

Figure S1. Comparison of up- and down-regulated Gene ontology(GO) enrichment terms of differentially expressed genes (DEGs) of *S. exigua* after exposure of MET.

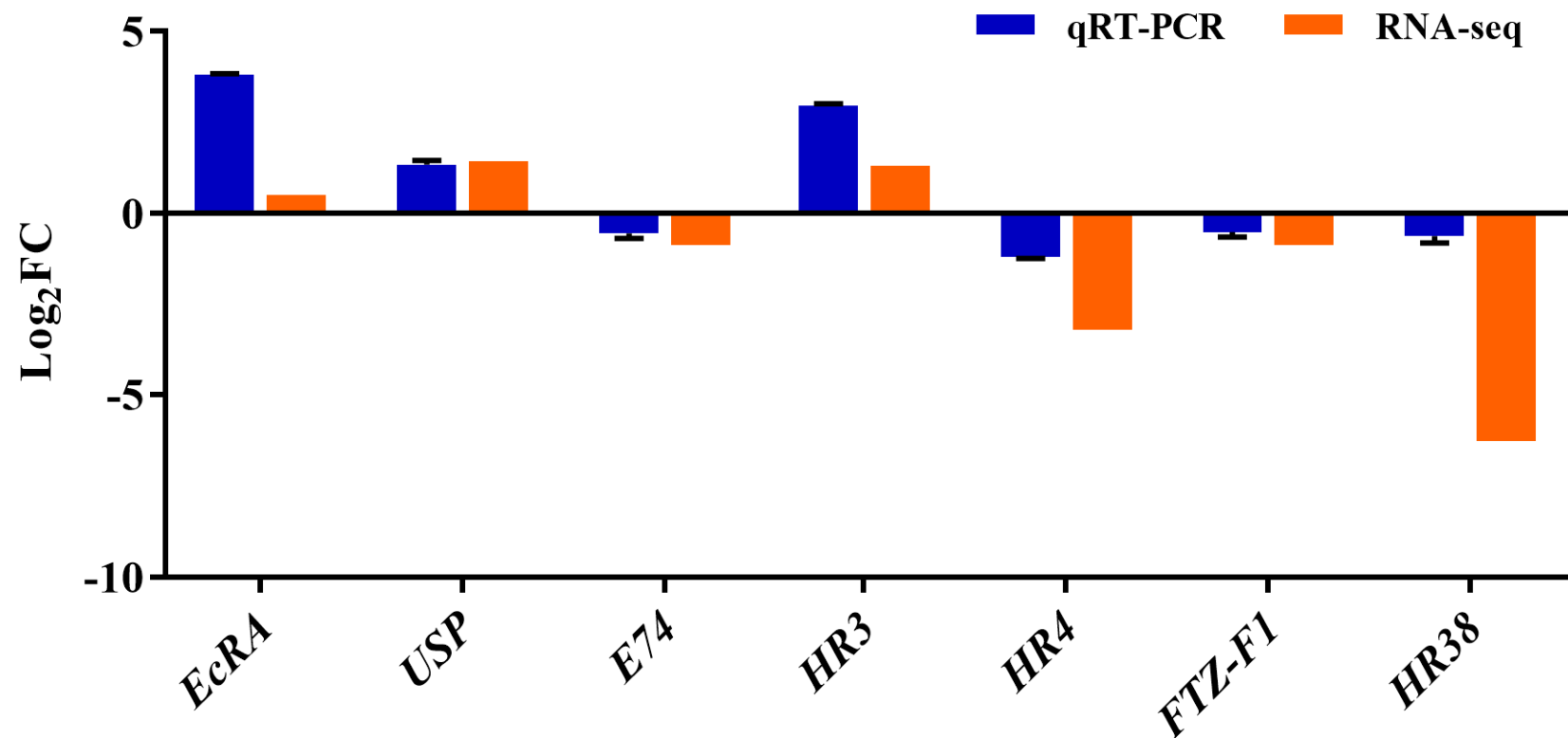


Figure S2. Prove transcriptome data according qPCR (Blue represent transcriptome date, orange represent qPCR). The bars represent the average (\pm SE) of biological repeats. Expression ratios of 7 candidate genes in log₂FC (The fold changes of the genes were calculated as the value of each FC comparison and are shown on the y-axis. Blue bars represent gene expression data ($2^{-\Delta\Delta C_t}$) that was obtained by qPCR analysis).

Table S1 Primer designer

Primer	Equation	R ²	Amplification efficiency	Forward Primer(5'-3')	Reverse Primer(5'-3')
<i>USP</i>	$y=-3.3143x+34.567$	0.99	97%	GTAGGTCATTGAACTGTAG	GACACCTACCTGACGATTA
<i>HR3</i>	$y=-3.3269x+32.564$	0.99	95%	GGTGATATAAGCAAGGTC	GTAGGTCATTGAACTGTAG
<i>EcRA</i>	$y=-3.3593x+33.527$	0.99	98%	GGAGCTATGTCTCGTCTG	AATCCTTTACACCCTTCACA
<i>FTZ-F1</i>	$y=-3.2212x+37.386$	0.99	104%	AACACAACGGAAGCGCTGCC	GGTGACGACTCTGGCGATGA
<i>HR4</i>	$y=-3.3597x+36.638$	0.98	98%	AGATACCAGCACGTCGTCGC	GATGGCAAGCAGGCGATGGT
<i>HR38</i>	$y=-3.3765x+32.309$	0.98	98%	AATGGACGAAGACTGCTA	ATGGAAGGTTGATGATATTGAT
<i>E74</i>	$y=-3.3888x+31.016$	0.99	97%	CACTGTTTCCTGGTTGTTGC	AGTCAGCAACAGCAACAACA
<i>TPS</i>	$y=-3.4958x+32.035$	0.99	93%	CGCTACACTTGAGTTGAA	ATTGGATGCTATTGAGGTT
<i>TREA</i>	$y=-3.4174x+30.393$	0.98	96%	ATTGGTGATTGGTAGTAAGT	GAAGCAGGTGGTATTATCA
<i>HK</i>	$y=-3.3729x+34.474$	0.99	98%	TTCTCTTGATTCTTCCAT	CACACGCTCTTATTATAG
<i>G6PI</i>	$y=-3.3048x+34.424$	0.98	101%	TACCTGACTTCTCTAACT	ATCTTACTAGCCAACCTC
<i>GFAT</i>	$y=-3.3493x+30.497$	0.99	99%	TCCATTGACATTCCATTA	ACTTATTGACATACGGTAA
<i>PGM</i>	$y=-3.2192x+31.904$	0.99	104%	GGACTGAAGATATTGTTAGAG	GAATACTGCTTGACATACTT
<i>UAP</i>	$y=-3.3597x+34.668$	0.98	98%	GGTGGTATTGTAGAAGAC	GGACTAATTGTGAAGACT
<i>CHSA</i>	$y=-3.3915x+33.309$	0.98	97%	CGCTCATACAGTTCTATA	CTTCATTCAACATCCATT
<i>SeGAPDH</i>	-	-	-	GACAACCACTCATCTATCTTCG	AACATTTATCTCTACAACGCAATC
<i>SeEF</i>	-	-	-	TGATGCCACAGACAAGAG	CCATTTCCACAAGTTCTACC
<i>dsEcRA</i>	-	-	-	ggatcctaatacgactcactatagg	ggatcctaatacgactcactatagg
	-	-	-	GTGTCGGTTGAAGAAATGTCT	CGCAACATCATCACCTCACT
<i>dsGFP</i>	-	-	-	ggatcctaatacgactcactatagg	ggatcctaatacgactcactatagg
	-	-	-	AAGGGCGAGGAGCTGTTACCG	CAGCAGGACCATGTGATCGCGC