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Supplemental information

Molecular basis of ocean acidification sensitivity and adaptation in *Mytilus galloprovincialis*

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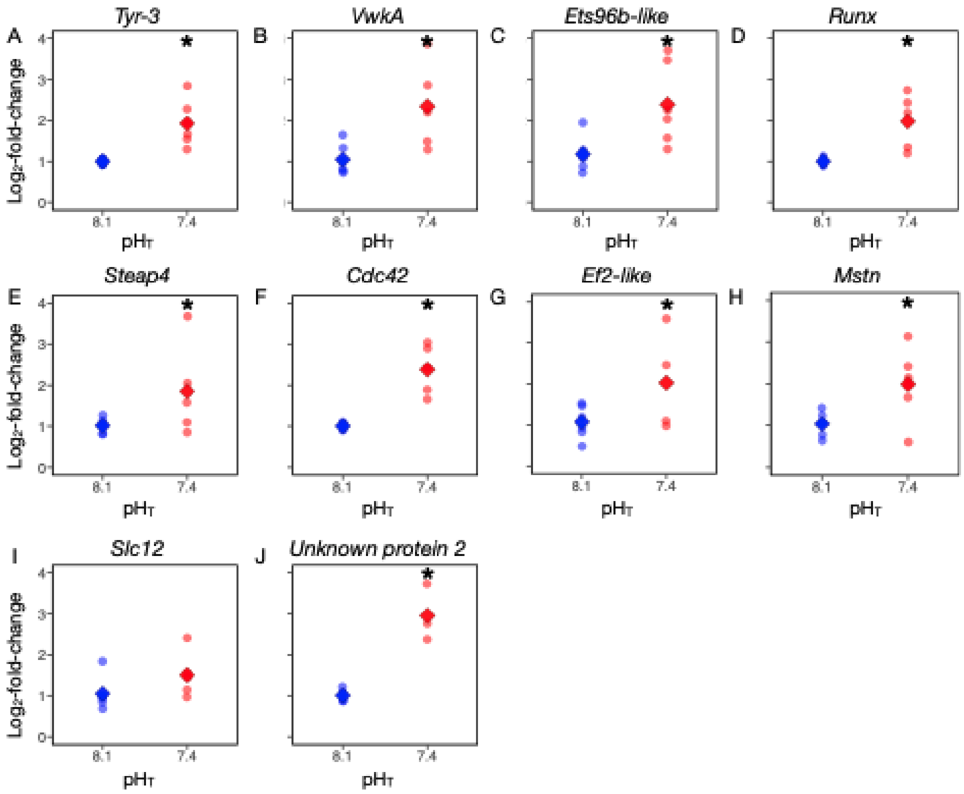

Figure S1 | Log$_2$-fold-expression at these genes identified as differentially expressed using RNA-sequencing, here determined via qPCR, relates to Table 1. Larvae were sampled at the trochophore stage at pH$_T$ 8.1 (in blue) or pH$_T$ 7.4 (in red, N = 6). Faded circles indicate values determined from individual replicate buckets, while diamonds correspond to treatment means. Asterisks indicate significant differences in expression between treatments ($p < 0.05$).

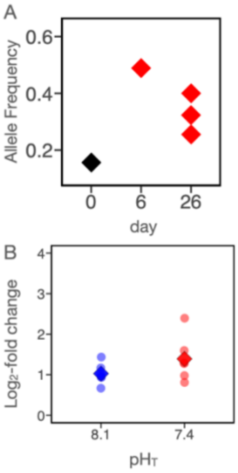

Figure S2 | Allele frequency dynamics and gene expression at *Tyr-1*, relates to Figure 3. (A) Allele frequency dynamics at *tyr-1*, a locus with significant signatures of selection (see STAR Methods), throughout development in low pH conditions. (B) Patterns of gene expression at *Tyr-1* in trochophore larvae in ambient and low pH conditions ($p > 0.05$).

Table S1 | Differentially expressed genes in trochophore larvae exposed to low pH conditions at the time of sampling, relates to Table 1. Gene IDs correspond to the transcriptome published by Moreira *et al.* (2015).

Gene ID	Gene name	Transcriptomics LogFC	Transcriptomics p-value (adj.)	qPCR p-value	Localization
Unigene26756_All	*ArfGap*	0.519	0.002	--	--
CL2533.Contig5_All	*Arih1*	0.684	0.028	0.047	not localized
Unigene36491_All	*Cbx8-like*	1.096	0.000	--	shell field
Unigene15921_All	*Cdc42*	1.224	0.000	0.002	--
Unigene35901_All	*Ef2-like*	0.708	0.021	0.038	shell field
Unigene19246_All	*Ets96b-like*	0.640	0.004	0.009	shell field
Unigene31791_All	*Impl2*	0.705	0.000	--	--
Unigene633_All	*Mstn*	0.970	0.003	0.026	muscle progenitors
CL14751.Contig1_All	*PrdX*	0.662	0.006	--	--
CL14297.Contig2_All	*Runx*	0.778	0.003	0.001	--
CL14297.Contig1_All	*Runx*	0.874	0.006	--	shell field
Unigene21137_All	*Slc12*	0.583	0.033	0.157	shell field
Unigene41251_All	*Steap4*	0.638	0.018	0.045	shell field
CL3552.Contig1_All	*Tob1*	0.700	0.048	--	--
CL1145.Contig4_All	*Tyr3*	0.761	0.013	0.001	shell field
CL7460.Contig2_All	*VwkA*	1.247	0.022	0.019	shell field
CL14268.Contig2_All	*Unknown protein 1*	1.665	0.000	0.001	--
CL4139.Contig1_All	*Unknown protein 2*	0.440	0.012	0.409	shell field
CL15076.Contig2_All	*Unknown protein 3*	1.548	0.000	--	shell field
CL15076.Contig1_All	*Unknown protein 3*	1.045	0.019	--	--
Unigene22287_All	*Unknown protein 4*	1.167	0.001	--	shell field
Unigene67129_All	*Unknown protein 5*	0.948	0.000	--	--
Unigene29772_All	*Unknown protein 6*	0.773	0.003	--	--
CL12151.Contig2_All	*Uknown protein 7*	0.846	0.000	--	--
Unigene97290_All	--	2.167	0.000	--	--
Unigene95225_All	--	0.499	0.003	--	--
Unigene94115_All	--	2.134	0.000	--	--
Unigene94108_All	--	2.066	0.000	--	--
Unigene92059_All	--	1.936	0.000	--	--
Unigene90028_All	--	1.764	0.000	--	--
Unigene87504_All	--	0.863	0.003	--	--
Unigene86350_All	--	0.323	0.048	--	--
Unigene84909_All	--	1.023	0.000	--	--
Unigene55968_All	--	0.671	0.001	--	--

Unigene36019_All	--	0.667	0.009	--	--
Unigene16595_All	--	1.012	0.000	--	--
Unigene11736_All	--	1.686	0.000	--	--
Unigene11735_All	--	1.535	0.000	--	--
CL3552.Contig2_All	--	0.866	0.000	--	--
CL2769.Contig2_All	--	-0.858	0.011	--	--

Table S2 | Primers used for qPCR, relates to Table 1. For the genes in which primers were designed directly from Gene ID corresponds to the associated gene ID in the Moreira *et al.* (2015) transcriptome. *Chi* required a longer sequence for qPCR primer design, so the *Chi* sequence from the Moreira *et al.* (2015) transcriptome was blasted to NCBI database to obtain sequences for primer design (the associated NCBI accession number is provided).

Gene ID	**Gene name**	**Sense**	**Primer**
CL12877.Contig1	*Unk-Hsp70-like*	F (5'-3')	GTAGTCGGTGGCCATTCAGA
		R (5'-3')	GCAAGAGATGGCTGTTTCGG
CL2533.Contig5	*Arih1*	F (5'-3')	ACTCCGGATGTTTGAAAGCAG
		R (5'-3')	GCCGTGTGTCTCTGTACTGT
CL1527.Contig2	*Trip11-like*	F (5'-3')	TCCTCTTCATCAGCTGTGCA
		R (5'-3')	CCTGATCACGCTGAGATGCT
CL1145.Contig4	*Tyr3*	F (5'-3')	CCCGAGCATGACATGGAGTT
		R (5'-3')	GATCATGGGCAGCTGTCTCA
MG827131	*Chi*	F (5'-3')	CAAGGGACAGGGTACAGCAG
		R (5'-3')	GTCCAACCACCCTTCTGTCC
Unigene35133	*Kif13*	F (5'-3')	CAGAAGCATTGGAGAGACGGA
		R (5'-3')	GCTCTCTCACGATCAGCATCA
Unigene633	*Mstn*	F (5'-3')	GCTCAACTTCCTCCAACGGA
		R (5'-3')	CCCACAGAAAAGCCTTCTCCA
CL14297.Contig2_All	*Runx*	F (5'-3')	CACGTATGCCAGACCTTCCA
		R (5'-3')	TCGCCAGAATAACGTTCGGT
Unigene19246	*Ets96b-like*	F (5'-3')	GTTCTCGTCTGCAAGCACTG
		R (5'-3')	AACAAAGTGTCCGGAAAACG
CL4139.Contig1	*Unknown protein 2*	F (5'-3')	ACGGAACACTTCACCCTGAC
		R (5'-3')	CGGAGAGAAAGCAACGAAAG
Unigene41251	*Steap4*	F (5'-3')	GTTTCGTTCCCATCCATGTC
		R (5'-3')	TCATGGGATCTCCCTACTGG
Unigene35901	*Ef2-like*	F (5'-3')	TGGCAAGACCACTCTCACTG
		R (5'-3')	CGTGAGACTCCTCCTTCTGG
CL7460.Contig2	*VwkA*	F (5'-3')	GAGGAGGTGATGGACCAGAA
		R (5'-3')	AGGATCGTGACCATTTGGAG
Unigene21137	*Slc12*	F (5'-3')	TATTGCGTGTGAAGGATGGA
		R (5'-3')	TTCCGTTGCTAGCATTTTCA

Unigene15921	*Cdc42*	F (5'-3')	GCCCGGAGACTTGTACGTAC
		R (5'-3')	GCTTACGCTCGGACATTTCG
Unigene31791	*Impl2*	F (5'-3')	TGTCTTCGTGTGCTGTTCCT
		R (5'-3')	AGCGAACGACCGAAGACAAT
CL14268.Contig2	*Unknown protein 1*	F (5'-3')	TCGAGCCAATTTCCGGTAAGT
		R (5'-3')	TCAACCGGACAATGGACCAA
CL4223.Contig1	*Tyr1*	F (5'-3')	TACCTGTGTCGGCTGCAATT
		R (5'-3')	GCAAAGGTTTTCGGGAAGGG

Table S3. Primers used for in situ hybridization, relates to Figure 2.

Contig	Gene	Sense	Primer
Unigene36491_All	*Cbx8-like*	F (5'-3')	ATGGAGAAGCAGACGGCATGT
		R (3'-5')	TCGTTAAAGTGCGTACAATG
CL14297.Contig2_All	*Runx*	F (5'-3')	ATGATGGAAGATTTATCCCTT
		R (3'-5')	GTATGGCCTCCAAACGGA
Unigene633_All	*Mstn*	F (5'-3')	ATGCAACAAATATCAACATTTT
		R (3'-5')	AGTACATCCACATCTCTCAA
Unigene19246_All	*Ets96b-like*	F (5'-3')	CAATGAGCTACGATAACATG
		R (3'-5')	GCGATGGTAACAAAATGATTAA
Unigene41251_All	*Steap4*	F (5'-3')	ATGATGAACAAAGAAAATAAACA
		R (3'-5')	AACCAAATTGGTTGCTCCAT
Unigene35901_All	*Ef2-like*	F (5'-3')	ATGGTAAACTTCACCATAGAA
		R (3'-5')	CACTGGACCAATGGGTCA
CL7460.Contig2_All	*VwkA*	F (5'-3')	ATGATCAAGGCAACACAATC
		R (3'-5')	AACACTAGGTAATCTTGCAG
CL2533.Contig5_All	*Arih1*	F (5'-3')	AGACATTTTCAACAACAGTTT
		R (3'-5')	TACTGTAAACTTTTTAGTGACT
Unigene21137_All	*Slc12*	F (5'-3')	ATGCTTGGTTACAAAACTGG
		R (3'-5')	AGAATAATATGTTAGTACGCT
CL1145.Contig4_All	*Tyr3*	F (5'-3')	ATGCGATTCTTTATACATGAAA
		R (3'-5')	TTGGTGGTTTTGGTACATGT
Unigene11975_All	*Chi*	F (5'-3')	CACCATGAATCTTAGAGGGATACAC
		R (3'-5')	TGAACATCCGGGTACATTATA
Unigene15921_All	*Cdc42*	F (5'-3')	CTAACCTGTTCACTTCGTC
		R (3'-5'	GCTTGCTCATGTTTATAAATA
CL4139. Contig1_All	*Unknown protein 2*	F (5'-3')	ATGAATTTAAAATCTGCTGATG
		R (3'-5'	CTGATCCAGGACTTTGTCA
CL15076. Contig2_All	*Unknown protein 3*	F (5'-3')	ATGTTGCTAGAACGAGACCT
		R (3'-5'	GAACAAAATTTGTATAGAATGTC

Unigene22287 _All	*Unknown protein 4*	F (5'-3')	AGAAATTTCTGAGGCCATCA
		R (3'-5'	CACATTTGACCGTTCCCAC
Unigene35133_All	*Kif13*	F (5'-3')	CTGGTCAGGAGAAATTATTTTC
		R (3'-5'	TTTCTTCTTAGCACTACTTGA
CL1527.Contig2_All	*Trip11-like*	F (5'-3')	ATGTCATGGATTGGGGGCA
		R (3'-5'	TTGGTCTTTCTCCTCTATAGA
CL12877.Contig1_All	*Unk-Hsp70-like*	F (5'-3')	ATGAGAGTTGTTAAATACTGTA
		R (3'-5'	GTCAAGTAAACAAAAGAAGC
CL4223.Contig1_All	*Tyr1*	F (5'-3')	GTTGGGATAAAACCTGCG
		R (3'-5'	ATAGCTCTGATATTTGATTCC