Supplementary Table S1. Specifically expressed genes under mild Al stress

Gene ID	Description	Average log_2FC value under mild				Average log_2FC value under			
		Al	Cd	Cu	Na	Al	Cd	Cu	Na
AT1G02310	mannan endo-1,4-beta-mannosidase 1	2.7	0.5	0.6	0.3	2.0	2.7	4.1	1.0
AT1G02470	SRPBCC ligand-binding domain-containing protein	2.5	0.1	-0.2	-0.4	0.6	0.7	1.1	-0.1
AT1G03170	protein FANTASTIC FOUR 2	3.7	1.5	1.6	0.3	1.0	1.1	0.5	0.7
AT1G05340	hypothetical protein	3.4	0.7	0.9	-0.2	1.8	1.3	2.4	0.8
AT1G10540	nucleobase-ascorbate transporter 8	2.4	0.6	0.0	0.2	0.2	0.4	0.6	0.3
AT1G11190	endonuclease 1	2.8	0.3	0.6	0.0	2.0	0.7	1.7	0.3
AT1G13310	Endosomal targeting BRO1-like domain-containing protein	2.3	0.7	-1.1	0.4	0.8	0.9	0.1	0.9
AT1G13340	Regulator of Vps4 activity in the MVB pathway protein	2.4	0.8	1.4	0.2	2.6	3.4	4.5	1.7
AT1G13520	hypothetical protein	2.7	1.8	1.8	0.4	1.4	3.0	3.9	1.8
AT1G13890	N-ethylmaleimide-sensitive factor adaptor protein 30	2.5	-0.1	-0.4	-0.2	0.5	0.3	0.5	0.2
AT1G15180	MATE efflux family protein	2.9	-1.0	-0.5	0.0	0.6	-0.5	0.2	-0.1
AT1G17310	MADS-box transcription factor family protein	3.4	1.2	1.7	-1.4	1.9	2.7	3.2	-0.6
AT1G17710	phosphoethanolamine/phosphocholine phosphatase	5.5	1.6	1.7	0.5	0.6	0.3	0.5	0.0
AT1G19610	defensin-like protein 19	4.2	0.7	1.5	0.7	-0.1	-0.3	1.4	0.1
AT1G20350	translocase inner membrane subunit 17-1	3.4	0.8	2.4	-0.5	0.2	0.6	0.6	0.5
AT1G21890	WAT1-related protein	3.1	1.7	0.1	-0.4	1.2	0.7	-0.3	0.2
AT1G23550	probable inactive poly [ADP-ribose] polymerase SRO2	2.7	0.4	0.5	0.2	2.3	2.0	2.8	0.6
AT1G25400	hypothetical protein	2.9	1.5	2.1	0.5	0.5	1.6	1.8	0.5
AT1G26560	beta glucosidase 40	2.3	0.7	1.2	0.3	0.0	0.5	0.1	0.1
AT1G27940	ABC transporter B family member 13	2.7	-2.1	-1.3	0.3	-0.1	-0.7	0.1	0.4
AT1G30220	putative inositol transporter 2	4.2	0.2	0.1	0.4	0.5	0.4	1.1	0.2
AT1G30740	FAD-binding and BBE domain-containing protein	2.5	0.1	0.5	-0.1	0.4	0.0	1.6	0.6
AT1G32940	Subtilase 3.5	3.0	1.8	1.7	0.1	0.3	0.8	1.5	0.0
AT1G35140	protein EXORDIUM LIKE 1	2.4	1.5	0.0	0.1	2.1	2.0	1.9	1.4
AT1G48000	myb domain protein 112	3.2	2.0	2.0	-0.2	3.1	3.7	3.5	1.6
AT1G51340	MATE efflux family protein	3.3	0.6	0.4	-0.1	0.2	0.0	0.2	0.1
AT1G51830	putative leucine-rich repeat protein kinase	2.2	1.4	1.0	-0.2	1.3	-2.1	-0.8	0.1
AT1G55780	hypothetical protein	3.3	1.1	0.4	0.3	2.6	1.0	1.7	2.6
AT1G57990	purine permease 18	2.5	1.3	1.1	0.3	1.8	2.7	4.0	1.1
AT1G62240	hypothetical protein	3.1	0.8	0.4	-0.4	0.1	0.7	1.3	0.3
AT1G66180	aspartyl protease family protein	2.6	1.6	0.8	-0.3	3.2	1.4	1.2	0.5
AT1G67070	mannose-6-phosphate isomerase	2.7	1.2	1.0	0.2	1.8	2.2	4.7	0.7
AT1G68320	R2R3-MYB transcription family	2.8	0.7	2.2	-0.2	0.5	0.6	0.9	0.3
AT1G69120	Floral homeotic protein APETALA 1	2.6	-0.3	2.4	-0.3	0.0	-0.3	0.4	0.2
AT1G69880	thioredoxin H8	2.8	0.0	1.0	1.0	0.5	0.9	3.1	0.5
AT1G70170	matrix metalloproteinase	2.6	1.4	1.3	0.4	2.0	1.8	2.6	1.2
AT1G72890	TIR-NBS class of disease resistance protein	3.8	1.0	1.0	0.2	2.6	1.9	2.1	0.1
AT1G74000	strictosidine synthase 3	2.4	0.5	1.5	0.4	1.1	1.1	3.8	1.4
AT1G74810	boron transporter 5	2.3	-0.3	-1.0	-1.1	-0.6	-0.3	-0.2	-0.8
AT1G75030	thaumatin-like protein 3	2.9	0.3	0.8	0.8	1.2	-0.1	-0.4	1.2
AT1G76650	calcium-binding protein CML38	2.5	1.0	1.4	0.1	1.7	3.2	4.4	2.1
AT1G78340	glutathione S-transferase TAU 22	2.7	0.9	-1.9	0.0	3.2	2.1	-0.1	2.0
AT1G80110	phloem protein 2-B11	2.4	0.2	0.1	-0.1	2.4	1.7	1.1	1.3
AT2G01300	hypothetical protein	3.1	0.9	0.6	-0.3	1.6	1.5	3.0	1.5
AT2G02270		2.9	0.8	0.7	-0.2	0.8	1.2	0.8	0.3
AT2G02300	phloem protein 2-B5	3.1	1.0	0.9	0.5	0.8	0.8	0.4	0.4
AT2G03850	late embryogenesis abundant protein (LEA) family protein	3.4	1.4	0.8	0.3	1.3	1.7	1.8	0.1
AT2G04460		2.5	0.9	2.4	0.0	-0.1	-0.2	0.3	-0.2
AT2G11810	Monogalactosyldiacylglycerol synthase 3	2.6	-0.1	0.0	0.1	0.6	-0.6	-0.2	-0.9
AT2G17500	auxin efflux carrier family protein	2.2	0.0	-0.1	0.0	2.3	0.6	1.3	1.0
AT2G18480	putative polyol transporter 3	3.5	1.1	0.1	0.3	2.8	-0.2	-0.1	0.9
AT2G18550	homeobox-leucine zipper protein ATHB-21	2.7	0.5	1.1	0.5	0.6	-0.1	1.9	0.0
AT2G19900	NADP-dependent malic enzyme 1	2.5	1.4	1.8	-0.1	2.0	1.5	2.4	0.3

AT2G21400	SHI-related sequence3	2.7	1.1	0.1	-0.8	0.6	0.5	0.3	0.1
AT2G25460	hypothetical protein	2.2	1.6	1.7	0.2	1.9	3.9	4.1	2.4
AT2G26480	UDP-glucosyl transferase 76D1	2.9	1.9	0.7	0.8	1.5	2.0	0.4	0.9
AT2G26690	nitrate transporter 1.4	2.7	-0.4	0.2	-0.1	1.9	0.2	1.1	-0.1
AT2G27535	ribosomal protein L10A family protein	2.9	0.2	0.1	0.6	0.0	1.4	0.1	0.9
AT2G27830	hypothetical protein	2.2	1.6	1.3	0.2	1.2	1.4	3.1	0.6
AT2G28700	protein agamous-like 46	3.8	1.9	0.5	0.6	0.2	0.1	0.3	0.1
AT2G29250	concanavalin A-like lectin protein kinase-like protein	2.7	2.1	1.2	0.7	0.1	-0.3	0.3	0.3
AT2G29380	highly ABA-induced PP2C protein 3	3.6	0.5	0.6	0.3	1.5	1.2	0.8	1.5
AT2G29450	glutathione S-transferase tau 5	2.7	0.5	1.9	0.7	2.4	2.9	4.6	1.8
AT2G30140	UDP-glycosyltransferase 87A2	2.1	1.8	1.0	0.3	2.4	3.6	3.9	1.6
AT2G31560	hypothetical protein	2.9	0.3	-0.4	0.2	1.6	0.4	1.1	0.8
AT2G32190	hypothetical protein	3.6	1.7	1.6	0.4	2.9	3.0	4.0	1.6
AT2G32660	receptor like protein 22	2.2	1.0	1.6	-0.1	0.5	2.7	3.7	0.7
AT2G32830	putative inorganic phosphate transporter 1-5	2.6	1.1	1.6	0.7	0.2	0.3	0.3	-0.1
AT2G33380	caleosin 3	3.4	-1.6	-1.0	0.5	1.5	0.3	1.3	0.2
AT2G35370	glycine decarboxylase complex protein H	2.5	0.3	1.3	0.3	0.3	1.2	0.5	0.2
AT2G36440	hypothetical protein	2.9	1.6	0.2	0.0	0.1	0.6	0.2	0.0
AT2G37330	protein aluminum sensitive 3	2.1	0.7	0.3	0.2	0.8	0.0	-0.2	-0.2
AT2G38790	hypothetical protein	3.9	1.0	1.4	0.2	1.8	1.5	1.9	1.5
AT2G39510	nodulin MtN21-like transporter family protein	6.2	0.3	0.1	1.2	1.9	1.4	0.3	-0.1
AT2G40880	cysteine proteinase inhibitor 3	3.1	0.6	-0.3	-0.2	2.2	1.5	1.2	1.2
AT2G41850	polygalacturonase ADPG2	3.1	-0.4	0.1	-0.3	0.6	1.2	2.3	0.8
AT2G44175	N-myristoyltransferase-related protein	2.9	-0.4	0.3	0.0	0.2	-0.1	0.0	-0.1
AT3G01290	SPFH/Band 7/PHB domain-containing membrane-associated protein	2.7	1.8	1.5	0.2	1.1	1.2	2.7	0.1
AT3G01830	putative calcium-binding protein CML40	2.5	1.8	1.4	0.7	2.1	3.3	4.3	3.6
AT3G01990	ACT domain-containing protein 6	2.5	1.1	1.3	0.2	0.7	1.9	1.5	-0.2
AT3G03640	beta glucosidase 25	3.6	0.7	0.1	-0.2	3.4	1.8	1.1	1.7
AT3G05400	sugar transporter ERD6-like 12	3.1	1.2	-0.9	0.1	0.4	0.1	0.9	0.0
AT3G06210	hypothetical protein	2.9	0.2	-0.3	-0.1	1.8	0.5	0.3	-0.1
AT3G06490	putative transcription factor MYB108	3.2	1.6	2.1	-0.6	2.1	4.0	4.2	2.0
AT3G08770	lipid-transfer protein 6	2.7	0.4	0.4	0.5	0.4	0.1	0.1	-0.1
AT3G08870	concanavalin A-like lectin protein kinase family protein	3.2	1.6	-0.3	0.6	-0.1	0.0	0.1	0.0
AT3G09220	laccase 7	2.6	1.9	1.6	0.4	0.6	0.5	1.5	0.8
AT3G14770	bidirectional sugar transporter SWEET2	2.8	0.0	1.2	-0.3	1.2	1.0	2.4	0.1
AT3G17520	late embryogenesis abundant protein (LEA) family protein	3.9	-1.1	-0.9	-0.9	-0.4	-0.1	-0.4	0.4
AT3G21790	UDP-glycosyltransferase 71B7	6.0	0.9	0.4	-0.5	1.7	0.3	3.0	0.2
AT3G22240	hypothetical protein	2.8	1.5	1.1	0.0	2.2	0.6	2.5	0.1
AT3G26740	CCR-like protein	2.8	0.1	0.1	0.2	0.5	0.2	2.2	0.3
AT3G27810	transcription factor MYB21	4.3	-0.1	2.1	-0.1	-0.3	-0.2	0.8	0.5
AT3G30842	pleiotropic drug resistance 10	2.4	0.4	0.3	0.4	0.1	0.2	0.0	0.1
AT3G44880	pheophorbide A oxygenase	2.8	0.9	1.0	0.0	0.8	1.4	2.0	0.1
AT3G48340	KDEL-tailed cysteine endopeptidase CEP2	3.7	0.7	0.8	-0.7	2.7	-1.0	-0.3	-0.4
AT3G48460	GDSL esterase/lipase	2.2	0.9	1.8	0.0	1.2	0.7	1.8	0.1
AT3G48520	cytochrome P450, family 94, subfamily B, polypeptide 3	3.9	1.1	1.6	0.7	0.4	1.1	3.2	0.8
AT3G51895	sulfate transporter 3;1	3.8	1.3	1.9	-0.4	2.9	1.0	1.4	0.3
AT3G52820	purple acid phosphatase 22	3.6	0.2	0.9	0.0	1.9	0.3	1.0	0.3
AT3G55790	hypothetical protein	2.8	1.9	0.2	-0.1	0.4	0.6	0.0	0.0
AT3G55910	hypothetical protein	2.2	-0.4	-0.2	-0.2	0.6	-0.1	0.8	-0.1
AT3G60130	beta glucosidase 16	2.2	0.1	0.7	0.0	1.9	1.8	2.4	0.4
AT3G61390	U-box domain-containing protein 36	2.7	0.4	0.2	0.1	1.7	2.0	2.8	1.5
AT3G61890	homeobox-leucine zipper protein ATHB-12	3.2	-0.9	-0.6	0.0	1.7	0.9	1.6	0.6
AT3G62730	hypothetical protein	3.2	-0.9	-0.8	0.4	0.8	0.0	0.3	0.6
AT3G63380	putative calcium-transporting ATPase 12	2.8	1.9	1.7	0.6	0.9	2.6	3.7	1.5
AT4G02170	hypothetical protein	2.3	1.4	0.1	-0.7	1.1	-0.2	-0.2	0.7
AT4G02280	sucrose synthase 3	3.1	0.5	0.5	0.3	0.7	0.4	1.2	0.3

AT4G04460	aspartic proteinase A3	2.3	-0.1	-0.1	-0.1	0.9	-1.2	-2.2	-0.2
AT4G04490	cysteine-rich receptor-like protein kinase 36	2.4	1.5	0.5	0.3	1.8	2.0	0.9	2.3
AT4G09120	putative RING-H2 finger protein ATL36	4.5	1.5	2.2	0.2	0.4	0.1	0.3	0.0
AT4G09940	P-loop containing nucleoside triphosphate hydrolases superfamily protein	2.5	0.2	-1.2	0.0	1.1	0.6	0.2	0.1
AT4G12870	Gamma interferon responsive lysosomal thiol (GILT) reductase family protein	2.7	1.2	1.4	0.8	1.5	-0.1	-0.8	-0.9
AT4G13250	probable chlorophyll(ide) b reductase NYC1	3.8	0.1	0.2	0.2	2.0	1.0	3.8	0.3
AT4G13920	receptor like protein 50	2.3	1.7	1.5	0.1	0.4	1.0	0.6	0.1
AT4G16620	nodulin MtN21 /EamA-like transporter family protein	2.6	0.3	-0.2	0.1	1.3	1.0	0.2	-0.2
AT4G18170	WRKY DNA-binding protein 28	2.5	1.8	1.9	0.1	1.5	2.2	3.7	1.3
AT4G18350	9-cis-epoxycarotenoid dioxygenase NCED2	5.1	1.3	1.3	0.3	2.1	0.8	2.4	1.0
AT4G19515		3.0	1.7	1.7	1.3	0.5	2.5	1.4	1.8
AT4G19810	Class V chitinase	2.9	1.6	0.6	0.7	1.7	2.9	1.9	1.3
AT4G19820	Glycosyl hydrolase family protein with chitinase insertion domain	2.8	1.6	0.6	0.7	0.8	1.9	0.6	0.4
AT4G21440	R2R3 family MYB transcription factor	3.4	0.9	-0.9	-0.7	0.2	1.2	0.8	0.0
AT4G21650	Subtilase family protein	2.5	0.4	1.4	-0.3	0.2	0.5	0.3	0.0
AT4G22070	WRKY DNA-binding protein 31	2.6	1.3	-0.1	0.8	2.0	1.9	1.9	1.5
AT4G24660	ZF-HD homeobox protein	3.2	-0.5	0.4	0.1	-0.1	0.1	0.3	0.0
AT4G24690	autophagy substrate NBR1	2.8	0.5	0.3	-0.1	2.1	1.8	2.0	0.3
AT4G28530	NAC domain containing protein 74	2.5	0.1	1.0	-0.3	0.6	0.0	0.2	-0.2
AT4G29640	cytidine/deoxycytidylate deaminase family protein	3.3	0.8	0.3	-0.9	0.1	0.6	0.7	-0.3
AT4G31330	hypothetical protein	2.5	2.0	-0.2	0.4	1.0	0.5	-0.4	-0.5
AT4G31710	glutamate receptor 2.4	2.8	-0.7	0.2	0.1	0.7	-0.5	0.2	0.1
AT4G33666	hypothetical protein	2.6	-0.4	-0.9	-0.1	1.3	0.4	0.9	0.2
AT4G34320	hypothetical protein	3.1	0.2	0.8	0.0	1.8	0.4	0.2	0.1
AT4G34330	hypothetical protein	3.0	0.1	0.8	0.1	1.8	0.2	0.5	0.2
AT4G34710	arginine decarboxylase 2	3.2	1.4	0.5	0.1	3.4	1.3	2.7	1.0
AT5G01300	putative phosphatidylethanolamine-binding protein	2.5	1.9	1.1	0.7	0.3	0.2	0.2	0.0
AT5G01640	prenylated RAB acceptor 1.B5	2.6	1.3	0.4	0.3	1.8	2.1	1.3	0.7
AT5G02020	hypothetical protein	2.3	1.6	1.8	0.4	1.1	1.5	1.9	0.4
AT5G03210	hypothetical protein	3.4	1.5	0.6	0.4	1.5	1.1	0.8	3.0
AT5G04120	phosphoglycerate mutase-like protein	4.3	0.4	2.2	1.3	0.9	0.1	0.3	0.6
AT5G06320	NDR1/HIN1-Like protein 3	3.8	1.6	1.1	0.3	2.8	3.4	4.0	1.8
AT5G09930	ABC transporter F family member 2	2.9	-0.1	-0.2	0.1	-0.3	-0.4	-0.3	-0.3
AT5G10120	putative ethylene insensitive 3-like 4 protein	3.0	0.5	0.1	-0.1	0.0	0.0	0.3	-0.1
AT5G10695	hypothetical protein	2.2	1.3	1.2	-0.1	1.6	2.6	3.0	1.6
AT5G11210	glutamate receptor 2.5	2.2	1.5	-0.3	0.3	1.2	2.0	1.6	0.9
AT5G11410	protein kinase family protein	2.9	1.7	0.9	0.5	0.0	0.2	0.5	0.2
AT5G11670	NADP-dependent malic enzyme 2	2.3	1.5	1.9	-0.1	2.1	1.8	2.6	0.3
AT5G13200	GRAM domain family protein	2.9	1.4	1.1	0.2	1.6	2.4	2.4	1.6
AT5G13670	nodulin MtN21-like transporter UMAMIT 15	2.4	-1.0	-0.4	-0.3	0.5	-0.2	0.3	0.5
AT5G16010	3-oxo-5-alpha-steroid 4-dehydrogenase family protein	4.0	1.1	0.5	-0.1	3.1	2.9	3.4	1.9
AT5G17860	calcium exchanger 7	4.0	1.6	0.8	-0.1	0.4	0.0	0.2	0.0
AT5G18170	glutamate dehydrogenase 1	2.3	1.1	0.9	0.4	2.3	-0.8	1.1	0.4
AT5G20000	AAA-type ATPase family protein	2.3	0.5	1.0	0.2	1.4	1.1	2.0	0.1
AT5G24860	flowering promoting factor 1	3.7	0.9	0.5	0.4	0.9	1.6	0.4	0.6
AT5G25460	hypothetical protein	3.1	1.1	1.4	0.2	2.6	-4.6	-2.7	-0.1
AT5G25910	receptor like protein 52	2.3	1.7	0.7	0.2	0.9	1.0	1.7	0.5
AT5G39520	hypothetical protein	7.6	1.4	1.4	0.2	2.4	1.1	2.6	-0.2
AT5G42800	dihydroflavonol-4-reductase	3.2	1.5	-1.1	0.1	0.0	0.4	-0.2	-0.1
AT5G43980	plasmodesmata-located protein 1	3.1	1.1	0.6	0.3	0.9	0.5	1.4	0.3
AT5G44390	FAD-binding Berberine family protein	3.4	0.8	-0.4	0.6	1.4	0.8	1.4	1.4
AT5G48180	nitrile specifier protein 5	2.8	0.0	-0.2	0.2	1.9	1.2	2.5	0.6
AT5G49350	glycine-rich protein	2.6	0.8	0.9	0.7	2.0	-0.9	-1.0	1.9
AT5G49690	UDP-glycosyltransferase 91C1	2.9	1.8	1.6	0.0	1.0	2.7	3.6	0.3

AT5G50130	Rossmann-fold NAD(P)-binding domain-containing protein	2.6	2.0	1.2	0.1	0.8	1.8	2.6	0.0
AT5G50360	hypothetical protein	3.2	-0.3	-0.3	-0.2	0.2	0.1	0.4	0.0
AT5G53820	Late embryogenesis abundant protein (LEA) family protein	2.8	1.6	0.5	0.4	1.9	2.9	0.7	3.6
AT5G56510	pumilio 12	3.2	1.0	1.1	0.8	0.0	-0.1	0.3	0.2
AT5G57560	xyloglucan endotransglucosylase/hydrolase protein 22	3.1	1.2	1.2	0.4	3.9	2.5	3.8	2.8
AT5G58070	temperature-induced lipocalin TIL1	2.2	0.0	-0.2	-0.2	1.5	0.2	0.9	0.6
AT5G58330	lactate/malate dehydrogenase family protein	2.6	0.5	0.4	0.3	0.9	0.3	2.1	0.9
AT5G58570	hypothetical protein	2.2	0.2	-0.6	-0.2	1.2	-0.3	-0.4	0.2
AT5G59230	transcription factor-related protein	2.5	2.5	2.1	0.3	-0.1	1.3	-0.2	-0.4
AT5G59390	XH/XS domain-containing protein	4.4	0.8	1.4	-0.2	0.6	0.3	0.8	0.3
AT5G59490	haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2.7	1.7	1.5	0.4	3.2	3.2	4.0	1.9
AT5G59820	high light responsive zinc finger protein ZAT12	3.5	1.6	1.7	0.4	1.6	2.4	2.4	1.7
AT5G61430	NAC domain containing protein 100	2.7	1.5	0.0	0.5	1.6	1.0	-0.3	0.9
AT5G62520	probable inactive poly [ADP-ribose] polymerase SRO5	2.4	1.3	0.6	-0.2	0.9	2.1	1.9	1.3
AT5G64210	alternative oxidase 2	3.0	0.3	0.7	-0.5	1.0	-0.5	-0.6	1.1
AT5G64490	pumilio homolog 26	2.7	0.4	0.5	0.0	0.1	0.3	-0.2	0.0
AT5G65100	Ethylene insensitive 3 family protein	2.7	0.5	-0.1	-0.8	0.4	-0.1	0.3	-0.1
AT5G65990	transmembrane amino acid transporter family protein	2.3	0.7	1.1	0.2	0.3	0.4	0.2	0.3
AT5G66700	homeobox-leucine zipper protein ATHB-53	2.3	1.7	0.5	-0.8	1.8	1.9	3.1	0.9

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