

Supplementary Table S1 The average electrical conductivity of substrate

NaCl Concentration	0.0%	0.2%	0.4%	0.6%	0.8%
Electrical Conductivity (dS m ⁻¹)					
The 1st Day	1.100	1.616	2.720	3.690	4.890
The 60th Day	1.183	1.645	2.680	3.573	4.572

Supplemental Table S2 Transcriptome comparion statistics

Samples_ID	All reads	Mapped reads	Mapped pair reads	Mapped broken-pair reads	Mapped unique reads	Mapped multi reads	Mapping ratio
401 ₀	47800427	21265641	11198366	10067275	20628629	637012	44.49%
401 ₆	46925138	21309391	11448032	9861359	20668223	641168	45.41%
T46 ₀	43434145	19289753	10350076	8939677	18713319	576434	44.41%
T46 ₆	50561810	22252762	11811456	10441306	21591536	661226	44.01%
T12 ₀	45666581	19875066	10345022	9530044	19276874	598192	43.52%
T12 ₆	64667540	29024640	15647984	13376656	28171096	853544	44.88%

Supplemental Table S3 The functional analysis of differential expressed genes in transgenic poplar under salty stress

Gene ID	Function description	Tair ID	log2FC	P-value
Genes associated to plant growth				
Potri.002G069800	SERINE DECARBOXYLASE 1	AT1G43710.1	1.94	4.15E-12
Potri.010G210000	PsbP-like protein 2	AT2G39470.1	1.40	4.25E-06
Potri.008G101500	Plant neutral invertase family protein	AT3G06500.1	2.22	9.11E-14
Potri.014G149700	pectin methylesterase 61	AT3G59010.1	1.16	2.94E-05
Potri.014G022900	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	AT3G16150.1	3.71	4.84E-20
Potri.007G089000	myo-inositol-1-phosphate synthase 2	AT2G22240.1	2.63	1.39E-26
Potri.008G144500	myo-inositol oxygenase 1	AT1G14520.2	3.11	1.55E-12
Potri.006G227500	Glycosyl hydrolases family 32 protein	AT3G13790.1	1.35	4.44E-05
Potri.001G449100	Glycosyl hydrolase superfamily protein	AT1G32860.1	1.35	0.000224
Potri.012G106500	Glycosyl hydrolase family 38 protein	AT5G13980.2	1.07	0.000336
Potri.015G132600	glycosyltransferase 18	AT5G62220.1	1.62	0.000464
Potri.005G072500	GCR2-like 1	AT5G65280.1	2.66	2.21E-17
Potri.016G025500	alpha-L-arabinofuranosidase 1	AT3G10740.1	1.41	0.000574
Potri.003G142000	3-ketoacyl-acyl carrier protein synthase I	AT5G46290.1	Inf	1.02E-16
Potri.019G028100	Photosystem I, PsaA/PsaB protein	ATCG00350.1	-2.99	2.09E-25
Potri.013G141800	Photosystem I, PsaA/PsaB protein	ATCG00350.1	-1.56	2.95E-08
Potri.003G065200	Photosystem I, PsaA/PsaB protein	ATCG00350.1	-1.62	0.002827
Potri.008G189700	Protein kinase superfamily protein	AT1G70460.1	-1.31	0.001041
Potri.002G083200	Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain	AT1G44446.1	-1.31	3.52E-12
Potri.011G075000	Chloroplast Ycf2;ATPase, AAA type, core	ATCG01280.1	-2.51	1.48E-13
Potri.014G118400	stachyose synthase	AT4G01970.1	1.53	2.97E-07

Potri.018G063500	sucrose synthase 4	AT3G43190.1	3.59	4.64E-23
Genes associated to wood property				
Potri.018G100500	NAD(P)-binding Rossmann-fold superfamily protein	AT2G23910.1	2.94	4.13E-25
Potri.018G081200	NAD(P)-binding Rossmann-fold superfamily protein	AT4G13250.1	1.29	9.54E-07
Potri.015G050200	NAD(P)-binding Rossmann-fold superfamily protein	AT1G75290.1	3.02	6.22E-24
Potri.010G129800	NAD(P)-binding Rossmann-fold superfamily protein	AT1G75290.1	1.39	7.48E-08
Potri.008G116500	NAD(P)-binding Rossmann-fold superfamily protein	AT1G75290.1	2.55	5.65E-19
Potri.006G178700	NAD(P)-binding Rossmann-fold superfamily protein	AT2G23910.1	2.37	8.65E-09
Potri.004G030700	NAD(P)-binding Rossmann-fold superfamily protein	AT1G61720.1	2.56	4.62E-22
Potri.001G140700	NAD(P)-binding Rossmann-fold superfamily protein	AT2G23910.1	3.31	1.12E-14
Potri.002G257900	cellulose synthase A4	AT5G44030.1	-1.12	4.21E-08
Potri.010G193100	Laccase/Diphenol oxidase family protein	AT2G38080.1	-1.12	0.004325
Potri.016G078300	cinnamyl alcohol dehydrogenase 6	AT4G37970.1	2.93	2.46E-08
Potri.019G130700	cinnamate-4-hydroxylase	AT2G30490.1	1.12	1.49E-05
Genes associated to plant reproduction				
Potri.012G024700	YELLOW STRIPE like 3	AT5G53550.2	1.78	2.00E-09
Potri.001G311300	white-brown complex homolog protein 11	AT1G17840.1	3.36	9.40E-27
Potri.014G120100	SET domain-containing protein	AT4G02020.1	1.21	0.000191
Potri.015G002300	pseudo-response regulator 5	AT5G24470.1	1.20	0.000387
Potri.010G169100	GDA1/CD39 nucleoside phosphatase family protein	AT2G02970.1	1.30	0.000366
Potri.010G081500	DNA repair family protein	AT3G22880.1	Inf	0.000352
Potri.012G062300	AGAMOUS-like 8	AT5G60910.1	2.44	3.69E-06
Potri.001G280200	Leucine-rich repeat protein kinase family protein	AT5G45840.2	-2.55	4.68E-15
Potri.005G155700	K-box region and MADS-box transcription factor family protein	AT2G22540.1	-3.43	8.47E-05

Inf: genes not expressed in line 401.

