

Supplemental Information

Genome-wide open chromatin regions and their effects on the regulation of silk protein genes in *Bombyx mori*

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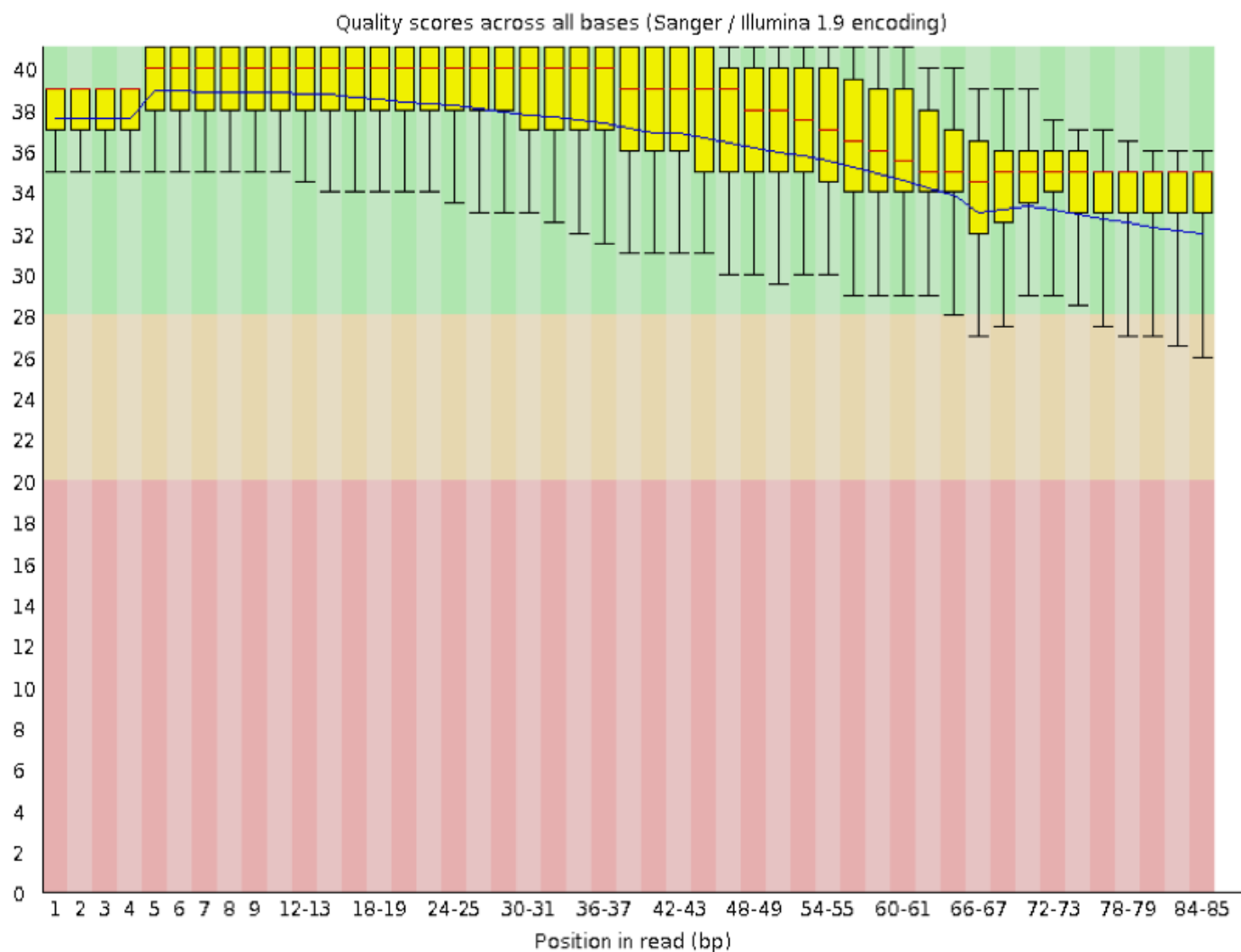
Supplementary Figure S6. Person correlation (PCC) of samples

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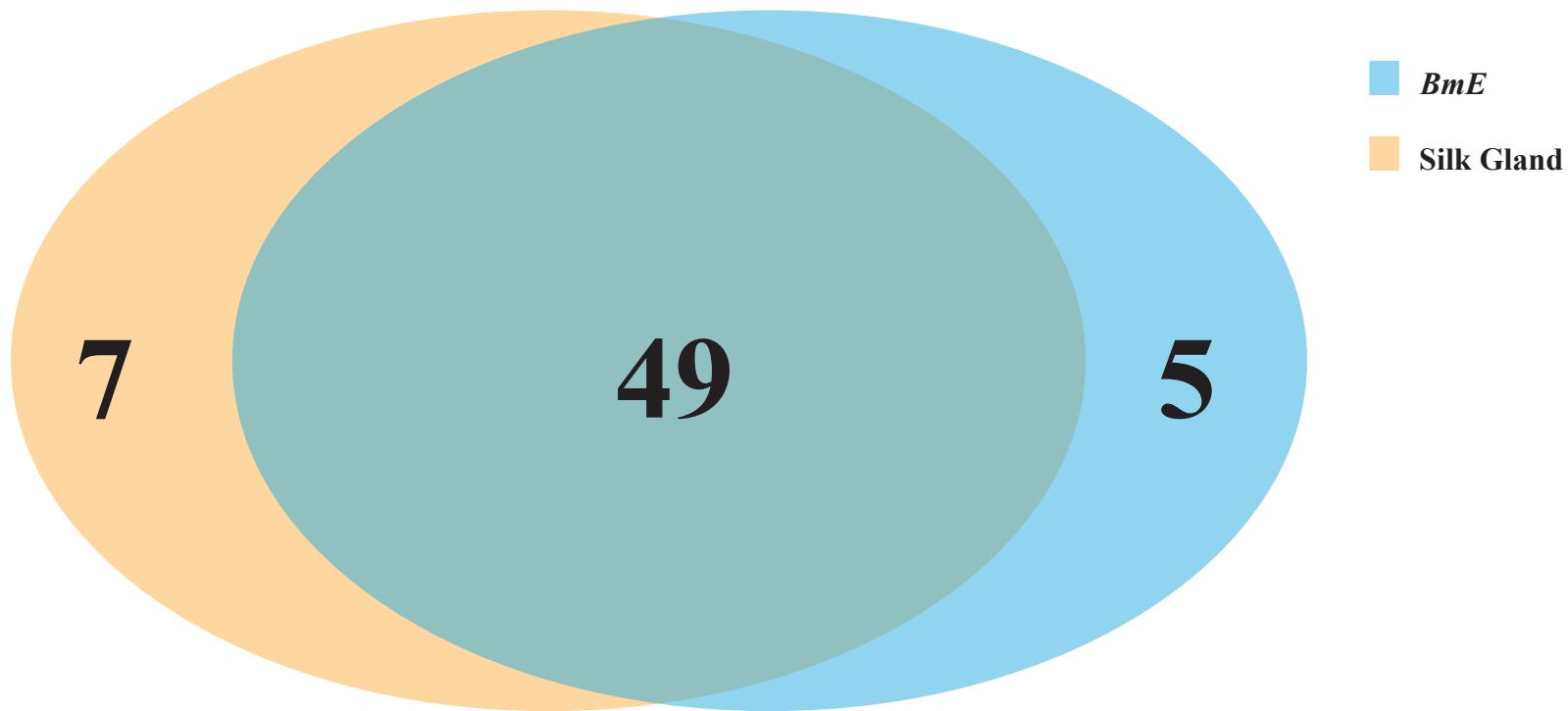
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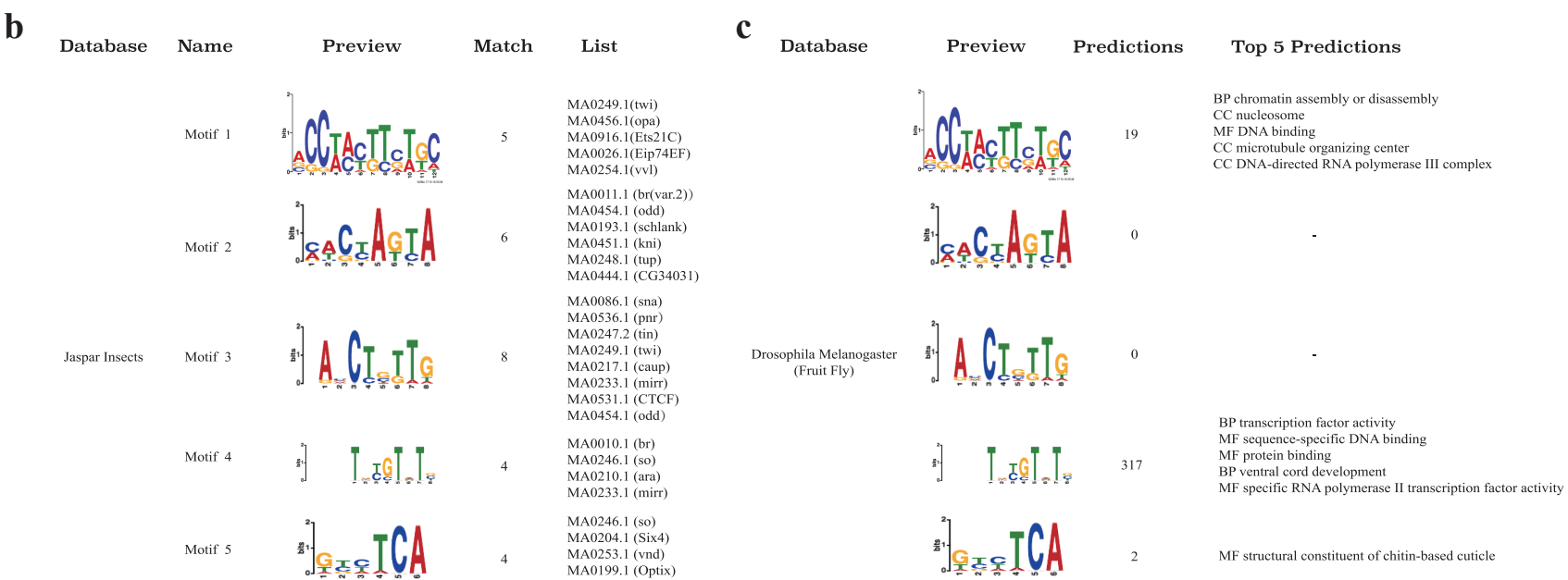
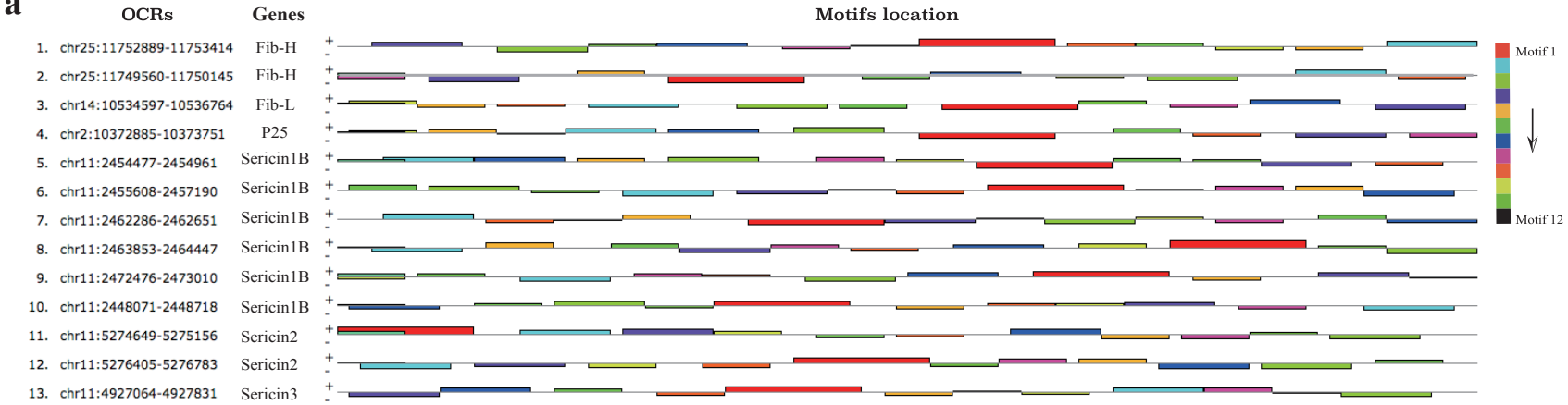
Supplementary Figure S10. GO annotation of silk gland and BmE Up-regulated DEGs



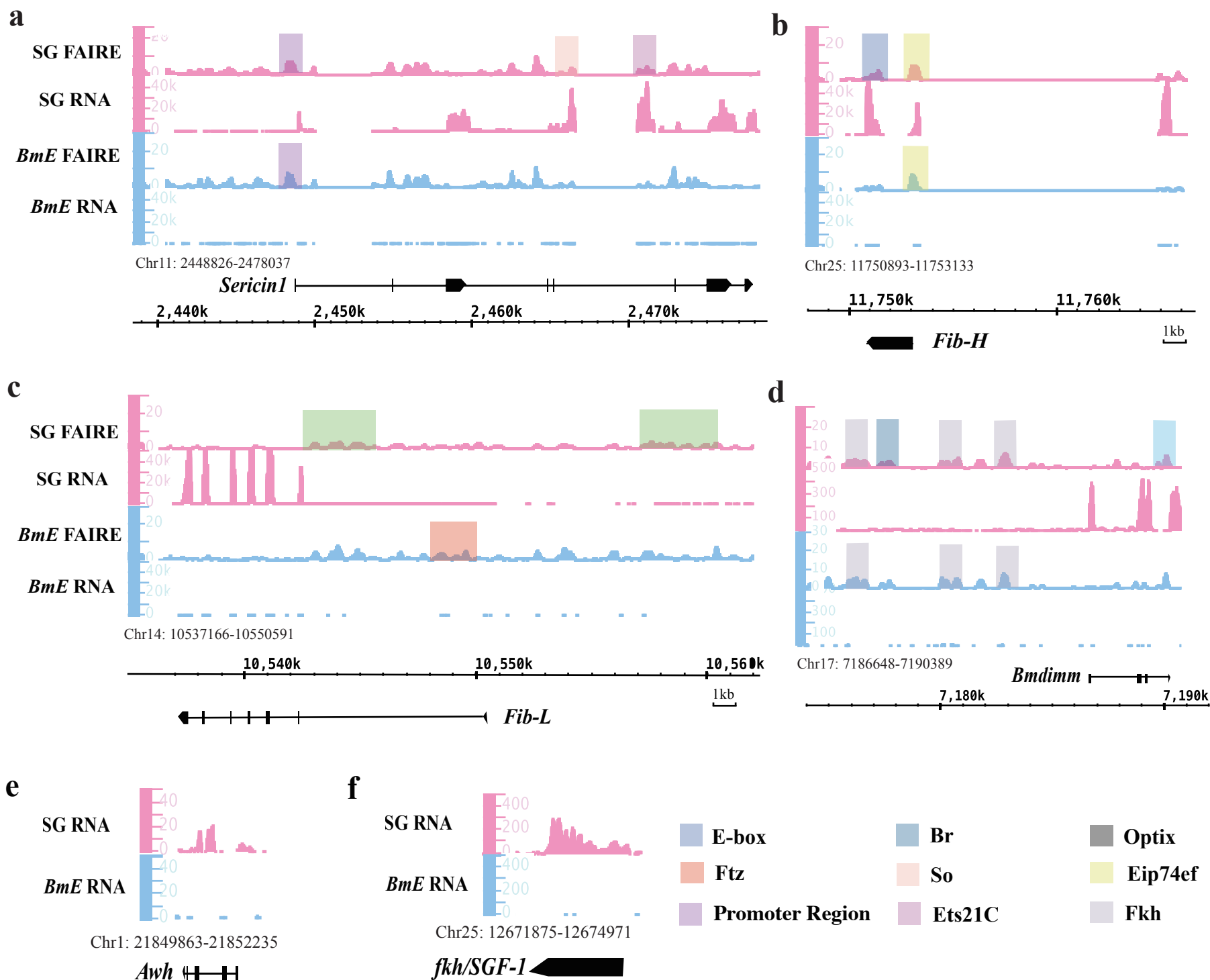
Supplementary Figure S1 Quality scores of all base. Almost all of the bases were high quality.



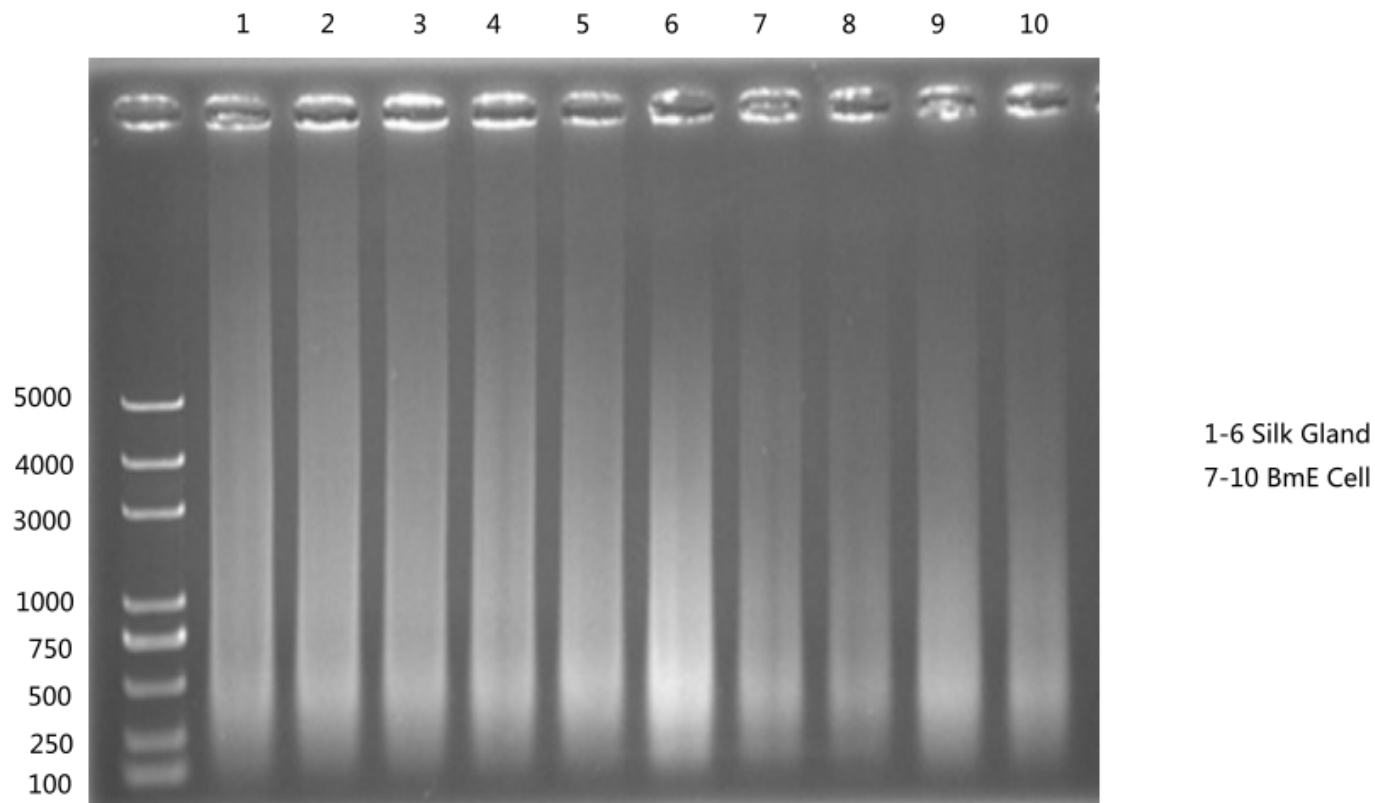
Supplementary Figure S2 venn graph of silk gland and BmE specific motifs. Blue was BmE and orange was silk gland.



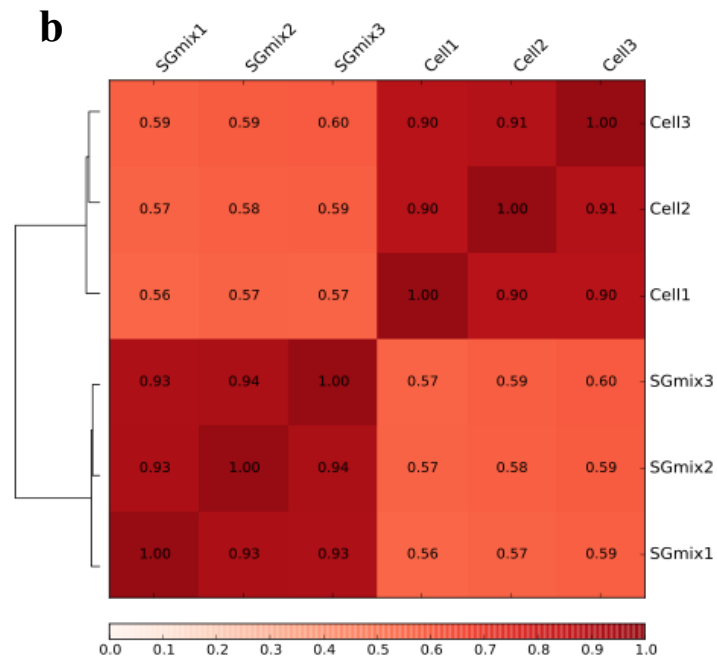
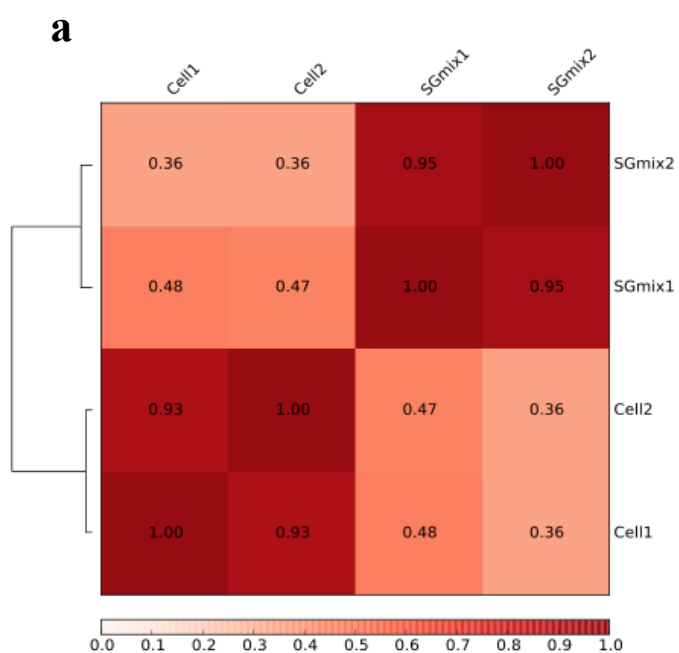
Supplementary Figure S3 A. Location of the new motifs in the open chromatin regions (OCRs). Different colors show different motifs. **B.** Known motifs similar to the newly discovered motifs. Here, we chose the E-value of the top 5 motifs. **C.** Gene ontolog annotation of the E-value of the top 5 newly discovered motifs.



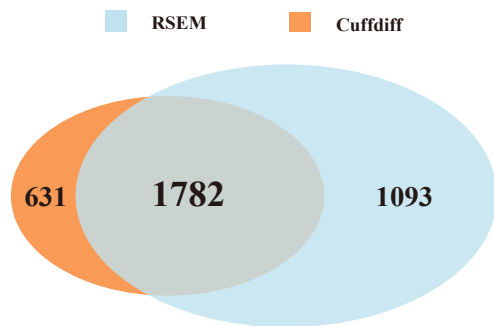
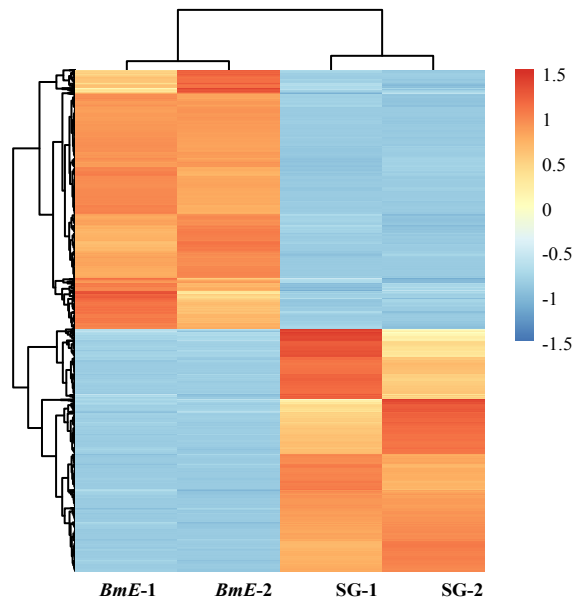
Supplementary Figure S4 FAIRE-seq and RNA-seq signal around *Fib-H*, *Sericin 1*, *Fib-L* and *Bmdimm* gene. Pink peaks are silk gland FAIRE-seq and RNA-seq peaks. Blue peaks are *BmE* FAIRE-seq and RNA-seq peaks. Other colored shadows show locations of known transcription factor binding sites, and one color corresponds to one transcription factor. A. *Sericin 1*. B. *Fib-H*. C. *Fib-L*. D. *Bmdimm*. E. RNA-seq signal peaks of *Awh*. F. RNA-seq signal peaks of *SGF-1*.



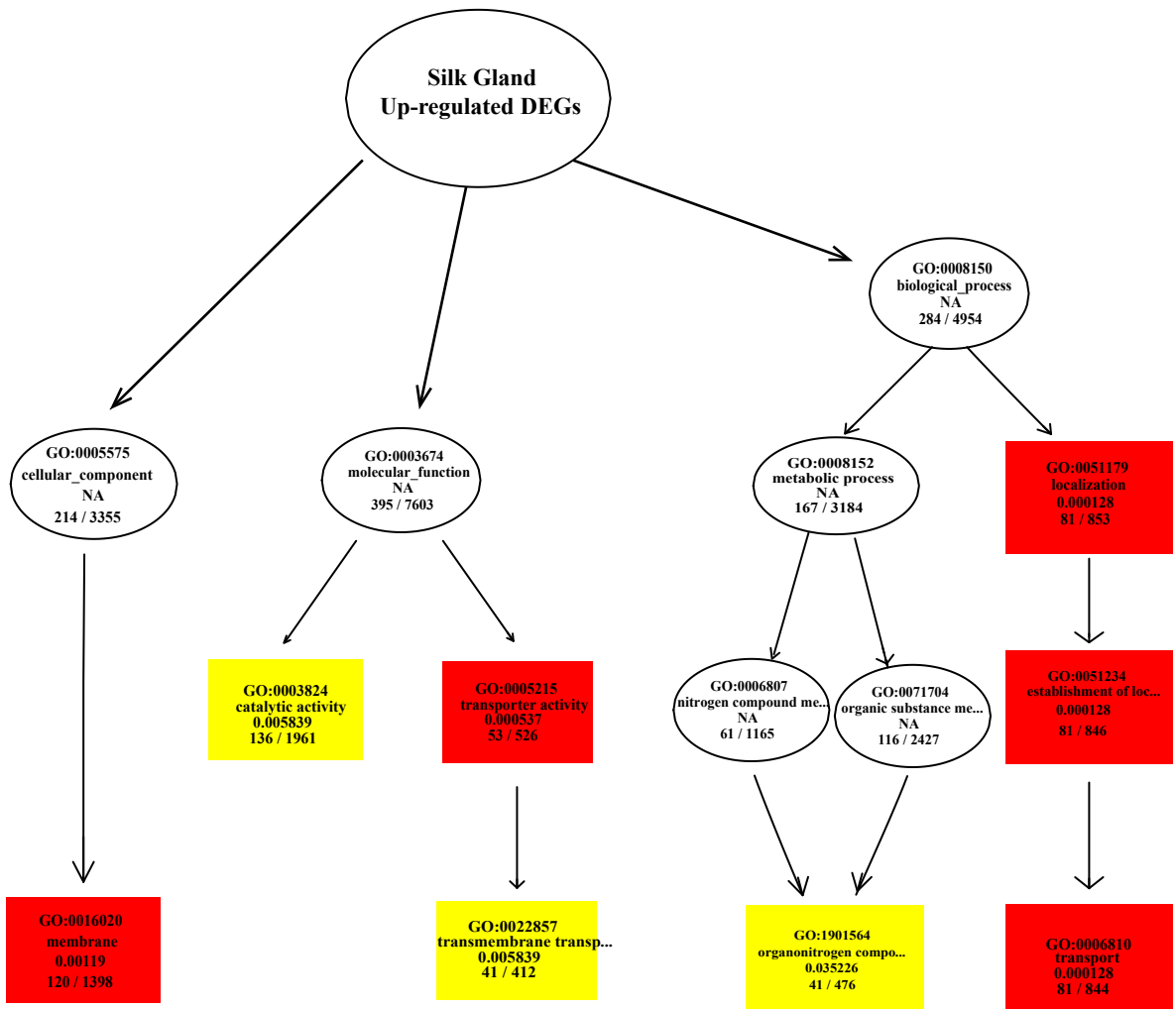
Supplementary Figure S5 DNA sonication agarose gel electrophoresis. The quantity control of FAIRE samples, 1,2,3,4,5,6 were the sonic crushing report of silk gland. 7,8,9,10 were BmE cell's. It indicated that the quantity of sonic crushing was very good, the main region of DNA was enriched in 250-500bp.



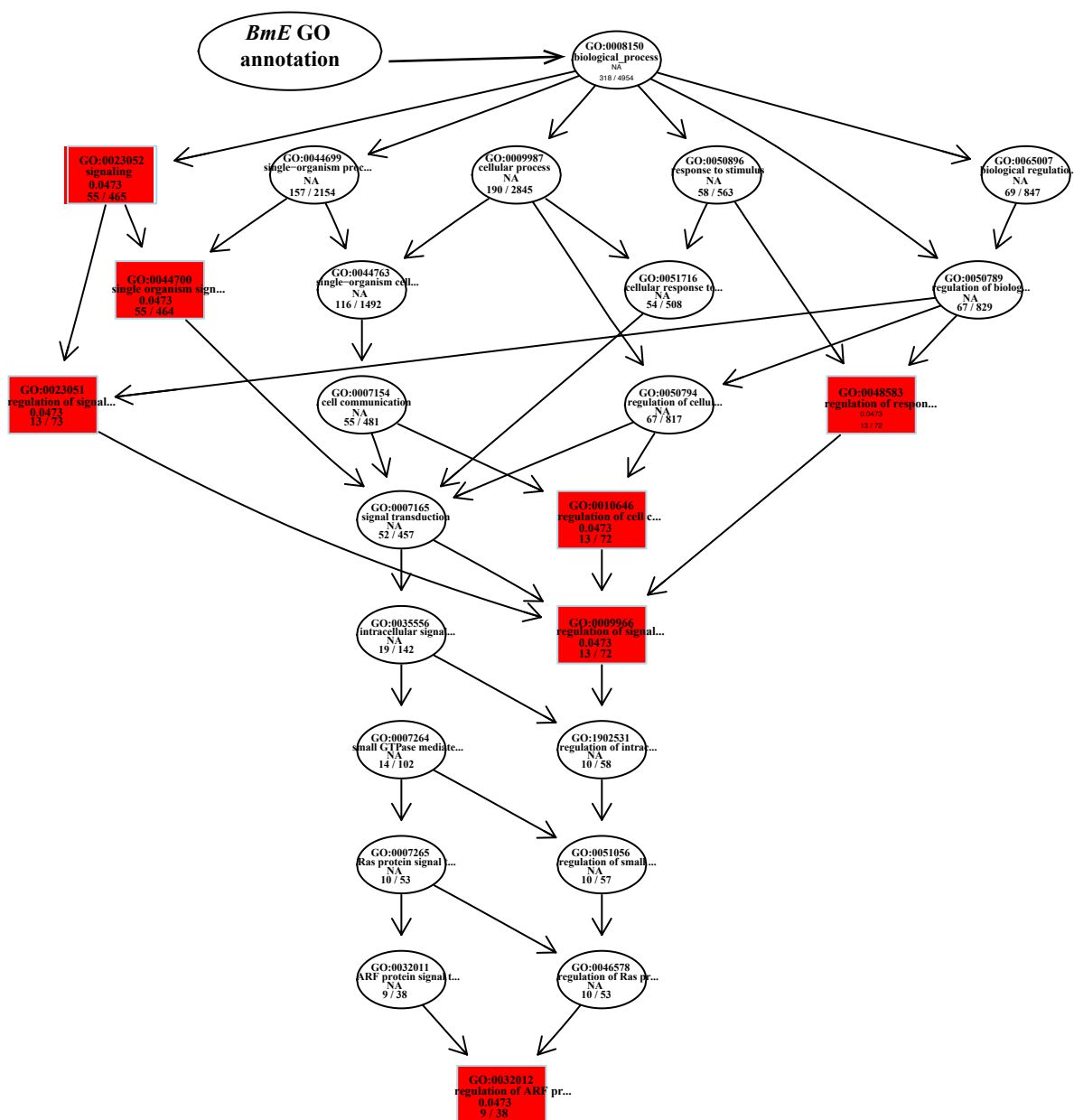
Supplementary Figure S6 Person correlation (PCC) of FAIRE-seq and RNA-seq samples. The color from light to dark indicated that the PCC was from low to high. Sample Cell was BmE cell, sample SG was silk gland. A. RNA-seq. B. FAIRE-seq.

a**b**

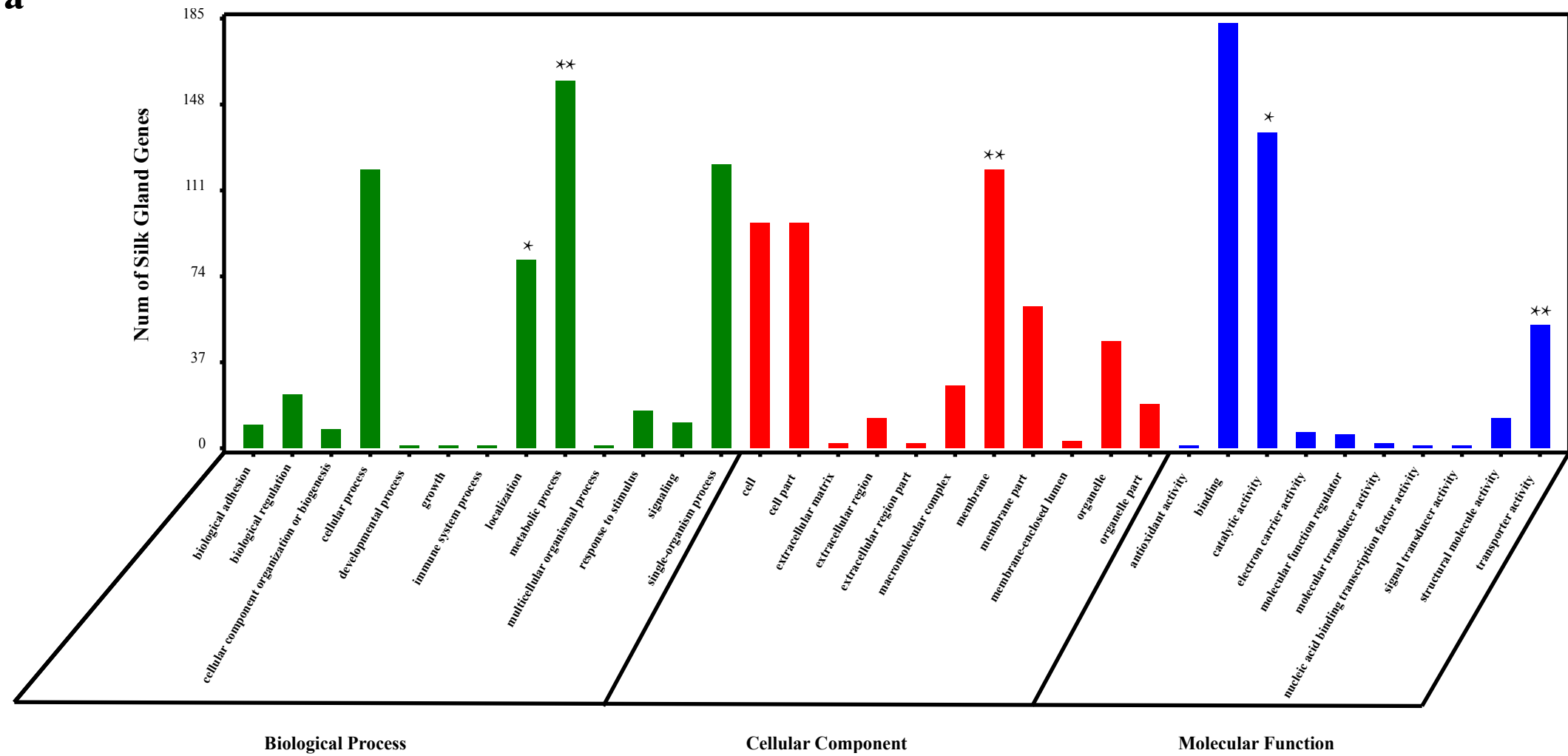
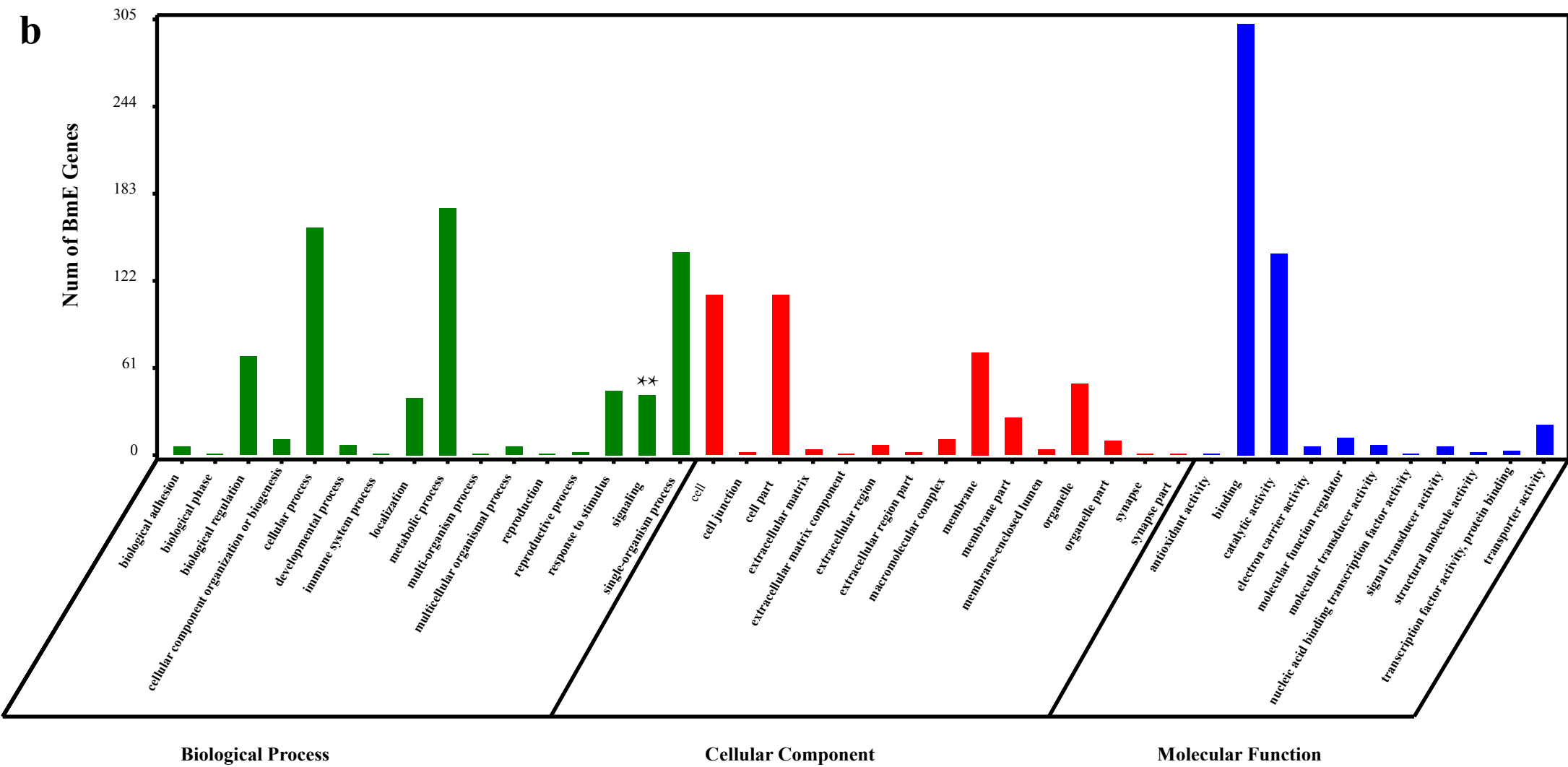
Supplementary Figure S7 Differentially expressed genes (DEGs) between silk gland and BmE. A. DEGs was generated by intersecting DEGs calculated by RSEM and Cuffdiff. The intersection was 1782. B. Heatmap of DEGs distribution in BmE and silk gland.



Supplementary Figure S8 Silk gland GO annotation Directed Acyclic Graphs. GO term in square was more remarkable than in ellipse. The red term was more remarkable than yellow. Each term was marked GO number, P-value, name and gene (DEG and background gene) number of enriched in this term. P-value <0.05 was remarkable.



Supplementary Figure S9 BmE GO annotation Directed Acyclic Graphs. GO term in square was more remarkable than in ellipse. The red term was more remarkable than yellow. Each term was marked GO number, P-value, name and gene (DEG and background gene) number of enriched in this term. P-value <0.05 was remarkable.

a**b**

Supplementary Figure S10 GO annotation of silk gland and BmE Up-regulated DEGs. Asterisk mean that term was P-value<0.05 and it was the remarkable term. Two asterisk was the most remarkable term. A. Silk gland DEGs GO annotation. B. BmE DEGs GO annotation.