

Table S1. A summary of the transcriptome sequence data.

Sample	Accession number	Raw reads	Clean reads	Clean bases (G)
Control_1	SAMN29837276	22 034 064	20 306 829	6.09
Control_2	SAMN29837277	23 780 173	22 603 668	6.78
Control_3	SAMN29837278	23 005 878	21 548 572	6.46
Treatment_1	SAMN29837279	23 116 935	22 020 532	6.61
Treatment_2	SAMN29837280	22 867 958	21 762 055	6.53
Treatment_3	SAMN29837281	22 998 135	22 006 280	6.60
Average	-	22 967 190	21 707 989	6.51

Table S3. Analysis of expression change of six selected target genes after normalized against a set of two reference genes [29].

Samples	Reference genes (reads count)		Target genes (reads count)						Total reads	Fold change against Control_1*					
	ATPA1	PMPCB	G1	G2	G3	G4	G5	G6		G1	G2	G3	G4	G5	G6
Control_1	9378.11	3458	198	360	111	1184.1	673	1914.38	20,306,829	-	-	-	-	-	-
Control_2	10550.84	3798	266	410	120	1445.01	1463.65	2538.26	22,603,668	1.21	1.14	1.08	1.10	1.96	1.19
Control_3	10405.61	3838	386	457.49	184	1396.76	842	2310.98	21,548,572	1.76	1.22	1.59	1.06	1.13	1.09
Treatment_1	10864.7	3836	632	1018	324	468.48	452	763.92	22,020,532	2.82	2.70	2.79	0.35	0.59	0.35
Treatment_2	10249.97	3653	726	973.03	368	470.46	439.03	772.88	21,762,055	3.41	2.70	3.31	0.37	0.61	0.38
Treatment_3	10236.77	3651	395	864.01	245	547.56	379	1128.28	21,762,055	1.86	2.40	2.20	0.43	0.52	0.55

* Fold change against Control_1 was calculated following Equation S1, Equation S2 and Equation S3 (Alexander et al., 2015^a).

$$\text{Equation S1: Normalized Count (NC)} = \frac{\text{Gene Count (Reference gene or Target gene)}}{\text{Total reads}};$$

$$\text{Equation S2: Stable gene normalizedcounts (SGNCs)} = \frac{\text{NC of target gene}}{\text{Geometricmean of NC of referencegenes}};$$

$$\text{Equation S3: Fold change against Control_1} = \frac{\text{SGNC of target gene (Control_2, Control_3, Treatment_1, Treatment_2 and Treatment_3)}}{\text{SGNC of target gene (Control_1)}}.$$

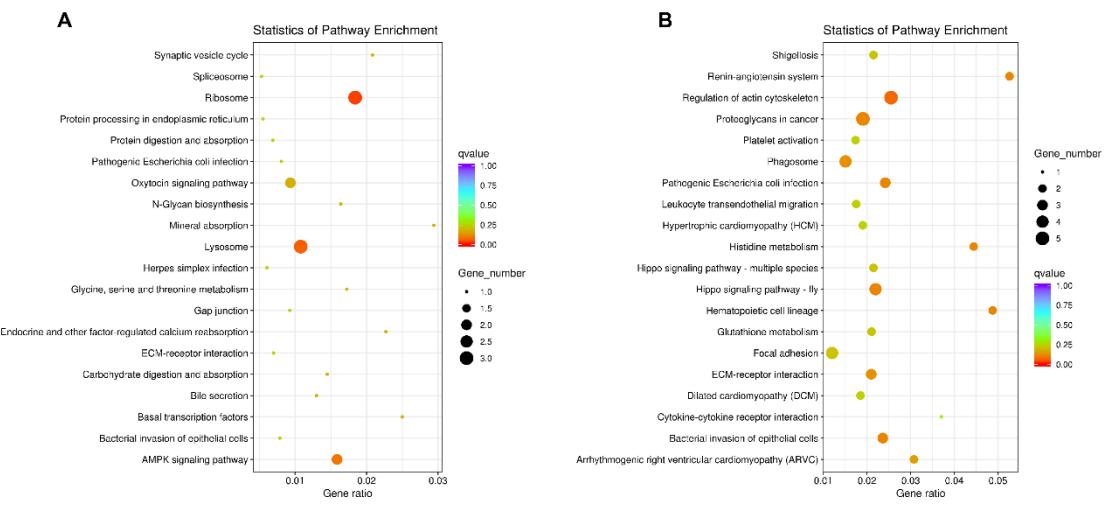


Figure S1. The 20 highest-ranking KEGG pathways associated with *M. mereritrix* DEGs

under different conditions. (a) up-regulated genes in the treatment group; (b) down-regulated genes in the treatment group.

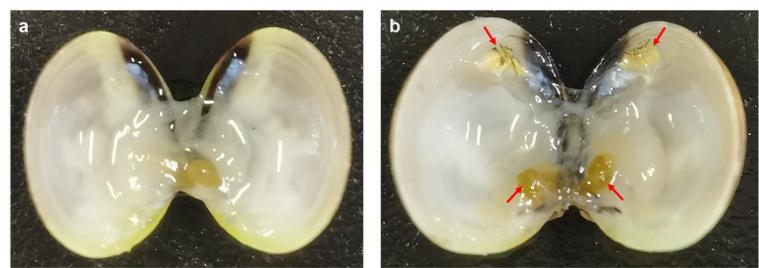


Figure S2. Photographs of the dissected clams. (a) control; (b) treatment.