

Gene Expression and Sensitivity in Response to Copper Stress in Rice Leaves. *Emi Sudo, Misao Itouga, Kayo Yoshida-Hatanaka, Yoshiro Ono, Hitoshi Sakakibara*

Supplementary Material

Table S1. Expression profiles of all Cu-responsive genes grown with 10, 45 or 130 μM of CuCl_2 .

Probe ID	Full length cDNA	Locus_id	Description ^a	Cu 10 μM		Cu 45 μM		Cu 130 μM		EC50 _F ^d (μM)	$ \log_2 F _{130}$ ^e
				F ^b	S.E. ^c	F	S.E.	F	S.E.		
defense (up-regulated)											
A_71_P105870	AK060724	LOC_Os02g41630	phenylalanine ammonia-lyase	1.02	0.13	1.70	0.99	2.01	0.58	96.84	1.01
A_71_P105867	AK068993	LOC_Os02g41680	phenylalanine ammonia-lyase	1.01	0.18	1.42	0.55	5.01	2.53	66.59	2.32
A_71_P105871	AK102817	LOC_Os02g41630	phenylalanine ammonia-lyase	1.19	0.13	1.82	0.88	2.26	0.50	79.62	1.17
A_71_P113211	AK067801	LOC_Os04g43800	phenylalanine ammonia-lyase	1.34	0.69	1.78	0.80	4.61	2.34	39.45	2.20
A_71_P126860	AK099443	LOC_Os11g02440	chalcone-flavonone isomerase	1.38	0.22	1.89	0.67	2.19	0.38	75.43	1.13
A_71_P104485	AK070746	LOC_Os02g08420	dihydroflavonol-4-reductase	1.07	0.41	1.32	1.06	2.23	1.32	116.44	1.16
A_71_P119630	AK065515	LOC_Os08g38910	caffeoyl-CoA O-methyltransferase 2	1.19	0.35	2.12	1.69	3.18	1.10	50.11	1.67
A_71_P115157	AK104994	LOC_Os05g25640	trans-cinnamate 4-monooxygenase	1.21	0.17	1.42	0.15	2.43	0.25	100.41	1.28
A_71_P123533	AK069308	LOC_Os10g02880	O-methyltransferase ZRP4	1.17	0.07	1.19	0.06	4.27	0.87	77.19	2.09
A_71_P122641	AK072740	LOC_Os09g17560	O-methyltransferase ZRP4	1.03	0.12	1.59	0.43	21.92	10.80	44.06	4.45
A_71_P111602	AK065090	LOC_Os04g59190	peroxidase 2 precursor	1.38	0.31	1.79	0.28	7.16	3.19	32.57	2.84
A_71_P113417	AK106200	LOC_Os05g04500	peroxidase 63 precursor	1.62	0.26	2.97	2.84	8.13	1.72	18.11	3.02
A_71_P117837	AK072862	LOC_Os07g47990	peroxidase 2 precursor	1.34	0.05	1.37	0.33	3.50	1.61	65.73	1.81
A_71_P103756	AK099241	LOC_Os01g22370	peroxidase 1 precursor	1.22	0.10	1.48	0.10	4.33	0.59	54.26	2.12
A_71_P120304	AK069503	LOC_Os08g02110	peroxidase 47 precursor	1.20	0.17	1.31	0.42	3.30	0.30	78.35	1.72
A_71_P117839	AK073202	LOC_Os07g48020	peroxidase 2 precursor	1.18	0.31	1.69	1.05	9.18	5.09	39.26	3.20
A_71_P103305	AK107822	LOC_Os01g72170	glutathione S-transferase	1.21	0.11	1.24	0.21	2.07	0.60	197.47	1.05
A_71_P125246	AK062653	LOC_Os11g47809	metallothionein-like protein 1	1.37	0.43	1.48	0.41	4.06	2.24	50.71	2.02
defense (down-regulated)											
A_71_P103051	AK103129	LOC_Os01g53330	anthocyanidin 5,3-O-glucosyltransferase	0.80	0.12	0.58	0.17	0.29	0.20	52.45	1.80
A_71_P119739	AK067868	LOC_Os08g07880	phosphopantothenate-cysteine ligase	0.61	0.06	0.48	0.06	0.43	0.04	43.90	1.23
A_71_P103162	AK062796	LOC_Os01g74300	metallothionein-like protein type 2	0.92	0.04	0.82	0.15	0.16	0.02	63.13	2.65
DNA, RNA modification, turnover (up-regulated)											
A_71_P100611	AK071917	LOC_Os01g03740	nuclease PA3	1.14	0.21	1.24	0.18	2.04	0.39	171.50	1.03
A_71_P103018	AK103534	LOC_Os01g21420	pre-mRNA-splicing factor SF2	1.47	0.37	1.50	0.65	2.20	0.18	132.94	1.14
A_71_P103546	AK058891	LOC_Os01g71690	recA protein, expressed	1.00	0.08	1.02	0.06	2.21	0.26	156.14	1.14
A_71_P120550	AK058502	LOC_Os08g33710	ribonuclease 3 precursor	1.20	0.14	1.27	0.17	2.80	0.59	99.88	1.48
DNA, RNA modification, turnover (down-regulated)											
A_71_P124729	AK103113	LOC_Os11g04390	heterogeneous nuclear ribonucleoprotein R	0.88	0.13	0.79	0.13	0.49	0.17	163.01	1.03
A_71_P108383	AK100035	LOC_Os03g55660	nucleoporin-like protein	0.83	0.14	0.64	0.11	0.43	0.13	93.44	1.20
A_71_P105782	AK067252	LOC_Os02g57010	ribonucleoprotein, chloroplast	0.92	0.13	0.84	0.08	0.49	0.10	167.00	1.02
A_71_P126172	AK071898	LOC_Os12g39380	transposon protein, putative, Mutator sub-class	0.72	0.16	0.66	0.21	0.47	0.08	132.91	1.10
A_71_P125725	AK059672	LOC_Os12g36400	transposon protein, putative, Pong sub-class	0.73	0.23	0.70	0.19	0.48	0.16	173.28	1.05
growth (up-regulated)											
A_71_P105893	AK072854	LOC_Os02g52560	galactoside 2-alpha-L-fucosyltransferase	1.24	0.10	1.30	0.25	2.09	0.48	177.01	1.06
A_71_P101403	AK100475	LOC_Os01g54620	CESA4 - cellulose synthase	1.28	0.31	1.79	1.27	3.01	0.87	55.30	1.59
A_71_P126612	AK059860	LOC_Os12g05260	phytosulfokines 5 precursor	1.01	0.17	1.14	0.13	3.30	0.23	96.28	1.72
A_71_P108939	AK105970	LOC_Os03g09230	xylogen protein 1	1.30	0.21	1.47	0.29	3.29	0.72	63.90	1.72

growth (down-regulated)											
A_71_P121749	AK070937	LOC_Os09g38768	cell division control protein 50	0.87	0.11	0.84	0.23	0.49	0.05	203.94	1.02
A_71_P109146	AK110743	LOC_Os03g02830	cell division control protein 50	0.73	0.11	0.63	0.05	0.48	0.12	125.46	1.06
metabolism (up-regulated)											
A_71_P123648	AK059063	LOC_Os10g25130	alanine aminotransferase 2	1.05	0.05	1.32	0.17	2.69	0.89	93.98	1.43
A_71_P115563	AK073364	LOC_Os06g01760	aldehyde dehydrogenase	1.52	0.17	1.62	0.31	3.54	0.26	43.67	1.82
A_71_P124200	AK061152	LOC_Os10g06720	aldose 1-epimerase	1.13	0.07	1.30	0.09	2.44	0.13	111.74	1.29
A_71_P105541	AK072245	LOC_Os02g01590	beta-fructofuranosidase 1 precursor	1.17	0.17	1.58	0.57	7.67	3.37	43.64	2.94
A_71_P125689	AK071599	LOC_Os12g16720	cytochrome P450 71A1	1.25	0.11	1.57	0.21	4.31	4.17	50.04	2.11
A_71_P125423	AK060292	LOC_Os11g18570	cytochrome P450 87A3	1.05	0.13	1.28	0.14	10.93	2.27	54.17	3.45
A_71_P114901	AK061050	LOC_Os05g33380	fructose-bisphosphate aldolase cytoplasmic isozyme	1.00	0.06	1.30	0.13	2.72	0.48	92.34	1.44
A_71_P108936	AK058750	LOC_Os03g09250	inositol-3-phosphate synthase	1.01	0.19	1.02	0.21	3.16	0.93	130.60	1.66
A_71_P126555	AK066737	LOC_Os12g37260	lipooxygenase 2.1, chloroplast precursor	3.06	0.97	3.70	1.79	18.41	3.28	4.86	4.20
A_71_P113429	AK062702	LOC_Os05g07890	lipase/lipooxygenase, PLAT/LH2	1.03	0.13	1.14	0.14	2.18	0.69	141.54	1.12
A_71_P103578	AK105208	LOC_Os01g62980	lipid binding protein	1.02	0.13	1.11	0.03	2.13	1.36	151.49	1.09
A_71_P119251	AK060951	LOC_Os07g09970	lipid binding protein	1.03	0.15	1.21	0.05	2.27	0.39	121.33	1.18
A_71_P107746	AK061537	LOC_Os03g57970	lipid transfer protein	1.61	0.47	3.57	1.06	5.01	0.60	17.29	2.32
A_71_P125078	AK061288	LOC_Os11g24070	nonspecific lipid-transfer protein 1 precursor	1.19	0.07	1.56	0.05	2.67	0.55	76.80	1.42
A_71_P125472	AK058896	LOC_Os11g02369	nonspecific lipid-transfer protein 2 precursor	1.64	0.43	1.79	0.26	3.58	1.84	32.98	1.84
A_71_P115043	AK062463	LOC_Os05g47700	nonspecific lipid-transfer protein precursor	1.57	0.08	2.13	0.35	4.72	0.46	25.88	2.24
A_71_P110178	AK058876	LOC_Os03g60090	methylenetetrahydrofolate reductase	1.19	0.13	1.47	0.18	2.28	0.79	104.13	1.19
A_71_P126897	AK065255	LOC_Os12g42876	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	1.06	0.19	1.53	0.25	2.15	0.28	100.54	1.10
A_71_P112860	AK108398	LOC_Os04g08550	NAD(P)H-dependent oxidoreductase	1.23	0.10	1.61	0.11	2.64	1.30	74.03	1.40
A_71_P125414	AK068268	LOC_Os11g09280	OsPDIL1-1 - Oryza sativa protein disulfide isomerase	1.36	0.03	1.91	0.13	2.27	0.45	69.60	1.18
A_71_P113641	AK105858	LOC_Os05g46510	polygalacturonase precursor	1.07	0.07	1.08	0.04	2.27	0.27	182.58	1.18
A_71_P116988	AK072921	LOC_Os06g42560	tryptophan synthase beta chain 2	1.28	0.26	1.41	0.11	2.44	0.46	103.42	1.29
metabolism (down-regulated)											
A_71_P111842	AK065943	LOC_Os04g39140	acetyltransferase, GNAT family protein	0.67	0.14	0.54	0.12	0.36	0.05	46.86	1.49
A_71_P124627	AK101288	LOC_Os11g10520	alcohol dehydrogenase 2	0.86	0.11	0.81	0.12	0.36	0.07	105.28	1.48
A_71_P105654	AK060824	LOC_Os02g43280	aldehyde dehydrogenase 3B1	0.94	0.04	0.81	0.03	0.44	0.02	124.39	1.19
A_71_P120663	AK072163	LOC_Os08g43390	cytochrome P450 78A3	0.77	0.04	0.56	0.03	0.15	0.02	36.47	2.72
A_71_P103251	AK067866	LOC_Os01g01120	E-1 enzyme	0.80	0.10	0.51	0.10	0.30	0.06	47.92	1.73
A_71_P122533	AK059603	LOC_Os09g15810	fold bifunctional protein	0.78	0.19	0.61	0.29	0.38	0.16	71.44	1.38
A_71_P120134	AK110716	LOC_Os08g37940	HAD-superfamily hydrolase subfamily IA, variant 3	0.99	0.26	0.80	0.19	0.22	0.13	76.47	2.16
A_71_P115741	AK065263	LOC_Os06g08090	heparanase-like protein 3 precursor	0.95	0.43	0.85	0.35	0.36	0.07	107.33	1.47
A_71_P106091	AK070107	LOC_Os02g07350	inositol-1-monophosphatase	0.87	0.16	0.81	0.11	0.45	0.04	148.69	1.15
A_71_P109112	AK067323	LOC_Os07g46310	magnesium-chelatase subunit H	0.84	0.07	0.78	0.07	0.33	0.09	89.09	1.60
A_71_P118096	AK112115	LOC_Os07g37840	monoglyceride lipase	0.65	0.05	0.62	0.10	0.44	0.04	100.64	1.17
A_71_P113163	AK066522	LOC_Os04g41340	4-nitrophenylphosphatase	0.85	0.32	0.76	0.23	0.35	0.16	91.38	1.51
A_71_P107837	AK065869	LOC_Os03g49510	phosphatidylinositol-4-phosphate 5-kinase 1 precursor	0.76	0.05	0.75	0.01	0.50	0.02	230.66	1.01
A_71_P124495	AK068167	LOC_Os11g05260	phosphoglycerate mutase	0.67	0.02	0.52	0.02	0.40	0.04	52.78	1.32
A_71_P105465	AK105848	LOC_Os02g06480	protein SCO1, mitochondrial precursor	0.96	0.33	0.88	0.34	0.42	0.07	130.05	1.27
photosynthesis (up-regulated)											
A_71_P114297	AK100910	LOC_Os05g50380	glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor	1.39	0.13	1.47	0.18	3.93	1.21	51.53	1.98
A_71_P116411	AK101836	LOC_Os06g49110	delta-aminolevulinic acid dehydratase, chloroplast	1.39	0.21	1.73	0.11	2.03	0.20	113.80	1.02

			precursor									
photosynthesis (down-regulated)												
A_71_P105099	AK062994	LOC_Os02g51470	ATP synthase delta chain, chloroplast precursor	0.96	0.16	0.87	0.08	0.45	0.10	140.05	1.15	
A_71_P115841	AK060904	LOC_Os06g21590	chlorophyll a-b binding protein 6A, chloroplast precursor	0.81	0.13	0.71	0.09	0.48	0.08	143.52	1.05	
A_71_P125058	AK061295	LOC_Os11g13890	chlorophyll a-b binding protein M9, chloroplast precursor	0.70	0.13	0.63	0.11	0.37	0.11	66.63	1.44	
A_71_P118301	AK109399	LOC_Os07g37550	chlorophyll a-b binding protein of LHClI type III, chloroplast precursor	0.69	0.11	0.58	0.06	0.40	0.11	64.58	1.32	
A_71_P121584	AK109203	LOC_Os09g32620	chloroplastic quinone-oxidoreductase	0.76	0.23	0.73	0.21	0.48	0.06	179.46	1.05	
A_71_P101901	AK066307	LOC_Os12g10604	cytochrome b/b6/petB family protein	0.61	0.10	0.54	0.06	0.32	0.11	34.08	1.66	
A_71_P126393	AK059037	LOC_Os12g08770	photosystem I reaction center subunit N, chloroplast precursor	0.73	0.08	0.67	0.07	0.40	0.14	89.00	1.33	
A_71_P114565	AK066345	LOC_Os05g43310	photosystem II reaction center W protein, chloroplast precursor	0.76	0.13	0.76	0.06	0.40	0.06	116.26	1.32	
A_71_P108389	AK058858	LOC_Os03g55720	plastoquinol-plastocyanin reductase	0.94	0.10	0.73	0.08	0.36	0.25	87.68	1.47	
A_71_P117917	AK069170	LOC_Os07g36080	oxygen-evolving enhancer protein 3-1, chloroplast precursor	0.93	0.09	0.80	0.05	0.30	0.12	84.61	1.76	
A_71_P117916	AK058793	LOC_Os07g36080	oxygen-evolving enhancer protein 3-1, chloroplast precursor	0.70	0.05	0.61	0.05	0.29	0.20	48.08	1.77	
A_71_P120166	AK058551	LOC_Os08g25734	glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor	0.86	0.20	0.84	0.16	0.47	0.15	191.25	1.08	
A_71_P124217	AK110705	LOC_Os06g39730	ribulose biphosphate carboxylase large chain, catalytic domain containing protein	0.76	0.27	0.73	0.13	0.50	0.12	203.68	1.01	
protein turnover (up-regulated)												
A_71_P123176	AK059434	LOC_Os10g27190	40S ribosomal protein S17-4	1.50	0.06	1.81	0.09	2.22	0.22	76.61	1.15	
A_71_P112526	AK068012	LOC_Os04g27860	40S ribosomal protein S27	1.18	0.06	1.57	0.04	2.03	0.22	117.84	1.02	
A_71_P103250	AK059844	LOC_Os01g01060	40S ribosomal protein S5	1.33	0.10	1.82	0.14	2.05	0.33	97.08	1.03	
A_71_P121513	AK064936	LOC_Os09g31180	60S ribosomal protein L9	1.11	0.03	1.64	0.07	2.13	0.32	97.20	1.09	
A_71_P124974	AK061884	LOC_Os11g08100	aspartic proteinase Asp1 precursor	1.33	0.26	1.64	0.78	2.18	0.76	99.43	1.12	
A_71_P121730	AK105666	LOC_Os09g30414	aspartic proteinase nepenthesin-2 precursor	1.03	0.20	1.68	0.21	3.02	0.72	71.77	1.59	
A_71_P101377	AK067257	LOC_Os01g03340	Bowman-Birk type bran trypsin inhibitor precursor	1.38	0.12	1.50	0.12	6.98	1.77	38.00	2.80	
A_71_P101369	AK070467	LOC_Os01g03310	Bowman-Birk type bran trypsin inhibitor precursor	1.11	0.45	1.55	0.46	3.70	1.50	62.48	1.89	
A_71_P107682	AK061464	LOC_Os03g08020	elongation factor 1-alpha	1.10	0.07	1.60	0.06	2.09	0.20	103.08	1.06	
A_71_P111054	AK105112	LOC_Os04g35140	subtilisin-like protease precursor	1.14	0.13	1.26	0.04	3.06	0.80	91.20	1.61	
protein turnover (down-regulated)												
A_71_P118909	AK062438	LOC_Os07g36940	eukaryotic translation initiation factor 4G	0.94	0.10	0.76	0.20	0.04	0.01	44.15	4.75	
A_71_P124668	AK103461	LOC_Os11g10750	serine carboxypeptidase F13S12.6 precursor	0.68	0.08	0.64	0.04	0.50	0.11	186.29	1.00	
A_71_P116063	AK105959	LOC_Os06g15400	threonine endopeptidase	0.89	0.06	0.69	0.03	0.28	0.02	67.60	1.85	
A_71_P100229	AK065381	LOC_Os01g12950	ubiquitin-conjugating enzyme	0.72	0.03	0.69	0.07	0.50	0.09	197.99	1.01	
A_71_P118288	AK070524	LOC_Os07g07240	ubiquitin-conjugating enzyme E2-17 kDa	0.88	0.33	0.77	0.31	0.49	0.03	156.61	1.02	
A_71_P111814	AK058755	LOC_Os04g58800	ubiquitin-conjugating enzyme spm2	0.75	0.08	0.60	0.01	0.32	0.02	54.81	1.65	
response to stress (up-regulated)												
A_71_P112980	AK100788	LOC_Os04g34600	ABA/WDS induced protein	1.47	0.04	1.88	0.19	2.17	0.22	75.04	1.12	
A_71_P115472	AK107775	LOC_Os06g07030	dehydration responsive element binding protein	1.17	0.21	1.64	0.45	4.35	0.15	51.96	2.12	
A_71_P126985	AK062422	LOC_Os09g35010	dehydration-responsive element-binding protein 1B	1.24	0.38	1.86	1.59	2.27	0.57	75.69	1.18	
A_71_P118699	AK106022	LOC_Os07g44250	disease resistance response protein 206	1.08	0.27	1.40	0.19	3.35	0.77	74.67	1.74	
A_71_P111503	AK071013	LOC_Os04g41680	endochitinase A precursor	1.09	0.10	1.14	0.26	2.45	0.37	140.75	1.29	

A_71_P114512	AK060312	LOC_Os05g42230	ER6 protein	1.03	0.02	1.16	0.08	2.37	0.12	125.23	1.24
A_71_P124122	AK065000	LOC_Os10g22520	glucan 1,3-beta-glucosidase precursor	1.14	0.49	1.40	0.28	4.57	3.06	60.04	2.19
A_71_P121735	AK061896	LOC_Os09g30418	heat shock protein 81-3	1.37	0.05	1.78	0.16	2.39	0.20	69.90	1.26
A_71_P126129	AK066682	LOC_Os12g14440	jasmonate-induced protein	1.63	0.84	1.99	1.18	11.92	7.51	21.62	3.58
A_71_P103425	AK062520	LOC_Os01g24710	salt stress-induced protein	1.16	0.29	1.28	0.04	6.20	0.97	56.61	2.63
A_71_P114369	AK070138	LOC_Os05g28740	universal stress protein	1.54	0.22	1.55	0.44	2.54	0.71	76.95	1.34
A_71_P114262	AK065866	LOC_Os05g15770	xylanase inhibitor protein 2 precursor	2.01	0.27	2.09	0.68	4.34	0.89	14.42	2.12
A_71_P114261	AK062114	LOC_Os05g15770	xylanase inhibitor protein 2 precursor	1.66	0.38	2.01	0.50	4.20	0.65	25.71	2.07
response to stress (down-regulated)											
A_71_P117292	AK099477	LOC_Os06g47800	disease resistance protein RGA3	0.77	0.08	0.61	0.06	0.27	0.03	50.42	1.87
A_71_P118794	AK065027	LOC_Os07g01630	disease resistance response protein 206	0.95	0.06	0.77	0.15	0.49	0.09	131.32	1.03
A_71_P122593	AK060664	LOC_Os09g37600	erwinia induced protein 1	0.94	0.05	0.76	0.04	0.43	0.05	111.86	1.20
signal transduction (up-regulated)											
A_71_P100175	AK067217	LOC_Os01g16030	ADP-ribosylation factor	1.04	0.15	1.65	0.62	3.11	0.79	70.94	1.64
A_71_P100901	AK065589	LOC_Os01g10890	CBL-interacting serine/threonine-protein kinase 15	1.45	0.65	1.61	0.41	2.80	0.59	61.28	1.49
A_71_P103829	AK106774	LOC_Os01g61610	gibberellin 20 oxidase 2	1.19	0.15	1.21	0.23	4.66	1.77	69.66	2.22
A_71_P107599	AK107136	LOC_Os03g57640	gibberellin receptor GID1L2	1.13	0.47	1.38	0.39	2.07	0.71	130.39	1.05
A_71_P126794	AK061124	LOC_Os12g04150	gibberellin receptor GID1L2	1.22	0.23	1.24	0.28	2.47	0.34	131.52	1.30
A_71_P115134	AK067214	LOC_Os05g31620	polcalcine Jun o 2	1.03	0.23	1.99	1.04	2.15	0.36	82.09	1.11
A_71_P112687	AK102285	LOC_Os04g44910	protein kinase	1.21	0.12	1.31	0.10	2.64	0.29	102.14	1.40
A_71_P117228	AK071637	LOC_Os06g48300	protein phosphatase 2C isoform epsilon	1.00	0.02	1.15	0.09	4.35	1.72	84.94	2.12
A_71_P106481	AK111620	LOC_Os02g13510	receptor-like protein kinase 5 precursor	1.12	0.18	1.18	0.18	2.14	0.93	169.85	1.10
A_71_P116780	AK105608	LOC_Os06g30130	serine/threonine-protein kinase receptor precursor	1.08	0.17	1.24	0.13	2.03	0.28	152.74	1.02
A_71_P102359	AK103756	LOC_Os01g07376	thioredoxin H-type	1.10	0.03	1.12	0.09	2.26	0.23	176.16	1.18
signal transduction (down-regulated)											
A_71_P117489	AK069024	LOC_Os06g16330	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor	0.78	0.09	0.67	0.10	0.48	0.03	134.97	1.06
A_71_P102248	AK102319	LOC_Os01g43100	catalytic/ protein phosphatase type 2C/ protein serine/threonine phosphatase	0.84	0.06	0.78	0.06	0.48	0.09	168.14	1.07
A_71_P109574	AK066541	LOC_Os03g22050	CBL-interacting serine/threonine-protein kinase 15	0.88	0.05	0.79	0.08	0.44	0.08	131.33	1.19
A_71_P128395	AK111510	LOC_Os03g43440	CBL-interacting serine/threonine-protein kinase 15	0.99	0.17	0.89	0.03	0.43	0.04	125.53	1.22
A_71_P118457	AK111594	LOC_Os07g43560	CRK10	0.66	0.07	0.60	0.07	0.26	0.02	39.45	1.93
A_71_P118458	AK111564	LOC_Os07g43570	CRK10	0.91	0.10	0.76	0.08	0.50	0.05	145.55	1.01
A_71_P118483	AK062716	LOC_Os07g42730	EF hand family protein	0.97	0.11	0.64	0.17	0.35	0.08	77.31	1.53
A_71_P117941	AK106266	LOC_Os07g06880	gibberellin receptor GID1L2	0.80	0.08	0.62	0.05	0.47	0.02	102.77	1.10
A_71_P102150	AK099645	LOC_Os01g07090	protein phosphatase 2C homolog 7	0.62	0.17	0.52	0.12	0.40	0.12	45.25	1.31
A_71_P103687	AK060605	LOC_Os01g70410	receptor protein kinase CRINKLY4 precursor	0.85	0.21	0.79	0.18	0.47	0.18	163.88	1.09
A_71_P108152	AK107160	LOC_Os03g61310	receptor-like protein kinase	0.73	0.02	0.67	0.12	0.48	0.08	144.42	1.07
A_71_P126328	AK069697	LOC_Os12g39630	serine/threonine-protein kinase SAPK9	0.85	0.26	0.71	0.06	0.48	0.02	133.71	1.05
transcription (up-regulated)											
A_71_P108394	AK105625	LOC_Os03g55590	DNA binding protein	1.34	0.18	2.07	0.63	2.32	0.64	60.31	1.22
A_71_P100096	AK107461	LOC_Os01g16810	DNA binding protein	1.05	0.10	1.07	0.09	2.30	0.33	171.75	1.20
A_71_P118965	AK073876	LOC_Os07g48550	NAC domain-containing protein 21/22	1.01	0.18	1.08	0.14	4.89	1.26	89.63	2.29
A_71_P105714	AK108454	LOC_Os02g34970	NAC domain-containing protein 78	1.04	0.25	1.28	0.10	2.87	0.86	92.62	1.52
A_71_P114849	AK109568	LOC_Os05g50610	OsWRKY8v2 - Superfamily of rice TFs having WRKY and zinc finger domains	1.32	0.35	1.35	0.61	2.55	0.63	106.17	1.35
A_71_P103952	AK062581	LOC_Os01g69830	teosinte glume architecture 1	1.01	0.32	1.20	0.48	2.33	0.75	110.12	1.22
A_71_P103396	AK064334	LOC_Os01g63980	TRANSPARENT TESTA 1 protein	1.10	0.02	1.19	0.08	2.24	0.40	147.77	1.17
transcription (down-regulated)											

A_71_P118455	AK070963	LOC_Os07g43530	amelogenin precursor like protein	0.54	0.20	0.35	0.14	0.32	0.18	12.43	1.66
A_71_P106994	AK058932	LOC_Os02g47560	DNA-binding protein SMUBP-2	0.48	0.14	0.39	0.08	0.35	0.04	6.96	1.53
A_71_P102267	AK067244	LOC_Os01g24070	GATA transcription factor 22	0.85	0.22	0.72	0.25	0.30	0.06	72.53	1.74
A_71_P113135	AK068202	LOC_Os04g19684	methyl-CpG binding domain containing protein	0.63	0.06	0.56	0.05	0.44	0.05	67.35	1.20
A_71_P105103	AK065868	LOC_Os02g51450	mTERF family protein	0.78	0.14	0.69	0.11	0.44	0.11	112.79	1.19
A_71_P120363	AK105596	LOC_Os08g10080	NAC domain-containing protein 21/22	0.86	0.51	0.60	0.11	0.38	0.15	72.85	1.41
A_71_P109284	AK060225	LOC_Os03g29970	nuclear transcription factor Y subunit B-3	0.94	0.14	0.86	0.09	0.42	0.09	129.52	1.26
A_71_P114145	AK070489	LOC_Os05g42130	protein MONOCULUM 1	0.98	0.36	0.84	0.27	0.33	0.14	96.85	1.60
A_71_P112651	AK066752	LOC_Os04g50100	RING-H2 finger protein ATLSG	0.62	0.08	0.58	0.09	0.38	0.02	51.45	1.41
A_71_P101855	AK071964	LOC_Os01g55750	TCP family transcription factor containing protein	0.75	0.08	0.66	0.09	0.50	0.06	157.96	1.01
A_71_P126137	AK072892	LOC_Os12g39110	zinc finger, C3HC4 type family protein	0.74	0.06	0.72	0.12	0.47	0.05	165.31	1.09
transport (up-regulated)											
A_71_P105105	AK108711	LOC_Os02g34580	ammonium transporter 2	1.06	0.15	1.35	0.23	2.47	0.98	99.19	1.30
A_71_P119764	AK065217	LOC_Os08g03350	LHT1	1.19	0.12	1.36	0.41	2.46	0.39	105.66	1.30
A_71_P117869	AK105311	LOC_Os07g33780	PDR-like ABC transporter	1.09	0.06	1.17	0.05	2.61	2.03	120.82	1.39
A_71_P127448	AK108393	LOC_Os05g27010	peptide transporter PTR2	1.17	0.11	1.33	0.18	2.22	0.23	129.86	1.15
A_71_P103242	AK063835	LOC_Os01g45640	tat pathway signal sequence family protein	1.02	0.35	1.04	0.11	7.43	1.10	86.01	2.89
A_71_P100920	AK103784	LOC_Os01g31980	transparent testa 12 protein	1.10	0.18	1.43	0.23	2.56	0.83	90.29	1.36
transport (down-regulated)											
A_71_P106018	AK100650	LOC_Os02g44980	amino acid transport protein	0.99	0.14	0.76	0.17	0.45	0.05	105.76	1.15
A_71_P116013	AK107472	LOC_Os06g12320	amino acid/polyamine transporter II	0.80	0.18	0.68	0.13	0.22	0.08	52.83	2.17
A_71_P115705	AK072617	LOC_Os06g03700	oligopeptide transporter 9	0.87	0.08	0.84	0.10	0.24	0.07	79.21	2.04
A_71_P104541	AK065840	LOC_Os02g46460	peptide transporter PTR2	0.74	0.28	0.57	0.26	0.29	0.11	47.76	1.77
A_71_P122896	AK066937	LOC_Os10g42900	peptide transporter PTR2	0.77	0.09	0.73	0.05	0.49	0.08	187.04	1.02
A_71_P114702	AK070558	LOC_Os05g34010	peptide transporter PTR2	0.90	0.04	0.77	0.08	0.48	0.09	142.11	1.06
A_71_P102553	AK066793	LOC_Os01g50616	phosphatidylinositol transporter/ transporter	0.75	0.10	0.68	0.07	0.44	0.02	114.02	1.18
A_71_P119359	AK066067	LOC_Os07g46780	tyrosine-specific transport protein	0.67	0.13	0.64	0.16	0.41	0.12	82.88	1.29
A_71_P123937	AK111957	LOC_Os10g38910	ABC-type Co ²⁺ transport system, permease component	0.91	0.05	0.73	0.06	0.44	0.05	108.67	1.19
A_71_P115940	AK105826	LOC_Os06g30730	ATPase, coupled to transmembrane movement of substances	0.99	0.10	0.75	0.14	0.48	0.00	111.94	1.05
A_71_P100064	AK065048	LOC_Os01g17214	carbohydrate transporter/ sugar porter/ transporter	0.86	0.49	0.63	0.11	0.22	0.11	52.97	2.16
A_71_P123327	AK071193	LOC_Os10g35140	permeases of the drug/metabolite transporter	0.82	0.01	0.68	0.01	0.50	0.00	142.34	1.01
A_71_P104342	AK071338	LOC_Os02g56510	phosphate transporter 1	0.59	0.18	0.54	0.21	0.42	0.12	48.47	1.27
A_71_P117558	AK067110	LOC_Os06g29790	phosphate transporter 1	0.55	0.07	0.48	0.03	0.27	0.05	19.82	1.90
A_71_P112325	AK070018	LOC_Os04g38026	sugar transport protein 5	0.74	0.10	0.63	0.02	0.37	0.03	71.48	1.42
A_71_P108667	AK067353	LOC_Os03g09930	sulfate transporter 2.1	0.53	0.17	0.39	0.09	0.10	0.03	14.91	3.36
A_71_P112060	AK072809	LOC_Os04g55800	sulfate transporter 3.3	0.90	0.21	0.84	0.25	0.49	0.07	173.25	1.04
A_71_P116372	AK063490	LOC_Os06g36450	transporter like protein	0.92	0.01	0.66	0.10	0.39	0.07	84.66	1.36
no categorized (up-regulated)											
A_71_P112689	AK110400	LOC_Os04g04330	ATP binding protein	1.91	0.18	1.99	0.19	2.91	0.32	20.17	1.54
A_71_P120258	AK059812	LOC_Os08g13440	germin-like protein subfamily 1 member 17 precursor	1.56	0.46	1.71	0.42	3.07	1.06	44.34	1.62
A_71_P117553	AK062457	LOC_Os06g21240	glycine-rich cell wall structural protein precursor	1.56	0.21	1.70	0.11	2.19	0.12	93.84	1.13
A_71_P115888	AK102441	LOC_Os06g28124	glycosyltransferase	1.06	0.42	1.16	0.36	2.20	0.45	145.19	1.14
A_71_P117935	AK065663	LOC_Os07g40870	igA FC receptor precursor	1.23	0.13	1.50	0.14	3.11	1.45	67.89	1.64
A_71_P117297	AK105605	LOC_Os06g37150	L-ascorbate oxidase precursor	1.05	0.13	1.60	0.50	2.78	0.63	76.27	1.48
A_71_P124858	AK060544	LOC_Os11g48060	monocopper oxidase-like protein SKS1 precursor	1.03	0.07	1.43	0.33	2.16	0.40	103.35	1.11
A_71_P119888	AK059493	LOC_Os08g37300	mucin-2 precursor	1.22	0.11	1.58	0.40	3.51	0.95	58.13	1.81

A_71_P119044	AK068499	LOC_Os07g46280	non-cyanogenic beta-glucosidase precursor	1.15	0.07	1.25	0.08	2.43	0.34	121.92	1.28
A_71_P110132	AK100934	LOC_Os03g15270	prMC3	1.50	0.19	1.82	0.88	2.05	0.60	102.37	1.03
A_71_P122990	AK102387	LOC_Os10g34840	ripening-related protein 3 precursor	1.04	0.23	1.47	0.22	2.07	0.37	108.02	1.05
A_71_P101334	AK065307	LOC_Os01g60860	spotted leaf protein 11	1.45	0.22	1.69	0.60	2.13	0.15	104.96	1.09
A_71_P105023	AK060001	LOC_Os02g33550	VAMP protein SEC22	1.16	0.13	2.33	0.82	2.41	0.41	60.26	1.27
A_71_P117663	AK105945	LOC_Os07g23660	vegetative cell wall protein gp1 precursor	1.07	0.19	1.14	0.04	2.63	2.10	123.98	1.39
A_71_P100986	AK062484	LOC_Os01g11600	conserved hypothetical protein	1.01	0.03	1.02	0.07	2.31	0.11	181.66	1.21
A_71_P100058	AK069098	LOC_Os01g15270	expressed protein	1.23	0.38	1.61	1.47	3.93	0.76	52.31	1.98
A_71_P123451	AK062449	LOC_Os10g41980	expressed protein	1.96	0.41	4.18	0.08	4.30	1.21	8.44	2.10
A_71_P117445	AK111637	LOC_Os06g51260	expressed protein	1.01	0.10	1.08	0.19	3.57	0.36	102.30	1.84
A_71_P125101	AK062973	LOC_Os11g30360	expressed protein	1.26	0.21	1.56	0.03	4.45	0.27	49.34	2.16
A_71_P123076	AK109893	LOC_Os10g28680	expressed protein	1.07	0.16	1.12	0.19	2.00	0.54	49.34	1.00
A_71_P102658	AK059855	LOC_Os01g51670	expressed protein	1.07	0.10	1.53	0.93	2.32	0.65	92.92	1.21
A_71_P124040	AK060177	LOC_Os10g13850	expressed protein	1.96	0.83	2.04	0.50	8.81	3.07	15.90	3.14
A_71_P116159	AK061129	LOC_Os06g39120	expressed protein	1.10	0.19	2.65	0.62	4.20	2.60	44.16	2.07
A_71_P119228	AK061478	LOC_Os07g23120	expressed protein	1.32	0.52	1.45	0.45	2.52	0.43	92.74	1.33
A_71_P123671	AK062588	LOC_Os10g36180	expressed protein	1.06	0.05	1.14	0.05	2.04	0.63	170.99	1.03
A_71_P117548	AK063903	LOC_Os06g38660	expressed protein	1.03	0.11	1.30	0.39	6.22	0.37	63.89	2.64
A_71_P103943	AK069808	LOC_Os01g69100	expressed protein	1.10	0.21	1.10	0.06	2.97	0.48	124.56	1.57
A_71_P112699	AK073181	LOC_Os04g49370	expressed protein	1.55	0.52	1.64	0.62	2.90	1.52	51.96	1.54
A_71_P110634	AK107276	LOC_Os03g51350	expressed protein	1.06	0.02	1.08	0.15	2.06	0.38	201.84	1.04
A_71_P113609	AK107732	LOC_Os05g50100	expressed protein	1.05	0.16	1.44	0.53	3.46	2.00	73.05	1.79
A_71_P111113	AK109364	LOC_Os04g39320	expressed protein	1.14	0.29	1.64	0.49	2.62	0.59	75.36	1.39
A_71_P100719	AK109646	LOC_Os01g02010	expressed protein	1.10	0.15	1.40	0.36	2.87	0.32	83.21	1.52
A_71_P114533	AK111244	LOC_Os05g11840	expressed protein	1.13	0.15	1.47	0.38	2.01	0.38	126.00	1.01
A_71_P101669	AK062919	LOC_Os01g73024	expressed protein	1.05	0.11	1.14	0.08	2.09	1.07	160.44	1.07
A_71_P118016	AK062637	LOC_Os07g09620	expressed protein	1.43	0.59	1.84	0.54	2.33	0.20	67.51	1.22
A_71_P110628	AK063718	LOC_Os03g51470	expressed protein	1.05	0.07	1.07	0.11	2.02	0.39	212.15	1.02
A_71_P125143	AK065205	LOC_Os11g30760	expressed protein	1.34	0.12	1.49	0.16	2.49	0.22	89.04	1.32
A_71_P108905	AK066091	LOC_Os03g10320	expressed protein	1.15	0.34	2.05	0.74	6.84	0.93	39.64	2.77
A_71_P126531	AK108198	LOC_Os12g05690	expressed protein	1.09	0.17	1.48	0.69	6.06	1.61	53.63	2.60
A_71_P101372	AK060800	not recognized		2.62	0.28	3.65	0.98	14.42	2.80	6.47	3.85
A_71_P125678	AK064494	no hit		1.16	0.07	1.21	0.07	2.17	0.37	169.57	1.12
A_71_P106932	AK105148	not recognized		1.40	0.23	1.46	0.26	3.40	0.50	58.80	1.77
A_71_P124017	AK106038	not recognized		1.02	0.13	1.03	0.22	2.08	0.13	204.62	1.06
A_71_P106253	AK060705	not recognized		1.09	0.23	1.64	0.59	2.13	0.82	96.31	1.09
A_71_P105425	AK070083	not recognized		1.05	0.20	1.42	0.60	2.28	0.54	100.95	1.19
A_71_P126644	AK065433	not recognized		1.18	0.13	1.37	0.17	5.48	1.27	54.63	2.45
A_71_P113466	AK069868	not recognized		1.30	0.07	1.46	0.04	2.28	0.80	112.60	1.19
A_71_P100291	AK070443	not recognized		1.13	0.31	1.93	0.32	6.01	0.23	43.26	2.59
A_71_P112511	AK068417	no hit		1.16	0.08	1.18	0.16	3.34	1.33	94.97	1.74

no categorized (down-regulated)

A_71_P102946	AK072165	LOC_Os01g51980	alliin lyase precursor	0.95	0.08	0.80	0.27	0.22	0.04	71.77	2.20
A_71_P105717	AK100703	LOC_Os02g34990	amino acid binding protein	0.80	0.04	0.75	0.06	0.43	0.04	126.67	1.22
A_71_P107535	AK099933	LOC_Os03g47620	ankyrin-1	0.99	0.05	0.84	0.19	0.23	0.02	80.52	2.11
A_71_P123898	AK070579	LOC_Os10g14870	ATFP3	0.76	0.12	0.74	0.04	0.36	0.05	91.89	1.46
A_71_P108101	AK065308	LOC_Os03g60910	ATP binding protein	0.75	0.02	0.69	0.07	0.48	0.11	151.21	1.06
A_71_P121046	AK111692	LOC_Os08g15060	ATP binding protein	0.92	0.16	0.90	0.12	0.38	0.05	138.58	1.39

A_71_P108751	AK063906	LOC_Os01g58000	ATP synthase epsilon chain	0.80	0.32	0.79	0.23	0.47	0.09	189.17	1.09
A_71_P108705	AK099538	LOC_Os03g01880	carboxy-lyase	0.70	0.12	0.59	0.06	0.40	0.04	67.76	1.33
A_71_P106598	AK066972	LOC_Os02g19650	catalytic/ hydrolase	0.66	0.07	0.65	0.05	0.30	0.03	51.07	1.73
A_71_P126207	AK071421	LOC_Os12g18110	cystinosin	0.78	0.17	0.67	0.17	0.23	0.02	51.48	2.12
A_71_P109730	AK063239	LOC_Os03g61360	epoxide hydrolase 2	0.89	0.09	0.66	0.17	0.44	0.11	98.29	1.19
A_71_P125307	AK071093	LOC_Os11g42800	kinesin-like protein KIF3A	0.89	0.05	0.87	0.14	0.34	0.04	111.82	1.56
A_71_P103020	AK067493	LOC_Os01g22980	lysosomal protective protein precursor	0.98	0.02	0.77	0.08	0.47	0.09	113.72	1.08
A_71_P101016	AK061954	LOC_Os01g08510	MAR binding filament-like protein 1	0.89	0.20	0.88	0.15	0.37	0.08	128.24	1.45
A_71_P102237	AK103941	LOC_Os01g61010	nodulin-like protein	0.62	0.11	0.60	0.05	0.41	0.04	69.86	1.28
A_71_P126283	AK063610	LOC_Os12g35340	OsGrx_C11 - glutaredoxin subgroup III	0.94	0.16	0.89	0.23	0.45	0.08	161.61	1.14
A_71_P102810	AK068523	LOC_Os01g12710	oxidoreductase	0.79	0.14	0.60	0.08	0.44	0.02	86.25	1.19
A_71_P111532	AK068663	LOC_Os04g46610	PAP fibrillin family protein	0.88	0.10	0.73	0.08	0.50	0.14	143.00	1.01
A_71_P111909	AK069628	LOC_Os04g43420	peptidoglycan binding domain containing protein	0.74	0.07	0.68	0.07	0.47	0.05	144.27	1.08
A_71_P124116	AK071673	LOC_Os10g05230	protein binding protein	0.69	0.05	0.66	0.05	0.47	0.03	149.78	1.08
A_71_P102917	AK065626	LOC_Os01g49770	protein binding protein	0.72	0.11	0.64	0.05	0.46	0.15	111.11	1.13
A_71_P102441	AK060416	LOC_Os01g67120	rhodanese-like domain containing protein	0.91	0.05	0.83	0.06	0.35	0.05	104.10	1.51
A_71_P113248	AK061666	LOC_Os04g33220	SAM domain family protein	0.75	0.13	0.59	0.14	0.40	0.09	69.43	1.34
A_71_P109620	AK104998	LOC_Os03g60240	SCAR-like protein 1	0.80	0.13	0.79	0.12	0.46	0.12	171.61	1.12
A_71_P102174	AK058392	LOC_Os01g42280	selenium-binding protein-like	0.96	0.14	0.81	0.14	0.37	0.06	102.94	1.42
A_71_P123068	AK063553	LOC_Os10g31930	shugoshin-1	0.95	0.06	0.91	0.04	0.49	0.04	187.60	1.02
A_71_P111510	AK064965	LOC_Os04g02620	steroid dehydrogenase let-767	0.95	0.30	0.86	0.15	0.35	0.03	109.24	1.49
A_71_P117796	AK061626	LOC_Os07g28610	thylakoid membrane phosphoprotein 14 kDa, chloroplast precursor	0.94	0.30	0.86	0.23	0.38	0.13	119.38	1.40
A_71_P126352	AK107649	LOC_Os12g42280	viviparous-14	0.89	0.18	0.68	0.17	0.30	0.08	70.56	1.72
A_71_P124448	AK073222	LOC_Os11g05400	expressed protein	0.77	0.18	0.65	0.21	0.49	0.18	135.99	1.03
A_71_P123826	AK108465	LOC_Os10g34700	expressed protein	0.75	0.04	0.49	0.11	0.29	0.08	40.87	1.81
A_71_P100590	AK102103	LOC_Os01g01890	expressed protein	0.87	0.05	0.67	0.10	0.29	0.09	65.35	1.78
A_71_P116695	AK107013	LOC_Os06g33330	expressed protein	0.78	0.07	0.67	0.12	0.46	0.06	118.98	1.12
A_71_P112379	AK060198	LOC_Os04g41150	expressed protein	0.99	0.22	0.81	0.21	0.50	0.19	122.08	1.01
A_71_P106860	AK072843	LOC_Os02g07820	expressed protein	0.70	0.17	0.65	0.03	0.29	0.05	52.85	1.77
A_71_P119311	AK102726	LOC_Os07g33270	expressed protein	0.85	0.42	0.68	0.45	0.48	0.42	120.82	1.07
A_71_P125320	AK099562	LOC_Os11g26890	expressed protein	0.70	0.11	0.67	0.07	0.49	0.09	189.35	1.02
A_71_P115554	AK068804	LOC_Os06g01790	expressed protein	0.90	0.14	0.77	0.11	0.39	0.10	102.16	1.38
A_71_P103833	AK067226	LOC_Os01g61630	expressed protein	0.86	0.06	0.65	0.08	0.38	0.04	79.80	1.40
A_71_P115207	AK066568	LOC_Os05g11064	expressed protein	0.86	0.16	0.71	0.16	0.40	0.18	95.79	1.33
A_71_P118481	AK100302	LOC_Os07g42714	expressed protein	0.76	0.11	0.61	0.09	0.49	0.13	117.07	1.03
A_71_P114807	AK065362	LOC_Os05g25400	expressed protein	0.78	0.08	0.66	0.05	0.26	0.01	54.51	1.93
A_71_P103134	AK059299	LOC_Os01g64270	expressed protein	0.95	0.17	0.83	0.13	0.36	0.13	103.17	1.47
A_71_P105785	AK061270	LOC_Os02g57030	expressed protein	0.99	0.13	0.81	0.23	0.48	0.11	121.74	1.06
A_71_P105784	AK061607	LOC_Os02g57020	expressed protein	0.87	0.17	0.77	0.15	0.48	0.17	147.97	1.07
A_71_P113838	AK062488	LOC_Os05g46470	expressed protein	0.75	0.07	0.74	0.02	0.15	0.04	45.07	2.75
A_71_P103799	AK064155	LOC_Os01g47130	expressed protein	0.77	0.03	0.66	0.06	0.42	0.13	94.20	1.26
A_71_P105814	AK065700	LOC_Os02g03670	expressed protein	0.78	0.11	0.65	0.09	0.31	0.13	60.92	1.71
A_71_P118154	AK067599	LOC_Os07g38230	expressed protein	0.75	0.06	0.69	0.01	0.44	0.04	119.46	1.18
A_71_P122416	AK067677	LOC_Os09g34140	expressed protein	0.89	0.19	0.79	0.09	0.39	0.26	109.65	1.35
A_71_P103688	AK067717	LOC_Os01g70400	expressed protein	0.84	0.08	0.77	0.05	0.44	0.13	137.19	1.17
A_71_P113677	AK067770	LOC_Os05g13860	expressed protein	0.78	0.16	0.75	0.24	0.48	0.14	185.22	1.05
A_71_P106877	AK068106	LOC_Os02g45460	expressed protein	0.93	0.12	0.75	0.11	0.35	0.15	89.61	1.50

A_71_P114716	AK068507	LOC_Os05g11260	expressed protein	0.75	0.31	0.72	0.24	0.33	0.16	74.68	1.60
A_71_P124304	AK072076	LOC_Os11g34110	expressed protein	0.97	0.16	0.71	0.15	0.41	0.29	94.16	1.30
A_71_P117052	AK099578	LOC_Os06g05950	expressed protein	0.75	0.06	0.64	0.08	0.39	0.09	76.12	1.37
A_71_P111917	AK105231	LOC_Os04g53180	expressed protein	0.82	0.32	0.54	0.03	0.22	0.22	44.56	2.17
A_71_P107530	AK109220	LOC_Os03g36960	expressed protein	0.92	0.15	0.78	0.15	0.45	0.11	124.84	1.16
A_71_P114138	AK110277	LOC_Os05g42100	expressed protein	0.93	0.14	0.72	0.14	0.48	0.15	121.65	1.05
A_71_P107316	AK066912	LOC_Os03g07360	expressed protein	0.93	0.20	0.78	0.07	0.44	0.06	118.37	1.18
A_71_P107483	AK059899	LOC_Os03g57349	expressed protein	0.76	0.12	0.63	0.11	0.49	0.12	126.95	1.04
A_71_P124007	AK062627	LOC_Os10g07450	expressed protein	0.58	0.09	0.50	0.05	0.42	0.09	39.53	1.24
A_71_P109121	AK063139	LOC_Os03g22519	expressed protein	0.84	0.13	0.74	0.19	0.49	0.07	158.15	1.03
A_71_P108384	AK063832	LOC_Os03g55770	expressed protein	0.53	0.03	0.45	0.02	0.19	0.02	16.20	2.42
A_71_P125815	AK109421	LOC_Os12g25180	expressed protein	0.75	0.09	0.69	0.17	0.39	0.07	88.56	1.37
A_71_P112638	AK058861	no hit		0.77	0.07	0.72	0.03	0.48	0.08	167.58	1.05
A_71_P128042	AK110284	not recognized		0.95	0.06	0.79	0.17	0.47	0.09	129.14	1.08
A_71_P125261	AK069449	not recognized		0.93	0.42	0.62	0.01	0.31	0.03	68.10	1.68
A_71_P126642	AK068287	no hit		0.73	0.16	0.68	0.12	0.50	0.13	181.33	1.01
A_71_P116868	AK111859	not recognized		0.66	0.10	0.65	0.06	0.45	0.09	120.51	1.15
A_71_P108341	AK102717	not recognized		0.73	0.06	0.65	0.10	0.50	0.06	156.05	1.01

^aDescriptions of each gene were annotated according to the TIGR database (<http://www.tigr.org/tdb/e2k1/osa1/>). Cu-responsive genes were also roughly classified into functional categories based partly on Gene Ontology Classification (<http://www.geneontology.org/>).

^{b,c}Values are means and S.E. of fold-change (F) calculated from triplicate data from different leaves.

^{d,e}Values are Cu sensitivities estimated from median effective concentrations for F (EC50_F), and the amplitude of expression change with the 130 μM treatment ($|\log_2 F|_{130}$). EC50_Fs were calculated by probit analysis (Finney, 1978).