

Supplementary Table S3. Specifically expressed genes under mild Cu 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
AT1G04580	aldehyde oxidase 4	0.9	-0.8	2.8	-0.4	-0.1	0.1	0.0	-0.1
AT1G05800	galactolipase DONGLE	0.9	1.1	2.7	0.2	0.4	2.5	3.5	0.9
AT1G06160	ethylene-responsive transcription factor ERF094	2.2	1.9	4.9	-0.8	0.1	2.3	2.1	0.2
AT1G09500	alcohol dehydrogenase-like protein	-0.3	-0.1	2.1	-0.2	0.7	0.2	1.2	0.6
AT1G15125	S-adenosyl-L-methionine-dependent methyltransferase	0.8	0.2	2.4	0.0	-0.2	-0.1	0.2	-0.1
AT1G15415	phosphatase 2A B'gamma subunit	1.3	1.1	2.4	1.0	0.5	2.1	2.8	0.6
AT1G15520	ABC transporter G family member 40	1.0	1.4	4.2	0.1	0.0	1.4	0.2	0.1
AT1G17380	protein TIFY 11A	1.4	0.2	2.5	0.1	1.8	3.0	4.2	2.5
AT1G18520	tetraspanin11	0.2	0.1	2.7	-0.2	-0.1	0.0	0.0	0.0
AT1G18710	myb domain protein 47	2.0	1.9	3.1	1.1	0.4	1.3	-0.2	1.2
AT1G19530	hypothetical protein	1.0	1.7	5.2	0.0	-0.1	0.5	4.3	0.3
AT1G19670	chlorophyllase 1	1.5	0.9	5.4	0.7	0.0	0.2	2.2	0.0
AT1G26700	MLO-like protein 14	-1.3	1.6	2.5	-1.1	0.1	0.0	0.4	-0.1
AT1G28370	ethylene-responsive transcription factor 11	0.8	1.7	2.9	-0.5	0.2	2.2	1.7	1.5
AT1G28480	glutaredoxin-GRX480	2.0	1.8	2.7	0.5	2.7	3.5	3.8	3.6
AT1G32350	alternative oxidase 1D	1.8	1.3	2.3	0.2	0.9	2.6	2.9	0.9
AT1G32960	Subtilase family protein SBT3.3	2.1	1.6	4.0	-0.5	0.4	1.0	1.5	0.3
AT1G35200		1.7	0.2	2.8	1.7	0.0	0.2	0.5	0.5
AT1G52120	jacalin-like lectin domain-containing protein	-1.5	2.1	2.9	-0.7	1.7	1.9	0.1	0.0
AT1G52400	beta glucosidase 18	0.6	1.6	4.3	0.3	0.7	1.2	3.5	1.4
AT1G52900	Toll-Interleukin-Resistance domain-containing protein	0.9	0.7	3.3	-0.4	0.0	1.1	1.1	0.0
AT1G61820	beta glucosidase 46	2.0	1.0	2.3	-0.3	1.6	3.0	5.8	1.3
AT1G63990	meiotic recombination protein SPO11-2	1.0	0.7	3.5	0.1	0.1	0.0	0.3	-0.2
AT1G65890	acyl activating enzyme 12	0.3	-0.2	2.9	0.0	-0.2	0.2	0.5	0.3
AT1G66040	putative E3 ubiquitin-protein ligase ORTHRUS 4	0.9	0.7	2.4	-0.1	0.4	0.6	2.0	-0.3
AT1G67000	probable receptor-like protein kinase	0.0	1.8	3.3	0.6	0.1	3.2	2.4	0.6
AT1G69150	cysteine/histidine-rich C1 domain-containing protein	0.7	1.1	2.2	0.1	-0.3	1.7	0.2	0.2
AT1G69930	glutathione S-transferase TAU 11	2.0	2.3	3.1	0.5	2.1	4.0	5.1	1.9
AT1G71695	peroxidase 12	0.1	0.7	2.4	-0.4	0.0	2.3	1.8	-0.4
AT1G72520	lipoxygenase 4	0.8	1.3	2.3	0.4	0.1	0.6	1.2	0.2
AT1G75040	pathogenesis-related protein 5	0.3	0.7	3.0	-0.1	0.4	2.8	0.8	0.7
AT1G76410	RING-H2 finger protein ATL8	1.4	0.3	3.3	-0.5	0.6	1.9	2.7	0.4
AT1G76640	calcium-binding protein CML39	2.3	0.9	3.1	0.2	1.6	2.0	2.4	1.7
AT1G80840	putative WRKY transcription factor 40	0.7	2.0	3.4	0.6	1.1	3.9	4.0	2.8
AT2G16660	Major facilitator superfamily protein	2.0	1.4	2.5	0.2	1.0	1.9	3.3	1.4
AT2G17330		0.3	-0.8	2.2	0.3	-0.2	-0.2	0.0	-0.1
AT2G22760		0.9	0.1	2.9	0.0	0.8	2.8	4.9	2.1
AT2G22860	phytosulfokine-beta	0.6	1.5	3.8	-0.3	0.6	4.3	3.8	2.2
AT2G31180	myb domain protein 14	0.2	0.9	2.7	0.3	0.0	0.7	1.0	0.4
AT2G31230	ethylene-responsive transcription factor 15	1.1	1.0	2.9	0.1	0.0	1.7	1.9	0.2
AT2G39030	L-ornithine N5-acetyltransferase NATA1	0.2	0.1	4.0	-0.4	0.0	0.5	5.5	-0.3
AT2G41180	VQ motif-containing protein	1.2	2.1	3.6	1.1	0.0	1.3	0.2	0.0
AT2G41810	hypothetical protein	-0.2	0.9	3.4	0.3	0.0	2.5	1.4	0.5
AT2G43920	putative thiol methyltransferase 1	0.7	0.8	3.2	0.1	1.8	3.1	1.7	0.0
AT2G44070	NagB/RpiA/CoA transferase-like superfamily protein	-0.2	1.5	4.2	-0.5	0.3	0.8	1.4	0.5
AT2G44790	uclacyanin 2	1.5	1.3	2.1	0.3	1.1	1.6	2.8	0.5
AT2G47780	Rubber elongation factor protein	-0.6	-0.6	2.4	0.0	0.2	0.5	0.2	0.1
AT2G47950	hypothetical protein	1.0	0.5	2.5	0.3	0.0	0.2	0.2	0.1
AT3G01970	WRKY DNA-binding protein 45	2.2	1.6	2.5	-0.2	0.6	1.6	2.1	0.2
AT3G04000	aldehyde reductase	0.8	0.7	2.5	0.0	0.1	0.6	0.5	0.1
AT3G04330	Kunitz family trypsin and protease inhibitor protein	-0.2	0.9	2.2	0.3	-1.4	-1.9	-0.2	-0.4
AT3G04720	pathogenesis-related 4	1.9	1.2	4.1	0.2	1.4	4.1	4.9	1.6
AT3G13640	ABC transporter E family member 1	2.2	1.7	2.5	0.9	0.3	1.5	2.3	0.3
AT3G17690	cyclic nucleotide gated channel 19	2.1	1.4	2.6	0.9	1.4	2.8	2.7	2.3

AT3G19550	hypothetical protein	0.3	0.3	3.8	0.1	0.1	1.0	2.1	1.5
AT3G19690	putative pathogenesis-related protein	0.2	0.9	4.3	-0.1	-0.6	1.3	1.9	-0.4
AT3G19700	leucine rich repeat kinase HAIKU 2	-0.2	2.0	2.4	-0.9	-0.1	-0.1	-0.1	-0.3
AT3G21040		0.8	-0.9	2.3	0.1	-0.1	0.1	0.3	-0.2
AT3G22250	UDP-glycosyltransferase 82A1	1.7	-0.8	2.8	-0.7	-0.2	0.4	3.0	-0.5
AT3G23550	MATE efflux family protein LAL5	0.6	1.2	3.5	0.3	0.0	1.4	2.2	0.5
AT3G26830	protein PHYTOALEXIN DEFICIENT 3	0.8	1.6	2.7	0.7	1.4	4.1	3.6	2.2
AT3G28380	ABC transporter B family member 17	0.9	2.0	3.5	-0.1	-0.1	-0.1	0.2	0.1
AT3G44460	basic leucine zipper transcription factor 67	0.1	0.6	3.1	-0.2	-0.4	0.2	0.5	-0.3
AT3G46110	hypothetical protein	1.2	2.0	2.2	0.2	1.6	4.4	3.9	1.9
AT3G49110	peroxidase 33	0.1	0.7	2.7	0.5	-0.3	1.5	2.5	0.5
AT3G49620	2-oxoacid-dependent dioxygenase-like protein DIN11	-0.9	1.5	6.6	1.4	-0.2	5.7	5.4	4.3
AT3G51810	Em-like protein GEA1	0.8	0.6	3.6	0.5	-0.6	0.3	0.3	0.7
AT3G53200	myb domain protein 27	1.2	1.6	3.0	-1.3	0.3	0.2	0.7	-0.3
AT3G55840	Hs1pro-1 protein	1.5	1.2	2.2	0.1	1.0	2.7	3.7	1.5
AT3G57260	beta 1,3-glucanase 2	-0.2	1.0	5.2	-0.8	0.0	3.0	1.3	2.2
AT3G59450	putative calcium-binding protein CML46	0.9	1.5	3.2	0.3	0.1	0.8	0.9	0.2
AT4G08770	peroxidase 37	1.4	1.2	2.8	0.0	1.5	2.5	3.3	0.8
AT4G08780	peroxidase 38	2.1	0.7	2.4	0.0	1.6	2.2	2.2	0.6
AT4G09690	cysteine/histidine-rich C1 domain-containing protein	0.6	2.5	2.7	0.6	0.2	0.2	0.5	-0.3
AT4G13310	cytochrome P450 71A20	1.1	0.7	3.2	-0.3	1.4	2.5	1.8	0.9
AT4G15280	UDP-glucosyl transferase 71B5	1.6	0.3	3.3	0.1	0.3	1.3	4.0	0.9
AT4G15670	monothiol glutaredoxin-S7	-0.9	-0.1	2.4	-0.3	0.0	0.1	0.4	0.1
AT4G15690	monothiol glutaredoxin-S5	-0.9	0.7	2.7	-1.5	-0.5	0.9	0.5	-0.6
AT4G15700	monothiol glutaredoxin-S3	-1.4	-0.5	3.6	-0.5	-0.4	0.1	0.6	-1.3
AT4G16000	hypothetical protein	-0.5	-0.6	3.0	-0.3	-0.1	0.7	0.7	0.0
AT4G17090	beta-amylase	2.1	2.3	3.2	-0.2	0.3	1.8	3.2	0.8
AT4G19000	INTERACTS WITH SPT6-like protein IWS2	-0.3	0.3	2.6	0.4	-0.5	-0.1	0.1	-0.8
AT4G23150	cysteine-rich receptor-like protein kinase 7	0.7	0.5	2.5	-0.4	0.5	2.6	0.6	0.7
AT4G23170	cysteine-rich receptor-like protein kinase 9	0.2	1.2	2.7	-0.4	0.1	2.3	1.5	0.3
AT4G23220	cysteine-rich receptor-like protein kinase 14	0.3	2.4	4.8	0.7	0.0	1.3	0.2	0.2
AT4G24350	phosphorylase family protein	1.7	0.9	5.4	-0.6	0.3	1.5	2.7	0.4
AT4G36670	putative polyol transporter 6	-2.1	-0.3	2.2	-0.6	-1.9	1.3	1.8	0.6
AT5G05600	oxidoreductase, 2OG-Fe(II) oxygenase family protein	2.0	1.2	3.0	-0.4	1.5	2.4	3.2	1.0
AT5G07310	ethylene-responsive transcription factor ERF115	2.6	0.9	3.0	0.7	0.3	1.6	3.4	1.2
AT5G16080	carboxylesterase 17	-0.3	0.4	2.5	-0.1	-0.1	1.3	1.5	0.8
AT5G18470	curculin-like (mannose-binding) lectin family protein	0.8	1.9	2.7	-0.6	2.5	4.3	3.5	2.2
AT5G19110	Eukaryotic aspartyl protease family protein	1.3	0.4	3.0	0.1	1.3	2.9	4.5	2.7
AT5G21960	ethylene-responsive transcription factor ERF016	1.4	0.7	3.1	0.1	-0.1	0.9	1.6	3.0
AT5G23660	bidirectional sugar transporter SWEET12	1.0	-0.5	3.6	0.8	-1.0	0.1	1.3	-0.8
AT5G24420	6-phosphogluconolactonase 5	0.3	-0.7	4.3	0.2	-0.1	0.3	0.6	0.0
AT5G24540	beta glucosidase 31	0.0	1.2	5.4	-0.1	0.2	2.8	1.0	1.8
AT5G26340	sugar transport protein 13	2.3	1.3	2.8	0.6	2.3	2.9	4.5	1.6
AT5G28510	beta glucosidase 24	1.8	0.7	4.1	-1.1	1.8	4.4	5.3	1.9
AT5G35735	putative auxin-responsive protein	1.1	1.4	2.3	0.2	1.2	4.1	4.3	1.8
AT5G36000	hypothetical protein	0.3	0.1	3.2	0.3	0.0	0.3	0.2	0.0
AT5G38540	Mannose-binding lectin superfamily protein	0.3	1.8	2.5	0.4	0.5	1.4	1.0	-0.2
AT5G38550	jacalin lectin family protein	-0.4	1.4	2.3	0.1	-0.2	0.7	0.2	-0.2
AT5G43410	ethylene-responsive transcription factor ERF096	-0.6	-1.2	4.9	0.0	0.0	1.4	1.5	1.7
AT5G44620	cytochrome P450, family 706, subfamily A, polypeptide 3	1.3	1.5	2.2	0.8	1.2	3.5	3.7	1.5
AT5G46370	two-pore potassium channel 2	1.1	1.7	2.9	0.1	-1.2	-1.8	-0.6	-1.0
AT5G48390	ZIP4-like protein	1.2	1.0	2.4	-0.1	0.7	2.2	1.8	0.2

AT5G52400	cytochrome P450, family 715, subfamily A, polypeptide 1	1.7	0.2	2.4	-0.5	0.2	2.0	3.6	1.0
AT5G59540	oxidoreductase, 2OG-Fe(II) oxygenase family protein	0.7	1.3	2.2	-1.1	1.8	3.4	2.9	0.3
AT5G61160	anthocyanin 5-aromatic acyltransferase 1	0.6	0.7	3.5	0.7	-0.2	1.6	2.2	0.6
AT5G61890	ethylene-responsive transcription factor ERF114	2.0	1.6	4.0	0.7	0.3	1.5	2.9	0.3
AT5G63900	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain	0.9	1.1	2.7	-0.3	-0.2	0.9	0.9	0.5
AT5G64990	RAB GTPase homolog H1A	1.7	1.9	2.9	0.1	0.3	2.1	1.5	0.1
AT5G65140		1.8	1.3	2.3	0.7	1.7	1.9	0.6	1.0
AT5G67080	mitogen-activated protein kinase kinase kinase 19	0.4	0.5	2.5	0.1	0.6	2.6	3.4	-0.1

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