$S4\ Table.\ Grafted\ watermelon\ reference\ genes\ ranked\ according\ to\ their\ expression\ stability\ as\ determined\ by\ geNorm\ in\ different\ sample\ sets.$

Scion samples under N, P starvation	Stability value (M)	Squash rootstock samples under N, P starvation	Stability value (M)	Bottle gourd rootstocks samples under N, P starvation	Stability value (M)	All scion and rootstocks under normal growth conditions	Stability value (M)
Cla-miR167c*	0.371	Cmo-miR167c*	0.118	Lsi-miR166b*	0.290	miR167c	0.747
Cla-miR167f*	0.371	Cmo-miR167f*	0.118	Lsi-U6*	0.290	miR166b	0.747
Cla-18S*	0.582	Cmo-miR166b	0.251	LsPP2A	0.399	miR167f	1.053
CLYLS8*	0.740	Cmo-miR167b	0.360	Lsi-miR167f	0.468	U6	1.437
Cla-miR82	0.776	Cmo-18S	0.473	Lsi-18S	0.502	18S	1.791
Cla-miR81	0.819	CmYLS8	0.525	Lsi-miR166u	0.528		
Cla-miR170	0.866	Cmo-miR319b	0.554	Lsi-miR167c	0.568		
Cla-U6	0.916	Cmo-U6	0.615	Lsi-miR398b	0.605		
Cla-miR169n-5p	0.969	CmPP2A	0.664				
Cla-miR166b	1.045	Cmo-miR160a	0.717				
		Cmo-miR3511-3p	0.786				

[&]quot;*": represents the optimal reference genes determined by pairwise variation analyses which are presented in Fig 3. The recommended threshold of 0.15 is adopted.