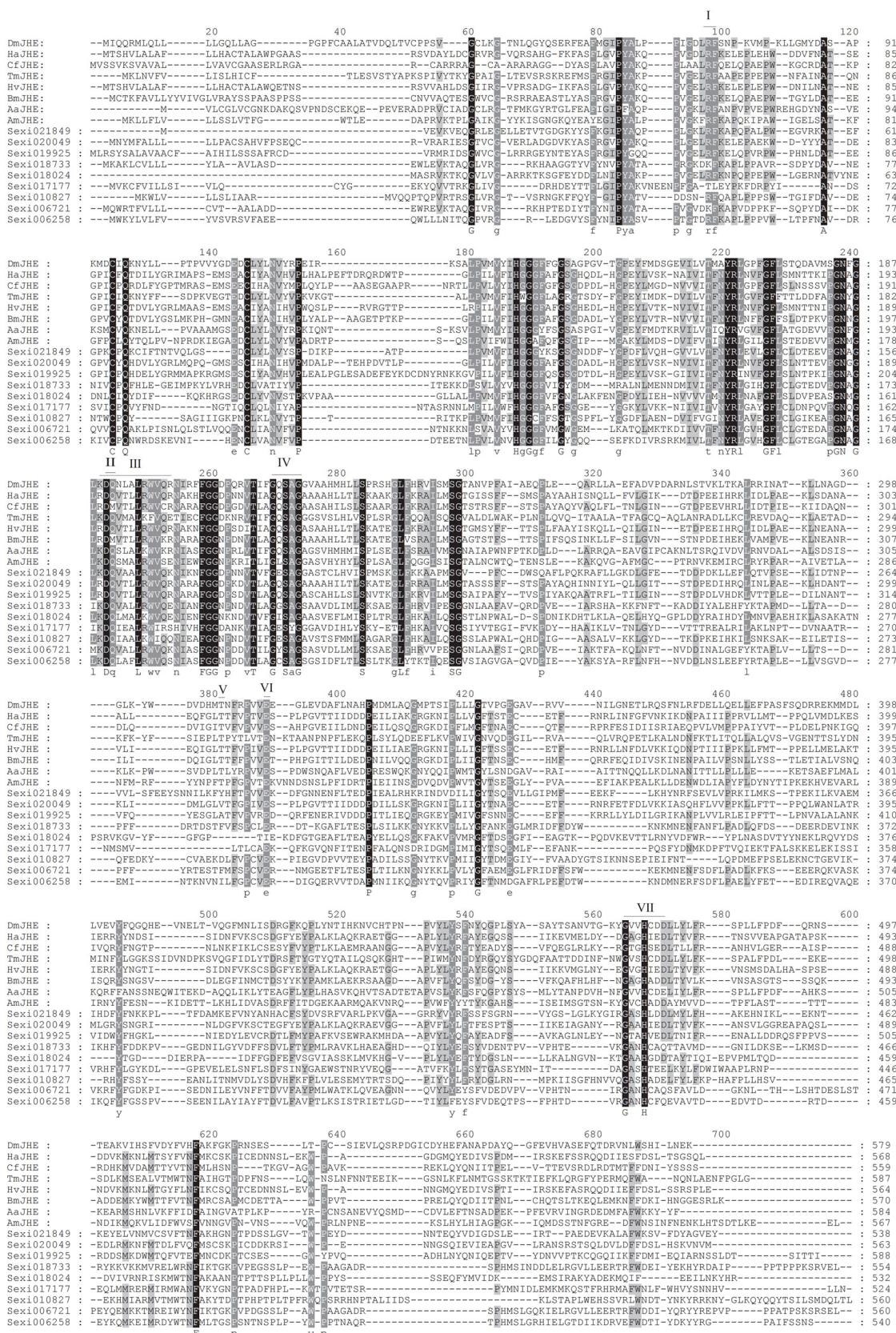


**Figure S1.** Verification of ten randomly selected differentially expressed gene using quantitative reverse transcriptase PCR.



**Table S1.** Conserved sequence motifs in the deduced *JHEs* and *JHELs* from various insect orders.

Source	Gene	SP <sup>a</sup>	Conservative Structural (Motif)							Others	
			RF	DQ	GQSAG	E	GxxHxxD	R/Kx(6)R/KxxR	T	MW (kDa)	pI
Diptera	NP_001163166	p	+ <sup>b</sup>	+	+	+	+	Kx(6)RxxxR	+	64.52	6.30
	EAT43357	a	+	+	+	+	GxxHxxE	Kx(6)RxxxR	+	65.19	6.67
Coleoptera	AAL41023	p	+	+	+	+	+	Kx(6)KxxxE	+	65.89	5.24
Hymenoptera	NP_001011563	p	+	+	GLSAG	+	+	Kx(6)RxxxE	+	63.91	6.52
	AEB77712	p	+	+	+	+	+	Rx(6)RxxxR	+	62.71	6.03
Lepidoptera	AAD34172	p	+	DM	+	+	+	Rx(6)RxxxR	+	61.32	7.49
	AAC38822	p	+	+	+	+	+	Rx(6)RxxxR	+	62.57	5.36
	AAR37335	p	+	DM	+	+	+	Rx(6)RxxxR	+	62.72	6.38
	Sexi020049	p	+	+	+	+	+	Rx(6)RxxxR	V	62.15	6.28
	Sexi019925	p	+	+	+	+	+	Rx(6)RxxxR	A	66.32	5.39
	Sexi021849	a	+	+	GESAG	+	+	Kx(6)RxxxK	Y	60.74	6.12
	Sexi018733	p	KF	+	GGSAG	+	GxxHxxQ	Kx(6)RxxxE	F	62.46	5.89
<i>S. exigua</i>	Sexi018024	a	+	+	GISAG	I	+	Kx(6)KxxxE	No(gap)	59.66	6.00
	Sexi017177	p	TL	+	GESAG	+	GxxHxxE	Kx(6)RxxxS	No(gap)	59.93	7.17
	Sexi010827	p	+	+	GESAG	+	GxxHxxE	Kx(6)KxxxQ	D	63.09	7.19
	Sexi006721	p	KF	+	GYSAG	+	GxxHxxQ	Kx(6)RxxxK	F	63.26	5.91
	Sexi006258	p	+	+	GCSAG	+	GxxHxxQ	Kx(6)RxxxS	I	61.19	4.53

<sup>a</sup> : 'SP' represents 'signal peptide'. 'p' and 'a' represent the 'presence' and 'absence' of the signal peptide, respectively. <sup>b</sup>: The "+" indicates that the consensus sequence is maintained. NP\_001163166.1 is the accession number of *DmJHE* (*Drosophila melanogaster*), EAT43357.2 of *AaJHE* (*Aedes aegypti*), AAL41023.1 of *TmJHE* (*Tenebrio molitor*), NP\_001011563.1 of *AmJHE* (*Apis mellifera*), AEB77712.1 of *HajHE* (*Helicoverpa armigera*), AAD34172.1 of *CfJHE* (*Choristoneura fumiferana*), AAC38822.1 of *HvJHE* (*Heliothis virescens*), and AAR37335.1 of *BmJHE* (*Bombyx mori*).

**Table S2.** Primers used for RT-qPCR.

Primer Name	Primer Sequence (5'-3')	Length of Product (bp)
$\beta$ -actin-F	CCAGCCTTCCTTCTGGGTAT	94
$\beta$ -actin-R	AGGTCTTACGGATGTCAACG	
Se021849-F	ATTCGGCCAAAATGTCCAC	173
Se021849-R	AATCGTCGTTACAGAGCCA	
Se018733-F	TGAAGTTACATGCGGAAGCTGGAC	81
Se018733-R	GCACCACAGGAGTATTCTCGTCAAC	
Se006721-F	TGTTACTGTTGCGTGACG	184
Se006721 -R	AATTTGGTGGGTCAACGGG	
Se006258-F	GTTCACTGTTCGCCGAAGAG	186
Se006258-R	GATCGACTGCATTGAACGGG	
Se002682-F	CATACGCCGAG TGGATGCTTC	100
Se002682-R	CATCTGATTGTGCCGTGTTGC	
Se013300-F	TGAGTTCCGGCAAAACAGAC	181
Se013300-R	GCCATGTCTCCCTGATCCT	
Se022490-F	TCTGACACCTACGCCAAAGA	181
Se022490-R	CCACAATGCGATCCAACCAT	
Se003449-F	CCGAAGACAACGGAGCCAAGAC	150
Se003449-R	GTTCACTGCTGCTGGTGTAC	
Se001306-F	TTTGCCTGCTTGTGTTGTGTTG	144
Se001306-R	AGCCTGGATCTGAGCGTCTGTG	
Se009605-F	CGAGAACAGAACGGCGTGAAG	93
Se009605-R	TGGTCAGAGTGTCTTAGCAGTC	