

Supplementary Table S2. Specifically expressed genes under mild Cd 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
AT1G01560	mitogen-activated protein kinase 11	1.7	2.7	1.7	0.7	-0.3	2.9	1.6	0.7
AT1G02220	NAC domain-containing protein 3	1.7	2.0	1.9	0.3	0.9	3.2	3.3	1.1
AT1G02250	NAC domain-containing protein 5	-0.1	2.4	1.5	-0.1	0.3	1.8	0.7	0.0
AT1G07400	class I heat shock protein	1.2	2.8	0.4	0.2	1.5	3.9	1.1	3.4
AT1G07440	NAD(P)-binding Rossmann-fold superfamily protein	-0.3	2.2	1.0	-0.2	0.1	0.7	0.0	0.0
AT1G07720	3-ketoacyl-CoA synthase 3	1.1	2.2	-0.2	0.0	0.6	1.4	0.1	1.4
AT1G14540	peroxidase 4	0.0	2.1	0.2	0.8	0.3	3.5	4.8	3.0
AT1G14880	cadmium resistance protein 1	-0.4	2.8	2.1	-0.5	0.4	1.6	0.5	-0.2
AT1G15630		2.1	3.6	2.1	-0.2	0.2	0.8	0.0	-0.3
AT1G15640	hypothetical protein	0.8	2.3	1.6	0.0	0.3	0.5	0.1	-0.1
AT1G16030	heat shock protein 70B	0.4	2.6	-0.1	0.0	1.0	2.9	1.5	0.8
AT1G21250	wall-associated receptor kinase 1	2.1	4.2	2.2	1.4	0.2	1.9	1.1	0.2
AT1G21945		1.3	2.6	0.0	0.1	-0.2	1.1	0.0	-0.3
AT1G22210	probable trehalose-phosphate phosphatase C	0.5	3.7	1.6	-0.3	-0.3	-0.3	-0.1	-0.2
AT1G35730	protein pumilio 9	2.0	2.8	0.6	-0.2	0.4	1.8	0.6	0.4
AT1G48720	hypothetical protein	1.1	2.8	-0.6	0.0	0.2	3.3	1.0	0.5
AT1G49750	leucine-rich repeat (LRR) family protein	0.9	2.1	0.7	-0.2	1.2	0.8	-0.5	0.7
AT1G51420	sucrose-phosphatase 1	0.7	2.0	1.4	0.2	1.3	2.0	1.6	0.9
AT1G59860	HSP20-like chaperone	1.5	2.0	0.5	0.2	0.4	2.3	0.5	1.5
AT1G60730	probable aldo-keto reductase 5	1.2	2.4	1.9	0.7	2.0	4.1	3.9	2.0
AT1G62580	flavin-containing monooxygenase FMO GS-OX-like 7	-0.3	2.6	-0.3	0.2	-0.3	0.5	-0.5	-0.7
AT1G66170	PHD finger protein MALE MEIOCYTE DEATH 1	0.1	2.3	0.6	0.4	0.0	0.7	0.1	0.1
AT1G66830	probable inactive leucine-rich repeat receptor-like protein kinase	1.5	3.4	2.4	-1.2	-0.1	-0.9	0.1	0.5
AT1G71000	chaperone DnaJ-domain containing protein	1.6	3.3	0.4	0.2	0.1	2.1	0.3	0.6
AT1G72910	Toll-Interleukin-Resistance domain-containing protein	0.7	3.5	0.8	1.1	0.0	1.4	0.6	0.0
AT1G74590	glutathione S-transferase TAU 10	1.9	2.0	0.8	0.9	1.6	3.0	3.1	2.1
AT2G02580	cytochrome P450 71B9	0.8	3.1	2.0	0.7	-0.3	0.3	-0.2	-0.1
AT2G13810	AGD2-like defense response protein 1	-0.7	4.1	1.7	1.1	0.6	2.7	0.2	0.6
AT2G19190	FLG22-induced receptor-like kinase 1	0.0	2.2	0.4	-0.7	-0.1	3.2	2.6	0.2
AT2G19500	cytokinin oxidase 2	-0.9	2.8	2.2	0.3	-0.7	-0.4	1.7	0.0
AT2G24600	Ankyrin repeat family protein	0.6	2.0	0.9	0.4	1.4	2.6	1.3	2.4
AT2G29110	glutamate receptor 2.8	-0.1	2.5	0.5	0.8	-0.1	0.9	0.0	1.0
AT2G29320	tropinone reductase-like protein	-0.4	2.4	0.7	-0.2	-0.1	0.0	0.1	0.7
AT2G30660		0.1	2.9	2.2	-0.3	0.6	1.3	0.1	-0.2
AT2G36690	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-3.5	2.0	1.3	0.2	-3.7	1.9	0.7	2.9
AT2G40750	WRKY DNA-binding protein 54	0.3	2.6	1.6	0.6	0.0	0.3	-0.3	-0.2
AT2G41090	calmodulin-like protein 10	0.5	2.7	0.9	0.2	1.5	1.6	0.4	0.6
AT2G43820	UDP-glucosyltransferase 74F2	-1.7	2.0	1.0	0.4	-1.0	0.4	-0.4	0.2
AT2G45550	cytochrome P450 76C4	0.2	2.6	1.7	0.4	0.0	1.0	0.3	-0.2
AT3G02840	hypothetical protein	1.6	2.2	2.1	0.7	1.4	4.0	4.8	3.6
AT3G03430	putative calcium-binding protein CML28	0.2	2.9	1.7	0.5	0.2	0.9	1.1	0.1
AT3G03800	syntaxin of plants 131	0.1	2.6	1.7	0.1	-0.1	0.1	0.3	-0.1
AT3G07600	heavy-metal-associated domain-containing protein	-0.7	2.1	0.9	0.8	-0.8	0.7	-0.1	0.0
AT3G12220	serine carboxypeptidase-like 16	0.4	2.5	2.0	0.0	1.3	0.8	0.7	-0.3
AT3G13090	multidrug resistance-associated protein 8	1.9	2.5	1.8	0.6	1.7	3.3	1.3	1.0
AT3G13100	ABC transporter C family member 7	1.7	2.7	1.9	1.0	2.3	3.8	2.2	1.6
AT3G16520	UDP-glucosyl transferase 88A1	1.8	2.4	2.0	0.2	0.1	0.3	0.4	0.1
AT3G22920	cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	1.9	2.9	1.0	0.3	0.3	1.0	0.7	0.1
AT3G29240	hypothetical protein	0.1	2.3	1.5	0.4	0.6	2.3	2.7	0.0
AT3G44350	putative NAC domain-containing protein 61	0.0	3.8	2.7	1.2	-0.1	0.9	0.2	1.2
AT3G45720	putative nitrate excretion transporter 7	1.3	2.8	2.0	-0.5	1.3	0.5	-0.7	-0.3

AT3G46680	UDP-glycosyltransferase 76E6	1.4	2.0	0.8	0.7	0.5	1.6	1.1	0.5
AT3G48790	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	1.0	2.2	1.2	-0.6	0.7	1.6	0.9	-0.4
AT3G48920	myb domain protein 45	1.9	1.9	0.4	0.2	1.0	0.9	0.6	0.2
AT3G49580	protein RESPONSE TO LOW SULFUR 1	1.9	3.9	1.7	0.2	0.6	2.7	1.9	0.0
AT3G50160		-1.0	2.8	1.9	0.3	-0.3	-0.1	-0.1	0.6
AT3G50170	hypothetical protein	1.9	2.3	1.7	-0.1	0.4	0.8	0.1	-0.3
AT3G50480	RPW8-like protein 4	-0.7	2.5	1.3	0.6	-0.1	2.5	1.6	2.0
AT3G54050	fructose-1,6-bisphosphatase	-0.4	3.6	2.6	-0.5	-0.3	1.4	1.5	-0.4
AT3G54070	ankyrin repeat-containing protein	-0.3	2.7	2.1	-0.3	-0.1	0.1	0.0	0.1
AT3G54150	S-adenosyl-L-methionine-dependent methyltransferase-like protein	2.1	2.5	2.2	0.9	3.1	4.1	4.5	2.1
AT3G56400	WRKY transcription factor 70	1.8	2.7	1.3	1.1	0.4	-0.6	-0.5	-0.1
AT3G57700	putative protein kinase	1.3	2.2	1.3	0.2	0.8	2.3	0.2	0.4
AT3G60160	multidrug resistance-associated protein 9	0.1	2.4	2.4	1.1	0.4	1.0	0.5	1.1
AT3G60970	putative ABC transporter C-15	0.1	2.7	1.7	1.0	0.3	1.0	0.0	0.8
AT4G04710	calcium-dependent protein kinase 22	0.0	2.4	1.1	-0.1	0.3	0.7	0.6	0.2
AT4G08620	sulfate transporter 1.1	-3.9	2.5	1.1	-1.1	-0.9	1.0	-0.2	-1.3
AT4G11890	receptor-like cytosolic kinase ARCK1	2.2	2.7	2.3	-0.2	1.3	2.2	0.5	1.3
AT4G13900		0.7	2.8	1.1	0.6	0.0	0.4	0.3	0.0
AT4G15530	pyruvate, phosphate dikinase 1	1.5	2.2	1.4	0.9	0.3	0.4	2.2	0.1
AT4G17785	transcription factor MYB39	0.6	2.7	1.9	0.2	0.7	3.1	2.6	1.3
AT4G18250	putative receptor serine/threonine kinase	1.2	2.2	2.0	0.4	0.8	2.6	2.0	1.1
	probable xyloglucan								
AT4G18990	endotransglucosylase/hydrolase protein 29	2.2	3.0	2.6	0.6	0.1	1.6	1.3	0.1
AT4G21366	protein kinase family protein	1.0	3.8	1.7	1.4	0.2	2.4	2.6	0.5
AT4G23180	cysteine-rich receptor-like protein kinase 10	0.2	2.4	1.8	0.2	0.4	2.9	1.5	0.7
AT4G23190		1.7	2.6	1.4	0.9	1.6	3.0	3.1	1.9
AT4G23260	cysteine-rich receptor-like protein kinase 18	1.7	3.6	2.6	0.2	0.4	2.0	1.2	0.6
AT4G25200	small heat shock protein 23.6	0.2	2.5	-0.6	-0.4	0.7	3.5	-0.1	3.5
AT4G27670	heat shock protein 21	0.7	3.8	1.0	-0.4	0.0	1.4	0.2	0.3
AT4G33050	calmodulin-binding protein	1.1	2.3	1.6	0.9	1.4	3.2	4.0	1.6
AT4G33870	putative peroxidase	2.2	2.8	0.6	-0.2	0.2	0.8	0.0	-0.6
AT4G34410	ethylene-responsive transcription factor ERF109	2.6	2.3	1.8	1.2	0.2	2.3	1.3	1.5
AT4G35070	SBP (S-ribonuclease binding protein) family protein	0.6	2.1	1.1	-0.1	0.0	0.3	0.7	0.2
AT4G38410	putative dehydrin	1.6	2.2	1.8	-0.3	1.4	0.9	0.0	1.1
AT4G39830	putative L-ascorbate oxidase	-0.1	2.2	1.1	-0.2	0.1	2.2	1.0	0.5
AT5G05220	hypothetical protein	1.6	3.5	1.7	0.3	-0.1	0.8	0.1	0.1
AT5G12020	class II heat shock protein 17.6	1.8	4.7	1.7	-0.2	0.2	2.5	0.7	3.0
AT5G12030	heat shock protein 17.6A	1.8	4.5	0.9	-1.5	0.1	2.1	0.8	2.6
AT5G17970	TIR-NBS-LRR class disease resistance protein	2.3	3.2	0.7	0.0	0.0	1.3	0.3	0.5
AT5G25250	Flotillin-like protein 1	1.5	2.4	1.8	0.6	0.1	1.6	1.2	0.6
AT5G37490	U-box domain-containing protein 21	0.5	2.1	0.3	0.8	0.2	1.9	2.3	1.2
AT5G39220	hydrolase, alpha/beta fold family protein	2.0	3.2	2.6	0.1	0.6	1.4	0.6	-0.3
AT5G39580	peroxidase 62	1.5	2.6	1.4	0.2	1.3	3.3	5.3	2.8
AT5G41740	TIR-NBS-LRR class disease resistance protein	1.3	2.1	1.7	0.6	0.4	1.9	2.1	1.4
AT5G42530	hypothetical protein	0.6	2.2	2.1	-0.3	0.2	-0.2	0.5	0.2
AT5G43450	1-aminocyclopropane-1-carboxylate oxidase-like protein	-2.2	2.1	-1.6	-0.1	0.0	2.2	1.5	2.0
AT5G44820	Nucleotide-diphospho-sugar transferase family protein	0.0	1.9	1.0	-0.5	0.2	2.9	1.7	0.7
AT5G45090	protein PHLOEM PROTEIN 2-LIKE A7	-1.7	2.2	1.6	0.7	-2.0	1.7	1.1	1.1
AT5G48700	putative small ubiquitin-related modifier 6	-2.0	2.2	2.3	-0.7	-0.1	0.1	0.2	0.0
AT5G48850	protein SULPHUR DEFICIENCY- INDUCED 1	0.7	2.7	0.6	-0.1	2.1	3.4	1.3	-0.7
AT5G52810	NAD(P)-binding Rossmann-fold superfamily protein	0.9	2.2	1.2	0.4	1.1	2.3	0.0	0.5

AT5G59580		2.2	2.5	2.1	0.1	1.4	1.8	1.0	1.0
AT5G59720	heat shock protein 18.2	0.9	2.7	-1.0	0.0	0.1	2.3	0.0	0.3
AT5G67340	ARM repeat superfamily protein	1.6	2.5	1.8	0.4	2.2	4.2	3.9	1.6

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