

Supplementary Materials

Supplementary Table:

Table S1. qPT-PCR primer sequence

Gene names	Primer-Forward (5'-3')	Primer-Reverse (5'-3')
Apple-Actin	TACTCAGCTTTGGCAATCCACATC	TGACCGAATGAGCAAGGAAATTACT
MYB 36	TGGTCTGCTATTGCTGCTCG	AAGTTGTTCAATTTGATGGTGGTG
MYB 14	GTGATGGCGGGGTCTGTC	AGGAGTTGTTGCATAGTCATTCCG
PP2C 24	GCTGGTGAAGGAGGAAGTGG	GAAGCTCGCAACGGCAAT
PP2C 77	GCTCAGGCAGTTGCTGTTCC	CGACTTCCACTCCCCGTTT
PYL 4	GACCATCGGCTGACGAATA	TTCTTGGTGTTTGGCTTATCG

Table S2. Summary of sequences analysis in apple leaves.

Sample	Raw Reads	Clean reads	Error (%)	Q20 (%)	Q30 (%)	GC content (%)
CK-0h-1	56551670	55765992	0.03	97.80	93.74	47.29
CK-0h-2	63476580	62495076	0.03	97.79	93.70	46.99
CK-0h-3	52584046	51258588	0.03	97.66	93.41	46.69
T-6h-1	54624528	53054810	0.03	97.86	93.86	46.87
T-6h-2	54077702	52735586	0.03	97.79	93.68	46.53
T-6h-3	56790426	55589402	0.03	97.85	93.81	46.48
T-24h-1	48749844	47944806	0.03	97.77	93.63	47.07
T-24h-2	50242364	49077578	0.03	97.7	93.48	46.79
T-24h-3	54245702	53252994	0.03	97.64	93.32	46.91
Total	498267772	487903916				

Note: Q20: The percentage of bases with a Phred value > 20; Q30: The percentage of bases with a Phred value > 30. CK-0h、T-6h、T-24h means: Control , severe drought was treated at 6h and severe drought was treated at 24h.

Table S3. BLAST analysis of unigenes against reference reads.

Sample name	Clean reads	Total mapped	Multiple mapped
CK_0h_1	55765992	48180250 (86.4%)	4658993 (8.35%)
CK_0h_2	62495076	48180250 (86.4%)	4658993 (8.35%)
CK_0h_3	51258588	48180250 (86.4%)	4658993 (8.35%)
T_6h_1	53054810	45424099 (85.62%)	4478437 (8.44%)
T_6h_2	52735586	45424099 (85.62%)	4478437 (8.44%)
T_6h_3	55589402	45424099 (85.62%)	4478437 (8.44%)
T_24h_1	47944806	41170023 (85.87%)	4545496 (9.48%)
T_24h_2	49077578	41170023 (85.87%)	4545496 (9.48%)
T_24h_3	53252994	41170023 (85.87%)	4545496 (9.48%)