

Table 1 Suppl. The expressional evaluation of selected genes by RT-qPCR after cold treatment. a - the cloned gene fragment from the SSH library, b - the sequence information based on *BLAST* of *Genbank*, c - the gene expression after cold *versus* control; **Bold** indicates the genes selected for further expressional analysis.

Clone name ^a	Annotation ^b	Average expression ratio ^c		
		2 ^{-ΔΔCT}	Miner	FPK-PCR
C3F05	No hits	10.7	6.54	13.42
C3B10	XM_002270764.1, PREDICTED: <i>Vitis vinifera</i> hypothetical protein LOC100251278 (LOC100251278), mRNA	4.06	3.94	8.07
C4A10	CU396690, <i>Eucalyptus gunnii</i> EST from cold-acclimated leaves	3.89	0.78	5.56
C4C10	no hits	2.78	4.02	4.4
C4D09	no hits	2.57	1.69	323.43
C3G02	XM_002518566.1, <i>Ricinus communis</i> chloroplast α-glucan water dikinase, putative, mRNA	2.53	2.44	1.97
C3D03	FP047165.1, FP047165 LG0AAC <i>Quercus petraea</i> cDNA clone LG0AAC21YL06RM1 similar to STIP_SOYBN heat shock protein STI. - <i>Glycine max</i> , mRNA sequence	1.85	2.29	0.66
C1D11	CU403091 LG0ABA <i>Eucalyptus gunnii</i> cDNA, mRNA sequence	1.53	1.17	0.33
7B5G12	CU223438.1, <i>Populus</i> EST from water stressed leaves	1.49	1.75	0.75
7B5G6	000001601152_C04.ab1 <i>Eucalyptus globulus</i> under low temperature, <i>Eucalyptus globulus</i> cDNA, mRNA sequence	1.43	0.8	1.47
C1E06	no hits	1.37	2.75	0.9
C4E11	no hits	1.32	1.16	1.09
C1E12	XM_002520565.1, <i>Ricinus communis</i> calcium-dependent protein kinase, putative, mRNA	1.29	2.13	1.9
7B7F2	000001601552_J09.ab1 <i>Eucalyptus globulus</i> under low temperature, <i>Eucalyptus globulus</i> cDNA, mRNA sequence	1.26	2.26	3.41
7B7G7	000001480352_L06.ab1 <i>Eucalyptus globulus</i> under low temperature, <i>Eucalyptus globulus</i> cDNA, mRNA sequence	1.26	2.44	1.35
C4B07	CU400336, <i>Eucalyptus gunnii</i> EST from cold-acclimated leaves	1.21	0.44	0.26
C1C08	CU396847 LG0ABA <i>Eucalyptus gunnii</i> cDNA, mRNA sequence	1.12	1.95	1.25
C2G10	CT988100 <i>Eucalyptus globulus</i> differentiating xylem RAIZ clone VC9, <i>Eucalyptus globulus</i> cDNA, mRNA sequence	1.11	0.98	0
C3G11	EH791239.1, LU01UID.1434 stem phloem fiber enriched library LU01, <i>Linum usitatissimum</i> cDNA clone FLAXSQ_RP_014_H08, mRNA sequence	1.11	0.71	0.94
7B7E9	CU400384, <i>Eucalyptus gunnii</i> EST from cold-acclimated leaves	1.09	1.76	2.82
C3E11	CT981368 <i>Eucalyptus gunnii</i> differentiating xylem AFOCEL clone 832 <i>Eucalyptus gunnii</i> cDNA, mRNA sequence	1.07	1.15	0.97
7B7H5	CU398105, <i>Eucalyptus gunnii</i> EST from cold-acclimated leaves	0.98	1.57	0.41
7B5F6	CU398227 LG0ABA <i>Eucalyptus gunnii</i> cDNA, mRNA sequence	0.97	1.15	1.31
7B5G10	CU402136 LG0ABA <i>Eucalyptus gunnii</i> cDNA, mRNA sequence	0.95	1.35	NA
C2G07	FC910008.1, IC0AAA60BG01RM1 IVIA1 <i>Citrus clementina</i> cDNA clone IC0AAA60BG01, mRNA sequence	0.95	1.23	0
C1E05	000001601852_K05.ab1 <i>Eucalyptus globulus</i> under low temperature <i>Eucalyptus globulus</i> cDNA, mRNA sequence	0.86	1.63	0.75
C4E12	XM_002302197.1, <i>Populus trichocarpa</i> predicted protein, mRNA	0.79	0.63	0.33
C1H05	No hits	0.75	0.63	0.59
C3D10	EY875778.1, CL06-C4-501-042-D09-CT.F Rangpur lime root, plant with water stress <i>Citrus limonia</i> cDNA, mRNA sequence	0.68	0.69	0.64
C3E02	FG828770.1, UCRVU04_CCNI13226_b1 Cowpea 524B mixed tissue and conditions cDNA Library UCRVU04-1-2 <i>Vigna unguiculata</i> cDNA clone CCNI13226.b1, mRNA sequence	0.49	0.43	NA
C2G01	XM_002274436.1, PREDICTED: <i>Vitis vinifera</i> hypothetical protein LOC100255131 (LOC100255131), mRNA	0.48	0.58	0.33
C2G12	000001603752_A16.ab1 <i>Eucalyptus globulus</i> under low temperature, <i>Eucalyptus globulus</i> cDNA, mRNA sequence	0.41	1.71	1.03
C2D06	CU401020 LG0ABA <i>Eucalyptus gunnii</i> cDNA, mRNA sequence	0.4	0.56	0.45
C3F10	000001480252_J18.ab1 <i>Eucalyptus globulus</i> under low temperature, <i>Eucalyptus globulus</i> cDNA, mRNA sequence	0.02	0.02	0.37