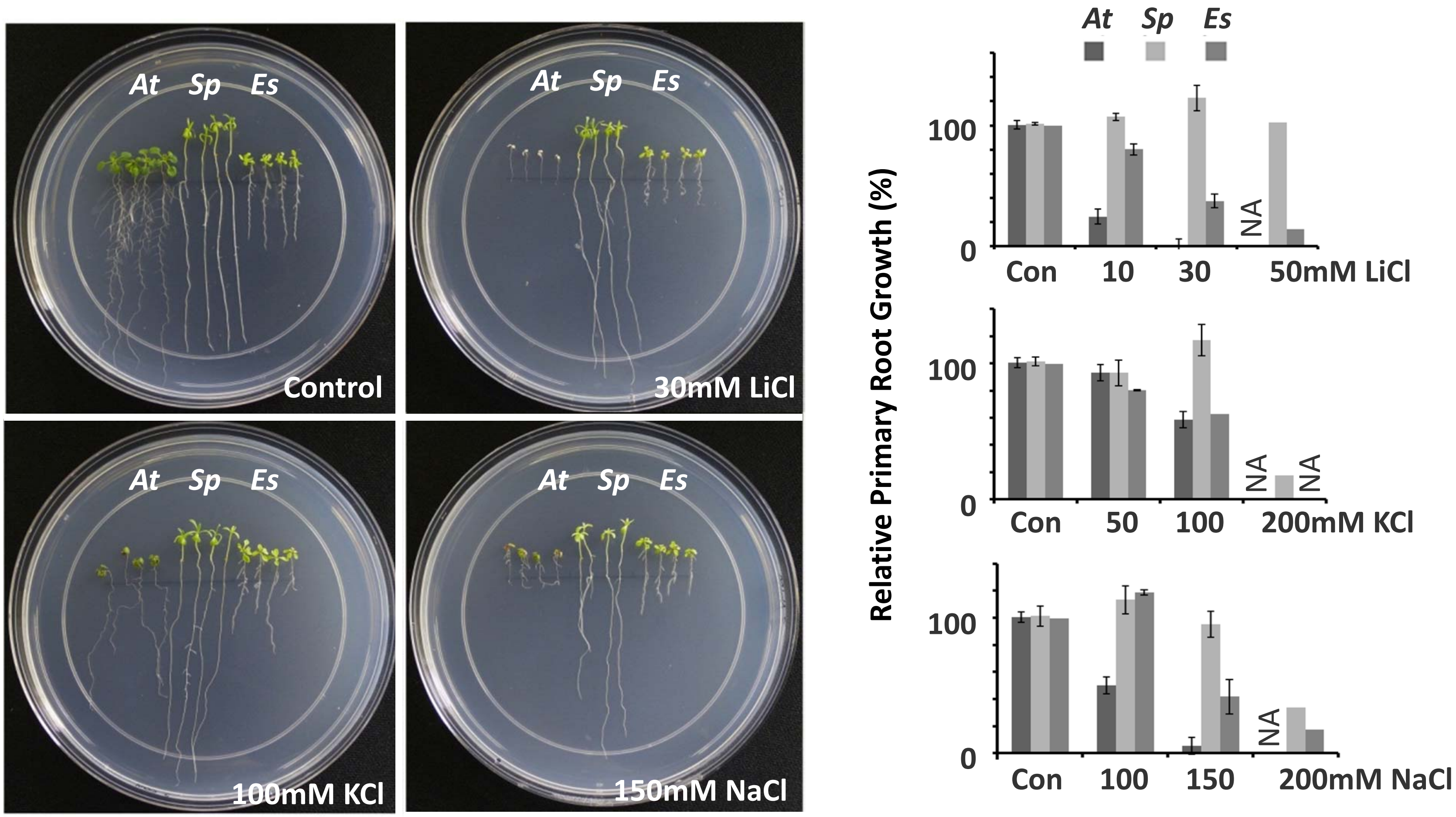
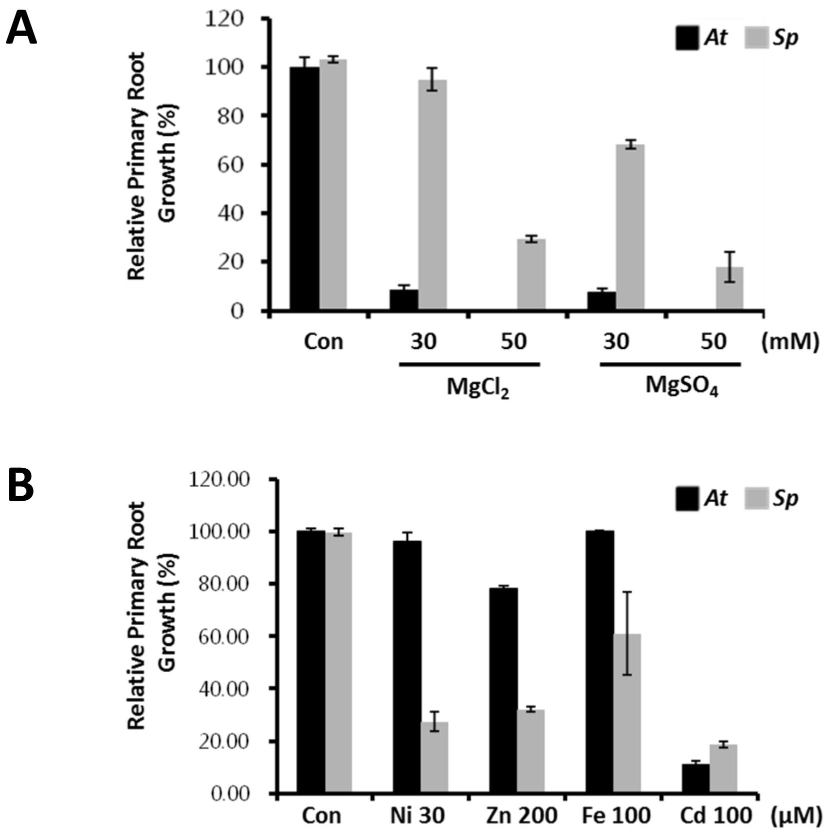
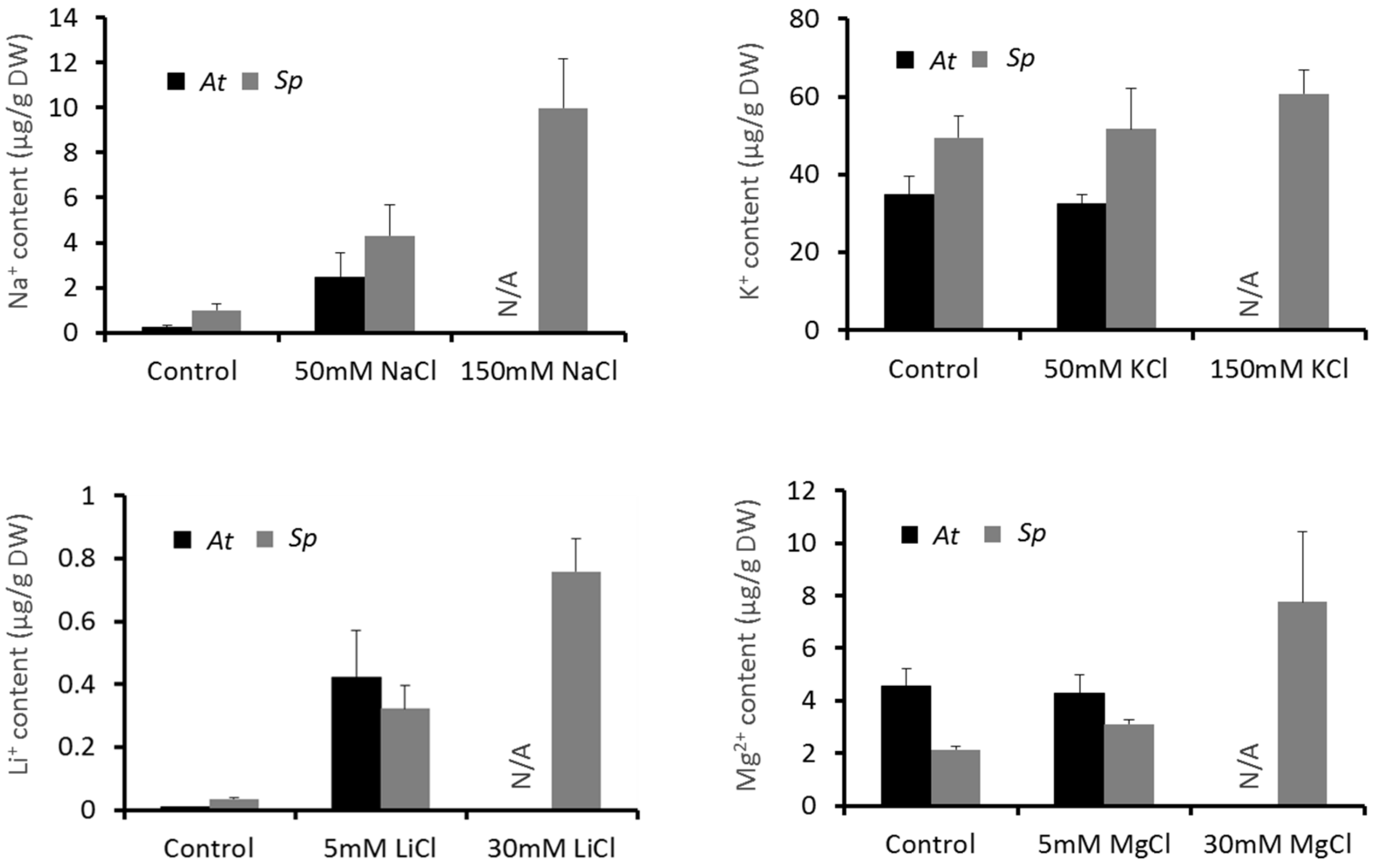
Contents



Supplemental Figure S1. Root growth comparison between *Arabidopsis thaliana* (At), *Schrenkiella parvula* (Sp) and *Eutrema salsugineum* (Es) Plant growth, treatments and measurements were done the same as for Figure 1B and 1C.

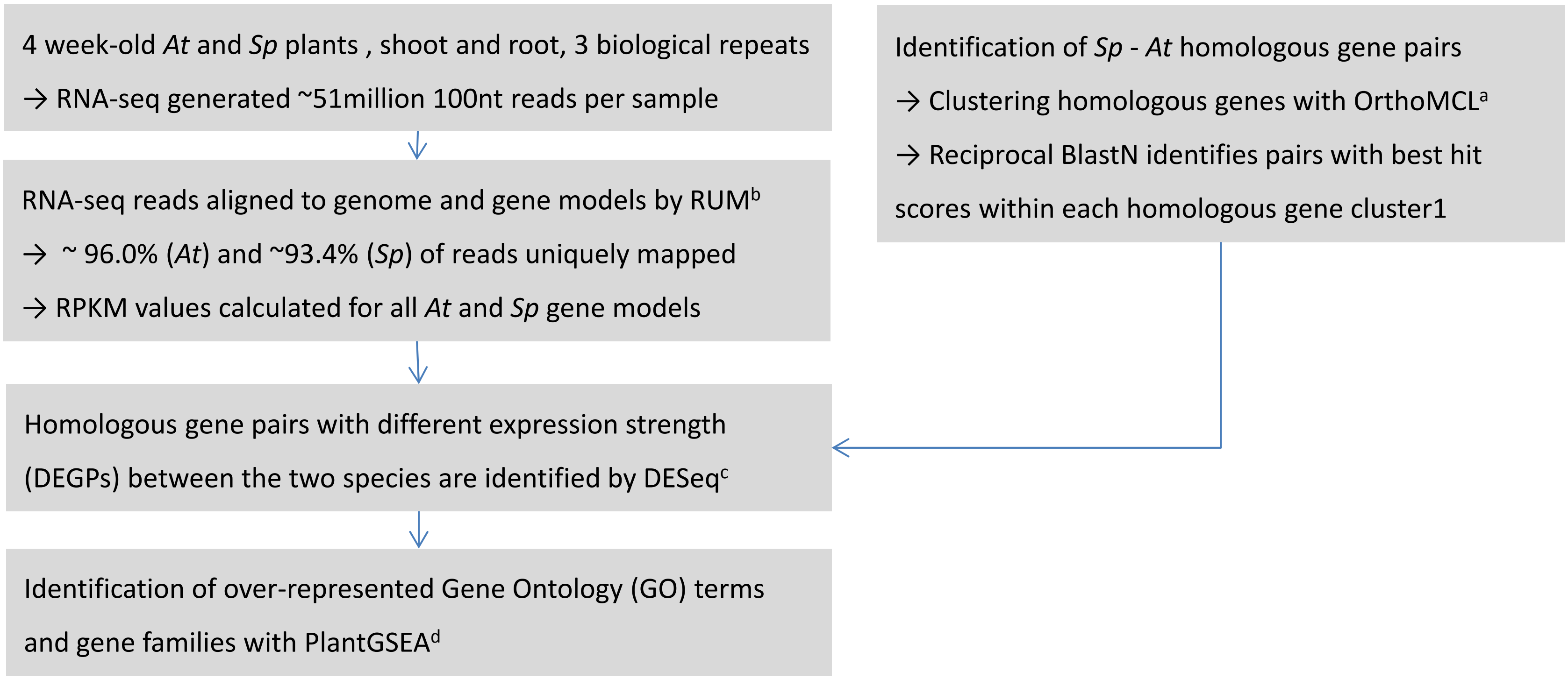


Supplemental Figure S2. Comparison of root growth of *A. thaliana* (At) and *S. parvula* (Sp) under different concentrations of salts and metal ions Plant growth, treatments and measurements were performed the same as for Figure 1B and 1C, with supplement of indicated concentrations of salts and metal ions.



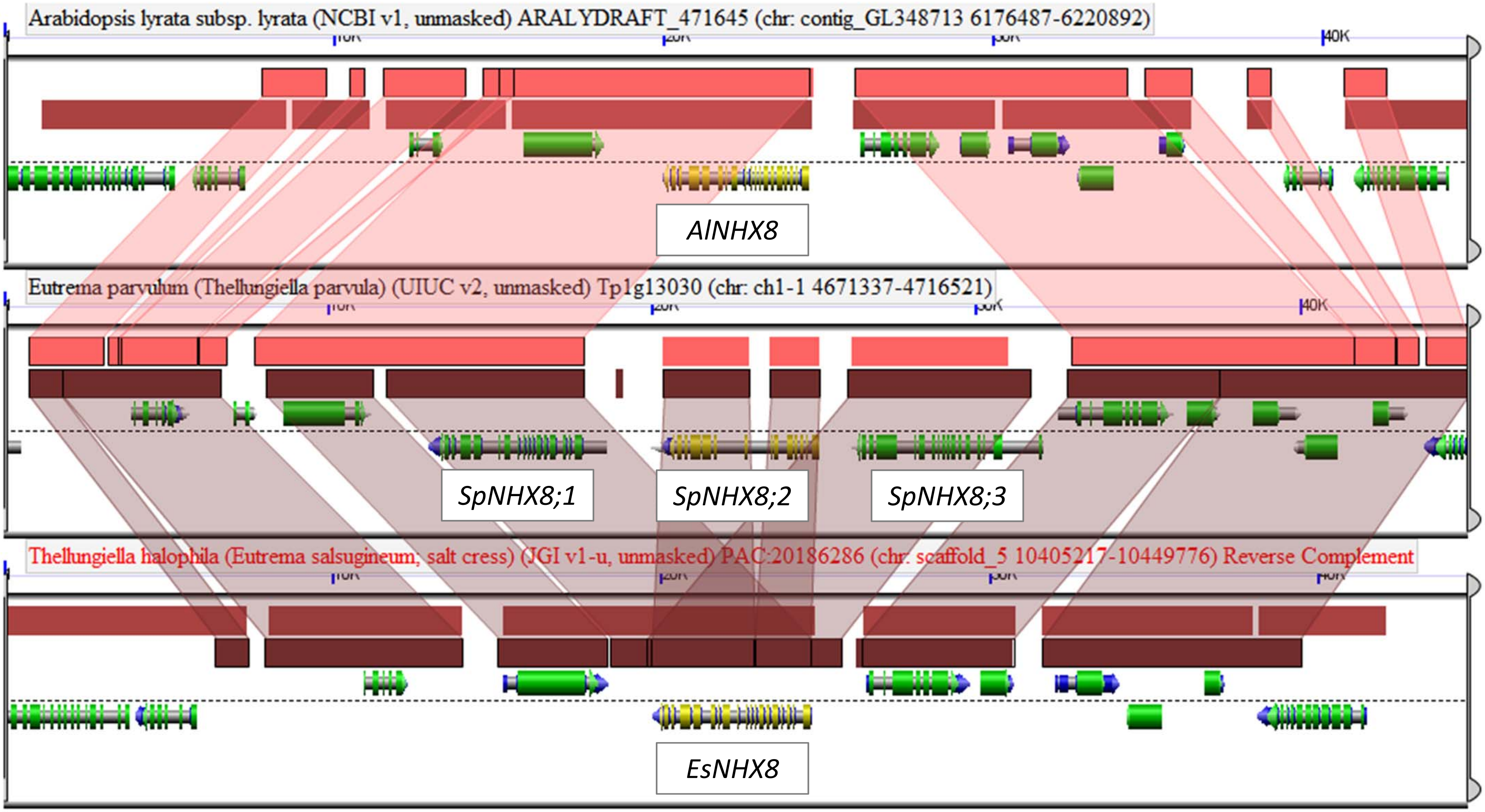
Supplemental Figure S3. Comparison of ion contents between *S. parvula* (Sp) and *A. thaliana* (At)

Plant growth and treatment were done essentially the same as Figure 1A, on root wash mix soil (see Methods) with addition of indicated concentrations of salts to the irrigation. After 2 weeks of salt treatment, 10 leaves of comparable developmental stages were harvested from individual plant, dried and digested in 0.6mL concentrated nitric acid (ultrapure grade, Mallinckrodt, St Louis, MO). Samples were diluted to 6mL, from which 1.2mL were used for analysis with Elan DRC-e ICP-MS (Inductively Coupled Plasma-Mass Spectrometry, PerkinElmer, Walthem, MA). Indium was used as internal standard. Error bars indicate standard deviations from 4 biological repeats.



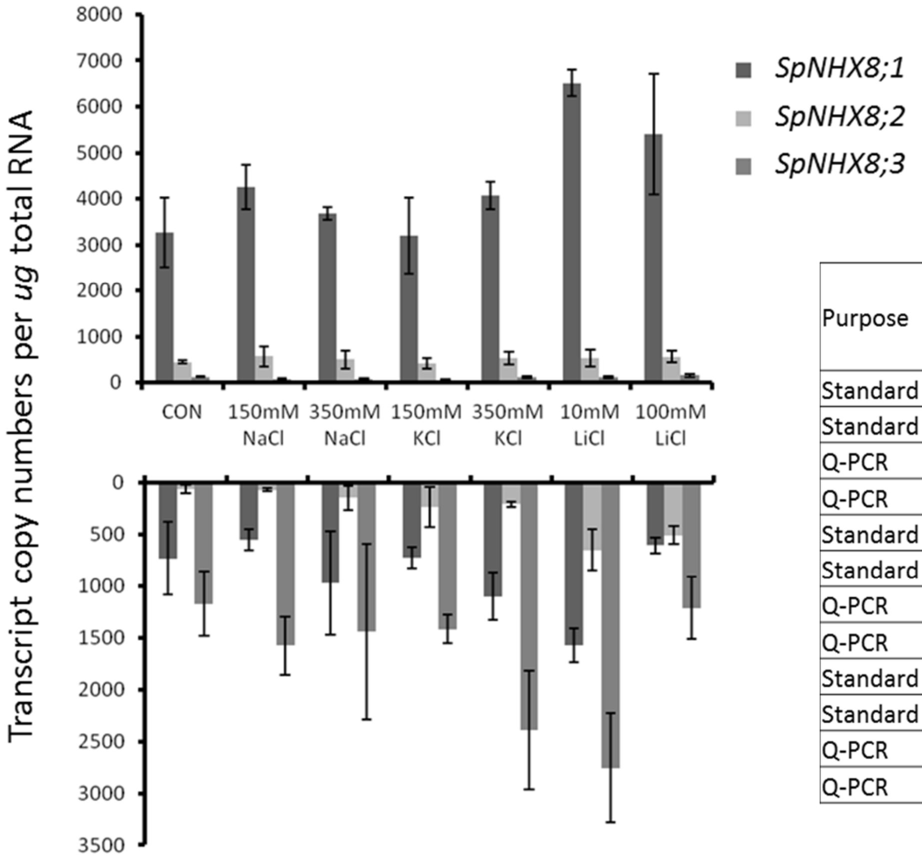
[a] Li et al (2003) [b] Grant et al (2011) [c] Anders and Huber (2010) [d] Yi et al (2013)

Supplemental Figure S4. Flowchart depicting the process of homologous gene pair identification, RNA-seq and downstream bioinformatics analyses.



Supplemental Figure S5. Comparison of genomic regions near *NHX8* loci of *Arabidopsis lyrata* (Al), *S. parvula* (Sp) and *E. salsugineum* (Es)

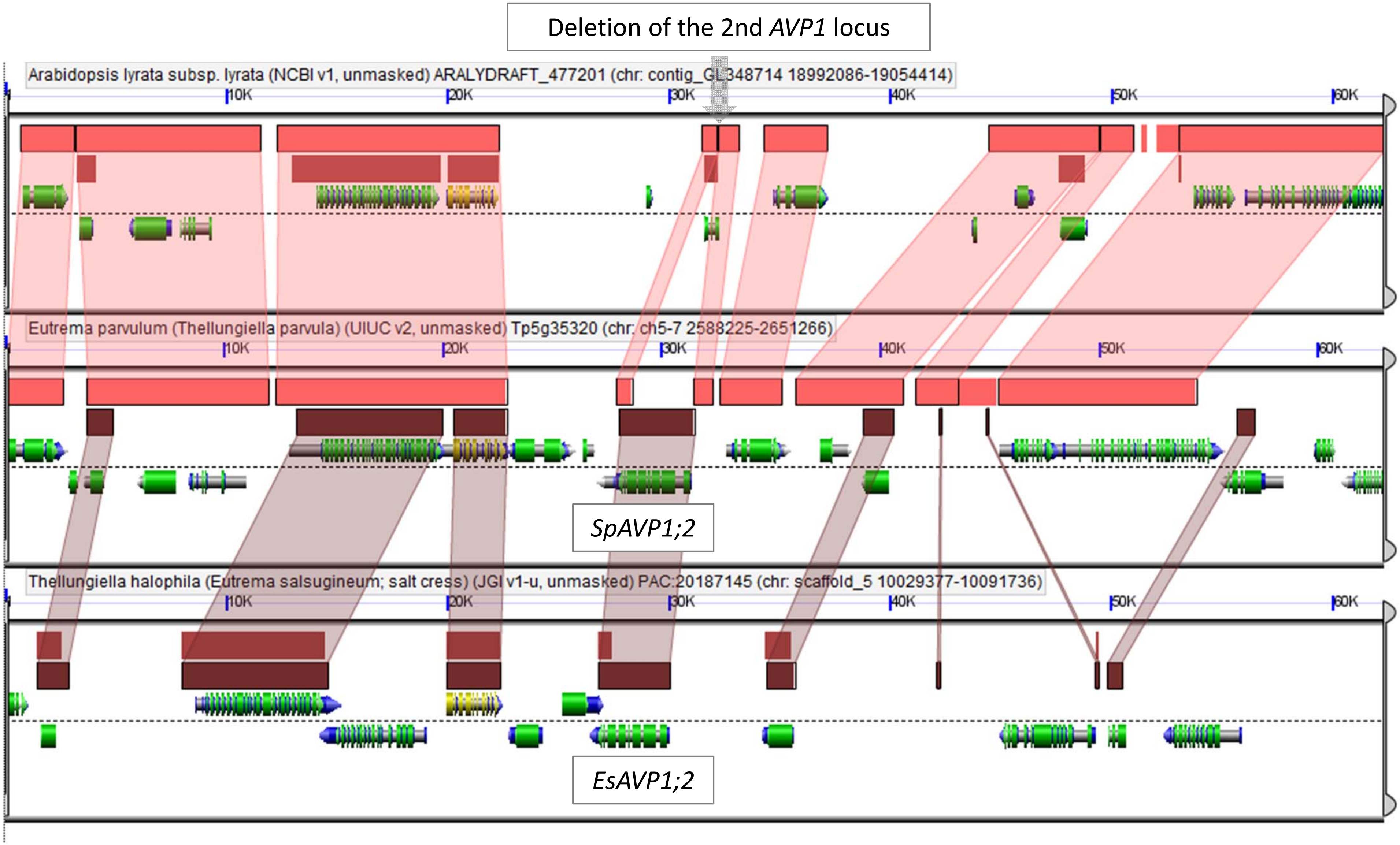
The pink and brown boxes indicate genomic regions showing sequence similarity, identified by LASTZ algorithm implemented in the CoGE GEvo (Lyon and Freeling, 2008). Gene models encoding NHX8 homologs were indicated with boxed gene IDs. The comparison and all settings are available through a permanent link provided by CoGE at: http://genomevolution.org/r/9tfh. Note that the duplication at the *NHX8* locus is found only in the lithium-tolerant *S. parvula*. The same genomic region of *A. thaliana* was presented in Figure 4B of the main text, in comparison with *S. parvula*. *E. salsugineum* genome is from Yang et al. (2013).



Purpose	Gene ID	Annotation	Direction	Starting position in the gene	Primer sequence
Standard	Sp1g13020	*SpNHX8;1*	Forward	628	GGTTCAGATCAGTGTAACGCTGTCC
Standard	Sp1g13020	*SpNHX8;1*	Reverse	1177	ACGAATTTCCACTTGATTGTTTTACAG
Q-PCR	Sp1g13020	*SpNHX8;1*	Forward	928	GGCGATCTTAGCAGTCAGATATCTCAC
Q-PCR	Sp1g13020	*SpNHX8;1*	Reverse	1056	GCCAAAACGACGTAGCAATGGGTAC
Standard	Sp1g13030	*SpNHX8;2*	Forward	19	TCGACGTTGCCGTACAGATCATTG
Standard	Sp1g13030	*SpNHX8;2*	Reverse	509	GCCACAGGATCGGTAGCACCTAAAA
Q-PCR	Sp1g13030	*SpNHX8;2*	Forward	382	GCTGGCCCTGGAGTTTTAATCTCTACC
Q-PCR	Sp1g13030	*SpNHX8;2*	Reverse	453	CCAGTCATATGGAAAAGTGAACTTCAGA
Standard	Sp1g13040	*SpNHX8;3*	Forward	116	AAAAGTCCGGTGAAGAGTGCTTTTC
Standard	Sp1g13040	*SpNHX8;3*	Reverse	582	CAATGATGTTTTCCAATCCCAGTTATAT
Q-PCR	Sp1g13040	*SpNHX8;3*	Forward	152	TTGTTGTCCATCCCATAATAAAAGGAG
Q-PCR	Sp1g13040	*SpNHX8;3*	Reverse	262	CGCTCTCCATTGAAAACGAAGAAGAA

Supplemental Figure S6. Quantitative RT-PCR analysis of transcript abundances of *NHX8* homologs in *S. parvula* (Sp)

Four-week old *S. parvula* plants, grown in the same manner as the Figure 2 in the main text, were treated with indicated concentration of different salts for 24 hours. RNA samples were prepared as described in Methods for preparation of RNA-seq samples. Reverse transcription was performed with 0.7ug of total RNAs using SuperScriptIII (Life Technology, Carlsbad, CA), to produce cDNA samples. The transcript copy numbers were determined using primers specific to each *SpNHX8* duplicates, as shown in the table. PCR fragments of about 500 nucleotides encompassing the amplicons used for quantitative real-time PCR (Q-PCR) were amplified from cDNA samples and cloned into pGemT-easy vector (Promega, Madison, WI). Q-PCR was performed on cDNA samples, as well as on serial dilutions of known amounts of the cloned PCR fragments as standards for copy numbers. Transcript copy numbers were deduced based on comparison of Q-PCR results between cDNA samples and standards. Error bars indicate standard deviation from three biological repeats.

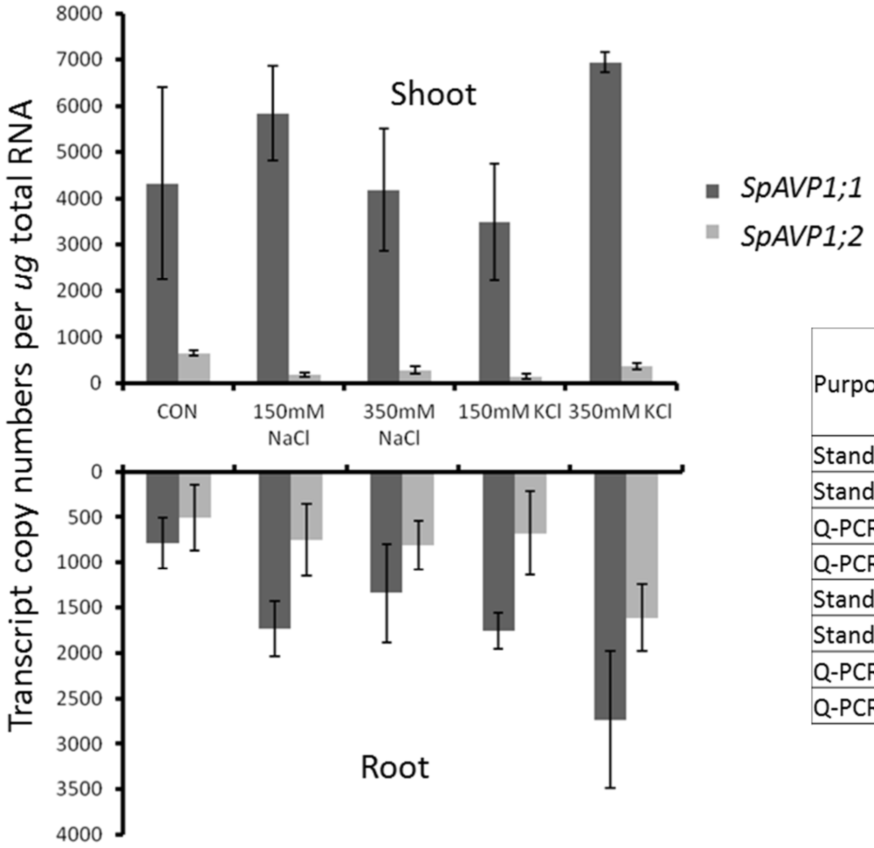


Deletion of the 2nd *AVP1* locus

SpAVP1;2

EsAVP1;2

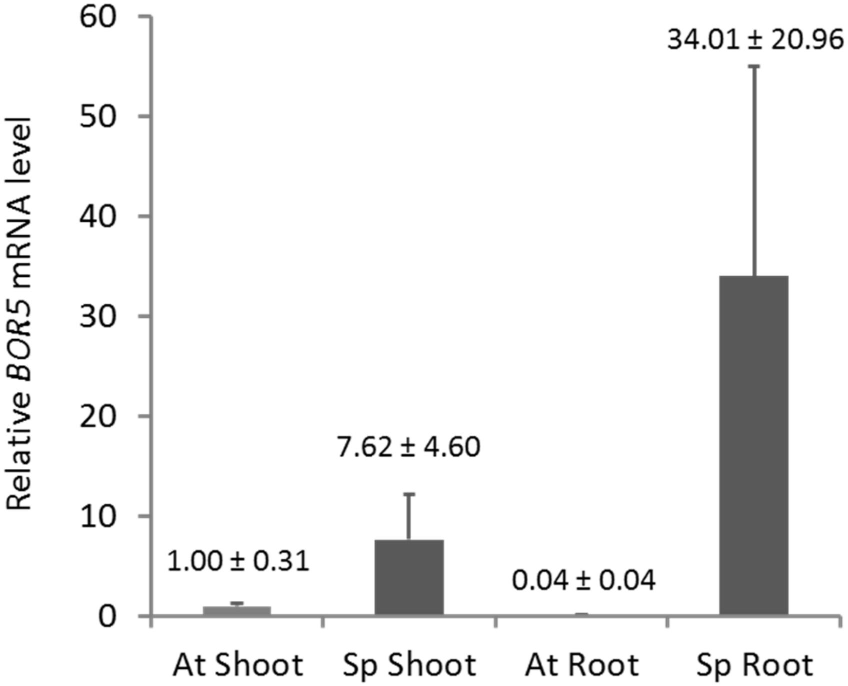
Supplemental Figure S7. Comparison of co-linear genomic regions near *AVP1;2* loci of *A. lyrata* (Al), *S. parvula* (Sp) and *E. salsugineum* (Es) The figure was generated in the same method as Figure S5, showing gene models encoding *AVP1;2* homologs with boxed gene IDs for Sp and Es, and deletion of the gene in Al. The comparison and all settings are available at: http://genomevolution.org/r/9tfs. Note that both halophytic species, Es and Sp, have kept the second *AVP1* copies, while both Arabidopsis species have deletions at the same loci. The same genomic region of *A. thaliana* was presented in Figure 5A of the main text, in comparison with *S. parvula*. *E. salsugineum* genome is from Yang et al. (2013).



Purpose	Gene ID	Annotation	Direction	Starting position in the gene	Primer sequence
Standard	Sp5g35350	*SpAVP1;1*	Forward	209	GTGGCGCGTCTTCTCTTTCTCAAG
Standard	Sp5g35350	*SpAVP1;1*	Reverse	701	AGCACCAAGAGACCGTTTGCAGC
Q-PCR	Sp5g35350	*SpAVP1;1*	Forward	209	GTGGCGCGTCTTCTCTTTCTCAAG
Q-PCR	Sp5g35350	*SpAVP1;1*	Reverse	348	AGAAGTTGCACCTTCGGATATAGCG
Standard	Sp1g13990	*SpAVP1;2*	Forward	235	AAGGTGCATCGTCTTCCGGTGGT
Standard	Sp1g13990	*SpAVP1;2*	Reverse	743	GGTAATGTAGAGCACCAACAGACCAC
Q-PCR	Sp1g13990	*SpAVP1;2*	Forward	235	AAGGTGCATCGTCTTCCGGTGGT
Q-PCR	Sp1g13990	*SpAVP1;2*	Reverse	381	ATGAAGTTGCACCTTCCGATATAGCA

Supplemental Figure S8. Quantitative RT-PCR analysis of transcript abundances of *AVP1* homologs in *S. parvula* (Sp)

See the legend of Figure S6 for experimental procedures and explanations.



Purpose	Gene ID	Annotation	Direction	Starting position in the gene*	Primer sequence
Q-PCR	Sp5g29940-At1g74810	*BOR5* (set 1)	Forward	1827	GGAGATCCCTGGAACTCCTAGA
Q-PCR	Sp5g29940-At1g74810	*BOR5* (set 1)	Reverse	1951	TGAGCTCGCCTCTGCTCGT
Q-PCR	Sp5g29940-At1g74810	*BOR5* (set 2)	Forward	1351	GGTTTCGATCCAGAGAAGCA
Q-PCR	Sp5g29940-At1g74810	*BOR5* (set 2)	Reverse	1427	TGCAACAGGTTGCTCACTCTCT
Q-PCR	Sp3g16870-At3g18780	*ACT2*	Forward	1224	GCAGCATGAAGATTAAGGTCGTT
Q-PCR	Sp3g16870-At3g18780	*ACT2*	Reverse	1330	GGAGATCCACATCTGCTGGAAT

*Positions in the At homologs. All primer sequences are conserved in the homologs of both species

Supplemental Figure S9. Quantitative RT-PCR comparing relative transcript abundances of *BOR5* homologs between *S. parvula* (Sp) and *A. thaliana* (At)

Relative expression levels are normalized with *ACT2* as the control and shown in a scale with the At Shoot data point as 1. All primers were designed to match both At and Sp sequences with the same amplicon length between species. Standard deviation is from four RT-PCR runs using two biological replicates and two different sets of *BOR5* primers.

Supplemental Table S1. *Summary of networks of GO terms over-represented in DEGP groups SpR and AtR*

Group	Network[a]	GO term[b]	Number (%) in DEGP group	Number (%) in background[c]	log(FDR)	Representative gene family
SpR (n=945)	1F	transporter activity	75 (7.9%)	1292 (4.6%)	-5.1	
		└ active transmembrane transporter activity	43 (4.6%)	597 (2.1%)	-5.4	
		└ antiporter activity	16 (1.7%)	145 (0.5%)	-4.5	
		└ monovalent cation:hydrogen antiporter activity	7 (0.7%)	45 (0.2%)	-3.2	
		└ substrate-specific transmembrane transporter activity	51 (5.4%)	820 (2.9%)	-4.5	
		└ amine transmembrane transporter activity	11 (1.2%)	77 (0.3%)	-4.3	
	2P	secondary metabolic process	70 (7.4%)	1242 (4.4%)	-4.5	
		└ isoprenoid metabolic process	37 (3.9%)	501 (1.8%)	-5.0	
		└ pigment metabolic process	32 (3.4%)	359 (1.3%)	-6.1	
		└ carotenoid metabolic process	13 (1.4%)	111 (0.4%)	-4.0	
		└ anthocyanin biosynthetic process	10 (1.1%)	63 (0.2%)	-4.3	
	3F	catalytic activity	392 (41.5%)	8760 (30.9%)	-6.2	
		└ esterase activity	55 (5.8%)	1040 (3.7%)	-3.1	
		└ oxidoreductase activity, acting on CH-OH group of donors	19 (2.0%)	217 (0.8%)	-3.8	
		└ acyltransferase activity	23 (2.4%)	298 (1.1%)	-3.7	
	4F	enzyme inhibitor activity	16 (1.7%)	188 (0.7%)	-3.2	
AtR (n=972)	1P	transport	180 (18.5%)	3566 (12.6%)	-5.7	
		└ cation transport	53 (5.5%)	813 (2.9%)	-4.9	
		└ metal ion transport	50 (5.1%)	576 (2.0%)	-8.2	
		└ inorganic anion transport	27 (2.8%)	267 (0.9%)	-6.1	
		└ nitrate transport	24 (2.5%)	207 (0.7%)	-6.5	
	2P	response to stimulus	299 (30.8%)	6237 (22.0%)	-6.5	
		└ defense response	98 (10.1%)	1628 (5.7%)	-6.5	
		└ innate immune response	53 (5.5%)	914 (3.2%)	-3.6	
		└ response to inorganic substance	68 (7.0%)	1078 (3.8%)	-5.5	
		└ response to nitrate	26 (2.7%)	199 (0.7%)	-8.1	
	3F	catalytic activity	415 (42.7%)	8760 (30.9%)	-7.7	
		└ glycosyltransferase activity	40 (4.1%)	590 (2.1%)	-4.2	Glycosyltransferase
		└ oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	45 (4.6%)	463 (1.6%)	-9.0	
	4F	transporter activity	76 (7.8%)	1292 (4.6%)	-5.0	
		└ substrate-specific transmembrane transporter activity	47 (4.8%)	820 (2.9%)	-3.2	
		└ amine transmembrane transporter activity	9 (0.9%)	77 (0.3%)	-2.9	
	5P	secondary metabolic process	72 (7.4%)	1242 (4.4%)	-4.6	
		cellular amino acid derivative metabolic process	44 (4.5%)	703 (2.5%)	-3.8	
		└ phenylpropanoid metabolic process	30 (3.1%)	396 (1.4%)	-4.2	
	6F	purine nucleoside binding	112 (11.5%)	2378 (8.4%)	-3.0	
		└ ADP binding	18 (1.9%)	168 (0.6%)	-4.6	TIR-NBS-LRR
	7F	heme binding	41 (4.2%)	377 (1.3%)	-9.7	Cytochrome P450

[a] P=Biological Process, F=Molecular Function; [b] GO terms best describing all branches of the network are selected ; [c] GO annotation of *A. thaliana* (TAIR10, n= 28,352) was used as the background.

Supplemental Table S2. *Summary of networks of GO terms over-represented in DEGP groups SpS and AtS*

Group	Network[a]	GO term[b]	Number (%) in DEGP group	Number (%) in background[c]	log(FDR)	Representative gene family
SpS (n=965)	1P	cell wall organization or biogenesis	61 (6.3%)	946 (3.3%)	-5.4	
		└ cell wall polysaccharide metabolic process	29 (3.0%)	227 (0.8%)	-8.8	
		└ xylan biosynthetic process	24 (2.5%)	182 (0.6%)	-7.7	
	2P	pollen tube development	24 (2.5%)	287 (1.0%)	-4.2	
		└ cell tip growth	25 (2.6%)	328 (1.2%)	-3.7	
	3P	actin filament-based process	23 (2.4%)	260 (0.9%)	-4.4	
		└ cytoskeleton-dependent intracellular transport	12 (1.2%)	82 (0.3%)	-4.6	
		└ xylem development	13 (1.3%)	82 (0.3%)	-5.4	
AtS (n=1,058)	1P	response to stimulus	341 (32.2%)	6237 (22.0%)	-9.1	
		└ defense response	127 (12.0%)	1628 (5.7%)	-12.8	TIR-NBS-LRR
		└ innate immune response	68 (6.4%)	914 (3.2%)	-6.7	
		└ cell death	35 (3.3%)	495 (1.7%)	-3.5	
		└ response to inorganic substance	85 (8.0%)	1078 (3.8%)	-9.3	
		└ response to nitrate	34 (3.2%)	199 (0.7%)	-12.6	
		└ response to metal ion	40 (3.8%)	608 (2.1%)	-3.2	
	2P	secondary metabolic process	73 (6.9%)	1242 (4.4%)	-3.7	
		cellular aromatic compound metabolic process	66 (6.2%)	1015 (3.6%)	-4.7	
		└ phenylpropanoid metabolic process	30 (2.8%)	396 (1.4%)	-3.6	
		└ auxin biosynthetic process	15 (1.4%)	123 (0.4%)	-4.2	
	3P	transport	191 (18.1%)	3566 (12.6%)	-5.4	
		└ amino acid transport	23 (2.2%)	266 (0.9%)	-3.7	
		└ metal ion transport	54 (5.1%)	576 (2.0%)	-8.7	
		└ nitrate transport	35 (3.3%)	207 (0.7%)	-12.9	
	4P	regulation of biological quality	91 (8.6%)	1609 (5.7%)	-3.9	
		└ ion homeostasis	25 (2.4%)	227 (0.8%)	-5.7	
		└ metal ion homeostasis	9 (0.9%)	51 (0.2%)	-4.0	
	5F	nucleotide binding	176 (16.6%)	3504 (12.4%)	-3.7	
		└ ADP binding	38 (3.6%)	168 (0.6%)	-18.3	TIR-NBS-LRR
	6F	catalytic activity	441 (41.7%)	8760 (30.9%)	-7.1	
		└ glycosyltransferase	40 (3.8%)	590 (2.1%)	-3.5	
	7P	regulation of defense response	41 (3.9%)	524 (1.8%)	-4.9	
		└ regulation of innate immune response	30 (2.8%)	412 (1.5%)	-3.3	
		└ negative regulation of defense response	24 (2.3%)	274 (1.0%)	-3.9	
	8F	heme binding	36 (3.4%)	377 (1.3%)	-6.3	Cytochrome P450
	9F	ligand-gated channel activity	6 (0.6%)	29 (0.1%)	-3.2	Glutamate receptor

[a] P=Biological Process, F=Molecular Function; [b] GO terms best describing all branches of the network are selected ; [c] GO annotation of *A. thaliana* (TAIR10, n= 28,352) was used as the background.

Supplemental Table S3. *List of salt or ion stress-related* A. thaliana *(At) qualitative trait loci*[a] *that are either included in DEGPs or showing CNVs in* S. parvula *(Sp)*

Keyword	At Locus	Name	Function	DEGP group	Copy number in *Sp*	Reference
Salt stress, Sodium, Potassium	At2g36270	ABA Insensitive 5 (ABI5)	Transcription factor	SpR	1	TAIR germplasm DB
	At1g15690	Arabidopsis Vacuolar Pyrophosphatase1 (AVP1)	Ion transport	-	2	Pasapula et al., 2011
	At4g33000	Calcineurin B-Like 10 (CBL10)	Ca^{2+} signaling	-	3	TAIR germplasm DB
	At2g39800	delta1-Pyrroline-5-Carboxylate Synthase 1 (P5CS1)	Proline synthesis	SpR	1	TAIR germplasm DB
	At4g10310	High-affinity K^+ Transporter 1 (HKT1)	Ion transport	SpS,AtR	2	TAIR germplasm DB
	At2g36490	Repressor of Silencing 1 (ROS1)	DNA demethylation	SpR	1	TAIR germplasm DB
	At2g01980	Salt Overly Sensitive 1 (SOS1)	Ion transport	SpR,SpS	1	TAIR germplasm DB
Lithium	At1g14660	Na^+/H^+ Exchanger 8 (NHX8)	Ion transport	SpR,SpS	3	An et al., 2007
Magnessium	At5g09690	Magnesium Transporter 7 (MGT7)	Ion transport	AtS	1	TAIR germplasm DB
Boron	At4g10380	NOD26-like Intrinsic Protein 5;1 (NIP5;1)	Ion transport	SpS	1	TAIR germplasm DB
	At1g80760	NOD26-like Intrinsic Protein 6;1 (NIP6;1)	Ion transport	-	2	TAIR germplasm DB

[a] At loci reported with salt or ion stress-related phenotypes when either mutated or over-expressed, curated by text mining with relevant keywords in TAIR germplasm database (DB) , the latest TAIR gene annotation, and the literature.

Supplemental Table S4. *Overview of ion transporter gene families in* S. parvula *(Sp) and* A. thaliana *(At)*

Ion transporter gene family[a]	# *Sp*[b]	# *At*	DEGPs / gene pairs (%)	SpR	SpS	AtR	AtS
Na^+ K^+ transporter (HKT1)	2	1	2 / 2 (100.0%)	0	1	0	1
Other anion transporter (DUR3, TDT, DiT2.2)	4	4	3 / 4 (75.0%)	0	0	2	1
K^+ channel (AKT1, KCOs, SKOR, GORK, KT)	17	16	6 / 15 (40.0%)	3	2	1	2
Sulphate transporter (SULTRs)	13	13	5 / 13 (38.5%)	3	3	1	0
Na^+-H^+ antiporter (NHXs, SOS1)	12	10	4 / 12 (33.3%)	2	2	0	1
Aquaporins (PIPs, TIPs, NIPs)	35	38	10 / 32 (31.3%)	5	5	3	0
K^+-efflux system (KEAs)	6	6	2 / 7 (28.6%)	2	0	0	0
Nitrate transporter (NRTs)	8	8	2 / 7 (28.6%)	0	0	1	2
Metal transporter (NRAMPs, ZIPs, MTPBs)	47	38	9 / 34 (26.5%)	3	1	5	4
Anion exchanger (BORs, HCO^{3-} transporters)	7	7	2 / 8 (25.0%)	1	1	1	0
Cation-H^+ antiporter (CHXs)	27	28	5 / 29 (17.2%)	3	4	1	1
Ammonium transporter (AMTs)	5	6	1 / 6 (16.7%)	1	0	0	0
Glutamate receptor (GLRs)	14	21	3 / 20 (15.0%)	0	0	3	0
Cyclic nucleotide gated channel (CNGCs)	21	20	2 / 18 (11.1%)	2	1	1	0
Mg^{2+}-transporter (MGTs, MRSs)	10	11	1 / 9 (11.1%)	0	0	0	1
P-type pump (ACAs, AHAs, HMAs, ECAs)	50	48	5 / 47 (10.6%)	0	1	3	3
Ca^{2+}-H^+ antiporter (CAXs)	10	11	1 / 11 (9.1%)	1	1	0	0
K^+-transporter (KUPs, TRH1)	18	13	1 / 14 (7.1%)	1	0	0	0
Phosphate transporter (PHTs)	20	18	1 / 17 (5.9%)	0	0	1	0
V-type pump (Vacuolar ATP synthase subunits)	28	27	1 / 29 (3.4%)	1	0	0	0
Cl^- channel (CLCs)	11	11	0 / 10 (0.0%)	0	0	0	0
Putative Ca^{2+} channel (SCAMPs, TPC1)	6	7	0 / 6 (0.0%)	0	0	0	0
F-type ATPase	5	5	0 / 4 (0.0%)	0	0	0	0
PPase (AVPs)	3	3	0 / 4 (0.0%)	0	0	0	0
Cation-Cl^- co-transporter (CCC)	1	1	0 / 1 (0.0%)	0	0	0	0
Mg^{2+}-H^+ exchanger (MHX)	1	1	0 / 1 (0.0%)	0	0	0	0
Total	381	372	66/360 (18.3%)				

[a] Ion transporter families are based on Maathuis *el al*. (2003);

[b] Based on *S. parvula* genome annotation version 2.0

Supplemental Table S5. *List of DEGPs encoding ion transporters and channels*

Ion transporter family	Annotation	Sp homolog	At homolog	Root			Shoot			DEGP group
				Mean Sp	Mean At	FDR (%)	Mean Sp	Mean At	FDR (%)	
Ammonium transporter (AMTs)	AMT1;5	Sp3g22070	At3g24290	**8802**	**47**	**4.8**	42	2	31.2	SpR
Anion exchanger (BORs, HCO^{3-} transporters)	BOR5	Sp5g29940	At1g74810	**10582**	**26**	**0.0**	**3841**	**794**	**0.3**	SpR, SpS
	HCO^{3-} transporter family	Sp5g01110	At3g62270	**351**	**2072**	**0.1**	268	600	18.7	AtR
Aquaporins (PIPs, TIPs, NIPs)	PIP1;5	Sp7g21310	At4g23400	**839**	**5902**	**0.5**	7046	11163	74.2	AtR
	PIP1A	Sp5g01970	At3g61430	22635	37225	49.4	**28705**	**8565**	**1.8**	SpS
	PIP2;5	Sp5g07610	At3g54820	**207**	**1088**	**0.2**	465	580	87.7	AtR
	PIP2E	Sp4g21370	At2g39010	**812**	**120**	**0.1**	10229	11519	97.5	SpR
	PIP3	Sp7g32870	At4g35100	22088	14938	67.5	**47832**	**15656**	**3.1**	SpS
	SIP1;2	Sp6g26010	At5g18290	**15**	**140**	**0.2**	88	114	90.3	AtR
	TIP2;3	Sp2g12160	At5g47450	**28456**	**8171**	**4.0**	157	181	97.8	SpR
	NIP5;1	Sp6g07050	At4g10380	4743	2917	53.5	**6459**	**985**	**0.0**	SpS
	TIP2;2	Sp7g16840	At4g17340	**1473**	**21246**	**0.0**	**19**	**4300**	**0.0**	AtR, AtS
Ca^{2+}-H^+ antiporter (CAXs)	CAX4	Sp6g40770	At5g01490	**1583**	**448**	**2.9**	**49**	**12**	**2.8**	SpR, SpS
Cation-H^+ antiporter (CHXs)	CHX24/25	Sp6g20150	At5g37060	**266**	**0**	**0.0**	**180**	**0**	**0.0**	SpR, SpS
			At5g58460*		**3**	**0.0**		**0**	**0.0**	
	CHX3	Sp6g22500	At5g22900	**2732**	**2**	**0.0**	**949**	**1**	**0.0**	SpR, SpS
Cyclic nucleotide gated channel (CNGCs)	DND1	Sp6g28680	At5g15410	**890**	**250**	**2.2**	8285	5364	56.2	SpR
	CNGC10/13	Sp6g01140	At1g01340	**1103**	**6026**	**1.1**	791	409	50.7	AtR
			At4g01010*		965	92.2		1239	70.0	
	CNGC9	Sp7g28440	At4g30560	**3018**	**519**	**0.1**	**3314**	**437**	**0.0**	SpR, SpS
Glutamate receptor (GLRs)	GLR1.1	Sp3g03080	At3g04110	61	390	7.7	**95**	**1397**	**0.4**	AtS
	GLR1.2/3/4	Sp2g18760	At5g48400*	**50**	138	75.4	**158**	214	93.2	AtS
			At5g48410		297	24.1		161	98.8	
			At3g07520		**574**	**0.0**		**778**	**0.4**	
	GLR2.1/2/3/4	Sp4g03690	At5g27100	478	1097	22.9	**2**	**477**	**0.0**	AtS
			At2g24720		1095	21.5		17	10.2	
			At2g24710		438	97.8		11	31.9	
			At4g31710		172	23.2		7	53.5	
	GLR3.3	Sp1g37300	At1g42540	705	1109	59.8	**742**	**2265**	**4.6**	AtS
K^+ channel (AKT1, KCOs, SKOR, GORK, KT)	GORK	Sp7g04660	At5g37500	2242	979	16.9	**4882**	**700**	**0.0**	SpS
	KCO1	Sp6g17550	At5g55630	618	949	60.4	**302**	**1405**	**0.4**	AtS
	KAT3	Sp7g30420	At4g32650	2582	2816	94.8	**57**	**505**	**0.0**	AtS
	KCO2	Sp2g11210	At5g46370	**422**	**52**	**0.1**	**141**	**7**	**0.0**	SpR, SpS
	KT5	Sp7g30270	At4g32500	**92**	**7**	**0.2**	**214**	**3**	**0.0**	SpR, SpS
	SKOR	Sp3g01880	At3g02850	**272**	**2188**	**0.0**	29	94	5.7	AtR
K^+-efflux system (KEAs)	KEA1	Sp1g00490	At1g01790	**6867**	**965**	**0.0**	10601	12926	90.2	SpR
		Sp1g00500*		2212		21.7	13075		99.2	
	KEA5	Sp2g02290	At5g51710	**1983**	**547**	**2.2**	1494	989	65.1	SpR
K^+-transporter (KUPs, TRH1)	KUP9	Sp7g12130	At4g19960	1901	**941**	57.6	4830	3181	84.9	SpR
		Sp7g18400*		**4540**		**0.8**	2636		85.9	

Supplemental Table S5. continued

Ion transporter family	Annotation	Sp homolog	At homolog	Root			Shoot			DEGP group
				Mean Sp	Mean At	FDR (%)	Mean Sp	Mean At	FDR (%)	
Metal transporter (NRAMPs, ZIPs, MTPBs)	Cation efflux family	Sp5g04660	At3g58060	**434**	**21**	**0.0**	**4**	**30**	**0.8**	SpR, AtS
	emb1513	Sp4g20220	At2g37920	**343**	**106**	**4.1**	1606	1533	97.7	SpR
	MTPB1	Sp4g12170	At2g29410	**304**	**69**	**2.8**	178	54	9.8	SpR
	NRAMP1	Sp5g34930	At1g80830	**494**	**7179**	**0.0**	**680**	**2465**	**1.4**	AtR, AtS
	NRAMP5	Sp7g17490	At4g18790	**255**	**1**	**0.0**	**119**	**1**	**0.0**	SpR, SpS
	NRAMP6	Sp1g14270	At1g15960	**444**	**2056**	**0.3**	**401**	**2300**	**0.1**	AtR, AtS
	ZIP2	Sp6g21230	At5g59520	**63**	**468**	**0.2**	**0**	**12**	**0.5**	AtR, AtS
	ZIP5	Sp1g04160	At1g05300	**57**	**927**	**0.1**	1255	1512	93.2	AtR
	ZIP6	Sp4g12640	At2g30080	**1664**	**468**	**2.6**	124	186	67.2	AtR
Mg^{2+}-transporter (MGTs, MRSs)	MGT7	Sp6g33680	At5g09690	674	833	87.2	**15**	**295**	**0.0**	AtS
Na^{+} K^{+} transporter (HKT1)	HKT1	Sp6g07110	At4g10310	**16**	**1627**	**0.0**	**1078**	**92**	**0.5**	SpS, AtR
		Sp6g07120*		**14**		**0.0**	**3**		**0.4**	
Na^{+}-H^{+} antiporter (NHXs, SOS1)	NHX8	Sp1g13020	At1g14660	1110	**506**	17.8	**5124**	**660**	**0.0**	SpR, SpS
		Sp1g13030*		1247		51.4	438		85.8	
		Sp1g13040		**3733**		**0.0**	484		74.2	
	SOS1	Sp2g13410	At2g01980	**8356**	**1828**	**0.3**	**11039**	**1628**	**0.0**	SpR, SpS
	NHX3	Sp6g17350	At5g55470	64	153	32.8	**7**	**305**	**0.0**	AtS
Nitrate transporter (NRTs)	NRT2.6	Sp5g16190	At3g45060	**4**	**838**	**0.0**	**0**	**226**	**0.0**	AtR, AtS
		Sp5g16200*		196		20.3	**6**		**0.1**	
	NRT3.1	Sp6g12300	At5g50200	9607	8439	92.9	**117**	**890**	**0.1**	AtS
Other anion transporter (DiT2.2,DUR3, TDT)	DiT2.2	Sp2g27340	At5g64280	**169**	**1102**	**0.0**	2144	3619	51.8	AtR
	DUR3	Sp1g01330	At1g02260	396	1120	7.4	**418**	**1569**	**1.6**	AtS
	TDT	Sp2g12290	At5g47560	**63**	**790**	**0.0**	4704	2955	58.2	AtR
Phosphate transporter (PHTs)	PHT1;3/5/6/7	Sp5g07750	At5g43360	**0**	**1475**	**4.5**	0	31	31.3	AtR
			At2g32830		14	41.5		189	18.3	
			At5g43340		0	100.0		5	84.6	
			At3g54700*		1	82.3		14	60.0	
P-type pump (ACAs, AHAs, HMAs, ECAs)	AHA10	Sp1g15390	At1g17260	**18**	**159**	**0.2**	49	165	13.6	AtR
	E1-E2 type ATPase family	Sp1g40710	At1g54280	185	61	14.7	**181**	**17**	**0.1**	SpS
	HA8	Sp5g18280	At3g42640	**0**	**1322**	**0.0**	**0**	**752**	**0.0**	AtR, AtS
	HMA2	Sp7g27960	At4g30110	1700	1355	85.1	**447**	**1670**	**1.6**	AtS
	HMA3	Sp7g27970	At4g30120	**11**	**225**	**0.0**	**8**	**76**	**0.5**	AtR, AtS
	HMA5	Sp2g01170*	At1g63440	**805**	**3524**	**0.6**	237	326	72.4	AtR
		Sp7g11650		**340**		**0.0**	482		71.7	
Sulphate transporter (SULTRs)	AST91	Sp1g20530	At1g23090	**1817**	**81**	**0.0**	4620	2054	19.5	SpR
	SULTR1;1	Sp6g09230	At4g08620	**0**	**581**	**0.0**	4	20	47.4	AtR
	SULTR3;2	Sp5g10370	At4g02700	**497**	**131**	**1.6**	**4178**	**130**	**0.0**	SpR, SpS
	SULTR3;5	Sp6g24790	At5g19600	1007	2201	60.0	**2042**	**252**	**3.5**	SpS
	SULTR4;2	Sp3g10650	At3g12520	**3929**	**311**	**0.0**	**3617**	**884**	**0.6**	SpR, SpS

Supplemental Table S6. Detailed information of homologous gene pairs shown in Figure 4

Figure	ID	Homologous gene pairs	Annotation	BLASTN best match	SV event	promoter sequence identity (%)	Root			Shoot		
							Mean *Sp*	Mean *At*	FDR (%)	Mean *Sp*	Mean *At*	FDR (%)
Fig4A	1	Sp1g00420-At1g01880	5'-3' exonuclease family	reciprocal		43.7	104	109	97.1	162	374	30.2
	2	Sp1g00430-At1g01860	PALEFACE 1 (PFC1)	reciprocal		62.1	278	402	69.0	782	1,266	56.3
	3	Sp1g00440-At1g01840	unknown protein	reciprocal		50.0	65	109	66.2	180	108	67.2
	4	Sp1g00450-At1g01830	ARM repeat superfamily	reciprocal		58.1	1,027	919	92.4	1,147	982	92.7
	5	Sp1g00460-At1g01820	peroxin 11c (PEX11C)	reciprocal		34.8	6,353	4,018	60.8	3,874	2,642	65.8
	6	Sp1g00470-At1g01810	unknown protein	reciprocal		58.1	51	46	99.6	31	52	78.4
	7	Sp1g00480-At1g01800	NAD(P)-binding Rossmann-fold superfamily	reciprocal		10.3	2,345	2,554	95.8	3,248	3,775	90.8
	KEA1	Sp1g00490-At1g01790	K$^+$ efflux antiporter 1 (KEA1)	Sp->At	TD (Sp)	15.3	**965**	**6,867**	**0.0**	12,926	10,601	90.2
		Sp1g00500-At1g01790		reciprocal		67.1		2,212	21.7		13,075	99.2
	8	Sp1g00510-At1g01780	GATA type zinc finger transcription factor family	reciprocal		80.9	**951**	**58**	**0.0**	**625**	**18**	**0.0**
	9	Sp1g00540-At1g01760	adenosine deaminases	reciprocal		70.0	287	535	42.4	210	446	31.3
	10	Sp1g00550-At1g01750	actin depolymerizing factor 11 (ADF11)	reciprocal		45.1	603	770	85.4	99	121	88.1
	11	Sp1g00560-At1g01740	Protein kinase with tetratricopeptide repeat domain	reciprocal		53.3	572	1,035	37.8	616	915	70.0
	12	Sp1g00570-At1g01730	unknown protein	reciprocal		57.7	1,529	1,234	85.3	1,113	802	73.7
Fig4B	1	Sp1g12980-At1g14620	DECOY (DECOY)	reciprocal		25.1	1,998	1,198	49.2	890	807	96.3
	2	Sp1g12990-At1g14630	unknown protein	reciprocal		68.1	295	1,037	17.9	114	290	33.3
	3	Sp1g13010-At1g14640	SWAP (Suppressor-of-White-APricot) domain	At->Sp	TD (At)	0.0	**1,095**	**5,571**	**0.1**	**458**	**4,050**	**0.0**
		Sp1g13010-At1g14650		reciprocal		39.6	5,691		100.0	3,750		97.6
	NHX8	Sp1g13020-At1g14660	Na$^+$/H$^+$ exchanger 8 (NHX8)	Sp->At	TD (Sp)	0.0	**506**	1,110	17.8	**660**	**5,124**	**0.0**
		Sp1g13030-At1g14660		reciprocal		8.4		1,247	51.4		438	85.8
		Sp1g13040-At1g14660		Sp->At		0.0		**3,733**	**0.0**		484	74.2
	4	Sp1g13050-At1g14670	Endomembrane protein 70 protein family	reciprocal		15.8	7,185	5,865	81.0	6,715	4,386	64.2
	5	Sp1g13060-At1g14680	unknown protein	reciprocal		76.3	56	28	64.3	68	12	10.1
	6	Sp1g13070-At1g14685	basic pentacysteine 2 (BPC2)	reciprocal		70.2	1,755	1,831	99.2	2,089	2,624	83.6
	7	Sp1g13080-At1g14686	ENTH/ANTH/VHS superfamily	reciprocal		41.7	5	10	87.3	3	8	84.9
Fig4C	1	Sp6g07060-At4g10360	TRAM/LAG1/CLN8 (TLC) lipid-sensing domain	reciprocal		54.9	1,565	769	31.2	1,548	1,149	77.3
	2	Sp6g07070-At4g10350	NAC domain containing 70 (NAC070)	reciprocal		68.3	124	195	82.8	2	0	84.2
	3	Sp6g07090-At4g10340	light harvesting complex of photosystem II 5 (LHCB5)	reciprocal		67.9	1,364	1,277	100.0	218,344	160,405	95.6
	4	Sp6g07100-At4g10330	glycine-rich protein	reciprocal		9.6	529	329	61.8	481	445	97.9
	-	Sp7g00280-At4g10320	tRNA synthetase class I (I, L, M and V) family	reciprocal	Tlc	0.0	8,168	8,841	96.3	7,131	6,355	94.7
	HKT1	Sp6g07110-At4g10310	high-affinity K$^+$ transporter 1 (HKT1)	Sp->At	TD (Sp)	13.2	**1,627**	**16**	**0.0**	**92**	**1,078**	**0.5**
		Sp6g07120-At4g10310		reciprocal		0.0		**14**	**0.0**		**3**	**0.4**
	CBL10	Sp6g07129-At4g33000	calcineurin B-like 10 (CBL10)	Sp->At	Tlc-TD (Sp)	0.0	117	64	58.6	1,520	1,139	88.2
		Sp6g07131-At4g33000		Sp->At		0.0		119	100.0		980	74.4
	5	Sp6g07140-At4g10300	RmlC-like cupins superfamily	reciprocal		4.1	276	402	72.2	5,261	4,899	99.3

Homologous gene pairs highlighted in Fig ure 4 are shaded gray.

Supplemental Table S7. Detailed information of homologous gene pairs shown in Figure 5

Figure	ID	Homologous gene pairs	Annotation	BLASTN best match	SV event	promoter sequence identity (%)	Root			Shoot		
							Mean *Sp*	Mean *At*	FDR (%)	Mean *Sp*	Mean *At*	FDR (%)
Fig5A upper panel	1	Sp5g35290-At1g80510	Transmembrane amino acid transporter family	reciprocal		64.6	589	1,279	26.9	986	1,106	95.1
	2	Sp5g35300-At1g80500*	SNARE-like superfamily protein	reciprocal		-	-	-	-	-	-	-
	3	Sp5g35310-At1g80490	TOPLESS-related 1 (TPR1)	reciprocal		71.0	6,798	10,764	54.4	3,870	6,278	54.3
	4	Sp5g35320-At1g80480	plastid transcriptionally active 17 (PTAC17)	reciprocal		62.3	1,178	1,824	57.9	6,494	6,278	100.0
	-	Sp5g35330-At4g33370	DEA(D/H)-box RNA helicase family	At->Sp	Tlc	0.0	**30**	**2,197**	**0.0**	**38**	**1,530**	**0.0**
	-	Sp5g35340-At2g26865	LOCATED IN: endomembrane system	reciprocal	Tlc	53.5	0	0	100.0	0	0	100.0
	AVP1	Sp5g35350-At1g15690	(*SpAVP1;2*)	Sp->At	Tlc	0.0	**21,806**	**6,264**	**1.7**	**43,620**	**3,510**	**0.0**
	5	Sp5g35360-At1g80460	nonhost resistance to P. s. phaseolicola 1 (NHO1)	reciprocal		40.3	5,578	2,284	13.3	3,154	1,943	55.1
	6	Sp5g35370-At1g80450	VQ motif-containing	reciprocal		65.6	291	200	72.2	305	191	60.8
	7	Sp5g35380-At1g80440	Galactose oxidase/kelch repeat superfamily	reciprocal		40.4	1,271	861	76.9	3,107	3,966	88.7
	8	Sp5g35390-At1g80420	ATXRCC1	reciprocal		59.1	901	919	100.0	1,274	813	60.2
	9	Sp5g35400-At1g80410	EMBRYO DEFECTIVE 2753 (EMB2753)	reciprocal		73.9	8,935	7,898	92.4	6,243	6,053	99.8
Fig5A lower panel	10	Sp1g13970-At1g15660	centromere protein C (CENP-C)	reciprocal		17.9	872	1,280	70.2	810	610	82.2
	11	Sp1g13980-At1g15670	Galactose oxidase/kelch repeat superfamily	reciprocal		37.8	4,083	2,766	87.0	1,002	348	54.3
	AVP1	Sp1g13990-At1g15690	AVP1 (*SpAVP1;1*)	reciprocal		52.5	21,806	30,195	73.9	43,620	59,813	72.8
	12	Sp1g14000-At1g15700	ATPC2	reciprocal		58.2	608	625	98.9	263	520	37.0
	13	Sp1g14010-At1g15710	prephenate dehydrogenase family	reciprocal		55.5	555	441	82.5	847	944	93.6
	14	Sp1g14020-At1g15730	Cobalamin biosynthesis CobW-like	reciprocal		22.8	589	489	94.8	2,340	1,323	45.8
	15	Sp1g14030-At1g15740	Leucine-rich repeat family	reciprocal		70.4	5,147	3,745	73.7	6,184	6,037	100.0
	16	Sp1g14040-At1g15750	TOPLESS (TPL)	reciprocal		83.1	10,725	8,159	77.7	8,527	6,083	71.8
Fig5B	1	Sp5g29900-At1g74790	catalytics	reciprocal		78.3	1,398	3,338	17.6	905	1,927	23.2
	-	Sp5g29910-At1g18950	DDT domain superfamily	Sp->At	Tlc	14.7	2,404	981	15.1	2,172	868	12.3
	2	Sp5g29920-At1g74800	Galactosyltransferase family	reciprocal		17.7	796	1,209	65.4	833	957	92.1
	-	Sp5g29930-At5g14200*	isopropylmalate dehydrogenase 1 (IMD1)	Sp->At	Tlc	-	-	-	-	-	-	-
	BOR5	Sp5g29940-At1g74810	BOR5	reciprocal		8.6	**26**	**10,582**	**0.0**	**794**	**3,841**	**0.3**
	3	Sp5g29950-At1g74820	RmlC-like cupins superfamily	reciprocal		58.8	1	1	100.0	0	0	100.0
	4	Sp5g29960-At1g74830	Protein of unknown protein function, DUF593	reciprocal		81.2	140	21	52.9	5	0	34.7
	5	Sp5g29970-At1g74840	Homeodomain-like superfamily	reciprocal		37.7	9,335	4,212	18.9	2,375	2,291	100.0
	6	Sp5g29980-At1g74850	plastid transcriptionally active 2 (PTAC2)	reciprocal		32.9	248	592	16.6	3,202	3,236	100.0

Homologous gene pairs highlighted in Figure 5 are shaded gray; * partial homology

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