Table S27. Stability analysis of the candidate reference genes during sweet pitaya fruit development. The values were calculated by the algorithms geNorm (M value), NormFinder (stability value), BestKeeper (standard deviation +/- crossing point value), the deltaCt method (average of standard deviation), and RefFinder (geometric mean of ranking values) from the cycle threshold (Ct) data. The lowest values indicate the most stable genes. The Ct data was recorded by qRT-PCR in a QIAquant 96 5 plex (QIAGEN) following the manufacturer's protocol. Abbreviations: Actin 7 (*StACT7*), alpha-tubulin (*StTUA*), elongation factor 1-alpha (*StEF1a*), COP1-interactive protein 1 (*StCIP1*), plasma membrane ATPase 4 (*StPMA4*), BEL1-like homeodomain protein 1 (*StBLH1*), polyubiquitin 3 (*StUBQ3*), and plastidic ATP/ADP-transporter (*StTLC1*). *S. thurberi* transcripts identified in this study were designated with the prefix "St" and the name of their best homologous match from other plant species.

Candidate reference gene	Algorithm				
	geNorm	NormFinder	BestKeeper	deltaCt method	RefFinder
StACT7	0.96	0.99	1.14	1.34	4.23
StTUA	0.74	0.51	0.75	1.10	1.68
StEF1a	0.74	0.45	0.87	1.07	1.32
StCIP1	1.23	1.06	1.06	1.41	6.09
StPMA4	1.16	1.01	1.49	1.35	6.16
StBLH1	1.31	1.27	1.49	1.54	7.74
StUBQ3	0.82	1.04	0.72	1.35	3.08
StTLC1	1.09	0.97	1.45	1.32	4.05