

Table S10. Model selection among one linear model and two non-linear models on the relationship between disease index and expression levels of *RKS1* in natural accessions. Green values indicate a better fit of the logarithmic function in comparison to the two other models. Yellow values indicate a better fit of the exponential function in comparison to the linear model. Similar results were obtained after excluding the Omo2-1 outlier accession (see Figure S13) from the statistical analyses.

accessions	expression	n	k	lm			exp			log		
				AIC	BIC	AICc	AIC	BIC	AICc	AIC	BIC	AICc
all	<i>RKS1-L</i>	88	2	121.06	128.50	121.20	119.64	127.07	119.78	115.45	122.88	115.59
all	<i>RKS1-L+S</i>	88	2	123.79	131.22	123.93	123.98	131.41	124.12	124.44	131.88	124.58
w/o stop codon	<i>RKS1-L</i>	75	2	106.97	113.93	107.14	103.63	110.58	103.80	99.78	106.74	99.95
w/o stop codon	<i>RKS1-L+S</i>	75	2	107.62	114.57	107.79	107.42	114.37	107.59	108.19	115.14	108.36
w/o additional S alleles	<i>RKS1-L</i>	72	2	93.60	100.43	93.77	93.16	99.99	93.33	94.07	100.90	94.24
w/o additional S alleles	<i>RKS1-L+S</i>	72	2	80.32	87.15	80.49	79.81	86.64	79.98	82.50	89.33	82.67

lm: linear model (disease \sim intercept + a*expression); exp: exponential function (disease \sim $Ae^{-k*expression}$); log: logarithmic function (disease \sim b*log(expression) + c). 'n' and 'k' denote the sample size and the number of parameters, respectively. AIC: Akaike's information criterion; BIC: Bayesian information criterion; AICc: corrected AICc.

accessions: 'all': all accessions for which expression level of *RKS1* is available; 'w/o stop codon': all accessions but accessions with the stop codon at the fourth amino-acid in *RKS1*; 'w/o additional S alleles': all accessions but accessions with the stop codon or belonging to the second S susceptible allele embedded in the R intergenic haplogroup.

expression: '*RKS1-L*': Relative gene expression (A.U.) of the *RKS1* long transcript; '*RKS1-L+S*': Relative gene expression (A.U.) of *RKS1* total mRNA.