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RESEARCH REPORT

Analysis of genes influencing the feeding of *Bombyx mori* by genome resequencing

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Abstract

Bombyx mori belonging to the Lepidoptera family of insects, is an oligophagous insect that feeds on mulberry leaves. But why the silkworm has a soft spot for mulberry leaves is still a scientific mystery. The existing silkworm genome assembly and annotation are not satisfactory, which limits further analysis of silkworm gene functions. We used next-generation and third-generation sequencing technology, Hic, and other new technologies to resequence and assemble the whole genome of *Bombyx mori Jiangsu*. Through Venn analysis, *Bombyx mori Jiangsu*, *Bombyx mori_JP* and *Bombyx mandarina* that eats mulberry leaves was compared with other 6 species, and the *Bombyx*-specific gene families were found. The positive selection analysis was used to find the positively selected genes among the *Bombyx mori Jiangsu*, *Bombyx mori_JP* and *Bombyx mandarina.* And then, GO and KEGG enrichment analysis were used to explore the functions of these genes, trying to find genes that affect silkworm feeding. The total amount of data obtained by next-generation, third-generation and Hi-C sequencing was 198.67 G, and the ratio of GC was 38.31%, with contig N50 of 3.75 Mb and scaffold N50 of 17.26 Mb. We found that UGT46A1, UGT33R1 and UGT33R2 were only found in *Bombyx mori Jiangsu*, *Bombyx mori_JP,* and *Bombyx mandarina*. And they were all involved in multiple pathways such as cytochrome P450 foreign body metabolism, starch and sucrose metabolism, and pentose and glucuronate conversion pathways. We found that cyclic nucleotide-gated cation channel subunit A-like (CNGA) was subject to positive selection and was involved in the olfactory transduction pathway.

Key Words: *Bombyx mori Jiangsu*; feeding habits; whole-genome sequencing; gene family cluster analysis; Venn analysis; positive selection analysis

Introduction

Bombyx mori (B. mori) is an important economic insect, and its diet plays an important role in silkworm cocoon production. Therefore, it is of great significance to the economic development of our country to study the molecular mechanism of feeding habits, cultivating polyphagous silkworm strains and developing artificial feeds that are more conducive to the growth of silkworms. Silkworm, as an oligophagous insect, only eats mulberry leaves under normal conditions. Mulberry leaves contain all the nutrients needed for silkworm growth and development (Fraenkel, 1959). Silkworm feeding on mulberry leaves is due to the presence of volatile feeding factors in mulberry leaves that can stimulate the feeding desire of silkworms (Xue, 2009), such as α,β-hexenal (Watanabe *et al.*, 1958), citral and linalool, etc., they act on the chemoreceptors of silkworms (Hsiao, 1969), causing positive feeding responses in silkworms. In addition, there are also contain biting factors such as β-sitosterol (Hamamura *et al.*, 1961) and swallowing factors such as cellulose. Isoquercitrin, quercetin, morin (Horie *et al*., 1962), polyphenolic acid (Hamamura and Naito, 1961), choline (Hayashiya, 1965), chlorogenic acid (Naito *et al.*, 1963, 1965), certain vegetable oils and fatty acids (Kato *et al.*, 1966), vanillin (Yamada *et al*., 1966) and so on in mulberry leaves can also promote the feeding of silkworms.

The monocular structure of silkworm larvae prevents silkworms from recognizing food (Chen, 2009), so silkworms do not rely on vision for feeding. Animals require a complex and powerful system of taste and smell to assess their food environment (Mack and Zhang, 2021). The colfactory atractan acting on the olfactory system can cause the silkworm to seek and recognize plants (Hsiao, 1969; Wilde, 2011), and the phagostimulant acting on the taste sensory system can affect the amount of food

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Table 1 Genes used for gene family clustering in each species

Species	Name	Number of Genes	Number of Gene families
Sfr	*Spodoptera frugiperda*	22086	19805
Aya	*Antheraea yamamai*	13610	11923
Bmj	*Bombyx mori Jiangsu*	13053	11923
Bmo	*Bombyx mori_JP*	16815	15776
Pxy	*Plutella xylostella*	17441	15287
Pra	*Pieris rapae*	12064	11578
Har	*Helicoverpa armigera*	13258	12634
Bma	*Bombyx mandarina*	12520	12118
Dpl	*Danaus plexippus*	14514	12286
Lde	*Leptinotarsa Decemlineata*	12671	10771
Tca	*Tribolium castaneum*	12786	11586
Ame	*Apis mellifera*	9881	9340
Aga	*Anopheles gambiae*	12311	10896
Aae	*Aedes aegypti*	14535	13356
Cel	*Caenorhabditis elegans*	20060	14320
Lhu	*Linepithema humile*	11428	10811
Dme	*Drosophila melanogaster*	13554	10774
Nvi	*Nasonia vitripennis*	12834	11086

eaten by silkworms (Fraenkel, 1959; Chapman, 2003). Therefore, silkworm food selection is based on the use of taste and smell-related chemical feedback from the nervous system to guide feeding behavior, ingest nutritious food that the body needs, and avoid toxic food (Zhang *et al.*, 2011; Kumar, 2018). Taste receptors can detect nutrients in the environment, and cellular sensors can monitor the levels of nutrients needed by cells. When certain substances are deficient, animals choose to contain corresponding food sources (Kim *et al.*, 2021). In addition, an animal's decision to accept or reject an expected food is also influenced by palatability, including smoothness and grit, the latter being influenced by particle size. Insects have the ability to discern the size of particles in their food and use this information to decide whether the food is attractive (Li and Montell, 2021).

As the most species and huge number of animals, insects are closely related to the development of human society, and the research of entomomics has been paid more and more attention. As an important data resource for insect molecular biology research, the genome sequences of various species have attracted much attention in current biological research. The rapid development of sequencing technology has brought entomology into the genome era, and the sequenced insect genome data are stored in various large-scale comprehensive databases. Since 2000, *Drosophila melanogaster (Dem)*, *Apis cerana Fabricius (Ace)*, *B. mori*, *Danaus plexippus (Dpl)*, *Acyrthosiphon pisum Harris (Api)*, *Plutella xylostella (Pxy), Nilaparvata lugens (Nlu)*, *Locusta migratoria (Lmi)* and other insect genomes have been deciphered, and the sequencing of insect genomes has shown an explosive growth trend in recent years. In 2004, the genome of the silkworm Dazao strain was firstly sequenced by shotgun. In 2008, the silkworm genome data was updated. Comparative genomics can be used to compare and analyze the genome sequences of different individuals of the same species and related species in terms of gene family, collinearity or gene structure, and explore the origin and evolution of genes in different species, and the amplification and loss of gene families, and analyze the genetic mechanism of important traits of species.

The current research on the molecular mechanism of silkworm's feeding preference for mulberry leaves is insufficient. With the development of sequencing technology and the improvement of various protein databases, it can help find the genes that determine the feeding habits of the silkworm. In this study, the genome of *Bombyx mori* strain Jiangsu was sequenced and assembled using next-generation sequencing (NGS), third-generation sequencing (TGS), and Hi-C technology. Through comparative genomics analysis, gene structures and

A

B

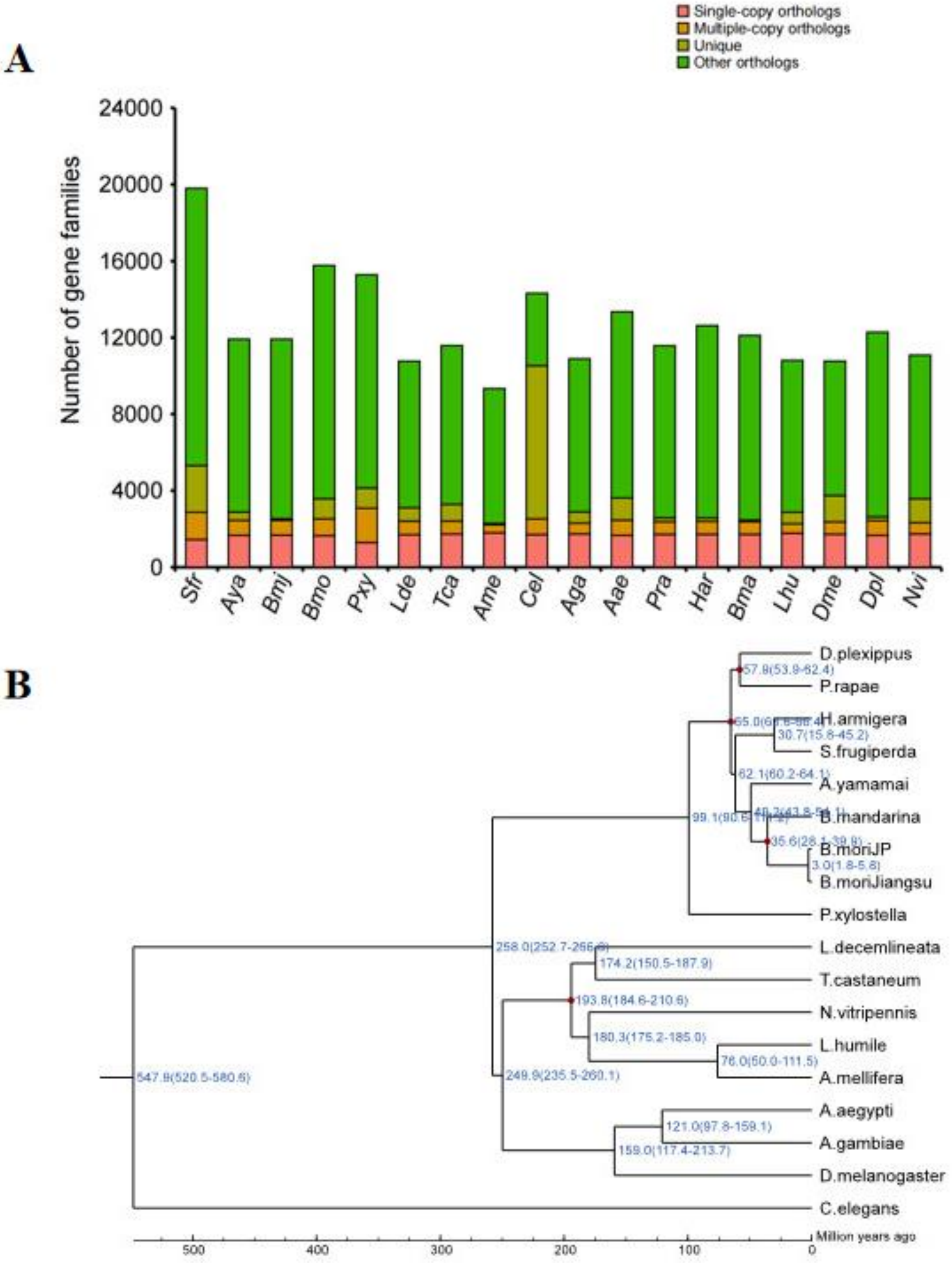

Fig. 1 The distribution of gene families in different species and estimation of species divergence time. (A) The horizontal axis showed 18 species, and the vertical axis was the number of corresponding gene families. (Pink) The number of gene families in the single-copy orthologs. (Yellow) The number of gene families in multiple-copy orthologs. (Dark yellow) The number of unique gene families in related species. (Green) The number of gene families in other orthologs. (B) Estimation of the divergence time between *Bombyx mori Jiangsu* and other 17 species. The number of the node position represented the divergence time of the species in millions of years, and the brackets indicated the confidence range of the divergence time

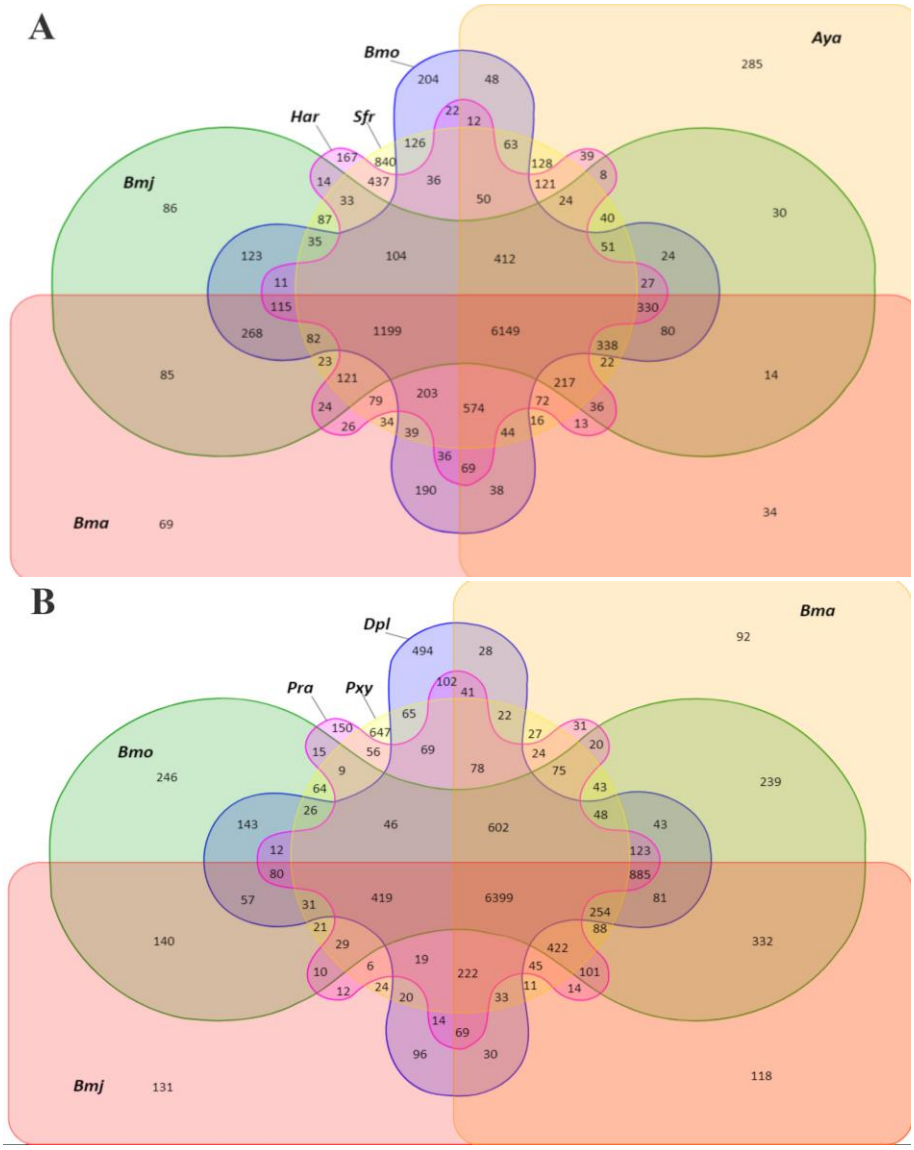

Fig. 2 Venn diagram of the gene family. (A) *Bmj*, *Bmo*, *Bma*, *Sfr*, *Har*, *Aya* gene family Venn diagram; (B) *Bmj*, *Bmo*, *Bma*, *Dpl*, *Pxy*, *Pra* gene family Venn diagram.Venn analysis was uesd to screen the gene families shared by *Bmj*, *Bmo* and *Bma* and remove all gene families of *Sfr*, *Har*, *Aya*, *Dpl*, *Pxy* and *Pra*

functions were annotated in order to find genes that affect silkworm feeding, particularly genes that affect the gustatory and olfactory processes of the silkworm. These results will provide essential information for future research of the silkworm genome. They will be of great significance for further research on the feeding habits of the silkworm and the promotion of the development of the sericulture industry.

Materials and methods

Sample preparation and whole-genome sequencing

Bombyx mori strain NB was raised in the laboratory of the School of Life Sciences, Jiangsu University. The posterior silk glands of the fifth-instar third-day larvae were taken and rinsed with PBS. The silkworm genome resequencing used NGS and TGS technology. NGS used DNAsecure Plant Kit (TIANGEN) to extract DNA. NEB Next® Ultra DNA Library Prep Kit (NEB, USA) was used to construct a library of qualified DNA samples, and index codes were added to each sequencing sample. The DNA was purified using the AMPure XP system (Beckman Coulter, Beverly, USA), the PCR products were purified, and the library quality was evaluated on the Agilent Bioanalyzer 2100 system. The Illumia Cluster Kit was used to cluster the qualified libraries on the cBot Cluster Generation System. After cluster generation, the library preparation was sequenced on the Illumina Hiseq platform, and 125/150/250 bp paired-end sequencing was generated. The DNA extraction of TGS adopted the SDS extraction method, and the qualified DNA samples were randomly broken into fragments of about 20 Kb, and the sticky ends of the fragments were turned into blunt ends. The two ends were connected to the single circular strand, and the two ends of the single strand were connected to the double strand's positive and negative strands. The two ends of the single strand were respectively connected to the positive and negative strands of the double-strand connected to the single circular strand. The two ends of the single strand were connected to the double strand's positive and negative strands to obtain a dumbbell-like structure, which completed the preparation of the third generation 20 Kb library (SMRTbell DNA library). The constructed library was sequenced through the PacBio Sequel platform. After self-correcting the third-generation data, FALCON (Branch 3.1) was used to perform a pure three-generation genome assembly. The corrected long reads were compared, and the string graph was generated according to the overlap connection, and the primary contig was formed. In order to find heterozygosity differences, FALCO-Unip analysis was used to reassemble 'haplotype fused' contigs into haplotigs and obtain the updated primary contigs and haplotigs that constitute diploids genome assembly then phased and classified these heterzygosity differences. Finally, for the assembly results of the previous step, the third-generation data was used to correct the assembly results based on quiver software, and then the second-generation data was used to perform secondary corrections based on pilon software to improve the accuracy of the assembly results and finally we obtained a high-quality consensus sequence. The obtained 10×Genomics Linked-reads data was aligned with the contig sequence assembled from the third-generation data. For contigs that were relatively close in actual distance, there were many Linked-reads that support their connection relationships; for contigs that were relatively far away, they lacked Linked-reads support, it could not be connected. FragScaff software (Version 140324) was used to extend contig and get the preliminary version of Scaffold. We compared the Hi-C data to the genome draft, performed comparison analysis, and performed clustering, sorting, and orientation according to the comparison results to assist the initial version of the genome to be upgraded to the chromosome level. Hi-C clean data was compared with the initial version through Burrows-Wheeler-Alignment (BWA) software. The contig/scaffold of the same kind was sorted and accurately oriented according to the mutual intensity of the two contigs and the position of the comparison of the mutual read. According to the link relationship provided by the restriction region and Hi-C data, the map was composed and the weight was calculated to obtain the final upgraded version. Finally, Core Eukaryotic Genes Mapping Approach (CEGMA) (http://korflab.ucdavis.edu/dataseda/cegma/) (Parra *et al.*, 2007) combined with softwares such as tblastn, genewise and geneid and Benchmarking Universal Single-Copy Orthologs(BUSCO) (http://busco.ezlab.org/) (Simão *et al.*, 2015), Augustus and hmmer were used to evaluate the assembled genome to ensure its consistency and integrity.

Gene family cluster analysis and species divergence time estimation

The OrthoMCL (http://orthomcl.org/orthomcl/) process (Li and L., 2003) was used to analyze *Bombyx mori Jiangsu* (*Bmj*), *Aedes aegypti* (*Aae*), Dme, *Anopheles gambiae* (*Aga*), *Apis mellifera* (*Ame*), *Nasonia vitripennis* (*Nvi*), *Tribolium castaneum* (*Tca*), *Leptinotarsa decemlineata* (*Lde*), *Pieris rapae* (*Pra*), *Antheraea yamamai* (*Aya*), *Bombyx mori_JP* (*Bmo*), *Bombyx mandarina* (*Bma*), *Spodoptera frugiperda* (*Sfr*), *Helicoverpa armigera* (*Har*), *Dpl, Linepithema humile* (*Lhu*), *Pxy, and Caenorhabditis elegans* (*Cel*) for gene family clusters. The gene information of each species was obtained from National Center for Biotechnology Information Search database (https://www.ncbi.nlm.nih.gov/), GigaDB (http://gigadb.org/), and SilkBase (http://silkbase.ab.a.u-tokyo.ac.jp/cgi-bin/index.cgi). The gene set of each species was filtered. When there were multiple alternatively spliced transcripts for a gene, only the transcript with the longest coding region was retained for further analysis; genes encoding proteins less than 30 amino acids were excluded. TreeFam software was employed to compare and cluster the results and 1.5 was used for the expansion coefficient (Li *et al.*, 2006). Mcmctree in the PAML (Yang, 2007) software package (http://abacus.gene.ucl.ac.uk/software/paml.html) was used to estimate the divergence time, where the time calibration point was, *Aya* and *Bmo*: 50-100 MYA; *Dpl*, *Tca*: 271.9-293.8 MYA; *Pxy*, *Bmj*: 97-190 MYA, time calibration point was taken from reference 26 (Tingcai Cheng *et al.*, 2017).

Venn analysis

In order to obtain genes that affect the feeding of silkworms, gene families from 9 species were selected, including *Bmj*, *Pra*, *Aya*, *Bmo*, *Bma*, *Sfr*, *Har*, *Dpl,* and *Pxy,* for comparison. Among them, *Bmj*, *Bmo,* and *Bma* eat mulberry leaves. *Pra*, *Aya*, *Sfr*, *Har*, *Dpl,* and *Pxy* do not eat mulberry leaves. According to the clustering results, the gene families shared by the three mulberry leaf-eating species were screened out through Venn analysis, and all gene families of the remaining six species were removed. The screened silkworm shared and unique gene families may contain genes that affect silkworm feeding. Since a Venn diagram can only count 6 species at most, we divided the 9 species into two groups, one group included *Bmj*, *Bmo*, *Bma*, *Sfr*, *Har,* and *Aya*; the other group had *Bmj*, *Bmo*, *Bma*, *Dpl*, *Pxy,* and *Pra*. The Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of these gene families was carried out to find the pathways related to feeding habits and then determine the genes that may affect the eating habits of the *B. mori*. KEGG information refered to https://www.kegg.jp/kegg/kegg1.html, the permission was provided by the Kanehisa laboratory (Kanehisa and Goto, 2000).

Positive selection analysis

Positive selection means that in a single-copy gene family, a particular gene is affected by environmental or human factors during the evolution process, and non-synonymous mutations occur at the amino acid level in order to adapt to changes in the environment. The probability of receiving a positive selection can be detected by calculating Ka/Ks through the maximum likelihood ratio. Among them, Ka/Ks refers to the ratio of non-synonymous mutation rate to synonymous mutation rate. If Ka/Ks>1, it is considered to have a positive selection effect; if Ka/Ks=1, it is considered that there is neutral selection; if Ka/Ks <1, it is considered to have purifying selection effect. We selected the species combination of *Bmj*, *Bmo,* and *Bma* in the foreground, *Pra*, *Aya*, *Sfr*, *Har*, *Dpl,* and *Pxy* in the background. MUSCLE software was used to perform multiple sequence comparisons of the protein sequences of the two species combinations. The two sets of protein sequence alignment results were filtered through Gblocks software to remove low-quality alignment regions. Then the filtered protein sequence alignment results were used as templates to generate multiple sequence alignment results corresponding to CDS (Castresana, 2000). The branch-site model (Yang and Rasmus, 2002; Zhang *et al.*, 2005) in the CODEML tool in PAML (Yang, 1997) for each gene family was used to conduct maximum likelihood analysis. The selection pressure analysis was carried out by pairwise comparison of the nested model of the null hypothesis and the alternative hypothesis. Model pairs were tested by the Likelihood ratio test (LRT) to determine whether the models have a significant difference. If P-value <0.05, it was considered that there was a significant difference between the two models. The empirical Bayes method (BEB) was used to calculate the posterior probability of the detected positive selection sites. The sites with the posterior probability> 95% when P<0.05 were considered to be credible positive selection sites. The GO and KEGG enrichment analysis of positive selection genes were performed to find pathways related to feeding habits. KEGG information refered to https://www.kegg.jp/kegg/kegg1.htm, the permission was provided by the Kanehisa laboratory (Kanehisa and Goto, 2000). The amino acid sites where positive selection occurred in related genes in the pathways were analyzed to determine genes that may affect silkworm eating mulberry leaves.

Results

Genome sequencing and assembly results

We sequenced and assembled the genome of the *Bmj* by using NGS, TGS, and Hi-C technology. According to the specific characteristics of the silkworm genome, the DNA insert is 350 bp. Paired-end sequencing was performed on both ends of these fragments on Ilumina Hiseq to obtain 64.81G whole-genome sequencing data (139.41×). The Hi-C strategy platform obtained a total sequencing volume of 83.78G, with a coverage depth of 180.21×; at the same time, the PacBio platform was used for sequencing with a total sequencing volume of 50.08G and a coverage depth of 107.72× (Table S1). The silkworm genome was assembled using the 198.67G sequencing data of the silkworm genome. The contig N50 of the silkworm genome reached 3.75Mbp, and the scaffold N50 reached 17.26 Mbp (Table S2). The GC

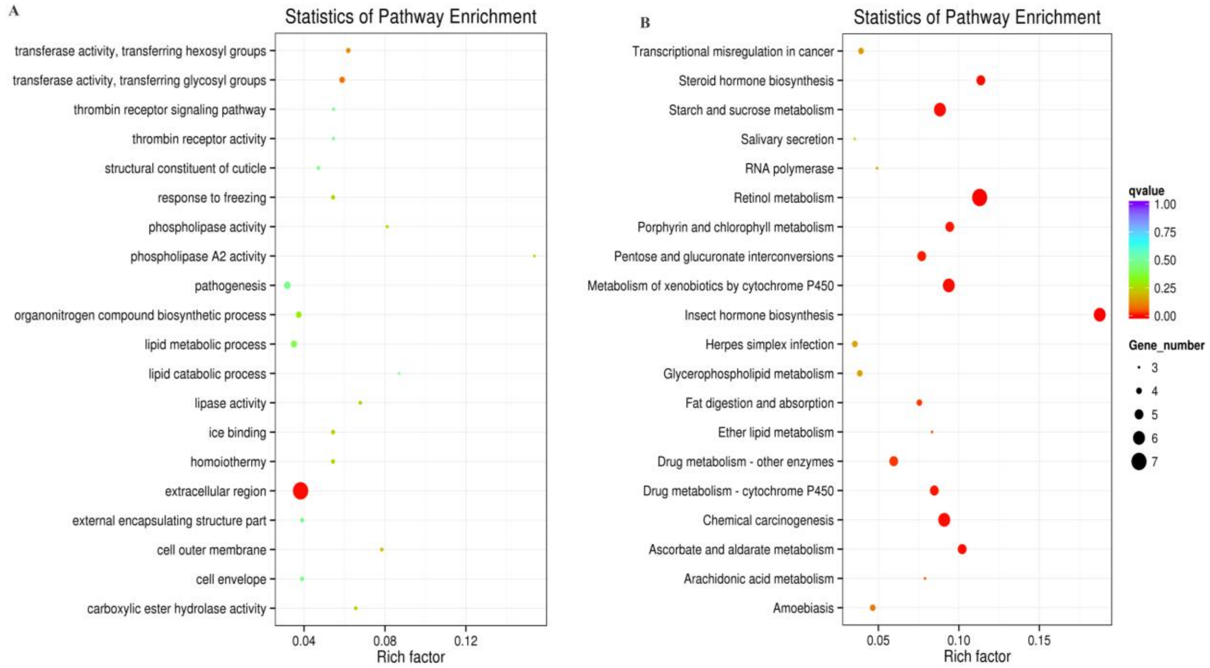

Fig. 3 GO and KEGG enrichment analysis of common genes in *Bombyx*-specific species. (A) GO enrichment analysis of common genes in *Bombyx*-specific species; (B) KEGG enrichment analysis of common genes in *Bombyx*-specific species. KEGG information refered to https,//www.kegg.jp/kegg/kegg1.htm, the permission was provided by the Kanehisa laboratory

Table 2 GO enrichment analysis resuits of common genes in Bombyx-specific species

GO Term	GO Class	Q value	Genes
extracellular region	CC	0.001869189	*low molecular mass 30 kDa lipoprotein 21G1-like; low molecular mass 30 kDa lipoprotein 19G1-like; low molecular mass 30 kDa lipoprotein 19G1-like; alcohol dehydrogenase precursor; uncharacterized protein; uncharacterized protein LOC101740086; uncharacterized protein LOC101739948; serine protease inhibitor 21 isoform X3; phospholipase A2-like; microvitellogenin-like; cuticular protein RR-2 motif 58 precursor; seroin 1 precursor; uncharacterized protein LOC101742341; RNA exonuclease 4-like; uncharacterized protein LOC101746057; uncharacterized protein LOC101736844; actin cytoskeleton-regulatory complex protein PAN1; microvitellogenin-like; low molecular 30 kDa lipoprotein PBMHP-12-like; glow molecular mass 30 kDa lipoprotein 19G1-like precursor; low molecular 30 kDa lipoprotein PBMHPC-19-like precursor; plasma kallikrein-like; uncharacterized protein LOC101743393; uncharacterized protein LOC105843019; uncharacterized protein LOC101742472; spherulin-2A-like; Low calcium response V antigen*
transferase activity, transferring glycosyl groups	MF	0.080585849	*UDP-glycosyltransferase UGT33R1 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glucosyltransferase precursor; UDP-glycosyltransferase UGT46A1; phospholipase A2-like isoform X1; cuticular protein glycine-rich 26 precursor; beta-1,4-galactosyltransferase 7-like*
transferase activity, transferring hexosyl groups	MF	0.120013148	*UDP-glycosyltransferase UGT33R1 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glucosyltransferase precursor ; UDP-glycosyltransferase UGT46A1; phospholipase A2-like isoform X1*
cell outer membrane	CC	0.202397931	*uncharacterized protein LOC101742377; sericin 2 isoform 1 precursor; uncharacterized protein LOC101737731; glow molecular mass 30 kDa lipoprotein 19G1-like precursor*
lipase activity	MF	0.237835251	*lipase member H-A-like; phospholipase A2-like; phospholipase A2-like isoform X1; pancreatic triacylglycerol lipase-like*

content is 38.31%, and the proportion of N is 0.000037%, which is an acceptable range (<10%) (Table S3). The comparison rate of all small fragment reads to the genome is about 98.92%, and the coverage rate is approximately 99.83%, indicating that the reads and the assembled genome have good consistency (Table S4). Samtools (http://samtools.sourceforge.net/) was used to sort the BWA comparison results by chromosome coordinates, duplicate reads were removed, Single Nucleotide Polymorphisms (SNP) Calling was performed, and the original results were filtered. The final SNP statistics showed that the heterozygous SNP ratio of the silkworm genome was 0.0528%, and the homozygous SNP ratio was 0.0001%, indicating that the assembly has a high single-base accuracy rate (Table S5). The CEGMA evaluation found that 223 (89.92%) of 248 core eukaryotic genes were complete (Table S6), and the BUSCO evaluation statistics of the *B. mori* genome showed that 1658 orthologous single-copy genes assembled 98.0% of the entire copy genes (Table S7), indicating that the assembly was relatively complete. The repetitive sequence library predicted by de novo was integrated with the homologous repetitive sequence database Repbase, and the *Bmj* genome was annotated with RepeatMasker software. The results showed that the Jiangsu silkworm genome contained 56.88% repeat sequences (Table S8). A total of 11,509 genes were predicted from the *Bmj*. The protein sequence obtained by gene structure prediction was compared with the known protein library, and 99.8% of the genes were able to predict the function (Table S9).

Gene family cluster analysis and species divergence time estimation

In order to reveal the genome characteristics of the *Bmj*, a genome-wide phylogenetic tree combining the sequenced genome of *Bmj* and published genomes of 17 other insect species was constructed, including *Aae*, *Dme*, *Aga*, *Ame*, *Nvi*, *Tca*, *Lde*, *Pra*, *Aya*, *Bmj*, *Bma*, *Sfr*, *Har*, *Dpl*, *Lhu*, *Pxy,* and *Cel*. The number of genes involved in the

Table 3 KEGG enrichment analysis results of common genes in Bombyx-specific species

MapTitle	Q value	Genes
Insect hormone biosynthesis	0.0000971	*calexcitin-2-like; uncharacterized protein LOC101742377; uncharacterized protein LOC101745533; uncharacterized protein LOC101743036; farnesol dehydrogenase-like isoform X1; uncharacterized protein LOC101738236*
Retinol metabolism	0.000202086	*UDP-glycosyltransferase UGT33R1 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] UDP-glucosyltransferase precursor; UDP-glycosyltransferase UGT46A1; 17-beta-hydroxysteroid dehydrogenase 14-like; 17-beta-hydroxysteroid dehydrogenase 14-like*
Metabolism of xenobiotics by cytochrome P450	0.001730997	*UDP-glycosyltransferase UGT33R1 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glucosyltransferase precursor; UDP-glycosyltransferase UGT46A1; carbonyl reductase [NADPH] 3-like*
Chemical carcinogenesis	0.001730997	*UDP-glycosyltransferase UGT33R1 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glucosyltransferase precursor; UDP-glycosyltransferase UGT46A1; carbonyl reductase [NADPH] 3-like*
Starch and sucrose metabolism	0.001730997	*UDP-glycosyltransferase UGT33R1 precursor; UDP-glycosyltransferase UGT33R2 precursor; UDP-glycosyltransferase UGT33R2 precursor; TPA, putative cuticle protein; UDP-glucosyltransferase precursor; UDP-glycosyltransferase UGT46A1*

comparison of each species is shown in Table 1. The gene family cluster analysis of protein-coding genes from these 18 species showed that there were 21904 gene families in the 18 species, and there were 650 single-copy gene families shared by all species (Fig. 1A). It could be seen from Fig. 1B that the divergence time of the clades of the *Bmj* and *Bmo* was about 3.0 million years. To be precise, the divergence time of *Bmj* and *Bmo* was far less than this length. This may be due to the result of artificial selection in the evolution process.

Venn analysis results

According to the Venn diagram (Fig. 2), the gene families of *Spr*, *Har*, *Aya*, *Dpl*, *Pxy,* and *Pra* that do not eat mulberry leaves are excluded. There are a total of 217 gene families shared by *Bmj*, *Bmo,* and *Bma* that eat mulberry leaves. GO enrichment analysis found that these 217 gene families had a total of 135 functional annotations (Table S10). The top five with the highest-ranking were extracellular region, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups, cell outer membrane, and lipase activity (Fig. 3A). The genes involved are shown in Table 2. KEGG enrichment results showed that these 217 gene families have 111 significant enrichment results (Table S11), of which insect hormone biosynthesis, retinol metabolism, metabolism of xenobiotics by cytochrome P450, chemical carcinogenesisand starch and sucrose metabolism had higher enrichment levels (Fig. 3B), the genes involved were shown in Table 3.

Positive selection analysis results

Bmj, *Bmo,* and *Bma* were set as foreground branches, *Spr*, *Har*, *Aya*, *Dpl*, *Pxy,* and *Pra* as background branches for positive selection analysis, and a total of 62 positive selection genes were identified. The functional enrichment analysis of genes subject to positive selection revealed a total of 19 terms in GO enrichment results (Table S12), but no terms related to eating habits were found (Fig. 4A). There were 22 valid results in KEGG (Table S13). The pathways related to eating habits included olfactory transduction, Glycolysis / Gluconeogenesis, and Galactose metabolism (Fig. 4B). The genes involved in the related pathways are shown in Table 4, and the amino acid positions where positive selection occurs are shown in Table S14.

Discussion

This study used NGS, TGS, and Hi-C technology to sequence and assembled the *Bmj* genome and annotated the gene structures and functions. Bioinformatics tools were used to compare the gene family information of *Bmj*, *Bmo*, *Bma*, *Spr*, *Har*, *Aya*, *Dpl*, *Pxy,* and *Pra*. It was found that *UDP-glycosyltransferase UGT46A1 (UGT46A1),*

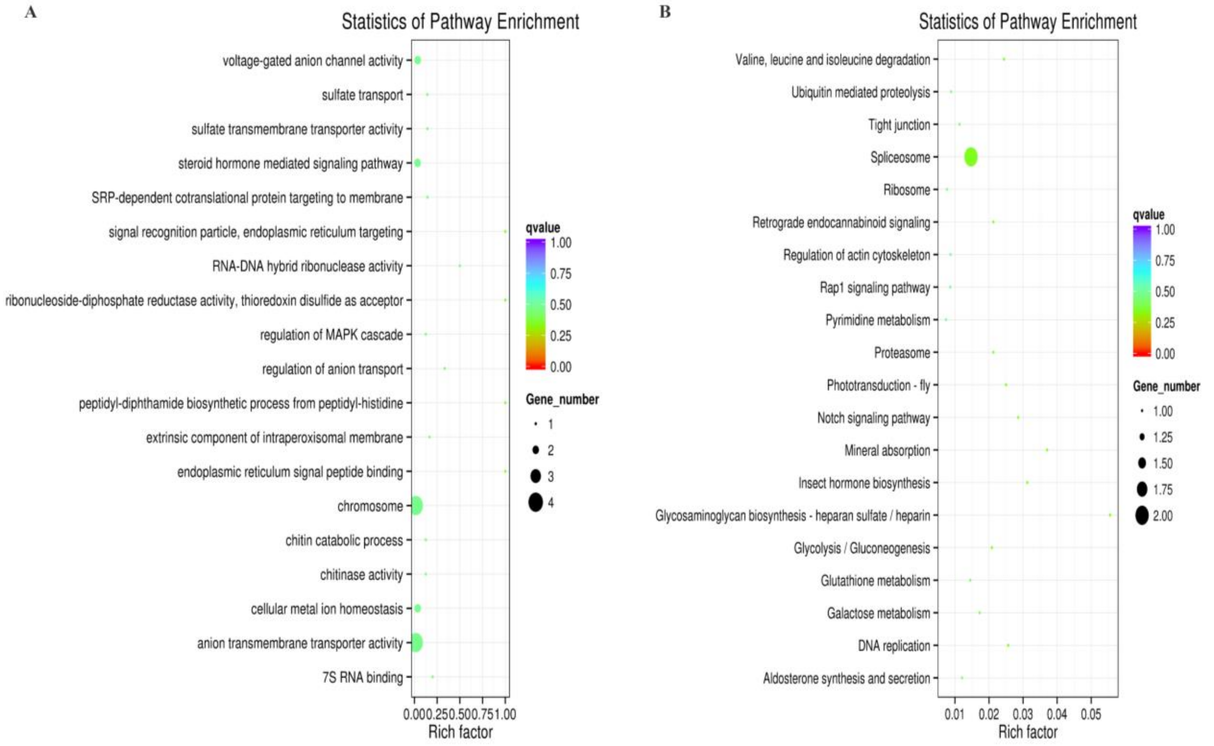

Fig. 4 GO and KEGG enrichment results of positive selection genes in *Bombyx mori Jiangsu*. (A) GO enrichment results of positive selection genes in *Bombyx mori Jiangsu*; (B) KEGG results of positive selection genes in *Bombyx mori Jiangsu*. KEGG information refered to https,//www.kegg.jp/kegg/kegg1.htm, the permission was provided by the Kanehisa laboratory

UDP-glycosyltransferase UGT33R1 (UGT33R1), and *UDP-glycosyltransferase UGT33R2 (UGT33R2)* only existed in species that ate mulberry leaves. GO and KEGG enrichment analysis showed that *UGT46A1*, *UGT33R1* and *UGT33R2* were involved in the most food-related pathways and were ranked high, including metabolism of xenobiotics by cytochrome P450, starch, and sucrose metabolism, and pentose and glucuronate interconversions, etc (Table S13, S14). UDP-glycosyltransferases (UGTs) are a superfamily of enzymes present in all life including plants, animals, fungi and bacteria, and even some viruses (Bock, 2016). UGT catalyzes the combination of uridine diphosphate (UDP) with various exogenous substances such as pollutants, food additives or drugs, and endogenous substances such as hormones, bilirubin, and bile acids, so that the receptor molecules are converted from hydrophobic to hydrophilic to facilitate their clearance (Tephly and Burchell, 1990). Exogenous metabolic enzymes (XMEs) such as GT, cytochrome P450 (CYP), carboxylesterase (COE) and glutathione transferase (GST) are involved in the detoxification of exogenous and endogenous active molecules and their removal from the body by catalyzing their biotransformation in inactive metabolites. Phase I enzymes (CYP, CE, etc.) catalyze functionalized chemical groups (-OH, -COOH, etc.) to form xenobiotics, and Phase II enzymes (GST, UGT, etc.) catalyze polar groups (glutathione, glucuronic acid, etc.), and their presence and activity against volatile odorant substrates have also been demonstrated in olfactory tissues (Nagashima and Touhara, 2010). A growing body of evidence demonstrated the primary function of these odor metabolizing enzymes (OMEs) in olfactory physiology. OME catalyzed odorant metabolism, removed odorants from the receptor surrounding environment to terminate the signal to maintain the highest sensitivity of detection and participated in the synthesis of metabolites, generating additional stimulatory signals that may be modulated (Nagashima and Touhara, 2010). Rane et al. compared the detoxification gene families (P450, GST, and carboxylesterases (CCE)) in 65 insect genomes and found a clear relationship between the number of P450, CCE, and GST genes and eating preferences. The size of the gene family related to the xenotoxic detoxification in insects may be related to the complexity of their diet and tendency to develop resistance to insecticides (Rane *et al.*, 2016). Then they examined the genomes of 160 insect species and found that omnivores and herbivores have more detoxification genes, while species that eat simpler tissues such as sap, nectar, and blood have relatively fewer detoxification genes (Rane *et al.*, 2019). In olfactory tissues, UGT has been demonstrated to have high glucuronic acid-binding activity for different odorants (Jedlitschky *et al.*, 1999) and to respond to a variety

Table 4 KEGG enrichment analysis of positive selection genes in silkworm

Map ID	Map Title	Q Value	Genes
map04740	Olfactory transduction	0.34567298	*cyclic nucleotide-gated cation channel subunit A-like*
map00010	Glycolysis / Gluconeogenesis	0.34567298	*aldose 1-epimerase-like*
map00052	Galactose metabolism	0.381133633	*aldose 1-epimerase-like*

of plant allelochemicals (Luque and O'Reilly, 2002). It was first demonstrated in *Spodoptera littoralis* that odor exposure modulates UGT expression, demonstrating that UGT has a specific role in olfaction (Bozzolan *et al.*, 2014). The enzymatic activity of UGT has been detected in insect brain, olfactory tissue, fat body, midgut and other tissues (Heydel *et al.*, 2010). These shreds of evidence all showed that UGT plays an important role in various dietary-related aspects such as olfactory, detoxification, and starch and sucrose metabolism in silkworms. Therefore, we speculate that *UGT46A1, UGT33R1, UGT33R2* may greatly affect the feeding habit of silkworm.

Through positive selection analysis and GO and KEGG functional enrichment, it was found that cyclic nucleotide-gated cation channel subunit A-like (CNGA) is the most likely gene in positive selection genes to affect the feeding habits of the silkworm. Cyclic nucleotide-gated (CNG) channels are non-selective cation channels, which were first identified in retinal photoreceptors (Haynes and Yau, 1985) and olfactory sensory neurons (Nakamura and Gold, 1987). The natural CNG channel is a heterotetramer formed by CNGA (A1, A2, A3, A4) and CNGB (B1, B3) subunits. CNGA plays an essential role in many signal transduction pathways, especially in the visual and olfactory sensory systems. After the surface receptors of competent cells receive light signals or chemical signals, the level of cyclic nucleotides in the cells will change, which in turn regulates the opening or closing of CNG channels (Varnum and Zagotta, 1996). The electrical signals generated by CNG channels activate downstream neurons so that mammals can sense changes in light and odor from the outside world (Bradley *et al.*, 2005). CNG channels are also involved in the transduction cascade of invertebrate photoreceptors and olfactory receptors (Baumann *et al.*, 1994). A cDNA encoding a putative CNG channel has been cloned from Drosophila. The N-terminal half of the predicted protein (CNGL) has a high degree of sequence similarity with the known CNG channel protein. Northern blot analysis showed that messenger RNA (mRNA) corresponding to the size of the cloned cDNA was expressed in the head of Drosophila. Immunolocalization studies have demonstrated that CNGL is expressed in the brain. These results indicate that CNGL channels may play a role in visual and olfactory information processing in the Drosophila nervous system (Miyazu *et al.*, 2010). Olfactory signal transduction is confirmed to include the following steps: After olfactory stimulation activates the binding of olfactory receptors, the tertiary structure of olfactory receptor proteins changes and the olfactory G protein (Golf) α subunit Golf is activated. The activation of Golf dissociates the β and γ subunits in the G protein and changes the intracellular ATP to cyclic adenosine monophosphate (Bakalyar and Reed, 1990). Intracellular cyclic adenosine monophosphate (cAMP) acts as a second messenger, opening CNG channels and causing extracellular Ca^{2+} influx and intracellular Ca^{2+} concentration to increase. This process opens Ca^{2+}/Cl^{-} gated channels and causes Cl^{-} efflux, causing the potential difference between the inside and outside of the olfactory receptor neuron membrane, producing membrane depolarization and the formation of nerve impulses (Sands and Palmer, 2008; Restrepo *et al.*, 2015). Many odorants have been shown to cause an increase in cAMP in olfactory neurons (Breer, 1993). Compounds that activate olfactory CNG channels will enhance the sense of smell and can be used to prepare foods that are more palatable to individuals with reduced olfactory function.

Conversely, compounds that inhibit olfactory CNG channels will inhibit smell and can be used to block modulators (Zoller *et al.*, 2002). CNG is indispensable in the process of olfactory signal transduction, so CNG may play an important role in the process of silkworm feeling the attraction of mulberry leaves. It is speculated that CNG may affect the silkworm olfactory information processing, thereby affecting the silkworm's feeding. It is known that mutations of phosphorylation sites in CNG can interfere with short-term adaptation and change odor sensitivity (O'Halloran *et al.*, 2017). We used NetPhos 3.1 Server to predict phosphorylation sites in silkworm CNGA and found that the presence of phosphorylation sites had a positive selection, which may be one of the reasons why silkworms changed their sensitivity to odor recognition and were attracted by the unique odor of mulberry leaves and thus eat mulberry leaves. Aldose 1-epimerase-like is a crucial enzyme of galactose metabolism (map00052). It is found in plants that may be involved in plant growth and control of defense responses against pathogen invasion and carbohydrate metabolism (Sheshukova *et al.*, 2017). However, this enzyme has not been studied in insects, and there are many positively selected amino acid sites, so it is not yet possible to judge whether it has an effect on the feeding habit of the silkworm. All the above inferences need further experimental verification.

Conclusions

This study compared the gene families of *Sfr*, *Har*, *Aya*, *Dpl*, *Pxy*, and *Pra* that did not eat mulberry leaves and *Bmj*, *Bmo*, *Bma* that ate mulberry leaves through resequencing and comparative genomics and found that *UGT46A1*, *UGT33R1,* and *UGT33R2* are genes unique to the silkworm, and may be involved in the process of silkworm odor recognition. *CNGA* is a positive selection gene, which may be involved in the process of silkworm olfactory transmission. *UGT46A1*, *UGT33R1, UGT33R2* and *CNGA* may be an important factor affecting silkworm feeding. These findings provide important materials and directions for in-depth analysis of the 'silkworm's feeding habits.

Availability of data and materials

All genome data is accessible on-line on the NCBI database through accession number PRJNA721561 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA721561/).

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Table S1 Statistics of silkworm genome sequencing data

Pair-end libraries	Insert size	Total data(G)	Read length(bp)	Sequence coverage(×)
Illumina reads	350bp	64.81	150	139.41
Pacbio reads	-	50.08	-	107.72
Hi-C	-	83.78	150	180.21
Total	-	198.67	-	427.34

Table S2 Silkworm genome assembly results

Sample ID	length		number	
	Contig**(bp)	Scaffold(bp)	Contig**	Scaffold
Total	455,441,876	455,458,976	241	70
Max	12,311,683	21,717,036	-	-
Number>=2000	-	-	241	70
N50	3,751,416	17,263,684	42	12
N60	2,941,879	16,129,543	57	15
N70	2,487,228	15,544,768	73	18
N80	1,833,732	14,680,109	95	21
N90	1,088,538	12,534,500	126	24

** Contig after scaffolding

Table S3 Statistics of base content in silkworm genome

	Number (bp)	% of genome
A	140500920	30.85
T	104438610	30.83
C	87251660	19.16
G	87250686	19.16
N	17100	0.000037%
Total (bp)	455458976	-
GC	174502346	38.31

* GC content of the genome without N

Table S4 Statistics of silkworm genome reads coverage

		Percentage
Reads	Mapping rate(%)	98.92
Genome	Average sequencing depth	123
	Coverage(%)	99.83
	Coverage at least 4X(%)	99.73
	Coverage at least 10X(%)	99.62
	Coverage at least 20X(%)	99.41

Note:
（1）mapping rate: the ratio of reads compared to the genome;
（2）Average sequence depth: the average depth of each base on the genome covered by reads;
（3）Coverage: the percentage of genome covered by reads;
（4）Coverage at least NX(%): the percentage of genome covered by NX reads.

Table S5 SNP statistics of silkworm genome

	Number	Percentage(%)
All SNP	239135	0.0529
Heterozygosis SNP	238736	0.0528
Homology SNP	399	0.0001

Table S6 CEGMA assessment results of silkworm genome

species	complete		Complete+partial	
	#Prots	%completeness	#Prots	%completeness
Bymbox mori	214	86.29	223	89.92

Note: （1）Complete: core gene >70% assembled;
（2）Complete + partial: partially assembled core gene;
（3）#Prots: the number of assembled core genes;
（4）% completeness: the percentage of assembled core genes in the core gene library.

Table S7 BUSCO assessment results of silkworm genome

Species	BUSCO notation assessment results
Bymbox mori	C:98.0%[S:97.2%,D:0.8%],F:0.5%,M:1.5%,n:1658

Note: C: Complete Single-Copy BUSCOs ; D: Complete Duplicated BUSCOs ; F: Fragmented BUSCOs ; M: Missing BUSCOs ; n: Total.

Table S8 Statistical results of repeated sequences

Type	Repeat Size(bp)	% of genome
Trf	7,535,223	1.65
Repeatmasker	252,412,824	55.42
Proteinmask	57,221,315	12.56
Total	259,068,541	56.88

Table S9 Statistical results of gene function annotation

	Number	Percent(%)
Total	11,509	-
Swissprot	8,809	76.50
Nr	11,204	97.30
KEGG	8,474	73.60
InterPro	11,399	99.00
GO	10,541	91.60
Pfam	8,523	74.10
Annotated	11,482	99.80
Unannotated	27	0.20

Table S10 GO enrichment analysis of common genes in *Bombyx*-specific species

GO_Term	GO_Class	P value	Genes
extracellular region	CC	0.00000956	*low molecular mass 30 kDa lipoprotein 21G1-like [Bombyx mori],low molecular mass 30 kDa lipoprotein 19G1-like [Bombyx mori], low molecular mass 30 kDa lipoprotein 19G1-like [Bombyx mori], alcohol dehydrogenase precursor [Bombyx mori], uncharacterized protein LOC101745266 [Bombyx mori],uncharacterized protein LOC101740086 [Bombyx mori],uncharacterized protein LOC101739948 [Bombyx mori],serine protease inhibitor 21 isoform X3 [Bombyx mori],phospholipase A2-like [Bombyx mori],microvitellogenin-like [Bombyx mori],cuticular protein RR-2 motif 58 precursor [Bombyx mori],seroin 1 precursor [Bombyx mori],uncharacterized protein LOC101742341 [Bombyx mori],RNA exonuclease 4-like [Bombyx mori],uncharacterized protein LOC101746057 [Bombyx mori],uncharacterized protein LOC101736844 [Bombyx mori],actin cytoskeleton-regulatory complex protein PAN1 [Bombyx mori],microvitellogenin-like [Bombyx mori],low molecular 30 kDa lipoprotein PBMHP-12-like [Bombyx mori],glow molecular mass 30 kDa lipoprotein 19G1-like precursor [Bombyx mori],low molecular 30 kDa lipoprotein PBMHPC-19-like precursor [Bombyx mori],plasma kallikrein-like [Bombyx mori],uncharacterized protein LOC101743393 [Bombyx mori],uncharacterized protein LOC105843019 [Bombyx mori],uncharacterized protein LOC101742472 [Bombyx mori],spherulin-2A-like [Bombyx mori],Low calcium response V antigen [Bombyx mori]*
transferase activity, transferring glycosyl groups	MF	0.002081246	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori],UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori],UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori],UDP-glucosyltransferase precursor [Bombyx mori],UDP-glycosyltransferase UGT46A1 [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori],cuticular protein glycine-rich 26 precursor [Bombyx mori],beta-1,4-galactosyltransferase 7-like [Bombyx mori]*
transferase activity, transferring hexosyl groups	MF	0.005827085	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori],UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori],UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori],UDP-glucosyltransferase precursor [Bombyx mori],UDP-glycosyltransferase UGT46A1 [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori]*
cell outer membrane	CC	0.010454439	*uncharacterized protein LOC101742377 [Bombyx mori],sericin 2 isoform 1 precursor [Bombyx mori],uncharacterized protein LOC101737731 [Bombyx mori],glow molecular mass 30 kDa lipoprotein 19G1-like precursor [Bombyx mori]*
lipase activity	MF	0.017171493	*lipase member H-A-like [Bombyx mori],phospholipase A2-like [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori],pancreatic triacylglycerol lipase-like [Bombyx mori]*
carboxylic ester hydrolase activity	MF	0.019188704	*lipase member H-A-like [Bombyx mori],phospholipase A2-like [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori],pancreatic triacylglycerol lipase-like [Bombyx mori]*
homoiothermy	BP	0.019327415	*antifreeze protein[Bombyx mori],angiomotin-like [Bombyx mori],vitelline membrane protein Vm26Ab-like [Bombyx mori],ice-structuring glycoprotein-like [Bombyx mori],calpain-B [Bombyx mori]*
ice binding	MF	0.019327415	*antifreeze protein[Bombyx mori],angiomotin-like [Bombyx mori],vitelline membrane protein Vm26Ab-like [Bombyx mori],ice-structuring glycoprotein-like [Bombyx mori],calpain-B [Bombyx mori]*
response to freezing	BP	0.019327415	*antifreeze protein[Bombyx mori],angiomotin-like [Bombyx mori],vitelline membrane protein Vm26Ab-like [Bombyx mori],ice-structuring glycoprotein-like [Bombyx mori],calpain-B [Bombyx mori]*
phospholipase A2 activity	MF	0.019410108	*phospholipase A2-like [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori]*
phospholipase activity	MF	0.023901444	*lipase member H-A-like [Bombyx mori],phospholipase A2-like [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori]*
tachykinin receptor signaling pathway	BP	0.025561348	*uncharacterized protein LOC101737931 [Bombyx mori],cuticle protein 6.4 [Bombyx mori]*
organonitrogen compound biosynthetic process	BP	0.02817645	*15-hydroxyprostaglandin dehydrogenase [NAD(+)]-like [Bombyx mori],collagenase-like [Bombyx mori],uncharacterized protein LOC105842596 [Bombyx mori],uncharacterized protein LOC105841445 [Bombyx mori],TPA: putative cuticle protein [Bombyx mori],uncharacterized protein LOC101747020 [Bombyx mori],putative cuticle protein CPH45 precursor [Bombyx mori], uncharacterized protein LOC101744973 [Bombyx mori]*
acid phosphatase activity	MF	0.028894576	*prostatic acid phosphatase-like [Bombyx mori],multiple inositol polyphosphate phosphatase 1-like [Bombyx mori]*

interleukin-6 receptor binding	MF	0.033333743	*alcohol dehydrogenase precursor [Bombyx mori]*
lactose synthase activity	MF	0.033333743	*phospholipase A2-like isoform X1 [Bombyx mori]*
lactose biosynthetic process	BP	0.033333743	*phospholipase A2-like isoform X1 [Bombyx mori]*
ferrous iron binding	MF	0.033333743	*extradiol ring-cleavage dioxygenase-like [Bombyx mori]*
lipid metabolic process	BP	0.041910497	*lipase 1-like [Bombyx mori],lipase 1-like [Bombyx mori],lipase member H-A-like [Bombyx mori],lipase member H-A-like [Bombyx mori],lipase member H-A-like [Bombyx mori],phospholipase A2-like [Bombyx mori],short-chain dehydrogenease/reductase-like protein [Danaus plexippus],phospholipase A2-like isoform X1 [Bombyx mori],pancreatic triacylglycerol lipase-like [Bombyx mori]*
structural constituent of cuticle	MF	0.054802939	*cuticular protein RR-2 motif 60 precursor [Bombyx mori],cuticular protein RR-2 motif 58 precursor [Bombyx mori],cuticular protein RR-1 motif 9 precursor [Bombyx mori],cuticular protein RR-2 motif 124 precursor [Bombyx mori]*
lipid catabolic process	BP	0.056445567	*phospholipase A2-like [Bombyx mori],phospholipase A2-like isoform X1 [Bombyx mori]*
pathogenesis	BP	0.06174495	*uncharacterized protein LOC101740086 [Bombyx mori],evm.model.Bomo_Chr11.201,phospholipase A2-like [Bombyx mori],uncharacterized protein LOC101742341 [Bombyx mori],RNA exonuclease 4-like [Bombyx mori],uncharacterized protein LOC101746057 [Bombyx mori],low molecular 30 kDa lipoprotein PBMHPC-19-like precursor [Bombyx mori],uncharacterized protein LOC105843019 [Bombyx mori],uncharacterized protein LOC101742472 [Bombyx mori],Low calcium response V antigen [Bombyx mori]*
cell envelope	CC	0.064680839	*alaserpin-like [Bombyx mori],uncharacterized protein LOC101742377 [Bombyx mori],sericin 2 isoform 1 precursor [Bombyx mori],uncharacterized protein LOC101737731 [Bombyx mori],glow molecular mass 30 kDa lipoprotein 19G1-like precursor [Bombyx mori]*
external encapsulating structure part	CC	0.064680839	*alaserpin-like [Bombyx mori],uncharacterized protein LOC101742377 [Bombyx mori],sericin 2 isoform 1 precursor [Bombyx mori],uncharacterized protein LOC101737731 [Bombyx mori],glow molecular mass 30 kDa lipoprotein 19G1-like precursor [Bombyx mori]*
thrombin receptor activity	MF	0.0649584	*uncharacterized protein LOC105842978 [Bombyx mori],putative uncharacterized protein DDB_G0282133 [Bombyx mori],uncharacterized protein LOC101743399 [Bombyx mori]*
thrombin receptor signaling pathway	BP	0.0649584	*uncharacterized protein LOC105842978 [Bombyx mori],putative uncharacterized protein DDB_G0282133 [Bombyx mori],uncharacterized protein LOC101743399 [Bombyx mori]*
adenosine kinase activity	MF	0.065561692	*collagenase-like [Bombyx mori]*
purine ribonucleoside salvage	BP	0.065561692	*collagenase-like [Bombyx mori]*
DNA transport	BP	0.065561692	*uncharacterized protein LOC101739948 [Bombyx mori]*
pericentriolar material	CC	0.065561692	*calexcitin-2-like [Bombyx mori]*
cell volume homeostasis	BP	0.065561692	*uncharacterized protein LOC101744296 [Bombyx mori]*

Table S11 KEGG enrichment analysis of common genes in *Bombyx*-specific species

MapTitle	Pvalue	Genes
Insect hormone biosynthesis	0.000000952	*calexcitin-2-like [Bombyx mori],uncharacterized protein LOC101742377 [Bombyx mori], uncharacterized protein LOC101745533 [Bombyx mori], uncharacterized protein LOC101743036 [Bombyx mori] ,farnesol dehydrogenase-like isoform X1 [Bombyx mori] ,uncharacterized protein LOC101738236 [Bombyx mori]*
Retinol metabolism	0.00000396	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori] UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori], 17-beta-hydroxysteroid dehydrogenase 14-like [Bombyx mori] , 17-beta-hydroxysteroid dehydrogenase 14-like [Bombyx mori]*
Metabolism of xenobiotics by cytochrome P450	0.0000601	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori] ,carbonyl reductase [NADPH] 3-like [Bombyx mori]*
Chemical carcinogenesis	0.0000716	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glucosyltransferase precursor [Bombyx mori] ,UDP-glycosyltransferase UGT46A1 [Bombyx mori] ,carbonyl reductase [NADPH] 3-like [Bombyx mori]*
Starch and sucrose metabolism	0.0000849	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], TPA: putative cuticle protein [Bombyx mori],UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Steroid hormone biosynthesis	0.000102613	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Ascorbate and aldarate metabolism	0.000172821	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Porphyrin and chlorophyll metabolism	0.000251556	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Drug metabolism - cytochrome P450	0.000417474	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glucosyltransferase precursor [Bombyx mori] ,UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Pentose and glucuronate interconversions	0.000655238	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Drug metabolism - other enzymes	0.002091395	*UDP-glycosyltransferase UGT33R1 precursor [Bombyx mori], UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori] ,UDP-glycosyltransferase UGT33R2 precursor [Bombyx mori], UDP-glucosyltransferase precursor [Bombyx mori], UDP-glycosyltransferase UGT46A1 [Bombyx mori]*
Fat digestion and absorption	0.002525354	*phospholipase A2-like [Bombyx mori] ,1-acyl-sn-glycerol-3-phosphate acyltransferase alpha-like [Bombyx mori] ,scavenger receptor class B member 1 like protein 15 [Bombyx mori], phospholipase A2-like isoform X1 [Bombyx mori]*
Tropane, piperidine and pyridine alkaloid biosynthesis	0.003151203	*short-chain dehydrogenease/reductase-like protein [Danaus plexippus] ,dehydrogenase/reductase SDR family member 2, mitochondrial-like [Bombyx mori]*

Ether lipid metabolism	0.006849896	*phospholipase A2-like [Bombyx mori] ,rRNA 2'-O-methyltransferase fibrillarin-like [Bombyx mori], phospholipase A2-like isoform X1 [Bombyx mori]*
Arachidonic acid metabolism	0.007969487	*phospholipase A2-like [Bombyx mori] ,phospholipase A2-like isoform X1 [Bombyx mori] ,carbonyl reductase [NADPH] 3-like [Bombyx mori]*
Amoebiasis	0.014034042	*serine protease inhibitor 21 isoform X3 [Bombyx mori], alaserpin-like [Bombyx mori] SCO-spondin [Bombyx mori], retrotransposon gag domain-containing protein 1-like [Ficedula albicollis]*
Linoleic acid metabolism	0.01781794	*phospholipase A2-like [Bombyx mori], phospholipase A2-like isoform X1 [Bombyx mori]*
Transcriptional misregulation in cancer	0.024704244	*15-hydroxyprostaglandin dehydrogenase [NAD(+)]-like [Bombyx mori] ,alcohol dehydrogenase precursor [Bombyx mori] ,15-hydroxyprostaglandin dehydrogenase [NAD(+)]-like [Bombyx mori] ,15-hydroxyprostaglandin dehydrogenase [NAD(+)]-like [Bombyx mori]*
Glycerophospholipid metabolism	0.026306467	*phospholipase A2-like [Bombyx mori], rRNA 2'-O-methyltransferase fibrillarin-like [Bombyx mori], 1-acyl-sn-glycerol-3-phosphate acyltransferase alpha-like [Bombyx mori] ,phospholipase A2-like isoform X1 [Bombyx mori]*
RNA polymerase	0.028505803	*cuticular protein RR-2 motif 60 precursor [Bombyx mori], cuticular protein RR-2 motif 58 precursor [Bombyx mori], cuticular protein RR-2 motif 124 precursor [Bombyx mori]*
Steroid biosynthesis	0.032255476	*lipase 1-like [Bombyx mori], lipase 1-like [Bombyx mori]*
Herpes simplex infection	0.034283226	*cuticular protein RR-2 motif 60 precursor [Bombyx mori] ,cuticular protein RR-2 motif 58 precursor [Bombyx mori] ,caspase-8-like [Bombyx mori] .cuticular protein RR-2 motif 124 precursor [Bombyx mori]*
alpha-Linolenic acid metabolism	0.034595265	*phospholipase A2-like [Bombyx mori] .phospholipase A2-like isoform X1 [Bombyx mori]*
Salivary secretion	0.065217254	*G-protein coupled receptor moody-like [Bombyx mori] ,Osteopontin ,sericin 1-like isoform X8 [Bombyx mori]*
Amino sugar and nucleotide sugar metabolism	0.080679888	*nose resistant to fluoxetine protein 6-like [Bombyx mori], N-acetylneuraminate lyase-like [Bombyx mori],N-acetylneuraminate lyase-like [Bombyx mori]*
Vascular smooth muscle contraction	0.086856672	*phospholipase A2-like [Bombyx mori], G-protein coupled receptor moody-like [Bombyx mori] ,phospholipase A2-like isoform X1 [Bombyx mori]*
Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	0.113961615	*beta-1,4-galactosyltransferase 7-like [Bombyx mori]*
Betalain biosynthesis	0.133264342	*extradiol ring-cleavage dioxygenase-like [Bombyx mori]*
Toxoplasmosis	0.135497312	*caspase-8-like [Bombyx mori] ,cuticular protein glycine-rich 19 precursor [Bombyx mori]*

Table S12 GO enrichment analysis of positive selection genes in silkworm

GO_Term	GO_Class	P value	Genes
signal recognition particle, endoplasmic reticulum targeting	CC	0.004766285	*signal recognition particle 14 kDa protein-like protein[Bombyx mori]*
endoplasmic reticulum signal peptide binding	MF	0.004766285	*signal recognition particle 14 kDa protein-like protein[Bombyx mori]*
ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor	MF	0.004766285	*ribonucleoside-diphosphate reductase large subunit [Bombyx mori]*
peptidyl-diphthamide biosynthetic process from peptidyl-histidine	BP	0.004766285	*diptheria toxin resistance protein[Bombyx mori]*
RNA-DNA hybrid ribonuclease activity	MF	0.009510249	*ribonuclease H2 subunit A[Bombyx mori]*
regulation of anion transport	BP	0.014231995	*26S proteasome non-ATPase regulatory subunit 6[Bombyx mori]*
7S RNA binding	MF	0.023609241	*signal recognition particle 14 kDa protein-like protein[Bombyx mori]*
voltage-gated anion channel activity	MF	0.028206301	*26S proteasome non-ATPase regulatory subunit 6[Bombyx mori],isovaleryl coenzyme A dehydrogenase[Bombyx mori]*
cellular metal ion homeostasis	BP	0.028206301	*uncharacterized LOC101746868[Bombyx mori],flavin-dependent monooxygenase FMO3 precursor[Bombyx mori]*
extrinsic component of intraperoxisomal membrane	CC	0.028264944	*calcium and integrin binding protein CIB[Bombyx mori]*
steroid hormone mediated signaling pathway	BP	0.031114487	*heparin sulfate O-sulfotransferase[Bombyx mori],apterous A splicing isoform type E[Bombyx mori]*
SRP-dependent cotranslational protein targeting to membrane	BP	0.032898834	*signal recognition particle 14 kDa protein-like protein[Bombyx mori]*
sulfate transport	BP	0.032898834	*prestin isoform X2[Bombyx mori]*
sulfate transmembrane transporter activity	MF	0.032898834	*prestin isoform X2[Bombyx mori]*
regulation of MAPK cascade	BP	0.037511014	*uncharacterized LOC101746868[Bombyx mori]*
chitinase activity	MF	0.037511014	*chitinase domain-containing protein 1[Bombyx mori]*
chitin catabolic process	BP	0.037511014	*chitinase domain-containing protein 1[Bombyx mori]*
anion transmembrane transporter activity	MF	0.038144162	*26S proteasome non-ATPase regulatory subunit 6[Bombyx mori],LOW QUALITY PROTEIN: protein CLEC16A[Bombyx mori],isovaleryl coenzyme A dehydrogenase,prestin isoform X2[Bombyx mori]*
chromosome	CC	0.038588406	*chromodomain-helicase-DNA-binding protein 1[Bombyx mori],signal recognition particle 14 kDa protein-like protein[Bombyx mori],peptidyl-prolyl cis-trans isomerase-like 4[Bombyx mori],aldose 1-epimerase-like[Bombyx mori]*

Table S13 KEGG enrichment analysis of positive selection genes in silkworm

MapTitle	Pvalue	Q value	Genes
Glycosaminoglycan biosynthesis - heparan sulfate / heparin	0.065807145	0.34567298	*heparin sulfate O-sulfotransferase[Bombyx mori]*
Protein export	0.086813143	0.34567298	*signal recognition particle 14 kDa protein-like protein[Bombyx mori]*
Spliceosome	0.091743986	0.34567298	*U2 small nuclear ribonucleoprotein auxiliary factor 2 [Bombyx mori]，inner centromere protein A[Bombyx mori]*
Mineral absorption	0.097147109	0.34567298	*zinc transporter 1[Bombyx mori]*
Insect hormone biosynthesis	0.114123927	0.34567298	*cytochrome P450[Bombyx mori]*
Notch signaling pathway	0.124163983	0.34567298	*protein numb isoform X1[Bombyx mori]*
DNA replication	0.137382666	0.34567298	*ribonuclease H2 subunit A [Bombyx mori]*
Phototransduction - fly	0.140657599	0.34567298	*sn1-specific diacylglycerol lipase beta[Bombyx mori]*
Valine, leucine and isoleucine degradation	0.143920718	0.34567298	*isovaleryl coenzyme A dehydrogenase[Bombyx mori]*
Olfactory transduction	0.150411676	0.34567298	*cyclic nucleotide-gated cation channel subunit A-like[Bombyx mori]*
Proteasome	0.163253593	0.34567298	*26S proteasome non-ATPase regulatory subunit 6[Bombyx mori]*
Retrograde endocannabinoid signaling	0.163253593	0.34567298	*esn1-specific diacylglycerol lipase beta[Bombyx mori]*
Glycolysis / Gluconeogenesis	0.166435138	0.34567298	*aldose 1-epimerase-like[Bombyx mori]*
Galactose metabolism	0.197624847	0.381133633	*aldose 1-epimerase-like[Bombyx mori]*
Glutathione metabolism	0.230652047	0.415173684	*ribonucleoside-diphosphate reductase large subunit[Bombyx mori]*
Aldosterone synthesis and secretion	0.270821318	0.452136217	*sn1-specific diacylglycerol lipase beta[Bombyx mori]*
Tight junction	0.284678359	0.452136217	*flavin-dependent monooxygenase FMO3 precursor[Bombyx mori]*
Ubiquitin mediated proteolysis	0.350292258	0.482989658	*F-box/WD repeat-containing protein 7 isoform X1[Bombyx mori]*
Regulation of actin cytoskeleton	0.35528663	0.482989658	*rho guanine nucleotide exchange factor 7[Bombyx mori]*
Rap1 signaling pathway	0.357770117	0.482989658	*flavin-dependent monooxygenase FMO3 precursor[Bombyx mori]*
Ribosome	0.393949097	0.497747803	*ribosomal protein S7[Bombyx mori]*
Pyrimidine metabolism	0.405572284	0.497747803	*ribonucleoside-diphosphate reductase large subunit[Bombyx mori]*

Table S14 Positive selection sites of genes related to feeding habit of *Bombyx mori Jiangsu*

Gene ID	Type	P value	Positive selection site
U2 small nuclear ribonucleoprotein auxiliary factor 2[Bombyx mori]	positive	0.000110954	2 G 0.991**;3 E 0.972*;5 K 0.614;382 C 0.775;404 F 0.933;406 E 0.980*;
PDZ domain-containing protein 8 isoform X1[Bombyx mori]	positive	4.37E-11	17 L 0.576;20 A 0.785;34 V 0.779;39 I 0.779;46 K 0.658;52 D 0.586;61 P 0.784;212 T 0.753;215 R 0.696;266 I 0.793;272 V 0.763;295 R 0.802;346 A 0.903;348 G 0.692;355 H 0.508;515 M 0.706;568 S 0.568;642 I 0.776;666 K 0.654;672 E 0.963*;696 W 0.850;732 P 0.666;805 E 0.556;819 R 0.786;839 V 0.999**;840 R 0.884;842 H 0.970*;866 N 0.859;886 I 0.652;923 E 0.790;929 D 0.793;960 C 0.688;971 I 0.811;972 H 0.969*;975 R 0.826;986 F 0.961*;987 A 0.920;988 A 0.998**;989 C 0.999**;990 A 0.998**;991 S 0.995**;992 T 0.813;993 W 0.998**;994 L 1.000**;995 A 0.986*;996 G 0.933;997 G 0.999**;998 G 0.996**;1002 L 0.566;1010 A 0.999**;1012 P 1.000**;1013 P 0.832;1014 D 0.740;1015 A 0.999**;1016 L 0.981*;1017 F 1.000**;1019 A 0.998**;1020 A 0.998**;1021 R 1.000**;1022 D 0.998**;1023 S 1.000**;1024 A 0.796;1026 Q 0.974*;1037 H 0.971*;1038 E 0.998**;1039 M 0.929;1040 L 0.993**;1041 L 0.991**;1042 A 0.803;1044 R 0.974*;1045 E 0.997**;1048 S 0.854;1054 C 0.794;1055 A 0.841;1073 F 0.506;1082 C 0.999**;1089 V 0.835;1090 Q 0.783;1091 Q 0.835;1092 R 0.999**;1093 A 0.995**;
flavin-dependent monooxygenase FMO3 precursor[Bombyx mori]	positive	0.000567658	5 R 0.995**;6 V 0.993**;7 C 0.830;8 V 0.993**;9 I 0.721;11 A 0.796;12 G 0.999**;13 A 0.755;14 A 0.827;15 G 0.999**;16 L 0.991**;17 C 0.746;18 A 0.997**;19 A 0.999**;20 R 0.798;21 H 0.611;22 L 0.708;23 L 0.992**;24 V 0.774;25 E 0.605;26 P 0.995**;28 V 0.749;29 S 0.945;30 Q 0.944;31 V 0.995**;32 D 0.529;33 I 0.992**;34 L 0.991**;35 E 0.999**;36 Q 0.995**;37 A 0.997**;38 D 0.718;39 Q 0.693;40 L 0.952*;41 G 0.999**;42 G 0.790;43 T 0.804;44 W 0.867;45 V 0.859;51 G 0.996**;52 Y 0.822;53 D 0.999**;54 D 0.983*;55 F 0.991**;56 G 0.991**;57 L 0.951*;59 I 0.994**;60 H 0.886;61 S 0.997**;62 S 0.840;65 K 0.993**;66 S 0.821;68 L 0.942;99 A 0.736;109 G 0.991**;112 K 0.562;115 K 0.592;121 Q 0.993**;137 T 0.884;212 I 0.578;244 V 0.818;251 A 0.740;256 G 0.992**;260 E 0.699;282 D 0.576;284 V 0.990*;328 V 0.691;331 M 0.693;356 A 0.819;372 E 0.738;373 K 0.990*;376 A 0.997**;379 A 0.833;382 A 0.780;385 R 0.767;389 S 0.845;391 L 0.611;393 K 0.988*;395 R 0.953*;396 E 0.986*;397 E 0.658;399 T 0.512;400 I 0.999**;401 R 0.727;404 N 0.608;407 K 0.903;408 D 0.844;411 Q 0.992**;415 K 0.716;416 I 0.812;420 N 0.607;421 T 0.999**;422 Y 0.805;423 A 0.894;424 I 0.993**;427 I 0.998**;428 S 0.997**;429 N 1.000**;430 G 1.000**;431 R 0.998**;432 Q 0.951*;
calcium and integrin binding protein CIB[Bombyx mori]	positive	0.000173765	89 Q 0.975*;94 R 0.668;166 P 0.787;171 T 0.764;211 Q 0.943;212 Y 0.999**;213 V 0.954*;214 - 0.959*;216 - 1.000**;
serine/threonine-protein kinase mig-15 isoform X2[Bombyx mori]	positive	1.29E-11	332 G 0.965*;556 P 0.882;570 G 0.960*;593 - 0.661;822 K 1.000**;929 L 0.885;1299 - 0.975*;1338 - 0.999**;1387 - 0.995**;1392 - 0.862;1410 - 0.989*;1411 - 0.966*;1413 - 0.997**;1419 - 0.999**;1420 - 0.999**;1423 - 0.965*;1425 - 0.999**;
gene12186	positive	1.11E-16	196 A 0.989*;199 D 0.988*;200 N 0.920;201 S 0.889;203 K 0.799;204 P 0.685;206 K 0.999**;207 K 0.974*;407 T 0.888;690 M 0.761;693 S 0.677;737 N 0.691;804 I 1.000**;805 S 0.752;806 L 0.994**;807 F 0.986*;
chromodomain-helicase-DNA-binding protein 1[Bombyx mori]	positive	0.001355458	83 S 0.641;99 S 0.652;441 Q 0.839;851 I 0.528;1043 M 0.637;1359 Q 0.806;1392 N 0.527;1429 K 0.515;1432 K 0.634;1595 K 0.706;1628 A 0.769;1670 E 0.683;1683 - 0.652;1858 P 0.867;
ataxin-10 isoform X1[Bombyx mori]	positive	1.75E-06	56 T 0.619;82 R 0.801;89 S 0.711;90 Y 0.713;95 L 0.623;140 S 0.793;184 T 0.745;214 V 0.702;299 S 0.828;377 A 0.608;394 N 0.599;396 P 0.660;435 N 0.665;439 V 0.669;456 K 0.535;457 F 0.690;461 I 0.887;466 N 0.551;469 G 0.628;477 P 0.819;478 I 0.947;485 L 0.594;488 V 0.556;504 R 0.645;537 N 0.519;559 L 0.619;564 R 0.698;586 L 0.755;587 K 0.538;609 T 0.580;622 V 0.515;663 A 0.526;675 N 0.641;677 L 0.775;678 P 1.000**;679 S 0.999**;680 V 1.000**;681 K 0.960*;682 I 0.997**;684 S 1.000**;685 P 0.817;687 S 0.976*;688 Q 0.997**;695 I 0.800;703 A 0.779;721 A 0.980*;727 A 0.867;730 C 0.879;731 W 0.876;732 K 0.996**;733 N

			0.998**;734 Q 0.839;736 N 0.967*;737 K 0.999**;738 K 0.999**;739 Q 1.000**;742 E 0.696;744 E 0.627;772 N 0.936;785 S 0.867;787 M 0.950;792 P 0.804;793 V 0.998**;794 D 0.783;795 N 0.995**;796 E 0.611;799 Q 1.000**;801 M 0.958*;802 G 0.845;804 T 0.998**;805 L 1.000**;806 H 1.000**;807 T 0.998**;808 D 0.651;809 P 0.999**;810 Q 0.699;811 G 1.000**;812 N 0.997**;813 T 0.999**;814 I 1.000**;815 K 0.998**;816 M 0.926;817 V 0.993**;820 S 0.784;822 G 1.000**;
26S proteasome non-ATPase regulatory subunit 6[Bombyx mori]	positive	1.51E-06	39 Q 0.958*;60 P 0.660;220 E 0.918;221 R 0.998**;222 H 0.993**;223 A 0.994**;224 L 0.823;225 Q 0.798;228 L 0.999**;229 R 0.695;230 R 0.999**;231 Q 0.611;232 G 1.000**;233 A 0.998**;234 A 0.760;235 V 0.753;236 Q 1.000**;237 A 0.749;238 L 0.814;239 R 0.997**;240 S 0.773;242 F 0.998**;243 P 0.977*;244 E 0.994**;245 L 0.838;246 R 1.000**;248 L 0.999**;251 S 1.000**;253 H 0.991**;254 E 0.738;255 C 1.000**;262 K 0.640;263 S 0.998**;264 L 0.680;265 A 0.999**;278 R 0.917;307 N 0.542;309 A 0.996**;310 D 0.923;311 T 0.999**;312 F 0.933;313 G 0.931;315 T 0.999**;319 V 0.745;
transmembrane protein 136-like[Bombyx mori]	positive	2.40E-09	23 F 0.832;28 Y 1.000**;30 W 0.698;32 V 0.579;33 E 0.847;34 E 0.510;35 A 1.000**;74 T 0.880;106 N 0.507;111 C 0.678;149 T 0.685;156 G 0.569;159 E 0.939;165 F 0.870;188 Y 0.824;232 S 0.551;233 R 0.732;236 D 0.979*;239 N 0.876;240 L 0.988*;241 C 0.974*;242 N 0.765;243 V 0.609;264 I 0.951*;
solute carrier family 35 member C2[Bombyx mori]	positive	0.005766172	5 K 0.959*;7 E 0.975*;9 L 0.973*;10 S 0.995**;22 N 0.609;29 V 0.585;40 L 0.975*;41 S 0.971*;42 L 0.838;43 I 0.758;44 A 0.977*;45 L 0.844;46 Y 0.998**;49 L 0.995**;50 S 0.912;51 I 0.764;52 G 0.967*;61 L 0.999**;62 R 0.711;66 F 0.676;94 G 0.991**;102 F 0.639;105 C 0.834;106 L 0.608;115 V 0.721;186 V 0.535;189 N 0.684;233 S 0.753;235 L 0.648;266 S 0.750;341 R 0.828;355 D 0.733;
diptheria toxin resistance protein[Bombyx mori]	positive	1.11E-06	2 - 1.000**;4 - 1.000**;5 - 0.865;6 - 0.999**;7 - 0.783;8 - 0.991**;9 - 1.000**;11 - 0.928;12 - 0.999**;14 - 1.000**;15 - 0.999**;16 - 1.000**;23 - 1.000**;24 - 0.888;26 - 0.883;27 - 0.978*;28 - 0.718;30 - 0.988*;31 - 1.000**;33 - 0.961*;34 - 0.990*;35 - 0.912;36 - 0.866;37 - 0.999**;38 - 0.998**;39 - 0.995**;40 - 0.875;44 - 0.900;45 - 0.815;46 - 0.822;48 - 0.547;49 - 0.999**;50 - 0.999**;51 - 0.992**;52 - 0.999**;55 - 0.998**;56 - 0.956*;57 - 0.951*;58 - 0.846;59 - 1.000**;60 - 0.999**;61 - 0.999**;62 - 0.959*;63 - 0.975*;65 - 0.999**;66 - 0.997**;67 - 0.948;68 - 0.932;69 - 0.984*;70 - 0.994**;71 - 0.888;72 - 0.746;73 - 0.993**;74 - 0.712;75 - 0.999**;76 - 0.783;77 - 0.993**;78 - 0.998**;79 - 0.998**;80 - 0.628;81 - 0.992**;82 - 0.994**;84 - 0.995**;85 - 0.836;86 - 0.855;87 - 0.999**;91 - 0.998**;92 - 1.000**;94 - 0.994**;95 - 0.786;96 - 1.000**;97 - 0.783;98 - 0.986*;99 - 1.000**;100 - 1.000**;101 - 0.999**;116 - 0.629;125 G 0.848;127 A 0.880;128 V 0.807;158 M 0.575;163 E 0.942;185 K 0.528;190 K 0.824;204 A 0.551;226 H 0.618;228 F 0.582;231 D 0.653;255 I 0.777;256 A 0.734;258 S 0.818;269 K 0.509;272 R 0.945;294 V 0.547;295 V 0.625;299 V 0.564;305 D 0.839;316 Q 0.625;335 V 0.987*;369 Y 0.807;375 V 0.656;384 Y 0.676;385 F 0.998**;403 C 0.506;407 H 0.871;412 T 0.746;420 K 0.855;424 T 0.813;427 D 0.504;434 K 0.696;439 K 0.574;446 S 0.991**;450 N 0.807;470 R 0.794;479 P 0.780;486 P 0.855;
sentrin-specific protease-like [Bombyx mori]	positive	4.62E-09	2 K 0.763;3 S 0.987*;4 V 0.803;5 V 0.974*;6 A 0.691;76 N 1.000**;78 R 1.000**;83 I 0.998**;118 L 0.712;120 S 0.574;149 V 0.941;153 E 0.934;164 W 0.699;233 D 0.523;253 S 0.913;435 R 0.547;461 Q 0.535;486 I 0.988*;510 T 0.552;578 R 0.612;645 S 0.910;714 A 0.638;
signal recognition particle 14 kDa protein-like protein [Bombyx mori]	positive	0.002525675	5 A 0.602;14 T 0.667;16 L 0.998**;17 F 0.898;18 Q 0.962*;19 K 0.997**;20 A 0.997**;21 R 0.966*;22 P 0.778;23 T 0.998**;24 G 0.927;25 S 0.998**;26 V 0.747;27 T 0.965*;28 M 0.993**;29 T 0.713;30 M 0.910;31 K 0.991**;36 R 0.999**;37 T 1.000**;40 Q 0.997**;57 I 0.627;79 S 0.951*;
leucine-rich repeat-containing protein AAC1 isoform X1 [Bombyx mori]	positive	0	3 Y 1.000**;5 F 0.610;6 N 0.991**;7 - 1.000**;8 Y 0.992**;11 G 0.897;12 P 0.853;14 N 0.626;16 F 0.997**;17 T 0.992**;30 T 0.783;32 I 0.981*;33 P 0.992**;34 P 0.649;35 P 0.998**;36 - 0.985*;37 - 0.967*;75 - 0.913;96 - 0.753;97 - 0.984*;98 P 0.994**;99 P 0.994**;100 P 0.997**;101 P 0.994**;103 F 0.979*;104 F 0.908;105 I 0.765;106 P 0.997**;107 S 0.989*;108 N 0.963*;109 - 0.993**;111 I 0.851;112 F 0.982*;113 S 0.968*;114 Q 0.997**;115 E 0.701;116 V 0.970*;117 T 0.977*;120 E 0.996**;121 F 1.000**;123 Q 0.991**;124 T 0.998**;125

			F 0.999**;127 R 0.607;128 I 0.973*;129 I 0.808;130 P 0.995**;131 P 0.990**;132 D 0.991**;133 Q 0.971*;140 E 0.586;142 - 0.521;143 I 0.993**;144 S 0.539;145 I 1.000**;146 S 1.000**;147 Q 0.873;148 V 1.000**;149 F 0.985*;150 H 0.797;152 L 0.997**;153 K 0.783;154 S 0.965*;155 I 1.000**;156 V 0.840;157 T 0.949;159 I 0.780;160 K 0.987*;162 L 0.999**;163 K 0.994**;164 D 0.999**;165 K 0.807;166 N 0.996**;167 E 0.914;168 I 0.909;171 Q 0.981*;172 E 0.998**;177 S 0.983*;178 S 0.974*;179 I 0.627;180 S 0.959*;182 E 0.920;183 E 0.682;208 G 0.917;209 T 0.721;306 N 0.707;321 E 0.992**;324 A 0.506;330 N 0.763;333 K 0.953*;405 D 0.699;406 V 0.943;414 I 0.617;423 V 0.829;
uncharacterized protein LOC101737699 isoform X1 [Bombyx mori]	positive	0.000362583	11 D 0.533;30 T 0.580;34 T 0.686;47 H 0.775;108 S 0.715;109 S 0.609;111 S 0.694;114 H 0.652;136 H 0.897;141 N 0.532;145 D 0.982*;146 S 0.994**;154 R 0.803;155 S 0.650;157 T 0.995**;158 S 0.676;161 P 0.811;174 Q 0.519;212 A 0.730;221 V 0.688;249 G 0.732;250 L 0.785;278 S 0.824;287 P 0.655;371 F 0.995**;372 S 0.665;373 G 0.812;374 S 0.596;375 S 0.994**;376 S 0.997**;379 S 0.999**;380 Y 0.994**;385 R 0.991**;386 R 0.916;399 A 0.898;400 Y 0.780;402 T 0.744;403 R 0.991**;404 G 1.000**;405 A 0.746;407 V 0.997**;408 R 0.838;409 I 0.999**;411 G 0.989*;412 A 0.776;413 D 0.998**;417 A 0.806;419 C 0.998**;420 S 0.790;421 R 0.997**;422 E 0.998**;423 A 0.956*;425 S 0.765;426 P 0.755;428 S 0.994**;429 S 0.834;430 S 0.997**;431 C 0.994**;433 D 0.997**;434 A 0.995**;436 T 0.640;437 T 0.999**;439 F 0.891;440 W 0.995**;441 N 0.997**;442 K 0.998**;443 K 0.988*;444 S 0.999**;445 W 0.998**;446 K 0.993**;447 K 0.722;448 I 0.994**;449 S 0.995**;451 F 0.998**;452 S 0.805;454 S 0.849;455 N 0.997**;456 S 0.699;457 I 0.996**;458 N 0.992**;459 K 0.990*;461 G 0.995**;462 L 0.792;463 T 0.930;464 G 0.524;498 - 0.599;499 - 0.623;501 L 0.983*;502 L 0.993**;503 V 0.991**;505 Y 0.995**;506 T 0.703;507 F 0.998**;508 R 0.721;509 R 0.871;510 K 0.993**;511 S 0.988*;512 G 0.984*;513 S 0.779;514 Q 0.994**;515 G 0.976*;516 S 0.803;517 Q 0.990*;519 K 0.992**;520 R 0.973*;521 R 0.974*;523 E 0.573;524 P 0.831;526 K 0.827;527 C 0.996**;528 D 0.986*;529 A 0.629;530 C 0.788;531 L 0.747;532 S 0.765;534 R 0.673;
chitinase domain-containing protein 1 [Bombyx mori]	positive	1.01E-09	2 K 0.874;4 I 0.827;7 I 0.964*;8 L 0.997**;9 Q 1.000**;10 V 1.000**;12 F 0.827;13 L 0.999**;18 V 1.000**;19 C 0.999**;44 N 0.817;48 D 0.674;49 R 1.000**;50 K 0.699;51 L 1.000**;52 V 0.891;53 D 0.819;54 E 0.732;55 A 0.998**;56 P 0.874;57 L 1.000**;58 A 0.899;59 K 0.999**;61 I 0.975*;62 I 0.831;63 K 1.000**;64 Y 0.999**;65 H 0.986*;66 A 1.000**;67 T 1.000**;68 Y 1.000**;69 H 0.999**;70 Q 0.999**;71 D 0.999**;72 V 1.000**;73 T 0.986*;74 T 1.000**;75 R 0.999**;76 N 0.757;77 F 0.901;79 N 1.000**;81 V 1.000**;82 L 1.000**;95 V 0.541;98 T 0.583;124 S 0.739;138 K 0.516;142 S 0.593;146 L 0.646;153 L 0.847;159 A 0.825;221 N 0.992**;224 D 0.514;234 F 0.678;243 F 0.689;280 R 0.695;296 R 0.751;312 A 0.772;326 L 0.997**;351 T 0.723;352 S 0.784;374 K 0.566;385 L 0.645;
putative WD repeat domain phosphoinositide-interacting protein [Danaus plexippus]	positive	0.000110226	65 S 0.964*;205 M 0.981*;251 A 0.978*;269 R 0.809;313 G 0.854;502 G 0.971*;504 L 0.746;512 L 0.515;524 P 0.608;664 R 0.979*;
inner centromere protein A [Bombyx mori]	positive	7.15E-13	2 - 1.000**;3 - 1.000**;4 - 1.000**;5 - 1.000**;6 - 0.894;7 - 1.000**;9 - 0.971*;10 - 1.000**;11 - 1.000**;12 - 0.985*;13 - 0.967*;14 - 1.000**;15 - 0.935;16 - 0.999**;17 - 0.997**;18 - 1.000**;19 - 0.987*;20 - 0.959*;21 - 0.749;22 - 0.875;23 - 0.954*;25 M 1.000**;26 S 1.000**;27 H 0.999**;28 L 1.000**;29 Y 1.000**;31 P 1.000**;32 W 1.000**;33 G 1.000**;34 T 0.995**;35 G 0.992**;36 E 0.947;37 K 0.868;38 Y 1.000**;39 S 0.903;40 N 1.000**;46 Q 0.898;47 T 0.995**;48 R 1.000**;49 N 0.863;50 Q 0.993**;51 F 0.970*;52 A 1.000**;53 S 0.997**;54 N 1.000**;55 L 1.000**;58 H 0.940;60 H 1.000**;61 A 0.999**;62 S 1.000**;63 Y 1.000**;65 Y 0.957*;71 E 1.000**;73 G 0.956*;74 Q 0.999**;86 R 0.997**;87 L 0.912;88 R 0.989*;89 S 1.000**;90 P 1.000**;91 S 0.890;92 L 0.960*;93 P 0.964*;94 P 1.000**;95 I 0.878;96 R 0.927;97 N 0.998**;98 V 0.993**;100 E 0.975*;101 T 0.982*;102 E 0.939;104 P 0.701;105 K 0.998**;107 E 0.998**;109 R 1.000**;134 A 0.983*;135 P 0.937;136 V 1.000**;137 L 1.000**;138 N 0.863;139 R 1.000**;140 N 1.000**;141 I 1.000**;143 S

			1.000**;144 A 1.000**;145 K 0.958*;166 V 0.711;193 E 0.845;194 N 0.604;203 S 0.909;204 N 0.533;209 M 0.826;212 G 0.998**;276 T 0.876;281 V 0.860;321 I 0.871;327 N 0.550;337 S 0.878;349 R 0.907;369 Q 0.954*;374 E 0.685;377 L 0.839;399 T 0.819;405 E 0.592;423 K 0.697;425 S 0.694;435 V 0.541;442 K 0.533;465 I 0.930;466 K 0.542;476 A 0.900;479 K 0.833;492 T 0.867;506 L 0.887;512 S 0.664;513 V 0.894;520 A 0.935;521 D 0.614;532 G 0.934;538 E 0.648;539 I 0.806;541 - 0.600;555 Q 0.758;559 N 0.988*;563 S 0.877;564 V 0.888;565 S 0.887;566 L 0.879;570 N 0.602;574 E 0.569;578 T 0.800;579 N 0.566;589 S 0.531;601 D 0.623;610 T 0.666;611 D 0.764;612 K 0.721;614 I 0.687;616 T 0.957*;628 S 0.794;640 H 0.579;660 E 0.783;690 I 0.691;697 Q 0.922;698 A 0.991**;716 A 0.507;730 N 0.998**;739 S 0.529;744 Q 0.733;763 F 0.937;766 S 0.782;774 N 0.870;776 N 0.877;812 D 0.674;815 S 0.771;816 E 0.570;825 D 0.643;831 K 0.514;838 T 0.822;842 E 0.913;847 K 0.551;862 K 0.692;
uncharacterized protein LOC101739083 isoform X2 [Bombyx mori]	positive	0	1 M 0.533;2 P 0.577;3 A 0.574;5 S 0.568;6 - 0.670;7 I 0.530;8 I 0.522;9 T 0.575;10 Y 0.592;11 - 0.670;12 F 0.571;13 Q 0.585;14 D 0.548;15 T 0.547;16 R 0.535;17 N 0.545;19 F 0.558;21 A 0.547;22 V 0.550;23 K 0.609;24 P 0.568;25 - 0.547;26 S 0.614;27 L 0.534;28 C 0.591;29 T 0.558;30 E 0.519;31 I 0.575;32 A 0.510;33 Q 0.556;34 P 0.584;35 V 0.670;36 G 0.548;37 Q 0.552;38 C 0.591;39 H 0.545;41 I 0.569;42 H 0.544;43 I 0.532;44 S 0.592;45 T 0.551;47 C 0.559;48 Y 0.572;49 Y 0.545;50 G 0.566;51 Y 0.559;52 H 0.517;53 S 0.521;54 T 0.570;56 T 0.600;57 A 0.628;58 E 0.557;59 N 0.568;60 V 0.524;61 Q 0.545;62 N 0.545;63 N 0.568;64 I 0.561;66 C 0.571;67 E 0.554;68 M 0.533;69 P 0.592;70 E 0.508;71 T 0.584;72 P 0.583;73 R 0.542;74 V 0.522;75 V 0.553;76 N 0.521;77 G 0.609;78 S 0.524;79 S 0.570;80 M 0.579;81 L 0.568;82 - 0.670;83 - 0.670;84 Q 0.670;85 A 0.568;86 G 0.559;87 S 0.556;88 R 0.535;90 R 0.535;91 C 0.512;92 A 0.547;94 N 0.511;95 S 0.548;96 D 0.574;97 Y 0.546;98 P 0.577;99 Q 0.585;100 S 0.551;101 K 0.542;102 R 0.572;103 I 0.566;104 R 0.608;105 E 0.508;106 E 1.000**;107 G 0.987*;108 - 1.000**;109 - 1.000**;110 - 0.944;111 - 1.000**;112 - 0.942;113 - 0.959*;114 - 0.670;115 - 1.000**;116 - 0.999**;117 - 0.556;118 - 0.947;119 - 1.000**;120 - 0.980*;121 - 0.939;122 - 0.999**;123 M 1.000**;124 V 1.000**;125 P 0.937;126 S 0.999**;127 T 0.994**;128 T 1.000**;129 H 0.981*;130 Y 1.000**;131 - 0.670;132 - 0.670;133 N 1.000**;134 P 1.000**;135 C 1.000**;136 L 1.000**;137 L 0.994**;138 R 1.000**;139 P 1.000**;140 T 0.985*;141 H 0.990**;142 N 1.000**;143 N 1.000**;144 P 0.991**;145 D 0.995**;146 I 1.000**;147 S 1.000**;148 R 1.000**;149 C 1.000**;150 L 0.999**;151 M 0.999**;152 V 0.999**;153 H 1.000**;154 M 1.000**;155 I 0.999**;
EH domain-containing protein 3 isoform X2 [Bombyx mori]	positive	0	141 P 0.539;323 G 0.795;488 - 0.961*;489 - 0.951*;490 - 0.918;491 - 0.995**;492 - 0.970*;493 L 0.916;494 L 0.963*;496 Y 0.979*;497 K 1.000**;498 M 1.000**;500 S 1.000**;501 N 0.992**;502 - 1.000**;503 L 0.940;504 L 1.000**;505 L 1.000**;506 F 0.999**;507 W 0.970*;508 E 0.992**;510 L 0.999**;511 L 0.995**;512 A 0.913;513 S 0.809;514 V 0.991**;515 - 0.914;516 - 1.000**;517 - 1.000**;518 - 0.991**;519 - 0.960*;520 - 0.999**;521 - 0.981*;522 - 0.999**;523 - 0.997**;524 - 0.912;526 - 1.000**;527 - 0.916;529 - 0.896;530 - 1.000**;531 - 0.988*;532 - 1.000**;533 - 0.924;534 - 1.000**;536 - 0.996**;603 - 1.000**;605 - 1.000**;606 - 1.000**;607 - 0.511;608 - 0.916;609 - 1.000**;610 - 0.953*;611 - 0.584;612 - 1.000**;613 - 0.957*;614 - 0.927;617 - 0.545;618 - 1.000**;619 - 0.999**;620 - 1.000**;
protein lin-28 homolog [Bombyx mori]	positive	0.00076189	25 G 0.987*;26 G 0.994**;27 N 0.515;28 A 0.989*;29 V 0.994**;30 P 0.980*;31 S 0.993**;109 I 0.810;140 S 0.784;143 S 0.995**;144 A 0.782;145 M 0.910;148 Q 0.529;151 H 0.533;158 K 0.927;198 I 0.639;216 S 0.983*;217 S 0.688;223 S 0.529;224 Q 0.996**;225 P 0.774;227 N 0.974*;229 P 0.589;
cyclic nucleotide-gated cation channel subunit A-like [Bombyx mori]	positive	0	36 - 0.945;38 - 0.951*;39 - 0.962*;40 - 0.966*;42 - 0.799;43 - 0.987*;44 - 0.938;45 - 0.955*;46 - 0.642;114 - 0.626;115 - 0.998**;116 - 0.944;117 - 0.988*;118 - 0.761;119 - 0.998**;516 K 0.569;633 A 0.961*;664 - 0.965*;730 R 0.660;749 S 0.979*;750 M 0.897;752 I 0.895;753 T 0.677;754 S 1.000**;755 M 0.987*;764 I 0.991**;765 R 0.967*;766 E 0.967*;767 R 1.000**;770 S 1.000**;771 L 0.997**;772 C 1.000**;773 V 0.966*;774 E 0.970*;775 R 0.999**;776 T 1.000**;777 P

			0.998**;778 S 1.000**;779 L 0.972*;780 L 1.000**;781 H 0.996**;782 I 0.691;783 A 1.000**;784 P 0.998**;785 E 0.961*;786 P 1.000**;787 R 0.977*;788 S 0.997**;789 K 0.997**;790 S 1.000**;791 L 0.970*;792 R 1.000**;793 L 1.000**;794 K 0.997**;795 R 0.978*;796 V 0.660;811 K 0.706;
ribosomal protein S7 [Bombyx mori]	positive	1.90E-13	140 D 1.000**;184 D 1.000**;185 T 0.977*;186 F 0.963*;187 Q 1.000**;188 S 1.000**;194 V 0.980*;195 Y 0.961*;196 K 0.997**;199 T 0.998**;200 G 1.000**;201 R 1.000**;202 E 1.000**;203 V 1.000**;204 T 0.958*;205 F 0.991**;206 E 1.000**;207 F 0.970*;208 P 1.000**;209 E 1.000**;210 P 1.000**;211 Y 0.972*;212 L 1.000**;
uncharacterized LOC101746868 [Bombyx mori]	positive	5.17E-13	1 - 0.582;2 - 0.582;3 - 0.591;4 M 0.583;5 T 0.579;6 S 0.586;7 T 0.577;8 V 0.577;9 I 0.575;10 K 0.575;11 Y 0.578;12 V 0.578;13 G 0.578;14 R 0.576;15 T 0.579;16 T 0.577;17 D 0.578;18 F 0.578;19 K 0.575;20 G 0.578;21 K 0.575;22 S 0.580;23 L 1.000**;24 W 1.000**;25 E 1.000**;26 I 1.000**;27 V 0.995**;28 G 0.994**;31 K 0.989*;33 C 0.999**;35 V 1.000**;37 R 1.000**;38 I 0.577;39 I 0.576;40 V 0.580;41 R 0.576;42 S 0.579;43 V 0.578;44 F 0.579;45 D 0.583;46 R 1.000**;47 Y 1.000**;48 P 1.000**;49 E 0.988*;50 P 1.000**;51 S 1.000**;52 F 1.000**;53 M 1.000**;54 K 1.000**;55 I 0.998**;56 V 0.996**;57 K 0.999**;58 V 1.000**;59 E 1.000**;60 T 1.000**;61 C 1.000**;62 P 1.000**;63 D 1.000**;64 E 0.996**;80 R 0.750;85 I 1.000**;95 P 0.756;103 N 0.644;106 A 0.863;107 K 0.548;112 A 0.506;114 D 0.530;117 T 0.824;135 K 0.842;148 Q 0.998**;149 M 0.995**;150 T 0.998**;151 S 0.579;152 L 0.579;153 S 0.592;154 M 0.575;155 P 0.580;156 L 0.580;157 S 0.576;158 Y 0.578;159 N 0.575;160 H 0.794;161 S 0.576;162 P 0.578;163 N 0.575;164 R 0.576;165 T 0.581;166 K 0.698;167 R 0.817;168 I 0.575;169 A 0.577;170 V 0.577;171 G 0.615;172 D 0.774;173 E 0.576;174 K 0.744;175 P 0.580;176 N 0.577;177 V 0.735;178 Q 0.815;179 F 0.578;180 S 0.581;181 M 0.575;182 G 0.578;183 L 0.579;184 G 0.578;185 K 0.575;186 P 0.578;187 V 1.000**;188 S 1.000**;189 P 1.000**;190 S 0.995**;191 L 0.999**;192 Y 0.578;193 E 0.734;194 G 0.578;195 I 0.580;196 P 0.579;197 L 0.578;198 N 0.582;
solute carrier family 35 member F5 isoform X2 [Bombyx mori]	positive	0.000504278	130 V 0.913;183 H 0.842;355 C 0.973*;410 S 0.948;412 Q 0.969*;424 L 0.559;498 S 0.952*;499 S 0.994**;
ribonuclease H2 subunit A [Bombyx mori]	positive	5.70E-06	97 S 0.905;123 H 0.533;318 P 0.963*;320 N 0.772;332 I 0.974*;333 S 0.974*;336 F 0.723;337 A 0.952*;338 P 0.969*;339 K 0.822;342 N 0.914;343 S 0.915;346 A 0.996**;429 K 0.847;432 K 0.986*;489 R 0.965*;490 H 0.866;492 T 1.000**;493 T 0.992**;575 N 0.999**;589 A 0.709;591 E 0.998**;
nudC domain-containing protein 1 [Bombyx mori]	positive	4.86E-05	18 H 0.608;205 Y 0.987*;332 P 0.693;333 S 0.698;436 M 0.949;534 A 0.999**;535 E 0.999**;536 L 0.982*;537 I 0.579;551 L 0.506;581 - 0.748;586 - 0.979*;
uncharacterized protein LOC101741203 [Bombyx mori]	positive	1.68E-05	1 - 0.758;2 M 1.000**;3 M 1.000**;4 N 0.751;5 S 1.000**;6 F 1.000**;7 R 0.978*;8 N 1.000**;9 T 0.996**;10 V 1.000**;11 K 1.000**;12 N 0.755;13 - 0.758;14 - 0.758;15 - 0.758;16 - 0.758;17 - 0.758;18 - 0.758;19 - 0.758;20 - 0.758;21 - 0.758;22 - 0.758;23 - 0.758;24 - 0.758;25 L 0.756;26 R 0.755;27 L 0.976*;28 L 0.852;29 N 0.752;30 F 0.855;31 T 0.753;32 N 0.754;33 V 0.950;34 V 0.755;35 K 0.921;36 S 0.775;37 V 0.756;38 T 0.753;39 E 0.996**;40 R 0.888;41 K 0.761;42 - 0.757;43 P 0.755;44 I 0.752;45 S 0.757;46 I 0.753;47 I 0.757;48 D 0.756;49 T 0.815;50 P 0.756;51 K 0.751;52 C 0.757;53 K 0.751;54 N 0.753;55 E 0.754;56 I 0.756;57 I 0.790;58 S 0.987*;59 N 0.882;60 V 0.759;61 G 0.754;62 I 0.758;63 L 0.756;64 S 0.758;65 F 0.754;66 A 0.761;67 P 0.755;68 R 0.755;69 S 0.874;70 I 0.782;71 G 0.755;72 V 0.869;73 E 0.753;74 I 0.753;75 S 0.756;76 E 0.753;77 K 0.753;78 P 0.755;79 L 0.757;80 N 0.757;81 S 0.754;82 K 0.758;83 V 0.756;84 K 0.752;85 Q 0.753;86 D 0.754;87 P 0.755;88 I 0.754;89 P 0.755;90 Y 0.754;91 V 0.756;92 P 0.755;93 I 0.752;94 V 0.968*;95 N 0.751;96 P 0.755;97 R 0.755;98 S 0.756;99 I 0.753;100 L 0.755;101 P 0.755;102 L 0.754;103 I 0.790;104 D 0.946;105 S 0.758;106 G 0.756;107 W 0.756;108 R 0.831;109 K 0.752;110 D 0.963*;111 E 0.753;112 I 0.753;113 G 0.755;114 L 0.755;115 P 0.755;116 S 0.756;117 V 0.756;118 R 0.758;119 Q 0.753;120 D 0.753;121 E 0.753;122 I 0.755;123 Q 0.753;124 A 0.754;125 A 0.756;126 R 0.753;127 L 0.756;128 I 0.753;129 V 0.754;130 I 0.753;131 R 0.753;132 K 0.753;133 K 0.751;134 K 0.752;135 M 0.750;136 R 0.752;137 K

			0.751;138 H 0.752;139 Q 0.753;140 R 0.753;141 K 0.753;142 K 0.752;143 L 0.754;144 W 0.756;145 K 0.752;146 K 0.755;147 M 0.750;148 R 0.753;149 Y 0.762;150 R 0.756;151 W 0.756;152 A 0.756;153 R 0.753;154 I 0.754;155 K 0.752;156 Q 0.753;157 R 0.755;158 R 0.755;159 Q 0.755;160 Q 0.753;161 I 0.756;162 K 0.751;163 E 0.753;164 K 0.751;165 I 0.767;166 F 0.754;167 Q 0.753;168 K 0.756;169 E 0.753;170 L 0.754;171 L 0.755;172 A 0.755;173 L 0.755;174 I 0.754;175 K 0.936;176 Q 0.778;177 A 0.754;178 N 0.751;179 E 0.753;180 F 0.755;181 S 0.756;182 A 0.754;183 E 0.753;184 A 0.774;185 Y 0.754;186 V 0.754;187 N 0.783;188 D 0.772;189 K 0.752;190 I 0.753;191 Q 0.756;192 R 0.923;193 A 0.755;194 N 0.752;195 H 0.947;196 T 0.755;197 P 0.755;198 L 0.972*;199 P 0.755;200 T 0.754;201 R 0.756;202 W 0.756;203 R 0.753;204 H 0.754;205 K 0.752;206 R 0.753;207 L 0.756;208 P 0.755;209 E 0.753;210 F 0.755;211 I 0.753;212 I 0.752;213 R 0.755;214 Q 0.753;215 L 0.755;216 L 0.754;217 G 0.755;218 I 0.753;219 D 0.754;220 K 0.752;221 K 0.751;222 I 0.754;223 N 0.751;224 Y 0.755;225 N 0.752;226 H 0.752;227 S 0.754;228 D 0.752;229 T 0.758;230 Y 0.755;231 K 0.751;232 A 0.755;
fragile X mental retardation syndrome-related protein 1-like [Bombyx mori]	positive	1.35E-11	61 V 0.965*;189 Q 0.750;295 K 0.512;346 V 0.657;351 R 0.895;376 A 0.891;426 G 0.994**;427 R 0.968*;428 R 0.952*;429 M 0.793;430 T 0.980*;431 P 0.988*;432 E 0.958*;433 L 0.995**;434 G 0.994**;435 E 0.936;436 E 0.988*;437 R 0.982*;438 G 0.791;439 E 0.906;441 G 0.970*;447 Y 0.594;449 P 0.849;451 G 0.722;453 R 0.968*;458 N 0.620;486 H 0.987*;
cytochrome P450 [Bombyx mori]	positive	2.41E-05	43 S 0.904;44 A 0.731;49 A 0.592;88 P 0.783;100 K 0.989*;153 D 0.998**;156 R 0.953*;158 H 0.996**;159 Q 0.996**;164 D 0.994**;166 N 0.998**;167 N 0.994**;319 N 0.535;388 A 0.524;495 S 0.733;541 S 0.587;551 E 0.746;
LOW QUALITY PROTEIN: protein CLEC16A [Bombyx mori]	positive	5.95E-06	234 A 0.806;353 S 0.617;634 P 0.640;787 R 0.758;822 A 0.574;1007 R 0.605;1115 N 0.993**;1116 D 0.994**;1129 L 0.567;1131 K 0.993**;1132 D 0.851;1165 S 0.734;1168 E 0.934;1169 D 0.975*;1174 N 0.929;1177 R 0.996**;1189 P 0.857;1191 P 0.678;1192 Q 0.962*;1195 P 0.855;1196 - 0.982*;1198 T 0.750;1199 S 0.989*;1200 S 0.734;1204 V 0.576;
uncharacterized protein LOC101735700 [Bombyx mori]	positive	0	46 - 0.999**;47 - 0.997**;48 - 1.000**;49 - 1.000**;50 - 1.000**;51 - 1.000**;52 - 0.999**;53 - 0.995**;54 - 1.000**;55 - 1.000**;56 - 1.000**;57 - 0.963*;58 - 0.873;60 - 0.986*;61 - 1.000**;63 - 0.989*;64 - 0.999**;65 - 1.000**;66 - 1.000**;73 - 0.572;165 - 0.642;233 - 0.646;246 - 0.752;256 - 0.521;394 - 0.731;588 V 0.600;750 S 0.755;1068 R 0.722;1122 R 0.592;1185 A 0.958*;1217 Y 0.698;
RING finger protein 113A [Bombyx mori]	positive	0.006139895	10 S 0.760;52 Q 0.915;53 P 0.915;63 A 0.764;70 V 0.566;72 I 0.636;73 D 0.922;112 R 0.671;138 V 0.510;210 S 0.998**;211 D 0.994**;212 Y 1.000**;214 H 0.679;215 G 0.858;216 W 0.977*;217 Q 0.712;218 L 0.883;219 E 0.670;220 R 0.653;231 A 0.526;241 V 0.616;253 I 0.840;256 N 0.655;257 N 0.752;259 T 1.000**;260 D 0.964*;261 P 0.844;263 V 0.799;264 T 0.996**;265 K 0.711;273 K 0.886;276 L 0.998**;277 D 0.576;278 N 0.975*;280 K 0.944;281 K 0.999**;282 S 0.996**;283 T 0.984*;284 R 0.998**;286 F 0.834;325 D 0.876;
retinoblastoma-binding protein 5 homolog [Bombyx mori]	positive	0	1183 R 0.976*;1331 T 0.998**;1332 T 0.999**;1333 W 1.000**;1334 K 0.968*;1335 K 0.992**;1342 G 1.000**;1343 E 0.977*;1344 Y 1.000**;1345 I 1.000**;1346 C 1.000**;1347 A 1.000**;1348 G 1.000**;1349 S 0.987*;1350 A 0.985*;1361 S 1.000**;1362 I 0.998**;1365 L 0.988*;1366 V 1.000**;1367 K 0.972*;1368 I 1.000**;1369 L 0.992**;1370 H 0.981*;1371 G 0.984*;1372 T 1.000**;1373 K 0.999**;1379 D 1.000**;1381 V 1.000**;1382 W 0.999**;1383 H 0.982*;1384 P 0.991**;1385 I 0.979*;1387 P 0.986*;1388 I 0.990**;1389 I 1.000**;1390 A 1.000**;1391 S 1.000**;1392 I 0.989*;1393 S 1.000**;1394 A 1.000**;1431 F 0.981*;1433 V 1.000**;1435 D 1.000**;1436 E 1.000**;1437 D 1.000**;1438 R 1.000**;1439 S 0.985*;1440 I 0.983*;1441 D 1.000**;1442 Q 1.000**;1443 T 0.994**;1445 E 0.999**;1446 S 0.991**;1447 R 1.000**;1448 N 0.988*;1449 D 0.999**;1450 E 1.000**;1451 E 1.000**;1453 E 0.989*;1460 V 1.000**;1461 D 0.992**;1462 V 1.000**;1463 T 0.985*;1464 S 1.000**;1465 C 1.000**;1466 E 1.000**;1467 P 0.999**;1468 V 1.000**;1469 A 1.000**;1470 A 1.000**;1471 F 1.000**;1473 S 0.986*;1474 S

			1.000**;1476 E 1.000**;1477 E 0.998**;1478 G 1.000**;1480 D 1.000**;1481 E 1.000**;1482 N 1.000**;1483 M 0.989*;1485 L 0.850;1486 F 1.000**;1487 L 0.989*;1488 P 0.986*;1489 I 0.989*;1490 A 1.000**;1491 P 0.985*;1492 E 0.992**;1493 I 1.000**;1494 E 0.998**;1495 D 0.999**;1496 P 0.991**;1498 D 1.000**;1500 W 1.000**;1501 A 1.000**;1502 A 0.986*;1503 T 0.985*;1504 Q 1.000**;1506 T 0.999**;1507 V 0.987*;1508 T 0.999**;1509 P 0.991**;1510 T 1.000**;1511 E 1.000**;1512 T 1.000**;1513 P 1.000**;1514 E 0.988*;1515 K 0.999**;1516 M 1.000**;1517 E 0.998**;1518 P 1.000**;1519 A 0.991**;1520 A 1.000**;1521 K 1.000**;1522 R 0.999**;1523 P 0.985*;1524 K 0.999**;1525 S 0.990**;1526 K 1.000**;1527 T 1.000**;1528 Y 1.000**;1529 D 0.999**;1530 I 0.999**;1531 S 1.000**;1532 L 0.991**;1533 K 1.000**;1534 I 1.000**;1535 A 0.995**;1537 P 0.984*;1538 E 1.000**;1539 Q 0.999**;1540 P 0.991**;1541 L 0.999**;1542 A 0.997**;1543 F 1.000**;1555 K 1.000**;1556 N 0.991**;1557 K 1.000**;1558 Q 1.000**;1559 A 1.000**;1560 A 1.000**;1561 G 1.000**;1562 S 1.000**;1563 K 0.976*;1565 V 0.987*;1566 A 0.986*;1567 G 1.000**;1568 R 1.000**;1569 P 1.000**;1570 R 0.992**;1571 K 0.991**;
IQ domain-containing protein G-like [Bombyx mori]	positive	5.54E-05	66 - 0.572;69 - 0.531;75 - 0.566;76 - 0.517;87 - 0.799;88 - 0.561;89 - 0.732;91 - 0.960*;92 - 0.872;93 - 0.942;95 - 0.929;97 - 0.664;98 - 0.545;101 - 0.920;102 - 0.906;104 - 0.690;105 - 0.924;106 - 0.555;108 - 0.559;110 - 0.877;113 - 0.553;114 - 0.573;118 - 0.535;119 - 0.562;125 - 0.510;126 - 0.946;127 - 0.658;141 - 0.571;145 - 0.518;146 - 0.539;152 - 0.952*;156 - 0.957*;164 - 0.605;168 - 0.705;172 - 0.573;175 - 0.753;179 - 0.933;194 - 0.514;217 V 0.680;222 I 0.669;252 Y 0.794;253 D 0.662;271 E 0.998**;273 I 0.693;274 K 0.993**;275 M 0.864;277 E 1.000**;278 L 0.996**;281 K 1.000**;292 Q 0.665;294 Y 0.987*;300 N 0.764;314 I 0.700;348 A 0.882;377 K 0.873;
leucine-rich repeat protein SHOC-2 [Bombyx mori]	positive	2.48E-05	2 V 0.999**;3 A 0.999**;4 H 0.691;5 K 0.922;6 Y 0.983*;7 A 0.936;9 A 0.935;10 A 0.925;11 A 0.934;12 L 0.988*;14 C 0.999**;15 A 0.999**;16 L 0.925;17 A 0.923;18 G 1.000**;29 A 0.925;30 M 0.978*;31 R 1.000**;32 R 0.994**;33 E 0.897;34 I 0.928;35 S 0.999**;36 P 0.999**;37 C 0.940;38 T 0.999**;40 R 1.000**;41 R 0.999**;43 D 0.893;44 A 0.998**;46 T 0.934;47 G 0.935;48 A 1.000**;49 I 0.998**;50 L 0.949;51 V 0.981*;52 V 1.000**;53 C 0.986*;56 I 0.915;57 N 0.814;58 S 0.920;61 E 0.999**;62 I 0.981*;63 S 0.999**;65 A 0.991**;66 L 0.999**;67 S 0.997**;68 N 0.924;69 K 0.999**;72 P 0.949;90 D 0.899;117 D 0.819;142 M 0.978*;177 V 0.903;189 K 0.838;192 R 0.895;198 A 0.761;211 S 0.881;236 D 0.832;241 I 0.910;246 I 0.731;247 T 0.694;261 K 0.997**;265 Q 0.928;270 E 0.897;284 G 0.900;285 A 0.892;291 K 0.885;306 A 0.892;307 E 0.834;325 Q 0.885;328 S 0.930;349 L 0.817;372 K 0.890;376 I 0.736;379 N 0.807;380 I 0.878;423 L 0.883;425 H 0.879;427 S 0.935;432 I 0.925;486 V 0.548;493 Q 0.878;560 V 0.853;568 V 0.847;569 I 0.878;571 Q 0.739;577 V 0.912;584 G 0.921;586 G 0.887;589 M 0.564;592 R 0.888;595 V 0.568;596 D 0.724;603 P 0.884;614 G 0.998**;615 T 0.737;618 G 0.928;623 E 0.816;628 L 0.886;629 P 0.921;631 V 0.751;632 L 0.865;633 E 0.823;636 V 0.911;640 P 0.910;643 T 0.937;644 N 0.830;651 D 0.826;653 R 0.972*;655 M 0.760;657 E 0.830;658 H 0.629;670 D 0.809;
ovarian serine protease isoform X1 [Bombyx mori]	positive	1.63E-09	74 C 0.778;218 K 0.550;236 D 0.649;310 H 0.783;336 G 0.946;369 P 0.613;456 E 0.957*;532 N 0.943;901 M 0.651;1017 P 0.904;1078 N 0.775;1209 T 0.536;1229 E 0.794;1346 E 0.954*;1497 L 0.730;1498 E 0.863;1516 R 0.636;1592 K 0.749;1598 K 0.852;1604 G 0.822;1674 N 0.780;1723 R 0.794;1867 E 0.971*;1884 Y 0.840;1900 D 0.935;1933 C 0.940;2045 H 0.833;2055 K 0.949;2072 I 0.548;2125 M 0.675;2138 G 0.800;
F-box/WD repeat-containing protein 7 isoform X1 [Bombyx mori]	positive	0.000126936	134 - 0.944;135 - 0.620;342 K 0.906;468 Y 0.792;519 A 0.598;561 S 0.891;878 V 0.875;
ribonucleoside-diphosphate reductase large subunit [Bombyx mori]	positive	0.0005413	2 M 1.000**;3 V 1.000**;4 G 0.920;5 K 0.890;6 T 0.995**;7 N 1.000**;8 K 0.999**;11 V 0.999**;13 K 1.000**;14 R 0.965*;15 D 0.933;55 I 0.926;107 S 0.823;110 Y 0.805;111 N 0.722;113 I 0.651;121 S 0.658;126 D 0.529;132 I 0.636;134 K 0.544;135 N 0.739;153 Y 0.905;229 I 0.605;307 I 0.616;353 N 0.621;355 N 0.739;357 S 0.896;373 E 0.687;377 A 0.874;381 K 0.810;384 Q 0.557;386 E

			0.596;415 Y 0.827;446 P 0.683;464 N 0.612;472 N 0.901;483 Q 0.813;504 M 0.984*;521 V 0.732;530 E 0.996**;571 Q 0.877;582 T 0.553;590 A 0.584;595 K 0.682;607 L 0.841;662 D 0.575;682 K 0.810;735 A 0.849;767 G 0.517;769 V 0.609;778 G 0.821;795 Q 0.901;
zinc transporter 1 [Bombyx mori]	positive	5.12E-05	2 A 0.999**;3 M 0.998**;4 K 0.847;5 E 0.976*;6 W 1.000**;7 L 0.661;8 Q 0.998**;9 W 0.999**;27 S 0.926;29 R 0.925;30 L 0.984*;32 A 1.000**;33 S 0.999**;35 F 0.970*;37 H 1.000**;38 S 1.000**;42 L 0.583;43 V 0.954*;44 D 0.999**;45 T 0.908;47 H 0.999**;48 S 0.999**;49 L 0.999**;50 C 1.000**;51 R 0.925;52 L 0.899;53 V 0.955*;62 Y 0.939;67 A 0.876;71 A 0.717;96 V 0.955*;99 A 0.999**;120 Q 0.935;138 L 0.849;184 T 0.999**;185 S 0.827;190 M 0.692;196 S 0.804;200 P 0.750;203 A 0.822;220 I 0.804;248 A 0.951*;257 L 0.520;282 S 0.830;289 S 0.809;317 L 0.693;325 A 0.578;328 D 0.806;339 A 0.651;344 A 0.811;357 T 0.730;
aldose 1-epimerase-like [Bombyx mori]	positive	1.28E-06	157 - 0.528;159 - 0.803;163 M 0.986*;164 A 0.654;165 D 0.847;166 N 0.659;171 - 0.654;172 - 0.558;173 - 0.782;174 - 0.894;176 - 0.591;178 - 0.840;181 - 0.652;184 - 0.886;188 - 0.639;194 - 0.534;205 - 0.533;210 - 0.527;211 - 0.819;212 - 0.746;420 S 1.000**;427 I 0.583;428 K 0.649;430 E 0.601;431 E 0.994**;432 V 0.965*;434 E 0.844;435 - 0.513;436 - 0.511;438 P 0.827;439 E 0.988*;441 - 0.685;442 P 0.998**;443 K 0.552;453 P 0.851;454 D 0.989*;455 V 0.997**;456 E 0.548;457 L 0.839;461 I 0.924;463 D 0.575;464 G 0.834;465 F 0.834;466 G 1.000**;467 F 0.996**;468 M 0.997**;469 P 0.998**;470 K 0.554;526 - 0.515;530 E 0.896;583 S 0.998**;584 G 0.858;587 K 0.567;588 K 1.000**;591 K 0.523;593 L 0.619;594 N 0.626;595 E 0.994**;619 A 0.810;620 K 0.621;621 S 0.898;622 P 0.861;623 C 1.000**;624 A 1.000**;625 S 0.852;626 S 1.000**;627 T 0.996**;629 I 1.000**;630 D 0.556;631 I 0.999**;632 V 0.997**;633 R 0.992**;634 R 0.974*;635 Y 0.996**;636 T 0.813;644 T 0.995**;646 Q 1.000**;649 T 0.860;736 R 0.801;783 T 0.830;793 N 0.769;807 E 0.940;841 A 0.980*;857 I 0.657;858 P 0.801;868 I 0.696;879 Q 0.632;891 L 0.588;893 V 0.805;900 M 0.823;954 E 0.989*;976 E 0.766;980 V 0.663;989 G 0.566;996 Y 0.878;1029 R 0.884;1030 N 0.626;1031 F 1.000**;1032 P 0.998**;1042 Y 0.801;1043 I 0.960*;1044 H 0.742;1046 I 0.993**;1048 Y 0.769;1052 I 0.994**;
rho guanine nucleotide exchange factor 7 [Plutella xylostella]	positive	3.61E-09	63 A 0.736;403 - 0.940;510 K 0.842;511 Y 0.963*;513 R 0.826;514 N 0.732;517 - 0.519;524 - 0.951*;525 - 0.798;526 - 0.621;760 N 0.984*;765 I 0.915;766 P 0.974*;768 R 0.792;772 L 0.511;773 N 0.879;775 D 0.902;779 R 0.631;780 R 0.803;781 S 0.960*;791 T 0.890;794 K 0.985*;797 G 0.950;799 R 0.849;801 Q 0.847;802 R 0.749;803 M 0.972*;804 S 0.974*;811 R 0.990*;813 Q 0.822;817 E 0.991**;819 C 0.960*;821 R 0.987*;822 S 0.961*;823 L 0.975*;824 C 0.976*;826 S 0.818;828 R 0.630;832 S 0.979*;834 V 0.991**;835 V 0.956*;836 G 0.955*;839 N 0.993**;840 L 0.813;844 D 0.967*;846 Q 0.948;847 E 0.977*;859 N 0.986*;861 S 0.985*;864 Q 0.962*;865 E 0.969*;866 K 0.593;874 S 0.513;877 N 0.876;878 L 0.695;879 S 0.983*;880 H 0.780;885 N 0.554;890 K 0.968*;894 S 0.982*;895 E 0.607;899 E 0.970*;900 T 0.973*;901 F 0.923;902 E 0.985*;907 C 0.879;909 S 0.948;910 P 0.983*;913 S 0.977*;914 T 0.985*;915 A 0.545;916 R 0.956*;917 T 0.964*;919 C 0.971*;920 V 0.518;921 T 0.527;922 S 0.975*;923 V 0.984*;924 T 0.967*;925 S 0.981*;927 N 0.958*;928 S 0.957*;929 L 0.966*;932 I 0.944;933 D 0.977*;935 S 0.980*;942 T 0.938;943 F 0.991**;944 A 0.864;945 A 0.975*;947 P 0.518;949 L 0.732;950 S 0.566;951 T 0.546;953 Q 0.795;956 R 0.628;958 S 0.989*;959 I 0.514;972 I 0.735;973 K 0.991**;974 P 0.982*;975 K 0.998**;976 P 0.976*;977 P 1.000**;978 P 1.000**;979 R 1.000**;980 I 0.992**;982 R 0.998**;983 K 0.911;985 S 1.000**;986 T 0.977*;987 H 0.941;988 L 0.837;989 E 1.000**;990 I 1.000**;991 P 0.997**;992 K 1.000**;993 N 1.000**;994 V 0.982*;995 R 0.999**;996 H 0.999**;997 Q 0.987*;1009 E 0.848;1017 Y 0.939;1022 Y 0.963*;1023 R 0.982*;1025 N 0.851;1027 E 0.976*;1030 S 0.793;1031 M 0.767;1032 K 0.642;1033 R 0.992**;1036 R 0.533;1038 N 0.903;1042 N 0.975*;1095 H 0.945;1097 W 0.960*;1098 M 0.635;
apterous A splicing isoform type E [Bombyx mori]	positive	0	1 - 0.628;2 - 0.628;3 - 0.628;4 - 0.628;5 - 0.628;6 - 0.628;7 - 0.628;8 - 0.628;9 - 0.629;10 - 0.628;11 - 0.628;12 - 0.628;13 - 0.628;14 - 0.628;15 - 0.628;16 - 0.628;17 - 0.628;18 - 0.628;19 - 0.628;20 - 0.628;21 - 0.628;22 - 0.628;23 - 0.628;24 - 0.628;25 - 0.628;26 -

	0.628;27 - 0.628;28 - 0.630;29 - 0.628;30 - 0.628;31 - 0.628;32 - 0.628;33 - 0.628;34 - 0.628;35 - 0.628;36 - 0.628;37 - 0.628;38 - 0.628;39 - 0.628;40 - 0.628;41 - 0.628;42 - 0.628;43 - 0.628;44 - 0.628;45 - 0.628;46 - 0.628;47 - 0.628;48 - 0.628;49 - 0.628;50 - 0.628;51 - 0.628;52 - 0.628;53 - 0.628;54 - 0.628;55 - 0.628;56 - 0.628;57 - 0.628;58 - 0.628;59 - 0.628;60 - 0.628;61 - 0.628;62 - 0.628;63 - 0.628;64 - 0.628;65 - 0.628;66 - 0.630;67 - 0.628;68 - 0.628;69 - 0.628;70 - 0.628;71 - 0.630;72 - 0.628;73 - 0.630;74 - 0.628;75 - 0.628;76 - 0.628;77 - 0.628;78 - 0.628;79 - 0.628;80 - 0.628;81 - 0.628;82 - 0.628;83 - 0.628;84 - 0.628;85 - 0.628;86 - 0.628;87 - 0.628;88 - 0.628;89 - 0.628;90 - 0.628;91 - 0.628;92 - 0.628;93 - 0.628;94 - 0.628;95 - 0.628;96 - 0.628;97 - 0.628;98 - 0.628;99 - 0.628;100 - 0.628;101 - 0.628;102 - 0.628;103 - 0.628;104 - 0.628;105 - 0.628;106 - 0.628;107 - 0.628;108 - 0.628;109 - 0.628;110 - 0.628;111 - 0.628;112 - 0.628;113 - 0.628;114 - 0.628;115 - 0.628;116 - 0.628;117 - 1.000**;118 - 0.628;119 - 1.000**;120 - 1.000**;121 - 0.997**;122 - 0.628;123 - 0.628;124 - 0.628;125 - 0.628;126 - 0.628;127 - 0.628;128 - 0.997**;129 - 0.997**;130 - 0.628;131 - 0.628;132 - 0.628;133 - 0.630;134 - 0.628;135 - 0.628;136 - 0.628;137 - 0.628;138 - 0.628;139 - 0.628;140 - 0.628;141 - 0.628;142 - 0.628;143 - 0.628;144 - 0.628;145 - 0.628;146 - 0.628;147 - 0.628;148 - 0.628;149 - 0.628;150 M 0.513;151 R 0.570;152 A 0.571;153 R 0.546;155 L 0.529;156 V 0.578;157 F 0.528;159 V 0.537;160 H 0.537;161 C 0.572;162 F 0.528;163 S 0.531;164 C 0.529;165 A 0.529;166 L 0.590;167 C 0.529;168 S 0.581;169 T 0.531;170 P 0.522;171 L 0.581;172 N 0.544;173 K 0.550;174 G 0.530;176 T 0.531;177 F 0.596;178 G 0.530;179 I 0.524;180 R 0.570;182 S 0.620;183 A 0.523;184 V 0.532;185 Y 0.576;186 C 0.529;187 R 0.532;188 L 0.577;189 H 0.537;190 Y 0.528;191 E 0.508;192 T 0.575;193 M 0.513;194 P 0.570;195 E 0.545;196 Y 0.528;197 G 0.581;198 A 0.570;199 H 0.537;200 M 0.513;201 A 0.524;202 V 0.537;203 P 0.527;204 G 0.577;205 P 0.522;206 P 0.527;207 Q 0.543;208 M 0.513;209 C 0.572;210 P 0.573;211 G 0.577;212 P 0.566;213 Y 0.528;214 - 0.628;215 S 0.529;216 G 0.581;217 P 0.527;218 P 0.573;219 A 0.527;220 G 0.534;221 P 0.566;223 Y 0.576;224 P 0.522;225 P 0.527;226 Y 0.528;227 P 0.527;228 S 0.551;229 P 0.527;231 F 0.528;232 S 0.531;233 R 0.576;234 V 0.532;236 T 0.534;237 D 0.540;238 V 0.537;239 P 0.567;240 K 0.550;241 G 0.530;242 P 0.527;243 F 0.645;244 F 0.569;246 G 0.530;247 G 0.527;248 S 0.572;249 A 0.529;250 P 0.522;251 P 0.573;252 P 0.527;253 R 0.588;254 Q 0.543;255 K 0.550;256 G 0.581;257 R 0.527;258 P 0.570;259 R 0.588;260 K 0.550;261 K 0.550;262 K 0.514;263 P 0.570;264 K 0.514;265 D 0.540;266 Q 0.543;268 I 0.524;269 M 0.513;270 T 0.526;271 A 0.571;273 L 0.545;274 D 0.628;275 L 0.628;276 N 0.628;277 A 0.628;278 E 0.635;279 Y 0.628;280 L 0.628;281 E 0.628;282 M 0.628;283 G 0.628;284 F 0.628;285 R 0.628;286 G 0.628;287 G 0.628;288 G 0.628;289 G 0.679;290 L 0.628;291 G 0.628;292 T 0.628;293 T 1.000**;294 S 0.996**;295 R 1.000**;296 T 0.575;297 K 0.996**;298 R 0.997**;299 M 0.999**;300 R 0.985*;301 T 1.000**;302 S 1.000**;303 F 1.000**;304 K 1.000**;305 H 1.000**;306 H 1.000**;307 Q 1.000**;308 L 1.000**;309 R 1.000**;310 T 1.000**;311 M 1.000**;312 K 0.996**;313 S 1.000**;314 Y 0.997**;315 F 0.997**;316 A 1.000**;317 I 0.996**;318 N 1.000**;319 H 0.628;320 N 0.628;321 P 1.000**;322 D 1.000**;323 A 1.000**;324 K 1.000**;325 D 1.000**;326 L 1.000**;327 K 1.000**;328 Q 1.000**;329 L 0.994**;330 S 0.626;331 Q 1.000**;332 K 0.998**;333 T 0.999**;334 G 1.000**;335 L 1.000**;336 P 0.996**;337 K 0.996**;338 R 1.000**;339 V 1.000**;340 L 1.000**;341 Q 1.000**;342 V 0.996**;343 W 0.542;344 F 0.996**;345 Q 0.628;346 N 0.628;347 A 0.628;348 R 0.628;349 A 0.628;350 K 0.628;351 W 0.542;352 R 1.000**;353 R 0.996**;354 M 0.999**;355 V 0.556;356 T 1.000**;357 K 1.000**;358 Q 1.000**;359 E 0.997**;360 N 0.995**;361 K 0.628;362 M 0.996**;363 A 0.999**;365 K 1.000**;366 C 1.000**;367 S 0.997**;368 P 1.000**;369 D 0.997**;370 G 0.996**;371 S 1.000**;372 L 0.554;373 E 1.000**;374 M 1.000**;375 D 0.997**;376 M 1.000**;377 Y 1.000**;378 H 1.000**;379 G 1.000**;380 P 1.000**;381 M 0.513;382 G 1.000**;383 S 1.000**;384 I

			1.000**;385 Q 0.999**;386 S 1.000**;387 L 1.000**;388 P 0.628;389 P 0.628;390 H 0.628;391 S 0.628;392 P 0.628;393 P 0.628;394 Y 0.628;395 S 0.628;396 V 0.628;397 M 0.628;398 G 0.628;399 G 0.628;400 P 0.628;401 P 0.628;402 S 0.628;403 P 0.628;404 N 0.628;405 S 0.628;406 L 0.628;407 D 0.648;408 C 0.572;409 P 1.000**;
E3 ubiquitin-protein ligase RING1 [Bombyx mori]	positive	0.000101585	390 R 0.703;443 T 0.936;446 V 0.687;494 S 0.988*;567 R 0.672;578 A 0.587;587 K 0.547;647 Y 0.997**;648 L 0.770;664 Y 0.995**;667 L 0.963*;668 N 0.914;669 F 0.691;671 I 0.995**;677 P 0.997**;682 P 0.738;693 N 0.700;699 V 0.739;700 N 0.913;701 K 0.991**;703 L 0.757;704 E 0.997**;705 M 1.000**;706 Y 0.995**;712 T 0.987*;
sn1-specific diacylglycerol lipase beta [Bombyx mori]	positive	2.22E-16	3 - 0.808;4 - 0.995**;5 - 0.994**;6 - 0.805;7 - 0.913;8 - 1.000**;9 - 0.816;10 - 1.000**;11 - 0.999**;13 - 0.905;15 - 1.000**;16 - 0.991**;17 - 0.939;18 - 1.000**;20 - 1.000**;21 - 1.000**;22 - 0.896;23 - 1.000**;25 - 0.999**;26 - 0.922;29 - 1.000**;30 - 0.987*;31 - 0.999**;33 - 1.000**;36 - 0.999**;291 E 0.866;369 R 0.609;385 S 0.735;430 A 0.924;481 F 0.585;487 A 0.949;619 V 0.563;635 K 0.962*;662 R 1.000**;663 M 0.999**;
gene3463	positive	2.97E-05	2 - 0.978*;3 - 1.000**;4 - 1.000**;5 - 0.971*;6 - 0.724;7 - 0.783;8 - 0.999**;9 - 0.996**;10 - 0.822;11 - 0.894;12 - 0.825;14 - 0.787;16 - 0.999**;17 - 0.998**;18 - 0.999**;19 - 1.000**;20 - 0.998**;21 - 0.837;22 - 0.958*;23 - 0.998**;24 - 0.981*;39 - 0.660;40 - 0.988*;41 - 0.839;42 - 0.848;44 - 0.907;45 - 0.999**;47 - 1.000**;102 - 0.797;105 - 0.784;106 - 0.997**;140 - 0.942;141 - 0.999**;142 - 0.997**;143 - 0.997**;206 E 0.682;251 T 0.994**;276 Q 0.743;281 M 0.911;289 I 0.506;294 S 0.779;302 S 0.748;365 K 0.546;366 A 0.575;371 L 0.826;378 K 0.918;379 C 0.996**;380 R 0.994**;396 P 0.786;415 T 0.653;435 L 0.570;439 H 0.817;469 N 0.507;477 D 0.697;478 T 0.770;484 V 0.687;
peptidyl-prolyl cis-trans isomerase-like 4 [Bombyx mori]	positive	0.00025426	64 Q 0.857;333 H 0.643;337 E 0.948;464 - 0.759;612 - 0.753;720 - 0.660;738 S 0.806;747 * 0.707;748 - 0.999**;751 - 0.741;756 - 0.843;766 - 0.540;
tetratricopeptide repeat protein 14 homolog isoform X2 [Bombyx mori]	positive	0.000105176	91 L 0.901;98 T 0.745;174 T 0.657;576 P 0.757;648 G 0.826;788 S 0.847;789 P 0.883;814 S 0.512;815 V 0.826;830 R 0.627;846 P 1.000**;847 S 0.953*;848 P 0.809;856 S 0.976*;858 R 0.867;859 R 0.996**;860 A 0.981*;1030 - 0.937;1112 - 0.847;1230 - 0.588;
LIM/homeobox protein Lhx3 isoform X4 [Bombyx mori]	positive	0.000284942	7 Y 0.995**;8 P 0.997**;9 G 0.835;10 V 0.802;11 E 0.886;13 A 0.816;15 L 0.994**;31 D 0.994**;33 R 0.996**;34 V 0.828;35 P 0.998**;36 P 0.771;37 I 0.828;38 Q 0.996**;39 L 0.997**;40 E 0.998**;47 L 0.795;49 E 0.601;51 F 0.758;63 S 0.743;104 M 0.771;106 S 0.777;126 K 0.739;133 A 0.988*;297 M 0.697;327 E 0.608;340 G 0.791;370 A 0.738;385 L 0.934;386 V 1.000**;387 Y 1.000**;436 P 0.676;437 H 0.622;438 H 0.989*;440 S 0.997**;441 P 0.784;442 R 0.513;
transmembrane protein 14C [Bombyx mori]	positive	2.75E-10	3 V 0.852;6 L 0.885;19 I 0.922;74 M 0.996**;88 R 0.954*;89 Y 1.000**;90 Y 1.000**;91 N 1.000**;92 G 1.000**;93 R 1.000**;94 K 0.997**;103 C 1.000**;104 L 0.988*;105 S 0.982*;106 V 1.000**;107 G 0.980*;108 M 0.962*;109 I 0.998**;111 K 1.000**;112 L 0.977*;113 L 1.000**;114 V 1.000**;116 N 1.000**;118 G 0.969*;119 S 0.978*;121 S 0.994**;122 P 0.989*;123 V 0.969*;124 P 1.000**;125 V 0.973*;126 K 1.000**;127 T 0.997**;128 G 0.991**;
TPA: putative cuticle protein [Bombyx mori]	positive	0	1 - 0.732;2 - 0.732;3 - 0.732;4 M 0.659;5 Q 0.570;6 S 0.612;7 M 0.717;8 I 0.946;9 F 0.564;11 A 0.647;15 C 0.549;18 Q 0.569;19 A 0.625;23 A 0.690;26 P 0.630;29 I 0.564;30 Q 0.587;32 S 0.552;33 P 0.630;34 D 0.546;35 G 0.596;36 K 0.646;42 P 0.630;43 E 0.522;44 V 0.641;47 A 0.606;48 K 0.629;51 H 0.584;52 Y 0.662;54 A 0.647;56 A 0.647;57 Q 0.587;59 S 0.612;60 S 0.608;61 G 0.625;62 H 0.584;64 A 0.647;65 W 0.662;66 A 0.677;68 - 0.732;69 - 0.732;70 - 0.732;71 - 0.732;72 - 0.732;73 G 0.649;74 A 0.523;76 Y 0.732;77 L 0.732;78 G 0.732;79 A 0.732;80 G 0.732;81 V 0.732;82 A 0.706;84 G 0.762;85 A 0.686;86 G 0.557;87 A 0.647;90 G 0.732;91 D 0.732;93 A 0.606;94 P 0.610;95 G 0.636;97 G 0.997**;98 L 1.000**;99 L 1.000**;100 K 1.000**;101 Y 1.000**;102 G 1.000**;103 P 1.000**;104 A 0.629;105 P 0.997**;106 L 0.994**;107 A 0.997**;108 H 0.651;109 D 0.732;110 G 0.521;111 R 0.631;112 V 0.997**;113 V 0.997**;114 D 0.732;115 T 1.000**;116 P 1.000**;117 E 0.999**;118 V 1.000**;119 A 0.997**;120

			H 1.000**;121 L 0.998**;122 K 1.000**;123 A 1.000**;124 A 0.997**;125 H 0.995**;126 I 1.000**;127 S 1.000**;128 A 1.000**;129 L 1.000**;130 S 0.996**;131 A 0.998**;132 A 1.000**;133 H 0.995**;134 A 0.998**;135 S 0.996**;136 A 1.000**;137 S 0.997**;138 H 0.999**;139 G 0.732;140 A 0.732;141 - 0.732;142 - 0.732;143 - 0.732;144 - 0.732;145 - 0.732;146 L 0.732;147 A 0.732;148 H 0.732;149 A 0.732;150 G 0.732;151 A 0.800;152 H 0.734;153 A 0.732;154 P 0.732;155 L 0.732;156 A 0.732;157 Y 0.732;158 A 0.732;159 A 0.753;160 P 0.732;161 L 0.732;162 G 0.732;163 H 0.732;164 G 0.732;165 A 0.992**;166 G 0.995**;167 Y 0.954*;168 G 0.744;169 A 0.996**;170 G 0.596;171 A 1.000**;172 G 0.732;173 Y 0.732;174 A 0.732;175 A 0.732;176 G 0.732;177 Y 0.732;178 G 0.732;179 K 0.646;180 W 0.662;181 T 1.000**;182 G 1.000**;184 Q 1.000**;185 A 0.996**;186 H 0.996**;187 I 0.998**;188 Q 1.000**;189 L 0.732;190 T 0.732;191 H 0.732;192 D 1.000**;193 G 1.000**;194 Q 1.000**;195 F 1.000**;196 V 0.626;197 V 1.000**;198 D 1.000**;199 T 0.536;200 P 0.539;201 E 0.998**;202 V 1.000**;203 Q 1.000**;204 H 1.000**;205 A 0.998**;206 R 0.732;207 A 0.998**;208 S 0.993**;210 L 1.000**;211 S 0.994**;212 Q 0.999**;213 Y 1.000**;214 A 0.924;215 A 0.991**;216 A 0.997**;218 H 1.000**;219 A 1.000**;220 A 0.995**;221 A 1.000**;222 A 1.000**;223 A 1.000**;224 - 0.732;225 - 0.732;226 - 0.732;227 - 0.732;228 P 0.539;229 E 1.000**;230 E 1.000**;231 P 1.000**;232 W 0.999**;233 A 1.000**;235 H 1.000**;236 G 0.996**;237 - 0.732;238 - 0.732;239 - 0.732;240 H 0.732;241 - 0.732;242 - 0.732;243 G 0.998**;244 W 1.000**;246 - 0.732;247 - 0.732;248 - 0.732;249 - 0.732;250 - 0.732;251 - 0.732;
uncharacterized protein LOC105381380, partial [Plutella xylostella]	positive	0.002199021	11 - 0.540;13 - 0.994**;14 - 0.998**;15 - 0.724;16 - 0.995**;18 - 0.557;19 - 0.671;48 - 0.831;50 - 0.808;51 - 0.994**;52 - 0.992**;54 - 0.811;82 - 0.548;94 - 0.529;103 - 0.923;104 - 0.945;106 - 0.528;108 - 0.811;135 - 0.528;136 - 0.827;137 - 0.922;138 - 0.713;139 - 0.739;140 - 0.994**;141 - 0.997**;142 - 0.901;143 - 0.996**;145 - 0.995**;147 - 0.740;148 - 0.998**;151 - 0.997**;152 - 1.000**;284 M 0.685;315 D 0.972*;344 G 0.611;346 C 0.995**;347 S 0.999**;348 P 0.827;349 K 0.733;358 L 0.681;359 P 0.993**;360 P 0.996**;363 - 0.989*;386 - 0.996**;387 - 0.606;388 - 0.989*;389 - 0.997**;399 - 0.503;438 D 0.997**;439 I 0.715;440 R 0.996**;442 G 0.997**;443 L 0.756;444 M 0.994**;446 M 1.000**;447 G 0.997**;449 D 0.993**;450 G 0.984*;451 V 0.995**;453 G 0.994**;454 P 0.783;455 F 0.792;456 G 0.995**;457 D 0.997**;458 D 0.993**;464 D 0.989*;466 A 0.993**;467 R 0.962*;468 G 0.995**;469 L 0.815;470 S 0.826;482 E 0.980*;484 D 0.552;486 E 0.996**;496 A 0.806;499 F 0.742;500 Q 0.845;507 T 0.996**;512 N 0.995**;513 D 0.556;515 R 0.999**;517 E 0.647;518 G 0.993**;519 I 0.768;520 I 0.725;521 S 0.995**;533 P 0.750;535 R 0.988*;537 G 0.996**;538 L 0.992**;539 I 0.984*;540 I 0.754;545 P 0.997**;546 Y 0.991**;548 T 0.704;549 T 0.998**;550 V 0.795;551 I 0.990*;555 T 0.818;556 A 0.991**;557 R 0.995**;558 D 0.673;560 E 0.995**;561 S 0.641;562 G 0.996**;563 D 0.977*;576 L 0.824;577 S 0.996**;578 G 0.808;580 S 0.847;584 N 0.899;585 R 0.923;586 S 0.995**;587 E 0.513;589 D 0.987*;591 R 0.993**;592 R 0.726;593 G 0.996**;595 R 0.979*;596 Q 0.843;597 M 0.999**;598 S 0.993**;599 G 0.990**;600 Y 0.707;601 R 0.963*;618 E 0.968*;619 S 0.770;620 E 0.968*;621 T 0.846;622 D 0.996**;623 S 0.879;624 Q 0.732;625 H 0.663;626 I 0.715;627 A 0.996**;628 T 0.995**;630 H 0.727;631 K 0.999**;633 A 0.989*;634 E 0.998**;635 E 0.944;636 C 0.997**;637 E 0.997**;638 G 0.822;640 S 0.994**;641 N 0.723;660 L 0.660;662 Q 0.994**;663 E 0.968*;664 R 0.572;665 G 0.794;666 P 0.842;667 E 0.715;668 - 0.903;669 G 0.718;670 S 0.513;671 E 0.981*;672 R 0.997**;673 R 0.973*;674 T 0.894;675 S 0.998**;676 G 0.992**;677 D 0.537;679 A 0.996**;680 F 0.770;681 P 0.994**;682 C 0.997**;683 S 0.999**;684 N 0.998**;685 S 0.977*;714 E 0.971*;725 S 0.713;726 L 0.726;727 L 0.993**;728 V 0.989*;729 P 0.834;730 Q 0.843;731 M 0.989*;732 L 0.870;733 C 0.770;734 R 0.992**;735 A 0.870;736 R 0.995**;737 A 0.813;738 L 0.772;739 V 0.996**;740 D 0.673;741 Y 0.727;743 P 0.806;745 I 0.660;746 Y 1.000**;758 I 0.995**;759 I 0.822;760 E 0.647;761 V 0.735;762 I 0.731;763 N 0.525;765 N 0.764;766 A 0.806;767 S 0.998**;768 G 0.976*;797 S 0.999**;798 R 1.000**;800 S 0.884;801 K 0.996**;831 M 0.537;834 A 0.761;854 Y 0.771;855 L

			0.999**;856 G 0.818;857 I 0.618;858 M 0.887;861 E 0.990*;862 H 0.993**;864 T 0.994**;867 L 0.723;868 A 0.997**;869 A 0.712;870 V 0.998**;878 C 0.904;881 G 0.897;882 E 0.823;888 G 0.996**;890 S 0.999**;891 S 0.995**;892 S 0.995**;893 E 0.515;894 G 0.995**;898 P 0.960*;899 F 0.770;901 R 0.809;903 Q 0.872;904 F 0.727;936 H 0.857;962 I 0.779;963 E 0.997**;964 R 0.981*;965 Y 0.998**;966 P 0.997**;977 S 0.630;999 K 0.994**;1000 F 0.770;1001 V 0.784;1002 A 0.800;1004 G 0.621;1005 E 0.524;
isovaleryl coenzyme A dehydrogenase [Bombyx mori]	positive	2.71E-11	212 P 0.600;380 G 0.951*;391 N 0.938;392 G 0.993**;394 I 0.959*;395 N 1.000**;396 D 1.000**;397 Y 0.945;398 P 0.954*;399 T 1.000**;402 G 1.000**;403 R 1.000**;405 L 0.946;406 R 0.928;407 D 0.917;408 A 0.949;409 K 0.960*;410 L 0.997**;411 Y 1.000**;418 E 1.000**;420 G 0.948;421 A 1.000**;422 G 0.968*;423 T 0.959*;425 E 1.000**;426 V 0.991**;427 R 0.947;428 R 1.000**;429 M 0.997**;430 L 0.992**;431 I 0.992**;435 L 0.992**;436 N 1.000**;437 S 0.866;440 K 0.945;
methyltransferase-like protein 16 homolog isoform X1 [Bombyx mori]	positive	7.05E-05	61 C 0.837;71 E 0.657;156 K 0.830;189 Q 0.998**;234 K 0.985*;307 V 0.558;417 D 0.999**;418 V 0.736;479 P 0.626;505 G 0.840;
prestin isoform X2 [Bombyx mori]	positive	0	20 E 0.703;21 G 0.878;25 T 0.984*;26 P 0.984*;27 D 0.699;29 E 0.991**;31 E 0.990*;32 K 0.782;33 L 0.957*;34 N 0.998**;35 P 0.998**;37 G 0.911;39 W 0.763;276 L 0.678;309 L 0.653;431 A 0.692;482 S 0.630;714 S 0.944;
protein numb isoform X1 [Bombyx mori]	positive	0	127 V 0.685;242 G 0.924;243 L 0.995**;244 T 0.828;279 A 0.506;280 D 0.631;281 A 0.616;340 A 0.504;366 F 0.929;367 A 1.000**;369 L 1.000**;370 N 1.000**;371 N 0.946;372 S 0.994**;391 P 1.000**;392 S 1.000**;395 E 1.000**;396 R 0.706;397 Q 0.980*;398 R 0.780;399 A 0.909;403 G 1.000**;404 S 1.000**;424 L 0.866;425 P 0.997**;427 V 0.658;428 V 0.594;429 K 0.995**;430 P 0.936;431 V 0.858;435 - 0.999**;436 - 0.987*;437 - 0.916;438 - 1.000**;439 - 0.950;440 - 0.884;
calcium uptake protein 1 homolog, mitochondrial-like [Bombyx mori]	positive	3.67E-09	2 Y 0.741;83 L 0.543;147 R 0.768;148 S 1.000**;155 I 0.805;157 R 0.560;162 V 0.940;163 K 0.733;164 L 1.000**;165 T 1.000**;167 G 1.000**;169 N 0.657;170 T 1.000**;172 I 0.614;182 A 0.926;183 I 0.506;187 M 0.995**;402 N 0.604;
probable hydroxyacid-oxoacid transhydrogenase, mitochondrial [Bombyx mori]	positive	1.83E-08	8 V 0.999**;9 F 1.000**;12 L 0.997**;13 R 0.997**;14 T 1.000**;17 V 0.910;29 G 0.974*;31 I 0.996**;32 Q 1.000**;33 V 0.952*;34 S 1.000**;35 N 0.944;36 A 0.967*;37 T 1.000**;38 P 0.967*;39 I 0.985*;40 K 1.000**;41 D 0.948;42 Y 0.961*;43 A 1.000**;44 F 0.968*;45 E 1.000**;82 V 0.890;114 S 0.940;121 K 0.579;134 V 0.844;151 S 0.950*;170 P 0.933;173 V 0.871;175 L 0.911;253 Y 0.941;296 Y 0.835;299 D 0.931;313 M 0.947;374 D 0.622;393 E 0.794;397 K 0.880;402 T 0.995**;405 K 0.999**;410 M 0.945;437 D 0.959*;438 R 0.965*;439 L 1.000**;441 K 0.971*;442 I 0.996**;446 S 0.704;448 T 0.943;458 D 0.789;
heparin sulfate O-sulfotransferase [Bombyx mori]	positive	5.36E-06	3 F 0.653;5 V 0.753;9 C 1.000**;10 L 0.992**;11 F 1.000**;12 S 0.878;13 C 1.000**;14 I 0.950;16 I 0.997**;17 I 0.999**;18 V 0.999**;19 L 0.978*;20 I 0.860;21 S 0.866;23 Y 1.000**;29 A 0.953*;31 L 0.935;36 R 0.998**;37 V 0.995**;38 R 0.994**;40 Y 0.755;43 L 0.537;44 Q 0.546;45 S 0.622;46 H 0.945;61 E 0.775;64 D 0.920;66 D 0.989*;85 V 0.637;123 K 0.684;227 Q 0.514;251 L 0.753;275 S 0.667;276 N 1.000**;277 K 0.998**;278 S 0.999**;279 H 0.996**;280 L 0.999**;281 R 0.973*;282 Q 0.997**;285 S 0.771;286 S 1.000**;287 K 0.576;288 I 0.996**;289 D 1.000**;290 P 0.826;291 I 0.920;293 A 0.847;294 T 0.999**;296 E 0.935;297 K 0.999**;299 Q 0.994**;300 Q 0.996**;301 S 0.855;302 I 0.594;303 V 0.869;307 W 0.998**;308 K 0.999**;309 M 0.525;310 E 0.699;312 E 0.606;313 L 0.957*;314 Y 0.996**;315 E 0.603;317 A 0.834;318 L 0.891;319 E 0.997**;320 Q 0.998**;321 F 0.997**;323 F 1.000**;372 K 0.962*;373 R 0.978*;374 K 0.773;375 L 0.858;377 V 0.809;378 K 0.780;379 E 0.820;380 A 0.998**;381 N 0.989*;382 N 0.774;383 V 0.811;385 Q 0.790;386 I 0.931;400 Y 0.754;403 E 0.626;404 K 0.576;405 I 0.891;406 R 0.955*;408 K 0.925;
sex combs on midleg [Bombyx mori]	positive	1.87E-07	263 P 0.716;530 K 0.836;538 S 0.807;604 A 0.968*;673 K 0.999**;674 N 0.995**;676 R 0.998**;677 H 0.963*;678 Y 0.981*;
fibrinogen C domain-containing protein 1-B-like [Bombyx mori]	positive	0	15 I 0.534;16 F 0.910;17 S 0.691;18 L 0.953*;20 V 0.964*;22 N 0.982*;25 K 0.943;26 K 0.542;27 E 0.706;29 A 0.528;30 R 1.000**;31 I 0.725;32 Q 0.991**;33 K 0.959*;35 I 0.716;37 D 0.934;38 E 0.845;40 E 0.980*;200 L 0.911;204 T 0.980*;205 G 0.696;206 R 0.565;207 G 0.964*;208 A 0.847;209 D 0.649;217 - 0.540;222 E 0.819;225 I

	0.590;233 M 0.587;234 S 0.928;241 M 0.503;242 I 0.774;247 R 0.970*;248 K 0.915;251 H 0.982*;255 T 0.937;257 H 0.986*;260 T 0.960*;261 N 0.850;264 T 0.985*;266 Y 0.987*;267 L 0.788;268 T 0.843;274 L 0.996**;277 S 0.945;280 S 0.990**;281 - 0.549;282 E 0.995**;283 A 0.988*;284 L 0.987*;286 D 0.827;287 A 0.978*;290 I 0.681;293 S 0.623;296 D 0.998**;300 H 0.847;301 S 0.567;302 V 0.996**;303 I 0.869;304 E 0.995**;305 R 0.918;307 E 0.869;308 H 0.964*;310 P 0.865;311 N 0.581;397 E 0.980*;508 H 0.806;618 N 0.574;720 S 0.621;

*Indicates that the posterior probability >0.95; **Indicates that the posterior probability >0.99.