SUPPLEMENTARY DATA

TABLE S1. Up-regulated genes in the *rad* mutant

Fold change (*rad*/WT) [a]	Locus ID[b]	Full-length cDNA accession no.[c]	Description[d]	Predicted functional classification	Data in Narsai *et al*. (2009)[e]	
					Fold change	Direction of regulation (24A vs 24N)
40.67	Os01g0944100	AK103482	Conserved hypothetical protein.	unknown	6.72	up
28.47	Os03g0762500	AK103002	Conserved hypothetical protein.	unknown	7.28	up
28.44	Os04g0206600	AK106302	UDP-glucuronosyl/UDP-glucosyltransferase family protein.	metabolism	1.52	down
28.29	Os07g0605800	AK105239	Similar to STF-1 (Fragment).	metabolism	1.26	down
25.22	Os03g0133000	AK107090	Similar to NAC-domain protein 14.	transcription	No Hit	No Hit
23.74	Os12g0555500	AK071613	Probenazole-inducible protein PBZ1.	stress	6.86	down
22.03	Os01g0172100	AK060343	Similar to Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT).	membrane protein	1.40	down (p<0.01)
21.27	Os01g0837200	AK062368	Conserved hypothetical protein.	unknown	68.76	up (p<0.01)
18.98	Os05g0438500	AK059951	Similar to Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase).	metabolism	14.89	down (p<0.01)
18.01	Os08g0502700	AK064774	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 domain containing protein.	metabolism	2.27	up
17.90	Os05g0324700	AK063581	Conserved hypothetical protein.	unknown	3.23	up

17.48	Os08g0502600	AK107730	Calcium-binding EF-hand domain containing protein.	ion binding	18.78	up (p<0.01)
15.86	Os03g0129100	AK098993	Seven transmembrane protein MLO2.	membrane protein	No Hit	No Hit
15.60	Os01g0627900	AK063764	Similar to Cytochrome P450 monooxygenase CYP72A5 (Fragment).	catalytic activity	1.12	down
15.45	Os07g0457800	AK102686	Conserved hypothetical protein.	unknown	1.07	up
14.93	Os06g0586000	AK063903	Conserved hypothetical protein.	unknown	No Hit	No Hit
14.82	Os03g0437200	AK059839	Zinc finger, C2H2-type domain containing protein.	ion binding	No Hit	No Hit
14.65	Os03g0218400	AK069202	Similar to Hexose transporter. (OsMST4)	membrane protein	4.61	up (p<0.01)
14.59	Os05g0571200	AK108389	Similar to WRKY transcription factor 19.	transcription	1.64	up (p<0.01)
14.53	Os10g0530900	AK103699	Similar to Glutathione S-transferase GST 30 (EC 2.5.1.18).	stress	27.31	down (p<0.01)
14.39	Os01g0864500	AK068115	Harpin-induced 1 domain containing protein.	unknown	1.73	up
14.17	Os10g0530900	AK059760	Similar to Glutathione S-transferase GST 30 (EC 2.5.1.18).	stress	27.31	down (p<0.01)
13.87	Os09g0535500	AK108282	Similar to RING-H2 finger protein ATL1R (RING-H2 finger protein ATL8).	protein binding	1.40	up
13.27	Os07g0604300	AK101860	Similar to Phytochelatin synthetase (Fragment).	detoxication	55.35	up (p<0.01)
12.47	Os04g0615200	AK063824	Conserved hypothetical protein.	unknown	3.07	down
12.39	Os01g0958200	AK107370	Curculin-like (mannose-binding) lectin domain containing protein.	signaling	2.73	up (p<0.01)

12.36	Os03g0737300	AK071016	HAD-superfamily phosphatase, subfamily IIIC domain containing protein.	catalytic activity	1.69	up
12.17	Os11g0702200	AK101155	Glycoside hydrolase, family 18 protein.	metabolism	10.63	up (p<0.01)
11.79	Os01g0783700	AK109278	Similar to EF-hand Ca2+-binding protein CCD1.	ion binding	3.32	up
11.71	Os02g0300700	AK069347	Similar to Eukaryotic translation initiation factor 1A (EIF-1A) (EIF-4C).	translation	1.00	up
11.43	Os03g0322200	AK062978	Conserved hypothetical protein.	unknown	2.84	down
10.77	Os06g0726200	AK061042	Endochitinase precursor (EC 3.2.1.14).	catalytic activity	5.82	down (p<0.01)
10.05	Os02g0275200	AK071664	Xyloglucan fucosyltransferase family protein.	cell elongation	1.91	up
9.98	Os04g0497000	AK109382	Similar to Allyl alcohol dehydrogenase.	metabolism	1.92	down
9.84	Os05g0506000	AK062012	Similar to MS5-like protein (Fragment).	unknown	1.84	down
9.74	Os03g0710000	AK060065	Protein of unknown function DUF292, eukaryotic domain containing protein.	unknown	No Hit	No Hit
9.63	Os09g0502500	AK109664	Alcohol dehydrogenase superfamily, zinc-containing protein.	metabolism	1.43	up
9.31	Os10g0497700	AK071225	Similar to Phytochelatin synthetase.	detoxication	1.78	down
9.14	Os01g0661800	AK103579	Conserved hypothetical protein.	unknown	1.00	down
9.02	Os09g0511600	AK105396	Glycoside hydrolase, family 1 protein.	metabolism	1.43	up
8.82	Os01g0826400	AK107199	WRKY transcription factor 24 (WRKY24).	transcription	1.74	up
8.71	Os01g0793900	AK062811	Conserved hypothetical protein.	unknown	1.42	down
8.53	Os01g0687400	AK106178	Similar to Chitinase (EC 3.2.1.14).	catalytic activity	1.30	down
8.53	Os02g0808800	AK064401	Similar to Cinnamoyl-CoA reductase (EC	metabolism	9.84	up

			1.2.1.44).			
8.52	Os05g0421600	AK107746	No apical meristem (NAM) protein domain containing protein.	transcription	1.26	down
8.46	Os08g0540900	AK111094	Conserved hypothetical protein.	unknown	4.75	up (p<0.01)
8.17	Os09g0367700	AK103316	Similar to GST6 protein (EC 2.5.1.18).	metabolism	2.19	down
8.13	Os11g0701000	AK103295	Class III chitinase homologue (OsChib3H-c).	catalytic activity	66.26	up (p<0.01)
8.05	Os08g0136700	AK073888	Protein of unknown function DUF26 domain containing protein.	unknown	9.97	up (p<0.01)
7.77	Os10g0444700	AK101170	Similar to Phosphate transporter 6.	membrane protein	1.95	down
7.76	Os01g0816100	AK073848	Similar to NAC domain protein.	transcription	2.11	up
7.70	Os07g0468200	AK103051	Conserved hypothetical protein.	unknown	No Hit	No Hit
7.68	Os07g0192000	AK065505	AAA ATPase domain containing protein.	ATP binding	1.93	up
7.68	Os10g0113000	AK109414	Similar to Chalcone reductase homologue (Fragment).	metabolism	1.02	down
7.38	Os05g0542800	AK106049	Pectin lyase fold/virulence factor domain containing protein.	cell elongation	4.72	up (p<0.01)
7.34	Os07g0244200	AK109746	Transferase family protein.	catalytic activity	2.54	down
7.28	Os04g0678400	AK107524	Zinc finger, Dof-type family protein.	transcription	4.48	up
7.26	Os09g0482800	AK063923	EF hand domain containing protein.	ion binding	5.39	up (p<0.01)
7.25	Os01g0720400	AK061237	HAD-superfamily subfamily IB hydrolase, hypothetical 1 protein.	catalytic activity	4.23	up
7.19	Os02g0758200	AK111266	Conserved hypothetical protein.	unknown	1.13	up
6.97	Os04g0547600	AK109141	Pathogenesis-related transcriptional factor and	transcription	3.92	up

			ERF domain containing protein.			
6.85	Os02g0211100	AK063336	Conserved hypothetical protein.	unknown	20.96	up (p<0.01)
6.80	Os11g0701400	AK106319	Chitinase (EC 3.2.1.14) III C10150-rice (EC 3.2.1.14).	catalytic activity	11.41	up (p<0.01)
6.77	Os01g0714600	AK059855	Conserved hypothetical protein.	unknown	2.81	up
6.72	Os07g0150700	AK069726	Similar to Serine/threonine kinase.	phosphorylation	2.15	down (p<0.01)
6.71	Os01g0186900	AK105331	Conserved hypothetical protein.	unknown	1.63	up
6.56	Os11g0701800	AK063939	Chitinase (EC 3.2.1.14) III C10701-rice (EC 3.2.1.14) (Class III chitinase homologue (OsChib3H-a)H-).	catalytic activity	48.30	up (p<0.01)
6.45	Os05g0542800	AK105858	Similar to polygalacturonase.	cell elongation	4.72	up (p<0.01)
6.43	Os02g0208400	AK073104	Conserved hypothetical protein.	unknown	No Hit	No Hit
6.24	Os10g0345100	AK069792	Multi antimicrobial extrusion protein MatE family protein.	membrane protein	1.04	down
6.19	Os01g0510200	AK062310	Conserved hypothetical protein.	unknown	1.24	down
6.09	Os02g0202200	AK107245	SPX, N-terminal domain containing protein.	stress	3.25	up
6.05	Os04g0604300	AK070734	Similar to Xyloglucan endotransglucosylase/hydrolase protein 24 precursor (EC 2.4.1.207) (At-XTH24) (XTH-24) (Meristem protein 5) (MERI-5 protein) (MERI5 protein) (Endo-xyloglucan transferase) (Xyloglucan endo-1,4-beta-D-glucanase) (OsXTH6).	cell elongation	2.08	up

6.03	Os06g0651000	AK065812	Similar to NADPH HC toxin reductase (Fragment).	detoxication	2.19	down
6.02	Os09g0482840	AK064644	EF hand domain containing protein.	ion binding	7.53	up
6.02	Os06g0200700	AK106950	Conserved hypothetical protein.	unknown	1.06	up
6.00	Os08g0540400	AK103306	Similar to Calcium-dependent protein kinase.	phosphorylation	No Hit	No Hit
5.99	Os07g0471300	AK069685	Similar to Argonaute 4 protein.	transcription	1.23	up
5.98	Os11g0702100	AK102505	Similar to Class III chitinase homologue (OsChib3H-h) (Fragment).	catalytic activity	2.62	up
5.93	Os02g0682300	AK107937	Zinc finger, RING-type domain containing protein.	protein binding	4.63	up
5.84	Os09g0511600	AK102869	Glycoside hydrolase, family 1 protein.	metabolism	1.43	up
5.73	Os10g0450900	AK064310	Similar to Glycine-rich cell wall structural protein 2 precursor (Osgrp-2).	cell elongation	1.40	up
5.73	Os11g0665600	AK110901	Helix-turn-helix, Fis-type domain containing protein.	transcription	1.13	up
5.71	Os02g0644000	AK101360	Similar to C13 endopeptidase NP1 (Fragment).	protein degradation	1.21	down
5.60	Os04g0450900	AK067842	Protein kinase PKN/PRK1, effector domain containing protein.	phosphorylation	1.43	up
5.59	Os01g0369700	AK063796	Similar to Glutathione S-transferase GST 8 (EC 2.5.1.18).	stress	4.68	down
5.59	Os08g0557600	AK102459	Similar to Monodehydroascorbate reductase (EC 1.6.5.4) (MDAR) (Ascorbate free radical	detoxication	8.50	down ($p<0.01$)

			reductase) (AFR reductase).			
5.59	Os01g0716500	AK101454	Methyltransferase type 12 domain containing protein.	metabolism	1.10	up
5.55	Os02g0209400	AK108109	Conserved hypothetical protein.	unknown	2.17	up
5.46	Os03g0230300	AK058934	Poly(ADP-ribose) polymerase, catalytic region domain containing protein.	DNA repair	3.17	up (p<0.01)
5.43	Os01g0584900	AK108522	WRKY transcription factor 28-like (WRKY5) (WRKY transcription factor 77).	transcription	No Hit	No Hit
5.41	Os06g0220500	AK063324	UDP-glucuronosyl/UDP-glucosyltransferase family protein.	metabolism	5.13	up (p<0.01)
5.32	Os12g0635400	AK063156	VQ domain containing protein.	unknown	2.01	up
5.31	Os10g0568900	AK103251	Haloacid dehalogenase-like hydrolase domain containing protein.	catalytic activity	1.23	down
5.27	Os03g0608000	AK111073	Conserved hypothetical protein.	unknown	1.82	down
5.26	Os04g0231800	AK068417	Conserved hypothetical protein.	unknown	1.06	up
5.23	Os12g0517200	AK111513	Mitochondrial ribosomal protein S10.	translation	1.05	up
5.17	Os03g0153900	AK106420	Aromatic-ring hydroxylase family protein.	metabolism	7.69	up (p<0.01)
5.11	Os10g0113000	AK059636	Similar to Chalcone reductase homologue (Fragment).	metabolism	1.02	down
5.09	Os10g0528400	AK061304	Glutathione S-transferase, N-terminal domain containing protein.	stress	1.78	down
5.08	Os02g0532500	AK059817	Germin family protein.	unknown	1.34	down

5.07	Os05g0198400	AK071272	Similar to Zinc transporter 4, chloroplast precursor (ZRT/IRT-like protein 4).	membrane protein	2.29	up
5.02	Os12g0555200	AK099157	Similar to Probenazole-inducible protein PBZ1.	stress	16.62	down
5.01	Os09g0483400	AK103890	Ubiquitin.	others	4.40	up (p<0.01)
4.99	Os08g0336200	AK111135	Conserved hypothetical protein.	unknown	3.26	up (p<0.01)
4.98	Os11g0701100	AK064356	Similar to Class III chitinase homologue (OsChib3H-h) (Fragment).	catalytic activity	4.24	up (p<0.01)
4.94	Os05g0522600	AK100082	Leucine-rich repeat, plant specific containing protein.	nucleotide binding	1.51	up
4.93	Os03g0388500	AK070350	Similar to Anther ethylene-upregulated protein ER1 (Fragment).	signaling	1.09	up
4.88	Os02g0173200	AK068418	VQ domain containing protein.	unknown	1.55	up
4.87	Os03g0281500	AK100137	Similar to Resistance protein candidate (Fragment).	unknown	No Hit	No Hit
4.86	Os03g0776900	AK107941	Similar to DNAJ protein-like.	others	1.44	down
4.82	Os10g0521100	AK064063	Similar to Actin-depolymerizing factor 6 (ADF-6) (AtADF6).	actin binding	2.91	up
4.77	Os03g0107700	AK063743	Similar to EL2 protein.	cell division	2.47	up
4.76	Os03g0230300	AK102303	Poly(ADP-ribose) polymerase, catalytic region domain containing protein.	DNA repair	3.17	up (p<0.01)
4.75	Os07g0516300	AK102726	Protein of unknown function DUF584 family protein.	unknown	1.42	down
4.75	Os01g0952900	AK104991	Conserved hypothetical protein.	unknown	No Hit	No Hit

4.71	Os03g0702000	AK105398	UDP-glucuronosyl/UDP-glucosyltransferase family protein.	metabolism	No Hit	No Hit
4.68	Os01g0740700	AK109635	Conserved hypothetical protein.	unknown	2.19	up
4.68	Os01g0135700	AK062711	EF-HAND 2 domain containing protein.	ion binding	1.26	up
4.67	Os05g0503300	AK073969	Similar to Sulfite reductase (Fragment).	metabolism	1.40	up
4.66	Os11g0141400	AK070778	Similar to Calmodulin-like protein CaML3.	ion binding	No Hit	No Hit
4.60	Os04g0401700	AK100669	Potassium transporter 1 (OsHAK1). Splice isoform 2.	membrane protein	6.62	down ($p<0.01$)
4.60	Os02g0181300	AK058773	Similar to WRKY transcription factor.	transcription	1.85	up
4.59	Os09g0480600	AK107853	Conserved hypothetical protein.	unknown	2.99	up ($p<0.01$)
4.59	Os10g0450900	AK064065	Similar to Glycine-rich cell wall structural protein 2 precursor (Osgrp-2).	cell elongation	1.40	up
4.57	Os10g0491000	AK100816	Plant Basic Secretory Protein family protein.	unknown	1.23	down
4.52	Os02g0756800	AK063605	Phosphate-induced protein 1 conserved region family protein.	unknown	2.50	up ($p<0.01$)
4.49	Os12g0268000	AK071599	Similar to Cytochrome P450 71A1 (EC 1.14.-.-) (CYPLXXIA1) (ARP-2).	metabolism	9.58	down ($p<0.01$)
4.47	Os02g0590800	AK060204	imilar to Serine/threonine-protein kinase Nek6.	phosphorylation	1.04	up
4.40	Os03g0305100	AK101765	Similar to AMP-binding protein.	catalytic activity	1.62	up
4.40	Os02g0327000	AK073631	C2 domain containing protein.	ion binding	5.69	up ($p<0.01$)
4.34	Os01g0498300	AK069247	Glycosyltransferase AER61	metabolism	5.35	up ($p<0.01$)
4.30	Os03g0141200	AK068968	Similar to Beta-amylase PCT-BMYI (EC 3.2.1.2).	metabolism	1.34	down

4.24	Os05g0194900	AK071798	Similar to Pyrophosphate-fructose-6-phosphate 1-phosphotransferase-like protein (Pyrophosphate-dependent phosphofructo-1-kinase-like protein).	metabolism	3.38	up ($p<0.01$)
4.23	Os03g0724600	AK063718	Conserved hypothetical protein.	unknown	1.09	up
4.20	Os03g0743900	AK099593	Similar to ATP sulfurylase.	metabolism	1.48	down ($p<0.01$)
4.18	Os04g0518400	AK067801	Similar to Phenylalanine ammonia-lyase (Fragment).	metabolism	2.56	up
4.14	Os02g0755900	AK104985	Similar to Glucosyltransferase (Fragment).	metabolism	12.01	down ($p<0.01$)
4.13	Os05g0402900	AK070554	Similar to EDGP.	protein degradation	2.39	up ($p<0.01$)
4.13	Os02g0188400	AK111118	Conserved hypothetical protein.	unknown	1.19	up
4.12	Os11g0701900	AK064281	Glycoside hydrolase, family 18 protein.	metabolism	5.26	up ($p<0.01$)
4.11	Os01g0948600	AK103603	Conserved hypothetical protein.	unknown	3.10	up
4.09	Os03g0133400	AK073032	Peptidoglycan-binding LysM domain containing protein.	cell elongation	2.55	down ($p<0.01$)
4.08	Os06g0621900	AK101940	Similar to Alpha-expansin OsEXPA16 (Fragment).	cell elongation	1.86	down
4.07	Os04g0450000	AK108406	Zinc finger, FYVE/PHD-type domain containing protein.	protein binding	1.75	down
4.07	Os10g0527800	AK063773	Similar to Tau class GST protein 3.	stress	2.95	down ($p<0.01$)
4.04	Os01g0955100	AK062671	Similar to Avr9/Cf-9 rapidly elicited protein 57 (Fragment).	ion binding	4.27	up
4.03	Os01g0383700	AK070583	Conserved hypothetical protein.	unknown	1.08	down

4.02	Os04g0565200	AK111866	Similar to Cis-zeatin O-glucosyltransferase 1 (EC 2.4.1.215) (cisZOG1).	hormone	9.58	down (p<0.01)
4.00	Os01g0850900	AK102887	SOUL heme-binding protein family protein.	metabolism	1.24	down
3.99	Os04g0209200	AK100406	Similar to Glutathione-conjugate transporter AtMRP4.	membrane protein	1.03	down
3.93	Os05g0414700	AK111590	Serine/threonine protein kinase domain containing protein.	phosphorylation	1.03	up
3.91	Os02g0465900	AK071205	ChaC-like protein family protein.	unknown	1.26	up
3.89	Os09g0385700	AK065210	Zinc finger, AN1-type domain containing protein.	ion binding	2.20	down
3.87	Os03g0773300	AK100394	Protein kinase, core domain containing protein.	phosphorylation	2.23	up
3.86	Os04g0398000	AK101501	Pathogenesis-related transcriptional factor and ERF domain containing protein.	transcription	1.09	up
3.84	Os06g0649000	AK106282	Similar to WRKY transcription factor 28.	transcription	2.85	up
3.83	Os01g0391100	AK108533	Similar to ATP-binding cassette, sub-family F, member 2 (Iron inhibited ABC transporter 2) (HUSSY-18).	unknown	1.00	down
3.83	Os03g0758000	AK069091	Similar to WRKY DNA binding protein.	transcription	1.13	up
3.73	Os05g0534400	AK101368	Similar to Calcineurin B-like protein 4 (SALT OVERLY SENSITIVE 3 protein).	ion binding	3.00	up (p<0.01)
3.73	Os07g0625400	AK073278	BTB/POZ fold domain containing protein.	protein binding	1.10	up

3.72	Os06g0506600	AK066232	Similar to Ubiquitin-conjugating enzyme E2-17 kDa 8 (EC 6.3.2.19) (Ubiquitin- protein ligase 8) (Ubiquitin carrier protein 8) (UBCAT4A).	protein degradation	1.37	up
3.72	Os03g0602300	AK101670	Cytochrome P450 85A1 (EC 1.14.-.-) (C6-oxidase) (OsDWARF) (Dwarf protein).	hormone	5.06	up ($p<0.01$)
3.71	Os03g0822400	AK070075	Conserved hypothetical protein.	unknown	1.33	up
3.70	Os06g0683400	AK111852	Similar to EF-hand Ca2+-binding protein CCD1.	ion binding	1.43	down
3.67	Os05g0187100	AK067988	Similar to Hexokinase.	metabolism	29.64	up ($p<0.01$)
3.63	Os05g0339200	AK111022	Conserved hypothetical protein.	unknown	1.22	up
3.61	Os01g0280500	AK103139	Similar to Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (p27(BBP)) (B(2)GCN homolog).	translation	1.80	up
3.61	Os05g0128200	AK099898	Similar to Transposable element Mu1 sequence.	others	1.13	up
3.57	Os09g0522000	AK062422	Similar to Dehydration-responsive element-binding protein 1B.	transcription	1.01	up
3.55	Os06g0215600	AK061212	Similar to Oxo-phytodienoic acid reductase.	hormone	1.58	down
3.52	Os04g0340100	AK062961	Conserved hypothetical protein.	unknown	No Hit	No Hit
3.52	Os01g0525800	AK073683	Similar to DVL5.	unknown	No Hit	No Hit
3.47	Os01g0689900	AK066381	Serine/threonine protein kinase-related domain containing protein	phosphorylation	1.17	down

3.47	Os04g0683700	AK105693	Similar to 4-coumarate-CoA ligase-like protein (Adenosine monophosphate binding protein 3 AMPBP3).	metabolism	2.60	up
3.40	Os07g0531200	AK111249	Conserved hypothetical protein.	unknown	1.06	down
3.39	Os04g0669800	AK067649	Methylthioribose kinase (EC 2.7.1.100).	hormone	4.78	down (p<0.01)
3.38	Os12g0278700	AK068027	Similar to Cystinosin homolog.	membrane protein	2.38	down (p<0.01)
3.36	Os02g0774200	AK064163	Conserved hypothetical protein.	unknown	1.75	down
3.35	Os08g0485000	AK073011	Similar to Phi-1 protein.	unknown	1.43	up
3.31	Os01g0631200	AK072497	Similar to Uroporphyrinogen III methyltransferase.	metabolism	4.22	down (p<0.01)
3.30	Os07g0646800	AK071716	Similar to Avr9/Cf-9 rapidly elicited protein 231.	metabolism	2.50	down (p<0.01)
3.30	Os01g0149200	AK069318	Conserved hypothetical protein.	unknown	1.02	up
3.29	Os04g0556300	AK062772	Glutathione peroxidase.	detoxication	2.16	down (p<0.01)
3.29	Os01g0795600	AK111059	Conserved hypothetical protein.	unknown	4.13	up
3.28	Os12g0190000	AK071188	Similar to VTC2.	unknown	3.23	down
3.25	Os09g0483100	AK107051	EF-Hand type domain containing protein.	ion binding	3.11	up
3.24	Os03g0147400	AK071480	Divalent ion symporter domain containing protein.	membrane protein	1.57	down
3.21	Os11g0502700	AK065205	Conserved hypothetical protein.	unknown	1.33	down
3.20	Os01g0830700	AK101671	Protein of unknown function DUF231, plant domain containing protein.	unknown	1.03	down
3.19	Os01g0660400	AK109270	Conserved hypothetical protein.	unknown	14.42	up (p<0.01)
3.18	Os01g0837800	AK064840	Similar to Cation diffusion facilitator 8.	membrane protein	2.25	down (p<0.01)

3.16	Os01g0261200	AK102808	No apical meristem (NAM) protein domain containing protein.	transcription	1.88	up (p<0.01)
3.15	Os05g0584200	AK061818	Similar to Late embryogenesis abundant protein Lea14-A.	unknown	2.05	up (p<0.01)
3.15	Os06g0602500	AK111737	Serine/threonine protein kinase-related domain containing protein	phosphorylation	1.09	up
3.14	Os07g0100200	AK073305	Similar to PDX1-like protein 4.	unknown	1.24	up
3.14	Os12g0147800	AK059860	Similar to Phytosulfokines 5 precursor (Secretory protein SH27A).	cell division	1.71	down (p<0.01)
3.13	Os02g0703600	AK067007	Similar to Cytochrome P450 90C1 (EC 1.14.-.-) (ROTUNDIFOLIA3).	hormone	1.44	up (p<0.01)
3.12	Os03g0245800	AK063618	Similar to Heat shock protein 26.	others	20.31	up (p<0.01)
3.12	Os03g0806600	AK070959	Conserved hypothetical protein.	unknown	1.43	up
3.12	Os06g0195800	AK111076	Conserved hypothetical protein.	unknown	3.15	up
3.11	Os04g0605100	AK061266	WRKY transcription factor 68.	transcription	1.32	down
3.11	Os11g0607200	AK111536	Protein kinase, core domain containing protein.	phosphorylation	1.63	up
3.10	Os07g0631700	AK105175	EF-Hand type domain containing protein.	ion binding	1.20	up
3.10	Os05g0380900	AK067214	Similar to Polcalcin Jun o 2 (Calcium-binding pollen allergen Jun o 2).	ion binding	4.01	up
3.10	Os07g0603600	AK071549	Similar to Avr9/Cf-9 rapidly elicited protein 246 (Fragment).	catalytic activity	1.44	up
3.09	Os05g0469800	AK100501	Pyruvate decarboxylase (EC 4.1.1.1)	metabolism	No Hit	No Hit
3.06	Os07g0486500	AK063998	RhoGAP domain containing protein.	signaling	1.58	up

3.06	Os04g0555300	AK103226	Major facilitator superfamily protein.	membrane protein	1.36	down
3.06	Os01g0916400	AK071710	Similar to Selenium binding protein.	stress	1.36	down
3.05	Os01g0689900	AK100606	Conserved hypothetical protein.	unknown	1.17	down
3.04	Os10g0419400	AK103834	Similar to SIPL.	unknown	11.87	down (p<0.01)
3.04	Os07g0596600	AK067238	Similar to Cdc2MsC protein.	cell division	1.23	down
3.04	Os04g0567700	AK064998	ORMDL family protein.	membrane protein	3.43	up (p<0.01)
3.03	Os03g0180900	AK073589	Tify domain containing protein.	stress	12.41	down (p<0.01)
3.02	Os08g0494300	AK066150	Copine domain containing protein.	protein binding	4.29	up (p<0.01)
3.01	Os03g0326500	AK058426	Similar to Thioredoxin-like 1.	detoxication	1.85	up
3.00	Os02g0819400	AK100921	Globin-like family protein.	unknown	1.50	up
3.00	Os03g0790500	AK107136	Alpha/beta hydrolase fold-3 domain containing protein.	metabolism	3.40	down
2.98	Os05g0580000	AK100910	Similar to ADP-glucose pyrophosphorylase (EC 2.7.7.27) (Fragment).	metabolism	1.47	down
2.96	Os04g0524600	AK069437	Oligopeptide transporter OPT superfamily protein.	membrane protein	1.00	down
2.95	Os03g0655400	AK059150	Similar to LIP5.	stress	1.36	up
2.95	Os03g0376100	AK060421	Similar to Cystathionine gamma-synthase (Fragment).	metabolism	1.95	up (p<0.01)
2.94	Os02g0631200	AK105924	Homeodomain-like containing protein.	transcription	2.85	up
2.91	Os02g0317500	AK102355	Cyclin-like F-box domain containing protein.	protein degradation	2.40	up (p<0.01)
2.89	Os01g0716800	AK101741	Endonuclease/exonuclease/phosphatase domain containing protein.	metabolism	4.43	up

2.89	Os05g0181800	AK066089	Conserved hypothetical protein.	unknown	3.48	up ($p<0.01$)
2.88	Os06g0219900	AK058704	Similar to Phi-1 protein.	unknown	3.85	up ($p<0.01$)
2.88	Os01g0647100	AK069624	ADP/ATP carrier protein family protein.	ATP binding	3.82	up ($p<0.01$)
2.87	Os03g0816700	AK107781	Protein of unknown function DUF567 family protein.	unknown	7.34	up ($p<0.01$)
2.86	Os08g0120600	AK104952	Similar to Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13).	metabolism	2.50	up
2.86	Os03g0244200	AK101837	Similar to Thaumatin-like protein.	stress	2.63	up ($p<0.01$)
2.86	Os01g0192000	AK100770	Similar to Zinc finger transcription factor.	ion binding	5.89	up ($p<0.01$)
2.86	Os04g0635000	AK062619	Conserved hypothetical protein.	unknown	1.53	up
2.85	Os01g0664100	AK065234	Conserved hypothetical protein.	unknown	1.24	down
2.85	Os06g0556000	AK102763	Similar to Amino acid carrier (Fragment).	membrane protein	2.85	up ($p<0.01$)
2.84	Os04g0119500	AK061898	Similar to Membrane related protein-like.	unknown	1.78	up
2.84	Os03g0752300	AK069303	Similar to K+ channel protein.	membrane protein	1.53	up
2.83	Os09g0438100	AK063180	Conserved hypothetical protein.	unknown	1.84	down
2.83	Os04g0591100	AK069139	Protein of unknown function DUF597 family protein.	unknown	1.80	up
2.82	Os02g0611200	AK070259	Similar to S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) (Induced stolen tip protein TUB13) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].	metabolism	1.25	down

2.82	Os03g0187600	AK068057	GRAM domain containing protein.	membrane protein	2.04	down
2.81	Os04g0550200	AK108473	Pathogenesis-related transcriptional factor and ERF domain containing protein.	transcription	1.52	up
2.80	Os01g0186900	AK105323	Similar to transposon protein CACTA, En/Spm sub-class.	others	1.63	up
2.80	Os01g0187900	AK071611	Similar to Transcription factor MYBS2.	transcription	1.34	up
2.80	Os09g0251800	AK061218	C2 calcium/lipid-binding region, CaLB domain containing protein.	ion binding	1.47	up
2.79	Os10g0431900	AK106265	Serine/threonine protein kinase-related domain containing protein.	phosphorylation	4.77	up
2.78	Os05g0110900	AK073169	Similar to Protein kinase APK1B, chloroplast precursor (EC 2.7.1.-).	signaling	1.11	up
2.77	Os01g0911700	AK073805	Similar to Regulatory protein viviparous-1.	transcription	5.10	up ($p<0.01$)
2.77	Os04g0461600	AK072586	Similar to Fw2.2.	unknown	1.03	down
2.77	Os12g0578400	AK060767	Glycoside hydrolase family 79, N-terminal protein.	metabolism	1.13	down
2.77	Os02g0118200	AK111716	Similar to Protein kinase APK1B, chloroplast precursor (EC 2.7.1.-).	signaling	1.14	up
2.75	Os04g0306400	AK103443	Ribose 5-phosphate isomerase family protein.	metabolism	1.05	up
2.74	Os09g0517600	AK101828	Similar to FH protein NFH1.	actin binding	2.29	up ($p<0.01$)
2.73	Os11g0536800	AK102704	Amidase family protein.	catalytic activity	1.02	down
2.73	Os04g0653600	AK059064	Similar to AINTEGUMENTA-like protein.	transcription	2.92	up ($p<0.01$)
2.72	Os07g0607800	AK106786	Conserved hypothetical protein.	unknown	1.05	down

2.72	Os04g0224900	AK058569	FAD dependent oxidoreductase family protein.	metabolism	3.56	down (p<0.01)
2.71	Os10g0407000	AK101494	Pectin lyase fold/virulence factor domain containing protein.	cell elongation	1.62	up (p<0.01)
2.71	Os10g0113100	AK103772	Aldo/keto reductase family protein.	metabolism	2.08	up (p<0.01)
2.70	Os10g0162000	AK062627	Conserved hypothetical protein.	unknown	1.67	up
2.70	Os10g0525500	AK063104	Similar to Glutathione S-transferase GSTU31 (Fragment).	stress	1.55	up
2.70	Os01g0110400	AK103194	Similar to Acetyl-CoA C-acetyltransferase.	metabolism	1.04	down
2.69	Os06g0192800	AK070038	Similar to RING-H2 finger protein ATL1R (RING-H2 finger protein ATL8).	protein binding	2.18	up
2.69	Os02g0726300	AK101321	Similar to AOBP (Ascorbate oxidase promoter-binding protein).	transcription	1.43	up
2.68	Os07g0438600	AK102261	Proteinase inhibitor I9, subtilisin propeptide domain containing protein.	catalytic activity	98.69	up (p<0.01)
2.67	Os10g0482900	AK071332	Thioredoxin fold domain containing protein.	detoxication	3.11	up
2.67	Os01g0575200	AK106333	Conserved hypothetical protein.	unknown	1.62	down
2.66	Os04g0493000	AK061664	Similar to H0425E08.14 protein.	unknown	1.19	up
2.66	Os03g0285800	AK067339	MAP Kinase. OsMAPK2	cell division	1.06	down
2.65	Os03g0440900	AK061730	Similar to LRR protein.	nucleotide binding	1.60	up
2.64	Os03g0676400	AK109228	VQ domain containing protein.	unknown	7.39	up (p<0.01)
2.63	Os10g0529400	AK102196	Similar to Tau class GST protein 4.	stress	No Hit	No Hit
2.63	Os08g0464400	AK073370	Zinc finger, RING-type domain containing protein.	protein binding	1.01	down

2.63	Os04g0684800	AK066799	Similar to CROC-1-like protein (Fragment).	catalytic activity	3.48	up
2.62	Os01g0719100	AK068005	Similar to PGPD14 protein.	protein binding	1.63	up
2.62	Os01g0797600	AK069262	Ethylene responsive element binding factor3 (OsERF3).	transcription	1.81	up
2.61	Os01g0165000	AK067313	DRE binding protein 2.	transcription	1.24	up
2.61	Os09g0440300	AK060757	Similar to Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1) (Matured fruit 60 kDa protein) (MF-60).	metabolism	1.99	down (p<0.01)
2.58	Os01g0246700	AK105509	Similar to WRKY transcription factor 1.	transcription	2.11	up
2.57	Os11g0158300	AK070475	Pentatricopeptide repeat containing protein.	nucleotide binding	1.12	up
2.57	Os02g0214900	AK071228	Similar to Histone deacetylase HDAC2.	transcription	1.08	up
2.57	Os07g0585500	AK070285	Conserved hypothetical protein.	unknown	1.63	down
2.57	Os06g0193400	AK065667	Similar to Helix-loop-helix protein homolog.	transcription	1.06	up
2.57	Os04g0119500	AK065035	Similar to Membrane related protein-like.	unknown	1.78	up
2.56	Os01g0845000	AK106438	Conserved hypothetical protein.	unknown	1.41	up
2.56	Os03g0128800	AK066570	Conserved hypothetical protein.	unknown	3.75	up
2.56	Os10g0463800	AK102352	Conserved hypothetical protein.	unknown	1.17	down
2.55	Os07g0557100	AK102045	Delayed-early response protein/equilibrative nucleoside transporter family protein.	membrane protein	1.93	up
2.54	Os10g0525000	AK099925	Cytochrome P450 family protein.	metabolism	1.67	down
2.54	Os05g0119300	AK068289	XYPPX repeat containing protein.	unknown	2.81	down (p<0.01)
2.53	Os07g0225300	AK073667	OsNAC3 protein.	transcription	1.53	up
2.50	Os05g0495300	AK067980	Conserved hypothetical protein.	unknown	1.71	up

2.50	Os02g0210700	AK111879	Protein kinase, core domain containing protein.	phosphorylation	20.07	up ($p<0.01$)

[a] Fold change shows the average expression ratio of three biological replicates and a colour swap for each replicate.

[b] Locus ID

[c] Full-length cDNA accession number

[d] Description in Rice Annotation Project Database (RAP-DB; http://rapdb.dna.affrc.go.jp/)

[e] Data was extracted from Narsai et al. (2009), *Plant Physiology* **151**: 306–322.