

Supplemental Table 1

Genes		Genes ID	Primers sequences	Genbank no.	Efficacy
Housekeeping genes			5'-AACCAAAATATCCGGAGTAAAAGA-3'		
	<i>EF1-α</i> (elongation factor 1-α)	VIT_206s0004g03240	5'-GAACTGGGTGCTTGATAGGC-3'	XM_002284888.3	100 %
	<i>39SRP</i> (39S ribosomal proteinL41-A)	VIT_218s0001g06410	5'-GATATAACAGGGAATACAGCAC-3'	XM_002285709.4	100 %
Photosynthesis	<i>CAB1</i> (chlorophyll a-b binding protein)	VIT_207s0005g02220	5'-GGAAATCAAGAACGGGCGTC-3'	XM_002273070.4	96.1 %
			5'-GCGTTGTTGTTCACTGGGTC-3'		
Defense	<i>CHIT1B</i> (chitinase class I basic)	VIT_203s0038g03400	5'-CCCAAGCCTTCTGCCATA-3'	NM_001280962.1	101.7 %
			5'-TGTGATAACACCAAAACCGGG-3'		
	<i>PR5</i> (thaumatin-like protein)	VIT_202s0025g04270	5'-TTTGATCATCCTTAGGGTAGCTGTAA-3'	XM_002282994.3	99.6 %
Secondary cell wall biogenesis	<i>FLA11</i> (fasciclin-like arabinogalactan protein 11)	VIT_208s0040g01970	5'-CGAAACCCCAAAGCCTAAGAA-3'	XM_002280793.2	98.7 %
			5'-GAAACACAAAGGGGTTGCA-3'		
Detoxification	<i>APX</i> (cytosolic ascorbate peroxidase)	VIT_208s0040g03150	5'-GGATTTGCTGATGCTGAGGAAC-3'	EU280159.1	97.2 %
			5'-ACCCAAATCACCGAGAAGCTCC-3'		
Stress tolerance	<i>GSTF9</i> (Glutathione S-transferase F9)	VIT_212s0028g00930	5'-GGAGCAGTGGCTAGAGTTGA-3'	XM_002283173.3	101.6 %
			5'-CATCTGCAGGAAACCCATCT-3'		
	<i>sHSP</i> (class I small heat shock protein)	VIT_206s0004g05770	5'-TCCTCGTGAAATGTGGGACC-3'	XM_002281470.3	90.4 %
	<i>PIP2-2</i> (plasma membrane 2-2 aquaporin)	VIT_203s0038g02520	5'-TCTCTATCCGGGCTTTGGC-3'	NM_001281028.1	93.4 %
Flavonoid/ isoflavonoid biosynthesis pathways			5'-GCTGTGCCTTGTGTAGCC-3'		
	<i>CHS</i> (chalcone synthase)	VIT_214s0068g00920	5'-CGAAGGAGCAATCGACGGA-3'	NM_001280950.1	99.6 %
Transcription factor			5'-GTCGCTGATGCCTATCGGAG-3'		
	<i>CRF2</i> (ethylene-responsive transcription factor CRF2)	VIT_202s0025g01055	5'-ACCTATGATACGGCGGAGGA-3'	XM_002271490.3	99.5 %
			5'-CACCGTCACCGGCTCTATTT-3'		