Scientific Reports

- Transcriptomic dissection of sexual differences in *Bemisia tabaci*, an invasive agricultural pest worldwide

Wen Xie[a1&], Litao Guo[b1&], Xiaoguo Jiao[c3], Nina Yang[d1], Xin Yang[e1], Qingjun Wu[f1], Shaoli Wang[g1], Xuguo Zhou[h2]*, Youjun Zhang[i1]*

[1]*Department of Plant Protection, Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, Beijing, 100081, P. R. China*
[2]*Department of Entomology, University of Kentucky, Lexington, KY 40546-0091, USA*
[3]*Hubei University, Wuhan, 430062, P. R. China*

[&] These authors contributed to this work equally

Email correspondence: [a]xiewen@caas.cn, [b]glt0629@163.com, [c]jiaoxg@hubu.edu.cn, [d]nina809@163.com, [e]hljdxyx@163.com, [f]wuqingjun@caas.cn, [g]wangshaoli@caas.cn, [h]xuguozhou@uky.edu, [i]zhangyoujun@caas.cn

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* Corresponding Authors:
Dr. Youjun Zhang
Department of Entomology, Institute of Vegetables and Flowers
Chinese Academy of Agricultural Sciences
12 Zhongguancun Nandajie, Haidian District
Beijing 100081, China
Phone: 86-10-82109518
Fax: 86-10-82109518
Email: zhangyj@mail.caas.net.cn

Dr. Xuguo "Joe" Zhou
Department of Entomology
University of Kentucky
S-225 Agricultural Science Center North
Lexington, KY 40546-0091
Phone: 859-257-3125
Fax: 859-323-1120
Email: xuguozhou@uky.edu

SUPPORTING INFORMATION

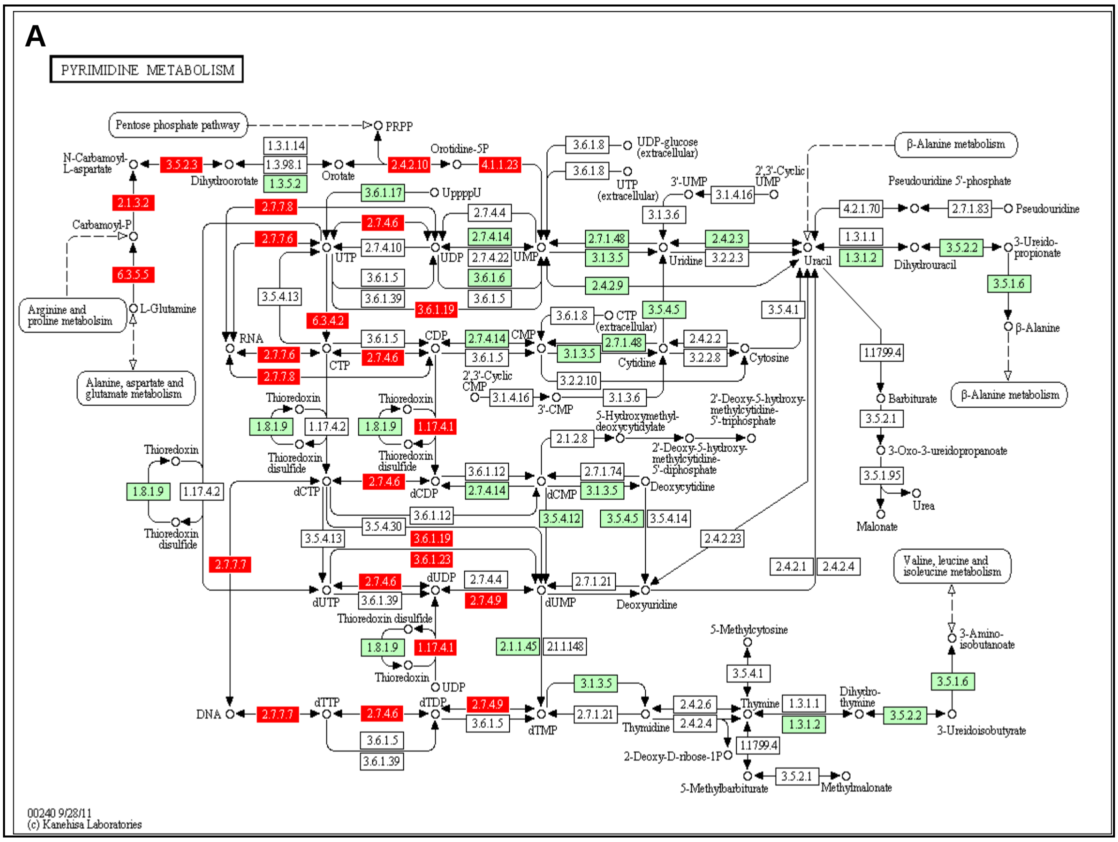
FIGURES

TABLES

Fig. S1. The enriched KEGG pathway analysis for female-biased genes relative to male.

A. Pyrimidine metabolism, **B**. Ribosome, **C**. mRNA surveillance pathway, **D**. Ribosome biogenesis in eukaryotes, **E**. RNA polymerase, **F**. RNA degradation. **G**. DNA replication. **H**. RNA transport.

KEGG pathway mapping (used *Acyrthosiphon pisum* as KEGG organisms) and further KEGG enrichment analysis using local server KOBAS 2.0, Q-value < 0.05 is chosen as enriched pathway. The red box denotes the female marker gene that could be annotated into a *Acyrthosiphon pisum* KEGG network.


A
PYRIMIDINE METABOLISM
Pentose phosphate pathway
PRPP
N-Carbamoyl-L-aspartate
Dihydroorotate
Orotate
Orotidine-5P
Carbamoyl-P
L-Glutamine
Arginine and proline metabolism
Alanine, aspartate and glutamate metabolism
UDP-glucose (extracellular)
UTP (extracellular)
3'-UMP
2',3'-Cyclic UMP
β-Alanine metabolism
Pseudouridine 5'-phosphate
Pseudouridine
UppppU
UTP
UDP
UMP
Uridine
Uracil
Dihydrouracil
3-Ureido-propionate
β-Alanine
RNA
CTP
CDP
CMP
CTP (extracellular)
Cytidine
Cytosine
2',3'-Cyclic CMP
3'-CMP
Thioredoxin
Thioredoxin disulfide
dCTP
dCDP
dCMP
Deoxycytidine
5-Hydroxymethyl-deoxycytidylate
2'-Deoxy-5-hydroxy-methylcytidine-5'-triphosphate
2'-Deoxy-5-hydroxy-methylcytidine-5'-diphosphate
Barbiturate
3-Oxo-3-ureidopropanoate
Urea
Malonate
dUTP
dUDP
dUMP
Deoxyuridine
Valine, leucine and isoleucine metabolism
5-Methylcytosine
3-Amino-isobutanoate
DNA
dTTP
dTDP
dTMP
Thymidine
Thymine
Dihydro-thymine
3-Ureidoisobutyrate
2-Deoxy-D-ribose-1P
5-Methylbarbiturate
Methylmalonate
3.5.2.3
2.1.3.2
6.3.5.5
1.3.1.14
1.3.98.1
1.3.5.2
2.4.2.10
4.1.1.23
3.6.1.17
3.6.1.8
3.1.3.6
3.1.4.16
4.2.1.70
2.7.1.83
1.3.1.1
1.3.1.2
3.5.2.2
3.5.1.6
2.7.7.8
2.7.7.6
2.7.4.6
2.7.4.10
3.6.1.5
3.6.1.39
3.5.4.13
6.3.4.2
3.6.1.19
2.7.4.4
2.7.4.14
2.7.4.22
3.6.1.6
2.7.1.48
3.1.3.5
2.4.2.3
3.2.2.3
2.4.2.9
3.5.4.5
3.5.4.1
2.4.2.2
3.2.2.8
3.2.2.10
1.17.99.4
3.5.2.1
3.5.1.95
1.8.1.9
1.17.4.2
1.17.4.1
2.7.1.74
3.6.1.12
3.5.4.12
3.5.4.14
3.5.4.30
3.6.1.23
2.7.7.7
2.4.2.23
2.4.2.1
2.4.2.4
2.7.1.21
2.7.4.9
2.1.1.45
2.1.1.148
2.4.2.6
00240 9/28/11
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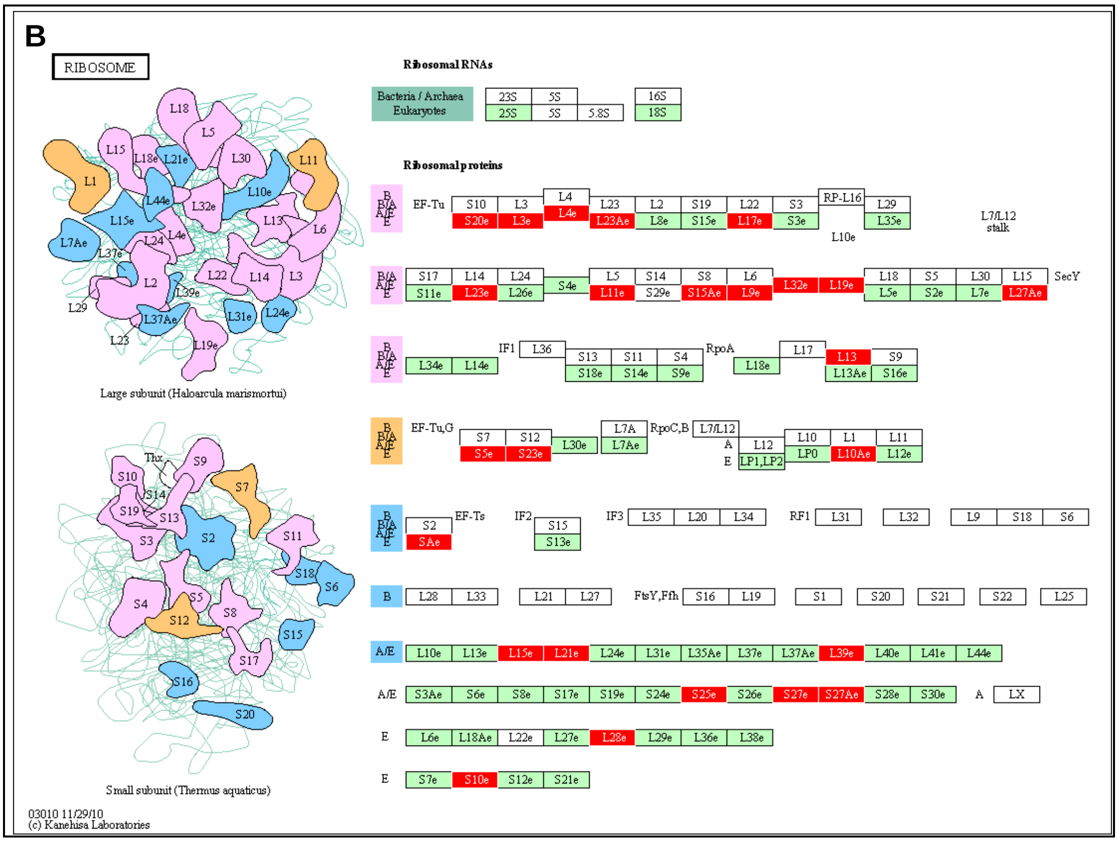
B
RIBOSOME
Large subunit (Haloarcula marismortui)
Small subunit (Thermus aquaticus)
Ribosomal RNAs
Bacteria / Archaea
Eukaryotes
23S
5S
16S
25S
5S
5.8S
18S
Ribosomal proteins
EF-Tu
EF-Tu,G
EF-Ts
IF1
IF2
IF3
RpoA
RpoC,B
RF1
SecY
FtsY,Ffh
RP-L16
L7/L12 stalk
L10e
S10
S20e
L3
L3e
L4
L4e
L23
L23Ae
L2
L8e
S19
S15e
L22
L17e
S3
S3e
L29
L35e
S17
S11e
L14
L23e
L24
L26e
S4e
L5
L11e
S14
S29e
S8
S15Ae
L6
L9e
L32e
L19e
L18
L5e
S5
S2e
L30
L7e
L15
L27Ae
L34e
L14e
L36
S13
S18e
S11
S14e
S4
S9e
L18e
L17
L13
L13Ae
S9
S16e
S7
S5e
S12
S23e
L30e
L7A
L7Ae
L7/L12
A
E
L12
LP1,LP2
L10
LP0
L1
L10Ae
L11
L12e
S2
SAe
S15
S13e
L35
L20
L34
L31
L32
L9
S18
S6
B
L28
L33
L21
L27
S16
L19
S1
S20
S21
S22
L25
A/E
L10e
L13e
L15e
L21e
L24e
L31e
L35Ae
L37e
L37Ae
L39e
L40e
L41e
L44e
S3Ae
S6e
S8e
S17e
S19e
S24e
S25e
S26e
S27e
S27Ae
S28e
S30e
LX
L6e
L18Ae
L22e
L27e
L28e
L29e
L36e
L38e
S7e
S10e
S12e
S21e
L18
L5
L15
L18e
L21e
L30
L11
L1
L44e
L32e
L10e
L15e
L13
L6
L7Ae
L37e
L24
L4e
L2
L22
L14
L3
L39e
L29
L37Ae
L31e
L24e
L23
L19e
S10
Thx
S9
S7
S14
S19
S13
S3
S2
S11
S18
S6
S4
S5
S12
S8
S15
S17
S16
S20
03010 11/29/10
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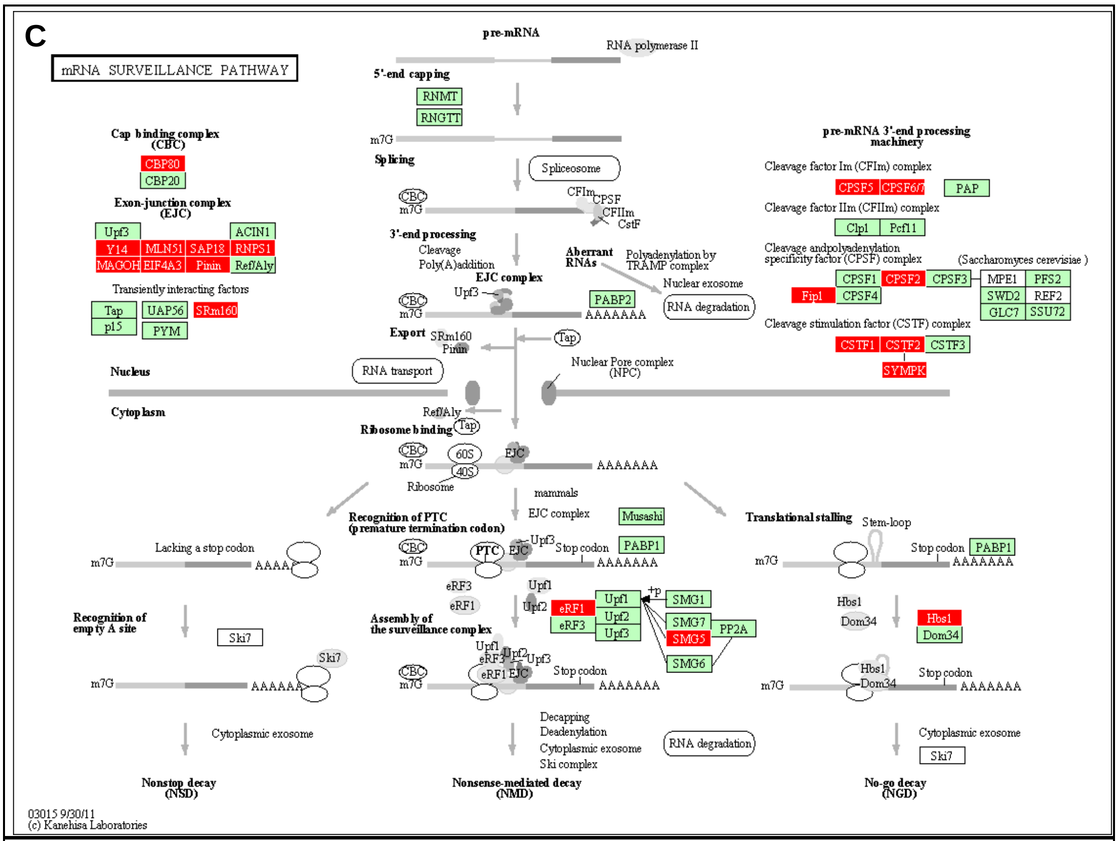
C
mRNA SURVEILLANCE PATHWAY
pre-mRNA
RNA polymerase II
5'-end capping
RNMT
RNGTT
m7G
Splicing
Spliceosome
Cap binding complex (CBC)
CBP80
CBP20
Exon-junction complex (EJC)
Upf3
ACIN1
Y14
MLN51
SAP18
RNPS1
MAGOH
EIF4A3
Pinin
Ref/Aly
Transiently interacting factors
Tap
UAP56
SRm160
p15
PYM
CBC
CFIm
CPSF
CFIIm
CstF
3'-end processing
Cleavage
Poly(A)addition
EJC complex
Aberrant RNAs
Polyadenylation by TRAMP complex
Nuclear exosome
RNA degradation
Upf3
PABP2
AAAAAAA
Export
SRm160
Pinin
Tap
Nucleus
RNA transport
Nuclear Pore complex (NPC)
Cytoplasm
Ref/Aly
Ribosome binding
60S
40S
EJC
Ribosome
AAAAAAA
pre-mRNA 3'-end processing machinery
Cleavage factor Im (CFIm) complex
CPSF5
CPSF6/7
PAP
Cleavage factor IIm (CFIIm) complex
Clp1
Pcf11
Cleavage and polyadenylation specificity factor (CPSF) complex
(Saccharomyces cerevisiae)
CPSF1
CPSF2
CPSF3
MPE1
PFS2
Fip1
CPSF4
SWD2
REF2
GLC7
SSU72
Cleavage stimulation factor (CSTF) complex
CSTF1
CSTF2
CSTF3
SYMPK
mammals
EJC complex
Musashi
Recognition of PTC (premature termination codon)
Translational stalling
Stem-loop
Lacking a stop codon
AAAA
PTC
Upf3
Stop codon
PABP1
Stop codon
PABP1
AAAAAAA
eRF3
Upf1
eRF1
Upf2
eRF1
Upf1
+p
SMG1
Recognition of empty A site
Assembly of the surveillance complex
eRF3
Upf2
SMG7
PP2A
Upf3
SMG5
Hbs1
Dom34
Hbs1
Dom34
Ski7
Ski7
SMG6
Upf1
eRF3
Upf2
Upf3
eRF1
Hbs1
Dom34
Stop codon
Stop codon
AAAAA
AAAAAAA
Cytoplasmic exosome
Decapping
Deadenylation
Cytoplasmic exosome
Ski complex
RNA degradation
Cytoplasmic exosome
Ski7
Nonstop decay (NSD)
Nonsense-mediated decay (NMD)
No-go decay (NGD)
03015 9/30/11
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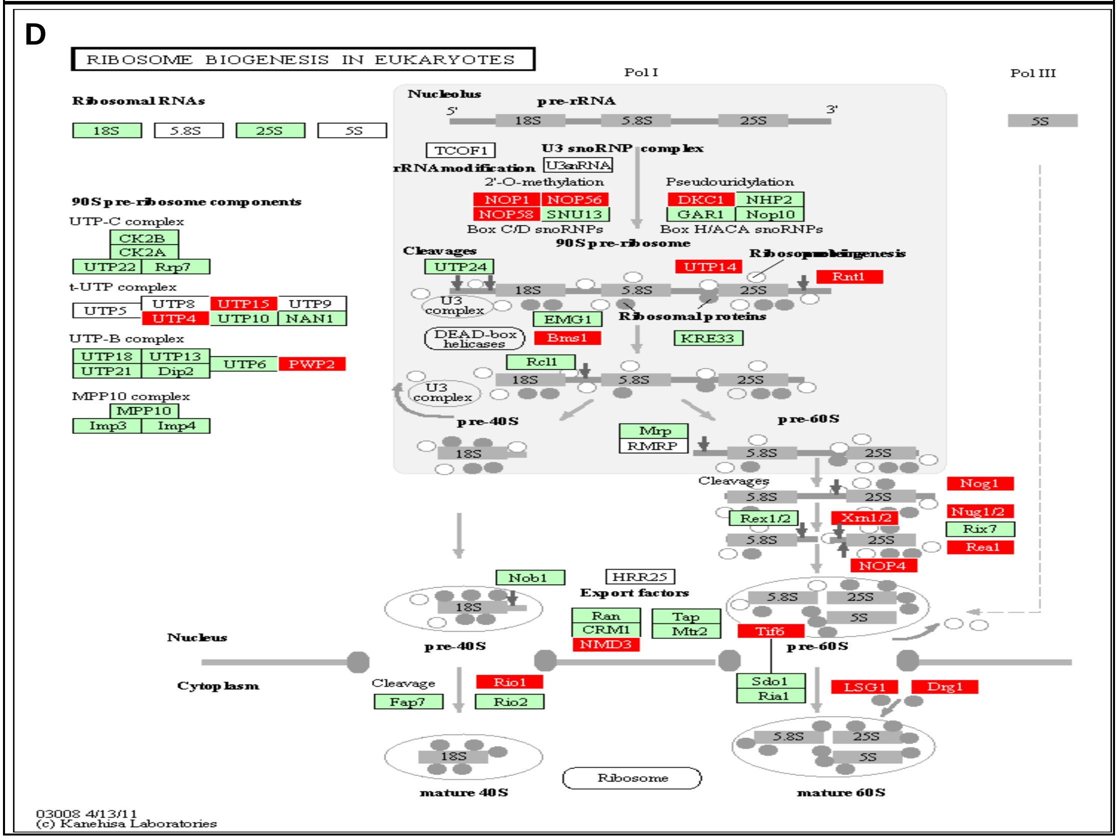
D
RIBOSOME BIOGENESIS IN EUKARYOTES
Pol I
Pol III
Ribosomal RNAs
18S
5.8S
25S
5S
Nucleolus
pre-rRNA
5'
3'
18S
5.8S
25S
5S
TCOF1
U3 snoRNP complex
rRNA modification
U3snRNA
2'-O-methylation
Pseudouridylation
NOP1
NOP56
DKC1
NHP2
NOP58
SNU13
GAR1
Nop10
Box C/D snoRNPs
Box H/ACA snoRNPs
90S pre-ribosome components
UTP-C complex
CK2B
CK2A
UTP22
Rrp7
t-UTP complex
UTP8
UTP15
UTP9
UTP5
UTP4
UTP10
NAN1
UTP-B complex
UTP18
UTP13
UTP21
Dip2
UTP6
PWP2
MPP10 complex
MPP10
Imp3
Imp4
90S pre-ribosome
Cleavages
UTP24
UTP14
Ribosome biogenesis
Rnt1
18S
5.8S
25S
U3 complex
EMG1
Ribosomal proteins
DEAD-box helicases
Bms1
KRE33
Rcl1
18S
5.8S
25S
U3 complex
pre-40S
pre-60S
Mrp
RMRP
18S
5.8S
25S
Cleavages
Nog1
5.8S
25S
Nug1/2
Rex1/2
Xrn1/2
Rix7
5.8S
25S
Rea1
NOP4
Nob1
HRR25
Export factors
18S
5.8S
25S
5S
Ran
Tap
CRM1
Mtr2
Tif6
NMD3
Nucleus
pre-40S
pre-60S
Cytoplasm
Cleavage
Rio1
Sdo1
LSG1
Drg1
Fap7
Rio2
Ria1
18S
5.8S
25S
5S
Ribosome
mature 40S
mature 60S
03008 4/13/11
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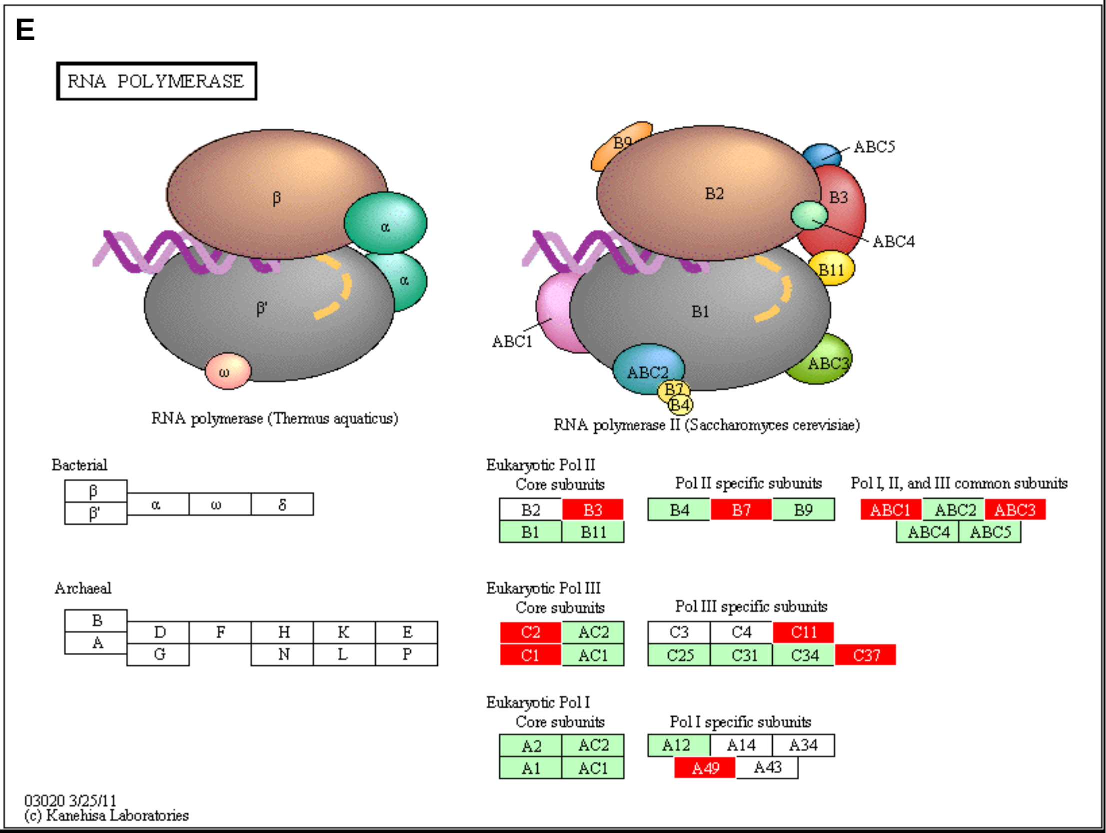
E
RNA POLYMERASE
β
α
α
β'
ω
RNA polymerase (Thermus aquaticus)
B9
ABC5
B2
B3
ABC4
B11
B1
ABC1
ABC2
B7
B4
ABC3
RNA polymerase II (Saccharomyces cerevisiae)
Bacterial
β
β'
α
ω
δ
Archaeal
B
A
D
G
F
H
N
K
L
E
P
Eukaryotic Pol II
Core subunits
B2
B3
B1
B11
Pol II specific subunits
B4
B7
B9
Pol I, II, and III common subunits
ABC1
ABC2
ABC3
ABC4
ABC5
Eukaryotic Pol III
Core subunits
C2
AC2
C1
AC1
Pol III specific subunits
C3
C4
C11
C25
C31
C34
C37
Eukaryotic Pol I
Core subunits
A2
AC2
A1
AC1
Pol I specific subunits
A12
A14
A34
A49
A43
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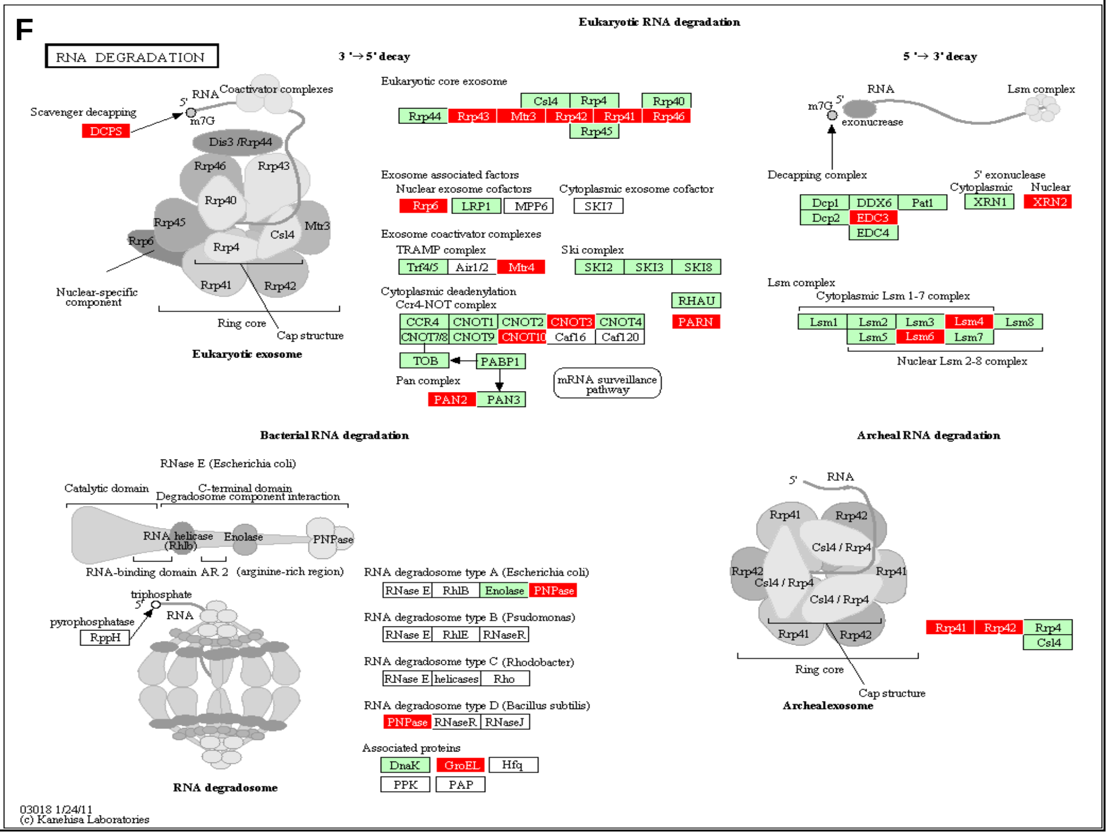
F
RNA DEGRADATION
Eukaryotic RNA degradation
3 '→ 5' decay
5 '→ 3' decay
Scavenger decapping
DCPS
5'
RNA
Coactivator complexes
m7G
Dis3 /Rrp44
Rrp46
Rrp43
Rrp40
Rrp45
Mtr3
Rrp6
Csl4
Rrp4
Rrp41
Rrp42
Nuclear-specific component
Ring core
Cap structure
Eukaryotic exosome
Eukaryotic core exosome
Csl4
Rrp4
Rrp40
Rrp44
Rrp43
Mtr3
Rrp42
Rrp41
Rrp46
Rrp45
Exosome associated factors
Nuclear exosome cofactors
Rrp6
LRP1
MPP6
Cytoplasmic exosome cofactor
SKI7
Exosome coactivator complexes
TRAMP complex
Trf4/5
Air1/2
Mtr4
Ski complex
SKI2
SKI3
SKI8
Cytoplasmic deadenylation
Ccr4-NOT complex
CCR4
CNOT1
CNOT2
CNOT3
CNOT4
CNOT7/8
CNOT9
CNOT10
Caf16
Caf120
RHAU
PARN
TOB
PABP1
Pan complex
PAN2
PAN3
mRNA surveillance pathway
RNA
Lsm complex
m7G
5'
exonucrease
Decapping complex
Dcp1
DDX6
Pat1
Dcp2
EDC3
EDC4
5' exonuclease
Cytoplasmic
Nuclear
XRN1
XRN2
Lsm complex
Cytoplasmic Lsm 1-7 complex
Lsm1
Lsm2
Lsm3
Lsm4
Lsm8
Lsm5
Lsm6
Lsm7
Nuclear Lsm 2-8 complex
Bacterial RNA degradation
RNase E (Escherichia coli)
Catalytic domain
C-terminal domain
Degradosome component interaction
RNA helicase (Rhlb)
Enolase
PNPase
RNA-binding domain
AR 2
(arginine-rich region)
triphosphate
5'
pyrophosphatase
RppH
RNA
RNA degradosome
RNA degradosome type A (Escherichia coli)
RNase E
RhlB
Enolase
PNPase
RNA degradosome type B (Psudomonas)
RNase E
RhlE
RNaseR
RNA degradosome type C (Rhodobacter)
RNase E
helicases
Rho
RNA degradosome type D (Bacillus subtilis)
PNPase
RNaseR
RNaseJ
Associated proteins
DnaK
GroEL
Hfq
PPK
PAP
Archeal RNA degradation
5'
RNA
Rrp41
Rrp42
Csl4 / Rrp4
Rrp42
Rrp41
Csl4 / Rrp4
Csl4 / Rrp4
Rrp41
Rrp42
Ring core
Cap structure
Archealexosome
Rrp41
Rrp42
Rrp4
Csl4
03018 1/24/11
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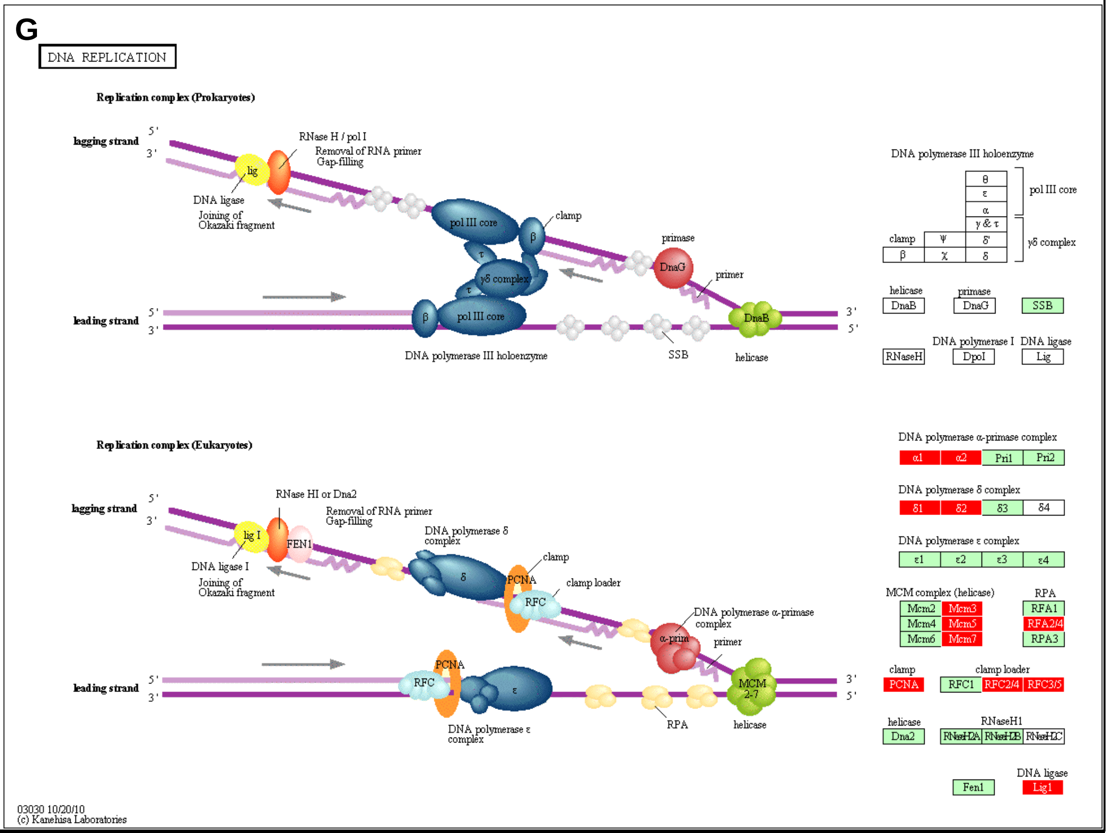
G


DNA REPLICATION
Replication complex (Prokaryotes)
lagging strand
leading strand
5'
3'
RNase H / pol I
Removal of RNA primer
Gap-filling
lig
DNA ligase
Joining of Okazaki fragment
pol III core
clamp
β
τ
γδ complex
primase
DnaG
primer
DnaB
helicase
SSB
DNA polymerase III holoenzyme
θ
ε
α
γ & τ
δ'
δ
ψ
χ
pol III core
γδ complex
DnaB
DnaG
DNA polymerase I
DNA ligase
RNaseH
DpoI
Lig
Replication complex (Eukaryotes)
RNase HI or Dna2
lig I
FEN1
DNA ligase I
DNA polymerase δ complex
PCNA
RFC
clamp loader
DNA polymerase α-primase complex
α-prim
MCM 2-7
RPA
DNA polymerase ε complex
DNA polymerase α-primase complex
α1
α2
Pri1
Pri2
DNA polymerase δ complex
δ1
δ2
δ3
δ4
DNA polymerase ε complex
ε1
ε2
ε3
ε4
MCM complex (helicase)
Mcm2
Mcm3
Mcm4
Mcm5
Mcm6
Mcm7
RFA1
RFA2/4
RPA3
RFC1
RFC2/4
RFC3/5
RNaseH1
Dna2
RNaseH2A
RNaseH2B
RNaseH2C
Fen1
Lig1
03030 10/20/10
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H

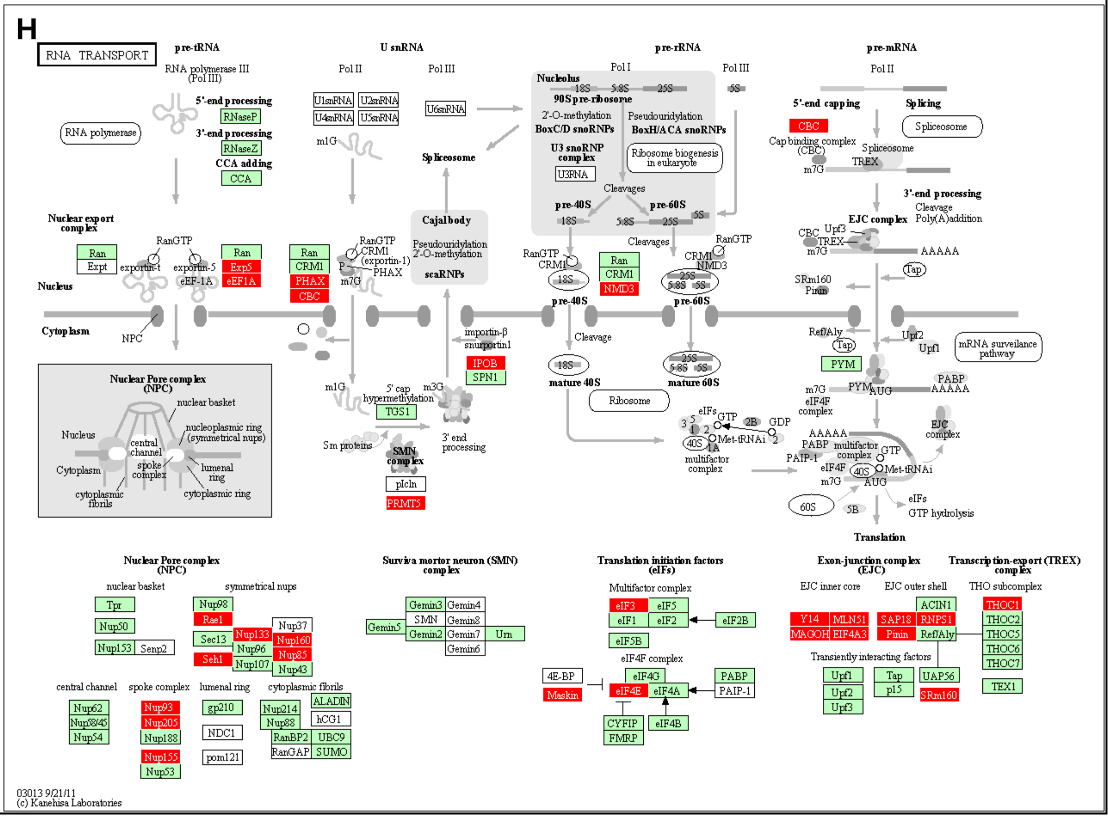
RNA TRANSPORT
pre-tRNA
RNA polymerase III (Pol III)
RNA polymerase
5'-end processing
RNaseP
3'-end processing
RNaseZ
CCA adding
CCA
U snRNA
Pol II
Pol III
U1snRNA
U2snRNA
U4snRNA
U5snRNA
U6snRNA
m1G
Spliceosome
Cajal body
Pseudouridylation
2'-O-methylation
scaRNPs
pre-rRNA
Nucleolus
Pol I
18S
5.8S
25S
5S
90S pre-ribosome
2'-O-methylation
Pseudouridylation
BoxC/D snoRNPs
BoxH/ACA snoRNPs
U3 snoRNP complex
U3RNA
Ribosome biogenesis in eukaryote
Cleavages
pre-40S
pre-60S
pre-mRNA
5'-end capping
CBC
Cap binding complex (CBC)
Splicing
Spliceosome
TREX
m7G
3'-end processing
Cleavage
Poly(A)addition
EJC complex
Upf3
AAAAA
Nuclear export complex
Ran
Expt
RanGTP
exportin-t
exportin-5
eEF-1A
Exp5
eEF1A
CRM1
PHAX
CBC
(exportin-1)
Nucleus
Cytoplasm
NPC
importin-β
snurportin1
IPOB
SPN1
m3G
5' cap hypermethylation
TGS1
Sm proteins
SMN complex
pICln
PRMT5
3' end processing
NMD3
Cleavage
mature 40S
mature 60S
Ribosome
SRm160
Pinin
Ref/Aly
Tap
Upf2
Upf1
mRNA surveillance pathway
PYM
AUG
PABP
eIF4F complex
eIFs
GTP
2B
GDP
40S
Met-tRNAi
multifactor complex
PAIP-1
60S
5B
GTP hydrolysis
Translation
Nuclear Pore complex (NPC)
nuclear basket
nucleoplasmic ring (symmetrical nups)
central channel
spoke complex
lumenal ring
cytoplasmic fibrils
cytoplasmic ring
Nuclear Pore complex (NPC)
nuclear basket
symmetrical nups
Tpr
Nup98
Nup37
Nup50
Rae1
Nup133
Nup160
Nup153
Senp2
Sec13
Nup96
Nup85
Seh1
Nup107
Nup43
central channel
spoke complex
lumenal ring
cytoplasmic fibrils
Nup62
Nup93
gp210
Nup214
ALADIN
Nup58/45
Nup205
Nup88
hCG1
Nup54
Nup188
NDC1
RanBP2
UBC9
Nup155
pom121
RanGAP
SUMO
Nup53
Survival motor neuron (SMN) complex
Gemin3
Gemin4
Gemin5
SMN
Gemin8
Gemin2
Gemin7
Urn
Gemin6
Translation initiation factors (eIFs)
Multifactor complex
eIF3
eIF5
eIF1
eIF2
eIF2B
eIF5B
eIF4F complex
4E-BP
eIF4G
PABP
Maskin
eIF4E
eIF4A
PAIP-1
CYFIP
eIF4B
FMRP
Exon-junction complex (EJC)
EJC inner core
EJC outer shell
Y14
MLN51
SAP18
RNPS1
MAGOH
EIF4A3
Pinin
Ref/Aly
ACIN1
Transiently interacting factors
Upf1
Tap
UAP56
Upf2
p15
SRm160
Upf3
Transcription-export (TREX) complex
THO subcomplex
THOC1
THOC2
THOC5
THOC6
THOC7
TEX1
03013 9/21/11
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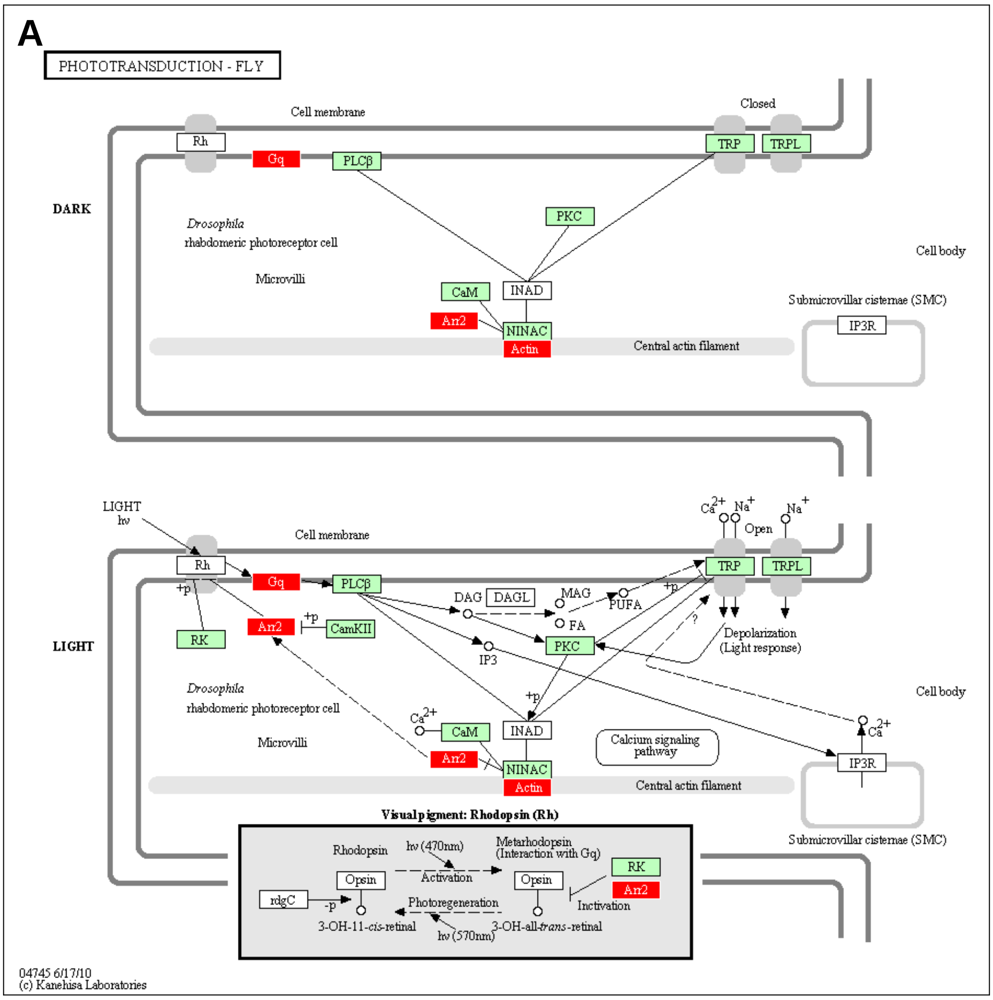
Fig. S2. The enriched KEGG pathway analysis for male-biased genes relative to female.

A. Phototransduction **-** fly, **B**. Lysosome, **C**. Nitrogen metabolism, **D**. Glycerophospholipid metabolism, **E**. Phagosome.

KEGG pathway mapping (used *Acyrthosiphon pisum* as KEGG organisms) and further KEGG enrichment analysis using local server KOBAS 2.0, Q-value < 0.05 is chosen as enriched pathway. The red box denotes the male marker gene that could be annotated into a *Acyrthosiphon pisum* KEGG network.


A
PHOTOTRANSDUCTION - FLY
DARK
Cell membrane
Closed
Rh
Gq
PLCβ
TRP
TRPL
PKC
Drosophila
rhabdomeric photoreceptor cell
Microvilli
Cell body
CaM
INAD
Arr2
NINAC
Actin
Submicrovillar cisternae (SMC)
IP3R
Central actin filament
LIGHT
LIGHT
hν
Cell membrane
Ca2+
Na+
Na+
Open
Rh
Gq
PLCβ
TRP
TRPL
+p
DAG
DAGL
MAG
PUFA
+p
FA
RK
Arr2
+p
CamKII
PKC
?
Depolarization
(Light response)
IP3
Cell body
+p
Ca2+
Ca2+
CaM
INAD
Calcium signaling pathway
Arr2
NINAC
IP3R
Actin
Central actin filament
Visual pigment: Rhodopsin (Rh)
Submicrovillar cisternae (SMC)
Rhodopsin
hν (470nm)
Metarhodopsin
(Interaction with Gq)
Activation
RK
Opsin
Opsin
Arr2
rdgC
-p
Photoregeneration
Inctivation
3-OH-11-cis-retinal
3-OH-all-trans-retinal
hν (570nm)
04745 6/17/10
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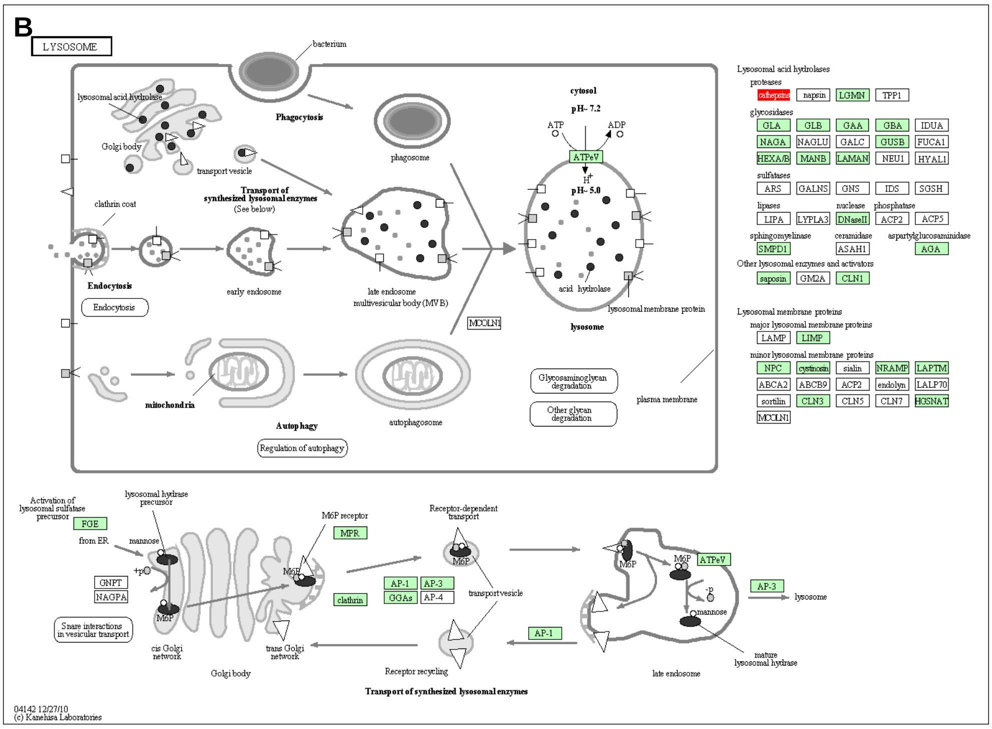
B
LYSOSOME
bacterium
lysosomal acid hydrolase
Phagocytosis
Golgi body
phagosome
transport vesicle
cytosol
pH~ 7.2
ATP
ADP
ATPeV
H+
pH~ 5.0
Transport of
synthesized lysosomal enzymes
(See below)
clathrin coat
Endocytosis
Endocytosis
early endosome
late endosome
multivesicular body (MVB)
acid hydrolase
lysosomal membrane protein
MCOLN1
lysosome
mitochondria
autophagosome
Autophagy
Regulation of autophagy
Glycosaminoglycan degradation
Other glycan degradation
plasma membrane
Lysosomal acid hydrolases
proteases
cathepsins
napsin
LGMN
TPP1
glycosidases
GLA
GLB
GAA
GBA
IDUA
NAGA
NAGLU
GALC
GUSB
FUCA1
HEXA/B
MANB
LAMAN
NEU1
HYAL1
sulfatases
ARS
GALNS
GNS
IDS
SGSH
lipases
LIPA
LYPLA3
nuclease
DNaseII
phosphatase
ACP2
ACP5
sphingomyelinase
SMPD1
ceramidase
ASAH1
aspartylglucosaminidase
AGA
Other lysosomal enzymes and activators
saposin
GM2A
CLN1
Lysosomal membrane proteins
major lysosomal membrane proteins
LAMP
LIMP
minor lysosomal membrane proteins
NPC
cystinosin
sialin
NRAMP
LAPTM
ABCA2
ABCB9
ACP2
endolyn
LALP70
sortilin
CLN3
CLN5
CLN7
HGSNAT
MCOLN1
Activation of lysosomal sulfatase precursor
FGE
lysosomal hydrase precursor
from ER
mannose
+p
GNPT
NAGPA
M6P
Snare interactions in vesicular transport
cis Golgi network
M6P receptor
MPR
M6P
clathrin
trans Golgi network
Golgi body
AP-1
AP-3
GGAs
AP-4
Receptor-dependent transport
M6P
transport vesicle
Receptor recycling
AP-1
M6P
M6P
ATPeV
-p
mannose
AP-3
lysosome
mature lysosomal hydrase
late endosome
Transport of synthesized lysosomal enzymes
04142 12/27/10
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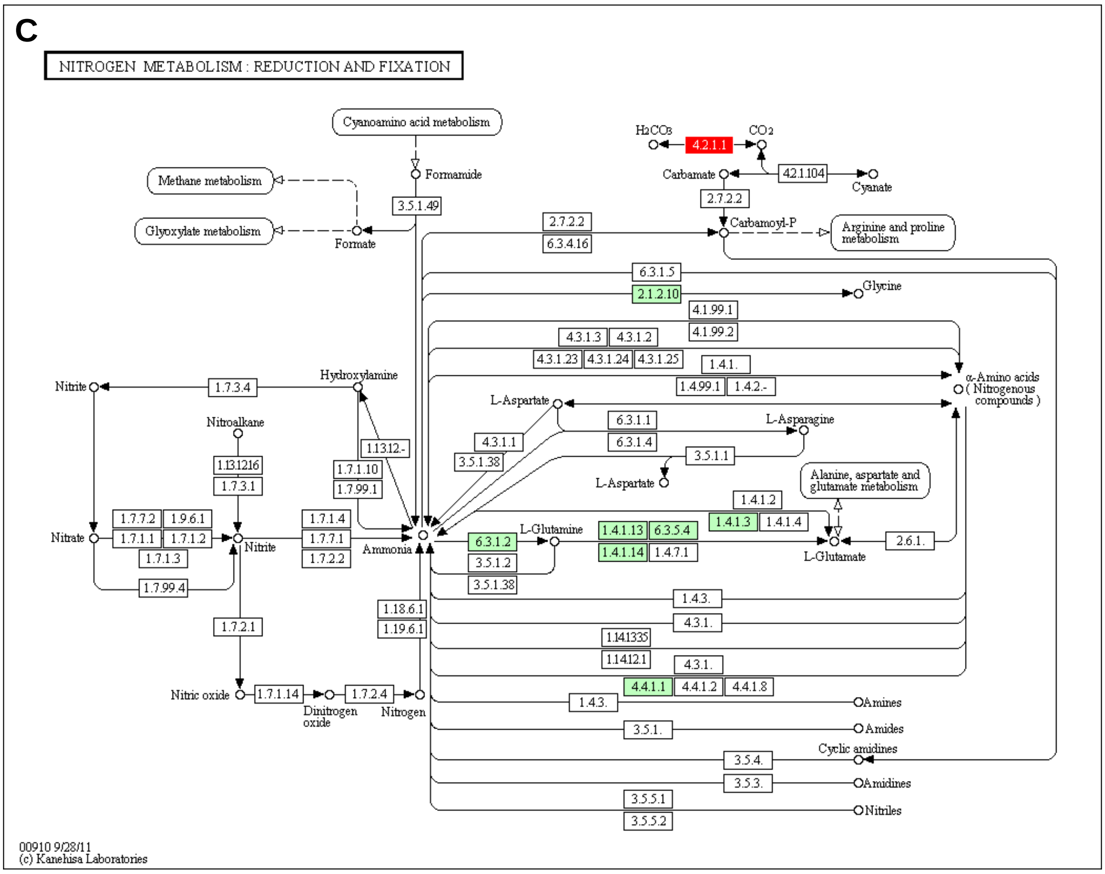
C
NITROGEN METABOLISM : REDUCTION AND FIXATION
Cyanoamino acid metabolism
Methane metabolism
Glyoxylate metabolism
Formamide
Formate
3.5.1.49
H2CO3
CO2
4.2.1.1
4.2.1.104
Carbamate
Cyanate
2.7.2.2
Carbamoyl-P
Arginine and proline metabolism
6.3.4.16
6.3.1.5
2.1.2.10
Glycine
4.1.99.1
4.1.99.2
4.3.1.3
4.3.1.2
4.3.1.23
4.3.1.24
4.3.1.25
1.4.1.
1.4.99.1
1.4.2.-
α-Amino acids (Nitrogenous compounds)
Nitrite
1.7.3.4
Hydroxylamine
Nitroalkane
1.13.12.16
1.7.3.1
1.13.12.-
1.7.1.10
1.7.99.1
L-Aspartate
6.3.1.1
6.3.1.4
L-Asparagine
4.3.1.1
3.5.1.38
3.5.1.1
L-Aspartate
Alanine, aspartate and glutamate metabolism
1.7.7.2
1.9.6.1
Nitrate
1.7.1.1
1.7.1.2
1.7.1.3
1.7.99.4
Nitrite
1.7.1.4
1.7.7.1
1.7.2.2
Ammonia
6.3.1.2
3.5.1.2
3.5.1.38
L-Glutamine
1.4.1.13
6.3.5.4
1.4.1.14
1.4.7.1
1.4.1.2
1.4.1.3
1.4.1.4
L-Glutamate
2.6.1.
1.4.3.
4.3.1.
1.18.6.1
1.19.6.1
1.14.13.35
1.14.12.1
4.3.1.
1.7.2.1
4.4.1.1
4.4.1.2
4.4.1.8
Nitric oxide
1.7.1.14
Dinitrogen oxide
1.7.2.4
Nitrogen
1.4.3.
Amines
3.5.1.
Amides
Cyclic amidines
3.5.4.
3.5.3.
Amidines
3.5.5.1
3.5.5.2
Nitriles
00910 9/28/11
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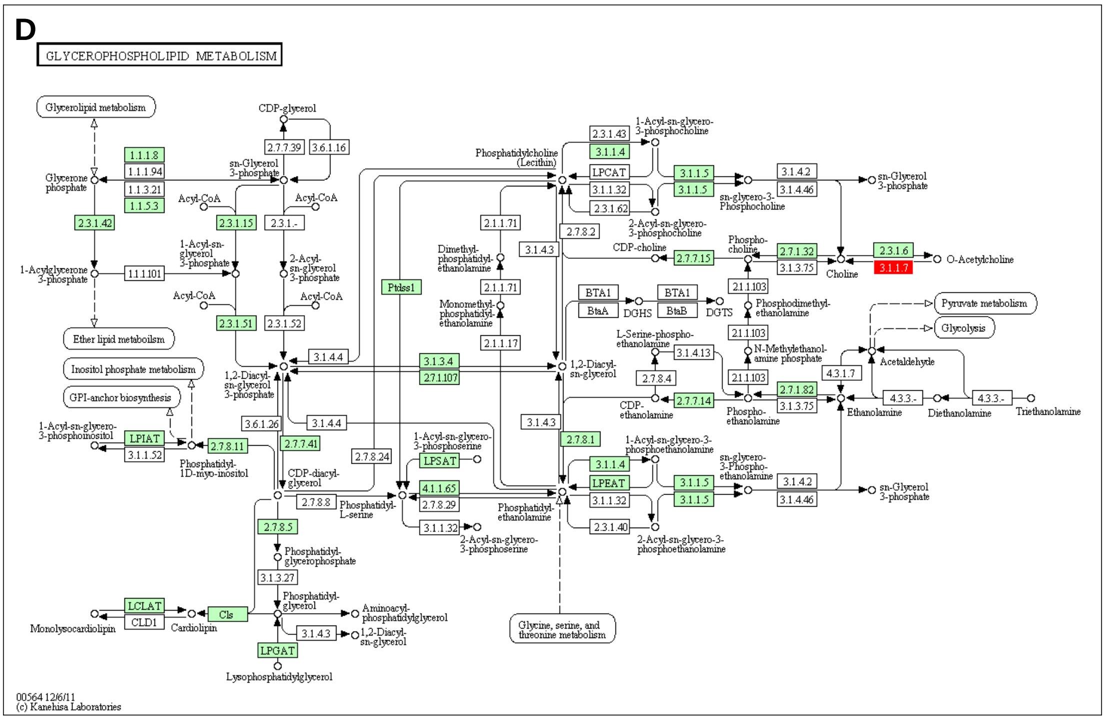
D
GLYCEROPHOSPHOLIPID METABOLISM
Glycerolipid metabolism
CDP-glycerol
2.7.7.39
3.6.1.16
1.1.1.8
1.1.1.94
1.1.3.21
1.1.5.3
Glycerone phosphate
sn-Glycerol 3-phosphate
2.3.1.42
Acyl-CoA
2.3.1.15
2.3.1.-
1-Acylglycerone 3-phosphate
1.1.1.101
1-Acyl-sn-glycerol 3-phosphate
2-Acyl-sn-glycerol 3-phosphate
Acyl-CoA
2.3.1.51
2.3.1.52
Ether lipid metabolism
Inositol phosphate metabolism
GPI-anchor biosynthesis
3.1.4.4
1,2-Diacyl-sn-glycerol 3-phosphate
3.6.1.26
1-Acyl-sn-glycero-3-phosphoinositol
LPIAT
3.1.1.52
2.7.8.11
Phosphatidyl-1D-myo-inositol
2.7.7.41
CDP-diacylglycerol
2.7.8.8
2.7.8.24
2.7.8.5
Phosphatidylglycerophosphate
3.1.3.27
Phosphatidylglycerol
LCLAT
CLD1
Cls
Monolysocardiolipin
Cardiolipin
LPGAT
Lysophosphatidylglycerol
3.1.4.3
Aminoacylphosphatidylglycerol
1,2-Diacyl-sn-glycerol
Phosphatidylcholine (Lecithin)
2.3.1.43
3.1.1.4
1-Acyl-sn-glycero-3-phosphocholine
LPCAT
3.1.1.32
2.3.1.62
3.1.1.5
sn-glycero-3-Phosphocholine
3.1.4.2
3.1.4.46
sn-Glycerol 3-phosphate
2-Acyl-sn-glycero-3-phosphocholine
2.7.8.2
CDP-choline
2.7.7.15
Phosphocholine
2.7.1.32
3.1.3.75
Choline
2.3.1.6
3.1.1.7
O-Acetylcholine
2.1.1.71
Dimethylphosphatidylethanolamine
3.1.4.3
Monomethylphosphatidylethanolamine
2.1.1.17
BTA1
BtaA
BtaB
DGHS
DGTS
2.1.1.103
Phosphodimethylethanolamine
Pyruvate metabolism
Glycolysis
L-Serine-phosphoethanolamine
3.1.4.13
N-Methylethanolamine phosphate
Acetaldehyde
Ptdss1
3.1.3.4
2.7.1.107
1,2-Diacyl-sn-glycerol
2.7.8.4
2.7.1.82
4.3.1.7
CDP-ethanolamine
2.7.7.14
Phosphoethanolamine
Ethanolamine
4.3.3.-
Diethanolamine
Triethanolamine
3.1.4.4
3.1.4.3
2.7.8.1
1-Acyl-sn-glycero-3-phosphoserine
LPSAT
4.1.1.65
2.7.8.29
Phosphatidyl-L-serine
Phosphatidylethanolamine
3.1.1.32
2-Acyl-sn-glycero-3-phosphoserine
1-Acyl-sn-glycero-3-phosphoethanolamine
LPEAT
3.1.1.4
sn-glycero-3-Phosphoethanolamine
2.3.1.40
2-Acyl-sn-glycero-3-phosphoethanolamine
Glycine, serine, and threonine metabolism
00564 12/6/11
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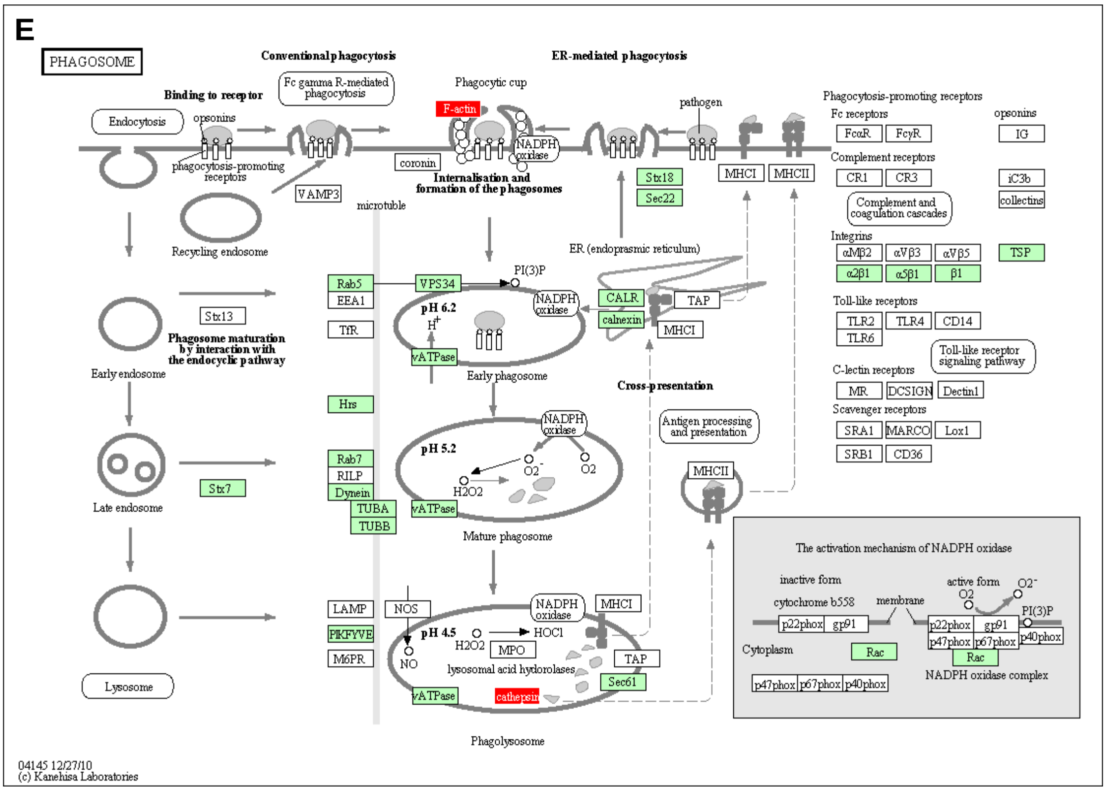
E
PHAGOSOME
Conventional phagocytosis
ER-mediated phagocytosis
Binding to receptor
Fc gamma R-mediated phagocytosis
Phagocytic cup
Endocytosis
opsonins
phagocytosis-promoting receptors
F-actin
NADPH oxidase
coronin
Internalisation and formation of the phagosomes
VAMP3
microtuble
Recycling endosome
pathogen
Stx18
Sec22
MHCI
MHCII
ER (endoprasmic reticulum)
Rab5
EEA1
VPS34
PI(3)P
Stx13
TfR
pH 6.2
H+
vATPase
CALR
calnexin
TAP
MHCI
Phagosome maturation by interaction with the endocyclic pathway
Early endosome
Early phagosome
Cross-presentation
Hrs
NADPH oxidase
Antigen processing and presentation
Rab7
RILP
Dynein
TUBA
TUBB
Stx7
Late endosome
pH 5.2
O2-
O2
H2O2
vATPase
Mature phagosome
MHCII
LAMP
NOS
PIKFYVE
M6PR
NADPH oxidase
MHCI
pH 4.5
H2O2
HOCl
MPO
NO
lysosomal acid hydrolases
TAP
Sec61
vATPase
cathepsin
Lysosome
Phagolysosome
Phagocytosis-promoting receptors
Fc receptors
FcαR
FcγR
opsonins
IG
Complement receptors
CR1
CR3
iC3b
collectins
Complement and coagulation cascades
Integrins
αMβ2
αVβ3
αVβ5
TSP
α2β1
α5β1
β1
Toll-like receptors
TLR2
TLR4
CD14
TLR6
Toll-like receptor signaling pathway
C-lectin receptors
MR
DCSIGN
Dectin1
Scavenger receptors
SRA1
MARCO
Lox1
SRB1
CD36
The activation mechanism of NADPH oxidase
inactive form
cytochrome b558
membrane
active form
O2
O2-
PI(3)P
p22phox
gp91
p22phox
gp91
p47phox
p67phox
p40phox
Cytoplasm
Rac
Rac
NADPH oxidase complex
p47phox
p67phox
p40phox
04145 12/27/10
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Fig. S3. The enriched GO analysis for female and male biased genes. A. Female enriched Go terms. B. Male enriched Go terms. GOSeq explicitly takes into account gene selection bias due to difference in gene lengths and thus numbers of overlapping sequencing reads. GOSeq is used for GO enrichment analysis, Q-value, 0.05 is chosen significant cutoff.

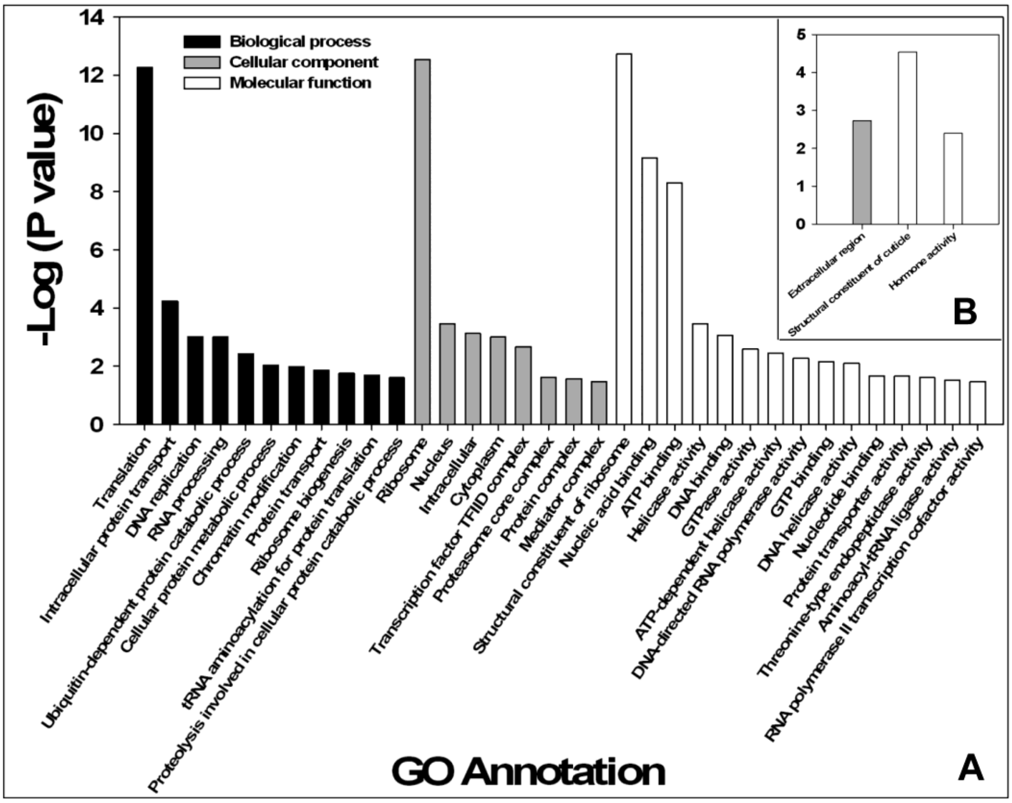

Fig. S4. Sequencing strategy.

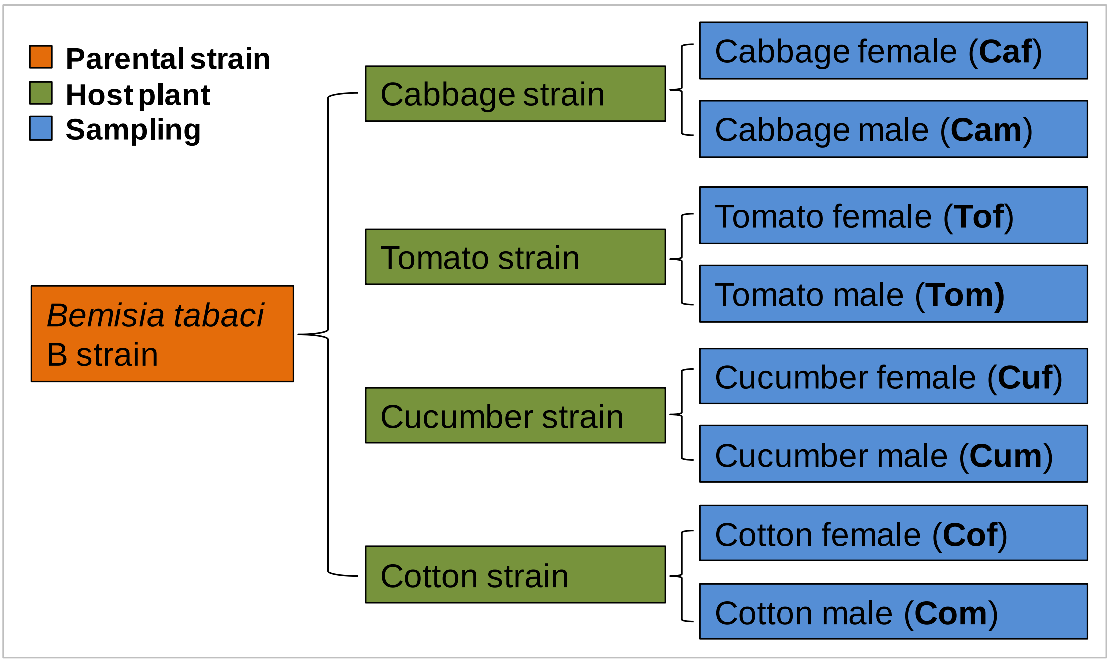

Table S1 Annotation of female-biased genes

Assembly ID	**NR database**
comp5946_c0_seq2	PREDICTED: hypothetical protein LOC409606 [Apis mellifera]
comp5566_c0_seq1	hypothetical protein SINV_80284 [Solenopsis invicta]
comp12946_c0_seq1	PREDICTED: hypothetical protein LOC100164170 [Acyrthosiphon pisum]
comp5546_c0_seq1	PREDICTED: ATP-dependent helicase brm-like [Acyrthosiphon pisum]
comp6965_c0_seq1	PREDICTED: f-box/LRR-repeat protein 2-like isoform 2 [Apis mellifera]
comp4175_c0_seq1	hypothetical protein BRAFLDRAFT_264350 [Branchiostoma floridae] gi|229290244|gb|EEN60925.1| hypothetical protein BRAFLDRAFT_264350 [Branchiostoma floridae]
comp5860_c0_seq1	hypothetical protein TcasGA2_TC010807 [Tribolium castaneum]
comp8187_c0_seq4	PREDICTED: e3 ubiquitin-protein ligase Rnf220-like [Apis mellifera]
comp3052_c0_seq1	PREDICTED: exocyst complex component 5-like [Apis mellifera]
comp4761_c0_seq1	PREDICTED: histone-arginine methyltransferase CARMER-like [Bombus terrestris]
comp1364_c0_seq1	Sec61 alpha 1 subunit [Acyrthosiphon pisum] gi|52630957|gb|AAU84942.1| probable transport protein Sec61 alpha subunit [Toxoptera citricida] >gi|89574501|gb|ABD76381.1| putative transport protein Sec61 alpha subunit [Acyrthosiphon pisum]
comp4895_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212515574|gb|EEB17698.1| conserved hypothetical protein [Pediculus humanus corporis]
comp7230_c0_seq2	hypothetical protein BRAFLDRAFT_114978 [Branchiostoma floridae] gi|229294780|gb|EEN65434.1| hypothetical protein BRAFLDRAFT_114978 [Branchiostoma floridae]
comp9683_c0_seq1	PREDICTED: MAGUK p55 subfamily member 6-like isoform 2 [Acyrthosiphon pisum]
comp4715_c0_seq1	PREDICTED: e3 ubiquitin-protein ligase TTC3-like [Xenopus (Silurana) tropicalis]
comp1319_c0_seq1	
comp4096_c0_seq1	PREDICTED: ATP-dependent RNA helicase Ddx1-like isoform 1 [Bombus terrestris]
comp8418_c0_seq1	hypothetical protein SINV_05940 [Solenopsis invicta]
comp1711_c0_seq1	GH19071 [Drosophila grimshawi] gi|193894137|gb|EDV93003.1| GH19071 [Drosophila grimshawi]
comp13751_c0_seq1	hypothetical protein SINV_09205 [Solenopsis invicta]
comp3946_c0_seq1	hypothetical protein SINV_10218 [Solenopsis invicta]
comp8186_c0_seq1	PREDICTED: similar to dehydrodolichyl diphosphate synthase [Tribolium castaneum] gi|270012136|gb|EFA08584.1| hypothetical protein TcasGA2_TC006239 [Tribolium castaneum]
comp4677_c0_seq1	hypothetical protein DAPPUDRAFT_194601 [Daphnia pulex]

comp11291_c0_seq1	PREDICTED: condensin-2 complex subunit D3-like [Bombus terrestris]
comp2918_c0_seq1	PREDICTED: high affinity copper uptake protein 1-like isoform 1 [Bombus terrestris] gi|340711491|ref|XP_003394309.1| PREDICTED: high affinity copper uptake protein 1-like isoform 2 [Bombus terrestris]
comp4553_c0_seq1	Sperm-associated antigen, putative [Pediculus humanus corporis] gi|212508991|gb|EEB12505.1| Sperm-associated antigen, putative [Pediculus humanus corporis]
comp5379_c0_seq1	hypothetical protein TcasGA2_TC004440 [Tribolium castaneum]
comp2855_c1_seq1	PREDICTED: sister chromatid cohesion protein PDS5 homolog B-A-like [Apis mellifera]
comp4814_c0_seq1	SWI/SNF-related matrix-associated actin-dependent regulator chromatin subfamily E member 1 [Acromyrmex echinatior]
comp5474_c0_seq1	PREDICTED: DNA-directed RNA polymerases I, II, and III subunit RPABC1-like [Apis mellifera] gi|340724888|ref|XP_003400810.1| PREDICTED: DNA-directed RNA polymerases I, II, and III subunit RPABC1-like [Bombus terrestris]
comp779_c0_seq1	
comp414_c0_seq1	
comp245_c0_seq1	putative peptidyl-prolyl cis-trans isomerase [Maconellicoccus hirsutus]
comp4452_c0_seq1	PREDICTED: similar to ubiquitin specific peptidase 14 [Tribolium castaneum] gi|270009745|gb|EFA06193.1| hypothetical protein TcasGA2_TC009042 [Tribolium castaneum]
comp146_c0_seq1	PREDICTED: 60S ribosomal protein L4-like [Bombus terrestris]
comp10171_c0_seq1	serine palmitoyltransferase, putative [Pediculus humanus corporis] gi|212510255|gb|EEB13466.1| serine palmitoyltransferase, putative [Pediculus humanus corporis]
comp4872_c0_seq1	PREDICTED: kinesin-like protein KIF23-like [Bombus terrestris]
comp9464_c0_seq1	farnesoic acid methyltransferase [Schistocerca gregaria]
comp1828_c0_seq1	PREDICTED: hypothetical protein LOC100639010 [Amphimedon queenslandica]
comp6906_c0_seq1	PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] gi|115925716|ref|XP_001197429.1| PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]
comp4945_c0_seq1	
comp4290_c0_seq1	hypothetical protein TcasGA2_TC000046 [Tribolium castaneum]
comp1339_c0_seq1	Deoxyuridine 5'-triphosphate nucleotidohydrolase [Camponotus floridanus]
comp2717_c0_seq1	PREDICTED: collagen alpha-1(IV) chain-like [Acyrthosiphon pisum]
comp328_c0_seq1	
comp8322_c0_seq1	EH domain-binding protein 1 [Acromyrmex echinatior]
comp2967_c0_seq1	PREDICTED: aspartyl-tRNA synthetase, cytoplasmic [Apis mellifera]

comp4287_c0_seq1	PREDICTED: hypothetical protein LOC100161450 [Acyrthosiphon pisum]
comp8000_c0_seq1	hypothetical protein AND_06034 [Anopheles darlingi]
comp2123_c0_seq1	Splicing factor 3B subunit, putative [Pediculus humanus corporis] gi|212510525|gb|EEB13688.1| Splicing factor 3B subunit, putative [Pediculus humanus corporis]
comp4596_c0_seq3	PREDICTED: similar to AGAP006448-PB [Tribolium castaneum] gi|270003022|gb|EEZ99469.1| hypothetical protein TcasGA2_TC000040 [Tribolium castaneum]
comp1389_c0_seq1	T-complex protein 1 subunit alpha [Culex quinquefasciatus] gi|167878016|gb|EDS41399.1| T-complex protein 1 subunit alpha [Culex quinquefasciatus]
comp3129_c0_seq1	PREDICTED: malignant T cell-amplified sequence 1-like [Apis mellifera]
comp4630_c0_seq1	PREDICTED: DENN domain-containing protein 2A-like [Acyrthosiphon pisum]
comp276_c0_seq1	
comp6076_c0_seq1	AGAP008908-PA [Anopheles gambiae str. PEST] gi|55235211|gb|EAA14867.2| AGAP008908-PA [Anopheles gambiae str. PEST]
comp251_c0_seq1	putative ribosomal protein S25 [Diaphorina citri]
comp7903_c0_seq9	PREDICTED: methylosome subunit pICln-like [Bombus terrestris]
comp3651_c0_seq1	PREDICTED: UDP-glucose:glycoprotein glucosyltransferase-like [Acyrthosiphon pisum]
comp4383_c0_seq1	PREDICTED: ATP-binding cassette sub-family G member 8-like isoform 1 [Acyrthosiphon pisum] gi|328718493|ref|XP_003246499.1| PREDICTED: ATP-binding cassette sub-family G member 8-like isoform 2 [Acyrthosiphon pisum]
comp1858_c0_seq1	ABC membrane transporter [Athalia rosae]
comp6943_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: gamma-tubulin complex component 3-like [Meleagris gallopavo]
comp5047_c0_seq1	PREDICTED: similar to CG11337 CG11337-PA [Tribolium castaneum] gi|270009999|gb|EFA06447.1| hypothetical protein TcasGA2_TC009329 [Tribolium castaneum]
comp9138_c0_seq1	PREDICTED: cleavage stimulation factor subunit 1-like isoform 1 [Bombus terrestris]
comp3883_c0_seq1	PREDICTED: rac GTPase-activating protein 1-like [Apis mellifera]
comp4140_c0_seq1	PREDICTED: ribonuclease 3-like [Bombus terrestris]
comp8427_c0_seq1	PREDICTED: PAB-dependent poly(A)-specific ribonuclease subunit 2-like [Acyrthosiphon pisum]
comp6518_c0_seq1	PREDICTED: mitotic checkpoint protein BUB3-like [Acyrthosiphon pisum]
comp2701_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: coiled-coil domain-containing protein 39-like [Bombus terrestris]
comp7198_c0_seq1	PREDICTED: DNA polymerase alpha catalytic subunit-like [Acyrthosiphon pisum]
comp5583_c0_seq1	CTP synthase [Nasonia vitripennis]
comp10714_c0_seq1	PREDICTED: similar to AGAP004271-PA [Tribolium castaneum] gi|270006251|gb|EFA02699.1| hypothetical protein TcasGA2_TC008421 [Tribolium castaneum]
comp5175_c0_seq3	conserved hypothetical protein [Pediculus humanus corporis] gi|212508158|gb|EEB11927.1| conserved hypothetical protein [Pediculus humanus corporis]

comp1151_c0_seq1	hypothetical protein SINV_07167 [Solenopsis invicta]
comp3329_c0_seq1	Signal recognition particle 14 kDa protein, putative [Pediculus humanus corporis] gi|212517121|gb|EEB19058.1| Signal recognition particle 14 kDa protein, putative [Pediculus humanus corporis]
comp1116_c0_seq2	hypothetical protein DAPPUDRAFT_218652 [Daphnia pulex]
comp2077_c0_seq1	
comp758_c1_seq4	GH14039 [Drosophila grimshawi] gi|193891834|gb|EDV90700.1| GH14039 [Drosophila grimshawi]
comp1458_c0_seq1	ribosomal protein L39, putative [Ixodes scapularis] gi|215510701|gb|EEC20154.1| ribosomal protein L39, putative [Ixodes scapularis]
comp6584_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212514903|gb|EEB17131.1| conserved hypothetical protein [Pediculus humanus corporis]
comp5881_c0_seq1	RNA-binding protein 28 [Camponotus floridanus]
comp2422_c0_seq2	AGAP007998-PA [Anopheles gambiae str. PEST] gi|116123253|gb|EAA12403.3| AGAP007998-PA [Anopheles gambiae str. PEST]
comp5456_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212505850|gb|EEB10208.1| conserved hypothetical protein [Pediculus humanus corporis]
comp97_c0_seq1	
comp1028_c0_seq1	PREDICTED: similar to eIF3-S9 [Tribolium castaneum] gi|270011918|gb|EFA08366.1| hypothetical protein TcasGA2_TC006009 [Tribolium castaneum]
comp3120_c0_seq1	PREDICTED: DNA ligase 1-like [Bombus terrestris]
comp2357_c0_seq1	WD-repeat protein YNL035C, putative [Pediculus humanus corporis] gi|212513065|gb|EEB15715.1| WD-repeat protein YNL035C, putative [Pediculus humanus corporis]
comp2796_c0_seq1	PREDICTED: similar to CG13472 CG13472-PA [Tribolium castaneum]
comp4899_c0_seq1	PREDICTED: similar to exosome component 8 [Tribolium castaneum] gi|270006123|gb|EFA02571.1| hypothetical protein TcasGA2_TC008282 [Tribolium castaneum]
comp5337_c0_seq1	PREDICTED: hypothetical protein LOC408574 isoform 1 [Apis mellifera]
comp3516_c0_seq1	
comp6743_c0_seq1	PREDICTED: seryl-tRNA synthetase, cytoplasmic-like [Acyrthosiphon pisum]
comp8270_c1_seq1	PREDICTED: transportin-1-like [Bombus terrestris]
comp6423_c0_seq1	hypothetical protein SINV_14041 [Solenopsis invicta]
comp9560_c0_seq1	PREDICTED: Bloom syndrome protein homolog [Acyrthosiphon pisum]
comp3911_c0_seq1	phosphatidylethanolamine binding protein isoform 2 [Bombyx mori] gi|95102826|gb|ABF51354.1| phosphatidylethanolamine binding protein isoform 2 [Bombyx mori]
comp5048_c0_seq1	Conserved oligomeric Golgi complex subunit 6 [Camponotus floridanus]
comp4282_c0_seq2	PREDICTED: hypothetical protein [Nasonia vitripennis]
comp5467_c0_seq1	hypothetical protein SINV_13915 [Solenopsis invicta]
comp4447_c0_seq1	PREDICTED: AP-3 complex subunit delta-1-like isoform 1 [Acyrthosiphon pisum]

comp6990_c0_seq1	PREDICTED: similar to AGAP001195-PA [Tribolium castaneum]
comp2132_c0_seq1	putative regulator of ribosome biosynthesis [Heliconius melpomene]
comp7456_c0_seq1	PREDICTED: probable tyrosyl-tRNA synthetase, mitochondrial-like [Acyrthosiphon pisum]
comp2094_c0_seq1	PREDICTED: growth/differentiation factor 3-like [Monodelphis domestica]
comp5712_c0_seq1	PREDICTED: hypothetical protein LOC100570013 [Acyrthosiphon pisum]
comp4842_c0_seq1	PHD finger protein 14 [Camponotus floridanus]
comp848_c0_seq1	PREDICTED: similar to aubergine [Nasonia vitripennis]
comp8352_c1_seq16	Collagen alpha-1(XV) chain [Acromyrmex echinatior]
comp6594_c0_seq1	PREDICTED: similar to CG3894 CG3894-PA [Tribolium castaneum] gi|270010902|gb|EFA07350.1| hypothetical protein TcasGA2_TC015949 [Tribolium castaneum]
comp10401_c0_seq1	PREDICTED: activating signal cointegrator 1 complex subunit 2-like [Bombus terrestris]
comp7828_c0_seq1	PREDICTED: similar to CG10470 CG10470-PA [Tribolium castaneum] gi|270007385|gb|EFA03833.1| hypothetical protein TcasGA2_TC013949 [Tribolium castaneum]
comp2469_c0_seq1	hypothetical protein TcasGA2_TC007276 [Tribolium castaneum]
comp5031_c0_seq1	Mitochondrial carrier-like protein 2 [Harpegnathos saltator]
comp3837_c0_seq2	PREDICTED: hypothetical protein LOC409240 [Apis mellifera]
comp5441_c0_seq1	PREDICTED: serine/threonine-protein kinase pelle-like [Acyrthosiphon pisum]
comp3834_c0_seq2	Arsenical pump-driving ATPase, putative [Pediculus humanus corporis] gi|212507576|gb|EEB11476.1| Arsenical pump-driving ATPase, putative [Pediculus humanus corporis]
comp2926_c1_seq2	
comp4158_c0_seq1	
comp3238_c0_seq1	Splicing factor, putative [Pediculus humanus corporis] gi|212513011|gb|EEB15661.1| Splicing factor, putative [Pediculus humanus corporis]
comp5092_c0_seq1	OTU domain-containing protein 6B [Acromyrmex echinatior]
comp4076_c0_seq1	PREDICTED: microfibrillar-associated protein 1 [Apis mellifera]
comp7996_c0_seq1	hypothetical protein TcasGA2_TC009196 [Tribolium castaneum]
comp4709_c0_seq1	FAD oxidoreductase [Culex quinquefasciatus] gi|167880398|gb|EDS43781.1| FAD oxidoreductase [Culex quinquefasciatus]
comp5152_c0_seq2	PREDICTED: similar to ran gtpase-activating protein [Tribolium castaneum] gi|270003723|gb|EFA00171.1| hypothetical protein TcasGA2_TC002993 [Tribolium castaneum]
comp1623_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212516897|gb|EEB18851.1| conserved hypothetical protein [Pediculus humanus corporis]
comp770_c0_seq1	hypothetical protein EAI_07906 [Harpegnathos saltator]

comp3260_c0_seq1	nuclear pore complex protein nup154, putative [Pediculus humanus corporis] gi|212512574|gb|EEB15317.1| nuclear pore complex protein nup154, putative [Pediculus humanus corporis]
comp4105_c0_seq1	PREDICTED: similar to cell division control protein [Tribolium castaneum] gi|270001087|gb|EEZ97534.1| hypothetical protein TcasGA2_TC011382 [Tribolium castaneum]
comp3751_c0_seq1	hypothetical protein SINV_02090 [Solenopsis invicta]
comp7210_c0_seq1	PREDICTED: protein scarlet-like [Bombus terrestris]
comp10534_c0_seq1	hypothetical protein TcasGA2_TC015253 [Tribolium castaneum]
comp5930_c0_seq2	PREDICTED: 10-formyltetrahydrofolate dehydrogenase-like [Acyrthosiphon pisum]
comp16622_c0_seq1	uridine diphosphate glucosyltransferase [Bombyx mori] gi|213494483|gb|ACJ48963.1| uridine diphosphate glucosyltransferase [Bombyx mori]
comp9762_c0_seq1	hypothetical protein SINV_00995 [Solenopsis invicta]
comp5382_c0_seq2	hypothetical protein DAPPUDRAFT_213756 [Daphnia pulex]
comp3859_c0_seq1	mitochondrial ribosomal protein S31 [Tribolium castaneum] gi|270010145|gb|EFA06593.1| hypothetical protein TcasGA2_TC009507 [Tribolium castaneum]
comp4619_c0_seq1	PREDICTED: similar to vesicle associated protein, putative [Tribolium castaneum]
comp413_c0_seq1	
comp3056_c1_seq1	
comp7983_c0_seq2	hypothetical protein BRAFLDRAFT_114907 [Branchiostoma floridae] gi|229295831|gb|EEN66475.1| hypothetical protein BRAFLDRAFT_114907 [Branchiostoma floridae]
comp6510_c0_seq1	PREDICTED: similar to cullin [Tribolium castaneum] gi|270008911|gb|EFA05359.1| hypothetical protein TcasGA2_TC015524 [Tribolium castaneum]
comp5484_c0_seq1	Exosome complex exonuclease RRP46 [Acromyrmex echinatior]
comp7152_c0_seq1	tRNA-dihydrouridine synthase 3-like [Harpegnathos saltator]
comp4489_c0_seq1	viral A-type inclusion protein, putative [Acyrthosiphon pisum] gi|239792807|dbj|BAH72702.1| ACYPI001034 [Acyrthosiphon pisum]
comp6687_c0_seq1	PREDICTED: BTB/POZ domain-containing protein KCTD3-like [Acyrthosiphon pisum]
comp4532_c0_seq1	AGAP008118-PA [Anopheles gambiae str. PEST] gi|157015001|gb|EAA12568.4| AGAP008118-PA [Anopheles gambiae str. PEST]
comp3451_c0_seq2	N-terminal acetyltransferase complex Ard1 subunit, putative [Pediculus humanus corporis] gi|212510022|gb|EEB13282.1| N-terminal acetyltransferase complex Ard1 subunit, putative [Pediculus humanus corporis]
comp3813_c0_seq1	hypothetical protein DAPPUDRAFT_60384 [Daphnia pulex]
comp7028_c0_seq2	Regulatory-associated protein of mTOR, putative [Pediculus humanus corporis] gi|212514611|gb|EEB16894.1| Regulatory-associated protein of mTOR, putative [Pediculus humanus corporis]

comp7138_c0_seq1	Mediator of RNA polymerase II transcription subunit 15 [Camponotus floridanus]
comp7672_c0_seq1	PREDICTED: bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial-like [Acyrthosiphon pisum]
comp6350_c0_seq1	hypothetical protein TcasGA2_TC010433 [Tribolium castaneum]
comp5248_c0_seq1	Transcription initiation factor TFIID subunit 12 [Camponotus floridanus]
comp6317_c0_seq1	DEAD box ATP-dependent RNA helicase, putative [Pediculus humanus corporis] gi|212509065|gb|EEB12562.1| DEAD box ATP-dependent RNA helicase, putative [Pediculus humanus corporis]
comp3371_c0_seq1	Rpd3 histone deacetylase [Nasonia vitripennis]
comp4559_c0_seq1	PREDICTED: BTB (POZ) domain containing 2-like [Saccoglossus kowalevskii]
comp10922_c0_seq1	PREDICTED: similar to CG5978 CG5978-PA [Tribolium castaneum] gi|270004611|gb|EFA01059.1| hypothetical protein TcasGA2_TC003977 [Tribolium castaneum]
comp1903_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212515794|gb|EEB17884.1| conserved hypothetical protein [Pediculus humanus corporis]
comp3512_c0_seq1	PREDICTED: coiled-coil domain-containing protein 6-like [Bombus terrestris]
comp4789_c0_seq1	116 kda U5 small nuclear ribonucleoprotein component [Aedes aegypti] gi|108872311|gb|EAT36536.1| 116 kda U5 small nuclear ribonucleoprotein component [Aedes aegypti]
comp10286_c0_seq1	hypothetical protein TcasGA2_TC003335 [Tribolium castaneum]
comp11549_c0_seq1	PREDICTED: protein melted-like isoform 1 [Acyrthosiphon pisum]
comp5664_c0_seq2	hypothetical protein SALIVA_1456 [Streptococcus salivarius JIM8777]
comp752_c0_seq1	
comp7112_c0_seq1	PREDICTED: zinc finger protein 160-like [Acyrthosiphon pisum]
comp5531_c0_seq1	PREDICTED: WD repeat-containing protein 18-like [Acyrthosiphon pisum]
comp3331_c0_seq1	hypothetical protein TcasGA2_TC013240 [Tribolium castaneum]
comp1332_c0_seq1	GJ13319 [Drosophila virilis] gi|194154378|gb|EDW69562.1| GJ13319 [Drosophila virilis]
comp1655_c0_seq1	PREDICTED: hypothetical protein LOC100161931 [Acyrthosiphon pisum]
comp7132_c0_seq3	conserved hypothetical protein [Pediculus humanus corporis] gi|212508467|gb|EEB12156.1| conserved hypothetical protein [Pediculus humanus corporis]
comp7636_c0_seq1	
comp4369_c0_seq2	PREDICTED: facilitated trehalose transporter Tret1-like [Acyrthosiphon pisum]
comp2907_c0_seq1	Fas (TNFRSF6) associated factor 1 [Tribolium castaneum]
comp2784_c1_seq1	
comp1331_c1_seq1	PREDICTED: polypyrimidine tract-binding protein 1-like isoform 1 [Acyrthosiphon pisum]

comp8368_c0_seq1	hypothetical protein Phum_PHUM202100 [Pediculus humanus corporis] gi|212509291|gb|EEB12717.1| hypothetical protein Phum_PHUM202100 [Pediculus humanus corporis]
comp2464_c0_seq1	PREDICTED: similar to 39S ribosomal protein L11, mitochondrial [Tribolium castaneum] gi|270010187|gb|EFA06635.1| hypothetical protein TcasGA2_TC009555 [Tribolium castaneum]
comp4264_c0_seq1	PREDICTED: facilitated trehalose transporter Tret1-like [Acyrthosiphon pisum]
comp281_c0_seq1	putative ribosomal protein L28 [Diaphorina citri]
comp6138_c0_seq1	sumo-1-activating enzyme E1a, putative [Pediculus humanus corporis] gi|212514229|gb|EEB16588.1| sumo-1-activating enzyme E1a, putative [Pediculus humanus corporis]
comp2400_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212505846|gb|EEB10204.1| conserved hypothetical protein [Pediculus humanus corporis]
comp4318_c0_seq1	cell division control protein [Aedes aegypti] gi|108879911|gb|EAT44136.1| cell division control protein [Aedes aegypti]
comp6198_c0_seq1	PREDICTED: similar to protein kinase protein [Tribolium castaneum] gi|270013600|gb|EFA10048.1| hypothetical protein TcasGA2_TC012222 [Tribolium castaneum]
comp4848_c0_seq1	PREDICTED: similar to alpha methylacyl-coa racemase [Tribolium castaneum] gi|270007738|gb|EFA04186.1| hypothetical protein TcasGA2_TC014435 [Tribolium castaneum]
comp6357_c0_seq1	PREDICTED: similar to CG10225 CG10225-PA [Tribolium castaneum] gi|270013975|gb|EFA10423.1| hypothetical protein TcasGA2_TC012664 [Tribolium castaneum]
comp11720_c0_seq1	PREDICTED: MGC80532 protein-like [Saccoglossus kowalevskii]
comp3323_c0_seq1	AGAP005961-PA [Anopheles gambiae str. PEST] gi|157015863|gb|EAA11702.5| AGAP005961-PA [Anopheles gambiae str. PEST]
comp2003_c0_seq1	PREDICTED: similar to proteasome beta subunit [Tribolium castaneum] gi|270003046|gb|EEZ99493.1| hypothetical protein TcasGA2_TC000069 [Tribolium castaneum]
comp4701_c0_seq1	PREDICTED: DNA repair protein RAD50 isoform 1 [Equus caballus]
comp8294_c0_seq1	PREDICTED: hypothetical protein LOC100577295 [Apis mellifera]
comp247_c0_seq1	60s ribosomal protein L19 [Glossina morsitans morsitans]
comp1985_c0_seq1	PREDICTED: similar to protein phosphatase 2c gamma [Nasonia vitripennis]
comp2939_c0_seq1	eukaryotic translation initiation factor 6 [Saccoglossus kowalevskii]
comp2546_c0_seq1	PREDICTED: similar to ribophorin ii [Nasonia vitripennis]
comp3678_c0_seq1	PREDICTED: similar to G protein pathway suppressor 1 [Tribolium castaneum] gi|270004016|gb|EFA00464.1| hypothetical protein TcasGA2_TC003322 [Tribolium castaneum]
comp214_c1_seq1	hypothetical protein SINV_08497 [Solenopsis invicta]
comp617_c0_seq1	PREDICTED: upstream activation factor subunit spp27-like [Acyrthosiphon pisum]

comp2409_c0_seq1	cAMP-regulated phosphoprotein, putative [Pediculus humanus corporis] gi|212506043|gb|EEB10359.1| cAMP-regulated phosphoprotein, putative [Pediculus humanus corporis]
comp3045_c0_seq1	PREDICTED: similar to pebble CG8114-PB [Tribolium castaneum]
comp622_c0_seq1	nucleosome assembly protein 1-like isoform 2 [Nasonia vitripennis]
comp6066_c0_seq1	epsin 4/enthoprotin, putative [Pediculus humanus corporis] gi|212505926|gb|EEB10272.1| epsin 4/enthoprotin, putative [Pediculus humanus corporis]
comp5598_c0_seq1	hypothetical protein TcasGA2_TC006403 [Tribolium castaneum]
comp4696_c0_seq1	Papain family cysteine protease containing protein [Tetrahymena thermophila] gi|89290066|gb|EAR88054.1| Papain family cysteine protease containing protein [Tetrahymena thermophila SB210]
comp20_c0_seq7	
comp2068_c0_seq1	Probable small nuclear ribonucleoprotein Sm D2 [Harpegnathos saltator] gi|322786953|gb|EFZ13177.1| hypothetical protein SINV_00701 [Solenopsis invicta]
comp3505_c0_seq1	sugar transporter [Culex quinquefasciatus] gi|167867183|gb|EDS30566.1| sugar transporter [Culex quinquefasciatus]
comp5759_c0_seq1	nucleoporin seh1, putative [Pediculus humanus corporis] gi|212509238|gb|EEB12683.1| nucleoporin seh1, putative [Pediculus humanus corporis]
comp11566_c0_seq1	sucrase [Acyrthosiphon pisum] gi|81159208|gb|ABB55878.1| sucrase [Acyrthosiphon pisum]
comp609_c0_seq2	PREDICTED: hypothetical protein [Nasonia vitripennis]
comp7178_c0_seq1	eukaryotic translation initiation factor 3 subunit, putative [Pediculus humanus corporis] gi|212514491|gb|EEB16805.1| eukaryotic translation initiation factor 3 subunit, putative [Pediculus humanus corporis]
comp5497_c0_seq1	PREDICTED: mitogen-activated protein kinase kinase kinase kinase 3-like isoform 1 [Acyrthosiphon pisum]
comp5918_c0_seq1	PREDICTED: prostatic acid phosphatase-like [Bombus terrestris]
comp6979_c0_seq1	PREDICTED: hypothetical protein LOC100642720 [Bombus terrestris]
comp1341_c0_seq3	Thioredoxin domain-containing protein 12 [Salmo salar] gi|221219350|gb|ACM08336.1| Thioredoxin domain-containing protein 12 precursor [Salmo salar]
comp7409_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212507988|gb|EEB11807.1| conserved hypothetical protein [Pediculus humanus corporis]
comp1297_c0_seq1	Interferon-inducible double stranded RNA-dependent protein kinase activator A [Camponotus floridanus]
comp7696_c0_seq1	PREDICTED: zinc finger protein 341-like [Apis mellifera]
comp715_c0_seq1	
comp4265_c0_seq1	Enhancer of rudimentary homolog [Caligus clemensi]
comp9389_c1_seq1	PREDICTED: similar to MGC79091 protein [Tribolium castaneum] gi|270009431|gb|EFA05879.1| hypothetical protein TcasGA2_TC008691 [Tribolium castaneum]

comp1541_c0_seq1	
comp9720_c0_seq1	PREDICTED: protein lin-9 homolog [Apis mellifera]
comp2259_c0_seq1	PREDICTED: similar to arsenite-resistance protein [Nasonia vitripennis]
comp105_c0_seq1	hexamerin 1 [Perla marginata]
comp1934_c0_seq1	
comp1215_c0_seq1	PREDICTED: hypothetical protein LOC100164801 isoform 2 [Acyrthosiphon pisum]
comp670_c0_seq1	PREDICTED: cytoplasmic aconitate hydratase-like [Acyrthosiphon pisum]
comp2897_c0_seq1	Sulfate permease, putative [Pediculus humanus corporis] gi|212509207|gb|EEB12660.1| Sulfate permease, putative [Pediculus humanus corporis]
comp2266_c1_seq1	PREDICTED: hamartin-like [Acyrthosiphon pisum]
comp7128_c0_seq1	hypothetical protein PMAA_098760 [Penicillium marneffei ATCC 18224] gi|210069195|gb|EEA23286.1| hypothetical protein PMAA_098760 [Penicillium marneffei ATCC 18224]
comp3047_c0_seq1	PREDICTED: hypothetical protein LOC725524 [Apis mellifera]
comp10959_c0_seq1	phosphatidylinositol glycan [Bombyx mori] gi|95103156|gb|ABF51519.1| phosphatidylinositol glycan [Bombyx mori]
comp585_c0_seq1	translation initiation factor 5a-like [Acyrthosiphon pisum] gi|239788242|dbj|BAH70809.1| ACYPI002632 [Acyrthosiphon pisum]
comp5411_c0_seq1	Ferrochelatase, mitochondrial [Camponotus floridanus]
comp3085_c0_seq1	Replication protein A 32 kDa subunit [Caligus rogercresseyi]
comp3683_c0_seq1	PREDICTED: similar to GA21647-PA [Nasonia vitripennis]
comp8104_c0_seq1	PREDICTED: protein fat-free homolog [Apis mellifera]
comp4147_c0_seq1	PREDICTED: myosin-XVIIIa-like isoform 1 [Bombus terrestris]
comp5315_c0_seq1	GM18925 [Drosophila sechellia] gi|194121868|gb|EDW43911.1| GM18925 [Drosophila sechellia]
comp6451_c0_seq2	PREDICTED: sodium/calcium exchanger 1-like [Acyrthosiphon pisum]
comp4326_c0_seq1	PREDICTED: coatomer subunit zeta-1 isoform 1 [Apis mellifera]
comp4143_c0_seq1	PREDICTED: DNA-directed RNA polymerase II subunit RPB3-like [Apis mellifera]
comp1556_c0_seq1	26S proteasome non-ATPase regulatory subunit, putative [Pediculus humanus corporis] gi|212512219|gb|EEB15027.1| 26S proteasome non-ATPase regulatory subunit, putative [Pediculus humanus corporis]
comp4459_c0_seq1	RhoA activator C11orf59-like protein [Acromyrmex echinatior]
comp1730_c0_seq1	26S protease regulatory subunit 6B, putative [Pediculus humanus corporis] gi|212511194|gb|EEB14227.1| 26S protease regulatory subunit 6B, putative [Pediculus humanus corporis]
comp11527_c0_seq1	PREDICTED: laccase-4-like [Bombus terrestris]
comp10948_c0_seq1	Tetratricopeptide repeat protein 35-B [Camponotus floridanus]
comp1214_c0_seq1	

comp6258_c0_seq2	eukaryotic translation initiation factor 4 gamma [Nasonia vitripennis]
comp4285_c0_seq6	PREDICTED: similar to sorting nexin isoform 1 [Tribolium castaneum] gi|270009518|gb|EFA05966.1| hypothetical protein TcasGA2_TC008785 [Tribolium castaneum]
comp1896_c0_seq1	Stathmin-4 [Acromyrmex echinatior]
comp3385_c0_seq1	eukaryotic translation initiation factor 2A [Nasonia vitripennis]
comp338_c0_seq1	vitellogenin [Nilaparvata lugens]
comp5037_c0_seq1	PREDICTED: cytoplasmic dynein 1 light intermediate chain 2 [Apis mellifera]
comp7649_c0_seq1	PREDICTED: GPN-loop GTPase 3-like [Apis mellifera]
comp4534_c0_seq1	PREDICTED: similar to AGAP008909-PA [Tribolium castaneum] gi|270016373|gb|EFA12819.1| hypothetical protein TcasGA2_TC001886 [Tribolium castaneum]
comp4033_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: nuclear pore complex protein Nup153-like [Bombus terrestris]
comp6367_c0_seq1	PREDICTED: ribosome biogenesis protein BOP1 homolog [Bombus terrestris]
comp4798_c0_seq1	clathrin coat assembly protein ap-1, putative [Pediculus humanus corporis] gi|212507089|gb|EEB11117.1| clathrin coat assembly protein ap-1, putative [Pediculus humanus corporis]
comp3656_c0_seq1	PREDICTED: similar to zinc finger protein [Tribolium castaneum] gi|270009543|gb|EFA05991.1| hypothetical protein TcasGA2_TC008817 [Tribolium castaneum]
comp5914_c0_seq1	hypothetical protein DAPPUDRAFT_319459 [Daphnia pulex]
comp324_c0_seq1	PREDICTED: 60S ribosomal protein L17-like [Acyrthosiphon pisum]
comp6707_c0_seq1	PREDICTED: hypothetical protein LOC100165548 isoform 2 [Acyrthosiphon pisum]
comp6458_c0_seq1	PREDICTED: similar to karyopherin alpha 6 [Tribolium castaneum] gi|270002024|gb|EEZ98471.1| hypothetical protein TcasGA2_TC000963 [Tribolium castaneum]
comp6210_c0_seq1	amidohydrolase [Spirosoma linguale DSM 74] gi|283819176|gb|ADB41014.1| amidohydrolase [Spirosoma linguale DSM 74]
comp2743_c0_seq1	
comp9641_c0_seq1	KRAB-zinc finger protein [Mus musculus]
comp1690_c0_seq1	Translocon-associated protein subunit alpha [Harpegnathos saltator]
comp5855_c0_seq1	RNA polymerase II-associated factor 1-like protein [Harpegnathos saltator]
comp687_c0_seq2	hypothetical protein TcasGA2_TC012700 [Tribolium castaneum]
comp59_c0_seq1	vitellogenin [Athalia rosae]
comp9436_c0_seq1	GF17194 [Drosophila ananassae] gi|313471310|sp|B3M098.1|MTNA_DROAN RecName: Full=Methylthioribose-1-phosphate isomerase; Short=M1Pi; Short=MTR-1-P isomerase; AltName: Full=S-methyl-5-thioribose-1-phosphate isomerase; AltName: Full=Translation initiation factor eIF-2B subunit alpha/beta/delta-like protein >gi|190626531|gb|EDV42055.1| GF17194 [Drosophila ananassae]

comp7204_c0_seq1	PREDICTED: hypothetical protein LOC100160456 [Acyrthosiphon pisum]
comp48_c0_seq1	PREDICTED: transcription initiation factor IIA subunit 1 isoform 2 [Apis mellifera]
comp4293_c0_seq1	glutamate carboxypeptidase [Culex quinquefasciatus] gi|167881720|gb|EDS45103.1| glutamate carboxypeptidase [Culex quinquefasciatus]
comp6097_c0_seq1	COP9 signalosome complex subunit, putative [Pediculus humanus corporis] gi|212514024|gb|EEB16413.1| COP9 signalosome complex subunit, putative [Pediculus humanus corporis]
comp326_c0_seq1	vitellogenin [Trigonotylus caelestialium]
comp7428_c0_seq1	target of rapamycin [Blattella germanica]
comp5273_c0_seq1	
comp7807_c0_seq1	hypothetical protein SINV_07805 [Solenopsis invicta]
comp7816_c0_seq2	PREDICTED: serine/threonine-protein kinase PAK 1-like [Acyrthosiphon pisum]
comp307_c0_seq2	
comp5040_c0_seq1	Histone deacetylase complex subunit SAP18 [Harpegnathos saltator]
comp189_c0_seq1	PREDICTED: similar to translation elongation factor 2 [Nasonia vitripennis]
comp6975_c0_seq1	Transcription initiation factor TFIID subunit 4 [Harpegnathos saltator]
comp8780_c0_seq1	S-phase kinase-associated protein 1 [Caligus rogercresseyi] gi|225710690|gb|ACO11191.1| S-phase kinase-associated protein 1 [Caligus rogercresseyi] >gi|225714348|gb|ACO13020.1| S-phase kinase-associated protein 1 [Lepeophtheirus salmonis] >gi|225719430|gb|ACO15561.1| S-phase kinase-associated protein 1 [Caligus clemensi] >gi|290561056|gb|ADD37930.1| S-phase kinase-associated protein 1 [Lepeophtheirus salmonis]
comp10588_c0_seq1	ankyrin repeat protein [Trichomonas vaginalis G3] gi|121891508|gb|EAX96837.1| ankyrin repeat protein, putative [Trichomonas vaginalis G3]
comp872_c0_seq3	zinc finger protein CCCH domain-containing protein, putative [Pediculus humanus corporis] gi|212508278|gb|EEB12026.1| zinc finger protein CCCH domain-containing protein, putative [Pediculus humanus corporis]
comp8984_c0_seq1	PREDICTED: cytochrome b5 reductase 3-like [Saccoglossus kowalevskii]
comp4017_c0_seq1	PREDICTED: dynamin related protein 1 isoform 1 [Apis mellifera]
comp5081_c0_seq1	PREDICTED: similar to histidine triad protein member [Tribolium castaneum]
comp2809_c0_seq1	N-acetyltransferase-like [Acyrthosiphon pisum] gi|239789332|dbj|BAH71296.1| ACYPI004487 [Acyrthosiphon pisum]
comp1848_c0_seq1	PREDICTED: ribosomal L1 domain-containing protein CG13096-like [Bombus terrestris]
comp509_c0_seq2	chemosensory protein 5 [Apis mellifera] gi|112031616|gb|ABH88173.1| chemosensory protein 5 [Apis mellifera]

comp4780_c0_seq1	PREDICTED: DNA-directed RNA polymerase III subunit RPC1-like [Bombus terrestris]
comp406_c0_seq4	PREDICTED: hypothetical protein LOC100650971 [Bombus terrestris]
comp7119_c0_seq1	Protein kinase C-binding protein 1 [Acromyrmex echinatior]
comp2036_c0_seq1	aldehyde dehydrogenase [Aedes aegypti] gi|108869413|gb|EAT33638.1| aldehyde dehydrogenase [Aedes aegypti]
comp1867_c0_seq1	PREDICTED: ubiquitin carboxyl-terminal hydrolase 3-like [Bombus terrestris]
comp223_c0_seq1	hypothetical protein SINV_04528 [Solenopsis invicta]
comp211_c0_seq1	60S ribosomal protein L23-like protein [Phlebotomus papatasi]
comp5455_c0_seq1	PREDICTED: PHD finger and CXXC domain-containing protein CG17446-like [Bombus terrestris]
comp7459_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp4272_c0_seq1	PREDICTED: probable dynactin subunit 2-like [Bombus terrestris]
comp2216_c0_seq1	Putative serine protease F56F10.1 [Camponotus floridanus]
comp5577_c0_seq1	PREDICTED: PMS1 protein homolog 1-like [Acyrthosiphon pisum]
comp5001_c0_seq1	hypothetical protein EAG_01480 [Camponotus floridanus]
comp9053_c0_seq1	PREDICTED: similar to coproporphyrinogen iii oxidase [Nasonia vitripennis]
comp5272_c0_seq1	
comp348_c0_seq4	putative ribosomal protein L11 [Maconellicoccus hirsutus]
comp8694_c0_seq1	AGAP005188-PA [Anopheles gambiae str. PEST] gi|157017129|gb|EAA09500.5| AGAP005188-PA [Anopheles gambiae str. PEST]
comp8774_c0_seq1	Pre-mRNA-splicing factor RBM22 [Camponotus floridanus]
comp4313_c0_seq1	PREDICTED: DNA-directed RNA polymerase III subunit RPC2-like [Bombus terrestris]
comp5189_c0_seq1	Protein transport protein Sec24B [Camponotus floridanus]
comp2754_c0_seq1	PREDICTED: zinc finger protein Xfin-like [Acyrthosiphon pisum]
comp2614_c0_seq1	hypothetical protein G5I_09090 [Acromyrmex echinatior]
comp2212_c0_seq1	PREDICTED: similar to predicted protein [Tribolium castaneum] gi|270012608|gb|EFA09056.1| hypothetical protein TcasGA2_TC006771 [Tribolium castaneum]
comp5737_c0_seq1	PREDICTED: hypothetical protein LOC100165457 [Acyrthosiphon pisum]
comp7090_c0_seq1	Probable JmjC domain-containing histone demethylation protein 3B [Camponotus floridanus]
comp8283_c0_seq1	PREDICTED: arginyl-tRNA--protein transferase 1 [Monodelphis domestica]
comp411_c0_seq1	lupus la ribonucleoprotein [Aedes aegypti] gi|108880822|gb|EAT45047.1| lupus la ribonucleoprotein [Aedes aegypti]

comp481_c0_seq1	60S ribosomal protein L9 [Aedes aegypti] gi|157116673|ref|XP_001652828.1| 60S ribosomal protein L9 [Aedes aegypti] >gi|157116675|ref|XP_001652829.1| 60S ribosomal protein L9 [Aedes aegypti] >gi|157116677|ref|XP_001652830.1| 60S ribosomal protein L9 [Aedes aegypti] >gi|94468812|gb|ABF18255.1| ribosomal protein L9 [Aedes aegypti] >gi|108876350|gb|EAT40575.1| 60S ribosomal protein L9 [Aedes aegypti] >gi|108876351|gb|EAT40576.1| 60S ribosomal protein L9 [Aedes aegypti] >gi|108876352|gb|EAT40577.1| 60S ribosomal protein L9 [Aedes aegypti] >gi|108876353|gb|EAT40578.1| 60S ribosomal protein L9 [Aedes aegypti]
comp1938_c0_seq1	predicted protein [Nematostella vectensis] gi|156222627|gb|EDO43469.1| predicted protein [Nematostella vectensis]
comp7510_c0_seq1	hypothetical protein TcasGA2_TC012601 [Tribolium castaneum]
comp1911_c0_seq1	hypothetical protein SINV_12193 [Solenopsis invicta]
comp8706_c0_seq1	PREDICTED: 26S proteasome non-ATPase regulatory subunit 10-like [Acyrthosiphon pisum]
comp4248_c0_seq1	DNA replication licensing factor MCM5 [Aedes aegypti] gi|108881751|gb|EAT45976.1| DNA replication licensing factor MCM5 [Aedes aegypti]
comp1414_c0_seq2	PREDICTED: hypothetical protein LOC551973 [Apis mellifera]
comp2067_c0_seq1	PREDICTED: similar to restricted expression proliferation associated protein-100 [Strongylocentrotus purpuratus] gi|115926901|ref|XP_001196535.1| PREDICTED: similar to restricted expression proliferation associated protein-100 [Strongylocentrotus purpuratus]
comp314_c0_seq1	vitellogenin [Trigonotylus caelestialium]
comp10244_c0_seq1	hypothetical protein AaeL_AAEL000965 [Aedes aegypti] gi|108883769|gb|EAT47994.1| conserved hypothetical protein [Aedes aegypti]
comp2965_c0_seq1	PREDICTED: THUMP domain-containing protein 1-like [Bombus terrestris]
comp5298_c0_seq1	phosphatidylethanolamine-binding protein [Branchiostoma belcheri tsingtauense]
comp5413_c0_seq1	pre-mRNA-splicing factor ATP-dependent RNA helicase prp16, putative [Pediculus humanus corporis] gi|212511335|gb|EEB14339.1| pre-mRNA-splicing factor ATP-dependent RNA helicase prp16, putative [Pediculus humanus corporis]
comp7161_c0_seq1	hypothetical protein LOC100135267 [Xenopus (Silurana) tropicalis] gi|163916166|gb|AAI57556.1| LOC100135267 protein [Xenopus (Silurana) tropicalis]
comp2269_c0_seq1	
comp4647_c0_seq1	PREDICTED: pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1-like [Bombus terrestris]
comp3430_c0_seq2	Protein CASC3 [Harpegnathos saltator]
comp3481_c0_seq1	import inner membrane translocase subunit TIM50-C, putative [Pediculus humanus corporis] gi|212513414|gb|EEB15991.1| import inner membrane translocase subunit TIM50-C, putative [Pediculus humanus corporis]

comp8033_c0_seq1	PREDICTED: WD repeat and HMG-box DNA-binding protein 1-like [Acyrthosiphon pisum]
comp5314_c0_seq1	Transcription initiation factor TFIID subunit 5 [Acromyrmex echinatior]
comp5008_c0_seq1	putative deoxyribose-phosphate aldolase [Gallus gallus] gi|53127188|emb|CAG31017.1| hypothetical protein RCJMB04_1j17 [Gallus gallus]
comp2654_c0_seq1	
comp8825_c0_seq1	PREDICTED: similar to GA18517-PA [Nasonia vitripennis]
comp3118_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp10936_c0_seq1	hypothetical protein SINV_06875 [Solenopsis invicta]
comp10587_c0_seq1	DNA repair and recombination protein RAD26, putative [Pediculus humanus corporis] gi|212510049|gb|EEB13301.1| DNA repair and recombination protein RAD26, putative [Pediculus humanus corporis]
comp3483_c0_seq1	splicing factor u2af large subunit [Aedes aegypti] gi|108881728|gb|EAT45953.1| splicing factor u2af large subunit [Aedes aegypti]
comp7239_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: DNA mismatch repair protein Msh2-like [Bombus terrestris]
comp4732_c0_seq1	PREDICTED: similar to GA21059-PA [Nasonia vitripennis]
comp337_c0_seq1	PREDICTED: similar to Haspin CG40080-PA [Tribolium castaneum]
comp8330_c0_seq1	PREDICTED: PH-interacting protein [Apis mellifera]
comp8989_c0_seq1	Metallophosphoesterase [Wolbachia endosymbiont of Culex quinquefasciatus Pel] gi|213019031|ref|ZP_03334838.1| Metallophosphoesterase [Wolbachia endosymbiont of Culex quinquefasciatus JHB] >gi|190357901|emb|CAQ55361.1| Metallophosphoesterase [Wolbachia endosymbiont of Culex quinquefasciatus Pel] >gi|212995140|gb|EEB55781.1| Metallophosphoesterase [Wolbachia endosymbiont of Culex quinquefasciatus JHB]
comp5482_c0_seq1	hypothetical protein AaeL_AAEL013304 [Aedes aegypti] gi|108870227|gb|EAT34452.1| conserved hypothetical protein [Aedes aegypti]
comp3121_c0_seq1	hypothetical protein DAPPUDRAFT_302851 [Daphnia pulex]
comp373_c1_seq3	
comp6845_c0_seq2	PREDICTED: similar to AGAP001629-PA [Tribolium castaneum] gi|270008427|gb|EFA04875.1| hypothetical protein TcasGA2_TC014933 [Tribolium castaneum]
comp3058_c0_seq2	
comp11869_c0_seq1	PREDICTED: hypothetical protein [Nasonia vitripennis]
comp7041_c0_seq1	hypothetical protein TcasGA2_TC014807 [Tribolium castaneum]
comp2406_c0_seq1	PREDICTED: similar to Parn-A protein [Tribolium castaneum] gi|270011407|gb|EFA07855.1| hypothetical protein TcasGA2_TC005425 [Tribolium castaneum]
comp3920_c0_seq1	hypothetical protein [Trichomonas vaginalis G3] gi|121890508|gb|EAX95880.1| hypothetical protein TVAG_008910 [Trichomonas vaginalis G3]

comp6309_c1_seq1	PREDICTED: similar to inhibitor of growth family, member 1 [Tribolium castaneum] gi|270005646|gb|EFA02094.1| hypothetical protein TcasGA2_TC007731 [Tribolium castaneum]
comp4381_c0_seq1	PREDICTED: Carbohydrate kinase domain-containing protein-like [Oryctolagus cuniculus]
comp2693_c0_seq1	PREDICTED: similar to GTP-binding protein [Tribolium castaneum] gi|270008006|gb|EFA04454.1| hypothetical protein TcasGA2_TC014758 [Tribolium castaneum]
comp1864_c0_seq1	PREDICTED: similar to metalloprotease [Tribolium castaneum] gi|270001475|gb|EEZ97922.1| hypothetical protein TcasGA2_TC000308 [Tribolium castaneum]
comp1173_c0_seq1	T-complex protein 1 subunit theta, putative [Pediculus humanus corporis] gi|212509512|gb|EEB12881.1| T-complex protein 1 subunit theta, putative [Pediculus humanus corporis]
comp7841_c0_seq1	serine/threonine-protein kinase VRK1, putative [Pediculus humanus corporis] gi|212515273|gb|EEB17444.1| serine/threonine-protein kinase VRK1, putative [Pediculus humanus corporis]
comp7498_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp2875_c0_seq1	GM16890 [Drosophila sechellia] gi|194130073|gb|EDW52116.1| GM16890 [Drosophila sechellia]
comp205_c0_seq1	PREDICTED: similar to ribosomal protein S5 [Nasonia vitripennis]
comp5982_c0_seq1	PREDICTED: similar to DNA replication licensing factor MCM3 [Tribolium castaneum] gi|270015933|gb|EFA12381.1| hypothetical protein TcasGA2_TC002088 [Tribolium castaneum]
comp447_c0_seq1	Inositol monophosphatase [Camponotus floridanus]
comp3219_c0_seq1	Ubiquitin carboxyl-terminal hydrolase 32 [Harpegnathos saltator]
comp5225_c0_seq1	PREDICTED: hypothetical protein LOC100636472 [Amphimedon queenslandica]
comp10352_c0_seq1	PREDICTED: bone morphogenetic protein 3-like [Oryctolagus cuniculus]
comp11047_c0_seq1	AGAP004465-PA [Anopheles gambiae str. PEST] gi|55240843|gb|EAA09266.2| AGAP004465-PA [Anopheles gambiae str. PEST]
comp3210_c0_seq4	glucose transporter, putative [Pediculus humanus corporis] gi|212517330|gb|EEB19241.1| glucose transporter, putative [Pediculus humanus corporis]
comp5462_c0_seq1	pre-mRNA-splicing factor clf-1, putative [Pediculus humanus corporis] gi|212509867|gb|EEB13153.1| pre-mRNA-splicing factor clf-1, putative [Pediculus humanus corporis]
comp8057_c0_seq1	hypothetical protein AaeL_AAEL002691 [Aedes aegypti] gi|108881878|gb|EAT46103.1| conserved hypothetical protein [Aedes aegypti]
comp4332_c0_seq1	Brain tumor protein [Harpegnathos saltator]
comp3447_c0_seq1	DnaJ domain containing protein [Heliconius melpomene]
comp3332_c0_seq1	N-myristoyltransferase, putative [Glyptapanteles indiensis]
comp6144_c0_seq1	PREDICTED: BAG family molecular chaperone regulator 2-like [Apis mellifera]

comp6807_c0_seq1	conserved hypothetical protein [Culex quinquefasciatus] gi|167862652|gb|EDS26035.1| conserved hypothetical protein [Culex quinquefasciatus]
comp6836_c0_seq1	hypothetical protein FOXB_13274 [Fusarium oxysporum Fo5176]
comp3555_c0_seq1	cell division cycle 20 [Acyrthosiphon pisum]
comp5641_c0_seq1	XPA-binding protein 1 [Culex quinquefasciatus] gi|167873024|gb|EDS36407.1| XPA-binding protein 1 [Culex quinquefasciatus]
comp3312_c0_seq1	JAB-MPN domain protein [Bombyx mori] gi|221579605|gb|ACM24339.1| JAB-MPN domain protein [Bombyx mori]
comp4545_c0_seq1	p21-activated protein kinase-interacting protein 1-like protein [Acromyrmex echinatior]
comp10743_c0_seq1	sentrin/sumo-specific protease, putative [Pediculus humanus corporis] gi|212518562|gb|EEB20308.1| sentrin/sumo-specific protease, putative [Pediculus humanus corporis]
comp392_c0_seq1	nucleoplasmin isoform 1-like protein [Maconellicoccus hirsutus]
comp3848_c0_seq1	Protein 4.1-like protein [Harpegnathos saltator]
comp7610_c0_seq1	PREDICTED: kanadaptin [Acyrthosiphon pisum]
comp1846_c0_seq1	PREDICTED: similar to proteasome zeta subunit [Tribolium castaneum] gi|270009423|gb|EFA05871.1| hypothetical protein TcasGA2_TC008671 [Tribolium castaneum]
comp9351_c0_seq1	PREDICTED: transcription elongation factor B polypeptide 3-like [Bombus terrestris]
comp178_c0_seq1	40S ribosomal protein S8 [Triatoma infestans]
comp1628_c0_seq1	hypothetical protein SINV_09873 [Solenopsis invicta]
comp6409_c0_seq2	Symplekin, putative [Pediculus humanus corporis] gi|212512753|gb|EEB15463.1| Symplekin, putative [Pediculus humanus corporis]
comp8083_c0_seq1	GA14724 [Drosophila pseudoobscura pseudoobscura] gi|198132043|gb|EAL28047.2| GA14724 [Drosophila pseudoobscura pseudoobscura]
comp5832_c0_seq1	PREDICTED: similar to lachesin [Tribolium castaneum] gi|270008732|gb|EFA05180.1| hypothetical protein TcasGA2_TC015310 [Tribolium castaneum]
comp556_c0_seq3	PREDICTED: ATP-dependent RNA helicase p62-like isoform 1 [Acyrthosiphon pisum]
comp8734_c0_seq1	PREDICTED: hypothetical protein LOC100161816 [Acyrthosiphon pisum]
comp9867_c0_seq1	PREDICTED: probable ATP-dependent RNA helicase DDX11-like [Acyrthosiphon pisum]
comp9088_c0_seq1	PREDICTED: WD40 repeat-containing protein SMU1-like isoform 1 [Apis mellifera]
comp2679_c0_seq1	GATAd [Tribolium castaneum]
comp4767_c0_seq1	PREDICTED: similar to Bm44 [Nasonia vitripennis]
comp551_c0_seq1	ribosomal protein L23A [Triatoma matogrossensis]
comp648_c0_seq1	PREDICTED: probable nucleolar GTP-binding protein 1-like [Acyrthosiphon pisum]
comp394_c0_seq1	vitellogenin [Trigonotylus caelestialium]
comp4244_c0_seq1	PREDICTED: protein LTV1 homolog [Acyrthosiphon pisum]
comp12137_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit beta-like [Bombus terrestris]

comp2966_c0_seq1	zinc finger protein 14 [Culex quinquefasciatus] gi|167876615|gb|EDS39998.1| zinc finger protein 14 [Culex quinquefasciatus]
comp4660_c0_seq1	
comp3722_c0_seq1	GI19579 [Drosophila mojavensis] gi|193909571|gb|EDW08438.1| GI19579 [Drosophila mojavensis]
comp8014_c0_seq1	Huntingtin [Camponotus floridanus]
comp5529_c0_seq1	PREDICTED: similar to replication factor C, 37-kDa subunit, putative [Tribolium castaneum] gi|270006308|gb|EFA02756.1| hypothetical protein TcasGA2_TC008489 [Tribolium castaneum]
comp233_c0_seq1	ribosomal protein S10 [Chrysomela tremulae]
comp1357_c0_seq2	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp11484_c0_seq1	Melanotransferrin [Camponotus floridanus]
comp5657_c0_seq4	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Q [Harpegnathos saltator]
comp369_c0_seq1	ribosomal protein S15Aa, isoform D [Drosophila melanogaster] gi|24641743|ref|NP_727690.1| ribosomal protein S15Aa, isoform A [Drosophila melanogaster] >gi|24641747|ref|NP_727692.1| ribosomal protein S15Aa, isoform C [Drosophila melanogaster] >gi|24641750|ref|NP_727693.1| ribosomal protein S15Aa, isoform E [Drosophila melanogaster] >gi|281360807|ref|NP_001162738.1| ribosomal protein S15Aa, isoform F [Drosophila melanogaster] >gi|125983534|ref|XP_001355532.1| GA15195 [Drosophila pseudoobscura pseudoobscura] >gi|194768000|ref|XP_001966102.1| GF19502 [Drosophila ananassae] >gi|194895562|ref|XP_001978283.1| GG19508 [Drosophila erecta] >gi|195059055|ref|XP_001995555.1| GH17815 [Drosophila grimshawi] >gi|195133640|ref|XP_002011247.1| GI16425 [Drosophila mojavensis] >gi|195168739|ref|XP_002025188.1| GL26726 [Drosophila persimilis] >gi|195352846|ref|XP_002042922.1| GM11496 [Drosophila sechellia] >gi|195398721|ref|XP_002057969.1| GJ15828 [Drosophila virilis] >gi|195456726|ref|XP_002075260.1| GK16027 [Drosophila willistoni] >gi|195478247|ref|XP_002100454.1| RpS15Aa [Drosophila yakuba] >gi|195566562|ref|XP_002106849.1| GD15889 [Drosophila simulans] >gi|1350954|sp|P48149.2|RS15A_DROME RecName: Full=40S ribosomal protein S15Aa >gi|60396627|sp|Q6XIM8.3|RS15A_DROYA RecName: Full=40S ribosomal protein S15a >gi|311606|emb|CAA79771.1| ribosomal
comp519_c0_seq1	10 kDa heat shock protein, putative [Pediculus humanus corporis] gi|212513354|gb|EEB15945.1| 10 kDa heat shock protein, putative [Pediculus humanus corporis]
comp3363_c0_seq1	PREDICTED: DNA-directed RNA polymerase III subunit RPC5-like [Bombus terrestris]
comp45_c0_seq1	elongation factor 1 alpha [Gryllus bimaculatus] gi|305377018|dbj|BAJ15872.1| elongation factor 1 alpha [Gryllus bimaculatus]
comp3074_c0_seq1	PREDICTED: similar to CG1078 CG1078-PA [Tribolium castaneum] gi|270006693|gb|EFA03141.1| hypothetical protein TcasGA2_TC013053 [Tribolium castaneum]
comp440_c0_seq6	ubiquitin-protein ligase/zinc ion binding protein [Triticum aestivum]

comp8334_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212508879|gb|EEB12439.1| conserved hypothetical protein [Pediculus humanus corporis]
comp9691_c0_seq1	golgi-specific brefeldin A-resistance guanine nucleotide exchange factor, putative [Pediculus humanus corporis] gi|212515878|gb|EEB17950.1| golgi-specific brefeldin A-resistance guanine nucleotide exchange factor, putative [Pediculus humanus corporis]
comp6255_c0_seq1	hypothetical protein SINV_05429 [Solenopsis invicta]
comp5609_c0_seq1	PREDICTED: u3 small nucleolar RNA-associated protein 15 homolog [Apis mellifera]
comp4595_c0_seq1	PREDICTED: signal recognition particle 72 kDa protein-like [Apis mellifera]
comp2854_c0_seq1	
comp6471_c0_seq2	PREDICTED: LOW QUALITY PROTEIN: integrator complex subunit 3 homolog [Bombus terrestris]
comp3330_c0_seq1	PREDICTED: c-Myc-binding protein-like [Bombus terrestris]
comp7200_c0_seq1	PREDICTED: lymphoid-specific helicase-like [Acyrthosiphon pisum]
comp576_c0_seq2	
comp2436_c0_seq1	PREDICTED: midasin-like [Bombus terrestris]
comp1739_c0_seq1	
comp4845_c0_seq1	secreted protein [Ixodes scapularis] gi|215505493|gb|EEC14987.1| secreted protein [Ixodes scapularis]
comp2791_c0_seq1	lysine-specific histone demethylase, putative [Ixodes scapularis] gi|215501670|gb|EEC11164.1| lysine-specific histone demethylase, putative [Ixodes scapularis]
comp7622_c0_seq3	PREDICTED: ethanolaminephosphotransferase 1-like [Acyrthosiphon pisum]
comp4324_c0_seq1	PREDICTED: 28S ribosomal protein S35, mitochondrial-like [Acyrthosiphon pisum]
comp7418_c0_seq1	PREDICTED: similar to Zinc finger protein 43 (Zinc finger protein 39) (Zinc protein HTF6) (Zinc finger protein KOX27) [Tribolium castaneum]
comp3888_c0_seq1	thymidine kinase-like [Acyrthosiphon pisum] gi|239790179|dbj|BAH71666.1| ACYPI006294 [Acyrthosiphon pisum]
comp5074_c0_seq1	
comp2325_c0_seq1	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP2-like [Acyrthosiphon pisum]
comp5454_c0_seq1	AGAP005341-PA [Anopheles gambiae str. PEST] gi|157015371|gb|EDO63649.1| AGAP005341-PA [Anopheles gambiae str. PEST]
comp194_c0_seq1	PREDICTED: similar to rap55 [Nasonia vitripennis]
comp5711_c0_seq1	PREDICTED: similar to Zinc finger RAD18 domain-containing protein C1orf124 [Tribolium castaneum] gi|270004629|gb|EFA01077.1| hypothetical protein TcasGA2_TC003998 [Tribolium castaneum]
comp2877_c0_seq1	hypothetical protein TcasGA2_TC006313 [Tribolium castaneum]
comp1610_c0_seq2	
comp1658_c0_seq1	
comp3073_c0_seq1	PREDICTED: putative U5 small nuclear ribonucleoprotein 200 kDa helicase-like [Bombus terrestris]

comp693_c0_seq1	PREDICTED: hypothetical protein LOC100168603 isoform 1 [Acyrthosiphon pisum] gi|328717699|ref|XP_003246281.1| PREDICTED: hypothetical protein LOC100168603 isoform 2 [Acyrthosiphon pisum]
comp8688_c0_seq1	hect E3 ubiquitin ligase, putative [Pediculus humanus corporis] gi|212512172|gb|EEB14993.1| hect E3 ubiquitin ligase, putative [Pediculus humanus corporis]
comp4142_c0_seq1	Peptidyl-prolyl cis-trans isomerase-like 4 [Acromyrmex echinatior]
comp2284_c0_seq1	39S ribosomal protein L13-like [Acyrthosiphon pisum] gi|239789841|dbj|BAH71519.1| ACYPI007195 [Acyrthosiphon pisum]
comp1166_c0_seq1	putative RNA polymerase II transcriptional coactivator [Antheraea yamamai]
comp3850_c0_seq1	formin 1,2/cappuccino, putative [Pediculus humanus corporis] gi|212518364|gb|EEB20117.1| formin 1,2/cappuccino, putative [Pediculus humanus corporis]
comp6512_c0_seq1	PREDICTED: transcription termination factor 2-like isoform 1 [Acyrthosiphon pisum] gi|328713458|ref|XP_003245082.1| PREDICTED: transcription termination factor 2-like isoform 2 [Acyrthosiphon pisum]
comp6779_c0_seq1	PREDICTED: facilitated trehalose transporter Tret1-like [Acyrthosiphon pisum]
comp5828_c0_seq1	Nuclear pore complex protein Nup133, putative [Pediculus humanus corporis] gi|212516399|gb|EEB18412.1| Nuclear pore complex protein Nup133, putative [Pediculus humanus corporis]
comp6009_c0_seq2	conserved hypothetical protein [Pediculus humanus corporis] gi|212515980|gb|EEB18045.1| conserved hypothetical protein [Pediculus humanus corporis]
comp243_c0_seq1	
comp3268_c0_seq1	
comp3755_c0_seq1	hypothetical protein BRAFLDRAFT_66468 [Branchiostoma floridae] gi|229282591|gb|EEN53340.1| hypothetical protein BRAFLDRAFT_66468 [Branchiostoma floridae]
comp5509_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212517725|gb|EEB19564.1| conserved hypothetical protein [Pediculus humanus corporis]
comp603_c0_seq1	Protein shuttle craft [Harpegnathos saltator]
comp3004_c0_seq1	PREDICTED: hypothetical protein LOC100166196 [Acyrthosiphon pisum]
comp8246_c0_seq1	PREDICTED: tripartite motif-containing 3-like [Saccoglossus kowalevskii]
comp3572_c0_seq2	PREDICTED: hypothetical protein LOC100651932 [Bombus terrestris]
comp1366_c0_seq1	hypothetical protein SINV_04585 [Solenopsis invicta]
comp9335_c0_seq1	protein EMSY, putative [Ixodes scapularis] gi|215499195|gb|EEC08689.1| protein EMSY, putative [Ixodes scapularis]
comp6148_c0_seq1	Probable cleavage and polyadenylation specificity factor subunit 2 [Camponotus floridanus]
comp3308_c0_seq1	translation initiation factor-3 (IF3), putative [Aedes aegypti] gi|108876153|gb|EAT40378.1| translation initiation factor-3 (IF3), putative [Aedes aegypti]

comp4643_c0_seq3	PREDICTED: patched domain-containing protein 3-like [Acyrthosiphon pisum]
comp8229_c0_seq1	PREDICTED: chromatin accessibility complex protein 1-like [Apis mellifera]
comp6245_c0_seq1	Wolframin [Camponotus floridanus]
comp3333_c0_seq1	hypothetical protein SINV_07726 [Solenopsis invicta]
comp6354_c0_seq2	PREDICTED: REST corepressor 3-like isoform 4 [Bombus terrestris]
comp6637_c0_seq1	daughter of sevenless-like [Nasonia vitripennis]
comp10431_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: tetratricopeptide repeat protein 28-like [Bombus terrestris]
comp4699_c0_seq1	hypothetical protein DAPPUDRAFT_300799 [Daphnia pulex]
comp6773_c0_seq1	PREDICTED: ragulator complex protein LAMTOR3-A-like [Apis mellifera]
comp2354_c0_seq1	Alpha-aminoadipic semialdehyde synthase, mitochondrial [Camponotus floridanus]
comp1356_c0_seq1	PREDICTED: SAFB-like transcription modulator-like [Apis mellifera]
comp4795_c0_seq1	fmr [Gryllus bimaculatus]
comp4199_c0_seq5	PREDICTED: splicing factor, arginine/serine-rich 18-like [Apis mellifera]
comp6221_c0_seq1	PREDICTED: similar to MGC84305 protein [Strongylocentrotus purpuratus] gi|115970867|ref|XP_001190992.1| PREDICTED: similar to MGC84305 protein [Strongylocentrotus purpuratus]
comp2928_c3_seq2	PREDICTED: probable ATP-dependent RNA helicase DDX52-like [Bombus terrestris]
comp1022_c0_seq1	PREDICTED: similar to chaperonin [Tribolium castaneum] gi|270002664|gb|EEZ99111.1| hypothetical protein TcasGA2_TC005004 [Tribolium castaneum]
comp792_c0_seq1	PREDICTED: proliferation-associated protein 2G4-like [Bombus terrestris]
comp5721_c0_seq1	GK10605 [Drosophila willistoni] gi|194164145|gb|EDW79046.1| GK10605 [Drosophila willistoni]
comp11284_c0_seq1	enhancer of filamentation 1 [Apis mellifera]
comp2998_c0_seq1	PREDICTED: similar to protein phosphatase-5 [Tribolium castaneum] gi|270009672|gb|EFA06120.1| hypothetical protein TcasGA2_TC008963 [Tribolium castaneum]
comp6968_c0_seq1	PREDICTED: nuclear pore complex protein Nup160 homolog [Acyrthosiphon pisum]
comp5540_c0_seq1	GE18291 [Drosophila yakuba] gi|194174027|gb|EDW87638.1| GE18291 [Drosophila yakuba]
comp5239_c0_seq1	THO complex subunit 1 [Harpegnathos saltator]
comp3933_c0_seq1	mex-3 protein [Tribolium castaneum] gi|218464687|emb|CAM28380.2| KH domain protein [Tribolium castaneum]
comp4289_c0_seq1	PREDICTED: probable ATP-dependent RNA helicase DDX28-like [Acyrthosiphon pisum]
comp1211_c0_seq4	structure specific recognition protein-like [Acyrthosiphon pisum]
comp5713_c0_seq1	GH22229 [Drosophila grimshawi] gi|193895784|gb|EDV94650.1| GH22229 [Drosophila grimshawi]

comp10204_c0_seq1	PREDICTED: similar to plexin A CG11081-PA [Tribolium castaneum] gi|270015104|gb|EFA11552.1| plexin A [Tribolium castaneum]
comp5616_c0_seq1	glycerol kinase [Aedes aegypti] gi|108879512|gb|EAT43737.1| glycerol kinase [Aedes aegypti]
comp2506_c0_seq1	Coatomer subunit beta', putative [Pediculus humanus corporis] gi|212508406|gb|EEB12118.1| Coatomer subunit beta', putative [Pediculus humanus corporis]
comp442_c0_seq1	ribosomal protein S29 [Chrysomela tremulae]
comp3276_c0_seq1	Ubiquitin thioesterase otubain-like [Camponotus floridanus]
comp3250_c0_seq1	PREDICTED: similar to delta-aminolevulinate dehydratase [Nasonia vitripennis]
comp4947_c0_seq1	PREDICTED: glutathione S-transferase omega-1-like [Bombus terrestris]
comp2482_c0_seq1	Guanine nucleotide-binding protein-like 1 [Camponotus floridanus]
comp1362_c0_seq2	PREDICTED: similar to GA11814-PA [Tribolium castaneum] gi|270004178|gb|EFA00626.1| hypothetical protein TcasGA2_TC003502 [Tribolium castaneum]
comp4544_c0_seq1	pentatricopeptide repeat domain 1 [Acyrthosiphon pisum]
comp9343_c0_seq1	hypothetical protein AaeL_AAEL011476 [Aedes aegypti] gi|94469314|gb|ABF18506.1| hypothetical conserved protein [Aedes aegypti] >gi|108872218|gb|EAT36443.1| conserved hypothetical protein [Aedes aegypti]
comp3218_c0_seq1	Cullin-associated NEDD8-dissociated protein, putative [Pediculus humanus corporis] gi|212518736|gb|EEB20457.1| Cullin-associated NEDD8-dissociated protein, putative [Pediculus humanus corporis]
comp11108_c0_seq1	
comp5371_c0_seq2	conserved hypothetical protein [Pediculus humanus corporis] gi|212508750|gb|EEB12347.1| conserved hypothetical protein [Pediculus humanus corporis]
comp1622_c1_seq1	RecName: Full=Heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog gi|10107|emb|CAA38481.1| mammalian A1, A2 /B1 hnRNP homologue [Schistocerca americana]
comp8897_c0_seq1	ornithine cyclodeaminase, putative [Pediculus humanus corporis] gi|212509614|gb|EEB12975.1| ornithine cyclodeaminase, putative [Pediculus humanus corporis]
comp318_c0_seq3	
comp6933_c0_seq1	PREDICTED: similar to CG3172-PA [Nasonia vitripennis]
comp3443_c0_seq1	hypothetical protein DAPPUDRAFT_218645 [Daphnia pulex]
comp3974_c0_seq1	hypothetical protein AND_13423 [Anopheles darlingi]
comp3386_c0_seq1	PREDICTED: similar to cleavage stimulation factor 64-kDa subunit [Nasonia vitripennis]
comp1849_c0_seq4	mcfdp2, putative [Pediculus humanus corporis] gi|212514434|gb|EEB16758.1| mcfdp2, putative [Pediculus humanus corporis]
comp2511_c0_seq1	PREDICTED: OV-16 antigen-like [Apis mellifera]
comp1659_c0_seq1	hypothetical protein SINV_11622 [Solenopsis invicta]
comp1195_c0_seq1	Protein bicaudal C [Harpegnathos saltator]
comp6834_c0_seq1	PREDICTED: hypothetical protein LOC100571834 [Acyrthosiphon pisum]

comp8066_c0_seq2	PREDICTED: hypothetical protein LOC100163498 isoform 1 [Acyrthosiphon pisum]
comp3002_c0_seq1	PREDICTED: kinesin-like protein KIF2A-like isoform 1 [Acyrthosiphon pisum]
comp4340_c0_seq1	PREDICTED: hypothetical protein LOC100162351 [Acyrthosiphon pisum]
comp5974_c0_seq1	Putative helicase Mov10l1 [Acromyrmex echinatior]
comp8094_c0_seq1	PREDICTED: similar to pinn [Tribolium castaneum]
comp136_c0_seq1	60S ribosomal protein L27a [Brugia malayi] gi|158601982|gb|EDP38710.1| 60S ribosomal protein L27a, putative [Brugia malayi]
comp2421_c0_seq1	PREDICTED: pescadillo homolog [Bombus terrestris]
comp6345_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Tribolium castaneum] gi|270012614|gb|EFA09062.1| hypothetical protein TcasGA2_TC006777 [Tribolium castaneum]
comp5534_c0_seq1	sin3a-associated protein sap130, putative [Pediculus humanus corporis] gi|212508545|gb|EEB12193.1| sin3a-associated protein sap130, putative [Pediculus humanus corporis]
comp5525_c0_seq1	hypothetical protein TcasGA2_TC030645 [Tribolium castaneum]
comp2359_c0_seq1	PREDICTED: similar to Rpt1 CG1341-PA [Tribolium castaneum] gi|270012350|gb|EFA08798.1| hypothetical protein TcasGA2_TC006492 [Tribolium castaneum]
comp4148_c0_seq1	Cell division cycle 2-like protein kinase 5 [Camponotus floridanus]
comp5062_c0_seq1	GH12492 [Drosophila grimshawi] gi|193900864|gb|EDV99730.1| GH12492 [Drosophila grimshawi]
comp1811_c0_seq1	PREDICTED: 26S proteasome non-ATPase regulatory subunit 2-like [Acyrthosiphon pisum]
comp4648_c0_seq1	PREDICTED: 39S ribosomal protein L44, mitochondrial-like [Acyrthosiphon pisum]
comp5564_c0_seq1	PREDICTED: similar to zinc finger, AN1 type domain 2B [Tribolium castaneum] gi|270005743|gb|EFA02191.1| hypothetical protein TcasGA2_TC007847 [Tribolium castaneum]
comp1191_c0_seq1	
comp982_c0_seq2	Putative glycerol kinase 3 [Camponotus floridanus]
comp6689_c0_seq1	G patch domain-containing protein 1-like protein [Acromyrmex echinatior]
comp13084_c0_seq3	PREDICTED: myosin-XV isoform 1 [Acyrthosiphon pisum]
comp5412_c0_seq1	PREDICTED: notchless protein homolog 1-like [Acyrthosiphon pisum]
comp16275_c0_seq1	Brefeldin A-inhibited guanine nucleotide-exchange protein, putative [Pediculus humanus corporis] gi|212509094|gb|EEB12582.1| Brefeldin A-inhibited guanine nucleotide-exchange protein, putative [Pediculus humanus corporis]
comp660_c0_seq1	E1b-55kD-associated protein, putative [Pediculus humanus corporis] gi|212508552|gb|EEB12200.1| E1b-55kD-associated protein, putative [Pediculus humanus corporis]
comp1263_c0_seq1	PREDICTED: similar to CG10206 [Nasonia vitripennis]
comp11663_c0_seq1	hypothetical protein TcasGA2_TC010431 [Tribolium castaneum]

comp2015_c0_seq1	PREDICTED: fumarylacetoacetate hydrolase domain-containing protein 2-like [Acyrthosiphon pisum]
comp5372_c0_seq1	PREDICTED: pre-mRNA branch site p14-like protein-like [Apis mellifera]
comp2057_c0_seq4	Blimp-1 [Tribolium castaneum]
comp7285_c0_seq2	PREDICTED: similar to MTA1-like CG2244-PB [Tribolium castaneum] gi|270009558|gb|EFA06006.1| hypothetical protein TcasGA2_TC008832 [Tribolium castaneum]
comp8465_c0_seq1	cytochrome P450 [Bemisia tabaci]
comp6413_c0_seq2	PREDICTED: DNA polymerase delta subunit 2-like [Acyrthosiphon pisum]
comp3126_c0_seq1	PREDICTED: similar to mitotic checkpoint protein and poly(a)+ RNA export protein [Nasonia vitripennis]
comp3455_c0_seq1	PREDICTED: similar to dolichyl-phosphate mannosyltransferase [Tribolium castaneum]
comp9468_c0_seq1	GK12556 [Drosophila willistoni] gi|194163804|gb|EDW78705.1| GK12556 [Drosophila willistoni]
comp196_c0_seq1	PREDICTED: similar to ribosome-associated protein P40 [Tribolium castaneum] gi|270012401|gb|EFA08849.1| hypothetical protein TcasGA2_TC006550 [Tribolium castaneum]
comp4961_c0_seq1	PREDICTED: similar to nuclear import 7 homolog [Tribolium castaneum] gi|270016870|gb|EFA13316.1| hypothetical protein TcasGA2_TC006900 [Tribolium castaneum]
comp4698_c0_seq1	conserved hypothetical protein [Rickettsia endosymbiont of Ixodes scapularis] gi|239922565|gb|EER22589.1| conserved hypothetical protein [Rickettsia endosymbiont of Ixodes scapularis]
comp9863_c0_seq2	PREDICTED: similar to procollagen-lysine,2-oxoglutarate 5-dioxygenase [Nasonia vitripennis]
comp10934_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212517537|gb|EEB19417.1| conserved hypothetical protein [Pediculus humanus corporis]
comp7172_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: cirhin-like [Bombus terrestris]
comp4401_c0_seq1	hypothetical protein AND_06035 [Anopheles darlingi]
comp5687_c0_seq1	PREDICTED: BRCA1-associated protein-like [Bombus terrestris]
comp8039_c0_seq1	conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA] gi|251847969|gb|EES75935.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39BFAA]
comp1829_c0_seq1	nucleolar phosphoprotein [Bombyx mori] gi|109706827|gb|ABG43000.1| nucleolar phosphoprotein [Bombyx mori]
comp1330_c0_seq1	uv excision repair protein rad23, putative [Pediculus humanus corporis] gi|212517628|gb|EEB19493.1| uv excision repair protein rad23, putative [Pediculus humanus corporis]
comp6288_c0_seq1	PREDICTED: similar to CG7488 CG7488-PA [Tribolium castaneum] gi|270011756|gb|EFA08204.1| hypothetical protein TcasGA2_TC005831 [Tribolium castaneum]
comp5247_c0_seq1	Fizzy-related protein-like protein [Harpegnathos saltator]
comp1411_c0_seq1	PREDICTED: similar to GA11007-PA [Nasonia vitripennis]
comp3645_c0_seq1	hypothetical protein SINV_01596 [Solenopsis invicta]
comp4999_c0_seq1	ACYPI001763 [Acyrthosiphon pisum]

comp1699_c0_seq1	PREDICTED: similar to formin 1,2/cappuccino [Tribolium castaneum] gi|270014279|gb|EFA10727.1| cappuccino [Tribolium castaneum]
comp6038_c0_seq1	PREDICTED: similar to pom1 [Nasonia vitripennis]
comp5494_c0_seq1	RNA-binding protein with serine-rich domain 1 [Dicentrarchus labrax]
comp1035_c0_seq1	PREDICTED: hypothetical protein LOC726887 [Apis mellifera]
comp1487_c0_seq1	viral A-type inclusion protein [Trichomonas vaginalis G3] gi|121905960|gb|EAY10879.1| viral A-type inclusion protein, putative [Trichomonas vaginalis G3]
comp7726_c0_seq1	PREDICTED: similar to virilizer CG3496-PA [Tribolium castaneum] gi|270003474|gb|EEZ99921.1| hypothetical protein TcasGA2_TC002713 [Tribolium castaneum]
comp6380_c0_seq1	PREDICTED: tetratricopeptide repeat protein 27-like [Acyrthosiphon pisum]
comp6180_c0_seq1	PREDICTED: similar to NC2alpha CG10318-PA [Tribolium castaneum]
comp8904_c0_seq1	GF18252 [Drosophila ananassae] gi|190627455|gb|EDV42979.1| GF18252 [Drosophila ananassae]
comp6113_c0_seq1	DNA polymerase delta catalytic subunit [Bemisia tabaci]
comp1347_c0_seq1	
comp3713_c0_seq1	COP9 signalosome complex subunit, putative [Pediculus humanus corporis] gi|212506922|gb|EEB10993.1| COP9 signalosome complex subunit, putative [Pediculus humanus corporis]
comp7875_c0_seq1	PREDICTED: tubulin gamma-1 chain isoform 1 [Apis mellifera]
comp5810_c0_seq1	inositol monophosphatase family domain containing protein [Pediculus humanus corporis] gi|212513972|gb|EEB16370.1| inositol monophosphatase family domain containing protein [Pediculus humanus corporis]
comp194_c0_seq2	PREDICTED: similar to rap55 [Nasonia vitripennis]
comp604_c0_seq1	PREDICTED: similar to eukaryotic translation initiation factor 3, theta subunit [Tribolium castaneum] gi|270013675|gb|EFA10123.1| hypothetical protein TcasGA2_TC012303 [Tribolium castaneum]
comp1715_c0_seq1	
comp318_c0_seq1	
comp7134_c0_seq1	PREDICTED: uncharacterized protein C12orf4 homolog [Apis mellifera]
comp2061_c0_seq1	eukaryotic translation initiation factor 3 subunit 12-like protein [Triatoma infestans]
comp4707_c0_seq1	PREDICTED: deoxynucleotidyltransferase terminal-interacting protein 2-like [Bombus terrestris]
comp7641_c0_seq1	Nucleoporin Nup37 [Camponotus floridanus]
comp7717_c0_seq1	
comp8148_c0_seq1	PREDICTED: similar to CG10903 CG10903-PA [Tribolium castaneum] gi|270008360|gb|EFA04808.1| hypothetical protein TcasGA2_TC014857 [Tribolium castaneum]
comp5488_c0_seq1	Nuclear nucleic acid-binding protein C1D [Camponotus floridanus]

comp5144_c0_seq1	GK18401 [Drosophila willistoni] gi|194171583|gb|EDW86484.1| GK18401 [Drosophila willistoni]
comp8981_c0_seq1	PREDICTED: similar to ENSANGP00000023686 [Nasonia vitripennis]
comp3486_c0_seq1	
comp6677_c0_seq1	secreted phosphatidylethanolamine binding protein [Glossina morsitans morsitans]
comp2058_c1_seq1	Folate receptor alpha precursor, putative [Pediculus humanus corporis] gi|212515246|gb|EEB17417.1| Folate receptor alpha precursor, putative [Pediculus humanus corporis]
comp179_c0_seq1	GJ17775 [Drosophila virilis] gi|194149287|gb|EDW64985.1| GJ17775 [Drosophila virilis]
comp5161_c0_seq1	wd-repeat protein [Aedes aegypti] gi|122106389|sp|Q17BB0.1|WDR12_AEDAE RecName: Full=Ribosome biogenesis protein WDR12 homolog >gi|108879311|gb|EAT43536.1| wd-repeat protein [Aedes aegypti]
comp10400_c0_seq1	phosphatidylethanolamine-binding protein [Aedes aegypti] gi|108870917|gb|EAT35142.1| phosphatidylethanolamine-binding protein [Aedes aegypti]
comp6000_c0_seq1	DEP domain containing 1a [Danio rerio]
comp2228_c0_seq1	
comp9008_c0_seq1	PREDICTED: cryptochrome-1-like [Bombus terrestris]
comp4165_c0_seq1	PREDICTED: similar to Phosphorylated adaptor for RNA export, putative [Tribolium castaneum] gi|270009528|gb|EFA05976.1| hypothetical protein TcasGA2_TC008802 [Tribolium castaneum]
comp7753_c0_seq1	Protein FAM50-like protein [Harpegnathos saltator]
comp8738_c0_seq1	probable O-sialoglycoprotein endopeptidase [Acyrthosiphon pisum] gi|239790727|dbj|BAH71906.1| ACYPI004911 [Acyrthosiphon pisum]
comp7575_c0_seq1	putative H3K9 methyltransferase [Lepisma saccharina]
comp3138_c0_seq1	PREDICTED: probable ATP-dependent RNA helicase pitchoune-like [Bombus terrestris]
comp41_c0_seq6	PREDICTED: similar to nucleolar KKE/D repeat protein; DmNOP56 [Nasonia vitripennis]
comp15893_c0_seq1	hypothetical protein Phum_PHUM299820 [Pediculus humanus corporis] gi|212511457|gb|EEB14436.1| hypothetical protein Phum_PHUM299820 [Pediculus humanus corporis]
comp1157_c0_seq1	transformer-2 sex-determining protein, putative [Pediculus humanus corporis] gi|212517371|gb|EEB19282.1| transformer-2 sex-determining protein, putative [Pediculus humanus corporis]
comp1586_c0_seq1	Tubulin beta-6 chain [Dicentrarchus labrax]
comp4903_c0_seq1	Metaxin-1, putative [Pediculus humanus corporis] gi|212513912|gb|EEB16319.1| Metaxin-1, putative [Pediculus humanus corporis]
comp10024_c0_seq1	Exosome component 10 [Acromyrmex echinatior]
comp4028_c0_seq1	ankyrin repeat protein [Trichomonas vaginalis G3] gi|121912377|gb|EAY17199.1| ankyrin repeat protein, putative [Trichomonas vaginalis G3]
comp4714_c0_seq1	PREDICTED: ruvB-like 2-like [Bombus terrestris]

comp5099_c0_seq1	NEDD8-activating enzyme E1 regulatory subunit [Camponotus floridanus]
comp9803_c0_seq1	PREDICTED: polyphosphoinositide phosphatase [Apis mellifera]
comp10399_c0_seq1	PREDICTED: DNA helicase INO80-like [Bombus terrestris]
comp6369_c0_seq1	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform 2 [Acyrthosiphon pisum]
comp11706_c1_seq1	PREDICTED: similar to tuberin [Tribolium castaneum]
comp2080_c0_seq1	Transcription factor GATA-4 [Camponotus floridanus]
comp906_c0_seq1	Hrp65 protein, putative [Pediculus humanus corporis] gi|212515645|gb|EEB17750.1| Hrp65 protein, putative [Pediculus humanus corporis]
comp13_c0_seq1	GA28568 [Drosophila pseudoobscura pseudoobscura] gi|198151215|gb|EDY74106.1| GA28568 [Drosophila pseudoobscura pseudoobscura]
comp1789_c0_seq1	PREDICTED: eukaryotic translation initiation factor 4H-like [Apis mellifera]
comp1400_c0_seq1	
comp4498_c0_seq1	
comp3328_c0_seq1	PREDICTED: similar to GA18228-PA [Nasonia vitripennis]
comp2963_c0_seq1	PREDICTED: hypothetical protein LOC100160600 [Acyrthosiphon pisum]
comp9159_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212517061|gb|EEB19008.1| conserved hypothetical protein [Pediculus humanus corporis]
comp2794_c0_seq1	PREDICTED: similar to histone H1 [Nasonia vitripennis]
comp2209_c0_seq1	hypothetical protein SINV_15099 [Solenopsis invicta]
comp5874_c0_seq1	PREDICTED: f-box only protein 22 [Macaca mulatta]
comp7349_c0_seq1	hypothetical protein DAPPUDRAFT_302493 [Daphnia pulex]
comp2948_c0_seq1	Coatomer subunit gamma-2, putative [Pediculus humanus corporis] gi|212511156|gb|EEB14189.1| Coatomer subunit gamma-2, putative [Pediculus humanus corporis]
comp12319_c0_seq1	zinc finger protein RTS2, putative [Pediculus humanus corporis] gi|212514394|gb|EEB16724.1| zinc finger protein RTS2, putative [Pediculus humanus corporis]
comp2864_c0_seq1	mitochondrial ribosomal protein L37 [Nasonia vitripennis]
comp11451_c0_seq1	PREDICTED: periodic tryptophan protein 2 homolog [Apis mellifera]
comp6284_c0_seq1	Exportin-2 [Harpegnathos saltator]
comp4382_c0_seq1	PREDICTED: sorting nexin-6-like [Acyrthosiphon pisum]
comp9893_c0_seq1	WD-repeat protein, putative [Pediculus humanus corporis] gi|212507706|gb|EEB11568.1| WD-repeat protein, putative [Pediculus humanus corporis]
comp7138_c0_seq2	PREDICTED: similar to DnaJ-like protein [Tribolium castaneum] gi|270007594|gb|EFA04042.1| hypothetical protein TcasGA2_TC014273 [Tribolium castaneum]
comp5322_c0_seq1	PREDICTED: protein spinster-like [Acyrthosiphon pisum]
comp2002_c0_seq1	clathrin coat associated protein ap-50 [Aedes aegypti] gi|108881420|gb|EAT45645.1| clathrin coat associated protein ap-50 [Aedes aegypti]
comp2625_c1_seq1	PREDICTED: hypothetical protein LOC100163820 [Acyrthosiphon pisum]
comp5367_c1_seq2	hypothetical protein TcasGA2_TC013167 [Tribolium castaneum]

comp686_c0_seq1	hypothetical protein DAPPUDRAFT_305914 [Daphnia pulex]
comp7962_c0_seq1	hypothetical protein TcasGA2_TC004421 [Tribolium castaneum]
comp175_c0_seq1	PREDICTED: ubiquitin-like protein 7-like [Apis mellifera]
comp169_c0_seq1	
comp2986_c0_seq1	hypothetical protein TcasGA2_TC012992 [Tribolium castaneum]
comp5470_c0_seq1	hypothetical protein TcasGA2_TC014492 [Tribolium castaneum]
comp6311_c0_seq1	double-strand break repair protein MRE11 [Culex quinquefasciatus] gi|167879929|gb|EDS43312.1| double-strand break repair protein MRE11 [Culex quinquefasciatus]
comp3146_c0_seq1	PREDICTED: hypothetical protein LOC408493 [Apis mellifera]
comp10892_c0_seq1	Transmembrane protein 104-like protein [Camponotus floridanus]
comp5934_c0_seq2	
comp2295_c0_seq1	PREDICTED: hypothetical protein, partial [Saccoglossus kowalevskii]
comp5146_c0_seq2	BMP and activin membrane-bound inhibitor [Xenopus laevis] gi|57921046|gb|AAH89131.1| Bambi-A protein [Xenopus laevis]
comp293_c0_seq1	60S ribosomal protein L21-like [Acyrthosiphon pisum] gi|239788244|dbj|BAH70810.1| ACYPI006688 [Acyrthosiphon pisum]
comp5124_c0_seq1	RNA-binding protein 26 [Acromyrmex echinatior]
comp8433_c0_seq2	STE20-like serine/threonine-protein kinase [Harpegnathos saltator]
comp3203_c0_seq1	PREDICTED: ribosomal RNA-processing protein 8-like [Acyrthosiphon pisum]
comp1880_c0_seq23	paramyosin, long form, putative [Pediculus humanus corporis] gi|212509963|gb|EEB13234.1| paramyosin, long form, putative [Pediculus humanus corporis]
comp2813_c0_seq1	PREDICTED: similar to lethal (1) G0004 CG11738-PA [Tribolium castaneum] gi|270010173|gb|EFA06621.1| hypothetical protein TcasGA2_TC009539 [Tribolium castaneum]
comp2318_c0_seq2	PREDICTED: similar to putative accessory gland protein [Tribolium castaneum] gi|270012410|gb|EFA08858.1| hypothetical protein TcasGA2_TC006559 [Tribolium castaneum]
comp6174_c0_seq2	PREDICTED: similar to GA19292-PA [Tribolium castaneum] gi|270001668|gb|EEZ98115.1| hypothetical protein TcasGA2_TC000533 [Tribolium castaneum]
comp4435_c0_seq1	PREDICTED: similar to host cell factor C1 [Tribolium castaneum]
comp6947_c0_seq1	
comp7082_c0_seq1	Mediator of RNA polymerase II transcription subunit 7 [Harpegnathos saltator]
comp12845_c0_seq1	hypothetical protein TcasGA2_TC006850 [Tribolium castaneum]
comp6130_c0_seq1	PREDICTED: transcription factor AP-2-beta-like [Acyrthosiphon pisum]
comp3421_c0_seq1	28S ribosomal protein S22, mitochondrial [Acromyrmex echinatior]

comp8302_c0_seq1	Transcription initiation factor TFIID subunit 6 [Camponotus floridanus]
comp3739_c0_seq1	PREDICTED: ubiquitin carboxyl-terminal hydrolase 5-like isoform 1 [Bombus terrestris]
comp4668_c0_seq1	Arfaptin-2 [Camponotus floridanus]
comp2805_c0_seq1	Brix domain-containing protein 1-like protein [Camponotus floridanus]
comp4261_c0_seq1	hypothetical protein AND_24115 [Anopheles darlingi]
comp3618_c0_seq1	Serine/threonine-protein kinase TAO1 [Acromyrmex echinatior]
comp6344_c0_seq1	DNA polymerase subunit gamma 1, mitochondrial [Culex quinquefasciatus] gi|167873869|gb|EDS37252.1| DNA polymerase subunit gamma 1, mitochondrial [Culex quinquefasciatus]
comp3341_c0_seq1	PREDICTED: hypothetical protein LOC100165888 [Acyrthosiphon pisum]
comp321_c0_seq1	
comp3174_c0_seq1	PREDICTED: similar to mitochondrial ribosomal protein S2 CG2937-PA [Tribolium castaneum] gi|270003534|gb|EEZ99981.1| hypothetical protein TcasGA2_TC002780 [Tribolium castaneum]
comp3839_c0_seq1	membrane-associated protein, putative [Pediculus humanus corporis] gi|212516187|gb|EEB18229.1| membrane-associated protein, putative [Pediculus humanus corporis]
comp6190_c0_seq1	PREDICTED: transcription initiation factor TFIID subunit 7 isoform 2 [Apis mellifera]
comp6688_c0_seq1	UPF0539 protein CG14977 [Harpegnathos saltator]
comp7430_c0_seq1	PREDICTED: centromere/kinetochore protein zw10 homolog [Apis mellifera]
comp485_c0_seq1	E3 ubiquitin ligase [Cimex lectularius]
comp7865_c0_seq1	hypothetical protein TcasGA2_TC009313 [Tribolium castaneum]
comp171_c0_seq2	
comp2569_c0_seq1	hypothetical protein AND_11649 [Anopheles darlingi]
comp4335_c0_seq1	mitochondrial import receptor subunit tom40 [Aedes aegypti] gi|108877122|gb|EAT41347.1| mitochondrial import receptor subunit tom40 [Aedes aegypti]
comp6332_c0_seq1	conserved hypothetical protein [Culex quinquefasciatus] gi|167862630|gb|EDS26013.1| conserved hypothetical protein [Culex quinquefasciatus]
comp234_c0_seq1	ribosomal protein S27 [Xenopsylla cheopis]
comp3706_c0_seq2	PREDICTED: similar to phosphoinositide-binding protein, putative [Tribolium castaneum] gi|270006674|gb|EFA03122.1| hypothetical protein TcasGA2_TC013032 [Tribolium castaneum]
comp1714_c0_seq1	PREDICTED: cyclin-A2-like [Acyrthosiphon pisum]
comp10676_c0_seq1	PREDICTED: ras association domain-containing protein 8-like [Acyrthosiphon pisum]
comp3775_c0_seq3	hypothetical protein SINV_04875 [Solenopsis invicta]
comp1088_c0_seq1	PREDICTED: similar to AGAP009694-PA [Tribolium castaneum] gi|270001410|gb|EEZ97857.1| hypothetical protein TcasGA2_TC000229 [Tribolium castaneum]
comp6985_c0_seq1	GD19864 [Drosophila simulans] gi|194198282|gb|EDX11858.1| GD19864 [Drosophila simulans]

comp4924_c0_seq1	PREDICTED: protein kibra-like isoform 1 [Acyrthosiphon pisum]
comp3745_c0_seq1	PREDICTED: similar to protein transport protein sec23 [Tribolium castaneum] gi|270009872|gb|EFA06320.1| hypothetical protein TcasGA2_TC009191 [Tribolium castaneum]
comp7448_c0_seq1	PREDICTED: nucleolar complex protein 4 homolog B-like isoform 1 [Bombus terrestris]
comp7770_c0_seq1	hypothetical protein SINV_04879 [Solenopsis invicta]
comp6913_c0_seq1	G-protein signaling modulator, putative [Pediculus humanus corporis] gi|212514168|gb|EEB16534.1| G-protein signaling modulator, putative [Pediculus humanus corporis]
comp8099_c0_seq1	PREDICTED: charged multivesicular body protein 6-like [Bombus terrestris]
comp3236_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: regulator of chromosome condensation-like [Bombus terrestris]
comp10971_c0_seq2	PREDICTED: neurogenic locus Notch protein [Apis mellifera]
comp7593_c0_seq1	PREDICTED: hypothetical protein LOC100575146 isoform 1 [Acyrthosiphon pisum] gi|328719833|ref|XP_003246874.1| PREDICTED: hypothetical protein LOC100575146 isoform 2 [Acyrthosiphon pisum] >gi|328719835|ref|XP_003246875.1| PREDICTED: hypothetical protein LOC100575146 isoform 3 [Acyrthosiphon pisum]
comp9158_c0_seq1	PREDICTED: similar to AGAP003463-PA [Tribolium castaneum]
comp4122_c0_seq1	Endoplasmic reticulum protein ERp29, putative [Pediculus humanus corporis] gi|212510717|gb|EEB13839.1| Endoplasmic reticulum protein ERp29, putative [Pediculus humanus corporis]
comp1984_c1_seq2	PREDICTED: similar to sumo ligase [Tribolium castaneum] gi|270010268|gb|EFA06716.1| hypothetical protein TcasGA2_TC009647 [Tribolium castaneum]
comp4106_c0_seq1	COP9 signalosome complex subunit, putative [Pediculus humanus corporis] gi|212506760|gb|EEB10874.1| COP9 signalosome complex subunit, putative [Pediculus humanus corporis]
comp12735_c0_seq1	PREDICTED: UVRAG-like protein-like [Bombus terrestris]
comp1593_c0_seq1	PREDICTED: similar to proteasome beta-subunit [Nasonia vitripennis]
comp5682_c0_seq1	DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide, putative [Pediculus humanus corporis] gi|212508897|gb|EEB12451.1| DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide, putative [Pediculus humanus corporis]
comp3764_c0_seq1	Ribosome production factor 1 [Lepeophtheirus salmonis]
comp9348_c0_seq1	hypothetical protein BRAFLDRAFT_283981 [Branchiostoma floridae] gi|229299324|gb|EEN69943.1| hypothetical protein BRAFLDRAFT_283981 [Branchiostoma floridae]
comp11431_c0_seq1	PREDICTED: endoplasmic reticulum metallopeptidase 1-like [Acyrthosiphon pisum]
comp6674_c0_seq1	GPI transamidase component PIG-T [Acromyrmex echinatior]

comp4501_c0_seq1	glucose dehydrogenase precursor, putative [Pediculus humanus corporis] gi|212514701|gb|EEB16960.1| glucose dehydrogenase precursor, putative [Pediculus humanus corporis]
comp6781_c0_seq1	RNA polymerase II subunit 7 [Nasonia vitripennis]
comp1038_c0_seq1	hypothetical protein Phum_PHUM300620 [Pediculus humanus corporis] gi|212511472|gb|EEB14447.1| hypothetical protein Phum_PHUM300620 [Pediculus humanus corporis]
comp6152_c0_seq1	PREDICTED: CTP synthase-like [Apis mellifera]
comp6397_c0_seq1	PREDICTED: hypothetical protein LOC725211 [Apis mellifera]
comp6673_c0_seq1	PREDICTED: similar to coiled-coil domain containing 134 [Tribolium castaneum] gi|270005764|gb|EFA02212.1| hypothetical protein TcasGA2_TC007871 [Tribolium castaneum]
comp1109_c0_seq1	Importin subunit beta-1 [Harpegnathos saltator]
comp6880_c0_seq1	
comp3456_c0_seq1	PREDICTED: similar to ENSANGP00000013045 [Nasonia vitripennis]
comp3856_c0_seq1	PREDICTED: cryptochrome-1-like [Acyrthosiphon pisum]
comp5058_c0_seq1	PREDICTED: e3 ubiquitin ligase RNF4-like [Monodelphis domestica]
comp2670_c0_seq1	Thymidylate kinase, putative [Aedes aegypti] gi|108883432|gb|EAT47657.1| Thymidylate kinase, putative [Aedes aegypti]
comp3660_c0_seq1	PREDICTED: similar to nonsense-mediated mrna decay protein [Tribolium castaneum] gi|270000793|gb|EEZ97240.1| hypothetical protein TcasGA2_TC011038 [Tribolium castaneum]
comp1630_c0_seq1	PREDICTED: similar to ebna2 binding protein P100 [Tribolium castaneum] gi|270003672|gb|EFA00120.1| hypothetical protein TcasGA2_TC002936 [Tribolium castaneum]
comp3885_c0_seq1	hypothetical protein SINV_15235 [Solenopsis invicta]
comp4056_c0_seq1	
comp11983_c0_seq1	PREDICTED: replication factor C subunit 5-like [Acyrthosiphon pisum]
comp4632_c0_seq1	PREDICTED: similar to GA19430-PA [Nasonia vitripennis]
comp216_c0_seq1	PREDICTED: similar to ribosomal protein L3e [Tribolium castaneum] gi|270011378|gb|EFA07826.1| hypothetical protein TcasGA2_TC005395 [Tribolium castaneum]
comp8165_c0_seq1	parafibromin, putative [Pediculus humanus corporis] gi|212512456|gb|EEB15219.1| parafibromin, putative [Pediculus humanus corporis]
comp3400_c0_seq1	
comp6224_c0_seq1	PREDICTED: similar to CG6697 CG6697-PA [Tribolium castaneum]
comp996_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit C-like [Bombus terrestris]
comp4286_c0_seq1	COP9 signalosome complex subunit 7A, putative [Pediculus humanus corporis] gi|212517618|gb|EEB19483.1| COP9 signalosome complex subunit 7A, putative [Pediculus humanus corporis]

comp6415_c0_seq1	PREDICTED: cyclic AMP response element-binding protein A-like [Acyrthosiphon pisum]
comp1799_c0_seq1	PREDICTED: similar to maintenance of killer 16 (mak16) protein [Nasonia vitripennis]
comp3024_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212508123|gb|EEB11911.1| conserved hypothetical protein [Pediculus humanus corporis]
comp2029_c0_seq1	PREDICTED: kinesin 8 [Apis mellifera]
comp11363_c0_seq1	PREDICTED: similar to beta-tubulin cofactor D [Tribolium castaneum] gi|270000809|gb|EEZ97256.1| hypothetical protein TcasGA2_TC011056 [Tribolium castaneum]
comp3537_c0_seq1	PREDICTED: prenylcysteine oxidase-like [Acyrthosiphon pisum]
comp5013_c0_seq1	hypothetical protein SINV_09004 [Solenopsis invicta]
comp10032_c0_seq1	PREDICTED: similar to CG1597 CG1597-PA [Tribolium castaneum] gi|270001063|gb|EEZ97510.1| hypothetical protein TcasGA2_TC011354 [Tribolium castaneum]
comp5969_c0_seq1	hypothetical protein LOC100168418 [Acyrthosiphon pisum] gi|239791114|dbj|BAH72068.1| ACYPI009121 [Acyrthosiphon pisum]
comp240_c0_seq1	putative ribosomal protein S23e [Graphocephala atropunctata]
comp2052_c0_seq1	PREDICTED: similar to aspartate aminotransferase [Nasonia vitripennis]
comp5216_c0_seq1	PREDICTED: similar to LD13710p [Nasonia vitripennis]
comp5895_c0_seq1	PREDICTED: similar to zinc binding dehydrogenase [Tribolium castaneum] gi|270012629|gb|EFA09077.1| hypothetical protein TcasGA2_TC006794 [Tribolium castaneum]
comp5603_c0_seq1	PREDICTED: similar to synaptobrevin [Tribolium castaneum] gi|270006153|gb|EFA02601.1| hypothetical protein TcasGA2_TC008320 [Tribolium castaneum]
comp2037_c0_seq1	GK20976 [Drosophila willistoni] gi|194157667|gb|EDW72568.1| GK20976 [Drosophila willistoni]
comp1013_c0_seq1	PREDICTED: ornithine aminotransferase, mitochondrial-like isoform 1 [Acyrthosiphon pisum] gi|328701505|ref|XP_003241621.1| PREDICTED: ornithine aminotransferase, mitochondrial-like isoform 2 [Acyrthosiphon pisum] >gi|328701507|ref|XP_003241622.1| PREDICTED: ornithine aminotransferase, mitochondrial-like isoform 3 [Acyrthosiphon pisum]
comp7637_c0_seq1	AGAP007923-PA [Anopheles gambiae str. PEST] gi|157015130|gb|EDO63606.1| AGAP007923-PA [Anopheles gambiae str. PEST]
comp12435_c0_seq1	Homeobox protein SIX4 [Acromyrmex echinatior]
comp7664_c0_seq1	PREDICTED: uncharacterized protein C19orf29-like isoform 1 [Bombus terrestris] gi|340713931|ref|XP_003395487.1| PREDICTED: uncharacterized protein C19orf29-like isoform 2 [Bombus terrestris]
comp1578_c0_seq1	PREDICTED: similar to CG3760 CG3760-PB [Tribolium castaneum] gi|270009679|gb|EFA06127.1| hypothetical protein TcasGA2_TC008970 [Tribolium castaneum]

comp1312_c0_seq1	clathrin heavy chain, putative [Pediculus humanus corporis] gi|212507343|gb|EEB11299.1| clathrin heavy chain, putative [Pediculus humanus corporis]
comp5780_c0_seq1	dihydrofolate reductase [Drosophila melanogaster]
comp4944_c0_seq1	hypothetical protein AaeL_AAEL006270 [Aedes aegypti] gi|108877937|gb|EAT42162.1| conserved hypothetical protein [Aedes aegypti]
comp5388_c0_seq1	
comp4841_c0_seq1	PREDICTED: furin-like protease 1, isoform 1-CRR-like [Acyrthosiphon pisum]
comp1473_c0_seq1	alakaline phosphatase 1 [Nilaparvata lugens]
comp263_c0_seq1	PREDICTED: similar to calcyclin binding protein [Tribolium castaneum] gi|270017125|gb|EFA13571.1| hypothetical protein TcasGA2_TC010306 [Tribolium castaneum]
comp998_c0_seq1	translocon-associated protein subunit delta precursor, putative [Pediculus humanus corporis] gi|212517119|gb|EEB19056.1| translocon-associated protein subunit delta precursor, putative [Pediculus humanus corporis]
comp273_c0_seq2	putative ubiquitin/ribosomal protein S27Ae fusion protein [Oncopeltus fasciatus]
comp105_c0_seq4	hypothetical protein AND_07297 [Anopheles darlingi]
comp9440_c0_seq1	PREDICTED: similar to kelch repeat protein isoform 1 [Tribolium castaneum] gi|270003222|gb|EEZ99669.1| hypothetical protein TcasGA2_TC002426 [Tribolium castaneum]
comp2134_c1_seq1	conserved hypothetical protein [Culex quinquefasciatus] gi|167872918|gb|EDS36301.1| conserved hypothetical protein [Culex quinquefasciatus]
comp3583_c0_seq1	hypothetical protein AND_02129 [Anopheles darlingi]
comp2358_c0_seq1	AGAP008604-PA [Anopheles gambiae str. PEST] gi|157016660|gb|EAL40245.2| AGAP008604-PA [Anopheles gambiae str. PEST]
comp9276_c0_seq1	Protein arginine N-methyltransferase 5 [Harpegnathos saltator]
comp4160_c0_seq1	AGAP007242-PA [Anopheles gambiae str. PEST] gi|116132312|gb|EAA04203.3| AGAP007242-PA [Anopheles gambiae str. PEST]
comp7797_c0_seq1	PREDICTED: vacuolar protein sorting-associated protein 13B-like [Acyrthosiphon pisum]
comp3636_c0_seq1	PREDICTED: tuberin [Apis mellifera]
comp9833_c0_seq1	PREDICTED: zinc finger protein 99-like [Acyrthosiphon pisum]
comp8341_c0_seq1	PREDICTED: mediator of RNA polymerase II transcription subunit 17 [Apis mellifera]
comp799_c0_seq1	hypothetical protein LOC100161110 [Acyrthosiphon pisum] gi|239799277|dbj|BAH70567.1| ACYPI002360 [Acyrthosiphon pisum]
comp11709_c0_seq1	Nucleoporin Ndc1, putative [Pediculus humanus corporis] gi|212516737|gb|EEB18711.1| Nucleoporin Ndc1, putative [Pediculus humanus corporis]
comp4706_c0_seq1	Spermine synthase [Camponotus floridanus]
comp1275_c0_seq1	hypothetical protein SINV_16053 [Solenopsis invicta]
comp2047_c0_seq1	Wiskott-Aldrich syndrome protein family member 3 [Harpegnathos saltator]

comp1384_c0_seq1	60 kDa heat shock protein, mitochondrial [Acromyrmex echinatior]
comp4986_c0_seq2	PREDICTED: spermatogenesis-associated protein 5-like [Apis mellifera]
comp5537_c0_seq2	PREDICTED: LOW QUALITY PROTEIN: actin-binding protein anillin [Apis mellifera]
comp3448_c0_seq1	PREDICTED: similar to AGAP003542-PA [Tribolium castaneum] gi|270002217|gb|EEZ98664.1| hypothetical protein TcasGA2_TC001195 [Tribolium castaneum]
comp1812_c0_seq1	PREDICTED: similar to LD23157p [Nasonia vitripennis]
comp381_c0_seq1	vitellogenin-2 [Plautia stali]
comp283_c0_seq1	PREDICTED: maternal protein exuperantia-like [Bombus terrestris]
comp2485_c0_seq2	cyclin B [Nasonia vitripennis]
comp4718_c0_seq1	rudimentary-like [Drosophila melanogaster] gi|76800654|sp|Q01637.2|PYR5_DROME RecName: Full=Uridine 5'-monophosphate synthase; Short=UMP synthase; AltName: Full=Rudimentary-like protein; Includes: RecName: Full=Orotate phosphoribosyltransferase; Short=OPRTase; Includes: RecName: Full=Orotidine 5'-phosphate decarboxylase; AltName: Full=OMPdecase >gi|7300695|gb|AAF55842.1| rudimentary-like [Drosophila melanogaster] >gi|16198241|gb|AAL13943.1| LD45235p [Drosophila melanogaster] >gi|220946406|gb|ACL85746.1| r-l-PA [synthetic construct] >gi|220956092|gb|ACL90589.1| r-l-PA [synthetic construct]
comp8512_c1_seq1	PREDICTED: protein FAM122A-like [Bombus terrestris]
comp3189_c0_seq1	PREDICTED: CWF19-like protein 2-like [Acyrthosiphon pisum]
comp2177_c0_seq1	
comp1511_c0_seq1	minifly protein, putative [Pediculus humanus corporis] gi|212515248|gb|EEB17419.1| minifly protein, putative [Pediculus humanus corporis]
comp2655_c0_seq1	PREDICTED: collagen alpha-1(IV) chain-like isoform 1 [Acyrthosiphon pisum] gi|328723517|ref|XP_003247862.1| PREDICTED: collagen alpha-1(IV) chain-like isoform 2 [Acyrthosiphon pisum]
comp2561_c0_seq1	PREDICTED: similar to Noa36 CG10009-PA [Tribolium castaneum] gi|270005496|gb|EFA01944.1| hypothetical protein TcasGA2_TC007558 [Tribolium castaneum]
comp4185_c0_seq2	PREDICTED: zinc finger protein 131-like [Acyrthosiphon pisum]
comp3842_c0_seq1	YjeF domain-containing protein, putative [Pediculus humanus corporis] gi|212510140|gb|EEB13365.1| YjeF domain-containing protein, putative [Pediculus humanus corporis]
comp10407_c0_seq2	conserved hypothetical protein [Pediculus humanus corporis] gi|212517234|gb|EEB19155.1| conserved hypothetical protein [Pediculus humanus corporis]
comp4312_c0_seq2	helicase with zinc finger protein domain helz, putative [Pediculus humanus corporis] gi|212508927|gb|EEB12468.1| helicase with zinc finger protein domain helz, putative [Pediculus humanus corporis]

comp3949_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212510047|gb|EEB13299.1| conserved hypothetical protein [Pediculus humanus corporis]
comp1763_c0_seq2	possible SD repeat-containing cell surface protein precursor [Pediococcus acidilactici DSM 20284] gi|304328006|gb|EFL95229.1| possible SD repeat-containing cell surface protein precursor [Pediococcus acidilactici DSM 20284]
comp12860_c0_seq1	Integrator complex subunit 12 [Harpegnathos saltator]
comp1888_c0_seq2	PREDICTED: similar to AGAP002077-PA [Tribolium castaneum]
comp3231_c0_seq1	PREDICTED: pontin protein isoform 1 [Apis mellifera]
comp634_c2_seq11	PREDICTED: tRNA pseudouridine synthase-like 1-like [Acyrthosiphon pisum]
comp4371_c0_seq1	GJ21580 [Drosophila virilis] gi|194144233|gb|EDW60629.1| GJ21580 [Drosophila virilis]
comp11237_c0_seq2	conserved hypothetical protein [Pediculus humanus corporis] gi|212513701|gb|EEB16172.1| conserved hypothetical protein [Pediculus humanus corporis]
comp7153_c0_seq1	PREDICTED: similar to GA11371-PA [Tribolium castaneum]
comp4807_c0_seq1	PREDICTED: exosome complex component MTR3-like [Bombus terrestris]
comp4949_c0_seq1	PREDICTED: puromycin-sensitive aminopeptidase-like [Acyrthosiphon pisum]
comp5574_c0_seq1	
comp3259_c0_seq1	
comp8555_c0_seq1	serine/threonine-protein phosphatase 6 catalytic subunit [Acyrthosiphon pisum] gi|239790702|dbj|BAH71896.1| ACYPI010064 [Acyrthosiphon pisum]
comp1965_c0_seq1	PREDICTED: importin-4-like [Apis mellifera]
comp2428_c1_seq1	Isoleucyl-tRNA synthetase, cytoplasmic [Harpegnathos saltator]
comp2592_c0_seq1	hypothetical protein SINV_10425 [Solenopsis invicta]
comp4742_c0_seq1	Nuclear pore complex protein Nup93, putative [Pediculus humanus corporis] gi|212517883|gb|EEB19712.1| Nuclear pore complex protein Nup93, putative [Pediculus humanus corporis]
comp3994_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp5998_c0_seq1	Membrane-associated protein Hem [Acromyrmex echinatior]
comp11113_c0_seq1	PREDICTED: zinc finger protein 91-like [Acyrthosiphon pisum]
comp4115_c0_seq1	PREDICTED: similar to ubiquitin fusion degradaton protein [Nasonia vitripennis]
comp7479_c0_seq1	Zinc finger protein ush [Harpegnathos saltator]
comp8939_c0_seq1	PREDICTED: sphingomyelin synthase-related 1-like [Bombus terrestris]
comp8499_c0_seq1	PREDICTED: LOW QUALITY PROTEIN: kinetochore-associated protein 1-like [Bombus terrestris]
comp4243_c0_seq2	COP9 signalosome complex subunit, putative [Pediculus humanus corporis] gi|212515414|gb|EEB17561.1| COP9 signalosome complex subunit, putative [Pediculus humanus corporis]

comp4969_c0_seq1	Inosine triphosphate pyrophosphatase, putative [Pediculus humanus corporis] gi|212515181|gb|EEB17362.1| Inosine triphosphate pyrophosphatase, putative [Pediculus humanus corporis]
comp6242_c0_seq2	PREDICTED: similar to AGAP002284-PA [Tribolium castaneum] gi|270006047|gb|EFA02495.1| hypothetical protein TcasGA2_TC008190 [Tribolium castaneum]
comp4748_c0_seq1	l-asparaginase i [Aedes aegypti] gi|108881762|gb|EAT45987.1| l-asparaginase i [Aedes aegypti]
comp5533_c0_seq2	PREDICTED: hypothetical protein LOC100649743 [Bombus terrestris]
comp484_c0_seq1	gamma-interferon-inducible lysosomal thiol reductase precursor, putative [Pediculus humanus corporis] gi|212518703|gb|EEB20424.1| gamma-interferon-inducible lysosomal thiol reductase precursor, putative [Pediculus humanus corporis]
comp470_c0_seq1	
comp3059_c0_seq1	Transforming acidic coiled-coil-containing protein 1 [Camponotus floridanus]
comp6724_c0_seq1	PREDICTED: hypothetical protein LOC100162750 isoform 1 [Acyrthosiphon pisum]
comp7991_c0_seq1	Ankyrin repeat and LEM domain-containing protein 2 [Harpegnathos saltator]
comp2611_c0_seq1	PREDICTED: hypothetical protein LOC100159253 isoform 1 [Acyrthosiphon pisum] gi|328716903|ref|XP_003246070.1| PREDICTED: hypothetical protein LOC100159253 isoform 2 [Acyrthosiphon pisum]
comp2486_c0_seq1	hypothetical protein Aasi_1441 [Candidatus Amoebophilus asiaticus 5a2] gi|189498184|gb|ACE06731.1| hypothetical protein Aasi_1441 [Candidatus Amoebophilus asiaticus 5a2]
comp7837_c0_seq1	PREDICTED: protein RSM22 homolog, mitochondrial-like [Acyrthosiphon pisum]
comp4832_c0_seq4	PREDICTED: hypothetical protein LOC725889 [Apis mellifera]
comp5894_c0_seq1	PREDICTED: similar to ATP-dependent transporter [Tribolium castaneum] gi|270013337|gb|EFA09785.1| hypothetical protein TcasGA2_TC011927 [Tribolium castaneum]
comp7999_c0_seq1	PREDICTED: similar to niemann-pick C1 [Tribolium castaneum]
comp8049_c0_seq1	AGAP003417-PA [Anopheles gambiae str. PEST]
comp5586_c0_seq1	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1-like [Bombus terrestris]
comp4316_c0_seq1	PREDICTED: actin-interacting protein 1-like isoform 2 [Acyrthosiphon pisum]
comp1702_c0_seq1	PREDICTED: similar to AGAP009119-PA [Tribolium castaneum] gi|270014189|gb|EFA10637.1| hypothetical protein TcasGA2_TC016274 [Tribolium castaneum]
comp9547_c0_seq1	Sorting nexin-13, putative [Pediculus humanus corporis] gi|212516139|gb|EEB18183.1| Sorting nexin-13, putative [Pediculus humanus corporis]
comp3324_c0_seq1	PREDICTED: pre-rRNA-processing protein TSR1 homolog [Apis mellifera]

comp4708_c0_seq1	hypothetical protein Phum_PHUM163860 [Pediculus humanus corporis] gi|212508546|gb|EEB12194.1| hypothetical protein Phum_PHUM163860 [Pediculus humanus corporis]
comp8468_c0_seq1	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Acromyrmex echinatior]
comp4224_c0_seq1	
comp3023_c0_seq1	Threonyl-tRNA synthetase, cytoplasmic, putative [Pediculus humanus corporis] gi|212518045|gb|EEB19847.1| Threonyl-tRNA synthetase, cytoplasmic, putative [Pediculus humanus corporis]
comp3804_c0_seq2	PREDICTED: similar to predicted protein [Tribolium castaneum] gi|270008010|gb|EFA04458.1| hypothetical protein TcasGA2_TC014762 [Tribolium castaneum]
comp124_c0_seq1	vitellogenin-3 [Plautia stali]
comp4569_c0_seq1	Augmenter of liver regeneration, putative [Pediculus humanus corporis] gi|212516556|gb|EEB18550.1| Augmenter of liver regeneration, putative [Pediculus humanus corporis]
comp1987_c0_seq1	PREDICTED: similar to CG3983 CG3983-PB [Tribolium castaneum] gi|270014031|gb|EFA10479.1| hypothetical protein TcasGA2_TC012725 [Tribolium castaneum]
comp3531_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp12_c0_seq1	vitellogenin [Lethocerus deyrollei]
comp40_c0_seq1	vitellogenin [Trigonotylus caelestialium]
comp5539_c0_seq1	Cullin-4B [Harpegnathos saltator]
comp3089_c0_seq1	hypothetical protein DAPPUDRAFT_306646 [Daphnia pulex]
comp2161_c0_seq1	Splicing factor U2Af 38 kDa subunit, putative [Pediculus humanus corporis] gi|212512324|gb|EEB15117.1| Splicing factor U2Af 38 kDa subunit, putative [Pediculus humanus corporis]
comp1851_c0_seq1	PREDICTED: similar to LD34072p [Nasonia vitripennis]
comp4781_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212516013|gb|EEB18072.1| conserved hypothetical protein [Pediculus humanus corporis]
comp3880_c0_seq1	syntaxin, putative [Aedes aegypti] gi|108879064|gb|EAT43289.1| syntaxin, putative [Aedes aegypti]
comp3222_c0_seq1	hypothetical protein SINV_05415 [Solenopsis invicta]
comp4595_c0_seq2	Signal recognition particle 72 kDa protein, putative [Pediculus humanus corporis] gi|212516466|gb|EEB18479.1| Signal recognition particle 72 kDa protein, putative [Pediculus humanus corporis]
comp6304_c0_seq1	PREDICTED: histone demethylase UTY-like, partial [Apis mellifera]
comp3423_c0_seq1	protein C20orf11, putative [Pediculus humanus corporis] gi|212508104|gb|EEB11900.1| protein C20orf11, putative [Pediculus humanus corporis]
comp7538_c0_seq1	tRNA-dihydrouridine synthase, putative [Pediculus humanus corporis] gi|212505672|gb|EEB10076.1| tRNA-dihydrouridine synthase, putative [Pediculus humanus corporis]
comp7808_c0_seq1	PREDICTED: u2 snRNP-associated SURP motif-containing protein-like [Apis mellifera]

comp4846_c0_seq1	PREDICTED: zinc finger protein 729-like [Danio rerio]
comp12057_c0_seq1	PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]
comp3765_c0_seq4	dorsal protein isoform A [Apis mellifera] gi|30351106|gb|AAP23055.1| dorsal protein [Apis mellifera]
comp7269_c0_seq1	PREDICTED: hypothetical protein LOC100166610 [Acyrthosiphon pisum]
comp1869_c0_seq1	guanine nucleotide-binding protein subunit beta-like [Microplitis mediator]
comp6003_c0_seq1	PREDICTED: similar to eIF2B-alpha protein [Nasonia vitripennis]
comp3696_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212508785|gb|EEB12373.1| conserved hypothetical protein [Pediculus humanus corporis]
comp3228_c0_seq1	PREDICTED: similar to signal peptidase complex subunit 3 [Tribolium castaneum] gi|270005949|gb|EFA02397.1| hypothetical protein TcasGA2_TC008077 [Tribolium castaneum]
comp3249_c0_seq1	oxidase, putative [Talaromyces stipitatus ATCC 10500] gi|218718404|gb|EED17824.1| oxidase, putative [Talaromyces stipitatus ATCC 10500]
comp7480_c0_seq1	aaa atpase [Aedes aegypti] gi|108874664|gb|EAT38889.1| aaa atpase [Aedes aegypti]
comp7528_c0_seq1	PREDICTED: hypothetical protein LOC100643403 [Bombus terrestris]
comp3106_c0_seq1	PREDICTED: probable ATP-dependent RNA helicase DDX23-like [Bombus terrestris]
comp5228_c0_seq1	hypothetical protein TcasGA2_TC010759 [Tribolium castaneum]
comp6969_c0_seq1	CCR4-NOT transcription complex subunit 3 [Camponotus floridanus]
comp7361_c0_seq1	PREDICTED: similar to myb-like, SWIRM and MPN domains 1 [Tribolium castaneum] gi|270013339|gb|EFA09787.1| hypothetical protein TcasGA2_TC011929 [Tribolium castaneum]
comp8101_c0_seq1	PREDICTED: similar to CG7371 CG7371-PA [Tribolium castaneum] gi|270006960|gb|EFA03408.1| hypothetical protein TcasGA2_TC013395 [Tribolium castaneum]
comp2525_c0_seq2	GK11710 [Drosophila willistoni] gi|194165871|gb|EDW80772.1| GK11710 [Drosophila willistoni]
comp1414_c0_seq1	PREDICTED: hypothetical protein LOC551973 [Apis mellifera]
comp909_c0_seq1	Unknown protein [Arabidopsis thaliana]
comp904_c0_seq1	PREDICTED: limkain-b1-like isoform 1 [Acyrthosiphon pisum]
comp482_c1_seq1	histone H2B.3, putative [Pediculus humanus corporis] gi|212516129|gb|EEB18173.1| histone H2B.3, putative [Pediculus humanus corporis]
comp4891_c0_seq1	PREDICTED: WD and tetratricopeptide repeats protein 1-like [Apis mellifera]
comp1785_c0_seq1	PREDICTED: hypothetical protein [Nasonia vitripennis]
comp1547_c0_seq1	Importin-7 [Camponotus floridanus]
comp6157_c0_seq1	Pterin-4-alpha-carbinolamine dehydratase 2 [Camponotus floridanus]

comp7391_c0_seq1	hypothetical protein Phum_PHUM521410 [Pediculus humanus corporis] gi|212516591|gb|EEB18585.1| hypothetical protein Phum_PHUM521410 [Pediculus humanus corporis]
comp2635_c1_seq1	hypothetical protein AaeL_AAEL005528 [Aedes aegypti] gi|108878769|gb|EAT42994.1| conserved hypothetical protein [Aedes aegypti]
comp3053_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212516481|gb|EEB18494.1| conserved hypothetical protein [Pediculus humanus corporis]
comp7288_c0_seq1	PREDICTED: lysosomal thioesterase PPT2 homolog isoform 2 [Apis mellifera]
comp3664_c0_seq1	Bromodomain-containing protein, putative [Pediculus humanus corporis] gi|212508638|gb|EEB12271.1| Bromodomain-containing protein, putative [Pediculus humanus corporis]
comp9959_c0_seq1	PREDICTED: protein downstream neighbor of son homolog [Acyrthosiphon pisum]
comp7312_c0_seq1	PREDICTED: similar to lethal (1) G0431 CG14788-PA [Tribolium castaneum] gi|270007374|gb|EFA03822.1| hypothetical protein TcasGA2_TC013937 [Tribolium castaneum]
comp7924_c0_seq1	Nuclear transcription factor Y subunit gamma [Camponotus floridanus]
comp1287_c0_seq1	
comp6388_c0_seq1	PREDICTED: hypothetical protein LOC100163939 [Acyrthosiphon pisum]
comp11361_c0_seq1	PREDICTED: similar to AGAP008858-PA [Tribolium castaneum] gi|270006798|gb|EFA03246.1| hypothetical protein TcasGA2_TC013179 [Tribolium castaneum]
comp1842_c0_seq3	PREDICTED: similar to CG10354 CG10354-PA [Tribolium castaneum]
comp9705_c0_seq1	PREDICTED: mothers against decapentaplegic homolog 6-like [Acyrthosiphon pisum]
comp4117_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212517283|gb|EEB19194.1| conserved hypothetical protein [Pediculus humanus corporis]
comp7899_c0_seq1	PREDICTED: integrator complex subunit 9-like [Bombus terrestris]
comp6577_c0_seq1	PREDICTED: similar to pcdc2/rp-8 (programmed cell death protein 2) [Nasonia vitripennis]
comp7740_c0_seq1	PREDICTED: transcription initiation factor TFIID subunit 2-like [Bombus terrestris]
comp3693_c0_seq1	PREDICTED: integrator complex subunit 11-like [Bombus terrestris]
comp8979_c0_seq1	Univin precursor, putative [Pediculus humanus corporis] gi|212508300|gb|EEB12039.1| Univin precursor, putative [Pediculus humanus corporis]
comp8272_c0_seq2	AGAP001236-PA [Anopheles gambiae str. PEST]
comp1684_c0_seq1	T-complex protein 1 subunit zeta [Acromyrmex echinatior]
comp3480_c0_seq1	
comp165_c0_seq1	putative ribosomal protein L32 [Maconellicoccus hirsutus]
comp5716_c0_seq1	PREDICTED: ras-related protein Rab-32-like [Bombus terrestris]
comp3736_c0_seq6	inhibitor of growth protein 3 [Apis mellifera]

comp1421_c0_seq1	hypothetical protein DAPPUDRAFT_191687 [Daphnia pulex]
comp8426_c0_seq1	PREDICTED: diphosphomevalonate decarboxylase-like [Bombus terrestris]
comp4764_c0_seq1	Apoptosis inhibitor, putative [Pediculus humanus corporis] gi|212506438|gb|EEB10656.1| Apoptosis inhibitor, putative [Pediculus humanus corporis]
comp3269_c0_seq1	PREDICTED: similar to LOC100049152 protein [Nasonia vitripennis]
comp2788_c0_seq1	Obg-like ATPase 1 [Acyrthosiphon pisum] gi|239788262|dbj|BAH70819.1| ACYPI52009 [Acyrthosiphon pisum] >gi|239788264|dbj|BAH70820.1| ACYPI52009 [Acyrthosiphon pisum] >gi|239788266|dbj|BAH70821.1| ACYPI52009 [Acyrthosiphon pisum] >gi|239788268|dbj|BAH70822.1| ACYPI52009 [Acyrthosiphon pisum] >gi|239788270|dbj|BAH70823.1| ACYPI52009 [Acyrthosiphon pisum] >gi|239788272|dbj|BAH70824.1| ACYPI52009 [Acyrthosiphon pisum]
comp204_c1_seq1	ribosomal protein L15e [Georissus sp. APV-2005]
comp746_c0_seq1	PREDICTED: similar to AGAP010331-PA [Tribolium castaneum]
comp2224_c0_seq2	PREDICTED: lysyl-tRNA synthetase-like isoform 3 [Acyrthosiphon pisum]
comp10854_c0_seq1	hypothetical protein TcasGA2_TC005383 [Tribolium castaneum]
comp1777_c0_seq1	PREDICTED: ubiquitin domain-containing protein 1-like [Acyrthosiphon pisum]
comp4792_c0_seq1	PREDICTED: similar to fidipidine [Tribolium castaneum]
comp7365_c0_seq1	PREDICTED: uncharacterized protein KIAA0528-like [Bombus terrestris]
comp9131_c0_seq1	sugar transporter 2 [Nilaparvata lugens]
comp5407_c0_seq1	PREDICTED: probable N(2),N(2)-dimethylguanosine tRNA methyltransferase-like isoform 1 [Acyrthosiphon pisum]
comp835_c0_seq1	GF11304 [Drosophila ananassae] gi|190622133|gb|EDV37657.1| GF11304 [Drosophila ananassae]
comp6_c0_seq1	vitellogenin [Athalia rosae]
comp4342_c0_seq1	GE20182 [Drosophila yakuba] gi|194180578|gb|EDW94189.1| GE20182 [Drosophila yakuba]
comp9984_c0_seq1	conserved hypothetical protein [Culex quinquefasciatus] gi|167867040|gb|EDS30423.1| conserved hypothetical protein [Culex quinquefasciatus]
comp6817_c0_seq1	Transmembrane protein 203 [Acromyrmex echinatior]
comp1092_c0_seq2	ribosomal protein L10Ae [Cicindela littoralis]
comp350_c0_seq1	90 kDa heat shock protein [Bemisia tabaci]
comp6601_c0_seq1	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform 1 [Acyrthosiphon pisum] gi|328704005|ref|XP_003242374.1| PREDICTED: glyoxylate reductase/hydroxypyruvate reductase-like isoform 2 [Acyrthosiphon pisum]
comp9124_c0_seq1	PREDICTED: hypothetical protein LOC100166285 [Acyrthosiphon pisum]

comp2416_c0_seq4	28S ribosomal protein S9, mitochondrial [Culex quinquefasciatus] gi|167870808|gb|EDS34191.1| 28S ribosomal protein S9, mitochondrial [Culex quinquefasciatus]
comp7132_c0_seq1	PREDICTED: similar to reserved [Tribolium castaneum]
comp2025_c0_seq1	PREDICTED: similar to small nuclear ribonucleoprotein at 69D CG10753-PA [Tribolium castaneum] gi|270016480|gb|EFA12926.1| hypothetical protein TcasGA2_TC010472 [Tribolium castaneum]
comp1403_c0_seq1	proliferating cell nuclear antigen [Litopenaeus vannamei] gi|339721489|gb|AEJ89928.1| proliferating cell nuclear antigen [Litopenaeus vannamei]
comp3226_c0_seq1	PREDICTED: similar to alcohol dehydrogenase [Nasonia vitripennis]
comp5686_c0_seq1	phosphatidylethanolamine-binding protein-like [Acyrthosiphon pisum] gi|239789027|dbj|BAH71163.1| ACYPI002878 [Acyrthosiphon pisum]
comp5637_c0_seq1	PREDICTED: la-related protein 7-like [Apis mellifera]
comp3958_c0_seq2	PREDICTED: protein transport protein Sec24C-like [Apis mellifera]
comp2713_c0_seq1	PREDICTED: mitochondrial import inner membrane translocase subunit TIM44-like isoform 1 [Apis mellifera]
comp6477_c0_seq1	E3 ubiquitin ligase triad3, putative [Pediculus humanus corporis] gi|212516216|gb|EEB18254.1| E3 ubiquitin ligase triad3, putative [Pediculus humanus corporis]
comp3369_c0_seq2	GK24233 [Drosophila willistoni] gi|194163131|gb|EDW78032.1| GK24233 [Drosophila willistoni]
comp4364_c0_seq1	COMPASS component SWD2, putative [Pediculus humanus corporis] gi|212510446|gb|EEB13631.1| COMPASS component SWD2, putative [Pediculus humanus corporis]
comp4665_c0_seq1	Probable ubiquitin carboxyl-terminal hydrolase FAF-X [Camponotus floridanus]
comp1818_c0_seq1	PREDICTED: similar to ubiquitin-activating enzyme E1 [Tribolium castaneum]
comp3198_c0_seq1	hypothetical protein TcasGA2_TC009771 [Tribolium castaneum]
comp2860_c0_seq1	PREDICTED: similar to 28S ribosomal protein S5 [Tribolium castaneum] gi|270010452|gb|EFA06900.1| hypothetical protein TcasGA2_TC009847 [Tribolium castaneum]
comp2694_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp1685_c0_seq1	PREDICTED: serine/threonine-protein kinase Nek7-like [Meleagris gallopavo]
comp1373_c0_seq1	PREDICTED: serine/threonine-protein kinase polo-like [Acyrthosiphon pisum]
comp3372_c0_seq1	PREDICTED: similar to protein disulfide isomerase [Nasonia vitripennis]
comp2267_c0_seq2	
comp4490_c0_seq1	PREDICTED: fatty acid 2-hydroxylase-like [Acyrthosiphon pisum]
comp2324_c0_seq1	hypothetical protein TcasGA2_TC002488 [Tribolium castaneum]
comp6516_c0_seq1	PREDICTED: similar to histone deacetylase [Tribolium castaneum] gi|270003320|gb|EEZ99767.1| hypothetical protein TcasGA2_TC002540 [Tribolium castaneum]

comp2048_c0_seq1	PREDICTED: similar to carbamoyl-phosphate synthase large chain [Tribolium castaneum] gi|270013749|gb|EFA10197.1| hypothetical protein TcasGA2_TC012392 [Tribolium castaneum]
comp5622_c0_seq3	DEAD-box helicase Dbp80 [Harpegnathos saltator]
comp4770_c0_seq2	PREDICTED: exportin-5-like [Bombus terrestris]
comp4349_c0_seq1	hypothetical protein G5I_04322 [Acromyrmex echinatior]
comp5263_c0_seq1	Breast cancer metastasis-suppressor, putative [Pediculus humanus corporis] gi|212511208|gb|EEB14241.1| Breast cancer metastasis-suppressor, putative [Pediculus humanus corporis]
comp1490_c0_seq1	follicle cell protein 3C [Blattella germanica]
comp1096_c0_seq1	Eukaryotic translation initiation factor 4E [Harpegnathos saltator]
comp4813_c0_seq1	
comp5300_c0_seq1	PREDICTED: lysine-specific demethylase NO66-like [Bombus terrestris]
comp3718_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212514728|gb|EEB16984.1| conserved hypothetical protein [Pediculus humanus corporis]
comp2439_c0_seq1	PREDICTED: DNA replication licensing factor mcm7-like isoform 1 [Acyrthosiphon pisum] gi|328710702|ref|XP_003244337.1| PREDICTED: DNA replication licensing factor mcm7-like isoform 2 [Acyrthosiphon pisum]
comp4439_c0_seq1	PREDICTED: Hermansky-Pudlak syndrome 1 protein homolog [Acyrthosiphon pisum]
comp12473_c0_seq1	zinc finger protein, putative [Pediculus humanus corporis] gi|212518778|gb|EEB20499.1| zinc finger protein, putative [Pediculus humanus corporis]
comp926_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Tribolium castaneum] gi|270007441|gb|EFA03889.1| hypothetical protein TcasGA2_TC014013 [Tribolium castaneum]
comp7548_c0_seq1	PREDICTED: similar to serine/threonine-protein kinase RIO1 [Tribolium castaneum] gi|270005675|gb|EFA02123.1| hypothetical protein TcasGA2_TC007772 [Tribolium castaneum]
comp1456_c0_seq1	DNA topoisomerase 1 [Camponotus floridanus]
comp4555_c0_seq1	DNA methyltransferase 1-associated protein 1 [Harpegnathos saltator]
comp9818_c0_seq1	coiled-coil domain-containing protein, putative [Pediculus humanus corporis] gi|212515961|gb|EEB18026.1| coiled-coil domain-containing protein, putative [Pediculus humanus corporis]
comp2001_c0_seq1	Tripeptidyl-peptidase 2 [Harpegnathos saltator]
comp8140_c0_seq1	PREDICTED: similar to CG12701 CG12701-PA [Tribolium castaneum] gi|270008254|gb|EFA04702.1| vielfaltig [Tribolium castaneum]
comp2936_c0_seq1	AGAP006818-PA [Anopheles gambiae str. PEST] gi|157020637|gb|EAA04227.4| AGAP006818-PA [Anopheles gambiae str. PEST]
comp9274_c0_seq1	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1-like [Acyrthosiphon pisum]
comp1367_c0_seq1	hypothetical protein SINV_01813 [Solenopsis invicta]

comp7622_c0_seq2	
comp7869_c0_seq1	B lymphoma Mo-MLV insertion region 1b [Danio rerio]
comp1955_c0_seq1	ACYPI007188 [Acyrthosiphon pisum]
comp5399_c0_seq1	Large neutral amino acids transporter small subunit 2 [Acromyrmex echinatior]
comp3932_c1_seq1	PREDICTED: hypothetical protein LOC100573509 isoform 1 [Acyrthosiphon pisum] gi|328708857|ref|XP_003243817.1| PREDICTED: hypothetical protein LOC100573509 isoform 2 [Acyrthosiphon pisum]
comp509_c0_seq1	GA27162 [Drosophila pseudoobscura pseudoobscura] gi|198131635|gb|EDY67919.1| GA27162 [Drosophila pseudoobscura pseudoobscura]
comp2504_c0_seq1	PREDICTED: gametogenetin-binding protein 2-like [Apis mellifera]
comp5992_c0_seq1	PREDICTED: hypothetical protein LOC100638831 [Amphimedon queenslandica]
comp2440_c0_seq1	hypothetical protein AaeL_AAEL010837 [Aedes aegypti] gi|108872915|gb|EAT37140.1| conserved hypothetical protein [Aedes aegypti]
comp6340_c0_seq1	PREDICTED: mitogen-activated protein kinase kinase kinase 9-like [Acyrthosiphon pisum]
comp9970_c0_seq1	hypothetical protein [Ictalurus punctatus]
comp8609_c0_seq1	GK12822 [Drosophila willistoni] gi|194170119|gb|EDW85020.1| GK12822 [Drosophila willistoni]
comp9333_c0_seq1	PREDICTED: similar to CG8311-PA [Nasonia vitripennis]
comp6462_c0_seq1	AGAP001319-PA [Anopheles gambiae str. PEST]
comp1688_c0_seq1	hypothetical protein TcasGA2_TC004080 [Tribolium castaneum]
comp9321_c0_seq1	cytochrome P450 [Bemisia tabaci]
comp1773_c1_seq1	PREDICTED: solute carrier family 35 member B1 homolog [Acyrthosiphon pisum]
comp1537_c0_seq1	PREDICTED: tRNA (uracil-5-)-methyltransferase homolog A-like [Acyrthosiphon pisum]
comp5084_c0_seq1	
comp6764_c0_seq2	hypothetical protein LOC100163911 [Acyrthosiphon pisum] gi|239792500|dbj|BAH72586.1| ACYPI004962 [Acyrthosiphon pisum]
comp8715_c0_seq1	PREDICTED: CD109 antigen-like [Acyrthosiphon pisum]
comp1091_c0_seq1	PREDICTED: stress-induced-phosphoprotein 1-like [Acyrthosiphon pisum]
comp867_c0_seq1	PREDICTED: tubulin beta chain-like [Amphimedon queenslandica]
comp1677_c0_seq7	Prefoldin subunit 6 [Acromyrmex echinatior]
comp4210_c0_seq1	phosphatidylethanolamine-binding protein [Aedes aegypti] gi|108870917|gb|EAT35142.1| phosphatidylethanolamine-binding protein [Aedes aegypti]
comp1241_c0_seq1	PREDICTED: t-complex protein 1 subunit gamma-like isoform 1 [Bombus terrestris]
comp3592_c0_seq1	
comp783_c0_seq1	PREDICTED: similar to diacylglycerol o-acyltransferase [Nasonia vitripennis]
comp7073_c0_seq1	PREDICTED: hypothetical protein LOC100649269 [Bombus terrestris]
comp11561_c0_seq2	hypothetical protein TcasGA2_TC014427 [Tribolium castaneum]

<table>
<tr><td>comp5200_c0_seq2</td><td>elongation factor ts [Aedes aegypti] gi|122069482|sp|Q17PI0.1|EFTS_AEDAE RecName: Full=Elongation factor Ts, mitochondrial; Short=EF-Ts; Short=EF-TsMt; Flags: Precursor >gi|108884412|gb|EAT48637.1| elongation factor ts [Aedes aegypti]</td></tr>
<tr><td>comp1229_c0_seq1</td><td>glycosyl-phosphatidyl-inositol-anchored protein [Bombyx mori] gi|87248139|gb|ABD36122.1| glycosyl-phosphatidyl-inositol-anchored protein [Bombyx mori]</td></tr>
<tr><td>comp4301_c0_seq1</td><td>WD repeat-containing protein 4 [Camponotus floridanus]</td></tr>
<tr><td>comp42_c0_seq1</td><td>putative pterin-4-alpha-carbinolamine dehydratase [Diaphorina citri]</td></tr>
<tr><td>comp4215_c0_seq1</td><td>PREDICTED: phenoloxidase subunit A3-like [Acyrthosiphon pisum]</td></tr>
<tr><td>comp828_c0_seq1</td><td>GJ20513 [Drosophila virilis] gi|194144659|gb|EDW61055.1| GJ20513 [Drosophila virilis]</td></tr>
<tr><td>comp3186_c0_seq1</td><td>PREDICTED: leucyl-tRNA synthetase, cytoplasmic-like isoform 1 [Apis mellifera]</td></tr>
<tr><td>comp6887_c0_seq1</td><td>conserved hypothetical protein [Pediculus humanus corporis] gi|212507728|gb|EEB11590.1| conserved hypothetical protein [Pediculus humanus corporis]</td></tr>
<tr><td>comp1009_c0_seq1</td><td>PREDICTED: f-box only protein 28-like [Apis mellifera]</td></tr>
<tr><td>comp5538_c0_seq1</td><td>AGAP009600-PA [Anopheles gambiae str. PEST] gi|157013889|gb|EAA14456.4| AGAP009600-PA [Anopheles gambiae str. PEST]</td></tr>
<tr><td>comp4088_c0_seq1</td><td>conserved hypothetical protein [Pediculus humanus corporis] gi|212509059|gb|EEB12556.1| conserved hypothetical protein [Pediculus humanus corporis]</td></tr>
<tr><td>comp7272_c0_seq1</td><td>hypothetical protein TcasGA2_TC009925 [Tribolium castaneum]</td></tr>
<tr><td>comp4234_c0_seq1</td><td>hypothetical protein TcasGA2_TC005972 [Tribolium castaneum]</td></tr>
<tr><td>comp1127_c0_seq1</td><td>hypothetical protein Phum_PHUM405430 [Pediculus humanus corporis] gi|212513603|gb|EEB16122.1| hypothetical protein Phum_PHUM405430 [Pediculus humanus corporis]</td></tr>
<tr><td>comp5123_c0_seq1</td><td>PREDICTED: similar to golgi phosphoprotein 3 (coat-protein GPP34) [Tribolium castaneum] gi|270014486|gb|EFA10934.1| hypothetical protein TcasGA2_TC001762 [Tribolium castaneum]</td></tr>
<tr><td>comp7840_c0_seq1</td><td>PREDICTED: exocyst complex component 6B-like isoform 2 [Bombus terrestris]</td></tr>
<tr><td>comp2862_c0_seq2</td><td>PREDICTED: u3 small nucleolar RNA-associated protein 14 homolog A-like [Apis mellifera]</td></tr>
<tr><td>comp6698_c0_seq1</td><td>hypothetical protein SINV_05401 [Solenopsis invicta]</td></tr>
<tr><td>comp3264_c0_seq1</td><td>Transcription elongation factor SPT5 [Camponotus floridanus]</td></tr>
<tr><td>comp4777_c0_seq1</td><td>PREDICTED: similar to ENSANGP00000014283 [Nasonia vitripennis]</td></tr>
<tr><td>comp2016_c0_seq3</td><td>PERQ amino acid-rich with GYF domain-containing protein 2 [Harpegnathos saltator]</td></tr>
<tr><td>comp8631_c0_seq1</td><td>PREDICTED: protein deltex [Apis mellifera]</td></tr>
<tr><td>comp9297_c0_seq1</td><td></td></tr>
<tr><td>comp2340_c0_seq1</td><td>PREDICTED: similar to proteasome alpha 4 subunit [Nasonia vitripennis]</td></tr>
</table>

comp9750_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212511663|gb|EEB14580.1| conserved hypothetical protein [Pediculus humanus corporis]
comp12510_c0_seq1	GA28568 [Drosophila pseudoobscura pseudoobscura] gi|198151215|gb|EDY74106.1| GA28568 [Drosophila pseudoobscura pseudoobscura]
comp3519_c0_seq1	PREDICTED: hypothetical protein LOC100163498 isoform 2 [Acyrthosiphon pisum]
comp2684_c0_seq1	PREDICTED: pentatricopeptide repeat-containing protein 2-like [Acyrthosiphon pisum]
comp3132_c0_seq1	translation elongation factor G [Halomonas sp. TD01] gi|338764053|gb|EGP19030.1| translation elongation factor G [Halomonas sp. TD01]
comp768_c0_seq1	PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Acyrthosiphon pisum]
comp563_c0_seq1	PREDICTED: importin subunit alpha-2-like [Bombus terrestris]

Table S2 Annotation of male-biased genes

Assembly ID	**NR database**
comp1796_c0_seq1	GG21229 [Drosophila erecta] gi|190651643|gb|EDV48898.1| GG21229 [Drosophila erecta]
comp8162_c0_seq2	hypothetical protein EAI_14722 [Harpegnathos saltator]
comp2863_c0_seq1	sugar transporter 7 [Nilaparvata lugens]
comp10931_c0_seq1	PREDICTED: JNK-interacting protein 1-like [Acyrthosiphon pisum]
comp72_c0_seq1	OS-D-like protein [Maconellicoccus hirsutus]
comp1098_c0_seq2	PREDICTED: similar to Zinc carboxypeptidase family protein [Tribolium castaneum]
comp4187_c0_seq1	
comp5819_c0_seq1	nicotinic acetylcholine receptor [Ctenocephalides felis]
comp5741_c0_seq1	PREDICTED: similar to CG3955-PA [Nasonia vitripennis]
comp6313_c0_seq2	
comp1380_c0_seq4	
comp68_c0_seq4	PREDICTED: myosin heavy chain, muscle isoform 1 [Acyrthosiphon pisum]
comp1964_c0_seq1	
comp743_c0_seq1	PREDICTED: hypothetical protein [Tribolium castaneum]
comp1130_c0_seq1	PREDICTED: sarcalumenin-like [Apis mellifera]
comp636_c0_seq1	PREDICTED: neurogenic locus notch homolog protein 1-like [Acyrthosiphon pisum]
comp9455_c0_seq4	PREDICTED: hypothetical protein LOC100650591 [Bombus terrestris]
comp1010_c0_seq1	
comp634_c2_seq1	hypothetical protein TcasGA2_TC009181 [Tribolium castaneum]
comp3944_c0_seq1	
comp2801_c0_seq1	RecName: Full=Hypertrehalosaemic prohormone; Contains: RecName: Full=Hypertrehalosaemic hormone; Short=HTH; AltName: Full=Hypertrehalosaemic neuropeptide; Contains: RecName: Full=Hypertrehalosaemic hormone precursor-related peptide; Flags: Precursor gi|1022716|gb|AAA79691.1| prepro-hypertrehalosemic hormone [Blaberus discoidalis]
comp1432_c0_seq1	
comp997_c0_seq1	
comp8888_c0_seq1	PREDICTED: hypothetical protein LOC100572071 [Acyrthosiphon
comp6912_c0_seq2	PREDICTED: hypothetical protein LOC100159668 [Acyrthosiphon
comp172_c0_seq1	
comp9334_c0_seq1	PREDICTED: similar to CG13375 CG13375-PA [Tribolium castaneum]
comp6702_c0_seq1	PREDICTED: similar to RAS-like, family 10, member B [Tribolium castaneum] gi|270008592|gb|EFA05040.1| hypothetical protein TcasGA2_TC015129 [Tribolium castaneum]
comp3545_c0_seq2	hypothetical protein SINV_03318 [Solenopsis invicta]
comp2174_c0_seq1	chemosensory protein-like [Acyrthosiphon pisum] gi|77415640|emb|CAJ01489.1| hypothetical protein [Acyrthosiphon pisum]
comp992_c0_seq1	PREDICTED: carbonic anhydrase 7-like [Acyrthosiphon pisum]
comp705_c0_seq1	
comp3725_c0_seq6	Arrestin-like protein [Camponotus floridanus]
comp7367_c0_seq1	cardioactive peptide isoform B [Rhodnius prolixus]
comp3840_c0_seq1	hypothetical protein TcasGA2_TC010074 [Tribolium castaneum]

comp5403_c0_seq1	PREDICTED: synaptic vesicular amine transporter-like isoform 2 [Acyrthosiphon pisum] gi|328709290|ref|XP_001945866.2| PREDICTED: synaptic vesicular amine transporter-like isoform 1 [Acyrthosiphon pisum]
comp7465_c0_seq1	hypothetical protein CAEBREN_13576 [Caenorhabditis brenneri]
comp149_c0_seq1	
comp388_c0_seq1	
comp706_c0_seq1	cysteine proteinase [Hypera postica]
comp2287_c0_seq2	AGAP005124-PC [Anopheles gambiae str. PEST] gi|157017072|gb|EAA09458.5| AGAP005124-PC [Anopheles gambiae str. PEST]
comp678_c0_seq1	
comp23_c0_seq1	secreted cathepsin F [Teladorsagia circumcincta]
comp8575_c0_seq1	hypothetical protein TcasGA2_TC003629 [Tribolium castaneum]
comp3102_c0_seq1	TPA: putative cuticle protein [Bombyx mori]
comp763_c0_seq1	
comp9143_c0_seq1	hypothetical protein TcasGA2_TC011452 [Tribolium castaneum]
comp758_c1_seq9	
comp185_c0_seq1	
comp464_c0_seq1	
comp3163_c0_seq1	PREDICTED: hypothetical protein LOC100568861 [Acyrthosiphon
comp13092_c0_seq1	PREDICTED: hypothetical protein LOC100577239 [Apis mellifera]
comp5477_c0_seq1	cytochrome P450 [Bemisia tabaci]
comp1104_c0_seq1	PREDICTED: alpha-tocopherol transfer protein-like [Bombus terrestris]
comp3540_c0_seq1	PREDICTED: hypothetical protein LOC100575897 isoform 1 [Acyrthosiphon pisum] gi|328698904|ref|XP_003240765.1| PREDICTED: hypothetical protein LOC100575897 isoform 2
comp9603_c0_seq1	hypothetical protein TcasGA2_TC001759 [Tribolium castaneum]
comp5821_c0_seq1	AChE2 [Bemisia tabaci] gi|157366848|gb|ABV45415.1| AChE2 [Bemisia tabaci]
comp913_c0_seq1	cathepsin L-like proteinase [Diabrotica virgifera virgifera]
comp1331_c5_seq3	
comp8517_c0_seq1	hypothetical protein Phum_PHUM258430 [Pediculus humanus corporis] gi|212510658|gb|EEB13794.1| hypothetical protein Phum_PHUM258430 [Pediculus humanus corporis]
comp5029_c0_seq1	PREDICTED: glycine receptor subunit beta-type 4-like [Acyrthosiphon pisum]
comp7526_c0_seq3	chitin binding peritrophin-A, putative [Pediculus humanus corporis] gi|212514415|gb|EEB16743.1| chitin binding peritrophin-A, putative [Pediculus humanus corporis]
comp4999_c1_seq1	AChE1 [Bemisia tabaci]
comp26_c0_seq1	myosin 3 light chain [Lonomia obliqua]
comp4400_c0_seq1	PREDICTED: hypothetical protein LOC100166909 [Acyrthosiphon
comp11_c0_seq3	
comp2334_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212506420|gb|EEB10638.1| conserved hypothetical protein [Pediculus humanus corporis]
comp5042_c0_seq3	PREDICTED: sodium- and chloride-dependent creatine transporter 1-like isoform 1 [Acyrthosiphon pisum] gi|328714515|ref|XP_003245380.1| PREDICTED: sodium- and chloride-dependent creatine transporter 1-like isoform 2 [Acyrthosiphon
comp1000_c0_seq2	
comp2955_c0_seq1	PREDICTED: hypothetical protein LOC100570172 [Acyrthosiphon
comp467_c0_seq1	

comp1544_c0_seq1	cuticular protein 58 [Acyrthosiphon pisum] gi|328710782|ref|XP_003244356.1| PREDICTED: hypothetical protein LOC100573511 [Acyrthosiphon pisum] >gi|239792554|dbj|BAH72607.1| ACYPI003073 [Acyrthosiphon
comp7388_c0_seq1	PREDICTED: hypothetical protein LOC100569264 [Acyrthosiphon
comp5240_c0_seq1	PREDICTED: similar to GA20722-PA [Tribolium castaneum]
comp4590_c0_seq1	
comp8703_c0_seq1	dual specificity protein phosphatase, putative [Pediculus humanus corporis] gi|212511054|gb|EEB14103.1| dual specificity protein phosphatase, putative [Pediculus humanus corporis]
comp2004_c0_seq1	PREDICTED: hypothetical protein LOC100160882 [Acyrthosiphon
comp1497_c0_seq1	
comp986_c0_seq1	hypothetical protein TcasGA2_TC010484 [Tribolium castaneum]
comp9234_c0_seq1	
comp634_c2_seq9	PREDICTED: hypothetical protein LOC100167699 [Acyrthosiphon
comp7085_c0_seq1	rab3 interacting molecule, putative [Pediculus humanus corporis] gi|212515720|gb|EEB17818.1| rab3 interacting molecule, putative [Pediculus humanus corporis]
comp1468_c0_seq2	Muscle M-line assembly protein unc-89 [Harpegnathos saltator]
comp7421_c0_seq1	PREDICTED: hypothetical protein LOC100163311 [Acyrthosiphon
comp820_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212516800|gb|EEB18768.1| conserved hypothetical protein [Pediculus humanus corporis]
comp4890_c0_seq1	
comp423_c0_seq1	PREDICTED: similar to peroxiredoxin [Nasonia vitripennis]
comp5082_c0_seq1	PREDICTED: similar to CG11044 CG11044-PA [Tribolium castaneum]
comp2949_c1_seq1	carboxylesterase [Laodelphax striatellus] gi|313667164|gb|ADR73025.1| carboxylesterase [Laodelphax
comp2564_c0_seq1	Glutamate decarboxylase [Camponotus floridanus]
comp1936_c0_seq6	
comp1055_c0_seq1	PREDICTED: hypothetical protein LOC100573041 [Acyrthosiphon
comp9943_c0_seq1	
comp43_c0_seq1	
comp257_c0_seq1	PREDICTED: glucose dehydrogenase [acceptor]-like [Acyrthosiphon pisum]
comp77_c6_seq83	
comp1383_c0_seq1	PREDICTED: hypothetical protein LOC100165870 [Acyrthosiphon
comp5532_c0_seq2	UGA suppressor tRNA-associated protein, putative [Pediculus humanus corporis] gi|212509888|gb|EEB13174.1| UGA suppressor tRNA-associated protein, putative [Pediculus humanus corporis]
comp3294_c0_seq1	allatostatin A prohormone precursor [Gryllus bimaculatus]
comp487_c0_seq3	L-xylulose reductase [Anoplopoma fimbria]
comp2445_c0_seq1	death-associated small cytoplasmic leucine-rich protein [Bombyx mori] gi|221579656|gb|ACM24345.1| death-associated small cytoplasmic leucine-rich protein [Bombyx mori]
comp7035_c0_seq1	PREDICTED: similar to DopEcR CG18314-PA [Tribolium castaneum] gi|270012800|gb|EFA09248.1| hypothetical protein TcasGA2_TC006457 [Tribolium castaneum]
comp988_c0_seq1	PREDICTED: prohormone-1-like [Bombus terrestris]
comp9062_c0_seq1	protein phosphatase-7 [Aedes aegypti] gi|108881203|gb|EAT45428.1| protein phosphatase-7 [Aedes aegypti]
comp1146_c0_seq2	leucomyosuppressin precursor [Blattella germanica]
comp4273_c1_seq1	

comp4398_c0_seq1	conserved hypothetical protein [Culex quinquefasciatus] gi|167882481|gb|EDS45864.1| conserved hypothetical protein [Culex quinquefasciatus]
comp3141_c0_seq1	PREDICTED: similar to papilin [Tribolium castaneum]
comp2265_c0_seq1	PREDICTED: trimeric intracellular cation channel type B-like [Apis mellifera]
comp7058_c0_seq1	RAB 3 and, putative [Pediculus humanus corporis] gi|212506265|gb|EEB10525.1| RAB 3 and, putative [Pediculus humanus corporis]
comp1095_c0_seq1	odorant binding protein 6 [Apolygus lucorum]
comp5120_c0_seq1	
comp1767_c0_seq1	hypothetical protein TcasGA2_TC000669 [Tribolium castaneum]
comp80_c0_seq1	
comp823_c0_seq3	hypothetical protein TcasGA2_TC011220 [Tribolium castaneum]
comp1837_c0_seq1	pathogenesis related gene 5 [Bupleurum kaoi]
comp7683_c0_seq1	PREDICTED: transmembrane and TPR repeat-containing protein 1-like [Bombus terrestris]
comp886_c0_seq1	hypothetical protein TcasGA2_TC008620 [Tribolium castaneum]
comp4045_c0_seq1	sodium channel, auxiliary protein, putative [Aedes aegypti] gi|108882513|gb|EAT46738.1| sodium channel, auxiliary protein, putative [Aedes aegypti]
comp4451_c0_seq2	Tubulin-specific chaperone cofactor E-like protein [Harpegnathos saltator]
comp7499_c0_seq1	PREDICTED: hypothetical protein LOC100574750 isoform 1 [Acyrthosiphon pisum] gi|328700245|ref|XP_003241194.1| PREDICTED: hypothetical protein LOC100574750 isoform 2
comp1841_c0_seq1	
comp1464_c0_seq1	
comp529_c0_seq1	
comp32_c0_seq1	
comp863_c0_seq1	
comp5879_c0_seq1	
comp3882_c0_seq1	
comp932_c0_seq1	
comp10069_c0_seq1	PREDICTED: hypothetical protein LOC100651767 [Bombus terrestris]
comp1274_c0_seq1	troponin C-like [Acyrthosiphon pisum] gi|239793671|dbj|BAH72939.1| ACYPI007505 [Acyrthosiphon pisum]
comp1418_c0_seq1	PREDICTED: facilitated trehalose transporter Tret1-like [Acyrthosiphon pisum]
comp4217_c0_seq2	
comp1566_c0_seq1	
comp4055_c0_seq1	PREDICTED: similar to IP17045p [Nasonia vitripennis]
comp10881_c0_seq1	PREDICTED: allatostatin-A receptor-like [Acyrthosiphon pisum]
comp4179_c0_seq1	
comp2810_c0_seq1	PREDICTED: putative fatty acyl-CoA reductase CG5065-like [Acyrthosiphon pisum]
comp466_c0_seq1	
comp7143_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Tribolium castaneum] gi|270011903|gb|EFA08351.1| hypothetical protein TcasGA2_TC005994 [Tribolium castaneum]
comp1320_c0_seq1	
comp235_c0_seq2	
comp4311_c0_seq1	PREDICTED: hypothetical protein LOC100167736 [Acyrthosiphon
comp10708_c0_seq1	PREDICTED: similar to CG34351 CG34351-PC [Tribolium castaneum]

comp581_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Tribolium castaneum] gi|270010967|gb|EFA07415.1| brain peptide ITGQGNRIF-like protein [Tribolium castaneum]
comp2305_c0_seq1	PREDICTED: hypothetical protein LOC100165710 [Acyrthosiphon
comp6279_c0_seq1	blue-sensitive opsin precursor [Dianemobius nigrofasciatus]
comp9957_c0_seq2	PREDICTED: hypothetical protein LOC100572072 [Acyrthosiphon
comp7826_c0_seq1	hypothetical protein TcasGA2_TC015574 [Tribolium castaneum]
comp1805_c0_seq1	
comp1394_c0_seq1	PREDICTED: probable maltase L-like [Acyrthosiphon pisum]
comp10637_c0_seq1	PREDICTED: similar to high-affinity serotonin transporter [Tribolium castaneum] gi|270016267|gb|EFA12713.1| hypothetical protein TcasGA2_TC002347 [Tribolium castaneum]
comp1555_c0_seq1	hypothetical protein TcasGA2_TC003200 [Tribolium castaneum]
comp3792_c0_seq1	
comp3068_c0_seq2	f-spondin [Aedes aegypti] gi|108876156|gb|EAT40381.1| f-spondin [Aedes aegypti]
comp248_c0_seq1	mitochondrial F1F0-ATP synthase subunit delta/ATP16 [Cimex lectularius]
comp1721_c0_seq1	ADP-ribose pyrophosphatase, mitochondrial [Camponotus floridanus]
comp5662_c0_seq1	
comp772_c0_seq2	PREDICTED: alpha-crystallin B chain-like isoform 3 [Acyrthosiphon pisum]
comp110_c0_seq1	myofilin isoform b [Acyrthosiphon pisum] gi|253735725|ref|NP_001156710.1| myofilin isoform b [Acyrthosiphon pisum] >gi|239793567|dbj|BAH72895.1| ACYPI002609 [Acyrthosiphon pisum]
comp1082_c0_seq1	
comp1124_c0_seq1	
comp1953_c0_seq1	
comp319_c0_seq1	
comp1790_c0_seq1	GI12142 [Drosophila mojavensis] gi|193919466|gb|EDW18333.1| GI12142 [Drosophila mojavensis]
comp5612_c0_seq1	odorant-binding protein 5 [Metopolophium dirhodum]
comp7159_c0_seq1	
comp6983_c0_seq1	PREDICTED: hypothetical protein LOC100650488 [Bombus terrestris]
comp144_c0_seq1	
comp2637_c0_seq1	PREDICTED: opsin, ultraviolet-sensitive-like [Acyrthosiphon pisum]
comp363_c0_seq1	
comp1046_c0_seq1	
comp3237_c0_seq3	Dopamine beta-hydroxylase precursor, putative [Pediculus humanus corporis] gi|212509498|gb|EEB12867.1| Dopamine beta-hydroxylase precursor, putative [Pediculus humanus corporis]
comp2370_c0_seq1	PREDICTED: short neuropeptide F-like isoform 1 [Acyrthosiphon pisum] gi|328721243|ref|XP_003247251.1| PREDICTED: short neuropeptide F-like isoform 2 [Acyrthosiphon pisum]
comp8100_c0_seq1	PREDICTED: hypothetical protein LOC100160452 [Acyrthosiphon
comp3054_c0_seq1	putative rhodopsin [Oncometopia nigricans]
comp3077_c0_seq1	
comp4388_c0_seq1	PREDICTED: similar to CG6329-PB [Nasonia vitripennis]
comp6798_c0_seq1	PREDICTED: similar to CG12541 CG12541-PB [Tribolium castaneum] gi|270014059|gb|EFA10507.1| hypothetical protein TcasGA2_TC012755 [Tribolium castaneum]

comp317_c0_seq3	GA27408 [Drosophila pseudoobscura pseudoobscura] gi|198132577|gb|EDY68326.1| GA27408 [Drosophila pseudoobscura pseudoobscura]
comp1549_c0_seq1	PREDICTED: BTB/POZ domain-containing protein KCTD16-like [Bombus terrestris]
comp1661_c0_seq1	cytochrome B5 [Culicoides sonorensis]
comp1507_c0_seq1	GF21209 [Drosophila ananassae] gi|190618724|gb|EDV34248.1| GF21209 [Drosophila ananassae]
comp1326_c0_seq1	hypothetical protein EAG_09069 [Camponotus floridanus]
comp2391_c0_seq1	PREDICTED: PQ-loop repeat-containing protein 1-like [Acyrthosiphon pisum]
comp2090_c0_seq1	arylalkylamine N-acetyltransferase-like [Acyrthosiphon pisum] gi|239788497|dbj|BAH70924.1| ACYPI002543 [Acyrthosiphon pisum]
comp3063_c1_seq1	cuticular protein [Tenebrio molitor]
comp3034_c0_seq3	PREDICTED: synapse-associated protein of 47 kDa-like isoform 2 [Acyrthosiphon pisum]
comp7374_c0_seq1	
comp2800_c0_seq1	PREDICTED: UDP-glucuronosyltransferase 2B14-like [Acyrthosiphon pisum]
comp895_c0_seq2	PREDICTED: similar to npdc-1 [Nasonia vitripennis]
comp16101_c0_seq2	PREDICTED: similar to CG34127 CG34127-PA [Tribolium castaneum]
comp2468_c0_seq1	PREDICTED: hypothetical protein LOC100168705 [Acyrthosiphon
comp9538_c0_seq1	sodium-dependent nutrient amino acid transporter, putative [Pediculus humanus corporis] gi|212505979|gb|EEB10310.1| sodium-dependent nutrient amino acid transporter, putative [Pediculus humanus corporis]
comp4373_c0_seq1	PREDICTED: hypothetical protein LOC100573179 [Acyrthosiphon
comp309_c0_seq1	cathepsin B-like proteinase [Triatoma vitticeps]
comp632_c1_seq3	
comp74_c0_seq1	
comp3066_c0_seq1	
comp7571_c1_seq1	stearoyl-coa desaturase-like [Acyrthosiphon pisum] gi|239791638|dbj|BAH72259.1| ACYPI006757 [Acyrthosiphon pisum]
comp9736_c0_seq1	
comp3051_c0_seq1	
comp11042_c0_seq1	PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]
comp6763_c0_seq1	F-box/LRR-repeat protein, putative [Pediculus humanus corporis] gi|212506146|gb|EEB10443.1| F-box/LRR-repeat protein, putative [Pediculus humanus corporis]
comp152_c0_seq1	hypothetical protein TcasGA2_TC010476 [Tribolium castaneum]
comp1054_c0_seq1	hypothetical protein EAG_04387 [Camponotus floridanus]
comp412_c0_seq1	troponin C-like [Acyrthosiphon pisum] gi|239790194|dbj|BAH71673.1| ACYPI007392 [Acyrthosiphon pisum]
comp10488_c0_seq1	
comp2281_c0_seq2	
comp6621_c0_seq1	GF24229 [Drosophila ananassae] gi|190624385|gb|EDV39909.1| GF24229 [Drosophila ananassae]
comp1286_c0_seq1	
comp11024_c0_seq1	PREDICTED: hypothetical protein LOC100161072 [Acyrthosiphon
comp1227_c0_seq1	
comp2109_c0_seq1	

comp110_c0_seq3	myofilin isoform b [Acyrthosiphon pisum] gi|253735725|ref|NP_001156710.1| myofilin isoform b [Acyrthosiphon pisum] >gi|239793567|dbj|BAH72895.1| ACYPI002609 [Acyrthosiphon pisum]
comp2556_c0_seq1	
comp2100_c0_seq1	hypothetical protein TcasGA2_TC007091 [Tribolium castaneum]
comp151_c0_seq1	PREDICTED: hypothetical protein LOC100159632 [Acyrthosiphon
comp4772_c0_seq1	
comp1572_c0_seq1	PREDICTED: similar to short-chain dehydrogenase [Nasonia
comp10332_c0_seq2	PREDICTED: potassium channel subfamily T member 1-like [Acyrthosiphon pisum]
comp1430_c0_seq2	PREDICTED: neuroendocrine convertase 1-like [Acyrthosiphon pisum]
comp1349_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212516655|gb|EEB18641.1| conserved hypothetical protein [Pediculus humanus corporis]
comp4361_c0_seq1	PREDICTED: facilitated trehalose transporter Tret1-like [Acyrthosiphon pisum]
comp7895_c0_seq1	PREDICTED: similar to CG7120 CG7120-PA [Tribolium castaneum] gi|270014094|gb|EFA10542.1| hypothetical protein TcasGA2_TC012797 [Tribolium castaneum]
comp448_c0_seq2	hypothetical protein TcasGA2_TC013580 [Tribolium castaneum]
comp3728_c0_seq1	PREDICTED: hypothetical protein LOC100572962 [Acyrthosiphon
comp1514_c0_seq1	hypothetical protein NEMVEDRAFT_v1g4783 [Nematostella vectensis] gi|156207529|gb|EDO29409.1| predicted protein [Nematostella
comp1756_c0_seq1	
comp135_c0_seq1	
comp475_c0_seq1	
comp5841_c0_seq1	AGAP008442-PA [Anopheles gambiae str. PEST] gi|157014809|gb|EAA12647.4| AGAP008442-PA [Anopheles gambiae str. PEST]
comp5465_c0_seq1	
comp2961_c0_seq1	hypothetical protein TcasGA2_TC009699 [Tribolium castaneum]
comp2033_c0_seq10	hypothetical protein LOC678510 [Apis mellifera] gi|89274060|dbj|BAE80739.1| GB15078 [Apis mellifera]
comp1065_c0_seq1	tachykinin precursor [Rhodnius prolixus]
comp13129_c0_seq1	hypothetical protein TcasGA2_TC011555 [Tribolium castaneum]
comp665_c0_seq2	PREDICTED: similar to CG32171-PD [Nasonia vitripennis]
comp1509_c0_seq1	uridine diphosphate glucosyltransferase [Bombyx mori] gi|213494483|gb|ACJ48963.1| uridine diphosphate glucosyltransferase [Bombyx mori]
comp2414_c0_seq1	cathepsin B [Acyrthosiphon pisum]
comp1706_c0_seq1	salivary secreted protein [Triatoma infestans]
comp1561_c0_seq1	GF13563 [Drosophila ananassae] gi|190622137|gb|EDV37661.1| GF13563 [Drosophila ananassae]
comp362_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212510636|gb|EEB13772.1| conserved hypothetical protein [Pediculus humanus corporis]
comp697_c0_seq1	PREDICTED: probable maltase H [Acyrthosiphon pisum]
comp1568_c0_seq7	conserved hypothetical protein [Pediculus humanus corporis] gi|212509245|gb|EEB12690.1| conserved hypothetical protein [Pediculus humanus corporis]
comp4337_c0_seq1	PREDICTED: hypothetical protein LOC100161965 [Acyrthosiphon pisum] gi|239789069|dbj|BAH71182.1| ACYPI003149 [Acyrthosiphon

comp2170_c0_seq3	RecName: Full=Diuretic hormone; Short=DH; AltName: Full=Diuretic peptide; Short=DP gi|265669|gb|AAB25411.1| CRF-related diuretic peptide [Periplaneta americana=cockroaches, Peptide, 46 aa]
comp445_c0_seq1	PREDICTED: uncharacterized family 31 glucosidase KIAA1161-like [Acyrthosiphon pisum]
comp5210_c0_seq1	PREDICTED: hypothetical protein LOC100163035 [Acyrthosiphon
comp1163_c0_seq1	
comp444_c0_seq2	
comp139_c2_seq11	
comp2902_c0_seq3	unknown [Populus trichocarpa x Populus deltoides]
comp1804_c0_seq1	carbonic anhydrase II, putative [Aedes aegypti] gi|108874595|gb|EAT38820.1| carbonic anhydrase II, putative [Aedes aegypti]
comp8079_c0_seq2	GE20711 [Drosophila yakuba] gi|194179610|gb|EDW93221.1| GE20711 [Drosophila yakuba]
comp6093_c0_seq1	
comp2957_c0_seq1	cuticular protein analogous to peritrophins 3-D1 [Tribolium castaneum] gi|268309022|gb|ACY95477.1| cuticular protein analogous to peritrophins 3-D1 [Tribolium castaneum] >gi|270000884|gb|EEZ97331.1| hypothetical protein
comp1208_c0_seq1	
comp1200_c0_seq1	
comp2943_c0_seq4	hypothetical protein TcasGA2_TC000583 [Tribolium castaneum]
comp4572_c0_seq1	cuticle protein-like protein [Triatoma matogrossensis]
comp5284_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212518410|gb|EEB20163.1| conserved hypothetical protein [Pediculus humanus corporis]
comp5028_c0_seq1	angiotensin converting enzyme [Locusta migratoria]
comp1867_c0_seq4	
comp1094_c0_seq1	PREDICTED: orcokinin peptides type A-like [Acyrthosiphon pisum]
comp10061_c0_seq2	PREDICTED: similar to cationic amino acid transporter 4 [Tribolium castaneum] gi|270012508|gb|EFA08956.1| hypothetical protein TcasGA2_TC006663 [Tribolium castaneum]
comp68_c0_seq3	PREDICTED: myosin heavy chain, muscle isoform 1 [Acyrthosiphon pisum]
comp949_c0_seq1	
comp2462_c0_seq1	hypothetical protein SINV_04886 [Solenopsis invicta]
comp9147_c0_seq1	PREDICTED: guanine nucleotide-binding protein subunit beta-2-like [Acyrthosiphon pisum]
comp590_c0_seq1	conserved hypothetical protein [Pediculus humanus corporis] gi|212518565|gb|EEB20311.1| conserved hypothetical protein [Pediculus humanus corporis]
comp325_c0_seq1	hypothetical protein TcasGA2_TC004676 [Tribolium castaneum]
comp2241_c0_seq1	hypothetical protein SINV_00593 [Solenopsis invicta]
comp4421_c0_seq1	
comp1381_c0_seq2	conserved hypothetical protein [Pediculus humanus corporis] gi|212507456|gb|EEB11401.1| conserved hypothetical protein [Pediculus humanus corporis]
comp3643_c0_seq2	PREDICTED: endoplasmic reticulum aminopeptidase 2-like [Acyrthosiphon pisum]
comp2151_c0_seq1	
comp2419_c0_seq1	
comp2899_c0_seq1	

comp1247_c0_seq1	GH14220 [Drosophila grimshawi] gi|193891727|gb|EDV90593.1| GH14220 [Drosophila grimshawi]
comp34_c0_seq1	actin related protein 1 [Acyrthosiphon pisum] gi|242011914|ref|XP_002426688.1| Actin, muscle [Pediculus humanus corporis] >gi|46561736|gb|AAT01073.1| putative muscle actin [Homalodisca vitripennis] >gi|52630959|gb|AAU84943.1| putative muscle actin [Toxoptera citricida] >gi|53830696|gb|AAU95191.1| putative muscle actin [Oncometopia nigricans] >gi|77158630|gb|ABA62321.1| beta-actin [Reticulitermes flavipes] >gi|91221295|gb|ABE27979.1| putative muscle actin [Lygus lineolaris] >gi|212510859|gb|EEB13950.1| Actin, muscle [Pediculus humanus corporis] >gi|326490788|dbj|BAJ90061.1| predicted protein [Hordeum vulgare subsp. vulgare]

Table S3 Summary of reciprocal best matched sequences (RBMs).

	The number of pairs of RBMs*	CPAG**
Caf***	31,658	22,976
Cam	42,150	
Cuf	35,692	12,903
Cum	17,929	
Tof	31,560	22,465
Tom	36,318	
Cof	26,169	12,066
Com	17,110	

"*": The number of pairs of reciprocal best matched sequences of female or male host sample corresponding to pooled assembly result.

"**": The number of communal pooled assembly genes, between female RBMs pairs and male RBMs pairs.

"***": Caf and Cam mean cabbage host female and male population, respectively, the same to other host population like cucumber (Cuf and Cum), tomato (Tof and Tom) and cotton (Cof and Com).

Table S4 Summary of the differentially expressed genes between sexes.

	Differential expression genes	Female specific[*]	Male specific [**]
Caf/Cam	8,434	5,597	2,837
Cuf/Cum	7,817	5,824	1,993
Tof/Tom	6,967	4,304	2,663
Cof/Com	5,151	3,213	1,938

“*”: Q-value < 0.05 and $\log_2$(Fold change) > 1; Fold change = normalized reads count in female sample / normalized reads count in male sample.

“**”: Q-value < 0.05 and $\log_2$(Fold change) < -1;.

Table S5 Primers used for the qRT-PCR analyses.

		qPCR primer	
Num	**Gene name**	**F**	**R**
1	comp324_c0_seq1	CCATCTACCTTGAACGCACTT	GCCATCCGCTACCTGAAA
2	comp7837_c0_seq1	CCCTTCATTCCAGCCTAAATC	GAGTCCACGCAATAGTATTCC
3	comp4718_c0_seq1	TCAGTCGTGCCTTCATTGG	CCTTCTCGCCTACTACAACC
4	comp2284_c0_seq1	TCTGCCTTTCTCAATCCCTCAC	GTAAGCCGTCTCCAACATCAAG
5	comp4969_c0_seq1	GTCTTCAAATCCAGCCAGTAG	ACACATCTCTATGCTTCAACG
6	comp4647_c0_seq1	GTGGCTGCTGTGTAGAAAC	AATCGGTGCTTATCAACGC
7	comp6157_c0_seq1	TCGCTACATCCTTCTTCTG	TTCTCCATCAATTAACCTCTTC
8	comp5682_c0_seq1	GATACATAGGCTGCTAGTTTGG	GGTGACTGGAATCCGATGG
9	comp146_c0_seq1	CTGTGAGGTCGGTGTTAGC	GTGGTCATGTTGGAAGATTCG
10	comp3174_c0_seq1	TTGGAGGAGCATAGAGGTG	CTAACAGGAGAGTCATCATTTC
11	comp348_c0_seq4	AGTGTATCGGGCTTTGGAG	CATCTGTGTTGGAGAATCTGG
12	comp6152_c0_seq1	CCGCATATAACGAACGCCATC	CACTGTCCCTCCTAACTCTACG
13	comp2670_c0_seq1	GCCACGACAACCACAAATAGC	CACAGCCTTCAAGCACGATAAG
14	comp1092_c0_seq2	CAGATTGGATTGAAGAACTATG	GGGATGTTGTTGGCTTTAG
15	comp551_c0_seq1	AGGACGGTGGAAACTAACAG	ATACAAGCGAGGTCACAAATAC
16	comp3004_c0_seq1	ACCAGACTCAATTACTCGCTTC	GTGCCTTGCTCTCAACTCAG
17	comp1458_c0_seq1	ACTTCAACTTGGTTCTCCTC	TGGCTGCTAAGAAGACTTTC
18	comp7178_c0_seq1	CACTTCGGTCAACAACAAC	CTCCACTTCTCCTTTCTCG
19	comp6413_c0_seq2	TGCCAAGAACAGCCACGAC	GCCTCTACCAAAGCGGACTC
20	comp293_c0_seq1	TTGCCAGTTCTTCCATGATACG	ACCTTCGCCCGAGATTTCC
21	comp6113_c0_seq1	TGACAACGCTGACACTGAG	CGTGCTGTATTGCCTTCTAATC
22	comp5525_c0_seq1	ATTGGAATAACTTGCGATGGTG	ACGGTTGCCTTTCTGGATG
23	comp481_c0_seq1	TCACAAAATGGTTCGGAAAG	TGAAATGATACAGTTGATGGG
24	comp247_c0_seq1	AATCCGTTGCCTTGTCATCC	GGTCGTCATCGTGGTATTGG
25	comp4313_c0_seq1	ACAAGACAGCCAACAGAAGG	CCGCATACATCCACATCAAAG
26	comp2936_c0_seq1	AATCACAGTGGAGACCTTCATC	TCTTCTTCTCTGGCAGTTTCG
27	comp1339_c0_seq1	CTGTGCCATCAAGGTTCTG	AATATCGGAGTTGTCGTCTTC
28	comp1421_c0_seq1	CTTCAGTAGCCATCGTATCG	ATCCTCCGCATCTTTGTTG
29	comp4282_c0_seq2	TTCACATCCATCTTCTATCAG	TTTCCTCTTTCAGCCAATG
30	comp3363_c0_seq1	AGGTCGTGAAGATGTAGATGAG	GGTGGGATGTGAAACTGAAAC
31	comp2860_c0_seq1	TCCGATTAACTATCTGATTAGG	CAACCAGTATCTTAGAGTCC
32	comp216_c0_seq1	TGCGAGACAATGACTTACG	CTAACGGAGAAGACCATCAC
33	comp4143_c0_seq1	TGATGAAGTAGTTGAACGAATC	AGTCAGCAGTGGTAACAAG
34	comp2864_c0_seq1	ATGTATGCTGGTCTGGATG	TACTGGTAGAAGGTGTTGAG
35	comp5047_c0_seq1	TCATCTGGTTTCTCTGTTG	AATGGTTCTTCGTCTATGG
36	comp4780_c0_seq1	CTGATGTTATTAGTGGAGTGTC	GGATGATACCTTGTGTTGTTG
37	comp7198_c0_seq1	TCTGCTTCTTGCTGGTTTGG	ACTGGATTGTGGATGATGATGG
38	comp5583_c0_seq1	AGTGATGGTGATGACGATGAC	GACGAAATGCTTCTGTGTATGG
39	comp5474_c0_seq1	CCTTCGGCAAAACAATCTTTAG	TTCAGGAGTCAGGACAACG
40	comp2048_c0_seq1	AGTTGCCAATGAGAGGATACG	GGAGCCAGGTGTGATGAAG
41	comp179_c0_seq1	TAGGGTTCTACTTCTACATTGG	CTGAATTAGCCTGCGTTTAC
42	comp3132_c0_seq1	ACAACTATGCCTGCTCCTAC	ATGGTAATGCCTGGTGATAATG

43	comp2416_c0_seq4	GGGAATGCTGAATAAAGTAGAC	CGACGAAATGGAAGAGACC
44	comp2464_c0_seq1	CCAACTGTGAACCGAGAGG	CGAAGAAACCACCCATAAGAG
45	comp11720_c0_seq1	AGTGGTATTCGTAGAGGCATAG	TCGGATGTGATGGCAATGG
46	comp6781_c0_seq1	TGTGATAACGGTCCAAGATG	TATGAGGGCAATCCAGAGG
47	comp3888_c0_seq1	TCTTGGTTCTCTGCTATTTGAC	ATCTTGGCGGATACACTGC
48	comp3885_c0_seq1	TTTGACATTCCGTGCGTTTG	TTGCCACTCCCGATATTGC
49	comp2955_c0_seq1	TCTTTGTGTCGGACTATCTC	GGTAGTAGGGTGCGTATTG
50	comp1247_c0_seq1	CCATAGTGTTACGCCTAAG	CTTCTTTCCAAGTCTCTCC
51	comp7526_c0_seq3	TGCCGTCAACACAGTAATAG	GACTTGCCATTCAACATCG
52	comp1544_c0_seq1	CCTCTCGTTCGCCTCTAAC	ATACTGTGCTTCGGCTTGG
53	comp9147_c0_seq1	GGATAAGACCGCACGACTATTC	TGAGCCACAGAGGAGATAGC
54	comp2957_c0_seq1	CGCCACGAAGAGCATCATC	CGGTCTTACGAGTACGATTAGC
55	comp6912_c0_seq2	GGTGGTGGTGGTGGCTCTG	GTGGTCGTAGTTGTGGTTGTGG
56	comp1326_c0_seq1	CAACCTGCTTTCAACTTCAC	CTCTCCACATTCCCAATCG
57	comp3063_c1_seq1	TTACCGTGAGCATCCTGAAC	AAACCCAATACCACTCCCAAG
58	comp2170_c0_seq3	GTCCACAGTCTGAGCAATCC	GTTAGTATCCGCCTTCGTATCC
59	comp4572_c0_seq1	GGACTACAGCGTTGAAACC	AACCAGACAAGGAGACACC
60	comp34_c0_seq1	GCTCGTTGTAGAAGGTGTGATG	CCCAGTCCAAGAGAGGTATCC
61	comp3725_c0_seq6	GGAGTACGAGATGACAATACC	CAAGTAATAAGGACCGAAGAGG
62	comp2801_c0_seq1	GAAGTTGACCTGGGCGTAG	TCTGAGAATCCGTGTCGTG
63	comp634_c2_seq9	CGGACAGGACGGAACAAAC	GACGACGGCGAAGTATTGG
64	comp3102_c0_seq1	GGCGATGTCGTTCAGGGTAG	GTGTGGGTCAGCGGTGTAG
	RPL29	TCGGAAAATTACCGTGAG	GAACTTGTGATCTACTCCTCTCGTG

Table S6 qRT-PCR validation and comparative analyses with RNAseq data.

		qRT-PCR analyses				RNA sequencing				
		Mean Δct (mean±se)		The expression ratio $2^{-\Delta\Delta ct}$		log2(Fold_change) normalized				
Number[$]	Gene name	Male	Female	Significance[#]	Female/Male	TofvsTom	CufvsCum	CafvsCam	CofvsCom	Average
1	comp324_c0_seq1	0.54±0.13	0.50±0.22		1.03 >1	2.434175564	2.11066551	1.76937032	1.06757522	1.845446653
2	comp7837_c0_seq1	5.2±0.03	5.7±0.07	**	0.71	1.884507783	4.649603558	2.65321818	4.56012342	3.436863235
3	comp4718_c0_seq1	6.9±0.03	6.2±0.1	**	1.62 > 1	4.110145092	4.662396584	3.63771135	4.49533044	4.23 > 2
4	comp2284_c0_seq1	5.2±0.02	4.6±0.09	**	1.52 > 1	1.905370666	2.026732393	1.34643919	1.74091719	1.754864859
5	comp4969_c0_seq1	5.6±0.06	6.0±0.1	*	0.76	1.484874081	3.725267827	1.70704817	5.7235477	3.16 > 2
6	comp4647_c0_seq1	5.8±0.02	6.4±0.1	**	0.66	1.092299629	3.466340257	1.10991284	3.38060518	2.26 > 2
7	comp6157_c0_seq1	6.7±0.16	6.0±0.08	*	1.62 > 1	2.28674517	7.52180926	2.50703971	3.11537516	3.86 > 2
8	comp5682_c0_seq1	4.7±0.15	4.8±0.1		0.93	1.827643684	2.039049343	1.71725161	2.87368804	2.11 > 2
9	comp146_c0_seq1	0.21±0.03	(-0.025)±0.11		1.18 > 1	2.539082832	2.173598267	1.99778794	1.12916724	1.959909069
10	comp3174_c0_seq1	2.7±0.14	3.7±0.06	**	0.4973333	1.727603953	2.749147686	1.95168696	1.64006837	2.02 > 2
11	comp348_c0_seq4	0.86±0.06	0.79±0.09		1.05 > 1	2.162156838	3.07692534	1.89976491	1.12833922	2.07 > 2
12	comp6152_c0_seq1	6.7±0.04	6.3±0.18		1.32 > 1	2.068661908	4.064844499	3.36327707	4.48695165	3.50 >2
13	comp2670_c0_seq1	3.7±0.18	3.8±0.2		0.9323333	1.723653108	3.626668444	1.97814485	1.23858091	2.14 > 2
14	comp1092_c0_seq2	3.0±0.07	1.5±0.11	***	2.83 > 1	2.448858975	2.998227813	2.156869	1.43617853	2.26 > 2
15	comp551_c0_seq1	2.4±0.14	2.1±0.13		1.23 > 1	2.300617036	4.124596936	2.20448327	2.25984483	2.72 > 2
16	comp3004_c0_seq1	6.1±0.10	6.0±0.14		1.07 > 1	1.603506088	1.66871238	1.72597186	2.42887599	1.85676658
17	comp1458_c0_seq1	0.83±0.04	0.36±0.2	***	1.39 > 1	1.183736829	4.345223664	1.70126759	1.38262817	2.15 > 2
18	comp7178_c0_seq1	2.0±0.13	4.6±0.03	***	0.16	2.152260737	3.486974619	1.36912631	5.07076688	3.02 > 2
19	comp6413_c0_seq2	6.8±0.09	6.5±0.1		1.23 > 1	1.763500579	5.587585272	2.5142291	3.12241799	3.25 > 2
20	comp293_c0_seq1	0.86±0.04	0.73±0.03		1.09 > 1	2.163277898	2.791766088	1.89228481	1.03505498	1.970595944
21	comp6113_c0_seq1	4.4±0.13	4.5±0.03		0.9273333	1.745751984	4.61890676	3.60882575	2.89640812	3.22 > 2
22	comp5525_c0_seq1	3.4±0.10	4.7±0.07	***	0.41	2.235408786	8.301428013	2.53649272	2.97098525	4.01 > 2
23	comp481_c0_seq1	1.1±0.05	0.38±0.03	***	1.65 > 1	2.224663907	3.487300484	2.03239627	1.10853312	2.21 > 2
24	comp247_c0_seq1	0.27±0.08	(-0.52)±0.04	***	1.73 > 1	2.291326738	3.104952879	1.96606158	1.10122783	2.12 > 2
25	comp4313_c0_seq1	6.5±0.02	5.2±0.00	***	2.46 > 1	3.685344493	5.981852458	3.57431979	5.44331889	4.67 > 2
26	comp2936_c0_seq1	5.6±0.12	4.8±0.05	**	1.74 > 1	2.105837969	3.923517935	3.35223981	3.55458164	3.23 > 2

27	comp1339_c0_seq1	4.1±0.0	2.7±0.03	***	2.64 > 1	2.663641106	3.232097803	3.45390368	2.32051782	2.92 > 2
28	comp1421_c0_seq1	4.5±0.14	4.4±0.13		1.07 > 1	3.058171011	2.540014039	4.17323746	2.14672537	2.98 > 2
29	comp4282_c0_seq2	4.3±0.08	4.2±0.23		1.07 >1	1.317777909	6.926031505	2.39992718	2.06947511	3.18 > 2
30	comp3363_c0_seq1	3.6±0.09	4.0±0.02	*	0.7573333	1.469916901	2.189646403	1.5298989	2.53695451	1.931604179
31	comp2860_c0_seq1	3.1±0.16	3.7±0.08	*	0.66	1.206966093	4.187950699	1.91561384	1.54689839	2.21 > 2
32	comp216_c0_seq1	1.3±0.02	0.71±0.04	***	1.51 > 1	2.631716362	2.018396754	2.02037846	1.24519539	1.978921741
33	comp4143_c0_seq1	4.9±0.11	4.9±0.16		1.00 > 1	2.626778727	2.369167592	2.24252003	2.14576759	2.35 > 2
34	comp2864_c0_seq1	4.5±0.06	4.5±0.3		1.00 > 1	1.750348158	2.967625375	2.05059631	1.49454676	2.07 > 2
35	comp5047_c0_seq1	6.5±0.24	6.2±0.18		1.23 >1	2.520964061	6.24362285	4.70236005	3.45683647	4.23 > 2
36	comp4780_c0_seq1	4.9±0.16	4.1±0.05	*	1.74 > 1	5.316148489	7.581432055	4.75949827	6.18922732	5.96 > 2
37	comp7198_c0_seq1	6.0±0.09	6.1±0.03		0.93	4.289305608	5.73445282	3.81793009	3.86619529	4.43 > 2
38	comp5583_c0_seq1	6.5±0.17	5.7±0.1	*	1.74 > 1	2.362931449	8.92186798	4.82894224	5.33159381	5.36 > 2
39	comp5474_c0_seq1	4.9±0.07	5.0±0.05		0.93	1.850255366	4.776982864	2.15793806	3.51351248	3.07 > 2
40	comp2048_c0_seq1	7.1±0.10	5.7±0.02	***	2.64 > 1	3.131345373	5.510866335	4.12546948	2.84294236	3.90 > 2
41	comp179_c0_seq1	1.4±0.03	0.52±0.03	***	1.84 > 1	1.631547209	5.210097714	1.88404314	2.70344938	2.86 > 2
42	comp3132_c0_seq1	1.4±0.18	1.1±0.03		1.23 > 1	1.910577509	7.990373961	1.67102784	1.61485444	3.30 > 2
43	comp2416_c0_seq4	3.5±0.12	3.8±0.05		0.81	1.238623438	3.021705111	1.40602694	1.29674179	1.74077432
44	comp2464_c0_seq1	2.9±0.11	3.6±0.05	**	0.62	1.01362746	2.830519343	1.35351647	1.0859038	1.570891769
45	comp11720_c0_seq1	8.2±0.04	7.7±0.12	***	1.41 > 1	6.554687029	4.206174458	3.89885075	4.15996451	4.70 > 2
46	comp6781_c0_seq1	7.3±0.15	7.5±0.00		0.87	1.618489518	3.275208043	2.07704967	6.23532585	3.30 > 2
47	comp3888_c0_seq1	6.9±0.18	5.4±0.00	**	2.83 > 1	2.244216271	3.805153537	4.10511613	2.82668456	3.25 > 2
48	comp3885_c0_seq1	8.3±0.2	6.1±0.06	***	4.59 > 1	3.025382723	6.850416924	3.57468795	4.95921547	4.60 > 2
					Male/Female					
49	comp2955_c0_seq1	2.2±0.03	6.4±0.14	***	18.4 > 1	-2.493729422	-3.16174065	-2.89677336	-1.8834825	(-2.61) < -2
50	comp1247_c0_seq1	(-1.4)±0.05	1.4±0.04	***	6.96 > 1	-2.026726664	-1.11056694	-4.66348629	-1.7798178	(-2.40) < -2
51	comp7526_c0_seq3	2.6±0.16	5.0±0.08	***	5.28 > 1	-1.278159541	-1.82997121	-3.6368774	-2.4345209	(-2.29) < -2
52	comp1544_c0_seq1	2.8±0.19	4.4±0.09	**	3.03 > 1	-2.901270922	-1.72130228	-4.65960214	-2.0629037	(-2.84) < -2
53	comp9147_c0_seq1	3.1±0.05	5.4±0.00	***	4.92 > 1	-1.945714422	-1.760486	-2.15488543	-2.3329349	(-2.05) < -2
54	comp2957_c0_seq1	3.4±0.12	5.6±0.1	***	4.59 > 1	-1.858174587	-1.99930586	-1.3728331	-1.9855221	-1.8
55	comp6912_c0_seq2	2.7±0.15	6.9±0.05	***	18.4 > 1	-3.384931938	-2.21276837	-2.3793914	-1.690391	(-2.42) < -2
56	comp1326_c0_seq1	1.8±0.05	4.7±0.1	***	7.46 > 1	-2.327329687	-1.83912669	-2.31347968	-2.3416269	(-2.21) < -2
57	comp3063_c1_seq1	0.7±0.1	4.2±0.1	***	11.3 > 1	-3.033413149	-2.61137519	-2.9367121	-2.4169628	(-2.75) < -2

58	comp2170_c0_seq3	7.7 ±0.1	7.5 ±0.1		0.871	-2.380423026	-2.05599787	-3.03948815	-2.4066335	(-2.47) < -2	
59	comp4572_c0_seq1	3.8 ±0.09	5.9 ±0.19	***	4.29 > 1	-2.398537969	-3.26974059	-6.44088776	-2.0725053	(-3.55) < -2	
60	comp34_c0_seq1	(-3.4) ±0.14	(-0.80) ±0.07	***	6.06 > 1	-1.389336008	-3.34592023	-2.56927462	-1.6409565	(-2.24) < -2	
61	comp3725_c0_seq6	1.4 ±0.06	4.5 ±0.00	***	8.57 > 1	-2.472388813	-1.42730154	-1.61923938	-1.700457		-1.8
62	comp2801_c0_seq1	3.0 ±0.1	5.8 ±0.05	***	6.96 > 1	-1.847586943	-1.16631338	-2.48064497	-2.2754671		-1.94
63	comp634_c2_seq9	5.1 ±0.15	8.0 ±0.2	***	7.46 > 1	-3.657515211	-2.40929013	-2.7401361	-3.6422711	(-3.11) < -2	
64	comp3102_c0_seq1	1.0 ±0.2	4.6 ±0.24	***	12.1 > 1	-1.787179932	-2.30957043	-7.51866243	-2.9313057	(-3.64) < -2	

"$": Number 1-48 is from female enriched genes and number 49-64 is from male enriched genes.

"#": * means P<0.05; ** means P<0.01; *** means P<0.001.