

Figure supplementary legends

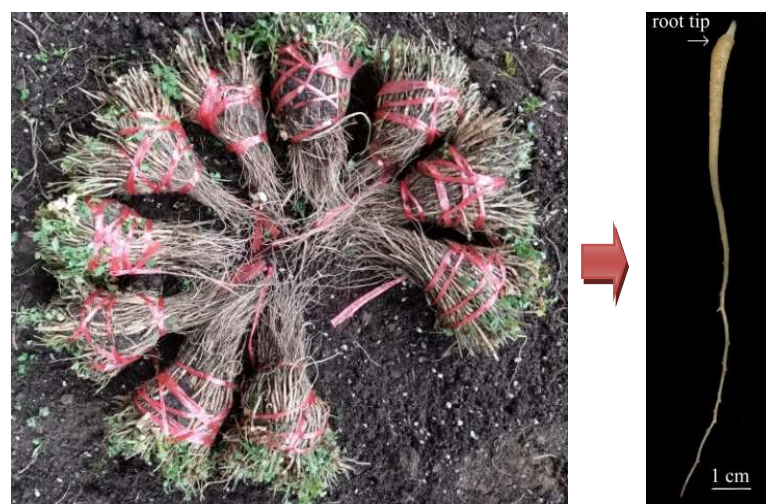


Figure S1. Morphological characteristic of *A. sinensis* seedlings.

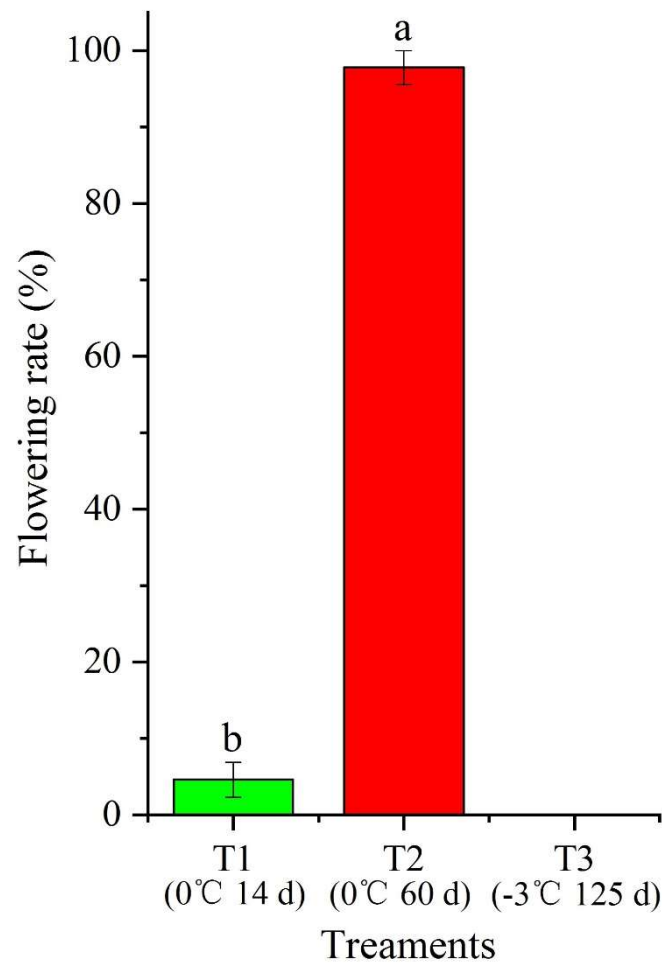


Figure S2. Flowering rate of *A. sinensis* after the seedlings stored at T1, T2 and T3. Different letters represent a significant difference ($p<0.05$) at different treatments.

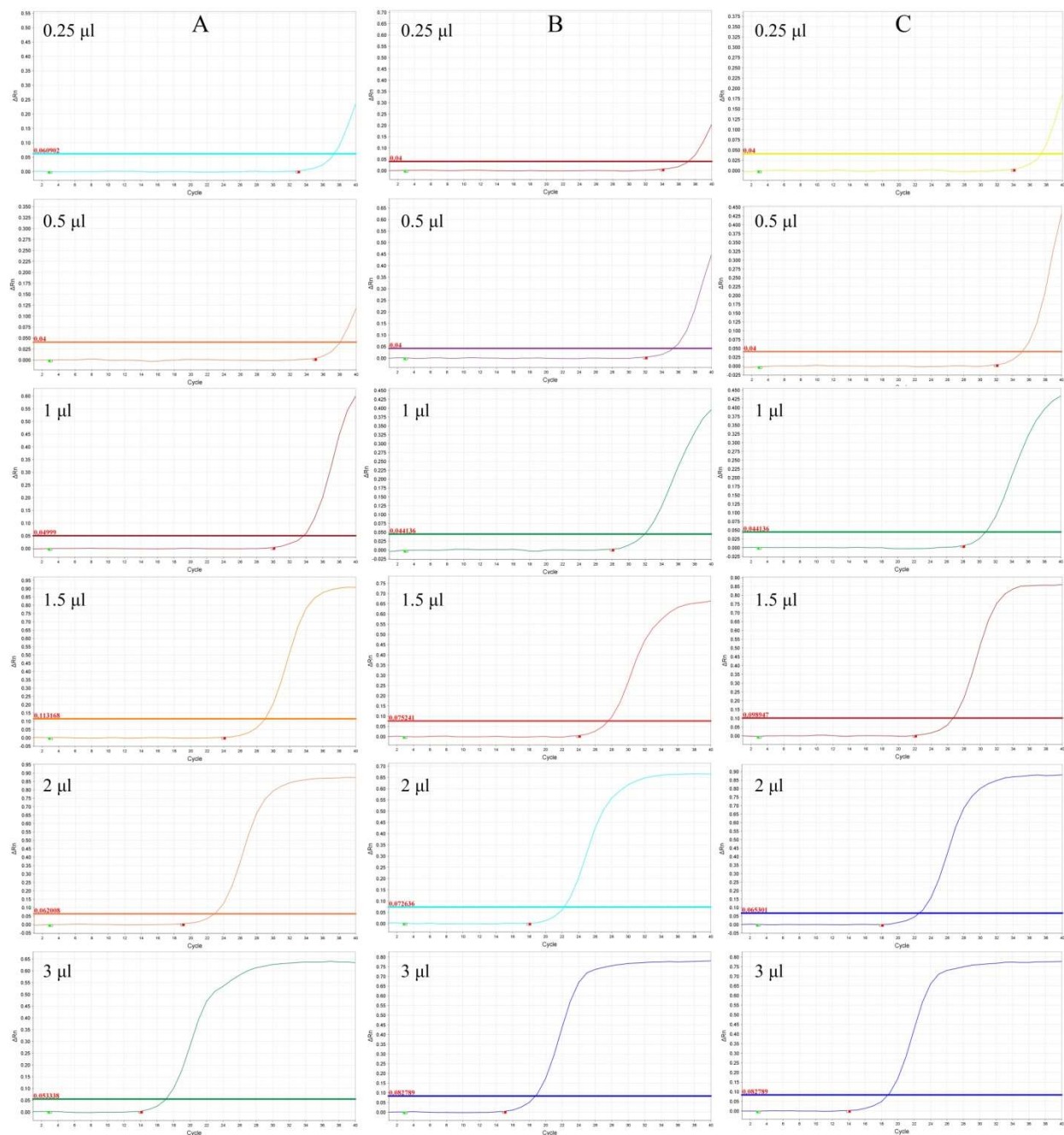


Figure S3. The cycle threshold (Ct) values of *ACT* gene at different volumes (0.25, 0.5, 1.0, 1.5, 2.0 and 3.0 µL) via PCR amplification with three replications.

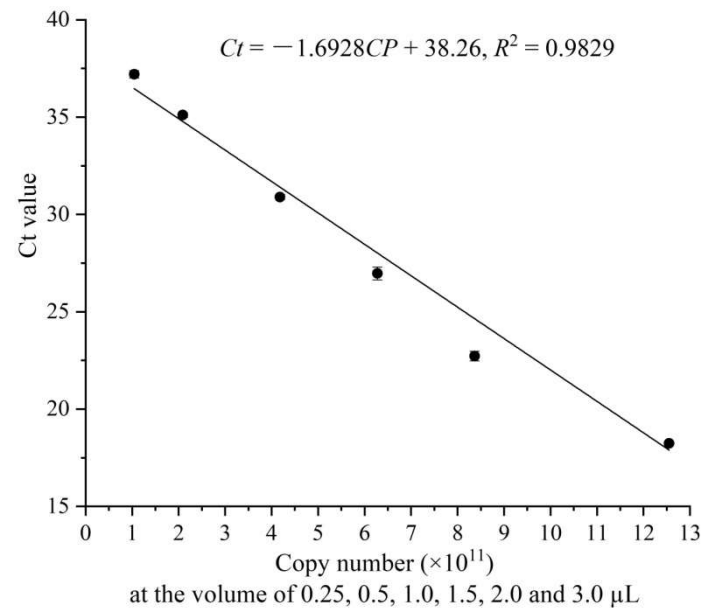


Figure S4. The standard curve of *ACT* gene.

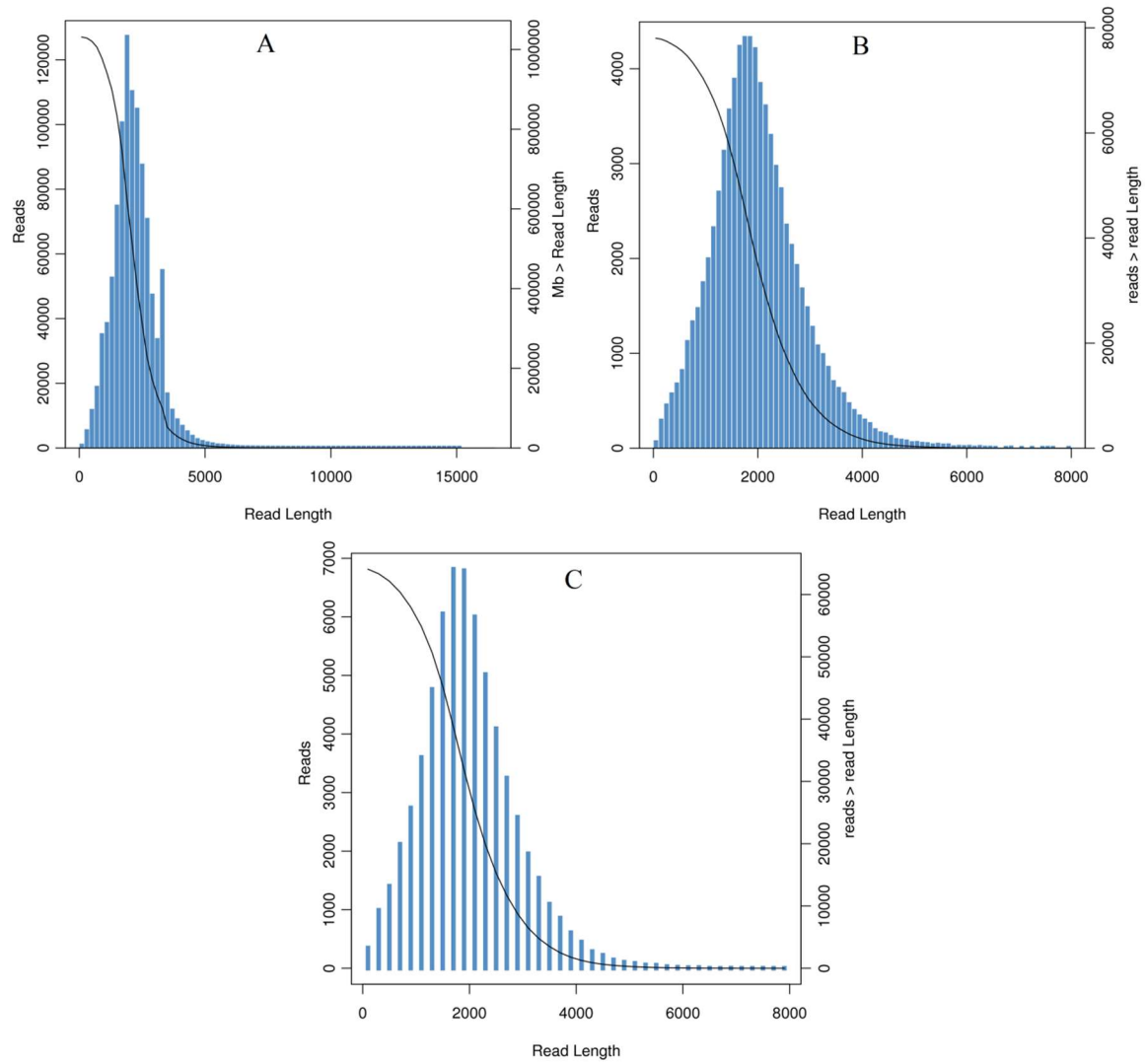


Figure S5. Number and length distribution of high-fidelity reads (A), polished high-quality isoforms (B) and full-length isoforms (C).

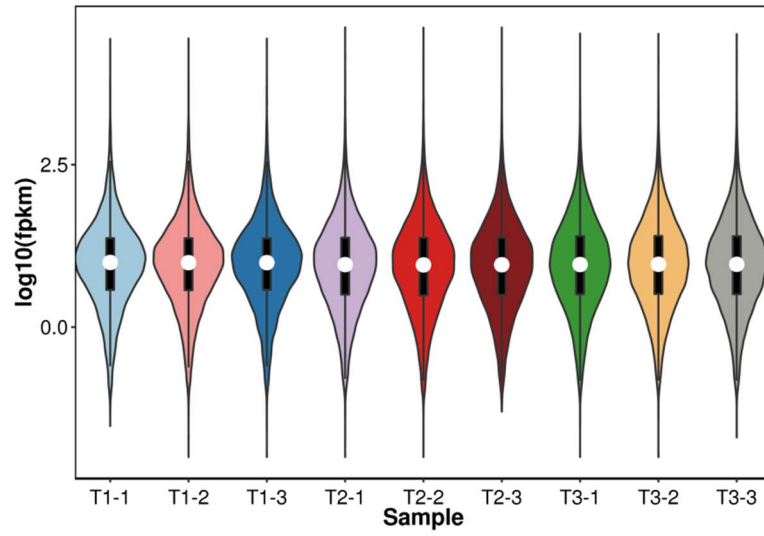


Figure S6. Violin plot of expression in T1, T2 and T3.

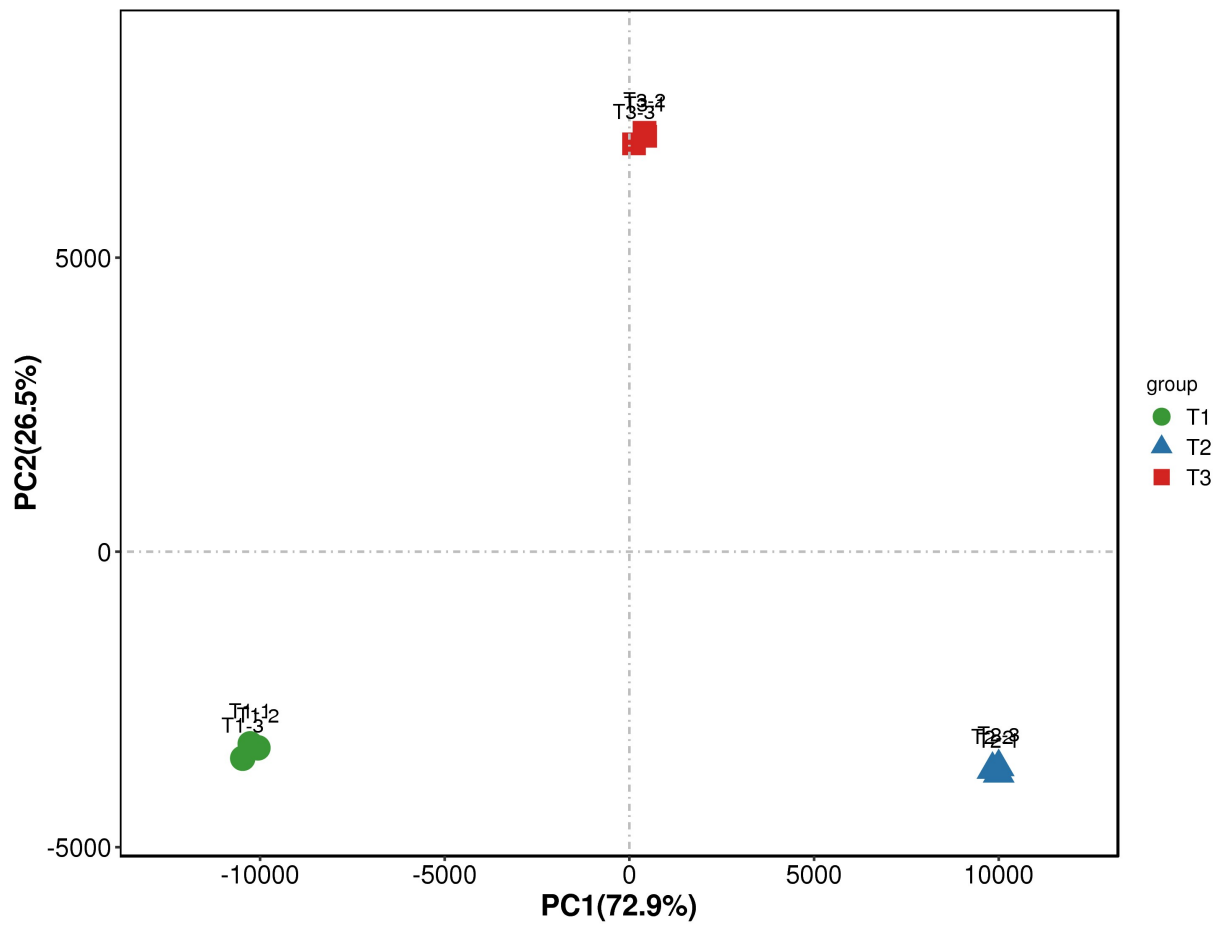


Figure S7. PCA analysis of T1, T2 and T3.

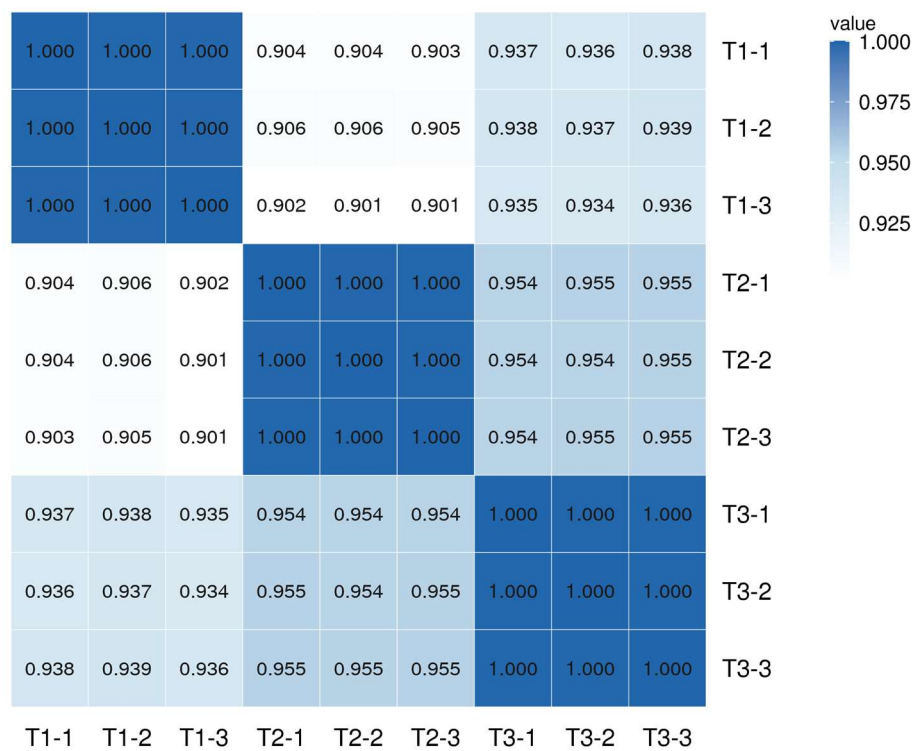


Figure S8. Pearson correlation analysis between T1, T2 and T3.

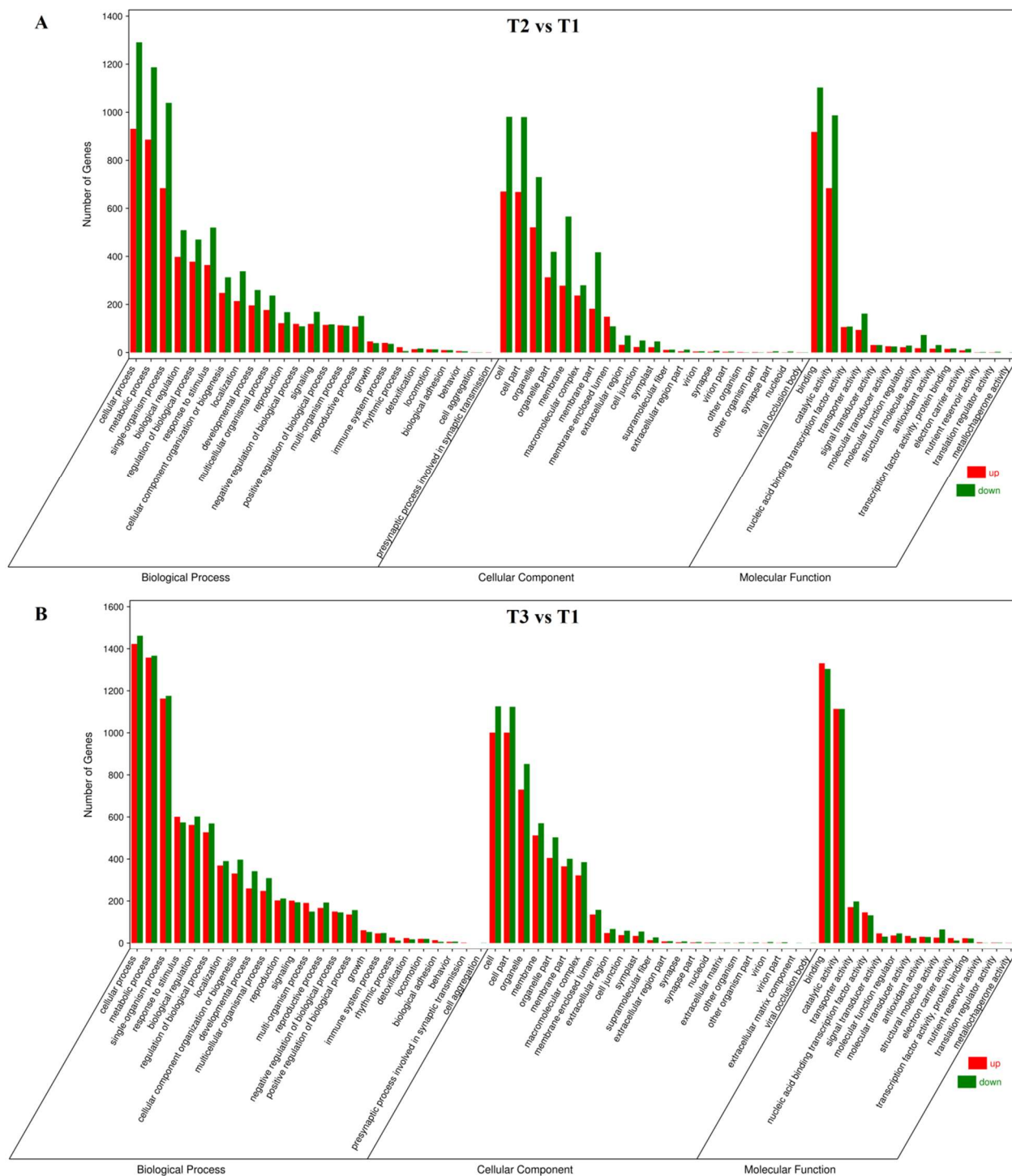


Figure S9. Gene Ontology (GO) enrichment of DEGs at T2 vs. T1 and T3 vs. T1.

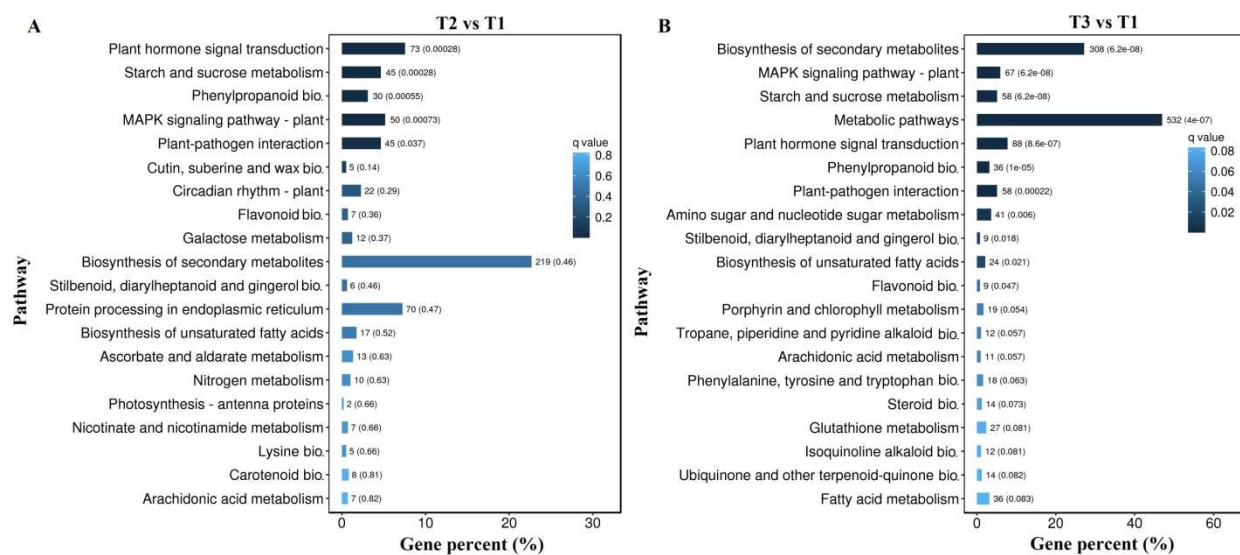


Figure S10. KEGG enrichment of DEGs at T2 vs. T1 and T3 vs. T1.

Table supplementary legends

Table S1. Sequences of primer used in qRT-PCR validation.

Gene name	Primer sequences (5' to 3')	Amplicon size (bp)
<i>ACT</i>	Forward: TGGTATTGTGCTGGATTCTGGT Reverse: TGAGATCACCACCAGCAAGG	109
FLC expression (15)		
<i>VIL1</i>	Forward: TAAGGACGCTCGACGTGTTG Reverse: TAGTTGAAACGCCACTCGCT	158
<i>VIL2</i>	Forward: TCAGATAGGTCCCCACGGAG Reverse: CTGCCCCAATGGTGGAAATCT	196
<i>VRN1-L</i>	Forward: GCGTATGTACTACCACCCACC Reverse: TTGCTTAACCCGACCCGAC	106
<i>FCA</i>	Forward: CTTCAACACCGGGTGGTTCT Reverse: TTGCGGCTTCGACTGGTTAT	122
<i>FLK</i>	Forward: GGGATAAACGCTGTTGGTGG Reverse: TAGGAGGCATGTCTGCAGGT	106
<i>FPA</i>	Forward: TTGGTGAGCTTGAGAGCGTT Reverse: GATTGCCCGCGACAGAAAAC	123
<i>FY</i>	Forward: TGCGATGCCGCTATCCATAC Reverse: TGTTGGAGCTGCTGAGCATT	174
<i>FLD</i>	Forward: AGGCTACCACCAAGCGTTAC Reverse: GGCAAGCACAAGAGTGTGTG	153
<i>LD</i>	Forward: ATAGTGGCTGGATGGTTGGC Reverse: CAGCATCAGGCAACTGTTTCG	198
<i>LHP1</i>	Forward: CTGTTTCGTCGAAAGCGTGTT Reverse: TACGCTTCCGCGATCTATGC	174
<i>MAF1</i>	Forward: GTGGTTCTTTGCTGGCTACC Reverse: TAACAACGCGCTTAAGCTTTCT	171
<i>VIP4</i>	Forward: ACTACGAGTCCCGACGTTCT Reverse: CGTCGGGATGATTTCGAAGC	151
<i>ATX2</i>	Forward: GATTTCGTGCTGAGCTTGGTG Reverse: TCATCCTCTCCACTTGCACT	122
<i>ARP6</i>	Forward: TGGAGCCACAGGACAACATAC Reverse: ATCTCCGGCACAAGGAAACG	138
<i>FRL3</i>	Forward: ATGCCAGCTCCTTGGTTACG Reverse: GTCACGAAGACCGAAAGCAC	112
Sucrose metabolism (3)		
<i>TPS1</i>	Forward: ACGCAGGGAGAATGGATGAC Reverse: AACGGGGTGTCTTTTCAGTG	103
<i>SUS3</i>	Forward: AGGGAAGTGGCAAACCTTGT Reverse: ACCGATAGAGCTCGCCATTG	181
<i>SPS</i>	Forward: GACGGTGAGAGGAATGATGGT Reverse: TGTGTCCCCTTCATGCCAAC	119
Hormone response (5)		
<i>GID1B</i>	Forward: AGCCCCAGACAACGAAACTC	118

	Reverse: GGAAGACGAATGGGCAAAGC	
<i>RAP2-7</i>	Forward: ACGCCGGTTGATTATCGGTT Reverse: CCACGATACTGCGAGCTTCT	116
<i>IAA13</i>	Forward: CTGCGATTGGACGAAAGGTG Reverse: CCCCTCCATGCTTGATCGTG	122
<i>ARF1</i>	Forward: ACTGTTTGCCCCATTGGAT Reverse: AGCATCACCAGCAACCAACT	179
<i>AHK3</i>	Forward: CGAACACATGGGGGTACAGG Reverse: CCGACTGCTGGTTGATTTGC	184
Circadian clock (2)		
<i>ELF3</i>	Forward: TGATGCCGAGTCTCGTGAAG Reverse: CTGTGCCGGACATCGAATCT	107
<i>COR27</i>	Forward: GGATTTGCATGGATCGCTGTC Reverse: GTCCAGCAACCATCACGAAG	123
Downstream floral integrators and meristem identity (6)		
<i>FTIP3</i>	Forward: GGACAAGGTTCCCGGATGTT Reverse: TCCTTGTTGGGTGCAACTCT	181
<i>FTIP7</i>	Forward: TGGGAAGGTGGTGTTCGATG Reverse: ATCACTATGCCATGCCTCGG	163
<i>SOC1</i>	Forward: GAGAAGGCTTGGGATCGTGTT Reverse: CTGCATTATCTGCTGCGAGG	159
<i>AGL65</i>	Forward: AGGTCTCACCAGATTTTGCCG Reverse: ATACGGGTGTTGGACTCTTGC	100
<i>SPL1</i>	Forward: AGCATCGCACCAAGACTCTC Reverse: TCCTATCTGTGCGGCTCTCT	113
<i>SOK2</i>	Forward: AACTGCTCCAAACACTCCAT Reverse: GTTGTCGTTTGCTTGTTCGG	176
Cold response (9)		
<i>PYL3</i>	Forward: GCTGCTCATCAGTGCTCTTCT Reverse: TTTTCGTGGCTGGAAGACCT	193
<i>ERF110</i>	Forward: ACCACTACAGCCACCTTGTC Reverse: ACTCTAGCAGCTTTGTGCGG	137
<i>ETR2</i>	Forward: TGCAGTGCTAGAAGAGTCGC Reverse: GAATTCCTTGCGTGGGTAGC	108
<i>COR413PM1</i>	Forward: AGGCGCGATGATCCTTATCTG Reverse: GAGGCGCGTATGTGTTCTG	129
<i>CRPK1</i>	Forward: GAAGCTGAGATGTTGCGGTTT Reverse: TTGCGAGGTGTAACGCCTAT	165
<i>MPK3</i>	Forward: TGGCGCTTACGGAATTGTCT Reverse: AGTTCGCTTCGCATCCATGT	109
<i>SRK2E</i>	Forward: GTATGCATCCGGAGGAGAGC Reverse: TCGCGGTGACATACTTGCAT	135
<i>PP2CA</i>	Forward: CGTTCTCCGGTGGAAGTCAT Reverse: CCTTGCACTTCATCGCAACC	186
<i>HAB1</i>	Forward: ATATTAGCCAGCGACGGTCTG Reverse: GTAACCGGCCCGTTCTTTCT	104

Table S2. The sequence details of the isoforms involved in the 104 co-expressed genes at T2 vs. T1 and T3 vs. T1. Note, the Table S2 is shown as a separate document of .txt format.

Table S3. DEGs involved in FLC expression at T2 vs. T1 and T3 vs. T1.

Gene name	Swiss-Prot ID	Protein name	FPKM value	
			T2/T1	T3/T1
Inhibiting FLC expression				
VIL1	Q9LHF5	VIN3-like protein 1	-1.28	-0.40
VIL2	Q9SUM4	VIN3-like protein 2	-1.43	-1.18
VRN1-L	A0A6P4B193	B3 domain-containing transcription factor VRN1-like	-0.55	2.07
FCA	O04425	Flowering time control protein FCA	0.85	2.47
FLK	Q9SR13	Flowering locus K homology domain	0.21	-0.42
FPA	Q8LPQ9	Flowering time control protein FPA	1.04	-1.15
FY	Q6NLV4	Flowering time control protein FY	0.29	-0.19
FLD	Q9CAE3	Protein FLOWERING LOCUS D	-0.77	-0.35
LD	Q38796	Homeobox protein LUMINIDEPENDENS	-1.17	-1.71
LHP1	Q944N1	Chromo domain protein LHP1	0.98	0.80
MAF1	Q7ZWL6	Repressor of RNA polymerase III transcription homolog MAF1	-1.41	-1.33
Activating FLC expression				
VIP4	Q9FNQ0	Protein LEO1 homolog	1.36	0.31
ATX2	P0CB22	Histone-lysine N-methyltransferase ATX2	0.31	-8.75
ATX4	Q9SUE7	Histone-lysine N-methyltransferase ATX4	0.11	-1.55
ATX5	Q8GZ42	Histone-lysine N-methyltransferase ATX5	0.34	-0.86
ARP6	Q8LGE3	Actin-related protein 6	-1.06	-1.10
PIE1	Q7X9V2	Protein PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1	0.37	1.78
FRL3	Q67ZB3	FRIGIDA-like protein 3	1.27	-1.48
FES1	Q84VG7	Protein FRIGIDA-ESSENTIAL 1	1.11	1.47
SUF4	Q9C5G0	Protein SUPPRESSOR OF FRI 4	2.31	1.17
Interacting FLC expression				
CLF	P93831	Histone-lysine N-methyltransferase CLF	-0.02	-0.56
FIE2	Q6ZJX0	Polycomb group protein FIE1	1.03	-0.92

Table S4. DEGs involved in sucrose metabolism at T2 vs. T1 and T3 vs. T1.

Gene name	Swiss-Prot ID	Protein name	FPKM value	
			T2/T1	T3/T1
<i>TPS1</i>	Q9SYM4	Alpha, alpha-trehalose-phosphate synthase 1	1.35	1.04
<i>TPS5</i>	O23617	Alpha, alpha-trehalose-phosphate synthase 5	-1.50	-1.42
<i>TPS7</i>	Q9LMI0	Probable alpha, alpha-trehalose-phosphate synthase 7	0.59	1.61
<i>TPS10</i>	O80738	Probable alpha, alpha-trehalose-phosphate synthase 10	3.22	3.12

<i>SUS2</i>	O24301	Sucrose synthase 2	-1.12	-1.55
<i>SUS3</i>	Q9M111	Sucrose synthase 3	1.11	-1.70
<i>SPS</i>	Q43845	Probable sucrose-phosphate synthase	-1.55	-2.92
<i>SPS1</i>	O22060	Probable sucrose-phosphate synthase 1	-1.00	-2.45
<i>PGMP</i>	Q9SCY0	Phosphoglucomutase, chloroplastic	-1.59	-1.00
<i>PGM1</i>	Q9ZSQ4	Phosphoglucomutase, cytoplasmic	-1.83	-3.19
<i>BAM1</i>	Q9LIR6	Beta-amylase 1, chloroplastic	-2.86	-1.88
<i>BAM3</i>	O23553	Beta-amylase 3, chloroplastic	-2.36	-1.67

Table S5. DEGs involved in hormone response at T2 vs. T1 and T3 vs. T1.

Gene name	Swiss-Prot ID	Protein name	FRPM value	
			T2/T1	T3/T1
Gibberellin				
<i>GID1B</i>	Q9LYC1	Gibberellin receptor GID1B	-0.28	5.56
Ethylene				
<i>RAP2-3</i>	P42736	Ethylene-responsive transcription factor RAP2-3	-2.44	-2.39
<i>RAP2-7</i>	Q9SK03	Ethylene-responsive transcription factor RAP2-7	-2.07	-0.74
Auxin				
<i>GH3.6</i>	Q9LSQ4	Indole-3-acetic acid-amido synthetase GH3.6	-2.67	-3.50
<i>LAX2</i>	Q9S836	Auxin transporter-like protein 2	-3.68	-5.37
<i>IAA8</i>	Q38826	Auxin-responsive protein IAA8	-1.46	-1.13
<i>IAA9</i>	Q38827	Auxin-responsive protein IAA9	-1.46	-1.25
<i>IAA12</i>	Q38830	Auxin-responsive protein IAA12	-2.60	-2.52
<i>IAA13</i>	Q38831	Auxin-responsive protein IAA13	-1.04	0.06
<i>IAA27</i>	Q9ZSY8	Auxin-responsive protein IAA27	-3.31	-4.02
<i>ARF1</i>	Q8L7G0	Auxin response factor 1	-1.26	-1.07
<i>ARF4</i>	Q9ZTX9	Auxin response factor 4	-1.33	-1.58
<i>ARF5</i>	P93024	Auxin response factor 5	-2.21	-1.54
<i>ARF6</i>	Q9ZTX8	Auxin response factor 6	1.02	1.04
<i>ARF19</i>	Q0D9R7	Auxin response factor 19	-1.75	-1.93
Cytokinin				
<i>AHK3</i>	Q9C5U1	Histidine kinase 3	2.42	2.25
<i>AHP1</i>	Q9ZNV9	Histidine-containing phosphotransfer protein 1	1.58	-0.12
<i>ARR2</i>	Q9ZWJ9	Two-component response regulator ARR2	-1.61	0.71

Table S6. DEGs involved in circadian clock at T2 vs. T1 and T3 vs. T1.

Gene name	Swiss-Prot ID	Protein name	FPKM value	
			T2/T1	T3/T1
<i>ELF3</i>	O82804	Protein EARLY FLOWERING 3	1.58	1.58
<i>COR27</i>	Q8L8T7	Cold-regulated protein 27	1.68	1.80

Table S7. DEGs involved in downstream floral integrators and meristem identity at T2 vs. T1 and T3 vs. T1.

Gene name	Swiss-Prot ID	Protein name	FRPM value	
			T2/T1	T3/T1
<i>FTIP3</i>	Q9M2R0	FT-interacting protein 3	2.40	1.55
<i>FTIP7</i>	Q60EW9	FT-interacting protein 7	1.27	1.59
<i>SOC1</i>	O64645	MADS-box protein SOC1	1.00	0.32
<i>AGL65</i>	Q7X9I0	Agamous-like MADS-box protein AGL65	-1.74	1.25
<i>SPL1</i>	Q9SMX9	Squamosa promoter-binding-like protein 1	1.19	-1.18
<i>SPL6</i>	Q94JW8	Squamosa promoter-binding-like protein 6	1.90	-2.31
<i>AP2</i>	P47927	Floral homeotic protein APETALA 2	-0.03	1.65
<i>AP2-1</i>	B8AXC3	APETALA2-like protein 1	-2.43	-1.53
<i>AP2-2</i>	B8AMA9	APETALA2-like protein 2	-1.51	-1.14
<i>AP2-3</i>	B8B8J2	APETALA2-like protein 3	-1.29	-0.24
<i>AIL5</i>	Q6PQQ3	AP2-like ethylene-responsive transcription factor AIL5	-1.84	1.22
<i>ANT</i>	Q38914	AP2-like ethylene-responsive transcription factor ANT	-1.36	-1.92
<i>At2g41710</i>	Q8GWK2	AP2-like ethylene-responsive transcription factor At2g41710	-1.84	-1.57
<i>TEM1</i>	Q9C6M5	AP2/ERF and B3 domain-containing transcription repressor TEM1	1.55	1.28
<i>SOK2</i>	Q9LX14	Protein SOSEKI 2	-3.63	3.03

Table S8. DEGs genes involved in cold response at T2 vs. T1 and T3 vs. T1.

Gene name	Swiss-Prot ID	Protein name	FRPM value	
			T2/T1	T3/T1
<i>PYL3</i>	Q6EN42	Absciscic acid receptor PYL3	1.13	1.30
<i>PYL4</i>	O80920	Absciscic acid receptor PYL4	1.15	7.36
<i>ERF3</i>	Q9SXS8	Ethylene-responsive transcription factor 3	1.30	1.16
<i>ERF5</i>	Q9LW48	Ethylene-responsive transcription factor 5	2.52	4.58
<i>ERF010</i>	Q9FH94	Ethylene-responsive transcription factor ERF010	1.84	2.25
<i>ERF011</i>	Q9SNE1	Ethylene-responsive transcription factor ERF011	1.28	1.42
<i>ERF13</i>	Q8L9K1	Ethylene-responsive transcription factor 13	1.93	0.65
<i>ERF110</i>	Q70II3	Ethylene-responsive transcription factor ERF110	1.79	3.32
<i>ERF118</i>	Q9CA27	Ethylene-responsive transcription factor ERF118	2.00	1.23
<i>ETR2</i>	Q0WPQ2	Ethylene receptor 2	2.17	1.92
<i>COR413PM1</i>	Q9XIM7	Cold-regulated 413 plasma membrane protein 1	1.10	-2.42
<i>COR413PM2</i>	Q9SVL6	Cold-regulated 413 plasma membrane protein 2	4.07	-3.29
<i>CRPK1</i>	Q93YN1	Cold-responsive protein kinase 1	-3.00	1.17
<i>MPK3</i>	Q39023	Mitogen-activated protein kinase 3	1.61	3.47
<i>MPK9</i>	Q9LV37	Mitogen-activated protein kinase 9	1.38	-1.07
<i>MPK16</i>	Q8W4J2	Mitogen-activated protein kinase 16	1.30	2.22
<i>YDA</i>	Q9CAD5	Mitogen-activated protein kinase kinase kinase YODA	-1.41	-2.57
<i>SRK2E</i>	Q940H6	Protein phosphatase 2C 70	1.25	0.48

<i>PP2CA</i>	P49598	Protein phosphatase 2C 3	-2.87	-4.23
<i>HAB1</i>	Q9CAJ0	Protein phosphatase 2C 16	-1.90	-5.44
<i>HAB2</i>	Q9LNP9	Protein phosphatase 2C 7	-3.51	-3.64
<i>KAPP</i>	P46014	Protein phosphatase 2C 37	1.48	-1.35
<i>PPC6-1</i>	Q9M8R7	Probable protein phosphatase 2C 33	1.01	1.31
<i>PPC6-7</i>	Q0WRB2	Probable protein phosphatase 2C 73	-1.19	-1.24
<i>PP2C27</i>	P93006	Probable protein phosphatase 2C 27	-1.88	1.48
<i>PP2C38</i>	Q9LHJ9	Probable protein phosphatase 2C 38	-2.25	1.39
<i>At2g30020</i>	O80871	Probable protein phosphatase 2C 25	1.75	2.70
<i>Os02g0799000</i>	Q69QZ0	Probable protein phosphatase 2C 27	2.87	2.02
<i>At3g15260</i>	Q9LDA7	Probable protein phosphatase 2C 39	-3.08	-3.72
<i>At3g16560</i>	Q9LUS8	Probable protein phosphatase 2C 40	1.61	2.82
<i>At3g62260</i>	Q3EAF9	Probable protein phosphatase 2C 49	-1.46	0.34
<i>Os06g0651600</i>	Q67UP9	Probable protein phosphatase 2C 58	1.24	-0.19
<i>At4g31860</i>	Q9SZ53	Probable protein phosphatase 2C 60	0.06	-0.99
<i>TGA2.2</i>	Q6IVC3	Transcription factor TGA2.2	-2.00	-0.96
<i>CDC5</i>	P92948	Cell division cycle 5-like protein	3.83	9.48