

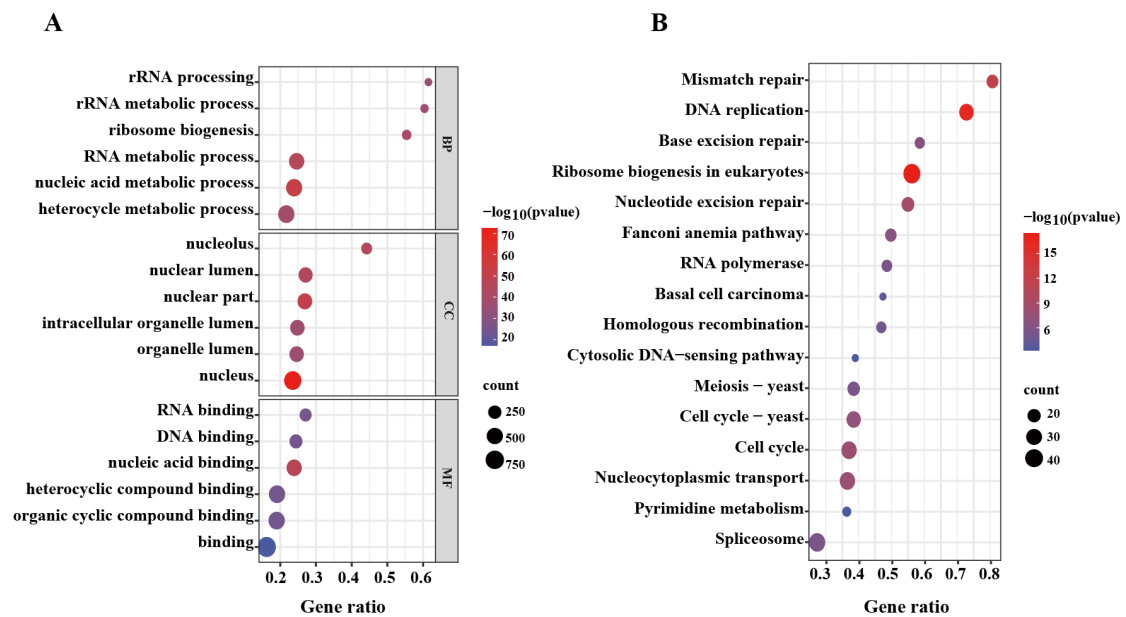


Figure S1. Functional enrichment analysis of differentially expressed gene (DEGs) in 2nd instar larvae. (A) The GO functional classification of the down-regulated DEGs, respectively. The distributions are summarized in three main categories: biological process (BP), molecular function (MF), and cellular component (CC). The x-axis indicates the gene ratio, which means the ratio of the differentially expressed gene number to the total gene number in a certain GO term and the y-axis indicates the different GO terms. (B) A bubble plot was constructed to illustrate the KEGG outcomes of down-regulated DEGs. GO: Gene Ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes.

Table S1. Primer sequences used in this study

Gene ID	Description	Sequence of primers (5'→3')	
CVE04043	Aldehyde dehydrogenase X, mitochondrial	Forward	CCAGAACTTTTGTCCACGCA
		Reverse	
CVE03410	Spermine oxidase	Forward	AAAACAGAGCACAAGCCCAA
		Reverse	
CVE11707	Acetyl-CoA acetyltransferase A	Forward	TAAGCAAGGGCAAAGGGA
		Reverse	GTAACGATGGACTCGGCGA
CVE07007	Asparagine synthetase	Forward	
		Reverse	ATTCGTGGTGCTCGCTGTC
CVE09703	Succinate-semialdehyde dehydrogenase	Forward	TTGCTTCAGTGCCCGACAT
		Reverse	CGAGACTCAGCCAGAGATTTTC
CVE04751	Alanine aminotransferase 2	Forward	ATGCCTCACGTTTGTAGCGGCA
		Reverse	TTGTGCCGCTACAAACGTGAGG
CVE03249	Glutamine synthetase 2 cytoplasmic	Forward	GTGGAGGAAAAGACAACGAAC
		Reverse	CAACGCATCACAGACAGAATAC
CVE06143	Probable phosphoserine aminotransferase	Forward	GCCGTCTGGAGTGACTGTTG
		Reverse	ACTTGGAAGGTCGGTGGTGT
CVE12326	Probable aspartate aminotransferase	Forward	CACGAGCAATGGAAGCAAAT
		Reverse	CAGCGAAGAGACGAGGAGC
CVE03669	D-3-phosphoglycerate dehydrogenase	Forward	TCCAACCAAAGACTTTCCAGC
		Reverse	CATCAATTTACCATCCGCA
CVE06125	Protein arginine N-methyltransferase 1	Forward	TTTGCGGTATCGAGGACCG
		Reverse	GCATTTGTGACGACTTGTTTAG
CVE05414	Fructose-bisphosphate aldolase	Forward	TGTCTAAACGCGCTACTCC
		Reverse	TTGTTCTTCTTGCCACCC
CVE07513	Putative cystathionine gamma-lyase 2	Forward	CGACCAACACCGAAGAAGG
		Reverse	ATTGCAGCGAGGCATGACT
CVE06146	Pyruvate kinase	Forward	CAAACATTCAAACCTTACCACAG
		Reverse	GCGATCCTAGCGTTCCACC
CVE00674	Probable 3-hydroxyisobutyrate	Forward	ACAGCAGCACAATAGACCCCT
		Reverse	CCTCGCTCCTACTACACCACC
MT459787	β -Tublin	Forward	CCTACTGGTCAAATGTTCCG
		Reverse	ATCACAGCCCTCAGACTCTCG

Table S2. Summary of the sequence assembly after Illumina sequencing

Sample	Raw Reads No.	Clean Reads No.	Clean Reads Rates (%)	Q30 (%)	Mapped Reads No.	Mapping Rate (%)	Total gene No.
L3d_1	43,689,408	43,347,108	99.22	91.03	40,860,077	94.26	10,320
L3d_2	45,300,788	44,926,410	99.17	93	42,846,864	95.37	10,409
L3d_3	39,758,812	39,366,212	99.01	93.05	37,690,094	95.74	10,369
L6d_1	37,957,852	37,318,858	98.32	92.8	35,199,046	94.32	10,598
L6d_2	45,616,030	44,727,398	98.05	93.1	41,943,498	93.78	10,510
L6d_3	37,899,682	36,946,384	97.48	90.63	32,748,199	88.64	10,726

Table S3 Data overview of RNA-Seq mapped to *C. vestalis* genome

Sample	Exon	Exon Rate (%)	Intron	Intron Rates (%)	Intergenic	Intergenic Rate (%)
L3d_1	4646004378	76.06	250787420	4.11	1211488535	19.83
L3d_2	4796433603	74.86	259396056	4.05	1351046758	31.09
L3d_3	4420379768	78.42	216355687	3.84	1000167192	17.74
L6d_1	3492295682	66.42	177905500	3.38	1587876990	30.20
L6d_2	4463010351	71.20	199687655	3.19	1605727966	25.61
L6d_3	3372008614	68.92	177753950	3.63	1342681245	27.44