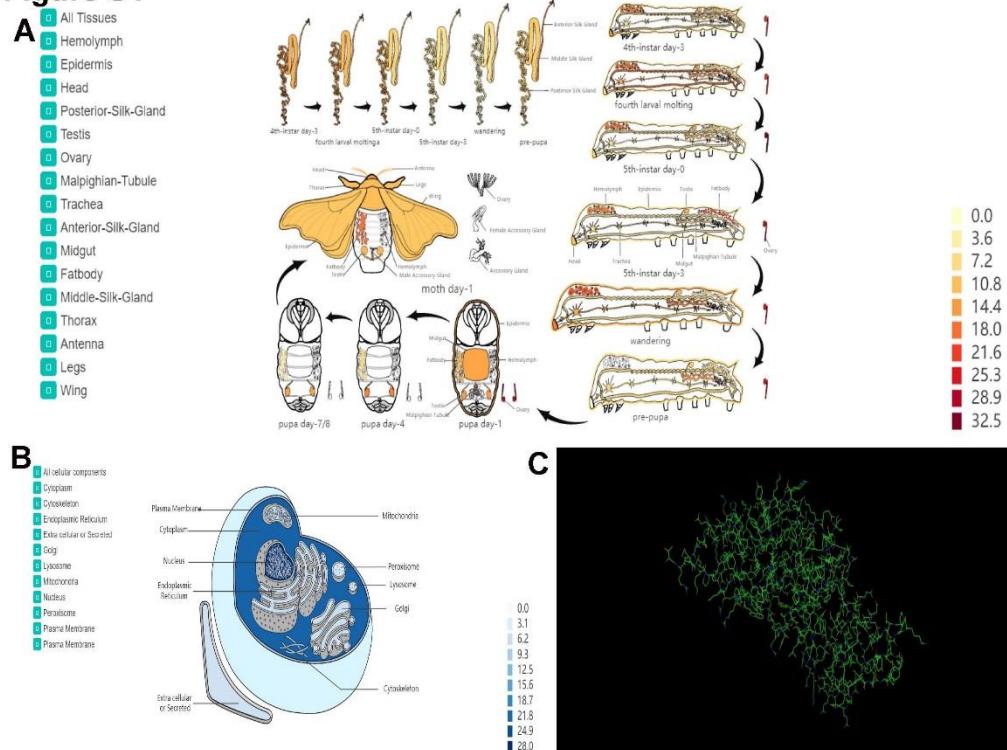


1 **Supplementary Materials:**2 **Figure S1:** Bioinformatics analysis of *BmTip60* in silkdatabase3.0.**Figure S1**

3

4 **Supplementary Figure S1.** Bioinformatics analysis of *BmTip60* in silkdatabase3.0. **(A)** The
5 expression values of *BmTip60* in 17 tissues at different growing stages (instar, larval, wandering,
6 pupa, and moth) is indicated by different colors. Light yellow: expression value is 0, deep red:
7 the highest expression value. **(B)** The predicted subcellular localization of *BmTip60*. **(C)** 3D model
8 of molecular structure of *BmTip60* protein, red color: α -helix, green color: β -sheet, and dark blue
9 color: random coil.

10 **Table S1: GeneIDs used in phylogenetic tree study****Table S1. GeneIDs used in phylogenetic tree**

Species	GeneID
<i>Acyrthosiphon pisum</i>	XP_008181995.1
<i>Aedes aegypti</i>	XP_021706851.1
<i>Amyelois transitella</i>	XP_013194528.1
<i>Apis dorsata</i>	XP_006618580.1
<i>Bemisia tabaci</i>	XP_018900801.1
<i>Bicyclus anynana</i>	XP_023947155.1

<i>Bombyx mori</i>	XP_004928298.1
<i>Caenorhabditis elegans</i>	NP_504796.1
<i>Ceratitis capitata</i>	XP_004530447.1
<i>Culex quinquefasciatus</i>	XP_001842875.1
<i>Drosophila melanogaster</i>	NP_001259234.1
<i>Fopius arisanus</i>	XP_011302800.1
<i>Helicoverpa armigera</i>	XP_021201592.1
<i>Homo sapiens</i>	NP_874369.1
<i>Leptinotarsa decemlineata</i>	XP_023025142.1
<i>Mus musculus</i>	NP_848752.1
<i>Ostrinia furnacalis</i>	XP_028156455.1
<i>Papilio polytes</i>	XP_013139927.1
<i>Papilio xuthus</i>	XP_013173093.1
<i>Plutella xylostella</i>	XP_011547865.1
<i>Saccharomyces cerevisiae</i>	EDZ69167.1
<i>Spodoptera litura</i>	XP_022826725.1
<i>Trichoplusia ni</i>	XP_026731014.1

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2

3 **Table S2:** The primers used in this study

4

Table S2. Primers used for vector construction

Primer name	Primer sequences ¹ (5' to 3')
<i>BmTip60-F</i>	CATGCC <u>ATGGCAATGAA</u> CGAAA <u>ATGATGATGAATTGACAAC</u> A
<i>BmTip60-R</i>	<u>CGGGGTACCTCACGTAGAATCGAGACCGAGGGAGAGGGTTAGGGATAGG</u> CTTACCCCATT <u>TCGCCCGTTAGACCAATCTT</u>
<i>BmAtg8-F</i>	<u>GGAAGATCTGAAATTCCAATACAAAGAAG</u>
<i>BmAtg8-R</i>	<u>CGGGGTACCTTAATTCCATAGACATTTCGTC</u>

5

6 ¹Sequences in underlined represent enzyme cutting sites. CCATGG indicated Nco I enzyme site, GGTACC indicated Kpn I enzyme site, AGATCT indicated Bgl II enzyme site.