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Comparative transcriptome analysis of *Eogammarus possjeticus* at different hydrostatic pressure and temperature exposures

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Table S3. Information of the primers used in quantitative real-time reverse transcription-PCR (qPCR) analysis (with *Rpl8* as internal control). PCC: Pearson correlation coefficients between qPCR and RNA-Seq.

Gene name	Gene ID	PCC	5'- 3' forward primer	5'- 3' reverse primer
<i>Rpl8</i>	Cluster-13637.43027		GCAGCAAGAAGATCCTCCCGTCCAA	ACACGGCAGGCAAACGAATCCAACG
<i>GS</i>	Cluster-13637.55967	0.90	GCCATCCACATATCGTCACCCAT	CACTCGCCAAAGACCAACATCCT
<i>PEPCK</i>	Cluster-13637.35569	0.86	ATTGTCTTTCCGGGTCAGGCTACGGT	AGTGAAGGAGTCATCATCGCCAGGT
Peroxidase	Cluster-13637.45510	0.99	AGGTGCCGTCTATGGTGCGGTATTT	CCACGAACAGGCTCTTCAGGTCAA
Crustin pm5	Cluster-13637.44495	0.96	ACGATGGCAGGCTTGCATGAGTG	TGTTGCTGGCGTGTGTAGTGGCT
Lysozyme	Cluster-13637.42497	0.90	TTACAACATTACCACCAACAAGG	ACCAGTCGGACAGAAACAGAGGCTA
<i>Hsp70</i>	Cluster-13637.44177	0.93	TCCACTGCTGGTGACACTCATCTT	ATCGGCACAGAGCTCCTCAAACCTA
<i>CA</i>	Cluster-13637.39561	0.98	GCTGCCCTGGTAGCGGTAGAAAT	TTGGATGACGCCCTGGGCCACGAAGAC
<i>A2M</i>	Cluster-13637.43635	0.89	GTAACGACGATCCCTGTTGAAAGA	AGAAACCAGAAGCACCCAAACCACT
<i>ATPIA</i>	Cluster-13637.41266	0.84	CATCGCTAAGGAGATCGCTCATTTT	ACATGTGGGCGACAGTCATACGGTT
<i>CALM</i>	Cluster-13637.38529	0.82	TCCACCTCCTCGTCTGTCAACTTCTC	GACGGTAACGGCACAATCGACTTCC
Peritrophin	Cluster-13637.45283	0.85	GAGCAACTACGAGTGTCCTCAAGCCA	CCATCTCCTCCGATTTCTCAGTGT
Clottable protein	Cluster-13637.43258	0.90	AGTTAGTCCGAATCCGCTCACAATC	CCTCACCAACATCACTTCTACCTCCTT
<i>IDH3</i>	Cluster-13637.43931	0.88	TTGTGCACGGCGGTGACTTTCTTAC	GCAATGGAATCTGCCTGAAGGGAAT
Enolase	Cluster-13637.42843	0.77	CTGCTCACTTCATTCCTCCACACC	GCTCAGAGAGGCTGGCCAAGTACAA
<i>HmgA</i>	Cluster-13637.51258	0.90	GATGGGTTTTGTACCTCTGTCTT	TGTCCATTTGGGAGTAGAAGCGA
Ring finger	Cluster-13637.39981	0.80	TTCAATCGAGGACGGAGAGATGGAC	CGAGTACGACAGCAGCAGCACAC
Vitellogenin	Cluster-13637.41706	0.97	AACTACTCAAGCAGAACCGAACATT	TCTTCAGTATCGGCTCCCTCAGTTG
<i>WAP</i>	Cluster-13637.37987	0.89	GCCTTCTGTCTCATGCAGGTGTAG	CTCGCTGTGCTGTGGTCTGTGT
<i>MDH</i>	Cluster-13637.45447	0.79	GCACCCTCCATCCCAAGGAAAACCT	TTCTTACCTCGGAGACAGGCACCC
<i>ATPeV0A</i>	Cluster-13637.35182	0.99	CAACAAGTTCACCTTCGGCTTCCAG	ACGCTCCTCAGCACCATCCACAGA
<i>ATPeV1B</i>	Cluster-13637.60972	0.96	ATGAAGGCTGTGGTGGGCGAAGAAG	CACACAAACCAATAAACCTACGAG
<i>ATPeV1C</i>	Cluster-13637.45517	0.99	CCTTGCTGAAGAGGGTGACCGAGAA	GGGAGACCTGGTGAAGAAAAGTGAC
<i>AMP</i>	Cluster-13637.45969	0.92	TTGGGTGAGTAAGGATTTCGATTGG	ACGCATACTTGGTAATGACGACTAA