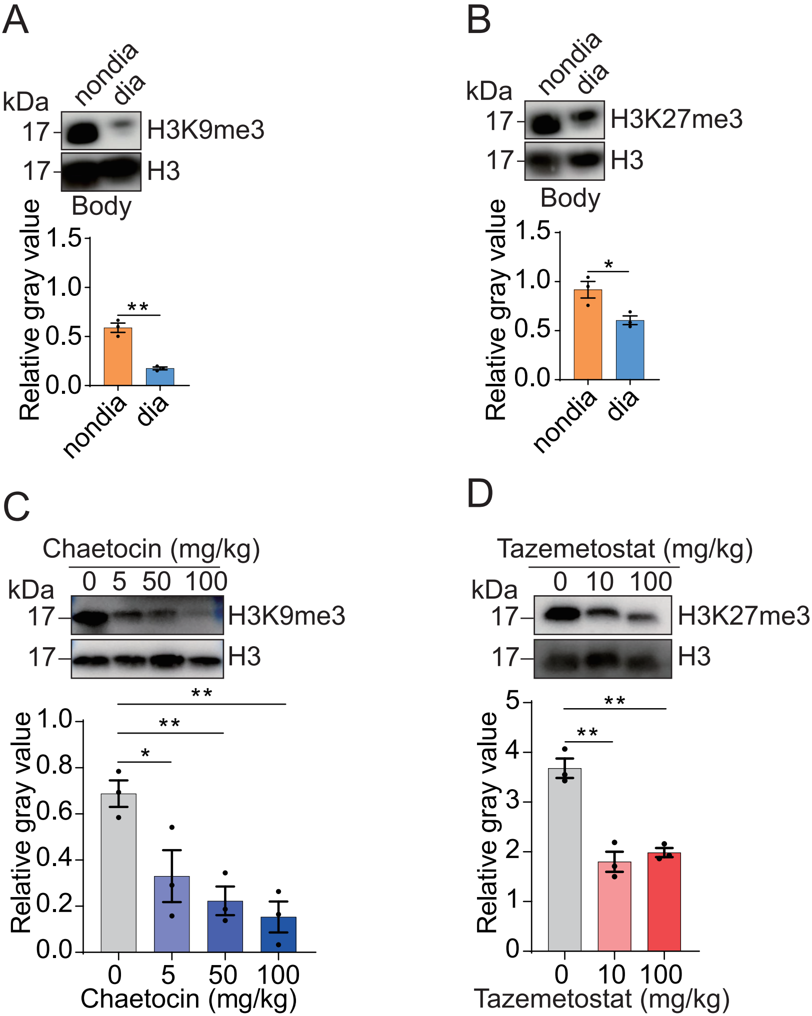
Supplementary Figures and Tables for

Genome-wide profiles of H3K9me3, H3K27me3 modifications and DNA methylation during diapause of Asia corn borer (*Ostrinia furnacalis*)

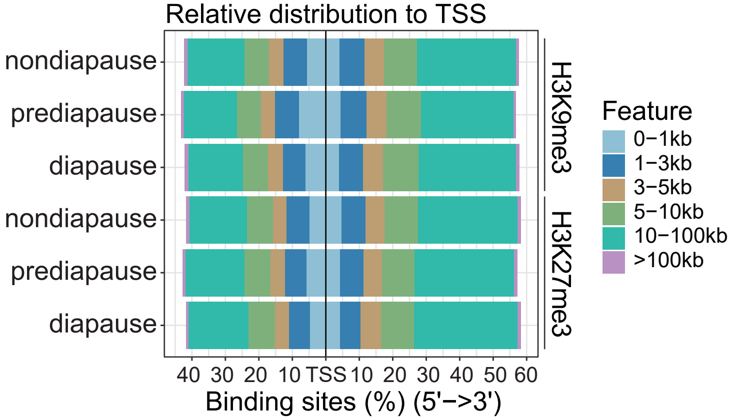
Supplemental_Fig_S1



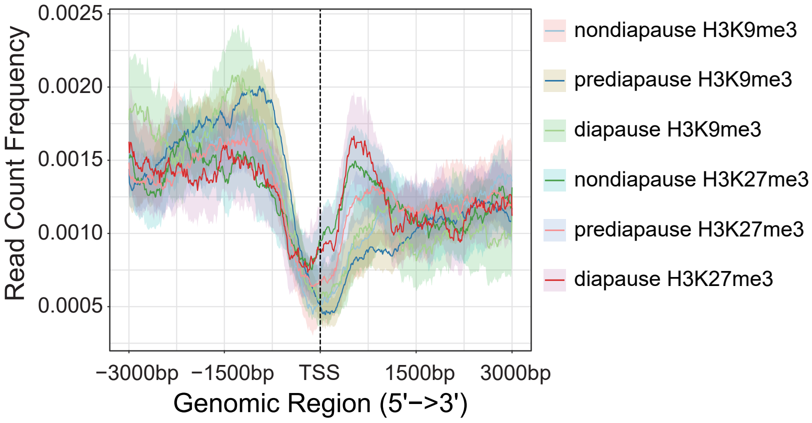
Supplemental Figure S1. H3K9me3 and H3K27me3 were also reduced in the body during diapause. (*A-B*) Western blot analysis of H3K9me3 and H3K27me3 of the body of Asian corn borer larvae using corresponding antibodies detecting the methylation of histone H3. The antibody against total H3 served as the loading control. The relative gray values of Western blot were measured using Image J. Statistical differences were measured using unpaired *t*-test, ** $p < 0.01$. Error bars show the mean ± SEM. (*C*) The effects of the SUV39H2-like inhibitor Chaetocin on H3K9me3 were dependent on the concentration. The relative gray values of Western blot were measured using Image J. Statistical differences were measured using unpaired *t*-test, * $p < 0.05$, ** $p < 0.01$. Error bars show the mean ± SEM. (*D*) The effects of the E(Z) inhibitor Tazemetostat on H3K27me3 were dependent on the concentration. The relative gray values of Western blot were measured using Image J. Statistical differences were measured using unpaired *t* test, ** $p < 0.01$, error bars show the mean ± SEM.

Supplemental_Fig_S2

A

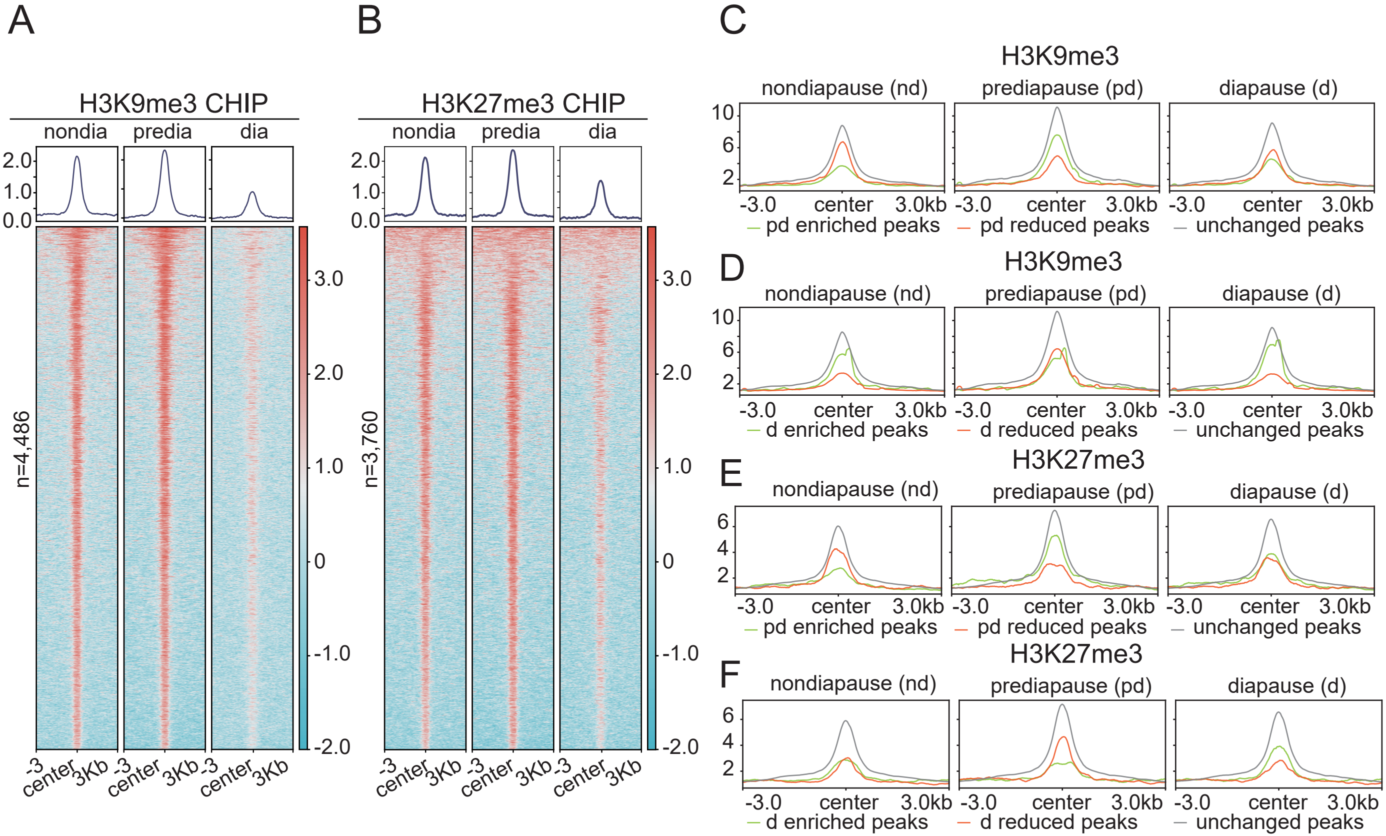


B



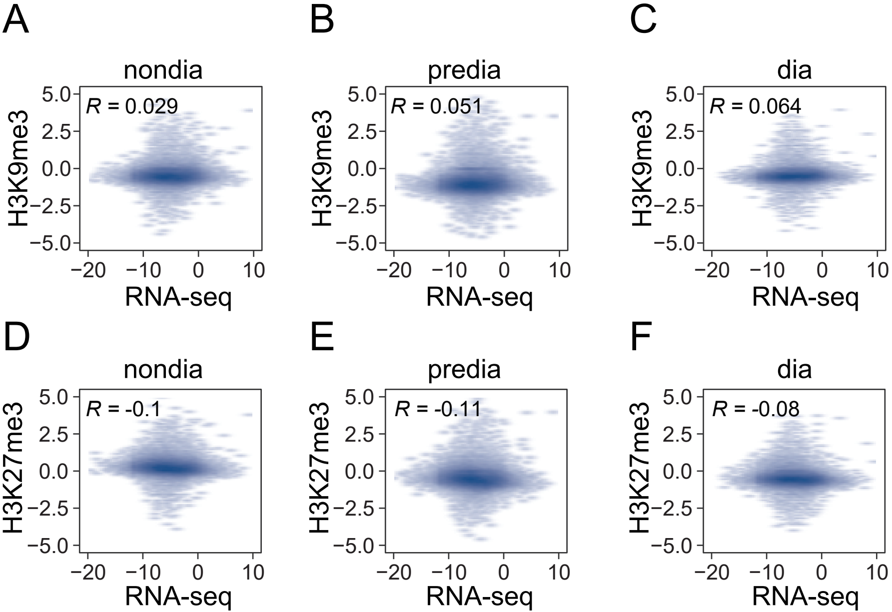
Supplemental Figure S2. Genomic distribution features of H3K9me3 and H3K27me3 modifications. (*A*) Distribution of the H3K9me3 and H3K27me3 peaks relative to the transcription start site (TSS). (*B*) Average profile of peaks of modifications in the TSS region (±3 kb). 95% confidence intervals were calculated for each cluster of genes.

Supplemental_Fig_S3



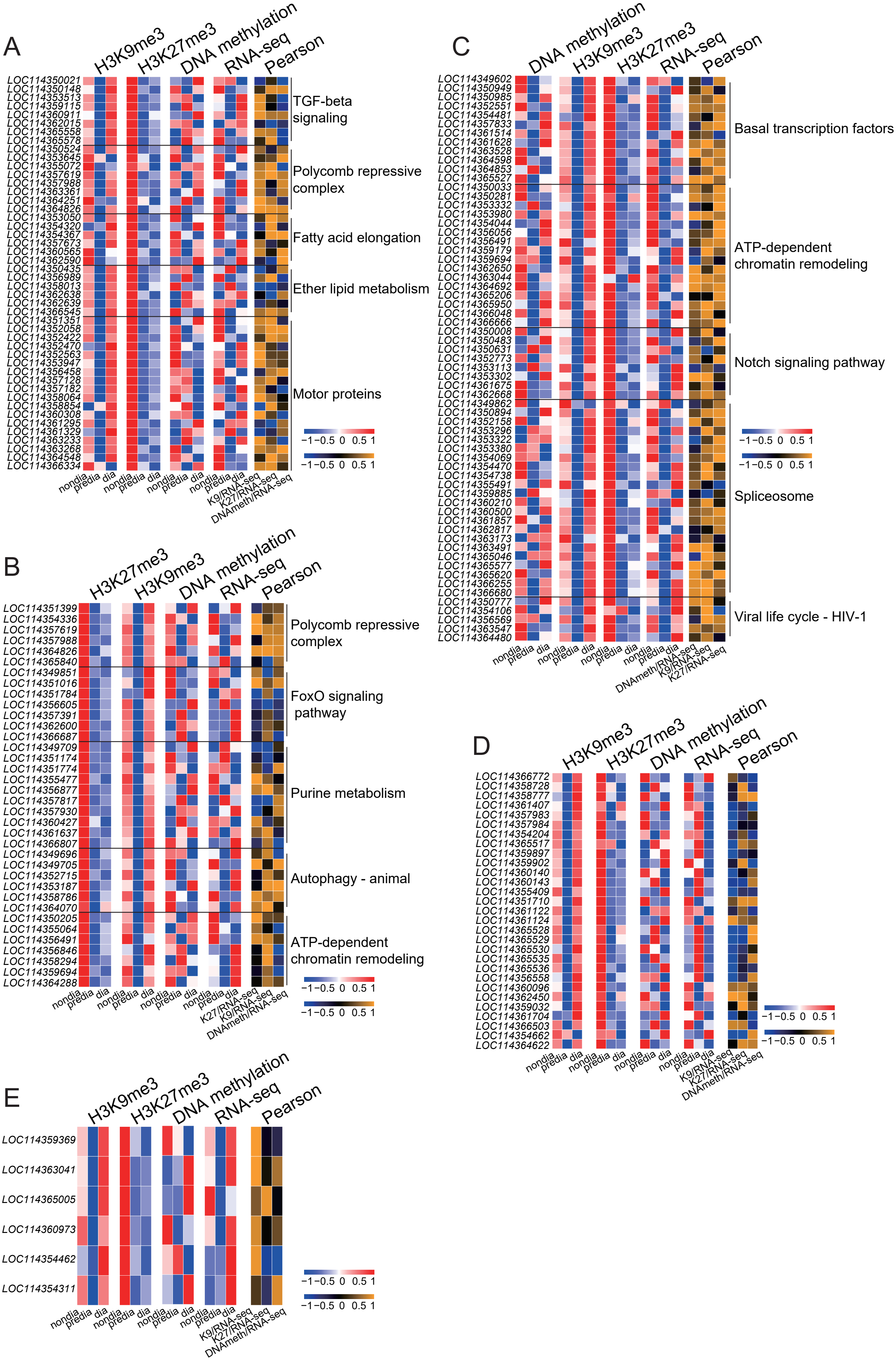
Supplemental Figure S3. The heatmap of ChIP-seq signals in the head of Asian corn borer larvae shows dynamic changes of H3K9me3 and H3K27me3 at different developmental stages. (*A*) Heatmap depicting H3K9me3 ChIP-seq signals in Asian corn borer larvae heads at nondiapause (left), prediapause (middle) or diapause (right) stages. The signals are centered around all H3K9me3 peaks in nondiapause larvae heads, with the peaks ordered vertically by signal strength. (*B*) Heatmap illustrating H3K27me3 ChIP-seq signals in Asian corn borer larvae heads at nondiapause (left), prediapause (middle) or diapause (right) stages. The signals are centered around all H3K27me3 peaks in nondiapause larvae heads. (*C-F*) Metaplot showing H3K9me3 and H3K27me3 ChIP-seq signals in Asian corn borer larvae heads at nondiapause (left), prediapause (middle) or diapause (right) stages, centered at statistically significant differential H3K9me3 and H3K27me3 peaks. The peaks are generated by comparing prediapause with nondiapause larvae (*C, E*) and comparing diapause with nondiapause larvae (*D, F*).

Supplemental_Fig_S4



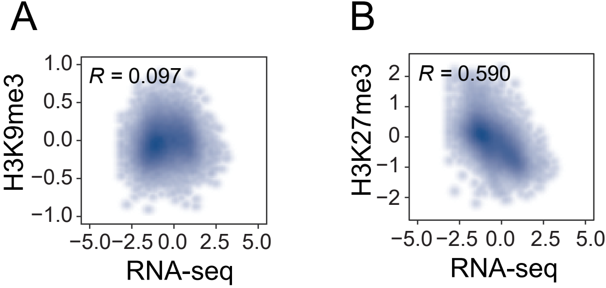
Supplemental Figure S4. There is no correlation between H3K9me3 or H3K27me3 and gene expression in the head of Asian corn borer larvae. (*A-C*) Genome-wide correlation plots of H3K9me3 and gene counts in nondiapause, prediapause and diapause stages. (*D-F*) Genome-wide correlation plots of H3K27me3 and gene counts in nondiapause, prediapause and diapause stages.

Supplemental_Fig_S5



Supplemental Figure S5. Epigenetic modifications regulate the expression levels of genes known to be important for diapause regulation. (*A-C*) Heatmaps showing the levels of the three chromosome modifications (rows 1-3), the gene expression levels (row 4) and the correlation between chromosomal modification and gene expression levels (row 5) of specific genes clustered to certain pathways. Clustered pathways selected from Fig. 6D were shown in A, B, C respectively. (*D*) Heatmaps showing the dynamics of the three chromosome modifications (rows 1-3), the gene expression levels (row 4) and the correlation between chromosomal modification and gene expression levels (row 5) of genes belonged to the juvenile hormone Pathway during Asian corn borer larvae diapause. (*E*) Heatmaps showing the dynamics of the three chromosome modifications (rows 1-3), the gene expression levels (row 4) and the correlation between chromosomal modification and gene expression levels (row 5) of clock genes during Asian corn borer larvae diapause.

Supplemental_Fig_S6



Supplemental Figure S6. Genome-wide correlation plots of H3K9me3 or H3K27me3 and gene counts in *B. mori*.

Supplemental_Table_S1

Fig.7A

Gene	Gene description
LOC114366772	4-nitrophenylphosphatase-like
LOC114358728	farnesol dehydrogenase-like
LOC114365517	juvenile hormone acid O-methyltransferase
LOC114365530	juvenile hormone esterase-like
LOC114360096	cholesterol 7-desaturase-like
LOC114362450	cholesterol 7-desaturase-like
LOC114359032	cytochrome P450 307a1

Supplemental Figure S5A

Gene	Gene description
LOC114350021	bone morphogenetic protein receptor type-1B
LOC114350148	uncharacterized *LOC114350148*
LOC114353513	mothers against decapentaplegic homolog 6
LOC114359115	iroquois-class homeodomain protein IRX-1-like
LOC114360911	activin receptor type-1-like
LOC114362015	cullin-1
LOC114365558	E3 ubiquitin-protein ligase SMURF1-like
LOC114365578	protein extra-macrochaetae
LOC114350524	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit
LOC114353645	testis-expressed protein 10 homolog
LOC114355072	ubiquitin carboxyl-terminal hydrolase calypso
LOC114357619	YY1-associated factor 2
LOC114357988	polycomb protein Sfmbt-like
LOC114363361	protein Jumonji
LOC114364251	transcription factor Dp-1
LOC114364826	WD repeat-containing protein 5
LOC114353050	very-long-chain 3-oxoacyl-CoA reductase
LOC114354320	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase hpo-8
LOC114354367	elongation of very long chain fatty acids protein AAEL008004-like
LOC114357673	elongation of very long chain fatty acids protein 7-like
LOC114360565	elongation of very long chain fatty acids protein AAEL008004
LOC114362590	elongation of very long chain fatty acids protein 6-like
LOC114350435	uncharacterized *LOC114350435*
LOC114356989	lissencephaly-1 homolog
LOC114358013	ethanolaminephosphotransferase 1-like
LOC114362638	putative phosphatidate phosphatase
LOC114362639	putative phosphatidate phosphatase
LOC114366545	phospholipid phosphatase 2-like
LOC114351351	kinesin-like protein unc-104
LOC114352058	dynein heavy chain, cytoplasmic
LOC114352422	unconventional myosin IC
LOC114352470	dynein light chain roadblock-type 1-like
LOC114352563	bicaudal D-related protein homolog
LOC114353947	kinesin-like protein KIF16B
LOC114356458	tropomyosin-2
LOC114357128	kinesin-like protein Klp10A
LOC114357182	dynactin subunit 1
LOC114358064	kinesin-like protein KIF3A
LOC114358854	dynein light chain 1, axonemal-like
LOC114360308	dynein heavy chain 3, axonemal
LOC114361295	dynein beta chain, ciliary-like
LOC114361329	uncharacterized *LOC114361329*
LOC114363233	tubulin beta-1 chain
LOC114363268	tubulin alpha chain
LOC114364548	kinesin-like protein KIN-5D
LOC114366334	kinesin-related protein 4-like

Supplemental Figure S5B

Gene	Gene description
LOC114351399	ubiquitin carboxyl-terminal hydrolase 7-like
LOC114354336	polyhomeotic-proximal chromatin protein-like
LOC114357619	YY1-associated factor 2
LOC114357988	polycomb protein Sfmbt-like
LOC114364826	WD repeat-containing protein 5
LOC114365840	polycomb protein suz12-B
LOC114349851	G2/mitotic-specific cyclin-B
LOC114351016	autophagy protein 12-like
LOC114351784	fork head domain transcription factor slp2-like
LOC114356605	gamma-aminobutyric acid receptor-associated protein
LOC114357391	catalase-like
LOC114362600	forkhead box protein O
LOC114366687	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3
LOC114349709	guanylate cyclase 32E
LOC114351174	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase-like
LOC114351774	bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase
LOC114355477	cAMP-specific 3',5'-cyclic phosphodiesterase
LOC114356877	adenylosuccinate synthetase
LOC114357817	xanthine dehydrogenase-like
LOC114357930	high affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8
LOC114360427	probable 3',5'-cyclic phosphodiesterase pde-5
LOC114361637	snake venom 5'-nucleotidase
LOC114366807	adenylate cyclase type 7-like
LOC114349696	MIP18 family protein galla-1
LOC114349705	phosphatidylinositol 3-kinase catalytic subunit type 3
LOC114352715	hypoxia-inducible factor 1-alpha-like
LOC114353187	high mobility group protein DSP1-like
LOC114358786	vacuole membrane protein 1
LOC114364070	TNF receptor-associated factor 4-like
LOC114350205	metastasis-associated protein MTA1
LOC114355064	uncharacterized *LOC114355064*
LOC114356491	mortality factor 4-like protein 1
LOC114356846	inorganic pyrophosphatase
LOC114358294	bromodomain adjacent to zinc finger domain protein 2B-like
LOC114359694	ubiquitin carboxyl-terminal hydrolase isozyme L5-like
LOC114364288	uncharacterized *LOC114364288*

Supplemental Figure S5C

Gene	Gene description
LOC114349602	TATA box-binding protein-like protein 1
LOC114350949	general transcription factor IIH subunit 1
LOC114350985	transcription initiation factor TFIID subunit 3
LOC114352551	transcription initiation factor TFIID subunit 11
LOC114354481	transcription initiation factor TFIID subunit 5
LOC114357833	general transcription factor IIH subunit 3
LOC114361514	general transcription factor IIF subunit 1
LOC114361628	general transcription and DNA repair factor IIH helicase subunit XPB
LOC114363528	transcription initiation factor TFIID subunit 6
LOC114364598	transcription initiation factor TFIID subunit 1
LOC114364853	transcription initiation factor TFIID subunit 4
LOC114365527	transcription initiation factor IIA subunit 1
LOC114350033	histone acetyltransferase Tip60
LOC114350281	actin-related protein 6
LOC114353332	ruvB-like helicase 1
LOC114353980	nucleosome-remodeling factor subunit NURF301
LOC114354044	probable histone-binding protein Caf1
LOC114356056	protein polybromo-1
LOC114356491	mortality factor 4-like protein 1
LOC114359179	uncharacterized *LOC114359179*
LOC114359694	ubiquitin carboxyl-terminal hydrolase isozyme L5-like
LOC114362650	bromodomain-containing protein 7
LOC114363044	YEATS domain-containing protein 4
LOC114364692	ATP-dependent helicase brm
LOC114365206	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1-A
LOC114365950	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-like
LOC114366048	chromatin complexes subunit BAP18-like
LOC114366666	transformation/transcription domain-associated protein
LOC114350008	histone deacetylase Rpd3
LOC114350483	C-terminal-binding protein
LOC114350631	fringe glycosyltransferase
LOC114352773	puff-specific protein Bx42
LOC114353113	corepressor interacting with RBPJ 1
LOC114353302	segment polarity protein dishevelled homolog DVL-3
LOC114361675	protein split ends-like
LOC114362668	CREB-binding protein-like
LOC114349862	survival of motor neuron-related-splicing factor 30
LOC114350894	ATP-dependent RNA helicase DBP2-A-like
LOC114352158	transformer-2 protein homolog beta
LOC114353296	U4/U6 small nuclear ribonucleoprotein Prp3
LOC114353322	serine/arginine-rich splicing factor 1A
LOC114353380	splicing factor 3A subunit 1
LOC114354069	pre-mRNA-splicing factor 38-like
LOC114354470	pre-mRNA-processing factor 40 homolog A
LOC114354738	THO complex subunit 2
LOC114355491	U2 small nuclear ribonucleoprotein A
LOC114357330	heat shock protein 68-like
LOC114359885	small nuclear ribonucleoprotein-associated protein B
LOC114360210	heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog
LOC114360500	putative pre-mRNA-splicing factor ATP-dependent RNA helicase PRP1
LOC114361857	cell division cycle 5-like protein
LOC114362817	U1 small nuclear ribonucleoprotein A
LOC114363173	U4/U6.U5 tri-snRNP-associated protein 2
LOC114363491	pre-mRNA-processing factor 6
LOC114365046	serine-arginine protein 55
LOC114365577	splicing factor 3B subunit 3
LOC114365620	WW domain-binding protein 11
LOC114366255	ATP-dependent RNA helicase dbp2-like
LOC114366680	putative U5 small nuclear ribonucleoprotein 200 kDa helicase
LOC114350777	RNA polymerase II elongation factor Ell
LOC114354106	GTP-binding nuclear protein Ran
LOC114356569	cleavage and polyadenylation specificity factor subunit CG7185
LOC114363547	E3 SUMO-protein ligase RanBP2-like
LOC114364480	cyclin-T

Supplemental Figure S5D

Gene	Gene description
LOC114366772	4-nitrophenylphosphatase-like
LOC114358728	farnesol dehydrogenase-like
LOC114358777	farnesol dehydrogenase-like
LOC114361407	farnesol dehydrogenase-like
LOC114357983	aldehyde dehydrogenase X, mitochondrial-like
LOC114357984	aldehyde dehydrogenase X, mitochondrial-like
LOC114354204	aldehyde dehydrogenase, mitochondrial
LOC114365517	juvenile hormone acid O-methyltransferase
LOC114359897	farnesoate epoxidase-like
LOC114359902	juvenile hormone epoxide hydrolase-like
LOC114360140	juvenile hormone epoxide hydrolase-like
LOC114360143	juvenile hormone epoxide hydrolase-like
LOC114355409	juvenile hormone epoxide hydrolase-like
LOC114351710	juvenile hormone epoxide hydrolase-like
LOC114361122	juvenile hormone esterase-like
LOC114361124	juvenile hormone esterase-like
LOC114365528	juvenile hormone esterase-like
LOC114365529	juvenile hormone esterase-like
LOC114365530	juvenile hormone esterase-like
LOC114365535	juvenile hormone esterase-like
LOC114365536	juvenile hormone esterase-like
LOC114356558	juvenile hormone esterase-like
LOC114360096	cholesterol 7-desaturase-like
LOC114362450	cholesterol 7-desaturase-like
LOC114359032	cytochrome P450 307a1
LOC114361704	cytochrome P450 306a1
LOC114366503	cytochrome P450 302a1, mitochondrial
LOC114354662	cytochrome P450 315a1, mitochondrial
LOC114364622	ecdysone 20-monooxygenase

Supplemental Figure S5E

Gene	Gene description
LOC114359369	circadian locomoter output cycles protein kaput-like
LOC114363041	protein cycle
LOC114365005	period circadian protein
LOC114360973	protein timeless
LOC114354462	cryptochrome-1
LOC114354311	cryptochrome-1-like

Supplemental table S1. Gene description corresponding to Fig.7 and Supplemental Fig. S5.

Supplemental_Table_S2

Primers	**Sequence (5’-3’)**
LOC114366772 F	GATCGGGCCAGTGAACGTAA
LOC114366772 R	CGAAGAACTCCCCTGAACCC
LOC114358728 F	TTAAGACGGCGGGGATTGAA
LOC114358728 R	ACCTGAATACTACGCGGTGC
LOC114365517 F	CTTCGACCTGCTCACTCCAG
LOC114365517 R	TGGTACGGCGATATGAACCG
LOC114365530 F	AAACTGGCCCCATTTGTCCT
LOC114365530 R	GGCACGTGGATGTTGATTCG
LOC114360096 F	ACAAAATCTTCGTGGGGGCT
LOC114360096 R	AAGCTCTTGCTGTTCTCGCT
LOC114362450 F	GATACAAGATACCCCCGCCG
LOC114362450 R	TGACCCAAGACATCCACTGC
LOC114359032 F	TTTGCGACTCGGGTATGGAG
LOC114359032 R	CCAATGCAGGTACGTTTGCC

Supplemental table S2. Primers used in this study.