

Comparative transcriptome analysis identifies MAPK signaling pathway associated with regulating ovarian lipid metabolism during vitellogenesis in the mud crab, *Scylla paramamosain*

Table S1. Specific primers used in qRT-PCR.

Gene ID	Gene information	Forward Sequence (5'-3')	Reverse Sequence (5'-3')	Length
Gene 1	Uncharacterized protein K02A2.6-like	CCACGACACCCATGTTGGTA	GGCATGGTCAACGCGTATTC	208bp
Gene 2	Catenin-like	GACCAGCTAGTCACCACCAC	TCTCCGAAGTATGCAGTGCC	185bp
Gene 3	Aggrecan core protein-like	AGAGAAGTGGTTCAGGCAGC	CCCATTCCCTCGTCATTGCT	110bp
Gene 4	Serine proteinase	GGCTGCAGGCATACATTGAC	AAGGTGCTGCCTACATGCTT	229bp
Gene 5	Proclotting enzyme-like	TGGACCAACGAAGAATGCGA	GTACACTCCGGGGTTTCCTG	210bp
Gene 6	Glucose transporter type-1 like	AGGCAGCCAAGGAGGAGATA	GACTGACTGGGGTGCATTGA	191bp
<i>Sp-Vg</i>	Vitellogenin	CGCAACCGCCACTGAAGAT	CCACCATGCTGCTCACGACT	204bp
<i>Sp-VgR</i>	Vitellogenin receptor	TTCTATACCAGGCCACTACC	TTTTCACTCCAAGCACACTC	252bp

Table S2. Raw data statistics table.

sample	Raw reads	Error rate (%)	Q30 (%)	GC content (%)
F_OV_1	50353638	0.0281	91.83	51.18
F_OV_2	59437014	0.0277	92.18	50.34
F_OV_3	52707876	0.0273	92.58	52.59
F_OV_4	56660064	0.0272	92.62	52.49
F_OV_5	53567568	0.0277	92.24	52.61
S_OV_3	63795672	0.028	92.01	52.67
S_OV_4	63846232	0.0275	92.33	51.86
S_OV_5	54671914	0.0281	91.92	50.53

Table S3. Clean data statistics table.

sample	Raw reads	Error rate (%)	Q30 (%)	GC content (%)
F_OV_1	48538534	0.026	93.34	51.09
F_OV_2	57552348	0.0257	93.63	50.18

F_OV_3	50772654	0.0251	94.2	52.56
F_OV_4	54877354	0.0251	94.13	52.38
F_OV_5	51673648	0.0254	93.9	52.43
S_OV_3	61434276	0.0256	93.7	52.5
S_OV_4	61793014	0.0254	93.86	51.62
S_OV_5	52576372	0.0257	93.65	50.23

Table S4. Information of eggNOG functional categories.

Type	Functional Categories	COG
INFORMATION STORAGE AND PROCESSING	[A] RNA processing and modification	169
INFORMATION STORAGE AND PROCESSING	[B] Chromatin structure and dynamics	126
METABOLISM	[C] Energy production and conversion	375
CELLULAR PROCESSES AND SIGNALING	[D] Cell cycle control, cell division, chromosome partitioning	239
METABOLISM	[E] Amino acid transport and metabolism	471
METABOLISM	[F] Nucleotide transport and metabolism	159
METABOLISM	[G] Carbohydrate transport and metabolism	580
METABOLISM	[H] Coenzyme transport and metabolism	135
METABOLISM	[I] Lipid transport and metabolism	336
INFORMATION STORAGE AND PROCESSING	[J] Translation, ribosomal structure and biogenesis	880
INFORMATION STORAGE AND PROCESSING	[K] Transcription	747
INFORMATION STORAGE AND PROCESSING	[L] Replication, recombination and repair	732
CELLULAR PROCESSES AND SIGNALING	[M] Cell wall/membrane/envelope biogenesis	104
CELLULAR PROCESSES AND SIGNALING	[N] Cell motility	7
CELLULAR PROCESSES AND SIGNALING	[O] Posttranslational modification, protein turnover, chaperones	1675
METABOLISM	[P] Inorganic ion transport and metabolism	328
METABOLISM	[Q] Secondary metabolites biosynthesis, transport and catabolism	166
POORLY CHARACTERIZED	[S] Function unknown	10996
CELLULAR PROCESSES AND SIGNALING	[T] Signal transduction mechanisms	1049
CELLULAR PROCESSES AND SIGNALING	[U] Intracellular trafficking, secretion, and vesicular transport	1419
CELLULAR PROCESSES AND SIGNALING	[V] Defense mechanisms	52

CELLULAR PROCESSES AND SIGNALING	[Y] Nuclear structure	1
CELLULAR PROCESSES AND SIGNALING	[Z] Cytoskeleton	696

Table S5. Information of functional proteins in PPI network.

Protein ID	Description
chic	Chickadee, isoform e; Profilin.
puc	Dual specificity phosphatase 10; Puckered, isoform A.
Drk	Protein enhancer of sevenless 2B.
msn	Misshapen, isoform A; JUN kinase kinase kinase activity; ATP binding.
alph	Alphabet, isoform E; Protein serine/threonine phosphatase activity.
lic	MAP kinase kinase activity; protein kinase activity; ATP binding.
Dsor1	Dual specificity mitogen-activated protein kinase kinase dSOR1.
Eip75B	Nuclear receptor subfamily 1 group d member 3; Ecdysone-induced protein 75B, isoform B.
Tak1	Mitogen-activated protein kinase kinase kinase 7.
Raf	Raf homolog serine/threonine-protein kinase phl.
aop	Ets DNA-binding protein pokkuri.
rl	Mitogen-activated protein kinase ERK-A.
csw	Tyrosine-protein phosphatase non-receptor type 11.
CG2107	Carnitine o-palmitoyltransferase 2; Carnitine O-palmitoyltransferase activity.
Desat1	Stearoyl-coa desaturase (delta-9 desaturase).
v(2)k05816	Fatty acid synthase, animal type.
Btk29A	Tyrosine-protein kinase Btk29A.
Eip78C	Nuclear receptor subfamily 1 group d member 3; Ecdysone-induced protein 78C.
gro	Groucho, isoform e.
ttk	Protein tramtrack, alpha isoform.
EcR	Ecdysone receptor.
sty	Protein sprouty homolog 2.
p38b	Mitogen-activated protein kinase 14B.
Ilk	Integrin linked kinase, isoform a.
Ubi-p5E	Ubiquitin-5E, isoform A; Protein tag.
whd	Carnitine O-palmitoyltransferase activity.
Mtl	Ras-related c3 botulinum toxin substrate 1; Mig-2-like GTPase Mtl.

Traf6	Tnf receptor-associated factor 6.
edl	ETS-domain lacking; Sequence-specific DNA binding; protein binding.
emb	Exportin-1; Receptor for the leucine-rich nuclear export signal (NES).
fabp	Fatty acid-binding protein 3.
peb	Ras-responsive element-binding protein 1.
Acs1	Acyl-CoA synthetase long-chain, isoform J; Long-chain fatty acid-CoA ligase activity.
usp	Protein ultraspiracle; Receptor for ecdysone.
ksr	Kinase suppressor of ras, isoform A; Protein kinase activity; ATP binding.
CG5009	Probable peroxisomal acyl-coenzyme A oxidase 1.
bsk	Mitogen-activated protein kinase 8/9/10 (c-jun n-terminal kinase).
dos	Protein daughter of sevenless.
Src42A	Src oncogene at 42a, isoform a; Tyrosine-protein kinase Src42A.
CG3961	Uncharacterized protein, isoform e; CG3961, isoform A; Long-chain fatty acid-CoA ligase activity.
