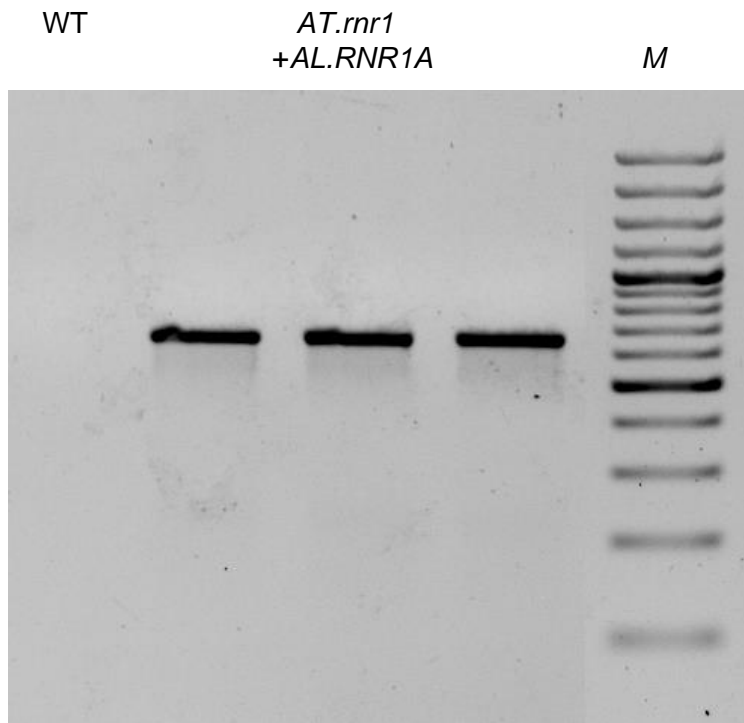


Supplemental Figure S1. Promoter sequences divergence analysis between expressologs and non-expressologs in the genetic redundant and species-specific functional categories (A) Promoter analyses of the gene group, where all the *A. lyrata* genes present within a gene group are genetically redundant to *A. thaliana* gene as predicted by gene expression analyses. For each *A. thaliana* and *A. lyrata* orthologous gene clusters we calculated the differences in promoter sequence divergence scores (delta d_{SM} scores) between the *A. lyrata* gene copies. For clusters with more than two *A. lyrata* gene copies we considered any two *A. lyrata* copies by random choice. In order to define the clusters that are closer in their d_{SM} values we have considered a threshold value of delta d_{SM} which has been shown by dotted line (<0.2). (B) Promoter analyses of the gene group, where all the *A. lyrata* genes present within a gene group are depicting species specific difference compared to *A. thaliana* gene as predicted by gene expression analyses. The other parameters used were the same as described in Figure S1A.



Supplemental Figure S2. Confirmation of the presence of the transgene insertion of *AL.RNR1A* in three independent transgenic plants by PCR analysis. An *AL.RNR1A*-specific primer pair (Table S4) was used to amplify a diagnostic fragment from genomic DNA, which was absent from an untransformed control plant (WT).

A

AT.TSO2 -----MPSMPEEPLLTPTPDRFCMFPIHYPIWEMY 31
 AL.TSO2A -----MPEEPLLTPTPDRFCMFPIHYPIWEMY 28
 AL.TSO2B -----MPSMPEEPILTPTPDRFCMFPIQYPQIWEMY 31
 HS.RRM2 SKTARRIFQEPTEPKTKAAAPGVEDEPLLRENPRRFVIFPIEYHDIWQMY 94
 SC.RNR2 DAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDKERTVLFPIKYHEIWQAY 100

TSO2-1 (D49>N)

AT.TSO2 KKAEASFWTAAEEVDLSQDNRDWNENSLNDGERHF~~I~~KHVLAFFAASDGVILE 81
 AL.TSO2A KKAEASFWTAAEEVDLSQDNRDWNENSLNDGERHF~~I~~KHVLAFFAASDGVILE 78
 AL.TSO2B KKAEASFWTAAEEVDLSQDNRDWNENSL~~S~~NDERHF~~I~~KHVLAFFAASDGVILE 81
 HS.RRM2 KKAEASFWTAAEEVDLSKDIQHVES-LKPEERYFISHVLAFFAASDGVINE 143
 SC.RNR2 KRAEASFWTAAEIDLKDIHDWNNRMNENERFFISRVLAFFAASDGVINE 150

TSO2-3 (R97>S)

AT.TSO2 NLASRFMSDVQVSEARAFYGFQIAIENIHSEMYSLLLDITYIKDNKERDHL 131
 AL.TSO2A NLASRFMSDVQVSEARAFYGFQIAIENIHSEMYSLLLDITYIKDNKERDHL 128
 AL.TSO2B NLSTRFMSDVQI~~I~~SEARAFYGFQIAIENIHSEMYSLLLDITYIKDNKERDHL 131
 HS.RRM2 NLVERFSQEVQITEARCFYGFQIAMENIHSEMYSLIDITYIKDPKEREFL 193
 SC.RNR2 NLVENFSTEVQIPEAKSFYGFQIMIENIHSETYSLLIDITYIKDPKESEFL 200

TSO2-2 (G170>S)

AT.TSO2 FRAIETIPCVAKKAQWAMKWIDG-SQTFAERIIAFACVEG~~I~~FFSGSFCSI 180
 AL.TSO2A FRAIETIPCVAKKAQWAMKWIDG-SQTFAERIIAFACVEG~~I~~FFSGSFCSI 177
 AL.TSO2B FRAIETIPCVTKKA~~E~~WAMKWING-SQSFAERIVAFACVEG~~I~~FFSGSFCSI 180
 HS.RRM2 FNAIETMPCVKKKADWALRWIGDKEATYGERVVAFAAVEG~~I~~FFSGSFASI 243
 SC.RNR2 FNAIHTIPEIGEKAEWALRWIQDADALFGERLVAFASIEG~~V~~FFSGSFASI 250

AT.TSO2 FWLKKRGLMPGLTFSNELISRDEGLHCDFACLLYTLLKTKLSEERVKSIV 230
 AL.TSO2A FWLKKRGLMPGLTFSNELISRDEGLHCDFACLLYTLLKTKLSEERVKSIV 227
 AL.TSO2B FWLKKRGLMPGLTFSNELISRDEGLHCDFACL~~I~~YSL~~L~~R~~T~~KL~~D~~EER~~L~~KSIV 230
 HS.RRM2 FWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFKHLVHKPSEERVREII 293
 SC.RNR2 FWLKKRGMPGLTFSNELICRDEGLHTDFACLLFAHLKKNKPDPAIVEKIV 300

AT.TSO2 CDAVEIEREFVCDALPCALVGMNRDLMSQYIEFVADRLLGALGYGKVVYGV 280
 AL.TSO2A CDAVEIEREFVCDALPCALVGMNRDLMSQYIEFVADRLLGALGYGKVVYGV 277
 AL.TSO2B CDAVEIEREFVCDALPCALVGMNRE~~L~~MSQYIEFVADRLL~~T~~ALG~~C~~GKVVYGV 280
 HS.RRM2 INAVRIEQEFLTEALPVKLI~~G~~MNCTLMKQYIEFVADRLL~~M~~LELGFSKVFRV 343
 SC.RNR2 TEAVEIEQRYFLDALPVALLGMNADLMNQYVEFVADRLLVAFGNKYYKV 350

AT.TSO2 TNPF~~D~~WMELISLQGKTNFF~~E~~KRVGDYQKASVMSVNGNGAF-DNHVFS~~L~~D 329
 AL.TSO2A TNPF~~D~~WMELISLQGKTNFF~~E~~KRVGDYQKASVMSVNGNGAF-DNHVFS~~L~~D 326
 AL.TSO2B SNPF~~D~~WMELISLQGKTNFF~~E~~KRVGEYQKASVMSVHGNAAFNDDHVFKLD 330
 HS.RRM2 ENPF~~D~~FMENISL~~E~~GKTNFF~~E~~KRVGEYQRMGMVSSP-----TENSFTLD 386
 SC.RNR2 ENPF~~D~~FMENISLAGKTNFF~~E~~KRVSDYQKAGVMSKS----TKQEAGAFTFN 396

B

```
AT.TSO2      TCA----CGTCAAAA-ATTCAAAA---CCCC--AAAACCCCTATAATCTCCTATATAAAAT 410
AL.TSO2A     CCT----CGACAAA-ATTCAAAA---CCCCAAAAACCCCTCTAATCTCCAGTATAAAAT 411
AL.TSO2B     CTAGGAGCGGGAAAATATTTTCACATTTCCCTCCTATATCCCCAAATTTTTCAAGATAAAAT 430

AT.TSO2      -ATTCAGCCCTAGATC--TTATAATTCATCAATCAAACAATCTCTTCAATCAAATTCTCTT 467
AL.TSO2A     -TTCATCCCTAGATC--TCATAATTCATCAATCAAATCATCTCTTCAATCACTTCTCTT 468
AL.TSO2B     ATCTCAATCACAGATCCATAATAATTCACACAAAAAAAAAACTCATAAATC-----TT 483

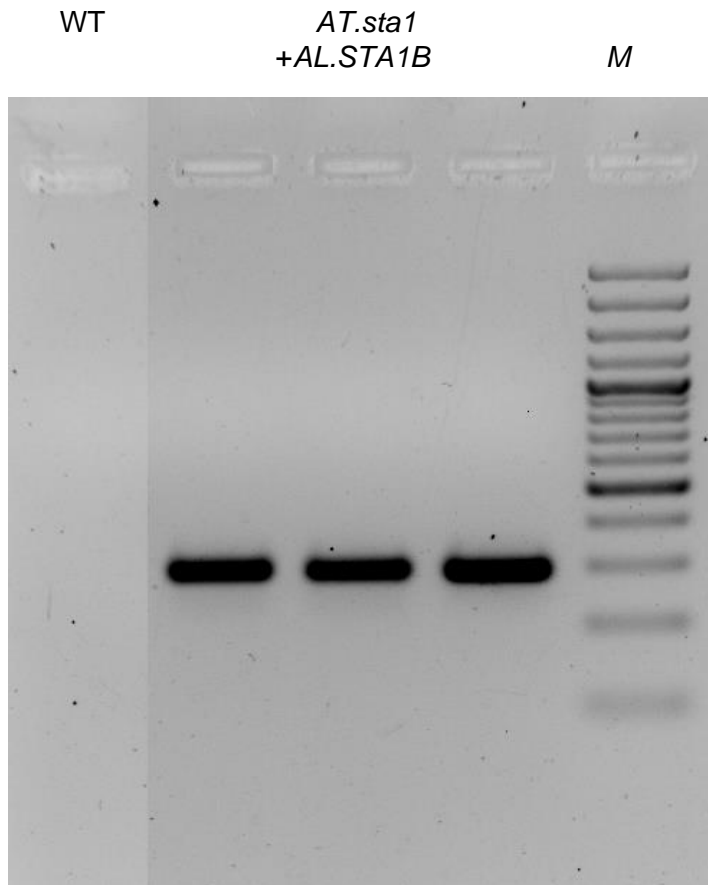
AT.TSO2      CTTCAATCAAATCTTCAA--TCCCTTCAAAGATG 500
AL.TSO2A     CTTCAATCAAATCTTCAAAGATGCCTTCAATG--- 500
AL.TSO2B     CTTCA-TAGAA-----AAA-----AATG--- 500
```

Supplemental Figure S3. Sequence alignments of *AT.TSO2* and *AL.TSO2* homologous genes. (A) Multiple sequence alignment of *AT.TSO2*, *AL.TSO2A*, *AL.TSO2B*, human (HS.RRM2, NP_001025) and *Saccharomyces cerevisiae* (SC.RNR2, NP_012508) sequences. The nucleotides highlighted in red are identified non-synonymous changes between *AT.TSO2* and *AL.TSO2A/AL.TSO2B*. Twenty eight non-synonymous changes were noticed between *AT.TSO2* and *AL.TSO2B*. Regions containing residues of important for enzymatic function are underlined (Philipps et al., 1995). Twenty-seven out of 28 amino acid changes for TSO2B are outside these regions indicating that gene function of TSO2B was probably not affected by these changes. The bold, underlined amino acids are three known TSO2 alleles in *Arabidopsis thaliana* (Wang and Liu, 2006). (B) Multiple alignment of 1000 bp upstream region of *AT.TSO2*, *AL.TSO2A* and *AL.TSO2B*. The bold, underlined sequence (CTCCTATATAAAATA) is the TATA box in the core promoter region of AT2G21790; while underlined region (TCTCTTCTTC) is the Y patch. Y Patch is a direction-sensitive plant core promoter element that appears around TSS.

atgggtgttctctcgattccaaacgtgaagaccatgtcgatcaatgtgaaccctagtgca
M V F L S I P N V K T M S I N V N P S A
accaccatctccgccttcgaacaattggtccatcaacgcactcatcttctcaacctctc
T T I S A F E Q L V H Q R T H L P Q P L
cttcgttactcgtctgtctccgcaacctagtcttgattcctccgatcctgcctgtta
L R Y S L C L R N P S L D S S D P A L L
tcggatctaggttttggcctttgtctacgggtactgttcatgtccctctaatacgggtgga
S D L G F G P L S T V L V H V P L I G G
gcggtccgcctcagcccctcttcaattcaaactatgtcgctgggttgggtcgtggggct
A A P P Q P L F N S N Y V A G L G R G A
acagggttactaccgctccgatattggtcctgctcgtgctgatggcgatgacgtgaat
T G F T T R S D I G P A R A D G D D V N
cacaagtttgatgactttgaagggatgatgcgggattgttcgctaatacggagtgatgat
H K F D D F E G N D A G L F A N A E C D
gacgaagacaaagaggtgacgccaattgataggaggaggaagacagaagagacatcgag
D E D K E A D A I D R R R R K D R R D I E
aattacagagcctccaaccctaaagtctgagcagtttgggtatctgaagagaaagttg
N Y R A S N P K V S E Q F V D L K R K L
catactttgtctgaggatgaatgggatagtttccagagattgggaattactcgcacggt
H T L S E D E W D S I P E I G N Y S H R
agcaagaagaagaggttggagagccttggcctgttctgacacgcttttgcaggaaaa
S K K K R F E S F V P V P D T L L Q E K
gggatcgtctcggccttaggcccaaatagcagagccgctgggtggatcgggagacgcatgg
G I V S A L G P N S R A A G G S E T P W
atagcttgacttcagtcgggtgaggaagaggttttctgttctctgaagccttgagag
I D L T S V G E G R G F L L S L K L E R
ttatcagattctcttccaggcgaactgttgggtatcctaaaggctacttaactgacctt
L S D S L S G Q T V V D P K G Y L T D L
aagaataaggaactaccaacgatgcagacatttttcatattaatagagctagaccctta
K N K E L T N D A D I F H I N R A R P L
ttaaagagtattacaacgtcgaatccaagaatccaatggctggattgctgctgcgaga
L K S I T Q S N P K N P N G W I A A A R
ctcgaggagagggctggtaaaaataaaagccgctagaactcagattcagaagggatgcaat
L E E R A A G K I K A A R T Q I Q K G C N
gagtgcccaaaacatgaggatgtttgggtgaggcttgatgctggccacaccggaggat
E C P K H E D V W V E A C M L A T P E D
gccaaagcgggtgattgcaatgggagtttaagcaataaccaactcgggtgaagctatgggtg
A K A V I A M G V K Q I P N S V K L W L
gaggctgcaaagttggaacatgatgaggataacaagagttaggggttggagaaaaggactg
E A A K L E H D E D N K S R V L R K G L
gagcatattccagactcgggttaggctatggaagactgttaaggacatggctaataagaa
E H I P D S V R L W K T V K D M A N K E
gatgcagtggttttgcctcacagagctgtggaatgctgcctctgcatccggagctatgg
D A V V L L H R A V E C C P L H P E L W
atggcgcttgcgaggcttgaacatacgaaaaacacaaaagaaagtgttgaacagagcgag
M A L A R L E T Y E K H K E S V E Q S E
agagaagctcccaagagcgggggatttggatcaccgctgctaagctagaggaagataa
R E A P Q G A G D L D H R C - A R G R -
tgggaataactactaaggttggaaagatcattgagaagggataaaatgctctgcagagaga
W E Y Y - G W K D H - E G Y K C S A E R
agaggttgcattgaccgggaaaagtggaggtctctgagagagccgggtatgtaacaacc
R G C H - P G K V E V S E R A G Y V T T
tgccaggaattattaagatcattattgggtttgaaagtcgatgaagaggatagaaagaaa
C Q A I I K I I I G F E V D E E D R K K
acttgggttgcctgatgcagaggagtcaagaagaggggttccatcgagactgcaagagca
T W V A D A E E C K K R G S I E T A R A
atatacgcacatgctcttaccgtgttcttactaagaaaagtatctggctgcgcagtttag
I Y A H A L T V F F T K K S I W L R S -

agaagagtcattgtagtatggagctctcttgatgccgtggtgcgtaaggctgtgacatacc
R R V M V V W S L L M P C C V R L - H T
tccctcaggtgaggttctctggctcatgtgtgccaaggagaagtggcttgctggagatg
S L R L R F S G S C V P R R S G L L E M
ttccagcagcccgtggcattctacaagaggctcatgccgcagttccaaactccgaggaaa
F Q Q P V A F Y K R L M P Q F Q T P R K
tctggcttgctgcttttaagctagagtttgagagcagggaggtggagagggcgaggatga
S G L L L L S - S L R A G R W R G R G -
ttctcgcgaaaagcaaggaaagaggaactactgggaggggtgtggatgaaatcagccattg
F S Q K Q G K E E L L G G C G - N Q P L
ttgagaggaactagggcaacgtagaggagaggagattgcttgaagaaggcgtgaaga
L R G N - A T - R R R G D C L K K A - R
aattcccagcattctcaagctttggttgatgcttggcagcttgggaaaggtttaggc
N S Q H S S S F G - C L G S L G K G L G
atctggaacaggccaagaaagcttacacatctggtttgagggcactgtcccagtgacac
I W N R P R K L T H L V - G T V P S A H
cattgtggctctcgctcgctgatattgaagagaaagtgaatgggctcaacaaagctcgtg
H C G S R S L I L K R K - M G S T K L V
tagttctcactctggccaggaagaaaaaccctaaggcggatgagctatggctagctgctg
- F S L W P G R K T L R R M S Y G - L L
ttcgtgttgaattagacatggcaacaagagagaagcagagcgttgatgtcaaaggccc
F V L K L D M A T R E K Q S A - C Q R P
tgcaagagtctcccaaaagtggtcttctcttggtgctgacatcgagatggcaccgcat
C K S L P K V V F S W L L T S R W H R H
gtctgctcccgcaaacgaagattgatgatgctctgaagaagtgtgtgaagaaggaggcgg
V C S R K R R L M M L - R S V - R R R R
cgcatgtcactgcaatggctcgccaagatctcctggcaagataggaaggtggataaagcca
R M S L Q W S P R S P G K I G R W I K P
gattgtggtttcaacggaccgtgaacgtcgaccagataatggagattttctgggccttgt
D C G F N G P - T S T Q I M E I S G P C
actacaaatttgaacttgaacatggctctgaggagaagcagaaggaggtgctgaccaaat
T T N L N L N M A L R R S R R R C - P N
gtgtggcgtctgagccaaagcacggtgagaagtggcaagccatatccaaagcgttgagaga
V W R L S Q S T V R S G K P Y P K R W R
atgccaccagcctgttgaagtcattcttgaagagagtggtgggttcattgacaaggaag
M P T S L L K S S - R E W W L H - Q G K
agcgtaaacaaactctaa
S V T N S

Supplemental Figure S4. Pseudogenization due to insertion of one A nucleotide at position 1352 (marked in red font and underlined), which causes premature insertion of the stop codon (-) in the *AL.STA1B* gene copy.

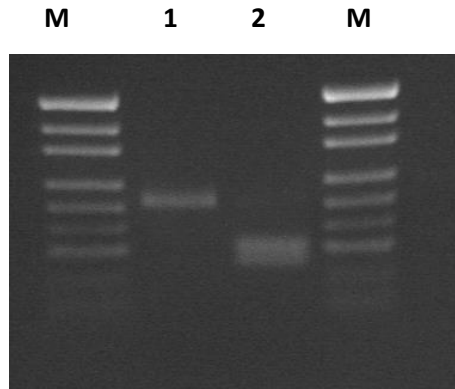


Supplemental Figure S5. Confirmation of the presence of the transgene insertion of *AL.STA1B* in three independent transgenic plants each by PCR analysis. An *AL.STA1B*-specific primer pair (Table S4) was used to amplify a diagnostic fragment from genomic DNA, which was absent from an untransformed control plant (WT).

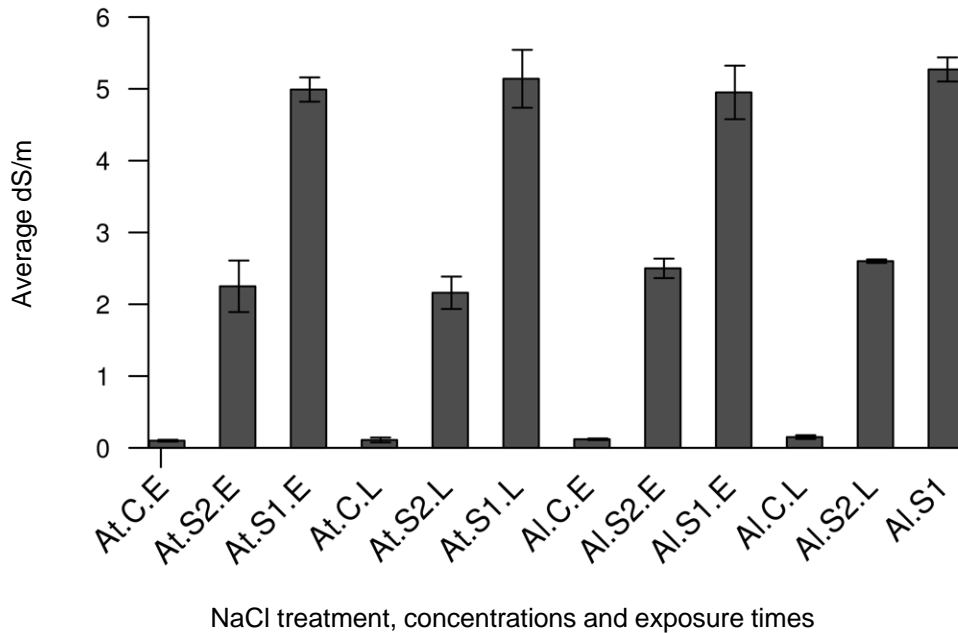
A

AL.MTP11ACDS	151	TGTCTTGGTTGTTTGG <u>GGTCCGGAAGACAATGTG</u> GCAGATTATTACCAGCA	200
		.	
AL.MTP11BCDS	151	TGTCTTGGTTGTTTGG <u>GGTCCGGAAGACAATGTA</u> GCAGATTATTACCAGCA	200
AL.MTP11ACDS	201	GCAAGTAGAGATGCTTGAGGGATTTACTGAAATGGATGAACTTGCAGAAC	250
		.	
AL.MTP11BCDS	201	GCAAGTAGAGATGCTTGAGGGCTTCACTGAAATGGATGAACTTGCAGAAC	250
AL.MTP11ACDS	251	<u>G</u> TGGCTTTGTTCCCTGGAATGTCAAAGGAAGAGCAGGATAATTTGGCTAAA	300
		.	
AL.MTP11BCDS	251	<u>G</u> CGGCTTTGTTCCCTGGAATGTCAAAGGAAGAGCAGGATAATTTGGCTAAA	300
AL.MTP11ACDS	301	AGCGAGACATTGGCGATTAGAATATCAAACATTGCAAACATG <u>CTTCTTTT</u>	350
		.	
AL.MTP11BCDS	301	AGTGAGACATTGGCGATTAGAATATCAAACATTGCAAACATG <u>GTTCTTTT</u>	350
AL.MTP11ACDS	351	<u>TGCTGCTAAAGTCT</u> ATGCTTCTGTCACAAGTGGCTCTTTAGCAATCATTG	400
		.	
AL.MTP11BCDS	351	<u>TGCTGCTAAAGTCT</u> ACGCTTCTGTCACAAGTGGCTCTTTAGCAATCATTG	400

B



Supplemental Figure S6. Distinction of *ALMTP11A* and *B* homologs. (A) Pairwise sequence comparison of the two *A. lyrata* MTP11A and B homologs to design gene specific primers (bold, underlined) for quantitative real time RT-PCR analyses. Presence of a restriction enzyme (*Aci* I) cut site (CCGC) was detected and underlined in the *AL.MTP11B* sequence, which is absent in the *AL.MTP11A* sequence. (B) To confirm specificity of the amplified PCR products both the amplified fragments were digested with *Aci* I. Only one fragment was noticed for *AL.MTP11A* (lane 1), while two fragments were noticed for *AL.MTP11B* (lane 2). This primer pair was used in the real-time RT-qPCR analyses to calculate expression patterns of these two homologs. M, DNA size marker (pUC19 digested with *Msp* I).



Supplemental Figure S7. Measurements of soil salinity for the stress assays used in the microarray based gene expression analyses. The abbreviations used: At.C.E- *A. thaliana*, control, early time point (3h); At.S2.E- *A. thaliana*, 250 mM NaCl, early time point (3h); At.S1.E- *A. thaliana*, 500 mM NaCl, early time point (3h); At.C.L- *A. thaliana*, control, late time point (27h); At.S2.L- *A. thaliana*, 250 mM NaCl, late time point (27h), At.S1.L- *A. thaliana*, 500 mM NaCl, late time point (27h); Al.C.E- *A. lyrata*, control, early time point (3h); Al.S2.E- *A. lyrata*, 250 mM NaCl, early time point (3h), Al.S1.E- *A. lyrata*, 500 mM NaCl; Al.C.L- *A. lyrata*, control, late time point (27h), Al.S2.L- *A. lyrata*, 250 mM NaCl, late time point (27h), Al.S1.L- *A. lyrata*, 500 mM NaCl, late time point (27h).