

Supplementary data:

Pleiotropic phenotypes of the salt-tolerant and cytosine hypomethylated *leafless inflorescence*, *evergreen dwarf* and *irregular leaf lamina* mutants of *Catharanthus roseus* possessing Mendelian inheritance

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Table 1. List of primers used for gene expression study.

Gene name	Forward primer sequence	Reverse primer sequence	Annealing temperature of the primer for amplification (°C)	No. of cycles used for amplification	Reference ^a
ABNORMAL LEAF SHAPE 2 (ALE2)	GGCGGAGAGTGTTCGCCGAG	CACTGTGGCACTGGCACCC	62.5	40	Tanaka <i>et al.</i> (2007)
ACETYL COA: 17-O-DEACETYLVINDOLINE 17-O-ACETYLTRANSFERSE (DAT)	ATGGAGTCAGGAAAAATATC	GAAACAAAATTGAAGTAGCTG	63.0	30	St-Pierre <i>et al.</i> (1999); Facchini (2001)
ACTIN-RELATED PROTEIN 4 (ARP4)	GCAAGGCTGGTTACGCCGGT	TGTGGATCCTCCACCGCAGTC	58.5	30	Kandasamy <i>et al.</i> (2005)
AGAMOUS-LIKE 24 (AGL24)	GGCGGAGTGTGTGATGAGCCA	GCCCAAGCTTCAGGGAAGTGTGG	56.5	30	Gregis <i>et al.</i> (2009)
AGAMOUS LIKE MADS-BOX PROTEIN 31 (AGL31)	GCTGTTCTCGTCGTCGCCG	ACGCTTCTTCCCACTGGCT	56.0	32	Ratcliffe <i>et al.</i> (2003)
ANTHRANILATE SYNTHASE (AS)	GGAATTCCCTTCTTGCTTACCGTTGT	GGAATTCCTAGCTTGTGTGGCAAGA	55.0	40	Li and Last (1996)
APETALA 2 (AP2)	ACGATGAGGAACCTCAATGCC	ATCAAACCCGGTGGTCTCAG	53.6	35	Ohto <i>et al.</i> (2009)
AP2-DOMAIN DNA-BINDING PROTEIN (ORCA3)	TTCCAGCTCGGAATTGACTT	ACTCTAACGGGTCCGGAAAT	53.6	30	Montiel <i>et al.</i> (2011)
<i>Arabidopsis thaliana</i> SEED GENE 3 (ATS3)	AACCAGAACCCGGTTTTCTCACTTGT	CAGACGGCCTTGGTGGAGGC	60.0	30	Nuccio and Thomas (1999)
ASYMMETRIC LEAVES 1 (AS1)	TTATCTTAAAGCCAGGGATCA	GAACACACTCTCGTACTCC	48.9	35	Koyama <i>et al.</i> (2010)
BASIC-LEUCINE ZIPPER (BZIP) TRANSCRIPTION FACTOR FAMILY PROTEIN (FD)	AGACCACGGGTTCTGCGCCT	CCTAGCCGGGAACGAGCTG	56.5	45	Abe <i>et al.</i> (2005)
CASEIN KINASE II BETA SUBUNIT (CKB2)	AACTGCAGGCTGGCGTCCAC	TCGTTCCCAACGAAGTTGCAGA	58.2	30	Sugano <i>et al.</i> (1998)
CHORISMATE MUTASE (CMU)	ATCAAAGCCACGCTCTGGAA	TATGCTTCGGGTGAGGGCTTG	56.0	45	Hu <i>et al.</i> (2009)
CHROMATIN REMODELLING PROTEIN 2 (CHR2)	TCTTCAAATGCTGGTGCAAG	AGCTTCAGCGTTATCCCTCCA	56.5	35	Tang <i>et al.</i> (2008)
CHROMATIN REMODELLING PROTEIN 5 (CHR5)	GATGGGGAAGTTTACGAGCA	GTCAATGCCCTTGTGAACCT	55.0	30	
CHROMATIN REMODELLING PROTEIN 11 (CHR11)	TGTTGCTCCAAAATCAACA	GCACAACTTCTTGTGGTCA	54.2	30	Huanca-Mamani <i>et al.</i> (2005)
CHROMOMETHYLASE 3 (CMT3)	AAGAGACCTGGACAAAAGGA	CCGAGCCGTGAAAATA CAGTT	56.6	35	Pillot <i>et al.</i> (2010)
COLD-REGULATED 15A (COR15A)	TCCTCCTTTCAITTCCTCAA	AGAATGTACGGGTGACCTGTG	52.0	30	Sokol <i>et al.</i> (2007)
CRYPTOCHROME 1 (CRY1)	CGAGGCCGGGGAAGAAAAGCG	TCCCGGCATCGACCAACGGGA	57.7	45	Lian <i>et al.</i> (2011)
CRYPTOCHROME 2 (CRY2)	GCGGCTGAAGCGAATTTGGGC	AGCTCGTGGCCATCGGGGAT	58.0	45	Kennedy <i>et al.</i> (2010); Liu <i>et al.</i> (2008)
CUP-SHAPED COTYLEDON1 (CUC1)	CCCCACGTACGCCACGTAC	AACGGCCACACACTCACGGC	57.0	38	Raman <i>et al.</i> (2008)

Table 1 (contd.)

Gene name	Forward primer sequence	Reverse primer sequence	Annealing temperature of the primer for amplification (°C)	No. of cycles used for amplification	Reference ^a
CYTOCHROME P450 REDUCTASE (CPR)	CCAGGGATGTCCACAGAACT	AAATTTTGCACATGGCCCTTC	53.3	35	Facchini (2001)
CYTOCHROME P450 72C1 (CYP72C1)	GCCGATTTTCTCCCTCGCAT	GCCAGGAATGTAGACGGGCTC	58.0	35	Nakamura <i>et al.</i> (2005)
DEFECTIVE IN RNA-DIRECTED DNA METHYLATION 1 (DRD1)	TGGCTGACGATCCTGGTGCGT	TGCTGTGCCCGGTTCTCTGC	60.0	40	Chan <i>et al.</i> (2006)
DEHYDRATION-RESPONSIVE ELEMENT-BINDING 1A (DREB1A)	CAGAGAAATCCGGATCCCAAT GAACTCATTTTCTGCT	CCGCACTCGAGGTCGACCCGT CGCATCACACATCTC	65.0	30	Sokol <i>et al.</i> (2007)
DEHYDRATION-RESPONSIVE ELEMENT-BINDING 2A (DREB2A)	GATCCGAATTCATGGCAG TTTATGATCAGAGTGG	CAGCATCGAGGTCGA CGGATCCTCTGTTTCAC	65.0	30	Sokol <i>et al.</i> (2007)
1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE (DXR)	TATTTTCGTTCTTGGATTCTCT	TAAGGTGTAAGAATAGGCA	63.0	30	St-Pierre and De Luca (1995)
DESACETOXYVINDOLINE-4-HYDROXYLASE (D4H)	AAGGACTTGAACITTTTCATGC	AACTTCCTTACCTTAATCCA	62.5	30	Facchini (2001)
DOMAIN REARRANGED METHYLTRANSFERASE 2 (DRM2)	CCCACCTGAGTTTGTGGACT	GCCTCCACCACGAGTATGAT	54.5	35	Henderson <i>et al.</i> (2010)
DWARF AND DELAYED FLOWERING 2 (DDF2)	TGCTCACGACGTGGGGGTTTC	CGGGCAGACATCAACGGGCTCCT	63.0	30	Magome <i>et al.</i> (2004)
EARLY FLOWERING 7 (ELF7)	CAGGTTGGAAGGGGGGAGCG	GGTGAGTAGGGCGTCGGCT	56.2	30	He <i>et al.</i> (2004)
EARLY FLOWERING 8 (ELF8)	GAGCGCCTTGAGCCCTTC	TGCCCGTGTCTTGTACCCGA	56.5	30	He <i>et al.</i> (2004)
EARLY FLOWERING IN SHORT DAYS (EFS)	ACTCGACCCGCTCCAAACCCGT	AGGAGAGGGATAGG AAAGAAAACGCA	62.4	30	Tang <i>et al.</i> (2012)
EMBRYO-DEFECTIVE-DEVELOPMENT 1 (EDD1)	CCGTTTCTCCGCCGCTGTT	AGCACCGGGCTCTCCCAGTT	62.0	40	Berg <i>et al.</i> (2005)
ESTERASE/LIPASE/THIOESTERASE (E/L/TH)	ACAGACCATCAATTCGAGCC	TCATCGTACCCCTGTTCGTA	53.6	30	
ETHYLENE RECEPTOR 1 (Cr ETR1)	ATTTGGTGGAAGTATGATGG	CCTGTCTGCGTTTGGCTGTTA	59.4	30	Dong <i>et al.</i> (2010)
FERTILIZATION INDEPENDENT SEED 2 (FIS2)	ACATGCAGAGCGGTGCGAGG	GGTCTTGGCGCAGATGAGACCG	55.0	45	Luo <i>et al.</i> (2000)
FLOWERING LOCUS D (FLD)	ATCAAACCGGTGGTTCTCAG	GGGTGTTTCCCTACCCTCCA	56.2	45	Yu <i>et al.</i> (2011)
FLOWERING LOCUS T (FT)	TCCTAGCAACCTCACCTCCGA	CCTCCGACGCACTCTCCCT	57.4	40	Abe <i>et al.</i> (2005)
FLOWERING TIME CONTROL PROTEIN (FY)	CCTGGTCCCCACCCCATCGCT	CCCGCAGACAGTGC GGTTGT	52.5	40	Henderson <i>et al.</i> (2005)
FLOWERING TIME CONTROL PROTEIN-RELATED/FCA	GCTTGAGGTACATG AGACGAGGAGC	ACAGGCCAATGTTT GGCAGCTCT	57.0	Baurle <i>et al.</i> (2007)	
GAMMA-RELATED (FCA)					
FLOWERING TIME CONTROL PROTEIN (FPA)	GCTGCCATGCAACCCACCAGC	AGCCTCTCTTGGTTCAGGCAA	56.3	40	Baurle <i>et al.</i> (2007)

Table 1 (contd.)

Gene name	Forward primer sequence	Reverse primer sequence	Annealing temperature of the primer for amplification (°C)	No. of cycles used for amplification	Reference ^a
GENERAL TRANSCRIPTION FACTOR GROUP E6 (GTE6)	GCAGGACCTTATGCGTCAAT	AGCATGGCAAATCTCATTTCC	56.5	35	Chua <i>et al.</i> (2005)
GERANIOL-10-HYDROXYLASE (GI0H)	TTGTACACTTCCATTCCATG	GAAATAGGACAGTTTGGCAC	62.3	30	St-Pierre and De Luca (1995); Facchini (2001)
GERANYL GERANYL PYROPHOSPHATE SYNTHASE (GGPS)	TCAATTACAACATGGGTTC	GTGAAAAGAAATTACCAGCTCA	60.2	30	St-Pierre and De Luca (1995)
GIBBERELLIN 20-OXIDASE (GA20OX1)	ATCATGGAGCTTCTGGGGCT	CTCTCGCTCTCGCTGTTTCCAC	57.0	35	Rieu <i>et al.</i> (2008)
GIGANTEA (GI)	GGGCTTTGGCAITGGAGAA	GCCCATCTTGGGGTTGAAGG	58.0	35	Jung <i>et al.</i> (2007)
GLYCINE-RICH PROTEIN 2B (ATGRP2B)	GTGCTCCCGTTACAGGGTAAC	ATCCCTTGCAAAGTGCCCGAG	55.6	30	Yang and Karison (2011)
HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 1 (HOS1)	AGCTCGTGGGAACAGCCAGC	TCCTCCTTCCCTTCAACGGCA	57.4	40	Dong <i>et al.</i> (2006)
HISTONE ACETYTRANSFERASE 3 (HAC3)	GATAGCCAGCAAAGAAAAGG	TCCGCAACAAAACATATCCAA	59.0	30	Earley <i>et al.</i> (2007)
HISTONE ACETYTRANSFERASE 5 (HAC5)	GAACAATCTTTGGCGTGT	CACCCACGATTTTCAACCT	59.2	30	
HISTONE ACETYTRANSFERASE 13 (HAC13)	GCTCCAGACGAAGCTATTG	AACCTTAACACGGGATGCAG	53.8	30	
HISTONE DEACETYLASE 9 (HDA9)	AGCCA GGGATCGACTAGGAT	CGGGTTTTGTTCTGCTTTCAT	56.0	35	
HISTONE DEACETYLASE 14 (HDA14)	GCCTGGAGGTT CAGGTGATA	AGGCAGGCAGTTTAAAGACGA	56.0	35	Zybailov <i>et al.</i> (2008)
HISTONE DEACETYLASE 19 (HDA19)	GATCATCGCAGCTTCTCCTC	ACGGGACAGTCTTACCAAC	53.2	30	Zhou <i>et al.</i> (2005); Chen and Wu (2010)
HISTONE DEACETYLASE 2A (HD2A)	CATGGAGTTCTGGGGAATTG	TCATCAACAGCTGGCTTCCAC	54.6	40	Ueno <i>et al.</i> (2007)
HISTONE MONO-UBIQUITINATION 2 (HUB2)	TCGGACGAGCCGATGCAGAA	CCCGGCACGAACACAAAGCA	56.5	35	Cao <i>et al.</i> (2008)
HUA ENHANCER 1 (HEN1)	GGCCTGTTCTGCCACCAGCA	TCGGTGGGGCCGCAAAAACA	59.4	40	Li <i>et al.</i> (2005)
KANADI (KAN)	GTAGCCTCCACGCCGGGTTT	TCGTGCCAATCTGGTCTGCCT	60.0	45	Wu <i>et al.</i> (2008)
LATE ELONGATED HYPOCOTYL (LHY)	CTGCACCGTCTGTTATGG	ACCGTTGTTCCAGGCTTTC	57.4	45	Park <i>et al.</i> (2010)
LEAFY (LFY)	CITTCGTTGGGAGCTTCTTG	CTGAAGAAGAACTCACGGC	53.8	45	Lee <i>et al.</i> (2008)
LEAFY COTYLEDON 2 (LEC2)	ATGGATCCTAACAAACATCG	AGCATCATCAGCTGTCTCTT	52.0	35	Willmann <i>et al.</i> (2011)
LEAFY PETIOLE (LEP)	GTTACATGTTTGGTGGCTCT	GAAACCTTGAGGAAAGAGT	52.8	35	Ward <i>et al.</i> (2006)
LIPID TRANSFER PROTEIN (LTP)	AGACTAGAAAACGACCCGGCAA	TGTTGCTGTAGAGGAAGACCG	53.7	45	Maldonado <i>et al.</i> (2002)
LSD1-LIKE1 (LDL1)	CCCTAATGGGGGAGCCTG	ACCCGCCACCCCGTCTATC	54.3	38	Jiang <i>et al.</i> (2007)
LSD1-LIKE2 (LDL2)	GGCCCTGCCITGGTGGCTT	TGCAACCACGTGGGACCTGC	54.0	35	Jiang <i>et al.</i> (2007)
LUMINIDEPENDENS (LD)	AGTTTTCCGTGCGGGCCAT	ACCTGGCGACTGTGATGCC	59.0	40	Doyle <i>et al.</i> (2009)
NUCLEAR RNA POLYMERASE D 1A (NRPD1A)	CCGGCATCTCCGTCGGAGC	ACCCCGAAATGCCCTTCGA	60.0	30	Eamens <i>et al.</i> (2008)
NUCLEAR RNA POLYMERASE D 1A (NRPD1B)	TCCCTGCCACCACAGCACT	GCCTGTCTGTGACCCAGCTT	60.0	30	Eamens <i>et al.</i> (2008)
MADS AFFECTING FLOWERING 1 (MAF1)	CCTCCGTGCGTGTGTGCTCG	TGGTGGTAATTGAGCAGCGGG	58.0	40	Ratcliffe <i>et al.</i> (2003)
MADS AFFECTING FLOWERING 5 (MAF5)	GGCGACAGCATGGCCAAAGATCA	AGAGTCTCCGGTGGGCTGTG	58.0	38	Caicedo <i>et al.</i> (2009); Kim <i>et al.</i> (2010)
MAP KINASE (Cr MAPK)	TCCTCGGTGGGTGAAATAC	CCGACAGACCACACATCAAT	58.3	30	Zhou <i>et al.</i> (2009)
METAL ION BINDING (FVE)	ACCGAGCGGAGGAAACCGGAG	GCTGCGGACCCCATCTGCAA	56.0	40	Pazhouhandeh <i>et al.</i> (2011)
NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR GROUP C					

Table 1 (contd.)

Gene name	Forward primer sequence	Reverse primer sequence	Annealing temperature of the primer for amplification (°C)	No. of cycles used for amplification	Reference ^a
2C-METHYL-D-ERYTHROL-2,4-CYCLODIPHOSPHATE SYNTHASE (MECS)	ATGGCTATGGCGACTTCTTT	GCCAAATGACATTGCCTATCT	55.5	30	St-Pierre and De Luca (1995)
O-METHYLTRANSFERASE (OMT)	ATGGACTTGGAAACTGCTGA	TCATGGATAAACTTCAATGG	62.8	32	St-Pierre and De Luca (1995); Facchini (2001)
METHYL-CpG-BINDING DOMAIN PROTEIN 8 (MBD8)	A ACTTCGGCGTCTCTCTCAG	GCTAGGGTTCGGAATCTTCC	60.0	35	Zemach and Grafi (2003)
METHYL-CpG-BINDING DOMAIN PROTEIN 10 (MBD10)	GGCTGAGGCTGAGAACAAAG	TGCTTCTGCGCTTTCATGTCG	59.3	35	Zemach and Grafi (2003)
METHYL-CpG-BINDING DOMAIN PROTEIN 11 (MBD11)	GATAAGAAATGGTCCCGGTGA	GCGATAATGCTCCGAGTAGG	52.0	40	Zemach and Grafi (2003)
miR156	TGACAGAAAGAGAGTGAGCAC	CGAACATGTACAGTCCATGGATAG	56	38	Park <i>et al.</i> (2009); Wu and Poethig (2006); Zhu <i>et al.</i> (2010)
miR159	ATTGGATTGAAGGGAGCTCCG	CGAACATGTACAGTCCATGGATAG	58	40	Allen <i>et al.</i> (2007); Patade and Suprasanna (2010); Zhu <i>et al.</i> (2010)
miR166	TCGGACCAGGCTTCATTCCTC	CGAACATGTACAGTCCATGGATAG	58	40	Bowman <i>et al.</i> (2004); Zhu <i>et al.</i> (2010)
miR171	GAGGTGAGCCGAGCCAATAIC	CGAACATGTACAGTCCATGGATAG	56	35	Hwang <i>et al.</i> (2011); Sire <i>et al.</i> (2009); Zhu <i>et al.</i> (2010)
miR319	TTGGA CTGAAAGGGAGTCCCT	CGAACATGTACAGTCCATGGATAG	58.0	38	Schommer <i>et al.</i> (2008); Zhu <i>et al.</i> (2010)
miR395	TTGAAAGTGTTTGGGGAACTC	CGAACATGTACAGTCCATGGATAG	58	35	Kawashima <i>et al.</i> (2009); Kim <i>et al.</i> (2010)
miR395c	ATGTTTTCTAGATTCCTCTG	ATCAGCCCCGGGAGTTCCCCC	58	40	Kim <i>et al.</i> (2010)
MULTICOPY SUPPRESSOR OF IRA1 (MSI)	TGGTGGCTTGGCTGTGCAACT	CAGGTGGGCCGTCTTCTGCG	60.2	35	Alexandre <i>et al.</i> (2009)
NUCLEAR FUSION DEFECTIVE 1 (NFD1)	GTCTCTGCTGTGGAAAGC	TTTGTGTGGCAAAAAGCTG	60.0	30	Portereiko <i>et al.</i> (2006)
ORESARA 1 (ORE1)	AAACCGGGCAGCAGAAAGCCG	CGTGAGACGACGAAACCGGTGA	56.0	30	Woo <i>et al.</i> (2004)
OSMOTIN-LIKE PROTEIN OSM34 (OSMOTIN)	ATGCTGCCACTATCGAGGTC	AGGACTCCACCACAGTCAAC	56.0	30	Sokol <i>et al.</i> (2007)
PATHOGENESIS RELATED (Cr PR)	GTGTTCAAAGGCGTTTGTCTT	AACTCTGGAITGGCTTGAACG	60.2	30	Pape <i>et al.</i> (2010)
PHAVOLUTA (PHV)	ACGTGCCCTGTGGCCCTCGTGA	AACTGCAGGCTGGCGTCCAC	61.1	40	Chandler <i>et al.</i> (2007)
PHD FINGER PROTEIN-LIKE PROTEIN (PHD)	TGGCACACCTCAGCCCCAAGA	GCAATGGAATTGCAGGAGGAGAGC	55.2	45	Lee <i>et al.</i> (2009)
PHENYLALANINE AMMONIA-LYASE (Cr PAL)	GCAATGCTCGTGAGAAATCA	ACATAACCCGCTTCCATCCAG	60.0	30	Olsen <i>et al.</i> (2008)

Table 1 (contd.)

Gene name	Forward primer sequence	Reverse primer sequence	Annealing temperature of the primer for amplification (°C)	No. of cycles used for amplification	Reference ^a
PHER1 (PHE1)	TGCGGTCATCCGTAGCCCGT	TGGGACAGATGCATCCACAACAGT	57.2	38	Villar <i>et al.</i> (2009)
PHOSPHENOLPYRUVATE CARBOXYLASE (PEPC)	TCAAATTACAACATGGGTTCC	GTGAAAGAAATTACCAGCTCA	56.8	35	Rademacher <i>et al.</i> (2002)
PHYTOCHROME A (PHYA)	AGCACCGCACAGCTGCCATT	GCCCTAGGAAAACCCGGCGTC	52.8	40	Jang <i>et al.</i> (2011)
PHYTOCHROME B (PHYB)	GCGTGACTCGCCTGCTGGAA	CCCCTAACGCAGCTGCACCG	56.5	40	Fernandez <i>et al.</i> (2005); Wang <i>et al.</i> (2010)
PHYTOCHROME C (PHYC)	CGTCGACGCAAAGCTACACGGA	AAAAGCCCCGGCAGCAGTCAC	57.1	38	Clack <i>et al.</i> (2009)
PHYTOCHROME D (PHYD)	TGCGCGGGAATGCTAGGGC	CCACACGAAACCGGTGACGCA	56.5	40	Fernandez <i>et al.</i> (2005)
PHYTOCHROME E (PHYE)	ACGTTCCATTCCCGTTGGCGT	AATCCTGCGGCAGCCACACG	55.8	40	Clack <i>et al.</i> (2009)
PHYTOCHROME AND FLOWERING TIME 1 (PFT1)	TCGAGAAAATCATCAGAGGAACCC	ATTGGGCTTTCCCGCATTTG	59.0	45	Kidd <i>et al.</i> (2009)
PROLINE-RICH FAMILY PROTEIN (PRF)	TCGCAAGCAGATTCCGCAAGA	AGCACCATCTGAGGAGATAGCA	58.0	35	Noh <i>et al.</i> (2004)
PROTEIN ARGININE METHYLTRANSFERASE 4A (PRMT4A)	AAGAGTTCACTCTCGCCTCCGT	CCGTTCCGGCAAGGCTGATCC	57.0	40	Niu <i>et al.</i> (2008)
PROTEIN ARGININE METHYLTRANSFERASE 4B (PRMT4B)	GCCACAGGCTGGTGCCAAAACA	TGCATCAACACACGGGCTGAGA	57.5	40	Niu <i>et al.</i> (2008)
RNA-DEPENDENT RNA POLYMERASE 2 (RDR2)	TCAGCGAGCCAACTGCGAGG	ATGCACCGCTTGCAATCGCCT	53.5	30	Brosnan <i>et al.</i> (2007)
REDUCED VERNALIZATION RESPONSE 1 (VRN1)	ACATGCCACGCCCTTTCTTCCA	ACGGGCGCGTTTGAAAGTGGT	58.0	30	Levy <i>et al.</i> (2002)
RELATIVE OF EARLY FLOWERING 6 (REF6)	AAGCGTTCCGGTCCGAGCTC	TCTTGCCTGGCACCCGCCCTTT	65.5	30	Yu <i>et al.</i> (2008)
RESPONSIVE TO DESSICATION 29A (RD29A)	GACTCCGGTCAATGAGAAAGGATCAA	ACAAACAGTGGAGCCAAAGTATTGT	59.0	30	Sokol <i>et al.</i> (2007)
REVOLUTA (REV)	TGGCTCCTGCCCCGGATTTC	AGCCTTGGCACAGACACCGC	58.0	40	Zhang <i>et al.</i> (2011)
RIBONUCLEASE/ TRANSCRIPTIONAL REPRESSOR (R/TR)	GCTGAGTTGGTGATCCCGTTC	CCCCGGTTCACCTCTAGCATA	54.1	30	
SECOLOGANIN SYNTHASE (SLS)	GCAGAAGAGTGAGCTTGTA	GGCTAATACATCACACAAGA	53.5	30	St-Pierre and De Luca (1995)
SERRATED LEAVES AND EARLY FLOWERING (SEF)	ATCGGACTCGTAAAGGTCGCT	CGACGAGAAAGACGAACTCGG	55.0	35	March-Diaz <i>et al.</i> (2007)
SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 14 (SPL14)	GAACCTTGTGCTGTCCCAIT	TGCAGATGAATTCCACCACAA	53.5	38	Stone <i>et al.</i> (2005)
STRICTOSIDINE SYNTHASE (STR)	CCTTCCATGCTCCGAATGC	CCATCGTCTCTTGAATCTG	59.0	30	Facchini (2001)
STRUCTURAL CONSTITUENT OF CYTOSKELETON (ATARP6)	CGGCGGCGAGTCATCGTCAT	ACGGTCGATTGGCGGGCGTA	62.5	30	Martin-Trillo <i>et al.</i> (2006)

Table 1 (contd.)

Gene name	Forward primer sequence	Reverse primer sequence	Annealing temperature of the primer for amplification (°C)	No. of cycles used for amplification	Reference ^a
SWINGER (SWN)	CACGCCGTGGATGCCTGT	GCGAGCCCACTGGTGCTT	55.0	35	Wang <i>et al.</i> (2006)
TABERSONINE	GCTTCAATCCACCAAGTTCCAT	TTTGCCACCAATTTCTTGACC	53.5	30	St-Pierre and De Luca (1995); Facchini (2001)
16-HYDROXYLASE (TI6H)	GGTACGCACGCITCCCCACA	ACGCGGGGTCTCCTCTCAGC	63.2	45	Legnatioli <i>et al.</i> (2009)
TIMING OF CAB EXPRESSION 1 (TOC1)	AGAGGTCGTGGTGAACATCC	TCAATGTGCAACAACCCACT	64.0	30	Takahashi <i>et al.</i> (2002)
TOPOISOMERASE1 (Ct-TOPO1) TRANSCRIPTION	TGGGAGACCTCCTGAGAAGC	ATACACCCAGGCTCGGAACA	56.0	30	Mathieu <i>et al.</i> (2003)
FACTOR IIIA (TFIIIA)	CAAAGTTTCCACACAGCACA	TTCTTCAGTTAGCCGATGAGC	54.3	30	St-Pierre and De Luca (1995); Facchini (2001)
TRYPTOPHAN DECARBOXYLASE (TDC)	TCGCGACCTGAATCGATCGGAA	CCCAGGTTGGTCTTTGCTG	57.2	40	Xu <i>et al.</i> (2009)
UBIQUITIN CARRIER PROTEIN 1 (UBC1)	CGCTAAGAGTGGCGTAGGAG	AGGGCTTGGAGCCGATAACT	54.1	35	Ward and Sze (1992)
VACUOLAR PROTON ATPase					
PROTEOLIPID SUBUNIT-LIKE PROTEIN (<i>Solanum tuberosum</i>) (ST)					
VERNALIZATION	CCCACGCCCCAGATGCACCAA	ATGGCTCCACCCGTCTGGGCT	58.0	30	Zhang <i>et al.</i> (2003)
INDEPENDENCE 3 (VIP3)	CCCACGCCCCAGATGCACCAA	ATGGCTCCACCCGTCTGGGCT	58.0	30	Zhang <i>et al.</i> (2003)
VERNALIZATION5/VIN3-LIKE (VEL2)	TCTGTCAAACGGACTGCGTGGC	TCTCGTTGCAGTCCAGTCCCT	56.0	30	Kim <i>et al.</i> (2010)
YELLOW-LEAF-SPECIFIC GENE 9 (YLS9)	GTGGCTGCTGCCCTCCTCAGC	TGGCCTTGGAAACGTTGGTGTGA	61.0	40	Yoshida <i>et al.</i> (2001)
Control ACTIN	TGAAATGTGACGTGGATATC	GCTGGAATGTGCTTAGAGA	62.0	30	Zhao <i>et al.</i> (2012)
Control Ubiquitin	AGGAGAGGGAGGCTGCTAAG	AACTTTGTTGAAAAGCGACAAT	60.1	35	Jian <i>et al.</i> (2008); Zhu <i>et al.</i> (2010)

^a = Gene sequences for primer designing were accessed from www.ncbi.nlm.nih.gov.

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