

Table S3.- Primer list specifying the genes used to corroborate results given by the transcriptomic approach. Eighteen primers were designed to obtain log₂-fold-change values. The list details sequences for each gene, gene id and the corresponding description based on BLAST result of the annotated sequence.

Gene id	Description	Tm (C°)	Primer	Sequence (5' -> 3')
GSVIVG01010629001	Ethylene responsive factor (ERF)	56.3	VvERF-s	CCT CCT TCA CAT TCC TCC TCA A
		52.5	VvERF-a	CTC CGA TAC CCA TTT ATT ACC TC
GSVIVG01025703001	Phenylalanine ammonia lyase (PAL)	56.7	VvPAL-s	AAG GTC AGG CAA GTT CTG GTA G
		61.8	vvpAL-a	ACC TCT TTG GGC AAA AGG GCC T
GSVIVG01031715001	Caffeoyl-CoA O-methyltransferase (CCOAMT)	60.2	VvCCOAMT-s	ATC GGC TAC GAC AAC ACC CTC T
		59.6	VvCCOAMT-a	CGT CAC CAA CCG GAA GCA TAC A
GSVIVG01028205001	S-adenosylmethionine synthase 5 (METK5)	54.5	VvMETK5-s	CAT CTT CCA TCT CAA CCC ATC A
		59.7	VvMETK5-a	CCC AGC CAC CGT AAG TGT CAA
GSVIVG01032744001	Laccase-12 (LAC12)	54.1	VvLAC12-s	GCA CCA TTT GAC AAT ACT ACC AC
		58.5	VvLAC12-a	CCG TGT CAT TGA AAG CAG GCA A
GSVIVG01033999001	BAHD acyltransferase DCR (DCR)	54.3	VvDCR-s	CCA CAA TTG CTT CAA ACA GTT CT
		60.9	VvDCR-a	TCC GTC TGC GAG TTC CGT GA
GSVIVG01009720001	3-methyladenine DNA glycosidase (JMT)	55.0	VvJMT-s	CTC CAT ACT ATG CAC CAA GTC C
		56.1	VvJMT-a	CCA TCA CCT CCA TCC CAA TCT A
GSVIVG01034174001	Metallothionein-like protein type 2 (MT2)	61.2	VvMT2-s	AGG AAA CTG CGG TTG TGG GTC T
		61.5	VvMT2-a	TGA TGG TCT CAG TGG TGG TGG C
GSVIVG01035962001	Chorismate mutase-2 (CM2)	56.7	VvCM2-s	TGC CTC TTC TTT CCT TCA CTC C
		54.2	VvCM2-a	AAG GTG GTA AAT CAT CTG GGA AA
GSVIVG01026477001	Polygalacturonase (PG)	57.9	VvPG-s	TCG GAG GGC TAT ACG GTA CAT G
		55.9	VvPG-a	AAA GGG TGA AAT TGC TGG TGA G
GSVIVG01016615001	Aquaporin TIP1 (TIP1)	59.6	VvTip1-s	TCT CCC TAT CCT CAG GCG TGT
		57.6	VvTip1-a	GGT GCA ATA ATG CCC AAG TTC C
GSVIVG01033651001	S-adenosylmethionine synthase 3 (METK3)	58.0	VvMETK3-s	TTG CAG AGG CAT TGG GTT TGT T
		57.0	VvMETK3-a	TCC GAT TTC CTC AGG CTT CTT G
GSVIVG01033677001	Aquaporin TIP11 (TIP11)	59.8	VvTIP11-s	AAG AAG GGC AAT TTG GGA AT
		59.9	VvTIP11-a	CCT CGT ACA CAA GTC CAG CA
GSVIVG01028402001	Cellulose synthase A catalytic subunit 7 [UDP-forming] (CESA7)	61.0	VvCESA7-s	AAA GAG AGC GGC TTT CAA GG
		60.1	VvCESA7-a	TCC AGC CAT TTC AAC TTT CC
GSVIVG01032968001	Chalcone synthase (CHSY)	60.1	VvCHSY-s	CCC GGT GCT GAC TAT CAA CT
		60.0	VvCHSY-a	AAT CCA GGT GGG TGT CAG AG
GSVIVG01027584001	Xylem serine proteinase (XSP1)	60.2	VvXSP1-s	TCA GAT ACC GGT TCG GAG AG
		60.2	VvXSP1-a	TTG TAT GTG GCG CTG TTG TT
GSVIVG01002109001	Probable mannitol dehydrogenase (MTDH)	60.1	VvMTDH-s	TGG TGT TGG GTG TAT GGT TG
		60.1	VvMTDH-a	TGT GAT CCC AGC ACA TAG GA
GSVIVG01009881001	Endoglucanase 10 (GUN10)	60.0	VvGUN10-s	TCG GAC TGC AAA GCT ATC CT
		60.0	VvGUN10-a	GGA TTG GGG TCC TTT GAT TT

