Supplementary Data

Title of article: A cotton miRNA is involved in regulation of plant response to salt stress

Running head: miRNVL5 and *GhCHR* involved in plant salt stress response

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Supplementary Data S1. Sequences of mature miRNVL5 (red) and its precursor (yellow)

Primary transcripts of miRNVL5

GATCTGGGCTTGGGTGCCTATAAATTCTTTAGGGGAAAAAGTAGGGCATCAGAGTGTATAGCCGAATATGCAAAAAGGCGAGGG
TGAGGGTGGAGTTTGAATCAAACAAGAAAATCATATTCTTACCTTCTTTTCTTCACAAATATCACAATAAAACATGGATGAAACT
ATCGATGCCCAAAGCTGCCTCTTGTATCGATGATAGAGTTCTATTATTGTGATATTAGTGAGGAACAAAAGGTATTGATATGAGG
TCGACGGCCATGACCAGATTCTGTCGGATATACACTCACCGTGTGCTGCGTACTGCTTTATTATCTTTGCCTC

Pre-miRNVL5

UUUCUUCACAAAUAUCACAAUAAAACAUGGAUGAAACUAUCGAUGCCCAAAGCUGCCUCUUGUAUCGAUGAUAGAGUUCUAU

UAUUGUGAUAUUAGUGAGGAAC

Mature miRNVL5
UUUCUUCACAAAUAUCACAAUA

Supplementary Data S2. Sequences of *GhCHR* and deduced amino acids of GhCHR

A: Sequences of *GhCHR* cDNA

ATGCTCTCGATCATTATATTTCTTCACTTGTAATCTTGCTTTTGGACTCTCTCTCTCTCTTTCCAATTTGTACTATACTTCAAACATTGAGTTTCAGTTTTTTTCTTCC
TACGTCAATGCAAAAAACCAAAGAGGAAGGAGAA**ATG**GAGGAGTCTAACAATTATGGCCACCAACATCCCCTGCTTCTTATCTTGAATCAAGACCAGCTGATC
CACAATCAAAGTGGTGTAACTCATTGCTCCAGGTGTGGGGAGAAGGTGTCTGCTCCATGTTTTTGCTGTGCGGAGCGCTGTGGGTTTTATGTCCACAAGGTATG
TGCCGAGGCACCTTTGGAGCTTAATCATCCTTTTCATACTCATCATCCTCTTCTTCTTATGCAAAATGCCCCTTATTCATCTGGACGGTACATTTGCAATTTTTGCG
ATAAAGACGGTAGTAAGTTTGTTTATCACTGCTCTTGCGGATTGGACTTTCATATTAAATGTGCTTTGTTTACATTTAATATTGCTGAGAATAATTTGAAAGAGCTT
GACCATGTTGCCCTTCAACATCCTTTGATTTCCACTGAAAACGGTGATGAAGAACTTGGAGACGTTAGTAAGTGCTTTGGATGTTGGGAACCATTAGCAAAGTA
TACACACTTTTCTCCTGACTGTGGATTTAATTTCCATGAGAAATGCGCTAAGCTTCCTTTCAAACTGAATCATGAGTGCCATCGCAAGCATCCTCTTGCTCTACAA
TTTAATAGCAAACGGCTCTCTTGCAAGATATGCAGAGAAACCAATCGAAAAACAGATCGCAGGCGTATAGGATTTGTTTATGGTTGTTCACCCTGTAAGTTTGCT
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CATGTGGTATGGAAGGAAGTTATGCTTCCTACATATGTTGTACATGCAACATTATGGTTCATAAAAAGTGCACTTCATTGCCGCGCATCATCAAAAGCAAGTGGC
ATGATCATCGCCTTTTTCACATATATTTCTTTCCGGATGAATTTACAAGTTCAGACTGCATGATTTGTCATGATGAAGTCGATCCAGAGCATGGTAGTTATTGCTGT
TCACATTGCAATATTACATTCCATGTGCGTTGTGTGACAGAGGATAAACGCTCATATTCAATAGTTTCACTAGAAAATGAAGATGAGATGCCCAATGAAAGTTCC
ATCATTGTTATTGAGAGCAACGATGCTGGAGAAGCTACAAAAATAAAGCATTTCAAGCATATGCATAATCTAATGTTAGGTCCCTTTGATGGAGGATACGAAAAT
AATTGCGACGGGTGTATGTTGCCAATCTCGGATCCATTTTACTACTGTTCAGAATGTGTTTTTTTTCTTCATAAAGCGTGTGCCGAGTTACCTAAGATGAAGAATG
TTTGGCATGAGTTGTGCCGAGAACCTCTTGCCCTTATTTCAGACAAAGTTTTTGAGTGTGCGAAATGTCGGCACATATCTAATACCTTTGCTTATGAATGTAGTG
AATGTGAGAGTAAGAGATGTCTCAGATGTGTGATTGTGCTTACCCCTGGTGCTCGAACATCTTTGAGACATGAGCACCCCCTCTTTTTCTACAAAGATTACCATG
GGCGCTGTGATGCTTGTGGTAATCTTACATTGGGAGCATTTTGTTGTAAGGATTGCAATTTTGTGCTACATTTTGGATGTTTTTCACTTCCAATTACAGCTCATCAC
AAATGTGATGAGCATCTTCTTTCACTCACTGCTCATAATGATAACAAATATTTAGAAAGTCATTATTGCGATATTTGTGAAGAAAGTCGAGATACAAATCGTTGGT
TTTATCATTGTGCAATATGCGATACTTCTGTTCATGTTAATTGTGTTCTTGGAAAATATCCATTCCTCAAACTTGGGAGCATATTTGAAGAAACAGATCATCCACAC
CCACTCACTATCGTGAAGAAGAAGTATTACTACCTTGATTGTAATAAATGCGGTAAGCCTTGTGAAGATTTATCTCTTGAGTGCTCAAAGTTGGAGTGTAAATATA
TTGTCCACTTGGATTGTGTAGTACACTACACTCTACGGTGTTTTTTGTGGTGGCGCATG**TAA**CAATTCAGATGTAATCATATTTGAAACCTATCACTTCATTTGTG
GGAAAACTAAAGAGTGGAGAACAGGGTTTGATCTTTGTCTTGTTGCTTGTGATGTTAGTGTTGTCATTGTAATTTGGTTTTTTTGACCTTTTAAGTTTTAAAGAA
ATGTCATGTAATAATCTTAAGTTGAAACTTGTGTGATTTGCATTGATGTGTGATTGTTGATTTTAGAATTTCTTGTAATATGGGAGTGTGGTTGTACCTACAACAAT
AAAGGTGTTGCTGGATGCTTCTCTTTGTTTCTTTATATAAGTTTTCTTG

Yellow letters: cleavage cite

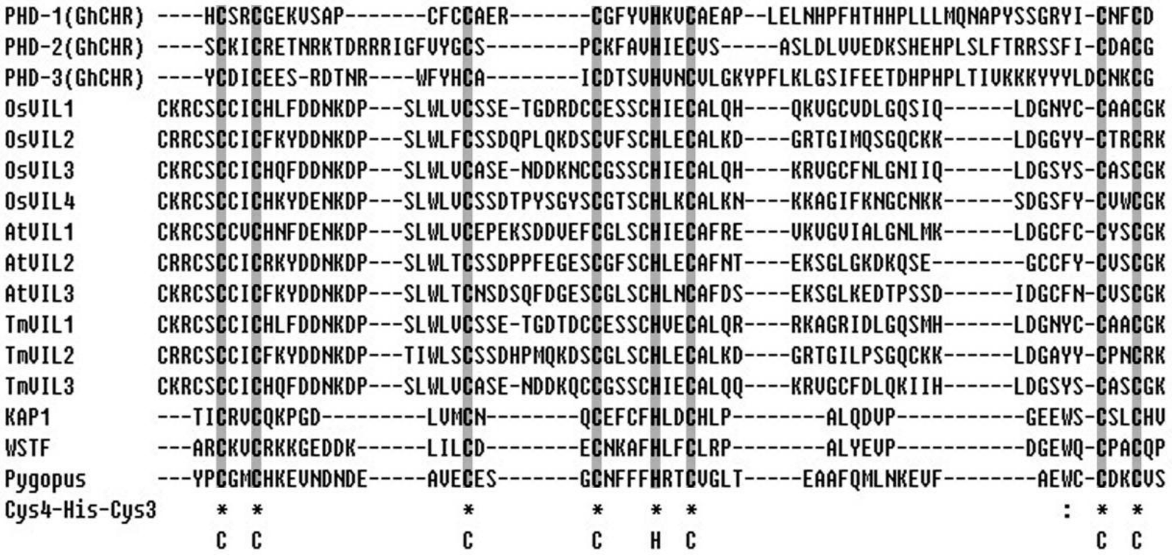
B: Deduced amino acids (677 aa) and domains of GhCHR

MEESNNYGHQHPLLLILNQDQLIHNQSGVTHCSRCGEKVSAPCFCCAERCGFYVHKVCAEAPLELNHPFHTHHPLLLMQNAPYSSGRYICNFCDKDGSKFV
YHCSCGLDFHIKCALFTFNIAENNLKELDHVALQHPLISTENGDEELGDVSKCFGCWEPLAKYTHFSPDCGFNFHEKCAKLPFKLNHECHRKHPLALQFNSK
RLSCKICRETNRKTDRRRIGFVYGCSPCKFAVHIECVSASLDLVVEDKSHEHPLSLFTRRSSFICDACGMEGSYASYICCTCNIMVHKKCTSLPRIIKSKWHDH
RLFHIYFFPDEFTSSDCMICHDEVDPEHGSYCCSHCNITFHVRCVTEDKRSYSIVSLENEDEMPNESSIIVIESNDAGEATKIKHFKHMHNLMLGPFDGGYENN
CDGCMLPISDPFYYCSECVFFLHKACAELPKMKNVWHELCREPLALISDKVFECAKCRHISNTFAYECSECESKRCLRCVIVLTPGARTSLRHEHPLFFYKDY
HGRCDACGNLTLGAFCCKDCNFVLHFGCFSLPITAHHKCDEHLLSLTAHNDNKYLESHYCDICEESRDTNRWFYHCAICDTSVHVNCVLGKYPFLKLGSIFE
ETDHPHPLTIVKKKYYYLDCNKCGKPCEDLSLECSKLECKYIVHLDCVVHYTLRCFLWWRM

PHD-type zinc finger domain
C1 domain

C: Comparison of amino acid sequence alignments between GhCHR and other species PHD (a), and GhCHR and other PHD-type finger proteins (b)

(a)



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PHD-1(GhCHR)  ----HCSRCGEKVSAP-------CFCCAER-------CGFYVHKVCAEAP--LELNHPFHTHHPLLLMQNAPYSSGRYI-CNFCD
PHD-2(GhCHR)  ----SCKICRETNRKTDRRRIGFVYGCS--------PCKFAVHIECVS-----ASLDLVVEDKSHEHPLSLFTRRSSFI-CDACG
PHD-3(GhCHR)  ----YCDICEES-RDTNR----WFYHCA--------ICDTSVHVNCVLGKYPFLKLGSIFEETDHPHPLTIVKKKYYYLDCNKCG
OsVIL1        CKRCSCCICHLFDDNKDP---SLWLVCSSE-TGDRDCCESSCHIECALQH----QKVGCVDLGQSIQ------LDGNYC-CAACGK
OsVIL2        CRRCSCCICFKYDDNKDP---SLWLFCSSDQPLQKDSCVFSCHLECALKD----GRTGIMQSGQCKK------LDGGYY-CTRCRK
OsVIL3        CKRCSCCICHQFDDNKDP---SLWLVCASE-NDDKNCCGSSCHIECALQH----KRVGCFNLGNIIQ------LDGSYS-CASCGK
OsVIL4        CKRCSCCICHKYDENKDP---SLWLVCSSDTPYSGYSCGTSCHLKCALKN----KKAGIFKNGCNKK------SDGSFY-CVWCGK
AtVIL1        CKRCSCCVCHNFDENKDP---SLWLVCEPEKSDDVEFCGLSCHIECAFRE----VKVGVIALGNLMK------LDGCFC-CYSCGK
AtVIL2        CRRCSCCICRKYDDNKDP---SLWLTCSSDPPFEGESCGFSCHLECAFNT----EKSGLGKDKQSE--------GCCFY-CVSCGK
AtVIL3        CKRCSCCICFKYDDNKDP---SLWLTCNSDSQFDGESCGLSCHLNCAFDS----EKSGLKEDTPSSD------IDGCFN-CVSCGK
TmVIL1        CKRCSCCICHLFDDNKDP---SLWLVCSSE-TGDTDCCESSCHVECALQR----RKAGRIDLGQSMH------LDGNYC-CAACGK
TmVIL2        CRRCSCCICFKYDDNKDP---TIWLSCSSDHPMQKDSCGLSCHLECALKD----GRTGILPSGQCKK------LDGAYY-CPNCRK
TmVIL3        CKRCSCCICHQFDDNKDP---SLWLVCASE-NDDKQCCGSSCHIECALQQ----KRVGCFDLQKIIH------LDGSYS-CASCGK
KAP1          ---TICRVCQKPGD---------LVMCN--------QCEFCFHLDCHLP--------ALQDVP-----------GEEWS-CSLCHV
WSTF          ---ARCKVCRKKGEDDK------LILCD--------ECNKAFHLFCLRP--------ALYEVP-----------DGEWQ-CPACQP
Pygopus       ---YPCGMCHKEVNDNDE-----AVECES-------GCNFFFHRTCVGLT-----EAAFQMLNKEVF--------AEWC-CDKCVS
Cys4-His-Cys3      *  *                 *          *    *  *                               :  *  *
                   C  C                 C          C    H  C                                  C  C
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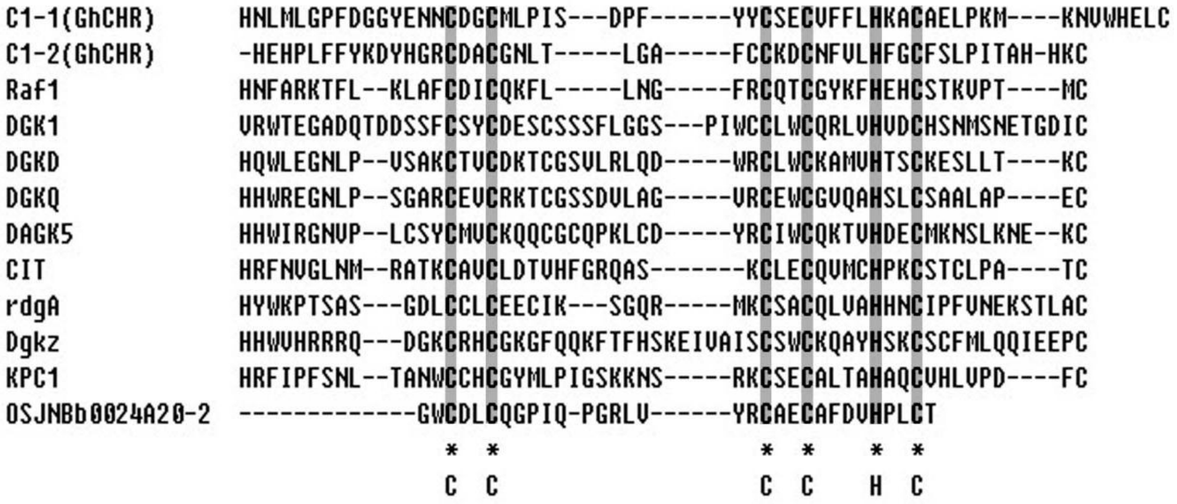
(b)



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C1-1(GhCHR)      HNLMLGPFDGGYENNCDGCMLPIS---DPF------YYCSECVFFLHKACAELPKM----KNVWHELC
C1-2(GhCHR)      -HEHPLFFYKDYHGRCDACGNLT-----LGA-----FCCKDCNFVLHFGCFSLPITAH-HKC
Raf1             HNFARKTFL--KLAFCDICQKFL-----LNG-----FRCQTCGYKFHEHCSTKVPT----MC
DGK1             VRWTEGADQTDDSSFCSYCDESCSSSFLGGS---PIWCCLWCQRLVHVDCHSNMSNETGDIC
DGKD             HQWLEGNLP--VSAKCTVCDKTCGSVLRLQD-----WRCLWCKAMVHTSCKESLLT----KC
DGKQ             HHWREGNLP--SGARCEVCRKTCGSSDVLAG-----VRCEWCGVQAHSLCSAALAP----EC
DAGK5            HHWIRGNVP--LCSYCMVCKQQCGCQPKLCD-----YRCIWCQKTVHDECMKNSLKNE--KC
CIT              HRFNVGLNM--RATKCAVCLDTVHFGRQAS-------KCLECQVMCHPKCSTCLPA----TC
rdgA             HYWKPTSAS---GDLCCLCEECIK---SGQR-----MKCSACQLVAHHNCIPFVNEKSTLAC
Dgkz             HHWVHRRRQ---DGKCRHCGKGFQQKFTFHSKEIVAISCSWCKQAYHSKCSCFMLQQIEEPC
KPC1             HRFIPFSNL--TANWCCHCGYMLPIGSKKNS-----RKCSECALTAHAQCVHLVPD----FC
OSJNBb0024A20-2  -------------GWCDLCQGPIQ-PGRLV------YRCAECAFDVHPLCT
                                *  *                   *  *    *  *
                                C  C                   C  C    H  C
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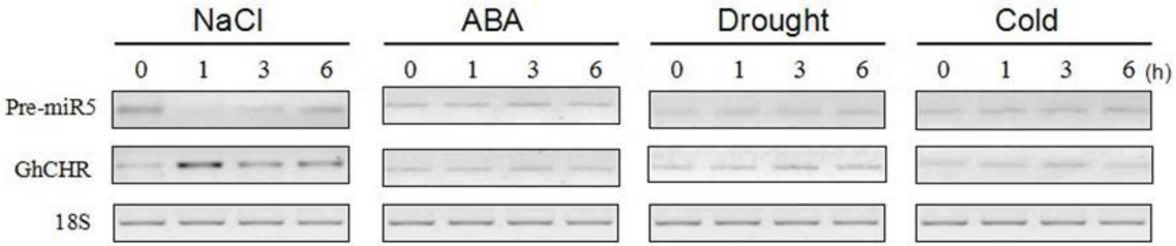
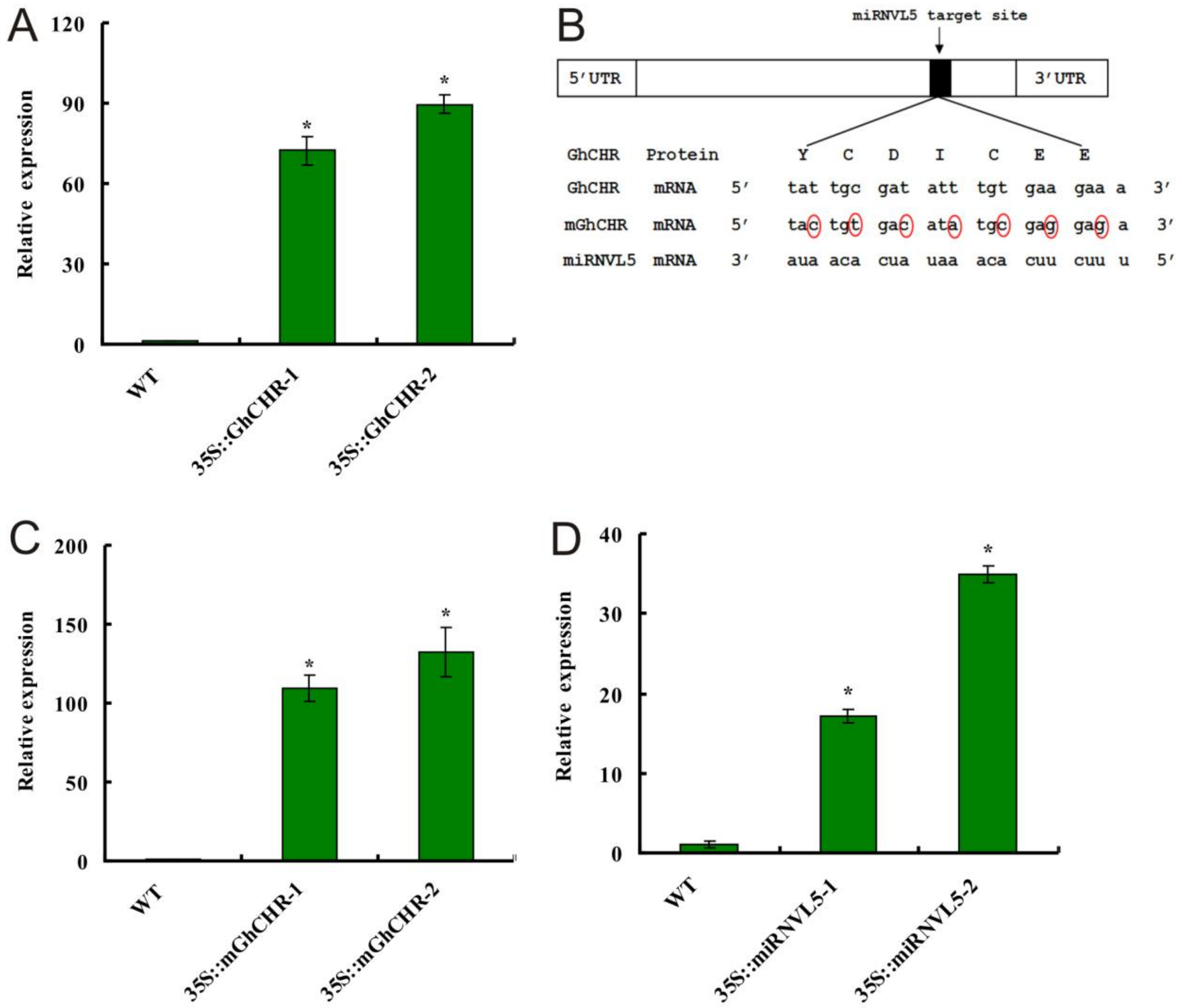


Supplementary Data S3. Effects of salinity, ABA, drought and cold stresses on expression of pre-miRNVL5 and *GhCHR* in seedlings of cotton (*Gossypium hirsutum*) plants. Two week-old cotton seedlings were treated with NaCl (0-400 mM) (A), ABA (100 μM), drought (20% polyethylene glycol 600) and cold (4 ℃) for 0, 1, 3 and 6 h. After that, total RNA was extracted and analyzed by semi-quantitative RT-PCR.



Supplementary Data S4. Expression of *GhCHR* and miRNVL5in transgenic Arabidopsis and wild type (WT). Transcripts in 4 week-old seedlings were analyzed using qRT-PCR. Values are the means ± standard deviation (SD). Means followed by different letters are significantly different at $p < 0.05$. A: qRT-PCR analysis of *GhCHR* mRNA in transgenic lines overexpressing *GhCHR* (*35S::GhCHR*). B: Base paring of miRNVL5 with its corresponding complementary site of *GhCHR* and miRNVL5-resistan form of *mGhCHR*. C: qRT-PCR analysis of *GhCHR* mRNA in transgenic lines overexpressing miRNVL5-resistant form (*35::mGhCHR*). D: qRT-PCR analysis of miRNVL5 in *35S::miRNVL5* Arabidopsis lines.

Supplementary Data S5 Differential expression of genes in WT and miRNVL5 under salt stress

AGI ID	Description	WT+S/WT (Up)	miR5+S/WT (Up)	miR5+S/WT+S (Down)
AT1G02460	Pectin lyase-like protein	3.8511736	3.8511736	1
PP2CA	protein phosphatase 2C 37	9.376997	9.376997	1
COL1	zinc finger protein CONSTANS-LIKE 1	2.462924	2.462924	1
42097	5'-adenylylsulfate reductase 3	2.8906884	2.8906884	1
AT2G26610	Transducin family protein / WD-40 repeat family protein	12.228756	12.225176	1.0002929
AT4G19200	proline-rich family protein	2.4270766	2.4259715	1.0004555
CCA1	protein CCA1	2.565155	2.563953	1.0004687
AT1G75000	GNS1/SUR4 membrane-like protein	2.718698	2.7173057	1.0005125
NAC053	NAC domain containing protein 53	2.3932486	2.3912387	1.0008405
AT4G26580	RING/U-box domain-containing protein	2.0456853	2.0437539	1.0009451
ABF1	abscisic acid-insensitive 5-like protein 4	3.1246445	3.121655	1.0009576
AT1G29640	hypothetical protein	3.9133673	3.9087703	1.001176
PIP2B	aquaporin PIP2-2	2.538842	2.5351675	1.0014493
AT5G18340	U-box domain-containing protein 48	2.4465628	2.442946	1.0014805
AT4G01280	myb family transcription factor	2.525326	2.5215228	1.0015084
AT2G42270	U5 small nuclear ribonucleoprotein helicase	2.3193634	2.3152368	1.0017824
AT5G08139	RING/U-box domain-containing protein	2.0949938	2.090961	1.0019288
AT1G24580	RING/U-box domain-containing protein	12.445006	12.416526	1.0022938
AT1G73390	Endosomal targeting BRO1-like domain-containing protein	4.4853163	4.4744835	1.002421
CK1	choline kinase 1	2.7362354	2.7288456	1.002708
EDA9	D-3-phosphoglycerate dehydrogenase	2.944129	2.9350524	1.0030925
ENODL2	early nodulin-like protein 2	3.8698719	3.857839	1.003119
PPCK1	phosphoenolpyruvate carboxylase kinase 1	2.0093555	2.0029452	1.0032005
AT1G60750	auxin-induced atb2-like protein	2.4820645	2.473724	1.0033717
AT4G29770	hypothetical protein	2.087976	2.0809488	1.003377
AT4G33550	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	2.221798	2.21298	1.0039847

AT1G53210	calcium-binding EF-hand domain-containing protein	2.1517618	2.143158	1.0040146
MPK19	mitogen-activated protein kinase 19	3.1702876	3.156023	1.0045198
AT3G04000	3-oxoacyl-[acyl-carrier protein] reductase	3.0724297	3.0579948	1.0047203
AT3G48990	AMP-dependent synthetase and ligase-like protein	2.0772448	2.0674515	1.0047369
AT2G13960	myb family transcription factor	9.235979	9.191244	1.0048671
AT4G19200	proline-rich family protein	2.1638145	2.1531277	1.0049634
AT5G18636	hypothetical protein	2.7230318	2.7093375	1.0050545
tic20-IV	translocon at the inner envelope membrane of chloroplasts 20-IV	2.1836915	2.1717591	1.0054944
AT5G17760	AAA-type ATPase family protein	2.7458513	2.730809	1.0055083
AT3G09440	protein heat shock protein 70-3	2.0231476	2.0119846	1.0055482
NAC053	NAC domain containing protein 53	2.3470216	2.3337862	1.0056711
AT5G59490	haloacid dehalogenase-like hydrolase domain-containing protein	3.3904226	3.3711092	1.0057291
ATGLR1.2	glutamate receptor 1.2	2.3588674	2.3444586	1.006146
UPL5	E3 ubiquitin-protein ligase UPL5	2.1834302	2.168924	1.0066881
AT5G02020	hypothetical protein	11.525537	11.445476	1.006995
AT1G71110	hypothetical protein	2.0834332	2.0675335	1.0076902
PP2CA	protein phosphatase 2C 37	7.3281417	7.2702947	1.0079566
DHAR2	glutathione S-transferase DHAR2	2.4653754	2.4451206	1.0082839
AT1G30080	glycosyl hydrolases family 17 domain-containing protein	2.5611393	2.5400572	1.0082998
AT3G59350	protein kinase family protein	2.2995615	2.2803025	1.0084459
AT3G62260	putative protein phosphatase 2C 49	4.2880135	4.2510805	1.0086879
DAR6	protein DA1-related 6	2.2634008	2.2436376	1.0088085
AT1G02820	late embryogenesis abundant 3-like protein	2.1471086	2.1279118	1.0090213
RD19	cysteine proteinase RD19a	2.0283031	2.0101342	1.0090387
AT3G57540	Remorin family protein	7.1788316	7.1140885	1.0091007
AT2G35990	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG2	2.5287726	2.505227	1.0093986
AT1G59860	HSP20-like chaperone	3.7089167	3.6736968	1.009587
AT3G25870	hypothetical protein	2.93942	2.9114687	1.0096004
VAMP725	vesicle-associated membrane protein 725	2.133735	2.1132956	1.0096718

AT1G22985	ethylene-responsive transcription factor ERF069	2.787973	2.7606752	1.009888
SHM7	serine hydroxymethyltransferase 7	3.0827909	3.0515614	1.010234
AT4G35720	hypothetical protein	2.086973	2.0638304	1.0112134
ATSAC1B	Phosphoinositide phosphatase-like protein	7.908695	7.816103	1.0118463
NAM	NAC domain-containing protein 18	2.25321	2.2268207	1.0118507
ADR1-L1	putative disease resistance protein ADR1-like 1	2.4015775	2.3734019	1.0118715
CRK15	cysteine-rich receptor-like protein kinase 15	2.1189244	2.0931818	1.0122982
MSS1	sugar transport protein 13	2.305659	2.277624	1.012309
AT2G39350	ABC transporter G family member 1	2.7211144	2.687994	1.0123217
AT4G31196	oxidoreductase	2.030236	2.0051348	1.0125184
AT2G38410	VHS and GAT domain-containing protein	2.4555843	2.4244428	1.0128448
EDA12	embryo sac development arrest 12 protein	7.1828237	7.0903234	1.013046
PIF7	transcription factor PIF7	2.2016892	2.1721625	1.0135932
BCB	blue copper protein	2.5548491	2.5201647	1.0137627
RHA2B	putative E3 ubiquitin-protein ligase RHA2B	2.2795956	2.2479763	1.0140657
RLP53	receptor like protein 53	7.283559	7.1805067	1.0143516
SAG13	senescence-associated protein 13	2.3223643	2.2894979	1.0143553
UGT76E11	UDP-glucosyl transferase 76E11	5.1533446	5.0795536	1.014527
AT1G10585	basic helix-loop-helix domain-containing protein	3.3822453	3.3334074	1.0146511
AT3G19240	Vacuolar import/degradation, Vid27-related protein	3.3131528	3.2649066	1.0147772
HAT22	homeobox-leucine zipper protein HAT22	2.389207	2.354345	1.0148073
AT2G38340	dehydration-responsive element-binding protein 2E	3.9656396	3.9065282	1.0151315
UGT73B5	UDP-glucosyl transferase 73B5	2.1340735	2.1016448	1.0154301
CK1	choline kinase 1	2.6714456	2.630302	1.0156422
AT4G38060	hypothetical protein	2.4016402	2.3627048	1.0164791
ZF2	zinc-finger protein 2	2.64291	2.5994618	1.0167143
AT3G24420	hydrolase, alpha/beta fold family protein	2.436751	2.396174	1.0169342
PUB18	U-box domain-containing protein 18	2.3034623	2.2643697	1.0172642
AT1G27200	hypothetical protein	2.1434767	2.1067092	1.0174525

AT2G32050	hypothetical protein	2.2732198	2.2334871	1.0177895
AT1G51440	phospholipase A1-Igamma3	3.06474	3.01049	1.0180203
NF-YC3	nuclear transcription factor Y subunit C-3	2.1136992	2.075388	1.0184599
AT3G11420	hypothetical protein	4.1061177	4.0280066	1.019392
ATAF1	NAC domain-containing protein 2	7.803936	7.6455226	1.0207198
AFP3	Ninja-family protein AFP3	7.935931	7.774674	1.0207413
EDL3	EID1-like F-box protein 3	19.152058	18.751087	1.0213839
AT1G07400	class I heat shock protein	4.0619917	3.9766335	1.021465
WIN2	putative protein phosphatase 2C 59	2.1175857	2.072628	1.0216911
AT4G11570	haloacid dehalogenase-like hydrolase domain-containing protein	2.1456683	2.0999494	1.0217716
EXLA3	expansin-like A3	2.2884552	2.2396479	1.0217924
AT1G54050	HSP20-like chaperone	3.875778	3.7923393	1.0220019
AT4G10510	Subtilase family protein	2.2687035	2.217894	1.0229089
RAP2.10	ethylene-responsive transcription factor RAP2-10	3.0793612	3.0101774	1.0229833
AT5G05220	hypothetical protein	4.3875866	4.2886567	1.0230678
AT1G01500	Erythronate-4-phosphate dehydrogenase-like protein	2.3210428	2.2678173	1.0234699
AT1G07500	hypothetical protein	3.0693867	2.9987595	1.0235522
UGT73B2	UDP-glucosyltransferase 73B2	4.6087947	4.5008173	1.0239906
AT1G47980	hypothetical protein	2.8899672	2.8211362	1.0243982
HSP18.2	heat shock protein 18.2	4.087278	3.9885936	1.0247416
ATMS1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2.1730587	2.1205006	1.0247856
AT4G27560	UDP-glycosyltransferase-like protein	2.9700515	2.8962984	1.0254647
MYB96	myb domain protein 96	3.9733384	3.872034	1.0261631
AT3G28600	AAA-type ATPase family protein	9.98129	9.7150345	1.0274066
ARSK1	root-specific kinase 1	2.7108495	2.638081	1.0275838
AT4G20320	putative CTP synthase	5.2255983	5.0851007	1.0276294
AT2G44970	alpha/beta-hydrolase domain-containing protein	2.2804449	2.2186573	1.0278491
RLP7	receptor like protein 7	2.444479	2.378092	1.0279161
AT4G20880	ethylene-responsive/regulated nuclear protein	2.1235487	2.0651104	1.028298

AT1G17745	D-3-phosphoglycerate dehydrogenase	2.1295612	2.0708272	1.0283625
TIP2;2	putative aquaporin TIP2-2	3.8160532	3.7107217	1.0283856
AT5G59760	hypothetical protein	4.4959984	4.3718934	1.0283871
AT1G52560	HSP20-like chaperone	3.9490964	3.8399632	1.0284203
AT5G52660	myb family transcription factor	3.3128285	3.2210765	1.028485
LEA	dehydrin LEA	5.4011555	5.251152	1.0285659
AT3G11580	AP2/B3 domain-containing protein	2.4127853	2.3455932	1.0286461
AT2G17500	auxin efflux carrier-like protein	3.1851935	3.0961902	1.028746
MYB34	myb domain protein 34	2.3322704	2.2660527	1.0292215
UBQ10	polyubiquitin 10	2.786512	2.706367	1.0296135
PGP11	P-glycoprotein 11	3.0322697	2.9405646	1.0311862
ACHT4	thioredoxin-like 1-1	2.567963	2.490058	1.0312864
AP4.3A	putative protein kinase	2.085008	2.0217278	1.0313001
ZF14	MATE efflux family protein	3.392985	3.289575	1.0314357
NAC004	NAC domain-containing protein 4	3.138707	3.0428414	1.0315052
AT4G30730	hypothetical protein	3.4569237	3.3512847	1.0315219
AT2G02870	F-box/kelch-repeat protein SKIP11	2.485128	2.408779	1.0316962
AT5G02950	PWWP domain-containing protein	2.3923345	2.3181143	1.0320175
ERD14	dehydrin ERD14	3.0535753	2.9585083	1.0321335
LEA4-5	late embryogenesis abundant protein 4-5	70.16928	67.976746	1.0322542
AT3G52310	ABC transporter G family member 27	4.669054	4.5207534	1.0328044
AT3G24090	putative glucosamine-fructose-6-phosphate aminotransferase	2.6950414	2.6086745	1.0331075
MTHSC70-2	mitochondrial HSO70 2	2.273379	2.199183	1.033738
RXW8	lipase/hydrolase	4.537028	4.3880157	1.0339588
42095	5'-adenylylsulfate reductase 1	2.3134131	2.2371266	1.0341003
AT3G54410	hypothetical protein	3.028638	2.9286673	1.0341351
AT1G69360	hypothetical protein	2.4258575	2.3456955	1.0341741
DAD1	putative phospholipase A1	40.62535	39.259502	1.0347903
AT2G45820	Remorin	2.2337618	2.1562598	1.0359428

SHM7	serine hydroxymethyltransferase 7	2.9380777	2.8361108	1.035953
AT5G15660	putative F-box protein	31.801104	30.683235	1.0364325
DREB1A	dehydration-responsive element-binding protein 1A	20.748535	20.01548	1.0366244
AT3G61390	U-box domain-containing protein 36	2.822859	2.7223542	1.0369184
ERD14	dehydrin ERD14	2.9464467	2.8405256	1.0372893
AZG1	adenine/guanine permease AZG1	2.1107266	2.0344384	1.0374985
AT1G51820	putative LRR receptor-like serine/threonine-protein kinase	2.153038	2.0751793	1.037519
ERD10	dehydrin ERD10	7.434529	7.161176	1.0381714
TPD1	tapetum determinant 1	2.1945825	2.11272	1.0387474
AT4G22758	hypothetical protein	3.7654164	3.6248004	1.0387927
RAP2.4	ethylene-responsive transcription factor RAP2-4	2.290185	2.2045991	1.0388216
ZFHD1	zinc finger homeodomain 1	5.742815	5.527686	1.0389184
PDE149	TerC integral membrane domain-containing protein	2.206762	2.1238978	1.0390152
AT1G76600	hypothetical protein	2.5434597	2.4468005	1.0395044
AT4G39130	Dehydrin family protein	2.8365617	2.7270586	1.0401542
ERD14	dehydrin ERD14	2.794719	2.6866918	1.0402082
NAC019	NAC domain-containing protein 19	18.601969	17.882786	1.0402164
AT4G38060	hypothetical protein	3.2814481	3.1544776	1.0402509
TRANS11	phospho-N-acetylmuramoyl-pentapeptide-transferase-like protein	2.9707701	2.8545206	1.0407248
AT2G25625	hypothetical protein	3.4894059	3.3510377	1.0412911
SVL4	protein SEUSS-like 4	9.069902	8.709818	1.0413424
AT3G54390	sequence-specific DNA binding transcription factor	2.3508694	2.2574918	1.0413634
AT5G42570	B-cell receptor-associated 31-like protein	2.5386002	2.4376693	1.0414047
DOF1	Dof zinc finger protein DOF1.7	2.5306518	2.4293928	1.0416808
AT1G66510	A1 cistron-splicing factor AAR2	2.4360616	2.3384948	1.041722
AT2G25625	hypothetical protein	3.126975	3.0007167	1.0420761
AT4G12430	haloacid dehalogenase-like hydrolase domain-containing protein	3.6481054	3.498471	1.0427713
AT3G17770	Dihydroxyacetone kinase	2.557847	2.451113	1.0435451
AT2G39050	hydroxyproline-rich glycoprotein-like protein	2.6351573	2.524984	1.0436333

MYB7	myb domain protein 7	2.6653318	2.5530968	1.0439605
NAC096	NAC domain containing protein 96	2.2527797	2.157145	1.0443338
GID1B	putative gibberellin receptor GID1L2	2.5090659	2.402426	1.0443884
AT1G03070	transmembrane BAX inhibitor motif-containing protein	4.3146095	4.1302834	1.044628
FLS6	flavonol synthase 6	9.640937	9.228193	1.0447264
AT1G30740	FAD-binding and BBE domain-containing protein	2.2573636	2.1606066	1.0447823
AGO2	Argonaute family protein	2.8815155	2.7564082	1.0453879
AT5G51845	putative defensin-like protein 270	4.399197	4.206629	1.0457773
AT2G43500	RWP-RK domain-containing protein	2.5931306	2.4795654	1.0458004
AT4G27560	UDP-glycosyltransferase-like protein	2.5244465	2.4135478	1.0459484
CER1	CER1 protein	11.520266	11.011364	1.046216
MYB49	myb domain protein 49	4.884303	4.6664867	1.0466768
SRC2	hypothetical protein	2.7642708	2.6404443	1.0468961
AT1G05870	hypothetical protein	2.7281206	2.6048303	1.0473315
AT2G11891	hypothetical protein	2.1433945	2.0463588	1.0474187
SQE3	squalene epoxidase 3	2.4253316	2.3154004	1.0474782
AER	2-alkenal reductase	3.6252341	3.4606345	1.0475634
UGT71B1	UDP-glucosyl transferase 71B1	2.3226805	2.2160804	1.048103
SULTR1;2	sulfate transporter 1.2	2.5374677	2.4203074	1.0484072
HSC70-1	heat shock 70kDa protein 1/8	2.6663823	2.542868	1.0485729
AT1G04770	male sterility MS5 family protein	2.356081	2.246075	1.048977
IDD16	ribonuclease P subunit RPR2	2.1817899	2.0798197	1.0490284
MSL4	mechanosensitive channel of small conductance-like 4	5.788264	5.5171256	1.0491449
AT1G64890	integral membrane transporter family protein	2.601712	2.4792342	1.0494015
CYP707A4	abscisic acid 8'-hydroxylase 4	2.132547	2.0312784	1.0498545
RPS6	TIR-NBS-LRR class disease resistance protein	2.1023562	2.0016375	1.0503182
HB6	homeobox-leucine zipper protein ATHB-6	2.7082658	2.578129	1.0504773
MPK7	mitogen-activated protein kinase 7	2.1140723	2.0122347	1.0506092
AT5G62570	calmodulin binding protein-like protein	2.5676963	2.4438956	1.0506572

PIP1B	aquaporin PIP1-2	2.3180606	2.2059562	1.0508189
AT1G52565	hypothetical protein	2.3055844	2.19376	1.0509739
CSLG2	cellulose synthase-like protein G2	3.0838733	2.9338973	1.0511184
AT5G64170	dentin sialophosphoprotein-like protein	2.2130706	2.1051278	1.0512761
AT2G18340	late embryogenesis abundant domain-containing protein	2.1147006	2.0111508	1.0514878
AT1G76980	hypothetical protein	2.8123887	2.6741426	1.0516974
ZIF1	zinc induced facilitator 1 proetin	3.110975	2.9576938	1.0518246
AT3G57380	Glycosyltransferase family 61 protein	2.409892	2.2910678	1.0518641
MAPKKK18	mitogen-activated protein kinase kinase kinase 18	25.252958	24.005972	1.0519449
AT1G78070	transducin/WD-40 repeat-containing protein	10.444754	9.928743	1.0519713
AT2G21640	hypothetical protein	2.6731732	2.5386388	1.0529947
AT1G23910	Polyketide cyclase/dehydrase and lipid transport superfamily protein	2.27979	2.163984	1.0535152
UGT73B1	UDP-glucosyl transferase 73B1	2.1177523	2.010077	1.0535678
APX2	L-ascorbate peroxidase	3.634633	3.446116	1.0547042
AT4G36010	pathogenesis-related thaumatin family protein	5.419246	5.1367607	1.0549929
AT4G38140	RING-H2 finger protein ATL18	6.913354	6.550641	1.0553706
PIP1A	aquaporin PIP1-1	2.2187233	2.1022868	1.0553856
AT1G25422	hypothetical protein	2.987772	2.8304152	1.0555949
CLPB3	casein lytic proteinase B3	2.1982732	2.082	1.0558468
KNAT4	homeobox protein knotted-1-like 4	2.9940197	2.8347874	1.0561708
AT3G17800	hypothetical protein	4.501618	4.25926	1.0569013
SYN1	Sister chromatid cohesion 1 protein 1	3.9127076	3.7018232	1.0569677
DIN2	beta-glucosidase 30	6.061409	5.7337604	1.0571438
AT2G18150	peroxidase 15	2.7225018	2.574692	1.0574087
AT1G80470	F-box/RNI-like/FBD-like domain-containing protein	2.8756359	2.7182093	1.0579156
PAP9	putative inactive purple acid phosphatase 9	3.4527707	3.2636433	1.0579498
CLPB4	casein lytic proteinase B4	2.6313922	2.4866662	1.0582008
RPS2	disease resistance protein RPS2	3.2098176	3.0331578	1.0582429
AT2G34930	disease resistance-like protein/LRR domain-containing protein	2.700568	2.5516407	1.0583653

AT3G15534	hypothetical protein	4.965611	4.6887016	1.0590588
MYB7	myb domain protein 7	2.4312901	2.2953107	1.0592422
ECT8	hypothetical protein	4.0277934	3.8013422	1.0595714
AT5G45350	proline-rich family protein	2.5937426	2.4461017	1.0603576
TIP2;2	putative aquaporin TIP2-2	3.3208447	3.131174	1.0605749
AT2G30766	hypothetical protein	3.0792818	2.902798	1.0607978
AT3G59940	F-box/kelch-repeat protein SKIP20	2.2889652	2.1575902	1.0608897
AT5G05220	hypothetical protein	4.0794907	3.844507	1.0611218
AT3G57010	strictosidine synthase family protein	2.7464938	2.5874424	1.0614705
MEE23	FAD-binding and BBE domain-containing protein	2.1637416	2.0374355	1.0619928
AT1G67360	Rubber elongation factor protein (REF)	4.6976347	4.423023	1.0620868
UBQ3	polyubiquitin 3	2.264334	2.1313214	1.0624084
AT1G22510	C3HC4-type RING finger protein	2.1807818	2.0501864	1.0636992
AT1G73920	alpha/beta-hydrolase domain-containing protein	2.3202865	2.1811295	1.0638006
RD21	cysteine proteinase RD21a	2.8973975	2.7222426	1.0643421
AOC2	allene oxide cyclase 2	3.2929387	3.093674	1.0644104
AT4G37900	hypothetical protein	2.3272543	2.1861815	1.0645293
AT2G33760	pentatricopeptide repeat-containing protein	5.4422894	5.110927	1.0648341
EYE	golgi complex component-related protein	2.134752	2.0045729	1.064941
AT1G07590	pentatricopeptide repeat-containing protein	3.039896	2.8531473	1.0654536
GSTU5	glutathione S-transferase 103-1A	2.619459	2.4583452	1.0655375
AT5G19875	hypothetical protein	4.5227294	4.243556	1.0657876
LOX3	lipoxygenase 3	3.768945	3.5356529	1.0659827
AT1G48100	polygalacturonase	13.797035	12.939905	1.0662392
AT1G29770	haloacid dehalogenase-like hydrolase	7.267861	6.8153076	1.0664024
NAC13	NAC domain protein 13	3.9953833	3.7463064	1.066486
ABF3	abscisic acid-insensitive 5-like protein 6	10.514151	9.854732	1.066914
AT2G45820	Remorin	2.2073405	2.0685737	1.0670832
TPS11	putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11	4.985386	4.6685877	1.0678574

ATHSP22.0	heat shock protein 22	3.4126785	3.192949	1.0688171
ATAF1	NAC domain-containing protein 2	6.087477	5.69482	1.0689499
AT5G15290	UPF0497 membrane protein	7.7149644	7.2065654	1.0705466
AT3G55880	Alpha/beta hydrolase related protein	2.7766178	2.591679	1.0713587
HB-12	homeobox-leucine zipper protein ATHB-12	13.968727	13.026286	1.0723492
CPuORF12	uncharacerized protein	2.8700905	2.675215	1.0728447
AT2G38010	neutral ceramidase	2.2595103	2.1058626	1.0729618
LOX3	lipoxygenase 3	3.8746355	3.6052625	1.0747166
BAM5	beta-amylase 5	2.6059222	2.4236841	1.0751905
AT5G39520	hypothetical protein	5.4412827	5.060069	1.0753376
AT1G52565	hypothetical protein	2.226828	2.0704837	1.0755111
AT3G10420	P-loop containing nucleoside triphosphate hydrolase family protein	2.4418359	2.269671	1.0758545
UGT84A3	UDP-glycosyltransferase-like protein	3.7606702	3.494789	1.0760794
PIP1A	aquaporin PIP1-1	3.027691	2.8127542	1.0764151
bZIP48	basic leucine-zipper 48	3.1331875	2.9102142	1.0766176
AT1G22190	ethylene-responsive transcription factor ERF058	2.1818144	2.0263586	1.0767169
GCN2	ABC transporter F family member 2	3.823038	3.5499985	1.0769126
KIN2	stress-induced protein KIN2	3.9331732	3.6516497	1.0770949
AT1G66060	hypothetical protein	2.6194832	2.431941	1.0771163
AT4G15248	B-box type zinc finger-containing protein	3.619552	3.3600433	1.0772337
AT2G23120	Late embryogenesis abundant protein, group 6	4.2996163	3.9904923	1.0774652
AT4G18920	hypothetical protein	2.256587	2.093631	1.0778341
AT4G32208	heat shock protein 70 (Hsp 70) family protein	2.8377366	2.6323247	1.0780344
AT1G04445	C2H2-like zinc finger protein	9.641439	8.940872	1.0783554
SULTR3;1	sulfate transporter 3.1	2.3150775	2.146839	1.0783658
CSLB06	cellulose synthase-like protein B6	5.8481655	5.420438	1.0789102
AT3G60920	hypothetical protein	3.8684766	3.5839863	1.0793781
ERD14	dehydrin ERD14	2.8049111	2.5981648	1.079574
AT3G55880	Alpha/beta hydrolase related protein	3.1726565	2.9385495	1.0796676

AT1G60190	U-box domain-containing protein 19	96.19778	89.055695	1.0801979
AT1G69610	hypothetical protein	3.7890317	3.507356	1.0803101
AT1G54590	splicing factor Prp18 domain-containing protein	7.586597	7.022058	1.080395
AT5G35380	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	2.8038387	2.5948436	1.0805426
AT2G21780	hypothetical protein	2.193757	2.0293975	1.0809894
MBF1C	multiprotein-bridging factor 1c	2.6308706	2.4329991	1.0813282
PLA IIIA	patatin-like protein 6	2.6280684	2.430138	1.0814482
AT3G15300	VQ motif-containing protein	2.2456489	2.0757844	1.0818315
AT1G12890	ethylene-responsive transcription factor ERF088	2.5051978	2.315633	1.0818629
COR27	cold regulated protein 27	3.7497182	3.4657764	1.0819273
AT2G42150	DNA-binding bromodomain-containing protein	5.098594	4.7124705	1.0819366
AT5G02020	hypothetical protein	13.475785	12.449713	1.0824174
AT4G18450	ethylene-responsive transcription factor ERF091	2.218155	2.0480103	1.0830779
AT3G62590	lipase class 3 family protein	2.9065497	2.682126	1.0836738
SULTR1;2	sulfate transporter 1.2	3.5805254	3.303942	1.0837132
LTI30	dehydrin Xero 2	6.7289324	6.208312	1.0838586
HB-7	homeobox-leucine zipper protein ATHB-7	10.941657	10.094676	1.0839038
AT3G27809	hypothetical protein	3.775923	3.4822826	1.0843241
PIP2;5	putative aquaporin PIP2-5	2.4176579	2.228294	1.0849816
KCS7	3-ketoacyl-CoA synthase 7	8.498386	7.83232	1.0850407
AT5G64820	hypothetical protein	3.3860774	3.1200974	1.0852473
AT5G61820	hypothetical protein	4.684759	4.315303	1.0856154
HVA22D	HVA22-like protein d	9.4661875	8.717894	1.0858343
AT3G11340	UDP-glycosyltransferase-like protein	2.2768667	2.0968046	1.0858746
ABF2	abscisic acid-insensitive 5-like protein 5	3.0393274	2.7985919	1.0860202
CPuORF17	hypothetical protein	2.8224933	2.5987694	1.0860884
AT3G04000	3-oxoacyl-[acyl-carrier protein] reductase	2.369836	2.1819413	1.0861136
BGLU31	beta glucosidase 31	2.633631	2.4239068	1.0865233
GAMMA-TIP	aquaporin TIP1-1	2.3673809	2.178098	1.0869029

TIL	outer membrane lipoprotein Blc	2.2303681	2.051126	1.0873872
AT4G09760	protein kinase family protein	2.3508086	2.161883	1.0873895
AT4G15420	ubiquitin fusion degradation UFD1 family protein	2.408962	2.214969	1.0875828
AT1G67930	Golgi transport complex-related protein	2.2906756	2.1057236	1.087833
ELIP1	chlorophyll A-B binding, early light-inducible protein	3.1024942	2.8519838	1.0878373
HSC70-1	heat shock 70kDa protein 1/8	2.6500301	2.4343956	1.0885782
AT5G10695	hypothetical protein	3.486533	3.2022347	1.0887812
AT2G47485	hypothetical protein	2.770049	2.5441642	1.0887855
AT5G04250	OTU-like cysteine protease family protein	3.8621643	3.5465868	1.0889806
LEA14	putative desiccation-related protein LEA14	4.545418	4.1724725	1.0893823
HSFA1E	heat stress transcription factor A-1e	2.6318514	2.414831	1.08987
AT4G09500	glycosyltransferase family protein	3.407868	3.1263695	1.09004
GGPS2	geranylgeranyl pyrophosphate synthase 4	2.385812	2.1885247	1.0901463
AT4G12000	SNARE associated Golgi family protein	7.142668	6.551284	1.0902699
AT4G27530	hypothetical protein	3.67228	3.365454	1.0911694
NSP5	nitrile specifier protein 5	3.9678423	3.6357746	1.0913334
AT1G62580	flavin-containing monooxygenase-like protein	2.4706762	2.2629018	1.0918176
AT5G37540	aspartyl protease family protein	2.2797387	2.0873702	1.0921583
AT5G54165	hypothetical protein	3.9274912	3.5951982	1.0924269
FER3	ferritin 3	2.383022	2.1813817	1.092437
AT4G03360	Ubiquitin family protein	15.917436	14.568823	1.0925685
AT4G05010	F-box protein	2.289121	2.094541	1.0928986
EGY3	ethylene-dependent gravitropism-deficient and yellow-green-like 3 protein	3.9212704	3.587466	1.0930474
PIA1	putative protein phosphatase 2C 20	33.434525	30.567135	1.0938064
RD19	cysteine proteinase RD19a	3.275001	2.993046	1.0942034
ddf2	dehydration-responsive element-binding protein 1E	10.690187	9.765122	1.0947316
WRKY67	putative WRKY transcription factor 67	4.573186	4.175745	1.0951785
AT3G21890	B-box type zinc finger-containing protein	11.611959	10.602055	1.0952556
CBF2	dehydration-responsive element-binding protein 1C	2.3685188	2.1622603	1.0953902

RCAR1	abscisic acid receptor PYL9	2.6494012	2.4186425	1.0954083
HAB1	protein phosphatase 2C 16	5.294006	4.8278966	1.0965451
AT2G03230	GCK domain-containing protein	2.4653292	2.2480142	1.0966698
AT4G21570	hypothetical protein	2.89608	2.640715	1.096703
AT1G11210	hypothetical protein	9.156326	8.34798	1.0968314
ABI1	protein phosphatase 2C 56	4.680163	4.2661414	1.0970482
AT3G16940	calmodulin-binding transcription activator	2.5954406	2.3657775	1.0970773
AT1G48060	F-box protein	2.643996	2.4080546	1.0979801
AT1G19400	Erythronate-4-phosphate dehydrogenase family protein	2.2089067	2.0115206	1.0981278
AT5G41460	hypothetical protein	2.3711069	2.1587813	1.0983543
AT5G09530	hydroxyproline-rich glycoprotein family protein	2.254214	2.0509565	1.0991039
BTI2	reticulon-like protein B2	2.5167036	2.287466	1.1002146
GA2OX6	gibberellin 2-oxidase 6	2.986143	2.7135289	1.1004648
SYP124	syntaxin-124	8.979209	8.152331	1.1014284
AT5G04760	duplicated SANT DNA-binding domain-containing protein	2.491902	2.2623425	1.1014699
CPUORF47	conserved peptide upstream open reading frame 47	3.4561515	3.1360335	1.1020772
AT1G51980	putative mitochondrial-processing peptidase subunit alpha-1	2.283489	2.070517	1.1028593
AT5G42570	B-cell receptor-associated 31-like protein	2.5675826	2.3276696	1.10307
AT5G58770	dehydrodolichyl diphosphate synthase 2	4.6569552	4.220825	1.1033281
AT4G30470	Rossmann-fold NAD(P)-binding domain-containing protein	2.3506145	2.1293979	1.103887
AT5G24870	RING/U-box domain-containing protein	2.70553	2.4488199	1.1048301
AT2G38905	Low temperature and salt responsive protein	2.7985535	2.5326588	1.1049864
AT1G07500	hypothetical protein	3.4931538	3.1610363	1.1050661
AT1G30320	Remorin family protein	2.9679046	2.68571	1.1050726
AT1G60590	Pectin lyase-like protein	3.0379233	2.747705	1.105622
AT1G73390	Endosomal targeting BRO1-like domain-containing protein	8.379757	7.579133	1.1056353
AT1G71000	chaperone DnaJ-domain containing protein	10.471182	9.4704	1.1056747
AGL91	protein agamous-like 91	4.339707	3.924932	1.1056769
AT3G27600	SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing	3.905098	3.531612	1.1057551

	protein			
AT5G60380	hypothetical protein	8.594811	7.770823	1.1060362
NCED2	9-cis-epoxycarotenoid dioxygenase NCED2	3.9880927	3.6055593	1.1060954
ASL9	LOB domain-containing protein 3	4.565558	4.1264467	1.106414
NF-YA5	nuclear transcription factor Y subunit A-5	3.0310512	2.7381244	1.1069809
ASY1	DNA-binding HORMA-like protein	2.7109363	2.4475882	1.107595
TRANS11	phospho-N-acetylmuramoyl-pentapeptide-transferase-like protein	2.6336493	2.3772244	1.1078674
CPK29	calcium-dependent protein kinase 29	3.6078553	3.2564929	1.107896
HSP90.1	heat shock protein 81-1	3.8554122	3.479851	1.1079245
SQP1	Squalene monooxygenase 1,1	2.6402576	2.3828425	1.1080285
AT1G70800	Calcium-dependent lipid-binding domain-containing protein	3.7590098	3.3919537	1.1082138
AT1G19970	ER lumen protein retaining receptor-like protein	2.6913168	2.428256	1.1083332
EGY3	ethylene-dependent gravitropism-deficient and yellow-green-like 3 protein	2.7199779	2.4530742	1.1088037
NAC032	NAC domain containing protein 32	9.1350155	8.234615	1.1093433
AT1G44414	hypothetical protein	3.1287968	2.820164	1.109438
AT5G52050	mate efflux domain-containing protein	4.49507	4.047531	1.1105708
AT5G40810	ubiquinol-cytochrome c reductase cytochrome c1 subunit	2.2238765	2.0017896	1.1109442
AT1G72660	P-loop containing nucleoside triphosphate hydrolase-like protein	4.7109413	4.239331	1.1112465
YSL7	putative metal-nicotianamine transporter YSL7	2.5842853	2.3253152	1.1113698
AT5G43420	RING-H2 finger protein ATL16	2.7108505	2.4379287	1.1119481
AT4G12400	putative stress-inducible protein	5.180419	4.654038	1.1131021
UGE2	UDP-D-glucose/UDP-D-galactose 4-epimerase 2	3.1685214	2.8459103	1.1133596
AT5G49525	hypothetical protein	2.654994	2.383753	1.1137873
AT2G47780	Rubber elongation factor protein (REF)	3.8944383	3.4942553	1.114526
NRT1.7	nitrate transporter 1.7	2.5847192	2.3187318	1.1147124
MSP2	microspore-specific promoter 2	3.9010472	3.4988353	1.1149559
AT5G27944	agamous-like MADS-box protein	2.4411774	2.1894739	1.1149608
AT5G64230	hypothetical protein	2.502667	2.2436116	1.1154635
AT1G30974	Plant thionin family protein	2.5117724	2.2517583	1.1154716

AT1G30810	transcription factor jumonji and C5HC2 type zinc finger domain-containing protein	9.998489	8.962871	1.1155454
AT1G21520	hypothetical protein	2.4652028	2.2086177	1.1161746
SSP4	SCP1-like small phosphatase 4	2.4435904	2.1890607	1.1162734
AFP1	Ninja-family protein AFP1	14.038125	12.572991	1.1165303
TAT3	tyrosine aminotransferase 3	2.4418836	2.186417	1.1168425
AT4G07965	hypothetical protein	2.9938674	2.6803935	1.1169506
PAP18	purple acid phosphatase 18	2.4045472	2.1508474	1.1179534
IAGLU	indole-3-acetate beta-D-glucosyltransferase	2.8249722	2.5258436	1.1184272
AT1G79520	Cation efflux family protein	10.307439	9.212973	1.1187962
MYB3	transcription factor MYB3	2.7521787	2.4588003	1.1193177
AT1G32560	Late embryogenesis abundant protein, group 1 protein	3.4346051	3.066657	1.1199834
AT5G43150	hypothetical protein	2.9843948	2.6646748	1.1199845
UPS4	ureide permease 4	6.8674507	6.131287	1.1200668
AT2G27950	RING/U-box domain-containing protein	2.4102888	2.1511004	1.120491
SPDS3	Spermine synthase	3.8041651	3.3943894	1.1207215
AT1G80120	protein LURP-one-related 5	3.4245472	3.0549684	1.1209763
AT2G02700	cysteine/histidine-rich C1 domain-containing protein	60.0329	53.547535	1.1211141
KIN1	stress-induced protein KIN1	4.1745033	3.7232132	1.1212097
AT1G64107	defensin-like protein 269	6.753621	6.0194573	1.121965
UKL5	putative uracil phosphoribosyltransferase	3.0219214	2.693337	1.121999
CYP71B19	cytochrome P450 71B19	2.2874086	2.0385659	1.1220676
AT3G17720	Pyridoxal phosphate-dependent transferase-like protein	2.6100678	2.325095	1.122564
AT1G73210	hypothetical protein	2.4479249	2.1790571	1.1233872
AT1G76530	auxin efflux carrier-like protein	3.3195662	2.9534101	1.1239773
AT2G20970	putative lipid binding protein	16.926514	15.056073	1.1242318
AT5G56980	hypothetical protein	2.546966	2.263982	1.1249938
ATSDI1	tetratricopeptide repeat domain-containing protein	11.46599	10.188228	1.1254156
AT5G43150	hypothetical protein	3.5275614	3.1269152	1.1281283

AT4G26701	DNA binding;DNA topoisomerase type Is	5.470082	4.8486066	1.128176
Fes1A	protein Fes1A	3.7226646	3.2995365	1.1282387
AT4G39290	putative F-box/kelch-repeat protein	5.49779	4.8712378	1.1286228
AT3G22910	Ca2+-transporting ATPase	2.6373618	2.3366885	1.128675
AT1G66760	MATE efflux family protein	3.1780279	2.8138998	1.1294035
RAP2.1	ethylene-responsive transcription factor RAP2-1	2.7282631	2.4153736	1.1295408
BGLU24	beta glucosidase 24	3.670711	3.2494323	1.1296469
PIRL7	plant intracellular ras group-related LRR 7	6.3823175	5.649216	1.1297705
AT5G64510	hypothetical protein	3.6039567	3.1899512	1.1297842
NF-YB2	nuclear transcription factor Y subunit B-2	5.5685863	4.9279227	1.1300069
RAP2.10	ethylene-responsive transcription factor RAP2-10	3.6580691	3.2363367	1.1303116
AT3G03440	armadillo/beta-catenin-like repeat-containing protein	2.6294067	2.32516	1.1308497
AT1G78230	Outer arm dynein light chain 1 protein	2.4190967	2.1385598	1.1311802
ELI3-2	cinnamyl alcohol dehydrogenase 8	4.4111104	3.8994024	1.1312274
UGT73C7	UDP-glucosyl transferase 73C7	3.97081	3.5094244	1.1314703
AT3G11420	hypothetical protein	2.3142252	2.0447903	1.1317666
AT3G04010	O-Glycosyl hydrolases family 17 protein	2.8786142	2.5432227	1.1318766
CPuORF17	hypothetical protein	2.9853773	2.6341498	1.1333362
MYB3	transcription factor MYB3	2.7550583	2.4307325	1.1334271
EP3	chitinase	3.6524053	3.2219176	1.1336123
NRT1.7	nitrate transporter 1.7	3.2098112	2.831233	1.1337149
AT4G30650	putative low temperature and salt responsive protein	2.7693224	2.4423711	1.1338663
LCR41	putative defensin-like protein 188	3.163851	2.7901034	1.1339548
KCS2	3-ketoacyl-CoA synthase 17	4.567396	4.0259647	1.1344849
KUOX1	KAR-UP oxidoreductase 1	2.5404394	2.238407	1.1349319
CYP707A2	abscisic acid 8'-hydroxylase 2	3.0646873	2.6995077	1.1352763
CT-BMY	beta-amylase 3	2.515654	2.2152412	1.1356118
AT5G61390	exonuclease-like protein	3.0060136	2.6459358	1.1360871
BAC2	Mitochondrial substrate carrier family protein	2.757571	2.4271889	1.1361171

SCL3	scarecrow-like protein 3	3.0417817	2.6770654	1.1362373
GSL09	callose synthase	2.3569984	2.0739677	1.1364683
RHA3A	RING-H2 finger protein ATL44	2.9229753	2.570964	1.136918
AT5G56050	hypothetical protein	2.9884002	2.6284368	1.1369495
AT5G55970	RING/U-box domain-containing protein	2.4136324	2.122509	1.1371601
AT4G01670	hypothetical protein	3.1676323	2.785141	1.1373329
AT2G16890	UDP-glycosyltransferase-like protein	2.9915586	2.629995	1.1374769
AT5G66460	mannan endo-1,4-beta-mannosidase 7	2.289298	2.0119407	1.1378555
ROF2	peptidylprolyl isomerase	3.9892845	3.5055943	1.1379766
AT4G14368	regulator of chromosome condensation repeat-containing protein	6.8302183	6.001751	1.1380376
FTSH6	cell division protease ftsH-6	5.19824	4.567351	1.1381302
TMAC2	Ninja-family protein AFP4	2.388018	2.097366	1.1385794
AT5G18130	hypothetical protein	2.4156818	2.119171	1.1399183
AT1G10400	UDP-glycosyltransferase-like protein	3.3557737	2.9413724	1.140887
AT5G35688	hypothetical protein	8.405684	7.367275	1.1409489
AT1G01240	hypothetical protein	2.3385165	2.0496173	1.1409527
OBP1	Dof zinc finger protein DOF3.4	2.393413	2.0965247	1.1416098
GolS3	galactinol synthase 3	3.146311	2.7558854	1.1416698
ERD4	Early-responsive to dehydration stress protein (ERD4)	2.3009179	2.015283	1.1417344
AT1G78070	transducin/WD-40 repeat-containing protein	9.190788	8.049211	1.1418248
AT3G28007	nodulin MtN3-like protein	5.447927	4.768594	1.1424599
HSP17.4	heat shock protein 17.4	7.0573945	6.1768003	1.1425648
AT1G05894	hypothetical protein	3.388619	2.965552	1.1426604
HAI2	protein phosphatase 2C 3	34.537853	30.197636	1.1437271
AT1G21790	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	5.582898	4.879698	1.1441073
AT1G64890	integral membrane transporter family protein	2.8663251	2.5047789	1.1443427
GSTU2	glutathione S-transferase	2.4722152	2.1597533	1.1446748
MTM1	manganese tracking factor for mitochondrial SOD2	3.016761	2.634924	1.1449139
AT5G41900	hydrolase, alpha/beta fold family protein	3.0837631	2.6906037	1.1461232

UGT73C1	cytokinin-O-glucosyltransferase 1	9.295618	8.108049	1.1464679
AT4G28140	ethylene-responsive transcription factor ERF054	17.248396	15.043074	1.1466006
FIB	putative plastid-lipid-associated protein 1	2.8548055	2.4893782	1.1467947
EXL2	protein EXORDIUM like 2	2.4644418	2.1482143	1.1472048
SKP2A	F-box protein SKP2A	3.0304663	2.6412368	1.1473664
AT3G18950	transducin/WD40 domain-containing protein	2.4769785	2.1587086	1.1474354
AT1G55530	RING/U-box domain-containing protein	2.3396761	2.038066	1.1479884
Fes1A	protein Fes1A	4.011439	3.4894564	1.1495885
AT5G20370	serine-rich protein-like protein	4.0062213	3.4840517	1.1498742
AT3G22090	hypothetical protein	3.1283014	2.720359	1.149959
JAZ5	protein TIFY 11A	2.682268	2.33031	1.1510347
AT1G47610	WD40 domain-containing protein	4.53364	3.9386642	1.1510602
AT5G51105	hypothetical protein	4.193425	3.6429195	1.1511166
CPuORF12	uncharacerized protein	2.6636357	2.3132586	1.1514647
AT3G20340	hypothetical protein	4.125132	3.5815918	1.1517594
RAP2.4	ethylene-responsive transcription factor RAP2-4	2.5177004	2.1854417	1.1520327
AT2G25460	hypothetical protein	3.412322	2.9572568	1.153881
AT3G55090	ABC transporter G family member 16	11.496925	9.956196	1.1547508
ANK	ankyrin repeat family protein	2.4409895	2.1135623	1.1549172
NTM1	NAC domain-containing protein 68	2.9816558	2.580267	1.155561
AT5G22545	hypothetical protein	2.614693	2.262353	1.1557405
AT4G05140	Nucleoside transporter family protein	2.7154884	2.349308	1.1558673
AT2G03460	galactose oxidase/kelch-like protein	4.3624864	3.77273	1.1563209
FLA3	fasciclin-like arabinogalactan protein 3	2.6533325	2.2942808	1.1564986
LCR18	putative defensin-like protein 184	2.8078706	2.4274669	1.1567081
WRKY48	putative WRKY transcription factor 48	2.6301003	2.2732198	1.1569934
ERD9	glutathione S-transferase	3.2355237	2.7964063	1.1570293
EDL3	EID1-like F-box protein 3	28.205553	24.375242	1.1571394
PP2-A10	phloem protein 2-A10	2.9851031	2.5793035	1.1573291

AT2G23120	Late embryogenesis abundant protein, group 6	3.494842	3.0162187	1.1586833
SR1	CBL-interacting serine/threonine-protein kinase 14	2.3380404	2.017549	1.1588517
AT2G33580	protein kinase family protein	2.9104564	2.5108294	1.1591613
AT1G63080	pentatricopeptide repeat-containing protein	4.5246625	3.903329	1.1591805
ALDH2B7	aldehyde dehydrogenase 2B7	2.8040714	2.4186425	1.1593575
AT5G56160	sec14p-like phosphatidylinositol transfer-like protein	2.525246	2.1775882	1.1596526
AT4G28150	hypothetical protein	3.1197178	2.6889803	1.1601863
AT2G03740	late embryogenesis abundant domain-containing protein	2.5336673	2.1835651	1.1603351
AT5G16380	hypothetical protein	2.4409008	2.1031597	1.1605874
NAP	NAC domain-containing protein 29	2.9324236	2.522935	1.1623064
MYB32	transcription factor MYB32	2.717108	2.3373356	1.1624808
ICS2	Isochorismate synthase 2	4.163741	3.5755196	1.1645136
AT2G41870	remorin-like protein	2.7869558	2.389041	1.1665584
ATS1	caleosin 1	7.1638966	6.1407948	1.1666074
AT1G76590	PLATZ transcription factor domain-containing protein	4.13343	3.541941	1.1669958
ERD9	glutathione S-transferase	2.834679	2.4289224	1.167052
AT5G41320	hypothetical protein	2.6564834	2.2758992	1.1672237
AT4G12000	SNARE associated Golgi family protein	6.2684655	5.3694634	1.1674286
IQD22	protein IQ-domain 22	2.4226606	2.0750697	1.1675081
AT1G24600	hypothetical protein	9.039624	7.741478	1.1676872
AT3G56790	RNA splicing factor-related protein	2.400503	2.0552382	1.1679925
AT4G16750	ethylene-responsive transcription factor ERF039	2.5704	2.2000365	1.1683443
AT1G19970	ER lumen protein retaining receptor-like protein	2.554572	2.1857524	1.1687381
AT3G60110	DNA-binding bromodomain-containing protein	2.814867	2.407082	1.1694105
AT4G22620	SAUR-like auxin-responsive protein	7.040787	6.0132275	1.1708833
GolS2	galactinol synthase 2	26.17591	22.323755	1.1725587
AT3G18490	aspartyl protease family protein	3.4763792	2.9635837	1.1730323
AT3G49130	SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein	16.063055	13.689824	1.1733572

CYP722A1	cytochrome P450, family 722, subfamily A, polypeptide 1	9.0365715	7.696871	1.1740578
TSPO	tryptophan-rich sensory protein-like protein	31.560072	26.87062	1.1745197
AT4G14225	putative zinc finger A20 and AN1 domain-containing stress-associated protein 8	7.8847184	6.710889	1.1749142
PKT3	3-ketoacyl-CoA thiolase 2	2.7685745	2.355512	1.1753601
AT1G20320	haloacid dehalogenase-like hydrolase	5.896794	5.0164056	1.1755018
NAC3	NAC domain-containing protein 55	2.585483	2.199372	1.1755551
AT3G03170	hypothetical protein	5.0182776	4.264526	1.1767493
AT3G15670	late embryogenesis abundant domain-containing protein	91.59765	77.83951	1.1767501
AT3G11325	acyltransferase	12.622323	10.726061	1.1767901
AT1G53540	HSP20-like chaperone	4.3957415	3.7338781	1.177259
AT5G41590	hypothetical protein	9.160335	7.7711697	1.1787587
AT2G24560	GDSL esterase/lipase	5.917697	5.0189447	1.179072
AT4G23493	hypothetical protein	2.8660429	2.4289641	1.1799445
AT3G63360	defensin-like protein 11	3.311968	2.8059034	1.1803572
AT1G05894	hypothetical protein	4.349819	3.6836681	1.1808391
AT5G01520	RING/U-box domain-containing protein	3.4943593	2.9582481	1.1812259
AT1G64380	ethylene-responsive transcription factor ERF061	9.978354	8.4469595	1.1812954
HVA22B	HVA22-like protein b	4.1888466	3.5449507	1.1816375
AT4G11570	haloacid dehalogenase-like hydrolase domain-containing protein	2.5987797	2.1988807	1.1818649
MYB112	myb domain protein 112	3.5083878	2.9673278	1.1823392
RPS2	disease resistance protein RPS2	3.745633	3.165398	1.1833055
DIN2	beta-glucosidase 30	7.4110255	6.262936	1.1833149
AT4G16146	cAMP-regulated phosphoprotein 19-related protein	2.8592908	2.4151773	1.1838845
COR413-PM1	cold regulated 413 plasma membrane 1	4.290205	3.620758	1.1848913
DGK1	diacylglycerol kinase1	3.280598	2.768559	1.1849477
ERD10	dehydrin ERD10	6.694911	5.6494923	1.1850464
AT1G55230	hypothetical protein	2.7906263	2.3547063	1.1851271
DREB2A	dehydration-responsive element-binding protein 2A	11.521972	9.719184	1.1854876
HSP70T-2	heat-shock protein 70T-2	3.89698	3.2847185	1.186397

AT3G51750	hypothetical protein	7.004666	5.9037676	1.1864738
AT5G35660	glycine-rich protein	2.874675	2.4203956	1.1876881
AT1G70130	concanavalin A-like lectin protein kinase	4.7565393	4.0023513	1.1884362
AT3G50390	transducin/WD40 domain-containing protein	2.6714907	2.2472682	1.1887724
BHLH92	transcription factor bHLH92	3.8179176	3.2106175	1.1891537
AT5G01880	RING-H2 finger protein ATL74	5.2359476	4.4027963	1.1892322
AT2G38240	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	5.7097354	4.799627	1.1896207
AT5G15180	peroxidase 56	3.0272627	2.542478	1.1906741
RKP	ubiquitination-promoting complex protein 1	2.8211074	2.3687906	1.1909485
AT5G40645	RPM1-interacting protein 4 (RIN4)	2.9687355	2.4923	1.191163
AT3G17770	Dihydroxyacetone kinase	4.526143	3.7982903	1.1916264
AT1G80320	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	2.6596525	2.2317133	1.1917537
AT2G27270	hypothetical protein	15.074888	12.642724	1.1923766
AT3G53820	C2H2 and C2HC zinc finger-containing protein	3.1731305	2.6602802	1.1927806
AT5G07610	F-box protein	2.4658613	2.0668488	1.1930535
AT1G62840	hypothetical protein	2.580371	2.1609244	1.1941051
AT1G74010	strictosidine synthase	2.5293808	2.118021	1.1942189
UGT73B3	UDP-glucosyl transferase 73B3	2.5483115	2.1306427	1.1960295
DGL	galactolipase DONGLE	3.177112	2.6549973	1.1966536
HFR1	transcription factor HFR1	3.320805	2.7745426	1.1968838
AT3G56260	hypothetical protein	6.1358604	5.1262045	1.1969597
ASY1	DNA-binding HORMA-like protein	2.6026511	2.1743505	1.1969787
AT1G54070	Dormancy/auxin associated family protein	2.8301773	2.3640933	1.1971512
AT1G62975	transcription factor bHLH125	2.5699496	2.1465564	1.197243
HAI1	protein phosphatase	66.85151	55.809277	1.1978565
AT4G35985	senescence/dehydration-associated protein	5.5125723	4.601352	1.1980331
42282	organic cation/carnitine transporter5	2.530406	2.1105773	1.1989164
CID11	CTC-interacting domain 11 protein	2.6687126	2.2241845	1.1998612
AT5G17460	hypothetical protein	15.283972	12.736639	1.2000003

HSFA6B	heat stress transcription factor A-6b	101.43073	84.51273	1.2001828
RAP2.4	ethylene-responsive transcription factor RAP2-4	2.423894	2.0164971	1.202032
SCL14	scarecrow-like protein 14	2.7286906	2.2689471	1.2026241
AT5G52390	PAR1 protein	4.3659196	3.6251192	1.204352
TET4	tetraspanin4	3.390391	2.8134413	1.2050692
HSFC1	heat stress transcription factor C-1	3.6190183	3.0010679	1.2059102
NAC089	NAC domain containing protein 89	2.56097	2.1230688	1.2062587
PMZ	zinc finger AN1 domain-containing stress-associated protein 12	3.311699	2.7452433	1.2063408
AT5G25450	ubiquinol-cytochrome c reductase subunit 7	3.0824528	2.5542884	1.2067754
AT4G15450	Senescence/dehydration-associated protein-like protein	2.4628475	2.0390902	1.207817
AT2G32235	hypothetical protein	3.6846604	3.049575	1.2082537
AT3G17770	Dihydroxyacetone kinase	3.0525408	2.5252383	1.208813
AT3G22275	hypothetical protein	6.5429745	5.412353	1.2088965
AT1G24330	U-box domain-containing protein 6	2.640151	2.1839197	1.2089049
DEAR3	ethylene-responsive transcription factor ERF008	2.5251458	2.0884163	1.2091198
AT4G16146	cAMP-regulated phosphoprotein 19-related protein	2.7725148	2.2923796	1.2094483
AT5G10410	putative clathrin assembly protein	3.0024548	2.4820235	1.2096803
AT3G29670	HXXXD-type acyl-transferase-like protein	6.8557076	5.6668735	1.2097867
AFP2	Ninja-family protein AFP2	3.103686	2.5640886	1.2104442
LCR3	defensin-like protein 141	6.9223948	5.7170963	1.2108235
AT1G33500	hypothetical protein	2.5536125	2.1060994	1.2124842
AT5G64230	hypothetical protein	2.6892807	2.215682	1.2137485
PP2-B1	F-box protein PP2-B1	2.7210875	2.2414415	1.21399
ERD7	senescence/dehydration related protein	9.682555	7.9756317	1.2140173
NSP5	nitrile specifier protein 5	2.6620235	2.192145	1.2143464
AT5G04170	putative calcium-binding protein CML50	2.8870714	2.3764293	1.2148778
GEX3	gamete-expressed 3	2.8451996	2.341688	1.2150209
MYB305	myb domain protein 305	13.399659	11.024014	1.2154973
AT4G06688	hypothetical protein	2.8483894	2.343368	1.2155108

CDT1	cadmium tolerance 1	2.9760635	2.446503	1.2164562
LEA18	late embryogenesis abundant group 1 protein	21.917835	18.008322	1.2170948
AT3G48240	octicosapeptide/Phox/Bem1p domain-containing protein	6.495038	5.3325987	1.2179874
AT4G33905	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	12.659516	10.3938	1.2179874
NTMC2T6.2	calcium-dependent lipid-binding domain-containing protein	4.165236	3.4179142	1.2186486
HAI3	putative protein phosphatase 2C 24	509.75458	418.1764	1.2189941
UBQ3	polyubiquitin 3	2.8028557	2.2989187	1.2192061
INVH	invertase H	3.67299	3.012369	1.2193029
NAC019	NAC domain-containing protein 19	19.593796	16.051931	1.2206504
AT1G11925	stigma-specific stig1-like protein	3.0285997	2.481085	1.2206755
AT3G17400	F-box protein	2.7180097	2.2264786	1.2207662
AT3G17770	Dihydroxyacetone kinase	3.8969157	3.1907916	1.2213006
CSLD1	cellulose synthase-like protein D1	13.635419	11.153275	1.2225485
ProT3	proline transporter 3	3.870038	3.1643646	1.2230064
UGE5	UDP-D-glucose/UDP-D-galactose 4-epimerase 5	3.1042955	2.5365236	1.2238386
AT5G13880	hypothetical protein	3.116898	2.5463667	1.2240571
AT5G13200	GEM-like protein 5	4.2727766	3.490663	1.2240586
BIM1	transcription factor BIM1	2.8531575	2.3283477	1.2254002
PP2-B11	F-box protein PP2-B11	4.6371756	3.7836304	1.2255889
MYB2	myb domain protein 2	3.3979163	2.7714539	1.2260411
EDA9	D-3-phosphoglycerate dehydrogenase	2.913004	2.374837	1.2266122
AT1G30280	chaperone DnaJ-domain-containing protein	2.7322283	2.2271342	1.226791
TIP2;2	putative aquaporin TIP2-2	2.9032602	2.3664594	1.2268372
AT4G38030	Rhamnogalacturonate lyase family protein	2.6018617	2.120687	1.2268956
ASL9	LOB domain-containing protein 3	5.2906547	4.308767	1.2278814
AT1G32860	glucan endo-1,3-beta-glucosidase 11	4.7005563	3.8278756	1.2279804
AT2G14290	F-box protein	4.78942	3.898029	1.2286775
AT2G21130	Peptidyl-prolyl cis-trans isomerase CYP19-2	3.3350537	2.7135038	1.229058
AT3G49200	O-acyltransferase (WSD1-like) family protein	2.9677339	2.4133499	1.2297155

AT1G07870	putative serine/threonine-protein kinase RLCKVII	2.4617667	2.0006943	1.2304562
RABA6b	RAB GTPase homolog A6B	3.0625	2.4872217	1.2312936
AT4G19870	putative F-box/kelch-repeat protein	2.8483589	2.3116186	1.2321924
AT4G14810	hypothetical protein	2.9126728	2.3599694	1.2341994
AT2G22590	UDP-glycosyltransferase-like protein	3.1921325	2.5859854	1.2343968
RD26	NAC domain-containing protein 72	13.311709	10.778733	1.2349976
LSU3	response to low sulfur 3 protein	11.908008	9.640079	1.2352605
MYB79	myb domain protein 79	40.918556	33.108242	1.2359024
BOR4	boron transporter 4	6.053803	4.8969693	1.2362345
GolS4	galactinol synthase 4	9.668084	7.8051867	1.2386743
AT1G52990	thioesterase-like protein	9.10927	7.3494678	1.2394463
AT4G29930	transcription factor bHLH27	5.7332225	4.623246	1.240086
AT1G32950	Subtilase-like protein	6.0159845	4.849748	1.2404737
AT5G24870	RING/U-box domain-containing protein	3.0807018	2.4777145	1.2433643
AT1G02030	C2H2-like zinc finger protein	3.409178	2.7363014	1.2459074
AT3G56080	dehydration-responsive protein-like protein	2.8349	2.2740946	1.246606
AT3G19920	hypothetical protein	4.509637	3.6174362	1.246639
AT4G35560	transducin/WD40 domain-containing protein	4.597613	3.682522	1.2484957
AT5G53710	hypothetical protein	46.123013	36.935677	1.2487388
LTI78	low-temperature-responsive protein 78/desiccation-responsive protein 29A	36.52818	29.240479	1.2492334
AT1G22290	14-3-3 family protein	2.9284112	2.3399024	1.25151
AT4G18280	glycine-rich cell wall protein-like protein	4.8712506	3.88465	1.2539741
NAP	NAC domain-containing protein 29	2.780815	2.2166123	1.2545338
AT1G23450	pentatricopeptide repeat-containing protein-like protein	3.007073	2.3953218	1.255394
AT5G53710	hypothetical protein	55.140335	43.880043	1.2566154
AT4G30350	heat shock-related protein	2.5273533	2.003382	1.2615434
AT5G59490	haloacid dehalogenase-like hydrolase domain-containing protein	2.7441437	2.1748896	1.2617394
AtIPCS1	inositol phosphorylceramide synthase 1	3.853695	3.0497243	1.2636207
AT2G29500	HSP20 family protein	3.5820584	2.833905	1.2640009

ABF3	abscisic acid-insensitive 5-like protein 6	8.007179	6.333902	1.264178
MAPKKK15	mitogen-activated protein kinase kinase kinase 15	3.2776606	2.59016	1.265428
AT4G22980	hypothetical protein	2.914517	2.3009543	1.2666557
AT1G79520	Cation efflux family protein	8.028088	6.334635	1.2673324
CYP89A5	cytochrome P450, family 89, subfamily A, polypeptide 5	2.8156412	2.2200599	1.2682728
AT1G75860	hypothetical protein	2.793068	2.2019744	1.2684379
AT1G80450	VQ motif-containing protein	2.6401143	2.0809405	1.268712
NF-YC2	nuclear transcription factor Y subunit C-2	4.605859	3.6295838	1.2689772
AT1G49450	WD40 domain-containing protein	34.732895	27.365553	1.2692196
LSU1	response to low sulfur 1 protein	8.9673	7.0602317	1.2701143
AT3G21320	hypothetical protein	3.2183516	2.5332966	1.2704203
AT2G04420	RNase H domain-containing protein	2.898132	2.2807863	1.2706723
AT1G51770	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	6.1049123	4.7996097	1.2719603
SIP4	CBL-interacting serine/threonine-protein kinase 11	6.2254243	4.887158	1.2738333
AT5G04250	OTU-like cysteine protease family protein	4.6075644	3.616297	1.2741112
COR47	dehydrin COR47	2.7671063	2.168047	1.276313
SKP2B	F-box/LRR-repeat protein 5	3.4377475	2.6929097	1.2765923
DREB2A	dehydration-responsive element-binding protein 2A	11.60414	9.089159	1.2767011
ZF2	zinc-finger protein 2	3.83027	2.999478	1.2769789
AT5G17850	Sodium/calcium exchanger family protein	11.147094	8.716741	1.2788144
HSA32	Aldolase-type TIM barrel family protein	3.2881532	2.5708604	1.2790089
AtS40-3	protein AtS40-3	4.334894	3.3881652	1.2794224
TIP2;3	aquaporin TIP2-3	21.143965	16.524345	1.2795645
RAN4	GTP-binding nuclear protein Ran-4	3.1913872	2.4940856	1.279582
CYP706A7	cytochrome P450, family 706, subfamily A, polypeptide 7	4.6979265	3.6708953	1.2797768
AT1G76470	Rossmann-fold NAD(P)-binding domain-containing protein	2.7645924	2.1569483	1.2817147
MSL5	mechanosensitive channel of small conductance-like 5	4.1471663	3.2338688	1.2824165
PDLP1	cysteine-rich repeat secretory protein 56	2.9130993	2.271473	1.2824715
AT4G34400	AP2/B3 domain-containing protein	4.6599145	3.6330838	1.2826334

AT2G34990	RING-H2 finger protein ATL38	4.2761064	3.3324423	1.2831749
AT5G23950	calcium-dependent lipid-binding domain-containing protein	4.0756063	3.1759741	1.2832619
AT1G64380	ethylene-responsive transcription factor ERF061	7.124656	5.54967	1.2837981
AT5G54420	hypothetical protein	2.966461	2.3100643	1.2841465
FH8	formin-like protein 8	2.8104384	2.1874723	1.284788
AT5G56160	sec14p-like phosphatidylinositol transfer-like protein	2.6635425	2.070697	1.2863023
AT3G49130	SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein	16.93192	13.1600485	1.2866153
AT3G61900	SAUR-like auxin-responsive protein	4.422149	3.436823	1.2866969
AT4G20320	putative CTP synthase	3.8301764	2.9729528	1.2883408
AT2G21320	B-box zinc finger-like protein	2.8001277	2.1732152	1.2884724
AT1G78840	putative F-box/FBD/LRR-repeat protein	2.6390636	2.0467825	1.2893717
AT2G25690	hypothetical protein	3.973685	3.0769622	1.2914313
AT3G53230	cell division control protein 48-D	4.5142794	3.4954522	1.2914722
MAPKKK17	mitogen-activated protein kinase kinase kinase 17	7.6180534	5.89711	1.2918283
AT5G38240	Protein kinase family protein	3.193938	2.47218	1.2919521
AT2G34030	calcium-binding EF-hand-containing protein	2.6133347	2.0216582	1.2926688
AT4G02950	Ubiquitin family protein	20.45135	15.81007	1.2935647
NAC080	NAC domain containing protein 80	6.628264	5.1162148	1.2955406
AT4G23450	RING/U-box domain-containing protein	3.5169442	2.7138069	1.2959449
MYB74	myb domain protein 74	9.845511	7.5962043	1.2961093
UGT75B1	indole-3-acetate beta-glucosyltransferase 1	4.5053596	3.4743507	1.2967486
UGT84A1	UDP-glycosyltransferase-like protein	2.8617415	2.2063003	1.2970771
MES9	methyl esterase 9	2.626153	2.0233161	1.297945
AT3G01830	putative calcium-binding protein CML40	7.5291576	5.798533	1.298459
TIP2;3	aquaporin TIP2-3	14.651527	11.274096	1.2995745
AT3G43270	pectinesterase 32	3.412841	2.6259933	1.299638
AT1G67856	RING/U-box domain-containing protein	8.415128	6.4617357	1.3023015
AT1G16850	hypothetical protein	7.184984	5.515233	1.3027526

AFP3	Ninja-family protein AFP3	7.427146	5.7004957	1.3028947
CYP81D1	cytochrome P450 CYP81D11	5.500738	4.2159734	1.3047374
AT2G40435	hypothetical protein	2.6752682	2.0501606	1.3049065
AT3G17130	plant invertase/pectin methylesterase inhibitor domain-containing protein	5.7310777	4.388123	1.306043
AT1G52855	hypothetical protein	6.411806	4.901335	1.3081754
CIPK18	CBL-interacting serine/threonine-protein kinase 18	2.975723	2.2736242	1.3088017
HSP70	heat shock protein 70-4	3.4307554	2.619421	1.3097382
AT4G39360	hypothetical protein	6.2939343	4.800522	1.3110938
AT5G35320	hypothetical protein	2.7345736	2.083586	1.3124361
LCR6	putative defensin-like protein 126	4.0966916	3.1182525	1.313778
AT1G68500	hypothetical protein	6.4678617	4.9194894	1.3147424
RLP33	receptor like protein 33	3.9084527	2.9716895	1.3152292
AT2G20625	hypothetical protein	8.549455	6.4991913	1.3154644
ABF3	abscisic acid-insensitive 5-like protein 6	7.0449123	5.3510985	1.3165357
ERF4	ethylene-responsive transcription factor 4	3.1781518	2.4132621	1.3169526
AT2G21237	hypothetical protein	4.2366695	3.2151127	1.3177359
AT4G39360	hypothetical protein	6.0873685	4.6191893	1.3178436
AT4G35655	putative nitrate-responsive NOI protein	7.0149503	5.318484	1.3189756
AT1G11925	stigma-specific stig1-like protein	2.7161043	2.0576062	1.320031
SNRK2.7	serine/threonine-protein kinase SRK2F	2.8907666	2.18977	1.3201236
TLP3	Tubby-like F-box protein 3	2.8254642	2.1402564	1.3201523
AT5G44065	hypothetical protein	4.289636	3.2486322	1.3204439
AT3G22920	peptidylprolyl isomerase	2.7625847	2.0899024	1.3218726
CYP71B10	cytochrome P450 71B10	4.0675874	3.0747805	1.3228871
AT3G03272	hypothetical protein	2.7888222	2.1079986	1.3229716
DEAR3	ethylene-responsive transcription factor ERF008	2.814374	2.1205456	1.3271934
UGT76E1	UDP-glucosyl transferase 76E1	4.152731	3.1269348	1.3280517
AT4G25433	peptidoglycan-binding LysM domain-containing protein	16.330198	12.29054	1.3286804
AT5G01200	duplicated SANT DNA-binding domain-containing protein	3.160988	2.3790386	1.328683

NCED9	9-cis-epoxycarotenoid dioxygenase NCED9	4.941269	3.7163959	1.3295863
AT5G05600	oxidoreductase, 2OG-Fe(II) oxygenase family protein	2.7006607	2.0252042	1.3335252
AT3G19240	Vacuolar import/degradation, Vid27-related protein	2.7784445	2.0789125	1.3364894
MYB41	myb domain protein 41	21.358395	15.972192	1.3372238
AT5G12010	hypothetical protein	3.6866632	2.75688	1.3372592
AT3G12977	no apical meristem-domain containing transcriptional regulator	2.9508674	2.206649	1.3372618
AT1G73510	hypothetical protein	12.784129	9.535602	1.3406734
NF-YC2	nuclear transcription factor Y subunit C-2	4.674577	3.4841218	1.3416802
SESA1	seed storage albumin 1	3.0451596	2.269434	1.3418145
NAC046	NAC domain containing protein 46	3.6959527	2.7542117	1.3419276
AT3G21660	UBX domain-containing protein	14.320535	10.664126	1.34287
MC3	metacaspase 3	3.0099447	2.2398033	1.3438432
AT3G17770	Dihydroxyacetone kinase	5.272687	3.9232934	1.3439441
SIP4	CBL-interacting serine/threonine-protein kinase 11	5.359159	3.9864373	1.344348
MAP65-8	microtubule-associated protein 65-8	3.2169602	2.3926167	1.3445363
AT3G22100	transcription factor bHLH117	4.939729	3.67149	1.345429
AT1G57590	Pectin lyase-like protein	4.048264	3.0080192	1.3458239
AT3G16800	putative protein phosphatase 2C 41	3.7878346	2.8143573	1.3458968
AT3G08750	F-box protein	25.784407	19.140497	1.3471128
AFP1	Ninja-family protein AFP1	8.242834	6.1154766	1.3478645
TET15	tetraspanin15	3.4233532	2.5366175	1.3495741
CPK15	calcium-dependent protein kinase 15	4.5184917	3.3443966	1.3510634
AT1G68620	alpha/beta-hydrolase domain-containing protein	3.3599057	2.4865115	1.3512528
AT4G01535	hypothetical protein	4.090873	3.0259984	1.3519086
TIP2;2	putative aquaporin TIP2-2	4.979997	3.681734	1.3526227
AT1G18830	transducin/WD-40 repeat-containing protein	3.545566	2.6203291	1.3530995
VHA-E2	V-type proton ATPase subunit E2	4.053068	2.9901192	1.355487
AT1G80160	lactoylglutathione lyase / glyoxalase I-like protein	2.8248732	2.078727	1.3589438
XERO1	dehydrin xero 1	4.9995604	3.6665835	1.3635473

AT5G44310	late embryogenesis abundant domain-containing protein	2.9486415	2.1577263	1.3665503
AT2G17660	RPM1-interacting protein 4-like protein	5.1581874	3.7727687	1.3672154
AT5G20690	leucine-rich repeat protein kinase-like protein	5.7099957	4.1738024	1.3680562
AT3G46070	C2H2-type zinc finger protein	3.4475856	2.51795	1.3692033
AT4G02655	hypothetical protein	6.925421	5.0545588	1.3701336
AT3G56260	hypothetical protein	7.0118327	5.116861	1.3703388
GA2OX7	gibberellin 2-beta-dioxygenase 7	6.182223	4.5108714	1.3705163
LSU1	response to low sulfur 1 protein	8.022602	5.8500137	1.3713819
AT1G32860	glucan endo-1,3-beta-glucosidase 11	3.3205132	2.4185865	1.3729147
AT3G52060	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	42.049057	30.565174	1.3757178
AT5G16980	2-alkenal reductase	2.9397154	2.1338406	1.377664
AT1G62975	transcription factor bHLH125	3.0153136	2.1886208	1.3777231
AT3G57760	protein kinase family protein	3.4525642	2.5043335	1.378636
MAN1	mannan endo-1,4-beta-mannosidase 1	8.835598	6.396333	1.3813535
AT3G04200	germin-like protein subfamily 1 member 6	6.383215	4.6198316	1.3816987
AT5G52660	myb family transcription factor	2.8170505	2.0336463	1.3852215
BTI2	reticulon-like protein B2	3.9919698	2.881146	1.3855493
AT1G30250	hypothetical protein	7.0630302	5.0945096	1.3864005
MAN1	mannan endo-1,4-beta-mannosidase 1	7.1563687	5.147941	1.3901418
AT5G11410	protein kinase family protein	2.9629235	2.1307383	1.3905619
AT1G19500	hypothetical protein	7.39062	5.3138976	1.3908097
MYB84	transcription factor RAX3	3.9424112	2.829031	1.3935553
AT2G34360	MATE efflux family protein	2.9155068	2.0892308	1.395493
AT3G56600	phosphatidylinositol 3- and 4-kinase-like protein	4.3211346	3.0882082	1.3992368
AT2G02061	nucleotide-diphospho-sugar transferase domain-containing protein	4.9957595	3.5681186	1.4001102
COR413IM1	cold regulated 314 inner membrane 1	5.4992332	3.9221673	1.4020904
AT4G30830	hypothetical protein	7.106876	5.06717	1.4025335
AT4G34400	AP2/B3 domain-containing protein	6.012957	4.2786427	1.4053422
ABI5	protein abscisic acid-insensitive 5	4.9324985	3.5068018	1.4065518

HOS3-1	GNS1/SUR4 membrane protein	3.6023514	2.5604708	1.4069098
AT5G16960	2-alkenal reductase	39.47992	28.044939	1.4077377
UGT76E12	UDP-glucosyl transferase 76E12	8.623215	6.1214056	1.4086984
AT5G24155	FAD/NAD(P)-binding oxidoreductase family protein	4.2844133	3.0365613	1.4109426
AT1G21722	hypothetical protein	10.492814	7.4293876	1.4123391
AT3G03341	hypothetical protein	42.769104	30.236946	1.4144651
AT3G27025	hypothetical protein	7.334677	5.183223	1.4150804
AT4G14730	Bax inhibitor-1 family protein	3.7547178	2.6523736	1.4156067
ABI2	protein phosphatase 2C 77	5.8843026	4.1531386	1.4168326
AT2G25890	Oleosin-like protein	6.4949746	4.574924	1.4196901
LTI78	low-temperature-responsive protein 78/desiccation-responsive protein 29A	40.03432	28.182861	1.4205201
MYB85	myb domain protein 85	3.320974	2.3377407	1.4205914
BAM1	beta-amylase 1	7.1663666	5.030447	1.4245983
ATZIP4	ZIP4-like protein	4.3318768	3.0354464	1.4270971
ASY1	DNA-binding HORMA-like protein	13.679837	9.559736	1.4309847
NIG1	transcription factor bHLH28	10.2736	7.176291	1.4316031
AT5G35110	hypothetical protein	3.0541728	2.130992	1.4332166
AT4G17550	MFS transporter, OPA family, solute carrier family 37	3.0122356	2.1005712	1.4340079
AT1G21940	hypothetical protein	10.148507	7.0765324	1.4341074
PDR10	ABC transporter G family member 38	3.6513178	2.5436463	1.435466
AT1G73510	hypothetical protein	17.931911	12.485918	1.4361707
AT1G07860	hypothetical protein	17.35277	12.074489	1.4371432
AT3G12510	MADS-box family protein	4.581384	3.1797743	1.4407892
AT3G20340	hypothetical protein	4.2654023	2.9597483	1.4411368
DREB2B	dehydration-responsive element-binding protein 2B	7.7986965	5.3975487	1.4448589
AT1G10585	basic helix-loop-helix domain-containing protein	3.556125	2.458095	1.4466996
AT2G38250	DNA-binding protein	3.4266055	2.3565593	1.4540715
AT3G12510	MADS-box family protein	4.4246726	3.0386868	1.4561136
JRG21	jasmonate-regulated protein	2.937831	2.0153737	1.4577103

AT3G14670	hypothetical protein	6.250919	4.286813	1.4581739
MYB121	myb proto-oncogene protein	74.905846	51.325943	1.459415
AT5G62360	plant invertase/pectin methylesterase inhibitor domain-containing protein	3.6481657	2.4994216	1.459604
AT5G16360	NC domain-containing protein-like protein	4.5939484	3.1471608	1.4597121
FLA14	fasciclin-like arabinogalactan protein 14	29.014442	19.86224	1.4607841
AT3G61900	SAUR-like auxin-responsive protein	4.8273764	3.2978225	1.4638072
AT4G12005	hypothetical protein	4.5561633	3.1072395	1.4663059
CYP94B3	cytochrome P450, family 94, subfamily B, polypeptide 3	7.3077326	4.982819	1.466586
CBF1	dehydration-responsive element-binding protein 1B	8.474016	5.7684813	1.4690204
AT3G12977	no apical meristem-domain containing transcriptional regulator	2.9781435	2.0259058	1.4700307
SVL3	protein SEUSS-like 3	11.535331	7.8440185	1.4705895
AT1G70640	octicosapeptide/Phox/Be.1 domain-containing protein	33.39988	22.6809	1.4725993
CYP89A6	cytochrome P450, family 87, subfamily A, polypeptide 6	5.053147	3.4141498	1.4800601
MYB102	MYB-like 102	10.73974	7.2555337	1.4802136
AT2G13640	transcription factor IIS-like protein	12.099832	8.16726	1.4815043
UPS4	ureide permease 4	6.290484	4.2409086	1.4832869
AT2G31930	hypothetical protein	3.276021	2.2051055	1.4856527
AT5G52940	hypothetical protein	4.2895584	2.8790214	1.4899362
EM1	Em-like protein GEA1	4.076982	2.7361567	1.4900397
AT2G31940	hypothetical protein	7.3791823	4.951629	1.4902534
ERD2	heat shock protein-70 cognate protein	3.422777	2.295	1.491406
RAP2.6	ethylene-responsive transcription factor RAP2-6	4.1466317	2.7714522	1.4961946
BOR4	boron transporter 4	12.349424	8.227757	1.5009466
CYP72A9	cytochrome P450, family 72, subfamily A, polypeptide 9	5.6798587	3.761273	1.5100895
AT3G15200	pentatricopeptide repeat-containing protein	3.095525	2.0426583	1.5154395
AT1G16515	hypothetical protein	4.3544683	2.872668	1.5158272
AT5G45630	hypothetical protein	7.229941	4.7679477	1.5163634
CIPK19	CBL-interacting serine/threonine-protein kinase 19	13.173505	8.676855	1.518235
AT3G27025	hypothetical protein	8.031424	5.28716	1.5190431

AT3G17130	plant invertase/pectin methylesterase inhibitor domain-containing protein	4.3692636	2.8723989	1.5211201
AT5G42053	hypothetical protein	4.0707297	2.675913	1.5212487
AT1G76530	auxin efflux carrier-like protein	3.7658942	2.4731598	1.5227056
NAC080	NAC domain containing protein 80	6.540648	4.29086	1.524321
DGK2	diacylglycerol kinase 2	3.2300851	2.1159668	1.5265293
AT1G69480	phosphate transporter PHO1-10	7.938423	5.1905036	1.529413
CDT1	cadmium tolerance 1	3.4548404	2.253353	1.5331998
AT2G04190	TRAF-like family protein	6.241515	4.061037	1.5369264
SAG29	senescence-associated protein 29	4.159686	2.7001376	1.540546
AT4G21930	hypothetical protein	17.028833	11.052691	1.5406957
APX1	L-ascorbate peroxidase	3.2338538	2.0928485	1.5451926
AT2G17660	RPM1-interacting protein 4-like protein	5.285411	3.4177897	1.5464412
MYB107	myb domain protein 107	4.867742	3.1425166	1.5489949
KNAT3	homeobox protein knotted-1-like 3	10.234946	6.5986586	1.5510646
AT1G57850	Toll-Interleukin-Resistance domain-containing protein	8.089746	5.210834	1.5524858
AT3G27210	hypothetical protein	3.2977266	2.1232457	1.5531536
AT1G55240	hypothetical protein	3.3325162	2.1442406	1.5541708
RAS1	response to ABA and salt 1	6.0293117	3.8519757	1.5652517
AT1G29680	hypothetical protein	28.237911	18.010012	1.5679008
FBW2	F-box protein FBW2	3.3434107	2.129072	1.5703605
AT3G62730	hypothetical protein	5.2821383	3.356498	1.5737052
AT5G24080	protein kinase family protein	27.669205	17.532507	1.5781659
MSL5	mechanosensitive channel of small conductance-like 5	6.357161	4.023804	1.5798882
AT2G34610	hypothetical protein	7.321857	4.630152	1.5813426
HSFA6B	heat stress transcription factor A-6b	3.1913033	2.0109563	1.5869582
PDR11	ABC transporter G family member 39	3.2026644	2.017856	1.5871621
AT4G30830	hypothetical protein	6.251365	3.9357727	1.588345
AT2G33280	major facilitator protein	6.872174	4.323966	1.5893217
AT1G62320	ERD (early-responsive to dehydration stress) family protein	3.5254471	2.2053263	1.5986056

AT1G05340	hypothetical protein	4.993011	3.1143792	1.6032122
AT1G14048	GCK domain-containing protein	4.39448	2.7285247	1.6105702
P5CS1	Gamma-glutamyl phosphate reductase	28.83455	17.824625	1.6176807
AT1G19490	bZIP transcription factor-like protein	4.0224957	2.4864063	1.6177951
RNS1	ribonuclease 1	3.2753043	2.0114527	1.6283277
AT1G56660	hypothetical protein	3.8419716	2.350414	1.6345935
AT2G01300	hypothetical protein	5.3740425	3.268434	1.6442255
AT3G23220	ethylene-responsive transcription factor ERF095	4.2497444	2.5539305	1.6640016
AT1G15010	hypothetical protein	3.8125608	2.2887805	1.6657608
AT5G03210	hypothetical protein	21.69327	12.97107	1.6724349
RRTF1	ethylene-responsive transcription factor ERF109	6.654209	3.9599447	1.6803793
AT4G21926	hypothetical protein	4.164758	2.4706843	1.68567
AT3G13130	hypothetical protein	4.610067	2.7076697	1.7025958
AT3G50373	hypothetical protein	4.856672	2.8348396	1.7132088
NAMT1	S-adenosyl-L-methionine-dependent methyltransferase-like protein	5.6540337	3.2949603	1.7159641
AT5G39560	F-box/kelch-repeat protein	8.194002	4.7654805	1.7194494
AT1G76965	hypothetical protein	11.157238	6.4663954	1.7254184
AT2G33690	Late embryogenesis abundant protein, group 6	5.1374893	2.9766388	1.7259364
AT1G77680	Ribonuclease II/R-like protein	4.6789036	2.6460967	1.7682285
CYP72A13	cytochrome P450, family 72, subfamily A, polypeptide 13	7.0993257	3.9592865	1.7930821
AT3G53040	putative late embryogenesis abundant protein	5.4607406	3.0329754	1.8004568
AT5G43285	defensin-like protein 217	4.8080454	2.6312218	1.8273052
AT5G62360	plant invertase/pectin methylesterase inhibitor domain-containing protein	4.706977	2.5645268	1.8354174
AT5G62360	plant invertase/pectin methylesterase inhibitor domain-containing protein	4.749228	2.5422428	1.8681254
AT1G80133	epidermal patterning factor-like protein 8	4.2646356	2.2712288	1.8776776
NAC080	NAC domain containing protein 80	9.045411	4.7808905	1.8919928
SIP1	putative galactinol--sucrose galactosyltransferase 5	7.5245953	3.9636688	1.8983915
SPS2F	sucrose phosphate synthase 2F	6.4162793	3.3616407	1.908675
AT3G09440	protein heat shock protein 70-3	4.013204	2.097905	1.9129581

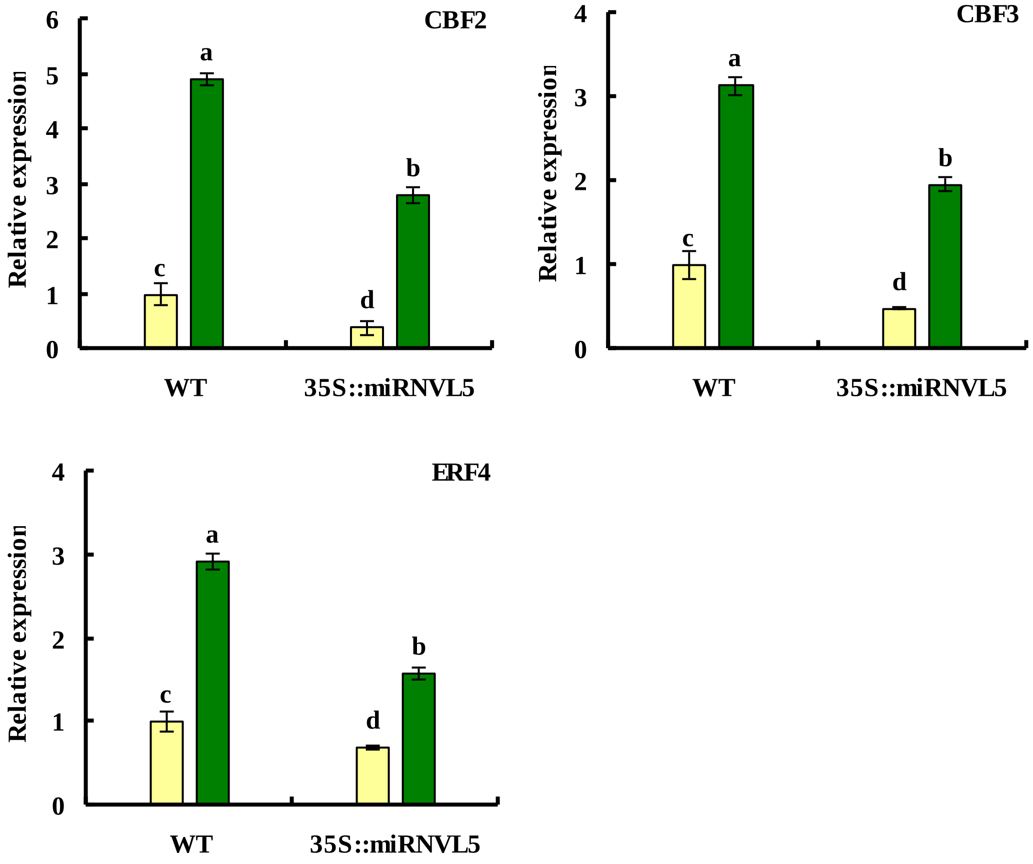
CBF4	dehydration-responsive element-binding protein 1D	31.357681	16.305992	1.9230771
AT5G62360	plant invertase/pectin methylesterase inhibitor domain-containing protein	4.368792	2.23942	1.9508588
HSP90.1	heat shock protein 81-1	4.804528	2.4238973	1.9821502
AT4G18650	transcription factor-related protein	8.718043	4.386015	1.9876912
AT1G30250	hypothetical protein	4.0762215	2.0505886	1.9878298

Supplementary Data S6. Categorization and abundance of degradome reads from the WT+S (wild-type Col-0, NaCl-free), MIR5-S (*35S::miRNVL5*, NaCl-free) and MIR5+S (*35S::miRNVL5*, NaCl-treated) libraries of wild-type and transgenic plants over-expressing miRNVL5. Clean reads are those after removal of low quality reads from raw data.

		WT+S	MIR5-S	MIR5+S
Raw reads	Total	30469415	24932306	27299578
Clean reads	Total	30200852	24739290	27064875
	Distinct reads	6682605	7785259	6118742
Reads mapping to cDNA	cDNA sense	17971327	16612018	17491882
	cDNA antisense	323197	374907	224288
	Total number	18294524	16986925	17716170
	Total % of clean reads	60.58%	68.66%	65.46%
	Distinct reads number	3734847	5266712	3641861
	Distinct reads % of clean reads	55.89%	67.65%	59.52%
Reads mapping to Genome	Total number	24750367	22232483	22361737
	Total % of clean reads	81.95%	89.87%	82.62%
	Distinct read number	4715269	6506758	4405498
	Distinct reads % of clean reads	70.56%	83.58%	72.00%

Supplementary Data S7. The number of differentially expressed genes in differential expression libraries as assessed by microarray.

Treatments/Control	Number of up-regulated genes	Number of down-regulated genes
miR5+S/Col-0+S	760	861
miR5+S/Col-0-S	3206	2938
miR5+S/miR5-S	2628	2442
miR5-S/Col-0-S	508	441
Col-0+S/Col-0-S	2815	2388



Supplementary Data S8. Validation of selected genes from microarray using qRT-PCR. Three week-old wild-type (WT) and *35S::miRNVLU5* seedlings were treated with 200 mM NaCl exposure for 1 h. Vertical bars represent SD of the mean with three replicates. Data with different letters are significant different (p<0.05).

Supplementary Data S9. Genes co-expressed with At2g44380

1	0.68	At2g44370*	Cysteine/Histidine-rich C1 domain family protein
2	0.61	At2g27660	Cysteine/Histidine-rich C1 domain family protein
4	0.59	At1g51850	Leucine-rich repeat protein kinase family protein
5	0.57	At3g55150	exocyst subunit exo70 family protein H1
5	0.54	At2g42350	RING/U-box superfamily protein
6	0.59	At1g51790	Leucine-rich repeat protein kinase family protein
8	0.58	At5g64100	Peroxidase superfamily protein
10	0.51	At5g43520	Cysteine/Histidine-rich C1 domain family protein
10	0.55	At2g39530	Uncharacterised protein family (UPF0497)
10	0.55	At3g51330*	Eukaryotic aspartyl protease family protein
11	0.53	At2g44790	uclacyanin 2

11	0.51	At2g39380	exocyst subunit exo70 family protein H2
12	0.51	At5g44910	Toll-Interleukin-Resistance (TIR) domain family protein
12	0.53	At3g46280	protein kinase-related
12	0.48	At3g46690**	UDP-Glycosyltransferase superfamily protein
12	0.5	At2g36690	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
12	0.51	At5g48430	Eukaryotic aspartyl protease family protein
13	0.54	At1g02360	Chitinase family protein
14	0.42	At4g32870**	Polyketide cyclase/dehydrase and lipid transport superfamily protein
15	0.54	At1g52200	PLAC8 family protein
16	0.5	At5g24230	Lipase class 3-related protein
16	0.49	At3g02240	
18	0.49	At5g53110	RING/U-box superfamily protein

18	0.48	At1g51860	Leucine-rich repeat protein kinase family protein
20	0.51	At5g44380	FAD-binding Berberine family protein
22	0.47	At4g32650	potassium channel in Arabidopsis thaliana 3
22	0.51	At2g44010	
22	0.38	At4g40070**	RING/U-box superfamily protein
25	0.47	At3g03000**	EF hand calcium-binding protein family
25	0.4	At2g29740	UDP-glucosyl transferase 71C2
25	0.47	At1g03850	Glutaredoxin family protein
25	0.47	At3g45410**	Concanavalin A-like lectin protein kinase family protein
26	0.49	At4g18430	RAB GTPase homolog A1E
26	0.44	At5g67450	zinc-finger protein 1
27	0.46	At4g01720	WRKY family transcription factor
28	0.43	At1g78000	sulfate transporter 1;2
29	0.5	At1g51800	Leucine-rich repeat protein kinase family protein

29	0.39	At5g06570	alpha/beta-Hydrolases superfamily protein
31	0.49	At2g39200	Seven transmembrane MLO family protein
32	0.39	At1g30110	nudix hydrolase homolog 25
33	0.43	At4g16350	calcineurin B-like protein 6
33	0.47	At2g42060	Cysteine/Histidine-rich C1 domain family protein
35	0.4	At1g14780	MAC/Perforin domain-containing protein
35	0.4	At2g29995	
36	0.46	At5g64120	Peroxidase superfamily protein
37	0.46	At2g35000**	RING/U-box superfamily protein
37	0.34	At1g13100**	cytochrome P450, family 71, subfamily B, polypeptide 29
37	0.44	At1g17860	Kunitz family trypsin and protease inhibitor protein
38	0.39	At1g22500	RING/U-box superfamily protein
40	0.5	At5g63600	flavonol synthase 5
42	0.45	At1g65610	Six-hairpin glycosidases superfamily protein

43	0.48	At1g30700**	FAD-binding Berberine family protein
43	0.41	At4g11530	cysteine-rich RLK (RECEPTOR-like protein kinase) 34
43	0.49	At4g20110	VACUOLAR SORTING RECEPTOR 7
45	0.47	At1g29280	WRKY DNA-binding protein 65
47	0.47	At2g21045	Rhodanese/Cell cycle control phosphatase superfamily protein
49	0.45	At4g25110	metacaspase 2
50	0.47	At3g09490	Tetratricopeptide repeat (TPR)-like superfamily protein

*genes that are predicted to interact with At2g44380
**genes that do not participate in the network

Supplementary Data S10. Primers used for this study by RT-PCR

Genes	Primers
Cotton-18S	F: 5’- TGAGAAACGGCTACCACA -3’ R: 5’- ACCCACCCTAAGTCCAAC -3’
(q)RT-Pre-miRNVL5	F: 5’- GATCTGGGCTTGGGTGCCTATAAAT -3’ R: 5’- AATAAAGCAGTACGCAGCACA -3’
5TF 5TR 5MF 5MR (GhCHR cDNA cloning)	5’- GAAGATCTATGGAGGAGTCTAACAATTA -3’ 5’ -GGACTAGTTTACATGCGCCACCACAAAA -3’ 5’- GCTCTAGAGATCTGGGCTTGGGTGCCT -3’ 5’- TCCCCCGGGGAGGCAAAGATAATAAAG -3’
RT- GhCHR	F: 5’- TCATCAAAAGCAAGTGGCA -3’ R: 5’- CTGAAATAAGGGCAAGAGGTT -3’
GhUB2	F: 5’- CAAGGAGGGTATCCCCCCA -3’ R: 5’- GCAGCCGCAACACCAAGTG -3’
qRT- GhCHR	F: 5’- CTTCTTTCACTCACTGCTCATA -3’ R: 5’- CCAACGATTTGTATCTCGACTT -3’
3'-RACE-Adapt	5’- GCGAGCACAGAATTAATACGACTCACTATAGGTTTTTTTTTTTTVN -3’
qRT-miRNVL5	5’- TTTCTTCACAAATATCACAATA -3’
3'-Outer	5’- GCGAGCACAGAATTAATACGACT -3’
Pre-miRNVL5	F: 5’- GCTCTAGAGATCTGGGCTTGGGTGCCT -3’ R: 5’- TCCCCCGGGGAGGCAAAGATAATAAAG -3’
ORF-GhCHR	F: 5’- GCTCTAGAATGGAGGAGTCTAACAATTATGGCC -3’ R: 5’- CGAGCTCTTACATGCGCCACCACAAAAAAC -3’

mGhCHR	F: 5’- AGTCATTACTGTGACATCTGCGAGGAGAGTCGAGATACAAATCGT -3’ R: 5’- TCTCGACTCTCCTCGCAGATGTCACAGTAATGACTTTCTAAATAT -3’
pBI121(JD)	5’- GCGAGAAAGGAAGGGAAGAAA -3’
Actin2	F: 5’- CATCAGGAAGGACTTGTACGG -3’ R: 5’- GATGGACCTGACTCGTCATAC -3’
qRT-RD29A	F: 5’- GTTACTGATCCCACCAAAGAAGA -3’ R: 5’- GGAGACTCATCAGTCACTTCCA -3’
qRT-RD22	F: 5’- AGGGCTGTTTCCACTGAGG -3’ R: 5’- CACCACAGATTTATCGTCAGACA -3’
qRT-KIN1	F: 5’- TGGAGCTGGAGCACAACA -3’ R: 5’- GACCCGAATCGCTACTTGTTC -3’
qRT-SOS1	F: 5’- CACTTCTGGGAAATGGTTGCA -3’ R: 5’- TGCCTTCAGCAATGACAACAC -3’
qRT-NHX1	F: 5’- GTATGGATTTTGGGGTGTTGTCATCA -3’ R: 5’- CAGCACAGTGGTGTTTGGTATGCT -3’
qRT-AVP1	F: 5’- GGGTCAAAACATCTACGGTGTGGAT -3’ R: 5’- GGAAACACCACTGCTGCTATTGGAA -3’
qRT-P5CS1	F: 5’- AGCAGCCTGTAATGCGATGG -3’ R: 5’- AAGTGACGCCTTTGGTTTGC -3’
qRT-CBF1	F: 5’- GCATGTCTCAACTTCGCTGA -3’ R: 5’- ATCGTCTCCTCCATGTCCAG -3’
qRT-CBF2	F: 5’- TGACGTGTCCTTATGGAGCTA -3’ R: 5’- CTGCACTCAAAAACATTTGCA -3’
qRT-CBF3	F: 5’- GATGACGACGTATCGTTATGGA -3’ R: 5’- TACACTCGTTTCTCAGTTTTACAAAC -3’
qRT-ERF4	F: 5’- TCAGCCTCCTCCTGTGACATC -3’ R: 5’- ACGACCGATGACGAATCAGAGT -3’

qRT-AT3G22920	F: 5’- CGTTGTGATCGGCAAAGTTGTT -3’ R: 5’- GGCGTCCTTGTTGTCGTAGTT -3’
qRT-AT3G49200	F: 5’- CATAGAGAACGCAAACGCAGAC -3’ R: 5’- CGGCTTGGAGGTGTCTAACG -3’