



Figure S1. The female reproductive system of *H. vigintioctopunctata*. A: representative picture which the reproductive system was dissected from the mated female in the dsGFP control group. B: representative picture which the reproductive system was dissected from the unmated female in the dsGFP control group. C: representative picture which the reproductive system was dissected from the mated female in the dsGFP/ dsRC2-like/dsPSHS-like treated groups which did not lay eggs. Lo: lateral oviduct; Sg: spermathecal gland; Tf: terminal filament; Mo: median oviduct; Sn: seminal node; Tr: trachea; Ov: ovariole.

Table S1. Gonadal development related genes in *H. vigintioctopunctata* ovary and testis transcriptomes

Genes	Matched species	Length (bp)	E value	Identity (%)
Oocyte meiosis				
adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98
anaphase-promoting complex subunit 4	<i>Anoplophora glabripennis</i>	2666	5.00E-53	65.92
PREDICTED: anaphase-promoting complex subunit 2	<i>Tribolium castaneum</i>	3131	2.00E-169	68.43
calcium-binding protein E63-1	<i>Anoplophora glabripennis</i>	615	8.00E-30	68.73
cell division cycle protein 23 homolog	<i>Anoplophora glabripennis</i>	1849	0	73.85
cell division cycle protein 27 homolog	<i>Anoplophora glabripennis</i>	3090	5.00E-91	69.22
cell division cycle protein 16 homolog	<i>Anoplophora glabripennis</i>	1855	5.00E-139	75.56
serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	<i>Leptinotarsa decemlineata</i>	2785	0	76.76
serine/threonine-protein kinase 10 isoform X3	<i>Anoplophora glabripennis</i>	4892	0	69.48
PREDICTED: serine/threonine-protein kinase mos	<i>Tribolium castaneum</i>	1708	7.00E-13	66.56

PREDICTED: serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform isoform X4	<i>Tribolium castaneum</i>	3501	0	73.59
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
14-3-3 protein epsilon	<i>Zootermopsis nevadensis</i>	1038	7.00E-146	75.53
14-3-3 protein zeta isoform X1	<i>Anoplophora glabripennis</i>	2161	0	83.52
structural maintenance of chromosomes protein 3	<i>Anoplophora glabripennis</i>	3851	0	75.59
PREDICTED: structural maintenance of chromosomes protein 1A	<i>Tribolium castaneum</i>	4067	0	74.69
beta-TrCP isoform X3	<i>Anoplophora glabripennis</i>	2114	0	76.69
FK506-binding protein 59	<i>Anoplophora glabripennis</i>	1584	2.00E-86	65.96
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
ribosomal protein S6 kinase 2 beta isoform X2	<i>Anoplophora glabripennis</i>	3142	0	71.32
mitotic checkpoint serine/threonine-protein kinase BUB1 beta	<i>Anoplophora glabripennis</i>	3658	2.00E-98	73.21

mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
separin	<i>Leptinotarsa decemlineata</i>	6148	3.00E-33	67.41
anaphase-promoting complex subunit 10	<i>Leptinotarsa decemlineata</i>	1072	2.00E-137	80.87
serine protease HTRA2, mitochondrial-like	<i>Leptinotarsa decemlineata</i>	1496	3.00E-31	72.62
rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
poly	<i>Onthophagus taurus</i>	4279	0	79.64
RING-box protein 1A	<i>Onthophagus taurus</i>	588	6.00E-89	81.16
Calmodulin	<i>Stylophora pistillata</i>	879	6.00E-05	80.77
protein phosphatase 1 catalytic subunit, partial	<i>Colaphellus bowringi</i>	1795	0	78.43
acid phosphatase, partial	<i>Cryptolaemus montrouzieri</i>	2868	0	87.05
PREDICTED: membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase-like	<i>Dendroctonus ponderosae</i>	2365	0.004	66.06
PREDICTED: 14-3-3 protein zeta isoform X3	<i>Dendroctonus ponderosae</i>	1175	2.00E-68	80.07
PREDICTED: cell division cycle protein 16 homolog	<i>Aethina tumida</i>	689	2.00E-37	71.72
PREDICTED: cyclin-dependent kinase 2-like	<i>Aethina tumida</i>	1454	2.00E-141	72.06
PREDICTED: uncharacterized protein LOC108739266	<i>Agrius planipennis</i>	1081	1.00E-53	74.77

PREDICTED: S-phase kinase-associated protein 1	<i>Agrilus planipennis</i>	305	6.00E-51	78.81
PREDICTED: S-phase kinase-associated protein 1 isoform X1	<i>Ceratosolen solmsi marchali</i>	845	3.00E-27	66.59
PREDICTED: inositol 1,4,5-trisphosphate receptor isoform X3	<i>Tribolium castaneum</i>	8858	0	73.04
PREDICTED: cullin-1	<i>Tribolium castaneum</i>	3231	0	74.24
PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X10	<i>Tribolium castaneum</i>	1504	0	75.42
PREDICTED: cytoplasmic polyadenylation element-binding protein 1-B	<i>Tribolium castaneum</i>	6685	2.00E-165	76.25
Ovarian steroidogenesis				
insulin-like receptor	<i>Anoplophora glabripennis</i>	7550	9.00E-143	72.23
adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	4.00E-103	70.96

rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
PREDICTED: guanine nucleotide-binding protein G	<i>Anoplophora glabripennis</i>	3377	1.00E-82	70.47
PREDICTED: scavenger receptor class B member 1-like	<i>Agrilus planipennis</i>	1994	6.00E-78	66.16
PREDICTED: probable cytochrome P450 303a1	<i>Tribolium castaneum</i>	795	2.00E-29	66.06
Progesterone-mediated oocyte maturation				
anaphase-promoting complex subunit 4	<i>Anoplophora glabripennis</i>	2666	5.00E-53	65.92
anaphase-promoting complex subunit 10	<i>Leptinotarsa decemlineata</i>	1072	2.00E-137	80.87
cell division cycle protein 23 homolog	<i>Anoplophora glabripennis</i>	1849	0	73.85
cell division cycle protein 27 homolog	<i>Anoplophora glabripennis</i>	3090	5.00E-91	69.22
heat shock protein 83-like	<i>Centruroides sculpturatus</i>	969	2.00E-135	72.55
heat shock protein 90	<i>Tribolium castaneum</i>	2435	0	76.23
PREDICTED: heat shock protein HSP 90-alpha-like	<i>Hyalella azteca</i>	1326	0	76.43
adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98

cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
mitotic checkpoint serine/threonine-protein kinase BUB1 beta	<i>Anoplophora glabripennis</i>	3658	2.00E-98	73.21
mitotic spindle assembly checkpoint protein MAD1-like	<i>Anoplophora glabripennis</i>	2604	3.00E-24	64.24
phosphatidylinositol 3-kinase regulatory subunit alpha isoform X2	<i>Anoplophora glabripennis</i>	8011	2.00E-69	64.9
probable ATP-dependent RNA helicase DDX27	<i>Anoplophora glabripennis</i>	2782	0	70.33
ribosomal protein S6 kinase 2 beta isoform X2	<i>Anoplophora glabripennis</i>	3142	0	71.32
raf homolog serine/threonine-protein kinase phl	<i>Anoplophora glabripennis</i>	3433	0	73.44
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09
RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35

protein enhancer of sevenless 2B	<i>Zootermopsis nevadensis</i>	1362	4.00E-36	67.17
PREDICTED: cell division cycle protein 16 homolog	<i>Aethina tumida</i>	689	2.00E-37	71.72
PREDICTED: cyclin-dependent kinase 2-like	<i>Aethina tumida</i>	1454	2.00E-141	72.06
PREDICTED: uncharacterized protein LOC108739266	<i>Agrilus planipennis</i>	1081	1.00E-53	74.77
PREDICTED: fizzy-related protein homolog	<i>Tribolium castaneum</i>	3134	0	73.3
PREDICTED: cytoplasmic polyadenylation element-binding protein 1-B	<i>Tribolium castaneum</i>	6685	2.00E-165	76.25
PREDICTED: anaphase-promoting complex subunit 2	<i>Tribolium castaneum</i>	3131	2.00E-169	68.43
PREDICTED: G protein alpha i subunit	<i>Tribolium castaneum</i>	3106	0	73.79
PREDICTED: serine/threonine-protein kinase mos	<i>Tribolium castaneum</i>	1708	7.00E-13	66.56
Estrogen signaling pathway				
testis-specific heat shock protein cognate 70-6	<i>Laodelphax striatella</i>	367	3.00E-13	73.28
heat shock protein 68	<i>Harmonia axyridis</i>	2242	0	78.25
heat shock protein 70	<i>Harmonia axyridis</i>	3004	0	73.57
heat shock protein 68-like	<i>Leptinotarsa decemlineata</i>	1720	0	75.03
heat shock protein 83-like	<i>Centruroides sculpturatus</i>	969	2.00E-135	72.55

heat shock protein 90	<i>Tribolium castaneum</i>	2435	0	76.23
heat shock 70 kDa protein cognate 4-like	<i>Centruroides sculpturatus</i>	2161	0	71.64
PREDICTED: heat shock 70 kDa protein cognate 2	<i>Tribolium castaneum</i>	744	8.00E-141	78.17
PREDICTED: heat shock 70 kDa protein cognate 4 isoform X2	<i>Megachile rotundata</i>	312	3.00E-23	85.11
PREDICTED: heat shock protein HSP 90-alpha-like	<i>Hyalella azteca</i>	1326	0	76.43
adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98
calcium-binding protein E63-1	<i>Anoplophora glabripennis</i>	615	8.00E-30	68.73
cyclic AMP-responsive element-binding protein 3-like protein 1	<i>Anoplophora glabripennis</i>	2996	3.00E-55	72.26
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
phosphatidylinositol 3-kinase regulatory subunit alpha isoform X2	<i>Anoplophora glabripennis</i>	8011	2.00E-69	64.9

G-protein alpha subunit	<i>Lissorhoptrus oryzophilus</i>	2446	0	79.53
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09
RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35
FK506-binding protein 59	<i>Anoplophora glabripennis</i>	1584	2.00E-86	65.96
uncharacterized protein LOC111511578	<i>Leptinotarsa decemlineata</i>	988	2.00E-08	69.54
protein son of sevenless isoform X2	<i>Leptinotarsa decemlineata</i>	5093	0	71.23
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
Calmodulin	<i>Stylophora pistillata</i>	879	6.00E-05	80.77
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
PREDICTED: LOW QUALITY PROTEIN: heat shock protein 68-like	<i>Aethina tumida</i>	1043	7.00E-146	73.66
PREDICTED: protein enhancer of sevenless 2B	<i>Tribolium castaneum</i>	636	4.00E-55	82.55
PREDICTED: inositol 1,4,5-trisphosphate receptor isoform X3	<i>Tribolium castaneum</i>	8858	0	73.04
PREDICTED: G protein alpha i subunit	<i>Tribolium castaneum</i>	3106	0	73.79

PREDICTED: SHC-transforming protein 1	<i>Tribolium castaneum</i>	5140	4.00E-130	69.36
PREDICTED: guanine nucleotide-binding protein G	<i>Tribolium castaneum</i>	4488	0	79.31
PREDICTED: endoplasmic	<i>Linepithema humile</i>	2719	6.00E-174	67.15
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
Prolactin signaling pathway				
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
phosphatidylinositol 3-kinase regulatory subunit alpha isoform X2	<i>Anoplophora glabripennis</i>	8011	2.00E-69	64.9
protein son of sevenless isoform X2	<i>Leptinotarsa decemlineata</i>	5093	0	71.23
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09
tyrosine hydroxylase	<i>Tribolium castaneum</i>	2123	0	69.58
RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35
suppressor of cytokine signaling 2	<i>Harmonia axyridis</i>	2643	2.00E-114	70.63
PREDICTED: G1/S-specific cyclin-D3-like	<i>Aethina tumida</i>	1476	3.00E-44	68
PREDICTED: nuclear factor NF-kappa-B p110 subunit	<i>Tribolium castaneum</i>	3301	3.00E-78	68.03

isoform X1

PREDICTED: SHC-transforming protein 1	<i>Tribolium castaneum</i>	5140	4.00E-130	69.36
PREDICTED: uncharacterized protein LOC662537	<i>Tribolium castaneum</i>	2939	5.00E-114	77.86
PREDICTED: BAG family molecular chaperone regulator 2	<i>Tribolium castaneum</i>	851	3.00E-71	71.92
PREDICTED: protein enhancer of sevenless 2B	<i>Tribolium castaneum</i>	636	4.00E-55	82.55

Thyroid hormone synthesis

adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
iodotyrosine deiodinase 1 isoform X1	<i>Anoplophora glabripennis</i>	1025	8.00E-64	70.48
cyclic AMP-responsive element-binding protein 3-like protein 1	<i>Anoplophora glabripennis</i>	2996	3.00E-55	72.26
low-density lipoprotein receptor class A domain-containing protein 3-like	<i>Anoplophora glabripennis</i>	2634	1.00E-54	71.91
rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
Protein Wnt-2-like Protein	<i>Tribolium castaneum</i>	2691	0	73.94
transcription termination factor 2-like	<i>Onthophagus taurus</i>	3187	2.00E-27	64.16

cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
PREDICTED: endoplasmin	<i>Linepithema humile</i>	2719	6.00E-174	67.15
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit beta-2-like	<i>Aethina tumida</i>	2892	2.00E-25	67.53
PREDICTED: probable phospholipid hydroperoxide glutathione peroxidase isoform X1	<i>Aethina tumida</i>	1230	2.00E-57	70.85
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98
PREDICTED: guanine nucleotide-binding protein G	<i>Tribolium castaneum</i>	4488	0	79.31
PREDICTED: inositol 1,4,5-trisphosphate receptor isoform X3	<i>Tribolium castaneum</i>	8858	0	73.04
Thyroid hormone signaling pathway				
testis-specific actin	<i>Rhipicephalus appendiculatus</i>	298	8.00E-85	82.83
actin, cytoplasmic A3a	<i>Ceratitis capitata</i>	1195	0	81.67
beta-actin	<i>Tigriopus japonicus</i>	1771	9.00E-173	90.07

PREDICTED: actin, cytoplasmic	<i>Tribolium castaneum</i>	667	1.00E-92	77.91
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
mediator of RNA polymerase II transcription subunit 13 isoform X3	<i>Anoplophora glabripennis</i>	7898	0	70.55
PREDICTED: mediator of RNA polymerase II transcription subunit 16 isoform X1	<i>Tribolium castaneum</i>	3031	0	67.7
PREDICTED: mediator of RNA polymerase II transcription subunit 17 isoform X2	<i>Tribolium castaneum</i>	2263	0	74.06
PREDICTED: mediator of RNA polymerase II transcription subunit 24	<i>Tribolium castaneum</i>	3506	0	68.31
solute carrier family 2, facilitated glucose transporter member 1	<i>Anoplophora glabripennis</i>	2568	2.00E-82	65.71
PREDICTED: solute carrier family 2, facilitated glucose transporter member 3-like isoform X2	<i>Ceratosolen solmsi marchali</i>	845	3.00E-14	67.93
histone deacetylase Rpd3 isoform X1	<i>Anoplophora glabripennis</i>	1908	0	78.01
hypoxia-inducible factor 1-alpha isoform X2	<i>Anoplophora glabripennis</i>	2366	2.00E-146	70.95
phosphatidylinositol 3-kinase regulatory subunit alpha isoform X2	<i>Anoplophora glabripennis</i>	8011	2.00E-69	64.9

protein decapentaplegic	<i>Anoplophora glabripennis</i>	3840	8.00E-52	74.03
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
transcriptional regulator Myc-1 isoform X2	<i>Anoplophora glabripennis</i>	3653	1.00E-24	74.18
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 isoform X1	<i>Anoplophora glabripennis</i>	3057	0	72.49
RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35
ultraspiracle 2 isoform	<i>Henosepilachna vigintioctopunctata</i>	2221	0	99.56
uncharacterized protein LOC111510921	<i>Leptinotarsa decemlineata</i>	1310	1.00E-17	74.34
mediator of RNA polymerase II transcription subunit 30-like	<i>Leptinotarsa decemlineata</i>	1185	1.00E-97	76.1
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09
glucose transporter type 1 isoform X4	<i>Onthophagus taurus</i>	2680	0	74.83
ras-like GTP-binding protein RHO	<i>Orbicella faveolata</i>	854	2.00E-10	83.08
steroid receptor coactivator	<i>Monochamus alternatus</i>	6138	0	67.81
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8

PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
PREDICTED: LOW QUALITY PROTEIN: histone deacetylase 3-like	<i>Aethina tumida</i>	3494	0	77.72
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit beta-2-like	<i>Aethina tumida</i>	2892	2.00E-25	67.53
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	<i>Tribolium castaneum</i>	4244	0	69.03
PREDICTED: 3-phosphoinositide-dependent protein kinase 1	<i>Tribolium castaneum</i>	1906	6.00E-27	67.01
PREDICTED: GATA-binding factor A isoform X2	<i>Tribolium castaneum</i>	2797	3.00E-109	72.24
PREDICTED: transcription factor GATA-4 isoform X1	<i>Tribolium castaneum</i>	2657	4.00E-88	80.34
PREDICTED: GTP-binding protein Rheb homolog	<i>Nicrophorus vespilloides</i>	2052	3.00E-97	76.4
Oxytocin signaling pathway				
testis-specific actin	<i>Rhipicephalus appendiculatus</i>	298	8.00E-85	82.83
actin, cytoplasmic A3a	<i>Ceratitis capitata</i>	1195	0	81.67
beta-actin	<i>Tigriopus japonicus</i>	1771	9.00E-173	90.07

PREDICTED: actin, cytoplasmic	<i>Tribolium castaneum</i>	667	1.00E-92	77.91
PREDICTED: testis-specific muscle calcium channel subunit alpha-1 isoform X2	<i>Nicrophorus vespilloides</i>	439	8.00E-53	75.83
protein phosphatase 1 catalytic subunit, partial	<i>Colaphellus bowringi</i>	1795	0	78.43
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X4	<i>Tribolium castaneum</i>	3143	0	69.69
adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98
calcium-binding protein E63-1	<i>Anoplophora glabripennis</i>	615	8.00E-30	68.73
PREDICTED: calcium/calmodulin-dependent protein kinase type 1	<i>Tribolium castaneum</i>	3330	0	79.48
PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X10	<i>Tribolium castaneum</i>	1504	0	75.42
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96

G-protein alpha subunit	<i>Lissorhoptrus oryzophilus</i>	2446	0	79.53
PREDICTED: G protein alpha i subunit	<i>Tribolium castaneum</i>	3106	0	73.79
FK506-binding protein 59	<i>Anoplophora glabripennis</i>	1584	2.00E-86	65.96
titin	<i>Anoplophora glabripennis</i>	3672	0	71.6
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
5'-AMP-activated protein kinase catalytic subunit alpha-2	<i>Dastarcus helophoroides</i>	2267	0	77.07
hypothetical protein YQE_10269, partial	<i>Dendroctonus ponderosae</i>	3681	1.00E-118	71.4
rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
ryanodine receptor	<i>Tribolium castaneum</i>	10129	0	74.66
acid phosphatase, partial	<i>Cryptolaemus montrouzieri</i>	2868	0	87.05
Calmodulin	<i>Stylophora pistillata</i>	879	6.00E-05	80.77
PREDICTED: guanine nucleotide-binding protein G	<i>Tribolium castaneum</i>	4488	0	79.31
PREDICTED: inositol 1,4,5-trisphosphate receptor isoform X3	<i>Tribolium castaneum</i>	8858	0	73.04

PREDICTED: head-specific guanylate cyclase	<i>Tribolium castaneum</i>	1161	2.00E-175	76.11
GnRH signaling pathway				
testis-specific PREDICTED: muscle calcium channel subunit alpha-1 isoform X2	<i>Nicrophorus vespilloides</i>	439	8.00E-53	75.83
testis-specific PREDICTED: cell division control protein 42 homolog	<i>Branchiostoma belcheri</i>	310	1.00E-30	80.42
adenylate cyclase type 8	<i>Anoplophora glabripennis</i>	1924	2.00E-164	69.83
PREDICTED: adenylate cyclase type 2 isoform X4	<i>Dendroctonus ponderosae</i>	2992	0	70.15
PREDICTED: adenylate cyclase type 3	<i>Tribolium castaneum</i>	2838	2.00E-174	71.98
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
matrix metalloproteinase 1 isoform 2 precursor	<i>Tribolium castaneum</i>	2544	7.00E-143	68.48
PREDICTED: matrix metalloproteinase-14-like isoform X1	<i>Nicrophorus vespilloides</i>	1143	1.00E-24	71.07
protein enhancer of sevenless 2B	<i>Zootermopsis nevadensis</i>	1362	4.00E-36	67.17
PREDICTED: protein enhancer of sevenless 2B	<i>Tribolium castaneum</i>	636	4.00E-55	82.55

calcium-binding protein E63-1	<i>Anoplophora glabripennis</i>	615	8.00E-30	68.73
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
rutabaga	<i>Tribolium castaneum</i>	7751	0	73.02
DNA excision repair protein ERCC-6-like isoform X3	<i>Leptinotarsa decemlineata</i>	1619	1.00E-115	70.59
protein son of sevenless isoform X2	<i>Leptinotarsa decemlineata</i>	5093	0	71.23
Calmodulin	<i>Stylophora pistillata</i>	879	6.00E-05	80.77
PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X10	<i>Tribolium castaneum</i>	1504	0	75.42
PREDICTED: guanine nucleotide-binding protein G	<i>Tribolium castaneum</i>	4488	0	79.31
PREDICTED: inositol 1,4,5-trisphosphate receptor isoform X3	<i>Tribolium castaneum</i>	8858	0	73.04
PREDICTED: cdc42 homolog	<i>Tribolium castaneum</i>	1786	3.00E-138	78.99
Apoptosis				
testis-specific probable multidrug resistance-associated protein lethal	<i>Diabrotica virgifera virgifera</i>	929	6.00E-39	73.18

testis-specific Cathepsin L1 precursor	<i>Caligus clemensi</i>	385	1.00E-31	73.61
testis-specific PREDICTED: cathepsin L1-like	<i>Aethina tumida</i>	1122	5.00E-15	67.32
testis-specific actin	<i>Rhipicephalus appendiculatus</i>	298	8.00E-85	82.83
actin, cytoplasmic A3a	<i>Ceratitidis capitata</i>	1195	0	81.67
beta-actin	<i>Tigriopus japonicus</i>	1771	9.00E-173	90.07
PREDICTED: actin, cytoplasmic	<i>Tribolium castaneum</i>	667	1.00E-92	77.91
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
tubulin alpha-4 chain-like	<i>Anoplophora glabripennis</i>	1526	0	74.4
phosphatidylinositol 3-kinase regulatory subunit alpha isoform X2	<i>Anoplophora glabripennis</i>	8011	2.00E-69	64.9
RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09
growth arrest and DNA damage-inducible protein GADD45 alpha	<i>Leptinotarsa decemlineata</i>	1125	2.00E-31	70.63
serine protease HTRA2, mitochondrial-like	<i>Leptinotarsa decemlineata</i>	1496	3.00E-31	72.62

PREDICTED: 3-phosphoinositide-dependent protein kinase 1	<i>Tribolium castaneum</i>	1906	6.00E-27	67.01
PREDICTED: nuclear factor NF-kappa-B p110 subunit isoform X1	<i>Tribolium castaneum</i>	3301	3.00E-78	68.03
PREDICTED: inositol 1,4,5-trisphosphate receptor isoform X3	<i>Tribolium castaneum</i>	8858	0	73.04
Apoptosis - fly				
raf homolog serine/threonine-protein kinase phl	<i>Anoplophora glabripennis</i>	3433	0	73.44
ultraspiracle 2 isoform	<i>Henosepilachna vigintioctopunctata</i>	2221	0	99.56
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
PREDICTED: mitogen-activated protein kinase kinase kinase 7-like isoform X1	<i>Agrilus planipennis</i>	1968	1.00E-74	69.19
serine protease HTRA2, mitochondrial-like	<i>Leptinotarsa decemlineata</i>	1496	3.00E-31	72.62
PREDICTED: serine/threonine-protein kinase 3 isoform X1	<i>Tribolium castaneum</i>	4285	0	73.78
Apoptosis - multiple species				
PREDICTED: S-phase kinase-associated protein 1 isoform X1	<i>Ceratosolen solmsi marchali</i>	845	3.00E-27	66.59

Steroid hormone biosynthesis

testis-specific UDP-glucuronosyltransferase 2B16-like isoform X1	<i>Anoplophora glabripennis</i>	629	3.00E-35	69.8
testis-specific PREDICTED: UDP-glucuronosyltransferase 2B2-like	<i>Nicrophorus vespilloides</i>	477	1.00E-06	80
uncharacterized protein LOC108903775	<i>Anoplophora glabripennis</i>	1273	9.00E-14	67.77
uncharacterized protein LOC108904558	<i>Anoplophora glabripennis</i>	1755	4.00E-07	77.11
uncharacterized protein LOC111515682	<i>Leptinotarsa decemlineata</i>	1338	2.00E-45	70.79
hypothetical protein D910_12170	<i>Dendroctonus ponderosae</i>	1589	7.00E-50	69.23
hypothetical protein TcasGA2_TC012282	<i>Tribolium castaneum</i>	1657	5.00E-14	65.04
UDP-glucuronosyltransferase 2B19 isoform X1	<i>Anoplophora glabripennis</i>	1995	5.00E-64	65.95
UDP-glucuronosyltransferase 2A3-like isoform X1	<i>Leptinotarsa decemlineata</i>	1930	1.00E-11	70.99
very-long-chain 3-oxoacyl-CoA reductase-B	<i>Leptinotarsa decemlineata</i>	1283	1.00E-48	65.71
PREDICTED: UDP-glucuronosyltransferase 1-1-like	<i>Agrilus planipennis</i>	660	1.00E-05	81.13
PREDICTED: UDP-glucuronosyltransferase 1-7 isoform X3	<i>Tribolium castaneum</i>	1323	4.00E-40	72.39
PREDICTED: UDP-glucuronosyltransferase 1-7C	<i>Tribolium castaneum</i>	834	8.00E-16	70.21

isoform X4

PREDICTED: UDP-glucuronosyltransferase 2B7-like	<i>Aethina tumida</i>	1878	3.00E-21	67.82
PREDICTED: UDP-glucuronosyltransferase 2B7 isoform X2	<i>Tribolium castaneum</i>	1670	6.00E-13	68.69
PREDICTED: UDP-glucuronosyltransferase 2B9	<i>Tribolium castaneum</i>	1250	2.00E-05	81.82
PREDICTED: UDP-glucuronosyltransferase 2B14	<i>Tribolium castaneum</i>	1913	8.00E-19	76.34
PREDICTED: UDP-glucuronosyltransferase 2B15-like	<i>Agrilus planipennis</i>	417	1.00E-11	76.29
PREDICTED: UDP-glucuronosyltransferase 2B17-like	<i>Dendroctonus ponderosae</i>	483	4.00E-07	71.3
PREDICTED: UDP-glucuronosyltransferase 2C1-like	<i>Tribolium castaneum</i>	1523	7.00E-26	72.35
PREDICTED: 2-hydroxyacylsphingosine 1-beta-galactosyltransferase-like	<i>Tribolium castaneum</i>	1795	1.00E-29	69.45

Homologous recombination

testis-specific PREDICTED: uncharacterized protein LOC106134883	<i>Amyelois transitella</i>	414	1.00E-135	85.82
testis-specific PREDICTED: uncharacterized protein LOC106140328	<i>Amyelois transitella</i>	271	6.00E-73	82.72
testis-specific PREDICTED: uncharacterized protein LOC109038256	<i>Bemisia tabaci</i>	336	6.00E-10	71.9

DNA repair protein RAD50 isoform X1	<i>Anoplophora glabripennis</i>	4231	7.00E-34	68.14
DNA repair protein RAD51 homolog 1	<i>Leptinotarsa decemlineata</i>	1294	0	76.06
DNA repair and recombination protein RAD54-like	<i>Anoplophora glabripennis</i>	429	6.00E-29	72.73
DNA topoisomerase 3-beta-1	<i>Anoplophora glabripennis</i>	3145	0	73.66
DNA polymerase delta small subunit	<i>Anoplophora glabripennis</i>	1805	2.00E-74	66.88
BRISC and BRCA1-A complex member 2	<i>Anoplophora glabripennis</i>	2183	8.00E-24	66.28
breast cancer type 2 susceptibility protein-like isoform X2	<i>Anoplophora glabripennis</i>	4335	1.00E-24	67.31
uncharacterized protein LOC111615589	<i>Centruroides sculpturatus</i>	1093	1.00E-05	68.66
PREDICTED: uncharacterized protein LOC106131883 isoform X1	<i>Amyelois transitella</i>	470	4.00E-28	69.23
PREDICTED: crossover junction endonuclease EME1	<i>Agrilus planipennis</i>	1985	2.00E-16	66.83
PREDICTED: single-stranded DNA-binding protein, mitochondrial	<i>Tribolium castaneum</i>	1323	4.00E-59	76.23
MAPK signaling pathway				
testis-specific mitogen-activated protein kinase kinase kinase 13-A	<i>Leptinotarsa decemlineata</i>	817	5.00E-07	72.73

testis-specific heat shock protein cognate 70-6	<i>Laodelphax striatella</i>	367	3.00E-13	73.28
testis-specific PREDICTED: cell division control protein 42 homolog	<i>Branchiostoma belcheri</i>	310	1.00E-30	80.42
testis-specific PREDICTED: TGF-beta receptor type-1 isoform X3	<i>Nicrophorus vespilloides</i>	353	2.00E-08	72.13
testis-specific PREDICTED: muscle calcium channel subunit alpha-1 isoform X2	<i>Nicrophorus vespilloides</i>	439	8.00E-53	75.83
heat shock protein 68	<i>Harmonia axyridis</i>	2242	0	78.25
heat shock protein 70	<i>Harmonia axyridis</i>	3004	0	73.57
heat shock protein 68-like	<i>Leptinotarsa decemlineata</i>	1720	0	75.03
PREDICTED: heat shock 70 kDa protein cognate 2	<i>Tribolium castaneum</i>	744	8.00E-141	78.17
PREDICTED: heat shock 70 kDa protein cognate 4 isoform X2	<i>Megachile rotundata</i>	312	3.00E-23	85.11
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	1.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13

PREDICTED: mitogen-activated protein kinase kinase kinase 7-like isoform X1	<i>Agrilus planipennis</i>	1968	1.00E-74	69.19
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
PREDICTED: dual specificity protein phosphatase 3	<i>Tribolium castaneum</i>	914	8.00E-53	68.37
MAP kinase-activated protein kinase 2	<i>Anoplophora glabripennis</i>	2384	0	77.83
MAP kinase-interacting serine/threonine-protein kinase 1	<i>Anoplophora glabripennis</i>	880	1.00E-117	76.35
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	<i>Anoplophora glabripennis</i>	3006	8.00E-57	69.07
transcriptional regulator Myc-1 isoform X2	<i>Anoplophora glabripennis</i>	3653	1.00E-24	74.18
ras-related C3 botulinum toxin substrate 1	<i>Anoplophora glabripennis</i>	2805	4.00E-136	78.21
raf homolog serine/threonine-protein kinase phl	<i>Anoplophora glabripennis</i>	3433	0	73.44
ribosomal protein S6 kinase 2 beta isoform X2	<i>Anoplophora glabripennis</i>	3142	0	71.32
DNA excision repair protein ERCC-6-like isoform X3	<i>Leptinotarsa decemlineata</i>	1619	1.00E-115	70.59
growth arrest and DNA damage-inducible protein GADD45 alpha	<i>Leptinotarsa decemlineata</i>	1125	2.00E-31	70.63
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09

protein son of sevenless isoform X2	<i>Leptinotarsa decemlineata</i>	5093	0	71.23
protein enhancer of sevenless 2B	<i>Zootermopsis nevadensis</i>	1362	4.00E-36	67.17
RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35
PREDICTED: LOW QUALITY PROTEIN: ras GTPase-activating protein 1-like	<i>Aethina tumida</i>	4518	0	74.04
PREDICTED: LOW QUALITY PROTEIN: heat shock protein 68-like	<i>Aethina tumida</i>	1043	7.00E-146	73.66
PREDICTED: zinc finger protein 2 homolog isoform X1	<i>Tribolium castaneum</i>	4028	2.00E-67	74.49
PREDICTED: serine/threonine-protein kinase mos	<i>Tribolium castaneum</i>	1708	7.00E-13	66.56
PREDICTED: serine/threonine-protein kinase 3 isoform X1	<i>Tribolium castaneum</i>	4285	0	73.78
PREDICTED: serine/threonine-protein kinase NLK isoform X1	<i>Tribolium castaneum</i>	3626	0	78.33
PREDICTED: serine/threonine-protein phosphatase 5	<i>Tribolium castaneum</i>	1774	0	71.26
PREDICTED: protein max isoform X3	<i>Tribolium castaneum</i>	1363	5.00E-70	73.66
PREDICTED: protein enhancer of sevenless 2B	<i>Tribolium castaneum</i>	636	4.00E-55	82.55
PREDICTED: adapter molecule Crk	<i>Tribolium castaneum</i>	1329	2.00E-128	72.72

PREDICTED: ras-like protein 3	<i>Tribolium castaneum</i>	4357	0	78.58
PREDICTED: nuclear factor NF-kappa-B p110 subunit isoform X1	<i>Tribolium castaneum</i>	3301	3.00E-78	68.03
PREDICTED: cdc42 homolog	<i>Tribolium castaneum</i>	1786	3.00E-138	78.99
PREDICTED: protein phosphatase 1A	<i>Tribolium castaneum</i>	4182	3.00E-168	74.23
PREDICTED: fizzy-related protein homolog	<i>Tribolium castaneum</i>	3134	0	73.3
MAPK signaling pathway - fly				
testis-specific PREDICTED: leucine-rich repeat-containing protein 24-like	<i>Nicrophorus vespilloides</i>	519	2.00E-11	72.44
sprouty	<i>Harmonia axyridis</i>	2358	0	82.6
<i>Agrilus planipennis</i>	<i>Agrilus planipennis</i>	2005	0	79.81
protein trunk	<i>Anoplophora glabripennis</i>	1337	2.00E-04	67.72
protein decapentaplegic	<i>Anoplophora glabripennis</i>	3840	8.00E-52	74.03
protein C-ets-2 isoform X1	<i>Anoplophora glabripennis</i>	3507	0	70.56
protein enhancer of sevenless 2B	<i>Zootermopsis nevadensis</i>	1362	4.00E-36	67.17
protein son of sevenless isoform X2	<i>Leptinotarsa decemlineata</i>	5093	0	71.23
raf homolog serine/threonine-protein kinase phl	<i>Anoplophora glabripennis</i>	3433	0	73.44

ras-related C3 botulinum toxin substrate 1	<i>Anoplophora glabripennis</i>	2805	4.00E-136	78.21
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
PREDICTED: mitogen-activated protein kinase kinase 7-like isoform X1	<i>Agrilus planipennis</i>	1968	1.00E-74	69.19
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
E3 ubiquitin-protein ligase SIAH1-like	<i>Anoplophora glabripennis</i>	1012	2.00E-15	65.37
receptor tyrosine kinase Torso-like protein	<i>Tribolium castaneum</i>	944	5.00E-05	72.63
uncharacterized protein LOC111504284	<i>Leptinotarsa decemlineata</i>	3305	4.00E-154	70.35
serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	<i>Leptinotarsa decemlineata</i>	2785	0	76.76
DNA excision repair protein ERCC-6-like isoform X3	<i>Leptinotarsa decemlineata</i>	1619	1.00E-115	70.59
PREDICTED: E3 ubiquitin-protein ligase SIAH1-like	<i>Aethina tumida</i>	2663	4.00E-172	77.66
PREDICTED: LOW QUALITY PROTEIN: ras GTPase-activating protein 1-like	<i>Aethina tumida</i>	4518	0	74.04
PREDICTED: LOW QUALITY PROTEIN: exportin-1	<i>Aethina tumida</i>	4508	0	71.34
PREDICTED: 14-3-3 protein zeta isoform X3	<i>Dendroctonus ponderosae</i>	1175	2.00E-68	80.07

PREDICTED: protein phosphatase 1A	<i>Tribolium castaneum</i>	4182	3.00E-168	74.23
PREDICTED: protein groucho isoform X4	<i>Tribolium castaneum</i>	2750	0	72.27
PREDICTED: tyrosine-protein kinase Btk29A isoform X1	<i>Tribolium castaneum</i>	2685	0	76.34
PREDICTED: SHC-transforming protein 1	<i>Tribolium castaneum</i>	5140	4.00E-130	69.36
PREDICTED: modulator of activity of ets isoform X1	<i>Tribolium castaneum</i>	1018	3.00E-15	68.3
PREDICTED: homeobox protein prospero isoform X2	<i>Tribolium castaneum</i>	3643	0	72.74
PREDICTED: zinc finger protein 2 homolog isoform X1	<i>Tribolium castaneum</i>	4028	2.00E-67	74.49
Ras signaling pathway				
testis-specific PREDICTED: LOW QUALITY PROTEIN: protein still life, isoform SIF type 1-like	<i>Aethina tumida</i>	2389	2.00E-29	74.07
testis-specific PREDICTED: protein still life, isoform SIF type 1 isoform X13	<i>Tribolium castaneum</i>	472	5.00E-98	76.91
testis-specific PREDICTED: cell division control protein 42 homolog	<i>Branchiostoma belcheri</i>	310	1.00E-30	80.42
cAMP-dependent protein kinase catalytic subunit alpha-like	<i>Leptinotarsa decemlineata</i>	770	3.00E-28	67.8
PREDICTED: cAMP-dependent protein kinase catalytic subunit-like	<i>Agrilus planipennis</i>	1362	6.00E-103	70.96

ras-like GTP-binding protein RHO	<i>Orbicella faveolata</i>	854	2.00E-10	83.08
PREDICTED: ras-like protein 2	<i>Harmonia axyridis</i>	430	0.008	92.59
PREDICTED: ras-like protein 3	<i>Tribolium castaneum</i>	4357	0	78.58
ras-related C3 botulinum toxin substrate 1	<i>Anoplophora glabripennis</i>	2805	4.00E-136	78.21
PREDICTED: ras-related protein Ral-a	<i>Tribolium castaneum</i>	2275	3.00E-100	73.32
mitogen-activated protein kinase 1	<i>Anoplophora glabripennis</i>	2301	0	77.13
5-hydroxytryptamine receptor 1-like	<i>Anoplophora glabripennis</i>	2157	0	73.52
leucine-rich repeat protein soc-2 homolog	<i>Anoplophora glabripennis</i>	3775	0	71.46
protein C-ets-2 isoform X1	<i>Anoplophora glabripennis</i>	3507	0	70.56
dual specificity mitogen-activated protein kinase kinase dSOR1	<i>Anoplophora glabripennis</i>	2118	0	78.13
vascular endothelial growth factor receptor 1 isoform X4	<i>Anoplophora glabripennis</i>	3248	1.00E-42	73.52
phosphatidylinositol 3-kinase regulatory subunit alpha isoform X2	<i>Anoplophora glabripennis</i>	8011	2.00E-69	64.9
BRCA1-associated protein isoform X2	<i>Anoplophora glabripennis</i>	2261	2.00E-165	69.74
insulin-like receptor	<i>Anoplophora glabripennis</i>	7550	9.00E-143	72.23
calcium-binding protein E63-1	<i>Anoplophora glabripennis</i>	615	8.00E-30	68.73

RNA-binding protein 41	<i>Harmonia axyridis</i>	2116	5.00E-20	65.35
protein son of sevenless isoform X2	<i>Leptinotarsa decemlineata</i>	5093	0	71.23
RAC serine/threonine-protein kinase isoform X2	<i>Leptinotarsa decemlineata</i>	2024	0	73.09
Calmodulin	<i>Stylophora pistillata</i>	879	6.00E-05	80.77
PREDICTED: vascular endothelial growth factor receptor 1 isoform X1	<i>Tribolium castaneum</i>	1926	2.00E-21	66.57
PREDICTED: vascular endothelial growth factor receptor 1 isoform X2	<i>Megachile rotundata</i>	465	3.00E-20	71.96
PREDICTED: LOW QUALITY PROTEIN: ras GTPase-activating protein 1-like	<i>Aethina tumida</i>	4518	0	74.04
PREDICTED: protein enhancer of sevenless 2B	<i>Tribolium castaneum</i>	636	4.00E-55	82.55
PREDICTED: ADP-ribosylation factor 6	<i>Tribolium castaneum</i>	3182	4.00E-82	72.8
PREDICTED: nuclear factor NF-kappa-B p110 subunit isoform X1	<i>Tribolium castaneum</i>	3301	3.00E-78	68.03
PREDICTED: cdc42 homolog	<i>Tribolium castaneum</i>	1786	3.00E-138	78.99
PREDICTED: glutamate [NMDA] receptor subunit 1 isoform X2	<i>Tribolium castaneum</i>	2932	0	71.43
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate	<i>Tribolium castaneum</i>	4244	0	69.03

phosphodiesterase gamma-1

PREDICTED: SHC-transforming protein 1	<i>Tribolium castaneum</i>	5140	4.00E-130	69.36
PREDICTED: zinc finger protein 2 homolog isoform X1	<i>Tribolium castaneum</i>	4028	2.00E-67	74.49
PREDICTED: group XIIA secretory phospholipase A2	<i>Aethina tumida</i>	1472	2.00E-85	71.66
PREDICTED: ralA-binding protein 1	<i>Aethina tumida</i>	2419	1.00E-127	69.26
PREDICTED: embryonic polarity protein dorsal-like isoform X3	<i>Agrilus planipennis</i>	3037	3.00E-111	71.07

Cell cycle

cell division cycle protein 16 homolog	<i>Anoplophora glabripennis</i>	1855	5.00E-139	75.56
cell division cycle protein 23 homolog	<i>Anoplophora glabripennis</i>	1849	0	73.85
cell division cycle protein 27 homolog	<i>Anoplophora glabripennis</i>	3090	5.00E-91	69.22
mitotic checkpoint serine/threonine-protein kinase BUB1 beta	<i>Anoplophora glabripennis</i>	3658	2.00E-98	73.21
mitotic spindle assembly checkpoint protein MAD1-like	<i>Anoplophora glabripennis</i>	2604	3.00E-24	64.24
14-3-3 protein epsilon	<i>Zootermopsis nevadensis</i>	1038	7.00E-146	75.53
14-3-3 protein zeta isoform X1	<i>Anoplophora glabripennis</i>	2161	0	83.52
PREDICTED: 14-3-3 protein zeta isoform X3	<i>Dendroctonus ponderosae</i>	1175	2.00E-68	80.07

anaphase-promoting complex subunit 4	<i>Anoplophora glabripennis</i>	2666	5.00E-53	65.92
anaphase-promoting complex subunit 10	<i>Leptinotarsa decemlineata</i>	1072	2.00E-137	80.87
PREDICTED: anaphase-promoting complex subunit 2	<i>Tribolium castaneum</i>	3131	2.00E-169	68.43
PREDICTED: cell division cycle protein 16 homolog	<i>Aethina tumida</i>	689	2.00E-37	71.72
structural maintenance of chromosomes protein 3	<i>Anoplophora glabripennis</i>	3851	0	75.59
PREDICTED: structural maintenance of chromosomes protein 1A	<i>Tribolium castaneum</i>	4067	0	74.69
dual specificity protein phosphatase CDC14B-like	<i>Anoplophora glabripennis</i>	2133	4.00E-116	69.17
histone deacetylase Rpd3 isoform X1	<i>Anoplophora glabripennis</i>	1908	0	78.01
transcriptional regulator Myc-1 isoform X2	<i>Anoplophora glabripennis</i>	3653	1.00E-24	74.18
probable ATP-dependent RNA helicase DDX27	<i>Anoplophora glabripennis</i>	2782	0	70.33
protein cortex-like	<i>Anoplophora glabripennis</i>	1877	0.11	95.83
growth arrest and DNA damage-inducible protein GADD45 alpha	<i>Leptinotarsa decemlineata</i>	1125	2.00E-31	70.63
RING-box protein 1A	<i>Onthophagus taurus</i>	588	6.00E-89	81.16
PREDICTED: G1/S-specific cyclin-D3-like	<i>Aethina tumida</i>	1476	3.00E-44	68
PREDICTED: cyclin-dependent kinase 2-like	<i>Aethina tumida</i>	1454	2.00E-141	72.06

PREDICTED: S-phase kinase-associated protein 1	<i>Agrilus planipennis</i>	305	6.00E-51	78.81
PREDICTED: S-phase kinase-associated protein 1 isoform X1	<i>Ceratosolen solmsi marchali</i>	845	3.00E-27	66.59
PREDICTED: cullin-1	<i>Tribolium castaneum</i>	3231	0	74.24
Insect hormone biosynthesis				
testis-specific aldehyde dehydrogenase, mitochondrial-like	<i>Mizuhopecten yessoensis</i>	331	2.00E-41	71.3
testis-specific PREDICTED: cytochrome P450 307a1-like	<i>Agrilus planipennis</i>	465	1.00E-22	69.93

Table S2. The C_t values of 29 tested unigenes for RT-qPCR analysis

Gene	Testis (C _t ± SE)	Ovary (C _t ± SE)
Testis-up-regulated unigenes		
TRINITY_DN36203_c0_g1	26.9213 ± 0.0269	--
TRINITY_DN36769_c0_g1	28.7448 ± 0.2658	--
TRINITY_DN32154_c0_g1	27.8281 ± 0.1527	--
TRINITY_DN34503_c0_g1	27.4787 ± 0.2203	--
TRINITY_DN3474_c0_g1	27.3564 ± 0.0576	--
TRINITY_DN34469_c0_g1	26.2939 ± 0.2123	--
TRINITY_DN38009_c0_g1	27.3262 ± 0.1442	--
TRINITY_DN37061_c0_g1	27.3928 ± 0.1300	--
TRINITY_DN38116_c0_g1	24.1200 ± 0.0146	--
TRINITY_DN39900_c0_g1	27.7148 ± 0.1271	--
TRINITY_DN36997_c0_g1	31.0963 ± 0.1055	--
TRINITY_DN36816_c1_g1	29.6950 ± 0.1461	--
TRINITY_DN40076_c0_g1	29.1139 ± 0.1323	--
TRINITY_DN37352_c0_g2	26.2067 ± 0.0948	--
TRINITY_DN28048_c0_g1	22.8569 ± 0.0961	37.2913 ± 0.1161
TRINITY_DN37903_c0_g1	25.0676 ± 0.1302	--
Ovary-up-regulated unigenes		
TRINITY_DN35620_c0_g2	--	27.7807 ± 0.2636
TRINITY_DN37242_c1_g2	--	30.9480 ± 0.3723
TRINITY_DN37127_c1_g1	--	31.0885 ± 0.1871
TRINITY_DN31659_c0_g1	--	30.9607 ± 0.2123
TRINITY_DN33161_c0_g1	--	30.2988 ± 0.2153

TRINITY_DN35988_c5_g2	--	31.1437 ± 0.1396
TRINITY_DN36847_c0_g3	37.3610 ± 0.2944	30.2949 ± 0.3812
TRINITY_DN32419_c0_g1	--	29.9618 ± 0.3918
TRINITY_DN37464_c0_g3	--	30.4087 ± 0.2826
TRINITY_DN38884_c0_g1	--	29.4363 ± 0.1464
TRINITY_DN24326_c0_g1	--	30.2033 ± 0.2681
TRINITY_DN40971_c0_g1	--	30.8122 ± 0.3285
TRINITY_DN34758_c0_g1	--	29.0019 ± 0.1400
<i>RPL13</i>	24.6785 ± 0.3439	23.2646 ± 0.0612

'--' cannot detect

Table S3. Primers used in semi-RT-qPCR and RT-qPCR for validation of differentially expressed genes.

Gene	Primer sequences (5'-3')	Length (bp)	FC (O/T)	Log2FC (O/T)	Annotation
Testis-up-regulated unigenes					
TRINITY_DN36203_c0_g1-F	GAGCGTCGGTACACATAAA	131	0.00	-15.66	arginine kinase
TRINITY_DN36203_c0_g1-R	GTACACGCCTTCTTCAGAC				
TRINITY_DN36769_c0_g1-F	GTTTGGTCTCTTGGAGTTGT	126	0.00	-15.62	testis-specific serine/threonine-protein kinase 3
TRINITY_DN36769_c0_g1-R	CGTTACTACTCGACCTGAAAG				
TRINITY_DN32154_c0_g1-F	CACAAGGAGGGAGCATTAT	112	0.00	-15.28	L-lactate dehydrogenase isoform X2
TRINITY_DN32154_c0_g1-R	TCAGTGATTCCGTTTGATCC				

TRINITY_DN34503_c0_g1-F	CACCTTACCTCCTGACGATA	118	0.00	-15.17	venom allergen 5-like
TRINITY_DN34503_c0_g1-R	ATGCCACAGTCTCTCATTTC				
TRINITY_DN3474_c0_g1-F	GCTCTACTTGGTGCCTAATC	144	0.00	-15.13	alpha-1,3/1,6-mannosyltransferase
TRINITY_DN3474_c0_g1-R	TCCACAAGAGGCATCATAAC				ALG2-like
TRINITY_DN34469_c0_g1-F	CCTCGAAAGCCTATCATTCC	124	0.00	-15.09	glandular kallikrein-3,
TRINITY_DN34469_c0_g1-R	CAGGTTGTGGTAGTGGATTT				submandibular-like
TRINITY_DN38009_c0_g1-F	TCCCAACTCAGACTGTTCTA	104	0.00	-15.08	proteasomal ubiquitin receptor
TRINITY_DN38009_c0_g1-R	GTGGACGTGTTTGGACTATT				ADRM1-like
TRINITY_DN37061_c0_g1-F	CAGGGACAAACAGACTTACC	100	0.00	-15.08	hypothetical protein AMK59
TRINITY_DN37061_c0_g1-R	ACTCCTCTACAGTGGCTATT				
TRINITY_DN38116_c0_g1-F	CAACTGCTCCCGTACTAAA	137	0.00	-14.76	parkin coregulated gene protein
TRINITY_DN38116_c0_g1-R	CCTCCTGTTCTTTCATCAA				homolog
TRINITY_DN39900_c0_g1-F	CGCTAAGAGCTGAGGACTA	128	0.00	-14.70	protein-glutamate O-methyltransferase
TRINITY_DN39900_c0_g1-R	TTGAAGCATTGTTGGACGA				
TRINITY_DN36997_c0_g1-F	CGAGTACACTGCCAACTT	104	0.00	-14.62	carnitine O-acetyltransferase-like
TRINITY_DN36997_c0_g1-R	CCATGTCCAACGGGTTATT				
TRINITY_DN36816_c1_g1-F	CCTCATTGGTGCATCTACTC	131	0.00	-14.59	NADP-dependent malic enzyme-like
TRINITY_DN36816_c1_g1-R	CCTGTGGTGTACATTCAGTT				
TRINITY_DN40076_c0_g1-F	GCATTCTCGCCTGGTATTT	107	0.00	-14.57	NADP-dependent malic enzyme-like
TRINITY_DN40076_c0_g1-R	GCGTCTTCTGCAGTACATT				
TRINITY_DN37352_c0_g2-F	CATCGGAGGAAAGCTGTATG	123	0.00	-14.53	cytosol aminopeptidase-like
TRINITY_DN37352_c0_g2-R	CCCAAACCTGCTACTGAAAT				
TRINITY_DN28048_c0_g1-F	ACAGTGTTCGAGATGAAA	118	0.00	-14.44	protein D3-like
TRINITY_DN28048_c0_g1-R	AGCCTTGGTACTCCTAAA				
TRINITY_DN37903_c0_g1-F	GAAGATGCAGCGAACAATTAC	137	0.00	-14.42	tubulin alpha-4 chain-like
TRINITY_DN37903_c0_g1-R	CCAAAGGAGTGGAAGACAAA				

Ovary-up-regulated unigenes					
TRINITY_DN35620_c0_g2-F	GCGAATGGAACGGAGAAT	134	2779.18	11.44	uncharacterized protein LOC108911198
TRINITY_DN35620_c0_g2-R	TCGGACACTCGTGAAGAA				
TRINITY_DN37242_c1_g2-F	AGGATTCGTGAGAACAAC	121	2047.99	11.00	uncharacterized protein LOC109609123
TRINITY_DN37242_c1_g2-R	GTCGACAACGGTTACCTTAC				
TRINITY_DN37127_c1_g1-F	TGTGGTTTGTGTGAAGTAGG	115	1725.60	10.75	uncharacterized protein LOC111513761
TRINITY_DN37127_c1_g1-R	CCTTTAGCAGGTCGTTTCATT				
TRINITY_DN31659_c0_g1-F	GACACACAGCTATGGTGAAG	123	1584.11	10.63	Pxs
TRINITY_DN31659_c0_g1-R	CGATTCTTAGGTTCCGTTGG				
TRINITY_DN33161_c0_g1-F	GCTCGCTGTGGTGATATAAA	140	1473.29	10.52	nuclear cap-binding protein subunit 2
TRINITY_DN33161_c0_g1-R	TCAAGATTCGTGCCGTTAAT				
TRINITY_DN35988_c5_g2-F	GTACCGCCTACCATTGTAAC	134	1469.59	10.52	ankyrin-1-like
TRINITY_DN35988_c5_g2-R	GGAACCCTCAGCTTAACTTC				
TRINITY_DN36847_c0_g3-F	CAGTTTGTACGATGCCTAT	121	1358.69	10.41	ceramide-1-phosphate transfer protein
TRINITY_DN36847_c0_g3-R	CAAACCTTTGCCAACAACCTC				
TRINITY_DN32419_c0_g1-F	CAGACTTCGACCACTTTCAT	110	1293.37	10.34	ras-like GTP-binding protein RHO
TRINITY_DN32419_c0_g1-R	TTACTTCAGGGAGCCATTTC				
TRINITY_DN37464_c0_g3-F	GCAACTCGGAATCTTGGTAG	143	1221.33	10.25	REST corepressor 2-like
TRINITY_DN37464_c0_g3-R	ACACAGTCCTCCCTCTTTAT				
TRINITY_DN38884_c0_g1-F	GATTTGCCGCAATACAAAT	128	1219.42	10.25	UDP-glucuronosyltransferase 1-7
TRINITY_DN38884_c0_g1-R	CTGTCCTGCTATGTGCTAAA				
TRINITY_DN24326_c0_g1-F	CGGACGATGAAGGAGATAGA	111	1149.35	10.17	uncharacterized protein LOC109609449
TRINITY_DN24326_c0_g1-R	CCGATGGACTTGGAGATGA				
TRINITY_DN40971_c0_g1-F	ACGGTATGATGACCCACA	117	1001.21	9.97	zinc finger protein 107-like
TRINITY_DN40971_c0_g1-R	GTCACGTA CTGCCTCTCT				
TRINITY_DN34758_c0_g1-F	CATCCCAGAAGAACCTGAAA	128	812.59	9.67	protein snail homolog Snai-like

TRINITY_DN34758_c0_g1-R

ATGAGGGTGGAGGAGAAATA

O/T: Ovary/Testis

Table S4. Primers used for dsRNA synthesise

Gene	Primer sequences (5'-3')	Length (bp)
dsRC2-like-F	taatagactcactatagggATGAAGACCCGGCTGAAAC	394
dsRC2-like-R	taatagactcactatagggAGCTCGCTTATTCGGTCAAA	
dsPSHS-like-F	taatagactcactatagggGGTGTATTATCCCCGAGCAA	398
dsPSHS-like-R	taatagactcactatagggGGTGTCTGTTCCCTGTCGT	