

Table S5. List of primers for RT-qPCR and transgenic tobacco (molecular characterization)

Primers ID	Accession ID	Functional Annotation ¹	Primers Main Features			
			Forward Primer (5'-3')	Reverse Primer (5'-3')	T _M (°C)	Amplicon Size (bp)
<i>GmNOA1</i>	Glyma.01G018000	Not Annotated 1	ACTTCCACACGAGAGAAGG	AAACTTTGCCAGCATCAGG	60	160
<i>GmFTH1</i>	Glyma.01G124500	Ferritin Heavy Chain (FTH1)	GCCTTGTTTGCGTACTTCG	AGGGAGGACTTGTGATTGG	60	163
<i>GmCYB5</i>	Glyma.03G259600	Cytochrome B5 Isoform A	GTTGACACTTCCACTCTTCC	TAGTACTGCAGGGCAAAGG	60	158
<i>GmUSP</i>	Glyma.04G107900	Universal Stress Protein Family (USP)	AGATTTGAAGCTGGATTTCGC	CTTGCTGCTGCTAGTTTCC	60	154
<i>GmALCD</i>	Glyma.04G240800	Alcohol Dehydrogenase Related	GCCATGATCTCAGCATTCG	TCTCCACAACAGAAGGAAGG	60	181
<i>GmNOA2</i>	Glyma.06G056000	Not Annotated 2	TCTGGTGTGTGTTGTTTAGC	AAGCGAAGTGGCAAATACC	60	167
<i>GmBAM5</i>	Glyma.06G301500	β-Amylase 5 Related	CTCTTATCCACAAAGCCAAGG	CTGGGACATCATTGTACTTGC	60	158
<i>GmBaBl</i>	Glyma.08G128100	Basic Blue Protein	GGACCTTTAACACCGTTACC	AGTCTGATCTGATCCTTCCC	60	178
<i>GmAPHO</i>	Glyma.08G200100	Acid Phosphatase Related	ACACCGTACTCTCTAATATCCC	GAAGCCAAGAGACAACAGC	60	155
<i>GmREMNI</i>	Glyma.09G139200	Remorin, N-terminal Region	TTCATCAGTTTCTGCATGGG	GCTCTTCTTTCTTCAGCTTCC	60	156
<i>GmDR4R</i>	Glyma.09G155500	DR4 Protein Related	GTGGTGGATTGAAACTAGGC	GGAGGATTCAGCACATAAGG	60	188
<i>GmCALN</i>	Glyma.10G147600	Calreticulin and Calnexin	GCTGGTTGAAGAAACATGGG	CGTCTTTGATTCAGCATCGG	60	175
<i>GmAND1</i>	Glyma.13G088700	Annexin D1 Related	GAGAAGGTTGTTTCGCTTGG	GGTGGTGTCTTAACAATAGC	60	162
<i>GmAUXA</i>	Glyma.13G237000	Dormancy/Auxin Associated Protein	CAGAAGACGTTGTCTGATGC	TAGACAGTGGGAGTGTTGG	60	188
<i>GmTYR</i>	Glyma.15G071200	Catechol Oxidase/Tyrosinase	TAGGTCAAGGGTTCAGAAGG	AAACCTCTTCCTCCTCTTCC	60	179
<i>GmTRPI</i>	Glyma.15G211500	Trypsin and Protease Inhibitor (Kunitz)	AAACCACGGGATCATACGG	CTGGAACATAACTGGGAGAGG	60	191
<i>GmBetV</i> ²	Glyma.17G030400	Pathogenesis Related Protein Bet v 1	TCGTTGAGGATGGAGAAACC	GTTTGGTATTCGACAGTGAGC	60	193
<i>GmGST</i>	Glyma.18G190300	Glutathione S Transferase	GAGGAGTTTGGCTTTGTGG	GCATAACTTCGTTGACAACTGG	60	151
<i>GmENOX</i>	Glyma.19G008500	Enone Oxidoreductase	AGAGTGGGAAGTAAAGTGAGG	AAATTGGAGGGTTTGTGAGC	60	152
<i>GmNOA3</i>	Glyma.19G114700	Not Annotated 3	AAGGAGGAGGAGCATAAGG	CTTGACTTTGTCTAGGAACCC	60	168
<i>GmCYP2</i> ³	Glyma.12G024700	CYP18-3 Related	CGGGACCAGTGTGCTTCTTCA	CCCCTCCACTACAAAGGCTCG	60	154
<i>GmERFIA</i> ³	Glyma.05G114900	Translation Factor	GACCTTCTTCGTTTCTCGCA	CGAACCTCTCAATCACACGC	60	161
<i>eGFP</i> ^{2,4}	MN623123.1 ⁵	Enhanced Green Fluorescent Protein	ACTTCAAGATCCGCCACAAC	GAACTCCAGCAGGACCATGT	60	179
<i>NtACT1</i> ^{2,3}	U60489.1 ⁵	<i>Nicotiana tabacum</i> Actin	AGCAAGGAAATTACCGCATTAGC	ACCTGCTGGAATGTGCTGAGA	60	125
<i>NtL25</i> ^{2,3}	L18908.1 ⁵	<i>Nicotiana tabacum</i> Ribosomal Protein L25	GCTAAGGTTGCCAAGGCTGTCAAG	GCACTAATACGAGGGTACTTGGGGTTTC	60	134

¹ For soybean genes, the assembly version used was *Glycine max* Wm82.a2.v1 (Phytozome 13).² Transgenic Tobacco Molecular Characterization³ Housekeeping/Reference Genes.⁴ Tobacco Transformation Marker.⁵ Accession ID from NCBI database.