SUPPLEMENTARY DATA

TABLE S2.Down-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)
0.09	Os03g0836800	AK061197	Similar to IAA-amino acid hydrolase 1 (EC 3.5.1.-).	hormone	243.5	down (p<0.01)
0.11	Os02g0178100	AK109630	CCT domain containing protein.	transcription	1.0	down
0.11	Os12g0111400	AK062951	Conserved hypothetical protein.	unknown	No Hit	No Hit
0.12	Os03g0738600	AK073529	Similar to Lipoxygenase L-2 (EC 1.13.11.12).	hormone	786.6	down (p<0.01)
0.13	Os05g0507000	AK108025	Conserved hypothetical protein.	unknown	56.5	down
0.14	Os11g0439600	AK069955	Similar to Nod factor binding lectin-nucleotide phosphohydrolase.	unknown	No Hit	No Hit
0.14	Os04g0496300	AK062810	Conserved hypothetical protein.	unknown	73.2	down (p<0.01)
0.14	Os06g0199000	AK106381	Similar to Glycine-rich cell wall structural protein 2 precursor.	cell elongation	51.7	up (p<0.01)
0.16	Os04g0413500	AK072276	Similar to Cell wall invertase 2. (OsCIN2.)	metabolism	3.5	down
0.16	Os09g0556800	AK101051	Conserved hypothetical protein.	unknown	41.5	down (p<0.01)
0.16	Os08g0389700	AK065108	Conserved hypothetical protein.	unknown	149.4	down (p<0.01)
0.16	Os11g0306400	AK106179	Similar to Herbicide safener binding protein.	unknown	13.3	down (p<0.01)
0.17	Os01g0348800	AK062553	Similar to Salt-stress induced protein (Salt protein).	stress	3.8	down (p<0.01)
0.17	Os05g0205100	AK111332	NLI interacting factor domain containing protein.	unknown	No Hit	No Hit
0.18	Os01g0191800	AK102360	Similar to Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora-B) (Fragment).	cell division	47.7	down (p<0.01)
0.18	Os03g0431100	AK058643	XYPPX repeat containing protein.	unknown	24.4	down (p<0.01)

0.19	Os10g0471100	AK100751	Wax-deficient anther1. Similar to CER1.	metabolism	7.3	down (p<0.01)
0.19	Os02g0699500	AK062786	Conserved hypothetical protein.	unknown	17.4	down (p<0.01)
0.20	Os01g0813800	AK067934	Glycoside hydrolase, family 1 protein.	metabolism	1.3	down
0.20	Os04g0563700	AK070211	CycB2;1.	cell division	32.7	down (p<0.01)
0.20	Os01g0176500	AK102552	Conserved hypothetical protein.	unknown	38.2	down (p<0.01)
0.20	Os03g0432100	AK065739	Similar to Orthophosphate dikinase precursor (EC 2.7.9.1).	photosynthesis	104.5	up (p<0.01)
0.21	Os12g0189300	AK068710	Pyruvate/Phosphoenolpyruvate kinase, catalytic core domain containing protein	metabolism	36.4	down (p<0.01)
0.21	Os09g0491100	AK066710	Similar to Beta-primeverosidase (EC 3.2.1.149).	metabolism	120.0	down (p<0.01)
0.21	Os02g0700100	AK102954	Similar to WD-repeat protein.	signaling	14.8	down (p<0.01)
0.21	Os10g0577400	AK064295	Conserved hypothetical protein.	unknown	55.9	down (p<0.01)
0.22	Os06g0726800	AK070518	CycB2;2.	cell division	30.9	down (p<0.01)
0.22	Os01g0756900	AK058427	Conserved hypothetical protein.	unknown	15.5	down (p<0.01)
0.23	Os02g0742800	AK106279	Conserved hypothetical protein.	unknown	49.2	down (p<0.01)
0.23	Os11g0171700	AK099115	Forkhead-associated domain containing protein.	protein binding	8.9	down (p<0.01)
0.24	Os06g0142200	AK105832	Early nodulin.	metabolism	1.3	up
0.24	Os12g0245700	AK107691	Conserved hypothetical protein.	unknown	5.8	down
0.24	Os02g0158100	AK058991	EF hand domain containing protein 1.	endocytosis	42.0	down (p<0.01)
0.24	Os04g0375900	AK101769	Kinesin, motor region domain containing protein.	cell division	28.8	down (p<0.01)
0.24	Os10g0498900	AK108732	Similar to Microtubule-associated protein EB1-like protein.	cell elongation	38.5	down (p<0.01)
0.25	Os01g0946100	AK072248	WD40-like domain containing protein.	nucleotide binding	10.6	down (p<0.01)
0.25	Os04g0559700	AK058323	Similar to Plasma membrane intrinsic protein.	membrane protein	1.2	down
0.25	Os09g0547200	AK073078	Protein of unknown function DUF292, eukaryotic	unknown	35.4	down (p<0.01)

			domain containing protein.			
0.25	Os02g0699700	AK072471	Similar to DNA topoisomerase II.	cell division	14.9	down (p<0.01)
0.26	Os07g0474300	AK108961	Conserved hypothetical protein.	unknown	11.7	down (p<0.01)
0.26	Os03g0128300	AK064718	Conserved hypothetical protein.	unknown	48.0	down (p<0.01)
0.26	Os08g0421800	AK103087	Similar to Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.-) (Arabidospsis NPK1-related protein kinase 1). Splice isoform 1S.	cell division	29.1	down (p<0.01)
0.26	Os03g0114000	AK063381	Similar to Kinesin.	cell division	22.4	down (p<0.01)
0.26	Os03g0288900	AK100329	Conserved hypothetical protein.	unknown	1.5	up
0.26	Os09g0484200	AK073885	Conserved hypothetical protein.	unknown	1.1	up
0.27	Os03g0297800	AK107121	Protein kinase-like domain containing protein.	phosphorylation	21.5	down (p<0.01)
0.27	Os04g0229100	AK071484	Similar to Sinapyl alcohol dehydrogenase.	metabolism	1.2	down
0.27	Os01g0972900	AK109536	Similar to Clone ZZD405 mRNA sequence. (Fragment).	unknown	14.9	down (p<0.01)
0.27	Os03g0765900	AK058858	PetM of cytochrome b6f complex subunit 7 family protein.	photosynthesis	2.2	down
0.27	Os03g0712100	AK106258	Cell division cycle-associated protein domain containing protein.	cell division	13.9	down (p<0.01)
0.28	Os03g0120000	AK101925	Conserved hypothetical protein.	unknown	7.0	down (p<0.01)
0.28	Os03g0780200	AK107920	Conserved hypothetical protein.	unknown	46.9	down (p<0.01)
0.28	Os03g0659800	AK062366	Conserved hypothetical protein.	unknown	25.8	down (p<0.01)
0.28	Os12g0263100	AK102127	Similar to Zinc finger, DHHC domain containing 4.	nucleotide binding	24.4	down (p<0.01)
0.29	Os05g0406800	AK062566	Leucine rich repeat, N-terminal domain containing protein.	nucleotide binding	7.7	down (p<0.01)
0.29	Os03g0183500	AK063042	Protein of unknown function DUF581 family	unknown	5.6	down (p<0.01)

			protein.			
0.29	Os01g0685900	AK064024	Similar to 65kD microtubule associated protein.	cell division	47.0	down (p<0.01)
0.29	Os02g0739700	AK111537	E2F Family domain containing protein.	cell division	34.1	down (p<0.01)
0.30	Os03g0165400	AK102192	Similar to Relative to SR12 protein (Fragment).	metabolism	1.9	down (p<0.01)
0.30	Os12g0120000	AK105399	Protein of unknown function DUF936, plant family protein.	unknown	No Hit	No Hit
0.30	Os06g0711900	AK105838	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein. (Os06t0711900-01)	unknown	3.6	down
0.30	Os02g0718100	AK109216	Conserved hypothetical protein.	unknown	6.2	down (p<0.01)
0.31	Os04g0228100	AK059410	Conserved hypothetical protein.	unknown	28.4	down (p<0.01)
0.31	Os09g0507500	AK071392	Similar to Peroxidase 55 precursor (EC 1.11.1.7) (Atperox P55) (ATP20a).	stress	1.2	down
0.31	Os01g0108800	AK102103	Protein of unknown function DUF936, plant family protein.	unknown	13.7	down (p<0.01)
0.31	Os11g0120200	AK101734	Protein of unknown function DUF936, plant family protein.	unknown	No Hit	No Hit
0.31	Os03g0162200	AK061605	Similar to Histone H2A.	cell division	37.4	down (p<0.01)
0.32	Os03g0238600	AK070684	Similar to Purple acid phosphatase.	unknown	1.0	up
0.32	Os07g0264100	AK065209	NAD(P)-binding domain containing protein	metabolism	13.4	down (p<0.01)
0.32	Os11g0150400	AK058243	Stress responsive alpha-beta barrel domain containing protein. Similar to pop3 peptide.	metabolism	1.7	down
0.32	Os02g0302700	AK060537	Similar to Nicotianamine aminotransferase A.	metabolism	27.4	down (p<0.01)
0.32	Os07g0659500	AK073537	Non-SMC condensin subunit, XCAP-D2/Cnd1 family protein.	cell division	16.1	down (p<0.01)

0.32	Os10g0544600	AK105882	Zinc finger, RING/FYVE/PHD-type domain containing protein.	protein binding	1.2	down
0.32	Os05g0497100	AK064293	Similar to SMC4 protein.	cell division	10.5	down (p<0.01)
0.32	Os01g0909400	AK068178	Protein of unknown function DUF868, plant family protein.	unknown	1.4	down
0.32	Os02g0658800	AK059638	Beta-expansin (OsEXPB11).	cell elongation	6.8	down (p<0.01)
0.32	Os01g0863500	AK111023	Conserved hypothetical protein.	unknown	3.4	down
0.33	Os11g0107700	AK073061	Similar to Leucine Rich Repeat family protein, expressed.	nucleotide binding	7.7	down (p<0.01)
0.33	Os06g0179000	AK065263	Glycoside hydrolase family 79, N-terminal protein.	metabolism	2.0	up (p<0.01)
0.33	Os05g0226900	AK100217	Similar to Repetitive proline rich protein.	unknown	No Hit	No Hit
0.33	Os01g0151700	AK099949	Similar to Short-chain dehydrogenase Tic32.	metabolism	17.9	down (p<0.01)
0.33	Os08g0199400	AK105852	Similar to Stearoyl-acyl carrier protein desaturse (EC 1.14.99.6) (Fragment).	metabolism	18.8	down (p<0.01)
0.33	Os08g0512600	AK059682	Protein cdc2 kinase (cdc2Os3).	cell division	21.3	down (p<0.01)
0.33	Os02g0193600	AK060499	Mitotic checkpoint serine/threonine protein kinase, Bub1 domain containing protein.	cell division	25.5	down (p<0.01)
0.33	Os08g0492000	AK100814	Similar to Glutathione transporter.	membrane protein	2.1	down
0.34	Os07g0448800	AK060712	Aquaporin.	membrane protein	1.1	down
0.34	Os01g0259400	AK102537	Armadillo-type fold domain containing protein.	unknown	12.6	down (p<0.01)
0.34	Os04g0644400	AK071989	Similar to Proline-rich-like protein.	unknown	No Hit	No Hit
0.34	Os04g0228400	AK069548	Expansin precursor (Alpha-expansin OsEXPA1).	cell elongation	1.4	down
0.34	Os07g0507200	AK102722	Targeting for Xklp2 family protein.	cell division	35.4	down (p<0.01)
0.34	Os02g0258200	AK070270	High mobility group box domain containing protein.	nucleotide binding	27.5	down (p<0.01)

0.34	Os08g0345800	AK058551	Similar to Glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPASE B) (Alpha-D-glucose-1-phosphate adenyl transferase).	metabolism	1.0	down
0.35	Os05g0585400	AK067538	Conserved hypothetical protein.	unknown	1.5	down
0.35	Os04g0530100	AK107184	Similar to Beta-expansin 1 precursor (AtEXPB1) (At-EXPB1) (Ath-ExpBeta-1.5) (OsEXPB17).	cell elongation	16.2	down
0.35	Os04g0105200	AK058807	Conserved hypothetical protein.	unknown	1.0	down
0.35	Os01g0963800	AK107518	Conserved hypothetical protein.	unknown	1.2	up
0.35	Os03g0119900	AK058741	Similar to histone H4.	cell division	No Hit	No Hit
0.35	Os02g0699700	AK063335	Similar to DNA topoisomerase II.	cell division	14.9	down ($p<0.01$)
0.35	Os05g0415700	AK102449	Glycoside hydrolase, family 20 protein.	metabolism	1.1	up
0.35	Os02g0511600	AK111241	Glycosyl transferase, family 31 protein.	metabolism	1.6	up ($p<0.01$)
0.35	Os03g0770900	AK106660	Conserved hypothetical protein.	unknown	28.2	down ($p<0.01$)
0.35	Os02g0218800	AK105964	Similar to Allene oxide synthase (EC 4.2.1.92).	hormone	57.7	down ($p<0.01$)
0.35	Os02g0794500	AK111818	Similar to Serine carboxypeptidase II precursor (EC 3.4.16.6) (Carboxypeptidase D) (Bri1 suppressor 1) [Contains: Serine carboxypeptidase II chain A; Serine carboxypeptidase II chain B].	protein degradation	1.4	down
0.36	Os02g0687900	AK064814	Peptidase S10, serine carboxypeptidase family protein.	protein degradation	1.8	down
0.36	Os09g0538500	AK105425	Similar to Male sterility MS5.	unknown	21.5	down ($p<0.01$)
0.36	Os02g0606700	AK063512	Conserved hypothetical protein.	unknown	28.0	down ($p<0.01$)
0.36	Os11g0549615	AK069660	Metallophosphoesterase domain containing protein.	unknown	3.4	down ($p<0.01$)

0.36	Os12g0433500	AK102130	Similar to Fused1 (Fragment).	unknown	19.5	down (p<0.01)
0.37	Os04g0583600	AK059019	Similar to histone H4.	cell division	No Hit	No Hit
0.37	Os03g0294600	AK110762	Similar to Importin-beta1.	membrane protein	15.9	down (p<0.01)
0.37	Os07g0638000	AK060298	Conserved hypothetical protein.	unknown	16.6	down (p<0.01)
0.37	Os05g0459400	AK073413	Kinesin, motor region domain containing protein.	cell division	29.4	down (p<0.01)
0.37	Os01g0662700	AK068152	Similar to Naphthoate synthase (EC 4.1.3.36).	metabolism	1.5	down
0.37	Os04g0505200	AK066703	Leucine-rich repeat, plant specific containing protein.	nucleotide binding	1.3	down
0.38	Os02g0178700	AK110943	Helix-loop-helix DNA-binding domain containing protein.	transcription	1.4	down
0.38	Os01g0814100	AK061173	Similar to Bindin (Fragment).	unknown	1.9	down
0.38	Os05g0512000	AK102433	Zinc finger, RING/FYVE/PHD-type domain containing protein.	protein binding	9.2	down (p<0.01)
0.38	Os05g0113900	AK074018	Similar to Histone H2A.	cell division	31.7	down (p<0.01)
0.38	Os06g0285400	AK067208	Similar to Serine/threonine-specific kinase like protein.	phosphorylation	39.0	down (p<0.01)
0.38	Os06g0514100	AK062831	Similar to Thionin Osthi1.	unknown	No Hit	No Hit
0.38	Os03g0314500	AK065474	Six-bladed beta-propeller, TolB-like domain containing protein.	metabolism	40.0	down (p<0.01)
0.38	Os10g0104900	AK112062	Similar to DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA methyltransferase I) (DNA MTase RnoIP) (MCMT) (M.RnoIP). Splice isoform 3.	transcription	48.0	down (p<0.01)
0.38	Os03g0767600	AK111226	BTB domain containing protein.	protein binding	No Hit	No Hit
0.39	Os05g0590000	AK070159	Peptidase A1, pepsin family protein.	protein degradation	1.0	down

0.39	Os02g0726700	AK068228	Helix-loop-helix DNA-binding domain containing protein.	transcription	1.0	up
0.39	Os05g0273800	AK060563	Similar to Soluble epoxide hydrolase.	metabolism	5.7	down ($p<0.01$)
0.39	Os12g0233100	AK108229	WW/Rsp5/WWP domain containing protein.	protein binding	2.3	down
0.39	Os04g0511700	AK102761	Conserved hypothetical protein.	unknown	15.0	down ($p<0.01$)
0.39	Os07g0551700	AK067424	Similar to Cellulose synthase (Fragment).	cell elongation	1.0	down
0.39	Os01g0748000	AK103720	Similar to Dynamin family protein.	cell division	14.5	down ($p<0.01$)
0.39	Os01g0243100	AK064212	Similar to Kinesin.	cell division	12.6	down ($p<0.01$)
0.39	Os04g0602500	AK058634	Similar to Pectin acetylesterase.	cell elongation	22.8	up ($p<0.01$)
0.39	Os03g0339700	AK073084	Protein of unknown function DUF827, plant family protein.	unknown	3.9	down
0.40	Os10g0457400	AK063553	Conserved hypothetical protein.	unknown	12.9	down ($p<0.01$)
0.40	Os07g0448800	AK103938	Aquaporin.	membrane protein	1.1	down
0.40	Os03g0214100	AK060582	Replication protein A1.	cell division	12.1	down ($p<0.01$)
0.40	Os01g0571100	AK068093	Similar to ZmGR2a protein.	hormone	2.9	down

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[a] Fold change shows 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.