

Table S1. Primer used for quantitative real-time PCR analysis.

Name	Accession number	Forward primer (5'–3')	Reverse primer ((5'–3')
<i>Acactin</i>	HQ148720	CTGGCCTACGTGGCACTTGACTT	CACTTCTGGGCAGCGGAACCTTT
<i>AcCCR</i>	Aco015695.1	TTCCTCCATCCAAAGTTCCC	CCGACAGCCGCACAAGA
<i>AcCCR</i>	Aco026870.1	ACGCCGCAAACCAAGAT	TTTACGGTCCTCCTTCCACA
<i>AcCCR</i>	Aco005397.1	GATTTGGAAGCGAAAGCAGC	GCGGTCACGGGCATAGTT
<i>AcCAD</i>	Aco001032.1	TCGGGATGAAAGTTACGG	CATTTGCTCAGGGTTGC
<i>AcCOMT</i>	Aco000946.1	CTACATTCATTACCACGAGA	CGAAAGCTGGGATAGTT
<i>AcCOMT</i>	Aco000839.1	TTACAAGACAATCGCTACA	TAGGGATAGAGTTGATAGTAGA
<i>Ac4CL</i>	Aco019975.1	TCGTTCAGGGCTATGGTATG	GTTTCAAAGTCAAGGCGGTA
<i>AcLAC</i>	Aco015409.1	TTCGCTGGGTTGTTGGC	TCGTCCGTTTACTGCTGTGAT
<i>AcPOD</i>	Aco002506.1	AAGGGTGAAGGCTAAAGTGG	GCATTGGGTGATGGCAGT
<i>AcPOD</i>	Aco008456.1	GGAGGAGGTTGAGCTATTTG	TGCTTTGGGACAGGTTTT
<i>AcF3H</i>	Aco027900.1	ATGGTGAAGGCAATGGGG	CGTTGGGGTCTTTGTGGC
<i>AcDFR</i>	Aco006769.1	GAGCACCAACGGTCAGAGT	AACAACAAGAGGTGGGATGA
<i>AcANR</i>	Aco010710.1	CAATCCTACGGTTGTGCG	CATCGAGCGGAGTCCAG
<i>AcGST</i>	Aco001260.1	ACGAGGACTTAGGCAACA	CAGGATGACCAGCGACT

Table S2. Summary of transcriptome data for pineapple fruit at YF, MF, and FMF stages.

Raw sequences and assembly statistics	
Raw reads (paired-end)	46284834 - 74558864
Clean reads (paired-end)	44474662 - 72092510
Retention rate	98.37% - 98.83%
Q20	98.11% - 98.29%
GC content percentage	50.41% - 53.45%
Rate of cleans reads pairs mapped to the reference genome	62.00% - 75.17%