

Supplemental Data. Li et al. (2008). The *Arabidopsis* NFYA5 transcription factor is regulated transcriptionally and posttranscriptionally to promote drought resistance.

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AT1G17590 VNAKQEHAI MRRRQ QAKLEAQN----KLIKARKPYLHESRHVHALR RPRGSGGRFLNTK
AT1G54160 VNAKQYHAILRRRKHRAKLEAQN----KLIKCRKPYLHESRHLHALR RARGSGGRFLNTK
AT1G72830 VNAKQYHAIMRRRQ QAKLEAQN----KLIKARKPYLHESRHVHALR RPRGSGGRFLNTK
AT2G34720 VNAKQYHGI LRRRQ SRAKLEARN----RAIKAKKPYMHESRHLHALR RPRGCGGRFLNTK
AT3G05690 VNAKQYHGI LRRRQ SRAKLEAVLDQKKLSRCRKPYMHESRHLHALR RPRGSGGRFLNTK
AT3G14020 VNAKQYQAILRRRERAKLEAQN----KLIKVRKPYLHESRHLHALR RVRGSGGRFLNTK
AT3G20910 VNAKQYQAILRRRQARAKAELEK----KLIKSRKPYLHESRHVHALR RPRGCGGRFAKKT
AT5G06510 VNAKQYHGI LRRRQ SRAKAEKLS----RCRKPYMHESRHLHALR RPRGSGGRFLNTK
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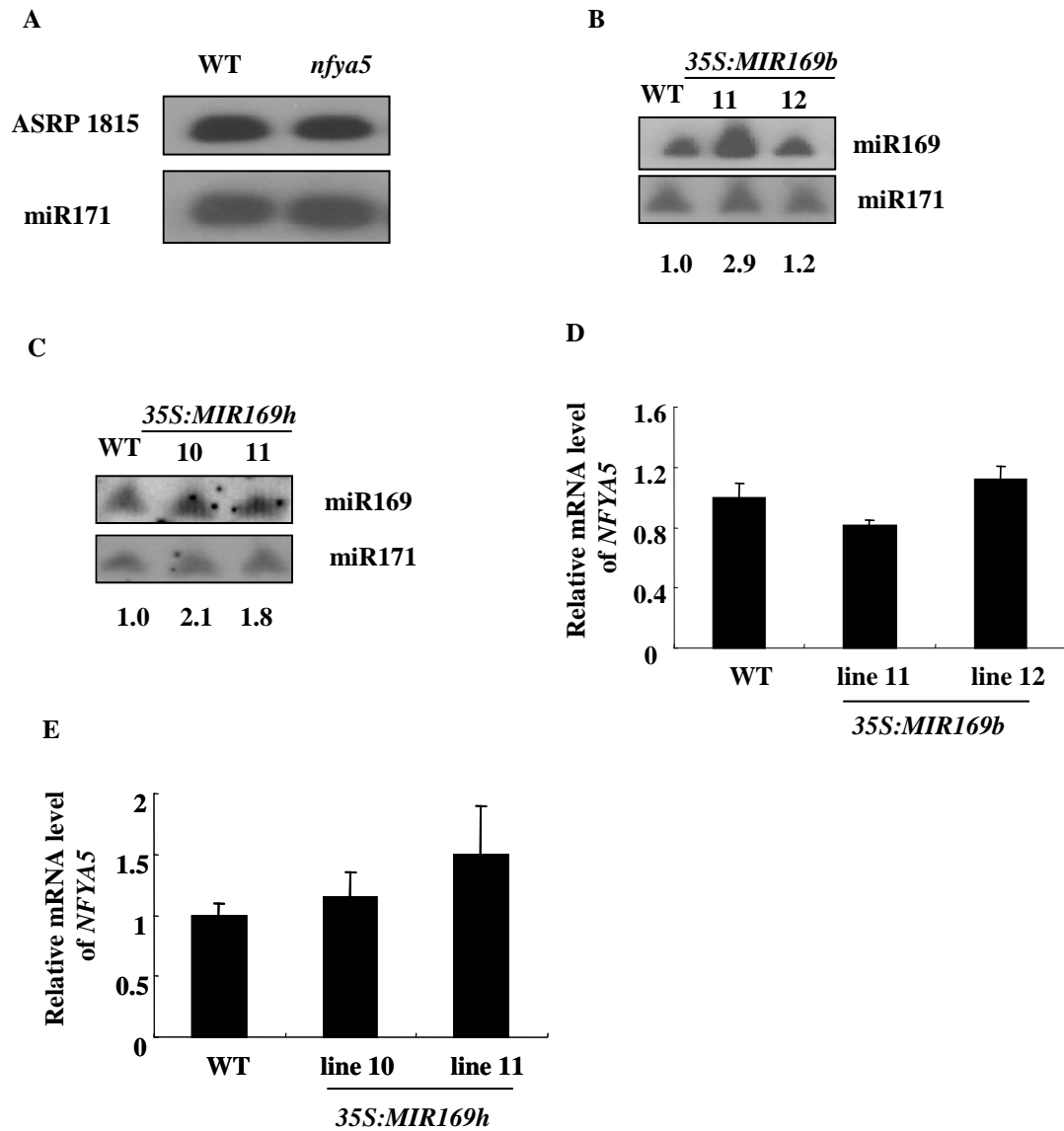
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NF-YC/NF-YB binding

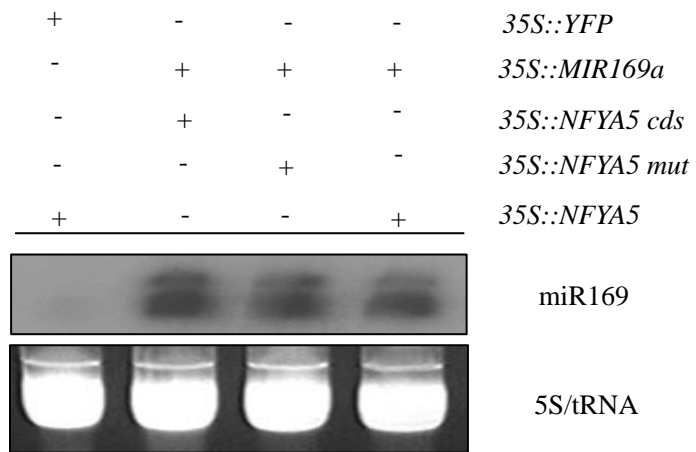
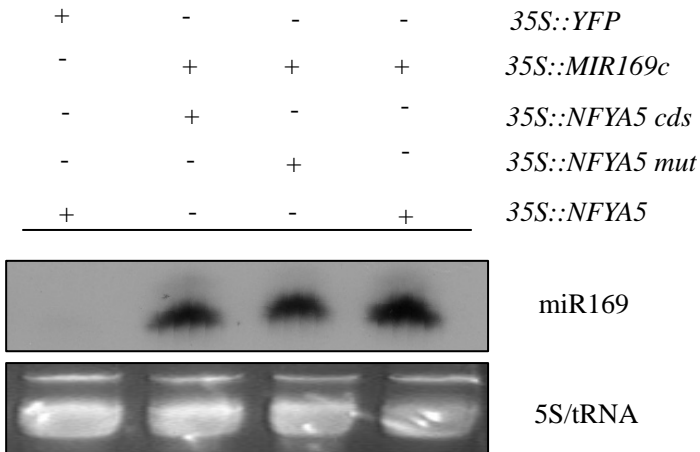
Linker

DNA binding

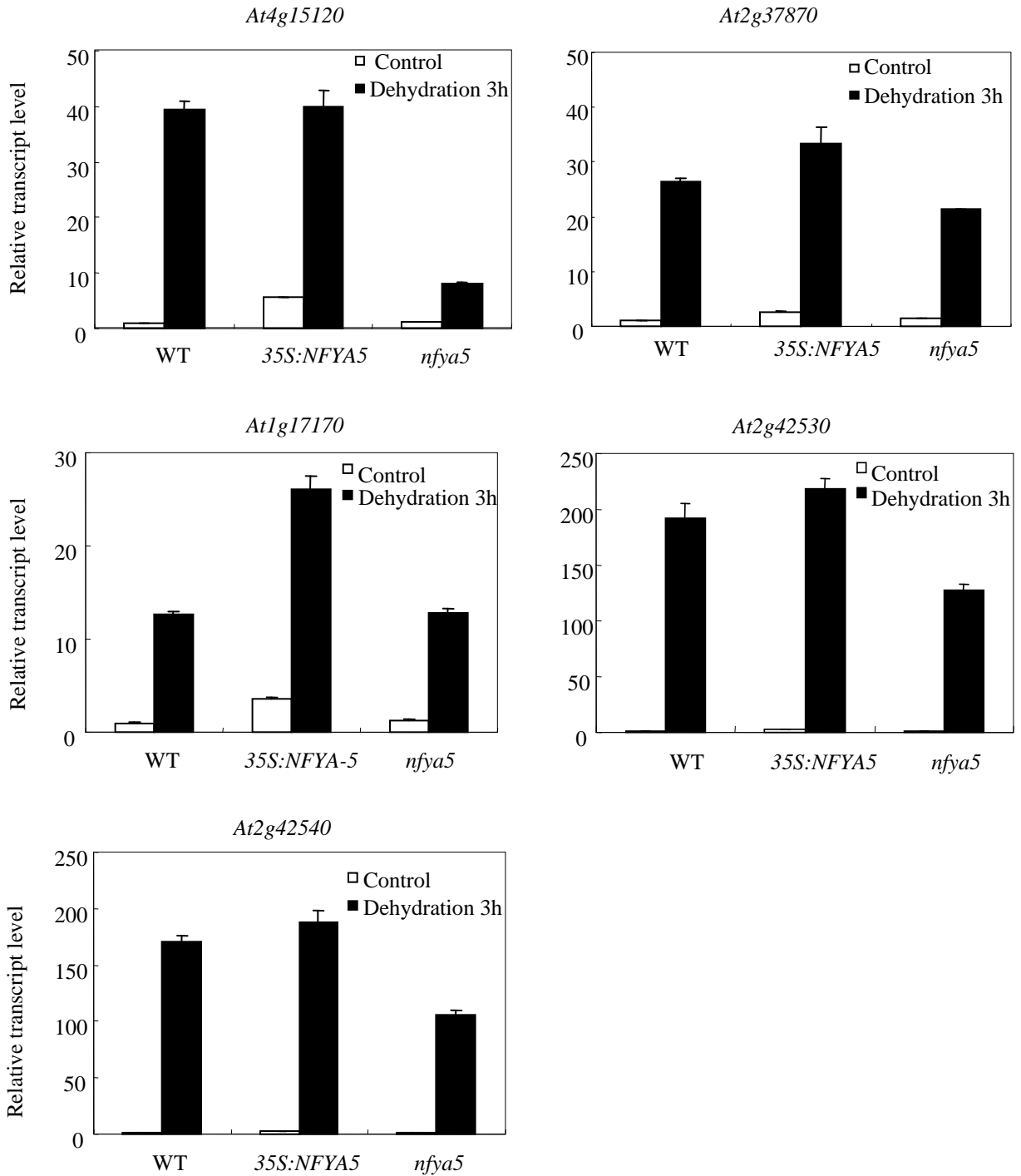
Supplemental Figure 1. Sequence alignment of the conserved domains in *Arabidopsis* NFYA family members.



Supplemental Figure 2. Analysis of miR169 (A-C) and *NFYA5* mRNA (D and E) levels in *nfyA5*, *35S:MIR169b* and *35S:MIR169h* transgenic plant lines. Real-time RT-PCR quantification of *NFYA5* transcript levels was normalized to the expression of *Tub 8*. Error bars represent standard errors (n=3).

A**B**

Supplemental Figure 3. Coexpression of various combinations of miR169 and *NFYA5* constructs in *N. benthamiana*. (A) Detection of miR169 in *N. benthamiana* coexpressing *MIR169a* and *NFYA5* constructs. (B) Detection of miR169 in *N. benthamiana* coexpressing *MIR169c* and *NFYA5* constructs.



Supplemental Figure 4. Analysis of transcript levels in the wild-type and 35S:NFYA5 transgenic plants. Real-time RT-PCR was used for analyzing the expression levels (normalized to the expression of *Tub8*) of indicated loci. Error bars represent standard errors for three independent experiments.

Supplemental Table S1. List of genes with expression changes (pfp<0.05) in the 35S:*NFYA5* transgenic plants from microarray analysis.

A. Genes with higher expression in *NFYA5* overexpression plants

Gene ID	Affy ID	Relative Expression Values (log ₂)				Definition
		WT1	WT2	OX1	OX2	
AT1G17170	262518_at	6.05	5.94	7.42	7.15	[AT1G17170]ATGSTU24 (Arabidopsis thaliana Glutathione S-transferase (class tau) 24); glutathione transferase
AT1G17180	262517_at	5.60	5.25	7.01	7.23	[AT1G17180]ATGSTU25 (Arabidopsis thaliana Glutathione S-transferase (class tau) 25); glutathione transferase
AT1G26380	261021_at	5.74	5.46	8.02	6.38	[AT1G26380]FAD-binding domain-containing protein
AT1G54160	263158_at	5.71	5.87	8.54	10.38	[AT1G54160]CCAAT-binding transcription factor (CBF-B/NF-YA) family protein
AT1G78340	260803_at	5.78	5.84	6.73	6.82	[AT1G78340]ATGSTU22 (Arabidopsis thaliana Glutathione S-transferase (class tau) 22); glutathione transferase
AT1G78370	260745_at	9.39	9.25	10.21	10.19	[AT1G78370]ATGSTU20 (Arabidopsis thaliana Glutathione S-transferase (class tau) 20); glutathione transferase
AT2G30750	267565_at	4.71	4.70	6.77	5.89	[AT2G30750]CYP71A12 (cytochrome P450, family 71, subfamily A, polypeptide 12); oxygen binding
AT2G37870	266098_at	7.18	7.00	8.59	8.57	[AT2G37870]protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT2G40670	266078_at	5.92	5.61	6.67	6.62	[AT2G40670]ARR16 (response regulator 16); transcription regulator/ two-component response regulator
AT2G41480	267101_at	5.81	5.76	6.92	7.03	[AT2G41480]peroxidase
AT2G42530	263495_at	8.28	8.28	9.40	9.36	[AT2G42530]cold-responsive protein / cold-regulated protein (cor15b)
AT2G42540	263497_at	9.42	9.60	10.52	10.77	[AT2G42540]COR15A (COLD-REGULATED 15A)
AT2G43570	260568_at	6.05	5.94	8.06	6.87	[AT2G43570]chitinase, putative
AT3G49580	252269_at	6.06	5.60	6.81	6.80	[AT3G49580]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49570.1); similar to unknown protein [Brassica rapa subsp. pekinensis] (GB:AAQ92331.1)

AT3G53400	251937_at	7.02	6.93	8.00	7.84	[AT3G53400]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03190.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABD32814.1); contains domain ARM repeat (SSF48371); contains domain no description (G3D.3.40.50.1860)
AT4G15210	245275_at	4.50	4.52	6.40	6.10	[AT4G15210]ATBETA-AMY (BETA-AMYLASE); beta-amylase
AT4G23600	254232_at	8.62	8.75	9.93	9.43	[AT4G23600]CORI3 (CORONATINE INDUCED 1, JASMONIC ACID RESPONSIVE 2); transaminase
AT5G38900	249481_at	4.89	4.89	6.60	5.50	[AT5G38900]DSBA oxidoreductase family protein
AT5G59310	247718_at	7.33	7.15	8.59	7.90	[AT5G59310]LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding
AT5G59320	247717_at	8.73	8.42	9.55	9.44	[AT5G59320]LTP3 (LIPID TRANSFER PROTEIN 3); lipid binding
AT5G65080	247224_at	4.70	4.76	5.96	6.01	[AT5G65080]MAF5 (MADS AFFECTING FLOWERING 5); transcription factor
ATCG00600	244966_at	6.17	7.28	8.22	8.70	[ATCG00600]Cytochrome b6-f complex, subunit V. Disruption of homologous gene in Chlamydomonas results in disruption of cytochrome b6-f complex.
ATCG00660	244970_at	6.63	6.76	7.69	7.55	[ATCG00660]encodes a chloroplast ribosomal protein L20, a constituent of the large subunit of the ribosomal complex
ATCG01000,ATCG01130	244993_s_at	9.34	9.95	10.72	10.95	[ATCG01000]hypothetical protein ,[ATCG01130]hypothetical protein

B. Genes with lower expression in *NFYA5* overexpression plants

Gene ID	Affy ID	Relative Expression Values (log ₂)				Definition
		WT1	WT2	OX1	OX2	
AT1G05250,AT1G05240	264567_s_at	8.36	8.40	7.30	7.65	[AT1G05250]peroxidase, putative ,[AT1G05240]peroxidase, putative
AT1G05260	264577_at	9.19	9.11	8.05	8.10	[AT1G05260]RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase
AT1G10770	262760_at	7.39	7.06	6.36	6.68	[AT1G10770]invertase/pectin methylesterase inhibitor family protein
AT1G13300	259365_at	6.49	6.43	5.60	5.71	[AT1G13300]myb family transcription factor
AT1G13670	256097_at	8.06	7.96	7.32	7.35	[AT1G13670]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69160.1)
AT1G19530	260668_at	12.05	12.09	11.49	11.24	[AT1G19530]unknown protein

AT1G29090	260890_at	6.00	5.51	5.08	4.74	[AT1G29090]peptidase C1A papain family protein
AT1G29500	259773_at	6.93	6.83	6.22	6.17	[AT1G29500]auxin-responsive protein, putative
AT1G49860	259813_at	6.89	6.84	5.93	6.42	[AT1G49860]ATGSTF14 (Arabidopsis thaliana Glutathione S-transferase (class phi) 14); glutathione transferase
AT1G51830	246375_at	6.75	6.75	5.43	6.04	[AT1G51830]ATP binding / kinase/ protein serine/threonine kinase
AT1G61590	265031_at	7.12	6.83	6.30	6.27	[AT1G61590]protein kinase, putative
AT1G64660	261957_at	9.65	9.61	9.27	8.63	[AT1G64660]ATMGL; catalytic/ methionine gamma-lyase
AT1G69490	256300_at	10.05	10.02	9.38	9.06	[AT1G69490]NAP (NAC-LIKE, ACTIVATED BY AP3/PI); transcription factor
AT1G70850	262260_at	10.73	10.87	9.82	10.04	[AT1G70850]Bet v I allergen family protein
AT1G73330	245736_at	11.27	11.46	10.70	10.62	[AT1G73330]ATDR4 (Arabidopsis thaliana drought-repressed 4)
AT1G76410	259982_at	9.16	9.18	8.78	8.19	[AT1G76410]ATL8; protein binding / zinc ion binding
AT1G78290	260774_at	8.46	8.28	7.57	7.41	[AT1G78290]serine/threonine protein kinase, putative
AT1G79360	264124_at	7.54	7.68	7.18	6.67	[AT1G79360]transporter-related
AT1G79840	260166_at	7.67	7.47	6.52	7.00	[AT1G79840]GL2 (GLABRA 2); DNA binding / transcription factor
AT1G80160	262047_at	8.73	8.76	8.17	7.80	[AT1G80160]lactoylglutathione lyase family protein / glyoxalase I family protein
AT1G80240	262045_at	7.94	7.85	6.80	7.00	[AT1G80240]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25460.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Galactose-binding like; (InterPro:IPR008979); contains InterPro domain Protein of unknown function DUF642; (InterPro:IPR006946)
AT2G01520	266353_at	10.53	10.75	9.48	9.56	[AT2G01520]major latex protein-related / MLP-related
AT2G01530	266330_at	11.06	11.12	10.16	10.35	[AT2G01530]major latex protein-related / MLP-related
AT2G01900	263596_at	5.12	4.89	4.26	4.39	[AT2G01900]endonuclease/exonuclease/phosphatase family protein
AT2G14580	266383_at	6.59	6.19	5.76	5.64	[AT2G14580]ATPRB1 (Arabidopsis thaliana basic pathogenesis-related protein 1)
AT2G17880	264788_at	9.52	9.54	8.82	8.94	[AT2G17880]DNAJ heat shock protein, putative
AT2G21540	263765_at	7.19	7.04	6.33	6.50	[AT2G21540]SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative
AT2G22860	266799_at	9.31	9.34	8.71	8.50	[AT2G22860]ATPSK2 (PHYTOSULFOKINE 2 PRECURSOR); growth factor

AT2G31980	265672_at	6.50	6.22	5.65	5.73	[AT2G31980]cysteine proteinase inhibitor-related
AT2G32300	266356_at	6.14	6.25	5.37	5.63	[AT2G32300]UCC1 (UCLACYANIN 1); copper ion binding
AT2G33815,AT2G33810	267460_at	7.37	6.85	6.13	6.05	[AT2G33815]other RNA ,[AT2G33810]SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); transcription factor
AT2G34180	267045_at	7.04	6.86	6.56	6.00	[AT2G34180]CIPK13 (CIPK13); kinase
AT2G34390,AT2G29870	267024_s_at	9.27	9.22	8.05	8.53	[AT2G34390]NIP2;1/NLM4 (NOD26-LIKE INTRINSIC PROTEIN 2;1); water channel ,[AT2G29870]major intrinsic family protein / MIP family protein
AT2G35270	266546_at	8.01	7.84	7.07	7.37	[AT2G35270]DNA-binding protein-related
AT2G35710	265841_at	6.65	6.72	5.82	5.99	[AT2G35710]glycogenin glucosyltransferase (glycogenin)-related
AT2G37750	267178_at	10.31	10.34	9.48	9.52	[AT2G37750]unknown protein
AT2G41260	266393_at	4.48	3.99	3.51	3.37	[AT2G41260]M17
AT2G44380	267385_at	9.53	9.44	8.65	8.85	[AT2G44380]DC1 domain-containing protein
AT2G45220	245148_at	9.54	9.53	9.13	8.48	[AT2G45220]pectinesterase family protein
AT2G46740	266711_at	7.98	7.86	7.02	6.99	[AT2G46740]FAD-binding domain-containing protein
AT3G02620,AT3G02610	258473_s_at	6.90	6.71	5.50	5.81	[AT3G02620]acyl-(acyl-carrier-protein) desaturase, putative / stearyl-ACP desaturase, putative ,[AT3G02610]acyl-[acyl-carrier-protein] desaturase
AT3G09220	259036_at	8.62	8.84	7.92	7.90	[AT3G09220]LAC7 (laccase 7); copper ion binding / oxidoreductase
AT3G11370	259260_at	4.94	4.99	4.16	4.32	[AT3G11370]DC1 domain-containing protein
AT3G13700,AT3G13710	256771_at	7.85	7.92	7.03	7.15	[AT3G13700]RNA-binding protein, putative ,[AT3G13710]prenylated rab acceptor (PRA1) family protein
AT3G14770	256548_at	9.22	9.28	8.57	8.43	[AT3G14770]nodulin MtN3 family protein
AT3G15440	258383_at	7.54	7.69	6.87	6.98	[AT3G15440]similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:AT3G15740.1)
AT3G16150	258338_at	10.03	10.03	9.22	8.63	[AT3G16150]L-asparaginase, putative / L-asparagine amidohydrolase, putative
AT3G18170	258143_at	6.54	6.02	5.31	5.82	[AT3G18170]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18180.1); similar to glycosyltransferase [Saccharum officinarum] (GB:CAI30073.1); contains InterPro domain Protein of unknown function DUF563; (InterPro:IPR007657)
AT3G20210	257130_at	4.72	4.77	3.87	3.91	[AT3G20210]DELTA-VPE (delta vacuolar processing enzyme); cysteine-type endopeptidase

AT3G21370	256814_at	5.48	5.35	4.78	4.70	[AT3G21370]glycosyl hydrolase family 1 protein
AT3G21720	257947_at	6.89	6.72	6.08	5.71	[AT3G21720]isocitrate lyase, putative
AT3G45730	252539_at	8.93	8.82	8.18	7.90	[AT3G45730]unknown protein
AT3G46270	252510_at	5.38	5.21	4.19	4.42	[AT3G46270]receptor protein kinase-related
AT3G48580	252320_at	5.99	6.32	5.29	5.24	[AT3G48580]xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
AT3G49160	252300_at	5.68	6.07	5.42	5.01	[AT3G49160]pyruvate kinase family protein
AT3G50970	252102_at	12.17	12.09	11.47	11.34	[AT3G50970]LTI30/XERO2 (LOW TEMPERATURE-INDUCED 30)
AT3G53250	251977_at	5.57	5.05	4.42	4.66	[AT3G53250]auxin-responsive family protein
AT3G59900	251436_at	7.04	6.92	5.89	6.42	[AT3G59900](ARGOS); unknown protein
AT3G62680	251226_at	6.33	6.37	5.35	5.23	[AT3G62680]PRP3 (PROLINE-RICH PROTEIN 3); structural constituent of cell wall
AT4G00680	255632_at	6.58	6.27	5.34	5.83	[AT4G00680]actin-depolymerizing factor, putative
AT4G01140	255608_at	5.74	5.69	4.99	4.86	[AT4G01140]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G08600.1); similar to Protein of unknown function DUF1191 [Medicago truncatula] (GB:ABE88654.1); contains InterPro domain Protein of unknown function DUF1191; (InterPro:IPR010605)
AT4G02270	255516_at	8.54	8.63	7.50	7.93	[AT4G02270]pollen Ole e 1 allergen and extensin family protein
AT4G04990	255252_at	6.11	6.05	5.37	5.42	[AT4G04990]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61260.1); similar to fiber expressed protein [Gossypium hirsutum] (GB:AAY85179.1); contains InterPro domain Protein of unknown function DUF761, plant; (InterPro:IPR008480)
AT4G08300	255127_at	6.90	6.68	6.03	6.21	[AT4G08300]nodulin MtN21 family protein
AT4G12550	254828_at	10.78	10.91	9.53	10.03	[AT4G12550]AIR1 (Auxin-Induced in Root cultures 1); lipid binding
AT4G14060	245267_at	5.34	5.40	4.87	4.51	[AT4G14060]major latex protein-related / MLP-related
AT4G14130	245325_at	10.28	10.31	9.71	9.39	[AT4G14130]XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting on glycosyl bonds
AT4G18510	254644_at	7.77	7.80	6.62	6.43	[AT4G18510]CLE2 (CLAVATA3/ESR-RELATED); receptor binding
AT4G25820	254044_at	7.73	7.29	6.17	6.61	[AT4G25820]XTR9 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 9); hydrolase, acting on glycosyl bonds
AT4G26010	253998_at	8.89	8.78	7.70	8.08	[AT4G26010]peroxidase, putative
AT4G26260	254001_at	8.97	9.10	8.41	8.06	[AT4G26260]MIOX4 (MYO-INOSITOL OXYGENASE 4)

AT4G27260	253908_at	8.23	8.45	7.67	7.62	[AT4G27260]GH3.5/WES1; indole-3-acetic acid amido synthetase
AT4G28520	253767_at	5.67	5.50	4.41	4.22	[AT4G28520]CRU3 (CRUCIFERIN 3); nutrient reservoir
AT4G28530	253774_at	5.67	5.90	4.81	5.35	[AT4G28530]ANAC074 (Arabidopsis NAC domain containing protein 74); transcription factor
AT4G30670	253582_at	7.90	8.11	6.94	7.32	[AT4G30670]unknown protein
AT4G32280	253423_at	6.21	5.78	5.33	5.33	[AT4G32280]IAA29 (indoleacetic acid-induced protein 29); transcription factor
AT4G37220	246251_at	7.93	7.73	7.05	6.82	[AT4G37220]stress-responsive protein, putative
AT4G39675	252882_at	11.34	11.35	10.72	10.49	[AT4G39675]unknown protein
AT4G40090	252833_at	5.88	5.83	5.02	5.27	[AT4G40090]AGP3 (ARABINOGALACTAN-PROTEIN 3)
AT5G02540	251013_at	7.74	7.75	6.56	7.19	[AT5G02540]short-chain dehydrogenase/reductase (SDR) family protein
AT5G02580	251012_at	5.88	5.57	5.04	5.02	[AT5G02580]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55240.1); similar to Os03g0280400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001049737.1); similar to Os05g0462000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055765.1); similar to Os01g0837600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044739.1); contains InterPro domain Conserved hypothetical protein 1589, plant; (InterPro:IPR006476)
AT5G04340	245711_at	8.32	8.28	7.77	7.49	[AT5G04340]C2H2; nucleic acid binding / transcription factor/ zinc ion binding
AT5G04960	250801_at	5.72	5.46	4.75	5.09	[AT5G04960]pectinesterase family protein
AT5G05500	250778_at	7.82	7.90	6.96	7.31	[AT5G05500]pollen Ole e 1 allergen and extensin family protein
AT5G10040	250464_at	8.86	8.62	8.41	7.37	[AT5G10040]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65207.1); similar to 80A08_3 [Brassica rapa subsp. pekinensis] (GB:AAZ67588.1)
AT5G12050	250327_at	8.62	8.71	7.68	8.23	[AT5G12050]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54200.1); similar to Os03g0175800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001049135.1); similar to ATP-dependent DNA helicase, putative [Plasmodium falciparum 3D7] (GB:NP_702167.1)
AT5G19890	246149_at	6.56	6.64	6.19	5.66	[AT5G19890]peroxidase, putative
AT5G23220	249848_at	6.52	6.60	5.85	5.54	[AT5G23220]isochorismatase hydrolase family protein

AT5G24410	249729_at	6.96	6.82	6.15	6.07	[AT5G24410]glucosamine/galactosamine-6-phosphate isomerase-related
AT5G25110	246922_at	8.28	8.05	7.14	7.40	[AT5G25110]CIPK25 (CBL-INTERACTING PROTEIN KINASE 25); kinase
AT5G39520	249454_at	5.89	5.73	5.27	5.00	[AT5G39520]similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39530.1); similar to hypothetical protein MtrDRAFT_AC119412g1v1 [Medicago truncatula] (GB:ABE86761.1)
AT5G43520	249097_at	9.51	9.54	8.45	8.93	[AT5G43520]DC1 domain-containing protein
AT5G44120	249082_at	7.32	7.33	4.34	3.83	[AT5G44120]CRA1 (CRUCIFERINA); nutrient reservoir
AT5G44260	249065_at	9.22	9.14	8.26	8.57	[AT5G44260]zinc finger (CCCH-type) family protein
AT5G44610	249009_at	8.79	8.49	7.89	8.08	[AT5G44610]DREPP plasma membrane polypeptide-related
AT5G47950	248723_at	6.70	6.86	5.72	6.16	[AT5G47950]transferase family protein
AT5G52050	248392_at	6.97	6.72	6.25	5.69	[AT5G52050]MATE efflux protein-related
AT5G53980	248208_at	5.47	5.45	4.69	4.83	[AT5G53980]ATHB52 (ARABIDOPSIS THALIANA HOMEBOX PROTEIN 52); transcription factor
AT5G57530	247871_at	5.59	5.39	4.35	4.87	[AT5G57530]xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
AT5G57760	247878_at	8.55	8.41	7.06	7.98	[AT5G57760]contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598)
AT5G58750	247778_at	5.47	5.03	4.52	4.66	[AT5G58750]wound-responsive protein-related
AT5G62860	247394_at	7.81	7.81	7.14	7.17	[AT5G62860]F-box family protein-related
AT5G67400	246991_at	8.34	8.29	7.45	7.55	[AT5G67400]peroxidase 73 (PER73) (P73) (PRXR11)
no_match	248636_at	6.60	6.50	5.64	5.64	[no_match]
no_match	261297_at	5.63	5.68	4.86	5.04	[no_match]

Supplemental Table 2. List of primers used in this study

Primer Name	Sequence (5'-3')
miR169a Forward	TGGGTATAGCTAGTGAAACGCG
miR169a Reverse	CCTTAGCTTGAGTTCTTGCGA
miR169b Forward	CTCCACTCCCTAAACCATCACAAC
miR169b Reverse	CTCATAACGGTCGATGTTAATCCGT
miR169c Forward	CTACATTCACAAACGAGAGAATT
miR169c Reverse	GCTCTACTTTAGCATCTCAACCA
miR169h Forward	GTAGTCTTGTGGGATACTCATCA
miR169h Reverse	ATCCCCAAATTTGGAGGCCAAACA
miR169i Forward	AAGGTGTCTCTGGGTTGAAAAT
miR169i Reverse	CCATGATCATTTCATGTGCGTGCCT
miR169j Forward	GAGAGCACATCCATGTGAGGAA
miR169j Reverse	GTCAGGCAAGTCATCCTTGGCT
miR169k Forward	CTCTTTGGCTATCTTGACATGCT
miR169k Reverse	CCAAGGAGACTGCCTGATGTCT
miR169l Forward	GAGAGCACATGAATGTAAGGCA
miR169l Reverse	AATAATGTGTAGACTCAGCCACAT
miR169l Reverse	CTTGCGGGTTAGGTTTCAGGCA
miR169m Reverse	GCCTCGAAATCATGAACATTATCT
miR169n Forward	AGAGAGCACATGCATGTATGGA
miR169n Reverse	GAAAAGTAGGTATAACATGGATGG
NFYA5 Forward	GAAGATTCATCTTGGGGAAACTC
NFYA5 Reverse	GAGCAGGAAACACAGAGTCTTGA
At4g15120 Forward	GGTTGGGTGTTTCCCGGCATCGGA
At4g15120 Reverse	GGCTTCTCCTAAGATCTGATCTCCA
At1g17170 Forward	CCTTCCCTCCGATCCTTACAAGA
At1g17170 Reverse	CAACCCAAGTTTCTTCTACGTTTCG
At2g37870 Forward	CGTTGAGGCGGCAGGTGAGTGT
At2g37870 Reverse	TGTAACGTCCACATCGCTTGCCA
At2g42530 Forward	TCAGTGGCATGGGTTCTTCTTCCA
At2g42530 Reverse	GAGGTCATCGAGGATGTTGCCGT
At2g42540 Forward	GTTCTCACTGGTATGGCTTCTT
At2g42540 Reverse	GTCTTTCGCTTCTCACCATCTGCT
18S Forward (tobacco)	AGGAATTGACGGAAGGGCA
18S Reverse (tobacco)	GTGCGGCCCCAGAACATCTAAG
Tub8 Forward	ATAACCGTTTCAAATCTCTCTCTC

Tub8 Reverse

TGCAAATCGTTCTCTCCTTG
