1 **Supplementary Materials**

2 **Table.S1.** Primer sets used in the transgenic overexpression.

3 **Table.S2.** Primer sets used in qRT-PCR.

4 **Figure S1.** Main economic characters of different silk-producing strain.

5 **Figure S2.** Expression of silk protein transcription factor in wild type and transgenic lines.

6 **Figure S3.** Overexpression of *BmJHBPd2* results in inhibition of JH catabolic enzyme in silk gland.

7

8

9

Gene	5'-3'
BmJHBPd2 F (*BamH* I)	GGATCCATGTGGACCGGTCTGTTTTTAGT
BmJHBPd2 R (*Not* I-Myc)	GCGGCCGCTTACAGATCCTCTTCTGAGATGAGTTTTTGTTCTTCGGGCATTAATTCGTCAA

10 **Table.S1.** Primer sets used in the transgenic overexpression. The underlined sequence is *BamH* I
11 restriction site, *Not* I restriction site and Myc tag sequence.

12

Gene	5'-3'
BmJHBPd2-F	TAGAAAAGGCTGTGTTTCGC
BmJHBPd2-R	ATGAGTGATCCGCAGATTT
BmfibH-F	TCTGTGTCATCTGCTTCATCTCG
BmfibH-R	TATCCAGGACGAAGTAAGAAACAA
BmfibL-F	ATACCGATTGGTCACATAACAG
BmfibL-R	GCAGATAGATGGGCGATAA
BmP25-F	AGCCGCTGTGGCAGTTTTG
BmP25-R	TAGGTGGCGTTGAAGTATGG
BmKr-h1-F	CTTCCTCCTACTCCACCT
BmKr-h1-R	GGCAACGAAATGTAATGT
BmMet1-F	AATCTTGCCACCAACAGC
BmMet1-R	ACCCAACGCACATCTTCT

BmMet2-F	<u>CCGAACCAACGCAGTATGTAA</u>
BmMet2-R	<u>ACGCACGACGCCAATGA</u>
BmSRC-F	<u>TCAAACGAGTCAAATAGGGTCA</u>
BmSRC-R	<u>GCGGTCGGTGGTAGGGTT</u>
Bmjhe-F	<u>ACAGATTGGCGGTTTTCGGA</u>
Bmjhe-R	<u>CCCTTAGCGGCATCAGACAT</u>
Bmjheh-F	<u>GGACTCTTCGGGTTAGTGATAA</u>
Bmjheh-R	<u>TGTGGTATTTCGTGCATTCC</u>
Bmdimm-F	<u>CGTGGAACCCGCATTTGTA</u>
Bmdimm-R	<u>AACCTCGGCAATCCAGTCG</u>
Bmsage-F	<u>AGCAATCACGAAGGTCCGC</u>
Bmsage-R	<u>CGTATCGTGGTTGGAGTCGT</u>
Bmsgf-1-F	<u>ATCCGACATTCGCTGTCCTT</u>
Bmsgf-1-R	<u>TGACGTCGCAAGAAACAACC</u>
BmEcR-F	<u>GCTGGTCTGATAACGGTGGCT</u>
BmEcR-R	<u>CAAGGATTCCGGCGACATAAC</u>
BmHR3-F	<u>TCAACGAGAAGACACCACGG</u>
BmHR3-R	<u>AGAAACATCCTGGGGCTTGC</u>
BmE75A-F	<u>GAAATTCCGCGCTATGAGGC</u>
BmE75A-R	<u>TTTTAGCGAGCACCGAATGC</u>
BmE74A-F	<u>AGCAGTCAACTGCAAGGGTA</u>
BmE74A-R	<u>GTGCCCGATCTAAGGAGTTG</u>
BmUSP-F	<u>AGAAGTGGACGTTCTTCGAG</u>
BmUSP-R	<u>GGTGGAACAGGTAGAGGTGC</u>
BmBrc-F	<u>TCGCTGACAAACACGCTG</u>
BmBrc-R	<u>ATGGTAAGAACGGCGGAC</u>

BmRPL3-2-F	TTCGTACTGGCTCTTCTCGT
BmRPL3-2-R	CAAAGTTGATAGCAATTCCCT

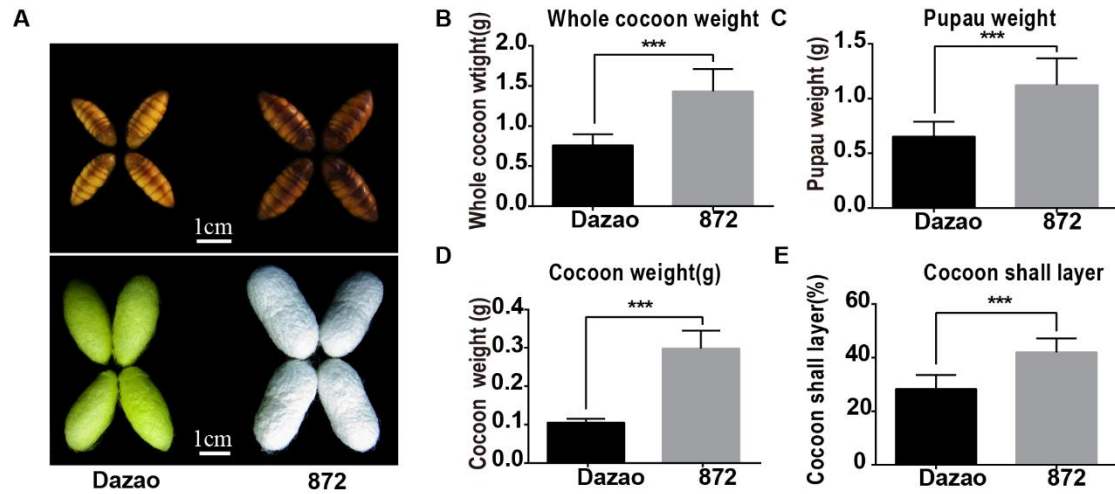13 **Table.S2**. Primer sets used in qRT-PCR.

14

15

16

17 **Figure S1**. Main economic characters of different silk-producing strain. A. Pupaus and cocoons of *Dazao*

18 and *S872*. B. Cocoon weight from *Dazao* and *S872*. C. Pupau weight from *Dazao* and *S872*. D. Cocoon

19 shell weight from *Dazao* and *S872*. D. Cocoon shell percentage from *Dazao* and *S872*. Data are means ±
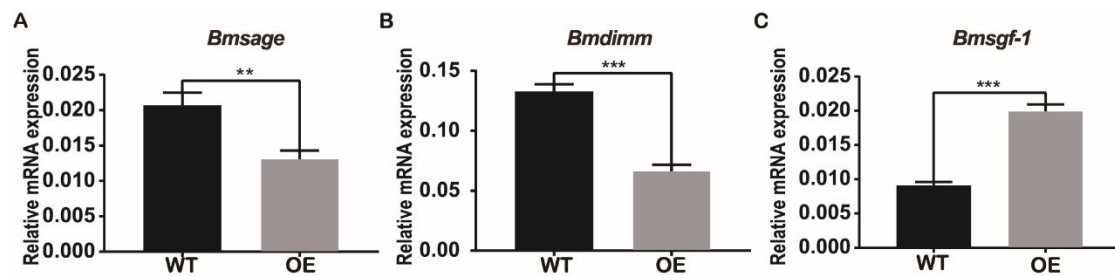
20 SD. ***$P < 0.001$.

21

22 **Figure S2**. Expression of silk protein transcription factor in wild type and transgenic lines. *BmRpl3*

23 expression was used as a control. Results are expressed as means S.D. of three independent experiments.

24 * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.
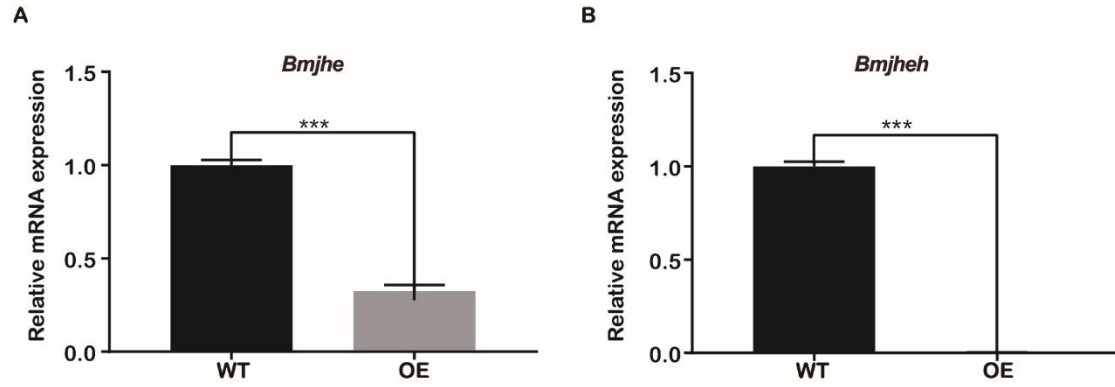
25

26

Figure S3. Overexpression of *BmJHBPd2* results in inhibition of JH catabolic enzyme in silk gland. The following JH catabolic enzyme related genes were selected: JHE(A) and JHEH(B). *BmRpl3* expression is shown as a control. Results are expressed as means S.D. of three independent experiments. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.