

Table 1 Suppl. Fragments per kilobase per million reads (FPKM) and fold changes of nine candidate reference genes. IB - inner petals of flowers at tight bud stage, OB - outer petals of flowers at the tight bud stage, IF - inner petals of flowers at the initial flowering stage, OF - outer petals of flowers at the initial flowering stage.

Gene name	Expression (FPKM)		IF	OF	Fold change		IF/OF	IB/OB	IF/OB	IB/OF
	IB	OB			IF/IB	OF/OB				
<i>ScACT1</i>	7.26	7.03	6.89	8.12	0.95	1.15	0.85	1.03	0.98	0.89
<i>ScACT2</i>	149.02	123.08	141.57	137.61	0.95	1.12	1.03	1.21	1.15	1.08
<i>ScEF</i>	121.94	110.80	95.54	106.44	0.78	0.96	0.90	1.10	0.86	1.15
<i>ScEIF</i>	128.25	123.17	101.25	105.40	0.79	0.86	0.96	1.04	0.82	1.22
<i>ScPGK</i>	29.47	25.14	33.14	33.47	1.12	1.33	0.99	1.17	1.32	0.88
<i>ScPP2A</i>	14.27	12.25	15.18	11.27	1.06	0.92	1.35	1.16	1.24	1.27
<i>ScRPL</i>	10.67	9.50	10.59	8.89	0.99	0.94	1.19	1.12	1.11	1.20
<i>ScTUB</i>	1.94	2.08	1.73	1.56	0.89	0.75	1.11	0.94	0.83	1.25
<i>ScUBC</i>	53.56	42.39	47.75	42.88	0.89	1.01	1.11	1.26	1.13	1.25

Table 2 Suppl. Reference gene primer information and amplicon characteristics.

Gene name	Primer sequence (5'-3')	Amplicon length [bp]	Amplification efficiency [%]	Regression coefficient (R ²)
<i>ScACT1</i>	F: CACGAGACCACATACAATTCCA R: TGATCCACCACTTAGCACAATG	87	100.8	0.9983
<i>ScACT2</i>	F: AGCATCCTGTTCTCCTTACTGA R: TGACACCATCACCAGAATCCA	180	97.7	0.9987
<i>ScEF</i>	F: ACCTGTCACATTGCTGTAAAGT R: TGGCTTGGTCGGAATCATCT	135	96.2	0.9997
<i>ScEIF</i>	F: ACTGGCTGACCGACAAGAT R: AACCTGCTGGACATCAATACC	167	97.4	0.9975
<i>ScPGK</i>	F: GAGTGTTGGCGATCTGTCTG R: TGTCGTCGGTGATGTTCTGA	104	99.2	0.9982
<i>ScPP2A</i>	F: GGATCGGTCGCTGTCTCAA R: CAATGGTTCCTCGTGTTCTTCT	157	95.4	0.9995
<i>ScRPL</i>	F: TCTGCCGAAGAGTGAATCTCA R: CCAACGCCTGAACATCAAGT	107	99.2	0.9985
<i>ScTUB</i>	F: CCGATGAGTGTATGGTTCTTGAC R: GGTGGCAGAGATGAGGTGATT	110	101.0	0.9992
<i>ScUBC</i>	F: TGACAGTGGACAAGAAGAAGATG R: CATTCCGAGATTGAGATTGAGATTC	153	99.3	0.9993

Table 3 Suppl. The expression stability rank of nine candidate reference genes generated by *geNorm*. M value - gene expression stability measure.

Rank	Total gene name	M value	Petals gene name	M value	Tissues gene name	M value
1	<i>ScEF</i> , <i>ScRPL</i>	0.534	<i>ScRPL</i> , <i>ScPP2A</i>	0.433	<i>ScEF</i> , <i>ScRPL</i>	0.543
3	<i>ScPP2A</i>	0.619	<i>ScEF</i>	0.457	<i>ScPP2A</i>	0.609
4	<i>ScTUB</i>	0.664	<i>ScEIF</i>	0.496	<i>ScTUB</i>	0.671
5	<i>ScACT1</i>	0.747	<i>ScACT1</i>	0.526	<i>ScUBC</i>	0.736
6	<i>ScUBC</i>	0.803	<i>ScTUB</i>	0.572	<i>ScACT1</i>	0.817
7	<i>ScACT2</i>	0.843	<i>ScACT2</i>	0.622	<i>ScACT2</i>	0.902
8	<i>ScEIF</i>	0.951	<i>ScUBC</i>	0.678	<i>ScEIF</i>	1.074
9	<i>ScPGK</i>	1.137	<i>ScPGK</i>	0.878	<i>ScPGK</i>	1.313

Table 4 Suppl. The expression stability rank of nine candidate reference genes generated by *NormFinder*.

Rank	Total gene name	stability value	Petals gene name	stability value	Tissues gene name	stability value
1	<i>ScEF</i>	0.225	<i>ScEF</i>	0.218	<i>ScEF</i>	0.234
2	<i>ScRPL</i>	0.287	<i>ScTUB</i>	0.227	<i>ScRPL</i>	0.305
3	<i>ScTUB</i>	0.354	<i>ScPP2A</i>	0.263	<i>ScPP2A</i>	0.319
4	<i>ScPP2A</i>	0.413	<i>ScRPL</i>	0.282	<i>ScTUB</i>	0.403
5	<i>ScUBC</i>	0.521	<i>ScEIF</i>	0.320	<i>ScUBC</i>	0.463
6	<i>ScACT1</i>	0.523	<i>ScACT1</i>	0.366	<i>ScACT1</i>	0.627
7	<i>ScACT2</i>	0.530	<i>ScACT2</i>	0.461	<i>ScACT2</i>	0.697
8	<i>ScEIF</i>	0.768	<i>ScUBC</i>	0.484	<i>ScEIF</i>	0.978
9	<i>ScPGK</i>	1.152	<i>ScPGK</i>	1.047	<i>ScPGK</i>	1.393

Table 5 Suppl. Overall stability of candidate reference genes according to the two evaluation algorithms.

Rank	Total gene name	overall ranking	Petals gene name	overall ranking	Tissues gene name	overall ranking
1	<i>ScEF</i>	1	<i>ScEF</i> , <i>ScPP2A</i>	2	<i>ScEF</i>	1
2	<i>ScRPL</i>	1.5	-	-	<i>ScRPL</i>	1.5
3	<i>ScPP2A</i> , <i>ScTUB</i>	3.5	<i>ScRPL</i>	2.5	<i>ScPP2A</i>	3
4	-	-	<i>ScTUB</i>	4	<i>ScTUB</i>	4
5	<i>ScACT1</i> , <i>ScUBC</i>	5.5	<i>ScEIF</i>	4.5	<i>ScUBC</i>	5
6	-	-	<i>ScACT1</i>	5.5	<i>ScACT1</i>	6
7	<i>ScACT2</i>	7	<i>ScACT2</i>	7	<i>ScACT2</i>	7
8	<i>ScEIF</i>	8	<i>ScUBC</i>	8	<i>ScEIF</i>	8
9	<i>ScPGK</i>	9	<i>ScPGK</i>	9	<i>ScPGK</i>	9

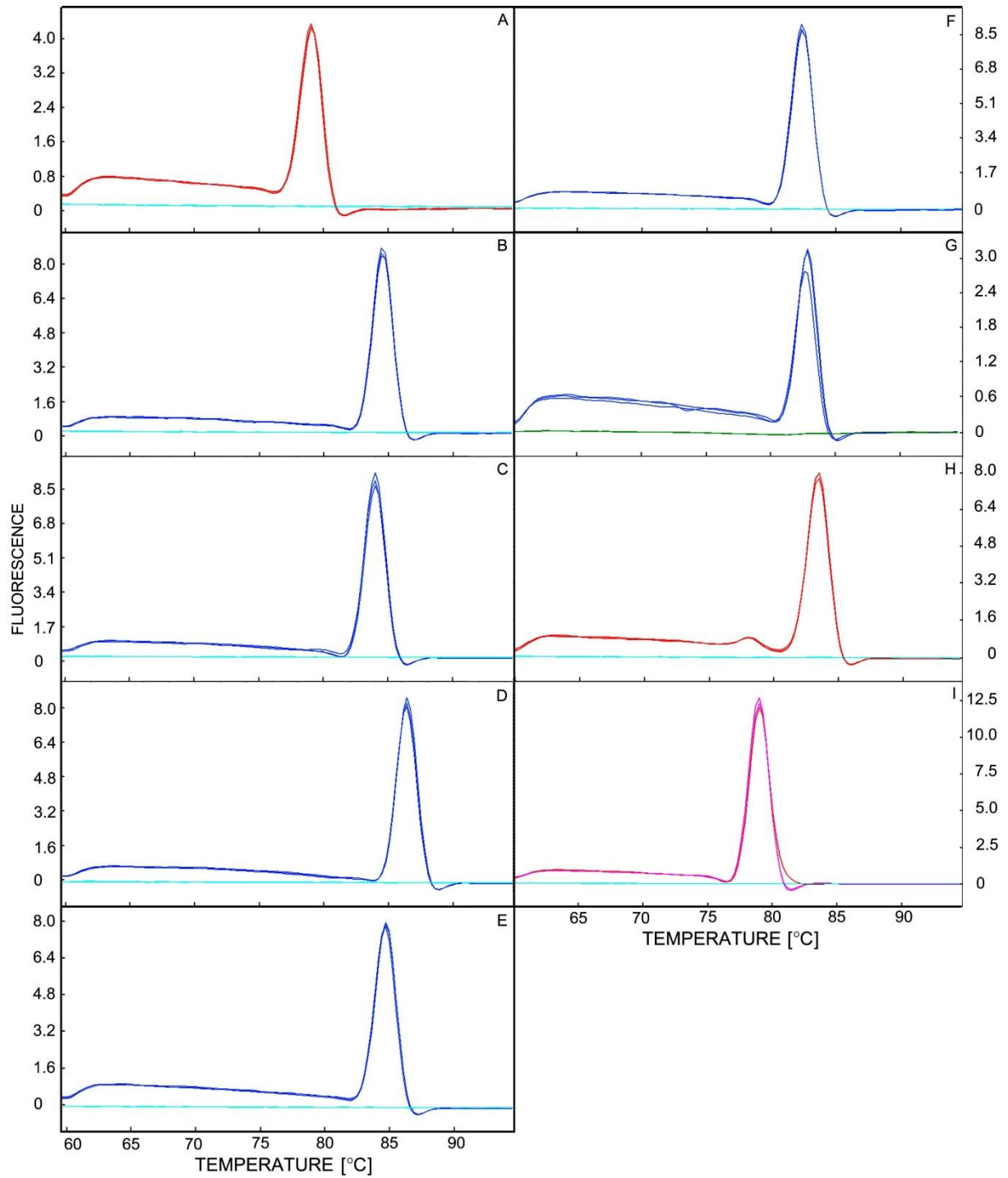


Fig. 1 Suppl. Melting curves of *Sinocalynthus chinensis* actin 1 (ScACT1) (A), ScACT2 (B), elongation factor 1-alpha (ScEF) (C), eukaryotic initiation factor (ScEIF) (D), phosphoglycerate kinase (ScPGK) (E), protein phosphatase 2a (ScPP2A) (F), 50S ribosomal protein L27 (ScRPL) (G), beta-tubulin (ScTUB) (H), and ubiquitin-conjugating enzyme (ScUBC) (I) with a single peak. There is no peak in the negative control.