

Figure S1. Evaluation of the specificity and amplification efficiency of the primer pairs. The specificity and efficiency of primer sets was determined by melting curve and standard analysis, respectively, and the length of qPCR products was visualized by agarose gel electrophoresis.

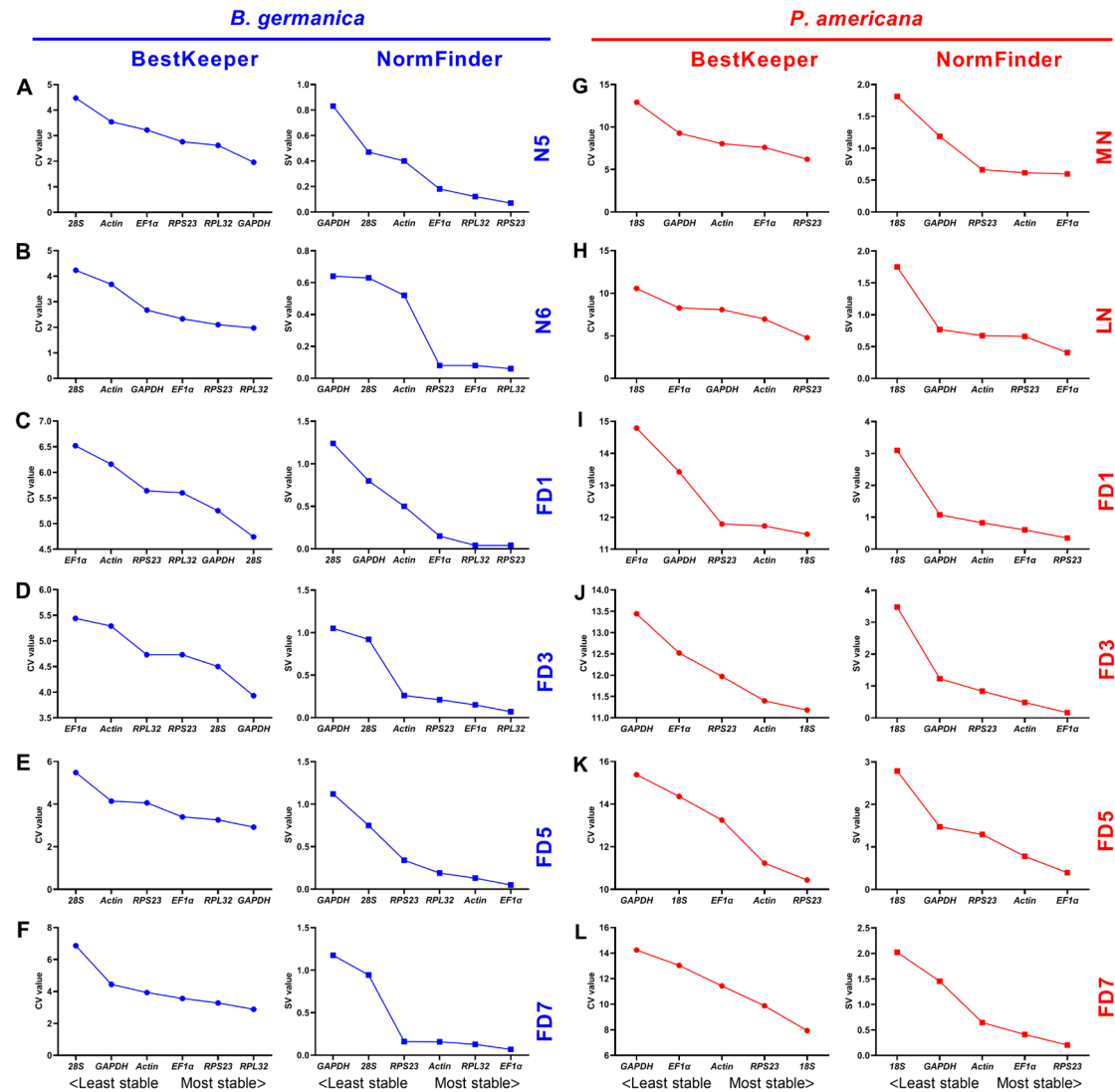


Figure S3. Expression stability rankings of candidate reference genes across various tissues at given developmental stages. The CV and SV values were calculated by BestKeeper and NormFinder algorithm, respectively, for candidate reference genes across various tissue types at the developmental stages of nymphs N5 (**A**) and N6 (**B**), and adults FD1 (**C**), FD3 (**D**), FD5 (**E**), and FD7 (**F**) in *B. germanica*. In *P. americana*, gene expression stability was calculated at the developmental stages of nymphs MN (**G**) and LN (**H**), and also adults FD1 (**I**), FD3 (**J**), FD5 (**K**), and FD7 (**L**).

Table S1. Primers used for evaluation of candidate reference genes in *B. germanica*.

Gene name	Primer sequences (forward and reverse)	Length of product (bp)	Amplification efficiency (%)	R ² of standard curve
<i>GAPDH</i>	F: CTGTTCCCAATGTGTCTGTT R: CTGCCTTACCTTTGCCTTA	87	95.49	0.998
<i>EF1α</i>	F: TGGAACTACTCCGACAAGAT R: TCAATGAGACACTTGCCTTC	85	95.38	0.999
<i>Actin5c</i>	F: TGAGACCACATACTCACTCCA R: CAATTCCAGGGTACATGGTG	104	92.37	0.998
<i>RPL32</i>	F: CAATCATGGAGAAAAGCCCAA R: TTCCTGTTGCTTCCATAACC	98	97.82	0.999
<i>RPS23</i>	F: AAACAGCCAAACAGTGCTAT R: CAATGTAGTTCAGGCAACCA	106	91.43	0.997
<i>28S</i>	F: ATCGTCAGAGCTGGGTATAG R: TATCCTGAGGGAACTTCGG	80	94.82	0.999

Table S2. Primers used for evaluation of candidate reference genes in *P. americana*.

Gene name	Primer sequences (forward and reverse)	Length of product (bp)	Amplification Efficiency (%)	R ² of standard curve
<i>GAPDH</i>	F: GGCCAGAATATCATACCAGC R: CGGAATGCCATACCAGTTAG	95	97.56	0.999
<i>EF1α</i>	F: AAGGAAGGAAAAGCTGATGG R: AGACGAAGAGGTTTCTCAGT	89	98.35	0.999
<i>Actin</i>	F: GCGATTTGACAGACTACCTC R: CTCCTTAATGTCACGCACAA	95	94.08	0.999
<i>RPS23</i>	F: TTCGGAAGTGTGTGAGAGTA R: CCACCAGGACTTCATCATTC	111	86.97	1.0
<i>18S</i>	F: AATGGAATAGGACCTCGGTT R: AATTTCACCTCTAACGTCGC	87	86.98	0.998