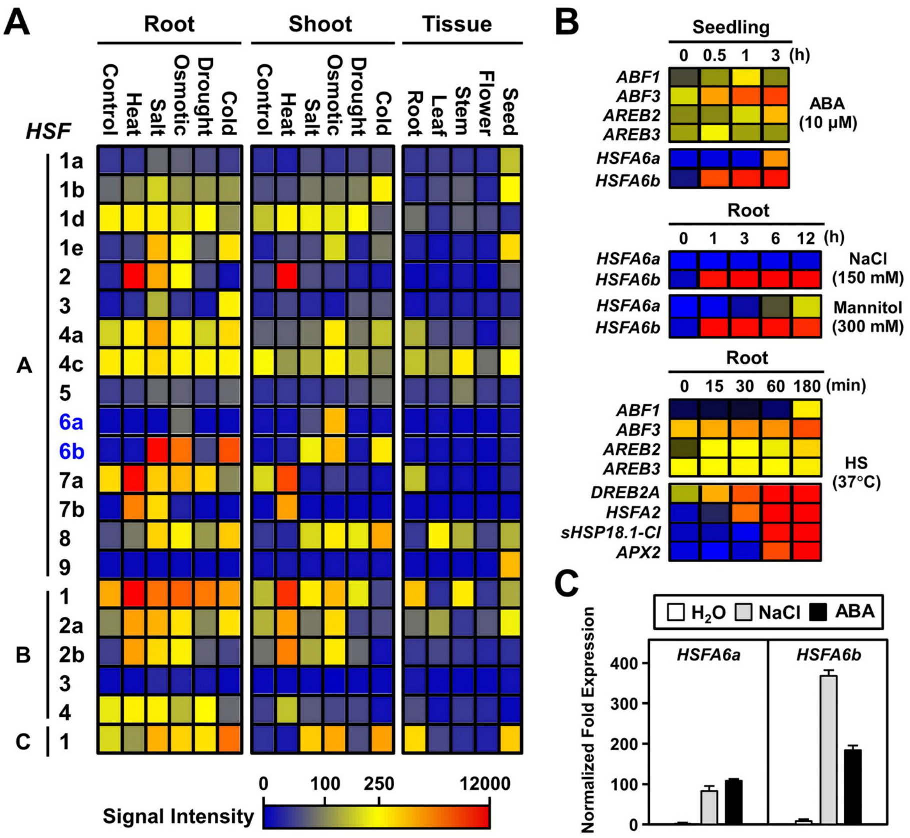
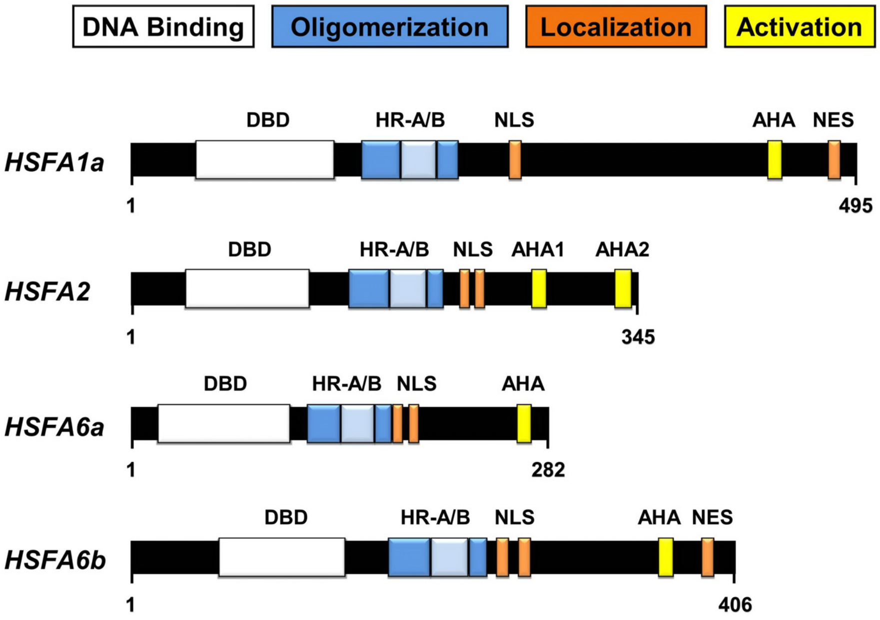
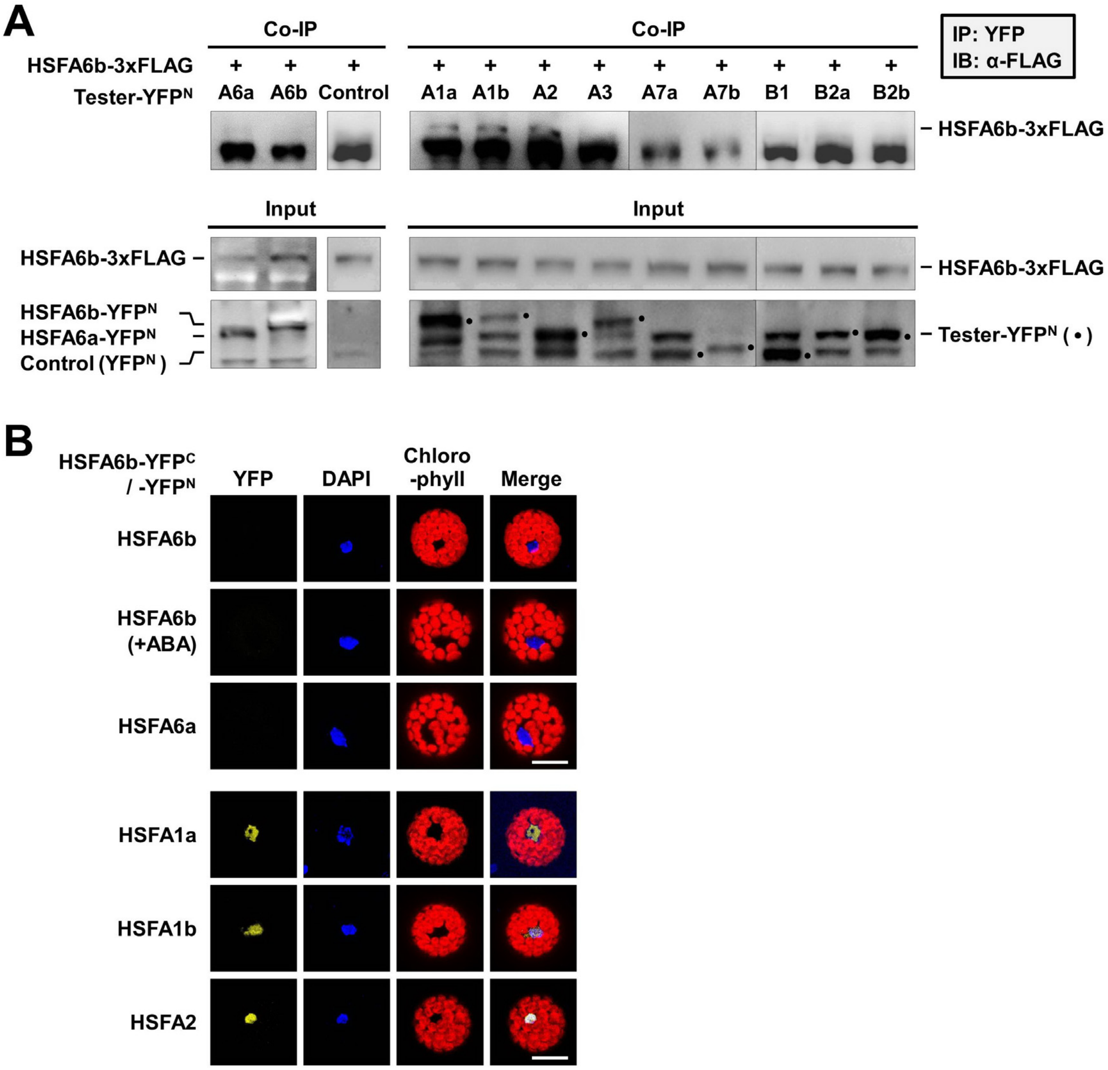


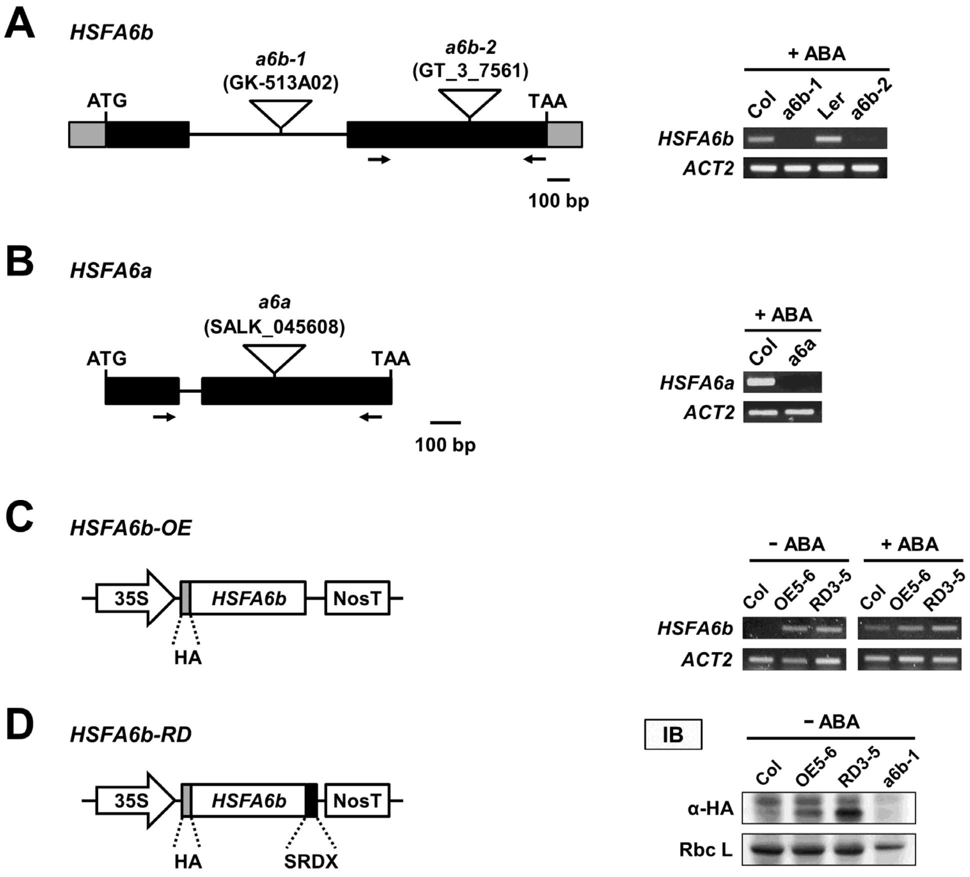
Supplemental Figure S1. The expression profiles of Arabidopsis 21 heat shock factor (HSF) genes under abiotic stresses and during development. (A and B) Normalized and averaged signals were analyzed as "heat maps" with GeneSpring 7.3 (Silicon Genetics). The color code of signal intensities corresponds to the abundance of transcripts, from low (blue) to high (red) expression. Root samples: 1-h heat stress (38°C in incubator); 6-h salt (150 mM NaCl), drought (15 min dry air stream until 10% loss of fresh weight) or osmotic (300 mM mannitol) stress; 12-h cold (4°C). Shoot samples: 1-h heat stress, 12-h salt, drought, cold or osmotic stress. Developmental samples: roots and leaves of 15-d-old plants; second stem internode, 21 days; flowers at stage 12; mature seeds at stage 10. The detailed microarray data was provided by the AtGenExpress consortium (http://www.arabidopsis.org/info/expression/ATGen_Express.jsp). The expression profiles of *HSFA6a, HSFA6b,* and *AREB/ABF* transcripts by time-series abiotic stresses and ABA treatment, as indicated. Note that the *AREB1* probe was not available in the ATH1 GeneChip. **(C)** Nine-d-old seedlings were incubated in H_2O containing 200 mM NaCl for 6 h or 10 μM ABA for 3 h. The transcription levels of *HSFA6a* and *HSFA6b* were analyzed by qRT-PCR. The fold expression was normalized relative to the *HSFA6a* level in H_2O treatment. Data are means ± SD of 3 biological replicates. *PP2A* was an internal control.



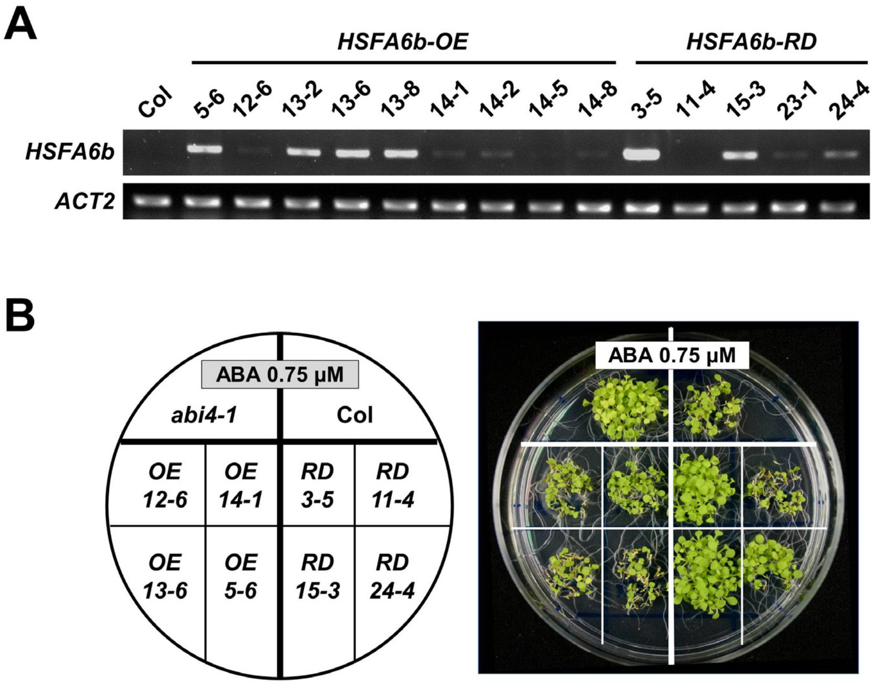
Supplemental Figure S2. Modular structures of Arabidopsis HSFs HSFA6a and HSFA6b. The well-studied class-A heat shock factors HSFA1a and HSFA2 were used as references for the conserved HSF signatures comparison. The block diagrams represent their conserved functional domains. N-terminal DNA-binding domain (DBD, white) is a helix-turn-helix motif, which binds to the HSEs of HS-responsive genes. HR-A/B (blue), a heptad-repeat region of hydrophobic amino acid residues, is required for homo- or hetero-oligomerization of HSFs. Nuclear-cytoplasmic shuttling sequence (brown), is a nuclear localization signal (NLS) and nuclear export signal (NES). AHA motifs (yellow), are a short domain enriched in aromatic and large hydrophobic amino acid residues embedded in an acidic surrounding, transcriptional activity of class-A HSFs. Adapted from Nover et al. (2001). HSFA6b harbors NLS and NES, but HSFA6a only contains NLS.



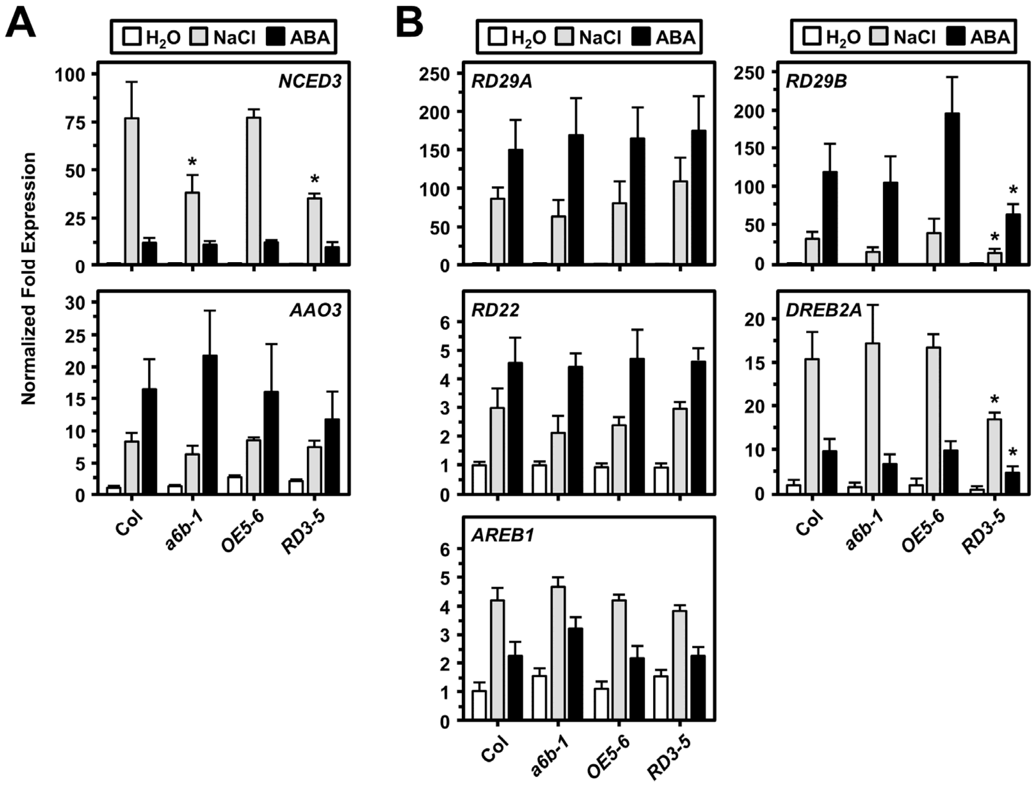
Supplemental Figure S3. Interaction of HSFA6b and different HSFs. (A) Co-immunoprecipitation (Co-IP) assay of HSFA6b-3XFLAG and tester (HSFs)-YFP^N in Arabidopsis leaf mesophyll protoplasts, as indicated. Immunoprecipitation (IP) with anti-GFP antibody and the interacted HSFA6b-3XFLAG were analyzed by immunoblotting (IB) with anti-FLAG antibody. Input protein (50%) was used as control of immunoblotting in the transfected cell lysates. **(B)** Confocal micrographs of protoplasts showing the interaction of HSFA6b-YFP^C and HSFs-YFP^N by using BiFC analysis without or with 10-µM ABA for 2 h treatment (+ABA), as indicated in **Figure 2**.



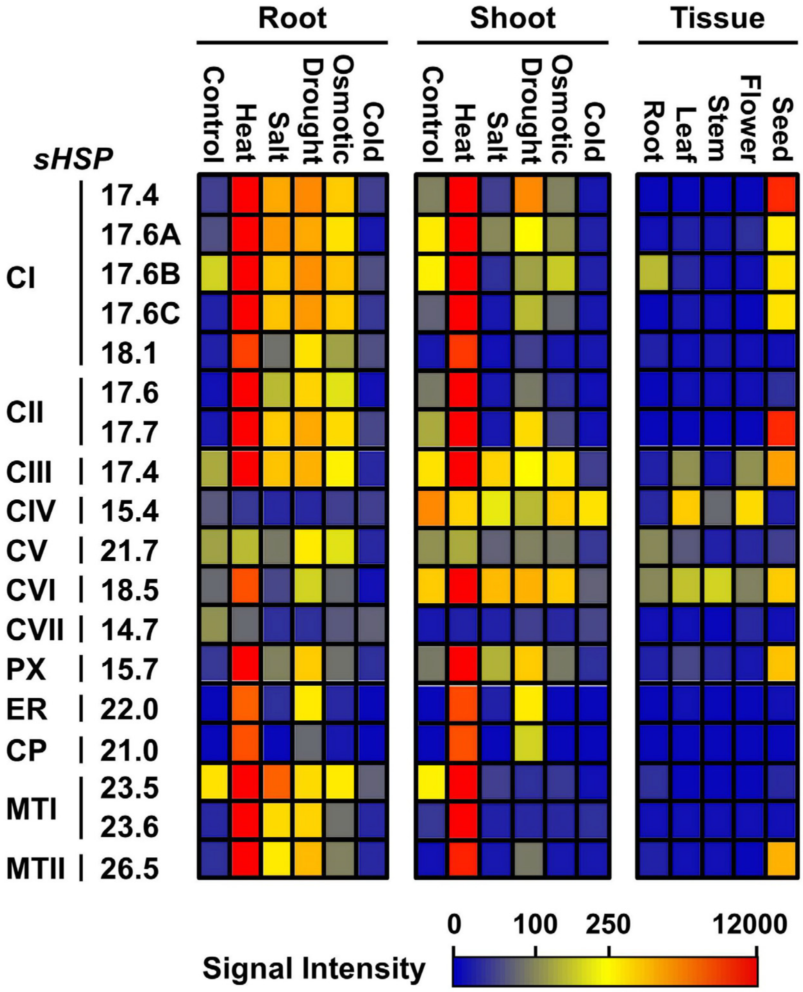
Supplemental Figure S4. Characterization of *HSFA6b* and *HSFA6b* T-DNA insertion, overexpression, and dominant-negative mutant lines. (A and B) Schematic maps of *HSFA6b* and *HSFA6a* gene structure and T-DNA insertion sites. Exon, UTR, and T-DNA are indicated by black, gray, and triangle, respectively. The specific primers for genotyping and RT-PCR are shown with black arrows. ATG and TAA are initiation and stop codons. **(C)** *HSFA6b*-overexpression line *HSFA6b-OE*. HSFA6b was fused with the hemagglutinin tag (HA; YPYDVPDYA) to the 5′ end and driven by the CaMV *35S* promoter. **(D)** *HSFA6b*-dominant-negative line *HSFA6b-RD*. The EAR-motif repression domain SRDX (GLDLDLELRLGFA) was fused to the 3′ end of the HA-HSFA6b. The expression level of *HSFA6a* and *HSFA6b* in wild-type, Col and Ler, plants and *HSFA6b* mutants *OE5-6* and *RD3-5* were analyzed by RT-PCR and immunoblotting (IB; with anti-HA antibody and the Rubisco large subunit, Rbc L, shown for equal loading). Plants without (-ABA) or with 3-h 20-µM ABA treatment (+ABA) are indicated. *ACT2* was a loading control for RT-PCR.



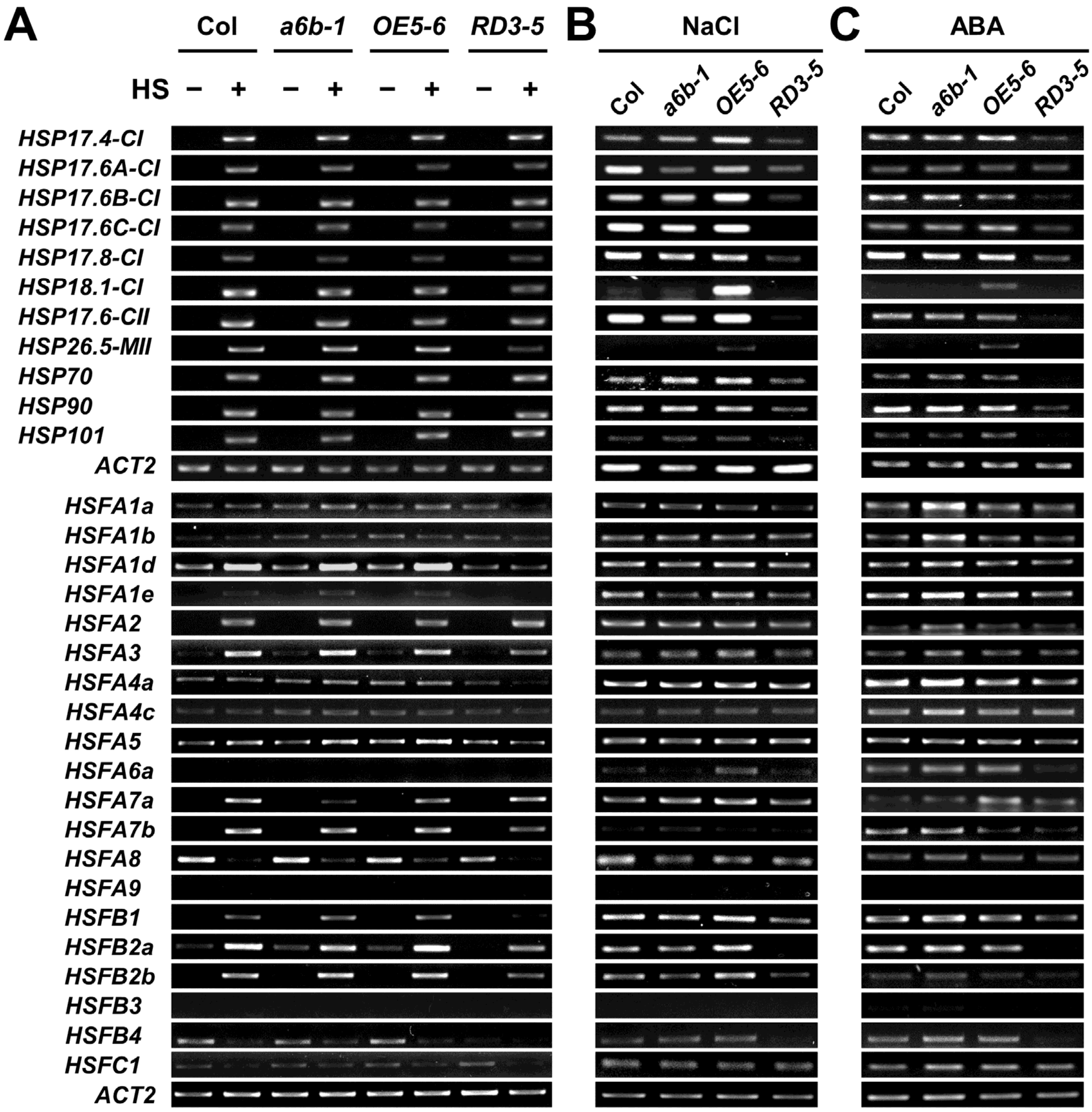
Supplemental Figure S5. The expression levels of *HSFA6b* and ABA sensitivity in *HSFA6b* mutant lines. (A) The *HSFA6b* transcription levels were analyzed by RT-PCR, under normal growth condition without ABA treatment, in *HSFA6b-OE* and *HSFA6b-RD* mutant lines. *ACT2* was a loading control. **(B)** Seeds with different expression levels of *HSFA6b*, as indicated in **panel A**, were planted in medium containing 0.75 µM ABA, and then photographed at day 12. *abi4-1*, an ABA insensitive mutant (Col ecotype), was used as reference.



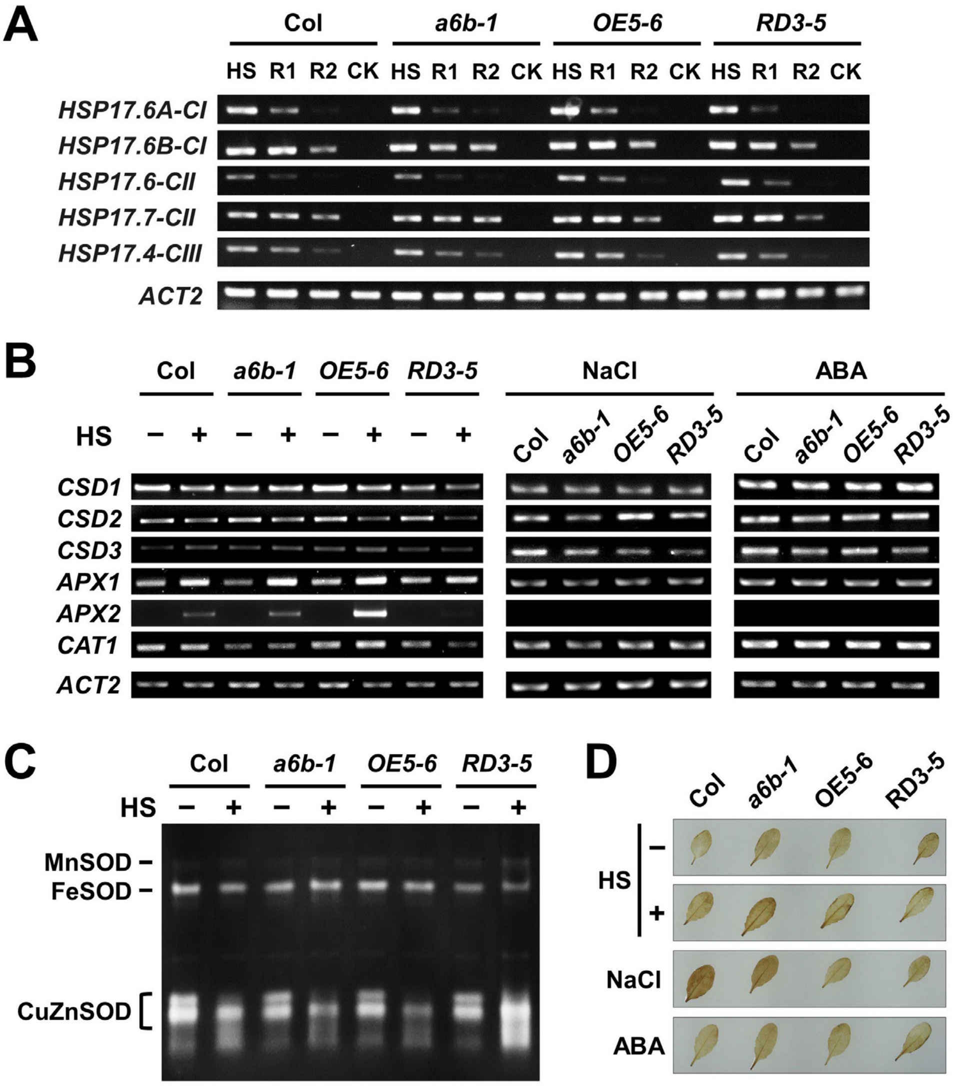
Supplemental Figure S6. The expression levels of ABA biosynthesis and responsive genes in response to salt and ABA treatments in *HSFA6b* mutants. (A and B) Nine-d-old seedlings were incubated in H_2O containing 200 mM NaCl for 6 h or 20 µM ABA for 3 h. The transcription levels of ABA biosynthesis genes *NCED3* and *AAO3*, ABA-responsive genes *RD29A*, *RD29B,* and *RD22*, as well as *DREB2A* and *AREB1,* were analyzed by qRT-PCR. The fold expression was normalized relative to that of Col H_2O treatment. Data are means ± SD of 3 biological replicates. *, Significant at $P < 0.05$ compared with Col. *PP2A* was an internal control.



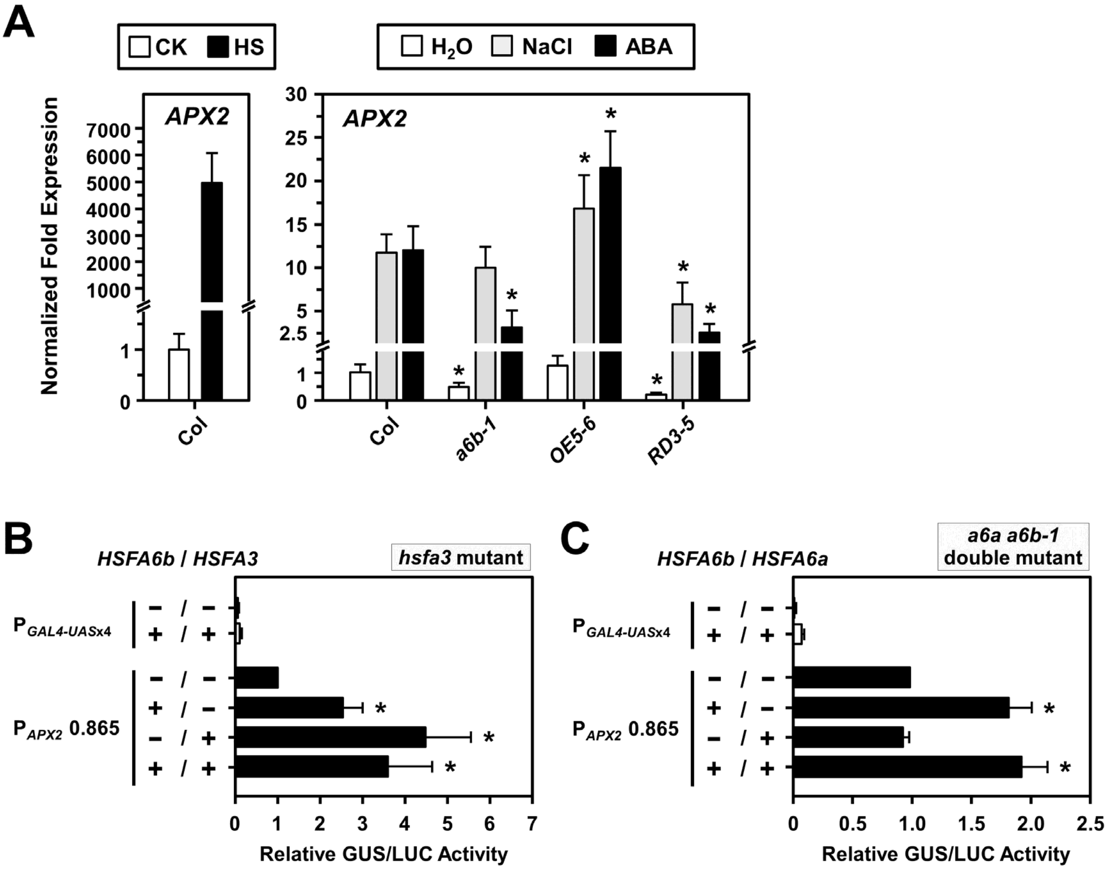
Supplemental Figure S7. The expression profiles of Arabidopsis 18 small heat shock protein (sHSP) genes under various abiotic stresses and during development. Normalized and averaged signals are presented as "heat maps", as indicated in **Supplemental Figure S1.** Because of the absence of a specific probe for *HSP17.8-CI*, only 18 sHSP genes are presented. The *HSP18.5-CIV*, *15.4-CV,* and *21.7-CVI* genes reported by Siddique et al. (2008) were revised as *HSP15.4-CIV*, *21.7-CV,* and *18.5-CVI*, respectively (Waters et al., 2008). CI to CVII (class I to VII subfamily), cytoplasmic/nuclear localization; CP, plastids; ER, endoplasmic reticulum; MT, mitochondria; PX, peroxisomes.



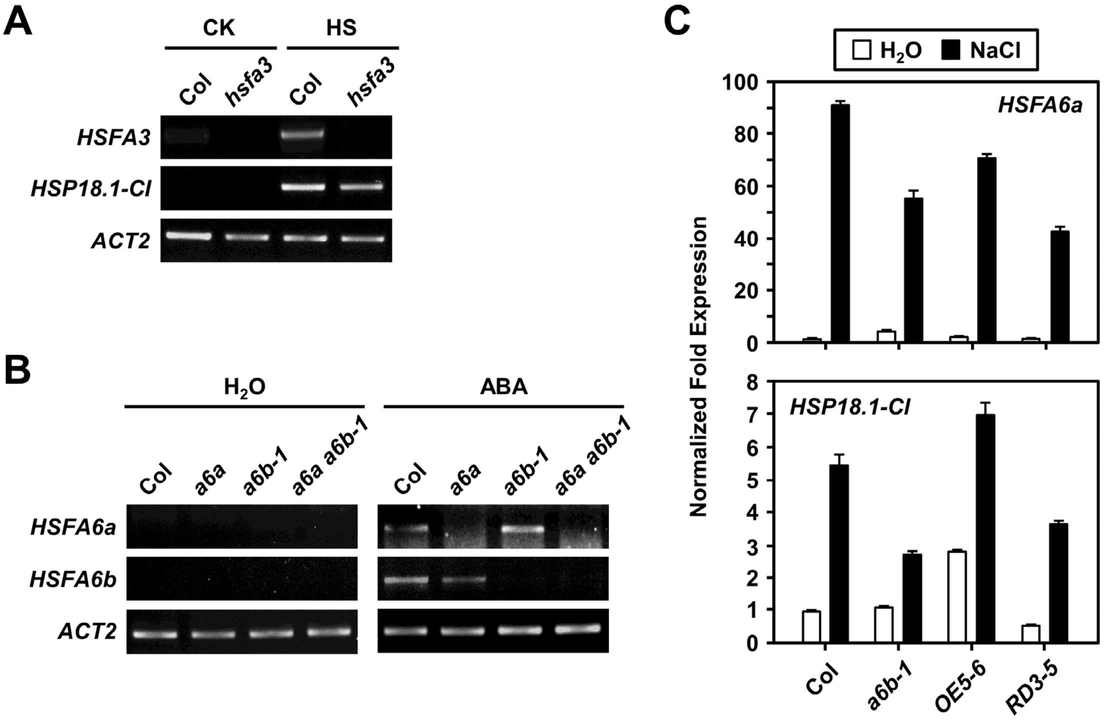
Supplemental Figure S8. The expression of HS-related genes in response to HS, salt, and ABA treatments in *HSFA6b* mutants. (A to C) Nine-d-old seedlings were treated without or with HS at 37°C for 1-h, incubated in H_2O containing 150-mM NaCl for 6 h, and incubated in H_2O containing 20-µM ABA for 3 h, respectively. The transcription levels of 11 *HSPs* and 20 *HSFs* were analyzed by RT-PCR. *ACT2* was a loading control.



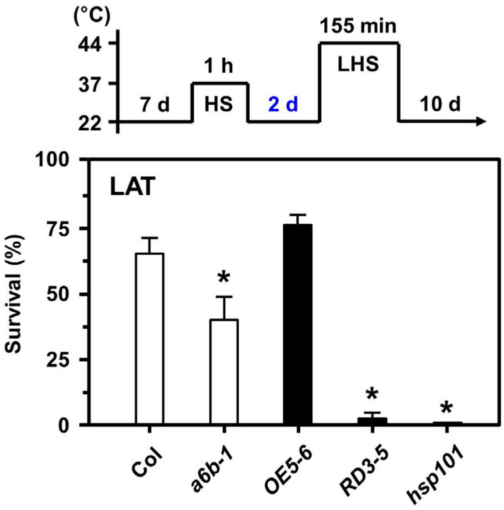
Supplemental Figure S9. The expression levels of HS and oxidative related genes, superoxide dismutase (SOD) activity, and H_2O_2 detection in response to HS, NaCl, and ABA treatments in *HSFA6b* mutants. Nine-d-old seedlings were treated without or with 1-h 37°C HS and then underwent recovery for 1 or 2 h (R1 and R2). The NaCl and ABA treatments, as indicated in **Supplemental Figure S8**. **(A and B)** The transcription levels of 5 HS-related and 6 oxidative-related genes were analyzed by RT-PCR, respectively. **(C)** In-gel CuZnSOD, FeSOD, and MnSOD activity assay. **(D)** H_2O_2 detection by DAB staining.



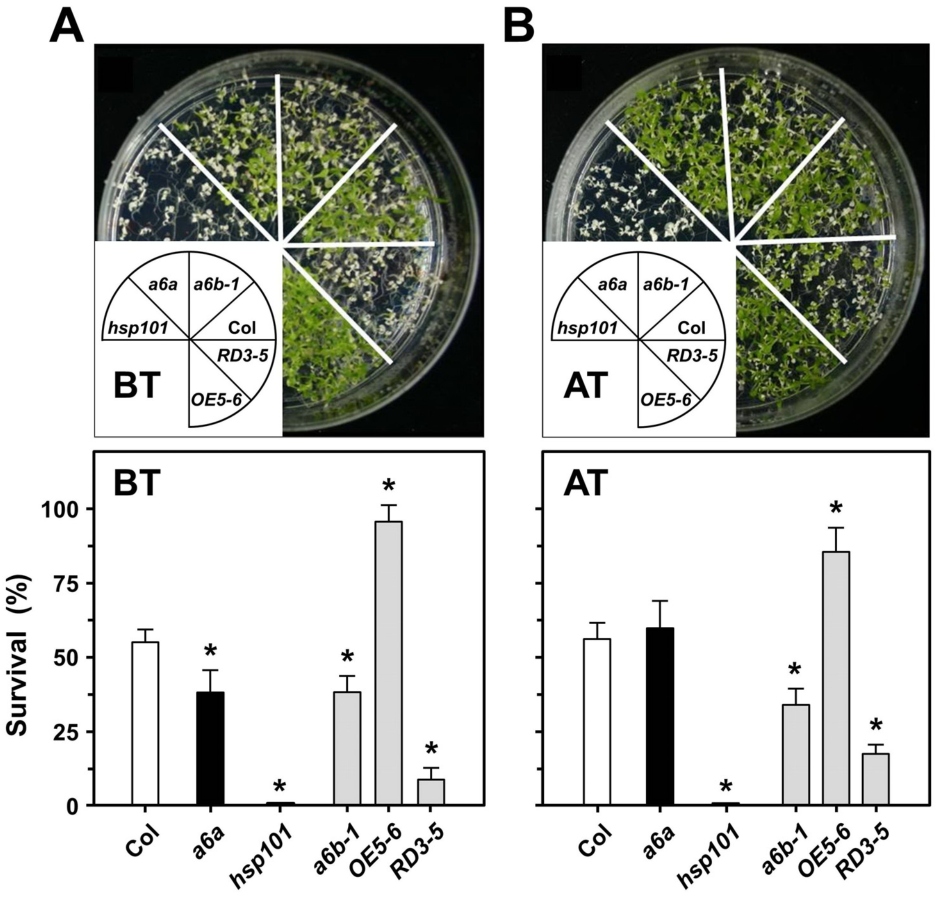
Supplemental Figure S10. The expression levels of *APX2* in response to HS, NaCl, and ABA treatment in *HSFA6b* mutants, as well as *HSFA6b* mediated *HSFA3* activation of the *APX2* promoter. (A) Nine-d-old seedlings were treated without (control) or with 1-h 37°C HS. The NaCl and ABA treatments are as indicated in **Supplemental Figure S8**. The transcription levels of *APX2* were analyzed by qRT-PCR. The fold expression was normalized to that of wild-type (Col) plants with mock (control or H_2O) treatment. Data are means ± SD of 3 independent replicates. *, Significant at $P < 0.05$ compared with the Col. *PP2A* was an internal control. **(B and C)** *hsfa3* and *hsfa6a hsfa6b* double (*a6a a6b-1*) mutant protoplasts were used for the transcriptional activation assay. $P_{GAL4\text{-}UASx4}$, was a control, and 0.856-kb length of the *APX2* promoter was fused with a *GUS* reporter gene, then transfected with or without effectors HSFA6b, HSFA3, and HSFA6a, as indicated. The fold expression was normalized to that with the transfection of P_{APX2} without effectors, as described in **Figure 4**. Data are means ± SD of 3 independent replicates. * $P < 0.05$.



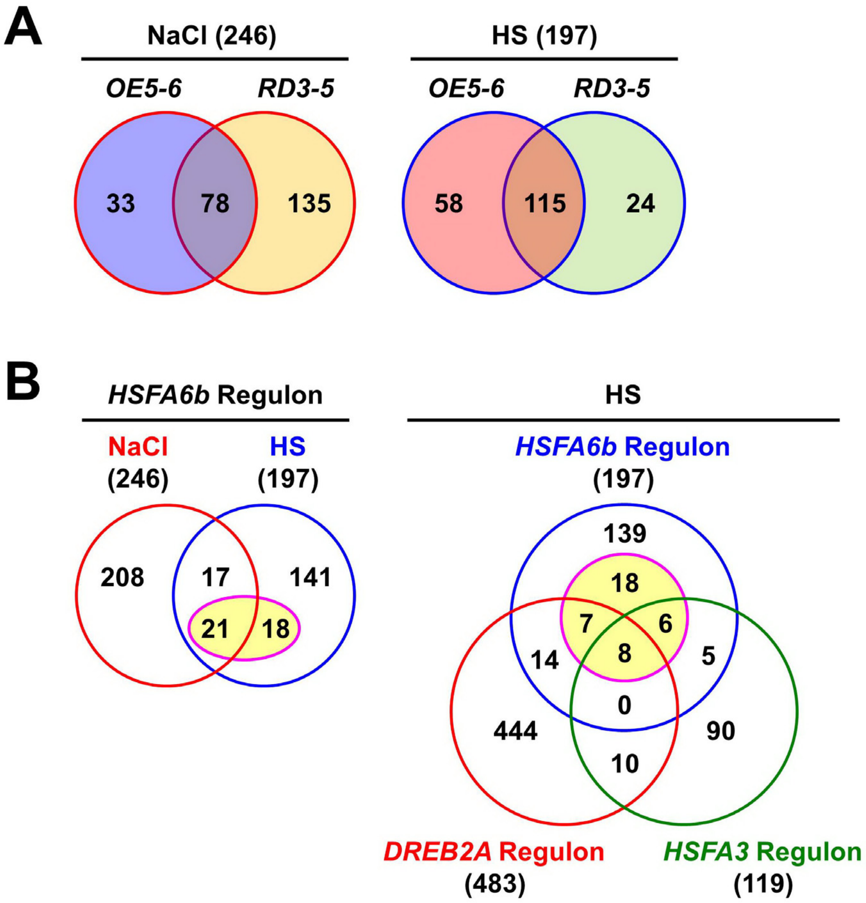
Supplemental Figure S11. Characterization of *hsfa3* and *hsfa6a hsfa6b* double mutant lines, as well as the *HSFA6a* and *HSP18.1-CI* transcription levels in response to NaCl treatment in *HSFA6b* mutants. The HS or ABA treatment was as indicated in **Supplemental Figure S8**. **(A and B)** The expression levels of *HSFA3*, *HSFA6a,* and *HSFA6b* in *hsfa3* (SALK_01117) and *a6a a6b-1* double mutant lines were analyzed by RT-PCR. *HSP18.1-CI*, used as a reference, is a HS-responsive gene. *ACT2* was a loading control. **(C)** The *HSFA6a* and *HSP18.1-CI* transcription levels in response to 200-mM NaCl for 6 h in *HSFA6b* mutants were analyzed by qRT-PCR. The fold expression was normalized to that of the *HSFA6a* level in Col H_2O treatment. Data are means ± SD of 3 biological replicates. *PP2A* was an internal control.



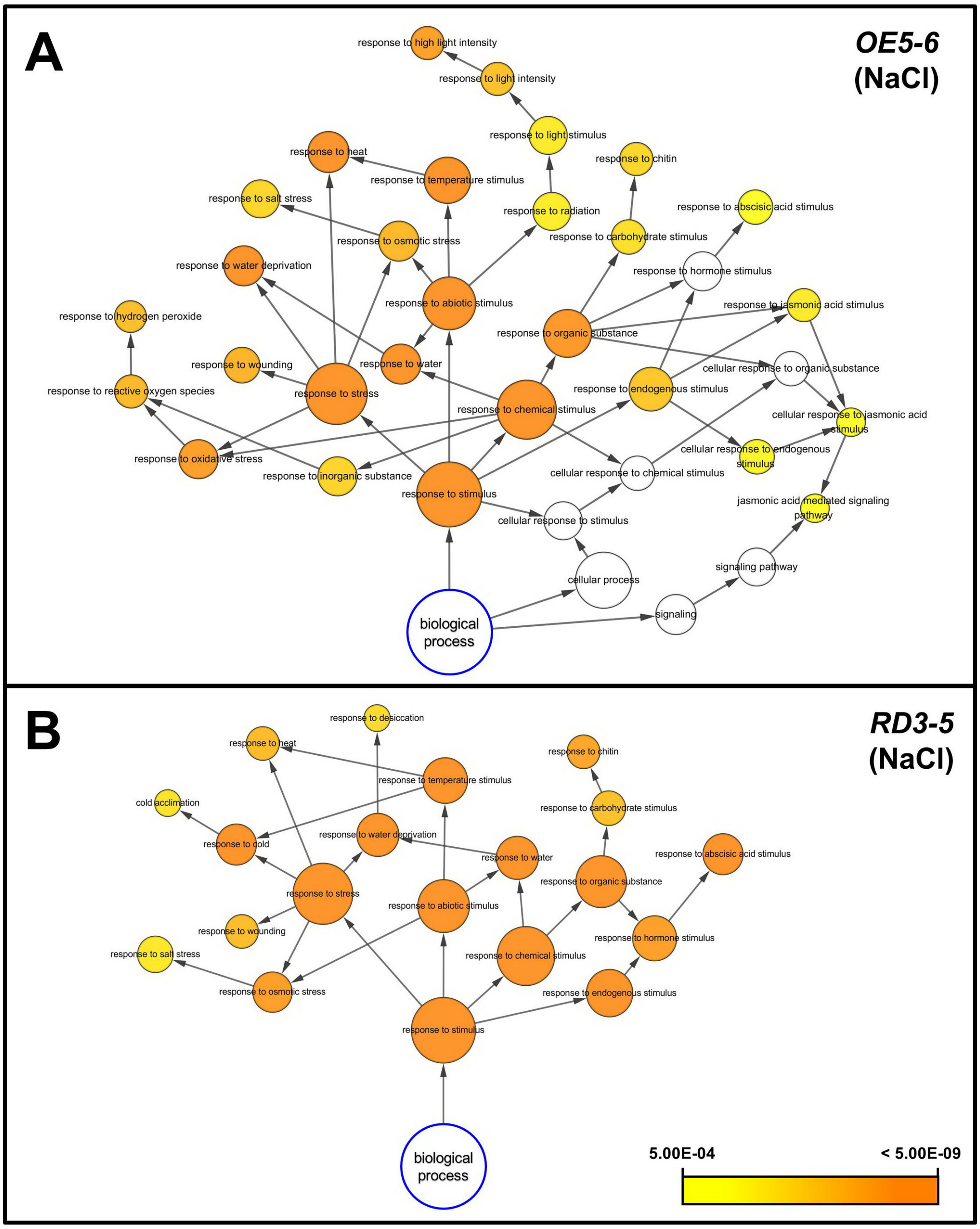
Supplemental Figure S12. Thermotolerance test in *HSFA6b* mutants. Seven-d-old seedlings were analyzed for long-term acquired thermotolerance (LAT). The pictogram shows the HS regime. Survival (%) was measured at day 10 after HS treatment, as described in **Figure 8**. Data are means ± SD of 3 independent replicates. *, Significant at $P < 0.05$ compared with the Col.



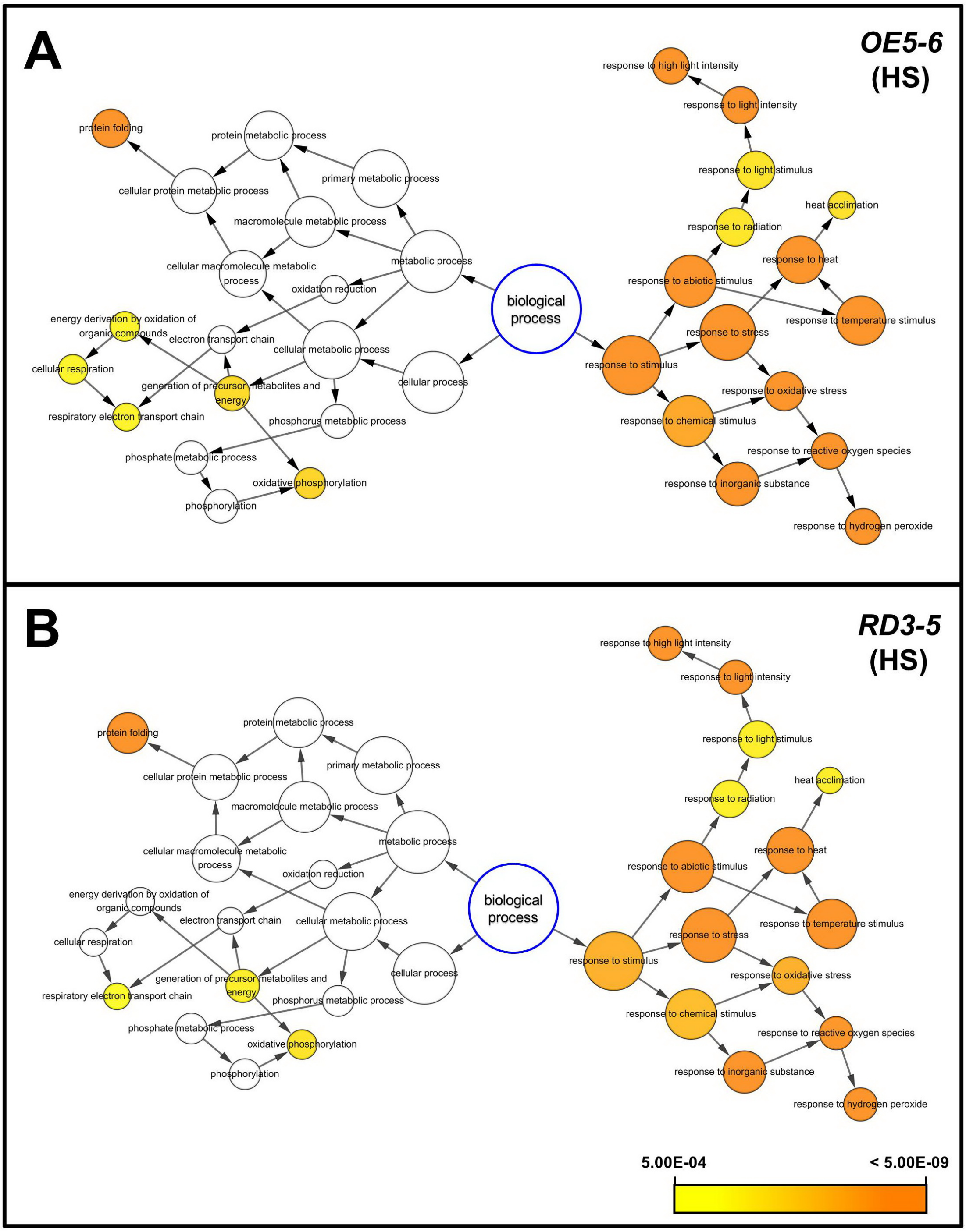
Supplemental Figure S13. Thermotolerance test in *HSFA6a* and *HSFA6b* mutants. (A and B) Nine-d-old seedlings were analyzed for BT and AT, respectively, as described in **Figure 8**. Seedlings were photographed **(top)** and survival (%) was measured **(bottom)**. Data are means ± SD of 3 independent replicates. *, Significant $P < 0.05$ compared with the Col.



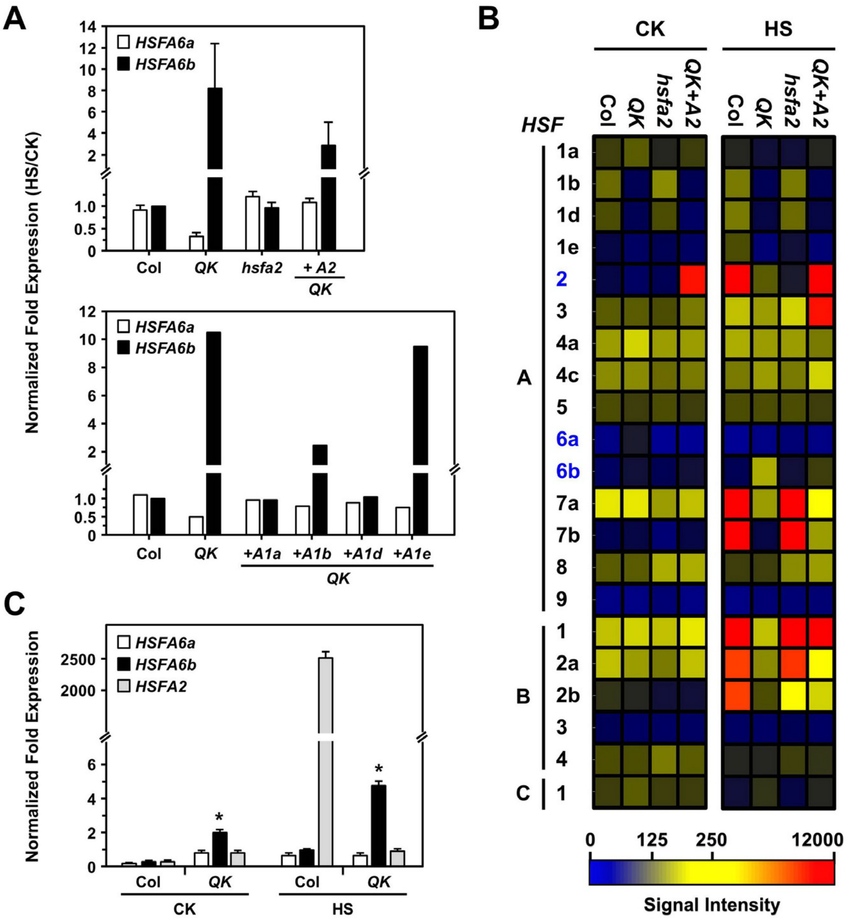
Supplemental Figure S14. Venn diagram of gene transcripts in response to salt or HS treatment in *HSFA6b* mutants. Venn diagram based on TAIR locus identifier. **(A)** The expression changed > 6-fold at $p < 0.10$, in *HSFA6b* mutants *OE5-6* and *RD3-5* with 150 mM NaCl for 6 h or 37°C HS for 1 h treatment, as compared with Col plants at 22°C-control treatment. **(B)** The top 39 DEGs with expression changed > 30-fold at $p < 0.05$ of the *HSFA6b* HS response regulon (highlighted in yellow) overlapping with NaCl-response regulon **(left)**, and the HS-response regulon of *DREB2A* and *HSFA3* **(right)** (Sakuma et al., 2006; Yoshida et al., 2008). At4g36990 and At4g36988 shared the same probeset number, 246214_at, in ATH1 GeneChip array.



Supplemental Figure S15. GO enrichment analysis of gene transcripts in response to salt treatment in *HSFA6b* mutants. (A and B) Network graphs of enriched GO terms in response to 150 mM NaCl for 6 h in *OE5-6* and *RD3-5* mutants, respectively, as indicated in **Supplemental Figure S14A**. The yellow to orange color of the circles correspond to the level of significance of the overrepresented GO category at $p \leq 5.00E-04$ according to a multiple *t* test with false discovery rate-corrected *p* value. The size of the circle is proportional to the number of genes in the category.



Supplemental Figure S16. GO enrichment analysis of gene transcripts in response to HS treatment in *HSFA6b* mutants. (A and B) Network graphs of enriched GO terms in response to 37°C HS for 1 h in *OE5-6* and *RD3-5* mutants, respectively, as indicated in **Supplemental Figures S14b and S15**.



Supplemental Figure S17. The expression levels of *HSFA6a* and *HSFA6b* in response to HS treatment in *hsfa1a/b/d/e* quadruple-KO (*QK*) and *hsfa2* mutant lines. (A) Wild-type Col, *QK,* and *hsfa2*, as well as the *QK* plants complemented (+) with *HSFA2* and different member of the *HSFA1s*, are as indicated. The 1-h 37°C treatment served as HS and 22°C treatment was a control (CK). The fold expression (HS/CK) was normalized to that of the *HSFA6b* level in Col. Normalized and averaged signals were collected from the Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo) from the National Center for Biotechnology Information (NCBI) accession number GSE26266 and GSE44655 (Liu et al., 2011; 2013). **(B)** The heat maps show the expression level of *HSFA6a* and *HSFA6b*, in addition to that of the HSFs. **(C)** The expression levels of *HSFA6a*, *HSFA6b,* and *HSFA2* were analyzed by qRT-PCR, which was normalized to that of the *HSFA6b* level in Col HS treatment. Data are means ± SD of 3 independent replicates. *, Significant at $P < 0.05$ (the *HSFA6b* level in *QK* compared with the Col).

Supplemental Table S1. Primers used for genotyping, cloning, RT-PCR and real-time quantitative PCR, as well as accession numbers can be found in the TAIR database.

Primer	**Sequence (5' to 3')**
Genotyping	
HSFA6a_Fw	GAACCAGAGACTTTTGCCCTAAT
HSFA6a_Rv	CTCCCCTTGTCCTTGATGCTC
HSFA6b-1_KO_Fw	TTGTCCGCCAGCTCAACACA
HSFA6b-1_KO_Rv	ACTCCCACCGATCCGGATTCACC
HSFA6b-2_KO_Fw	GGCAAAAGCATCTCCTCAAG
HSFA6b-2_KO_Rv	CTTCCCAAAAACCTTCACCA
HSPs	
HSP17.4-CI_Fw	AAATACGCCAACGCACATAA
HSP17.4-CI_Rv	AACTATCAATGGATCAAAACACTC
HSP17.6A-CI_Fw	AACTTCAATTCCCGTCATCG
HSP17.6A-CI_Rv	ATCCAAATACACACATTTCTCCAC
HSP17.6B-CI_Fw	CTTGCCTGGATTGAAGAAGG
HSP17.6B-CI_Rv	AGGATCAAATGTATCCGATACATC
HSP17.6C-CI_Fw	GATTGGAGGGAGACACCTGA
HSP17.6C-CI_Rv	ACAAAGCACACTCTTATTAAGATT
HSP17.8-CI_Fw	AAACATCGGCGATAACGAAC
HSP17.8-CI_Rv	AATATAAAGGCCTTGCTTAATTAT
HSP18.2-CI_Fw	ACGTCTTTGATCCGTTCTCG

HSP18.2-CI_Rv	ATTCATAACACAACAAGCCAAG
HSP17.6-CII_Fw	GACCCGCAACAACCCTTCAC
HSP17.6-CII_Rv	ACCATATCCCTCACGCATTCC
HSP26.5-MII_Fw	TCACTCCCACCCTAAATGAG
HSP26.5-MII_Rv	TTCTCCGTCCTAGGAATCAC
HSP70b_Fw (70-5)	AGACAATCAACCAGGCGTTCT
HSP70b_Rv (70-5)	TCGCCTTCTCAATCTTCTGCT
HSP90.1_Fw	GCGAGGTCTGGAACAAAAGAG
HSP90.1_Rv	ATCGGTTTCTGCTTGTTGATG
HSP101_Fw	ACCGAGAAGAAGTCCTCTGGC
HSP101_Rv	TTTCCCACGAAGCTTCTCAAC
HSFs	
HSFA1a_Fw	CGAGGCCAATAAGAAGCGGAGACT
HSFA1a_Rv	CTGAATCGGGACTGAACCACCATC
HSFA1b_Fw	ACCGCCAGATTGTTAGATA
HSFA1b_Rv	CCGGGCAGCTTAGGGACTC
HSFA1d_Fw	CGGCGATGATGGTTTCCTTCTA
HSFA1d_Rv	TTGTCCCATCCATTTTGTTCCTG
HSFA1e_Fw	GTGGGTGCGTGCGTTGAAGT
HSFA1e_Rv	GAAGCCTGCAGGAATGGATGAAA
HSFA2_Fw	TGAGGCAACAGCAACACAGC
HSFA2_Rv	CAAAGGCGAACCAACCAAATCT
HSFA3_Fw	TGGAAAAGGCGAGAAAGAAGTT

HSFA3_Rv	TTGGCGTATTATCATCATCAC
HSFA4a_Fw	GCCAGGGCTTGCTTTGAAC
HSFA4a_Rv	TCCGGCTTTATCTTTATCGTCTTT
HSFA4c_Fw	ACGGAATCAGAAAGACGGAGCAT
HSFA4c_Rv	GAGCAGGCGCAGTAACGGTAAC
HSFA5_Fw	CACGCCTCCTTCTTCCAACCTACT
HSFA5_Rv	CGCGTCTCGAGCTACCACTACTAT
HSFA7a_Fw	AGATGGGAATTTGCAAACGAA
HSFA7a_Rv	TCCCAGAAACCATCATCCAACT
HSFA7b_Fw	TCCCCTCCTTCGCTTAACTACTCT
HSFA7b_Rv	ACCCGTCGTAAGCTCCCTCTC
HSFA8_Fw	CAGGAGGTGACGGATACTAAGA
HSFA8_Rv	GAAGGGCTCAACAACAAAAG
HSFA9_Fw	GAAGCGAGTACCACCACCACGACA
HSFA9_Rv	TATCCTCCCATTTACATCCATTGA
HSFB1_Fw	ACGGCGGGGAAATGTGTTGTTGT
HSFB1_Rv	CTTTTCATCCCGGTCCCTCTTTTT
HSFB2a_Fw	GTACCGGATCGATGGGAGTTTTC
HSFB2a_Rv	ACCGCCGTCGTCTTCACCT
HSFB2b_Fw	CGCCGGGAATAGTGGTGGAAGTAG
HSFB2b_Rv	CCGCAGGCGAAGAATTAGACGATA
HSFB3_Fw	GTTCGCCAGCTCAATACTTACG
HSFB3_Rv	AGCCCTTCATCTTCTTCATCATC

HSFB4_Fw	GAAATCCACCGCCGTAAAACATC
HSFB4_Rv	AGTGGCATTGACAGTGGCAGTATT
HSFC1_Fw	CGGACCGGTGGGAGTTTG
HSFC1_Rv	ATGACGGCGACGGTGTTGATGAT
Oxidative stress responsive genes	
APX1_Fw	CAATGAGGTTTCCGGCTGAGCAAGC
APX1_Rv	CTGCAGTTAAGCATCAGCAAACCCAAGC
APX2_Fw	AGCCTTCAACGATTTCCAGAAG
APX2_Rv	TCGAATCCTGAACGCTCCTT
CAT1_Fw	CAGTCTCACCTAAAAATCGC
CAT1_Rv	ACTTGGGATTCGGTTTCAAT
CSD1_Fw	TCTGAGCTCATGGCGAAAGGAGTTGCAGTTTTG
CSD1_Rv	TTAGCCCTGGAGACCAATGATGC
CSD2_Fw	TCTCCCGGGATGGCTGCCACCAACACAATCC
CSD2_Rv	TCTGGATCCGAGCGGCGTCAAGCCAATCA
CSD3_Fw	TCTGAGCTCATGGAAGCTCCTAGAGGAAATCTGAGAG
CSD3_Rv	TCTCCCGGGTAGTTTAGCATCCGCAGATGATTGAAGT
Cloning	
HSFA6b_cDNA_Fw	TCTGTCGACTATGGATCCTTCATTTAGGTT
HSFA6b_cDNA_Rv	TCTCTGCAGTTAATTAGTGTGTGAACTAG
HA_Fw	TCTCCCGGGATGTACCCATACGATGTTCCA
HSFA6b_ORF_Rv	TCTCCCGGGATTAGTGTGTGAACTAGAA
HSFA6b_ORF_Fw	ATGGATCCTTCATTTAGGTTCATTA

HSFA6b_ORF_Rv	ATTAGTGTGTGAACTAGAACCCAAA
AREB1_Fw	AAGTCGACATGGATGGTAGTATGAATTTG
AREB1_Rv	AAGGATCCTCACCAAGGTCCCG
ProHSFA6b_1.0_Fw	CTCGAGGTTTAAAAAATTGGATAACAACAC
ProHSFA6b_1.0_Rv	CCATGGGGTTTTAAATTTAAACAAAGATTTTTTTAT
ProHSFA6b_1.7_Fw	CTCGAGTTCAATTTTCTCGTTATTGTTTTTAGG
ProHSFA6b_1.7_Rv	CCATGGGGTTTTAAATTTAAACAAAGATTTTTTTAT
ProHSP18.1_1.0_Fw	GGATCCATTTGCAGTGTTATGAGTGAATTTT
ProHSP18.1_1.0_Rv	CTC GAGTGTTCGTTGCTTTTCGGGAGACTTTT
ProDREB2A_1.0_Fw	CTCGAGTAAAATGGACGACACCCATCCAAT
ProDREB2A_1.0_Rv	CCATGGAAGGAAGACAAAGTATCTACGGAGT
ProAPX2_0.856_Fw	AAGGATCCTAATCTCGTCTGCTTTGG
ProAPX2_0.856_Rv	AACCATGGTTTTTTCAAATTCGCTTCC
Real-time Quantitative PCR	
qHSFA2_Fw	CAGCGTTGGATGTGAAAGTG
qHSFA2_Rv	CAGCGTTGGATGTGAAAGTG
qHSFA6a_Fw	CAGCGTTGGATGTGAAAGTG
qHSFA6a_Rv	CAGCGTTGGATGTGAAAGTG
qHSFA6b_Fw	GTGATGAAAGTGGTTATGGGAATG
qHSFA6b_Rv	TCCGACATCTCGAATTCAGACAT
qRD22_Fw	ATTGTGCGACGTCTTTGGAGT
qRD22_Rw	TGCGTTCTTCTTAGCCACCTC
qRD29A_Fw	TGGATCTGAAGAACGAATCTGATATC

qRD29A_Rv	GGTCTTCCCTTCGCCAGAA
qRD29B_Fw	AGTCGCCACGGTCCGTTGAAG
qRD29B_Rv	CCGCCACTGCCTCCCAACTC
qNCED3_Fw	AGCCGCCATTATCGTCTTCTC
qNCED3_Rv	GGAGTGTGAAGCGCAGATGAA
qAAO3_Fw	TCCATCATGGACTGCTCCTTC
qAAO3_Rv	CGAGACACTAGCGCCAAGAAA
qDREB2A_Fw	GACCTAAATGGCGACGATGT
qDREB2A_Rv	TCGAGCTGAAACGGAGGTAT
qAREB1_Fw	GAGAGAAGGCAAAGGAGAATGA
qAREB1_Rv	CTTCAAGCTCCACGGTGTAAG
qAPX2_Fw	CGGGTTTGCTGACAAGGAGTA
qAPX2_Rv	GAGGGAACAAGAATCAAGGAGGTA
qHSP18.1_Fw	AAGGCAACAATGGAGAATGG
qHSP18.1_Rv	GCACACAAGCTTTTTATTTGACA
ChIP	
qPCR_Fw	ATTTTAAAAAGGTTTAAACT
qPCR_Rv	TCCGTTCGACGAGTGTCCTC
18S rDNA_Fw	CCTGCGGCTTAATTTGACTC
18S rDNA_Rv	GACAAATCGCTCCACCAACT
Controls	
UBQ10_Fw	GATCTTTGCCGGAAAACAATTGGAGGATGGT
UBQ10_Rv	CGACTTGTCATTAGAAAGAAAGAGATAACAGG

ACT2_Fw	ATGAAGCACAATCCAAGAGAGGTATTCTTA
ACT2_Rv	GAGCTTCTCCTTGATGTCTCTTACAATTTC
qPP2A_Fw	CCTGCGGTAATAACTGCATCT
qPP2A_Rv	CTTCACTTAGCTCCACCAAGCA

Sequence data in this article can be found in the TAIR database under the following accession numbers: AAO3 (At2g27150), APX1 (At1g07890), APX2 (At3g09640), AREB1/ABF2 (At1g45249), CAT1 (At1g20630), CSD1 (At1g08830), CSD2 (At2g28190), CSD3 (At5g18100), DREB2A (At5g05410), NCED3 (At3g14440), RD22 (At5g25610), RD29A (At5g52310), RD29B (At5g52300).

HSP genes: HSP17.4-CI (At3g46230), HSP17.6A-CI (At1g59860), HSP17.6B-CI (At2g29500), HSP17.6C-CI (At1g53540), HSP17.8-CI (At1g07400), HSP18.2-CI (At5g59720), HSP17.6-CII (At5g12020), HSP26.5-MII (At1g52560), HSP70b (At1g16030), HSP90.1 (At5g52640), HSP101 (At1g74310).

HSF genes: HSFA1a (At4g17750), HSFA1b (At5g16820), HSFA1d (At1g32330), HSFA1e (At3g02990), HSFA2 (At2g26150), HSFA3 (At5g03270), HSFA4a (At4g18880), HSFA4c (At5g45710), HSFA5 (At4g13980), HSFA7a (At3g51910), HSFA7b (At3g63350), HSFA8 (At1g67970), HSFA9 (At5g54070), HSFB1 (At4g36990), HSFB2a (At5g62020), HSFB2b (At4g11660), HSFB3 (At2g41690), HSFB4 (At1g46264), HSFC1 (At3g24520).

Supplementrary Table S2. Differential expression genes (DEGs) whose expression changed more than 6 fold a *p* value of < 0.10 in transgenic plants harboring HSFA6b-OE, HSFA6b-RD under CK, Salt or HS conditions compared with wild type plants at 22°C as a control were selectec

Treatment	CK		CK		CK		SALT		SALT		SALT		HS		HS		HS					
line	WT		HSFA6b-OE		HSFA6b-RD		WT		HSFA6b-OE		HSFA6b-RD		WT		HSFA6b-OE		HSFA6b-RD					
Locus Identifier	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Normalized	*p* -value	Symbol	Array Element	Gene Function	shared the same array element
ATMG00640	0.97	0.92	1.20	0.59	1.04	0.94	2.08	0.11	1.74	0.17	3.76	0.37	9.70	0.02	10.49	0.01	10.10	0.03	ORF25	244901_at	Hydrogen ion transporting ATP synthases, rotational mechanism;zinc ion binding	
ATMG00660	0.99	0.95	1.03	0.84	0.87	0.47	1.19	0.77	1.16	0.68	2.91	0.40	6.73	0.07	10.27	0.00	11.23	0.01	ORF149	244903_at	Unknown protein	
ATMG00690	1.00	1.00	1.20	0.37	1.30	0.50	2.20	0.29	1.64	0.49	4.89	0.37	22.01	0.00	24.79	0.02	26.16	0.01	ORF240A	244906_at	Unknown protein	
ATMG00990	0.99	0.96	1.09	0.73	0.93	0.89	1.13	0.28	1.01	0.94	1.62	0.38	5.55	0.02	6.32	0.05	7.88	0.02	NAD3	244920_s_at	NADH dehydrogenase subunit 3	AT2G07751
AT2G07751	0.99	0.96	1.09	0.73	0.93	0.89	1.13	0.28	1.01	0.94	1.62	0.38	5.55	0.02	6.32	0.05	7.88	0.02		244920_s_at	NADH:ubiquinone/plastoquinone oxidoreductase, chain 3 protein	ATMG00990
ATMG01000	1.00	0.98	0.80	0.56	0.90	0.87	0.60	0.06	0.49	0.15	1.03	0.86	4.88	0.16	5.62	0.02	7.91	0.06	ORF114	244921_s_at	Unknown protein	
ATMG00070	0.97	0.93	0.97	0.89	0.97	0.97	1.43	0.37	1.09	0.78	1.97	0.42	15.90	0.05	14.73	0.00	15.18	0.02	NAD9	244943_at	NADH dehydrogenase subunit 9	
ATMG00160	0.96	0.91	1.12	0.86	1.28	0.60	3.77	0.02	3.00	0.13	5.67	0.24	11.49	0.08	13.98	0.04	12.83	0.05	COX2	244950_at	Cytochrome oxidase 2	
AT2G26530	0.98	0.94	0.93	0.11	0.66	0.11	13.53	0.02	13.60	0.00	14.18	0.00	1.31	0.43	0.72	0.27	0.74	0.40	AR781	245041_at	Protein of unknown function (DUF1645)	
AT2G23170	0.99	0.95	0.72	0.53	0.87	0.46	32.70	0.08	44.35	0.04	55.24	0.03	1.31	0.70	0.59	0.29	2.86	0.06	GH3.3	245076_at	Auxin-responsive GH3 family protein	
AT2G47600	1.00	0.99	1.06	0.54	1.16	0.31	6.74	0.08	5.84	0.07	11.46	0.04	0.89	0.23	0.75	0.05	0.79	0.10	MHX1	245127_at	Magnesium/proton exchanger	
AT4G17615	1.00	0.99	1.04	0.53	0.82	0.55	8.32	0.04	10.04	0.00	7.92	0.03	3.05	0.14	3.19	0.10	2.23	0.01	SCABP5	245251_at	Calcineurin B-like protein 1	
AT4G17500	0.99	0.96	1.19	0.33	1.27	0.32	16.12	0.04	14.58	0.07	15.98	0.03	3.08	0.09	0.96	0.68	1.82	0.02	ERF-1	245252_at	Ethylene responsive element binding factor 1	
AT4G16660	0.99	0.95	0.91	0.28	0.94	0.86	0.46	0.22	0.51	0.03	0.44	0.02	7.32	0.03	10.83	0.01	5.58	0.07		245293_at	Heat shock protein 70 (Hsp 70) family protein	
AT4G15420	1.00	0.98	0.78	0.11	1.05	0.63	4.93	0.12	4.37	0.01	3.02	0.03	27.80	0.01	18.46	0.01	20.50	0.03		245313_at	Ubiquitin fusion degradation UFD1 family protein	
AT4G16500	0.99	0.96	1.36	0.17	1.15	0.23	1.39	0.21	1.23	0.10	0.93	0.84	17.36	0.01	19.75	0.01	9.59	0.02		245323_at	Cystatin/monellin superfamily protein	
AT4G17460	0.97	0.93	0.95	0.88	1.10	0.43	0.55	0.45	0.76	0.54	0.16	0.09	0.70	0.46	0.46	0.02	1.00	0.99	HAT1	245362_at	Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein	
AT4G14270	1.00	0.97	0.72	0.23	1.16	0.39	1.57	0.31	1.61	0.33	1.15	0.71	8.26	0.03	4.55	0.02	6.49	0.02		245602_at	Containing PAM2 motif protein	
AT5G22060	0.99	0.95	0.98	0.90	0.95	0.86	3.08	0.20	2.88	0.17	2.72	0.07	7.64	0.05	8.11	0.03	8.48	0.02	J2	245686_at	DNAJ homologue 2	
AT5G04250	1.00	1.00	1.00	1.00	1.01	0.97	9.89	0.19	10.21	0.09	14.40	0.04	3.95	0.12	4.25	0.02	2.65	0.20		245699_at	Cysteine proteinases superfamily protein	
AT1G73500	0.96	0.91	1.22	0.58	1.03	0.93	16.06	0.05	13.04	0.06	9.32	0.03	2.43	0.16	1.19	0.53	0.88	0.05	MKK9	245731_at	MAP kinase kinase 9	
AT1G73480	0.97	0.92	1.01	0.92	1.15	0.70	15.27	0.08	13.37	0.08	13.22	0.08	6.32	0.14	6.91	0.02	3.71	0.11		245734_at	alpha/beta-Hydrolases superfamily protein	
AT1G73540	0.98	0.94	0.87	0.05	0.66	0.12	6.74	0.02	6.60	0.06	7.90	0.00	2.70	0.18	1.25	0.39	1.66	0.09	NUDT21	245777_at	Nudix hydrolase homolog 21	
AT5G09440	1.00	0.98	0.97	0.34	1.12	0.71	4.21	0.26	3.40	0.17	13.02	0.06	2.32	0.08	1.48	0.00	2.38	0.03	EXL4	245885_at	EXORDIUM like 4	
AT5G28500	1.00	0.99	1.06	0.56	0.80	0.26	0.20	0.22	0.25	0.06	0.16	0.01	0.35	0.12	0.43	0.02	0.38	0.06		245952_at	Unknown protein	
AT5G42020	1.00	0.99	0.96	0.84	0.76	0.58	0.48	0.04	0.50	0.04	0.51	0.09	5.53	0.02	6.74	0.00	5.54	0.03	BIP2	245956_s_at	Heat shock protein 70 (Hsp 70) family protein	AT5G28540
AT5G28540	1.00	0.99	0.96	0.84	0.76	0.58	0.48	0.04	0.50	0.04	0.51	0.09	5.53	0.02	6.74	0.00	5.54	0.03	BIP1	245956_s_at	Heat shock protein 70 (Hsp 70) family protein	AT5G42020
AT5G20630	0.95	0.90	0.64	0.36	0.39	0.41	0.17	0.01	0.32	0.09	0.05	0.05	0.65	0.48	1.00	0.99	0.42	0.09	GLP3B	246004_at	Germin 3	
AT5G10695	0.95	0.90	1.10	0.76	0.84	0.80	9.07	0.04	7.60	0.02	3.31	0.06	113.47	0.01	83.39	0.01	82.34	0.03		246018_at	Unknown protein	
AT5G08380	0.99	0.96	1.11	0.66	1.13	0.46	0.58	0.12	0.94	0.59	0.65	0.57	3.68	0.13	11.49	0.03	3.00	0.13	AGAL1	246055_at	alpha-Galactosidase 1	
AT5G20150	0.99	0.96	1.53	0.58	0.98	0.97	14.78	0.04	14.92	0.04	12.39	0.06	6.70	0.00	5.61	0.03	8.98	0.04	SPX1	246071_at	SPX domain gene 1	
AT4G36988	0.97	0.92	1.60	0.20	0.52	0.14	5.36	0.06	8.94	0.06	3.44	0.00	77.52	0.01	74.90	0.01	57.55	0.01	CPuORF49	246214_at	Conserved peptide upstream open reading frame 49	AT4G36990
AT4G36990	0.97	0.92	1.60	0.20	0.52	0.14	5.36	0.06	8.94	0.06	3.44	0.00	77.52	0.01	74.90	0.01	57.55	0.01	HSFB1	246214_at	Heat shock factor 4	AT4G36988
AT3G51890	1.00	0.98	1.38	0.09	1.15	0.77	5.82	0.14	5.64	0.01	6.60	0.03	0.80	0.79	0.49	0.16	0.60	0.32		246305_at	Clathrin light chain protein	
AT3G51790	1.00	0.99	1.15	0.58	1.25	0.26	1.13	0.19	1.13	0.31	0.92	0.65	5.87	0.04	6.15	0.03	4.10	0.06	TG1	246309_at	Transmembrane protein G1P-related 1	
AT5G15970	0.98	0.94	1.10	0.63	0.42	0.09	7.93	0.09	7.27	0.05	11.73	0.01	2.15	0.05	3.26	0.02	0.91	0.14	KIN2	246481_s_at	Stress-responsive protein (KIN2) / stress-induced protein (KIN2) / cold-responsive protein (COR6.6) / cold-regulated protein (COF	AT5G15960
AT5G15960	0.98	0.94	1.10	0.63	0.42	0.09	7.93	0.09	7.27	0.05	11.73	0.01	2.15	0.05	3.26	0.02	0.91	0.14	KIN1	246481_s_at	Stress-responsive protein (KIN1) / stress-induced protein (KIN1)	AT5G15970
AT5G15450	1.00	0.98	1.33	0.24	0.77	0.14	2.18	0.25	2.35	0.06	0.86	0.55	15.63	0.01	14.02	0.02	12.05	0.04	CLPB3	246554_at	Casein lytic proteinase B3	
AT5G35320	0.99	0.95	1.03	0.85	1.08	0.32	13.94	0.05	12.89	0.04	6.27	0.03	92.65	0.02	80.82	0.01	85.69	0.03		246612_at	Unknown protein	
AT5G27520	1.00	0.97	1.18	0.41	1.25	0.48	10.41	0.06	10.84	0.08	12.36	0.01	1.63	0.08	1.60	0.08	1.57	0.05	PNC2	246779_at	Peroxisomal adenine nucleotide carrier 2	
AT5G25510	1.00	0.98	0.93	0.18	0.80	0.58	0.23	0.04	0.23	0.04	0.16	0.04	0.23	0.03	0.58	0.03	0.41	0.15		246907_at	Protein phosphatase 2A regulatory B subunit family protein	
AT5G25460	0.99	0.96	1.03	0.84	1.20	0.09	0.21	0.04	0.22	0.02	0.13	0.08	0.39	0.16	0.26	0.00	0.34	0.02		246919_at	Protein of unknown function, DUF642	
AT5G25450	1.00	0.97	1.83	0.03	1.09	0.41	12.33	0.07	12.46	0.02	5.45	0.05	98.55	0.00	74.69	0.01	78.50	0.03		246944_at	Cytochrome bd ubiquinol oxidase, 14kDa subunit	
AT5G64310	0.99	0.97	0.83	0.18	0.85	0.80	4.19	0.09	5.30	0.12	4.96	0.04	7.29	0.07	4.88	0.04	9.43	0.02	AGP1	247279_at	Arabinogalactan protein 1	
AT5G63790	0.99	0.97	1.17	0.01	1.10	0.13	27.47	0.02	25.93	0.01	29.39	0.01	1.82	0.06	1.55	0.05	1.63	0.06	NAC102	247351_at	NAC domain containing protein 102	
AT5G62470	1.00	0.99	0.91	0.40	1.06	0.14	11.33	0.05	13.46	0.05	13.70	0.02	1.46	0.13	0.98	0.93	1.87	0.15	MYBCOV1	247455_at	Myb domain protein 96	
AT5G62020	0.99	0.95	1.05	0.89	0.33	0.12	5.14	0.18	6.68	0.13	1.09	0.63	8.77	0.05	9.06	0.02	5.07	0.04	HSFB2A	247509_at	Heat shock transcription factor B2A	
AT5G61510	1.00	0.99	0.97	0.14	0.92	0.62	1.88	0.11	2.19	0.13	1.34	0.08	6.23	0.04	6.58	0.00	4.15	0.01		247513_at	GroES-like zinc-binding alcohol dehydrogenase family protein	
AT5G59720	1.00	0.97	7.05	0.02	0.72	0.22	4.64	0.00	6.94	0.08	1.20	0.42	259.01	0.00	225.01	0.00	195.59	0.02	HSP18.2	247691_at	Heat shock protein 18.1	
AT5G58590	1.00	0.98	0.91	0.34	1.23	0.16	2.05	0.09	1.47	0.10	1.41	0.26	9.94	0.03	10.98	0.01	8.67	0.01	RANBP1	247771_at	RAN binding protein 1	
AT5G58770	1.00	0.97	1.66	0.18	0.90	0.55	6.14	0.21	7.19	0.14	4.45	0.15	24.64	0.08	31.03	0.04	16.55	0.01		247780_at	Undecaprenyl pyrophosphate synthetase family protein	
AT5G58787	1.00	0.98	0.81	0.17	0.66	0.06	0.71	0.47	1.13	0.22	0.50	0.19	10.32	0.04	11.38	0.01	4.75	0.04		247792_at	RING/U-box superfamily protein	
AT5G57910	0.96	0.91	1.07	0.63	0.72	0.12	6.35	0.29	4.87	0.31	10.92	0.05	2.87	0.05	4.91	0.04	1.90	0.19		247835_at	Unknown protein	
AT5G58120	0.99	0.96	1.08	0.86	0.77	0.57	8.28	0.02	9.86	0.01	10.50	0.01	2.36	0.45	2.41	0.01	2.53	0.02		247848_at	Disease resistance protein (TIR-NBS-LRR class) family	
AT5G58070	1.00	0.98	1.46	0.07	0.42	0.05	3.01	0.05	3.71	0.02	1.13	0.33	8.93	0.02	8.01	0.01	5.34	0.06	TIL	247851_at	Temperature-induced lipocalin	
AT5G57900	0.99	0.96	0.89	0.67	1.02	0.87	4.62	0.31	3.98	0.25	8.33	0.01	1.39	0.36	1.74	0.00	1.32	0.33	SKIP1	247863_at	SKP1 interacting partner 1	
AT5G57050	0.99	0.96	0.88	0.56	0.69	0.03	5.08	0.31	5.96	0.20	6.66	0.01	2.05	0.20	2.40	0.08	1.33	0.08	ABI2	247957_at	Protein phosphatase 2C family protein	
AT5G56540	1.00	0.98	0.90	0.69	0.85	0.60	0.10	0.08	0.13	0.03	0.07	0.04	0.93	0.56	0.85	0.24	1.00	0.94	AGP14	247965_at	Arabinogalactan protein 14	
AT5G56000	1.00	1.00	0.87	0.49	0.90	0.80	3.74	0.04	3.87	0.00	2.40	0.01	9.21	0.03	8.57	0.04	9.01	0.06	HSP81.4	248043_s_at	Heat shock protein 81.4	AT5G56010
AT5G56010	1.00	1.00	0.87	0.49	0.90	0.80	3.74	0.04	3.87	0.00	2.40	0.01	9.21	0.03	8.57	0.04	9.01	0.06	HSP81.3	248043_s_at	Heat shock protein 81-3	AT5G56000
AT5G56030	0.99	0.96	0.99	0.91	0.74	0.43	6.31	0.02	6.39	0.02	4.57	0.08	24.90	0.01	20.95	0.00	20.16	0.04	HSP90.2	248045_at	Heat shock protein 81-2	
AT5G55050	1.00	0.98	1.70	0.18	0.70	0.08	0.89	0.30	1.68	0.15	0.67	0.59	9.31	0.06	11.79	0.01	3.08	0.04		248118_at	GDSL-like Lipase/Acylhydrolase superfamily protein	
AT5G54080	1.00	0.99	0.84	0.24	1.41	0.29	5.59	0.20	5.24	0.08	8.12	0.02	1.61	0.45	0.60	0.02	1.01	0.93	HGO	248193_at	Homogentisate 1,2-dioxygenase	
AT5G54170	0.98	0.94	1.19	0.29	1.16	0.11	7.91	0.05	7.66	0.04	8.85	0.05	2.22	0.26	3.09	0.06	3.82	0.14		248199_at	Polyketide cyclase/dehydrase and lipid transport superfamily protein	
AT5G53400	0.98	0.94	1.29	0.36	1.30	0.21	3.65	0.09	3.43	0.02	1.90	0.00	18.09	0.01	16.42	0.01	15.20	0.00	BOB1	248258_at	HSP20-like chaperones superfamily protein	
AT5G52640	1.00	0.99	1.13	0.49	0.69	0.03	49.50	0.01	51.41	0.00	24.06	0.05	176.39	0.00	149.88	0.01	134.73	0.03	HSP90.1	248332_at	Heat shock protein 90.1	
AT5G52310	1.00	1.00	0.85	0.67	0.39	0.22	5.98	0.12	9.29	0.08	11.59	0.04	2.83	0.05	4.45	0.10	2.31	0.22	RD29A	248337_at	Low-temperature-responsive protein 78 (LTI78) / desiccation-responsive protein 29A (RD29A)	
AT5G51740	0.99	0.96	0.83	0.01	0.99	0.96	1.37	0.41	1.39	0.21	1.48	0.05	18.32	0.04	16.48	0.01	10.94	0.01		248426_at	Peptidase family M48 family protein	
AT5G50915	1.00	0.99	1.21	0.20	1.91	0.12	2.32	0.19	2.71	0.05	2.69	0.04	2.78	0.48	3.18	0.02	7.34	0.00		248460_at	basic Helix-Loop-Helix (bHLH) DNA-binding superfamily protein	
AT5G48570	1.00	0.99	1.33	0.06	0.53	0.21	45.26	0.03	46.35	0.01	11.95	0.00	143.37	0.00	128.58	0.01	117.63	0.02	ROF2	248657_at	FKBP-type peptidyl-prolyl cis-trans isomerase family protein	
AT5G47610	0.98	0.93	1.29	0.36	0.41	0.20	1.44	0.61	2.19	0.37	0.29	0.10	28.57	0.06	30.47	0.01	22.71	0.03		248759_at	RING/U-box superfamily protein	
AT5G47830	0.99	0.97	0.91	0.60	0.77	0.13	4.82	0.08	4.35	0.03	2.15	0.21	22.23	0.04	17.62	0.00	18.01	0.01		248774_at	Unknown protein	
AT5G45950	0.99	0.96	0.98	0.86	0.75	0.27	0.13	0.01	0.17	0.16	0.14	0.05	0.46	0.13	0.56	0.18	0.56	0.06		248921_at	GDSL-like Lipase/Acylhydrolase superfamily protein	
AT5G44680	0.98	0.93	0.92	0.78	0.53	0.28	0.10	0.10	0.11	0.02	0.04	0.02	0.44	0.23	0.42	0.07	0.43	0.08		249008_at	DNA glycosylase superfamily protein	
AT5G43170	0.99	0.97	1.41	0.16	0.88	0.50	2.34	0.04	3.06	0.03	2.20	0.04	47.00	0.00	50.63	0.01	9.32	0.04	ZF3	249139_at	Zinc-finger protein 3	
AT5G42150	1.00	1.00	0.96	0.55	0.73	0.33	1.05	0.87	1.23	0.53	0.56	0.11	16.05	0.03	16.00	0.00	11.41	0.01		249233_at	Glutathione S-transferase family protein	
AT5G40780	0.98	0.94	1.27	0.47	1.70	0.18	3.66	0.21	5.02	0.11	7.51	0.03	0.55	0.28	0.48	0.15	0.67	0.08	LHT1	249346_at	Lysine histidine transporter 1	
AT5G40420	0.99	0.95	1.74	0.26	0.56	0.07	0.13	0.06	0.21	0.05	0.09	0.09	0.88	0.54	1.44	0.05	0.93	0.67	OLEO2	249353_at	Oleosin 2	
AT5G39320	1.00	0.98	0.98	0.91	0.73	0.61	0.25	0.24	0.27	0.11	0.16	0.03	0.40	0.11	0.47	0.11	0.50	0.07		249469_at	UDP-glucose 6-dehydrogenase family protein	
AT5G38895	0.96	0.91	1.34	0.32	0.86	0.50	3.72	0.15	4.01	0.03	2.90	0.15	7.64	0.07	8.21	0.04	3.81	0.04		249483_at	RING/U-box superfamily protein	

AT5G23050	0.99	0.96	1.02	0.95	1.20	0.49	4.77	0.22	4.05	0.24	7.13	0.02	0.90	0.83	0.83	0.06	0.82	0.23	AAE17	249869_at	Acyl-activating enzyme 17	
AT5G22480	0.99	0.95	0.72	0.02	0.94	0.40	1.94	0.22	1.62	0.10	1.10	0.53	9.98	0.05	8.24	0.07	6.74	0.02		249888_s_at	ZPR1 zinc-finger domain protein	AT5G37340
AT5G37340	0.99	0.95	0.72	0.02	0.94	0.40	1.94	0.22	1.62	0.10	1.10	0.53	9.98	0.05	8.24	0.07	6.74	0.02		249888_s_at	ZPR1 zinc-finger domain protein	AT5G22480
AT5G22580	0.98	0.94	0.99	0.96	0.94	0.87	0.19	0.20	0.23	0.19	0.13	0.09	1.20	0.06	0.68	0.07	0.80	0.55		249894_at	Stress responsive A/B Barrel Domain	
AT5G18060	0.99	0.96	0.91	0.89	1.47	0.40	1.40	0.53	1.72	0.45	0.20	0.13	0.31	0.01	0.15	0.05	0.39	0.16		250012_x_at	SAUR-like auxin-responsive protein family	
AT5G18040	1.00	0.98	1.05	0.86	1.10	0.66	4.05	0.22	4.08	0.10	2.99	0.00	9.53	0.04	8.31	0.06	7.82	0.04		250013_at	Unknown protein	
AT5G17850	1.00	0.98	1.06	0.22	0.73	0.37	12.30	0.00	12.81	0.01	11.68	0.01	3.43	0.08	4.37	0.05	3.92	0.14		250053_at	Sodium/calcium exchanger family protein	
AT5G16650	1.00	0.99	1.05	0.70	1.19	0.43	4.88	0.15	4.37	0.11	6.79	0.05	1.23	0.16	1.50	0.30	1.45	0.01		250079_at	Chaperone DnaJ-domain superfamily protein	
AT5G12110	1.00	0.99	1.85	0.00	0.51	0.06	4.12	0.05	6.52	0.06	0.60	0.47	38.62	0.02	35.94	0.00	26.57	0.02		250304_at	Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6	
AT5G11680	0.99	0.95	0.96	0.62	0.91	0.58	1.86	0.03	2.05	0.02	1.92	0.04	18.22	0.04	16.99	0.01	12.78	0.00		250332_at	Unknown protein	
AT5G11650	1.00	0.98	1.04	0.87	1.00	0.96	4.75	0.11	4.90	0.09	8.10	0.00	2.04	0.31	1.42	0.10	2.65	0.02		250335_at	alpha/beta-Hydrolases superfamily protein	
AT5G11420	0.99	0.96	1.00	0.96	0.88	0.54	0.20	0.03	0.21	0.02	0.16	0.06	0.69	0.09	0.44	0.01	0.46	0.03		250366_at	Protein of unknown function, DUF642	
AT5G10550	1.00	0.99	1.13	0.11	1.12	0.68	1.57	0.05	2.62	0.02	1.67	0.04	7.34	0.04	4.52	0.01	9.04	0.05	GTE2	250424_at	Global transcription factor group E2	
AT5G09530	0.97	0.92	1.64	0.05	0.18	0.00	0.15	0.09	0.11	0.23	0.05	0.05	0.36	0.20	0.98	0.92	0.10	0.02	PRP10	250500_at	Hydroxyproline-rich glycoprotein family protein	
AT5G09590	0.99	0.95	0.97	0.01	0.81	0.22	7.69	0.00	9.04	0.01	4.75	0.04	80.59	0.01	71.41	0.00	68.11	0.02	MTHSC70-2	250502_at	Mitochondrial HSO70 2	
AT5G07330	0.94	0.89	1.84	0.05	0.33	0.20	0.88	0.68	1.57	0.59	0.27	0.36	34.75	0.04	47.23	0.00	12.62	0.01		250624_at	Unknown protein	
AT5G07030	0.97	0.92	0.88	0.43	0.59	0.45	0.15	0.09	0.16	0.12	0.10	0.03	0.32	0.00	0.54	0.44	0.40	0.06		250661_at	Eukaryotic aspartyl protease family protein	
AT5G05960	1.00	0.99	0.91	0.54	0.31	0.17	0.09	0.08	0.12	0.15	0.06	0.01	0.53	0.08	0.55	0.12	0.25	0.01		250764_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	
AT5G05410	0.99	0.96	1.30	0.01	0.64	0.07	85.07	0.02	95.38	0.00	56.15	0.02	66.95	0.02	35.83	0.00	37.61	0.05	DREB2A	250781_at	DRE-binding protein 2A	
AT5G04980	1.00	1.00	0.91	0.61	0.78	0.18	1.11	0.52	1.21	0.33	0.93	0.66	6.63	0.11	11.85	0.00	2.33	0.06		250803_at	DNAse I-like superfamily protein	
AT5G03340	0.99	0.96	0.94	0.66	1.14	0.31	2.61	0.06	2.12	0.00	1.42	0.05	5.29	0.05	6.27	0.06	3.99	0.03		250899_at	ATPase, AAA-type, CDC48 protein	
AT5G02760	0.94	0.89	0.88	0.75	1.10	0.54	0.54	0.42	0.73	0.53	0.12	0.08	0.37	0.50	0.10	0.01	0.38	0.18		251017_at	Protein phosphatase 2C family protein	
AT5G02020	0.98	0.93	0.82	0.51	1.42	0.04	13.75	0.15	14.86	0.10	26.95	0.03	1.05	0.95	0.91	0.55	1.10	0.32	SIS	251039_at	Encodes a protein involved in salt tolerance, names SIS (Salt Induced Serine rich).	
AT5G01870	0.92	0.87	0.80	0.63	0.40	0.43	0.08	0.12	0.07	0.09	0.08	0.24	0.26	0.18	0.91	0.39	0.42	0.05		251065_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	
AT5G01990	0.99	0.97	0.96	0.77	0.67	0.22	1.30	0.45	1.58	0.26	0.79	0.06	10.17	0.04	9.19	0.06	5.08	0.05		251078_at	Auxin efflux carrier family protein	
AT5G01600	1.00	0.99	0.72	0.11	1.13	0.79	4.84	0.04	5.04	0.03	6.51	0.01	1.53	0.70	2.14	0.06	2.60	0.04	FER1	251109_at	Ferretin 1	
AT3G63310	0.99	0.95	0.94	0.64	0.92	0.67	2.04	0.21	1.93	0.06	1.58	0.01	6.73	0.04	6.35	0.00	4.47	0.02	BIL4	251163_at	Bax inhibitor-1 family protein	
AT3G62260	1.00	0.97	1.31	0.38	1.13	0.35	9.59	0.11	9.87	0.12	10.35	0.01	22.49	0.01	19.50	0.00	12.77	0.03		251259_at	Protein phosphatase 2C family protein	
AT3G61820	1.00	0.97	0.82	0.29	0.60	0.27	0.19	0.14	0.20	0.08	0.15	0.02	0.15	0.07	0.15	0.05	0.16	0.02		251287_at	Eukaryotic aspartyl protease family protein	
AT2G45470	1.00	0.99	0.87	0.03	1.04	0.73	0.07	0.13	0.09	0.07	0.05	0.02	0.27	0.10	0.25	0.13	0.32	0.04	FLA8	251395_at	FASCICLIN-like arabinogalactan protein 8	
AT3G60250	1.00	0.99	0.89	0.11	1.05	0.34	0.96	0.68	0.99	0.40	0.85	0.07	3.74	0.02	6.15	0.01	2.27	0.11	CKB3	251411_at	Casein kinase II beta chain 3	
AT5G33355	0.99	0.95	0.91	0.82	1.07	0.76	9.03	0.26	11.16	0.18	10.25	0.05	2.55	0.22	1.21	0.03	1.71	0.07		251438_s_at	Defensin-like (DEFL) family protein	AT3G59930
AT3G59930	0.99	0.95	0.91	0.82	1.07	0.76	9.03	0.26	11.16	0.18	10.25	0.05	2.55	0.22	1.21	0.03	1.71	0.07		251438_s_at	Encodes a defensin-like (DEFL) family protein	AT5G33355
AT3G58990	1.00	1.00	0.87	0.68	0.89	0.68	0.08	0.23	0.11	0.14	0.12	0.03	0.22	0.24	0.54	0.12	0.60	0.02	IPMI1	251524_at	Isopropylmalate isomerase 1	
AT3G57010	0.98	0.94	0.78	0.37	0.32	0.06	0.17	0.11	0.11	0.10	0.13	0.04	0.31	0.00	0.78	0.57	0.42	0.09		251668_at	Calcium-dependent phosphotriesterase superfamily protein	
AT3G54400	1.00	1.00	0.92	0.55	0.86	0.51	0.14	0.06	0.13	0.01	0.12	0.02	0.35	0.05	0.64	0.15	0.80	0.07		251899_at	Eukaryotic aspartyl protease family protein	
AT3G53810	1.00	0.97	1.01	0.96	0.99	0.94	1.11	0.67	1.23	0.51	1.17	0.71	3.21	0.13	6.83	0.03	3.03	0.02		251910_at	Concanavalin A-like lectin protein kinase family protein	
AT3G53180	1.00	0.97	1.07	0.34	1.14	0.23	5.32	0.15	5.11	0.05	8.96	0.01	0.85	0.41	0.98	0.69	0.98	0.69	NODGS	251973_at	Glutamate-ammonia ligases;catalytics;glutamate-ammonia ligases	
AT3G53230	1.00	0.98	0.92	0.44	0.78	0.19	8.45	0.08	8.49	0.03	5.00	0.04	19.94	0.00	19.05	0.02	16.22	0.00		251975_at	ATPase, AAA-type, CDC48 protein	
AT3G52940	0.98	0.94	0.92	0.83	0.78	0.15	0.22	0.18	0.26	0.26	0.12	0.07	0.62	0.37	0.64	0.00	0.69	0.06	HYD2	251995_at	Ergosterol biosynthesis ERG4/ERG24 family	
AT3G51910	0.99	0.96	0.91	0.24	1.06	0.70	4.60	0.01	4.32	0.02	2.65	0.04	34.01	0.01	25.64	0.02	30.31	0.03	HSFA7A	252081_at	Heat shock transcription factor A7A	
AT3G50970	1.00	0.97	0.99	0.92	0.55	0.12	3.97	0.11	4.82	0.18	5.07	0.05	6.50	0.02	6.88	0.02	4.55	0.08	XERO2	252102_at	Dehydrin family protein	
AT3G50260	0.98	0.94	1.02	0.59	1.24	0.29	8.65	0.01	6.63	0.01	12.95	0.01	4.23	0.08	1.79	0.11	2.87	0.09	DEAR1	252214_at	Cooperatively regulated by ethylene and jasmonate 1	
AT3G49780	1.00	0.97	1.20	0.44	0.60	0.20	6.22	0.02	6.95	0.05	4.71	0.04	3.65	0.00	2.78	0.03	1.13	0.47	PSK4	252234_at	Phytosulfokine 4 precursor	
AT3G46600	1.00	0.99	0.80	0.34	1.04	0.59	6.59	0.09	6.51	0.08	9.29	0.02	1.84	0.17	1.10	0.59	1.93	0.07		252483_at	GRAS family transcription factor	
AT3G45300	1.00	0.98	0.90	0.48	1.59	0.29	5.42	0.21	5.34	0.15	8.89	0.01	0.85	0.81	0.50	0.12	0.70	0.02	IVDH	252570_at	Isovaleryl-CoA-dehydrogenase	
AT3G44990	0.97	0.92	1.13	0.68	0.17	0.13	0.15	0.23	0.29	0.24	0.05	0.08	0.41	0.16	1.11	0.41	0.17	0.03	XTR8	252607_at	Xyloglucan endo-transglycosylase-related 8	
AT3G44110	1.00	0.98	1.08	0.23	1.00	0.93	2.38	0.11	2.28	0.11	2.04	0.19	9.72	0.00	8.15	0.01	7.84	0.02	J3	252670_at	DNAJ homologue 3	
AT3G43800	0.99	0.97	0.95	0.08	0.71	0.06	0.19	0.17	0.21	0.18	0.13	0.03	0.46	0.06	0.49	0.02	0.65	0.32	GSTU27	252712_at	Glutathione S-transferase tau 27	
AT4G36010	0.99	0.96	0.87	0.73	0.53	0.11	1.67	0.35	1.99	0.27	1.41	0.57	32.51	0.05	13.15	0.05	13.89	0.05		253104_at	Pathogenesis-related thaumatin superfamily protein	
AT4G35985	0.99	0.97	0.99	0.96	1.17	0.61	13.69	0.06	13.31	0.04	10.10	0.02	2.82	0.04	2.04	0.21	2.57	0.06		253113_at	Senescence/dehydration-associated protein-related	
AT4G34760	0.98	0.94	0.87	0.54	1.25	0.04	0.69	0.26	1.01	0.98	0.12	0.04	0.21	0.11	0.14	0.01	0.54	0.11		253255_at	SAUR-like auxin-responsive protein family	
AT4G33660	0.98	0.94	0.96	0.89	1.00	0.99	1.00	0.99	1.31	0.46	0.90	0.71	14.02	0.07	15.16	0.02	10.15	0.02		253302_at	Unknown protein	
AT4G33550	0.98	0.94	0.96	0.80	0.21	0.17	0.13	0.11	0.17	0.01	0.06	0.08	0.21	0.35	1.15	0.15	0.34	0.04		253344_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	
AT4G33220	0.97	0.92	1.00	1.00	1.42	0.31	0.17	0.13	0.14	0.09	0.26	0.02	0.29	0.04	0.20	0.02	0.44	0.16	PME44	253372_at	Pectin methylesterase 44	
AT4G33150	1.00	0.97	1.23	0.23	0.97	0.78	4.72	0.33	4.01	0.29	9.72	0.01	0.60	0.35	0.72	0.35	0.52	0.05	SDH	253373_at	Lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme	
AT4G30670	1.00	1.00	1.07	0.71	0.67	0.17	0.15	0.02	0.16	0.03	0.15	0.09	1.43	0.02	0.63	0.18	0.65	0.05		253582_at	Putative membrane lipoprotein	
AT4G30490	1.00	0.99	1.05	0.83	0.81	0.07	10.03	0.14	11.16	0.04	8.29	0.02	4.88	0.14	4.84	0.02	3.84	0.04		253630_at	AFG1-like ATPase family protein	
AT4G30470	0.97	0.93	1.20	0.29	1.12	0.75	9.02	0.08	8.63	0.10	10.59	0.04	1.68	0.27	2.34	0.03	2.09	0.01		253638_at	NAD(P)-binding Rossmann-fold superfamily protein	
AT4G30020	0.99	0.95	0.88	0.49	0.83	0.57	0.19	0.14	0.24	0.17	0.15	0.07	0.20	0.00	0.45	0.07	0.33	0.02		253650_at	PA-domain containing subtilase family protein	
AT4G29330	0.98	0.94	1.05	0.65	1.28	0.15	1.81	0.32	1.87	0.15	1.27	0.01	24.42	0.01	18.85	0.01	16.69	0.00	DER1	253712_at	DERLIN-1	
AT4G29020	1.00	0.98	1.11	0.07	0.96	0.71	0.15	0.03	0.18	0.03	0.10	0.03	1.01	0.92	1.04	0.10	0.92	0.57		253754_at	Glycine-rich protein	
AT4G28390	0.99	0.96	1.59	0.17	1.15	0.39	1.23	0.55	1.64	0.09	1.28	0.28	9.39	0.06	12.51	0.04	6.40	0.07	AAC3	253776_at	ADP/ATP carrier 3	
AT4G28480	1.00	0.97	1.07	0.26	0.91	0.33	1.01	0.94	1.13	0.16	0.68	0.05	7.49	0.04	6.95	0.01	5.42	0.00		253778_at	DNAJ heat shock family protein	
AT4G27680	1.00	0.97	1.20	0.17	1.08	0.39	2.74	0.23	2.61	0.07	2.31	0.17	7.05	0.03	8.03	0.01	5.45	0.01		253861_at	P-loop containing nucleoside triphosphate hydrolases superfamily protein	
AT4G27410	0.99	0.97	1.07	0.19	0.99	0.98	15.43	0.11	16.79	0.06	14.74	0.02	3.40	0.08	3.82	0.00	1.82	0.16	RD26	253872_at	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	
AT4G26500	1.00	0.99	1.06	0.44	1.06	0.54	0.66	0.46	0.60	0.34	0.47	0.12	8.29	0.04	9.36	0.01	5.66	0.06	SUFE1	253972_at	Chloroplast sulfur E	
AT4G26270	1.00	0.99	0.94	0.77	0.74	0.32	1.45	0.14	1.66	0.18	0.91	0.64	34.58	0.02	30.64	0.03	21.60	0.05	PFK3	253987_at	Phosphofructokinase 3	
AT4G26080	1.00	0.99	0.89	0.21	1.00	0.98	7.19	0.20	7.17	0.09	7.59	0.02	1.35	0.28	1.24	0.15	0.83	0.13	ABI1	253994_at	Protein phosphatase 2C family protein	
AT4G25340	0.97	0.92	1.14	0.47	0.87	0.79	0.76	0.58	0.86	0.70	0.50	0.24	32.27	0.01	30.23	0.00	20.23	0.00	FKBP53	254076_at	FK506 BINDING PROTEIN 53	
AT4G24780	0.99	0.96	0.94	0.72	0.61	0.43	0.13	0.16	0.14	0.08	0.19	0.10	0.18	0.01	0.20	0.02	0.23	0.05		254119_at	Pectin lyase-like superfamily protein	
AT4G24280	0.99	0.95	1.33	0.05	0.97	0.89	1.23	0.49	1.27	0.37	0.87	0.56	4.93	0.05	9.34	0.02	4.16	0.00	cpHsc70-1	254148_at	Chloroplast heat shock protein 70-1	
AT4G24380	1.00	0.99	1.33	0.19	0.76	0.31	18.27	0.02	18.86	0.03	16.76	0.04	4.13	0.29	2.69	0.02	4.59	0.05		254158_at	Unknown protein	
AT4G23570	0.95	0.90	0.94	0.69	1.23	0.46	7.65	0.13	7.42	0.11	6.26	0.14	43.25	0.05	30.51	0.00	37.74	0.02	SGT1A	254211_at	Phosphatase-related	
AT4G23060	1.00	0.98	0.80	0.46	1.09	0.51	5.65	0.04	5.66	0.06	6.92	0.00	0.33	0.47	0.56	0.04	0.57	0.29	IQD22	254293_at	IQ-domain 22	
AT4G22340	0.99	0.96	0.92	0.70	0.72	0.03	1.36	0.03	1.53	0.07	1.17	0.60	6.73	0.11	11.45	0.04	3.70	0.08	CDS2	254360_at	Cytidinediphosphate diacylglycerol synthase 2	
AT4G21840	0.99	0.96	1.18	0.67	0.97	0.95	18.06	0.03	17.92	0.01	15.86	0.04	0.88	0.65	1.19	0.45	1.61	0.06	MSRB8	254385_s_at	Methionine sulfoxide reductase B8	AT4G21830
AT4G21830	0.99	0.96	1.18	0.67	0.97	0.95	18.06	0.03	17.92	0.01	15.86	0.04	0.88	0.65	1.19	0.45	1.61	0.06	MSRB7	254385_s_at	Methionine sulfoxide reductase B7	AT4G21840
AT4G21580	0.99	0.97	1.18	0.18	0.98	0.51	2.81	0.22	2.36	0.21	3.07	0.04	6.96	0.09	7.69	0.01	4.44	0.06		254393_at	Oxidoreductase, zinc-binding dehydrogenase family protein	
AT4G21310	1.00	0.97	1.04	0.03	0.94	0.85	0.60	0.03	0.81	0.29	0.82	0.47	4.74	0.10	6.19	0.01	2.54	0.08		254402_at	Protein of unknown function (DUF1218)	
AT4G21090	0.98	0.94	1.11	0.06	1.11	0.24	1.75	0.04	2.00	0.08	1.69	0.19	10.08	0.06	11.00	0.03	6.13	0.02	MFDX2	254451_at	Mitochondrial ferredoxin 2	
AT4G19170	1.00	0.99	0.84	0.18	0.95	0.84	0.17	0.21	0.17	0.17	0.15	0.05	0.34	0.35	0.27	0.06	0.30	0.02	NCED4	254564_at	nine-cis-Epoxycarotenoid dioxygenase 4	
AT4G18280	1.00	1.00	1.07	0.77	0.54	0.23	15.46	0.03	20.60	0.00	7.61	0.03	3.99	0.13	4.82	0.04	0.89	0.02		254667_at	Glycine-rich cell wall protein-related	
AT4G13890	1.00	0.97	0.98	0.45	0.83	0.52	0.14	0.14	0.16	0.10	0.15	0.02	0.41	0.02	0.52	0.19	0.58	0.15	SHM5	254740_s_at	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	AT4G13930
AT4G13930	1.00	0.97	0.98	0.45	0.83	0.52	0.14	0.14	0.16	0.10	0.15	0.02	0.41	0.02	0.52	0.19	0.58	0.15	SHM4	254740_s_at	Serine hydroxymethyltransferase 4	AT4G13890
AT4G13180	1.00	0.97	1.18	0.50	1.01	0.98	5.02	0.04	4.25	0.09	3.16	0.19	4.35	0.05	6.21	0.04	3.78	0.04		254759_at	NAD(P)-binding Rossmann-fold superfamily protein	

AT4G12880	1.00	0.99	1.10	0.46	0.95	0.71	0.10	0.18	0.13	0.14	0.10	0.05	0.79	0.21	0.88	0.57	0.61	0.05	ENODL19	254789_at	Early nodulin-like protein 19	
AT4G12400	1.00	0.98	1.19	0.41	0.99	0.98	32.71	0.06	30.27	0.05	13.00	0.05	171.53	0.00	152.08	0.00	145.27	0.01	HOP3	254839_at	Stress-inducible protein, putative	
AT4G12000	0.98	0.94	0.85	0.67	0.97	0.14	6.12	0.14	6.00	0.15	6.05	0.09	1.38	0.30	1.72	0.12	2.42	0.08		254850_at	SNARE associated Golgi protein family	
AT4G11740	1.00	0.99	1.04	0.03	1.02	0.86	1.14	0.50	1.29	0.02	0.93	0.45	6.98	0.04	6.47	0.01	4.32	0.07	SAY1	254891_at	Ubiquitin-like superfamily protein	
AT4G11310	0.99	0.96	0.76	0.29	0.39	0.05	0.23	0.08	0.23	0.01	0.13	0.00	0.18	0.02	0.10	0.02	0.07	0.01		254915_s_at	Papain family cysteine protease	AT4G11320
AT4G11320	0.99	0.96	0.76	0.29	0.39	0.05	0.23	0.08	0.23	0.01	0.13	0.00	0.18	0.02	0.10	0.02	0.07	0.01		254915_s_at	Papain family cysteine protease	AT4G11310
AT4G11280	1.00	0.99	0.93	0.73	0.97	0.65	17.07	0.02	16.83	0.06	22.03	0.03	5.35	0.05	2.12	0.29	8.88	0.10	ACS6	254926_at	1-Aminocyclopropane-1-carboxylic acid (acc) synthase 6	
AT4G10070	1.00	0.99	1.10	0.10	1.07	0.02	6.91	0.05	5.94	0.05	6.48	0.02	0.87	0.36	0.97	0.78	0.84	0.64		255009_at	KH domain-containing protein	
AT4G10040	0.97	0.93	1.08	0.66	0.65	0.28	1.41	0.55	1.78	0.44	1.53	0.41	7.67	0.05	7.03	0.04	5.90	0.01	CYTC-2	255011_at	Cytochrome c-2	
AT4G09150	1.00	1.00	1.21	0.42	1.31	0.20	5.57	0.07	6.75	0.03	2.88	0.02	17.32	0.02	14.70	0.02	13.23	0.00		255077_at	T-complex protein 11	
AT4G08685	1.00	0.99	1.09	0.31	0.96	0.16	0.16	0.07	0.18	0.14	0.13	0.01	1.00	1.00	0.92	0.25	0.89	0.63	SAH7	255104_at	Pollen Ole e 1 allergen and extensin family protein	
AT4G05020	0.98	0.94	1.05	0.75	0.88	0.60	0.87	0.83	1.35	0.29	1.57	0.12	3.63	0.05	6.08	0.03	3.78	0.06	NDB2	255259_at	NAD(P)H dehydrogenase B2	
AT4G03320	0.99	0.97	1.24	0.09	0.82	0.20	1.47	0.56	1.28	0.40	1.40	0.39	6.68	0.01	6.31	0.01	4.13	0.06	Tic20-IV	255430_at	Translocon at the inner envelope membrane of chloroplasts 20-IV	
AT4G01026	1.00	0.97	0.90	0.21	1.05	0.45	9.24	0.16	9.12	0.10	13.10	0.05	3.50	0.03	2.62	0.10	2.44	0.22	RCAR2	255602_at	PYR1-like 7	
AT4G00760	1.00	1.00	1.09	0.43	0.98	0.25	3.16	0.12	3.07	0.05	4.60	0.07	5.16	0.11	7.54	0.01	4.27	0.09	PRR8	255639_at	Pseudo-response regulator 8	
AT4G00550	0.98	0.93	0.91	0.65	0.76	0.15	1.14	0.43	1.18	0.17	1.19	0.02	14.26	0.01	19.79	0.00	7.31	0.02	DGD2	255681_at	Digalactosyl diacylglycerol deficient 2	
AT3G29575	0.97	0.92	0.74	0.21	1.21	0.58	5.31	0.23	5.73	0.16	8.34	0.05	0.72	0.45	1.11	0.36	0.92	0.10	AFP3	255723_at	ABI five binding protein 3	
AT1G25400	0.96	0.91	0.84	0.69	1.90	0.31	8.99	0.15	8.92	0.12	10.95	0.07	4.60	0.04	2.52	0.07	3.69	0.21		255733_at	Unknown protein	
AT2G33590	0.98	0.93	1.12	0.42	1.05	0.81	3.66	0.33	4.23	0.21	3.43	0.21	24.98	0.05	24.62	0.00	16.82	0.00		255787_at	NAD(P)-binding Rossmann-fold superfamily protein	
AT2G33380	0.98	0.93	0.91	0.68	1.03	0.90	22.11	0.21	21.33	0.19	62.46	0.02	0.79	0.89	2.74	0.11	1.61	0.02	RD20	255795_at	Caleosin-related family protein	
AT1G66940	0.98	0.94	1.19	0.74	0.70	0.26	0.19	0.18	0.23	0.20	0.10	0.05	0.41	0.44	0.65	0.04	0.48	0.17		255856_at	Protein kinase-related	
AT1G17870	1.00	0.99	1.91	0.16	0.50	0.08	4.96	0.19	7.21	0.05	1.11	0.61	32.09	0.06	34.92	0.01	34.07	0.02	EGY3	255891_at	Ethylene-dependent gravitropism-deficient and yellow-green-like 3	
AT1G22190	0.99	0.96	1.25	0.01	1.22	0.05	5.62	0.13	4.72	0.17	7.41	0.00	1.38	0.59	1.24	0.29	2.43	0.02	RAP2.4	255926_at	Integrase-type DNA-binding superfamily protein	
AT1G12710	0.99	0.96	1.09	0.55	1.33	0.59	2.38	0.34	2.50	0.14	1.36	0.01	6.36	0.04	6.20	0.08	1.77	0.23	PP2-A12	255931_at	Phloem protein 2-A12	
AT1G19180	1.00	1.00	1.20	0.39	0.60	0.35	23.06	0.02	19.79	0.00	18.07	0.05	1.87	0.23	1.17	0.26	0.64	0.26	TIFY10A	256017_at	Jasmonate-zim-domain protein 1	
AT1G13690	1.00	0.99	0.86	0.12	1.04	0.56	0.56	0.23	0.60	0.34	0.40	0.11	11.57	0.05	14.76	0.01	6.12	0.00	ATE1	256068_at	ATPase E1	
AT1G20693	0.99	0.95	1.08	0.42	1.04	0.95	0.24	0.09	0.30	0.13	0.15	0.07	0.70	0.68	0.25	0.01	0.25	0.03	NFD2	256091_at	High mobility group B2	
AT1G20823	0.98	0.93	1.05	0.75	1.33	0.29	2.51	0.11	2.91	0.01	3.11	0.05	3.61	0.01	2.30	0.02	6.30	0.07		256093_at	RING/U-box superfamily protein	
AT1G48750	1.00	0.98	1.04	0.83	0.26	0.13	0.22	0.16	0.20	0.13	0.08	0.01	0.47	0.20	0.85	0.32	0.29	0.03		256145_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	
AT1G51780	1.00	0.98	1.24	0.08	0.97	0.91	8.94	0.01	6.34	0.02	9.64	0.01	0.52	0.05	1.48	0.18	1.14	0.31	ILL5	256178_s_at	IAA-leucine resistant (ILR)-like gene 5	AT1G51760
AT1G51760	1.00	0.98	1.24	0.08	0.97	0.91	8.94	0.01	6.34	0.02	9.64	0.01	0.52	0.05	1.48	0.18	1.14	0.31	JR3	256178_s_at	Peptidase M20/M25/M40 family protein	AT1G51780
AT3G12610	0.99	0.96	1.14	0.11	0.92	0.05	0.08	0.13	0.09	0.03	0.07	0.03	0.36	0.07	0.26	0.03	0.37	0.06	DRT100	256237_at	Leucine-rich repeat (LRR) family protein	
AT3G12580	0.97	0.93	1.49	0.00	0.41	0.18	34.48	0.04	42.84	0.01	19.39	0.03	83.76	0.01	75.19	0.01	68.70	0.03	HSP70	256245_at	Heat shock protein 70	
AT1G72060	0.98	0.94	0.87	0.65	1.81	0.02	28.19	0.15	22.24	0.12	53.27	0.03	1.48	0.27	0.90	0.19	1.36	0.23		256337_at	Serine-type endopeptidase inhibitors	
AT3G10985	1.00	0.99	0.89	0.20	1.40	0.03	5.41	0.19	4.28	0.20	6.61	0.03	1.48	0.14	0.87	0.02	1.94	0.11	WI12	256433_at	Senescence associated gene 20	
AT1G75230	1.00	0.98	1.34	0.13	1.22	0.50	4.83	0.03	5.43	0.02	7.23	0.05	1.55	0.36	0.85	0.68	1.51	0.22		256457_at	DNA glycosylase superfamily protein	
AT1G66100	0.96	0.91	0.69	0.46	0.31	0.26	0.33	0.14	0.20	0.04	0.18	0.25	0.82	0.85	0.29	0.05	0.16	0.08		256527_at	Plant thionin	
AT3G12050	0.98	0.94	1.01	0.84	1.02	0.80	5.43	0.07	5.97	0.02	3.25	0.01	35.77	0.00	30.38	0.01	28.28	0.02		256663_at	aha1 Domain-containing protein	
AT3G23920	0.98	0.93	1.23	0.34	0.92	0.32	7.39	0.24	7.22	0.17	11.46	0.05	8.55	0.16	14.78	0.02	9.86	0.02	TR-BAMY	256861_at	beta-Amylase 1	
AT3G22600	0.97	0.93	1.21	0.21	0.49	0.21	0.21	0.00	0.20	0.01	0.08	0.09	0.52	0.20	1.12	0.18	0.31	0.07		256933_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	
AT3G13470	1.00	0.98	1.02	0.90	1.06	0.92	2.32	0.04	2.44	0.04	2.69	0.19	18.01	0.02	16.62	0.01	14.81	0.03	CPN60beta2	256983_at	TCP-1/CPN60 chaperonin family protein	
AT3G25830	1.00	0.98	1.26	0.13	0.46	0.04	0.44	0.16	0.47	0.10	0.17	0.18	0.25	0.14	0.35	0.00	0.13	0.00	TPS-CIN	256994_s_at	Terpene synthase-like sequence-1,8-cineole	AT3G25820
AT3G25820	1.00	0.98	1.26	0.13	0.46	0.04	0.44	0.16	0.47	0.10	0.17	0.18	0.25	0.14	0.35	0.00	0.13	0.00	TPS-CIN	256994_s_at	Terpene synthase-like sequence-1,8-cineole	AT3G25830
AT3G19580	1.00	0.98	1.25	0.01	0.96	0.89	9.71	0.06	11.36	0.09	12.33	0.01	2.07	0.02	3.08	0.02	1.62	0.30	ZF2	257022_at	Zinc-finger protein 2	
AT3G19240	1.00	0.97	1.11	0.43	1.08	0.40	6.42	0.00	6.35	0.05	5.39	0.06	1.75	0.06	1.03	0.32	1.27	0.24		257029_at	Vacuolar import/degradation, Vid27-related protein	
AT3G15210	0.99	0.96	0.98	0.47	0.86	0.56	7.47	0.02	7.99	0.05	6.87	0.02	1.73	0.28	1.11	0.36	1.14	0.34	RAP2.5	257053_at	Ethylene responsive element binding factor 4	
AT3G14220	0.98	0.94	0.99	0.91	1.17	0.36	0.20	0.13	0.28	0.08	0.16	0.07	0.65	0.48	0.97	0.59	0.82	0.35		257072_at	GDSL-like Lipase/Acylhydrolase superfamily protein	
AT3G28040	1.00	0.98	1.04	0.87	0.74	0.21	0.09	0.06	0.12	0.01	0.11	0.00	0.08	0.00	0.22	0.02	0.12	0.04		257297_at	Leucine-rich receptor-like protein kinase family protein	
ATMG01360	1.00	1.00	0.96	0.79	1.27	0.27	1.32	0.12	1.41	0.64	2.52	0.39	7.73	0.04	7.47	0.05	7.54	0.01	COX1	257333_at	Cytochrome oxidase	
ATMG01370	0.99	0.95	1.14	0.59	1.39	0.31	0.23	0.02	0.21	0.09	0.43	0.37	6.17	0.03	6.81	0.01	8.87	0.02	ORF111D	257334_at	Unknown protein	
ATMG00040	0.99	0.96	1.06	0.88	1.02	0.79	1.94	0.43	1.15	0.61	3.43	0.37	5.89	0.07	6.20	0.00	7.47	0.02	ORF315	257339_s_at	ATP synthase subunit C family protein	AT2G07671;ATMG01080
ATMG01080	0.99	0.96	1.06	0.88	1.02	0.79	1.94	0.43	1.15	0.61	3.43	0.37	5.89	0.07	6.20	0.00	7.47	0.02	ATP9	257339_s_at	Mitochondrial F0-ATPase subunit 9	ATMG00040;AT2G07671
AT2G07671	0.99	0.96	1.06	0.88	1.02	0.79	1.94	0.43	1.15	0.61	3.43	0.37	5.89	0.07	6.20	0.00	7.47	0.02		257339_s_at	ATP synthase subunit C family protein	ATMG00040;ATMG01080
AT3G20370	0.99	0.96	1.21	0.30	0.89	0.33	0.12	0.10	0.14	0.06	0.09	0.04	0.35	0.03	0.40	0.01	0.33	0.01		257673_at	TRAF-like family protein	
AT3G18370	1.00	0.99	1.28	0.31	1.12	0.48	1.09	0.58	1.18	0.35	1.12	0.47	3.99	0.01	9.67	0.02	2.27	0.16	SYTF	257734_at	C2 domain-containing protein	
AT3G25230	0.98	0.94	0.88	0.06	0.92	0.74	4.48	0.12	4.76	0.12	2.72	0.02	34.39	0.02	33.16	0.01	31.95	0.03	ROF1	257822_at	Rotamase FKBP 1	
AT3G21190	1.00	0.99	0.92	0.40	0.69	0.34	0.13	0.06	0.16	0.00	0.14	0.07	0.28	0.04	0.41	0.03	0.48	0.02		258040_at	O-fucosyltransferase family protein	
AT3G24500	0.97	0.92	1.39	0.65	0.62	0.16	86.33	0.04	85.07	0.01	35.92	0.01	240.40	0.01	190.96	0.00	184.66	0.03	MBF1C	258133_at	Multiprotein bridging factor 1C	
AT3G15770	1.00	0.99	1.48	0.19	1.04	0.66	8.55	0.10	6.77	0.10	6.52	0.04	7.16	0.07	5.40	0.04	4.70	0.01		258262_at	Unknown protein	
AT3G16050	0.99	0.95	0.86	0.58	1.26	0.65	14.86	0.06	15.43	0.00	6.92	0.05	162.86	0.00	149.22	0.00	147.97	0.03	PDX1.2	258336_at	Pyridoxine biosynthesis 1.2	
AT3G15500	0.95	0.90	0.76	0.56	1.47	0.54	48.82	0.08	38.34	0.08	55.57	0.02	1.71	0.22	0.84	0.47	0.78	0.61	NAC3	258395_at	NAC domain containing protein 3	
AT3G17611	0.97	0.92	0.99	0.97	1.06	0.09	1.85	0.34	2.00	0.18	0.99	0.97	19.55	0.01	19.21	0.01	14.32	0.04	RBL14	258406_at	RHOMBOID-like protein 14	
AT3G06035	1.00	0.98	0.78	0.03	0.52	0.22	0.13	0.11	0.16	0.05	0.15	0.01	0.33	0.01	0.36	0.02	0.37	0.09		258470_at	Glycoprotein membrane precursor GPI-anchored	
AT3G06500	1.00	0.97	1.12	0.00	1.36	0.44	12.95	0.11	9.01	0.06	16.77	0.04	1.75	0.05	0.95	0.28	1.28	0.35	A/N-InvC	258507_at	Plant neutral invertase family protein	
AT3G08720	1.00	0.97	1.10	0.25	1.20	0.52	14.95	0.08	14.61	0.08	22.04	0.00	1.64	0.35	1.97	0.03	2.13	0.06	S6K2	258682_at	Serine/threonine protein kinase 2	
AT3G04710	0.97	0.93	1.14	0.19	1.03	0.89	4.13	0.06	4.52	0.02	2.67	0.01	28.55	0.02	19.05	0.00	17.20	0.01	TPR10	258794_at	Ankyrin repeat family protein	
AT3G04070	0.99	0.97	1.09	0.73	0.84	0.15	8.43	0.08	8.56	0.07	10.38	0.00	0.52	0.20	0.67	0.18	0.90	0.78	NAC047	258809_at	NAC domain containing protein 47	
AT3G03950	0.99	0.96	0.95	0.66	0.84	0.43	1.76	0.11	1.69	0.11	1.52	0.26	4.32	0.05	12.44	0.01	3.01	0.11	ECT1	258812_at	Evolutionarily conserved C-terminal region 1	
AT3G07090	1.00	0.97	0.99	0.83	0.74	0.40	9.43	0.08	9.97	0.07	5.61	0.04	45.97	0.00	37.63	0.01	41.28	0.03		258830_at	PPPDE putative thiol peptidase family protein	
AT3G03270	1.00	0.98	1.24	0.07	0.28	0.04	1.38	0.74	1.99	0.58	0.20	0.06	17.84	0.01	14.77	0.01	4.26	0.03		258879_at	Adenine nucleotide alpha hydrolases-like superfamily protein	
AT3G10525	1.00	0.98	1.09	0.66	0.54	0.04	0.24	0.01	0.29	0.19	0.16	0.03	0.34	0.40	0.65	0.03	0.40	0.17	SMR1	258919_at	LOSS OF GIANT CELLS FROM ORGANS	
AT3G10020	0.98	0.94	1.09	0.11	0.76	0.59	9.00	0.03	10.15	0.01	2.56	0.01	21.08	0.00	18.10	0.01	16.42	0.04		258939_at	Unknown protein	
AT3G09440	1.00	0.98	1.06	0.59	0.94	0.44	15.75	0.03	12.69	0.09	9.01	0.08	56.78	0.02	49.70	0.02	47.36	0.02		258979_at	Heat shock protein 70 (Hsp 70) family protein	
AT3G09350	0.99	0.95	1.17	0.57	1.42	0.25	108.66	0.02	93.26	0.02	76.75	0.00	187.54	0.01	155.87	0.00	165.78	0.02	Fes1A	259037_at	Fes1A	
AT3G07770	1.00	1.00	1.13	0.53	1.00	0.96	1.31	0.23	1.62	0.05	1.40	0.05	10.58	0.03	11.47	0.02	10.64	0.02	HSP89.1	259248_at	Heat shock protein 89.1	
AT1G02400	0.99	0.97	1.08	0.77	1.15	0.17	34.85	0.02	36.81	0.00	37.01	0.02	1.78	0.23	1.91	0.06	3.31	0.06	GA2OX6	259445_at	Gibberellin 2-oxidase 6	
AT1G20450	0.98	0.94	1.10	0.67	0.80	0.66	6.54	0.01	6.91	0.01	6.04	0.02	5.81	0.06	5.23	0.02	3.66	0.01	LTI45	259516_at	Dehydrin family protein	
AT1G20640	1.00	0.98	1.05	0.76	0.75	0.11	1.74	0.14	2.07	0.05	0.76	0.19	8.55	0.00	7.49	0.02	6.40	0.03		259540_at	Plant regulator RWP-RK family protein	
AT1G20440	0.99	0.95	1.14	0.57	0.80	0.65	4.96	0.11	4.87	0.04	5.94	0.05	7.11	0.01	5.74	0.01	4.04	0.01	RD17	259570_at	Cold-regulated 47	
AT1G63180	1.00	0.97	0.80	0.39	1.10	0.52	5.80	0.11	5.95	0.08	8.80	0.03	0.95	0.90	0.99	0.75	1.11	0.71	UGE3	259694_at	UDP-D-glucose/UDP-D-galactose 4-epimerase 3	
AT1G77450	0.98	0.94	1.04	0.92	1.00	1.00	15.40	0.15	14.62	0.11	22.70	0.00	1.31	0.17	1.82	0.04	1.88	0.04	NAC032	259705_at	NAC domain containing protein 32	
AT1G64390	0.99	0.95	0.76	0.16	0.65	0.42	0.17	0.25	0.19	0.20	0.14	0.07	0.13	0.03	0.15	0.04	0.15	0.03	GH9C2	259736_at	Glycosyl hydrolase 9C2	
AT1G29510	0.99	0.95	0.80	0.61	1.05	0.87	1.82	0.12	2.12	0.17	0.15	0.08	0.44	0.10	0.29	0.12	0.57	0.27	SAUR68	259783_at	SAUR-like auxin-responsive protein family	
AT1G29660	1.00	0.98	1.02	0.94	0.76	0.26	0.19	0.11	0.29	0.01	0.16	0.03	0.56	0.19	0.75	0.05	0.62	0.14		259786_at	GDSL-like Lipase/Acylhydrolase superfamily protein	
AT1G29395	0.98	0.93	0.66	0.16	1.42	0.35	5.63	0.21	5.70	0.19	7.42	0.06	1.39	0.76	0.28	0.04	0.32	0.10	COR414-TM1	259789_at	COLD REGULATED 314 INNER MEMBRANE 1	
AT1G76600	0.98	0.93	0.85	0.69	1.94	0.26	25.04	0.01	23.82	0.05	24.22	0.01	2.97	0.18	1.32	0.46	2.88	0.11		259979_at	Unknown protein	

AT1G30070	1.00	0.98	0.96	0.51	1.06	0.61	15.65	0.10	12.33	0.08	5.80	0.00	142.27	0.01	113.05	0.00	130.83	0.01		260025_at	SGS domain-containing protein	
AT1G73190	0.95	0.90	1.52	0.14	0.54	0.02	0.08	0.03	0.13	0.01	0.06	0.08	0.73	0.14	1.67	0.15	1.17	0.42	TIP3;1	260088_at	Aquaporin-like superfamily protein	
AT1G70700	0.99	0.97	0.78	0.06	0.97	0.91	7.11	0.02	7.02	0.02	5.66	0.02	0.67	0.78	1.25	0.10	1.49	0.19	TIFY7	260205_at	TIFY domain/Divergent CCT motif family protein	
AT1G74670	0.99	0.95	0.97	0.36	0.84	0.08	0.10	0.04	0.11	0.05	0.04	0.05	0.76	0.12	0.34	0.13	0.43	0.14	GASA6	260221_at	Gibberellin-regulated family protein	
AT1G74320	1.00	0.99	0.87	0.06	0.86	0.35	2.25	0.13	2.72	0.03	0.94	0.21	9.06	0.03	6.30	0.01	6.60	0.01		260244_at	Protein kinase superfamily protein	
AT1G80480	0.99	0.96	0.99	0.94	0.99	0.98	1.48	0.19	1.57	0.23	1.17	0.50	7.30	0.05	6.93	0.01	3.31	0.07	PTAC17	260283_at	Plastid transcriptionally active 17	
AT1G70590	1.00	0.98	1.10	0.31	1.04	0.86	6.03	0.02	5.93	0.02	6.35	0.03	3.18	0.08	1.93	0.11	2.10	0.02		260310_at	F-box family protein	
AT1G69690	1.00	0.97	0.74	0.31	0.88	0.68	0.21	0.09	0.20	0.18	0.16	0.04	0.49	0.12	0.41	0.11	0.46	0.02	TCP15	260371_at	TCP family transcription factor	
AT1G68140	1.00	0.97	0.85	0.51	0.97	0.86	1.28	0.56	1.46	0.27	1.57	0.06	8.07	0.08	12.15	0.02	4.29	0.08		260436_at	Protein of unknown function (DUF1644)	
AT2G43500	0.99	0.96	1.00	0.97	0.77	0.32	1.37	0.05	1.68	0.23	1.17	0.18	5.80	0.08	9.97	0.04	2.51	0.08		260540_at	Plant regulator RWP-RK family protein	
AT1G78370	1.00	0.98	1.04	0.88	1.15	0.55	0.06	0.29	0.07	0.24	0.05	0.02	0.35	0.39	0.98	0.90	1.41	0.22	GSTU20	260745_at	Glutathione S-transferase TAU 20	
AT1G06760	1.00	1.00	0.95	0.73	1.01	0.67	0.23	0.07	0.26	0.06	0.22	0.01	0.11	0.09	0.18	0.02	0.16	0.04		260830_at	Winged-helix DNA-binding transcription factor family protein	
AT1G21460	0.98	0.93	0.99	0.96	0.38	0.09	0.95	0.92	1.37	0.54	0.43	0.16	2.73	0.25	8.34	0.05	0.65	0.06	SWEET1	260876_at	Nodulin MtN3 family protein	
AT1G02660	0.94	0.89	0.82	0.69	1.45	0.56	8.50	0.10	7.62	0.09	7.94	0.09	1.48	0.25	0.70	0.10	1.31	0.21		260915_at	alpha/beta-Hydrolases superfamily protein	
AT1G45130	1.00	0.99	0.86	0.25	0.91	0.32	0.16	0.02	0.19	0.04	0.11	0.00	1.23	0.28	1.28	0.23	0.89	0.56	BGAL5	260944_at	beta-Galactosidase 5	
AT1G26560	0.96	0.91	1.00	0.99	0.74	0.50	6.20	0.06	6.52	0.08	5.33	0.04	0.46	0.58	1.13	0.15	0.77	0.18	BGLU40	261016_at	beta-Glucosidase 40	
AT1G07350	0.99	0.95	0.95	0.81	1.02	0.43	12.86	0.08	12.75	0.03	8.63	0.00	48.95	0.02	43.22	0.00	37.32	0.02	SR45a	261081_at	RNA-binding (RRM/RBD/RNP motifs) family protein	
AT1G26800	1.00	1.00	0.95	0.17	1.23	0.36	10.17	0.03	10.86	0.02	3.92	0.04	48.05	0.00	40.84	0.01	35.43	0.02		261265_at	RING/U-box superfamily protein	
AT1G14360	0.98	0.93	0.85	0.03	0.89	0.69	1.56	0.09	1.32	0.12	1.30	0.17	13.88	0.03	13.44	0.00	9.90	0.03	UTR3	261485_at	UDP-galactose transporter 3	
AT1G28400	1.00	0.98	0.95	0.54	0.52	0.20	0.07	0.19	0.09	0.12	0.06	0.07	0.13	0.04	0.26	0.02	0.14	0.01		261500_at	Unknown protein	
AT1G71697	0.99	0.95	1.03	0.84	0.69	0.16	3.66	0.10	4.19	0.13	6.14	0.02	1.58	0.11	0.92	0.09	0.95	0.86	CK1	261506_at	Choline kinase 1	
AT1G01720	0.90	0.86	0.85	0.30	0.86	0.44	19.03	0.09	22.52	0.05	16.48	0.03	14.57	0.04	8.63	0.03	13.71	0.04	ATAF1	261564_at	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	
AT1G49750	0.99	0.97	0.84	0.07	0.54	0.12	0.17	0.29	0.21	0.17	0.12	0.06	0.54	0.13	0.65	0.08	0.48	0.10		261598_at	Leucine-rich repeat (LRR) family protein	
AT1G49975	0.99	0.97	0.94	0.20	0.86	0.16	0.29	0.14	0.40	0.00	0.16	0.03	0.29	0.02	0.38	0.08	0.40	0.11		261638_at	Unknown protein	
AT1G27730	0.97	0.92	1.01	0.97	1.58	0.34	27.16	0.01	25.92	0.02	22.09	0.03	19.22	0.01	11.06	0.05	12.96	0.02	ZAT10	261648_at	Salt tolerance zinc finger	
AT1G01940	1.00	0.98	0.98	0.03	1.02	0.70	1.02	0.90	0.85	0.58	0.73	0.36	17.85	0.04	14.16	0.00	8.61	0.03		261655_at	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	
AT1G18330	0.99	0.95	1.08	0.59	1.63	0.12	5.25	0.13	7.80	0.08	1.82	0.18	8.64	0.09	6.21	0.03	7.94	0.00	RVE7	261663_at	Homeodomain-like superfamily protein	
AT1G32640	1.00	0.97	1.16	0.34	0.88	0.11	10.73	0.05	11.59	0.01	11.76	0.03	0.91	0.89	0.49	0.31	0.83	0.01	ZBF1	261713_at	Basic helix-loop-helix (bHLH) DNA-binding family protein	
AT1G30510	0.98	0.94	1.23	0.26	0.82	0.57	0.20	0.28	0.25	0.25	0.15	0.05	0.47	0.06	0.79	0.20	0.76	0.15	RFNR2	261806_at	Root FNR 2	
AT1G16030	1.00	0.99	1.16	0.22	0.98	0.74	26.67	0.03	34.48	0.03	6.63	0.18	340.51	0.00	301.70	0.01	286.78	0.02	HSP70b	261838_at	Heat shock protein 70B	
AT1G80840	0.99	0.97	1.02	0.89	2.09	0.02	15.84	0.05	13.64	0.00	18.01	0.00	1.89	0.14	0.90	0.45	2.87	0.03	WRKY40	261892_at	WRKY DNA-binding protein 40	
AT1G64650	1.00	1.00	0.83	0.04	0.86	0.55	0.16	0.08	0.20	0.11	0.12	0.02	0.48	0.17	0.38	0.05	0.53	0.02		261944_at	Major facilitator superfamily protein	
AT1G64660	0.99	0.96	1.03	0.08	1.15	0.02	6.28	0.18	5.22	0.15	6.55	0.01	0.80	0.34	1.22	0.37	0.76	0.49	MGL	261957_at	Methionine gamma-lyase	
AT1G79920	0.99	0.95	1.14	0.32	1.09	0.66	2.59	0.10	2.89	0.07	1.43	0.33	18.86	0.03	15.85	0.00	13.91	0.01	HSP70-15	262054_s_at	Heat shock protein 70 (Hsp 70) family protein	AT1G79930
AT1G79930	0.99	0.95	1.14	0.32	1.09	0.66	2.59	0.10	2.89	0.07	1.43	0.33	18.86	0.03	15.85	0.00	13.91	0.01	HSP91	262054_s_at	Heat shock protein 91	AT1G79920
AT1G02820	1.00	0.97	1.31	0.17	1.16	0.14	1.08	0.69	0.99	0.83	2.43	0.52	0.71	0.92	6.70	0.07	4.32	0.10		262113_at	Late embryogenesis abundant 3 (LEA3) family protein	
AT1G02900	1.00	0.97	0.99	0.84	0.62	0.01	0.20	0.05	0.18	0.05	0.14	0.03	0.42	0.08	0.45	0.05	0.25	0.04	RALFL1	262131_at	Rapid alkalinization factor 1	
AT1G78070	0.94	0.89	0.93	0.76	0.61	0.21	26.42	0.07	28.64	0.08	27.59	0.05	4.80	0.03	2.18	0.34	3.24	0.01		262164_at	Transducin/WD40 repeat-like superfamily protein	
AT1G74950	0.99	0.96	1.06	0.56	0.98	0.75	16.17	0.01	15.20	0.01	16.21	0.01	1.00	0.99	0.89	0.20	0.92	0.29	TIFY10B	262171_at	TIFY domain/Divergent CCT motif family protein	
AT1G74680	0.99	0.96	0.82	0.21	0.97	0.94	0.59	0.15	0.62	0.22	0.59	0.09	0.33	0.19	0.23	0.00	0.16	0.07		262223_at	Exostosin family protein	
AT1G68585	1.00	0.97	1.22	0.18	0.62	0.22	0.79	0.58	0.89	0.41	0.70	0.32	4.50	0.13	6.58	0.00	3.86	0.06		262286_at	Unknown protein	
AT1G73080	1.00	1.00	0.84	0.44	1.01	0.91	8.76	0.04	6.89	0.03	9.51	0.02	0.81	0.30	1.10	0.47	0.95	0.55	PEPR1	262360_at	PEP1 receptor 1	
AT1G11320	1.00	0.98	0.99	0.82	1.04	0.80	0.83	0.42	0.70	0.46	0.71	0.10	5.83	0.00	6.74	0.03	2.77	0.03		262450_at	Unknown protein	
AT1G21680	0.97	0.93	0.89	0.51	1.67	0.32	9.00	0.06	8.39	0.02	11.61	0.02	2.83	0.39	1.03	0.85	1.22	0.11		262505_at	DPP6 N-terminal domain-like protein	
AT1G31335	0.99	0.95	1.09	0.41	1.06	0.77	0.56	0.28	0.64	0.24	0.44	0.20	9.91	0.09	13.14	0.00	4.64	0.00		262558_at	Unknown protein	
AT1G15410	1.00	0.97	0.99	0.95	0.71	0.13	0.51	0.12	0.68	0.33	0.30	0.09	5.79	0.11	7.29	0.01	2.16	0.07		262582_at	Aspartate-glutamate racemase family	
AT1G15260	0.99	0.96	1.02	0.92	0.94	0.52	0.11	0.07	0.12	0.03	0.12	0.03	0.31	0.07	0.24	0.04	0.28	0.03		262598_at	Unknown protein	
AT1G13990	0.99	0.97	1.16	0.46	1.20	0.68	4.43	0.16	3.75	0.05	6.01	0.01	2.31	0.26	1.45	0.16	1.10	0.21		262607_at	Unknown protein	
AT1G06620	1.00	1.00	1.13	0.19	1.14	0.59	11.81	0.03	14.60	0.05	14.36	0.01	1.17	0.58	1.05	0.56	1.59	0.17		262616_at	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	
AT1G06570	0.99	0.96	0.89	0.23	1.47	0.29	4.97	0.22	4.03	0.18	8.92	0.03	1.01	0.93	0.79	0.05	1.12	0.51	PDS1	262635_at	Phytoene desaturation 1	
AT1G75860	1.00	0.98	0.90	0.66	1.09	0.41	1.74	0.13	2.08	0.29	1.43	0.34	11.42	0.01	6.23	0.04	8.21	0.01		262677_at	Unknown protein	
AT1G62740	0.99	0.97	1.02	0.66	0.91	0.73	4.05	0.12	4.08	0.09	2.13	0.03	12.64	0.01	12.19	0.02	10.08	0.00	HOP2	262691_at	Stress-inducible protein, putative	
AT1G75820	1.00	0.99	0.82	0.48	0.73	0.21	0.38	0.25	0.44	0.28	0.28	0.15	0.22	0.21	0.24	0.03	0.14	0.05	FLO5	262728_at	Leucine-rich receptor-like protein kinase family protein	
AT1G16370	0.99	0.96	1.18	0.48	1.59	0.28	7.50	0.02	8.42	0.03	8.14	0.06	0.87	0.55	0.56	0.26	0.71	0.18	OCT_6	262756_at	Organic cation/carnitine transporter 6	
AT1G11660	1.00	0.98	1.04	0.55	0.84	0.18	0.93	0.85	1.17	0.63	0.84	0.37	8.75	0.08	20.24	0.00	4.82	0.09		262814_at	Heat shock protein 70 (Hsp 70) family protein	
AT1G14780	1.00	0.98	1.35	0.25	0.87	0.50	8.87	0.05	11.13	0.05	9.43	0.00	2.05	0.21	1.51	0.31	1.48	0.10		262887_at	MAC/Perforin domain-containing protein	
AT1G23330	1.00	0.98	1.02	0.88	0.63	0.23	0.67	0.02	0.73	0.07	0.62	0.12	2.17	0.26	6.69	0.03	1.24	0.22		263010_at	Alpha/Beta-Hydrolases superfamily protein	
AT1G54050	1.00	1.00	0.98	0.78	1.32	0.31	71.51	0.00	71.52	0.00	36.53	0.03	195.21	0.00	156.21	0.00	151.22	0.02	HSP17.4	263150_at	HSP20-like chaperones superfamily protein	
AT1G54010	1.00	0.98	1.25	0.52	0.76	0.64	0.13	0.22	0.12	0.05	0.14	0.04	0.31	0.14	0.46	0.11	0.44	0.04		263153_s_at	GDSL-like Lipase/Acylhydrolase superfamily protein	AT1G54000
AT1G54000	1.00	0.98	1.25	0.52	0.76	0.64	0.13	0.22	0.12	0.05	0.14	0.04	0.31	0.14	0.46	0.11	0.44	0.04	GLL22	263153_s_at	GDSL-like Lipase/Acylhydrolase superfamily protein	AT1G54010
AT1G54100	1.00	0.99	0.90	0.19	1.29	0.44	3.87	0.17	3.58	0.10	6.28	0.02	1.00	0.99	0.81	0.25	0.77	0.38	ALDH7B4	263157_at	Aldehyde dehydrogenase 7B4	
AT1G03070	0.96	0.91	1.12	0.58	1.09	0.73	3.70	0.25	6.19	0.10	0.85	0.77	168.09	0.03	180.81	0.02	119.03	0.01		263164_at	Bax inhibitor-1 family protein	
AT1G05575	1.00	0.98	1.15	0.40	1.09	0.72	8.75	0.04	9.42	0.08	6.29	0.00	4.67	0.11	3.46	0.07	3.61	0.01		263182_at	Unknown protein	
AT2G38820	1.00	0.99	0.99	0.96	1.81	0.18	6.46	0.17	6.57	0.04	6.06	0.05	1.72	0.19	2.46	0.06	2.23	0.04		263265_at	Protein of unknown function (DUF506)	
AT2G47180	0.99	0.95	1.32	0.30	0.54	0.18	5.21	0.18	6.87	0.00	1.82	0.17	34.01	0.00	29.85	0.00	26.19	0.04	GOLS1	263320_at	Galactinol synthase 1	
AT2G40140	0.99	0.96	0.91	0.37	1.04	0.85	4.83	0.14	4.90	0.09	7.28	0.07	2.34	0.23	1.84	0.05	2.58	0.03	ZFAR1	263379_at	Zinc finger (CCCH-type) family protein	
AT2G22230	1.00	0.98	0.77	0.12	1.07	0.65	0.17	0.18	0.19	0.09	0.16	0.03	0.71	0.28	0.79	0.08	1.16	0.27		263432_at	Thioesterase superfamily protein	
AT2G22240	1.00	0.99	1.23	0.07	0.35	0.13	1.47	0.70	2.63	0.32	0.79	0.10	15.20	0.04	18.43	0.00	9.33	0.00	MIPS2	263433_at	Myo-inositol-1-phosphate synthase 2	
AT2G31945	1.00	0.98	0.94	0.43	0.99	0.95	9.61	0.29	8.74	0.18	19.02	0.05	1.26	0.43	1.30	0.13	1.07	0.93		263475_at	Unknown protein	
AT2G42540	0.85	0.83	1.17	0.80	0.67	0.51	16.09	0.26	21.45	0.20	40.84	0.06	1.83	0.25	1.97	0.25	0.63	0.10	COR15A	263497_at	Cold-regulated 15a	
AT2G07675	0.97	0.92	1.74	0.42	1.29	0.70	1.78	0.40	1.26	0.31	2.69	0.26	12.03	0.00	14.75	0.05	17.03	0.02		263502_s_at	Ribosomal protein S12/S23 family protein	ATMG00980
ATMG00980	0.97	0.92	1.74	0.42	1.29	0.70	1.78	0.40	1.26	0.31	2.69	0.26	12.03	0.00	14.75	0.05	17.03	0.02	RPSL2	263502_s_at	Ribosomal protein L2	AT2G07675
ATMG00730	0.98	0.94	1.14	0.66	1.59	0.14	2.55	0.12	2.66	0.15	3.77	0.28	11.60	0.03	13.05	0.03	15.76	0.04	COX3	263509_s_at	Cytochrome c oxidase subunit 3	AT2G07687
AT2G07687	0.98	0.94	1.14	0.66	1.59	0.14	2.55	0.12	2.66	0.15	3.77	0.28	11.60	0.03	13.05	0.03	15.76	0.04		263509_s_at	Cytochrome c oxidase, subunit III	ATMG00730
AT2G04780	1.00	0.98	0.97	0.61	0.97	0.84	0.15	0.08	0.15	0.03	0.13	0.02	0.43	0.07	0.47	0.03	0.49	0.08	FLA7	263628_at	FASCICLIN-like arabinoogalactan 7	
AT2G21940	1.00	1.00	1.03	0.90	0.80	0.06	2.07	0.30	2.16	0.20	1.02	0.68	9.69	0.04	10.80	0.03	6.50	0.07	SK1	263897_at	Shikimate kinase 1	
AT2G36460	1.00	0.98	1.04	0.72	1.05	0.06	2.49	0.01	2.46	0.10	0.95	0.46	15.65	0.06	14.85	0.02	10.81	0.00		263921_at	Aldolase superfamily protein	
AT2G35930	0.99	0.96	0.92	0.81	0.81	0.02	8.22	0.03	10.72	0.03	8.17	0.01	1.40	0.67	1.17	0.25	1.63	0.28	PUB23	263935_at	Plant U-box 23	
AT2G35860	1.00	0.98	0.89	0.73	0.70	0.20	0.14	0.12	0.24	0.17	0.15	0.01	0.40	0.15	0.40	0.07	0.34	0.02	FLA16	263942_at	FASCICLIN-like arabinogalactan protein 16 precursor	
AT1G79160	0.98	0.94	1.16	0.07	1.12	0.56	5.48	0.07	4.39	0.14	6.10	0.05	1.21	0.59	0.81	0.14	1.38	0.25		264130_at	Unknown protein	
AT1G02090	1.00	0.98	1.06	0.36	1.25	0.29	1.54	0.13	1.39	0.09	1.04	0.50	11.03	0.03	6.78	0.04	5.67	0.00	FUS5	264150_at	Proteasome component (PCI) domain protein	
AT1G60190	0.92	0.88	1.06	0.42	0.70	0.57	32.74	0.11	45.82	0.04	22.10	0.03	2.53	0.27	5.06	0.00	1.50	0.11	PUB19	264217_at	ARM repeat superfamily protein	
AT1G60140	0.99	0.96	1.11	0.03	1.91	0.17	5.79	0.10	6.01	0.01	7.15	0.05	0.81	0.74	0.70	0.00	0.75	0.38	TPS10	264246_at	Trehalose phosphate synthase	
AT1G61890	1.00	0.99	0.98	0.91	1.04	0.81	13.30	0.01	12.06	0.01	13.12	0.02	1.78	0.54	1.52	0.05	1.89	0.07		264289_at	MATE efflux family protein	
AT1G04130	0.99	0.97	0.88	0.50	0.85	0.32	1.55	0.01	1.87	0.01	1.11	0.28	10.15	0.02	12.32	0.02	8.41	0.04	TPR2	264331_at	Tetratricopeptide repeat (TPR)-like superfamily protein	
AT1G12090	0.99	0.95	0.94	0.77	0.98	0.91	0.11	0.14	0.10	0.03	0.05	0.00	0.76	0.21	0.28	0.04	0.29	0.02	ELP	264371_at	Extensin-like protein	

AT1G11960	0.98	0.93	0.87	0.51	1.10	0.69	10.24	0.06	11.15	0.03	9.81	0.02	3.82	0.09	1.72	0.11	2.54	0.22		264389_at	ERD (early-responsive to dehydration stress) family protein	
AT1G10170	1.00	0.97	0.87	0.14	0.88	0.54	2.95	0.09	2.98	0.05	2.38	0.04	9.01	0.13	6.03	0.09	6.90	0.01	NFXL1	264460_at	NF-X-like 1	
AT1G10230	1.00	0.97	1.14	0.06	1.29	0.09	1.71	0.08	1.63	0.03	1.45	0.05	8.08	0.01	8.61	0.02	7.14	0.01	SK18	264465_at	SKP1-like 18	
AT1G30820	1.00	0.98	0.93	0.19	1.82	0.26	5.33	0.09	6.50	0.06	6.45	0.03	0.60	0.41	0.67	0.30	0.84	0.15		264529_at	CTP synthase family protein	
AT1G05260	1.00	0.99	1.02	0.78	0.84	0.72	0.15	0.13	0.19	0.10	0.15	0.02	0.82	0.62	0.49	0.19	0.91	0.13	RCI3A	264577_at	Peroxidase superfamily protein	
AT1G05340	1.00	0.99	1.28	0.14	0.73	0.50	12.75	0.20	8.14	0.20	13.39	0.13	3.78	0.04	6.44	0.02	2.32	0.08		264580_at	Unknown protein	
AT1G09750	1.00	0.99	0.89	0.27	1.20	0.08	0.14	0.18	0.17	0.02	0.12	0.03	0.36	0.22	0.40	0.14	0.59	0.07		264672_at	Eukaryotic aspartyl protease family protein	
AT1G22985	1.00	0.97	0.85	0.04	0.74	0.20	2.74	0.10	2.60	0.00	1.94	0.05	18.27	0.01	13.02	0.02	10.79	0.04	CRF7	264726_at	Integrase-type DNA-binding superfamily protein	
AT2G17840	1.00	0.99	0.86	0.62	0.67	0.44	19.23	0.03	22.70	0.01	20.85	0.02	2.60	0.13	0.86	0.05	1.24	0.26	ERD7	264787_at	Senescence/dehydration-associated protein-related	
AT2G17900	1.00	0.98	1.04	0.52	1.08	0.48	2.06	0.21	1.60	0.25	1.68	0.10	13.75	0.02	11.27	0.05	9.54	0.09	SDG37	264814_at	SET domain group 37	
AT1G23180	1.00	0.98	1.17	0.21	1.21	0.25	1.59	0.02	1.51	0.13	0.90	0.74	12.41	0.03	14.31	0.01	8.12	0.01		264890_at	ARM repeat superfamily protein	
AT1G60660	1.00	1.00	0.90	0.47	0.85	0.33	0.15	0.19	0.19	0.12	0.15	0.01	0.31	0.08	0.36	0.04	0.46	0.01	CB5LP	264926_at	cytochrome B5-like protein	
AT1G77120	1.00	0.99	0.96	0.37	0.28	0.04	5.78	0.00	6.45	0.01	4.43	0.16	1.58	0.26	2.50	0.04	0.68	0.26	ADH1	264953_at	alcohol dehydrogenase 1	
AT1G77000	0.99	0.95	1.01	0.80	1.21	0.48	4.54	0.23	4.33	0.10	5.22	0.03	10.42	0.02	9.49	0.01	7.76	0.02	SKP2B	264957_at	RNI-like superfamily protein	
AT1G67360	0.99	0.95	1.56	0.27	0.54	0.03	4.29	0.28	11.14	0.12	0.42	0.09	75.03	0.01	68.90	0.00	49.41	0.02		264968_at	Rubber elongation factor protein (REF)	
AT1G03870	0.92	0.87	0.87	0.75	0.86	0.58	0.13	0.06	0.14	0.11	0.05	0.06	0.66	0.51	0.45	0.06	0.69	0.18	FLA9	265066_at	FASCICLIN-like arabinoogalactan 9	
AT1G55530	0.97	0.93	0.85	0.33	0.92	0.51	4.89	0.19	6.16	0.07	2.82	0.08	14.58	0.06	13.00	0.01	13.13	0.03		265077_at	RING/U-box superfamily protein	
AT1G23710	1.00	0.97	1.24	0.13	1.01	0.75	13.30	0.04	14.38	0.10	16.73	0.04	2.60	0.16	1.85	0.14	2.91	0.06		265184_at	Protein of unknown function (DUF1645)	
AT2G07698	1.00	0.97	0.95	0.53	1.54	0.02	3.34	0.18	3.07	0.23	5.87	0.23	14.24	0.00	13.92	0.03	13.97	0.00		265228_s_at	ATPase, F1 complex, alpha subunit protein	ATMG01190
ATMG01190	1.00	0.97	0.95	0.53	1.54	0.02	3.34	0.18	3.07	0.23	5.87	0.23	14.24	0.00	13.92	0.03	13.97	0.00	ATP1	265228_s_at	ATP synthase subunit 1	AT2G07698
AT2G18370	0.98	0.94	1.06	0.70	0.40	0.09	0.23	0.10	0.19	0.12	0.10	0.09	0.44	0.03	0.56	0.14	0.28	0.03		265334_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	
AT2G05790	1.00	0.97	0.90	0.16	1.11	0.66	0.17	0.16	0.20	0.09	0.13	0.07	0.49	0.14	0.51	0.04	0.54	0.05		265377_at	O-Glycosyl hydrolases family 17 protein	
AT2G46510	0.94	0.89	0.73	0.50	0.79	0.07	10.38	0.02	11.20	0.02	11.76	0.08	0.60	0.41	0.69	0.17	0.95	0.79	AIB	265452_at	ABA-inducible BHLH-type transcription factor	
AT2G06050	0.96	0.91	0.87	0.17	0.83	0.13	5.47	0.17	5.37	0.11	6.39	0.08	0.75	0.61	3.01	0.05	1.64	0.04	OPR3	265530_at	Oxophytodienoate-reductase 3	
AT2G32120	0.99	0.97	0.99	0.95	0.87	0.17	12.06	0.11	10.86	0.03	2.93	0.14	126.82	0.01	104.49	0.01	96.54	0.03	HSP70T-2	265675_at	Heat-shock protein 70T-2	
AT2G32150	0.99	0.96	0.86	0.18	1.52	0.33	5.64	0.04	4.40	0.03	6.53	0.00	2.25	0.27	0.91	0.60	1.36	0.17		265680_at	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	
AT2G32100	0.95	0.90	0.94	0.80	0.66	0.24	0.11	0.17	0.12	0.09	0.06	0.05	0.12	0.22	0.19	0.02	0.19	0.16	OFP16	265724_at	Ovate family protein 16	
AT2G24100	0.97	0.93	1.05	0.55	0.80	0.45	9.71	0.09	13.09	0.06	5.94	0.12	15.03	0.00	10.87	0.02	12.10	0.03	ASG1	265999_at	Unknown protein	
AT2G07699	0.97	0.92	1.17	0.61	1.62	0.30	1.15	0.79	1.12	0.76	2.40	0.45	20.45	0.00	24.12	0.02	23.72	0.01		266012_s_at	Pseudogene, similar to ATPase subunit 6	ATMG00410;AT2G07741;ATMG01170
ATMG00410	0.97	0.92	1.17	0.61	1.62	0.30	1.15	0.79	1.12	0.76	2.40	0.45	20.45	0.00	24.12	0.02	23.72	0.01	ATP6-1	266012_s_at	ATPase subunit 6-1	AT2G07699;AT2G07741;ATMG01170
AT2G07741	0.97	0.92	1.17	0.61	1.62	0.30	1.15	0.79	1.12	0.76	2.40	0.45	20.45	0.00	24.12	0.02	23.72	0.01		266012_s_at	ATPase, F0 complex, subunit A protein	AT2G07699;ATMG00410;ATMG01170
ATMG01170	0.97	0.92	1.17	0.61	1.62	0.30	1.15	0.79	1.12	0.76	2.40	0.45	20.45	0.00	24.12	0.02	23.72	0.01	ATP6-2	266012_s_at	ATPase, F0 complex, subunit A protein	AT2G07699;ATMG00410;AT2G07741
ATMG00220	0.99	0.95	1.29	0.25	0.87	0.23	3.45	0.12	2.99	0.17	5.96	0.25	9.02	0.04	10.23	0.01	9.80	0.02	COB	266045_s_at	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	AT2G07727
AT2G07727	0.99	0.95	1.29	0.25	0.87	0.23	3.45	0.12	2.99	0.17	5.96	0.25	9.02	0.04	10.23	0.01	9.80	0.02		266045_s_at	Di-haem cytochrome, transmembrane;Cytochrome b/b6, C-terminal	ATMG00220
AT2G28120	0.96	0.92	0.86	0.59	1.92	0.27	4.99	0.22	3.06	0.16	8.94	0.04	1.08	0.77	0.52	0.29	1.13	0.45		266140_at	Major facilitator superfamily protein	
AT2G38870	0.99	0.96	1.30	0.36	1.23	0.63	4.49	0.02	4.83	0.01	7.85	0.02	1.15	0.68	1.80	0.06	2.07	0.01		266168_at	Serine protease inhibitor, potato inhibitor I-type family protein	
AT2G27830	1.00	0.98	0.94	0.28	1.32	0.34	10.99	0.14	8.31	0.13	11.63	0.03	2.16	0.19	0.77	0.49	1.56	0.20		266259_at	Unknown protein	
AT2G27580	1.00	0.97	1.46	0.18	1.33	0.38	2.28	0.20	2.53	0.13	1.08	0.51	11.17	0.02	10.06	0.01	9.16	0.00		266261_at	A20/AN1-like zinc finger family protein	
AT2G29340	1.00	0.98	1.02	0.77	1.70	0.01	2.93	0.13	3.10	0.07	6.46	0.03	1.37	0.62	1.30	0.06	2.44	0.10		266265_at	NAD-dependent epimerase/dehydratase family protein	
AT2G29500	0.92	0.87	2.25	0.23	0.58	0.47	15.64	0.00	19.44	0.00	3.34	0.20	134.48	0.00	120.65	0.00	104.98	0.03	HSP17.6B	266294_at	HSP20-like chaperones superfamily protein	
AT2G29450	1.00	0.99	1.04	0.91	0.92	0.84	11.33	0.03	11.83	0.05	7.45	0.04	19.18	0.05	15.07	0.02	13.86	0.04	GSTU5	266299_at	Glutathione S-transferase tau 5	
AT2G27080	1.00	0.98	0.96	0.82	0.96	0.34	8.66	0.05	11.58	0.02	9.50	0.01	6.21	0.06	2.09	0.15	8.19	0.02		266316_at	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	
AT2G46690	0.99	0.96	0.96	0.49	0.78	0.07	0.73	0.36	0.75	0.31	0.55	0.27	0.17	0.02	0.22	0.05	0.11	0.06		266322_at	SAUR-like auxin-responsive protein family	
AT2G47730	1.00	0.99	0.94	0.66	1.28	0.04	4.36	0.11	4.19	0.04	3.43	0.08	8.09	0.02	6.65	0.01	6.21	0.04	GSTF8	266461_at	Glutathione S-transferase phi 8	
AT2G47780	0.96	0.91	1.11	0.28	1.76	0.06	3.56	0.46	5.32	0.27	9.02	0.07	0.92	0.64	2.22	0.14	1.94	0.05		266503_at	Rubber elongation factor protein (REF)	
AT2G46270	0.97	0.93	0.82	0.70	0.86	0.71	6.72	0.23	7.75	0.19	9.21	0.02	1.00	0.99	1.27	0.20	1.08	0.03	GBF3	266555_at	G-box binding factor 3	
AT2G14890	1.00	0.98	0.70	0.20	1.08	0.02	0.18	0.13	0.18	0.02	0.14	0.02	0.62	0.19	0.69	0.08	0.81	0.03	AGP9	266588_at	Arabinogalactan protein 9	
AT2G28950	0.99	0.97	0.88	0.16	0.89	0.39	0.13	0.14	0.12	0.11	0.12	0.02	0.23	0.08	0.37	0.09	0.45	0.06	EXPA6	266790_at	Expansin A6	
AT2G30010	0.96	0.91	1.23	0.59	0.51	0.07	0.14	0.15	0.14	0.07	0.07	0.04	0.37	0.37	0.36	0.04	0.27	0.11	TBL45	266805_at	Trichome birefringence-like 45	
AT2G30000	1.00	0.99	0.91	0.39	1.12	0.11	1.73	0.11	1.23	0.38	1.23	0.52	16.15	0.02	18.46	0.01	10.18	0.01		266806_at	PHF5-like protein	
AT2G30040	1.00	0.98	1.13	0.71	1.01	0.96	26.05	0.03	27.95	0.04	21.89	0.02	1.14	0.71	1.66	0.09	0.74	0.60	MAPKKK14	266832_at	Mitogen-activated protein kinase kinase kinase 14	
AT2G26140	0.99	0.97	0.92	0.52	0.96	0.78	0.86	0.65	0.90	0.08	0.77	0.31	5.92	0.08	7.14	0.01	5.71	0.02	FTSH4	266842_at	FTSH protease 4	
AT2G45920	1.00	1.00	1.11	0.35	1.21	0.07	5.49	0.07	5.21	0.02	7.39	0.00	0.97	0.26	0.79	0.21	0.95	0.72		266910_at	U-box domain-containing protein	
AT2G34490	0.98	0.94	1.21	0.51	0.69	0.14	0.08	0.20	0.10	0.11	0.11	0.04	0.37	0.24	0.74	0.17	0.68	0.17	CYP710A2	266996_at	Cytochrome P450, family 710, subfamily A, polypeptide 2	
AT2G38470	0.99	0.95	1.46	0.01	1.28	0.01	8.53	0.02	8.57	0.03	11.06	0.05	2.98	0.10	1.57	0.04	2.56	0.18	WRKY33	267028_at	WRKY DNA-binding protein 33	
AT2G38380	0.99	0.96	1.34	0.39	0.44	0.37	0.31	0.11	0.33	0.14	0.15	0.03	0.82	0.59	0.53	0.28	0.35	0.01		267053_s_at	Peroxidase superfamily protein	AT2G38390
AT2G38390	0.99	0.96	1.34	0.39	0.44	0.37	0.31	0.11	0.33	0.14	0.15	0.03	0.82	0.59	0.53	0.28	0.35	0.01		267053_s_at	Peroxidase superfamily protein	AT2G38380
AT2G38360	1.00	1.00	1.03	0.84	0.58	0.43	0.22	0.10	0.27	0.23	0.16	0.04	0.91	0.74	0.81	0.52	0.79	0.43	PRA1.B4	267055_at	Prenylated RAB acceptor 1.B4	
AT2G41160	1.00	1.00	1.03	0.56	0.92	0.08	3.36	0.16	3.08	0.17	2.24	0.13	13.78	0.04	11.61	0.01	10.08	0.04		267073_at	Ubiquitin-associated (UBA) protein	
AT2G41190	0.99	0.95	2.02	0.18	0.94	0.55	2.39	0.58	4.50	0.37	1.92	0.09	3.62	0.15	10.19	0.02	1.56	0.35		267080_at	Transmembrane amino acid transporter family protein	
AT2G30250	0.95	0.90	1.11	0.76	0.95	0.90	7.86	0.10	7.70	0.07	7.47	0.04	1.79	0.17	1.25	0.51	1.15	0.73	WRKY25	267246_at	WRKY DNA-binding protein 25	
AT2G19310	0.99	0.95	1.98	0.13	0.83	0.30	9.58	0.08	9.98	0.05	4.16	0.06	56.67	0.00	44.68	0.01	41.74	0.02	HSP18.5	267336_at	HSP20-like chaperones superfamily protein	
AT2G39980	1.00	0.98	1.15	0.62	1.59	0.36	11.12	0.10	10.41	0.04	11.80	0.07	3.16	0.17	1.11	0.79	1.83	0.32		267337_at	HXXXD-type acyl-transferase family protein	
AT2G40000	0.96	0.91	0.84	0.73	1.66	0.20	11.59	0.02	10.47	0.04	13.13	0.05	5.44	0.14	2.76	0.07	4.37	0.02	HSPRO2	267357_at	Ortholog of sugar beet HS1 PRO-1 2	
AT2G02710	0.98	0.94	0.83	0.18	1.42	0.46	5.49	0.10	4.77	0.04	6.46	0.05	1.08	0.60	0.71	0.08	0.68	0.27	PLPC	267477_at	PAS/LOV protein B	
AT2G30540	0.99	0.95	0.90	0.20	1.86	0.13	4.01	0.03	3.26	0.02	8.23	0.08	0.69	0.40	0.72	0.09	5.16	0.04		267497_at	Thioredoxin superfamily protein	

Supplemental Table S3. Enriched GO terms in differential expression genes (DEGs) expression changed more than 6 fold in transgenic plants harboring HSFA6B-OE and HSFA6b-RD under Salr or HS treatment. Enriched GO terms were identified using BiNGO and GO_full annotation (Maere et al. , 2005). Significantly overepresented terms with a *p* -value less than 5.00E-04 following a Benjamini and Hochberg false discovery rate correction are shown. BP, biological process. CC, cellular component. MF, moleculare function.

(A) Transgenic plants harboring HSFA6b-OE in SALT condition

GO ID	GO Type	GO description	corrected p-value
6950	BP	response to stress	1.17E-19
42221	BP	response to chemical stimulus	1.88E-17
50896	BP	response to stimulus	1.28E-16
9266	BP	response to temperature stimulus	2.57E-15
9408	BP	response to heat	2.16E-14
9628	BP	response to abiotic stimulus	1.21E-13
9414	BP	response to water deprivation	5.69E-11
9415	BP	response to water	8.48E-11
10033	BP	response to organic substance	7.78E-09
6979	BP	response to oxidative stress	1.96E-08
9644	BP	response to high light intensity	2.04E-08
9611	BP	response to wounding	1.63E-07
6970	BP	response to osmotic stress	2.44E-07
302	BP	response to reactive oxygen species	2.89E-07
42542	BP	response to hydrogene peroxide	5.58E-07
9642	BP	response to light intensity	7.09E-07
9719	BP	response to endogenous substance	1.24E-06
10035	BP	response to inorganic substance	5.71E-06
10200	BP	response to chitin	6.39E-06
9651	BP	response to salt stress	6.43E-06
9743	BP	response to carbohydrate stimulus	1.63E-05
9416	BP	response to light stimulus	5.76E-05
9753	BP	response to jasmonic acid stimulus	5.76E-05
9314	BP	response to radiation	7.40E-05
71495	BP	cellular response to endogenous stimulus	2.01E-04
9737	BP	response to abscisic acid stimulus	3.17E-04
9867	BP	jasmonic acid mediated signaling pathway	3.76E-04
71395	BP	cellular response to jasmonic acid stimulus	3.76E-04
16563	MF	transcription activator activity	3.87E-04

(B) Transgenic plants harboring HSFA6b-RD in SALT condition

GO ID	GO Type	GO description	corrected p-value
9414	BP	response to water deprivation	3.69E-18
6950	BP	response to stress	3.69E-18
9415	BP	response to water	3.69E-18
9266	BP	response to temperature stimulus	1.31E-16
42221	BP	response to chemical stimulus	2.01E-16
50896	BP	response to stimulus	7.49E-14
10033	BP	response to organic substance	1.34E-13
9628	BP	response to abiotic stimulus	1.78E-13
9409	BP	response to cold	3.99E-13
9737	BP	response to abscisic acid stimulus	3.61E-12
9719	BP	response to endogenous substance	2.03E-10
6970	BP	response to osmotic stress	1.60E-08
9725	BP	response to hormone stimulus	1.98E-08
10200	BP	response to chitin	3.46E-08
9408	BP	response to heat	3.84E-07
9611	BP	response to wounding	4.22E-07
9743	BP	response to carbohydrate stimulus	7.74E-07
9269	BP	response to desiccation	1.07E-05
9631	BP	cold acclimation	2.37E-05
9651	BP	response to salt stress	4.12E-05

(C) Transgenic plants harboring HSFA6b-OE in HS condition

GO ID	GO Type	GO description	corrected p-value
9408	BP	response to heat	1.99E-28
9266	BP	response to temperature stimulus	8.84E-24
6457	BP	protein folding	1.18E-13
9628	BP	response to abiotic stimulus	4.64E-13
9644	BP	response to high light intensity	5.85E-12
42542	BP	response to hydrogene peroxide	1.67E-10
6950	BP	response to stress	2.74E-10
10035	BP	response to inorganic substance	5.93E-10
9642	BP	response to light intensity	1.05E-09
302	BP	response to reactive oxygen species	7.05E-09
50896	BP	response to stimulus	1.04E-07
6979	BP	response to oxidative stress	1.05E-07
42221	BP	response to chemical stimulus	4.17E-07
6119	BP	oxidative phosphorylation	3.06E-05
10286	BP	heat acclimation	7.82E-05
9416	BP	response to light stimulus	8.80E-05
6091	BP	generation of precursor metabolites and energy	8.80E-05
9314	BP	response to radiation	1.09E-04
22904	BP	respiratory electron transport chain	3.55E-04
5618	CC	cell wall	8.93E-05
30312	CC	external encapsulating structure	9.30E-05
30554	MF	adenyl nucleotide binding	1.24E-04
1883	MF	purine nucleotide binding	1.24E-04
1882	MF	nucleotide binding	1.25E-04
5524	MF	ATP binding	1.52E-04
32559	MF	adenyl ribonucleotide binding	1.52E-04

(D) Transgenic plants harboring HSFA6b-RD in HS condition

GO ID	GO Type	GO description	corrected p-value
9408	BP	response to heat	5.29E-28
9266	BP	response to temperature stimulus	1.28E-20
42542	BP	response to hydrogene peroxide	3.32E-13
9644	BP	response to high light intensity	4.23E-13
9628	BP	response to abiotic stimulus	1.76E-12
9642	BP	response to light intensity	2.20E-12
6950	BP	response to stress	4.67E-12
302	BP	response to reactive oxygen species	1.55E-11
10035	BP	response to inorganic substance	4.10E-11
6457	BP	protein folding	1.83E-09
6979	BP	response to oxidative stress	3.56E-09
50896	BP	response to stimulus	3.59E-09
42221	BP	response to chemical stimulus	3.83E-08
6119	BP	oxidative phosphorylation	5.60E-06
6091	BP	generation of precursor metabolites and energy	9.30E-06
10286	BP	heat acclimation	2.24E-05
9416	BP	response to light stimulus	2.63E-05
9314	BP	response to radiation	3.56E-05
22904	BP	respiratory electron transport chain	1.50E-04
15980	BP	energy derivation by oxidation of organic compounds	1.71E-04
45333	BP	cellular respiration	1.71E-04

Supplementrary TableS4. The top 39 DEGs with levels changed > 30-fold at *p* < 0.05 in HSFA6b mutants OE5-6 and RD3-5 after 150 mM NaCl for 6 h or 37°C HS for 1 h treatment as compared with the Col control (CK) treatment.

Treatment	**CK**		**CK**		**CK**		**SALT**		**SALT**		**SALT**		**HS**		**HS**		**HS**				
line	**WT**		**AtHSFA6b-OE**		**AtHSFA6b-RD**		**WT**		**AtHSFA6b-OE**		**AtHSFA6b-RD**		**WT**		**AtHSFA6b-OE**		**AtHSFA6b-RD**				
Locus Identifier	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Normalized**	***p* -value**	**Symbol**	**Array Element**	**Gene Function**
AT2G19310	0.99	0.95	1.98	0.13	0.83	0.30	9.58	0.08	9.98	0.05	4.16	0.06	56.67	0.00	44.68	0.01	41.74	0.02	HSP18.5	267336_at	HSP20-like chaperones superfamily protein
AT5G25450	1.00	0.97	1.83	0.03	1.09	0.41	12.33	0.07	12.46	0.02	5.45	0.05	98.55	0.00	74.69	0.01	78.50	0.03		246944_at	Cytochrome bd ubiquinol oxidase, 14kDa subunit
AT2G29500	0.92	0.87	2.25	0.23	0.58	0.47	15.64	0.00	19.44	0.00	3.34	0.20	134.48	0.00	120.65	0.00	104.98	0.03	HSP17.6B	266294_at	HSP20-like chaperones superfamily protein
AT2G47180	0.99	0.95	1.32	0.30	0.54	0.18	5.21	0.18	6.87	0.00	1.82	0.17	34.01	0.00	29.85	0.00	26.19	0.04	GOLS1	263320_at	Galactinol synthase 1
AT4G36990	0.97	0.92	1.60	0.20	0.52	0.14	5.36	0.06	8.94	0.06	3.44	0.00	77.52	0.01	74.90	0.01	57.55	0.01	HSFB1	246214_at	Heat shock transcription factor B1
AT5G58770	1.00	0.97	1.66	0.18	0.90	0.55	6.14	0.21	7.19	0.14	4.45	0.15	24.64	0.08	31.03	0.04	16.55	0.01		247780_at	Undecaprenyl pyrophosphate synthetase family protein
AT2G32120	0.99	0.97	0.99	0.95	0.87	0.17	12.06	0.11	10.86	0.03	2.93	0.14	126.82	0.01	104.49	0.01	96.54	0.03	HSP70T-2	265675_at	Heat-shock protein 70T-2
AT5G10695	0.95	0.90	1.10	0.76	0.84	0.80	9.07	0.04	7.60	0.02	3.31	0.06	113.47	0.01	83.39	0.01	82.34	0.03		246018_at	Unknown protein
AT3G25230	0.98	0.94	0.88	0.06	0.92	0.74	4.48	0.12	4.76	0.12	2.72	0.02	34.39	0.02	33.16	0.01	31.95	0.03	ROF1	257822_at	Rotamase FKBP 1
AT3G51910	0.99	0.96	0.91	0.24	1.06	0.70	4.60	0.01	4.32	0.02	2.65	0.04	34.01	0.01	25.64	0.02	30.31	0.03	HSFA7A	252081_at	Heat shock transcription factor A7A
AT1G16030	1.00	0.99	1.16	0.22	0.98	0.74	26.67	0.03	34.48	0.03	6.63	0.18	340.51	0.00	301.70	0.01	286.78	0.02	HSP70b	261838_at	Heat shock protein 70B
AT1G26800	1.00	1.00	0.95	0.17	1.23	0.36	10.17	0.03	10.86	0.02	3.92	0.04	48.05	0.00	40.84	0.01	35.43	0.02		261265_at	RING/U-box superfamily protein
AT1G30070	1.00	0.98	0.96	0.51	1.06	0.61	15.65	0.10	12.33	0.08	5.80	0.00	142.27	0.01	113.05	0.00	130.83	0.01		260025_at	SGS domain-containing protein
AT5G35320	0.99	0.95	1.03	0.85	1.08	0.32	13.94	0.05	12.89	0.04	6.27	0.03	92.65	0.02	80.82	0.01	85.69	0.03		246612_at	Unknown protein
AT3G16050	0.99	0.95	0.86	0.58	1.26	0.65	14.86	0.06	15.43	0.00	6.92	0.05	162.86	0.00	149.22	0.00	147.97	0.03	PDX1.2	258336_at	Pyridoxine biosynthesis 1.2
AT3G12050	0.98	0.94	1.01	0.84	1.02	0.80	5.43	0.07	5.97	0.02	3.25	0.01	35.77	0.00	30.38	0.01	28.28	0.02		256663_at	aha1 domain-containing protein
AT5G09590	0.99	0.95	0.97	0.01	0.81	0.22	7.69	0.00	9.04	0.01	4.75	0.04	80.59	0.01	71.41	0.00	68.11	0.02	MTHSC70-2	250502_at	Mitochondrial HSO70 2
AT1G07350	0.99	0.95	0.95	0.81	1.02	0.43	12.86	0.08	12.75	0.03	8.63	0.00	48.95	0.02	43.22	0.00	37.32	0.02	SR45a	261081_at	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G09440	1.00	0.98	1.06	0.59	0.94	0.44	15.75	0.03	12.69	0.09	9.01	0.08	56.78	0.02	49.70	0.02	47.36	0.02		258979_at	Heat shock protein 70 (Hsp 70) family protein
AT4G12400	1.00	0.98	1.19	0.41	0.99	0.98	32.71	0.06	30.27	0.05	13.00	0.05	171.53	0.00	152.08	0.00	145.27	0.01	HOP3	254839_at	Stress-inducible protein, putative
AT3G07090	1.00	0.97	0.99	0.83	0.74	0.40	9.43	0.08	9.97	0.07	5.61	0.04	45.97	0.00	37.63	0.01	41.28	0.03		258830_at	PPPDE putative thiol peptidase family protein
AT4G23570	0.95	0.90	0.94	0.69	1.23	0.46	7.65	0.13	7.42	0.11	6.26	0.14	43.25	0.05	30.51	0.00	37.74	0.02	SGT1A	254211_at	Phosphatase-related
AT1G54050	1.00	1.00	0.98	0.78	1.32	0.31	71.51	0.00	71.52	0.00	36.53	0.03	195.21	0.00	156.21	0.00	151.22	0.02	HSP17.4	263150_at	HSP20-like chaperones superfamily protein
AT3G09350	0.99	0.95	1.17	0.57	1.42	0.25	108.66	0.02	93.26	0.02	76.75	0.00	187.54	0.01	155.87	0.00	165.78	0.02	Fes1A	259037_at	Fes1A
AT3G24500	0.97	0.92	1.39	0.65	0.62	0.16	86.33	0.04	85.07	0.01	35.92	0.01	240.40	0.01	190.96	0.00	184.66	0.03	MBF1C	258133_at	Multiprotein bridging factor 1C
AT5G52640	1.00	0.99	1.13	0.49	0.69	0.03	49.50	0.01	51.41	0.00	24.06	0.05	176.39	0.00	149.88	0.01	134.73	0.03	HSP90.1	248332_at	Heat shock protein 90.1
AT3G12580	0.97	0.93	1.49	0.00	0.41	0.18	34.48	0.04	42.84	0.01	19.39	0.03	83.76	0.01	75.19	0.01	68.70	0.03	HSP70	256245_at	Heat shock protein 70
AT5G48570	1.00	0.99	1.33	0.06	0.53	0.21	45.26	0.03	46.35	0.01	11.95	0.00	143.37	0.00	128.58	0.01	117.63	0.02	ROF2	248657_at	FKBP-type peptidyl-prolyl cis-trans isomerase family protein
AT5G05410	0.99	0.96	1.30	0.01	0.64	0.07	85.07	0.02	95.38	0.00	56.15	0.02	66.95	0.02	35.83	0.00	37.61	0.05	DREB2A	250781_at	DRE-binding protein 2A
AT1G67360	0.99	0.95	1.56	0.27	0.54	0.03	4.29	0.28	11.14	0.12	0.42	0.09	75.03	0.01	68.90	0.00	49.41	0.02		264968_at	Rubber elongation factor protein (REF)
AT5G12110	1.00	0.99	1.85	0.00	0.51	0.06	4.12	0.05	6.52	0.06	0.60	0.47	38.62	0.02	35.94	0.00	26.57	0.02		250304_at	Glutathione S-transferase
AT1G17870	1.00	0.99	1.91	0.16	0.50	0.08	4.96	0.19	7.21	0.05	1.11	0.61	32.09	0.06	34.92	0.01	34.07	0.02	EGY3	255891_at	Ethylene-dependent gravitropism-deficient and yellow-green-like 3
AT1G03070	0.96	0.91	1.12	*0.58*	1.09	0.73	3.70	0.25	6.19	0.10	0.85	0.77	168.09	0.03	180.81	0.02	119.03	0.01		263164_at	Bax inhibitor-1 family protein
AT4G26270	1.00	0.99	0.94	0.77	0.74	0.32	1.45	0.14	1.66	0.18	0.91	0.64	34.58	0.02	30.64	0.03	21.60	0.05	PFK3	253987_at	Phosphofructokinase 3
AT5G47610	0.98	0.93	1.29	0.36	0.41	0.20	1.44	0.61	2.19	0.37	0.29	0.10	28.57	0.06	30.47	0.01	22.71	0.03		248759_at	RING/U-box superfamily protein
AT5G59720	1.00	0.97	7.05	0.02	0.72	0.22	4.64	0.00	6.94	0.08	1.20	0.42	259.01	0.00	225.01	0.00	195.59	0.02	HSP18.1	247691_at	Heat shock protein 18.2
AT4G25340	0.97	0.92	1.14	0.47	0.87	0.79	0.76	0.58	0.86	0.70	0.50	0.24	32.27	0.01	30.23	0.00	20.23	0.00	FKBP53	254076_at	FK506 BINDING PROTEIN 53
AT5G43170	0.99	0.97	1.41	0.16	0.88	0.50	2.34	0.04	3.06	0.03	2.20	0.04	47.00	0.00	50.63	0.01	9.32	0.04	ZF3	249139_at	Zinc-finger protein 3