Supplemental Table S1. Summary of *Arabidopsis thaliana* and *A. lyrata* array design features

Array features	***A. thaliana***	***A. lyrata ssp. lyrata***
Agilent design Id	029132	030951
Design format	8X60K	8X60K
Number of biological probes	43603	32386
Number of replicated probes	50 X 5	477 X 10
Mean probe length (bp)	60	60
Agilent controls on array	1319	1319
% filled by selected probe group	71.64	61.09
Total number of features on array	62976	62976
Total % filled	100	100

Supplemental Table S3. *A. thaliana* mutants used in this study for genetic complementation with *A. lyrata* homologs. The complemented plants were phenotyped according to the conditions described in the original reference.

Gene	Annotation	Mutant name	Nature of mutation	Phenotype	Genetic background	Reference	Utility in our complementation assay
AT2G21790	Ribonucleotide reductase 1/RNR1	*crinkled leaves 8 (cls8-1)*	Point mutation. Missense G>A substitution/ G718>E.	First developing true leaves emerge bleached, subsequent leaves emerge curled with bleached edges, matured rosette leaves become crinkled and show patches of white pits on the surface	Columbia	Garton et al. (2007) Plant Journal 50: 118–127	Used in complementation assay.
AT3G27060	Ribonucleaotide reductase 2/TSO2	*tso2-1*	Point mutation. Missense change: D49>N.	White sectors in green organs, uneven thickness, rough surfaces, irregular margins of leaves or floral organs, sepals rough and uneven, stamens occasionally exhibited carpel characteristics indicating homeotic transformation.	Landsberg *erecta*	Wang and Liu (2006) Plant Cell 18: 350-365	Used in complementation assay.
AT2G39450	Manganese transporter 11/MTP11	*N859636, SALK_025271*	T-DNA insertion	On nutrient agar supplied with Mn^{2+} concentrations ranged from basal to toxic levels, the mutant was more sensitive to Mn^{2+} than the wild type, as determined by significantly reduced shoot dry weights.	Columbia	Delhaize et al. (2007) The Plant Journal 51: 198–210	Used in complementation assay.
AT4G03430	Stabilized 1/STA1	*sta1-1*	In-frame deletion of two amino acids: 1249 to 1254 bp from the translation initiation site/ 417C, 418P	*sta1-1* plants showed many developmental and stress-related phenotypes, smaller in size and heights than the wild-type plants. Mutant leaves were more serrated with a pointed leaf tip. The mutant was more sensitive to ABA.	Columbia gl1	Lee et al. (2006) Plant Cell 18: 1736–1749	Used in complementation assay.

Supplemental Table S4. Oligonucleotides used in this study for different purposes.

*Since, the promoter and 3' UTR region of *AL.MTP11A* and *B* are sequentially highly similar, we used the same oligonucleotide pairs to amplify both homologs.

Target gene	Gene identifier	Oligo name	5'-3' sequence	Amplified product length	Purpose
AL.RNR1A	Al_scaffold_0007_128	AL.CLSA.GW.F	GGGGACAAGTTTGTACAAAAAAGCAGGCTaaagacgacaaaacaaaacg	6.3 Kb	Gene amplification- GATEWAY cloning
AL.RNR1A	Al_scaffold_0007_128	AL.CLSA.GW.R	GGGGACCACTTTGTACAAGAAAGCTGGGtctgagatttgaggatgagg	-	Gene amplification- GATEWAY cloning
AL.RNR1B	fgenesh2_kg.4__104__AT2G21790.1	AL.CLSB.GW.F	GGGGACAAGTTTGTACAAAAAAGCAGGCTaagaggtgcgttgaagtcta	6.5 Kb	Gene amplification- GATEWAY cloning
AL.RNR1B	fgenesh2_kg.4__104__AT2G21790.1	AL.CLSB.GW.R	GGGGACCACTTTGTACAAGAAAGCTGGGTaagttccacaaaatcctcct	-	Gene amplification- GATEWAY cloning
AL.TSO2A	fgenesh2_kg.5__483__AT3G27060.1	AL.TSO2A.GW.F	GGGGACAAGTTTGTACAAAAAAGCAGGCTgttcacaaacatggcttagg	3.73 Kb	Gene amplification- GATEWAY cloning
AL.TSO2A	fgenesh2_kg.5__483__AT3G27060.1	AL.TSO2A.GW.R	GGGGACCACTTTGTACAAGAAAGCTGGGtccaatctataaaacacaaaaca	-	Gene amplification- GATEWAY cloning
AL.TSO2B	scaffold_703867.1	AL.TSO2B.GW.F	GGGGACAAGTTTGTACAAAAAAGCAGGCTcatctgaatcatggtccttt	3.58 Kb	Gene amplification- GATEWAY cloning
AL.TSO2B	scaffold_703867.1	AL.TSO2B.GW.R	GGGGACCACTTTGTACAAGAAAGCTGGGTaactcggccatatcaactta	-	Gene amplification- GATEWAY cloning
AL.STA1A	fgenesh2_kg.6__3353__AT4G03430.1	AL.STA1A.GW.F2	GGGGACAAGTTTGTACAAAAAAGCAGGCTggtcttggtaataacgtcca	5.78 Kb	Gene amplification- GATEWAY cloning
AL.STA1A	fgenesh2_kg.6__3353__AT4G03430.1	AL.STA1A.GW.R2	GGGGACCACTTTGTACAAGAAAGCTGGGTcaacatatcccgttgtttct	-	Gene amplification- GATEWAY cloning
AL.STA1B	scaffold_700051.1	AL.STA1B.GW.F	GGGGACAAGTTTGTACAAAAAAGCAGGCTagaattgggggacttaaca	5.8 Kb	Gene amplification- GATEWAY cloning
AL.STA1B	scaffold_700051.1	AL.STA1B.GW.R	GGGGACCACTTTGTACAAGAAAGCTGGGTaaactcaagttcgatccgta	-	Gene amplification- GATEWAY cloning
AL.MTP11*	-	AL.MTP11GW.F	GGGGACAAGTTTGTACAAAAAAGCAGGCTgatggagtggaaacagaaga	4.9 Kb	Gene amplification- GATEWAY cloning

AL.MTP11*	-	AL.MTP11GW.R	GGGGACCACTTTGTACAAGAAAGCTGGGTggtgagaatcagagtgagga	-	Gene amplification- GATEWAY cloning
AL.MTP11A	fgenesh2_kg.4__2026__AT2G39450.1	AL.MTP11A.RT.F1	GGTCCGGAAGACAATGTG	199 bp	RT-qPCR- gene expression assay
AL.MTP11A	fgenesh2_kg.4__2026__AT2G39450.1	AL.MTP11A.RT.R	AGACTTTAGCAGCAAAAAGAAG		RT-qPCR- gene expression assay
AL.MTP11B	fgenesh2_kg.463__5__AT2G39450.1	AL.MTP11B.RT.F1	GGTCCGGAAGACAATGTA	199 bp	RT-qPCR- gene expression assay
AL.MTP11B	fgenesh2_kg.463__5__AT2G39450.1	AL.MTP11B.RT.R	AGACTTTAGCAGCAAAAAGAAC		RT-qPCR- gene expression assay
AL.UBQ5	fgenesh2_kg.5__2722__AT3G62250.1.1	AL.UBQ5_fnew	GATGGATCTGGAAAAGTTCAG	168 bp	RT-qPCR -reference gene for *A. lyrata*
AL.UBQ5	fgenesh2_kg.5__2722__AT3G62250.1.1	AL.UBQ5_rnew	AGCGGTTGCTAGAACAGATC	-	RT-qPCR reference gene for *A. lyrata*
AL.S16	fgenesh2_kg.6__1842__AT2G09990.1.1	AL.S16qRT_f	TTTACGCCATCCGGCAGAGTAT	186 bp	RT-qPCR reference gene for *A. lyrata*
AL.S16	fgenesh2_kg.6__1842__AT2G09990.1.1	AL.S16qRT_r	GGAAACGAGCACGAGCAC	-	RT-qPCR reference gene for *A. lyrata*
At.mtp11 TDNA line	-	SALK_025271.LP	AATCTGCAATCCAAGTGTTGC		Genotyping
At.mtp11 TDNA line	-	SALK_025271.RP	CTGCTCGAGTTTCACGGTAAC		Genotyping
AL.RNR1A	Al_scaffold_0007_128	AL_CLSA_F	ATGGTTCTATCGTGAATGTCAAG	650 bp	PCR assay to confirm transgene insertion
AL.RNR1A	Al_scaffold_0007_128	AL_CLSA_R	TTGTCTCGTTGTCTTCTTCTGTTG	-	PCR assay to confirm transgene insertion
AL.STA1B	scaffold_700051.1	AL_STA1-B_F	AGTTAGAGAAGAGTCATGGTAGTAT	300 bp	PCR assay to confirm transgene insertion
AL.STA1B	scaffold_700051.1	AL_STA1-B_R	TTCATCCACACCCTCCCAGTAGT	-	PCR assay to confirm transgene insertion

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