Legends for Supplementary Figures

Fig. S1. Expression profiling of *BmHP1a* and *BmHP1b*.

The *BmHP1a* (A) and *BmHP1b* (B) mRNA expression levels in 17 different tissues from day three fifth-instar larvae. RT-qPCR was performed using total RNA from the brain (BR), prothoracic gland (PG), salivary gland (SG), fat body (FB), trachea (TR), hemocyte (HC), testis (TES), ovary (OV), anterior silkgland (ASG), middle silkgland (MSG), posterior silkgland (PSG), foregut (FG), midgut (MG), hindgut (HG), Malpighian tubules (MT), integument (IG), and BmN4 cells (BmN). *rp49* was used as an internal control.

Fig. S2. BmHP1a enrichment for 121 well-annotated silkworm transposons.

We mapped the ChIP-seq data from BmHP1a-BmN4 and pIZ-BmN4 (control) cells to 121 well-annotated silkworm transposons. Transposons shown in red letters are known to belong to the telomere-specific transposon family.

Fig. S3. Four additional histone marks and RNA polymerase II binding for Fig. 2.

The ChIP-seq data for one euchromatic mark (H3K27ac), two heterochromatic marks (H3K27me3, H3K36me3), one enhancer mark (H3K4me1) and RNA polymerase II (Pol2)-binding sites were added to Fig. 2A.

Fig. S4. An example of a BmHP1a-binding locus observed on chromosome 23.

(A) The BmHP1a-binding locus on chromosome 23: 9,344,991–9,366,591. The mapped reads were visualized using the Genome studio (Illumina). The BmHP1a binding region is indicated by the orange box. At this locus, BmHP1a binds to the upstream region of two head-to-head located genes, *BGIBMGA011491 and BGIBMGA011523*.

(B–C) ChIP-qPCR experiments. The ChIP-seq data in Fig. S4A were validated by ChIP-qPCR. The locations of the primers are indicated in Fig. S4A. The BmHP1a binding region is indicated by the orange box. The data are shown as means ± SD (n = 3). ** $P < 0.01$ with Student's *t*-test.

Fig. S5. Expression levels of the gene groups classified according to the distance between each gene and the nearest BmHP1a peak.

The data are shown as *box-and-whisker* diagrams. The boxes represent the medians and the 25th–75th percentile ranges of the expression levels. The *whiskers* indicate the most extreme data points, which were no more than 1.5-fold beyond the interquartile ranges represented by the *boxes*. Data were subjected to pair-wise *t*-tests for all combinations. Statistically significant values ($P < 0.05$) are indicated by different letters.

Fig. S6. RT-qPCR analysis of the genes that were examined in Fig. 6B–D following treatment of NIAS-Bm-M1 cells with *BmHP1a* siRNA.

(A) RT-qPCR analysis of the five genes examined in Fig. 6B in *BmHP1a* siRNA-transfected NIAS-Bm-M1 cells.

(B) RT-qPCR analysis of the five genes examined in Fig. 6C in *BmHP1a* siRNA-transfected NIAS-Bm-M1 cells.

(C) RT-qPCR analysis of the five genes examined in Fig. 6D in *BmHP1a* siRNA-transfected NIAS-Bm-M1 cells.

* $P < 0.05$, ** $P < 0.01$ with Student's *t*-test. The data are shown as means ± SD (n = 3).

Fig. S7. RT-qPCR analysis of the genes that were examined in Fig. 6B–D following treatment of BmVF cells with *BmHP1a* siRNA.

(A) RT-qPCR analysis of the five genes examined in Fig. 6B in *BmHP1a* siRNA-transfected BmVF cells.

(B) RT-qPCR analysis of the five genes examined in Fig. 6C in *BmHP1a* siRNA-transfected BmVF cells.

(C) RT-qPCR analysis of the five genes examined in Fig. 6D in *BmHP1a* siRNA-transfected BmVF cells.

* $P < 0.05$, ** $P < 0.01$ with Student's *t*-test. The data are shown as means ± SD (n = 3).

Fig. S8. RT-qPCR analysis of the genes that were selected in Fig. 2A and Fig. S4 following treatment with *BmHP1a* siRNA.

RT-qPCR analysis of the four genes examined in Fig. 2A and Fig. S4 in *BmHP1a* siRNA-transfected cells.

* $P < 0.05$, ** $P < 0.01$ with Student's *t*-test. The data are shown as means ± SD (n = 6).

Fig. S9. The levels of BmHP1a binding.

The median of BmHP1a-binding level at 50-base resolution in a 2-kb region from the first nucleotide of the upregulated (red line), unchanged (black line) and downregulated (blue line) genes in the *BmHP1a*-depleted cells was shown in the upper panel. The raw data within 0.5-kb regions from the first nucleotide of the genes are shown in the lower panel as *box-and-whisker* diagrams. The boxes represent the medians and the 25th–75th percentile ranges of the modification levels. The *whiskers* indicate the most extreme data points, which were no more than 1.5-fold beyond the interquartile ranges represented by the *boxes*. * $P < 0.05$ with Student's *t*-test.

Fig. S10. Tissue distributions of BmHP1a-regulated genes.

The tissue distributions of upregulated (A) or downregulated (B) genes in *BmHP1a*-depleted cells were examined in a BLAST analysis, using the expressed sequence tags from 15 full-length cDNA libraries (Table S2).

Fig. S11. RT-qPCR analysis of the genes that were examined in Fig. 6B–D following treatment with *BmHP1b* siRNA.

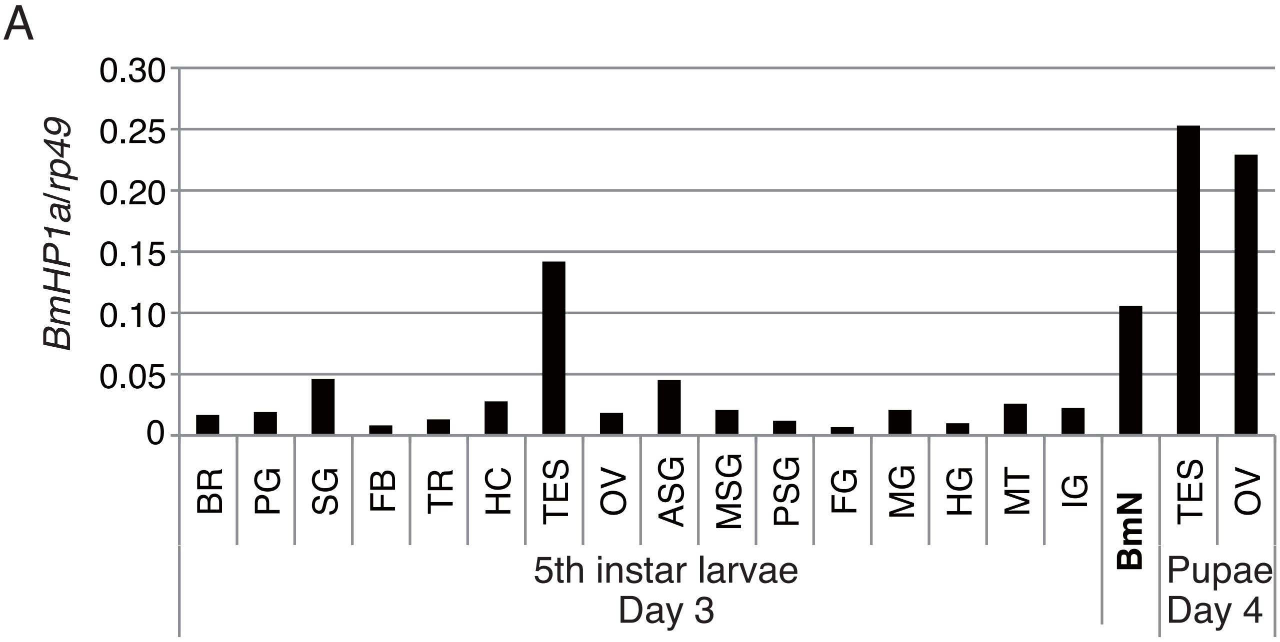
(A) RT-qPCR analysis of the five genes examined in Fig. 6B in *BmHP1b* siRNA-transfected cells.

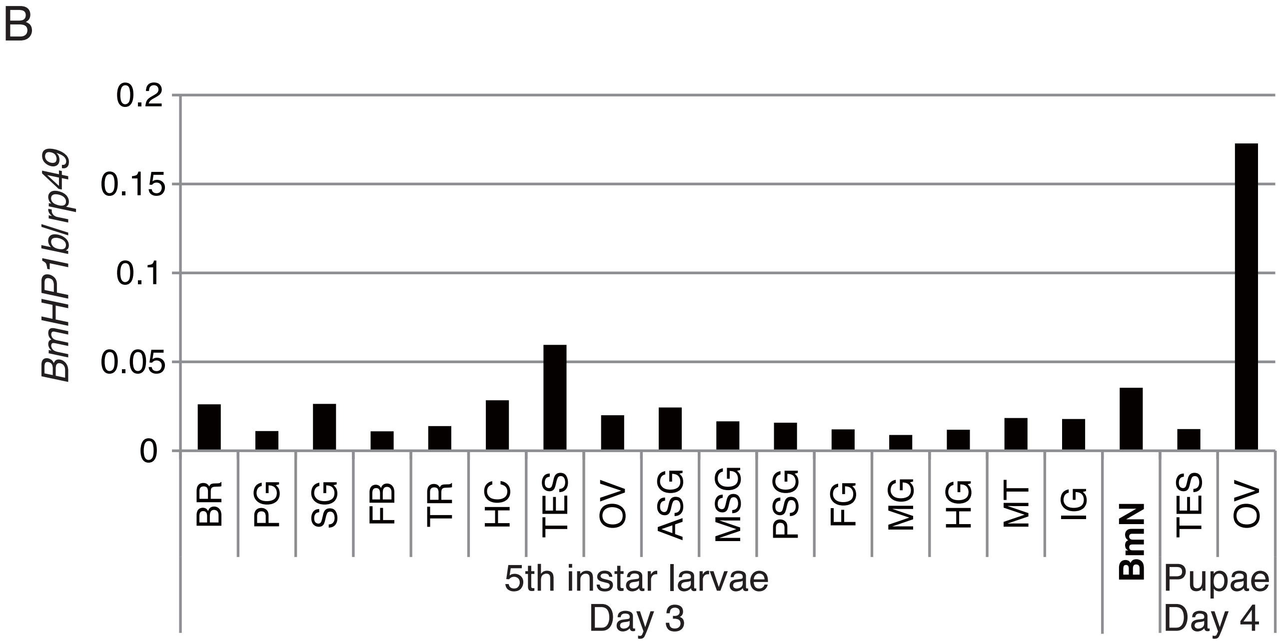
(B) RT-qPCR analysis of the five genes examined in Fig. 6C in *BmHP1b* siRNA-transfected cells.

(C) RT-qPCR analysis of the five genes examined in Fig. 6D in *BmHP1b* siRNA-transfected cells.

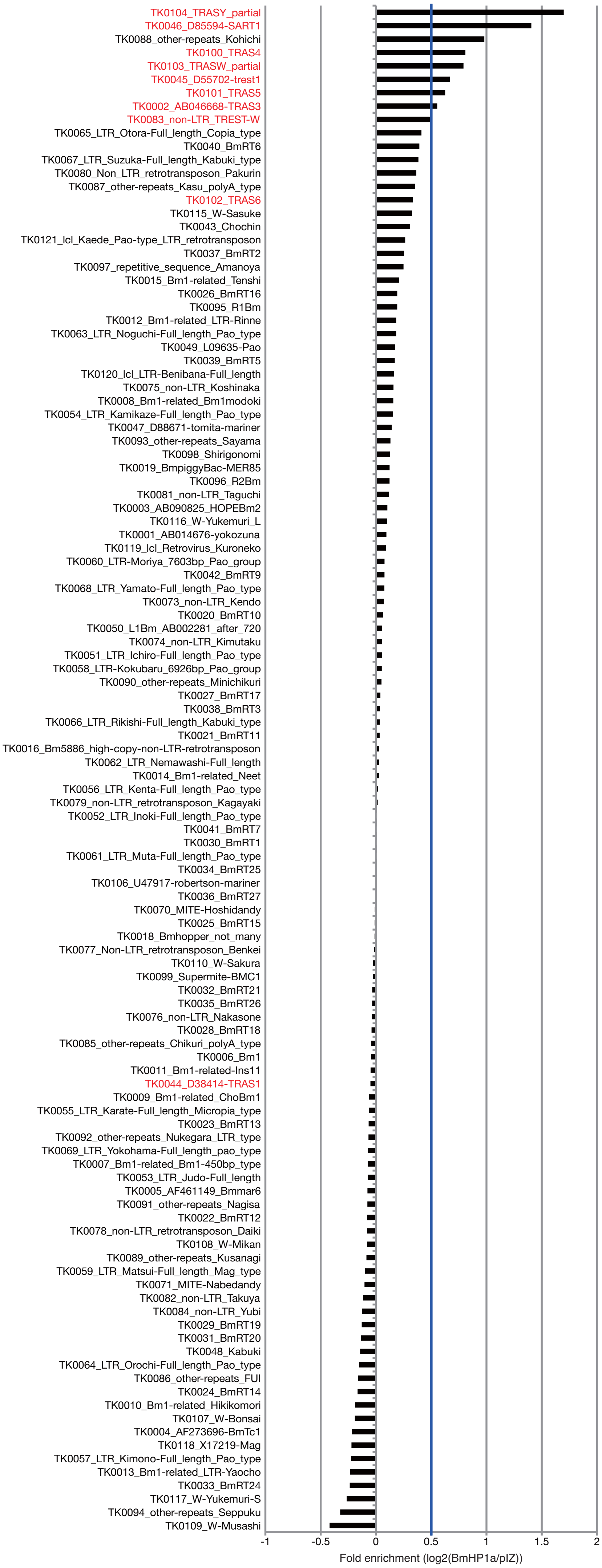
* $P < 0.05$, ** $P < 0.01$ with Student's *t*-test. The data are shown as means ± SD ($n = 6$).

Shoji et al., Fig. S1

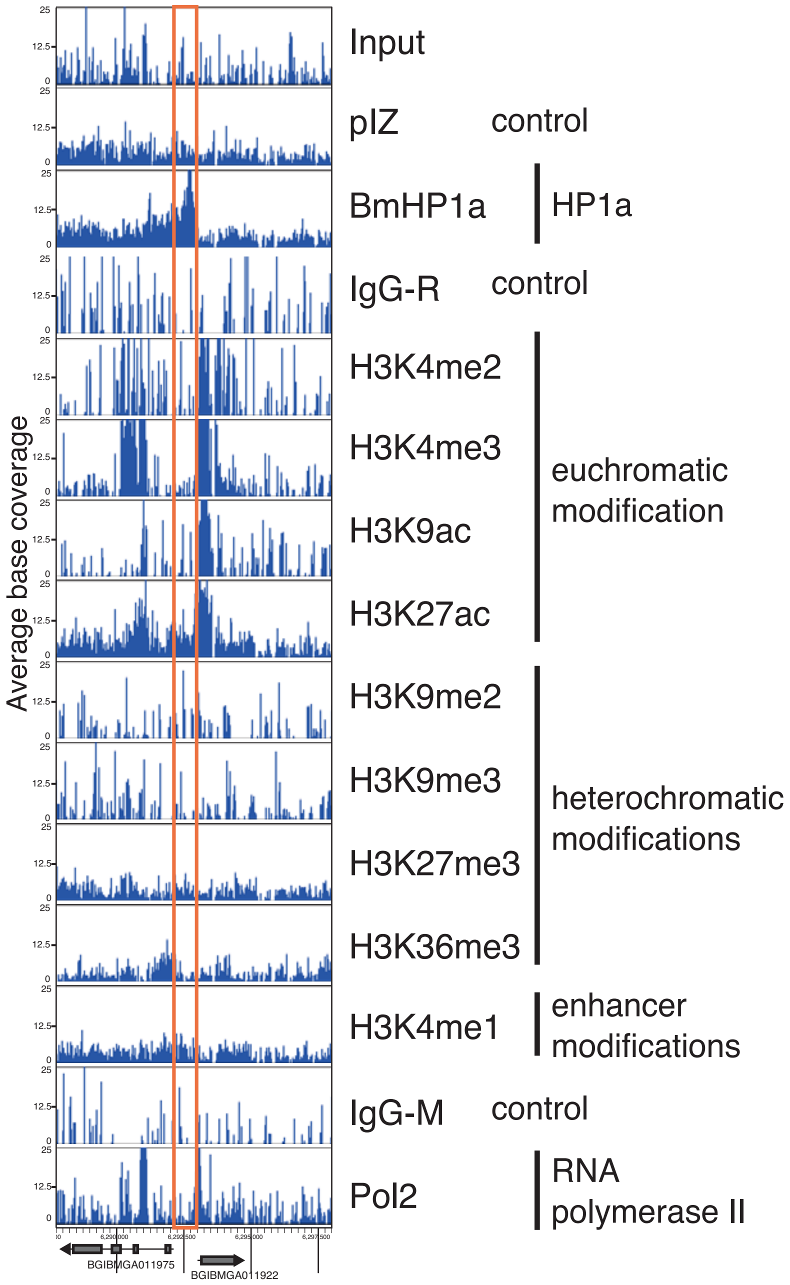




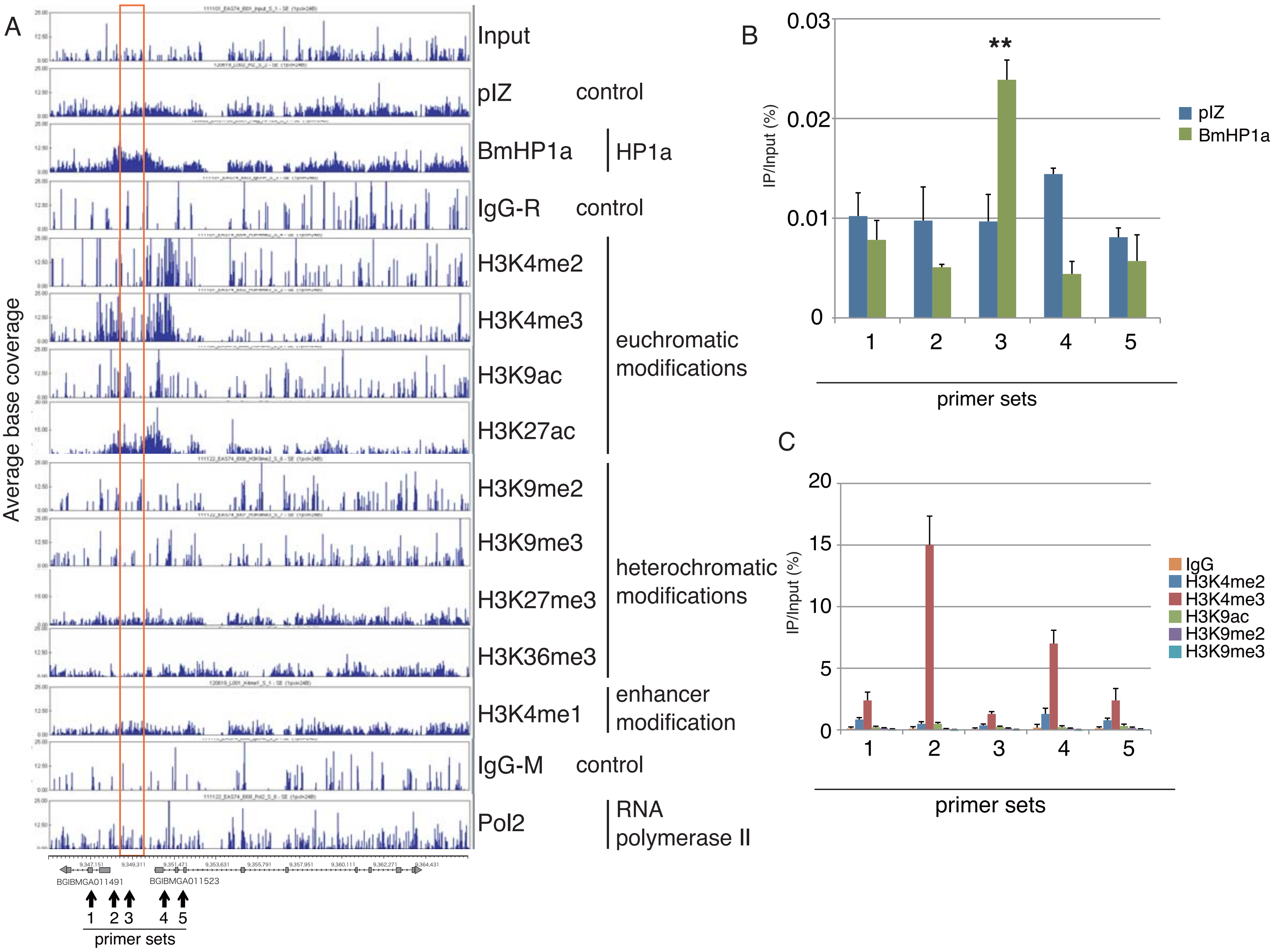
Shoji et al., Fig. S2



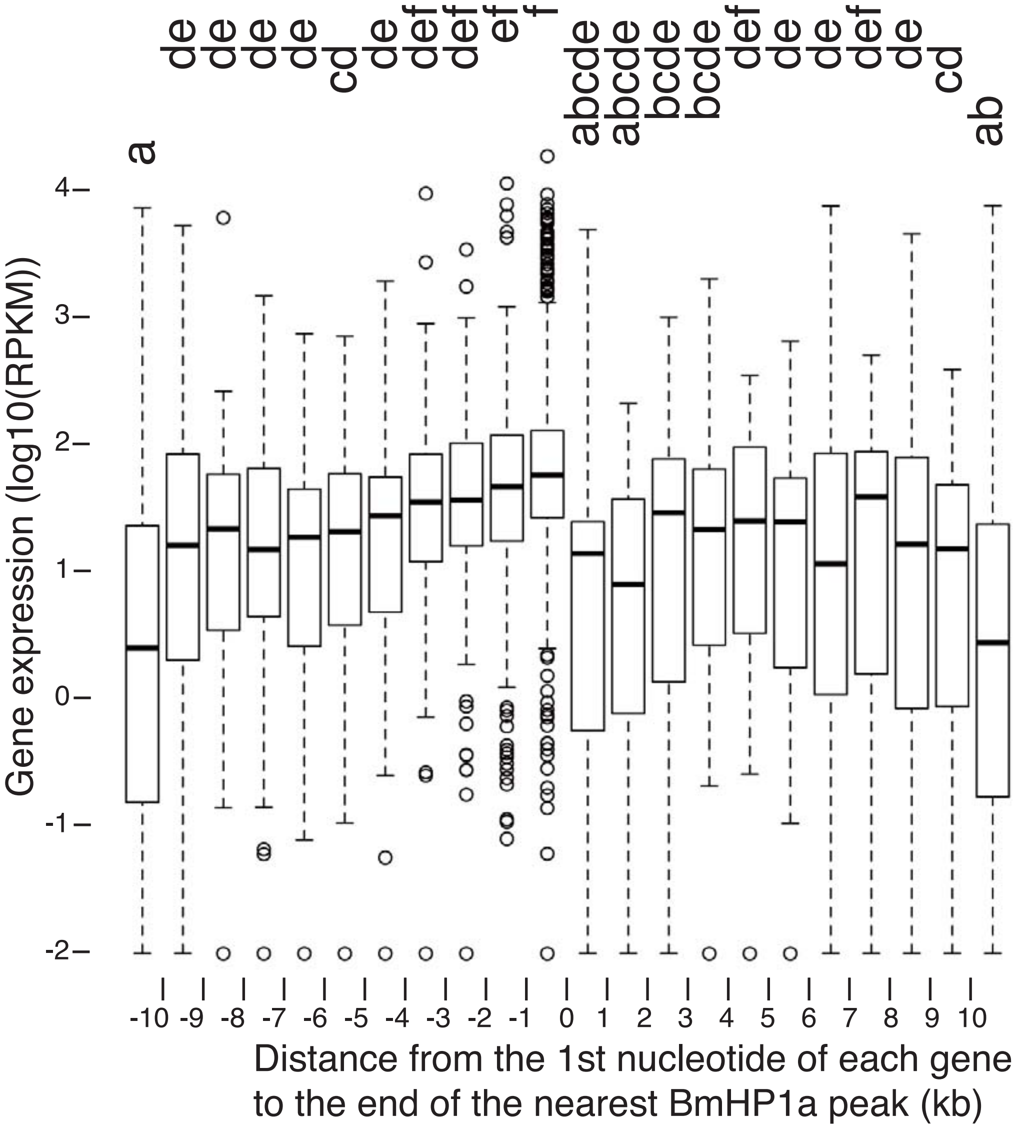
Shoji et al., Fig. S3



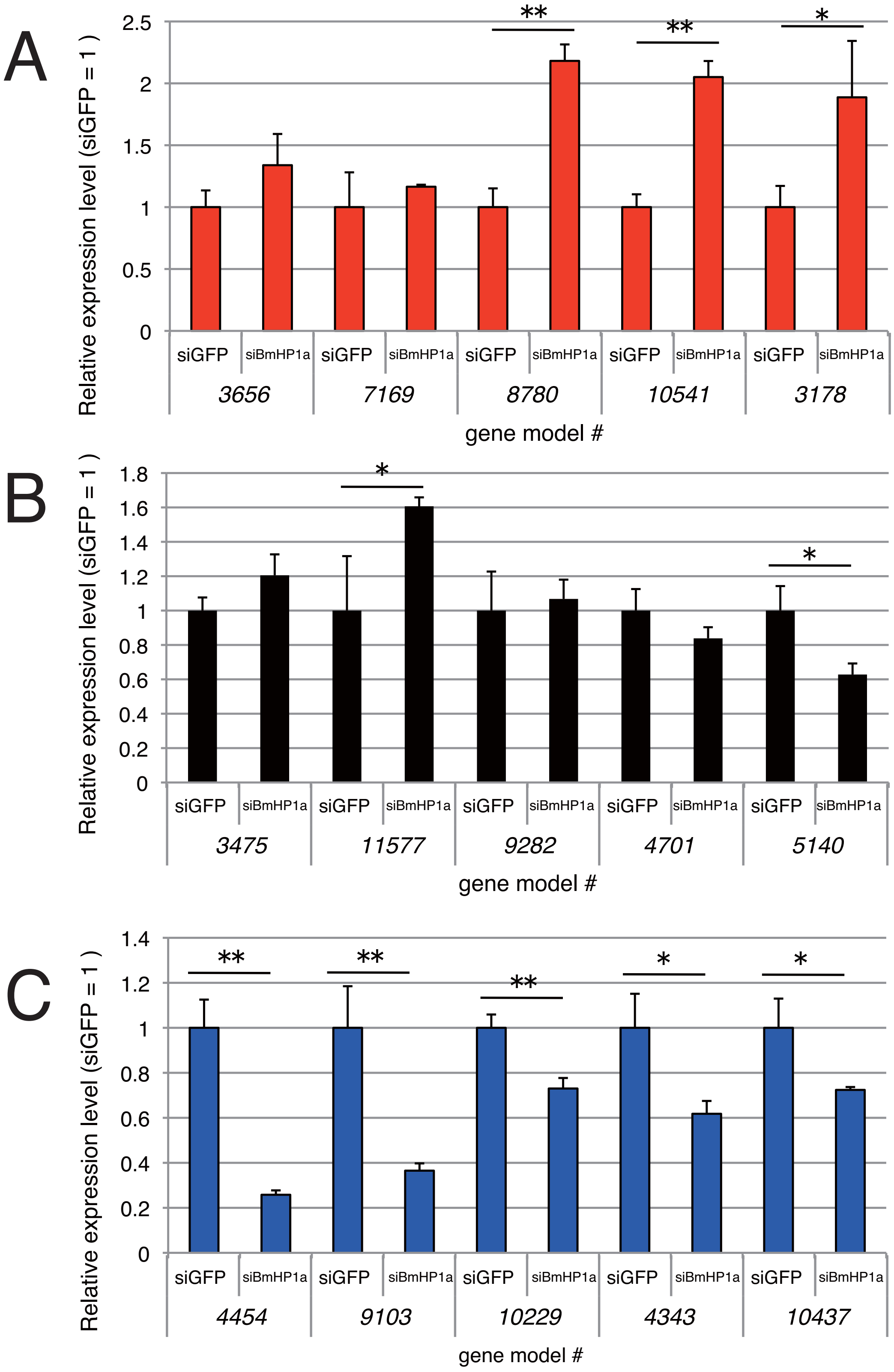
Shoji et al., Fig. S4



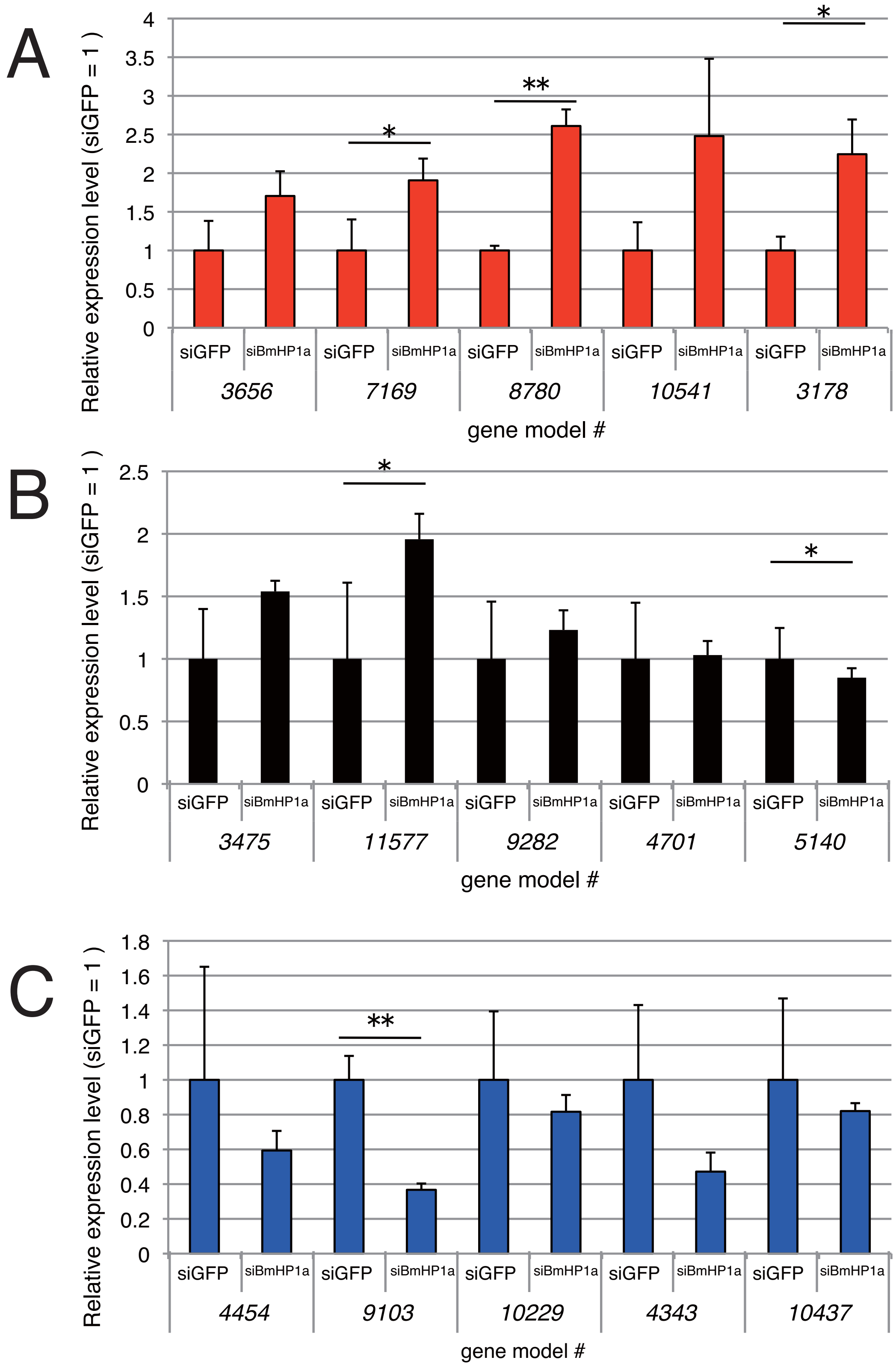
Shoji et al., Fig. S5



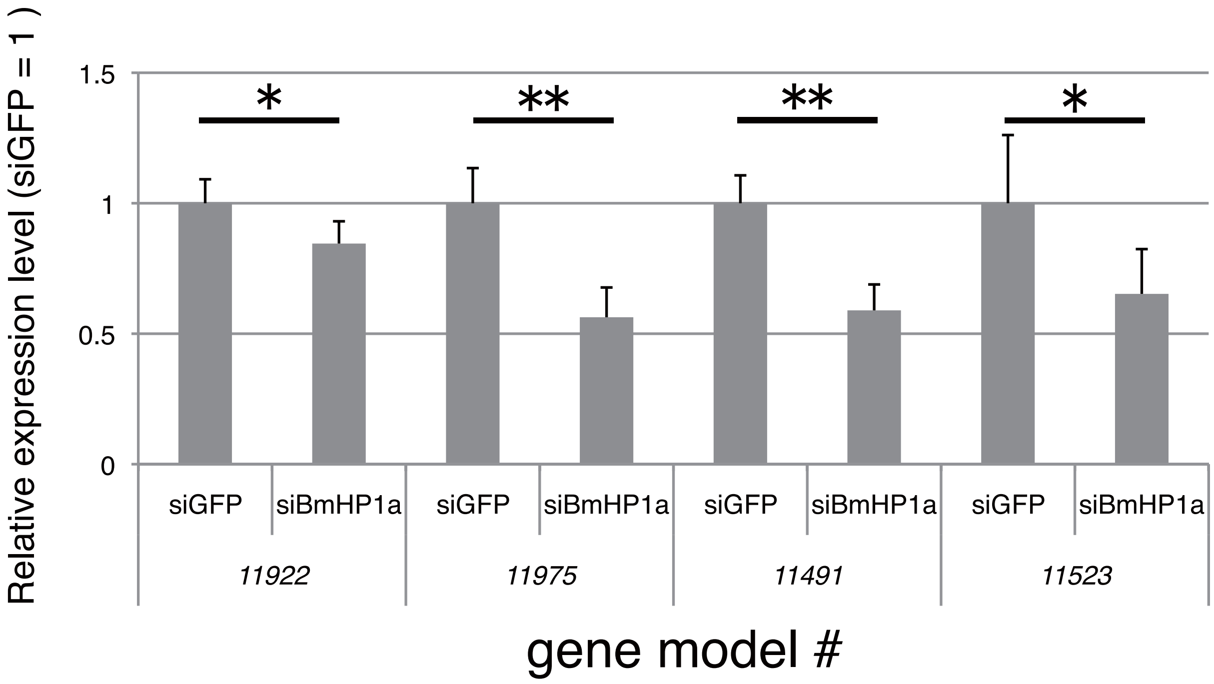
Shoji et al., Fig. S6



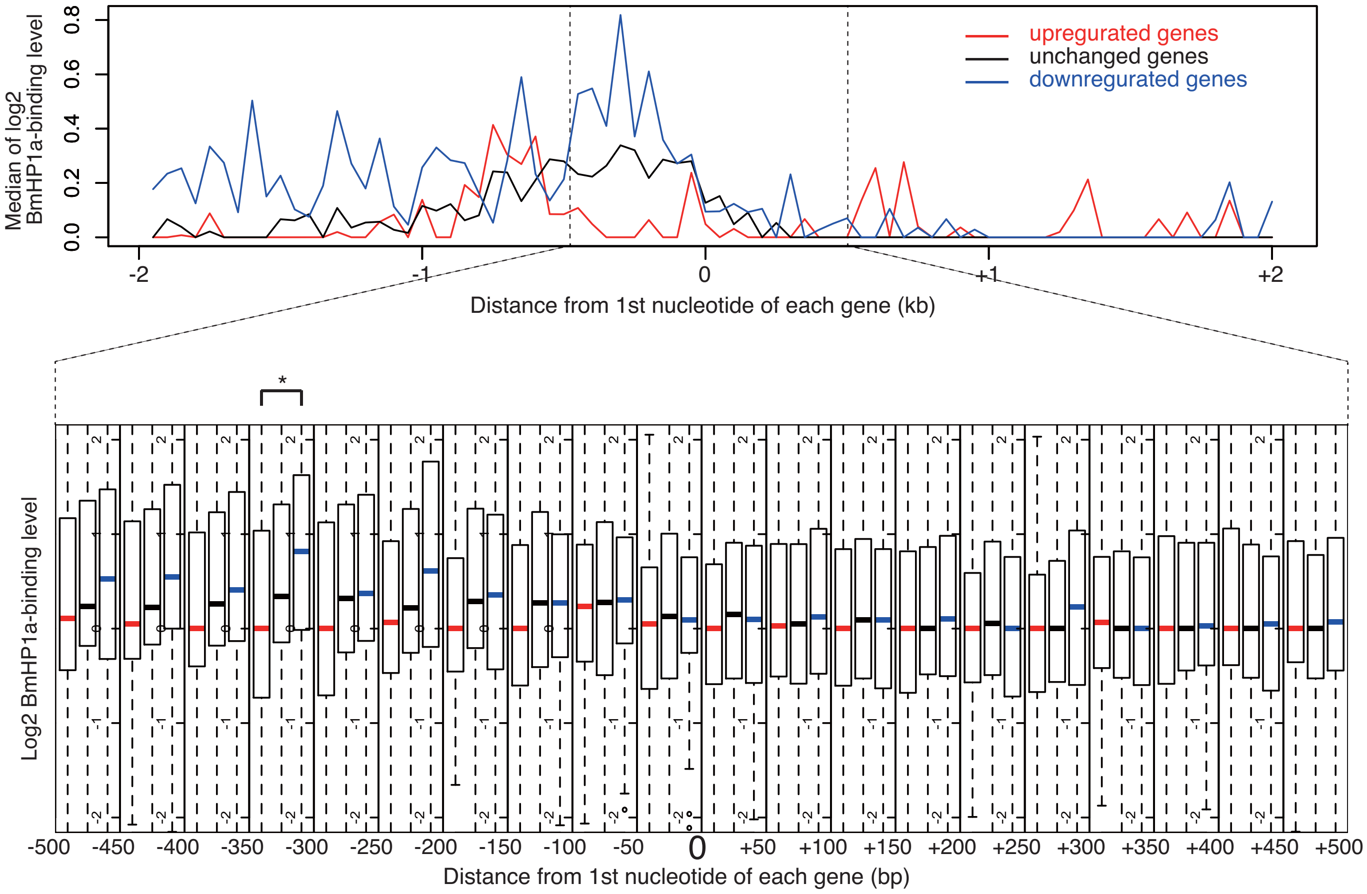
Shoji et al., Fig. S7



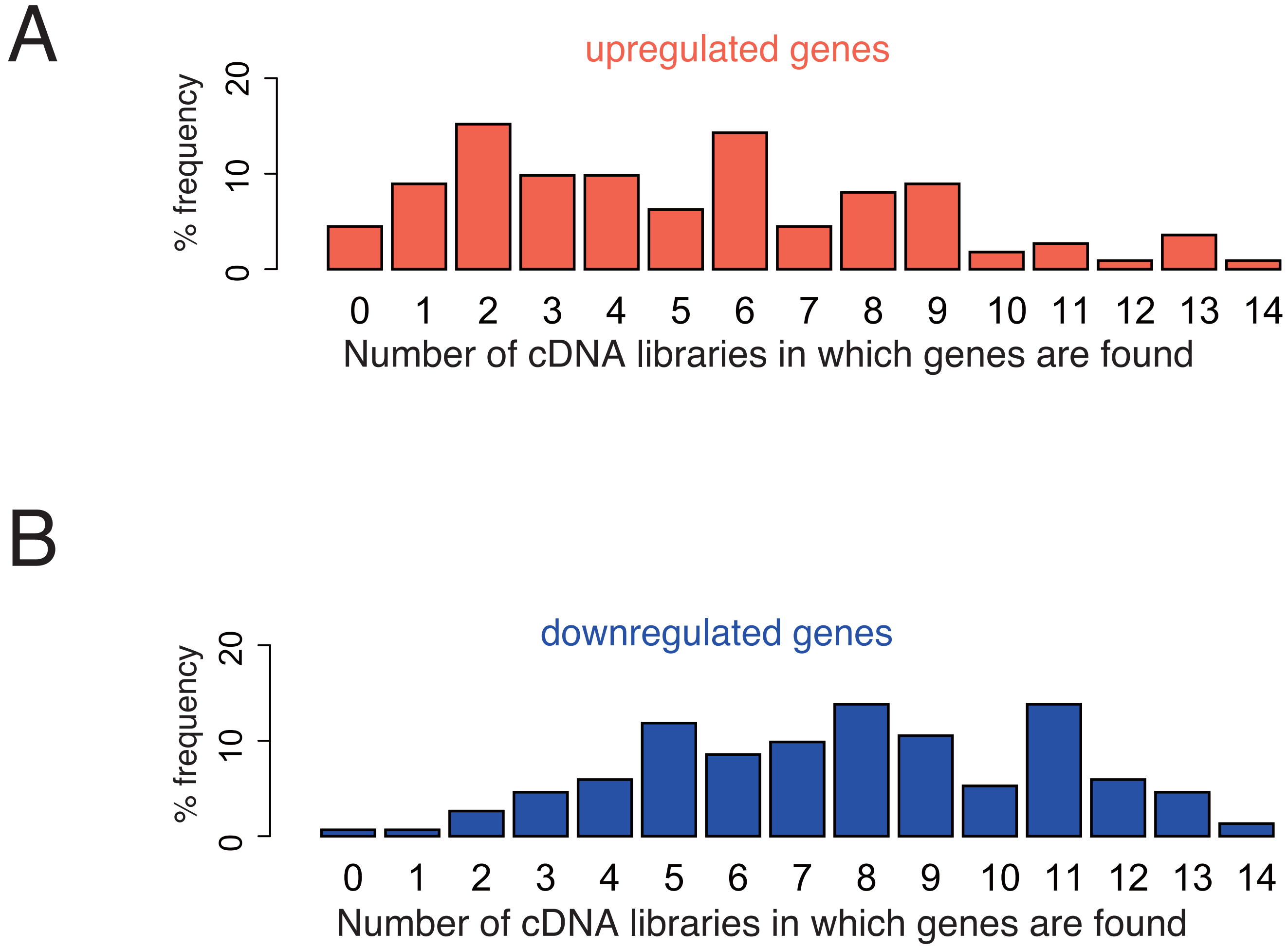
Shoji et al., Fig. S8



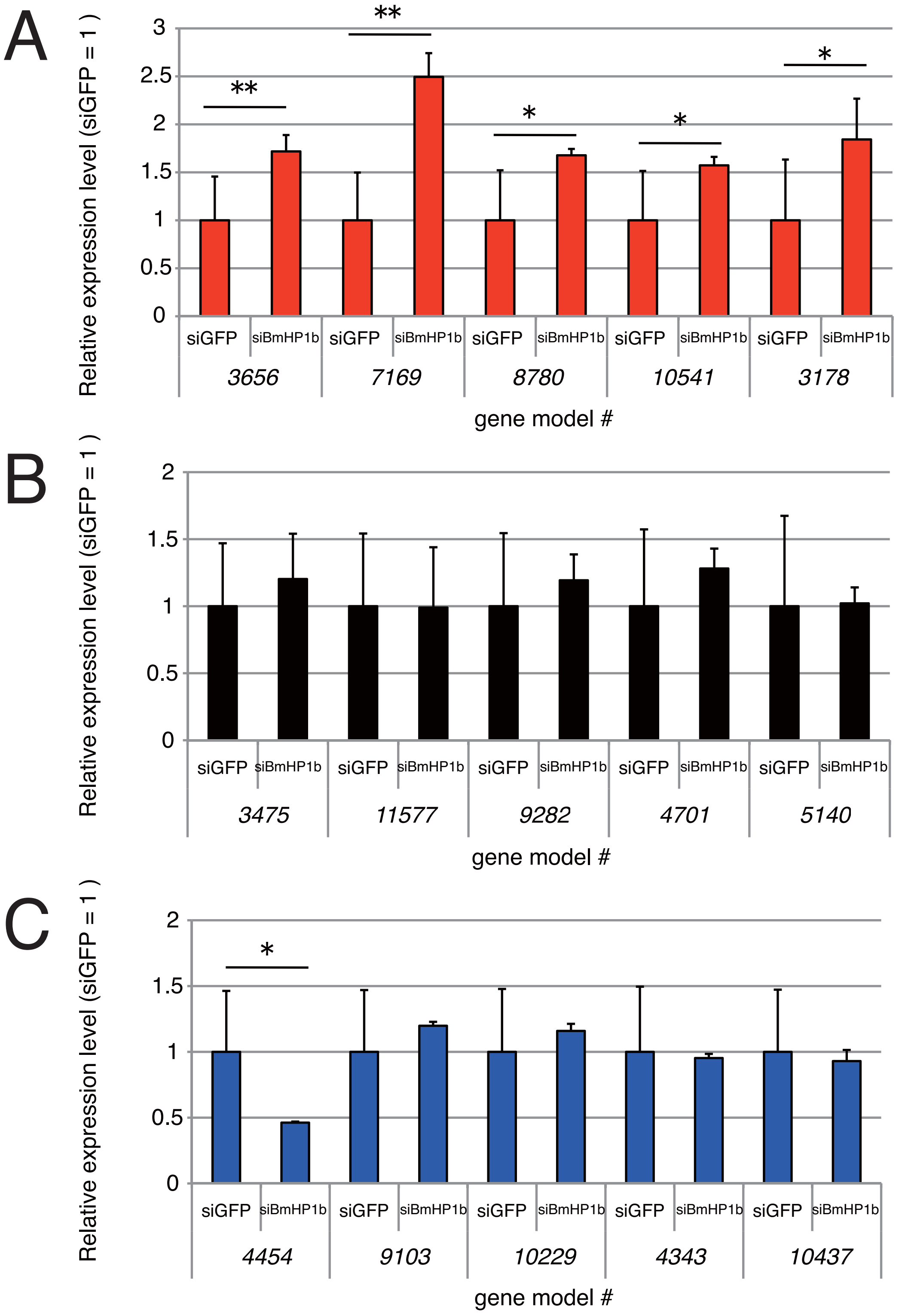
Shoji et al., Fig. S9



Shoji et al., Fig. S10



Shoji et al., Fig. S11



Supplementary Table 1. Oligonucleotide used in this study.

Primer name	Primer sequence (5'-3')	purpose
11922-1F	GAAGCAGTTGATATCCACGAAAC	ChIP-qPCR
11922-1R	GGGTTGTGTAATTCCATTCTGTG	
11922-2F	TCTGAGGGGTTACTTATTGGACA	
11922-2R	ACATGGCAAGAAGATTCAGCTA	
11922-3F	AGCCATCGTGTGGAATATAGATG	
11922-3R	CAGTCTAAAACGAGCAAGAGTCAA	
11922-4F	CAGTCATGTCAACAGTCGGTAAA	
11922-4R	GAAACACTCCCTCAGGATCTTTT	
11922-5F	CTGGAAAATCTATCCGTGCAGTA	
11922-5R	TGCAATGGTCGTAGTCTAACTCA	
11491-1F	TCAATGAAATAGTTAACTTACCA	
11491-1R	CCCGGGTTTTAAGAATGAAGATC	
11491-2F	GGCGCAGTTTACCAACATAAA	
11491-2R	ATCATCGGTCGAGACGAAAA	
11491-3F	CTCCTCACGTTACCCCAAAA	
11491-3R	GCAAACTAACGGAAGTGCAA	
11491-4F	ATCCTGGCCAACTCAAACAG	
11491-4R	CCGCCCGTCAAATCTAAATA	
11491-5F	TTGATAAAAAATTGATGGTAATT	
11491-5R	TCAAGTGCAGCAGCGTGGGCGCA	
BGIBMGA003656-F	CGAACATACGAACACCCTAGAAG	qPCR
BGIBMGA003656-R	GTTTGTACCGCCGTATACATCAT	
BGIBMGA007169-F	GACCGAGTACAAATTGGTGGTT	
BGIBMGA007169-R	GTCTCTCATCGCCGAATACTCTT	
BGIBMGA008780-F	ATGAAGGTGTATGCTCTCATCGT	
BGIBMGA008780-R	CTACAACGTGGTTGTCCTTGAAT	
BGIBMGA010541-F	TGACAGTCCTTATCAAGGAGGAG	
BGIBMGA010541-R	AGAGCAACACTTTGGATATGGTG	
BGIBMGA003178-F	GGTCGTAGCAGTCAACCTTATTG	

BGIBMGA003178-R	TGTCCGGAGAATAAGTAGACCAA
BGIBMGA003475-F	GAATCATCCAGCAGTATCACCTC
BGIBMGA003475-R	GACGCTCTTCCTTTATCTTAGCTG
BGIBMGA011577-F	GCTGAGAAAGATGAACAAGAGGA
BGIBMGA011577-R	GGTATCCAAGCGAAGTCCTAGAT
BGIBMGA009282-F	CAACCCTCGATACATAGAGGACA
BGIBMGA009282-R	ACTCTTCGTAGATTTGCGGTAAG
BGIBMGA004701-F	GTACCTCGGTAACTCCACCAAC
BGIBMGA004701-R	ATCTTATAGCCTGAGGGAAGTGC
BGIBMGA005140-F	TCTTAATTCGGTGGGATACTGTG
BGIBMGA005140-R	CTTTCTTCGTTCTTCCTCTTCG
BGIBMGA004454-F	CTCTGAGCAAGGATCTAGACCAA
BGIBMGA004454-R	TCTGTAGCATCGTCAGATGAGAA
BGIBMGA009103-F	ACACTTATGGAGGCCAAGTTGTA
BGIBMGA009103-R	CGTCACGTTTGAGAATCCTTTAC
BGIBMGA010229-F	GACCCTCATCAATTTCACTTGTC
BGIBMGA010229-R	TAGCACGCAACTCTAACCTTTTC
BGIBMGA004343-F	GGTATGAGGATCACCCAACATAA
BGIBMGA004343-R	CTGGAGTGAAGTCTGCATTACCT
BGIBMGA010437-F	AAATCACAACTGGGTCTTGGAAG
BGIBMGA010437-R	CCTTATGCGCCTTCTGTAGTTTT
BGIBMGA11922-F	CGGTAAAGTGATTAAGTGCTTGG
BGIBMGA11922-R	GAAACACTCCCTCAGGATCTTTT
BGIBMGA11975-F	GATATTGTAACCTGCCCACTCAG
BGIBMGA11975-R	GAAGCAGTTGATATCCACGAAAC
BGIBMGA11491-F	TTCTCCAGATGTAGTTGGAAAGC
BGIBMGA11491-R	CCCTACCATAACTGCACGTAAAA
BGIBMGA11523-F	CGCCTAAAGATCTATCAGAAGCA
BGIBMGA11523-R	GTTATTGGACTCTCCATGCACTC

siRNA name	siRNA sequence (5'-3')	purpose
siGFP-guide	AUAGACGUUGUGGCUGUUGUA	RNAi

siGFP-passenger	CAACAGCCACAACGUCUAUUU
siBmHP1a-guide	CAGUUCUGGUAGGAAAGGUCG
siBmHP1a-passenger	ACCUUUCCUACCAGAACUGUU
siBmHP1b-guide	UCAGCUUCUUUCUUCUUUCUU
siBmHP1b-passenger	GAAAGAAGAAAGAAGCUGAUU

Supplementary Table 2. Full length cDNA libraries used for Fig. S10.

Name of full-length cDNA library	No. of Clones	Vector	Method
BmN (cultured cell)	20736	pCMVFL	Oligo-cap
fe8d (embryo day 8)	18731	pGCAP10	V-cap
fwd (wing disc, 5th larva)	24960	pCMVFL	Oligo-cap
MFB (fat body, microbe-infected)	10368	pGCAP1	G-cap
bmmt (malpighian tubule, 5th larva)	10534	pGCAP10	V-cap
bmnc (cultured cell, NPV infected; 20hr postinfection)	10281	pGCAP10	V-cap
bmov (ovary, pupa day 4)	10708	pGCAP10	V-cap
bmte (testis, pupa day 4)	10723	pGCAP10	V-cap
famL (antenna & maxillary glalea, 5th larva)	25972	pGCAP10	V-cap
fcaL (corpora allata-cardiaca, 5th larva)	33462	pGCAP1	G-cap
fner (nerve system + brain, 5th larva)	37074	pGCAP10	V-cap
fmgV (midgut, 5th larva)	38020	pGCAP10	V-cap
ftes (testis, 5th larva)	29669	pGCAP10	V-cap
fufe (unfertilized egg)	17095	pGCAP10	V-cap
fwgP (wing, pupa day 2–8)	17521	pGCAP10	V-cap

Supplementary Table 3 (A) Annotation list of downregulated genes selected in Fig. 6A

genemodel names	annotation	e.value	RPKM(siHP1a) /RPKM(siGFP)
BGIBMGA004454	low molecular mass 30 kDa lipoprotein 21G1-like precursor [Bombyx mori]	1e-179,	0.08101521
BGIBMGA006109	BmHP1a	8e-91,	0.122335689
BGIBMGA009103	sterol carrier protein x [Bombyx mori]	0.0,	0.512934047
BGIBMGA010229	PREDICTED: uncharacterized protein C31H12.03c-like [Bombyx mori]	7e-171,	0.546441258
BGIBMGA004343	death-related protein [Bombyx mori]	2e-67,	0.569799602
BGIBMGA010437	PREDICTED: tubulin-specific chaperone C-like [Bombyx mori]	0.0,	0.605804028
BGIBMGA012125	uncharacterized protein LOC100216501 [Bombyx mori]	6e-118,	0.609788981
BGIBMGA010450	no hit		0.611755647
BGIBMGA006574	heat shock 70 kDa protein 14-like [Bombyx mori]	0.0,	0.616839054
BGIBMGA003356	PREDICTED: HIG1 domain family member 1A, mitochondrial-like isoform [Bom	1e-51,	0.623584191
BGIBMGA013201	14-3-3 epsilon protein [Bombyx mori]	0.0,	0.628240196
BGIBMGA003466	PREDICTED: FUN14 domain-containing protein 1A-like isoform X1 [Bombyx m	8e-89,	0.632056115
BGIBMGA006865	creb [Bombyx mori]	0.0,	0.632205099
BGIBMGA011668	SoxE [Bombyx mori]	6e-123,	0.633168491
BGIBMGA006779	PREDICTED: probable protein phosphatase CG10417-like [Bombyx mori]	0.0,	0.635689466
BGIBMGA013782	PREDICTED: uncharacterized protein LOC101746461 [Bombyx mori]	7e-73,	0.655997284
BGIBMGA007844	PREDICTED: surfeit locus protein 6 homolog [Bombyx mori]	1e-43,	0.661998892
BGIBMGA006158	prohibitin protein WPH [Bombyx mori]	0.0,	0.666196218
BGIBMGA012537	mitochondrial ribosomal protein L32 [Bombyx mori]	3e-143,	0.671096729
BGIBMGA004834	PREDICTED: RRP15-like protein-like isoform X1 [Bombyx mori]	4e-141,	0.673895709
BGIBMGA000243	PREDICTED: protein FAM32A-like [Bombyx mori]	5e-47,	0.676344678
BGIBMGA011450	uncharacterized protein LOC692929 [Bombyx mori]	2e-115,	0.676983287
BGIBMGA004250	PREDICTED: protein PXR1-like [Bombyx mori]	1e-58,	0.680299462
BGIBMGA005564	PREDICTED: ribosome biogenesis regulatory protein homolog [Bombyx mori]	0.0,	0.680749704
BGIBMGA008501	PREDICTED: LOW QUALITY PROTEIN: serine/threonine-protein phosphatase [	9e-177,	0.681532007
BGIBMGA004635	nucleolar phosphoprotein [Bombyx mori]	1e-90,	0.683895144
BGIBMGA005372	PREDICTED: LDLR chaperone boca-like isoform X1 [Bombyx mori]	4e-106,	0.684003287
BGIBMGA011922	alcohol dehydrogenase [Bombyx mori]	0.0,	0.684484824
BGIBMGA007941	PREDICTED: BTB/POZ and MATH domain-containing protein 2-like [Bombyx	6e-159,	0.688337694
BGIBMGA012298	6-phosphogluconate dehydrogenase [Bombyx mori]	0.0,	0.68835626
BGIBMGA005495	PREDICTED: PRKR-interacting protein 1 homolog [Bombyx mori]	5e-86,	0.694816662
BGIBMGA009021	PREDICTED: calcyclin-binding protein-like [Bombyx mori]	1e-157,	0.695660552
BGIBMGA012559	PREDICTED: U3 small nucleolar RNA-associated protein 18 homolog [Bombyx	0.0,	0.695690706
BGIBMGA010225	peroxisomal biogenesis factor 3 [Bombyx mori]	0.0,	0.697521138
BGIBMGA006105	PREDICTED: rRNA-processing protein UTP23 homolog isoform X1 [Bombyx m	1e-106,	0.699270952
BGIBMGA011004	DDRGK domain-containing protein 1 precursor [Bombyx mori]	1e-63,	0.700016742
BGIBMGA000177	PREDICTED: transmembrane protein 70 homolog, mitochondrial-like [Bombyx	6e-157,	0.700447787
BGIBMGA012045	small nuclear ribonucleoprotein protein F [Bombyx mori]	1e-52,	0.703583863
BGIBMGA007107	TPR-repeat protein [Bombyx mori]	0.0,	0.704903515
BGIBMGA006980	PREDICTED: nucleolar protein 12-like [Bombyx mori]	1e-90,	0.709179107
BGIBMGA012508	RNA binding motif protein X-linked 2 [Bombyx mori]	7e-51,	0.709574009
BGIBMGA000029	nucleolar protein family A member 2 [Bombyx mori]	1e-100,	0.710415541
BGIBMGA000664	uncharacterized protein LOC692928 [Bombyx mori]	8e-96,	0.710900253
BGIBMGA012122	PREDICTED: esterase FE4-like [Bombyx mori]	0.0,	0.712063046
BGIBMGA008675	PREDICTED: probable 28S ribosomal protein S26, mitochondrial-like [Bombyx	9e-156,	0.712079177
BGIBMGA011070	PREDICTED: THO complex subunit 7 homolog isoform X1 [Bombyx mori]	1e-133,	0.714418819
BGIBMGA006022	PREDICTED: la protein homolog isoform X1 [Bombyx mori]	0.0,	0.717607935
BGIBMGA005023	PREDICTED: cell growth-regulating nucleolar protein-like isoform [Bombyx mo	0.0,	0.71844501
BGIBMGA008532	N-acetyltransferase [Bombyx mori]	4e-137,	0.719538206
BGIBMGA000990	PREDICTED: exonuclease 3'-5' domain-containing protein 1-like [Bombyx mori	4e-173,	0.720246495
BGIBMGA009133	beta-tubulin [Bombyx mori]	0.0,	0.720447058
BGIBMGA008650	PREDICTED: cyclin-dependent kinases regulatory subunit 1-like [Bombyx mori]	3e-65,	0.720557139
BGIBMGA014593	PREDICTED: alpha-ketoglutarate-dependent dioxygenase alkB homolog [Bom	0.0,	0.722971148
BGIBMGA000382	nuclear migration protein nudC [Bombyx mori]	6e-104,	0.723479907
BGIBMGA007224	PREDICTED: 28 kDa heat- and acid-stable phosphoprotein-like [Bombyx mori]	7e-46,	0.724038669
BGIBMGA001627	no hit		0.727797495
BGIBMGA013785	PREDICTED: uncharacterized protein LOC101746975 [Bombyx mori]	3e-103,	0.728450461
BGIBMGA011314	DnaJ-8 [Bombyx mori]	0.0,	0.730150666
BGIBMGA011253	PREDICTED: 26S proteasome complex subunit DSS1-like [Bombyx mori]	2e-31,	0.735777287
BGIBMGA000122	no hit		0.736365903
BGIBMGA007405	PREDICTED: PEST proteolytic signal-containing nuclear protein-like [Bombyx	1e-61,	0.738379836
BGIBMGA011019	endothelial-monocyte activating polypeptide II [Bombyx mori]	9e-156,	0.739695838
BGIBMGA005319	PREDICTED: density-regulated protein-like [Bombyx mori]	3e-109,	0.741907625
BGIBMGA011334	thymosin isoform 1 [Bombyx mori]	6e-95,	0.742606311
BGIBMGA008899	U6 snRNA-associated Sm-like protein [Bombyx mori]	4e-82,	0.742937823
BGIBMGA007263	PREDICTED: ribosomal L1 domain-containing protein CG13096-like [Bombyx	0.0,	0.743485571
BGIBMGA011531	PREDICTED: uncharacterized protein LOC101743953 [Bombyx mori]	0.0,	0.744715559
BGIBMGA007010	PREDICTED: charged multivesicular body protein 6-A-like [Bombyx mori]	1e-97,	0.744715828
BGIBMGA007297	PREDICTED: protein SDA1 homolog [Bombyx mori]	0.0,	0.744991911
BGIBMGA011092	PREDICTED: ribosome production factor 2 homolog [Bombyx mori]	0.0,	0.746774281
BGIBMGA003153	DnaJ (Hsp40) homolog 3 [Bombyx mori]	0.0,	0.7482602

BGIBMGA010827	PREDICTED: exosome complex component CSL4-like [Bombyx mori]	2e-163,	0.750182514
BGIBMGA003562	NADH dehydrogenase 1 alpha subcomplex subunit 5 [Bombyx mori]	1e-72,	0.750976902
BGIBMGA013713	transport protein Sec61 gamma subunit [Bombyx mori]	3e-32,	0.752148186
BGIBMGA010278	PIN2/TRF1-interacting protein [Bombyx mori]	1e-75,	0.752955428
BGIBMGA010375	no hit		0.754965973
BGIBMGA012220	PREDICTED: tetratricopeptide repeat protein 1-like [Bombyx mori]	0.0,	0.755670836
BGIBMGA004850	ubiquitin-conjugating enzyme E2 J1-like [Bombyx mori]	0.0,	0.755674486
BGIBMGA011143	PREDICTED: uncharacterized protein LOC101742884 [Bombyx mori]	0.0,	0.756451237
BGIBMGA014064	PREDICTED: RNA-binding protein pno1-like [Bombyx mori]	9e-156,	0.756866299
BGIBMGA011919	PREDICTED: ribosomal RNA-processing protein 7 homolog A-like	3e-88,	0.757323197
BGIBMGA013514	PREDICTED: coiled-coil domain-containing protein 124-like isoform	1e-100,	0.757368301
BGIBMGA001363	40S ribosomal protein S21 [Bombyx mori]	7e-55,	0.760819988
BGIBMGA004540	heat shock protein hsp 19.9 [Bombyx mori]	1e-129,	0.761054352
BGIBMGA008493	PREDICTED: LSM domain-containing protein 1-like [Bombyx mori]	8e-78,	0.761302254
BGIBMGA012126	PREDICTED: eukaryotic translation initiation factor 3 subunit [Bombyx mori]	0.0,	0.763599101
BGIBMGA008648	PREDICTED: dystrophin, isoform D-like [Bombyx mori]	1e-146,	0.764952454
BGIBMGA005160	PREDICTED: probable cardiolipin synthase-like [Bombyx mori]	0.0,	0.765944096
BGIBMGA012474	PREDICTED: huntingtin-interacting protein K-like [Bombyx mori]	6e-80,	0.766051654
BGIBMGA007192	no hit		0.766118747
BGIBMGA003699	PREDICTED: LIN1-like protein-like [Bombyx mori]	1e-72,	0.767301601
BGIBMGA001189	PREDICTED: uncharacterized protein LOC101739083 isoform X3 [Bombyx mor	9e-80,	0.767367538
BGIBMGA005939	PREDICTED: protein CWC15 homolog [Bombyx mori]	2e-136,	0.767664559
BGIBMGA001136	signal peptidase complex subunit 3 [Bombyx mori]	1e-73,	0.768999151
BGIBMGA009041	PREDICTED: zinc finger HIT domain-containing protein 1-like [Bombyx mori]	5e-58,	0.769600194
BGIBMGA012931	PREDICTED: protein windbeutel-like [Bombyx mori]	2e-173,	0.770533823
BGIBMGA003609	PREDICTED: adenylate kinase isoenzyme 6 homolog [Bombyx mori]	2e-131,	0.770601763
BGIBMGA000374	PREDICTED: sentrin-specific protease 6-like isoform X2 [Bombyx mori]	0.0,	0.770715896
BGIBMGA011798	PREDICTED: leukocyte receptor cluster member 1 homolog [Bombyx mori]	0.0,	0.770886205
BGIBMGA009987	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex [Bombyx	2e-72,	0.774068599
BGIBMGA011782	PREDICTED: putative RNA exonuclease NEF-sp-like [Bombyx mori]	0.0,	0.774341396
BGIBMGA006849	PREDICTED: protein RER1-like isoform X1 [Bombyx mori]	2e-102,	0.774586895
BGIBMGA000921	PREDICTED: ER membrane protein complex subunit 10-like isoform [Bombyx r	6e-147,	0.774783249
BGIBMGA002481	PREDICTED: LOW QUALITY PROTEIN: cell division cycle 5-like protein-like [Bo	0.0,	0.776602491
BGIBMGA000918	S-phase kinase-associated protein [Bombyx mori]	3e-102,	0.779635282
BGIBMGA006789	PREDICTED: malectin-like [Bombyx mori]	0.0,	0.780219484
BGIBMGA008451	PREDICTED: inositol-trisphosphate 3-kinase B-like [Bombyx mori]	0.0,	0.780294126
BGIBMGA005928	ribosomal protein L35 [Bombyx mori]	1e-68,	0.780317404
BGIBMGA006805	PREDICTED: probable cytosolic iron-sulfur protein assembly protein [Bombyx r	0.0,	0.780457451
BGIBMGA006376	p23-like protein [Bombyx mori]	3e-109,	0.780785602
BGIBMGA010930	rRNA processing protein Ebp2 [Bombyx mori]	4e-168,	0.780822395
BGIBMGA010199	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP2-like [Bombyx mori]	6e-88,	0.780921455
BGIBMGA007493	PREDICTED: transcription factor A, mitochondrial-like [Bombyx mori]	2e-101,	0.781546588
BGIBMGA003923	ribosomal protein S24 [Bombyx mori]	4e-85,	0.782159531
BGIBMGA008301	PREDICTED: 39S ribosomal protein L14, mitochondrial-like [Bombyx mori]	2e-73,	0.78351005
BGIBMGA003669	eukaryotic translation initiation factor 3 subunit E [Bombyx mori]	0.0,	0.783791376
BGIBMGA012563	PREDICTED: uncharacterized protein LOC101740540 [Bombyx mori]	0.0,	0.785131137
BGIBMGA000926	transaldolase [Bombyx mori]	0.0,	0.785593652
BGIBMGA012505	PREDICTED: thioredoxin domain-containing protein-like isoform [Bombyx mori]	0.0,	0.786988854
BGIBMGA011975	PREDICTED: nucleolar protein 11-like [Bombyx mori]	0.0,	0.78702801
BGIBMGA011296	PREDICTED: UPF0562 protein C7orf55-like [Bombyx mori]	3e-53,	0.787288566
BGIBMGA013131	PREDICTED: apolipoprotein D-like [Bombyx mori]	3e-155,	0.787394718
BGIBMGA000381	nuclear migration protein nudC [Bombyx mori]	5e-89,	0.7874625
BGIBMGA014046	PREDICTED: pre-rRNA processing protein FTSJ3-like [Bombyx mori]	0.0,	0.788407664
BGIBMGA012708	PREDICTED: spermine synthase-like [Bombyx mori]	3e-109,	0.788603949
BGIBMGA005381	PREDICTED: KRR1 small subunit processome component homolog [Bombyx m	0.0,	0.789949448
BGIBMGA010723	small nuclear ribonucleoprotein sm d2 [Bombyx mori]	5e-60,	0.791432585
BGIBMGA000440	PREDICTED: 39S ribosomal protein L47, mitochondrial-like [Bombyx mori]	0.0,	0.791545306
BGIBMGA011779	PREDICTED: probable prefoldin subunit 4-like [Bombyx mori]	4e-94,	0.791867536
BGIBMGA007043	PREDICTED: signal peptidase complex subunit 1-like [Bombyx mori]	3e-42,	0.792523287
BGIBMGA010337	PREDICTED: RNA polymerase II transcriptional coactivator-like [Bombyx mori]	1e-49,	0.792821992
BGIBMGA006735	PREDICTED: ribosome maturation protein SBDS-like [Bombyx mori]	0.0,	0.79341164
BGIBMGA006711	RNA binding motif protein 18 [Bombyx mori]	2e-102,	0.794263931
BGIBMGA010651	PREDICTED: coiled-coil domain-containing protein 97-like [Bombyx mori]	0.0,	0.794830437
BGIBMGA010845	PREDICTED: protein BCCIP homolog [Bombyx mori]	8e-177,	0.794948922
BGIBMGA000399	ribosomal protein L20 [Bombyx mori]	4e-116,	0.795040314
BGIBMGA001954	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like isoform [Bombyx	3e-47,	0.796269044
BGIBMGA002439	PREDICTED: uncharacterized protein C9orf114 homolog isoform X1 [Bombyx r	0.0,	0.796412424
BGIBMGA008477	PREDICTED: 39S ribosomal protein L17, mitochondrial-like [Bombyx mori]	5e-150,	0.796432247
BGIBMGA010487	ribosomal protein L36A [Bombyx mori]	1e-51,	0.796599336
BGIBMGA001829	PREDICTED: RNA exonuclease 4-like [Bombyx mori]	3e-15,	0.796802395
BGIBMGA003544	ubiquinol-cytochrome C reductase complex 14kD subunit [Bombyx mori]	5e-54,	0.797259428
BGIBMGA009685	PREDICTED: transcriptional regulator ATRX homolog isoform X1 [Bombyx mori]	0.0,	0.797867295
BGIBMGA003070	PREDICTED: mitochondrial import inner membrane translocase subunit [Bomb	2e-62,	0.797998321
BGIBMGA007068	PREDICTED: U6 snRNA-associated Sm-like protein LSm5-like [Bombyx mori]	6e-54,	0.798209501

BGIBMGA006964	PREDICTED: ATP-binding cassette sub-family F member 3-like [Bombyx mori]	0.0,	0.798324304
BGIBMGA010234	DNA-directed RNA polymerase subunit 6-like protein [Bombyx mori]	2e-65,	0.798481574
BGIBMGA010262	dynein molecular motor protein light chain 1 [Bombyx mori]	3e-73,	0.798662512
BGIBMGA006783	tRNA (guanine-N(7)-)-methyltransferase [Bombyx mori]	3e-118,	0.798958607
BGIBMGA003456	PREDICTED: regulator of microtubule dynamics protein 1-like isoform [Bombyx	5e-176,	0.799691624
BGIBMGA013451	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex [Bombyx	1e-47,	0.799716096
BGIBMGA006752	PREDICTED: DNA-directed RNA polymerase II subunit RPB11-like [Bombyx m	1e-82,	0.799876534

Supplementary Table 3(B) Annotation list of upregulated genes selected in Fig. 6A

genemodel names	annotation	e.value	RPKM(siHP1a)/ RPKM(siGFP)
BGIBMGA000119	PREDICTED: porphobilinogen deaminase-like [Bombyx mori]	0.0,	1.297359696
BGIBMGA000120	PREDICTED: vacuolar protein sorting-associated protein 26-like	0.0,	1.358466043
BGIBMGA000132	neutral alpha-glucosidase AB-like precursor [Bombyx mori]	0.0,	1.201527709
BGIBMGA000447	PREDICTED: vesicle-fusing ATPase 1 [Bombyx mori]	0.0,	1.241107522
BGIBMGA000516	PREDICTED: insulin-like growth factor 2 mRNA-binding protein [Bombyx mori]	0.0,	1.345981827
BGIBMGA000528	PREDICTED: eukaryotic translation initiation factor 4 gamma 3-like [Bombyx mo	0.0,	1.300253158
BGIBMGA000629	PREDICTED: cold shock domain-containing protein E1-like isoform [Bombyx m	0.0,	1.388441393
BGIBMGA000672	PREDICTED: probable citrate synthase 1, mitochondrial-like [Bombyx mori]	0.0,	1.219720971
BGIBMGA000714	PREDICTED: proton-coupled amino acid transporter 1-like [Bombyx mori]	0.0,	1.350599706
BGIBMGA000808	PREDICTED: LOW QUALITY PROTEIN: 5'-3' exoribonuclease 2 homolog [Bomb	0.0,	1.264804405
BGIBMGA001126	PREDICTED: rab proteins geranylgeranyltransferase component A [Bombyx mo	0.0,	1.246884653
BGIBMGA001266	sprouty [Bombyx mori]	2e-84,	1.301340647
BGIBMGA001646	PREDICTED: uncharacterized protein LOC101741044 [Bombyx mori]	0.0,	1.452842621
BGIBMGA001735	PREDICTED: titin-like [Bombyx mori]	3e-128,	1.24330091
BGIBMGA001751	PREDICTED: multiple coagulation factor deficiency protein 2 homolog [Bombyx	7e-106,	1.395446743
BGIBMGA001787	PREDICTED: uncharacterized protein LOC101738779 [Bombyx mori]	0.0,	1.691149166
BGIBMGA001934	PREDICTED: dystroglycan-like isoform X4 [Bombyx mori]	0.0,	1.355362994
BGIBMGA001935	PREDICTED: dystroglycan-like isoform X4 [Bombyx mori]	0.0,	1.204332237
BGIBMGA002004	ATP-binding cassette sub-family F member 2 [Bombyx mori]	0.0,	1.426946366
BGIBMGA002012	PREDICTED: importin-7-like isoform X1 [Bombyx mori]	0.0,	1.337931173
BGIBMGA002013	PREDICTED: importin-7-like isoform X2 [Bombyx mori]	0.0,	1.226088923
BGIBMGA002504	PREDICTED: GTP-binding protein SAR1b-like isoform X1 [Bombyx mori]	4e-142,	1.283919596
BGIBMGA002551	PREDICTED: zinc finger protein 1-like [Bombyx mori]	0.0,	1.448775271
BGIBMGA002773	annexin B13 [Bombyx mori]	0.0,	1.300896395
BGIBMGA002779	PREDICTED: FACT complex subunit spt16-like [Bombyx mori]	0.0,	1.383967033
BGIBMGA002930	PREDICTED: uncharacterized protein LOC101744916 isoform X1 [Bombyx mori	0.0,	1.461357063
BGIBMGA002972	PREDICTED: LOW QUALITY PROTEIN: importin subunit beta-1-like [Bombyx m	0.0,	1.251251846
BGIBMGA003014	PREDICTED: cytochrome b5-like [Bombyx mori]	6e-102,	1.213711479
BGIBMGA003178	PREDICTED: large neutral amino acids transporter small subunit [Bombyx mori]	0.0,	2.015558599
BGIBMGA003506	PREDICTED: uncharacterized protein LOC101740603 [Bombyx mori]	0.0,	1.20347463
BGIBMGA003656	cystathionine gamma-lyase [Bombyx mori]	0.0,	1.835476064
BGIBMGA003681	YKI2 [Bombyx mori]	8e-75,	1.409123618
BGIBMGA003682	YKI3, partial [Bombyx mori]	3e-132,	1.255321028
BGIBMGA003704	heat shock factor-d [Bombyx mori]	0.0,	1.207047817
BGIBMGA003742	PREDICTED: phospholipid scramblase 1-like isoform X1 [Bombyx mori]	3e-161,	1.213099112
BGIBMGA004021	G protein alpha subunit Go isoform 1 [Bombyx mori]	3e-99,	1.414760612
BGIBMGA004022	guanine nucleotide-binding protein G(o) subunit alpha 1 isoform [Bombyx mori]	3e-144,	1.311164656
BGIBMGA004126	PREDICTED: ankyrin repeat and LEM domain-containing protein 1-like [Bombyx	0.0,	1.442294799
BGIBMGA004626	heterotrimeric guanine nucleotide-binding protein beta subunit [Bombyx mori]	0.0,	1.332672182
BGIBMGA004819	calcium-binding protein p22 [Bombyx mori]	7e-92,	1.252564761
BGIBMGA004852	PREDICTED: protein transport protein Sec23A-like isoform X1 [Bombyx mori]	0.0,	1.285763523
BGIBMGA004857	PREDICTED: adenylosuccinate synthetase-like [Bombyx mori]	5e-44,	1.227170808
BGIBMGA004972	PREDICTED: ETS-like protein pointed, isoform P2/D-like [Bombyx mori]	2e-99,	1.270838546
BGIBMGA004973	no hit		1.210475785
BGIBMGA004989	PREDICTED: uncharacterized protein LOC101738733 isoform X1[Bombyx mori]	0.0,	1.24721232
BGIBMGA005058	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Bomby	0.0,	1.20234357
BGIBMGA005068	PREDICTED: uncharacterized protein LOC101742323 [Bombyx mori]	0.0,	1.497033882
BGIBMGA005115	small GTP-binding protein [Bombyx mori]	4e-151,	1.232576649
BGIBMGA005468	PREDICTED: clustered mitochondria protein homolog [Bombyx mori]	0.0,	1.336506289
BGIBMGA005834	cactus [Bombyx mori]	0.0,	1.237287189
BGIBMGA005861	no hit	9.00E-106	1.290194138
BGIBMGA006045	small GTP binding protein RAB5 [Bombyx mori]	6e-151,	1.356162152
BGIBMGA006475	PREDICTED: ras-related C3 botulinum toxin substrate 1-like isoform [Bombyx m	2e-89,	1.225155291
BGIBMGA006518	PREDICTED: peroxidase-like isoform X1 [Bombyx mori]	0.0,	1.330959502
BGIBMGA006590	PREDICTED: syntaxin-1A-like isoform X4 [Bombyx mori]	6e-161,	1.37189894
BGIBMGA006627	PREDICTED: RNA polymerase I-specific transcription initiation [Bombyx mori]	0.0,	1.246019054
BGIBMGA006766	ecdysone receptor isoform B2 [Bombyx mori]	2e-81,	1.673188165
BGIBMGA006809	kinesin heavy chain [Bombyx mori]	0.0,	1.276999662
BGIBMGA006959	PREDICTED: armadillo segment polarity protein-like [Bombyx mori]	0.0,	1.240659279
BGIBMGA007012	PREDICTED: extracellular serine/threonine protein kinase FAM20C-like [Bombyx	0.0,	1.34282547
BGIBMGA007110	PREDICTED: ras-related C3 botulinum toxin substrate 1-like [Bombyx mori]	6e-135,	1.282917484
BGIBMGA007133	PREDICTED: TATA-binding protein-associated factor 172-like [Bombyx mori]	0.0,	1.309619906
BGIBMGA007159	PREDICTED: probable isocitrate dehydrogenase [NAD] subunit alpha [Bombyx	9e-81,	1.234550042
BGIBMGA007169	ras-like protein 1 [Bombyx mori]	4e-134,	1.843636686

BGIBMGA007418	adenosine kinase [Bombyx mori]	0.0,	1.226732907
BGIBMGA007519	PREDICTED: E3 ubiquitin-protein ligase hyd-like [Bombyx mori]	0.0,	1.317251515
BGIBMGA007808	DnaJ (Hsp40) homolog 7 [Bombyx mori]	2e-104,	1.340274128
BGIBMGA007948	PREDICTED: spectrin alpha chain-like [Bombyx mori]	0.0,	1.232294941
BGIBMGA007964	PREDICTED: nucleolin-like isoform X2 [Bombyx mori]	6e-73,	1.255099632
BGIBMGA008337	PREDICTED: protein TIS11-like isoform X2 [Bombyx mori]	7e-101,	1.306793549
BGIBMGA008425	PREDICTED: LOW QUALITY PROTEIN: 26S proteasome non-ATPase regulatory	0.0,	1.236959738
BGIBMGA008498	PREDICTED: synaptobrevin homolog YKT6-like [Bombyx mori]	7e-148,	1.29029656
BGIBMGA008780	ferritin precursor [Bombyx mori]	4e-169,	1.870931229
BGIBMGA008927	PREDICTED: probable actin-related protein 2/3 complex subunit [Bombyx mori]	0.0,	1.213975049
BGIBMGA009049	PREDICTED: niemann-Pick C1 protein-like isoform X1 [Bombyx mori]	0.0,	1.331433542
BGIBMGA009223	PREDICTED: LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase UBR1-like [B	0.0,	1.36724741
BGIBMGA009227	no hit		1.457972499
BGIBMGA009248	PREDICTED: T-complex protein 11-like protein 1-like [Bombyx mori]	0.0,	1.268345293
BGIBMGA009282	PREDICTED: protein kinase C and casein kinase substrate in neurons [Bombyx	0.0,	1.350100658
BGIBMGA009770	ced-6 protein [Bombyx mori]	0.0,	1.344875175
BGIBMGA009941	PREDICTED: ubiquitin carboxyl-terminal hydrolase 5-like [Bombyx mori]	0.0,	1.261981919
BGIBMGA010176	PREDICTED: uncharacterized protein LOC101740250 [Bombyx mori]	0.0,	1.210275242
BGIBMGA010365	uncharacterized protein LOC692518 [Bombyx mori]	0.0,	1.260135785
BGIBMGA010406	argonaute 2 [Bombyx mori]	0.0,	1.327604648
BGIBMGA010541	PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa-like isoform [Bombyx mo	4e-71,	1.939143944
BGIBMGA010576	PREDICTED: protein numb-like isoform X1 [Bombyx mori]	0.0,	1.209777418
BGIBMGA010744	PREDICTED: zinc finger protein on ecdysone puffs-like [Bombyx mori]	0.0,	1.257138107
BGIBMGA010926	PREDICTED: dual specificity testis-specific protein kinase 2-like [Bombyx mori]	1e-82,	1.282391009
BGIBMGA011089	sex combs on midleg [Bombyx mori]	0.0,	1.323249689
BGIBMGA011144	PREDICTED: peroxisomal biogenesis factor 19-like [Bombyx mori]	3e-177,	1.322123409
BGIBMGA011364	PREDICTED: choline/ethanolamine kinase-like isoform X3 [Bombyx mori]	0.0,	1.247990477
BGIBMGA011427	PREDICTED: uncharacterized protein LOC101738318 [Bombyx mori]	0.0,	1.345443442
BGIBMGA011543	dicer-2 [Bombyx mori]	0.0,	1.399939728
BGIBMGA011577	PREDICTED: uncharacterized protein LOC101738278 [Bombyx mori]	0.0,	1.268092435
BGIBMGA011594	PREDICTED: serine proteinase stubble-like [Bombyx mori]	0.0,	1.245325038
BGIBMGA011754	PREDICTED: probable ATP-dependent RNA helicase DDX17-like isoform [Bomb	0.0,	1.24092286
BGIBMGA011809	PREDICTED: zinc transporter ZIP11-like [Bombyx mori]	2e-162,	1.361396196
BGIBMGA011963	PREDICTED: ubiquitin-conjugating enzyme E2 W-like isoform X2 [Bombyx mori]	2e-49,	1.281012432
BGIBMGA011982	PREDICTED: LOW QUALITY PROTEIN: low-density lipoprotein receptor-related	0.0,	1.436874655
BGIBMGA012192	PREDICTED: U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein-like [Bo	1e-55,	1.361703097
BGIBMGA012428	hnRNPA/B-like 28 [Bombyx mori]	2e-50,	1.232321139
BGIBMGA012428	no hit	1.00E-114	1.401722905
BGIBMGA012560	glycerol-3-phosphate dehydrogenase-1 [Bombyx mori]	0.0,	1.259662046
BGIBMGA012935	clathrin heavy chain [Bombyx mori]	0.0,	1.395128299
BGIBMGA013231	protein phosphatase 1 catalytic subunit [Bombyx mori]	1e-97,	1.274741666
BGIBMGA013312	PREDICTED: LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase CBL-like [Bo	4e-128,	1.274401083
BGIBMGA013313	PREDICTED: LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase CBL-like [Bo	7e-158,	1.460250456
BGIBMGA013510	ribonucleoside diphosphate reductase small subunit [Bombyx mori]	0.0,	1.334397578
BGIBMGA013960	PREDICTED: probable ATP-dependent RNA helicase ddx17-like [Bombyx mori]	9e-143,	1.331078583
BGIBMGA014091	PREDICTED: uncharacterized protein LOC101736214, partial [Bombyx mori]	3e-160,	1.266487751
BGIBMGA014106	PREDICTED: SUZ domain-containing protein 1-like [Bombyx mori]	8e-140,	1.221177005
BGIBMGA014456	PREDICTED: uncharacterized protein LOC101739986 [Bombyx mori]	7e-158,	1.375421636