

Supplementary Table S4. Specifically expressed genes under mild Na stress

Gene ID	Description	Average log ₂ FC value under mild				Average log ₂ FC value under			
		Al	Cd	Cu	Na	Al	Cd	Cu	Na
AT1G02920	glutathione S-transferase F7	-0.2	1.8	2.1	1.5	0.9	4.0	4.1	1.9
AT1G07690	hypothetical protein	0.0	1.0	1.7	1.5	-1.1	-1.3	-0.7	-1.3
AT1G15330	Cystathionine beta-synthase (CBS) protein	-1.2	0.2	0.8	2.0	-0.5	-0.3	1.2	0.1
AT1G17615	Disease resistance protein (TIR-NBS class)	1.7	1.0	-0.5	1.5	0.5	0.4	0.5	0.1
AT1G48590	calcium-dependent lipid-binding family protein	0.6	0.6	-0.5	1.9	0.0	0.4	0.3	0.3
AT1G65800	receptor-like serine/threonine-protein kinase SD1-6	-0.2	0.3	0.5	1.3	0.2	1.2	0.2	0.5
AT1G66700	SABATH family methyltransferase PXMT1	0.9	0.4	1.2	2.3	0.1	0.6	0.6	1.0
AT1G75830	PLANT DEFENSIN 1.1	0.3	0.1	0.2	1.8	0.0	0.4	0.5	0.1
AT1G77910	hypothetical protein	-1.1	-0.8	-1.1	1.2	-0.3	0.7	-0.1	0.3
AT1G78410	VQ motif-containing protein	1.0	1.0	1.3	1.2	1.7	2.7	1.8	1.7
AT1G79130	SAUR-like auxin-responsive protein	-2.7	-2.5	-2.0	1.3	-0.1	-0.4	0.1	-0.2
AT2G03460	galactose oxidase/kelch-like protein	0.0	0.3	0.5	1.4	0.0	0.2	0.2	0.1
AT2G10940	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-0.2	0.0	-0.4	2.8	-0.1	0.0	0.2	-0.1
AT2G29220	putative inactive L-type lectin-domain containing receptor kinase III.1	2.2	1.8	-0.3	1.7	0.2	-0.4	0.0	1.1
AT2G33790	arabinogalactan protein 30	-0.5	-0.2	1.9	1.1	-2.1	-3.2	-3.4	-0.1
AT3G05780	lon protease 3	-2.7	-2.4	-1.5	1.8	-0.9	-1.9	-1.7	-0.5
AT3G05790	lon protease 4	-2.3	-2.3	-2.6	1.8	0.1	0.2	-0.9	0.0
AT4G05076		0.5	-0.4	0.0	1.0	-0.1	0.3	0.2	-0.1
AT4G12170	thioredoxin family protein	0.0	-0.5	0.9	1.5	0.1	-0.3	0.5	0.4
AT4G17980	NAC domain containing protein 71	2.0	1.9	1.0	2.0	0.4	0.2	0.4	0.2
AT4G26200	1-aminocyclopropane-1-carboxylate synthase 7	0.3	1.7	-0.8	1.4	1.1	3.5	1.7	3.1
AT4G26260	myo-inositol oxygenase 4	-2.8	0.5	0.1	1.4	-1.2	-1.4	2.8	-0.2
AT4G27550	putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 4	0.1	0.6	0.1	1.3	0.2	0.9	0.1	0.4
AT4G36850	PQ-loop repeat family protein / transmembrane family protein	-5.7	-6.8	-6.0	1.3	-1.0	-2.9	-2.8	0.3
AT5G07610	F-box protein	2.2	0.5	2.0	1.2	0.3	0.2	0.2	1.3
AT5G11930	Thioredoxin superfamily protein	0.4	-0.5	-0.8	1.2	0.7	0.2	-0.3	0.3
AT5G22390	hypothetical protein	0.3	0.2	0.4	1.8	0.0	0.0	0.0	1.1
AT5G28470	probable peptide/nitrate transporter	2.0	1.3	1.1	1.8	-0.1	0.0	0.1	0.0
AT5G37730	hypothetical protein	2.0	2.0	-0.2	1.4	0.1	0.6	0.1	-0.3
AT5G57220	cytochrome P450, family 81, subfamily F, polypeptide 2	-0.7	1.1	0.6	1.5	0.2	3.5	3.8	2.7
AT5G58780	Z,E-mixed heptaprenyl diphosphate synthase	0.3	-0.8	-1.3	1.3	-0.4	-1.3	-0.3	-0.2
AT5G61470	C2H2-like zinc finger protein	-1.1	0.1	-0.3	2.0	-0.1	0.2	-0.1	-0.1
AT5G65600	concanavalin A-like lectin kinase-like protein	1.3	2.0	2.1	1.4	0.5	3.4	3.1	1.5

Averaged values of fold change in three microarray replicates were shown.