

Fig. S1. Expression stability values for seven reference genes calculated by geNorm software among different treatments

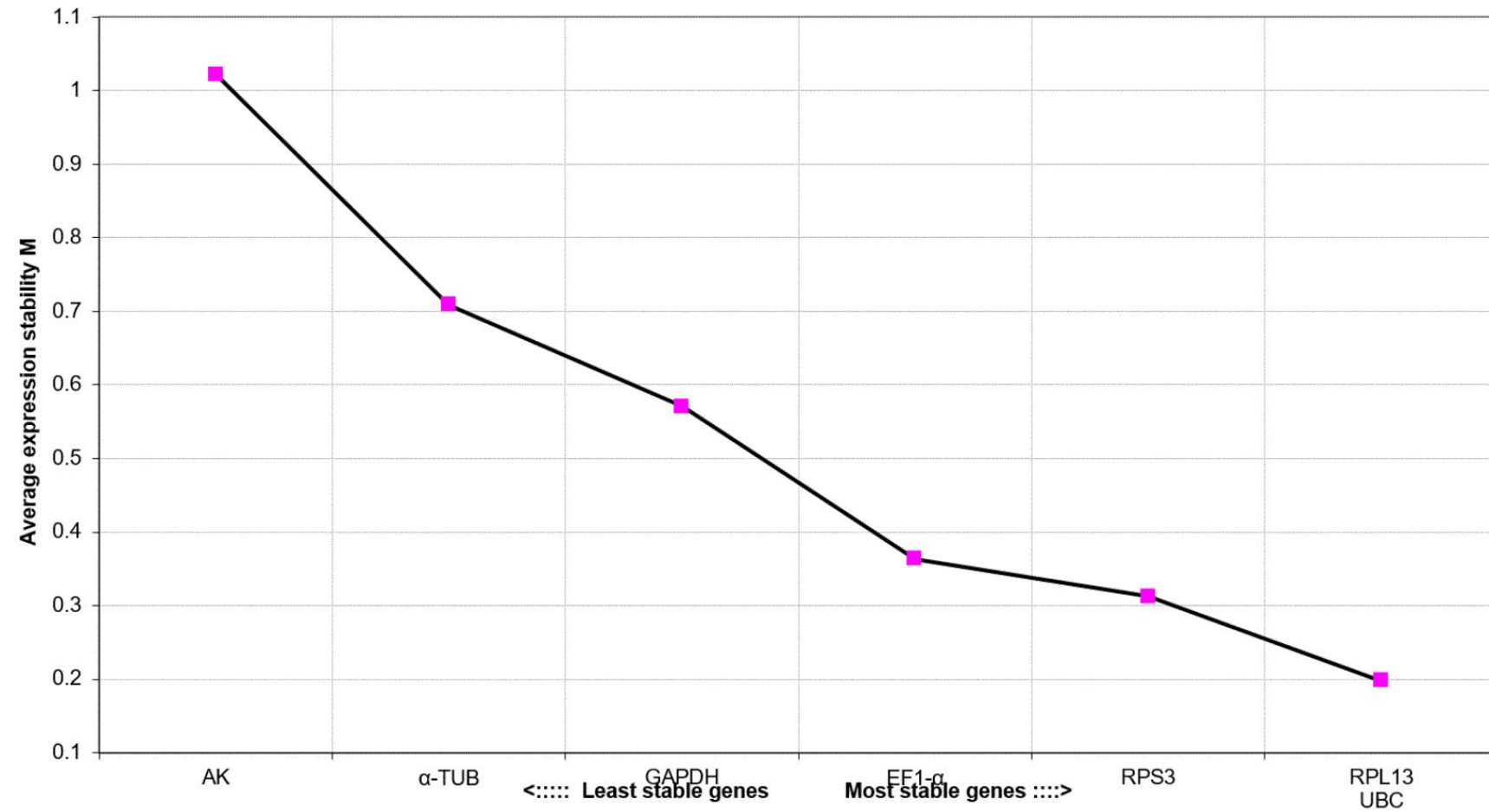


Fig. S2. Pairwise variation (V_n $n + 1$) between normalization factors after stepwise inclusion of stable reference genes from the most stably expressed genes

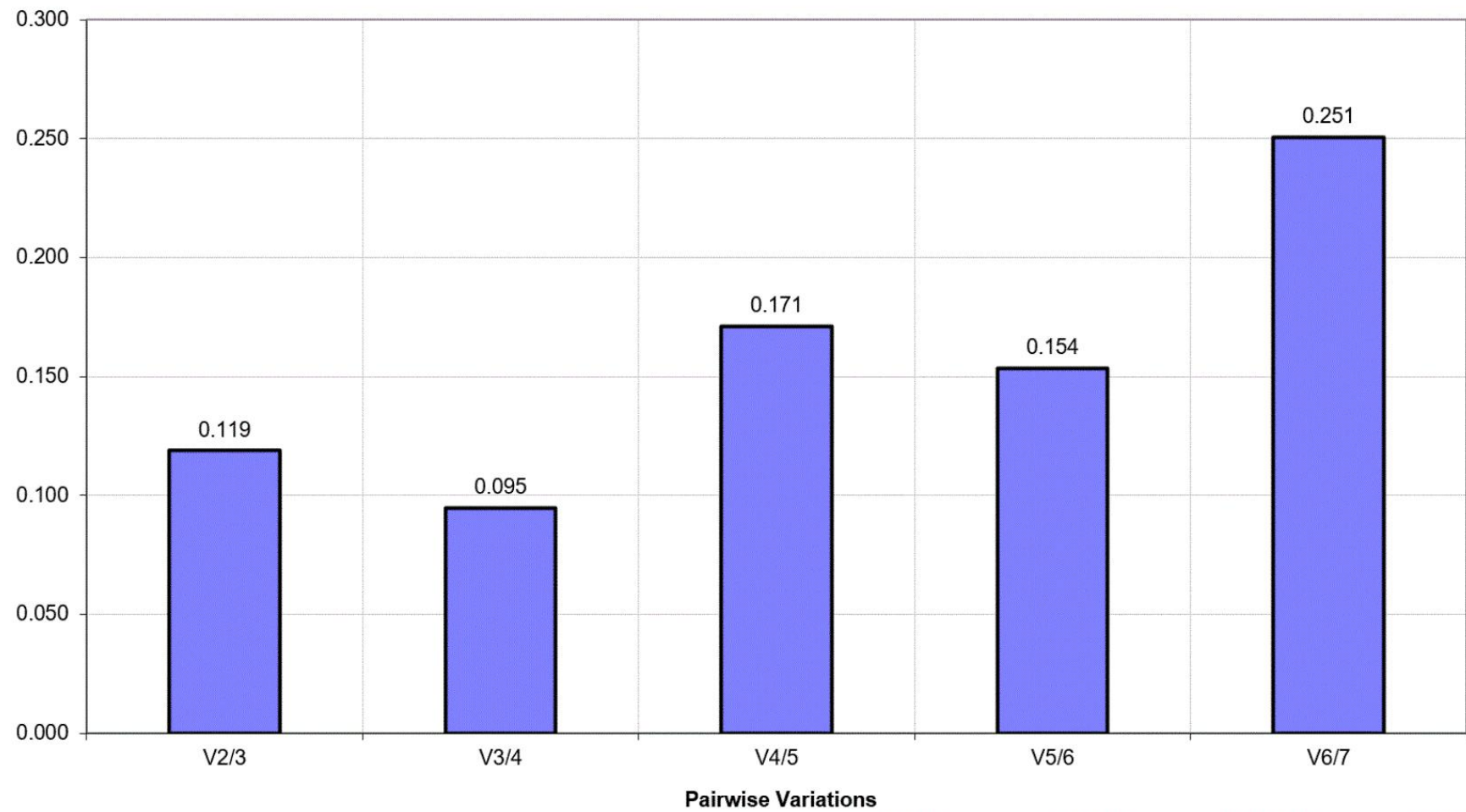


Fig. S3. The ranking order of the expression stability value of candidate reference genes in different tissues of *S. bifasciatus* calculated by NormFinder

Gene name	Stability value	Best gene	UBC
α -TUB	0.713		
GAPDH	0.416		
RPL13	0.192		
RPS3	0.311		
UBC	0.069		
EF1- α	0.241		
AK	1.206		

NormFinder

Getting Started

Select input data: Sheet1!\$A\$13:\$I\$20

Data selected

☒ Sample names (first row) included

☒ Gene names (first column) included

☐ Group identifier (last row) included

☒ Log transform data
(natural base (e) logarithm)

☒ Simple output only

Go

Exit