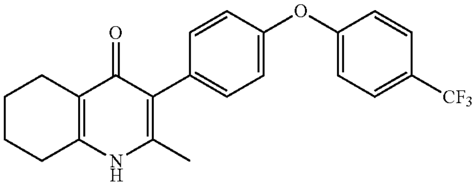
[0929] Protocol adapted from Fomovska, et. al. (Fomovska A, Huang Q, El Bissati K, Mui E J, Witola W H, Cheng G, et al. Novel N-Benzoyl-2-Hydroxybenzamide Disrupts Unique Parasite Secretory Pathway. Antimicrob Agents Chemother [Internet]. 2012 May [cited 2015 Jul. 8];56(5):2666-82; Fomovska A, Wood R D, Mui E, Dubey J P, Ferreira L R, Hickman M R, et al. Salicylanilide inhibitors of *Toxoplasma gondii*. J Med Chem. 2012 Oct. 11;55(19):8375-91.). Human foreskin fibroblasts (HFF) were cultured on a flat, clear-bottomed, black 96-well plate to 90% to 100% confluence. IMDM (1×, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS [gibco, Denmark]) was removed from each well and replaced with IMDM-C(1×, [+] glutamine, [+] 25 mM HEPES, [−] Phenol red, 10% FBS)[gibco, Denmark]). Type I RH parasites expressing Yellow Fluorescent Protein (RH-YFP) were lysed from host cells by double passage through a 27-gauge needle. Parasites were counted and diluted to 32,000/mL in IMDM-C. Fibroblast cultures were infected with 3200 tachyzoites of the Type I RH strain expressing Yellow Fluorescent Protein (RH-YFP) and returned to incubator at 37° C. for 1-2 hours to allow for infection(Gubbels M-J, Li C. Striepen B. High-Throughput Growth Assay for *Toxoplasma gondii* Using Yellow Fluorescent Protein. Antimicrob Agents Chemother [Internet]. 2003 January [cited 2015 Jul. 8];47(1):309-16.). Various concentrations of the compounds were made using IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. Controls included pyrimethamine/sulfadiazine (current standard of treatment), 0.1% DMSO only, fibroblast only, and an untreated YFP gradient with 2 fold dilutions of the parasite. Cells were incubated at 37° C. for 72 hours. Plates were read using a fluorimeter (Synergy H4 Hybrid Reader, BioTek) to ascertain the amount of yellow fluorescent protein, in relative fluorescence units (RFU), as a measure of parasite burden after treatment. Data was collected using Gen5 software. IC50 was calculated by graphical analysis in Excel.

In Vitro Challenge Assay for Bradyzoites

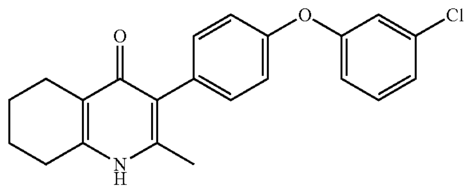
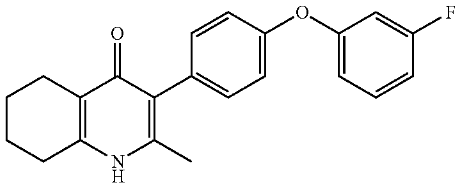
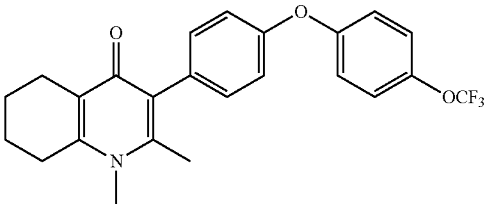
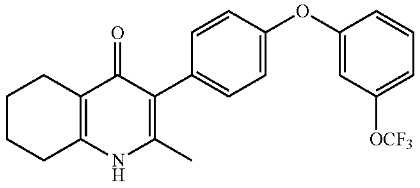
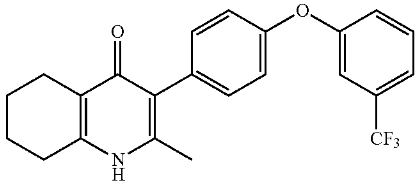
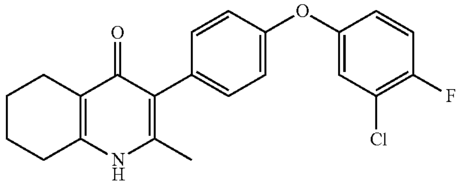
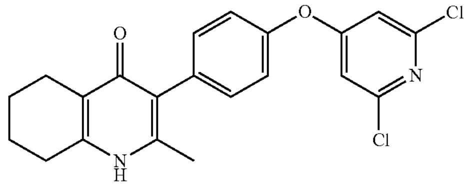
[0930] HFF cells were grown in IMDM (1×, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS, [gibco, Denmark]) on removable, sterile glass disks in the bottom of a clear, flat-bottomed 24-well plate. Cultures were infected with 3x104 parasites (EGS strain) per well, in 0.5 mL media and plate was returned to incubator at 37° C. overnight. The following day, the media was removed and clear IMDM and compounds were added to making various concentrations of the drug, to a total volume of 0.5 mL. 2 wells were filled with media only, as a control. Plates were returned to the 37° C. incubator for 72 hours, and checked once every 24 hours. If tachyzoites were visible in the control before 72 hours, the cells were fixed and stained. Cells were fixed using 4% paraformaldehyde and stained with Fluorescein-labeled Dolichos Biflorus Agglutinin, DAPI, and BAG1. Disks were removed and mounted onto glass slides and visualized using microscopy (Nikon T17). Slides were scanned using a CRi Pannoramic Scan Whole Slide Scanner and viewed using Panoramic Viewer Software. Effects of the compounds were quantified by counting cysts in the controls and treated cells. Cysts and persisting organisms were counted in a representative field of view and then multiplied by a factor determined by the total area of the disk in order to estimate the number of cysts and organisms in each condition. Data was collected using Gen5 software. IC50 was calculated by graphical analysis in Excel.

ID	Structure	Tachy IC_{50} μM	Brady IC_{50} μM	Pf D6 IC_{50} μM
MJM136		1.0-10.0	>10	0.2
MJM141		1.0-10.0	1.0-10.0	0.16
JAG006		>1	N.D.	0.29
JAG013		>1	N.D.	1.31
JAG014		>1	N.D.	0.71
JAG015		>1	N.D.	>20
MJM170		0.03	1.0-10.0	0.01

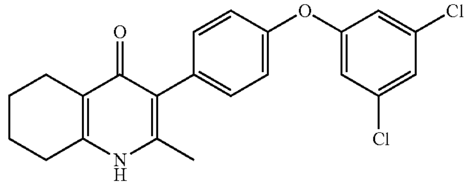
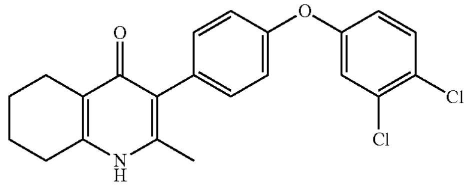
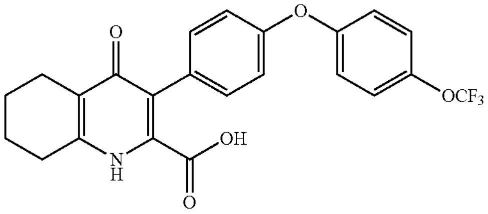
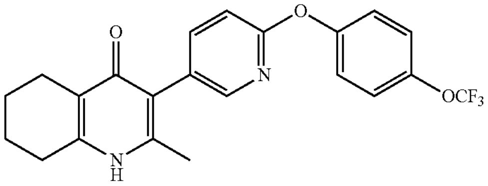
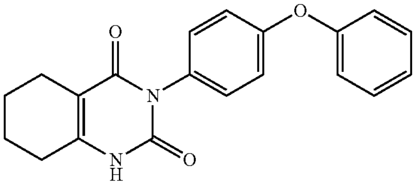
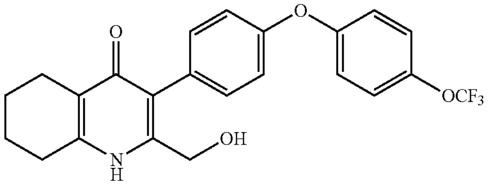
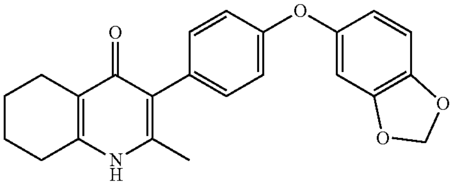
-continued

ID	Structure	Tachy IC_{50} µM	Brady IC_{50} µM	Pf D6 IC_{50} µM
JAG21		0.09	N.D.	0.01435
JAG039		7.6	N.D.	9.595
JAG046		>10	N.D.	6.716
JAG047		>10	N.D.	3.746
JAG50		0.055	N.D.	0.04664
JAG58		0.04- 0.08	N.D.	Awaiting Testing
JAG63		0.1- 0.3	N.D.	Awaiting Testing

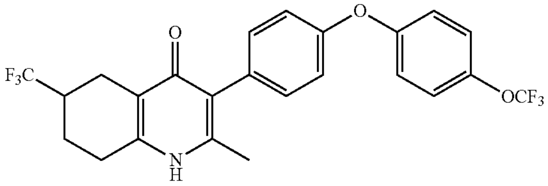
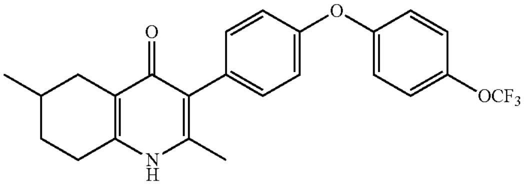
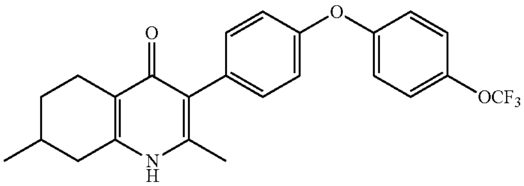
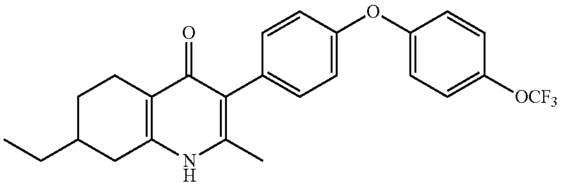
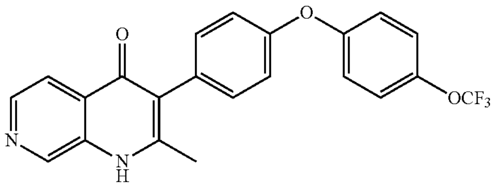
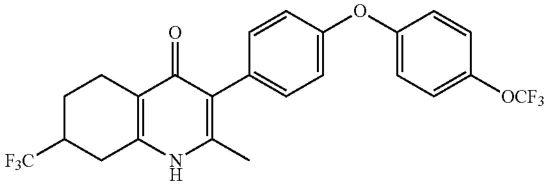
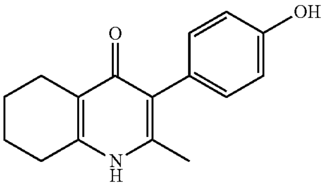
-continued

ID	Structure	Tachy IC_{50} μM	Brady IC_{50} μM	Pf D6 IC_{50} μM
JAG062		0.016	N.D.	N.D.
JAG069		0.02	N.D.	N.D.
JAG023		1	N.D.	N.D.
AS006/ JAG143		0.06- 0.08	N.D.	N.D.
AS012/ JAG144		0.3	N.D .	N.D.
AS021/ JAG145		0.08	N.D.	N.D.
AS034/ JAG148		0.1- 0.5	N.D.	N.D.

-continued

ID	Structure	Tachy IC_{50} μM	Brady IC_{50} μM	Pf D6 IC_{50} μM
AS022		0.02- 0.04	N.D.	N.D.
JAG084		0.04- 0.08	N.D.	N.D.
JAG091		>1	N.D.	N.D.
JAG092		1	N.D.	N.D.
JAG095		>10	N.D.	N.D.
JAG099		0.32	N.D.	N.D.
AS032		0.1- 0.3	N.D.	N.D.

-continued

ID	Structure	Tachy IC_{50} μM	Brady IC_{50} μM	Pf D6 IC_{50} μM
JAG100		>10	N.D.	N.D.
JAG106		~1	N.D.	N.D.
JAG107		1	N.D.	N.D.
JAG121		0.1	N.D.	N.D.
JAG129		0.1	N.D.	N.D.
JAG162		0.5	N.D.	N.D.
JAG094		1	N.D.	N.D.

Biological Activity Studies

Malaria In Vitro Studies:

[0931] D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. These assays were performed using standard protocols.

Compound Activity Against *Plasmodium falciparum:*

[0932] Compound activity against *P. falciparum*, a causative agent of malaria, was tested using the Malaria SYBR Green I—Based Fluorescence (MSF) Assay. This; microtiter plate drug sensitivity assay uses the presence of malarial DNA as a measure of parasitic proliferation in the presence of antimalarial drugs or experimental compounds based on modifications of previously described methods known in the art. As the intercalation of SYBR Green I dye and its resulting fluorescence is relative to parasite growth, a test compound that inhibits the growth of the parasite will result in a lower fluorescence. Selected compounds were examined for activity against four strains of *P. falciparum*: D6 (CDC/Sierra Leone), a drugsensitive strain readily killed by chloroquine, TM91-C235, a multi-drug resistant strain resistant to chloroquine, W2, a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone.

Example 5: Effect of Active Forms of *T. gondii* on Transcriptomes, Proteomes and Mechanisms Whereby this Occurs and Reflection of the Same Type of Damage to Neuronal Cells in Circulating Biomarkers from Children

[0933] Since we found signature pathways reflecting influence of the bradyzoite stage (characteristic of the chronic *Toxoplasma gondii* infection) in primary human neuronal stem cells in tissue culture on pathways of neurodevelopment, neuroplasticity, and neurotoxicity, we asked whether the active form of the parasite would also affect those pathways. It did. We found alterations in pathways similar to those shown with EGS bradyzoites in transcriptomics and proteomics (FIG. **19** with explanatory figure legends and methods). These abnormalities suggested that there might be circulating biomarkers reflecting such damage to neuronal cells in patients. In that context we then asked whether serum biomarkers from ill children would reflect neuronal damage and neurodegeneration.

Methods.

[0934] Biomarkers: Serum collection was from children in the National Collaborative Congenital ToxoplasmosisStudy (NCCCTS). Children have serum drawn at each visit. Sera characterized were obtained at a visit when new seizures

ID	Parasite strains	SYBR Green D6 IC50 (uM)	SYBR D6 R^2	SYBR Green C235 IC50 (uM)	SYBR TM91C235 R^2
MJM129	D6, C235, W2, C2B	0.03	0.94	0.07	0.94
MJM136	D6, C235, W2, C2B	0.20	0.99	0.58	0.98
MJM141	D6, C235, W2, C2B	0.16	0.96	0.57	0.95
MJM170	D6, C235, W2, C2B	0.01	0.98	0.03	0.99
JAG006	D6, C235, W2, C2B	0.29	0.90	0.88	0.92
JAG013	D6, C235, W2, C2B	1.31	0.98	2.60	0.96
JAG014	D6, C235, W2, C2B	0.71	0.94	1.35	0.99
JAG015	D6, C235, W2, C2B	>20	N/A	>20	N/A
JM10	D6, C235, W2, C2B	0.88	0.94	4.48	0.97
JAG021	D6, C235, W2, C2B	0.01435	0.9572	0.06164	0.9706
JAG047	D6, C235, W2, C2B	3.746	0.9738	12.56	0.9218
JAG046	D6, C235, W2, C2B	6.716	0.9844	>20	N/A
JAG039	D6, C235, W2, C2B	9.595	0.9532	>20	N/A
JAG050	D6, C235, W2, C2B	0.04664	0.9138	0.06913	0.9562
RG38	D6, C235, W2, C2B	2.884	0.8936	13.66	0.8338

ID	Parasite strains	SYBR Green W2 IC50 (uM)	SYBR W2 R^2	SYBR Green C2B IC50 (uM)	SYBR C2B R^2
MJM129	D6, C235, W2, C2B	0.08	0.93	0.01	0.94
MJM136	D6, C235, W2, C2B	0.55	0.98	0.38	0.99
MJM141	D6, C235, W2, C2B	0.63	0.88	0.48	0.95
MJM170	D6, C235, W2, C2B	0.03	0.99	0.01	0.99
JAG006	D6, C235, W2, C2B	2.46	0.92	1.66	0.94
JAG013	D6, C235, W2, C2B	2.35	0.96	1.39	0.94
JAG014	D6, C235, W2, C2B	1.27	0.99	0.92	0.98
JAG015	D6, C235, W2, C2B	>20	N/A	>20	N/A
JM10	D6, C235, W2, C2B	5.36	0.90	6.75	0.81
JAG021	D6, C235, W2, C2B	0.05518	0.9727	0.04042	0.9847
JAG047	D6, C235, W2, C2B	9.072	0.9358	7.781	0.9575
JAG046	D6, C235, W2, C2B	>20	N/A	>20	N/A
JAG039	D6, C235, W2, C2B	>20	N/A	>20	N/A
JAG050	D6, C235, W2, C2B	0.03136	0.9693	0.03635	0.9427
RG38	D6, C235, W2, C2B	9.245	0.7954	>20	N/A

were noted for ill children. These sera were analyzed with nano proteomic and miR analyses as described earlier by Hood, Wang et al. This was done using a panel of markers known to be abnormal in patients with Alzheimer's and other neurodegenerative diseases. This was done to determine whether the same biomarkers present in serum or plasma from persons with these neurodegenerative disease might be present in sera from the ill children. The children are described more fully in the figure legend.

[0935] Murine Study of Apolipoprotein A1:

[0936] Wildtype mice on a C57B16/J background, mice in which the Apolipoprotein A1 gene was knocked out (Apo A1−/−) were utilized in this experiment. They were immunized with an attenuated strain of the RH strain of *Toxoplasma* in which ribosomal proteins small subunit 13 was placed under the control of a tetracycline repressor by placing 4 tet 0 elements in the promoter and a tetracycline regulatable repressor with YFP was stably transfected. This immunized the mice and subsequently the mice were challenged with the Me49 strain *T. gondii* and cysts were counted or luminescence in brain measured.

[0937] EGS and Canonical Type 1,2,3 Transcriptomics Details and Type 1, 2, 3 Proteomics, Analysis of Alternatively Spliced Genes, and Immunoflurescense Studies:

[0938] Details of the specific genes with altered transcription caused by EGS in Example 1 are discussed above. Trascriptomics were carried out as described in Example 1.

[0939] iTRAQ data from *T. gondii* infected cell cultures. Protein quantified, extracted, subjected to mass spectroscopy, and sequence analysis from each flask, ~180-190 ug proteins were extracted and 50 ug were used for 8-plex iTRAQ. A raw table listing relative ratios for all peptide identified in 8 samples was created. The ratio should be 0.125 (1.000/8) if one peptide/protein evenly distributes in 8 samples. Ratios of peptides from the same proteins are then calculated to protein ratios. A "Ratio to Channel 0" then included a total of 4,367 proteins identified with iTRAQ ratio. The protein ratios crossed 8 samples (4 conditions in duplicates) and were raw data from mass spec and converted to ratios against Channel 0, i.e. Control sample. They are then normalized and ratios made. "Prot with high score" has 3,359 proteins identified by more than 1 peptide and with ProteinProphet probability >0.8 (=FDR<1%). Among these 3,3359 proteins with high confidence, 10 proteins up>2-fold in either of the 3 infected cells vs. controls, while 28 proteins down >2-fold were identified. Occurrence of differences in alternative splicing between infected and uninfected cells was done with rMATS. Method for IFA are as described in Example 1. The antibodies are to SAG1, P50-NFkB.

Results:

[0940] Human serum biomarkers in ill congenitally infected children reflect *T. gondii* infection and neuronal damage. Three pairs of children were studied. In each demographically-matched pair, one child had severe disease and the other had mild or no clinical illness. Each child had serum stored from evaluations at the same ages. The second pair are dizygotic, discordant twins. Each of the three ill children had new myoclonic-"infantile" spasms, or hypsarrhythmic seizures. For two, this was associated with a rise in or high *T. gondii* specific IgG antibody titers (FIG. **19***a*). IgG was not measured for the third ill child. A panel of nanoproteomics and miR sequencing was performed on serum obtained at the time of this new illness. The two ill children diagnosed more recently had T2 weighted abnormalities on brain MRIs similar to active inflammatory and parasitic caused brain disease seen in a murine model. Ill children compared with their paired healthy controls had alterations in miRs and increases in serum proteins associated with neurodegeneration, inflammation, a misfolded protein response and protein misfolding. Elevated proteins included clusterin, and oxytocin (FIG. **19** *b-d*). PGLYRP2 (N-acetylmuramoyl-L-alanine amidase) and Apolipoprotein B1 were depressed. miR-17-92, which *T. gondii* RH strain markedly increases in HFF cultures, also was increased in sera of the ill children, as was miR-124 (FIG. **19***b,c*). miR-124 is associated with neurodegeneration This indicates active brain destruction by the parasite or the response to it. These circulating proteins and miRs are clinically useful biomarkers to identify active toxoplasmic brain (and possibly retinal) disease.

[0941] To determine whether the presence of one of these biomarkers could be confirmed, a murine model was used. In this example of biomarkers in a murine experiment recapitulating the data of biomarkers in the serum of the ill children, APOA1 knockout and wild type mice were infected with *Toxoplasma*. The wild type and uninfected mice had less radiance from luciferase parasites and fewer cysts, and less immunologic reaction to the lower parasite burden in brain (data not shown). This demonstrates that the circulating ApoA1 diminishing in the boys who were ill as a biomarker. This provides evidence that these biomarkers that were abnormal in the children had counterparts in murine models.

[0942] To determine whether similar pathways as were abnormal in EGS Example 1 were perturbed by the canonical U.S./European types of parasites and mechanisms whereby this might occur, transcriptomics, proteomics, analysis of alternately spliced genes and immunoflueresce were also performed. Experimental data showed similar perturbation of pathways by canonical U.S./European type parasites that infected the children with the biomarkers through similar transcriptomics analyses demonstrating biological effect of Type I,II,III parasites on localization of NFkB, STAT 3 and STAT 6 in primary human neuronal stem cells. These abnormalities are caused by the canonical U.S. and European types of parasites growing as tachyzoites in the human primary neuronal stem cells and monocytic cells. These finding along with those demonstrated by the Omic studies of EGS (Example 1) suggest a mechanism whereby circulating biomarkers reflecting damage to neuronal cells in patients can occur. Placed in this context, we hypothesize that serum biomarkers from ill children reflect neuronal damage and neurodegeneration, as confirmed by our murine models, and findings seen in tissue culture and/or in patients.

DISCUSSION

[0943] The signature pathways we noted in studies of human primary neuronal stem cells which reflected abnormalities and gene products associated with neurodegenerative disease and the mechanisms whereby *T. gondii* can cause such pathology prompted study of biomarkers in a small number of ill versus well children. Biomarkers of active brain *T. gondii* infection in humans were found. The serum biomarkers shown in FIG. **19** are increased (e.g., clusterin, oxytocin, amyloid, and mir 17-92 and mir 124) or diminished, including PGLYRP2 (N-acetylmuramoyl-L-alanine amidase) and Apolipooprotein-A1 which are indicative of infection. These are consistent with the transcriptome demonstrating signature pathways in GO slim and KEGG analyses with effect on ribosomes, alternative splicing and neurodegenerative diseases, including Alzheimer's disease, Huntingtons disease, and Parkinson's disease by encysted EGS, and for example pathways of response to oxidative stress, regulation of apoptosis, and alternative splicing of toll receptors that were abnormal in the same cells infected by the canonical US/European parasites (active tachyzoites) that the children had. Other manifestations of active disease in the brain diminished with treatment and are not abnormal in the dizygotic healthy twin of one child or demographically matched well children. This is consistent with these biomarkers being selected to be assayed with MiR sequencing and proteomics based on their differences in diseases of neurodegeneration. These ill children had developed new seizures, elevations in antibody titer, elevated cerebrospinal fluid protein in one child, and abnormal T2 weighted alterations in T2 weighted brain magnetic resonance imaging. The biomarkers that were characteristic of neurodegeneration in the ill children and when diminished were associated with greater severity of disease in a murine model will be useful to monitor disease and response to treatment of disease due to this parasite. Restoration to normal values being indicative of favorable response to treatment and presence may also mark recrudescence of disease. ApoA1 may also be a useful treatment.

```
                        SEQUENCE LISTING


<160> NUMBER OF SEQ ID NOS: 27

<210> SEQ ID NO 1
<211> LENGTH: 54
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

Gly Gly Asn Arg Pro His Tyr His Val Ala Lys Gln Glu Trp Arg Val
1               5                   10                  15

Arg Tyr Tyr Met Asn Gly Lys Arg Lys Met Arg Thr Tyr Ser Ala Lys
            20                  25                  30

Phe Tyr Gly Tyr Glu Thr Ala His Thr Met Ala Glu Asp Phe Ala His
        35                  40                  45

Tyr Val Asp Lys His Glu
    50


<210> SEQ ID NO 2
<211> LENGTH: 2406
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

Met Ala Ala Pro Ala Pro Ser Ala Glu Ala Arg Pro Ala Lys Arg Arg
1               5                   10                  15

Cys Phe Pro Leu Pro Arg Glu Thr Pro Val Ser Ser Glu Asp Glu Thr
            20                  25                  30

Arg Lys Thr Leu Gln His Asp Thr Leu Gly Cys Leu Pro Arg Ser Ser
        35                  40                  45

Ser Gly Gln Pro Glu Leu Ala Ala Ala Ser Ala Ala Ser Gln Val Gly
    50                  55                  60

His Leu Ser Ser Ala Ala Leu Leu Gln Leu Val Gln Thr Gln Ser Ala
65                  70                  75                  80

Gly Gly Val Pro Gln Ala Val Leu Arg Asn Leu Phe Ser Ser Ile His
                85                  90                  95

Arg Asn Pro Lys Pro Leu Pro Ala Asn Ala Leu Ala Ala Thr Pro Asn
            100                 105                 110

Ser Ser Leu Tyr Ala Ser Leu Thr Ser Leu Ser Ser Ala Ala Ala Leu
        115                 120                 125

Pro Gly Ala Gly Pro Ala Tyr Ser Gln Ala Pro Ser Pro Ala Ser Ala
    130                 135                 140

Asp Leu Leu Gln Ser Glu Gln Phe Gly Ser Ala Ala Lys Asn Pro Ser
```

-continued

```
145                 150                 155                 160

Pro Asn Glu Ala Ser Pro Ile Leu Ala Leu Leu Gly Glu Ala Ala Arg
                165                 170                 175

Ala Ala Thr Thr Pro Arg Thr Val Pro Ala Leu Ser Ala Val Cys Pro
            180                 185                 190

Ala Ala Ser Ser Gly Val Ser Leu Pro Ser Ala Ser Asp Thr Leu Ala
        195                 200                 205

Leu Ala Gln Ser Ser Leu Ser Ser Ser Thr Gly Cys Ala Ser Asp Val
    210                 215                 220

Lys Ala Ser Arg Pro Glu Glu His Pro Ala Phe Ala Ser Gly Thr Ala
225                 230                 235                 240

Asn Arg Gln Ser Leu Leu Gln Ala Leu Leu Leu Ser Thr Ala Pro Leu
                245                 250                 255

Ala Phe Ser Gly Pro Ser Leu Ser Ser Ala Ser Thr Thr Leu Pro Ala
            260                 265                 270

Ser Ser Gly Ala Val Ser Ser Arg Asn Ala Gly Ala Tyr Gln Phe Glu
        275                 280                 285

Arg Leu Leu Gln Ala Glu Ala Ala Lys Val Lys Ala Leu Leu Pro Asn
    290                 295                 300

Ala Thr Ser Lys Ser Met Ser Gln Ser Ser Val Pro Gln Arg Asp Leu
305                 310                 315                 320

Thr Arg Lys Thr Ser Leu Phe Pro Asp Pro Arg Gly Leu Ser Ala Asp
                325                 330                 335

Asp Ala Ser Arg Arg Tyr Asn Thr Arg Gly Ala Asn Ser Gly Gly Ala
            340                 345                 350

Gly Leu Arg Arg Gly Thr Gly Val His Ala Thr Thr Glu Gln Ser Gly
        355                 360                 365

Ala Leu Asp Ala Gly Glu Arg Thr Arg Pro Phe Gly Ala Gly Glu Asp
    370                 375                 380

Glu Ser Ala Gln Gly Lys Pro Asp Ser Arg Gly Arg Gln Arg Pro Gly
385                 390                 395                 400

Ala Leu Asp Ala Ser Asn Ile Leu Gly Leu Leu Ala Ala Phe Gln Pro
                405                 410                 415

Ser Gln Ala Pro Ala Ile Arg Asp Leu Ser Ala Pro Ser His Leu Ser
            420                 425                 430

Ala Ala Ala Thr Gly Ala Leu Pro Leu Thr Ala Ser Phe Thr Ala Ser
        435                 440                 445

Ala Leu Ala Ser Ser Gln Cys Leu Pro Ala Gly Thr Pro Ala Ser Ser
    450                 455                 460

Ser Ala Ser Pro Pro Phe Ser Glu Val Leu Ser Thr Thr Glu Glu Ser
465                 470                 475                 480

Ser Thr Thr Lys Glu Thr Asp Ala Ser Ala Ser Thr Leu Leu Ala Phe
                485                 490                 495

Leu Gln Lys Tyr Ser Ala Val Ser Gly Leu Gly Gly Ala Ser Asp Phe
            500                 505                 510

Leu Gly Gln Leu Gln Gly Lys Ser Ser Leu Pro Pro Leu Ser Leu Ala
        515                 520                 525

Glu Pro Ser Ser Ala Leu Pro Ser Ser Phe Leu Gly Gly Ser Asp Gly
    530                 535                 540

Gly Thr Ile Asp Thr Arg Asn Gly Asn Gly Glu Lys Thr Thr Pro Pro
545                 550                 555                 560
```

-continued

```
Ile His Leu Phe Gln Ser Ala Phe Arg Ile Pro Ser Pro Ser Gln Gln
                565                 570                 575

Asn Leu Leu Asp Ala Leu Leu Ala Ser Ser Cys Thr Thr Ala Thr Ser
            580                 585                 590

Arg Ser Asp Gly Ser Gly Asn Leu Gly Cys Pro Val Val Asp Glu Arg
        595                 600                 605

Asn Ala Lys Leu Ala Gly Pro Ala His Pro Leu Pro Cys Ser Phe Pro
    610                 615                 620

Gln Ile Ser Ser Ser Ser Gly Glu Pro Gly Arg Lys Thr Gly Gly Arg
625                 630                 635                 640

Val His Arg Gln Gly Thr Ser Gln Ser Gly Gly Arg Val Arg Ser Gly
                645                 650                 655

Lys Asn Gly Gly Ser Ala Ala Pro Pro Arg Gln Ser Ser Ser Glu Asn
            660                 665                 670

Val Pro Ser Thr Pro Thr Val Ser Ser His Glu Ala Pro His Arg Ala
        675                 680                 685

Gly Phe Pro Ser Gln Thr Pro Tyr Glu Leu Ser Ala Ser Pro Ser His
    690                 695                 700

Gln Leu Asp Leu Leu Arg Leu Gly Ala Phe Leu Gly Gly Ala Gly Lys
705                 710                 715                 720

Gln Asp Ala Ser Val His Ser Asp Glu Thr Gly Thr Leu Ser Gly Glu
                725                 730                 735

Pro Ser His Arg Ser Cys Ser Leu Ser Arg Gly Leu Thr Gln Glu Ser
            740                 745                 750

Val Leu Gln Leu Ser Asp Thr Thr Ser Thr Ser Arg Glu Gly Glu Pro
        755                 760                 765

Asn Glu Pro Ser Gln Gly Cys Val Asn Val Ala Ala Ser Leu Pro Ala
    770                 775                 780

Phe Gly Pro Gln Pro Ser Ser Gly Ala Ala Lys Ala Arg Glu Gly Arg
785                 790                 795                 800

Arg Gly Ala Gly Gly Ala Gly Ala Ala Pro Pro Val Pro Leu Arg Ala
                805                 810                 815

Asp Val Thr Leu Gly Gly Asn Arg Pro His Tyr His Val Ala Lys Gln
            820                 825                 830

Glu Trp Arg Val Arg Tyr Tyr Met Asn Gly Lys Arg Lys Met Arg Thr
        835                 840                 845

Tyr Ser Ala Lys Phe Tyr Gly Tyr Glu Thr Ala His Thr Met Ala Glu
    850                 855                 860

Asp Phe Ala His Tyr Val Asp Lys His Glu Ala Leu Pro Asp Ser Met
865                 870                 875                 880

Met Met Thr Ala Met Met Leu Gln Ala Gln Ala Asn Ser Ala Ala Ser
                885                 890                 895

Ser Gly Gln Thr Val Pro Leu Ala Arg Gly Ile Arg Ala Ser Ser Ala
            900                 905                 910

Ser Ala Gly Ala Gly Gly His Val Ser Lys Ser Ala Thr Lys Gly Ser
        915                 920                 925

Val Ala Ala Ser Ser Glu Gly Ser Thr Ser Met Gly Ser Asp Ala Thr
    930                 935                 940

Arg Ser Gln Glu Gly Glu Ala Ala Glu Leu Cys Pro Leu Ala Ala Gly
945                 950                 955                 960
```

-continued

```
Leu Ser Arg Pro Leu Ala Ser Met His Ser Ala Ala Gly Asn Ala Val
                965                 970                 975

Ala Gln Gly Arg Gln Glu Ser Lys Glu Glu Ala Pro Gly Gly Gln Ala
            980                 985                 990

Trp Phe Gly Glu Pro Gly Lys Phe  Arg Ala Ser Ser Glu  Ala Ala Leu
        995                 1000                 1005

Cys Gly  Ser Gly Ser Ser Ala  Glu Gly Arg Asp Gly  His Glu Ser
    1010                 1015                 1020

Glu Val  Leu Trp Ala Thr Leu  Gly Lys Val His Asp  Ala Ser Gln
    1025                 1030                 1035

Gly Lys  Lys Ile Lys Pro Glu  Lys Pro Leu Thr Val  Ala Arg Gly
    1040                 1045                 1050

Arg Leu  Ala Leu Gly Ala Glu  Asp Lys Ser Gln Asn  Leu Gly Val
    1055                 1060                 1065

Asp Leu  Gly Asp Ser Gly Gly  Ala Gln Gly Leu Pro  Gly Val Arg
    1070                 1075                 1080

Gln Pro  Arg Gln Met Lys Asn  Ser Glu Glu Cys Ser  Leu Arg Asp
    1085                 1090                 1095

Ser Asp  Lys Gly Met Ala Leu  Ser Lys Arg Phe Gly  Phe Leu Pro
    1100                 1105                 1110

Ser Gln  Thr Pro Ser Cys Asp  Ser Met Thr Leu Pro  Phe Pro Gly
    1115                 1120                 1125

Gly Phe  Asp Ala Leu Ser Leu  Ser Ser Ala Leu Ser  Ser Cys Ala
    1130                 1135                 1140

Ser Leu  Pro Val Ala His Glu  Gly Asn Asn Phe Gln  Lys Gly His
    1145                 1150                 1155

Thr Gly  Asp Ile Val Ala Leu  Ala Ser Gln Ser Gly  Thr Gln Arg
    1160                 1165                 1170

Pro Ala  Ser Val Val Leu Ser  Arg Asp Ala Asn Val  Ser Gly Ser
    1175                 1180                 1185

Ser Pro  Ser His Pro Thr Trp  Gln Arg Glu Gly Ala  Ala Val Ser
    1190                 1195                 1200

Gly Arg  Ala Asp Glu Phe Ser  Ser Leu Ser Val Thr  Pro Ser Thr
    1205                 1210                 1215

Val Pro  Leu Ser Ser Phe Thr  Met Glu Asp Ile Lys  Gly Glu Glu
    1220                 1225                 1230

Gly Asp  Pro Ser Arg Arg Phe  Ala Leu Val Gly Glu  Ser Met Lys
    1235                 1240                 1245

Asn Val  Ser Ala Pro Glu Val  Gln Ala Leu Phe Pro  Thr Ser Ser
    1250                 1255                 1260

Ile Ala  Asn Ala Glu Leu Leu  Pro Val Asp Phe Leu  His Ser Asn
    1265                 1270                 1275

Ser Cys  Ser Ala Asp Lys Leu  Glu Ser Ser Ile Pro  Arg Gly Leu
    1280                 1285                 1290

Ala Gly  Asn Asn Pro Ser Met  Thr Ala Thr Ala Val  Ala Ala Thr
    1295                 1300                 1305

Ala Val  Ser His Gln Ile Phe  Asp Thr Ile Thr Leu  Phe Gly Glu
    1310                 1315                 1320

Phe Leu  Arg Glu Phe Ala Lys  Glu Lys Val Asn Glu  Phe His Glu
    1325                 1330                 1335

Tyr Gly  Leu Glu Ala Ser Pro  Leu Thr Val Glu Ala  Ser Pro Glu
```

-continued

```
    1340                 1345                 1350

Val Ser  Leu Phe Gly Lys Ala  Thr Phe Gly Arg Cys  Pro Val Ala
    1355                 1360                 1365

Gly Gly  Ser Thr Pro Ala Gly  Ile Ser Lys Met Ser  Gly Glu Thr
    1370                 1375                 1380

Leu Ser  Gly Leu Ser Ala Ser  Glu Leu Ser Leu Val  Ser Ala Arg
    1385                 1390                 1395

Thr Asn  Thr Thr Thr Gly Glu  Glu Gln Phe Ala Leu  Ala Arg Gly
    1400                 1405                 1410

Leu Phe  Pro Gly Asp Ser Glu  Gly Asp Arg Asp Glu  Lys Lys Pro
    1415                 1420                 1425

Gln Leu  Ser Gln Gln Glu Leu  Leu Val Leu Ser His  Ala Leu Val
    1430                 1435                 1440

Asn Leu  Thr Ser Ser Thr Tyr  Val Leu Met His Thr  Leu Lys Ala
    1445                 1450                 1455

Ser Leu  Ser Lys Ser Thr Glu  Ala Val Gln Leu His  Gln Pro Leu
    1460                 1465                 1470

Leu Glu  Ala Ala Ser Glu Ala  Lys Ala Thr Asp Glu  Ala Lys Thr
    1475                 1480                 1485

Arg Glu  Glu Gln Glu Ser Ser  Glu Cys Asp His Glu  Tyr Pro Pro
    1490                 1495                 1500

Gly Ser  Ser Leu Glu Ala Thr  Thr Gly Ala Leu Pro  Phe Arg Leu
    1505                 1510                 1515

Ser Pro  Ala Leu Ser Ala Ser  Ser Lys Asp Leu Pro  Ser Leu Ser
    1520                 1525                 1530

Ala Ser  Ala Ser Leu Glu Ser  Val Thr Pro Phe Ala  Gly Leu Pro
    1535                 1540                 1545

Leu Glu  Glu Gly Thr Leu Ser  Ala Ser Val Gly Leu  Ala Ser Ser
    1550                 1555                 1560

Asp Asp  Glu His Asp Thr Ser  Leu Leu Phe Lys Thr  Glu Ala Ala
    1565                 1570                 1575

Lys Lys  Arg Ser Leu Phe Ser  Thr Ala Ala Asp Gly  Asp Glu Ser
    1580                 1585                 1590

Arg Thr  Tyr Asn Asp Gly Leu  Gly Gln Pro Met Glu  Glu Glu Ile
    1595                 1600                 1605

Arg Ser  Cys Val Ser Thr Ser  Cys Gly Glu Ala Val  Ala Thr Thr
    1610                 1615                 1620

Thr Leu  Ser Ala Ile Gly Pro  Gly Thr Gly Ala Ser  Gly Ala Leu
    1625                 1630                 1635

Leu Asp  Ser Glu Ser Arg Glu  Ser Leu Gly Glu Lys  Pro Gly Ala
    1640                 1645                 1650

Ala Leu  Arg Ala Gly Ala His  Thr Pro Ala Pro Ser  Arg Ala Pro
    1655                 1660                 1665

Thr Pro  Ser Arg Thr Phe Ser  Phe Thr Ser Ser Ser  Thr Ala Thr
    1670                 1675                 1680

Ser Ala  Ala Leu Leu Cys Asp  Ser Asn Val Val His  Glu Lys Leu
    1685                 1690                 1695

Ser Ala  Gln Gly Lys Asp Ser  Glu Ala Gly Glu Arg  Lys Gly Asp
    1700                 1705                 1710

Ser Glu  Lys Glu Glu Glu Val  Glu Met Trp Lys Glu  Glu Asp Glu
    1715                 1720                 1725
```

-continued

```
Glu Val  Gln Arg Cys Thr Gly  Ser Ala Glu Thr Asp  Ser Thr Glu
    1730                 1735                 1740

Ala Thr  Arg Gly Glu Glu Ala  Trp Arg Arg Gly Lys  Gln Ser Glu
    1745                 1750                 1755

Lys Lys  Pro Ser Val Ile Thr  Thr Ala Leu Asn Leu  Leu Glu Thr
    1760                 1765                 1770

His Arg  His Leu Ala Leu Thr  Ile Ser Gln Leu Lys  Arg Pro Val
    1775                 1780                 1785

Ala Gln  Gln Leu Arg Phe Ile  Leu Pro Ile Ala Ala  Pro Gln Leu
    1790                 1795                 1800

Leu Pro  Cys Ile Leu Pro Pro  Ala Ser Phe Gln Gly  Thr Gly Glu
    1805                 1810                 1815

Ser Gly  Asp Gly Lys Ala Glu  Ala Glu Ala Lys Gly  Ser Ser Ser
    1820                 1825                 1830

Leu Gly  Gln Val Leu Glu Thr  Ala Leu Gly His Gly  Thr Arg Leu
    1835                 1840                 1845

Ala Pro  Ser Ala Ser Ala Met  Val Pro Pro Arg Lys  Asp Glu Ala
    1850                 1855                 1860

Ala Ser  Ala Val Pro Glu Ala  Lys Thr Leu Thr Gly  Leu Ala Asn
    1865                 1870                 1875

Ala Gly  Val Thr Arg Glu Ala  Ala Ser Arg Thr Leu  Glu Ala Glu
    1880                 1885                 1890

Gln Val  Ser Arg Lys Arg Ser  Arg Glu Glu Val Val  Asp Ser Glu
    1895                 1900                 1905

Thr Ala  Gly Asp Glu Gly Asp  Met Glu Asn Val Pro  Glu Thr Arg
    1910                 1915                 1920

Asp Gly  Thr Thr Arg Pro Gly  Ser Arg Gln Tyr Asp  Thr Ser Pro
    1925                 1930                 1935

Ser Asn  Asp Gly Thr Lys Pro  Pro Ala Thr Ala Lys  Ser Arg Val
    1940                 1945                 1950

Ile Arg  Asp Gln Ala Ala Leu  Glu Arg Leu Leu Leu  Ala Pro Phe
    1955                 1960                 1965

Gln Asp  Thr Pro Thr Cys Ser  Cys Thr Asp Arg Pro  Cys Pro Cys
    1970                 1975                 1980

Asp Arg  Gln Gln Val Ala Asp  Met Ile Tyr Leu Phe  Tyr Ala Val
    1985                 1990                 1995

Pro Ala  Arg Gln Gln Ala Glu  Ser Ser Lys Glu Gly  Ser Thr Gln
    2000                 2005                 2010

Arg Leu  Gln Phe Ala Ala Arg  Asp Thr Asn Glu Arg  Lys Asp Ala
    2015                 2020                 2025

Arg Thr  Gly Glu Glu Thr Gln  Gly Gly Glu Thr Glu  Ala Lys Glu
    2030                 2035                 2040

Val Ile  Arg Asp Pro Glu Glu  Arg Gly Val Cys Glu  Gly Ser Ser
    2045                 2050                 2055

Ser Gln  Asn Ala His Thr Gln  Phe Asp Ala Glu Thr  Ala Ser Ser
    2060                 2065                 2070

Ser Met  Ser Ser Asp Pro Arg  Ala Asp Lys Glu Ser  Asn Ala Gln
    2075                 2080                 2085

Asp Ala  His Met Ala Asp Lys  Thr Ser Phe Val Ser  Asp Leu Pro
    2090                 2095                 2100
```

-continued

```
Gln Pro  Ser Gly Glu Phe Ala  Pro Ser Leu Leu Ser  Glu Thr Ser
    2105                 2110                 2115

Leu Asp  Val Ala Met Ala Asp  Ser Arg Gly Thr Pro  Ser Glu Ile
    2120                 2125                 2130

His Gly  Phe Phe Thr Arg Ser  Asp Glu Gln Lys Arg  Ala Ser Phe
    2135                 2140                 2145

Ser Ser  Ser Ser Leu Leu Ala  Ala Gly His Ala Val  Ala Ser Phe
    2150                 2155                 2160

Ser Ser  Ser Leu Ala Gly Val  Val Ser Gly Ala Gly  Glu Arg Arg
    2165                 2170                 2175

Glu Cys  Ala Gly Pro Ser Leu  Gly Asp Leu Ser Thr  Ile Gly Leu
    2180                 2185                 2190

Leu Ser  Leu Ser Tyr Pro Ala  Met Leu Ala Phe Ile  Leu Pro Leu
    2195                 2200                 2205

Gln Ser  Leu Leu His Thr Val  Ser Gly Met Ile Leu  Thr Leu His
    2210                 2215                 2220

Lys Lys  Leu Ile His Arg Phe  Ile Cys Ala His Leu  Arg Leu Val
    2225                 2230                 2235

Leu Asp  Asp Asp Met Arg Arg  Pro Ala Gly Gly Ala  Leu Lys Ser
    2240                 2245                 2250

Arg Gly  Ala His Gly Asp Thr  Glu Ala Ala Glu Ala  Gln Val Glu
    2255                 2260                 2265

Arg Arg  Arg Arg Glu His Glu  Arg Glu Glu Thr Thr  Asn Leu Ala
    2270                 2275                 2280

Ile Gly  Tyr Arg Glu Gly Asn  Ala Glu Ala Ala Asn  Thr Phe Pro
    2285                 2290                 2295

Leu Val  Asp Thr Val Ser Ser  Leu Leu Ser Pro Gly  Ser Leu Arg
    2300                 2305                 2310

Gln Glu  Asn Ser Glu Val Glu  Arg Arg Asp Asn Asp  Glu Glu Arg
    2315                 2320                 2325

Leu Glu  Leu Ile Thr Gly Ile  Ala Arg Glu Ser Pro  Lys Pro Ser
    2330                 2335                 2340

Glu Lys  Asp Ser Val Ser Pro  Phe Leu Ser Thr Ala  Pro Cys Pro
    2345                 2350                 2355

Gly Thr  Glu Ala Glu Ser Ser  Asp Cys Ser Ala Ser  Ser Ala Cys
    2360                 2365                 2370

Ser Gly  Thr Pro Thr Glu Gly  Thr Glu Gly Gly Glu  Thr Gly Asp
    2375                 2380                 2385

Ile Ala  Ser Phe Leu Ser Pro  Ser Gly Glu Val Lys  Gln Thr Ile
    2390                 2395                 2400

Met Leu  Ala
    2405


<210> SEQ ID NO 3
<211> LENGTH: 1217
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

tatccagttg cccggctctg tctaccttct tctcgatgta gcggcggcgt tctgtgttcc      60

ttagagcgag tccacgcacc agcctcgtgg agtcgaacag ttttcgccag agcggggaca     120

gccggtggaa gacagaacag gagggattca ccgtcacctc gtttgcttcc ttctggtgat     180
```

-continued

```
ggagggaata agccgacaga ctcacttctt aacagttcat ggcagagggg caacgacgtc    240

accatccagc tttccattca cttaaccgca caagcgttct gctcgttagt caagcctcac    300

tcgccagtcg aaagccatta aaagttcgcg tttctggctc tcgtttgtgc cggaagtctg    360

ccaaagcaaa caaaggatct gaaaccgagt agcagtgaac gcgtgacagt gcagaggggt    420

gcccgcgtcg gcgtcctctc tgtccacgaa cagccacaat tctcatcacg agaagtcctc    480

ctcccctgga tcttcctcca gttccccatg actgcctccg gttctcgcac ggacggcgat    540

ccgccttcac gctccccggc ctttgccagt tttgtgcaag aaggtcgccc gtcttattct    600

tgtcacgttc cctgtatcta ctcggttcac tgcgctctac agaagctctt cttcgccttc    660

tactgatcag tgcactctac gagatgcact atcatcagtc ctgaactcca tgtttgggtg    720

gaaacctggg cgtgctgtgt cgcagcgagt cgcgagattg ccggcctgtc gacgagttcc    780

cgtttttcct gcactggcta cagcgtagcg gcttcgcctg ctcactggcg acggtactgg    840

ccgcacggtt tcacgatcct gaggtcggcg agatgcccct gtctggcgag gccttttgtc    900

tacgcagcga cctctgtcta ctagagaaag gcagaaggcc ggagcgtttt ctcagatgtg    960

ctactctttg tcttctgcga tcttccgtgc gttcagctgt gcttttgcca aaggagacct   1020

gtgtgcagag gacttcgctg ctaaaaagca gaagagtgcg cggcgtgtgt agctcagtgg   1080

catttcggga ctcggtcttg cgtcgttcgc gactggacgt cgtcgtctgt gagagcgtca   1140

aactagggag aaggggcggg ccagagcgtt cggaaaatta tctgcaaagc ccaggtcccg   1200

tatgatattc aaaaaag                                                  1217


<210> SEQ ID NO 4
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1               5                   10                  15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
            20                  25                  30

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
        35                  40                  45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
    50                  55                  60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
65                  70                  75                  80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
                85                  90                  95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
            100                 105                 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
        115                 120                 125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
    130                 135                 140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
145                 150                 155                 160

Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
```

-continued

```
                165                 170                 175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
            180                 185                 190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
        195                 200                 205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
    210                 215                 220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
225                 230                 235                 240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
                245                 250                 255

Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
            260                 265


<210> SEQ ID NO 5
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

agtgttctcg aaaccatgct aacac                                           25


<210> SEQ ID NO 6
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

cctcttacct cagttacaat ttata                                           25


<210> SEQ ID NO 7
<211> LENGTH: 968
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met Leu Ser Arg Arg Cys Lys Arg Ser Ser Ala Glu Asp Ser Gly Ala
1               5                   10                  15

Asn Glu Val Gly Ala Asn Ala Asp Gln Ser Lys Arg Leu Arg His Ser
            20                  25                  30

Leu Asp Ser Ile Ile Glu Lys Gly Gly Asp Pro Val Asn His Asp Ser
        35                  40                  45

Ala Met Leu Leu Asp Cys Ala Pro Thr Gln Thr Gly Arg Ala Phe Ala
    50                  55                  60

Phe Leu Ser Met Pro Ala Pro Ile Glu Pro Ser Gly Asn Glu Glu Ser
65                  70                  75                  80

Ala Pro Ala Val His Arg Asp Ser Gly Val Gly Gly Ile Asp Tyr Pro
                85                  90                  95

Arg Pro Val Ala Ser Ile Ser Val Glu Ser Ser Ser Gln Val Val Ala
            100                 105                 110

Pro Arg Asp Glu Asn Pro Ser Ala Ser Tyr Gln Arg Arg Gly Asp Ser
        115                 120                 125

Pro Pro Ser Leu Arg Asn Gly Gly Asp Arg Gln Glu Arg Lys Arg Thr
    130                 135                 140

Ala Val Ala Pro Glu Ala Asn Glu Pro Gln Asp Asn Glu Thr Lys Asn
```

-continued

```
145                 150                 155                 160

Glu Glu Trp Leu Gln Leu Ala Arg Leu Lys Pro Lys Val Glu Gly Val
                165                 170                 175

Cys Phe Asp Arg Phe Phe Arg Arg Trp Val Ala Lys Arg Ala Gly Leu
            180                 185                 190

Lys Lys Val Tyr Phe Pro Val Tyr Lys Tyr Gly Phe Asp Arg Ala Tyr
        195                 200                 205

Glu Leu Ala Val Ala Thr Arg Arg Gly Leu Glu Asn Asp Ala Ala Ala
    210                 215                 220

Gly Ile Arg Ala Val Gly Ala Leu Arg Pro Arg Ile Ser Glu Ala Ala
225                 230                 235                 240

Gly Cys Thr Ser Ser Pro Gly Met Leu Ser Glu Asp Ala Cys Pro Glu
                245                 250                 255

Lys Pro Pro Val Pro Val Gln Pro Pro Arg Thr Leu Ser Thr Arg Ala
            260                 265                 270

Thr Ala Ala Gln Ala Glu Val Lys Ser Gly Asp Ser Ala Glu Ser Thr
        275                 280                 285

Lys Asn Asp Ser Glu Gly Ala His Val Leu Glu Gly Ala Glu Leu Gln
    290                 295                 300

Thr Pro Glu Arg Ser Thr Ser Asn Thr Ile Cys Trp Ala Thr Ala Ala
305                 310                 315                 320

Glu Gly Ser Ile Ser Lys Thr Asp Gly Phe Gln Asn Arg Ser Ser Pro
                325                 330                 335

Ser Gly Phe Gly His Gly Ser Arg Asn Lys Pro Glu Leu Ser Gln Gln
            340                 345                 350

Lys Val Glu Thr Thr Ser Arg Gly Ile Arg Ser Ala Ser Ala Ser Cys
        355                 360                 365

Asn Arg Glu Lys Asp Gln Gly Gly Ser Ala Cys Ser Val Leu Ser Ile
    370                 375                 380

Ala Ser Phe Ser Leu Ser Gln Ile Asp Glu Glu Leu Glu Gly Ile Asn
385                 390                 395                 400

Asp Glu Ala Tyr Glu Ala Glu Arg Leu Gln Ala Asp Glu Asp Arg Ser
                405                 410                 415

His Ala Pro Ala Ala Ser His Gly Glu Gly Gly Thr Ser Ala Gly Glu
            420                 425                 430

Ser Thr Ala Ala Ser Thr Thr Gly Ser Glu Asp Ser Gly Pro Leu Arg
        435                 440                 445

Ala Ala Thr Ser Pro Leu Met Phe Pro Gln Gly Ser Glu Gly Ser Ala
    450                 455                 460

Ser Ser Ala Ser Thr Glu Ile Met Val Leu Asp Asp Glu Ser Met Gln
465                 470                 475                 480

Gln Ala Leu Val Thr Ala Ser Ala Glu Thr Leu Asn Lys Leu Arg Ser
                485                 490                 495

Thr Leu Pro Ala Gly Val His Phe Asp Phe Ala Ser Lys Arg Trp Phe
            500                 505                 510

Ala Val Tyr Ser Ser His Glu Ser Pro Glu Ala Thr Gln Arg Asp Pro
        515                 520                 525

Val Arg Pro Lys Glu Arg Val Arg Ile Phe Asp Pro Thr Gln Tyr Glu
    530                 535                 540

Gly Ser Met Leu Lys Ala Phe His Ala Cys Arg Ser Phe Cys Gly Ser
545                 550                 555                 560
```

-continued

```
Val Glu Ala Gly Ala Ser Asp Trp Asp Ser Val Pro Gln Leu Val Pro
                565                 570                 575

Glu Gln Arg Lys Gln Gly Glu Cys Gln Asp Thr Ser Gly Ser Ser Asp
            580                 585                 590

Gln Gly Ala Asn Arg Leu Ser Pro Thr Glu Thr Glu Asn Pro Pro Thr
        595                 600                 605

Ala Asp His Pro Arg Ser Leu Ser Ala Thr Thr Arg Pro Glu Gly Ser
    610                 615                 620

Leu Glu Gln Thr Gln His Pro Gln Arg Asn Arg Gly Ile Leu Gly Ile
625                 630                 635                 640

Gln Pro Gly Glu Thr Glu Gly Leu Gln Val Pro Ser Asn Gly His Gly
                645                 650                 655

Val Asn Ala Gly Asp Ile Glu Thr Asn Leu Leu Asp Ala Glu Phe Gly
            660                 665                 670

Ser Glu Thr Arg Ala Arg Thr Thr Ala Leu Pro His Leu Arg Arg Ser
        675                 680                 685

Gln Arg Arg Ala Asp Pro Ala Arg Ser Val His Ser Asn Thr Phe Ala
    690                 695                 700

Gly Gln Glu Leu His Gln Ser Pro Lys Pro Gly Asn Gln Thr Ser Arg
705                 710                 715                 720

Gly Glu Ser Gly Arg Ser Ser Leu Arg Arg Lys Asn Gln Val Ser Thr
                725                 730                 735

Asn Glu Lys Gly Leu Pro Gly Glu Gly Gly Cys Arg Thr Asp Glu Lys
            740                 745                 750

Ser Lys Gln Val Ser Tyr Val Ser Phe Ser Glu Pro Ile Thr Val Arg
        755                 760                 765

Tyr Gln Gln Val Pro Thr Glu Ser Ala Ser Thr Arg Gly Cys Ser Gln
    770                 775                 780

Arg Arg Pro Gln Asn Ala Glu Glu Leu Glu Asp Arg Arg Ser Pro Leu
785                 790                 795                 800

Thr Arg Gln Glu Glu Arg Thr Glu Ser Asp Pro Arg Thr Thr Ala Gly
                805                 810                 815

Leu Cys Gln Glu Asn Pro His Pro Ser Tyr Arg Phe Leu Arg Gln Gln
            820                 825                 830

Ser Arg Glu Leu Ala Val Arg Cys Leu Leu Val Ile Phe Gly Asn Leu
        835                 840                 845

Ala Asp Val Cys Thr Pro Ala Leu Phe Arg Leu Phe Pro Gln Asp Arg
    850                 855                 860

Cys Arg Arg Val Arg Ala Val Leu Gln His Arg Asp Leu Leu Gln Ser
865                 870                 875                 880

Gly Lys His Thr Arg Val Leu Leu Ser Ala Tyr Phe Gln Leu Phe Trp
                885                 890                 895

Pro Leu Leu Glu Thr Arg Thr Leu Pro Gln His Tyr Ser Ala Asp Tyr
            900                 905                 910

Ile Arg Arg Leu Leu Asn Gly Met His Asn Val Ala Ala Met His Lys
        915                 920                 925

Ser Leu Phe Pro Glu Tyr Pro Leu Arg Gly Glu Leu Asp Asn Arg Glu
    930                 935                 940

Gly Pro Tyr Ala Phe Leu Asp Asp Thr Ala Ala Glu Gly Ile Asn Phe
945                 950                 955                 960
```

-continued

```
Phe Glu Thr Asp Phe Asp Glu Pro
                965


<210> SEQ ID NO 8
<211> LENGTH: 425
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Ala Tyr Gln Arg Arg Arg Ala Ala Ala Cys Thr Ile Glu Val Ser
1               5                   10                  15

Arg Asp Leu Phe Ser Pro Glu Arg Asn Leu His Asp Asn Phe Ser Ser
            20                  25                  30

Leu Ala Ile Thr Met Ala Phe Arg Thr Val Ser Lys Val Leu Pro Thr
        35                  40                  45

Leu Ser His Cys Phe Pro Gly Pro Leu Ser Val Ala Ala Ser Ser Ser
    50                  55                  60

Leu Pro Gly His Ser Lys Gly Glu Glu Ser Val Pro Cys Arg Val His
65                  70                  75                  80

Arg Ser Phe Arg Leu Ser Pro Val Ala Asp His Glu Ala Glu Ala Leu
                85                  90                  95

Ser Gly Ser Gly Asn Asp Thr Ser Gly Cys Ser Gln Arg Asp Arg Phe
            100                 105                 110

Cys Ala Gly Asn Gly Ser Asp Cys Lys Ala Arg Arg Thr Ser Asp Gly
        115                 120                 125

Asn Gly Ser Pro Pro Thr Asn Ala Arg Met Ser Glu Lys Leu Ser Leu
    130                 135                 140

Phe Lys Asn His Ala Tyr Ser Cys Leu Glu Gln Arg Ala Cys Pro Ala
145                 150                 155                 160

Ser Asn Arg Asn Leu Gly Asp Thr Ala Ala Cys Pro Leu Ser Ala Phe
                165                 170                 175

Cys Arg Ser Leu Val Arg Arg Thr Pro Ser Arg Leu Trp Leu Pro Pro
            180                 185                 190

Gln Cys Ser Leu Leu Ser Gly Cys Ser Ala Arg Ser Cys Pro Pro Lys
        195                 200                 205

Ile Ser Val Arg Ala Thr Asn Gly Ala Ser Glu Gln Ala Ser Trp Gln
    210                 215                 220

Asp Phe His Pro Ala Leu Gly Arg Ala Val Val Pro Leu Ser Leu Ser
225                 230                 235                 240

Gly Arg Gly Thr Ala Gly Thr His Leu Val Arg Lys Phe Gly Thr Gln
                245                 250                 255

Arg Val Val Gln Lys Arg Arg His Gln Met Arg Ile Leu His Pro Ala
            260                 265                 270

Gln Thr Ala Tyr Val Pro Val Glu Gln Arg Pro Pro Pro Ile Pro His
        275                 280                 285

Ser Leu Thr Ala Ser Ser Thr Val Lys Arg Leu Leu Asn Asn Asn Thr
    290                 295                 300

Val Ala Ala Lys Glu Ala Ala Lys Arg Ile Asn Trp Gly Ala Tyr Ile
305                 310                 315                 320

Ser His Gln Arg Gly Val Arg Trp His Pro Gln Gly Ala Trp Arg Val
                325                 330                 335

Gln Phe Ser Arg Arg Asn His Glu Arg Asn Phe Phe Val Arg Cys Glu
            340                 345                 350
```

-continued

```
Cys Tyr Phe Arg Val Gly Thr Tyr Gly Phe Gln Met Ala Lys Asp Leu
        355                 360                 365

Ala Ile Arg Tyr Arg Gln Arg Leu Glu Lys Glu Trp Glu Glu Leu Gln
    370                 375                 380

Glu Gln Trp Thr Lys Leu Asp Ile Leu Glu Ala Glu Gln Arg Ala Lys
385                 390                 395                 400

Tyr Lys Glu Lys Arg Glu Glu His Leu Leu Leu Gly Ala Gly Glu Glu
                405                 410                 415

Pro Glu Leu His Ser Arg Arg Ser Lys
            420                 425


<210> SEQ ID NO 9
<211> LENGTH: 2674
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Met Asp Gly Ser Gly Glu Ser Ser Gly His Leu Phe Lys Pro Gly His
1               5                   10                  15

Gly Glu Ala Arg Val Ser Val His Arg Gly Ser Leu Thr Asp Ser Gly
            20                  25                  30

Ser Leu Pro Ala Ala Ser Arg Cys His Ser Gln Asp Asn Lys Leu Ser
        35                  40                  45

Leu Pro Cys Ala Gly Ser Met Leu Pro Ala Ser Ser Gly Arg Phe Ser
    50                  55                  60

Cys Asp Ser Ala Leu Phe Gly Gly Pro Val Asp Ser Ala Cys Ser Ser
65                  70                  75                  80

Asp Trp Thr Pro Val Val Ser Pro Ser Arg Asp Leu Ser Ala Asp Gly
                85                  90                  95

Thr Asp Ser Ser Ser Val Ser Gly Ser Arg Gly Ser Ser Leu Pro Phe
            100                 105                 110

Gly Ser Pro Thr Ser Ala Leu Leu Arg Pro Ser Ser Glu Ala Ser Ala
        115                 120                 125

Asn Phe Pro Arg Leu His Lys Ser Val His Ala Leu Asp Asp Lys Met
    130                 135                 140

Arg Gly Leu Asp Ala Gln Leu Tyr Val Arg Pro His Gln Thr Leu Pro
145                 150                 155                 160

Leu Gln Pro Arg Leu Arg Glu Thr Asp Leu Cys Arg Asn Gly Glu Asp
                165                 170                 175

Gly Arg Pro Gly Lys Phe Asp Ser Pro His Leu Gly Ser Ser Ala Gly
            180                 185                 190

Pro Tyr Gly His Ser Phe Leu Ala Asn Pro Gln Leu Thr Pro Phe Val
        195                 200                 205

Pro Gln His Leu Ser Ser Ser Pro Pro Gln Pro Val Leu Ser Pro Pro
    210                 215                 220

Gly Glu Glu Gly Arg Asn Ser Ala Ala Phe Gly Lys Thr Val Ser Arg
225                 230                 235                 240

Leu Asn Thr Gly Gly Gly Glu Arg Gln Asp Ser Ser Glu Asp Gln Val
                245                 250                 255

Gly Gly Thr Gly Arg Gln Ser Asp Gln Ala Thr Lys Ala Asn Ser Gly
            260                 265                 270

Ser Thr Pro Ala Gly Cys Ala Gln Thr Ala Gly Leu Leu Thr Asp Val
```

-continued

```
        275                 280                 285

Gln Ser Ser Gly Thr Asn Val Glu His Gly Arg Glu His Phe Ser Thr
    290                 295                 300

Pro Gln Lys Pro Ala Asp Gly Ser Ala Arg Thr Cys Gly Phe Arg Glu
305                 310                 315                 320

Thr Arg Val Ser Pro Ser Asn Ser Ser Leu Pro Arg Thr Ala Cys Arg
                325                 330                 335

Ser Arg Leu Asp Ala Phe Leu Pro Gln Lys Ser Val Ser Pro Asp His
            340                 345                 350

Glu His Val Arg Gly Thr Gly Gly Ala Arg Ala Phe Val Gly Gly Asp
        355                 360                 365

Ser Pro Phe Pro Glu Lys Pro Asp Thr Leu Pro Ala Thr Val Thr Ala
    370                 375                 380

Glu Leu Ala Thr Glu Ala Pro Pro Ala Ser Arg Asp Pro Pro Val Glu
385                 390                 395                 400

Glu Phe Pro Gly Ala His Glu Leu Glu Ser Leu Pro Pro Pro His Val
                405                 410                 415

Asn Ser Gly Arg Pro Pro Ile Gly Glu Lys Asp Gly Ala Ala Ala Ser
            420                 425                 430

Pro Gly Val Ser Arg Leu Pro Ser Gln Glu Arg Val His Thr Leu Leu
        435                 440                 445

Tyr Pro Asn Glu Lys Asp Ala Ser Ser Leu Ser Arg Cys Cys Pro Ser
    450                 455                 460

Ser Met Gln Pro Pro Pro Ala Gly Pro Arg Gln Glu Glu Ala Arg Ser
465                 470                 475                 480

Phe Ser Val Ser Ala Ala Ser Ala Pro Gly Ala Pro Pro Gly Ile Val
                485                 490                 495

Tyr Gln Ala Ser Ala Cys Ala Ser Pro Ala Thr Val Ala Ser Phe Ala
            500                 505                 510

Thr Pro Leu Thr Thr Pro Val Gly Ala Ser Ala Gln Ser Glu Pro Ala
        515                 520                 525

Ala Leu His Ala His Ser Arg Ser Arg Thr Gly Ala His Pro Glu Ala
    530                 535                 540

Leu Pro Pro Gly Val Pro Gly Val Thr Ser Gln Leu Gly Arg Gly Ala
545                 550                 555                 560

Arg Gly Asp Arg Glu Thr Leu Ala Gly Gly Ala Arg Pro Gly Gln Asp
                565                 570                 575

Gly Val Cys Glu Arg Arg Gly Asp Val Ala Arg Gly Arg Leu Gly Gly
            580                 585                 590

Val Ser Val Ala Gly Asp Glu Ala Ala Glu Gly Thr Ser His Lys Ala
        595                 600                 605

Ala Leu Glu Gly Ala Tyr Val Gln Asp Gly Cys Ser Pro Gln Pro Leu
    610                 615                 620

Asn Pro His Ala Pro Ser Gly Ile Ser Ala Pro Thr Asn Gly Ser Ser
625                 630                 635                 640

Glu Leu Ala Ser Ser Ala Ile Pro Ala Ser Thr Cys His Asp Ala Phe
                645                 650                 655

Val Arg Ser Pro Val Ser Gly Ser Asp Cys Met Ser Val Ala Asn Pro
            660                 665                 670

Gly Gly Pro Pro Gly Ala Leu Gly Gly Leu Phe Pro Ser Pro Arg Gly
        675                 680                 685
```

-continued

```
Pro Ser Gly Pro Arg Pro Thr Pro His Pro Ala Gln Met Ala Phe Ala
    690                 695                 700

Phe Val Gly Gln Gln Pro Val Phe Pro Gly Phe Asp Ala Ser Gln Pro
705                 710                 715                 720

Ala Gly Ser Thr Phe Gln Tyr Pro Pro Ile Arg Gly Ala Val Ser Gly
                725                 730                 735

Val Ser Pro Pro Pro Pro Met His Pro Ser Ser Phe Ala Gln Pro Val
            740                 745                 750

Trp Ser Pro Thr Ser Val Pro Ser Ser Ser Val Ser Ser Ser Val Ser
        755                 760                 765

Ser Ser Gly Val Ser Ser Ser Ala Pro Pro Pro Leu Ala Val Gly Phe
    770                 775                 780

Gln Asn Pro Cys Pro Trp Arg Pro Thr Ala Pro Arg Asp Arg Ser Glu
785                 790                 795                 800

Gly Gly Ala Gly Ser Pro Gly Val Ser Cys Gly Ser Ala Pro Pro Ala
                805                 810                 815

Pro Thr His Pro Thr Gly Lys Gly Gly Ala Ala Gly Arg Ala Gly Lys
            820                 825                 830

Gln Leu Gly Gln Ala Thr Arg Phe Leu Ser Ser Val Ser Gly Val Val
        835                 840                 845

Tyr Asp Lys Gly Gly Glu Lys Trp Ile Ala Arg Trp Ser Glu Asn Gly
    850                 855                 860

Lys Pro Phe Lys Lys Thr Phe Ala Val Gly Lys His Gly Phe Asp Ala
865                 870                 875                 880

Ala Arg Lys Met Ala Glu Asp Cys Arg Leu Gln Ala Leu Tyr Ala Lys
                885                 890                 895

Arg Trp Asn Ser Ala Ser Gly Leu Pro Ala Ser Phe Ser Lys Ser Asn
            900                 905                 910

Ser Leu Gly Arg Ser Thr Pro Gly Asp Arg Gly Lys Thr Glu Ser Thr
        915                 920                 925

Asn Ser Ala Lys Cys Lys Arg Asp Thr Ser Gly Glu Ser Gly Cys Thr
    930                 935                 940

Asp Thr Gly Leu Arg Ser Leu His Met Gly Gly Ala Gly Asp Leu Ser
945                 950                 955                 960

Ser Leu Gly His Pro Gly Thr Pro Pro Arg Asp Gln Glu Gly Ala Pro
                965                 970                 975

Ala Ser Phe Leu Leu Glu Gly Thr Gly Val Val Arg Ser Ser Gln Val
            980                 985                 990

Gln Thr Pro Phe Arg Leu Tyr Asp  Ser Val Pro Ser Pro  Leu Arg Ser
        995                 1000                 1005

Gly Asp  Ala Leu Gly Ala Gln  Arg Gly Leu Val Pro  Gln Leu Leu
    1010                 1015                 1020

Asn Asn  Ala Leu Val Gly Val  Pro Phe Ala Pro Pro  Pro Gly Ala
    1025                 1030                 1035

Ser His  Ser Gly Cys Ser Ala  Ala Leu Pro Pro Gly  Pro Gly Ala
    1040                 1045                 1050

Pro Val  Gln Val Ser Ser Pro  His Thr Gly Phe Val  Ala Pro Ala
    1055                 1060                 1065

Asp Val  Asp Ala Pro Pro Arg  Asp Gly Leu Glu Gly  Leu Gly Gly
    1070                 1075                 1080
```

-continued

```
Ala Ala  Glu Val Ser Pro Gln  Ile Ala Val Gln Asp  Gly Gly Lys
    1085                 1090                 1095

Lys Gly  Glu Gly Leu Leu Gly  Ser Ala Ser Leu Ser  Val Arg Arg
    1100                 1105                 1110

Arg Arg  Lys Arg Glu Pro Asp  Glu Lys Phe Ser Pro  Gly Glu Ser
    1115                 1120                 1125

Asn Ala  Ala Val Lys Lys Thr  Pro Arg Pro Gly Ser  Phe His Pro
    1130                 1135                 1140

His Ser  Cys Pro Gly Ser Glu  Gly Phe Arg Ser His  Asp Gly Pro
    1145                 1150                 1155

Gly Asp  Ser Thr Glu Ala Arg  Cys Ala Gly Leu Pro  Ala Phe Gln
    1160                 1165                 1170

His Ala  Thr Ala Pro Ser Ser  Val Cys Trp Pro Ser  Thr Ala Ser
    1175                 1180                 1185

Leu Pro  Ser Leu Asp Lys Ala  Gly Gln Arg Ala Glu  His Ala Gly
    1190                 1195                 1200

Pro Ser  Ala Phe Ser Ser Phe  Ser Ser Val Gln Gln  Ser Pro Gly
    1205                 1210                 1215

Ser Val  Glu Thr Trp Arg Pro  Glu Gly Asp Gly Gly  Pro Ala Ser
    1220                 1225                 1230

Pro Ala  Arg Asp Ala Gly Arg  Arg Gly Ala Glu Ser  Glu Glu Arg
    1235                 1240                 1245

Glu Thr  Gly Glu Leu Ala Gly  Pro Phe Ala Gly Val  Ser Ala Ser
    1250                 1255                 1260

Ala Gly  Ser Ala Ser Arg Lys  Gly Gln Gln Lys Gln  Leu Thr Arg
    1265                 1270                 1275

Gln Ile  Gln Arg Gln Gln Gln  Leu Tyr Arg Gln Gln  Glu Ala Leu
    1280                 1285                 1290

Leu Gln  Asn Gln Glu Glu Leu  Phe Ser Arg Leu Leu  Arg Arg Arg
    1295                 1300                 1305

Ser Arg  Gln Glu Arg Ser Asp  Val Arg Arg Arg Met  Gln Arg Asp
    1310                 1315                 1320

Val Ser  Ser Leu Arg Arg Leu  Pro Ala Met Leu Leu  Ser Pro Leu
    1325                 1330                 1335

Arg Asp  Thr Leu Val Ala Ser  Ala Ala Arg Leu Pro  Leu Ala Thr
    1340                 1345                 1350

Arg Gly  Thr Lys Arg Glu Ser  Gln Lys Glu Arg Arg  Asp Cys Gly
    1355                 1360                 1365

Ala Gly  Ile Gly Gly Glu Thr  Ala Ser Glu Lys Lys  Glu Met Ala
    1370                 1375                 1380

Glu Pro  Val Arg Val His Arg  Arg Asp Arg Gly Gly  Ala Arg Asp
    1385                 1390                 1395

Glu Glu  Lys Pro Ser Thr Glu  Gly Val Arg Gln Ala  Asp Pro Lys
    1400                 1405                 1410

Gly Arg  Lys Ala Glu Gly Phe  Pro Thr Trp Val Ile  Pro Pro Asn
    1415                 1420                 1425

Glu Glu  Leu Lys Ala Ala Gln  Val Leu Arg Ala Leu  Arg Val Gln
    1430                 1435                 1440

Arg Arg  Ala Ala Ala Arg Glu  Gly Lys Leu Leu Glu  Ser Leu Leu
    1445                 1450                 1455

Val His  Arg Gly Glu Gly Glu  Gly Thr Phe Ser Glu  Glu Thr Glu
```

-continued

```
    1460                 1465                 1470

Gly Asn  Thr Gly Ile Glu Asp  Ala Gly Thr Glu Ser  Asp Ala Thr
    1475                 1480                 1485

Val Thr  Gln Glu Thr Ala Glu  Lys Val Val Glu Asn  Val Gln Lys
    1490                 1495                 1500

Met Glu  Glu Leu Glu Ser Lys  Val Glu Lys Glu Asn  Glu Arg Arg
    1505                 1510                 1515

Arg Glu  Ala Glu Asp Glu Thr  Pro Lys Gln Ser Ser  Glu Glu Ala
    1520                 1525                 1530

Pro Gly  Val Gln Gln Ser Pro  His Lys Leu Ser Thr  Asn Asn Glu
    1535                 1540                 1545

Asn Asp  Ala Ser Pro Gln Lys  Leu Thr Lys Ser Val  Arg Phe Ala
    1550                 1555                 1560

Glu Ser  Val Ala Gly Ser Ser  Ser Ala Val Gln Thr  Ala Gly Ala
    1565                 1570                 1575

Ala Asp  Glu Glu Pro Leu Ala  Thr Glu Thr Leu Glu  Gly Arg Arg
    1580                 1585                 1590

Val Gly  Gly Ile Pro Val Pro  Ala Thr Ser Ser Pro  Ala Pro Val
    1595                 1600                 1605

Phe Pro  Cys Thr Ala Ala Gln  Leu Gly Asp Leu Cys  Met Asp Thr
    1610                 1615                 1620

Leu Tyr  Ala Leu Gly Thr Val  Arg Pro Gln Trp Arg  Arg Gln Asp
    1625                 1630                 1635

His Arg  Arg Ala Phe Gly Trp  His Leu Ser Gln Ile  Lys Pro Asp
    1640                 1645                 1650

Leu Ile  Leu Pro Ser Leu His  Ala Ser Arg Val Leu  Arg Arg Leu
    1655                 1660                 1665

Ser Pro  Arg Pro Ser Asn Ala  Val Glu Phe Pro Arg  Glu Glu Leu
    1670                 1675                 1680

Ala Ala  Ala Ser Ser Ala Ala  Gly Leu Val Tyr Gly  Glu Gly Leu
    1685                 1690                 1695

Ser Ser  His His Thr Leu Arg  Ser Tyr Val Asp Ala  Phe Arg Pro
    1700                 1705                 1710

Leu Phe  Ser Ser Pro Ser Ser  Pro Pro Leu Glu Phe  Leu His Leu
    1715                 1720                 1725

Ser Ser  Gly Asp Leu Leu Met  Ser Leu Trp Gln Leu  Glu Glu Gly
    1730                 1735                 1740

Gly Arg  Ala Ala Val Ile Asp  Asn Val Leu Leu Ala  Leu Asp Ala
    1745                 1750                 1755

Leu Tyr  Glu Arg His Thr Gly  Arg Arg Leu Arg Gly  Thr Ala Pro
    1760                 1765                 1770

Pro Pro  Phe Ala Val Ser Ser  Pro Ser Ser Ala Pro  Ser Ser Leu
    1775                 1780                 1785

Phe Ala  Leu Ala His Leu Gln  Gly Gly Ala Thr Ser  Thr Thr Pro
    1790                 1795                 1800

Leu Pro  Ala Thr Ala Leu Pro  Ser Pro Pro Phe Pro  Arg Val Ser
    1805                 1810                 1815

Ser Ala  Pro Asp Ser Pro Val  Phe Ala Pro Asp Ala  Ser His Gly
    1820                 1825                 1830

Pro Ser  Gln Arg Arg Gln Val  Ser Pro His Val Thr  Phe Glu Thr
    1835                 1840                 1845
```

-continued

```
Pro Pro  Thr His Pro Arg Asp  Arg Asp Ser Glu Thr  Ser Val Glu
    1850                 1855                 1860

Arg Asn  Ala Ser Pro Glu Ala  Ser Pro Gln Ala Ala  Thr Leu Ala
    1865                 1870                 1875

Ala Pro  Ala Pro Cys Asp Gly  Asp Arg Glu Glu Asn  Phe Val Leu
    1880                 1885                 1890

Ala Tyr  Asn Pro Glu Ala Lys  Ala Leu Arg Gln Val  Asn Phe Leu
    1895                 1900                 1905

Ala Val  Gly Val Arg Val Phe  Leu His Leu Glu Val  Val Glu Glu
    1910                 1915                 1920

Met Leu  His Leu Gln Ala Lys  Met Gln Arg Thr Pro  Gly Arg Asp
    1925                 1930                 1935

Asp Arg  Ala Thr Ala Ser Ser  Gly Pro Ser Val Asp  Asp Gly Ser
    1940                 1945                 1950

Gly Leu  Met Thr Ser Leu Pro  Ser Thr Cys Ser Gly  Val Ser Gly
    1955                 1960                 1965

Lys Lys  Asp Pro Met His Trp  Ser Ala Leu Phe Val  Thr Val Pro
    1970                 1975                 1980

Ala Pro  Ser Val Ser Thr Ala  Ala Ser Lys Pro Leu  Phe Val Val
    1985                 1990                 1995

Ala Glu  Met Val Asp Arg Arg  Leu Gln Val Pro Cys  Gly Glu Gln
    2000                 2005                 2010

Leu Leu  Phe Arg Pro Leu Pro  Leu Ser Pro Ala Ala  Pro Ser Ala
    2015                 2020                 2025

Leu Leu  Ala Phe Ala Pro Ala  Arg Val Cys Gln Leu  Leu Arg Ala
    2030                 2035                 2040

Gly Ala  Met Cys Leu Thr Arg  Phe Thr Glu Lys Glu  Gly Gly Lys
    2045                 2050                 2055

Arg Pro  Arg Gly Ser Ala Gln  Arg Cys Ser Ala Ala  Ser Ser Phe
    2060                 2065                 2070

Phe Tyr  Ser Pro Pro Pro Leu  Asp Leu Ser His Leu  Ala Ser Phe
    2075                 2080                 2085

Ala Pro  Ala Ala Ser Thr Leu  Thr Pro Pro Ser Ser  Pro Ala Ser
    2090                 2095                 2100

Ser Pro  Ser Ala Ser Ala Ser  Gln Thr Gly Pro Gly  Arg Ala Lys
    2105                 2110                 2115

Ser Arg  Gly Thr Ser Pro Val  Gly Pro Glu Ser Pro  Glu Ala Ala
    2120                 2125                 2130

Ser Thr  Thr Ser Asp Gly Leu  Ala Val Pro Gly Ser  Ala Ser Ala
    2135                 2140                 2145

Val Ser  Thr Pro Gly Val Pro  Ala Gly Ala Ser Gly  Ala Ser Leu
    2150                 2155                 2160

Gly Ala  Pro Ala Pro Ser Pro  Met Ala Ser Pro Gly  Gly Ser Pro
    2165                 2170                 2175

Gly Arg  Pro Pro Lys Pro Val  Cys Cys Pro Ala Ala  Pro Gly Ile
    2180                 2185                 2190

Glu Thr  Ala Trp Arg Cys Lys  Cys Ser His Arg Arg  His Glu Leu
    2195                 2200                 2205

Gln Leu  Glu Ile Lys Gln Lys  Leu Arg Gln Asp Lys  Lys Arg Cys
    2210                 2215                 2220
```

-continued

```
Leu Ala  Leu Ile Arg Glu Tyr  Pro Asp Leu Ser Leu  Leu Val Gly
    2225                 2230                 2235

Ala Pro  Pro Ala Thr Pro Arg  Glu Lys Glu Thr Gly  Ala Lys Arg
    2240                 2245                 2250

Gln Ala  Pro Glu Gly Arg Arg  Thr Ala Thr Pro Ser  Gly Ser Gly
    2255                 2260                 2265

Thr Leu  Thr Ala Lys Gly Gly  Asp Leu Gln Gly Ser  Thr Pro Ser
    2270                 2275                 2280

Gly Ala  Gly Leu Leu Ser Leu  Ala Arg Thr Ser Gln  Leu Glu Met
    2285                 2290                 2295

Leu Ala  Tyr Leu Val Glu Val  Asp Pro Trp Lys Tyr  Ala Lys Asn
    2300                 2305                 2310

Arg Gln  Asp Ala Pro Lys Pro  Glu Glu Ile Pro Gly  Leu Leu Ala
    2315                 2320                 2325

Lys Tyr  Lys Ala Ala Val Arg  Thr Ala Glu Tyr Gly  Arg Met Leu
    2330                 2335                 2340

Gln Lys  Trp Arg Ala Gly Gln  Ser Arg Glu Asp Glu  Gly Arg Gly
    2345                 2350                 2355

Gly Ala  Asp Gly Arg Lys Glu  Gly Asp Gly Leu Leu  Ser Pro Thr
    2360                 2365                 2370

Ala Ser  Pro Pro Ser Arg Arg  Lys Gln Gly Lys Asp  Ser Ser Pro
    2375                 2380                 2385

Asn Ser  Ala Ser Ser Gln Ala  Ser Gly Pro Ala Pro  Ser Pro Ser
    2390                 2395                 2400

Leu Ser  Pro Gly Ala Gly Ala  Ala Ala Val Leu Glu  Ala Glu Lys
    2405                 2410                 2415

Pro Glu  Pro Gln Ser Pro Gln  Glu Ser Pro Cys Pro  Leu Glu Pro
    2420                 2425                 2430

Ala Ala  Gly Gln Glu Pro Arg  Ala Thr Ser Ser Ala  Leu Pro Ala
    2435                 2440                 2445

Gly Ser  Pro Pro Trp Ala Leu  Pro Leu Val Pro Pro  Gly Gly Ser
    2450                 2455                 2460

Pro Arg  Ala Ser Val Ser Pro  Ser Val Leu Glu Glu  Leu Leu Arg
    2465                 2470                 2475

Ile Gln  Thr Ala Met Ser Gln  Leu Ala Ile Gly Thr  Ala Ile Cys
    2480                 2485                 2490

Val Arg  Val Lys Ala Leu Leu  Gly Leu Pro Ala Gly  Ala Glu Gln
    2495                 2500                 2505

His Ile  Arg Gly Val Val Thr  Arg Asn Ala Leu Lys  Phe Pro Trp
    2510                 2515                 2520

Glu Lys  Pro Ala Ala Pro Gln  Val Gln Ala Ala Gly  Pro Ser Val
    2525                 2530                 2535

Gly Ala  Ser Arg Thr Ser Pro  Ser Arg Arg Leu Ser  Gly Gly Val
    2540                 2545                 2550

Leu Pro  Gly Asp Glu Ala Gly  Glu Arg Arg Glu Lys  Gly Gly Ala
    2555                 2560                 2565

Arg Arg  Gly Val Ala Glu Gly  Asp Thr Glu Lys Lys  Glu Asp Glu
    2570                 2575                 2580

Gly Thr  Ala Leu Cys Ala Gly  Ser Arg Glu Thr Glu  Ala Asp Gly
    2585                 2590                 2595

Ala Gly  Tyr Leu Thr Leu Ser  Leu Asn Asn Arg Lys  Glu Glu Phe
```

-continued

```
    2600                 2605                 2610

Ile Leu  Ser Phe Arg Glu Val  Gln Cys Leu Val Ala  Gln Asp Asp
    2615                 2620                 2625

Leu Arg  Leu Val Arg Thr Arg  Ala Arg Gln Trp Val  Ser Ser Phe
    2630                 2635                 2640

Gly Pro  Gln Pro Ser Ala Asp  Arg Lys Gly Glu Arg  Glu Glu Glu
    2645                 2650                 2655

Lys Glu  Thr Gly Gly Arg Thr  Arg Lys Phe Val Val  Asp Glu Asp
    2660                 2665                 2670

Phe


<210> SEQ ID NO 10
<211> LENGTH: 2282
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Met Asp Ser Gly Arg Asp Val Lys Asp Gly Thr Ala Gly Ser Arg Pro
1               5                   10                  15

Lys Asp Gly Gly Asp Gly Val Gly Glu Thr Arg Ala Ser Gly Arg Glu
            20                  25                  30

Ser Glu Glu Arg Ser Leu Gln Leu Glu Ala Asn Glu Cys Pro Gly Ala
        35                  40                  45

Val Met Ser Arg Arg Glu Asp Glu Ala Glu Pro Gln Ser Ser Pro Ser
    50                  55                  60

Ser Ser Pro Pro Arg Glu Glu Gly Pro Gln Asn Val Asp Asp Ala Asp
65                  70                  75                  80

Thr Ala Asn Gly Ser Gly Glu Ala Gly Leu Gln Arg Pro Pro Gln Lys
                85                  90                  95

Arg Arg Leu Glu Gln Gly Leu Glu Ala Glu Ala Gly Val Gly Ser Ser
            100                 105                 110

Arg Val Glu Glu Val Glu Ala Val Cys Arg Lys Arg Pro Ala Phe Ser
        115                 120                 125

Gly Val Ala Asp Ala Phe Leu Glu Arg Pro Val Thr Leu Lys Asn Ser
    130                 135                 140

Ser Glu Glu Asp Ala Ala Arg Leu Ser Gly Asp Asp Ala Ala Gly Ala
145                 150                 155                 160

Ser Leu Leu Ser Val Arg Ser Ala Gly Ala Leu Thr Gly Asp Phe Pro
                165                 170                 175

Ser Ser Ser Ser Arg Leu Pro Ala Met Leu Ser Gly Ala Arg Gly Glu
            180                 185                 190

Asn Ala Glu Glu Ser Val Arg Asp Ala His Thr Pro Ala Gln Asp Ser
        195                 200                 205

Arg Asp Ser Ala Leu Ala Ser Phe Ala Pro Thr Leu Ala Pro Gly Gln
    210                 215                 220

Glu Ser Glu Tyr Thr Arg Ala Lys Leu Trp Ser Ile Glu Lys Ala Phe
225                 230                 235                 240

Asp Ala Phe Leu Ala Asp Gln Lys Ala Asn Gly Arg Arg Gln Gly Ser
                245                 250                 255

Arg Ser Met Arg Glu Pro Ser His Ala His Pro Gly Leu Ser Ala Glu
            260                 265                 270

Arg Glu Thr Ser Ser Gly Ala Ser Ala Ala Thr Ser Asp Leu Ser Arg
```

-continued

```
        275                 280                 285

Glu Asp Val Glu Glu Leu Phe Arg Gln His Gly Val Ser Pro Arg Glu
    290                 295                 300

Leu Val Arg Met Leu Ser Gly Arg Arg Asp Gly Pro Gly Thr Ser Pro
305                 310                 315                 320

Glu Glu Leu Arg Ala Ala Val Ala Trp Ala Arg Gln Leu Phe Pro Ala
                325                 330                 335

Ala Pro Arg Ser Pro Ser Glu Leu Arg Met Tyr Leu Gln Arg Ala Val
            340                 345                 350

Leu Asp Arg Gln Lys Arg Leu Arg Glu Arg Trp Gly Ala Glu Ala Asn
        355                 360                 365

Pro Cys Gly Asp Ala Ser Val Tyr Gly Asp Glu Lys Leu Arg Glu His
    370                 375                 380

Leu Ser Asp Leu Ser Ala Phe Met Pro His Leu Asp Ala Gly Arg Glu
385                 390                 395                 400

Val Tyr Met Gln Trp Gln Arg Ser Arg Gly Arg Arg Asp Phe Asp Ala
                405                 410                 415

Phe Val Arg Pro Pro Gly Leu Thr Pro Phe Arg Asp Ser Ser Ser Arg
            420                 425                 430

Gln Gly Asp Phe Ala Ala Ser Pro Leu Tyr Ser Phe Ser Ser Arg Thr
        435                 440                 445

Pro Trp Ala Ser Ala Cys Lys Glu Ala Ser Thr Pro Pro Ala Ala Lys
    450                 455                 460

Gln Gln Ala Pro Pro Pro Ser Leu Trp Asn Leu Pro Asn Arg Pro Gln
465                 470                 475                 480

Pro Tyr Thr Leu Ala Asp Val Gln Glu Ala Met Glu Gly Pro Glu Gly
                485                 490                 495

Val Leu Arg Val Ala Arg Pro Leu Thr Gly Phe Gly Glu Asp Ala Glu
            500                 505                 510

Ser Leu Ser Phe Ala Ser Leu Pro Lys Gly Ala Glu Thr Leu Phe Trp
        515                 520                 525

Ser Ser Gly Arg Gly Leu Tyr Phe Leu Arg His Leu Glu Arg Thr Lys
    530                 535                 540

Ala Gly Glu His Asp Val Val Gly Glu Ala Gly Val Trp Val Ala Ala
545                 550                 555                 560

Ser Glu Glu Glu Phe Gly Gly Phe Ile Ile His Arg Lys Phe Ser Val
                565                 570                 575

Ala Lys Phe Gly Phe Glu Arg Ala Lys Met Leu Ala Cys Arg Trp Tyr
            580                 585                 590

Asn Asp Arg Gln Glu Ala Arg Arg Gly Gln His Ala Leu Pro His Arg
        595                 600                 605

Glu Lys Pro Lys Gly Ile Met Ser Ser Asp Arg Pro Leu Ser Arg Glu
    610                 615                 620

Ala Ala Pro Glu Ala Ser Arg Phe Ser Ala Ser Arg Ala Gly Glu Leu
625                 630                 635                 640

Ser Gly Lys Ala Gln Glu Ala Pro Lys Ser Thr Gly Gly Thr Ala Ala
                645                 650                 655

Glu His Pro Arg Ala Ser Gln Lys Cys Arg Val Met Asp Thr Thr Cys
            660                 665                 670

Pro Val Pro Gly Val Arg Tyr Asp Ser Arg Asp Arg Ala Trp Leu Ala
        675                 680                 685
```

-continued

```
Thr Trp His Asp Gly Val Arg Gln Tyr Lys Arg Cys Phe Ser Ile Lys
    690                 695                 700

Lys Tyr Gly Phe Ala Lys Ala Lys Glu Cys Ala Ile Arg Met Lys Met
705                 710                 715                 720

Ser Leu Val Gly Gln Pro Gly Val Ser Gln Ser Gly Arg Gln Ala Pro
                725                 730                 735

Phe Pro Val Arg Pro Phe Thr Ser Arg Ala Cys Ser Pro Leu Gln Asp
            740                 745                 750

Phe Phe Arg Glu Gly Asp Arg Arg Val Ala Ala Ser Ser Phe Ser Leu
        755                 760                 765

Leu Pro Ser Gly Arg Gly Glu Pro Arg Gly Ser Leu Gly Ser Ser Gln
    770                 775                 780

Gly Ala Asp Asp Glu Arg Ser Lys Pro Gln Ser Cys Arg Gly Leu Val
785                 790                 795                 800

Glu Gln Leu Leu Ala Arg Phe Gln Asp Ser Glu Gly Phe Thr Arg Gly
                805                 810                 815

Leu Pro Gly Asp Asp Glu Asn Arg Gly Lys Arg Leu Ser Lys Gln Ala
            820                 825                 830

Gln Asp Asp Phe Gln Ser Trp Arg Pro Pro Pro Gly Ala Arg Phe Gly
        835                 840                 845

Ser Ala Ala Gln Ala Ser Arg His Ser Thr Asp Glu Val Gly Gly Phe
    850                 855                 860

Ala Gly Phe Pro Gly Phe Ala Ala Ser His Cys Gly Glu Lys Pro Gly
865                 870                 875                 880

Gly Glu Gly Pro Ser Phe Leu Gln Lys Ser Gly Phe Val Gln Glu Asn
                885                 890                 895

Ala Phe Ser Pro Pro Ser Glu Arg Phe Glu Thr Gly Val His Arg Arg
            900                 905                 910

Val Pro Ser Leu Ser Ser Glu Leu Ala Asn Pro Gln Val Thr Glu Glu
        915                 920                 925

Val Glu Glu Phe Leu Phe Ser Leu Ser Thr Arg Ala Arg Gln Ser Leu
    930                 935                 940

Leu Ala Ser Leu Arg Arg Gly Ala Glu Asp Ser Arg Arg Ser Ala Trp
945                 950                 955                 960

Pro Gly Ala Ser Arg Asp Cys His Thr Gly Ala Gly Thr Pro Gly Gly
                965                 970                 975

Thr Asp Val Ala Asp Arg Arg Ala Thr Arg Glu Thr Arg Arg Asp Arg
            980                 985                 990

Glu Gly Glu Glu Ser Thr Ser Glu  Asp Gly Thr Val Arg  Arg Glu Thr
        995                 1000                 1005

Asp Ala  Gly Ala Val Ser Pro  Asp Glu Val Ser Arg  Ala Asn Ala
    1010                 1015                 1020

Glu Glu  Arg Ala Ala Gly Glu  Lys Thr Arg Ser Ser  Glu Arg Ile
    1025                 1030                 1035

Trp Thr  Gly Glu Gly Glu Arg  Ser Ala Gly Asp Arg  Asp Asp Lys
    1040                 1045                 1050

Gly Glu  Gly Glu Gly Gly Gly  Gly Val Val Glu Gly  Arg Thr Glu
    1055                 1060                 1065

Lys Gly  Gly Asp Asp Asp Lys  Lys Pro Gly Glu Glu  Glu Ser Ala
    1070                 1075                 1080
```

-continued

```
Glu Arg  Glu Glu Glu Leu Lys  Asn Asp Ala Tyr Ala  Tyr Phe Thr
    1085                 1090                 1095

His Leu  Thr Asn Arg Glu Trp  Asp Leu Leu Asp Tyr  Leu Asp Thr
    1100                 1105                 1110

Leu Asp  Phe Glu Thr Val Asp  Leu Asp Ala Val Met  Pro Phe Ile
    1115                 1120                 1125

Asn Gln  Val Pro Lys Val Arg  Gly Val Cys Phe Asp  Arg Lys Gly
    1130                 1135                 1140

Leu Tyr  Trp Ile Ser Gln Trp  His Ser Gln Gln Lys  Lys His Arg
    1145                 1150                 1155

Glu Trp  Phe Gly Val Lys Arg  Leu Gly Phe Arg Lys  Ala Trp Ala
    1160                 1165                 1170

Leu Ala  Val Cys Val Arg Arg  Asp Ala Glu Lys Val  Glu Asp Glu
    1175                 1180                 1185

Pro Val  Asp Tyr Pro Lys Leu  Pro Asp Tyr Glu Glu  Val Leu Gly
    1190                 1195                 1200

Val Thr  Tyr Ala Arg Phe Ala  Ser Gly Arg Tyr Trp  Val Ala His
    1205                 1210                 1215

Tyr Met  Arg Pro Ala Ala Pro  Ser Ser Gly Cys Leu  Gly Ser Val
    1220                 1225                 1230

Gly Arg  Lys Leu Phe Pro Val  Ser Glu Ser Ser Phe  Glu Glu Ala
    1235                 1240                 1245

Arg Ser  Gln Ala Val Ala Val  Ala Thr Ala Phe Pro  Leu Pro Leu
    1250                 1255                 1260

Ala Phe  Phe Val Asp Pro Glu  Arg Arg Ala Thr Ser  Ala Phe Glu
    1265                 1270                 1275

Ser Ala  Arg Ala Glu Asn Leu  Gln Gly Asp Lys Gln  Val Leu Leu
    1280                 1285                 1290

Ser Lys  Asn Cys Leu Phe Asn  Val Phe Thr Trp Leu  Asn Gly Gly
    1295                 1300                 1305

Ala Ser  Trp Thr Asn Val Arg  Arg Trp Ala His Ala  Lys Arg Met
    1310                 1315                 1320

Gln Leu  Ala Glu Asp Asp Trp  Pro Gln Gln Phe Phe  Ser Leu Pro
    1325                 1330                 1335

Ser Pro  Ala Lys Gly Asp Ser  Phe Ala Glu Ala Glu  Lys Glu Arg
    1340                 1345                 1350

Ala Glu  Glu Arg Thr Gly Gly  Glu Glu Val Lys Ala  Asn Ser Ala
    1355                 1360                 1365

Ser Arg  Ala Ala Ala Lys Ser  Glu Trp Pro Val Ala  Ser Thr Thr
    1370                 1375                 1380

Ser Pro  Ala Glu Asp Leu Ala  Ser Ser Gly Ser Pro  Arg Asp Leu
    1385                 1390                 1395

Gln Lys  Leu Ser Pro Leu Leu  Ala Asp Ser Ser Leu  Thr Lys Glu
    1400                 1405                 1410

Leu Leu  Gly Gly Asp Arg Glu  Leu Gly Asn Ala Met  Asp Gly Ala
    1415                 1420                 1425

Arg Gly  Pro Arg Gly Leu Asp  Thr Ala Lys Gly Arg  Ala Lys Asp
    1430                 1435                 1440

Glu Glu  Arg Leu Thr Ala Lys  Asp Ala Glu Ser Arg  Gln Ala Thr
    1445                 1450                 1455

Leu Pro  Gly Gly Arg Ala Ala  His Gly Gly Gly Val  Gly Gly Ser
```

-continued

```
    1460                1465                1470

Leu Gly  Thr Ala Cys Glu Glu  Glu Leu Asp Glu Pro  Leu Ser Pro
    1475                1480                1485

Leu Asp  Ile Glu Ser Ile Val  Ala Asp Ala Tyr Glu  Ser Phe Ser
    1490                1495                1500

Asp Glu  Asp Ala Glu Gly Glu  Gly Asp Gly Gly Lys  Pro Gly Lys
    1505                1510                1515

Arg Ile  Arg Leu Pro Lys Ile  Gly Gly Val Tyr Tyr  Lys Arg Asp
    1520                1525                1530

Gly Asn  Tyr Lys Ala Trp Ala  Ala Ser Trp His Ile  Gln Gly Lys
    1535                1540                1545

Arg Thr  Arg Arg Tyr Phe Thr  Val Lys Lys His Gly  Phe Arg Asn
    1550                1555                1560

Ala Tyr  Leu Lys Ala Val Arg  Ala Arg Arg Glu Ala  Glu Arg His
    1565                1570                1575

Glu Gly  Ile Ser Val Lys His  Arg His His Ala Leu  Val Pro Gly
    1580                1585                1590

His Pro  Gly Asn Met Leu Gly  Ala Ser Lys Val Cys  Ala Glu Ser
    1595                1600                1605

His Glu  Val Ser Gly Phe Pro  His Gly Asp Glu Asp  Ser Arg Leu
    1610                1615                1620

Thr Arg  Gly Gly Ala Ser His  Ala Ala Val Ala Pro  Gly Arg Val
    1625                1630                1635

Asn Arg  Glu Arg Ser Val Ala  Leu Val Asp Arg Ala  Thr Lys Asp
    1640                1645                1650

Asp Glu  Asp Asp Glu Arg Asp  Leu Gln Arg Glu Lys  Thr Gly Ala
    1655                1660                1665

Gly Gly  Gly Glu Ala Cys Ser  Gly Glu Ser Val Lys  Val Ala Leu
    1670                1675                1680

Gly Thr  Arg His Asp Ser Phe  Ser Asp Gly Ser Cys  Arg Thr Leu
    1685                1690                1695

Asp Lys  Leu Ser Thr Gln Phe  Glu Gln Lys Pro Arg  Gly Gly Ala
    1700                1705                1710

Gly Glu  Glu Ala Glu His Pro  Thr Arg Lys Gln Gly  Gln Glu Thr
    1715                1720                1725

Gly Gly  Val Asp Glu Pro Leu  Ser Arg Ala Ala Ser  Ile Val Gly
    1730                1735                1740

Gly Arg  Glu Val Arg Leu Thr  Ser Gly Val Ser Val  His Leu Thr
    1745                1750                1755

Pro Leu  Glu Arg Val Ala Lys  Ala Val Asp Val Asp  Leu Lys Glu
    1760                1765                1770

Leu Thr  Asp Arg Val Ser Arg  Ala Ala Phe Arg Gly  Gly Asp Ser
    1775                1780                1785

Arg Leu  Phe His Arg Thr Val  Asp Asn Cys Glu Gly  Glu Ala Asp
    1790                1795                1800

Glu Val  Ala Gln Gly Leu Asp  Thr His Arg Glu Asp  Val Asp Val
    1805                1810                1815

Thr Arg  Asn Leu Glu Phe Ala  Met Ala Arg Glu Thr  Leu Asp Val
    1820                1825                1830

Leu Leu  Ser Asp Leu Tyr Ser  Val Val Ala Lys Leu  Ser Gly Ala
    1835                1840                1845
```

-continued

```
Gly Arg  Trp Thr Ser Leu Val  Ser Pro Thr Ala Ala  Glu Ala Glu
    1850                 1855                 1860

Pro Leu  Val Ser Ala Trp Asp  Arg Ser Ala Arg Glu  Glu Arg Arg
    1865                 1870                 1875

Glu Lys  Phe Glu Asp Thr Asn  Ala Ala Ser Asp Glu  Pro Gly Tyr
    1880                 1885                 1890

Pro Thr  Ser Ser Ala Gln Ile  His Val Ala Ile Gln  Leu Val Val
    1895                 1900                 1905

Ile Lys  His Tyr Leu Ala Thr  Val Arg Thr Ala Asn  Arg Val Glu
    1910                 1915                 1920

Gln Ile  Ala Pro Leu Leu Ala  Leu Phe Glu Pro Cys  Ile Lys Gln
    1925                 1930                 1935

Gly Met  Leu Pro His Glu Cys  Ala Leu Pro Arg Leu  Arg Trp Leu
    1940                 1945                 1950

Val Cys  Gln Leu Cys Arg Ala  Ser Leu Pro Trp Leu  Asp Glu Ser
    1955                 1960                 1965

Asp Val  Leu Thr Asp Ala Leu  Leu Tyr Arg His Leu  Glu Glu Leu
    1970                 1975                 1980

Val Glu  Thr Glu Glu Ala Glu  Ala Pro Gln Glu Gly  Val Pro Pro
    1985                 1990                 1995

Gly Gly  Gln Ile Val Phe Ser  Ala Gly Phe Ala Glu  Gly Asn Ser
    2000                 2005                 2010

Thr Val  Ala Ser Arg Asn Val  Phe Thr Gly Glu Ser  Arg Val Ala
    2015                 2020                 2025

Gly Gly  Phe Arg Thr Asp Ser  Glu Lys Glu Ser Gly  Ile Asp Asp
    2030                 2035                 2040

Arg Asp  Glu Ala Ser Leu Ala  Ala Leu Ile Cys Leu  Pro Gly Lys
    2045                 2050                 2055

Gly Lys  Lys Leu Arg Glu Glu  Ala Asp Val Glu Lys  Asp Asp Thr
    2060                 2065                 2070

Ser Ala  Ser Leu Asn Cys Glu  Ser Gly Lys Lys Thr  Glu Ala Glu
    2075                 2080                 2085

Ser Gln  His Ser Arg Ser Pro  Thr Glu Val Ala Ala  Ser Ser Val
    2090                 2095                 2100

Ser Gly  Ser Glu Gly Lys Asp  Gly Ser Ser Asp Asn  Glu Arg Ser
    2105                 2110                 2115

Gly Asp  Ala Asp Asp Ala Thr  Glu Gly Ser Glu Lys  Cys Glu Lys
    2120                 2125                 2130

Thr Arg  Gly Gly Asp Gln Arg  Arg Ala Ala Pro Arg  Thr Ser Ser
    2135                 2140                 2145

Ala Ser  Thr Ala Ser Gly Glu  Thr Pro Glu Lys Ser  Lys Asn Arg
    2150                 2155                 2160

Gly Ser  Asp Ala Leu Lys Gly  Lys Asn Glu Gly Gly  Ala Thr Gly
    2165                 2170                 2175

Thr Ser  Gly Glu Gln Arg Asp  Asp Glu Asp Arg Asp  Leu Glu Asn
    2180                 2185                 2190

Val Glu  Ile Ser Lys Asp Thr  Arg Ala Gly Ser Gly  Gly Arg Arg
    2195                 2200                 2205

Arg Thr  Gly Glu Arg Arg Gly  Gln Arg Phe Cys Ala  Ser Gly Gly
    2210                 2215                 2220
```

-continued

```
Glu Leu  Arg Val Ser Glu Glu  Ser Pro Asp Arg Ala  Lys Thr Glu
    2225                 2230                 2235

Lys Ser  Lys Gly Glu Pro Val  Arg Asp Ser Leu Ser  Pro Asp Ala
    2240                 2245                 2250

Ser Ser  Arg Leu Pro Ser Arg  Cys Gly Thr Pro Pro  Pro Ala Ala
    2255                 2260                 2265

Ala Thr  Gly Ser Cys Ala Thr  Val Glu Ser Asp Val  Pro Ala
    2270                 2275                 2280


<210> SEQ ID NO 11
<211> LENGTH: 3236
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Thr Thr Val Ser Arg Ala His Ala Ser Arg Ser Arg Arg Lys Ser
1               5                   10                  15

Arg Asp Glu Asp Ser Glu Gly Ser Ser Leu Pro Ala Val Gly Ile His
            20                  25                  30

Glu Thr Gln Ser Pro Val Phe Ser Arg Glu Gly His Glu Gly Asp Arg
        35                  40                  45

Ala Ala Gln Pro Glu Asp Val Val Ala Ala Glu Ser His Ser Asn Pro
    50                  55                  60

Gln Trp Pro Thr Pro Leu Asp Thr Gly Phe Asp Lys Gly Ala Pro Pro
65                  70                  75                  80

Leu Gly Cys Ser Arg Ser Glu Glu Leu Arg Ser Pro Pro Met Ala Ser
                85                  90                  95

Gly Ser Phe His Gly Ser Gly Thr Gly Gly Asp Gly Gly Cys Leu Leu
            100                 105                 110

Ser Leu Glu Ala His Ala Val Ser Lys Asp Ser Glu Arg Gln Val Asn
        115                 120                 125

Ser Gly Leu Pro Gly Gly Gly Asp Glu Ile Ser Gly Arg Leu Ser Pro
    130                 135                 140

Ser Cys Ala Ser Leu Pro Leu Val Ala Ala Ala Leu Ser Pro Val Glu
145                 150                 155                 160

Asp Thr Arg Leu Glu Arg Asp Ser Ser Ile Pro Val Leu Lys Pro Ser
                165                 170                 175

Leu Ser Ile Pro Asn Leu Leu Val Thr Ser Pro Ser Leu Thr Ser Val
            180                 185                 190

Ser Tyr Val Cys Glu Ala Asp Arg Ser Ala Glu Gly Lys Ala Pro Ser
        195                 200                 205

Met Asp Ala Leu Pro Pro Ser His Ser Ala Ala Pro Glu Ser Gly Leu
    210                 215                 220

Trp Arg Glu Cys Asp Glu Arg Gly Lys Asn Ser Phe Phe Ser Ser Gly
225                 230                 235                 240

Leu Pro Ala His Pro Glu Gly Asn Gly Glu Arg Ala Gly Glu Gly Gln
                245                 250                 255

Asp Pro Arg Ser Gly Asp Phe Glu Thr Pro Glu Glu Ala Ala Phe Ser
            260                 265                 270

Val Gln Arg Ile Leu Gln Glu Ser Glu Glu Leu Phe Leu Leu Ser Gly
        275                 280                 285

Cys Ala Arg Glu Asp Arg Gly Gly Glu Ser Asp Ala Ala Phe Lys Thr
    290                 295                 300
```

-continued

```
Met Thr Arg Ser Glu Gly Ala Phe Ser Arg Glu Pro Ala His Arg His
305                 310                 315                 320

Ala Phe Ala Lys Pro Gly Asn Gly Gly Glu Ser Glu Pro Phe Met Ser
                325                 330                 335

Ile Asp Glu Glu Arg Ala Ala Ser Pro Ser Ala Ser Gly Pro Ser Ser
            340                 345                 350

Tyr Ala Phe Leu Ser Phe Glu Glu Thr Ser Ala Gly Ser Arg Arg Ser
        355                 360                 365

Pro Asp Ala Gln Ser Pro Pro Leu Ser Gly His Leu Ser Asp Gly Asp
    370                 375                 380

Arg Thr Gln Arg Lys Ala Gly Glu Arg Phe Leu Glu Asp Pro Arg Gly
385                 390                 395                 400

Asn Leu Lys Arg Ser Arg Ser Pro Leu Ile Ala Arg Asp Cys Asn Arg
                405                 410                 415

Ser Leu Gly Thr Cys Asp Ser Ser Leu Thr Thr Arg Gly Pro Val Ala
            420                 425                 430

Ser Asp Thr Ser Pro Arg Arg Gly Tyr Thr Asp Gln Trp His Ser His
        435                 440                 445

Arg Lys Ala Gln Ser Pro Gly Arg Phe Arg Arg Thr Asn Thr Glu Gly
    450                 455                 460

Asn Ala Thr Pro Val Asp Ser Gln Ser Ser Pro Pro Ser Lys Lys Arg
465                 470                 475                 480

Cys Cys Leu Ala Glu Arg Phe Ala Phe Glu Arg Arg Arg Gln Pro Pro
                485                 490                 495

Val Pro Leu Pro Ser Val Ala Ser Ala Val Ala Ala Ala Leu Ala Gln
            500                 505                 510

Phe Pro Pro Gly Ala Cys Thr Ala Ala Val Glu Arg Ala Asp Asp Val
        515                 520                 525

Pro Pro Glu Gly Ser Gly Asn Gly Val Leu Pro Gly Gly Glu Val Ser
    530                 535                 540

Asp Leu Ser Leu Ser Asp Arg Lys Ser Gly Ala Ser Pro Arg Gln Thr
545                 550                 555                 560

Leu Asp Thr Phe Leu Pro Ala Lys Gly Ala Ser Ala Ala Leu Lys Gln
                565                 570                 575

Glu Gly Ser Ser Ser Glu Ile Gly Glu Gly Cys Pro Ala Ser Asp Asp
            580                 585                 590

Ala Ala Val Ala Ala Thr Leu Ser Gly Trp Lys Arg Gly Arg Gly Pro
        595                 600                 605

Arg Ser Gly Cys Val Ser Gly Ser Ser Arg Ala Ser Ser Leu Glu His
    610                 615                 620

Ala Gly Ala Arg Arg Arg Ser Gly Val Glu Arg Lys Arg Arg Glu Lys
625                 630                 635                 640

Arg Lys Ala Ala Leu Ala Thr Ala Ala Val Val Ser Ala Ser Val Arg
                645                 650                 655

Arg Leu Ala Leu Val Ala Ala Pro Cys Leu Val Glu Asn Thr Leu Arg
            660                 665                 670

Gln Trp Trp Arg Leu Gln Glu Gln Val Gly Asp Glu Leu Asp Asn Gly
        675                 680                 685

Gly Val Ser Glu Glu Gln Thr Thr Gly Arg Ser Gly Arg Arg Thr Gly
    690                 695                 700
```

-continued

```
Lys Asn Pro Ile Val Gly Gly Arg Val Lys Glu Gly Glu Gln Ser Val
705                 710                 715                 720

Arg Leu Glu Ile Glu Arg Ser Gly Asp Ser Pro Arg Asn Thr Ala Lys
                725                 730                 735

Thr Glu Pro Gly Asp Gln Gly Ala Ala Gln Gly Gln Gly Gly Pro Glu
            740                 745                 750

Gln Ile Ala Glu Asn Glu Ser Gly Thr Glu Arg Met Glu Thr Ser Gln
        755                 760                 765

Thr Lys Gln Glu Ala Gln Asp Leu Pro Leu His Arg Glu Ala Ala Ser
    770                 775                 780

Ala Ser Ala Thr Pro Phe Ile Pro Glu Gly Arg Thr Gln Glu Arg Asp
785                 790                 795                 800

Ser Tyr Leu Arg Val Thr Leu Phe Ala Ala Ser Gln Val Leu Asn Ser
                805                 810                 815

Gly Gln Phe Arg Gln Ala Ile Arg Met Phe Pro Gly Ala Asp Ser Pro
            820                 825                 830

Arg Gly Asp Gln Arg Ser Arg Cys Val Val Arg Val Tyr Lys Gln Ser
        835                 840                 845

Leu Arg Lys Arg Arg Leu Ser Gly Asp Arg Asn Arg Arg Val Gly Glu
    850                 855                 860

Asp Gly Asn Leu Val Ser Val Ser Leu Arg Asp Leu Leu Ala Asn Ser
865                 870                 875                 880

Gly Glu Asp Trp Glu Pro Ser Ser Pro Ser Ala Ala Thr Arg Pro Leu
                885                 890                 895

Pro Leu Ala Pro Ser Ala Leu Ser Ala His Gln Ala Arg Ser Ser Phe
            900                 905                 910

Gly Ser Phe Ser Arg Arg Ser Ala Glu Gly Val Pro Gly Pro Ser Pro
        915                 920                 925

Trp Gly Gly Asp Cys Ser Pro Thr Ala Ala Arg Ser Pro Leu Pro Leu
    930                 935                 940

Ser Thr Ser His Asp Leu Arg Arg Arg Arg Val Cys Pro Pro Arg Arg
945                 950                 955                 960

Arg Tyr Ser Pro Ser Glu Ser Val His Ser Ser Asp Gly Arg Gly Gly
                965                 970                 975

Ala Cys Ala Ile Ala Ala Lys Lys Pro Lys Gly Arg Arg Ser Arg Gly
            980                 985                 990

Arg Glu Glu Gln Thr Arg Glu Glu  Val Ser Glu Ser Arg  Cys Ser Thr
        995                 1000                 1005

Pro Arg  Ser Cys Ser Ser Val  Arg Tyr Ala Val Ser  Asp Gly Ser
    1010                 1015                 1020

Pro Ala  Ser Ser Arg Ala His  Leu Gly Arg Pro Asp  Asp Glu Gly
    1025                 1030                 1035

Asp Glu  Arg Met Thr Gly Gly  Gln Arg Thr Pro Arg  Gly Thr Pro
    1040                 1045                 1050

Gln Glu  Gly Glu Asp Ser Asp  Phe Leu Pro Ala Gly  Met Ser Gly
    1055                 1060                 1065

Leu Arg  Gly Gly Thr Leu Pro  Leu Asp Gln Leu Gly  Glu Arg Ser
    1070                 1075                 1080

Arg Ser  Ala Glu Arg Trp Met  Pro Ala Pro Ser Val  Ala Val Val
    1085                 1090                 1095

Pro Phe  Ala Pro Asn Ile Leu  Ala Lys Lys His Ala  Glu Asp Val
```

-continued

```
    1100                1105                1110

Glu Asn  Gln Leu Asp Gly Gly  Lys Met Ser Leu Asp  Gly Val Gly
    1115                1120                1125

Gln Lys  Glu Cys Gly Leu Val  Glu Thr Gly Asp Thr  Gly Glu Gln
    1130                1135                1140

Glu Ala  Ala Val Ala Ala Ser  Glu Lys Arg Arg Pro  Leu Glu Ala
    1145                1150                1155

Gln Thr  Pro Gly Arg His Gly  Thr Thr Val Leu Met  Lys Gly Glu
    1160                1165                1170

Gly Leu  Leu Ala Gly Arg Thr  Ser Glu Val Asp Gly  Asp Arg Thr
    1175                1180                1185

Gly Glu  Lys Thr Thr Gln Ile  Ser Pro Phe Ser Glu  Ala Thr Gly
    1190                1195                1200

Ile Cys  Ile Leu Arg Arg Ser  Pro Arg Arg Val Gln  Ser Asn Ser
    1205                1210                1215

Ser Glu  Ala Ser Arg Thr Ala  Val Arg Ser Thr Glu  Gly Leu Glu
    1220                1225                1230

Thr Ser  Asp Lys Leu Gly Val  Asp Val Gly Thr Thr  Asn Lys Glu
    1235                1240                1245

Ala Asp  Ser Phe Ser Ala Ser  Cys Asp Ser Pro Arg  Asp Ser Leu
    1250                1255                1260

Glu Arg  Asn Val Gly Glu Ile  Val Ala Ile Trp Ala  Arg Ala Arg
    1265                1270                1275

Asp Ala  Lys Gln Gly Gly Arg  Ile Arg Arg Arg Val  Trp Leu Pro
    1280                1285                1290

Pro Gly  Met Ala Thr His Gly  Gly His Glu Gly Asn  Glu Gln Asn
    1295                1300                1305

Asn Glu  Ala Ile Cys Gly Gly  Gly Ala Thr Pro Met  Met Lys Thr
    1310                1315                1320

Glu Arg  Ala Met Glu Glu Gly  Arg Gly Asp Ala Lys  Thr His Pro
    1325                1330                1335

Val Gly  Gly Thr Tyr Ala Glu  Thr Glu Lys Lys Val  Val Asp Glu
    1340                1345                1350

Met Lys  Ala Trp Trp Ser Lys  Leu Thr Cys Ala Ser  Val Glu Ala
    1355                1360                1365

Val Pro  Val Gln Thr Leu Thr  Leu Asp Asp Phe Ala  Arg Ala Phe
    1370                1375                1380

Ser Thr  Val Ala Asn Arg Ala  Val Asp Leu Leu Cys  Leu Ala Phe
    1385                1390                1395

Arg Ala  Arg Gly Ala Gly Pro  Val Phe Arg Pro Val  Leu Ser Ser
    1400                1405                1410

Ser Pro  Lys Gln Gln Gly Asn  Ser Pro Gln Pro Glu  Ser Glu Asp
    1415                1420                1425

Val Glu  Thr Arg Ile Glu Thr  Tyr Arg Gln Gln Val  Arg Arg Leu
    1430                1435                1440

Tyr Arg  Arg Arg Gln Gln Leu  His Glu Ala Thr Gly  Asn Ser Pro
    1445                1450                1455

Phe Ser  Ser Ser Arg Val Gly  Gly Ala Leu Gln Arg  Arg Ile Gly
    1460                1465                1470

Glu Leu  Gln Arg Leu Arg Glu  Ala His Gly Arg Val  Asp Ile Pro
    1475                1480                1485
```

-continued

```
Asn Glu  Gly Pro Arg Arg Glu  Glu Asp Ser Glu Lys  Cys Pro Ala
    1490                 1495                 1500

Ser Leu  Trp Asp Val Pro Leu  Arg Gln Arg Lys Gln  Gly Arg Lys
    1505                 1510                 1515

Arg Val  Ser Pro Trp Tyr Ser  Val Gly Val Arg Trp  Leu Ala Asp
    1520                 1525                 1530

Phe Ser  Ala Phe Glu Tyr Phe  Val Val Lys Asn Tyr  Arg Lys Glu
    1535                 1540                 1545

Asp Leu  Gly Ala Thr Val Ser  Leu Ser Asn Arg Gly  Glu Ala Ser
    1550                 1555                 1560

Asp Thr  Thr Trp Ser Val Asp  Gly Thr Gly Ser Gln  Arg Ala Pro
    1565                 1570                 1575

Val Pro  Cys Leu Ser Arg Ala  Gly Thr Pro Arg Thr  Val Ser Pro
    1580                 1585                 1590

Ser Pro  Pro Ser Ala Asp Ala  Met Asn Leu Trp Ala  Gln Ala Tyr
    1595                 1600                 1605

Ala Pro  Ser Leu Asn Gln Pro  Arg Gly Met Ser Pro  Ala Thr Thr
    1610                 1615                 1620

Pro Pro  Leu Ser Glu Ser Ala  Thr Pro Arg Gly Asn  Val Ser Pro
    1625                 1630                 1635

Pro Phe  Ser Glu Ala Ser Ser  Ser Gly Gln Arg Gly  Lys Lys Val
    1640                 1645                 1650

Ala Pro  Gly Pro Ser Ala Asp  Glu Lys Lys Asp Glu  Asp Tyr Gln
    1655                 1660                 1665

Ser Ala  Gly Ser Leu Arg Trp  Glu Val Asp Gly Gly  Gln Arg Arg
    1670                 1675                 1680

Gln Val  Gln Val Arg Ser Arg  Leu Leu Leu His Glu  Leu Leu Gln
    1685                 1690                 1695

Pro Pro  Ser Leu Asp Ala Thr  Gly Leu Arg Thr Ala  Leu Val Leu
    1700                 1705                 1710

Ile Val  Leu Arg Leu Gln Arg  Phe Leu Arg Leu Lys  Glu Gly Gly
    1715                 1720                 1725

Val Asn  Asn Arg Gly Arg Gly  Gln Arg Ser Glu Arg  Lys Arg Arg
    1730                 1735                 1740

Cys Arg  Ala Met Pro Pro Ile  Phe Ile Phe Arg Asp  Asp Ser Asn
    1745                 1750                 1755

Ala Phe  Gln Glu Ala Leu Leu  Ala Lys Lys Leu Asp  Ile Arg Leu
    1760                 1765                 1770

Asp Ser  Asp Ser Pro His Thr  Asp Val Pro Ser Arg  Arg Ser Leu
    1775                 1780                 1785

Asp Gly  Glu Val Gly Asp Glu  Arg Arg Arg Leu Arg  Ser Val Lys
    1790                 1795                 1800

Pro Thr  Asn Ser Asn Asp Leu  Ser Asp Glu Arg Gly  Pro Pro Pro
    1805                 1810                 1815

Pro Ser  Thr Met Ser Pro His  Ser Leu Gly Ser Gly  Pro Cys Asp
    1820                 1825                 1830

Thr Gln  Glu Gly Val Gln Asn  Leu Gln Gln Asp Ala  Ser Leu Phe
    1835                 1840                 1845

Ser Pro  Ala Leu Ala Gln Gly  Gln Ala His Ala His  Thr Asp Ala
    1850                 1855                 1860
```

-continued

```
Val Pro  Gly Ala Arg His Asp  Asp Val Leu Pro Arg  Ser Pro Arg
    1865                 1870                 1875

Phe Pro  Val Val Asp Ala Gly  Pro Glu Glu Thr Pro  Arg Pro Glu
    1880                 1885                 1890

Val Glu  Ser Met Leu Asp Ser  Glu Ser Gly Asp Pro  Thr Gly Leu
    1895                 1900                 1905

Gly Gln  Ala Ser Arg Arg Arg  Trp Arg Gly Arg Gly  Ser Arg Thr
    1910                 1915                 1920

Ser Val  Gln Arg Thr Val Ser  Thr Cys Leu His Glu  Asp His Ser
    1925                 1930                 1935

Gly Asp  Lys Thr Pro Arg Glu  Glu Thr Phe Gly Gly  Asp Ala Ala
    1940                 1945                 1950

Ser Leu  Leu Arg Val Ala Ser  Ser Val Pro Pro Ser  Thr Cys Ser
    1955                 1960                 1965

Ser Pro  Gln Ser Ser Ser Gly  Gly Arg Arg Glu Arg  Gly Arg Arg
    1970                 1975                 1980

Gly Val  Arg Gly Arg Arg Gly  Arg Gly Arg Leu Ile  Ser Gln Gln
    1985                 1990                 1995

Gly Ser  Ser Leu Leu Gly Gln  Thr Val Ser Ala Gly  Ala Leu Ser
    2000                 2005                 2010

Ser Gly  Asp Thr Ala Gly Ala  Ile Ser Thr Glu Gly  Glu Asn Arg
    2015                 2020                 2025

Arg Asn  Ala Val Arg Pro Gly  Ala Leu Glu His Ser  Asp Glu Asp
    2030                 2035                 2040

Lys Glu  Asp Leu Ser Ala Ser  Ser Pro Pro Ser Asp  Asp Gly Ile
    2045                 2050                 2055

Ser Gln  Arg Ser Ser Gly Ser  Gln Gly Asp Ser Ser  Ser Ser Gly
    2060                 2065                 2070

Gly Pro  Ser Ser Glu Ala Cys  Arg Lys Thr Thr Ser  His Val Ala
    2075                 2080                 2085

Ala Lys  Ala Asp Ser Ala Ser  Pro Arg Ala Leu His  Pro Ser Ala
    2090                 2095                 2100

Arg Pro  Gln Pro Arg Gly Thr  Ala Ser Trp Thr Pro  Gly Gly Glu
    2105                 2110                 2115

Pro Ala  Val Ser Gly Val Gln  His Pro Ser Ala Leu  Thr Pro Ser
    2120                 2125                 2130

Pro Ser  Arg Gly Arg Phe Ser  Glu Asp Asn Val Ala  Ser Arg Val
    2135                 2140                 2145

Ser Arg  Val Ser Ser Val Gly  Ala Leu Leu Arg Ser  Arg Cys Val
    2150                 2155                 2160

Val Gly  Glu Glu Gln Lys Glu  Thr Gln Asn Ser Cys  Ser Leu Trp
    2165                 2170                 2175

Val Val  Glu Lys Gly Ala Leu  Glu Pro Phe Trp Trp  Arg Thr Ala
    2180                 2185                 2190

Ser Ala  Val Gly Cys Val Ser  Ala Gly Arg Arg Asp  His Ser Asp
    2195                 2200                 2205

Lys Asp  Ala Asn Arg Leu Phe  Leu Ala Asp Lys Glu  Ala Gly Thr
    2210                 2215                 2220

Gly Pro  Leu Gln Asp Phe Val  Leu Pro Asp Phe Ser  Gly Ser Ala
    2225                 2230                 2235

Arg Glu  Ile His Gly Asp Glu  Arg Gly Ser Asp Ser  Asp Ala Ser
```

-continued

```
    2240                2245                2250

Cys Lys  Ser Ala Ala Leu Ser  Thr Thr Ser Asp Ser  Ser Gly Ile
    2255                2260                2265

Ser Glu  Val Ser Leu Asp Leu  Glu Ser Thr Val Gln  Glu Val Ala
    2270                2275                2280

Leu Gly  Thr Ile Leu Ser Ser  Ala Leu Ser Ala Leu  His Gly Lys
    2285                2290                2295

Thr Gly  Asp Gly Asp Thr Gln  Glu Ser Asp Ala Glu  Arg Glu Ala
    2300                2305                2310

Asn Ala  Asp Asp Gly Ser Ala  Thr Gly Val Asn Glu  Lys Asp Leu
    2315                2320                2325

Arg Gly  Glu Ser Arg Pro Glu  Leu Pro Ser Pro Ile  Pro Gly Lys
    2330                2335                2340

Asp Glu  Leu Gly Ser Gln Glu  Glu Gly Lys Thr Ala  Ser Ser Leu
    2345                2350                2355

Pro Ser  Val Lys Ala Glu Gln  Gly Gly Ser Glu Arg  Gly Gly Ala
    2360                2365                2370

Asp Glu  Ile Val Lys Lys Ala  Thr Ser Val Leu Arg  Ala Cys Lys
    2375                2380                2385

Asp Pro  Asp Glu Ala Thr Ser  Thr Ser Leu Val Pro  Glu Gly Glu
    2390                2395                2400

Asp Glu  Asn Asp Ala Cys Gly  Ala Leu Glu Pro Asp  Ser Leu Val
    2405                2410                2415

Ser Val  Ser Ala Leu Gly Glu  Ser Ser Glu Glu Leu  Phe Thr Glu
    2420                2425                2430

Val Pro  Gln Asn Glu Lys Glu  Leu Lys Lys Thr Leu  Gln His Val
    2435                2440                2445

Asp Pro  Arg Leu Cys Gln Gln  Met Leu His Gly Gly  Leu Cys Phe
    2450                2455                2460

Ile Arg  Thr Tyr Val Asp Leu  Glu Thr Lys Lys Glu  Ser Leu Gln
    2465                2470                2475

Ala Gly  Pro Phe Ala Ala Lys  Arg Arg Arg Val Ala  Gln Leu Leu
    2480                2485                2490

Arg Gly  Leu Gln Gly Leu Phe  Asp Ala Leu Glu Ser  Val Arg Glu
    2495                2500                2505

Arg Glu  Gly Asp Asp Leu Ser  Gly Glu His Glu Gly  Asp Ser Ala
    2510                2515                2520

Ser Gly  Gly Leu Phe Thr Ala  Glu Gln Glu Lys Glu  Gly Ala Asp
    2525                2530                2535

Lys Val  Ser Gly Asp Arg Glu  Asn Ala Gly Glu Arg  Gly Gln Lys
    2540                2545                2550

Thr Ala  Ala Glu Thr Gly Asp  Gln Lys Ala Ser Ile  Glu Asp Ala
    2555                2560                2565

Val Ala  Ala Ala Phe Cys Arg  Arg Val Gly Ala Ala  Ile Ala Thr
    2570                2575                2580

Glu Thr  Cys Gly Ser Ile Gln  Thr Val Phe Pro Glu  Ile Gly Glu
    2585                2590                2595

Ala Tyr  Asp Val Glu Asp Ser  Val Ala Arg Leu Gly  Ala Pro Pro
    2600                2605                2610

Arg Ala  Pro Val Arg Thr Arg  Arg Glu Cys Thr Gly  Thr Gly Phe
    2615                2620                2625
```

-continued

```
Thr Ser  Thr Ala Ala Leu Pro  Glu Pro Arg Gly Glu  Asp Gly Arg
    2630                 2635                 2640

Lys Gln  Glu Thr Ser Glu Pro  Leu Gly Val Glu Ala  Ala Asp Lys
    2645                 2650                 2655

Thr Asp  Ile Gln Gly Glu Tyr  Ala Gln Glu Ser Glu  His Thr Trp
    2660                 2665                 2670

Thr Gln  Glu Met Gly Arg Lys  Ala Ser Leu Phe Leu  Ser Gly Thr
    2675                 2680                 2685

Leu Glu  Leu Ala Gln Leu Lys  Glu Glu Gln Gln Val  Glu Glu Leu
    2690                 2695                 2700

Gln Gly  Glu Gly Asp Pro Leu  Thr Ser Phe Leu Leu  Pro Ser Asp
    2705                 2710                 2715

Gln Ser  Asp Ser Thr Lys Lys  Ala Asn Glu Glu Cys  Met Gly Gly
    2720                 2725                 2730

Arg Thr  Ala Arg Glu Leu Tyr  Ala Glu Arg Glu Glu  Asp Val Lys
    2735                 2740                 2745

Thr Leu  Gly Arg Arg Arg Glu  Ala Gln Thr Glu Ser  Arg Ala Arg
    2750                 2755                 2760

Gly Pro  His Val Asp Ser Ser  Ala Glu Ala Ala Ser  Val Ala Gln
    2765                 2770                 2775

Gly Asp  Glu Gly Gly Glu Glu  Ala Arg Lys Arg Lys  Lys Asp Glu
    2780                 2785                 2790

Lys Arg  Glu Lys Arg Ser Gly  Asn Ala Phe Leu Asp  Ala Leu Leu
    2795                 2800                 2805

Glu Pro  Ala Leu Arg Glu Asp  Val Gly Arg Ala Phe  Leu Thr Asp
    2810                 2815                 2820

Phe Gly  Ser Gln Ala Pro Gln  Asn Ser Thr Asp Ala  Gly Lys Pro
    2825                 2830                 2835

Ile Phe  Leu Ser Pro Cys Val  Phe Gly Val Arg Gly  Gly Ala Arg
    2840                 2845                 2850

Trp Lys  Lys Leu Gly Leu Phe  Asn Asp Glu Ala Gln  Arg Glu Gly
    2855                 2860                 2865

Thr Glu  Ser Ser Pro Trp Arg  Asn Asp Cys Ser Asp  Pro Met Ser
    2870                 2875                 2880

Tyr Arg  Ala Asp Ala Pro His  Thr Trp Arg Arg His  Glu Gly Leu
    2885                 2890                 2895

Leu Trp  Gly Gly Ser Arg His  Ala Ala Ser Ala Leu  Arg His His
    2900                 2905                 2910

Gly Arg  Lys Ser Pro Ala Phe  Leu Ser Pro Gln Trp  Glu Asp Asp
    2915                 2920                 2925

Glu Arg  Leu Ser Leu Ser Ser  Ser Ala Asp Glu Arg  Gly Tyr Thr
    2930                 2935                 2940

Ser Ser  Gly Ser Glu Arg Phe  Leu Ser Ile Pro Thr  Arg Arg Lys
    2945                 2950                 2955

Tyr Gly  Leu Arg Phe Gln Arg  Arg Ser Thr Lys Thr  Gly Arg Ala
    2960                 2965                 2970

Pro Ser  Pro Thr Ala Gly Arg  Ser Ser Val Asn Arg  Ser Gly Trp
    2975                 2980                 2985

Arg Glu  Thr Leu Arg Pro Ser  Ser Gly Phe Ser Gly  Glu Glu Thr
    2990                 2995                 3000
```

-continued

```
Pro Arg  Ser Leu Ser Ser Arg  Arg Arg Arg Gly Gly  Leu Gly Gly
    3005                 3010                 3015

Ser Ser  Pro Thr Ala Phe Arg  Pro Pro Met Thr Arg  Ala Ala Thr
    3020                 3025                 3030

Gly Lys  Ala Ala Ala Cys Val  Arg His Gly Asp Gly  Asp Glu Cys
    3035                 3040                 3045

Ala Glu  Pro Asp Ser Gln Phe  Gly Ala Phe Gly Ser  Ala Asp Leu
    3050                 3055                 3060

Gly Leu  Ser Asp Arg Arg Gly  Glu Ala Gly Glu Ala  Asp Thr Arg
    3065                 3070                 3075

Glu Glu  Lys Ala Gly Gly Ser  Ala Arg His Gly Lys  Arg Gly Ser
    3080                 3085                 3090

Gly Val  Arg Ser Gly Gly Ala  Arg Glu Ala Gly Ser  Asp Ala Gly
    3095                 3100                 3105

Thr Asp  Thr Leu Trp Val Ala  Pro Gly Ser Gly Pro  Asn Thr Cys
    3110                 3115                 3120

Arg Ser  Gly Arg Lys Ser Pro  Ala Ala Ala Ala Leu  Ser Ser Leu
    3125                 3130                 3135

Pro Thr  Gly Val Tyr Phe Asp  Ala Ser Arg Lys Leu  Trp Arg Cys
    3140                 3145                 3150

Gln Trp  Arg Glu Asn Gly Arg  Phe Lys Thr Lys Gly  Phe Ser Leu
    3155                 3160                 3165

Asn Val  Tyr Lys Thr Leu Lys  Glu Ala Arg Arg Ala  Cys Val Val
    3170                 3175                 3180

Tyr Arg  Cys Leu Met Gly Gly  Trp Glu Val Asp Pro  Arg Trp Leu
    3185                 3190                 3195

Gly Pro  Asp Asp Asp Glu Gln  Asp Asn Ser Gly Gly  Ala Asp Glu
    3200                 3205                 3210

Val Gly  Arg Pro Val Pro Ser  Asp Gly Ile Ser Asp  Val Val Gly
    3215                 3220                 3225

Glu Ala  Arg Arg Lys Gly Glu  Tyr
    3230                 3235


<210> SEQ ID NO 12
<211> LENGTH: 1670
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Ile Asn Leu His Gln Leu Phe Arg Val Phe Ser Arg Val Ser Ser
1               5                   10                  15

Ser Ala Ser Asp Pro Ser Ala Ser Asn Pro Ser Pro Ala Ser Leu Val
            20                  25                  30

Ser Val Pro Ala Leu Gln Thr Leu Ser Phe Pro Ala Leu Gln Gln Gln
        35                  40                  45

Asp Leu Leu Ala Ser Leu Ala Ala Ala Ser Leu Pro Gly Pro Asp Ser
    50                  55                  60

Val Thr Met Ser Ser Ser Pro Thr Ser Val Leu Asn Ser Ser Phe Cys
65                  70                  75                  80

Ser Leu Pro Ser Ser Arg Lys Pro Ala Ala Leu Pro Phe Pro Ala Thr
                85                  90                  95

Ser Pro Lys Thr Pro His Leu Ser Asp Ser Phe Pro Ala Ser Ala Ile
            100                 105                 110
```

-continued

```
Ser Gly Pro Ser Ser Pro Gly Leu Gln Glu Leu Leu Ala Ser Pro Glu
        115                 120                 125

Leu Ala Ala Ala Ala Leu Ala Ser Leu Gln Lys Gln Gln Leu Arg Leu
    130                 135                 140

Ala Leu Gly Thr Glu Arg Gly Gly Cys Gly Ala Arg Gly Asp Glu His
145                 150                 155                 160

Leu His Ser Ile Leu Leu Gln His Lys Ala Thr Ser Glu Asn Ala Met
                165                 170                 175

Arg Trp Ser Trp His Ala Gly Arg Asp Gly Ala Gln Glu Leu Asp Thr
            180                 185                 190

Val Pro Glu Thr Phe Asp Leu Pro Leu Ser Leu Ser Ser Phe Leu Gly
        195                 200                 205

Val Ala Pro Gln Gln Pro Ser Ser Leu Pro Arg Ser Ser Leu Leu Pro
    210                 215                 220

Pro Thr Asp Phe Ser Leu Thr Asp Gly Thr Leu Arg Val Ser Ser Ser
225                 230                 235                 240

Met Leu Pro Ala Leu Ala Thr Gly Ser Glu Ser Gly Ser Ser Arg Gly
                245                 250                 255

Leu Asn Ser Ala Gln Ala Ser Pro Ser Phe Ser Ser Leu Arg Gly Pro
            260                 265                 270

Pro Val Ser Val Pro Glu Glu Glu Val Ser Gly Ser Leu Glu Gly Ser
        275                 280                 285

Pro Gly Pro Phe Ser Ser Gly His Pro Pro Ala Ala Pro Ser His Pro
    290                 295                 300

Cys Ser Thr Val Ser Gly Ala Asp Thr Gln Glu Ala Glu Pro Pro Leu
305                 310                 315                 320

Leu Thr Leu Val Ala Val Asn Thr Pro Asp Ala Gln Asp Pro Ala Val
                325                 330                 335

Asp Gly Ala Ser Leu Cys Ala Ser Lys Glu Gly Met Arg Thr Ser Ser
            340                 345                 350

Ala Asp Leu Gly Asp Ser Leu Leu Ala Pro Pro Gly His Gly Ser Ala
        355                 360                 365

Ala Pro Leu Pro Gly Arg His Leu Gly Ser Asp Ala Thr Arg Thr Thr
    370                 375                 380

Thr Thr Thr Gly Ser Gly Ala Pro Glu Ser Pro Ser Leu Pro Leu Ala
385                 390                 395                 400

Arg Gly Asp Cys Glu Gly Ala Glu Arg Gly Leu Ala Leu Leu Glu Ala
                405                 410                 415

Pro Val Asn Gly Phe Asn Leu Ala Ala Ser Gln Ser Val Leu Gly Gly
            420                 425                 430

Phe Ala Ala Asp Thr Arg Gly Glu Ala Gly Glu Lys Gly Ile Ala Pro
        435                 440                 445

Gln Ser Arg Lys Ala Arg Lys Pro Gly Thr Ala Val Glu Thr Ala Gly
    450                 455                 460

Ala Pro Glu Ala Val Arg Arg Gly Arg Ala Ala Cys Asn Gly Glu Ala
465                 470                 475                 480

Glu Thr Thr Gly Leu Glu Thr Ala Pro Gln Gln Val Ser Thr Ser Glu
                485                 490                 495

Glu Thr Ala Lys Ser Gly Arg Glu Leu Ala Cys Ala Arg Ala Gly Met
            500                 505                 510
```

-continued

```
Asp Glu Glu Glu Asp Ala Ala Phe Pro Ser His Val Val Ser Glu Phe
        515                 520                 525

Arg Gly Pro Pro Glu Ile Ser Asn Val Phe Asn Asp Leu Asp Cys Ser
    530                 535                 540

Ser Ala Val Glu Arg Pro Gln Gly Cys Leu Gln His Ala Ala Val Gln
545                 550                 555                 560

Pro Phe Leu Pro Ala Val Ala Pro Glu Val Arg Pro Ser Ala Thr Thr
                565                 570                 575

Ala Gly Arg Thr Pro Met Gly Leu Trp Ser Glu Ala Gly Arg Val Ser
            580                 585                 590

Ser Leu Glu Thr Asp Thr Ala Glu Ile Gly Arg Arg Leu Asp Gly Glu
        595                 600                 605

Ser Ser Gly Ser Pro Asp Arg Trp Gly Asp Ala Arg Leu Ser Ser Pro
    610                 615                 620

Asp Ser Val Pro Ser Ser Ala Asp Val Pro Val Pro Ser Arg Pro Gln
625                 630                 635                 640

Cys Gln Glu Gln Val Pro Gln Val Asp Pro Asp Ser Ser His Pro Leu
                645                 650                 655

Phe Ala Ser Cys Ser Ala Gly Ser Ser Ser Thr Ala Gly Ser Ala Ser
            660                 665                 670

Ala Leu Ala Gly Leu Ala Ser Pro Phe Pro Pro Pro Lys Ser Pro Lys
        675                 680                 685

Thr Gly Ala Asn Asp Pro Arg Met Thr Pro Ser Glu Gly Glu Met Arg
    690                 695                 700

Ala Val Ser Gly Ala Pro Pro Ser Leu His Met Ser Pro Pro Ile Pro
705                 710                 715                 720

Pro Leu Ala Leu Gln Asp Ser Phe Gly Glu Cys Thr Ala Ser Ser Leu
                725                 730                 735

Ala Gly Val Asp Ala Pro Glu Ala Thr Ala Gly Gly Leu Ala Glu Gly
            740                 745                 750

Val Ala Thr Gly Gly Gly Ser Asp Ser Val Gly Glu Gly Arg Leu Pro
        755                 760                 765

Gly Ala Ala Ser Leu Glu Val Pro Ser Ser Pro Ser Ala Leu Leu Ser
    770                 775                 780

Gly Ala Pro Ala Ser Leu Leu Leu Leu Leu Arg Asn Gly Gln Ser Gly
785                 790                 795                 800

Ala Ala Ala Leu Val Ala Ala Met Gln Gln His Gln Ala Leu Ser Gly
                805                 810                 815

Asp Ala Glu Glu Ala Leu Glu Ala Val Leu Ala Gly Gly Ser Asn Val
            820                 825                 830

Gly Asp Met Ala Asn Ser Ser Arg Gly Leu Glu Thr Val Gly Asp Gly
        835                 840                 845

Thr Arg Gly Ser Ala His Thr Thr His Ala Ala His Ser Ser Gly Arg
    850                 855                 860

Asn Ala Val Gly Ala Cys Pro Ala Pro Asp Arg Glu Gly Glu Thr Val
865                 870                 875                 880

Ala Val Pro Thr Ser Val Leu Thr Asn Asn Pro Ala Ser Thr Ser Lys
                885                 890                 895

Thr Met Pro Ser Val Tyr Ser Thr Pro Ala Ser Ala Gly Leu Ser Leu
            900                 905                 910

Thr Ser Ser Ser Thr Pro Pro Val Leu Pro Thr Pro Asn Pro Gly Ala
```

-continued

```
        915                 920                 925

Gly Met Pro Pro Leu Ala Ser Ala His Ala Ala Ser Pro Ala Val Pro
    930                 935                 940

Gly Asp Ala Asn Leu Gln Ser Leu Phe Phe Trp Ala Pro Gln Ala Cys
945                 950                 955                 960

Pro Leu Gln Pro Gly Ala Leu Ala Val Asp Ala Ser Ala Ser Ser Cys
                965                 970                 975

Gly Gly Val Gly Ser Cys Asn Gly Gly Pro Ala Pro Pro Gly Pro Ser
            980                 985                 990

Pro Val Ala Glu Leu Leu Asp Ala  Ser Gly Ser Gly Pro  Phe Gly Ala
        995                 1000                 1005

Ala Gly  Ser Gly Ala Gln Leu  Ala Ala Gly Pro Phe  Gly Ala Ala
    1010                 1015                 1020

Thr Pro  Ala Ser Ala Thr Phe  Gln Gln Gln Leu Leu  Leu Leu Ser
    1025                 1030                 1035

Ala Ala  Phe Asp Gln Ile Gly  Ser Ser Ser Phe Pro  Val Val Gly
    1040                 1045                 1050

Gly Glu  Asn Phe Ile Gly Tyr  Ser Ala Leu Ser Ala  Ala Arg Pro
    1055                 1060                 1065

Asp Ala  Ser Asp Leu Ser Ala  Ser Gly Gly Pro Pro  Ala Ser Leu
    1070                 1075                 1080

Pro Val  Leu Leu Ala Ala Ala  Asn Ala Gly Val Gly  Pro Gly Ala
    1085                 1090                 1095

Ala Gly  Val Gly Asp Gln Pro  Asp Phe Leu Ala Leu  Leu Gly Gly
    1100                 1105                 1110

Gly Ser  Ala Ser Arg Glu Gly  Ala Arg Asp Pro Val  Gly Gly Glu
    1115                 1120                 1125

Leu Gly  Gly Ala Gly Asn Ser  Ala Thr Ser Met Lys  Gly Val Lys
    1130                 1135                 1140

Arg Gln  Phe Val Gln Asn Gly  His Gly Thr Ala Ser  Gln Thr His
    1145                 1150                 1155

Pro Glu  Glu Asn Thr Gln Gly  Pro Gly Arg Ser Ala  Ala Val Val
    1160                 1165                 1170

Gly Arg  Ala Thr Lys Lys Gln  Arg Arg Gly Pro Pro  His Ser Gly
    1175                 1180                 1185

Ala Ala  Val Ser Ser Gly Ala  Pro Ser Gly Val Leu  Ala Val Pro
    1190                 1195                 1200

Gly Cys  Leu Gly Pro Pro Ser  Val Ala Lys Gly Pro  Gly Ser Asp
    1205                 1210                 1215

Glu Phe  Asn Leu Gln Gln Leu  Gln Gln Ser Arg Asp  Ser Arg His
    1220                 1225                 1230

Ser Ala  Asp Asn Ala Ser Gly  Ile Pro Asn Trp Pro  Pro Val Phe
    1235                 1240                 1245

Ser Asn  Gly Asn His Thr Leu  Gly Val Gly Thr Arg  Ser Pro Ser
    1250                 1255                 1260

Pro Ser  Val Cys Ser Ile Ser  His Asp Ala Gly Phe  Phe Gly Ala
    1265                 1270                 1275

Ser Gly  Ser Asn His Ala Gly  Ser Leu Ser Thr Pro  Val Cys Leu
    1280                 1285                 1290

Pro Gln  Leu Pro Gly Ala Ala  Ser Ala Ser Glu Gly  Pro Cys Glu
    1295                 1300                 1305
```

-continued

```
Ala Gln  Gln Thr Pro Pro Gly  Ser Ile Pro Glu Ala  Thr Thr Leu
    1310                 1315                 1320

Gly Gly  Leu Ser Ala Ala Ser  Gly Asn Pro Asn Ser  Thr Phe Ser
    1325                 1330                 1335

Val Ser  Ala Gly Gly Gly Val  Ala Pro Ala Ile Leu  Asn Leu Ser
    1340                 1345                 1350

Ser Ala  Ser Arg Thr Ser Ser  Gln Thr Ser Pro Cys  Cys Pro Thr
    1355                 1360                 1365

Ala Pro  Gly Ser Leu Leu Ser  Gly Gly Ser Gly Pro  Ala Leu Phe
    1370                 1375                 1380

Phe Ala  Gly Pro Pro Ser Pro  Leu Gln Lys Ala Pro  Val Tyr Ala
    1385                 1390                 1395

Gly Gly  Ser Gly Ser Val Cys  Ala Ser Ser Gly Asp  Ala Ile Ala
    1400                 1405                 1410

Ala Ala  Ala Leu Leu His Leu  Arg Thr Leu Gln Gln  Leu Gln Glu
    1415                 1420                 1425

Leu Gln  Arg His Phe Gln Arg  Pro Gly Ser Leu Pro  Pro Ala Val
    1430                 1435                 1440

Thr Pro  Ala Cys Leu Pro Ser  Gly Val Ala Gly Cys  Ser Pro Ala
    1445                 1450                 1455

Gly Leu  Gly Ala Ser Thr Pro  Gly Thr His Ser Val  Val Cys Asn
    1460                 1465                 1470

Ser Ser  Ala Ser Pro Val Pro  Gly Ala Ser Arg Val  Pro Arg Arg
    1475                 1480                 1485

Pro Asp  Gly Arg Gly Thr Gly  Gly Ala Gly Gly Asp  Pro Gly Pro
    1490                 1495                 1500

Ser Lys  Arg Gly Ser Val Ser  Val Ser Pro Ser Ala  Gln Gln Phe
    1505                 1510                 1515

Val Leu  Leu Gln Leu Lys Gln  Gln Gln Pro Gly Ser  His Gly Asn
    1520                 1525                 1530

Ala Leu  Ser Leu Gly Thr Gln  Gly Asn Ser Ser Asn  Pro Ala Pro
    1535                 1540                 1545

Ala Gly  Gly Ala Gly Ala Pro  Gln Gln His His Pro  Gly Val Cys
    1550                 1555                 1560

Tyr Ser  Pro Pro Lys Asp Val  Trp Arg Ala Arg Ile  Thr Val Asp
    1565                 1570                 1575

Gly Arg  Gln His Glu Gln Gln  Phe Ser Val Lys Arg  His Gly Phe
    1580                 1585                 1590

Glu Glu  Ala Arg Leu Leu Ala  Val Gln Trp Arg Ala  His Met Glu
    1595                 1600                 1605

Asn Leu  Arg Leu Gly Gly Ala  Ala Lys Gly Lys Gly  Asn Ala Ser
    1610                 1615                 1620

Ala Ser  Ser Ala Ser Ala Ala  Thr Ala Thr Ser Gln  Gly Ser Ser
    1625                 1630                 1635

Gln Ser  Ser His Gln Pro Pro  Leu Gly Ser Leu Met  Val Ser Gly
    1640                 1645                 1650

Asn Ser  Gly Met Ser Gly Pro  Gly Ala Gly Pro Leu  Ala Asn Arg
    1655                 1660                 1665

Gly Leu
    1670
```

```
<210> SEQ ID NO 13
<211> LENGTH: 2330
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

Met Ser Asp Tyr Ala Pro Ser Arg Phe Ala Ser Pro Pro Gly Asn Ala
1               5                   10                  15

His Pro Lys Ser Pro Leu Phe Ala Arg Pro His Ser Cys Arg Glu Met
            20                  25                  30

Glu Thr Arg Ala Ser Val Gly Thr Ser Arg Gly Ser Arg Gln Pro Leu
        35                  40                  45

Cys Leu Arg Gly Ser Pro His Gly Cys Leu Ser Pro Gln Lys Gly Gln
    50                  55                  60

Asp Arg Leu Pro Ser Phe Ser Pro Leu Arg Thr Gln Pro Thr Leu Leu
65                  70                  75                  80

Ser Pro Pro Phe Pro Ser Lys Gly Cys Phe Ser Ser Cys Leu Pro Ser
                85                  90                  95

Ser Gln Ala Phe Thr Ser His Arg Ala Arg Gly Pro Ser Pro Glu Val
            100                 105                 110

His Ala Val Ser Ala Asp Ala Ser Thr Ser Ser Ser Pro Ile Ser Pro
        115                 120                 125

Ala Ser Arg Ser Ala Ser Glu Gln Gln Pro Arg Arg Glu Met Cys Ser
    130                 135                 140

Pro Pro Gly Ala Ser Ser Asp Ser Thr Ser Pro Thr Gly Ser Ser Ser
145                 150                 155                 160

Cys Ser Ala Glu Gln Asp Asp Val Leu Cys Phe Arg Gln Arg Phe His
                165                 170                 175

Leu Pro Pro Leu Leu His Leu Ser Thr Ser Arg Lys Arg Leu Arg Glu
            180                 185                 190

Glu Asp Ala Ser Ala Ser Ala Cys Ile Ser Ser Leu Gly Asn Leu Pro
        195                 200                 205

Leu Asp Val Asp Thr Lys Arg Arg Arg Gln Glu Tyr Asp Arg Leu Ser
    210                 215                 220

Thr Ala Ser Leu Ser Ser Phe Arg Ser Pro Lys Thr Pro Arg Leu Pro
225                 230                 235                 240

Ser Cys Leu Ala Arg Arg Asp Pro Glu Glu Ser His Ala Asp Leu Ser
                245                 250                 255

Glu Ser Arg Thr Phe Leu Gln Arg Leu Glu Ala Ala Gly Gln Ser Arg
            260                 265                 270

Lys Gly Asp Thr Ser Arg Glu Thr Ile Glu Ala Asp Glu Lys Lys Val
        275                 280                 285

Leu Ser Thr His Ser Thr Asp Thr Ser Val Gln Arg Ser Pro Ser Glu
    290                 295                 300

Ser Ala Glu Arg Arg Ser Phe Gly Lys Arg Ser Asp Pro Asn Asn Gly
305                 310                 315                 320

Leu Pro Met Ala His Ser Pro Thr Pro Phe Thr Ser Lys Arg Thr Asp
                325                 330                 335

Leu Gly His Ala Leu Asp Asn Ala Leu Ser Met Arg Ala Ala Ser Arg
            340                 345                 350

Cys Gly Phe Pro Gly Pro Ala Glu Ala Thr Val Ala Pro Ala Ala Ser
        355                 360                 365
```

-continued

```
Gly Ala Ser Arg Thr Ala Ser Pro Leu Pro Phe Thr Val Pro Val Val
    370                 375                 380

Leu Ala Ala Ser Pro Pro Thr Met Pro Ser Ala Cys Ser Pro Asp Leu
385                 390                 395                 400

Cys Arg Ala Ser Thr Ser Pro Leu Ser Cys Ala Gly Val Ser Ser Leu
                405                 410                 415

Asp Ala Pro Gln Ala Val Gly Arg Arg Ser Glu Val Ala Ala Cys Val
            420                 425                 430

Ser Pro Ala Ala Ser Glu Glu Thr Val Gly Asp Thr Arg Glu His Ala
        435                 440                 445

Asp Leu Ser Ser Pro Val Ala Trp Pro Val Ala Cys Leu Ala Ser Ser
    450                 455                 460

Pro Gly Val Ala Lys Lys Pro Leu Asp Leu Gln Ile Asp Pro Glu Gln
465                 470                 475                 480

Pro Arg Gly Asn Asp Lys Leu Val Glu Pro Glu Phe Pro Gly Gly Thr
                485                 490                 495

Ala Ala Val Ser Glu Ser Ala Pro Val Ala Gly Ala Asp Ala Pro Arg
            500                 505                 510

Leu Cys Asp Tyr Gly Leu Ser Glu Ala Gly Val Leu Pro Ala Ser Gly
        515                 520                 525

Pro Trp Leu Arg Lys Pro Asn Pro Met Leu Thr Pro Asp Thr Glu Trp
    530                 535                 540

Ala Ala Pro Ser Ser Gln Glu Asp Arg Ala Cys Thr Gln Lys Glu Thr
545                 550                 555                 560

Ser Ala Ala Arg Leu Ala Pro Asn Leu Leu Tyr Arg Gln Ala Asp Ala
                565                 570                 575

Ala Ala Asp Asn Val Thr Lys Gly His Glu Asp Asp Ser Gln Phe Pro
            580                 585                 590

Leu Arg Ser Gly Ser Phe Thr Ser Ser Ala Val Ala Cys Pro Ser Pro
        595                 600                 605

Pro Asp Val Gln Ala Asp Ser Glu Ala Ala Cys Thr Trp Gly Thr Pro
    610                 615                 620

Gly Asn Gly Asp Thr Cys Glu Ser Thr Gly Gly Trp Arg Gly Ala Thr
625                 630                 635                 640

Asn Val Glu Ala His Thr Cys Leu Thr Gly Glu Asp Gly Ser Arg Tyr
                645                 650                 655

Gly Leu Gln Gly Pro Leu Ser Gln Asp Ser Pro Phe Gln Pro Pro Leu
            660                 665                 670

Pro Ser Met Arg Pro Val His Phe Gly Gly Phe Glu Ala Trp Gly Gly
        675                 680                 685

Asn Ser Glu Ala Ser Gln Gly Asp Ala Gln Gly Leu Gln Phe Pro Arg
    690                 695                 700

Val Glu Arg Phe Ser Ser Arg Arg Thr Glu His Gly Ser Glu Gly Gly
705                 710                 715                 720

Phe Cys Gly Gln Leu Ala Gly Glu Leu Leu Pro Thr Ser Thr Ser Gly
                725                 730                 735

Gln Pro His Ser Gln His Val Ala Asp Leu Glu Ser His Thr Gly Ala
            740                 745                 750

Val Phe Ala Ser Cys Asp Pro Ala Met His Ala His Ala Ser Leu Tyr
        755                 760                 765
```

-continued

```
Gly Tyr Pro Gly Ala Phe Tyr Asn Ser Phe Gly Thr Ala Ser Ser Ile
    770                 775                 780

Phe Asp Leu Thr Gln Pro Pro Gln Ala Phe Leu Tyr Gly Gly Thr Tyr
785                 790                 795                 800

Gly Asn Asn Gly Pro Asp Asp Tyr Cys Val His Arg Thr Asn Ser Thr
                805                 810                 815

Ser Cys Gln Gly Phe Thr Ala Pro Asp Asn Ile Ser Thr Gly Thr Leu
            820                 825                 830

Asn Thr Ala Asp Ala Gln Gln Glu Trp Thr Thr Pro Ala Pro Val Ser
        835                 840                 845

Asp Ala Ala Val Gly His Trp Glu Thr Ser Asp Phe Gly Pro Gln His
    850                 855                 860

Leu Asn Gly Arg Ala Ser Ser Ser Val Pro Asp His Gly Gly Gly Leu
865                 870                 875                 880

Pro Phe Gly Gly Asn Gly Asn Ser Trp Gly Thr Ser Gly Asn Gly Asp
                885                 890                 895

Ala Trp Gly Thr Pro Gly Asn Gly Asp Thr Cys Glu Ser Thr Gly Gly
            900                 905                 910

Trp Arg Gly Thr Thr Asn Val Glu Gly His Thr Cys Leu Thr Gly Glu
        915                 920                 925

Asp Gly Ser Arg Tyr Gly Leu Gln Ala Pro Leu Ser Gln Asp Ser Pro
    930                 935                 940

Tyr Gln Pro Pro Leu Pro Pro Met Gln Pro Val His Phe Ala Asn Phe
945                 950                 955                 960

Tyr Ser Ala Cys Phe Pro Pro Leu Pro Pro Pro Pro Val Phe Pro Gly
                965                 970                 975

Ile Gly Cys Val Ser Ala Ser Tyr Pro Asp Ile Leu Leu Pro Gln Ala
            980                 985                 990

Arg Phe Leu Ser Gln Ser Cys Pro  Gly Pro Pro Ser Val  Leu Arg Cys
        995                 1000                1005

Pro Pro  Pro Ala Ala Leu Leu  Arg Gly Ser Ser Pro  Leu Asp Cys
    1010                 1015                 1020

Trp Ser  Leu Pro Ala Leu Pro  Ser Leu Pro Arg Ile  Pro Ser Asp
    1025                 1030                 1035

Phe Ala  Ser Asp Pro Ala Ser  Val Pro Leu Pro Ala  Ala Val Gln
    1040                 1045                 1050

Asn Leu  Pro Glu Asp Ser Pro  Arg Leu Arg Leu Pro  Cys Gln Gly
    1055                 1060                 1065

Ala Ser  Thr Arg Asp Gln Ser  Pro Leu Gln Tyr Glu  Gly Asn Phe
    1070                 1075                 1080

Gly Gly  Ser Asp Glu Val Leu  Arg Pro Gln Val Glu  Val Ala Glu
    1085                 1090                 1095

Asn Arg  Gly Thr Pro Asn Phe  Leu Ala Ala Ser Tyr  Ser Leu Leu
    1100                 1105                 1110

Gly Ala  Phe Ser Cys Glu Gly  Asp Asn Arg Asp Asn  Glu Tyr Glu
    1115                 1120                 1125

Thr Gln  Leu Trp Gln Gln Leu  Asn Glu Ser Gly Glu  Leu Gly Val
    1130                 1135                 1140

Ser Gly  Leu Pro Gln Pro Tyr  Ser Val Glu Glu Gly  Arg Arg Gln
    1145                 1150                 1155

Glu Leu  Gln Ser Pro Tyr Pro  Ala Pro Tyr Glu Asn  Ile Pro Tyr
```

-continued

```
    1160                1165                1170

Ser Thr  Pro Ser Tyr Asn Ser  Val Ser Tyr Thr Ala  Ala Ser Lys
    1175                1180                1185

Asp Arg  Leu Val Gly Asp Asn  Thr Ala Tyr Asn Gly  Ala Ala Tyr
    1190                1195                1200

Cys Pro  Phe Tyr Gly Gly Ser  Gly Met Tyr Glu Thr  Pro Gln Arg
    1205                1210                1215

Ser Glu  Glu Asn Ser Leu Tyr  Ser Ala Asp Pro Gln  Val His Phe
    1220                1225                1230

Ser Glu  Ser Glu Lys Thr Gly  Ser Ser Asp Ser Phe  Pro Tyr Ser
    1235                1240                1245

Phe Phe  Ser Leu Gly Thr Pro  Ala Leu Tyr Pro Gly  Gly Ser Leu
    1250                1255                1260

Gln Thr  Gly Ala His Leu Glu  Glu Val Pro Gly Ser  Gly Asp Ala
    1265                1270                1275

Glu Gly  Ser Ala Trp Ser Pro  Ser Leu Glu Ser Arg  Arg Leu Arg
    1280                1285                1290

Gly Arg  Thr Arg Ser Pro His  Ala Gln Ser Pro Asn  Ser Asn Arg
    1295                1300                1305

Ser Arg  Gly Ala Ala Trp Thr  Phe Ser Pro Ala Ser  Leu Pro Phe
    1310                1315                1320

Glu Val  Pro Ala Ala Ala Lys  Ala Ser Gly Arg Lys  Arg Arg Ala
    1325                1330                1335

Pro Gly  Ser Leu Pro Ala Gln  Thr Asp Arg Gly His  Lys Asp Phe
    1340                1345                1350

Leu Leu  Glu Leu Leu Ala Ser  Arg Leu Glu Pro Val  Lys Gly Val
    1355                1360                1365

His Met  Asp Arg Leu Arg Lys  Thr Trp Val Ala Ser  Trp Leu Val
    1370                1375                1380

Gly Lys  Arg Arg Ile Thr Arg  Ile Phe Ser Phe Gln  Lys Phe Gly
    1385                1390                1395

Phe Phe  Gly Ala Arg Glu Gln  Ala Ile Arg His Arg  Arg Glu Ala
    1400                1405                1410

Leu Leu  Asn Pro Glu Leu Asp  Asn Ser Glu Arg Arg  Glu Ala Leu
    1415                1420                1425

Ala Asn  Val Glu Arg Ala Thr  Asp Asp Glu Leu Gln  Gln Ala Ala
    1430                1435                1440

Asp Ala  Leu Pro Phe Val Val  Gly Val Thr Tyr His  Arg Ala Ser
    1445                1450                1455

Arg Cys  Trp Val Ala Asn His  Arg Lys Pro Met Gly  Lys Ile Val
    1460                1465                1470

Gln Arg  Lys Lys Phe Ala Val  Ala Glu Leu Gly Phe  Leu Glu Ala
    1475                1480                1485

Arg Tyr  His Ala Ala Val Met  Met Phe Cys Trp Asn  Lys Gln Gly
    1490                1495                1500

Arg Thr  Gln Glu Pro Glu Asp  Tyr Asp Gln Gly Ala  Thr Glu Ala
    1505                1510                1515

Phe Asn  Ser Arg Gln Val Pro  Gln Arg Pro Gly Asp  Asp Arg Ala
    1520                1525                1530

Phe Glu  Phe Ser His Pro Thr  Cys Ser Glu Asn Glu  Pro Leu Tyr
    1535                1540                1545
```

-continued

```
Thr Leu  Lys Ala Leu Asp Ser  Gly Thr Cys Asp Asp  Ala Met Val
    1550                 1555                 1560

Leu Leu  Ala Phe Ile Cys Gly  Ser Pro Trp Arg Lys  Ile Cys Arg
    1565                 1570                 1575

Gly Gln  Gln Cys Gly Asp Asp  Pro Thr Leu Leu Glu  Ala Ala Ser
    1580                 1585                 1590

Thr Ile  Gln Thr Glu Lys Ser  Leu Trp Arg Thr Arg  Val Lys Ser
    1595                 1600                 1605

Ala Ala  Asp Glu Val Arg Glu  Gly Pro Gln Arg Arg  Leu Glu Gly
    1610                 1615                 1620

Thr Asp  Ala Gly Asp Ser Gly  Ala Phe Pro Arg Gly  Gln Ser Pro
    1625                 1630                 1635

Glu Lys  Gly Arg Pro Arg Arg  Arg Arg Lys Thr Ala  Thr Leu Arg
    1640                 1645                 1650

Glu Gln  Glu Asp Val Thr Glu  Asp Lys Thr Glu Asp  Gly Arg Glu
    1655                 1660                 1665

Asp Lys  Thr Glu Asp Gly Gly  Glu Asp Lys Thr Glu  Asp Gly Gly
    1670                 1675                 1680

Glu Asp  Gly Arg Glu Asp Glu  Gly Glu Asp Glu Gly  Glu Asp Pro
    1685                 1690                 1695

Gly His  Gly Trp Gly Glu Arg  Arg Arg Cys Arg Lys  Ser Asp Arg
    1700                 1705                 1710

Glu Asn  Ala Gly Glu Ala Glu  Arg Gly Gln Lys Arg  Glu Lys Arg
    1715                 1720                 1725

Gln Gln  Ser Glu Gly Arg Cys  Val Val Ala Glu Val  Asp Leu Arg
    1730                 1735                 1740

Asp Ala  Lys Asp Thr Val Val  Arg Arg Asn Arg Val  Ala Arg Arg
    1745                 1750                 1755

Glu Gly  Leu Glu Thr Gly Phe  Gly Lys Lys Asn Ala  Lys Ser Gly
    1760                 1765                 1770

Ala Glu  Ser Cys Leu Ser Gln  Thr Pro Ala Leu Gly  Pro Ser Ser
    1775                 1780                 1785

Pro Pro  Phe Pro Val Ser Phe  Lys Lys Arg Arg Lys  Ser Ser Ser
    1790                 1795                 1800

Arg Glu  Ala Asp Leu Arg Gln  Ser Arg Pro Arg Arg  His Arg Asn
    1805                 1810                 1815

Asp Thr  Glu Glu Ala Arg Ser  Ile Cys Glu Asp Ser  Pro Ser Ser
    1820                 1825                 1830

Glu Val  Ala Pro Thr Pro Ala  Ser Ser Ser Phe Ser  Pro Ala Ala
    1835                 1840                 1845

Ser Leu  Ser Ser Asp Gly Ser  Arg Leu Gly Ser His  Asn His Asp
    1850                 1855                 1860

Leu Thr  Asp Ser Gly Arg Ser  Ala Ser Val Ser Arg  Gly Arg Ser
    1865                 1870                 1875

Thr Asp  Phe Ser Met Phe Ala  Gly Leu Pro Tyr Leu  Lys Ser Leu
    1880                 1885                 1890

Glu Ser  Asn Thr Arg Phe Val  Pro Pro Ser Arg Pro  Gly Glu Ser
    1895                 1900                 1905

Gly Leu  Pro Asn Val Tyr Ala  Ser Tyr Asn Ser Gly  Leu Ala Phe
    1910                 1915                 1920
```

-continued

```
Glu Ala  Asn Arg Pro Cys Pro  Leu Ala Phe Asp Ser  Arg Ala Asp
    1925                 1930                 1935

Pro Thr  Gly Trp Pro His Thr  Phe Pro His Pro Ala  Glu Ala Tyr
    1940                 1945                 1950

Gly Ser  Gly Ile Ala Ser Trp  Thr Pro Asn Ala Asn  Gly Phe Phe
    1955                 1960                 1965

Glu Ser  Leu Ala Tyr Thr Gly  Asn Leu Glu Glu Leu  Arg Asp Leu
    1970                 1975                 1980

Cys Gly  Arg Thr Pro Asp Ala  Arg Asp Ser Ser Asp  His Trp Gln
    1985                 1990                 1995

Glu Ala  Ala Ala Ala Ala Ser  Ser Arg Leu Pro Leu  Arg Pro Pro
    2000                 2005                 2010

Ala Val  His Ser Trp Gln Asp  Ala Pro Cys Ala Lys  Asp Pro Ala
    2015                 2020                 2025

Pro Cys  Val Glu Leu Ala Arg  Asp Glu Cys Leu Ala  Gly Gly Asp
    2030                 2035                 2040

Arg Gln  Thr Cys Arg Phe His  Ser Ala Phe Asp Ser  Ala Asp Ala
    2045                 2050                 2055

Gly Asp  Tyr Lys Phe Asn Thr  Asp Ala Arg Cys Leu  Arg Gly Pro
    2060                 2065                 2070

Thr Phe  Asn Pro His Ser Asn  Ala Val Ala Thr Leu  Arg Arg Glu
    2075                 2080                 2085

Gln Glu  Ala Ala Arg Gly Ala  Ser Gly Gln Thr Pro  Ser Phe Phe
    2090                 2095                 2100

Phe Pro  Arg Leu Val Pro Val  Ala Gln Thr Asp Trp  Glu Ala Asp
    2105                 2110                 2115

Pro Gly  Arg Gly Ser Gly Asp  Ser Leu Ser Ala Pro  His Glu Ala
    2120                 2125                 2130

Gly Glu  Ala Val Gly Val Glu  Gly Ser Glu Gly Ala  Pro Cys Glu
    2135                 2140                 2145

Trp Asn  Phe Glu Arg Asp Ala  His Pro Val Ile Leu  Pro Thr Ser
    2150                 2155                 2160

Asn Cys  Ser His Gly His Glu  Arg Leu Ala Ser Ser  Asn Ala Phe
    2165                 2170                 2175

Thr Glu  Ala Lys Gln Arg Asn  Ala Leu Arg Cys Thr  Pro Gln Glu
    2180                 2185                 2190

Thr Val  Gly Gly Val Asn Glu  Asn Gly Ser Pro Leu  Phe Ser Thr
    2195                 2200                 2205

His Arg  Asp Ala Pro Glu Ala  Met Ser Ala Leu Thr  Glu Val Ser
    2210                 2215                 2220

Asp Arg  Glu Thr Gln Arg Gly  Pro Ala Val Leu Gln  Ser Gly Asn
    2225                 2230                 2235

Thr Glu  Ala Leu Leu Gln Asp  Ser Thr Ser Asn Ser  Ala Ser Pro
    2240                 2245                 2250

Thr Gln  Arg Arg Ala His Gly  Leu Asp Pro Glu Pro  Asp Glu Ser
    2255                 2260                 2265

Lys Ala  Arg Gly Glu Arg Ser  Lys Glu Glu Asp Arg  Glu Thr Leu
    2270                 2275                 2280

Arg Thr  Glu Ala Pro Ser Lys  Gly Arg Lys Gln Ile  Leu Ser Pro
    2285                 2290                 2295

Pro Thr  Glu Arg Asn Ser Met  Tyr Gly Glu Ala Met  Ser Ile Asp
```

-continued

```
    2300                 2305                 2310

Arg Gln  Val Ser Ala Leu Pro  Thr Leu Leu Ser His  Gly Thr Ala
    2315                 2320                 2325

Phe Pro
    2330


<210> SEQ ID NO 14
<211> LENGTH: 1438
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

Met Ala Ala Ala Ser Pro Pro Ala Gln Pro Leu Gly Ala Thr Ser Pro
1               5                   10                  15

Cys Thr Phe Ser Pro Pro Cys Ser Phe Ser Pro Ser Asp Thr Cys Ser
            20                  25                  30

Val Phe Phe Ala Thr Pro Ser Arg Ala Val Ser Ala Val Pro Glu Leu
        35                  40                  45

Pro Ala Thr Ser Ser Ala Gln Leu Pro Glu Arg Thr Arg Leu Arg Asn
    50                  55                  60

Arg Ser Ile Gln Ser Ala Ser Thr Thr Glu Ala Ser Pro Phe Val Asp
65                  70                  75                  80

Ser Ala Ser Leu Phe Pro Glu Ser Leu Ser Glu Ala Pro Lys Ala Val
                85                  90                  95

Ser Val Asp Gly Glu Ser Arg Arg Thr Arg Glu Arg Arg Arg Lys Ser
            100                 105                 110

Arg Ser Leu Leu Ala Ala Ala Glu Glu Thr Pro Glu Ala Thr Ala Ala
        115                 120                 125

Ser Pro Asn Gly Ser Ser Ser Glu Ile Ser Asp Glu Ala Ser Thr Phe
    130                 135                 140

Val Leu Thr Pro Ala Thr Ala Ser Leu Ala Pro Ala Ala Leu Pro Pro
145                 150                 155                 160

Phe Met Thr Glu Arg Ser Asp Pro Thr Glu Lys Lys Tyr Glu Ala Gln
                165                 170                 175

Asn Met Gln Val Thr Ala Val Glu Pro Val Gly Leu Ala Pro Arg Ser
            180                 185                 190

Ala Ser Arg Ser Glu Leu Gly Asp Ala Glu Ser Leu Ser Ala Gly Lys
        195                 200                 205

Ser Gly Leu Gln Gly Glu Ser Ala Ala Pro Thr Ala Ala Leu Glu Ala
    210                 215                 220

Asp Ala Gly Glu Thr Arg Leu Glu Thr Gly Leu Ala Gly Glu Pro Val
225                 230                 235                 240

Asn Ser Ser Ser Glu Gly Val Gly Tyr Gly Gly Asp Glu Gln Thr Val
                245                 250                 255

Ala Gly Glu Thr Arg Glu Pro Gly Thr Ala Glu Glu Lys Leu Gly Asp
            260                 265                 270

Leu Lys Pro Glu Val Arg Pro Arg Phe His Ala Tyr Ala Glu Gln Asp
        275                 280                 285

Val Cys Ala Trp Ala Thr Ser Met Leu Ala Arg Lys Glu Leu Arg Lys
    290                 295                 300

Leu Lys Ala Ala Ala Val Lys Leu Glu Gly Asp Arg Met Pro Arg Ser
305                 310                 315                 320
```

-continued

```
Asp Val Val Gly Leu Tyr Phe Lys Lys His Arg Pro Cys Trp Ser Val
                325                 330                 335

Asp Tyr His Thr Arg Gln Gly Lys Arg Lys Thr Val Glu Phe Phe Val
            340                 345                 350

Pro Asp Leu Ser Arg Glu Thr Ile Glu Leu Val Leu Val His Ala Ile
        355                 360                 365

Glu Cys Arg Lys Tyr Met Pro Arg Arg Phe Asp Gln Ala Pro Ala Phe
    370                 375                 380

Val Pro Glu Pro Asp Asp Thr Thr Ser Gly Met Pro Tyr Arg Tyr Gly
385                 390                 395                 400

Ala Arg Leu Leu Ser Pro Lys Val Leu Ala Trp Ile Val Glu Asn Thr
                405                 410                 415

Asn Gly Ser Gly Arg Thr Ser Gln His Gly His Gly Gln Ser Arg Arg
            420                 425                 430

Leu Glu Gly Asp Lys Val Gly Glu Gly Asp Ala Gly Ala Gln Leu Leu
        435                 440                 445

Ser Gly Pro Ala Gly Ile Asp Ala Phe Gly Ser Arg Ser Pro Arg Ala
    450                 455                 460

Gly Phe Ala Arg Gln Arg Asp Asn Asn Ser Arg Arg Gln Gly Lys Ala
465                 470                 475                 480

Ser Gly Cys Arg Pro Gly Ala Asp Leu Ala Thr Ser Ser Glu Glu Lys
                485                 490                 495

Ala Thr Arg Glu Gly Glu Thr Glu Leu Pro Gly Gly Ser Ala Gly Pro
            500                 505                 510

Gly Ser Val Pro Ala Gly Thr Ala Tyr Gly Asp Tyr Ala Arg Gln Leu
        515                 520                 525

Pro Ser Glu Gly Tyr Gln Thr Pro Pro Thr Met Glu Gly Arg Met Thr
    530                 535                 540

Pro Ala Gly Leu Leu Ser Gly Gln Glu Phe Gly His Gly Gln Gly Met
545                 550                 555                 560

Gln Gly Ala Gly Val Met Trp Arg Asp Asp Pro Arg Gln Ala Leu Gln
                565                 570                 575

Ala Met Pro Gln Pro Leu Asn Leu Ala Pro His Ala Thr Pro Phe Met
            580                 585                 590

Ser Arg Ala Gly Gly Leu Tyr Asp Gln Arg Glu Ala Ser Val Glu Pro
        595                 600                 605

Gly Arg Asp Val Tyr Pro Val His Tyr Pro Thr Pro Tyr Ala Tyr Gly
    610                 615                 620

Pro Gly Ile Pro Ala Asp Ala Gly Ala Pro Ser Ala Gly Pro Gly Pro
625                 630                 635                 640

Tyr Pro His Gln Phe Pro Ser Gly Gly Ala Gly Tyr Val Val Asn Gly
                645                 650                 655

Arg Val Pro Asp Ser Ala Asp His Glu Ala His Ser Pro Arg Ser Pro
            660                 665                 670

Glu Ser Tyr Trp Gly Pro Gln Ala Gly Ser Gln Gly Ala Glu Asp Lys
        675                 680                 685

Asp Cys Gln Val Val Gly Cys Met Leu Pro Asn Gly Ser Glu Met Ala
    690                 695                 700

Met Arg Arg Met Glu Ser Tyr Val Gly Asp Arg Asp Asn Leu Arg Gly
705                 710                 715                 720

Ser Ala Ala Phe Ala Gly Asp Gly Arg Thr Gln Ala Glu Gly Leu Ser
```

-continued

```
                725                 730                 735

Pro Gln Cys Glu Pro Asn Ala Lys Arg Arg Arg Leu Gln Ala Gly Gly
            740                 745                 750

Asp Gly Ser Asn Gly Gly Leu Glu Ala Ser Gly Pro Glu Arg Pro Phe
        755                 760                 765

Pro Gly Ser Gln Met Leu Gln Pro Ser Asp Glu Trp Ala Arg Asn Gly
    770                 775                 780

Gln Arg Ala Phe Ala Val Gln Pro Gly Thr Gly Gly Arg Thr Phe Met
785                 790                 795                 800

Asn Gly Gly Phe Arg Gln Pro Gly Pro Glu Asp Ala Arg Gln Pro Leu
                805                 810                 815

Leu Leu Ser Ser Ala Pro Tyr Ser Pro Pro Ser Val Phe Pro Ala Ala
            820                 825                 830

Pro Pro His Leu Ser His Ala Val Arg Leu Pro Pro Gly Ser Ser Asp
        835                 840                 845

Ala Ala His Arg Thr Pro Met Ser Gly Ala Ala Gly Cys Ala Ser Pro
    850                 855                 860

Val Ala Ser Ala Phe Arg Lys Glu Ala Glu Ala Ser Glu Trp Pro Ser
865                 870                 875                 880

Asn Glu Val Tyr Gly Ser Pro Gln Ala Phe Pro Asp Lys Ala Asn Ala
                885                 890                 895

Phe Ala Lys Gly Val Thr Leu Pro Arg Arg Gln Ser Phe Ala Phe Ser
            900                 905                 910

Asp Ala Gly Leu Pro Thr Pro Thr Thr Ser Pro His His Gly Ser Tyr
        915                 920                 925

Cys Ala Ser Thr Ile Ala Ser Ser Ser Pro Lys Ser Ala Ser Pro Val
    930                 935                 940

Ser Gln Ser Gly Cys Phe Pro Cys Asp Phe Tyr Pro Ala Thr Ala His
945                 950                 955                 960

Tyr Ser Gly Pro Gly Val Glu Thr Pro Ser Asp Val Ser Ser Phe Val
                965                 970                 975

Pro Ala Pro Ala Glu Thr Ala Glu Gln Gln Ile His Gly Ala Gly Gln
            980                 985                 990

Ala Ala Val Lys Thr Pro Glu Ser  Gly Leu His Met Pro  Ser Ser Gly
        995                 1000                 1005

Trp Pro  Gln Gln Ala Ser Val  Pro Gly Ala His Gly  Ala Glu Phe
    1010                 1015                 1020

Tyr Ala  Ser Arg Ala Phe Ala  Asn Gly Ala His Ala  Pro Ser Leu
    1025                 1030                 1035

Ser Leu  Arg Pro Ser Trp Arg  Tyr Pro Gly Gly Glu  Arg Ser Glu
    1040                 1045                 1050

Gly Asp  Leu Thr Thr Gln Glu  Gln Asn Ala Pro Ala  Gly Ala Ser
    1055                 1060                 1065

Pro Ser  Ser Pro Val Trp Ser  Gly Asn Thr Gly Val  Cys Thr Thr
    1070                 1075                 1080

Glu Gly  Cys Gly Val Trp Leu  Glu Asn Arg Gln Ala  Ala Gly Ser
    1085                 1090                 1095

Val Glu  Gly Ala Ala Asp Pro  Gly Val Gln Gly Ser  Ala Cys Met
    1100                 1105                 1110

Gln Gly  Lys Pro Gln Glu Gly  Gly Arg Cys Ser Pro  Glu Pro Ala
    1115                 1120                 1125
```

-continued

Leu Gly Val Arg Arg Pro Ala Glu Phe Ala Gly Ala Pro Val Gly
1130 1135 1140

Ala Cys Arg Ala Val Glu Asp Arg Thr Met Thr Gly Glu Arg Gly
1145 1150 1155

Ala Trp Gly Asn Glu Ala Arg Arg Glu Thr Val Thr Gly Asp Gln
1160 1165 1170

Glu Cys Cys Gly Asp Gln Ala Arg Asp Pro Met Val Phe Ser His
1175 1180 1185

Met Gly Ser Arg Ala Glu Leu Ser Gly Phe Asp Asp Gly Ser Glu
1190 1195 1200

Leu Pro Pro Ala Ser Pro Leu Asn Glu Cys Met His Pro Leu Gly
1205 1210 1215

Lys Pro Gly Ser Arg Ile Phe Pro Glu Phe Gly Ala Trp Pro Gly
1220 1225 1230

Ser Pro Pro His Glu Gly Ser Phe Val Gln Glu Phe Asp Ile Phe
1235 1240 1245

Lys Glu Asn Gly Glu Gly Ala Ala Gly Ala Val Asp Asp Ala Met
1250 1255 1260

Ala Leu Trp Pro Asn Gly Gly Ala Phe Gly Gln Arg Thr Asp Pro
1265 1270 1275

Leu Ala His Glu Glu Glu Lys Glu Gly Glu Leu Trp Lys Gly Gln
1280 1285 1290

Pro Thr Pro Phe Cys Ser Ser Pro Ala Leu Trp Cys Val Cys Pro
1295 1300 1305

Val Glu His Thr Arg Glu Phe Asp Val Met Asp Met Val Thr Leu
1310 1315 1320

Pro Asp Leu Ser His Thr Ala Gly Pro Val Ser Arg Pro Leu Pro
1325 1330 1335

Asn Ala Pro Leu Cys Gly Gly Cys Val Val Ala Gly Val Gly Glu
1340 1345 1350

Ala Gln Ala Gly Asp Gly Glu Ser Lys Gln Gly Ala Lys Leu Ala
1355 1360 1365

Pro Asp Ser Gln His Leu His Gly Gly Ala Ala Asn Pro Gly Ala
1370 1375 1380

Val Gly Lys Leu Val Thr Asp Glu Thr Ala Gln Thr Ser Gly Arg
1385 1390 1395

Glu Gln His Pro Gly Glu Gly Asp Ser Thr Glu Gln Arg Leu Ser
1400 1405 1410

Gly Leu Ala Ala Arg Ala Thr Pro Gln Arg Glu Thr Lys Arg Pro
1415 1420 1425

Gly Pro Ser Arg Arg Thr Glu Gly Glu Leu
1430 1435

<210> SEQ ID NO 15
<211> LENGTH: 3817
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Asp Phe Glu Arg Gly Glu Ser Pro Gly Asp Ser Arg Gly Ser Val
1 5 10 15

Ala Phe Leu His His Thr Glu Lys Leu Glu Arg Leu Pro Gly Thr Gly

-continued

```
            20                  25                  30

Glu Thr Thr Ile Arg Gly Met Ser Phe Thr Pro Pro Tyr Ile Cys Met
        35                  40                  45

Glu Arg Pro Pro Arg Ala Asn Cys Glu Ala Leu Arg Leu Lys Ser Pro
    50                  55                  60

Pro Glu Asn Arg Ala Phe Ser Ser Arg Ser Glu Ser Pro Ser Pro Thr
65                  70                  75                  80

Pro Phe Ala Arg Glu Cys Ala Ser Leu Gly Leu Val Trp Gly Asp Glu
                85                  90                  95

Gly Thr Arg Ala Gly Leu Leu Arg Thr Arg Leu Phe Thr Pro Pro Asp
            100                 105                 110

His Thr Pro His Leu Leu Ala Glu Thr Gly Ala Ser Cys Leu Glu Asp
        115                 120                 125

Leu Phe Pro Gly Thr Val Pro Gln Leu Leu Ser His Leu Pro Ser Pro
    130                 135                 140

Pro Pro Val Pro Gly Val Ala Arg Ala Ser Arg Ser Ser Ser Pro Leu
145                 150                 155                 160

Ala Gly Gly Ser Ser Leu Ala Cys Ala Ser Pro Trp Pro Arg Ser Ala
                165                 170                 175

Thr Pro Phe Phe Ala Ala Asn Met Pro Ala Leu Leu Pro Gly Arg Gly
            180                 185                 190

Pro Met Arg Val Thr Lys Trp Leu Asp Gly Gln Val Ser Asp Pro Gln
        195                 200                 205

Ser Asp Ser Cys Leu Arg Gly Gly Ala Ser Arg Val Glu Arg Ala Ala
    210                 215                 220

Ala Leu Leu Cys Gly Arg Ser Glu Glu Glu Gln Glu Arg Glu Arg Ser
225                 230                 235                 240

Val Asp Glu Arg Arg Leu Arg Lys Ala Ile Gly Val Thr Asp Glu Asp
                245                 250                 255

Glu Ser Glu Arg Glu Arg Glu Thr Glu Gly Gly Val His Glu Arg Leu
            260                 265                 270

Ser Arg Cys Ala Ala Ala Thr Ala Ala Asp Arg Ala Asn Asn Leu Leu
        275                 280                 285

Gly Leu Gly Val Glu Arg Gly Pro Glu Val Ala Gly Gly Arg Leu Gly
    290                 295                 300

Gly Tyr Trp Thr Thr Glu Ser Glu Val Tyr Pro Gln Arg Ile Gly Glu
305                 310                 315                 320

Leu Glu Gly Glu Gly Leu Gly Ser Pro Asp Pro Val Ala Ala Ser Ala
                325                 330                 335

Leu Val Thr Ala Val Gln Asp Ser Arg Glu Asn Leu Asn Cys Leu Thr
            340                 345                 350

Gly Val Leu Thr Thr Leu Arg Leu Ser Ser Arg Asp Ser Glu Gly Asp
        355                 360                 365

Phe Asp Leu Pro Leu Phe Val Gln Ser Arg Lys Trp Arg Ala Lys Tyr
    370                 375                 380

Asn Arg Arg Ser Leu Asp Leu Lys Gly Thr Val Ala Arg Ser Lys Ala
385                 390                 395                 400

Leu Gly Tyr Pro Ala Gly Leu Gln Ile Pro Glu Thr Tyr Arg Asp Leu
                405                 410                 415

Lys Asn Cys Met Gln Arg Pro Pro Ser Ile Asp Ala Ala Asp Ser Arg
            420                 425                 430
```

-continued

```
Ala Trp Arg Ser Ala Glu Ala Pro Arg Ala Ala Lys Lys Val Phe Ser
        435                 440                 445

Glu Gly Arg Arg Ala Thr Asp Arg Asp Glu Gln Val Ala Phe Val Glu
    450                 455                 460

Asp Glu Val Thr Glu Gln Leu Leu Phe Asn Ala Asn Ala Ala Val Glu
465                 470                 475                 480

Gly Thr Thr Leu Tyr Asn Asn Leu Leu Cys Lys Tyr Gly Leu Glu Thr
                485                 490                 495

Arg Cys Phe Ser Thr Ser Ser Ala Pro Gly Asn Thr Ala Phe Glu Ser
            500                 505                 510

Arg Leu Ala Arg Ser Asp Ala Asp Pro Thr Ala Ser Ser Gln Ser Ala
        515                 520                 525

Ser Ala Leu Ser His Ala Ala Val Ser Pro Ser Leu Ala Ser Ala Leu
    530                 535                 540

Pro Val Ser Ser Leu Leu Leu Glu Asp Ala Ala Asp Ala Val Gly Asp
545                 550                 555                 560

Arg Ser Glu Leu Glu Thr Gly Ser Gln Ala Glu Ala Ala Ile Pro Thr
                565                 570                 575

Ser Glu Ala Ser Cys Met Arg Arg Glu Lys His Val Gly Glu Glu Ser
            580                 585                 590

Arg Ala Asp Lys Gly Ala Phe Leu Arg Ser Ala Ser Asp Ser Thr His
        595                 600                 605

Ala Glu Glu Asp Gly Leu Ser Gly Gly Lys Asp Ala Ser Ser Arg Glu
    610                 615                 620

Gly Gly Ser Glu Glu Arg Glu Glu Ala Ala His Glu Ala Ala Asp Ser
625                 630                 635                 640

Leu Trp Ser Leu Val Leu Asn Arg Asn Ile Ala Ala Leu Pro Gly Phe
                645                 650                 655

Met Thr Val Gly Arg Tyr Glu Cys Asp Leu Leu Pro Lys Arg Ser Ala
            660                 665                 670

Phe Ser Arg Lys Gln Leu Ala Gly Leu Val Ala Gly Ser Arg Pro Leu
        675                 680                 685

Pro Val Leu Pro Ser Ser Ser Asp Thr Pro Gly Ser Ala Ser Thr Glu
    690                 695                 700

Leu Leu Ala Glu Arg Val Ala Cys Ala Leu Thr Leu Asp Glu Gly Glu
705                 710                 715                 720

Ala Trp Asn Pro Ser Asp Ala Ser Asp Leu Asp Asp Phe Leu Glu Ser
                725                 730                 735

Ser Cys Ala Pro Asn Ala Leu Arg Arg Gly Arg Gln Ala Val Val Pro
            740                 745                 750

Val Arg Gly Ala Arg Arg Arg Arg Gly Ala Asp Leu Gly Leu Ser Pro
        755                 760                 765

Pro Pro Ser Ser Pro Ala Val Arg Cys Arg Ser Leu Val Arg Trp Ser
    770                 775                 780

Gln Gln Arg Pro Phe Phe Ser Asn Val Ser Ala Cys Ala Gly Ala Ala
785                 790                 795                 800

Asp Ser Arg Arg Glu Glu Trp Lys Asp Ala Gly Lys Val Ala Lys Pro
                805                 810                 815

Gly Ser Glu Ser Ala Leu Thr Ser Arg Asp Leu His Ala Ser Thr Gly
            820                 825                 830
```

-continued

```
Leu Val Asn Ala Ala Leu Asp Ser Ser Glu Gln Lys Ser Gly Glu Arg
        835                 840                 845

Glu Ser Ser Leu Ser Pro Gln Glu Arg Ile Leu Thr Gln Val Lys Lys
    850                 855                 860

Glu Leu Glu Asp Glu Arg Val Arg Glu Lys Gln Thr Ile Arg Asp Lys
865                 870                 875                 880

Asp Ser Glu Lys Gly Gln Gly Gly Glu Ser Asn His His Met Pro Gly
                885                 890                 895

Thr Ala Asn Gly Gln Arg Thr Pro Asn Glu Gly Glu Ala Pro Met Glu
            900                 905                 910

Thr Glu Glu Ala Pro Thr Leu Glu Pro Ser Asn Gly Met His Arg Asp
        915                 920                 925

Gly Gln Asp Ala Gly Ala Arg Met His Ser Ser Ser Thr Arg Ala Leu
    930                 935                 940

Glu Gly Ala Val Glu Asp Glu Pro Lys Val Thr Leu Pro Asp Lys Asp
945                 950                 955                 960

Glu Pro His Ala Ser Ala Leu Cys Gly Glu Arg Glu Lys Gln Arg Gln
                965                 970                 975

Ser Phe Phe Ser Ser Val Ser Ser Arg Glu Asp Ala Gln Asp Glu Asp
            980                 985                 990

Ser Arg Trp Cys Val Ala Gly Gly  Met Tyr Asn Gly Trp  Lys Gly Thr
        995                 1000                 1005

Tyr Asp  Val Trp Ile Tyr Arg  Arg Val Ser Ala Ala  Leu Arg Glu
    1010                 1015                 1020

Gly Lys  Gly Glu Glu Glu Lys  Arg Arg Glu Gly Glu  Lys Arg Lys
    1025                 1030                 1035

Thr Gly  Lys Gly Lys Gln Ser  Val His Thr Ala Ser  Leu Gly Ala
    1040                 1045                 1050

Gly Gly  Ala Gln Gly Leu Ser  Pro Gly Glu Thr Gln  Ala Ser Gly
    1055                 1060                 1065

Leu Ala  Pro Gly Ser Thr Pro  Leu Gly Ser Ala Gly  Thr Leu Ser
    1070                 1075                 1080

Ala Gly  Arg Asn Gly Glu Glu  Thr Arg Glu Ser Thr  Gly Ser Pro
    1085                 1090                 1095

Ala Gly  Ala Phe Ala Ser Ser  Ser Ser Leu Ala Ala  Lys Gly Gln
    1100                 1105                 1110

Asn Gly  His Ala Ser Val Glu  Asp Leu Lys Thr Gln  Lys Glu Glu
    1115                 1120                 1125

Ser Leu  Gly Cys Val Leu Ser  Ala Ser Ala Leu Pro  Leu Asn Pro
    1130                 1135                 1140

His Ser  Gly Glu Thr Arg Glu  Asp Ser Ala Gly Arg  Asp Glu Glu
    1145                 1150                 1155

Lys Gly  Glu Glu Arg Glu Arg  Asp Glu Asn Glu Pro  Pro Leu Tyr
    1160                 1165                 1170

Glu Trp  Arg Val Lys Arg Phe  Ser Ala Leu Ile His  Gly His Glu
    1175                 1180                 1185

Lys Ala  Ser Arg Leu Ala Cys  Lys Tyr Cys Val Tyr  Leu Glu Arg
    1190                 1195                 1200

Phe Gly  Arg Ile Arg Gly Arg  Leu Ser Ile Cys Ser  Thr Cys Cys
    1205                 1210                 1215

Arg Asp  Ala Cys Ser Gly Cys  Met Pro Ser Lys Lys  Arg Ala Ala
```

-continued

```
    1220                1225                1230

Gly Ala  Asp Phe Ser Pro His  Cys Arg Asn Gly Arg  Asp Ala Gly
    1235                1240                1245

Val Gly  Gly Ala Gly Arg Ala  Pro Lys Arg Arg Val  Gln Ala Lys
    1250                1255                1260

Lys Gly  Ala Ala Gly Ala Ala  Gly Val Cys Gly Asp  Arg Ala Arg
    1265                1270                1275

Lys Gly  Lys Gly Glu Asp Glu  Pro Glu Arg Asp Gly  Leu Asp Arg
    1280                1285                1290

Arg Glu  Glu Gly Gly Thr Pro  Ser Ser Lys Gln Thr  Ala Glu Arg
    1295                1300                1305

Arg Gly  Ala Ala Lys Lys Glu  Gly Arg Glu Glu Asp  Asp Arg Val
    1310                1315                1320

Asp Gly  Lys Gly Thr Ser Leu  Ser Leu Glu Asn Asn  Ser Phe Glu
    1325                1330                1335

Ser Ser  Cys Pro Ala Met Arg  Ser Ser Leu Arg Ala  Ser Phe Glu
    1340                1345                1350

Val Lys  Gly Pro Leu Ser Pro  Ser Ser Ala Asp Asp  Arg Pro Asn
    1355                1360                1365

Glu Gly  Ala Ala Gly Arg Gly  Ala Pro Pro Gly Ser  Glu Gly Pro
    1370                1375                1380

Ser Arg  Asp Leu Ala Leu Arg  Ser His Ser Phe Ser  Ser Ala Ser
    1385                1390                1395

Ser Ser  Arg Lys Ser Ala Lys  Asn Ala Ala Glu Ser  Leu Arg Arg
    1400                1405                1410

Ile Ala  Gly Pro Leu Phe Arg  Ser Ser Gly Asp Leu  Thr Ala Ser
    1415                1420                1425

Gln Leu  Gly Ala Glu Thr Glu  Glu Ser Asp Val Leu  Gln Asp Val
    1430                1435                1440

Phe Glu  Leu Tyr Ser Glu Ala  Gly Glu Ala Trp Glu  Thr Cys Thr
    1445                1450                1455

Thr Pro  Val Ser Phe Ser Pro  Ser Leu Ser Val Ala  Ser Arg Asp
    1460                1465                1470

Thr Leu  Val Val Leu Gly Gly  Ser Gln Thr Thr Ala  Val Ala Arg
    1475                1480                1485

Leu Asp  Ser Gly Lys Met Ser  Glu Ala Val Arg Arg  Ser Ser Asn
    1490                1495                1500

Ala Leu  Ser Ala Ala Ala Ser  Ser Phe Pro Lys Gly  Lys Gly Phe
    1505                1510                1515

Gly Gly  Ala Ser Lys Lys Thr  Asp Ser Val Thr Leu  Ser Phe Leu
    1520                1525                1530

Ala Arg  Val Cys Arg Asn Leu  Arg Met Phe Leu Leu  Leu Cys Gln
    1535                1540                1545

His Asn  Thr Val Ala Gly Gly  Leu Pro Gly Asp Ser  Lys Cys Val
    1550                1555                1560

Cys Arg  Ala Gln Ser Gly Pro  Gly Gly Ala Gly Leu  Ala Gly Ala
    1565                1570                1575

Asp Gly  Arg Ala Pro Gly Asp  Leu Gly Asp Ser Lys  Gly Thr Ala
    1580                1585                1590

Ile Ala  Arg Gly Pro Gly Gly  Ala Ala Gly Arg Ala  His Gly Ser
    1595                1600                1605
```

-continued

```
Glu Pro  Trp Ala Ser Pro Asn  Tyr Thr Gly Gly Pro  Phe Phe Pro
    1610                 1615                 1620

Pro Ala  Gly Ser Ala Pro Ser  Gly Trp Pro Pro Val  Ala Gln Ala
    1625                 1630                 1635

Asn Ser  Arg Pro Glu Val Leu  Ser Ala Ile Gln Gly  Ala Gln Gly
    1640                 1645                 1650

Gln Gly  Pro His Val Ala His  Ser Leu Arg Leu Ala  Ala Ser Leu
    1655                 1660                 1665

Ser Pro  Ala Gln Thr Thr Ser  Glu Ser Phe Leu Ala  Pro Glu Ser
    1670                 1675                 1680

Phe Ala  Ala Gly Val Arg Pro  Leu Leu Glu Gly Ser  Leu Ser Val
    1685                 1690                 1695

Leu Ile  Pro Glu Glu Pro Gln  Val Gly Leu Gly Pro  Ser Ala Gly
    1700                 1705                 1710

Gln Gln  Leu Ala Ser Ser Ser  Leu Ser Pro Gly Val  Ser Val Lys
    1715                 1720                 1725

Ala Glu  Pro Ser Ser Tyr Phe  Gln Ser Ala Gln Gly  Thr Cys Arg
    1730                 1735                 1740

Asp Val  Ser Ala Gly Ala Arg  Thr Ala Met Pro Ser  Ser Phe Leu
    1745                 1750                 1755

Glu Gln  Gly Arg Pro Gly Ala  Ala Pro Gly His Ala  Pro Ser Gly
    1760                 1765                 1770

Val Gly  Arg Cys Pro Pro Gln  Gly Arg Asp Ala Ser  Pro Gly Cys
    1775                 1780                 1785

Pro Gly  Phe Arg Thr Pro Pro  Ala Gly Phe Asp Gly  Pro Ser Ser
    1790                 1795                 1800

Ser Gly  Ala Gly Tyr Ser Leu  Ser Pro Tyr Gly Tyr  Pro Gly Thr
    1805                 1810                 1815

Glu Ile  Ser Pro His Leu Ala  Pro Phe Phe Pro Glu  Pro Tyr Arg
    1820                 1825                 1830

Arg Phe  Arg Glu Ser Arg Gly  Gly Pro Ala Trp Ile  His Ser Pro
    1835                 1840                 1845

Gly Ser  Val Asp Val Pro Ser  Ser Gly Leu Gln Ser  Pro Phe Thr
    1850                 1855                 1860

Gly Phe  His Ala Thr Ser Gly  Ser Ser Pro Pro Arg  Leu Gly Pro
    1865                 1870                 1875

Ser Glu  Gly Ala Ser Phe Ala  Glu Ala Ser Pro Arg  Ala Leu Ala
    1880                 1885                 1890

Gly Asp  Leu Gly Pro Ala Gly  Phe Leu Gly Ala Ser  Ala Gly Ala
    1895                 1900                 1905

Pro Ala  Ala Glu Gly Arg Gly  Pro Leu Phe Asp Pro  Ser Ala Glu
    1910                 1915                 1920

Gly Glu  Gly Lys Phe Ala Pro  Asp Ala Gly Ala Leu  Gly Thr Val
    1925                 1930                 1935

Glu Gly  Pro Ala Asp Cys Arg  Thr Gln Gly Glu Thr  Gly Arg Thr
    1940                 1945                 1950

Ala Asp  Glu Asp Glu Lys Lys  Lys Ala Lys Lys Ala  Lys Lys His
    1955                 1960                 1965

Gly Arg  Ile Thr Asp Ile Glu  Glu Arg Leu Ala Arg  Glu Glu Pro
    1970                 1975                 1980
```

-continued

```
Tyr Asp  Val Val Glu Glu Gly  Asp Asp Pro Glu Pro  Thr Arg Gln
    1985                 1990                 1995

Leu Gly  Leu Glu Ala Thr Glu  Lys Glu Gln Asp Val  Pro Arg Ser
    2000                 2005                 2010

Gly Asp  Ser Lys Ser Pro Asp  Gln Asp Ser Pro Gly  Gln Pro Ala
    2015                 2020                 2025

Asp Ile  Met His Gly Tyr Phe  Lys Ala Arg Val Arg  Asn Arg Arg
    2030                 2035                 2040

Val Lys  Asp Gly Leu Leu Leu  Arg Met Thr Ala Val  Leu Val Gly
    2045                 2050                 2055

Lys Gly  Phe Tyr Asp Leu Glu  Thr Val Glu Pro Gly  Ala Pro Arg
    2060                 2065                 2070

Arg Arg  Gly Gly Trp Gly Glu  Ser Gly Glu Glu Glu  Glu Glu Ser
    2075                 2080                 2085

Glu Thr  Lys Tyr Leu Phe Ser  Asn Pro Ala Ser Gln  Lys Pro Cys
    2090                 2095                 2100

Asp Phe  Ile Leu Tyr Phe Asp  Thr Arg Glu Asn Arg  Asp Ala Ser
    2105                 2110                 2115

Val Ala  Ile Leu Asn Gln Ala  Leu Pro Ala Pro Pro  Pro Arg Leu
    2120                 2125                 2130

Pro Pro  Lys Asn Gly Glu Ser  Gln Ala Arg Arg Thr  Leu Arg Gln
    2135                 2140                 2145

Leu Tyr  Asp His Phe Leu Glu  Pro Lys Cys Gln Cys  Leu Glu Asp
    2150                 2155                 2160

Lys Thr  Leu Lys Val Lys His  Gly Val Ile Asn Leu  Leu Gly Phe
    2165                 2170                 2175

Pro Arg  Leu Tyr Val Lys Leu  His Cys Ser Met Ser  Trp Asp Glu
    2180                 2185                 2190

Arg Leu  Ser Leu Phe Ser Ser  Phe Leu His Trp Leu  Cys Arg Glu
    2195                 2200                 2205

Asp Asp  Ser Gln Pro Pro Pro  Trp Ser Ser Pro Glu  Leu His Pro
    2210                 2215                 2220

Glu Leu  Leu Ala Tyr Leu Val  Asp Leu Gly Arg Lys  Gly Phe Ala
    2225                 2230                 2235

Ser Gly  Gly Ala Ala Thr Thr  Ala Val Val Asn Ala  Pro Asp Leu
    2240                 2245                 2250

Pro Leu  Asp Asp Ser Ala Leu  Ser Lys Lys Asn Ala  Ala Leu Ile
    2255                 2260                 2265

Arg Ala  Tyr Met Gln Gln Asp  Thr Gly Ala Ser Gly  Pro Ser Gly
    2270                 2275                 2280

Ser Val  Gly Ala Thr Ser Ser  Asp Pro Glu Ala Pro  Arg Lys Asp
    2285                 2290                 2295

Asp Glu  Ala Glu Glu Gly Glu  Lys Asp Asp Ser Asn  Ala Ala Leu
    2300                 2305                 2310

Val Glu  Gly Pro Ala Pro Glu  Thr Ser Gly Asp Ser  Thr Gly Ala
    2315                 2320                 2325

Ala Gln  Pro Cys Gly Lys Gly  Arg Glu Glu Arg Glu  Ala Gly Asp
    2330                 2335                 2340

Lys Arg  Gly Pro Gly Asn Glu  Gly Cys Gly Lys Gly  Asp Gly Phe
    2345                 2350                 2355

Gly Ser  Pro Val Ala Val Ala  Gly Thr Thr Ala Ala  Pro Gly Glu
```

-continued

```
    2360                2365                2370

Thr Glu  Ser Val Ser Cys Pro  Ser Ser Thr Ser Gly  Gly Gly Ala
    2375                2380                2385

Ser Ser  Ala Leu Ser Ser Gly  Pro Ser Asp Ser Ala  Ala Ala Pro
    2390                2395                2400

Asp Gly  Cys Glu Ser Ser Pro  Val Ala Leu Glu Ser  Ala Ser Leu
    2405                2410                2415

Leu Ser  Phe Ser Pro Ser Ala  Ala Arg Ala Glu Val  Leu Thr Val
    2420                2425                2430

Pro Gly  Val Gly Leu Val Asn  Phe Ser Leu Pro Asp  Gly Val Lys
    2435                2440                2445

Phe Asp  Lys Ser Lys Leu Ala  Phe Arg Cys Tyr Trp  Arg Glu Gly
    2450                2455                2460

His Ala  Gly Val Val Thr Val  Gly Ala Gly Ala Ala  Val Ser Pro
    2465                2470                2475

Ser Ser  Gly Ala Gly Thr Phe  Val Pro Ser Arg Pro  Thr Val Cys
    2480                2485                2490

Thr Ala  Gln Asn Lys Ser Arg  Thr Phe Ser Cys Arg  Lys Tyr Gly
    2495                2500                2505

Leu Tyr  Gln Ser Arg Val Leu  Ala Leu Gln Ala Arg  Leu Leu Ser
    2510                2515                2520

Glu Leu  Leu Trp Pro Gln Pro  Pro Ser Pro Ala Arg  Leu Arg Val
    2525                2530                2535

Ser Ala  Met Ala Ala Val Val  Tyr Gly Leu Ile Ala  Ala Pro Met
    2540                2545                2550

Pro Phe  Thr Asp Pro Trp Gln  Ala Val Cys Gly Val  Ser Val Ala
    2555                2560                2565

Glu Asp  Ala Leu Arg Gln Arg  Arg Glu Val Trp Lys  Asn Leu Leu
    2570                2575                2580

Asp Pro  Arg Gln Arg Arg Pro  Ala Pro Ala Pro Ile  Ser Gln Leu
    2585                2590                2595

Ser Leu  Pro Pro Val Ser Gly  Pro Pro His Ala Ser  Ser Ala Thr
    2600                2605                2610

Gln Glu  Leu Pro Asn Arg Pro  Gly Thr Pro Trp Pro  Gly Gln Glu
    2615                2620                2625

Thr Val  Cys Gly Ala Arg Gly  Pro Ala Pro Gly Leu  Ala Ser Ala
    2630                2635                2640

Trp Ala  Thr Tyr Gly Asn Pro  Gly Asp Arg Asp Ala  Ala Glu Pro
    2645                2650                2655

Gln Ser  Thr Tyr Val Gly Arg  Gly Pro Ala Gly Ala  Glu Gly Pro
    2660                2665                2670

Gly Gly  Gly Ile Ala Val His  Arg Glu Trp Ala Arg  Asn Ser Gly
    2675                2680                2685

Ser Glu  Ala Ala Gln Pro Cys  Gln Phe Gly Arg Ala  Val Glu Arg
    2690                2695                2700

Pro Val  Pro Gly Pro Gln Ser  Ser Leu Gly Pro Gly  Gly Asp Asn
    2705                2710                2715

Arg Gly  Asp His Met Ala Tyr  Asp Gln Ser Pro Ala  Gly Pro Ala
    2720                2725                2730

Ser Asn  Ala Pro Gly Pro Thr  Pro Pro Phe Val Gly  Pro Phe Ser
    2735                2740                2745
```

-continued

```
Pro Gly  Leu Val Leu Arg His  Gly Pro Pro Ala Phe  Ser Gln Asp
    2750                 2755                 2760

Pro Ser  Leu His Arg Pro Pro  Phe Ala Ala Gly Thr  Gly Pro Ala
    2765                 2770                 2775

Gly Gln  Arg Leu Ala Ser Asp  Ser Pro Tyr Pro Leu  Lys Asn Glu
    2780                 2785                 2790

Ala Ser  Pro Gln Leu Ala Met  Ala His Ala Pro Gly  Phe Glu Asn
    2795                 2800                 2805

Ser Asp  Gly Phe Gln Gly Glu  Gln Pro Leu Ala Lys  Gln Arg Lys
    2810                 2815                 2820

Ile Glu  Gly Ala Ser Asp Arg  Pro Val Pro Asp Glu  Gly Gln Val
    2825                 2830                 2835

Leu Gly  Thr Ile Ser His Gly  Lys Ser Pro Ala Ala  Arg Pro Val
    2840                 2845                 2850

Asp Gly  Asp Phe Ala Pro Asp  Gly Arg Ser Pro Leu  Phe Ser Gln
    2855                 2860                 2865

Asp Ala  Ser Gly Val Gly Gly  Gly Arg Pro Ser Gly  Val Gly Gly
    2870                 2875                 2880

Gln Leu  Ala Ala Gly Gly Lys  Gly His Phe Ala Thr  Ala Pro Phe
    2885                 2890                 2895

Gly Ser  Gly Thr Leu Pro Thr  Thr Arg Gly Pro Ser  Gln Pro Gly
    2900                 2905                 2910

Gly Asp  Gly Leu Ser His Arg  Ser Gly Thr Glu Pro  Ala Ala Ala
    2915                 2920                 2925

Tyr Ser  Ser Pro Ala Gly Ala  Ala Tyr Pro Ser Ala  Ser Asn Ala
    2930                 2935                 2940

Ser Pro  Ile Tyr Gly Ala Ala  Pro Lys Arg Glu Gly  Asp Ser Pro
    2945                 2950                 2955

Phe Gly  Pro Ala Pro Pro Ser  Gly Tyr Cys Arg Pro  Gly Ser Pro
    2960                 2965                 2970

Ala Val  Asp Pro Lys Leu Pro  Gly Ser Val Pro Ser  Ser Gly Asn
    2975                 2980                 2985

Leu Asp  Ser Val Asn Tyr Gly  Ser Phe Phe Pro Gly  Gln Gln Ala
    2990                 2995                 3000

Pro Gln  Gly Asp Gly Arg Ile  Ala Pro Trp Gly Ser  Gly His Val
    3005                 3010                 3015

Gly Ala  Pro Arg Gly Glu Ala  Arg Gly Ser Glu Arg  Val Gly His
    3020                 3025                 3030

Ala Gly  Ala Ser Arg Gly Leu  Thr Gly His Glu Leu  Glu Glu Gly
    3035                 3040                 3045

Gln Gly  Gly Pro Gly Glu Glu  Gly Ala Gly Arg Glu  Arg Gln Arg
    3050                 3055                 3060

Lys Arg  Arg Lys Ser Ala Met  Ser Met Ser Ser Gln  Gly Glu Asn
    3065                 3070                 3075

Thr Pro  Leu Phe Ala Pro Thr  Ser Leu Pro Pro Val  Pro Phe Ala
    3080                 3085                 3090

Ser Gly  Asp Ser Leu Ala Asp  Gly Ser Gly Ser Asp  Phe Gly Gln
    3095                 3100                 3105

Gln Leu  Gly Pro Pro Phe Ser  His Gly Ser His Ala  Pro Pro Phe
    3110                 3115                 3120
```

-continued

```
Pro Glu  Ala Asn Ala Val Gly  Ser Gln His Phe Thr  Ala Asp Asn
    3125                 3130                 3135

Leu Glu  Thr Pro Gly Leu Pro  Ala Glu Leu Gly Gly  Gly Asp Gly
    3140                 3145                 3150

Arg Arg  Gln Ser Gly Ser Thr  His Glu Glu Val Ser  Gly Pro Arg
    3155                 3160                 3165

Ala Gly  Gly Glu Lys Gly Glu  Phe Ser Leu Glu Gly  Ala Pro Gln
    3170                 3175                 3180

Ala Ala  Ala Gln Gln Leu Ser  Ala Glu Thr Leu Thr  Phe Leu Leu
    3185                 3190                 3195

Gly Thr  Asn Val Val Trp Glu  Glu Asn Glu Lys Arg  Trp Arg Val
    3200                 3205                 3210

Gln Val  Arg Pro Pro Ser Pro  Arg Gly Cys Asp Gly  Glu Gly Ala
    3215                 3220                 3225

Asp Gly  Lys Leu Gly Gly Glu  Lys Lys Lys Arg Lys  Arg Asp Gly
    3230                 3235                 3240

Phe Ser  Ala Gly Gly Glu Arg  Arg Arg Ser Ser Thr  Gly Asn Glu
    3245                 3250                 3255

Pro Asp  Asp Gln His Lys Ala  Gly Thr Leu Glu Trp  Val Ser Met
    3260                 3265                 3270

Ala Gln  Leu His Gln Ala Gln  Lys Leu Gln Asn Gln  Leu Val Gly
    3275                 3280                 3285

Lys Met  Glu Arg Gly Lys Gly  Glu Gly Gly Asp Glu  Glu Arg Leu
    3290                 3295                 3300

Gly Gly  Asp Gly Arg Gly Asn  Ile Phe Phe Asp Ala  Asn Gly Ser
    3305                 3310                 3315

Asp Glu  Asn Ala Lys Lys Ala  Ala Leu Leu Lys Ala  Arg Arg Trp
    3320                 3325                 3330

Leu Arg  Arg Arg Ile Val Gln  Gly Gln Ile Leu Val  Thr Gly Leu
    3335                 3340                 3345

Ser Arg  Asp Gly Leu Phe Ser  Ser Arg Pro Asp Glu  Pro Glu Arg
    3350                 3355                 3360

Ser Ser  Ser Val Ser Thr Gly  Ala Phe Thr Gly Ser  Ser Pro Asn
    3365                 3370                 3375

Asp Lys  Pro Thr Asp Leu Asn  Ala Ala Val Pro Pro  Leu Ser Pro
    3380                 3385                 3390

Phe Phe  Ser Pro Ile Pro Phe  Gly Ala Thr Thr Ala  Pro His Arg
    3395                 3400                 3405

Pro Ser  Pro Gly Phe Tyr Pro  Pro Ala Pro Ala His  Pro Thr Glu
    3410                 3415                 3420

Asp Gly  Cys Arg Pro Pro Met  Pro Ala Pro Val Pro  Met His Ala
    3425                 3430                 3435

Pro Gln  Gly Pro Val Asp Ser  Arg Thr Tyr Arg Gly  Ala Arg Pro
    3440                 3445                 3450

Val Tyr  Pro Gly Ser Asp Val  Thr Pro Gln Thr Cys  His Gly Val
    3455                 3460                 3465

Arg Pro  Glu Ser Met Gln Glu  Glu Gly Arg Ala Ala  Leu Leu Ala
    3470                 3475                 3480

Glu Gln  Gly Ser Ala Phe Phe  Val Ser Gly Asp Gly  Lys Gly Asp
    3485                 3490                 3495

Asn Arg  Gly Ala Thr Val Gly  Gln Ile Arg Gln Gly  Thr Val Arg
```

-continued

```
    3500                3505                3510

Val Met  Gln Ser Gln Thr Ala  Ser Gln Ser Leu Asp  Gln Gly Phe
    3515                3520                3525

Asp Leu  Pro His Pro Pro Ala  Pro Gly Pro Ala Tyr  Arg Gly Val
    3530                3535                3540

Pro Val  Gly His Gly Pro Ser  Gly Pro Tyr Tyr Leu  Asn Gly Gly
    3545                3550                3555

Cys Val  Ala Gln Arg Pro Tyr  Ala Thr Phe Ser Asn  Leu Ala Gly
    3560                3565                3570

Pro Val  Gln Gly Ser Phe Pro  Pro Leu Glu Phe Ser  Asn Gly Gly
    3575                3580                3585

Leu Pro  Thr Thr Ala Leu Gly  Arg Arg Gly Ser Asp  Ser Gly Pro
    3590                3595                3600

Gln Gly  Ala Gly Arg Asn Ala  Ser Gln Met Gln Pro  Gly Phe Ala
    3605                3610                3615

Ser Arg  Pro His Gly Pro Glu  Arg Leu Gly Arg Glu  Ser Ala Pro
    3620                3625                3630

Gln Ser  Gly Ala Pro Pro Gly  Phe Ser Pro His Ala  His Gly Arg
    3635                3640                3645

Gly Glu  Arg Asp Arg Pro Ser  Phe Ser Gly Ala Thr  Thr Met Pro
    3650                3655                3660

Leu Ala  Ser Leu Thr Ala Phe  Ser His Pro Ala Ala  Gly Pro Met
    3665                3670                3675

Phe Val  Gly Thr Glu Gly Arg  Gly Gln Gln Gly Asp  Ile His Pro
    3680                3685                3690

Asn Leu  Cys Gly Val Ala Pro  Val Gly Gly Pro Arg  Gly Pro Ala
    3695                3700                3705

His Ala  Pro Met Pro Ala Tyr  Gly Pro Gly Gly Ala  Ala Gly Pro
    3710                3715                3720

Pro Arg  Asp Asp Arg Arg Ala  Glu Gly Gly Ala Pro  Gly Val Ser
    3725                3730                3735

His Ser  Asp Ile Phe Leu Ala  Asn Asp Arg Arg Leu  His Pro Glu
    3740                3745                3750

Met Cys  Leu His Ser Ala Pro  Ser Trp Gly Pro Ala  Gly Thr Phe
    3755                3760                3765

Ala Ser  Pro Asp Asn Arg Gln  Asn Ala Glu Pro Trp  Pro Ala Ala
    3770                3775                3780

His Ala  Ser Ser Asn Asn Phe  Phe Asp Tyr Thr Gly  Val Asn Met
    3785                3790                3795

Pro Ala  Ala Gly Pro Pro Ile  Gln Leu Asp Trp Ser  Lys Val Arg
    3800                3805                3810

Gly Ala  Gly Gly
    3815


<210> SEQ ID NO 16
<211> LENGTH: 432
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

Met Asp Arg Ala Gly Leu Leu Phe Leu Arg Gly Ala Ala Gly Pro Gly
1               5                   10                  15
```

-continued

```
Pro Leu Lys Cys Phe Gly Pro Arg Val Glu Ala Phe Ser Gly Ser Ile
            20                  25                  30

Ser Leu Leu Ser Leu Asp Ser Arg Gly Pro Thr Pro Phe Arg Thr Pro
        35                  40                  45

Phe His Thr Thr Ser Ala Leu Ser Lys Ser Arg Gln Pro Pro Lys Glu
    50                  55                  60

Ser Pro Glu Ser Ala Ala Ala Cys Thr Phe Ser Pro Leu Phe Pro Ser
65                  70                  75                  80

Pro Val Arg Ala Ser Pro His Arg Asn Leu Leu Gly Ala Arg Val Ser
                85                  90                  95

Val Pro Cys Lys Pro Leu Ala Cys Val Gly Ala Pro Lys Arg Arg His
            100                 105                 110

Gly Glu Thr Ser Asp Gly Phe Ser Ser Arg Ala Ala Val Ala Ala Glu
        115                 120                 125

Ala Leu Pro Pro Trp Pro Ser Asp Phe Leu Gln Ser Glu Glu Ile Ala
    130                 135                 140

Val Asp Ser Pro Gln Lys Pro Thr Gly Phe Ser Arg Pro Ser Asn Ala
145                 150                 155                 160

Arg Val Ser Pro Ala Pro Asn Ala Trp Glu Ala Ala Ala Val Phe Arg
                165                 170                 175

Arg Leu His Ala Phe Asp Ser Gly Leu Arg Gly Asp Ala Ser Gly Ala
            180                 185                 190

Phe Ala Ala Ser Ala Thr Cys Gly Cys Leu Ala Ala Ala Ser Arg Arg
        195                 200                 205

Asn Pro Cys Leu Pro Ala Tyr Gln Leu Ser Trp Asn Leu Leu Gln Ala
    210                 215                 220

Arg Met Phe Gly Gly Arg Ala Gly Gly Leu Lys Arg Arg Lys Pro Arg
225                 230                 235                 240

Arg Asp Pro Gly Arg Val Ile Gln Ser Gly Met Gly Arg Arg Gln Glu
                245                 250                 255

Phe Phe Trp Pro Glu Lys Ala Arg Arg Thr Arg Val Pro Leu Tyr Gln
            260                 265                 270

Asn Ser Arg Pro Asn Leu Val Tyr Asp Gln Arg Phe Arg Arg Phe Met
        275                 280                 285

Cys Met Trp Tyr Ala Asn Gly Val Gln Val Phe Arg Pro Phe Ser Cys
    290                 295                 300

Arg Gly Arg Arg Gly Gly Arg Gly Lys Glu Gly Leu Pro Asp Gly Leu
305                 310                 315                 320

Gly Ile Gly Arg Gly Ser Gly Thr Trp Glu Arg Ala Arg Ala Lys Ala
                325                 330                 335

Val Val Leu Leu Lys Gln Leu Gln Arg Gln Gly His Leu Asp Arg Leu
            340                 345                 350

Ala Lys Pro Asp Val Thr Arg Ser Gly Val Arg Gly Val Tyr Phe Asp
        355                 360                 365

Thr Glu Glu Lys Leu Trp Val Ala Thr Trp Asn Glu His Gly Leu Arg
    370                 375                 380

Arg Phe Lys Ala Phe Pro Thr Met Glu Met Gly Phe Asp Ala Ala Tyr
385                 390                 395                 400

Gln Ala Ala Val Ala Val Arg Arg Gln Lys Leu Arg Glu Asn Tyr Ile
                405                 410                 415

Phe Ser Met Gln Arg Asn Arg Lys Lys Ser Gly Arg Pro Pro Phe Lys
```

-continued

```
            420                 425                 430


<210> SEQ ID NO 17
<211> LENGTH: 1919
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Glu Leu Pro Asp Gln Ala Ala Tyr Gly Arg Gln Leu Ala Lys Arg
1               5                   10                  15

Arg Arg Leu Ser Ala Ser Glu Glu Glu Ala Thr Leu Ala Ser Lys Asn
            20                  25                  30

Asp Gly Lys Glu Gly Leu Gln Glu Pro Ala Gly Ala Thr Ala Gly His
        35                  40                  45

Leu Leu Pro Ala Glu Glu Pro Gly Gln Tyr Thr Pro Glu His Thr Glu
    50                  55                  60

Gly Arg Arg Glu Phe Arg Arg His Pro Val Val Leu Pro Gly Gly Gly
65                  70                  75                  80

Arg Lys Ala Ala Ser Tyr Gly Leu Ile Ala Val Gly Gly Gly Asp Ser
                85                  90                  95

Leu Arg Ala Ser Arg Arg Thr Arg Ser Ser Ala Ser Ile Glu Thr Ser
            100                 105                 110

Ala Glu Glu Lys Glu Thr Tyr Thr Ser Pro Glu Leu Gly Pro Gly Ala
        115                 120                 125

Ser Trp Ser Val Ser Thr Val Lys Gly Ser Lys Gly Arg Ser Asp Glu
    130                 135                 140

Glu Gly Arg Ala Gly Lys Arg Ala Gly Ala Cys Ala Ala Arg Asp Ser
145                 150                 155                 160

Ala Ala Gly Ser Arg Thr Leu Ala Gln Ala His Arg Gly Ala Asp Glu
                165                 170                 175

Glu Arg Met Pro Pro His Ser Pro Ala Arg Asp Gly Ser His Gln Val
            180                 185                 190

Cys Trp Asp Ser Asp Ala Leu Pro Ser Pro Tyr Asp Leu Gly Leu Ser
        195                 200                 205

Glu Ala Asp Asp Glu Glu Val Ser Pro Gln Lys Glu Ala Leu Ala Glu
    210                 215                 220

Lys Asn Gly Leu Val Leu Phe Ala Glu Gln Ser Leu Gln Gly Val Gly
225                 230                 235                 240

Leu Ala Thr Leu Thr Val Pro Ser Gly Ala Thr Ser Ser Lys Gly Ala
                245                 250                 255

Phe Ser Ala Gly Ser Pro Phe Leu Pro Gly Ser Gly Thr Thr Ala Ser
            260                 265                 270

Pro Arg Ser Pro Val Pro Arg Gly Asp Lys Ser Leu Gly Asp Gly Ser
        275                 280                 285

Val Gly Ser Asp Asp Val Ser Ala Lys Ala Ser Pro His Ala His His
    290                 295                 300

Asn Val Thr Ala Gly Ala Asp Ala Ser Gln Ser Ser Glu Asp Ala Phe
305                 310                 315                 320

Phe Pro Ala Ala Pro Pro Gly Gly Val Pro Gly Thr Leu Thr Val Glu
                325                 330                 335

Asp Leu Leu Thr Met Pro Glu Arg Arg Gln Asp Pro Glu Ala Glu Lys
            340                 345                 350
```

-continued

```
Ala Ala Lys Thr Asp Phe Asp Cys Leu Ala Ala Leu Ile Gln Asp Ala
        355                 360                 365

Leu Gly Glu Ala Gly Gly Ala Ala Gly Arg Val Ala Pro Lys Arg Arg
    370                 375                 380

Cys Arg Thr Leu Gly Ala Gly Phe Asn Pro Thr His Ser Ala Arg Pro
385                 390                 395                 400

Gly Ser Gly Ser Val Ala Gly Leu Glu Ala Pro Gly Ala Leu Gly Arg
                405                 410                 415

Glu Leu Asp Ala Leu Val Ala Gly Gly Ser Pro Glu Glu Ser Arg Ala
            420                 425                 430

Asp Leu Glu Pro Asp Gly Gln Ala Ala Gly Ala Ser Trp Gln Glu Ser
        435                 440                 445

Leu His Leu Gln Tyr Asp Thr Arg Asn Gly Gly Thr Tyr Glu Glu Asp
    450                 455                 460

Leu Asp Ser Ala Ser Leu Ser Phe Leu Leu Gly His Ser Glu Gly Ser
465                 470                 475                 480

Glu Lys Gly Pro Ala Leu Ser Ala Ser Ala Gly Ala Ser Thr Ala Ala
                485                 490                 495

Ser Val Ser Ser Phe Phe Pro Ser Glu Ala Ala Cys Gly Val Tyr Ala
            500                 505                 510

Pro Gly Gln His Gly Arg Pro Thr Gln Ser Gln Asp Pro Ala Lys Glu
        515                 520                 525

Arg Gln Arg Arg Leu Ala Arg Asp Arg Glu Thr Leu Asn Leu Ser Ala
    530                 535                 540

Gln Ile Ala Ala Arg Phe Lys Ser Cys Arg Thr Glu Asp Val Met Arg
545                 550                 555                 560

Leu Phe Arg Arg Tyr Leu Ala Val Ser Ser Arg Gln Val Arg Asp Pro
                565                 570                 575

Ala Thr Leu Glu Arg Val Val Ala Ala Cys Cys Tyr Ile Ser Ser Arg
            580                 585                 590

Gln Ala Met Asp Gly Leu Ser Leu Ser Asp Ile Cys His Glu Met Asp
        595                 600                 605

Ala Ser Asn Gly Gln Asp Leu Phe Ala Ala Gly Cys Glu Ala Arg Gly
    610                 615                 620

Lys Lys Leu Ala Asp Gly Glu Gly Met Gly Arg Gly Glu Ser Asp Arg
625                 630                 635                 640

Glu Arg Ala Gly Gly Ala His Ala Ser Met Arg Cys Lys Ser Leu Gly
                645                 650                 655

Lys Trp Val Val Arg Ile Cys Arg Lys Leu Gln Leu Gln Ala Leu Pro
            660                 665                 670

Asp Lys Asp Asp Asp Pro Glu Glu Arg Ala Asn Arg Val Leu Ala Arg
        675                 680                 685

Val Lys Gln Leu Leu Ile Ala Lys Met Glu Glu Glu Glu Gln Arg Arg
    690                 695                 700

Pro Gln Leu Val Asn Ala Phe Val Arg Ala Thr Gln Ser Ala Val Glu
705                 710                 715                 720

Lys Gln Arg Leu Lys Ala Glu Gly Asp Arg Ser Glu Ala Asp Ser Leu
                725                 730                 735

Ala Ser Leu Glu Ser Leu Leu Gly Asp Glu Ala Arg Arg Ala Asp Ala
            740                 745                 750

Arg Ala Asp Ala Glu Ala Arg Arg Gln Thr Pro Ala Glu Ala Gln Leu
```

-continued

```
        755                 760                 765

Gly Asp Phe Leu Asp Gly His Gln Gly Gly Glu Lys Thr Gly Arg Val
    770                 775                 780

Ser Ser Ala Arg Ile Asn Gly Arg Ala Ala Glu Ala Ser Pro Ala Pro
785                 790                 795                 800

Pro Ala Pro Gln Gly Ser Thr Ala Pro Ala Asp Ser Thr Pro Ala Ala
                805                 810                 815

Gly Ser Glu Glu Arg Gln Ala Leu Asn Ala Ile Glu Glu Leu Leu Ala
            820                 825                 830

Gln Val Thr Gly Gly Ser Asn Leu Asp Cys Phe Gly Ser Ala Thr Leu
        835                 840                 845

Ala Ala Val Asp Ser Asp Leu Ala Ser Gly Thr Ser His Val Asp Arg
    850                 855                 860

Glu Ser Cys Ala Arg Leu Arg Arg Leu Asp Lys Ser Gly Arg Asp Ala
865                 870                 875                 880

Phe Ala Ala Asp Ala Asp Gly Pro Glu Arg Pro Thr Glu Asn Glu Val
                885                 890                 895

Glu Pro Glu Ala Arg Pro Gly Ala Ala Gly Val Leu Ala Glu Asp Val
            900                 905                 910

Asp Glu Ala Ser Met Ala Leu Thr Pro Asn Pro Asp Asp Arg Ser Ser
        915                 920                 925

Ser Ala Ser Gly Asp Ala Ala Glu Pro Val Ala Ser Ile Arg Leu Glu
    930                 935                 940

Gln Arg Glu Glu Lys Asn Gly Asp Ala Ser Gly Leu Ser Leu Asp Ile
945                 950                 955                 960

Cys Pro Ser Leu Phe Asp Pro Val Asp Met Pro Ala Leu Ser Ala Ser
                965                 970                 975

Ser Glu Gly Asp Ser Gly Asp Ser Ser Pro Phe Ser Pro Ile Leu Thr
            980                 985                 990

Ser Leu Leu Ser Ala Ser Leu Pro  Pro Ser Glu Thr Leu  Ala Gln Ala
        995                 1000                1005

Lys Asp  Met Gln Pro Ala Ala  Arg Leu Gln Leu Gln  Arg Phe Thr
    1010                 1015                1020

Trp Leu  Gln Lys Met Arg Ala  Glu Ala Leu Glu Lys  Leu Lys Lys
    1025                 1030                1035

Glu Lys  Glu Ala Val Phe Arg  Gly Leu Val Leu Leu  Gln Arg Ile
    1040                 1045                1050

Leu Gln  Leu Phe Tyr Asp Val  Lys Gln Gly Glu Ser  Asp Gly Glu
    1055                 1060                1065

Arg Glu  Asp Gly Glu Asp Gly  Glu Gly Lys Lys Arg  Gln Lys Gly
    1070                 1075                1080

Trp Thr  Glu Glu Asp Pro Leu  Asp Lys Arg Trp Arg  Ala Arg Gly
    1085                 1090                1095

Arg Cys  Asp Ala Val Ser Leu  Ala Ser Leu Ile Ile  Ile Val Phe
    1100                 1105                1110

Lys Trp  Met Gln Ile Pro Ile  Pro Gln Arg Ile Ala  Leu Asp Ala
    1115                 1120                1125

Leu His  Val Asp Arg Lys Ser  Val Tyr Lys Arg Arg  Leu Glu Gln
    1130                 1135                1140

Met His  Ile Leu Lys Thr Leu  Phe Gly His Leu Arg  Gly Met Val
    1145                 1150                1155
```

-continued

```
Glu Lys  Lys Asp Gly Ser Ser  Ser Ser Ala Leu Ala  Glu Glu Leu
    1160                 1165                 1170

Lys Ala  Ser Leu Pro Pro His  Leu Ala Ser Leu Leu  Gln Gln Val
    1175                 1180                 1185

Val Gly  Asn Pro Ala Thr Met  Gln Arg Leu Leu Ala  Leu Ala Asp
    1190                 1195                 1200

Glu Glu  Glu Glu Leu Gly Asn  Phe Ile Ser Ser Gln  Ser Leu Gly
    1205                 1210                 1215

Ser Asp  Gly Glu Ser Gly Lys  Ala Ser Ala Gly Leu  Gly Gly Val
    1220                 1225                 1230

Pro Pro  Pro Ala Ala Ala Ala  Ser Pro Thr Pro Val  Lys Thr Ser
    1235                 1240                 1245

Gln Ala  Ser Phe His Pro Gln  Ala Pro Ala Ala Ser  Ser Pro Glu
    1250                 1255                 1260

Ser Ser  Ala Pro Ser Val Ala  Val Glu Pro Glu Gln  Asp Ala Ala
    1265                 1270                 1275

Ser Ser  Ser Phe Leu Ala Ala  Ile Leu Ala Glu Val  Ala Ala Glu
    1280                 1285                 1290

Arg Glu  Val Gly Ala Val Lys  Thr Arg Gly Pro Gly  Asp Ala Glu
    1295                 1300                 1305

Arg Thr  Ala Ala Glu Leu Gly  Phe Gln Thr Arg Lys  Lys Arg Arg
    1310                 1315                 1320

Val Ser  Glu Leu Asn Ala Gln  Arg Ser Pro Asp Asn  Gly Leu Gly
    1325                 1330                 1335

Ser Asp  Leu Tyr Asp Glu Asp  Arg Glu Ala Ser Ser  Ala Val Pro
    1340                 1345                 1350

Val Ala  Ser Pro Leu Ala Asn  Leu Cys Ser Ser Leu  Ser Ser Ser
    1355                 1360                 1365

Ser His  Arg Asn Pro Ser Glu  Met Ala Ala Val Ala  Ser Val Ala
    1370                 1375                 1380

Pro Ser  Pro Arg Ala Ala Arg  His Pro Arg Ala Pro  Asp Glu Met
    1385                 1390                 1395

Thr Leu  Gln Gly Leu Ala Val  Gly Lys Asp Ala Gly  Thr Pro Arg
    1400                 1405                 1410

Gln Ala  Gly Gly Tyr Ala Gly  Thr Phe Leu Pro Gly  Asp Gly Asp
    1415                 1420                 1425

Arg Val  Ser Glu Gly Glu Asp  Gly Arg Ser Glu Arg  Val Arg Ala
    1430                 1435                 1440

Arg Phe  Leu Ala Glu Arg Gly  Ser Met Asp Ala Ser  Ser Ser Phe
    1445                 1450                 1455

Ala Leu  Gly Phe Ser Leu Ala  Glu Ala Leu Leu Arg  His Gly Phe
    1460                 1465                 1470

Cys Leu  Pro Ser Pro Ser Asp  Pro Pro Ala Gly Leu  Ala Asp Ala
    1475                 1480                 1485

Gln Phe  Ala Thr Gly Asp Leu  Leu Arg Asp Gly Gly  Ser Ser Ser
    1490                 1495                 1500

Gly Glu  Arg Ala Leu Arg Met  Gln Pro Glu Gly Phe  Ser Ala Thr
    1505                 1510                 1515

Arg Gly  Ser Arg Pro Ala Val  Ala Pro Gly Pro Ala  Gly Phe Gly
    1520                 1525                 1530
```

-continued

```
Ile Gln  Ala Glu Ala Glu His  Glu Gly Arg Gly Asp  Val Asn Ser
    1535                 1540                 1545

Thr Asp  Val Ile Phe Ser Asn  Arg Ala Thr Arg Asp  Ile Ile Ala
    1550                 1555                 1560

Ser Phe  Leu Ala Ser Ala Ser  Thr Glu Gly His Pro  Gly Thr Ala
    1565                 1570                 1575

Ser Leu  Thr Gly Arg Gly Leu  Glu Asp Gly Arg Ser  Pro Arg Leu
    1580                 1585                 1590

Arg Gly  Pro Leu Ala Ala Val  Pro Lys Ala Val Ser  Gln Ala Asp
    1595                 1600                 1605

Arg Gly  Pro Gly Arg Phe Asn  Arg Gly Ala Ser Gly  Ser Cys Arg
    1610                 1615                 1620

Gln Pro  Ser Ser Arg Ser Pro  Pro Leu Pro Val Ser  Pro Tyr Arg
    1625                 1630                 1635

Gly Arg  Thr Gly Asp Ser Ser  Arg Gln Arg Pro Leu  Ser Pro Ser
    1640                 1645                 1650

Ser Leu  Phe Ala Ala Ala Ala  Ser Met Ala Gly Val  Leu Pro Gly
    1655                 1660                 1665

Pro Leu  Pro Ser Ser Arg Ser  Ala Gly Ser Ser Ala  Leu Ser Pro
    1670                 1675                 1680

Gly Val  Glu Arg Ser Pro Arg  Glu Arg Val Ala Ala  Gln Ala Leu
    1685                 1690                 1695

Glu Ala  Thr Arg Arg Gly Asp  Val Asp Asp Arg Ser  Leu His Pro
    1700                 1705                 1710

Ser Ser  Ser Val Ser Ala Val  Arg Ser Leu Leu Pro  Ala Glu Pro
    1715                 1720                 1725

Ala Leu  Gly Gly Ala Ser Pro  Phe Ala Ser Ser Ala  Leu Ala Met
    1730                 1735                 1740

Gly Leu  Pro Glu Ala Gly Ala  Ser Gln Ala Gly Ala  Asp Ala Pro
    1745                 1750                 1755

Leu Ala  Ser Pro Ser Ile Ala  Leu Ala Thr Val Ala  His Leu Lys
    1760                 1765                 1770

Ala Ala  Glu Lys Ala Leu Leu  Asp Ser Val Pro Asp  Ser Ala Arg
    1775                 1780                 1785

Val Val  Ser Leu Gln Phe Glu  Arg Thr Gln Gln Arg  Trp Val Cys
    1790                 1795                 1800

Lys Trp  Gln Arg His Lys Pro  Ala Gly Ala Pro Ala  Asn Arg Lys
    1805                 1810                 1815

Glu Pro  Trp His Arg Arg Cys  Phe Ser Val Ile Lys  Tyr Gly Tyr
    1820                 1825                 1830

Glu Gly  Ala His Ala Leu Ala  Ala Ala Val Ala Lys  Lys Leu Arg
    1835                 1840                 1845

Asp Gly  Arg Arg Ala Leu Leu  Gln Lys Gln Arg Arg  Leu Glu Glu
    1850                 1855                 1860

Glu Gly  Leu Ala Glu Ala Glu  Glu Ala Pro Arg Asp  Glu Glu Glu
    1865                 1870                 1875

Val Gly  Asp Ala Glu Asp Glu  Glu Pro Leu Gly Ala  Ala Glu Glu
    1880                 1885                 1890

Ala Glu  Glu Thr Val Ser Pro  Arg Val Asp Ala Gly  Gly Asp Arg
    1895                 1900                 1905

Ser Ala  Ser Gly Ser Ala Glu  Ala Gly Lys Gln
```

-continued

```
    1910                1915


<210> SEQ ID NO 18
<211> LENGTH: 485
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Met Cys Val Lys Lys Glu Gly Gly Asp Gly Lys Arg Gly Asn Glu Lys
1               5                   10                  15

Asn Gln Val Asn Asp Lys Gly Val Lys Arg Thr Gly Arg Asp Val Glu
            20                  25                  30

Ser Arg His Ala Pro Ser Val Pro His Leu Glu Lys Leu Val Asp Met
        35                  40                  45

Ala Met Val Tyr Ser Ser Cys Leu Pro Pro Cys Asp Ser Ser Gln Gly
    50                  55                  60

Gly Asp Gly Glu Arg Val Lys Arg Asn Ala Gly Ala Lys Arg Lys Gln
65                  70                  75                  80

Gly Gln Gly Glu Ser Gln Asp Arg Leu Lys Ala Leu His Asp Ser His
                85                  90                  95

Pro Leu Gln Cys Val Trp Tyr Leu Glu Ser Ser Pro Ala Thr Asn Ile
            100                 105                 110

Thr Leu Pro Ser Glu Ser Gly Ser Leu Lys Ser Pro Ser Ser Pro Ser
        115                 120                 125

Lys Arg Ala Ser Pro Asp Arg Val Met Glu Val Ser Ala Ser Leu Cys
    130                 135                 140

Lys Glu Glu Gln Lys Arg Arg Glu Gly Pro Arg Glu Gly Gln Trp Cys
145                 150                 155                 160

Cys Ser Trp Ser Phe Pro Arg Gly Arg Pro Thr Gly Thr Lys Phe Ser
                165                 170                 175

Val Lys Leu Phe Gly Tyr Glu Glu Ala Lys Arg Leu Ala Leu Tyr Thr
            180                 185                 190

Ala Leu Tyr Ala Tyr Ser Pro Glu Glu Arg Cys Asp Val Leu Gln Glu
        195                 200                 205

Leu Ile Asp Glu Val Leu Ala Thr Ala Ser Ser Ala Ser Leu Ser Ala
    210                 215                 220

Ser His Leu Pro Asn Pro Glu Arg Phe Pro Ala Ile Leu Glu Leu Gln
225                 230                 235                 240

Pro Gln Pro Leu Ser Leu Ser Ser Ser Leu Ser Pro Ser Leu Cys Val
                245                 250                 255

Arg Leu Asp Ala Cys Ala Phe Pro Ser Pro Val Leu Ser Gly Ser Pro
            260                 265                 270

Leu Cys Ser Ser Pro Gly Leu Ser Ser Arg Gly Arg Asn Gly Ser Lys
        275                 280                 285

Ala Ala Arg Glu Thr Leu Ser Ile Asp Arg Gly Ile Arg Leu Ser Ser
    290                 295                 300

Gln Ser Ser Ala Ser Ser Asn Ala Met Pro Ser Gln Phe Pro Gln Arg
305                 310                 315                 320

Trp Gln Ala Thr Glu Val Arg Met Ser Leu Leu Cys Arg Ser Ser Phe
                325                 330                 335

Arg Ala Ser Arg Arg Arg Glu Gly Gly Asn His Gly Glu Ala Glu Ala
            340                 345                 350
```

-continued

```
Glu Ala Lys Arg Ala Gly Gln Thr Arg Glu Lys Thr Gly Arg Arg Asp
        355                 360                 365

Lys Gly Asn His Pro His Asp Leu Ser Val Asn Asn Arg Lys Glu Pro
    370                 375                 380

Asn Lys Leu Glu Lys Ser His Ser Ser Cys Ser Pro Arg Arg Ser Leu
385                 390                 395                 400

Phe Ser Ser Ile Gln Val Gln Gln Asp Glu Arg Ser Gly Gly Arg Leu
                405                 410                 415

Leu His Gly Phe Arg Gly Asp Met Glu Glu Gly Lys Arg Ala Ser Arg
            420                 425                 430

Ala Asn Lys His Val Glu Ala Lys Lys Gly Glu Val Thr Gly Arg Arg
        435                 440                 445

Lys Gly Val Cys Gly Gly Ala Leu Phe Gly Cys Phe Pro Ala Arg Arg
    450                 455                 460

Gly Arg Glu Arg Gly Glu Asp Glu Gly Glu Arg Glu Lys Ala Gly Gln
465                 470                 475                 480

Val Asn Ala Gln His
                485


<210> SEQ ID NO 19
<211> LENGTH: 3837
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Ala Phe Ala Pro Arg Thr Ser Pro Arg Leu Ser Ala Gly Ala Gly
1               5                   10                  15

Gly Pro Ser Glu Ala Ser Arg Gly Gly Thr Ala Ala Gly Ala Pro Leu
            20                  25                  30

Gly Pro Val Glu Thr Pro Thr Gly Arg Glu Pro Ser Ser Pro Phe Leu
        35                  40                  45

Arg Ser Ala Ser Ala Lys Arg Val Thr Arg Ala Arg Ala Gly Phe Leu
    50                  55                  60

Ala Ser Ser Pro Asp Asn Gln Ser Arg Ser Thr Ser Pro Leu Arg Pro
65                  70                  75                  80

Ala Asp Ala Leu Arg Ile Ser Glu Ala Ser Ser Ala Ser Ala Pro Gly
                85                  90                  95

Val Arg Arg Ser Leu Arg Ala Ser Asn Ala Arg Pro Pro Val Ser Ala
            100                 105                 110

Ser Arg Gly Leu Met Gly Lys Ala Gly Glu Glu Gly Glu Gly Ala Ser
        115                 120                 125

Gly Gly Gly Arg Pro Gly Gly Ala Arg Arg Thr Ser Gly Gly Gly Glu
    130                 135                 140

Asp Val Cys Ala Ser Pro Arg Asp Ile Ser Tyr Arg Asp Lys Gly Ala
145                 150                 155                 160

Gly Gly Asp Ala Thr Ala Ser Ser Asn Ser Gln Ser Pro Ser Ser Val
                165                 170                 175

Asp Ala Ala Val Ser Ser Ser Tyr Ser Val Ala Ser Ser Val Ser Ser
            180                 185                 190

Pro Pro Ala Ser Ser Leu Ser Ser Ala Leu Ser Ser Ser Phe Ser Ser
        195                 200                 205

Ser Thr Leu Ser Arg Ser Gly Ser Ser Val Cys Pro Arg Ala Thr Ser
    210                 215                 220
```

-continued

```
Ala Val Ser Ala Thr Leu Gln Gln Gly Glu Arg Ser Gln Glu Ser Ser
225                 230                 235                 240

Leu Leu Ala Gly Glu Arg Glu Thr Asp Arg Asp Ala Asn Arg Pro Gln
                245                 250                 255

Arg Glu Thr Asp Glu Gly Gln Gly Ala Lys Ser Glu Thr Asp Arg Ala
            260                 265                 270

Pro Glu Asp Asp Arg Gly Arg Ser Arg Arg Gly Ser Ala Ser Pro Val
        275                 280                 285

Gln Gly Pro Phe Ser Pro Arg Gly Phe Phe Ser Asn Ala Val Thr Lys
    290                 295                 300

Glu Asn Ser Ala Tyr Pro Ala Thr Ser Gly Gln Ser Gly Gln Glu Val
305                 310                 315                 320

Gly Cys Arg Pro Asn Ser Thr Leu Ser Ser Val Ser Val Cys Ser Leu
                325                 330                 335

Ser Ser Arg Pro Pro Ser Thr Leu Ala Ser Asp Gln Leu Leu Ser Val
            340                 345                 350

Pro Asn Gly Asp Ala Ser Thr Val Ser Thr Ser Ser Pro Ser Leu Ser
        355                 360                 365

Cys Ser Cys Ser Ser Phe Ser Ser Ser Ser Ser Ser Leu Ser Ser Ser
    370                 375                 380

Ser Leu Leu Ser Ser Ser Pro Leu Ser Ser Thr Pro Ser Ser Phe Phe
385                 390                 395                 400

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ala Ser Val Ala Pro Pro Gly
                405                 410                 415

Glu Gly Lys Gly Arg Pro Pro Val Arg Ser Gly Arg Gly Ala Cys Pro
            420                 425                 430

Arg Lys Pro Ala Gly Pro Pro Pro Arg Leu Cys Val Pro Tyr Gln Cys
        435                 440                 445

Gln Phe Asn Val Glu Lys Arg Glu Trp Arg Ala Arg Tyr Leu Phe Arg
    450                 455                 460

Gly Gln Lys Lys Met Arg Val Phe Ser Leu Ala Arg Tyr Ser Pro Glu
465                 470                 475                 480

Val Ala Val Ser Leu Ala Glu Leu Phe Leu Thr Phe Leu Ala Asp Asn
                485                 490                 495

Asp Gly Ile Pro Arg Ser Glu Val Ile Ala Tyr Trp Ala Glu Thr Leu
            500                 505                 510

Ala Arg Gly Pro Val Thr Ala Thr Thr Gly Thr Asn Pro Lys Gly Gly
        515                 520                 525

Asn Leu Leu Gly Pro Gly Ala Ser Glu Glu Glu Thr Val Gly Gly Glu
    530                 535                 540

Gly Gly Glu Asp Ala Glu Ser Arg Ala Ala Glu Lys Glu Arg Glu Glu
545                 550                 555                 560

Glu Gly Lys Ala Ser Ser Ser Ser Gly Ser Ser Asp Gln Asn Ile Thr
                565                 570                 575

Arg Val Glu Ser Ser Glu Ala Lys Glu Asp Gly Glu Glu Asn Ser Ala
            580                 585                 590

Ser Ser Lys Pro Pro Gly Ala Ala Ser Ala Ala Thr Glu Pro Ala Gly
        595                 600                 605

Gly Asp Ala Asp Gly Arg Pro Gly Arg Ala Ala Ser Gly Pro Gly Asp
    610                 615                 620
```

-continued

```
Ala Cys Arg Ser Val Thr Ser Thr Glu Thr Glu Ala Ala Val Ala Val
625                 630                 635                 640

Ala Pro Glu Ala Lys Gly Gly Pro Ser Ser Asp Val Ser Cys Thr Leu
                645                 650                 655

Asp Lys Ser Arg Glu Ser Arg Gly Asn Gly Val Ala Gly Lys Arg Glu
            660                 665                 670

Asn Pro Ala Trp Ala Val Ser Pro Ser Ser Phe Ala Ala Phe Val Glu
        675                 680                 685

Thr Ala Lys Ala Arg Gln Trp Val Thr Glu Ala Ser Arg Leu Gln Ala
    690                 695                 700

Ala Ser Leu Pro Pro Leu Ala Pro Ala Glu Arg Pro Ala Arg Pro Pro
705                 710                 715                 720

Ile Leu Pro Thr Leu Ala Ser Ser Arg Ala Arg Arg Cys Thr Ser His
                725                 730                 735

Ser Leu Ile Ser Gly Leu Ser Ala Arg Glu Gly Ser Gln Arg Thr Val
            740                 745                 750

Ser Gln Gly Asp Ser Leu Ser Pro Ala Ser Gly Leu Ala Gly Glu Pro
        755                 760                 765

Gly Ala Val Arg Glu Ala Glu Gly Arg Glu Ala Ile Ala Val Asp Asp
    770                 775                 780

Glu Thr Gly Gly Glu His Arg Asp Phe Pro His Ser Gln Gly Pro Ala
785                 790                 795                 800

Gly Arg Gly Arg Leu Ala Gly Ala Arg Pro Ser Ser Ser Asp Met Arg
                805                 810                 815

Gly Glu Lys Arg Gly Arg Arg Ala Leu Arg Glu Gly Glu Ser Lys Arg
            820                 825                 830

Pro Cys Arg Arg Arg Glu Asp Leu Lys Ser Glu Glu Gly Gln Arg Glu
        835                 840                 845

Arg Arg Arg Arg Asp Thr Ala Trp Pro Ala Gly Arg Arg Glu Ala Ser
    850                 855                 860

His Gly Arg Gln Asp Ser Arg Val Lys Glu Glu Thr Pro Ala Pro Asp
865                 870                 875                 880

Ala Gly Ala Ala Leu Ala Leu Asp Gly Arg Ala Ala Ala Ala Arg Asp
                885                 890                 895

Arg Pro Gln Lys Ala Pro Ser Pro Phe Gly Thr Pro Glu Ala Leu Ser
            900                 905                 910

Ser Ser Leu Thr Gly Ser Gly Leu His Pro Asp Gly Arg Asn Pro His
        915                 920                 925

Gly His Pro Ala Leu Arg Val Lys Leu Ala Ala Gly Arg Gly Asn Gly
    930                 935                 940

Leu Leu Ala Ala Ser Pro Ala Ser Pro Ser Ser Ala Ser His Ala Ser
945                 950                 955                 960

Ser Leu Ala Ser Pro Ser Ala Ser Trp His Ala Ala Gln Gly Glu Ala
                965                 970                 975

Glu Ile Pro Gly Ala Ser Thr Gly Phe Val Asp Ser Pro Cys Ser Ala
            980                 985                 990

Asn Gly Ser Leu Asp Asp Ser Gly  Leu Gly Gly Pro Ala  Ala Ala Leu
        995                 1000                 1005

Gln Lys  Ser Trp Arg Asp Arg  Lys Arg Asn Arg Lys  Lys Leu Ser
    1010                 1015                 1020

Lys Ser  Met His Arg Lys Ser  Leu Ala Ser Leu Gly  Met Arg Ala
```

-continued

```
    1025                1030                1035

Pro Pro  Gln Asn Ala Cys Leu  Ala Asp Pro Ser Asp  Val Gly Leu
    1040                1045                1050

Gly Val  Gln Met Pro Ser Asp  Ala Gly Thr Val Pro  Gly Ile Ser
    1055                1060                1065

Pro Pro  Ser Phe Gly Ala Ser  Glu Gln Lys Ala Ser  Ser Ser Ala
    1070                1075                1080

Leu Gly  Leu Ala Phe Arg Ala  Ser Ser Ser Phe Ser  Pro Lys Asn
    1085                1090                1095

Gly Asp  Val Glu Pro Ala Gly  Arg Asn Pro Pro Gln  Phe Leu Pro
    1100                1105                1110

Thr Ala  Ser Val Gln Arg Ala  Asp Pro Pro Gly Thr  Gly Ala Pro
    1115                1120                1125

Pro Ser  Gln Gln Val Val Ser  Ser Ala Ser Pro Cys  Ser Pro Ser
    1130                1135                1140

Ala Leu  Ala Ala Thr Ala Ser  Pro Gly Ala Cys Arg  Gly Gly Ala
    1145                1150                1155

Ser Arg  Asn Gly Asp Pro Gln  Gly Glu Arg Phe Ser  Phe Pro Ala
    1160                1165                1170

Ser Pro  Thr Ser Gln Tyr Arg  Trp Tyr Ala His Pro  Asp Gly Gly
    1175                1180                1185

Ala Thr  Gly Pro Ser Cys Cys  Arg Gln His Val Gly  Gly Ser Gly
    1190                1195                1200

Gly Gly  Gly Trp Pro Val Val  Trp Leu Lys Gln Leu  Glu Met Ala
    1205                1210                1215

Val Asn  Gly Pro Pro Lys Phe  Cys Ser Tyr Val Glu  Ala Val Asp
    1220                1225                1230

Lys His  Leu Arg Leu Gly Gly  Leu Arg Arg Pro Val  Ala Phe Leu
    1235                1240                1245

Pro Leu  Ala Ser Arg Pro Ala  Ser Pro Thr Gly Leu  Gly Gly Gly
    1250                1255                1260

Leu Gly  Ala Pro Gly Pro Ala  Leu Arg Gln Ala Ser  Glu Lys Ala
    1265                1270                1275

Leu Ala  Ala Glu Gly Arg Gln  Gly Gln Asn Glu Glu  Lys Gln Val
    1280                1285                1290

Gly Trp  Lys Ser Ala Thr Gly  Ser Lys Ala Gly Met  Phe Gln Gly
    1295                1300                1305

Asp Ser  Gly Glu Thr Thr Ser  Glu Arg Gly Ala Glu  Glu Ala Glu
    1310                1315                1320

Gly Thr  Gly Gly Gly Arg Arg  Gly Ile Leu Gly Lys  Glu Glu Glu
    1325                1330                1335

Asp Arg  Asn Gly Gly Glu Gly  Glu Lys Ala Ala Thr  Pro Thr Met
    1340                1345                1350

Gly Gly  Ala Ser Pro Ala Ala  Ser Asp Asp Ala Leu  Ser Pro Met
    1355                1360                1365

Lys Ala  Asp Arg Pro Ala Glu  Ala Leu Gly Thr Gly  Gly Ser Ala
    1370                1375                1380

Pro Thr  His Ala Asp Ser Arg  Arg Ala Pro Gly Met  Pro Glu Gly
    1385                1390                1395

Glu Lys  Met Thr Gly Pro Ser  Lys Glu Gln Glu Met  Ala Glu Ala
    1400                1405                1410
```

-continued

```
Gly Glu  Arg Asp Arg Cys Glu  Arg Ser Leu Glu Arg  Asn Ala Glu
    1415                 1420                 1425

Leu Val  Leu Lys Glu Asn Val  Ser Met Thr Ser Ala  Ser Asp Val
    1430                 1435                 1440

Ser Glu  Ala Ala Glu Glu Lys  Gly Ala Pro Lys Lys  Leu Ala Ser
    1445                 1450                 1455

Ser Pro  His Ser Val Glu Ser  Pro Cys Gly Arg Thr  Ala Glu Lys
    1460                 1465                 1470

Thr Gly  Thr Leu Asn Thr Ser  Glu Lys Gly Glu Asn  Thr Arg Thr
    1475                 1480                 1485

Ala Glu  Gly Asp Asp Pro Gly  Thr Thr Ile Val Lys  Glu Glu Phe
    1490                 1495                 1500

Pro Leu  Leu Pro Ala Pro Glu  Thr Pro Val Thr Val  Thr Ala Gln
    1505                 1510                 1515

Asp Leu  Leu Ser Pro Thr Val  Tyr Thr Pro Arg Trp  Gln Ala Thr
    1520                 1525                 1530

Val Gly  Lys Ser Leu Glu Leu  Gly Ser Leu Asn Cys  Glu Lys Ser
    1535                 1540                 1545

Cys Glu  Arg Gly His Trp Ala  Asp Ala Ser Ala Cys  Asp Leu Glu
    1550                 1555                 1560

Thr Lys  Asp Leu Arg Leu Pro  Glu Asp Asn Lys Ser  Glu Glu Leu
    1565                 1570                 1575

Lys Lys  Glu Thr Gly Met Phe  Leu Gly Val Glu Gly  Glu Gln Val
    1580                 1585                 1590

Glu Glu  Ala Lys Ser Ser Lys  Glu Ala Phe Ser Pro  Glu Glu Arg
    1595                 1600                 1605

Glu Arg  Glu Glu Gln Lys Glu  Ser Ser Lys Ala Ala  Gly Gly Gly
    1610                 1615                 1620

Asp Ser  Cys Arg Thr Pro Arg  Gln Gln Glu Ala Thr  Pro Arg Ala
    1625                 1630                 1635

Ser Glu  Glu Cys Gln Pro Glu  Ser Arg Ile Asp Met  Lys Val Ser
    1640                 1645                 1650

Pro Asn  Thr Glu Met Met Val  Glu Lys Leu Glu Glu  Thr Arg Val
    1655                 1660                 1665

Gln Asn  Thr Glu Glu Pro Glu  Lys Val Glu Glu Lys  Glu Glu Gly
    1670                 1675                 1680

Gly Ser  Val Cys Arg Asp Val  Ser Val Ala Ser Pro  Leu Glu Ser
    1685                 1690                 1695

Pro Asn  Ser Arg Leu Ser Glu  Lys Gly Asp Gln Ser  Glu Thr Pro
    1700                 1705                 1710

Ala Gly  Val Ala Pro Pro Ser  Ser Ser Ala Leu Glu  Ala Arg Ala
    1715                 1720                 1725

Gly Arg  Asp Ser Ala Leu Leu  Ser Ala Ser Leu Pro  Leu Ser Pro
    1730                 1735                 1740

Arg Ala  Ser Cys Pro Pro Thr  Gln Ser Ala Ser Pro  Ala Ser Arg
    1745                 1750                 1755

Asp Pro  Thr Pro Ala Ser Leu  Arg Val Ser Ser Val  Ala Ser Gly
    1760                 1765                 1770

Asp Arg  Asn Gly Pro Thr Gly  Ile Leu Phe Arg Pro  Leu Ser Ser
    1775                 1780                 1785
```

-continued

```
Pro His  Lys Arg Val Ser Phe  Cys Leu Arg Gly Gly  Ala Glu Pro
    1790                 1795                 1800

Pro Gln  Arg Pro Leu Ser Glu  Ala Val Pro Tyr Pro  Leu Asn Ala
    1805                 1810                 1815

Arg Leu  Gln Glu Ile Val Ser  Arg Phe Arg Leu Leu  Gln Gly Val
    1820                 1825                 1830

Ser Ala  Ala Arg Val Ser Ser  His Gly Lys Gly Glu  Thr Ser Ser
    1835                 1840                 1845

Gln Ala  Thr Pro Lys Ala Val  Gln Gly Glu Ala Thr  Val Lys Glu
    1850                 1855                 1860

Lys Ala  Thr Val Thr Pro Thr  Glu Ser Ala Lys Ser  Leu Ala Gly
    1865                 1870                 1875

Gly Gln  Ala Glu Thr Glu Lys  Gly Glu Ser Pro Ser  Gly Ala Glu
    1880                 1885                 1890

Ala Ala  Thr Gln Lys Ala Asp  Glu Lys Glu Lys Thr  Pro Asp Thr
    1895                 1900                 1905

Asp Ala  Thr Gln Ser Arg Ser  Thr Ser Ser Gly Phe  Glu Thr Gln
    1910                 1915                 1920

Glu Ala  Lys Thr Ala Pro Ala  Ser Ile Leu Pro Ala  Ser Ser Leu
    1925                 1930                 1935

Pro Ser  Ser Asp Arg Pro Ser  Ala Ser Cys Ser Asp  Thr His Ala
    1940                 1945                 1950

Ser Arg  Asp Ala Val Pro Leu  Ala Ser Ser Pro Ser  Ser Ser Ser
    1955                 1960                 1965

Ser Pro  Ala Leu Arg Arg Cys  Ser Val Arg Gly Lys  Asp Leu Val
    1970                 1975                 1980

Ser Ala  Pro Val Asp Ser Phe  Ser Glu Gly Asp Ser  Ser Asp Ala
    1985                 1990                 1995

Arg Pro  Phe Val Ser Val Arg  Asp Leu Ala Val Lys  Leu Tyr Arg
    2000                 2005                 2010

Trp Leu  Glu Gln Gly Glu Gly  Leu Pro Ala Ala Ala  Gly Glu Pro
    2015                 2020                 2025

Gln Gly  Ala Cys Gly Val Gly  Ala Lys Ala Gln Ala  Arg Glu Ala
    2030                 2035                 2040

Leu Arg  Ile Asp Thr Val Pro  Phe Ile Ser Arg Trp  Arg Gln Met
    2045                 2050                 2055

Leu Glu  Arg Ser Leu Ser Ile  Ala Ser Asp Leu Arg  Lys Leu Asp
    2060                 2065                 2070

Leu Gln  Val Val His Leu Val  Glu Leu Thr Glu Ala  Leu His Ile
    2075                 2080                 2085

Ala Val  Tyr Ile Cys Gly Gln  Leu Arg Arg Arg Leu  Arg Glu Gly
    2090                 2095                 2100

Ala Ala  Pro Asp Ala Gly Ala  Ala Glu Asp Leu Ala  Pro Val Asp
    2105                 2110                 2115

Val Asp  Asp Pro Arg Gly Cys  Ser Gln Gln Ser Gly  Asp Thr Arg
    2120                 2125                 2130

Asp Ser  Ser Ser Pro Ala Thr  Pro Gly Gly Arg Leu  Ala Gly Gly
    2135                 2140                 2145

Ala Gly  Gly Ala Ala Thr Ser  Pro Lys Gly Gln Ala  Phe Ala Pro
    2150                 2155                 2160

Arg Gly  Gly Glu Gly Glu Ile  Lys Pro Gln Glu Thr  Gly Asn Ser
```

-continued

```
    2165                2170                2175

Gly Asp  Ser Lys Ala Glu Gly  Lys Glu Ala Ser Gly  Asp Ala Asn
    2180                2185                2190

Thr Ser  Glu Gly Lys Arg Leu  Ser Gly Glu Val Asp  Lys Thr Ala
    2195                2200                2205

Glu Val  Glu Thr Ala Gly Ser  Glu Asp Ile Asn Val  Glu Arg Gly
    2210                2215                2220

Val Pro  Gly Ala Gln Ala Glu  Thr Ala Arg Thr Glu  Met Asn Gly
    2225                2230                2235

Gly Val  Val Lys Gly Gln Glu  Thr Ser Gly Asp Ile  Leu Ser Val
    2240                2245                2250

Gly Ser  Ser Gln Val Leu Ser  Leu Ser Ser Pro Ser  Leu Ser His
    2255                2260                2265

Leu Ala  Ser Ser Ser Gly Lys  Gly Pro Leu Lys Pro  Thr Ser Ser
    2270                2275                2280

Pro Ser  Ser Ser Leu Tyr Ala  Leu Ser Pro Ser Ser  Ser Ala Ala
    2285                2290                2295

Ser Pro  Phe Ser Ala Gln Leu  Ala Ser Pro Ser Ser  His Ala Pro
    2300                2305                2310

Leu Ser  Leu Ser Phe Arg Ser  Ser Ser Ser Pro Thr  Ser Leu Ser
    2315                2320                2325

Ser Pro  Leu Ala Ser Tyr Pro  Phe Pro Gln Thr Leu  Gln Gln Thr
    2330                2335                2340

Ser Ala  Ser Pro Ser Ser Ser  Ala Ser Ala Arg Pro  Ser Cys Ala
    2345                2350                2355

Ser Val  Lys Pro Leu Arg Glu  Ala Gly Asp Leu Val  Arg Ala Ala
    2360                2365                2370

Ala Arg  Ala Ala Leu Glu Gln  Ala Gln Val Phe Gly  Val Gly Gly
    2375                2380                2385

Lys Leu  Ser Asp Ala Thr His  Gln Leu Ala Ala Arg  Val Thr Val
    2390                2395                2400

Ala Val  Arg Ala Ala Met Leu  Ala Lys Gly Glu Gly  Gly Leu Thr
    2405                2410                2415

Arg Gly  Asp Val Asp Leu Leu  Val Glu Glu Thr Glu  Arg Phe Val
    2420                2425                2430

Arg Glu  Ala Arg Phe Lys Ala  Gln Glu Thr Ala Ala  Glu Thr Thr
    2435                2440                2445

Ala Leu  Pro Asp Gly Val Ala  Glu Val Val Ser Ser  Glu Ala Gly
    2450                2455                2460

Leu Gly  Leu Gln Thr Thr Asn  His Ala Pro Val Ser  Pro Ala Ala
    2465                2470                2475

Ala Pro  Ser Ala Gly Gly Ala  Phe Ala Gly Leu Thr  Glu Ala Val
    2480                2485                2490

Glu Val  Glu Ala Arg Gln Leu  Pro Glu Ala Ser Glu  Arg Val Gly
    2495                2500                2505

Arg Val  Ser Ser Pro Arg Gly  Ser Leu Gly Phe Glu  Ala Met Asp
    2510                2515                2520

Leu Ala  Gly Glu Leu His Leu  Val Lys Val Leu Asn  Ala Phe His
    2525                2530                2535

Arg His  Thr Glu Cys Leu Met  Asn Glu Arg Glu Arg  Leu Ile Gln
    2540                2545                2550
```

-continued

```
Ala Thr  Asn Glu Asp Leu Ser  Phe Leu Leu His Ala  Met Glu Leu
    2555                 2560                 2565

Ala Leu  Pro Ser Gly Leu Asp  Thr Pro Leu Leu Ser  Ile Leu Glu
    2570                 2575                 2580

Gly Asp  Val Asp Ile Leu Pro  Pro Leu Pro Pro Pro  Asn Val Glu
    2585                 2590                 2595

Ala Leu  Ile Tyr Leu His Ala  Val Ser Leu Ala Gln  Ala Asp Ala
    2600                 2605                 2610

Ser Ala  Ser Pro Ser Ser Pro  Ser Ala Val Ala Pro  Cys Leu Leu
    2615                 2620                 2625

Ser Pro  Ser Ala Arg Leu Leu  Leu Ala His Phe Ala  Gly Ala Ser
    2630                 2635                 2640

Pro Thr  Ala Gly Gly Leu Gly  Gly Asp Ser Ala Lys  Gly Arg Thr
    2645                 2650                 2655

Met Ser  Ser Phe Pro Gly Arg  Pro Gly Glu Glu Arg  His Arg Ala
    2660                 2665                 2670

Asp Glu  Arg Lys Gly Ser Val  Leu Pro Val Arg Arg  Gly Arg Pro
    2675                 2680                 2685

Pro Ser  Ser Ala Arg Leu Asn  Ala Leu Arg Arg Leu  His Ala Val
    2690                 2695                 2700

Gly Glu  Pro Ala Ala Asp Ala  Gly Leu Asp Thr Val  Asn Gly Arg
    2705                 2710                 2715

Phe Arg  Ser Lys Arg Leu Arg  Ala Met Ser Gln Glu  Glu Glu Ala
    2720                 2725                 2730

Arg Arg  Ala Ala Thr His Ala  Ser Pro Thr Ile Pro  Tyr Pro Leu
    2735                 2740                 2745

Ser Arg  Tyr Leu His Arg Pro  Pro Arg Leu Leu Ser  Pro Thr Asp
    2750                 2755                 2760

Ala Gly  His Phe Ala Ser Ser  Tyr Ser Ser Pro Leu  Ser His Pro
    2765                 2770                 2775

Leu Ser  Lys Gly Ser Ser Leu  Thr Ser Pro Lys Arg  Gln Arg Arg
    2780                 2785                 2790

Ser Val  Cys Ser Glu Ala Pro  Glu His Glu Arg Lys  Asn Leu Arg
    2795                 2800                 2805

Ser Leu  Phe Lys Ser Pro Ser  Ala Gln Arg Glu Glu  Ala Pro Arg
    2810                 2815                 2820

Ser Leu  Thr Arg Pro Phe Gly  Pro Leu Lys Gly Glu  Gly Phe Ser
    2825                 2830                 2835

Pro Ala  Ser Leu Gly Thr Leu  Gly Ser Arg Arg Gln  Ser Glu Leu
    2840                 2845                 2850

Gly Ile  Arg Arg Arg Asp Ala  Leu Val Ala Phe Pro  Pro Ala Gly
    2855                 2860                 2865

Met Pro  Cys His Pro Ala Ser  Pro Gly Arg Arg Leu  Glu Arg Pro
    2870                 2875                 2880

Arg Val  Asp Gly Ala Asp Met  Asp Gly Glu Arg Arg  Arg Arg Thr
    2885                 2890                 2895

Arg Cys  Ala Gly Asp Arg Leu  Glu Glu Arg Arg Arg  Pro Leu Gly
    2900                 2905                 2910

Pro Val  Tyr Ile Pro Thr Lys  Val Arg Asp Pro Ala  Thr Gly Arg
    2915                 2920                 2925
```

-continued

```
Val Ala  Val Cys Ala Cys Asp  Thr Glu Arg Gly Glu  Arg Val Arg
    2930                 2935                 2940

Lys Val  Gln Leu Phe Glu Lys  Pro His Val Gly Ala  Phe Trp Cys
    2945                 2950                 2955

Ala Arg  Tyr Gly Pro Asn Asp  Glu Phe Val Arg Cys  Phe Ser Ile
    2960                 2965                 2970

Glu Lys  Val Gly Ser Leu Lys  Ala Leu Val Ser Ala  Val Arg Phe
    2975                 2980                 2985

Arg Gln  Tyr Val Thr Gly His  Ser Leu Gly Tyr Gly  Val Gly Asn
    2990                 2995                 3000

Cys Val  Pro Val Glu Thr Ile  Arg Ser Ala Gly Arg  Arg Asp Arg
    3005                 3010                 3015

Asn Gly  Asp Val Ala Pro Asp  Arg Pro Leu Lys Gln  Ala Ala Ala
    3020                 3025                 3030

Ser Pro  Pro Pro Ala Gly Val  Ala Gly Ala Leu Gly  Arg Gly Glu
    3035                 3040                 3045

Val Gly  Gln Ala Gln Asp Glu  Ser Gly Glu Thr Arg  Asp Ala Val
    3050                 3055                 3060

Glu Glu  Glu Gly Arg Gly Gln  Glu Pro Leu Gly Ser  Gly Glu Gly
    3065                 3070                 3075

Ala Ser  Gly Val Ala Ala Lys  Glu Gly His Gly Ser  Ser Arg Gly
    3080                 3085                 3090

Glu Gly  Glu Gly Ala Glu Gly  Arg Thr Asp Ser Ala  Ala Gly Ser
    3095                 3100                 3105

Thr Ala  Gly Asp Arg Ser Thr  Glu Asp Ser Ser Arg  Leu Leu Ser
    3110                 3115                 3120

Glu Gly  Arg Asp Ala Lys His  Gly Ser Ser Pro Ala  Gly Gly Ser
    3125                 3130                 3135

Glu Ala  Leu Ala Pro Gly Gly  Glu His Ala Leu Ala  Glu Gly Ser
    3140                 3145                 3150

Glu Lys  Val Gly Arg Ala Gln  Glu Thr Glu Ala Arg  Lys Glu Asp
    3155                 3160                 3165

Leu Arg  Thr Ser Gln Asn Glu  Thr His Ser Gly Glu  Asp Val Ser
    3170                 3175                 3180

Ser Leu  Asn Glu Lys Ala Leu  Asp Ser Pro Arg Ser  Ser Ala Pro
    3185                 3190                 3195

Gln Gly  Lys Ser Asp Gln Gly  Arg Glu Pro Ile Ala  Leu Arg Ile
    3200                 3205                 3210

Arg Ser  Thr Leu Pro Pro Ser  Glu Val Asp Lys Gln  Glu Ala Ala
    3215                 3220                 3225

Gly Gln  Gly Gly Ser Ala Ser  Glu Leu Ala Phe Pro  Thr Gly Val
    3230                 3235                 3240

Ser Leu  Ala Ser Pro Val Ser  Pro Phe Ser Ala Leu  Ala Arg Ser
    3245                 3250                 3255

Pro Ile  Ser Ala Arg Ala Ser  Ser Val Ser Pro Gly  Ala Cys Asp
    3260                 3265                 3270

Arg Pro  Asp Val Ser Arg Arg  His Ser Gly Ser Ser  Asp Glu Ala
    3275                 3280                 3285

Ser Glu  Ala Leu Trp Asp Leu  Gly Glu Asp Leu Gly  Phe Ala Gly
    3290                 3295                 3300

Asp Asp  Ala Asn Phe Pro Phe  Leu Asp Ser Glu Asn  Ser Ala Leu
```

-continued

```
    3305                3310                3315

Leu Phe  Ala Pro Pro Arg His  Leu Met Ser Pro Gly  Ser Ala Ser
    3320                3325                3330

Pro Thr  Gly Gly Gly Leu Gly  Ile His Tyr Asp Lys  Thr Lys His
    3335                3340                3345

Arg Trp  Lys Ala Thr Trp Thr  Thr Leu Asp Gly Gln  Arg Ala Ser
    3350                3355                3360

Thr Ser  Phe Ser Val Lys Val  Leu Gly Met Glu Arg  Ala Arg Glu
    3365                3370                3375

Leu Ala  Leu Glu Ala Arg Gln  Arg Ala Leu Ala Gly  Leu Asp Pro
    3380                3385                3390

Arg Glu  Val Arg Asp Glu Met  Val Ala Gly Gly Ala  Ala Ala Arg
    3395                3400                3405

Asp Arg  Glu Arg Glu Arg Gly  Arg Gln Asp Gly Arg  Arg Glu Gly
    3410                3415                3420

Ser Glu  Arg Arg Val Gly Phe  Glu Ala Glu Ala Glu  Gly Thr Glu
    3425                3430                3435

Ala Ala  Ser Glu Arg Leu Arg  Arg Arg Gly Glu Arg  Glu Asp Gly
    3440                3445                3450

Asp Glu  Glu Arg Arg Arg Lys  Lys Thr Arg Gly Asp  Glu Leu Arg
    3455                3460                3465

Gly Ala  Glu Gly Asp Arg Glu  Glu Arg Glu Leu Arg  Arg Arg Lys
    3470                3475                3480

Thr Ser  Glu Glu Arg Arg Lys  Gly Lys Asn Glu Ala  Ala Lys Asn
    3485                3490                3495

Glu Ala  Ala Lys Asn Glu Ala  Ala Lys Asn Glu Gly  Gly Lys Gly
    3500                3505                3510

Glu Thr  Trp Lys Val Arg Glu  Gly Gly Lys Thr Pro  Leu Gly Val
    3515                3520                3525

Lys Ser  His Arg Ala Lys Val  Val Gly Gln Thr Val  Glu Arg Arg
    3530                3535                3540

Gly Glu  Glu Arg Arg Arg Asp  Leu Arg Gly Ser Arg  Arg Glu Glu
    3545                3550                3555

Gly Lys  Thr Val Trp Gly Gln  Glu Gln Asp Ala Glu  His Gln Val
    3560                3565                3570

Phe Glu  Gly Val Lys Glu Asp  Asp Asn Glu Arg Gly  Arg Arg Arg
    3575                3580                3585

Glu Arg  Arg Arg Phe Glu Glu  Arg Asp Ser Leu Arg  Gly Ser His
    3590                3595                3600

Gly Ala  Thr Pro Ser Asp Glu  Gln Arg Gln Met Arg  Arg Gln Thr
    3605                3610                3615

Ile Leu  Gly Ser Arg Glu Val  Asp Gly Lys Pro Leu  Ser Phe Asp
    3620                3625                3630

Asp Thr  His Arg Val Asp Ala  Gln Leu Gly Ile Gln  Asn Glu Val
    3635                3640                3645

Ala Phe  Pro Gly Pro Gln Gly  Val Gly Gly Ala Gly  Asn Ser Leu
    3650                3655                3660

Gln Phe  Gly Arg Glu Gly Glu  Arg Phe Ala Ser Ser  Ser Pro Val
    3665                3670                3675

Ala Phe  Leu Arg Thr Lys Glu  Glu Asp Glu Glu Ile  Val Glu Val
    3680                3685                3690
```

-continued

```
Phe Leu  Thr Pro Glu Gly Ser  Gly Ser Glu Arg Asp  Lys Ala Ser
    3695                 3700                 3705

Ser Val  Ser Ala Ser Ser Ala  Pro Arg Asp Ser Arg  Pro Ala Ser
    3710                 3715                 3720

Pro Arg  Leu Arg Ala Ser Arg  Leu Arg Glu Ser Ala  Arg Leu Gln
    3725                 3730                 3735

Arg Arg  Leu Glu Glu Ala Glu  Val His Asp Arg Gly  Ser Arg Pro
    3740                 3745                 3750

Leu Arg  Pro Glu Glu Arg Arg  Val Ala Lys Arg His  Val Ala Glu
    3755                 3760                 3765

Glu Asn  Val Asp Ala Thr Phe  Ser Ala Gly Ala Gly  Gly Thr Lys
    3770                 3775                 3780

Lys Ile  Arg Pro His Ser Ser  His Asp Phe Ser Ala  Glu Gly Leu
    3785                 3790                 3795

Ser Lys  Phe Gln Glu Leu Leu  Thr Trp Asp Cys Glu  Val Glu Ile
    3800                 3805                 3810

Asp Gly  Thr Asp Ala His Val  Trp Arg Ala Val Ala  Ala Leu Pro
    3815                 3820                 3825

Gly Pro  Arg Pro Arg Pro Arg  Tyr Val
    3830                 3835


<210> SEQ ID NO 20
<211> LENGTH: 1292
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Cys Gln Glu Arg Lys Pro Arg Glu Leu Ser Leu Arg Asn Asn Ser
1               5                   10                  15

Arg Ala Arg Glu Arg Arg Gly Ser Lys Leu Glu Pro Gly Val Ser Cys
            20                  25                  30

Leu Ser Leu Ser Ala Cys Pro Ser Val Ala Pro Asn Asp Arg Gly Gly
        35                  40                  45

Val Thr Thr Pro Arg Ser Leu His Ala Trp Thr Arg Glu Val Ser Ala
    50                  55                  60

Cys Arg Leu Pro Arg Gln Gln Val Ser Arg Pro Leu Pro Arg Arg Ser
65                  70                  75                  80

Leu Ser Arg Pro Arg Ser Glu Pro Asp Ala Ser Pro Val Lys Gly Pro
                85                  90                  95

Gly Gln Arg Val Glu Ala Ser Ala Val Glu Gly Gly Pro Ser Ala Ser
            100                 105                 110

Ser Ala Glu Arg Leu Gln Val Asp Asp Gly Leu Ala Ala Met Arg Lys
        115                 120                 125

Thr Lys Lys Gly Lys Gly Glu Glu Gly Gly Glu Glu Thr Glu Arg Trp
    130                 135                 140

Ala Thr Gln Ala Val Glu Gln Gln Gly Thr Leu Lys Pro Ala Gly Glu
145                 150                 155                 160

Glu Thr Ala Val Pro Gly Ala Ser Glu Arg Ser Ala Ser Pro Gln Gln
                165                 170                 175

Ala Met Glu Gly Ser Cys Gly Val Glu Thr Pro Glu Thr Phe Phe Gly
            180                 185                 190

Val Ser Thr Gly Asn Ser Gln Gly Ser Pro Ser Pro Glu Ser Val Ala
```

-continued

```
        195                 200                 205

Gly Glu Glu Ala Arg Pro Glu Arg Glu Asn Ala Glu Lys Ser Ala Thr
    210                 215                 220

Gly Gly Ser Ala Ser Lys Ala Lys Lys Pro Ser Arg Glu Ser Ala Arg
225                 230                 235                 240

Arg Pro Asp Thr Ala Leu Ile Asp Arg His Leu Ile Ala Ala Ser Pro
                245                 250                 255

Ser Pro Ser Ser Ala Arg Arg Ser Ser Thr Cys Ser Pro Ser Pro His
            260                 265                 270

Ser Arg Glu Gly Glu Asp Lys Pro Gly Ser Gly Ala Pro Pro Ala Ser
        275                 280                 285

Ser Pro Ser Ala Asn Ala Gly Ala Leu Glu Pro Ala Glu Lys Gly Thr
    290                 295                 300

Leu Gly Ser Pro Pro Gln Asp Val Leu Pro Ala Leu Pro Ala Ser Ser
305                 310                 315                 320

Ser Ser Pro Ser Thr Gly Gly Gly Ser Pro Leu Ser Pro Pro Pro Gly
                325                 330                 335

Gln Ala Pro Arg Ala Glu Ser Gly Ala Pro Gly Ser Gly Ala Leu Ser
            340                 345                 350

Leu Arg Arg Ser Leu Arg His Arg Gln Pro Val Arg Pro Ala Ala Ile
        355                 360                 365

Ala Val Ser Pro Leu Gly Gly Pro Gly Ser Ser Leu Ser Ser Arg Ser
    370                 375                 380

Ala Ser Pro Thr Arg Arg Gly Gly Val Ser Pro Cys Gly Pro Ala Thr
385                 390                 395                 400

Ala Val Gly Lys Gly Ala Gly Ala Ala Ser Gly Ala Ala Ala Leu Pro
                405                 410                 415

Gly Val Gly Ala Lys Ala Pro Pro Ser Ala Thr Pro Leu Ala Gly Leu
            420                 425                 430

Ser Gly Arg Ser Leu Leu Ala Ser Val Ser Pro Ser Ala Ala Ala Leu
        435                 440                 445

Gly Pro Gly Ala Pro Gly Lys Lys Lys Ala Gly Gln Val Gln Gly Ala
    450                 455                 460

Ala Lys Ala Arg Gly Ala Pro Pro Phe Val Leu Ala Glu Tyr Trp Pro
465                 470                 475                 480

Gly Val Thr Leu Asp Glu Met Glu Lys Gly Glu Leu Ser Trp Ala Arg
                485                 490                 495

Ala Ala Ala Gly Leu Pro Leu Pro Ala Ser Pro His Lys Val Pro Gly
            500                 505                 510

Gly Pro Ala Pro Pro Val Gly Gly Pro Pro Ala Arg Asp Glu Asp Ser
        515                 520                 525

Val Ala Ala Cys Ala Gly Glu Lys Gly Lys Glu Lys Ala Phe Leu Gly
    530                 535                 540

Ser Gly Arg Ser Gln Ala Ala Gln Gly Leu Pro Gly Ile Asp Ala Val
545                 550                 555                 560

Ala Ala Ala Cys Trp Gly Gly Ala Gly Val Asp Ser Arg Val Leu Ala
                565                 570                 575

Pro Ala Glu Gly Glu Ala Ser Gly Ala Phe Gly Pro Gly Gly Glu Lys
            580                 585                 590

Lys Lys Val His Ala Ser Ser Asp Ser Ser Gly Gly Ser Arg Ala Ala
        595                 600                 605
```

-continued

```
Leu Gly Gly Arg Ala Ser Val Gln Gly Lys Ala Arg Lys Pro Ala Gly
    610                 615                 620

Trp Glu Glu Glu Arg Gly Arg Arg Asp Asp Arg Ser Arg Gly Arg Arg
625                 630                 635                 640

Asp Glu Thr Asp Gly Pro Arg Phe Asp Val Thr Trp Phe Val Asp Asp
                645                 650                 655

Ser Pro Leu Ala His Thr Arg Lys Arg Thr Arg Trp Asp Ser Leu Trp
            660                 665                 670

Val Arg Pro Ala Ser Pro Val Arg Val Val Gly Asp Ser Ala Pro Glu
        675                 680                 685

Glu Ser Pro Glu Arg Arg Glu Gly Gly Gly Arg Ala Pro Asp Leu Gln
    690                 695                 700

Ala Ser Met Ala Lys Arg Arg Thr Ala Asp Ser Gly Leu Glu Glu Glu
705                 710                 715                 720

Ala Gln Val Glu Arg Gly Phe Ser Ser Ser Asp Ser Asp Asp Cys Asp
                725                 730                 735

Trp His Leu Pro Thr Arg Thr Val Ser Ser Ser Leu Ala Pro Phe Ala
            740                 745                 750

Ala Ser Lys Ala His Leu Val Pro Arg Cys Cys Tyr Cys Leu Leu Pro
        755                 760                 765

Arg Arg Leu Pro Gly Arg His Thr Glu Ala Gly Gly Pro Pro Arg Asp
    770                 775                 780

Leu Leu Gly Trp Ser Thr Ser Val Glu Ser Glu Glu Thr Arg Gly Arg
785                 790                 795                 800

Tyr Leu Gln Leu Tyr Cys Ala Cys Thr Lys Arg Pro Phe Gly Glu Ser
                805                 810                 815

Val Leu Gln Gly Ala Ala Gly Arg Arg Gly Leu Leu Leu Pro Val Ala
            820                 825                 830

Thr Asn Ala Leu Leu Tyr Ser Val Arg Arg Val Ala Leu Asp Gly Ala
        835                 840                 845

Ala Ser Glu Gln Lys Ser Glu Ala Leu Pro Thr Ser Ala Val Ser Arg
    850                 855                 860

Pro Ser Ser Ala Val Arg Ala Arg Ser Ser Cys Ala Ser Ser Gly Cys
865                 870                 875                 880

Asp Asp Gly Arg Ala Glu Val Ala Pro Gly Ala Pro Ala Glu Thr Ile
                885                 890                 895

Tyr Arg Trp Arg Asp Pro Cys Thr Leu Gln Thr Phe Ser Ser Ser Leu
            900                 905                 910

Asp Arg Ile Gln Gly Ser Leu Ala Ala Thr Ala Ala Val Ala Ala Ala
        915                 920                 925

Ala Glu Ser Ala Gly Lys Pro Val Ala Phe Leu Pro Arg Leu Tyr Trp
    930                 935                 940

Asp Ser Gln Ala Asp Cys Tyr Ile Ala Ser Cys Leu Arg Trp Glu Glu
945                 950                 955                 960

Glu Ala Gln Pro Thr Pro Ala Ala Glu Arg Gly Glu Lys Arg Asn Gly
                965                 970                 975

Val Glu Arg Pro Ala Glu Ala Arg Glu Arg Gly Arg Asp Glu Lys Lys
            980                 985                 990

Pro Glu Asp Pro Ser Val Pro Gly  Leu Arg Arg Arg Ser  Leu Lys Leu
        995                 1000                 1005
```

-continued

Leu Gln Lys Lys Phe Ser Val Ala Phe Leu Gly Asp Ala Lys Ala
1010 1015 1020

His Phe Tyr Ala Ser Glu Trp Leu Lys Trp Gln His Lys Gly Gln
1025 1030 1035

Arg Met Met Asp Glu Glu Asp Arg Arg Gln Glu Val Ala Arg Gln
1040 1045 1050

Met Leu Leu Val Ser Pro Leu Leu Ala Gly Arg Lys Ala Pro Ala
1055 1060 1065

Lys Ala Pro Gly Gly Cys Ser Lys Lys Ala Ser Ser Leu Ser Ala
1070 1075 1080

Ala Gln Leu Ala Leu Ala Ser Gly Arg Pro Leu Thr Pro Glu Glu
1085 1090 1095

Glu Ala Glu Leu Lys Arg Gln Leu Glu Asn Lys Glu Arg Gln Lys
1100 1105 1110

Lys Gln Lys Leu Leu Arg Gln Gln Trp Arg Arg Gln Gln Ala Arg
1115 1120 1125

Glu Ala Lys Leu Arg Leu Arg Glu Ala Glu Ala Ala Ala Ala Ala
1130 1135 1140

Ala Ala Ala Ala Gly Ala Pro Ser Ala Pro Gly Thr Thr Gly Ala
1145 1150 1155

Ser Gln Thr Arg Ser Pro Gln Ser Gln Gln Lys Ser Glu Ser Leu
1160 1165 1170

Pro Val Leu Arg Ser Lys Thr Glu Val Leu Gln Pro Ser Pro Gly
1175 1180 1185

Ala Ser Phe Ala Pro Ala Ser Ser Arg Ser Thr Leu Pro Ala Gly
1190 1195 1200

Glu Ser Gly Ala Ala Pro Cys Glu Gly Val Gly Thr Arg Arg Ser
1205 1210 1215

Ala Ala Ser Ala Thr Ser Val Ala Pro Glu Lys Val Thr Gly Arg
1220 1225 1230

Lys Ser Glu Thr Ala Arg Asp Ala Ala Ser Ala Ser Leu Glu Ala
1235 1240 1245

Ala Lys Ser Thr Met Val Thr Arg Gly Gly Gly Arg Gly Ser Ser
1250 1255 1260

Val Val Ala Val Thr Arg Ser Thr Ser Ser Pro Ser Gly Arg Ala
1265 1270 1275

Ala Ser Val Ala Ser Ser Thr Leu Gly Gly Phe Gly Ala Arg
1280 1285 1290

<210> SEQ ID NO 21
<211> LENGTH: 2406
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

Met Ala Ala Pro Ala Pro Ser Ala Glu Ala Arg Pro Ala Lys Arg Arg
1 5 10 15

Cys Phe Pro Leu Pro Arg Glu Thr Pro Val Ser Ser Glu Asp Glu Thr
20 25 30

Arg Lys Thr Leu Gln His Asp Thr Leu Gly Cys Leu Pro Arg Ser Ser
35 40 45

Ser Gly Gln Pro Glu Leu Ala Ala Ala Ser Ala Ala Ser Gln Val Gly
50 55 60

-continued

```
His Leu Ser Ser Ala Ala Leu Leu Gln Leu Val Gln Thr Gln Ser Ala
65                  70                  75                  80

Gly Gly Val Pro Gln Ala Val Leu Arg Asn Leu Phe Ser Ser Ile His
                85                  90                  95

Arg Asn Pro Lys Pro Leu Pro Ala Asn Ala Leu Ala Ala Thr Pro Asn
            100                 105                 110

Ser Ser Leu Tyr Ala Ser Leu Thr Ser Leu Ser Ser Ala Ala Ala Leu
        115                 120                 125

Pro Gly Ala Gly Pro Ala Tyr Ser Gln Ala Pro Ser Pro Ala Ser Ala
    130                 135                 140

Asp Leu Leu Gln Ser Glu Gln Phe Arg Ser Ala Ala Lys Asn Pro Ser
145                 150                 155                 160

Pro Asn Glu Ala Ser Pro Ile Leu Ala Leu Leu Gly Glu Ala Ala Arg
                165                 170                 175

Ala Ala Thr Thr Pro Arg Thr Val Pro Ala Leu Ser Ala Val Cys Pro
            180                 185                 190

Ala Ala Ser Ser Gly Val Ser Leu Pro Pro Ala Ser Asp Thr Leu Ala
        195                 200                 205

Leu Ala Gln Ser Ser Leu Ser Ser Ser Thr Gly Cys Ala Ser Asp Val
    210                 215                 220

Lys Ala Ser Arg Pro Glu Glu His Pro Ala Phe Ala Ser Gly Thr Ala
225                 230                 235                 240

Asn Arg Gln Ser Leu Leu Gln Ala Leu Leu Leu Ser Thr Ala Pro Leu
                245                 250                 255

Ala Phe Ser Gly Pro Ser Leu Ser Ser Ala Ser Thr Thr Leu Pro Ala
            260                 265                 270

Ser Ser Gly Ala Val Ser Ser Arg Asn Ala Gly Ala Tyr Gln Phe Glu
        275                 280                 285

Arg Leu Leu Gln Ala Glu Ala Ala Lys Val Lys Ala Leu Leu Pro Asn
    290                 295                 300

Thr Thr Ser Lys Ser Met Ser Gln Ser Ser Val Pro Gln Arg Asp Leu
305                 310                 315                 320

Thr Arg Lys Thr Ser Leu Phe Pro Asp Pro Arg Gly Leu Ser Ala Asp
                325                 330                 335

Asp Ala Ser Arg Arg Tyr Asn Thr Arg Gly Ala Asn Ser Gly Gly Ala
            340                 345                 350

Gly Leu Arg Arg Gly Thr Gly Val His Ala Thr Thr Glu Gln Ser Gly
        355                 360                 365

Ala Leu Asp Ala Gly Glu Arg Thr Arg Pro Phe Gly Ala Gly Glu Asp
    370                 375                 380

Glu Ser Ala Gln Gly Lys Pro Asp Ser Arg Gly Arg Gln Arg Pro Gly
385                 390                 395                 400

Ala Leu Asp Ala Ser Asn Ile Leu Gly Leu Leu Ala Ala Phe Gln Pro
                405                 410                 415

Ser Gln Ala Pro Ala Ile Arg Asp Leu Ser Ala Pro Ser His Leu Ser
            420                 425                 430

Ala Ala Ala Thr Gly Ala Leu Pro Leu Thr Ala Ser Phe Thr Ala Ser
        435                 440                 445

Ala Leu Ala Ser Ser Gln Cys Leu Pro Ala Gly Thr Pro Ala Ser Ser
    450                 455                 460
```

-continued

```
Ser Ala Ser Pro Pro Phe Ser Glu Val Leu Ser Thr Thr Glu Glu Ser
465                 470                 475                 480

Ser Thr Thr Lys Glu Thr Asp Ala Ser Ala Ser Thr Leu Leu Ala Phe
                485                 490                 495

Leu Gln Lys Tyr Ser Ala Val Ser Gly Leu Gly Gly Ala Ser Asp Phe
            500                 505                 510

Leu Gly Gln Leu Gln Gly Lys Thr Ser Leu Pro Pro Leu Ser Leu Ala
        515                 520                 525

Glu Pro Ser Ser Ala Leu Pro Ser Ser Phe Leu Gly Gly Ser Asp Gly
    530                 535                 540

Gly Thr Ile Asp Thr Arg Asn Gly Asn Gly Glu Lys Thr Thr Pro Pro
545                 550                 555                 560

Ile His Leu Phe Gln Ser Ala Phe Arg Met Pro Ser Pro Ser Gln Gln
                565                 570                 575

Asn Leu Leu Asp Ala Leu Leu Ala Ser Ser Cys Thr Thr Ala Thr Ser
            580                 585                 590

Arg Ser Asp Gly Ser Gly Asn Leu Gly Cys Pro Val Val Asp Glu Arg
        595                 600                 605

Asn Ala Lys Leu Ala Gly Pro Ala His Pro Leu Pro Cys Ser Phe Pro
    610                 615                 620

Gln Ile Ser Ser Ser Ser Gly Glu Pro Gly Arg Lys Thr Gly Gly Arg
625                 630                 635                 640

Val His Arg Gln Gly Thr Ser Gln Ser Gly Gly Arg Val Arg Ser Gly
                645                 650                 655

Lys Asn Gly Gly Ser Ala Ala Pro Pro Arg Gln Ser Ser Ser Asp Asn
            660                 665                 670

Val Pro Ser Thr Pro Thr Val Ser Ser His Glu Ala Pro His Arg Ala
        675                 680                 685

Gly Phe Pro Ser Gln Thr Pro Tyr Glu Leu Ser Ala Ser Pro Ser His
    690                 695                 700

Gln Leu Asp Leu Leu Arg Leu Gly Ala Phe Leu Gly Gly Ala Gly Lys
705                 710                 715                 720

Gln Asp Ala Ser Val His Ser Asp Glu Thr Gly Thr Leu Ser Gly Glu
                725                 730                 735

Pro Ser His Arg Ser Cys Ser Leu Ser Arg Gly Leu Thr Gln Glu Ser
            740                 745                 750

Val Leu Gln Leu Ser Asp Thr Thr Ser Thr Ser Arg Glu Gly Glu Pro
        755                 760                 765

Asn Glu Pro Ser Gln Gly Cys Val Asn Val Ala Ala Ser Leu Pro Ala
    770                 775                 780

Phe Gly Pro Gln Pro Ser Ser Gly Ala Ala Lys Ala Arg Glu Gly Arg
785                 790                 795                 800

Arg Gly Ala Gly Gly Ala Gly Ala Ala Pro Pro Val Pro Leu Arg Ala
                805                 810                 815

Asp Val Thr Leu Gly Gly Asn Arg Pro His Tyr His Val Ala Lys Gln
            820                 825                 830

Glu Trp Arg Val Arg Tyr Tyr Met Asn Gly Lys Arg Lys Met Arg Thr
        835                 840                 845

Tyr Ser Ala Lys Phe Tyr Gly Tyr Glu Thr Ala His Thr Met Ala Glu
    850                 855                 860

Asp Phe Ala His Tyr Val Asp Lys His Glu Ala Leu Pro Asp Ser Met
```

-continued

```
865                 870                 875                 880

Met Met Thr Ala Met Met Leu Gln Ala Gln Ala Asn Ser Ala Ala Ser
                885                 890                 895

Ser Gly Gln Thr Val Pro Leu Ala Arg Gly Ile Arg Ala Ser Ser Ala
            900                 905                 910

Ser Thr Gly Ala Gly Gly His Val Ser Lys Ser Ala Thr Lys Gly Ser
        915                 920                 925

Val Ala Ala Ser Ser Glu Gly Ser Thr Ser Met Gly Ser Asp Ala Thr
    930                 935                 940

Arg Ser Gln Glu Gly Glu Ala Ala Glu Leu Cys Pro Leu Ala Ala Gly
945                 950                 955                 960

Leu Ser Arg Pro Leu Ala Ser Met His Ser Ala Ala Gly Asn Ala Val
                965                 970                 975

Ala Gln Gly Arg Gln Glu Ser Lys Glu Glu Ala Pro Gly Gly Gln Ala
            980                 985                 990

Trp Phe Gly Glu Pro Gly Lys Phe  Arg Ala Ser Ser Glu  Ala Ala Leu
        995                 1000                1005

Cys Gly  Ser Gly Ser Ser Ala  Glu Gly Arg Asp Gly  His Glu Ser
    1010                 1015                 1020

Glu Val  Leu Trp Ala Thr Leu  Gly Lys Val His Asp  Ala Ser Gln
    1025                 1030                 1035

Gly Lys  Lys Ile Lys Pro Glu  Lys Pro Leu Thr Val  Ala Arg Gly
    1040                 1045                 1050

Arg Leu  Ala Leu Gly Ala Glu  Asp Lys Ser Gln Asn  Leu Gly Val
    1055                 1060                 1065

Asp Leu  Val Asp Ser Gly Glu  Ala Gln Gly Leu Pro  Gly Val Arg
    1070                 1075                 1080

Gln Pro  Arg Gln Met Lys Asn  Ser Glu Glu Cys Ser  Leu Arg Asp
    1085                 1090                 1095

Ser Asp  Lys Gly Met Ala Leu  Ser Lys Arg Phe Gly  Phe Leu Pro
    1100                 1105                 1110

Ser Gln  Thr Pro Ser Cys Asp  Ser Met Thr Leu Pro  Phe Pro Gly
    1115                 1120                 1125

Gly Phe  Asp Ala Leu Ser Leu  Ser Ser Ala Leu Ser  Ser Cys Ala
    1130                 1135                 1140

Ser Leu  Pro Val Ala His Glu  Gly Asn Asn Phe Gln  Lys Gly His
    1145                 1150                 1155

Thr Gly  Asp Ile Val Ala Leu  Ala Ser Gln Ser Gly  Thr Gln Arg
    1160                 1165                 1170

Pro Ala  Ser Val Val Leu Ser  Arg Asp Ala Asn Val  Ser Gly Ser
    1175                 1180                 1185

Ser Pro  Ser His Pro Thr Trp  Gln Arg Glu Gly Ala  Ala Val Ser
    1190                 1195                 1200

Gly Arg  Ala Asp Glu Phe Ser  Ser Leu Ser Val Thr  Pro Ser Thr
    1205                 1210                 1215

Val Pro  Leu Ser Ser Phe Thr  Met Glu Asp Ile Lys  Gly Glu Lys
    1220                 1225                 1230

Gly Asp  Pro Ser Arg Arg Phe  Ala Leu Val Gly Glu  Ser Met Lys
    1235                 1240                 1245

Asn Val  Ser Ala Pro Glu Val  Gln Ala Leu Phe Pro  Thr Ser Ser
    1250                 1255                 1260
```

-continued

```
Ile Ala  Asn Ala Glu Leu Leu  Pro Val Asp Phe Leu  His Ser Asn
    1265                 1270                 1275

Ser Cys  Ser Ala Asp Lys Leu  Glu Ser Ser Ile Pro  Arg Gly Leu
    1280                 1285                 1290

Ala Gly  Asn Asn Pro Ser Met  Thr Ala Thr Ala Val  Ala Ala Thr
    1295                 1300                 1305

Ala Val  Ser His Gln Ile Phe  Asp Thr Ile Thr Leu  Phe Gly Glu
    1310                 1315                 1320

Phe Leu  Arg Glu Phe Ala Lys  Glu Lys Val Asn Glu  Phe His Glu
    1325                 1330                 1335

Tyr Gly  Leu Glu Ala Ser Pro  Leu Thr Val Glu Ala  Ser Ser Glu
    1340                 1345                 1350

Val Ser  Leu Phe Gly Lys Ala  Thr Phe Gly Arg Cys  Pro Val Ala
    1355                 1360                 1365

Gly Gly  Ser Thr Pro Ala Gly  Ile Ser Lys Met Ser  Gly Glu Thr
    1370                 1375                 1380

Leu Ser  Gly Leu Ser Ala Ser  Glu Leu Ser Leu Val  Ser Ala Arg
    1385                 1390                 1395

Thr Asn  Thr Thr Thr Gly Glu  Glu Gln Phe Ala Leu  Ala Arg Gly
    1400                 1405                 1410

Leu Phe  Pro Gly Asp Ser Glu  Gly Asp Arg Asp Glu  Lys Lys Pro
    1415                 1420                 1425

Gln Leu  Ser Gln Gln Glu Leu  Leu Val Leu Ser His  Ala Leu Val
    1430                 1435                 1440

Asn Leu  Thr Ser Ser Thr Tyr  Val Leu Met His Thr  Leu Lys Ala
    1445                 1450                 1455

Ser Leu  Ser Lys Ser Thr Glu  Ala Val Gln Leu His  Gln Pro Leu
    1460                 1465                 1470

Leu Glu  Ala Ala Ser Glu Ala  Lys Ala Thr Asp Glu  Ala Lys Thr
    1475                 1480                 1485

Arg Glu  Glu Gln Glu Ser Ser  Glu Cys Asp His Glu  Tyr Pro Pro
    1490                 1495                 1500

Arg Ser  Ser Leu Glu Ala Thr  Thr Gly Ala Leu Pro  Phe Arg Leu
    1505                 1510                 1515

Ser Pro  Ala Leu Ser Ala Ser  Ser Lys Asp Leu Pro  Ser Leu Ser
    1520                 1525                 1530

Ala Ser  Ala Ser Leu Glu Ser  Val Thr Pro Phe Ala  Gly Leu Pro
    1535                 1540                 1545

Leu Glu  Glu Gly Thr Leu Ser  Ala Ser Val Gly Leu  Ala Ser Ser
    1550                 1555                 1560

Asp Asp  Glu His Asp Thr Ser  Leu Leu Phe Lys Thr  Glu Ala Ala
    1565                 1570                 1575

Lys Lys  Arg Ser Leu Phe Ser  Thr Ala Ala Asp Gly  Asp Glu Ser
    1580                 1585                 1590

Arg Thr  Tyr Asn Asp Gly Leu  Gly Gln Pro Met Glu  Glu Glu Ile
    1595                 1600                 1605

Arg Ser  Cys Val Ser Thr Ser  Cys Gly Glu Ala Val  Ala Thr Thr
    1610                 1615                 1620

Thr Leu  Ser Ala Ile Gly Pro  Gly Thr Gly Ala Ser  Gly Ala Leu
    1625                 1630                 1635
```

-continued

```
Leu Asp  Ser Glu Ser Arg Glu  Ser Leu Gly Glu Lys  Pro Gly Ala
    1640                 1645                 1650

Ala Leu  Arg Ala Gly Ala His  Thr Pro Ala Pro Ser  Arg Ala Pro
    1655                 1660                 1665

Thr Pro  Ser Arg Thr Phe Ser  Phe Thr Ser Ser Ser  Thr Ala Thr
    1670                 1675                 1680

Ser Ala  Ala Leu Leu Cys Asp  Ser Asn Val Val His  Glu Lys Leu
    1685                 1690                 1695

Arg Ala  Gln Gly Lys Asp Ser  Glu Ala Gly Glu Arg  Lys Gly Asp
    1700                 1705                 1710

Ser Glu  Lys Glu Glu Glu Val  Glu Met Trp Lys Glu  Glu Asp Glu
    1715                 1720                 1725

Glu Val  Gln Arg Cys Thr Gly  Ser Ala Glu Thr Asp  Ser Thr Glu
    1730                 1735                 1740

Ala Thr  Arg Gly Glu Glu Ala  Trp Arg Arg Gly Lys  Gln Ser Glu
    1745                 1750                 1755

Lys Lys  Pro Ser Val Ile Thr  Thr Ala Leu Asn Leu  Leu Glu Thr
    1760                 1765                 1770

His Arg  His Leu Ala Leu Thr  Ile Ser Gln Leu Lys  Arg Pro Val
    1775                 1780                 1785

Ala Gln  Gln Leu Arg Phe Ile  Leu Pro Ile Ala Ala  Pro Gln Leu
    1790                 1795                 1800

Leu Pro  Cys Ile Leu Pro Pro  Ala Ser Phe Gln Gly  Pro Gly Glu
    1805                 1810                 1815

Ser Gly  Asp Gly Lys Ala Glu  Ala Glu Ala Lys Gly  Ser Ser Ser
    1820                 1825                 1830

Leu Gly  Gln Val Leu Glu Thr  Ala Leu Gly His Gly  Thr Arg Leu
    1835                 1840                 1845

Ala Pro  Ser Ala Ser Ala Met  Val Pro Pro Arg Lys  Asp Glu Ala
    1850                 1855                 1860

Ala Ser  Ala Val Pro Glu Ala  Lys Thr Phe Thr Gly  Leu Ala Asn
    1865                 1870                 1875

Ala Gly  Val Met Arg Glu Ala  Ala Ser Arg Thr Leu  Glu Ala Glu
    1880                 1885                 1890

Gln Val  Ser Arg Lys Arg Ser  Arg Glu Glu Val Val  Asp Ser Glu
    1895                 1900                 1905

Thr Ala  Gly Asp Glu Gly Asp  Met Glu Asn Val Pro  Glu Thr Leu
    1910                 1915                 1920

Asp Ala  Thr Thr Ser Pro Gly  Ser Arg Gln Tyr Asp  Lys Ser Pro
    1925                 1930                 1935

Ser Asn  Gly Gly Thr Lys Pro  Pro Ala Thr Ala Lys  Ser Arg Val
    1940                 1945                 1950

Ile Arg  Asp Gln Ala Ala Leu  Glu Arg Leu Leu Leu  Ala Pro Phe
    1955                 1960                 1965

Gln Asp  Thr Pro Thr Cys Ser  Cys Thr Asp Arg Pro  Cys Pro Cys
    1970                 1975                 1980

Asp Arg  Gln Gln Val Ala Asp  Met Ile Tyr Leu Phe  Tyr Ala Val
    1985                 1990                 1995

Pro Ala  Arg Gln Gln Ala Glu  Ser Ser Lys Glu Gly  Ser Thr Gln
    2000                 2005                 2010

Arg Leu  Gln Phe Ala Ala Arg  Asp Thr Asn Glu Arg  Lys Asp Ala
```

-continued

```
    2015                2020                2025

Arg Thr  Gly Glu Glu Thr Gln  Gly Gly Glu Thr Glu  Ala Lys Glu
    2030                2035                2040

Val Ile  Arg Asp Pro Glu Glu  Arg Gly Val Cys Glu  Gly Ser Ser
    2045                2050                2055

Ser Gln  Asn Ala His Thr Gln  Phe Asp Ala Glu Thr  Ala Ser Ser
    2060                2065                2070

Ser Met  Ser Ser Asp Pro Arg  Ala Asp Lys Glu Ser  Asn Ala Gln
    2075                2080                2085

Asp Ala  His Met Ala Asp Lys  Thr Ser Phe Val Ser  Asp Leu Pro
    2090                2095                2100

Gln Pro  Ser Gly Glu Phe Ala  Pro Ser Leu Leu Ser  Glu Thr Ser
    2105                2110                2115

Leu Asp  Val Ala Met Ala Asp  Ser Arg Gly Thr Thr  Ser Glu Ile
    2120                2125                2130

His Gly  Phe Phe Thr Arg Ser  Asp Glu Gln Lys Arg  Ala Ser Phe
    2135                2140                2145

Ser Ser  Ser Ser Leu Leu Ala  Ala Gly His Ala Val  Ala Ser Phe
    2150                2155                2160

Ser Ser  Ser Leu Ala Gly Val  Val Ser Gly Ala Gly  Glu Arg Arg
    2165                2170                2175

Glu Cys  Ala Gly Pro Ser Leu  Gly Asp Leu Ser Thr  Ile Gly Leu
    2180                2185                2190

Leu Ser  Leu Ser Tyr Pro Ala  Met Leu Ala Phe Ile  Leu Pro Leu
    2195                2200                2205

Gln Ser  Leu Leu His Met Val  Ser Gly Met Ile Leu  Thr Leu His
    2210                2215                2220

Lys Lys  Leu Ile His Arg Phe  Ile Cys Ala His Leu  Arg Leu Val
    2225                2230                2235

Leu Asp  Asp Asp Met Arg Arg  Pro Ala Gly Gly Ala  Leu Lys Ser
    2240                2245                2250

Arg Gly  Ala His Gly Asp Thr  Glu Ala Ala Glu Ala  Gln Val Glu
    2255                2260                2265

Arg Arg  Arg Arg Glu His Glu  Arg Glu Glu Thr Thr  Asn Leu Ala
    2270                2275                2280

Ile Gly  Tyr Arg Glu Gly Asn  Ala Glu Ala Ser Asn  Thr Phe Pro
    2285                2290                2295

Leu Val  Asp Thr Val Ser Ser  Leu Leu Ser Pro Gly  Ser Leu Arg
    2300                2305                2310

Gln Glu  Asn Ser Glu Val Glu  Arg Arg Asp Asn Asp  Glu Glu Arg
    2315                2320                2325

Leu Glu  Leu Ile Thr Gly Ile  Ala Arg Glu Ser Pro  Lys Pro Ser
    2330                2335                2340

Glu Lys  Asp Ser Val Ser Pro  Phe Leu Ser Thr Ala  Pro Cys Pro
    2345                2350                2355

Gly Thr  Glu Ala Glu Ser Ser  Asp Cys Ser Ala Ser  Ser Ala Cys
    2360                2365                2370

Ser Gly  Thr Pro Thr Glu Gly  Thr Glu Gly Gly Glu  Thr Gly Asp
    2375                2380                2385

Ile Ala  Ser Phe Leu Ser Pro  Ser Gly Asp Val Lys  Gln Thr Ile
    2390                2395                2400
```

-continued

```
Met Leu  Ala
    2405


<210> SEQ ID NO 22
<211> LENGTH: 711
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Pro Leu Lys Thr Ser Trp His Cys Ser Cys Asn Ala Thr Phe Pro
1               5                   10                  15

Gly Asp Leu Leu Met Val Val Ala Asn His Asp Arg Val Gly Asn Trp
            20                  25                  30

Asn Pro Gln Asn Ser Val Val Leu Ser Thr Asp Ala Ser Ser Phe Pro
        35                  40                  45

Thr Trp Arg Ser Gly Glu Val Cys Phe Asp Glu Gln Gln Pro Val Arg
    50                  55                  60

Leu Glu Tyr Lys Leu Ile Ile Arg Arg Ala Ser Gly Glu Ile Tyr Trp
65                  70                  75                  80

Glu Pro Ile Pro Thr Asn Arg Val Val Thr Leu Thr Ala Asn Thr Ser
                85                  90                  95

Ser Val Ile Glu Asn Val Trp Gly Ser Leu Ala Thr Cys Ser Ile Thr
            100                 105                 110

Phe Phe Pro Leu Gln Pro Ile Pro Ser Pro Ser Phe Tyr Lys His Ala
        115                 120                 125

Glu Arg Thr Lys Lys Glu Ala Ser Ser Val His Leu His Ser Ala Ser
    130                 135                 140

Ile Ser Asp Asp Ser Gly Ser Asp Thr Gly Thr Cys Ser Gln Val Asp
145                 150                 155                 160

Glu Ser Arg Thr Gln Arg Asn Val Arg Gly Gln Pro Ala Ser Val Gly
                165                 170                 175

Thr Gly Lys Ala Thr Ala Ala Glu Arg Gly Gly Lys Gly Tyr Val Met
            180                 185                 190

Pro His His Gln Cys Ser Thr Ser Gln Arg Arg His Ser Ile Ser Thr
        195                 200                 205

Gln Ala Ala Asp Glu Ala Ala Gly Gly Gly Asn Arg Val Ser Phe Lys
    210                 215                 220

Arg Ser Ala Phe Ile Leu Ala Asn Thr Gly Pro Ile Thr Asn Tyr Tyr
225                 230                 235                 240

Thr Val Ser Lys Thr Ile Gly Arg Gly Thr Trp Gly Glu Val Lys Leu
                245                 250                 255

Val Ile Asp Asn Gly Thr Gly Ala Arg Arg Ala Ala Lys Lys Ile Pro
            260                 265                 270

Lys Cys Tyr Val Glu Asp Ala Asp Arg Phe Arg Gln Glu Ile Glu Ile
        275                 280                 285

Met Lys Ser Leu Asp His Pro Asn Ile Val Arg Leu Tyr Glu Thr Phe
    290                 295                 300

Glu Asp Met Thr Asp Phe Tyr Leu Val Met Glu Tyr Cys Thr Gly Gly
305                 310                 315                 320

Glu Leu Phe Asp Arg Leu Val His Gln Gly Val Phe Thr Glu Ala Leu
                325                 330                 335

Ala Cys Arg Ile Met Arg Gln Ile Leu Ala Ala Val Ala Tyr Cys His
```

-continued

```
            340                 345                 350

Ala His Arg Val Ala His Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe
        355                 360                 365

Leu His Asp Asn Pro Glu Ser Pro Ile Lys Leu Ile Asp Phe Gly Leu
    370                 375                 380

Ala Ala Arg Phe Lys Ser Gly Gln Pro Met Arg Thr Arg Ala Gly Thr
385                 390                 395                 400

Pro Tyr Tyr Val Ser Pro Gln Val Leu Glu Gly Arg Tyr Gly Pro Glu
                405                 410                 415

Cys Asp Val Trp Ser Ala Gly Val Met Met Tyr Ile Leu Leu Cys Gly
            420                 425                 430

Tyr Pro Pro Phe Asn Ala Pro Ser Asp Arg Ala Ile Met Asn Lys Val
        435                 440                 445

Arg Ala Gly His Tyr Thr Phe Pro Asp Ser Glu Trp Ser Arg Val Ser
    450                 455                 460

Leu Gln Ala Lys Asp Leu Ile Ser Arg Leu Leu Asp Arg His Pro Arg
465                 470                 475                 480

Thr Arg Ile Ser Ala Glu Gln Ala Leu Arg His Ala Trp Phe Ala Met
                485                 490                 495

His Ala Pro Gly Asp His Phe Glu Pro Leu Gly Leu Asp Ile Leu Ser
            500                 505                 510

Lys Phe Arg Arg Phe Gln Gly Leu Ser Arg Leu Lys Lys Leu Ala Leu
        515                 520                 525

Thr Val Ile Ala Gln His Leu Glu Asp Ser Glu Ile Glu Gly Leu Lys
    530                 535                 540

Asn Leu Phe Thr Gln Leu Asp Thr Glu Gly Asp Gly Val Leu Thr Val
545                 550                 555                 560

Glu Glu Ile Arg Lys Gly Ile Glu Arg Ser Gly Val His Leu Pro Pro
                565                 570                 575

Asp Met Val Leu Glu Asp Val Leu Arg Glu Val Asp Thr Ala Gly Thr
            580                 585                 590

Gly Ser Ile Asp Tyr Thr Glu Phe Ile Ala Ala Cys Leu His Gln Ser
        595                 600                 605

His Tyr Ile Arg Glu Glu Ala Cys Arg Ala Ala Phe Arg Val Leu Asp
    610                 615                 620

Ile Asn Gly Asp Gly Leu Val Ser Ala Gln Glu Leu Arg Gln Val Phe
625                 630                 635                 640

His Met Ala Gly Asp Leu Glu Thr Asp Ala Ala Ala Glu Leu Leu Glu
                645                 650                 655

Ala Asp Ala Asp Gly Asp Gly His Ile Thr Phe Asp Glu Phe Cys Gly
            660                 665                 670

Leu Met Arg Lys Val Pro Ser Leu Ala Leu Val Thr Glu His Thr Val
        675                 680                 685

Ser Met Met Arg Arg Thr Cys Ser Arg Thr Asn Ile Ser Glu Ala Ser
    690                 695                 700

Leu Thr Pro Arg Ala Thr Gly
705                 710


<210> SEQ ID NO 23
<211> LENGTH: 368
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
```

-continued

```
<400> SEQUENCE: 23

Met Val Ser Arg Thr Leu Ser Leu Ser Met Ser Leu Phe Arg Ala His
1               5                   10                  15

Leu Val Phe Tyr Arg Cys Ala Leu Asn Leu Asn Ser Ser Tyr Asn Phe
            20                  25                  30

Gly Phe Leu Val Ala Met Thr Phe Val Leu Gln Ile Ile Thr Gly Ile
        35                  40                  45

Thr Leu Ala Phe Arg Tyr Thr Ser Glu Ala Ser Cys Ala Phe Ala Ser
    50                  55                  60

Val Gln His Leu Val Arg Glu Val Ala Ala Gly Trp Glu Phe Arg Met
65                  70                  75                  80

Leu His Ala Thr Thr Ala Ser Phe Val Phe Leu Cys Ile Leu Ile His
                85                  90                  95

Met Thr Arg Gly Leu Tyr Asn Trp Ser Tyr Ser Tyr Leu Thr Thr Ala
            100                 105                 110

Trp Met Ser Gly Leu Val Leu Tyr Leu Leu Thr Ile Ala Thr Ala Phe
        115                 120                 125

Leu Gly Tyr Val Leu Pro Trp Gly Gln Met Ser Phe Trp Gly Ala Thr
    130                 135                 140

Val Ile Thr Asn Leu Leu Ser Pro Ile Pro Tyr Leu Val Pro Trp Leu
145                 150                 155                 160

Leu Gly Gly Tyr Tyr Val Ser Asp Val Thr Leu Lys Arg Phe Phe Val
                165                 170                 175

Leu His Phe Ile Leu Pro Phe Ile Gly Cys Ile Ile Ile Val Leu His
            180                 185                 190

Ile Phe Tyr Leu His Leu Asn Gly Ser Ser Asn Pro Ala Gly Ile Asp
        195                 200                 205

Thr Ala Leu Lys Val Ala Phe Tyr Pro His Met Leu Met Thr Asp Ala
    210                 215                 220

Lys Cys Leu Ser Tyr Leu Ile Gly Leu Ile Phe Leu Gln Ala Ala Phe
225                 230                 235                 240

Gly Leu Met Glu Leu Ser His Pro Asp Asn Ser Ile Pro Val Asn Arg
                245                 250                 255

Phe Val Thr Pro Leu His Ile Val Pro Glu Trp Tyr Phe Leu Ala Tyr
            260                 265                 270

Tyr Ala Val Leu Lys Val Ile Pro Ser Lys Thr Gly Gly Leu Leu Val
        275                 280                 285

Phe Met Ser Ser Leu Ile Asn Leu Gly Leu Leu Ser Glu Ile Arg Ala
    290                 295                 300

Leu Asn Thr Arg Met Leu Ile Arg Gln Gln Phe Met Thr Arg Asn Val
305                 310                 315                 320

Val Ser Gly Trp Val Ile Ile Trp Val Tyr Ser Met Ile Phe Leu Ile
                325                 330                 335

Ile Ile Gly Ser Ala Ile Pro Gln Ala Thr Tyr Ile Leu Tyr Gly Arg
            340                 345                 350

Leu Ala Thr Ile Leu Tyr Leu Thr Thr Gly Leu Val Leu Cys Leu Tyr
        355                 360                 365


<210> SEQ ID NO 24
<211> LENGTH: 84
<212> TYPE: PRT
```

-continued

```
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

Lys Leu Cys Lys Tyr His His Phe Leu Cys Ser Leu Thr Ser Gln Leu
1               5                   10                  15

Ser Tyr Leu Ile Gly Leu Ile Phe Leu Gln Ala Ala Phe Gly Leu Met
            20                  25                  30

Glu Leu Ser His Pro Asp Asn Ser Ile Pro Val Asn Arg Phe Val Thr
        35                  40                  45

Pro Leu His Ile Val Pro Glu Trp Tyr Phe Leu Ala Tyr Tyr Ala Val
    50                  55                  60

Leu Lys Val Ile Pro Ser Lys Thr Gly Gly Leu Leu Val Phe Met Ser
65                  70                  75                  80

Ser Thr Cys Gln


<210> SEQ ID NO 25
<211> LENGTH: 244
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Ile Ala Val His His His Pro Thr Gly Leu Leu Lys Thr Ala Lys
1               5                   10                  15

Ser Val Gly Phe Gln Tyr Pro Thr Thr Leu Arg Leu Phe His Ile Gly
            20                  25                  30

Tyr Val Leu Gly Val Ile Tyr Gly Leu Leu Leu Ser Leu Val Leu Thr
        35                  40                  45

Ala Arg Glu Asn Tyr Tyr Ser Asp Ala Ser Met Ile Ser Thr Ile Val
    50                  55                  60

Leu Gly Val Ile Ile Ser Glu Thr Gly Leu Phe Ile Ser Phe Phe Trp
65                  70                  75                  80

Gly Val Tyr Thr Thr Ser Trp Thr Thr Gly Leu Asp Leu Glu Gly Leu
                85                  90                  95

Cys Leu Pro Asp Pro Ser Ser Ile Val Leu Phe Met Thr Ile Met Leu
            100                 105                 110

Ser Ala Leu Ser Ile Val Val Ser Ser Val Tyr Leu Lys Asn Gln His
        115                 120                 125

Leu Tyr Thr Ser Cys Thr Asn Ile Met Ile Phe Thr Leu Val Val Ser
    130                 135                 140

Phe Leu Met Leu Val Cys Thr Glu Tyr Leu Gly Leu Ser Ile Tyr Ile
145                 150                 155                 160

Asn Asp Asn Gly Phe Gly Asn Gly Leu Phe Ile Leu Thr Gly Ile His
                165                 170                 175

Phe Ser His Val Ile Val Gly Ala Ile Leu Gly Phe Phe Asn Gln Gly
            180                 185                 190

Met Tyr Ser Ser Leu Val Thr Tyr Leu Pro Val Asn Cys Ile Thr Leu
        195                 200                 205

Ser Lys Cys Lys Gly Thr Leu Cys Lys Ile Phe Ser Glu Pro Phe Thr
    210                 215                 220

Ile Leu Tyr Leu His Phe Val Glu Ala Val Trp Ile Met Ile His Val
225                 230                 235                 240

Thr Phe Tyr Leu
```

```
<210> SEQ ID NO 26
<211> LENGTH: 156
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

Met Ser Leu Phe Arg Ala His Leu Val Phe Tyr Arg Cys Ala Leu Asn
1               5                   10                  15

Leu Asn Ser Ser Tyr Asn Phe Gly Phe Leu Val Ala Met Thr Phe Val
            20                  25                  30

Leu Gln Ile Ile Thr Gly Ile Thr Leu Ala Phe Arg Tyr Thr Ser Glu
        35                  40                  45

Ala Ser Cys Ala Phe Ala Ser Val Gln His Leu Val Arg Glu Val Ala
    50                  55                  60

Ala Gly Trp Glu Phe Arg Met Leu His Ala Thr Thr Ala Ser Phe Val
65                  70                  75                  80

Phe Leu Cys Ile Leu Ile His Met Thr Arg Gly Leu Tyr Asn Trp Ser
                85                  90                  95

Tyr Ser Tyr Leu Thr Thr Ala Trp Met Ser Gly Leu Val Leu Tyr Leu
            100                 105                 110

Leu Thr Ile Ala Thr Ala Phe Leu Gly Tyr Ala Thr Ser Asn Tyr Thr
        115                 120                 125

Thr Leu Cys Gln Glu Gly Ser Gln Ile Thr Leu Ile Ile Phe Val Ile
    130                 135                 140

Leu Ile His Gly Val Gln Leu Val Leu Phe Leu Gln
145                 150                 155


<210> SEQ ID NO 27
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

Trp Ala His His Met Met Thr Val Gly Leu Glu Val Asp Thr Arg Ala
1               5                   10                  15

Tyr Phe Ser Ala Met Thr Ile Met Ile Ala Ile Pro Thr Gly Thr Lys
            20                  25                  30

Ile Phe Asn Trp Leu Gly Thr Tyr Met Ala Ser His Asn Thr Thr Arg
        35                  40                  45

Thr Ile Asp Leu Trp Ala Ala Leu Cys Phe Ile Leu Leu Phe Thr Leu
    50                  55                  60

Gly Gly Thr Thr Gly Val Val Met Gly Asn Ala Gly Met Asp Ile Ala
65                  70                  75                  80

Leu His Asp Thr Tyr Tyr Ile Val Ala His Phe His Phe Val Leu Ser
                85                  90                  95

Leu Gly Ala Ile Leu Ala Thr Ile Cys Gly Phe Val Phe Tyr Ser Lys
            100                 105                 110

Asp Met Phe Gly Asp Thr Leu Asn Leu Phe His Val Asn Thr Gly Ser
        115                 120                 125

Ser Pro Tyr Leu Asn Ile Trp Phe Val Val Phe Leu Ala Ser Ile Met
    130                 135                 140

Leu Ile Phe Leu Pro Met His Ile Leu Gly Phe Asn Val Met Pro Arg
145                 150                 155                 160
```

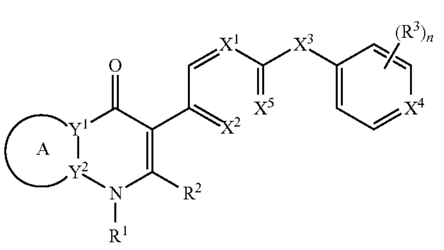
-continued

```
Arg Ile Pro Asp Tyr Pro Asp Tyr Leu Cys Tyr Ile Asn Thr Trp Cys
                165                 170                 175

Ser Ile Val Gln Leu Val Val Tyr Thr Pro Gln Lys Lys Leu Ile Asn
            180                 185                 190

Asn Pro Val Ser Glu Met Ile Thr Pro Ser Thr Met Val Leu Ile Ile
        195                 200                 205

Leu Ala Ser Glu Tyr Tyr Ser Tyr Leu Thr Thr Ala Trp Met Ser Gly
    210                 215                 220

Leu Val Leu Tyr Leu Leu Thr Ile Ala Thr Ala Phe Leu Gly Tyr Val
225                 230                 235                 240

Leu Pro Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Asn
                245                 250                 255

Leu Leu Ser Pro Ile Pro Tyr Leu Val Pro Trp Leu Leu Gly Gly Tyr
            260                 265                 270

Tyr Val Ser Asp Val Thr Leu Lys Arg Phe Phe Val Leu His Phe Ile
        275                 280                 285

Leu Pro Phe Ile Gly Cys Ile Ile Ile Val Leu His Ile Phe Tyr Leu
    290                 295                 300

His Leu Asn Gly Ser Ser Asn Pro Ala Gly Ile Asp Thr Ala Leu Lys
305                 310                 315                 320

Val Ala Phe Tyr Pro His Met Leu Met Thr Asp Ala Lys Cys Leu Ser
                325                 330                 335

Tyr Leu Ile Gly Leu Ile Phe Leu Gln Ala Ala Phe Gly Leu Met Glu
            340                 345                 350

Leu Ser His Pro Asp Asn Ser Ile Pro Val Asn Arg Phe Val Thr Pro
        355                 360                 365

Leu His Ile Val Pro Glu Trp Tyr Phe Leu Ala Tyr Tyr Ala Val Leu
    370                 375                 380

Lys Val Ile Pro Ser Lys Thr Gly Gly Leu Leu Val Phe Met Ser Ser
385                 390                 395                 400

Thr Cys Gln
```

1. A compound of the structure of

(a) Formula (I):

(I)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

Y^1 is C or N;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^3 is O, N(R), S or C_{1-3}alkyl;

X^4 is C or N;

X^5 is C or N;

R^1 is hydrogen or C_{1-3}alkyl;

R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

n is 0, 1, 2, 3 or 4;

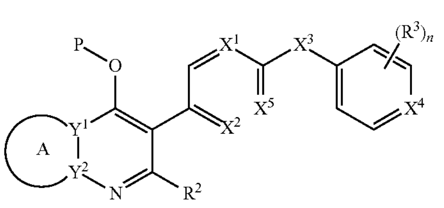
each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C_{1-3}alkyl; or

(b) compound of the structure of Formula (I-p):

(I-p)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

Y^1 is C or N;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^3 is O, N(R), S or C_{1-3}alkyl;

X^5 is C or N;

P is —C(O)OR', —C(O)R', —C(O)NR'2, wherein R' is hydrogen, C_{1-3}alkyl or —CH_2OR;

R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR, —C(O)OR or —CH_2OP;

P is —C(O)OR', —C(O)R', —C(O)NR'2 or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C_{1-3}alkyl;

n is 0, 1, 2, 3 or 4;

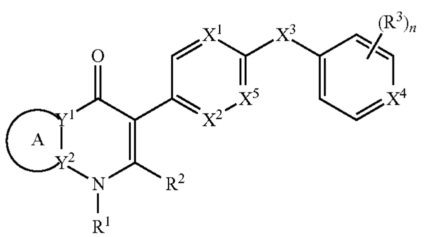
each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C_{1-3}alkyl.

2. The compound of claim 1, having the structure of (I):

(I)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

Y^1 is C or N;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^3 is O, N(R), S or C_{1-3}alkyl;

X^4 is C or N;

X^5 is C or N;

R^1 is hydrogen or C_{1-3}alkyl;

R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

n is 0, 1, 2, 3 or 4;

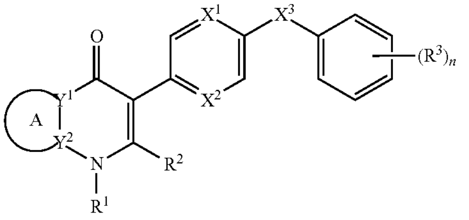
each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5;

or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C_{1-3}alkyl.

3. The compound of claim 1, having the structure of (Ia):

(Ia)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

Y^1 is C or N;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^3 is O, N(R), S or C_{1-3}alkyl;

R^1 is hydrogen or C_{1-3}alkyl;

R^2 is hydrogen, C_{1-3}alkyl or —C(O)OR;

n is 0, 1, 2, 3 or 4;

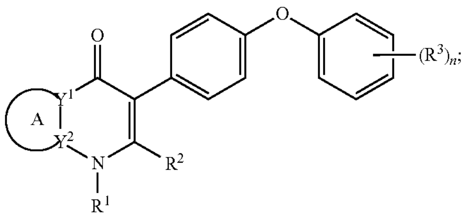
each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5; and

each R is independently hydrogen or C_{1-3}alkyl.

4. The compound of claim **3**, having

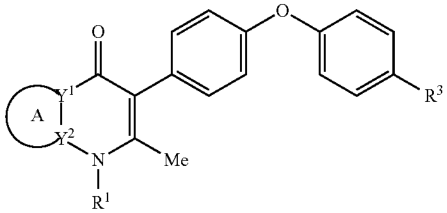
(a) the structure of Formula (Ib):

(Ib)



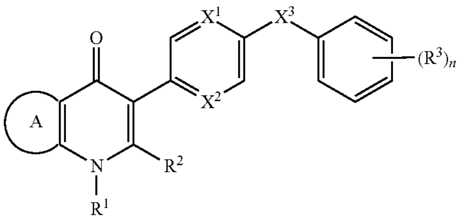
(b) the structure of Formula (Ic):

(Ic)



(c) the structure of Formula (II):

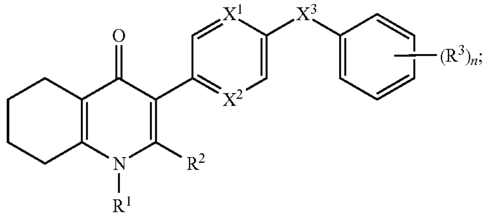
(II)



wherein ring A combines with the carbon atoms with which it is attached to form a C_{3-7} cycloalkenyl;

(d) the structure of Formula (IIa):

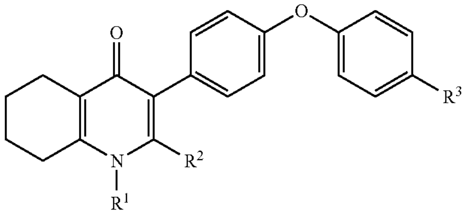
(IIa)



or

(e) the structure of Formula (IIa-1):

(IIa-1)

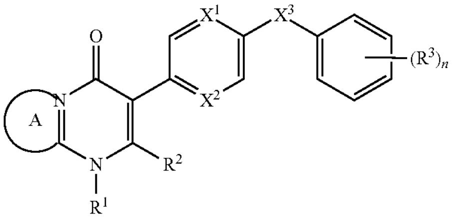


wherein R^3 is hydrogen, halogen, C_{1-3}alkyl or C_{1-3}haloalkyl.

5-8. (canceled)

9. The compound of claim **3**, having the structure of Formula (III):

(III)

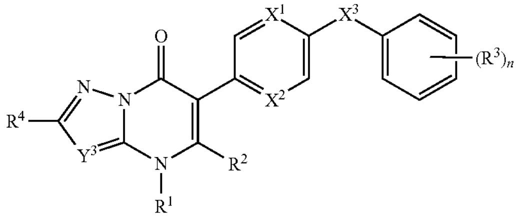


wherein

ring A combines with the nitrogen atom and carbon atom with which it is attached to form a heteroaryl ring.

10. The compound of claim **9**, having the structure of Formula (IIIa):

(IIIa)



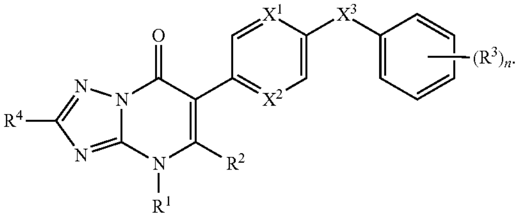
wherein

Y^3 is $C(R^5)$ or N; and

R^4 and R^5 are independently hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl.

11. The compound of claim **10**, having the structure of Formula (IIIb):

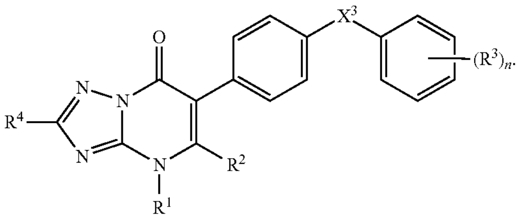
(IIIb)



12. The compound of claim **11**, wherein R^4 is hydrogen or C_{1-3}alkyl.

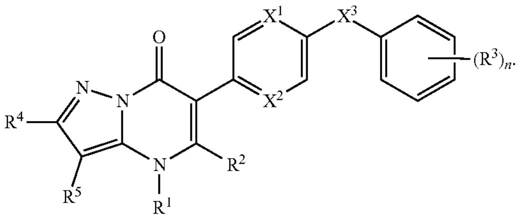
13. The compound of claim **11**, having the structure of Formula (IIIb-1):

(IIIb-1)



14. The compound of claim **10**, having the structure of Formula (IIIc):

(IIIc)



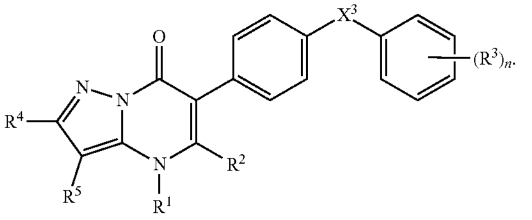
15. The compound of claim **14**, wherein

R^4 is hydrogen or C_{1-3}alkylor phenyl; and

R^5 is hydrogen or cyano.

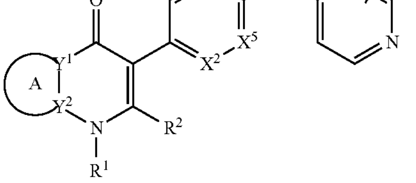
16. The compound of claim **14**, having the structure of Formula (IIIc-1):

(IIIc-1)



17. The compound of claim **1**, having the structure of Formula (IV):

(IV)



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y^1 and Y_2 to form a C_{3-7}cycloalkenyl or heteroaryl ring,

wherein the C_{3-7}cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR, cyano or phenyl;

Y^1 is C or N;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3}alkyl, C_{1-3}alkoxy or C_{1-3}haloalkyl;

X^3 is O, N(R), S or C_{1-3}alkyl;

X^3 is C or N;

X^5 is C or N;

R^1 is hydrogen or C_{1-3}alkyl;

R^2 is hydrogen, C_{1-3}alkyl, C_{1-3}haloalkyl, —CH_2OH, —CH_2OR or —C(O)OR;

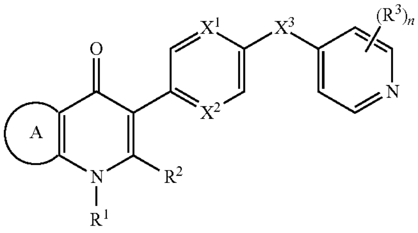
n is 0, 1, 2, 3 or 4;

each R^3 is independently halogen, C_{1-3}alkyl, C_{1-3}alkoxy, C_{1-3}haloalkyl, —O—C_{1-3}haloalkyl, —S—C_{1-3}haloalkyl, —C(O)OR or SF_5; and

each R is independently hydrogen or C_{1-3}alkyl.

18. The compound of claim **17**, having the structure of Formula (IVa):

(IVa)

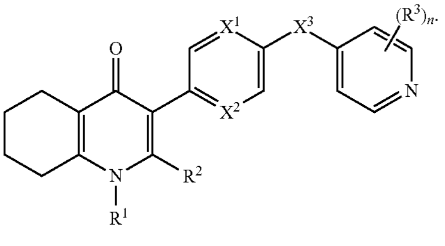


wherein

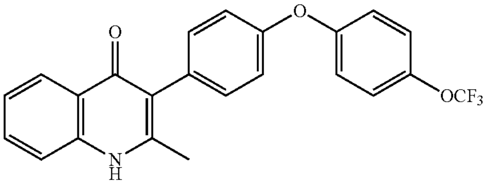
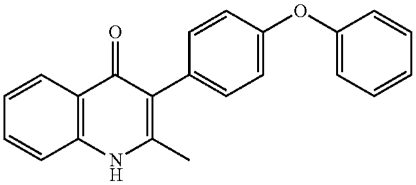
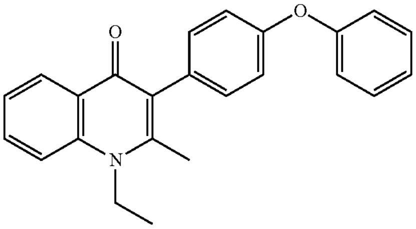
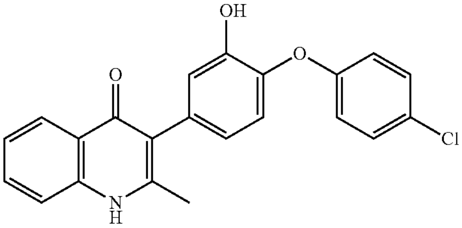
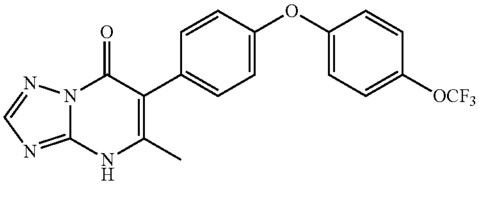
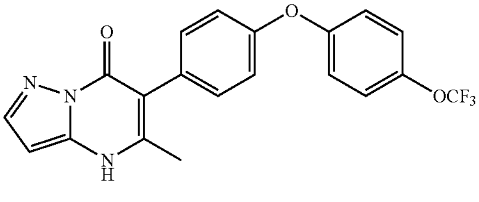
ring A combines with the carbon atoms with which it is attached to form a C_{3-7}cycloalkenyl.

19. The compound of claim **17**, having the structure of Formula (IVb):

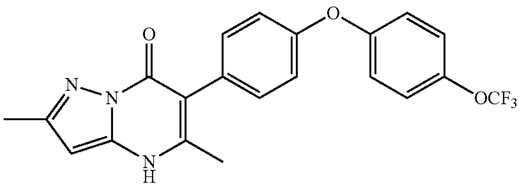
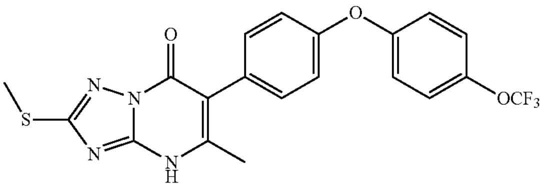
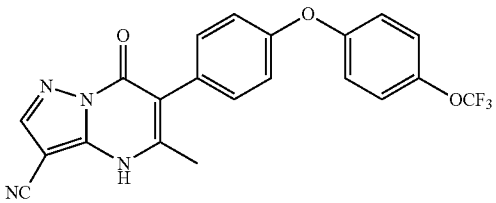
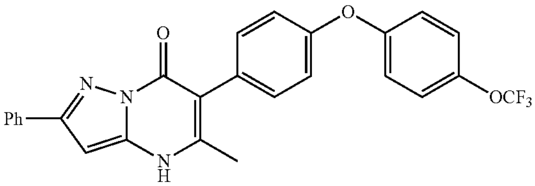
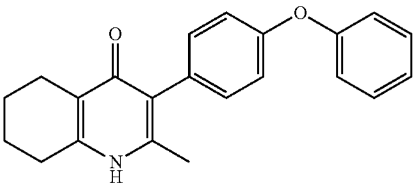
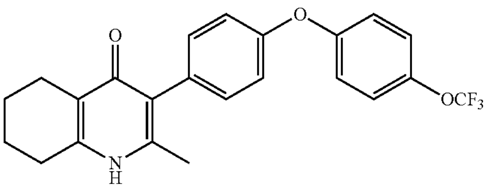
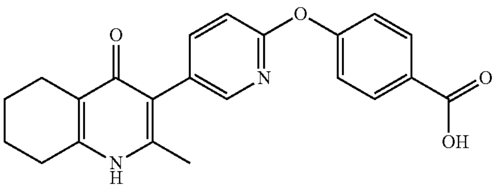
(IVb)



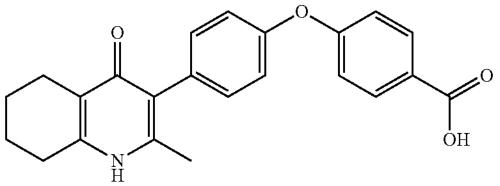
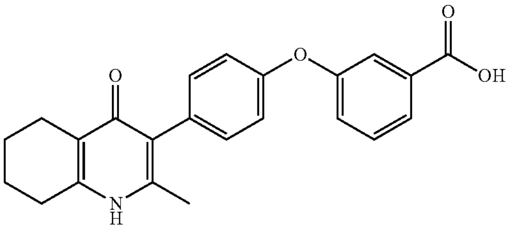
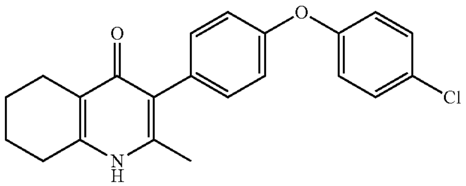
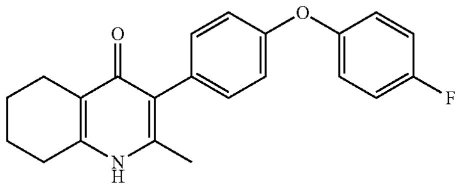
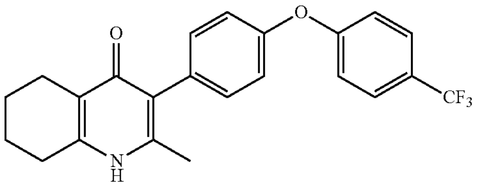
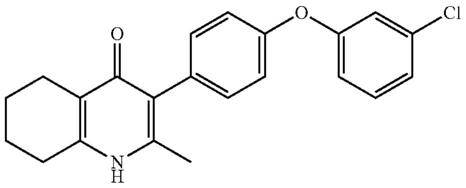
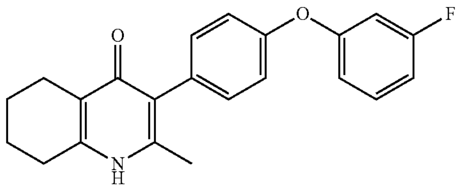
20. A compound that is:

No.	ID	Structure	Name
		ELQ-type systems	
PA1	MJM102/ MJM113 (ELQ-271)		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)quinolin-4(1H)-one
PA2	MJM 129		2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one
PA3	JM10		1-ethyl-2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one
PA4	RG38		3-(4-(4-chlorophenoxy)-3-hydroxyphenyl)-2-methylquinolin-4(1H)-one
		5,6-fused pyridone systems	
1	MJM136		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
2	MJM141		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

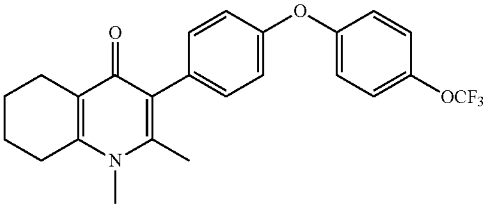
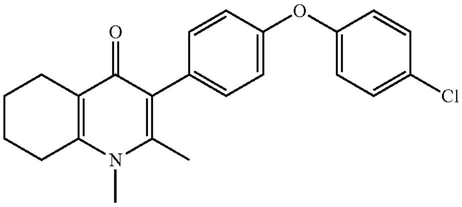
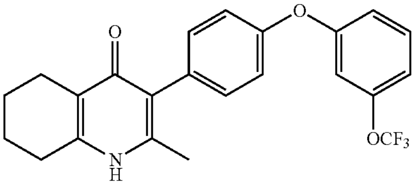
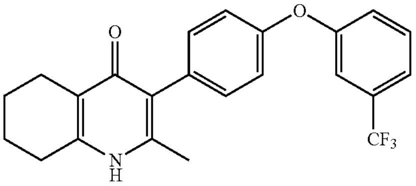
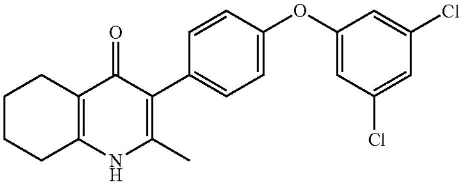
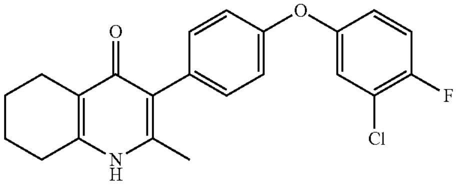
-continued

No.	ID	Structure	Name
3	JAG006		2,5-dimethyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
4	JAG013		5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
5	JAG014		5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile
6	JAG015		5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
		Tetrahydroquinolones (THQ)	
7	MJM170		2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
8	JAG21		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
9	JAG039		4-((5-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)pyridin-2-yl)oxy)benzoic acid

-continued

No.	ID	Structure	Name
10	JAG046		4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
11	JAG047		3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
12	JAG50		3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
13	JAG58		3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
14	JAG63		2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
15	JAG062		3-(4-(3-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
16	JAG067		3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

No.	ID	Structure	Name
17	JAG023		1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
18	JAG077		3-(4-(4-chlorophenoxy)phenyl)-1,2-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
19	AS006		2-methyl-3-(4-(3-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
20	AS0012		2-methyl-3-(4-(3-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
21	AS021		3-(4-(3,5-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
22	AS022		3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one

5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

2,5-dimethyl-4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one

5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile

5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

methyl 3-((5-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate

4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid

3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-(4-(4-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
2-Methyl-3-4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-(4-(3-Chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-(4-(3-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
1,2-dimethyl-3-4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4-one
3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-[4-(3-chloro-4-fluorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
3{-4-[(2,6-dichloropyridin-4-yl)oxy]phenyl}-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
3-[4-(3, 5-dichlorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4(1H)-one
3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3 (4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-(6-(4-Trifluoromethoxyphenoxy)pyrdin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinolin-(4-one
3-(4-Phenonxyphenyl)-1,2,3,4,5,6,7,8-octahydroquinazoline-2,4,dione
3 (4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(methylhydroxy)-5,6,7,8-tetrahydroquinolin-4(1H)-one
3-[4-(2H-1,3-benzodioxol-5-yloxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
6-Ethyl-3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3 (4-(4-Trifluoromethoxyphenoxy)phenyl)-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
3 (4-(4-Trifluoromethoxyphenoxy)phenyl)-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
7-Ethyl-2-methyl-3 (4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
3 (4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-napthyrid-4(1H)-one
7-Trifluromethyl-2-methyl-3 (4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof.

21. (canceled)

22. The compound of claim **1** that is 2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one, or a pharmaceutically acceptable salt thereof.

23. A pharmaceutical composition comprising a compound of claim **1** and a pharmaceutically acceptable diluent, excipient, or carrier.

24. A method for treating an apicomplexan parasitic infection, comprising administering to a subject (such as a human subject) in need thereof an amount effective to treat the infection of the compound or pharmaceutical composition of claim **1**.

25-34. (canceled)

35. An invention selected from the group consisting of:

(a) a method for monitoring treatment of an apicomplexan parasitic infection, such as *T. gondii* infection (including but not limited to any of the treatments of claims **24-34**), comprising monitoring expression, protein in serum or plasma, and/or activity of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or all of the markers listed in FIGS. **1-2** in a subject (such as a human subject) being treated for an apicomplexan parasitic infection, wherein a decrease or increase in expression and/or presence and/or activity of the one or more markers indicates that the treatment is effective;

(b) a cell line infected with an apicomplexan parasite, wherein the apicomplexan parasite genome comprises a gene encoding an Apetela 2 IV-4 protein with an M=>I modification at residue 570 ("AP2 IV-4 M570I") compared to its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470);

(c) a method for treating an apicomplexan parasite infection (such as a *T. gondii* infection), comprising administering to a subject in need thereof an amount effective to treat the infection of an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of 1 or more of the up-regulated genes listed in FIG. **1** or FIG. **2**;

(d) a method for identifying test compounds for apicomplexan parasite therapy, comprising identifying test compounds that reduce expression (for up-regulated genes), or increase expression (for down-regulated genes) of 1 or more of the apicomplexan parasite genes in FIGS. **3-5**;

(e) a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIGS. **3-5**, complements thereof, or their expression products, or functional equivalents thereof wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in the EGS strain of *T. gondii* after infection of human fibroblasts, human neuronal stem cells or human monocytic lineage cells; and

(f) a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIG. **1-2**, complements thereof, or their expression products, or functional equivalents thereof, wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in human fibroblasts, human neuronal stem cells or human monocytic lineage cells after infection with *T. gondii*, including but not limited to infection with the EGS strain of *T. gondii*.

36-76. (canceled)

* * * * *