

Supplementary Methods

Determination of sorbitol content

Sorbitol contents were determined by gas chromatography-mass spectrometer (GC-MS) following the protocol described by Bartolozzi, *et al.* [1]. In detail, 0.3 g of phloem sap and leaf was dissolved in 1 ml of 80 % methanol. The mixture was incubated in a water bath at 70 °C for 30 min, followed by ultrasonic treatment for 45 min, and then centrifuged at 3000 rpm for 20 min. After centrifugation supernatant was collected in a 5 ml round bottom flask and the above-followed extraction was repeated twice. Afterwards, 0.1 ml of internal standard solution (2.5% methyl- α -D-glucose) was added and final volume was achieved by 80 % methanol. The solution was taken into a 10 ml Eppendorf tube and centrifugation at 12000rpm for 30 min, and 0.5 ml of supernatant was sampled into a 2 ml Eppendorf tube and evaporated at 60 °C for 2 h. The residue was dissolved in 0.8 ml of hydroxylamine hydrochloride solution in pyridine (20 mg/ml), incubated at 75 °C for 1 h, and then cooled to room temperature. Subsequently, 0.4 ml of hexamethyldisilazane and 0.2 ml of trimethylchlorosilane were added and the mixture was incubated at 70 °C for 2 h. The samples were then kept overnight at room temperature, followed by centrifugation at 12000 rpm for 30 min. The supernatant was then subjected to gas chromatography analysis using GC-MS Ultra-ITQ1100 autosampler (Thermo-Fisher, USA).

Reference

1. Bartolozzi, F.; Bertazza, G.; Bassi, D.; Cristoferi, G. Simultaneous determination of soluble sugars and organic acids as their trimethylsilyl derivatives in apricot fruits by gas-liquid chromatography. *Journal of chromatography A* **1997**, 758, 99-107.

Table S1 Comparison of nutrients concentration in bud samples (normal bud and wizened bud), and soil samples (orchard soil and normal range).

Nutrients	Bud		Soil	
	Normal bud	Wizened bud	Orchard Soil	Normal range
N (mg/kg)	10076.76±275.74	10027.47±117.79	64.46±7.80	45<
P (mg/kg)	1494.52±45.56	1297.12±148.88	32.34±4.80	20-75
K (mg/kg)	7082.73±160.38*	4271.43±239.13	221.81±23.10	50-300
Ca (mg/kg)	9705.66±117.31	9542.44±1425.10	1352.74±88.87	1000-2000
Mg (mg/kg)	2038.48±27.14*	1419.21±99.35	206.24±13.63•	60-180
S (mg/kg)	459.39±5.70	439.53±26.61	111.72±3.05	<240
Fe (mg/kg)	34.88±6.79	33.60±9.54	31.81±1.64	5-50
Mn (mg/kg)	57.00±3.81	58.58±1.13	35.53±6.57	8-50
B (mg/kg)	40.86±1.02*	20.93±1.37	0.19±0.02•	0.5-2
Cu (mg/kg)	29.42±1.55	29.64±0.93	3.60±0.66	1-12
Zn (mg/kg)	40.55±0.20	40.62±2.39	2.86±0.22	3-20

Values are means of three replicates ±SD. '*' in each table cell indicates significant differences between normal bud and wizened bud (*t*-test, $P<0.05$). '•' in each table cell indicates the nutrient concentration of soil is out of the normal range. C/N: the ratio of total carbon concentration and total nitrogen concentration.

Table S2 The gene names and corresponding gene IDs in this study, and primers designed for qRT-PCR validation.

Gene name	Gene ID	Primer sequence
<i>PpySDH</i>	Ppy07g2595.1-F	AGCCGCTTATTACTCACC
	Ppy07g2595.1-R	GCTTCCACAAATGCCTAC
<i>PpyPL18.1</i>	Ppy14g1420.1-F	ATCCACGGACTGAACATACA
	Ppy14g1420.1-R	CGCATCAATCAACCCATC
<i>PpyPG1</i>	Ppy02g2733.1-F	GATTCCCAGGCATTTACG
	Ppy02g2733.1-R	TTGGCTTCAGTTGATAGACC
<i>PpyPG2</i>	Ppy17g2590.1-F	ATTGCCCTGAGGTTCTTC
	Ppy17g2590.1-R	CCATCTGTATTGGACTTT
<i>PpyPL18.2</i>	Ppy06g1334.1-F	ATTTATGGGTCCACTGCG
	Ppy06g1334.1-R	GCTATTGATTGTAGGGTCTGC
<i>PpyWRKY24.1</i>	Ppy01g1216.1-F	CAGATTCCACCCGACATT
	Ppy01g1216.1-R	CCGCCTTCCTTCTATTCT
<i>PpyWRKY70</i>	Ppy01g1522.1-F	ACAGTAGCCTCGGACAAA
	Ppy01g1522.1-R	CTGAGATTCACAGGGATTAG
<i>PpyCUC1.1</i>	Ppy06g1884.1-F	CTGGTTGGGATGAAGAAA
	Ppy06g1884.1-R	CTGATGGGAGGATGTGGT
<i>PpyMYB67</i>	Ppy10g1108.1-F	CTCAGATAGCCAAGCATT
	Ppy10g1108.1-R	GAGAAGATTGTGGGTGTT
<i>PpyMYB39.2</i>	Ppy01g0320.1-F	ATACCCAACACCCACAAA
	Ppy01g0320.1-R	CACGGGAGGAGTCACAGA
<i>PpyMYB39.1</i>	Ppy15g2679.1-F	TCGGACAGACAATGAAAT
	Ppy15g2679.1-R	AGAGCTAGAACATGAGGC
<i>PpyHT4</i>	Ppy16g1297.1-F	GGCAAGTTGGAGGAAGGA
	Ppy16g1297.1-R	GCCGAGTAGAGGGAAAGCA
<i>PpyHT2</i>	Ppy16g1295.1-F	GATTGTTGAGGCAAGTCG
	Ppy16g1295.1-R	GCAGAGTAGAGGGAAAGCA
<i>PpyHT1</i>	Ppy13g1850.1-F	TCGGAGATTGCACCCACA
	Ppy13g1850.1-R	CAAACCCAGCGATAACCT
<i>PpyHT3</i>	Ppy16g1296.1-F	GCATCATACACAACCAGA
	Ppy16g1296.1-R	AAGTAAGAGCCTCCCAAT
<i>PpyPMEI3</i>	Ppy11g2629.1-F	TTCTCGTCGTCGCTGGTA
	Ppy11g2629.1-R	GCTTCTCGGGTCCTCTC
<i>PpyPMEI1</i>	Ppy13g1628.1-F	TTCTGGTGGCAATGGTAG
	Ppy13g1628.1-R	GTCTTCTTATAGTCGGTGGG
<i>PpyPMEI4</i>	Ppy16g1085.1-F	CTTCTGGTGGCGATGCTA
	Ppy16g1085.1-R	TCTTTCAAAGTGTCCGAGTT

<i>PpyPME12</i>	Ppy13g1629.1-F	ATCAACAATAAGCGTAGCC
	Ppy13g1629.1-R	CACTCCCTCCTTCACATAA
<i>PpyPME3</i>	Ppy09g1413.1-F	CAGACGGCACTGGAACT
	Ppy09g1413.1-R	CTCACCAACCGCAGCAAC
<i>PpyWRKY24.2</i>	Ppy07g1557.1-F	TGGCTCTGCTGGACTAT
	Ppy07g1557.1-R	TTCTTGACGGCTTCTGT
<i>PpyCUC1.2</i>	Ppy14g1928.1-F	TGGCTCTGCTGGACTAT
	Ppy14g1928.1-R	TTCTTGACGGCTTCTGT
<i>PpyMYB86</i>	Ppy14g1480.1-F	TATGATGAAACGGAGGA
	Ppy14g1480.1-R	TTGGTACGGTGGTATTGA
<i>PpyMYB36</i>	Ppy15g0537.1-F	CTTGGAGGGAGGTTAGT
	Ppy15g0537.1-R	AGTAGCGGCATAGGAAAT
ACTIN	PpyPP2A-F	CTCACGGTTGTGGCAACTC
	PpyPP2A-R	TATGACCACCTCCGCTTCCA

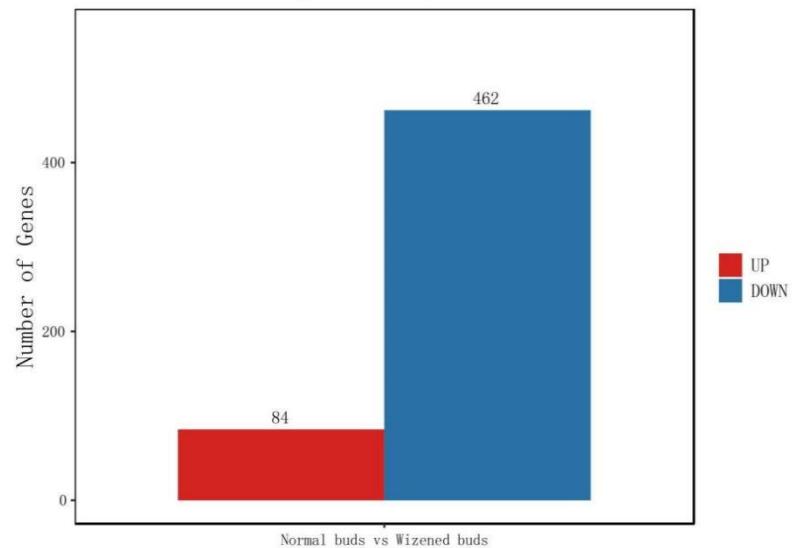


Figure S1 The number of differentially expressed genes in wizened buds compared with normal buds.