

Table 1 Suppl. Primer sequences of genes selected for real-time quantitative PCR.

Gene name or ID	Forward sequence (5'-3')	Reverse sequence (5'-3')
<i>Actin</i>	AAACGGCTACCACATCCA	CACCAGACTTGCCCTCCA
MELO3C013203	TCTTTCGTCCCTCACCTT	CAGCTCCTCTGCATACTTTC
MELO3C012015	AACTGTACGGCAACATCCA	CAACTCCCAACTGAATAATG
MELO3C020630	GACGCCGTTCATGGTGAATCC	CTGTGCGTCGAACATGTTTCGTA
MELO3C010936	GAGGACATTAACAAGACC	CCATCATACTCAACCATCAAGG
MELO3C021622	GGACCACGACACCTTCTC	CTTCCATCCTCCCACTTC
MELO3C014574	GGTGACATTGTGAGAAGAGTGAT	CAGCCATTAGAGGTGTTGTC
MELO3C003275	TTCGTTGAGGGATGCGATGG	TCGGCACAAGAAACAACACC
MELO3C007596	GCGGAACTCATCTCAAAGGA	TCCCGTCACAATCACATCCA

Table 2 Suppl. The throughput and quality of *Illumina* sequencing the melon transcriptome. CK - control samples; chilling stress - samples exposed to chilling treatment (6 °C); chilling stress + SNP - samples exposed to chilling stress and 200 µM NO donor sodium nitroprusside (SNP). Three independent replications.

Sample	Raw reads	Clean reads	Clean reads [%]	Mapped genes	Total mapping ratio [%]	Uniquely mapping ratio [%]
CK1	48 651 732	44 880 600	92.24	32 594 698	89.09	87.85
CK2	45 119 702	41 472 800	91.91	26 923 442	82.44	81.46
CK3	46 574 456	42 939 192	92.19	29 914 428	87.35	86.26
Chilling stress1	47 252 734	43 565 120	92.19	31 224 824	88.80	87.43
Chilling stress 2	46 303 700	42 702 238	92.22	30 592 528	88.89	87.74
Chilling stress 3	43 434 630	40 171 756	92.48	28 281 278	89.52	88.42
Chilling stress + SNP1	45 302 596	40 911 316	90.30	24 889 102	79.42	78.54
Chilling stress + SNP2	44 894 210	40 770 706	90.81	24 420 196	78.89	78.05
Chilling stress + SNP3	45 291 470	41 932 292	92.58	27 324 516	82.42	81.48

Table 3 Suppl. Analysis of sequencing data quality. Q20, Q30 - proportion of bases with a mass no less than 20 or 30, respectively, after filtration, GC - percentage of bases G and C in the total base number after filtration, CK - control samples; chilling stress - samples exposed to chilling treatment (6 °C); chilling stress + SNP - samples exposed to chilling stress and 200 µM NO donor sodium nitroprusside (SNP) Three independent replications.

Sample	Q20 [%]	Q30 [%]	GC content [%]
CK1	96.55	91.84	43.91
CK2	96.65	92.11	44.85
CK3	96.69	92.10	43.71
Chilling stress1	96.88	92.44	43.77
Chilling stress 2	96.89	92.50	43.56
Chilling stress 3	96.81	92.28	43.20
Chilling stress + SNP1	96.44	91.82	45.29
Chilling stress + SNP2	96.41	91.63	44.64
Chilling stress + SNP3	96.59	91.81	45.29

Table 4 Suppl. A list of differentially expressed genes related to sugar metabolism. CK - controls, CS - plants subjected to chilling stress, CN - plants treated with sodium nitroprusside and subjected to chilling, U - up regulation, D - down regulation.

Gene ID	Description	Fold change			P value		
		CK vs. CS	CS vs. CN	CK vs. CN	CK vs. CS	CS vs. CN	CK vs. CN
MELO3C010186	UDP-glucuronate 4-epimerase	4.32 ^(U)	-2.13	2.16	5.82E-06	2.98E-02	3.11E-01
MELO3C008095	β -glucosidase	2.08 ^(U)	-0.91	1.16	1.03E-04	2.56E-02	1.80E-02
MELO3C020591	glucuronosyltransferase	1.54 ^(U)	-0.49	1.04	1.77E-05	2.18E-01	5.89E-03
MELO3C027332	UDP-glucuronate 4-epimerase	1.31 ^(U)	-0.12	1.17 ^(U)	1.30E-03	7.45E-01	1.02E-03
MELO3C019691	α -1,4-galacturonosyl transferase	1.29 ^(U)	-0.97	0.31	2.57E-06	3.16E-03	3.24E-01
MELO3C014574	hexokinase	1.12 ^(U)	-0.60	0.52	2.59E-06	2.97E-01	4.24E-01
MELO3C017588	trehalose 6-phosphate phosphatase	-1.21 ^(D)	0.34	-0.88	1.36E-03	1.98E-01	3.51E-02
MELO3C013203	fructose-bisphosphate aldolase, class I	-2.16 ^(D)	2.33 ^(U)	0.17	9.23E-06	1.55E-08	7.76E-01
MELO3C011801	fructose-bisphosphate aldolase, class I	-2.01 ^(D)	2.14 ^(U)	0.13	1.35E-04	4.28E-04	8.11E-01
MELO3C012015	fructose-bisphosphate aldolase, class I	-1.90 ^(D)	3.73 ^(U)	1.82 ^(U)	8.03E-06	1.58E-42	2.91E-06
MELO3C015214	β -glucosidase	-1.08 ^(D)	0.62	-0.47	1.19E-08	2.58E-01	4.14E-01
MELO3C018794	β -amylase	-1.28 ^(D)	0.97	-0.31	1.79E-06	9.94E-03	4.95E-01
MELO3C020630	glucan endo-1,3- β -glucosidase	-1.01 ^(D)	2.22 ^(U)	1.20 ^(U)	2.65E-05	1.70E-09	2.12E-03
MELO3C023110	raffinose synthase	-1.53 ^(D)	1.68 ^(U)	0.15	1.04E-03	1.93E-11	7.74E-01
MELO3C023335	β -galactosidase	-1.82 ^(D)	0.30	-1.53	3.07E-05	5.67E-01	6.27E-03
MELO3C026170	6-phosphofructokinase 1	1.20 ^(D)	0.70	-0.50	7.43E-04	1.20E-02	1.38E-01
MELO3C006362	β -amylase	0.38	-1.11 ^(D)	-0.74	2.46E-01	1.51E-07	3.15E-02
MELO3C020244	UTP-glucose-1-phosphate uridylyltransferase	-0.38	0.04	-0.34	4.70E-02	8.47E-01	1.89E-01
MELO3C023310	glucose-1-phosphate adenyltransferase	0.91	-3.19 ^(D)	-2.29 ^(D)	1.33E-02	2.06E-12	3.53E-05
MELO3C010936	glucose-6-phosphate isomerase	-0.80	0.48	-0.32	9.28E-05	1.87E-02	1.99E-01
MELO3C021622	triosephosphate isomerase	1.03	0.28	1.29	4.63E-02	4.83E-01	1.64E-02
MELO3C016119	UDP-glucose 4,6-dehydratase	1.19	-0.73	0.44	5.24E-03	3.52E-02	3.46E-01

Table 5 Suppl. Fold changes in expression of defense-response genes with significant ($P < 0.01$) differential expression (≥ 2.0 -fold). (CK - controls, CS - plants subjected to chilling stress, CN - plants treated with sodium nitroprusside and subjected to chilling).

Gene ID	Description	CK vs. CS	CS vs. CN	CK vs. CN
MELO3C004579	EREBP-like factor	3.24	-0.62	2.62
MELO3C020166	WRKY transcription factor 2	2.44	-1.26	1.17
MELO3C003275	peroxidase	3.50	-2.06	1.44
MELO3C007596	auxin responsive GH3 gene family	5.29	-1.97	3.30
MELO3C014224	phenylalanine ammonia-lyase	2.91	-3.38	-0.48
MELO3C005476	auxin-responsive protein IAA	3.26	-1.47	1.78
MELO3C002483	gibberellin 2-oxidase	3.68	-1.57	2.10
MELO3C008314	abscisic acid receptor PYR/PYL family	3.93	-2.90	1.03
MELO3C005502	EREBP-like factor	3.63	-2.90	2.57
MELO3C026265	myb proto-oncogene protein	2.93	-2.00	0.92
MELO3C014229	phenylalanine ammonia lyase	2.32	-1.56	0.75
MELO3C027346	auxin responsive GH3 gene family	2.30	-1.00	1.32
MELO3C016219	abscisic acid 8'-hydroxylase	2.08	-1.49	0.58
MELO3C017219	flavonoid 3'-monooxygenase	2.65	-36.24	-0.60
MELO3C014228	phenylalanine ammonia-lyase	2.23	-0.74	1.48
MELO3C017940	EREBP-like factor	2.47	-1.96	0.50
MELO3C018394	abscisic acid receptor PYR/PYL family	2.31	-2.07	0.22
MELO3C012971	photosystem I subunit VI	-2.01	2.15	0.13
MELO3C011576	zinc-finger protein CONSTANS	-3.66	3.53	0.13
MELO3C011865	light-harvesting complex I chlorophyll a/b binding protein 2	-2.50	2.41	-0.10