

Table S1. List of GA up-regulated probes.

Probe#	ID	Accession	WT-GA	WT+GA	WT±GA*	Annotation
1	Os09g0457600	CI048168	9.59	17.03	2.51	RAMy3B
2	Os09g0473600	AK065236	10.63	18.05	2.61	RAMy3E
3	Os08g0473600	AK103413	10.61	17.99	2.22	RAMy3E
4	Os02g0765400	M81144	10.79	17.94	2.15	RAMy1C
5	Os10g0805000	AK068643	6.37	13.30	2.09	Metallophosphoesterase domain containing protein.
6	Os07g0600000	AK062055	6.53	12.22	1.98	Hypothetical protein.
7	Os04g0538400	AK108230	7.12	13.68	1.98	Nodulin 21 (N-21).
8	Os02g0740400	AK070261	10.73	17.03	1.90	Lipolytic enzyme, G-D-S-L family protein.
9	Os02g0740400	AK099325	10.74	17.02	1.89	Lipolytic enzyme, G-D-S-L family protein.
10	Os10g0842500	AK068515	4.74	10.91	1.86	Laccase (EC 1.10.3.2).
11	Os10g0357400	AK063489	4.76	10.89	1.85	RAMy1B
12	Os04g0441700	AK072763	3.94	9.99	1.82	Conserved hypothetical protein.
13	Os08g0473600	AK064300	11.62	17.45	1.76	RAMy3E
14	Os04g0227500	AK104227	9.65	15.45	1.75	DSBA oxidoreductase family protein.
15	Os04g0227500	AK060352	9.43	15.19	1.74	DSBA oxidoreductase family protein.
16	Os04g0227500	AK059943	8.19	13.87	1.71	DSBA oxidoreductase family protein.
17	Os03g0248500	CI557828	6.04	11.61	1.68	(No Hit)
18	Os03g0248500	CI557828	6.06	11.62	1.67	(No Hit)
19	Os05g0289700	AK108917	4.43	9.62	1.65	Xylan endohydrolase isoenzyme X-1 (EC 3.2.1.8).
20	Os12g0131900	Os12g0131900	7.49	12.98	1.65	MYST1 protein (Fragment).
21	Os02g0659900	CI436459	7.77	13.25	1.65	(No Hit)
22	Os03g0327700	AK120305	8.25	13.68	1.64	Hypothetical protein.
23	Os04g0515900	AK062055	6.80	12.70	1.63	NAM1/CLC2-like protein.
24	Os05g0523300	AK071192	6.47	11.81	1.61	AUX/IAA protein family protein.
25	Os01g0134800	AK063402	5.75	11.06	1.60	(1,4)-beta-xylan endohydrolase, isoenzyme X-II (EC 3.2.1.8) (Fragment).
26	Os01g0165500	AK122083	4.15	9.46	1.60	Conserved hypothetical protein.
27	Os05g0514000	CI260287	4.45	9.79	1.59	Lipase, class 3 family protein.
28	Os10g0323500	AK071372	4.50	9.79	1.59	Beta-glucosidase.
29	Os02g0721100	AK108167	4.11	9.25	1.55	Ubiquitin-conjugating enzyme E2-17 kDa 11 (EC 6.3.2.19) (Ubiquitin carrier protein 11).
30	Os06g0143100	AK121057	9.18	14.29	1.54	Hypothetical protein.
31	Os04g0521100	AK109499	4.59	9.70	1.52	Plasma membrane intrinsic protein (Aquaporin).
32	Os03g0102700	AF261275	4.37	9.46	1.53	Beta-expansin precursor.
33	Os09g0457800	AK101358	9.63	14.69	1.52	RAMy3C
34	Os01g0878900	AK104652	6.48	11.53	1.52	4,5-DOPA dioxygenase extradiol.
35	Os02g0225200	CI537771	4.41	9.62	1.51	HAD-superfamily subfamily 1B hydrolase, hypothetical 1 protein.
36	Os01g0878900	AK104545	6.41	11.39	1.50	4,5-DOPA dioxygenase extradiol.
37	Os01g0878900	AK060927	6.34	11.31	1.49	4,5-DOPA dioxygenase extradiol.
38	Os02g0665500	AK109040	6.69	11.64	1.49	Protein kinase domain containing protein.
39	Os03g0159100	AK109495	6.34	11.20	1.49	Protein kinase APK18 (EC 2.7.1.1).
40	Os01g0704000	AK061237	11.44	16.38	1.49	HAD-superfamily subfamily 1B hydrolase, hypothetical 1 protein.
41	Os01g0878900	AK104601	6.24	11.17	1.49	4,5-DOPA dioxygenase extradiol.
42	Os01g0878900	AK104432	6.12	11.05	1.48	4,5-DOPA dioxygenase extradiol.
43	Os03g0165500	CI206378	5.67	10.80	1.48	Cyclin-like F-box domain containing protein.
44	Os01g0165400	AK101691	4.98	9.66	1.47	Conserved hypothetical protein.
45	Os01g0878900	AK104462	6.11	10.97	1.46	4,5-DOPA dioxygenase extradiol.
46	Os11g0139400	AK107562	6.45	11.25	1.44	Conserved hypothetical protein.
47	Os09g0479900	CI269495	10.63	15.33	1.42	Peptidase S8 and S53, subtilisin, kexin, sedoimin domain containing protein.
48	Os01g0772100	CI463933	8.74	13.98	1.38	LOB domain protein 30.
49	Os03g0658800	AK109467	6.70	11.29	1.38	Multi antimicrobial extrusion protein MatE family protein.
50	Os01g0212400	AK066468	7.05	11.59	1.37	Calcium-binding EF-hand domain containing protein.
51	Os01g0731100	AK106037	4.81	9.31	1.36	Conserved hypothetical protein.
52	Os06g0280100	AK119420	4.50	9.69	1.35	Phytase.
53	Os08g0475100	AK105839	10.10	14.49	1.32	Esterase/lipase/thioesterase domain containing protein.
54	Os05g0574100	AK106699	6.99	11.38	1.32	Lipase, class 3 family protein.
55	Os11g0253300	AK071495	11.81	16.20	1.32	Peptidase C1A, papain family protein.
56	Os12g0463300	AK058988	7.49	11.98	1.31	(No Hit)
57	Os08g0124600	CI405888	7.65	12.00	1.31	(No Hit)
58	Os08g0459300	AK060409	8.84	13.19	1.31	Allergen V5/tpx-1 related family protein.
59	Os02g0481400	CI405888	7.69	12.03	1.31	(No Hit)
60	Os02g0510700	CI386159	6.08	11.41	1.30	(No Hit)
61	Os04g0280700	CI405888	7.80	12.11	1.30	(No Hit)
62	Os08g0289400	CI405888	7.65	11.96	1.30	Zn-finger, CCHC type domain containing protein.
63	Os02g0120500	AK119580	4.81	9.11	1.29	Basic helix-loop-helix dimerization region bHLH domain containing protein.
64	Os01g0731100	AK109495	6.40	11.20	1.29	Conserved hypothetical protein.
65	Os02g0577500	CI405888	7.48	11.78	1.29	(No Hit)
66	Os01g0731100	AK061471	5.00	9.28	1.29	Conserved hypothetical protein.
67	Os02g0769900	Os02g0769900	10.53	14.79	1.28	Glycoside hydrolase, family 5 protein.
68	Os03g0102700	AK061423	3.80	8.05	1.28	Beta-expansin precursor.
69	Os01g0163400	CI405888	7.50	11.75	1.28	(No Hit)
70	Os09g0518200	AK121725	9.62	13.85	1.27	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
71	Os06g0519100	AK058759	4.82	9.05	1.27	Hypothetical protein.
72	Os03g0549900	CI386359	6.05	12.28	1.27	(No Hit)
73	Os10g1074000	AK065945	5.52	9.74	1.27	Nodulin-like domain containing protein.
74	Os01g0281600	AK062646	7.06	11.28	1.27	Plastocyanin-like domain containing protein.
75	Os11g0134100	Os11g0134100	6.79	11.01	1.27	Rhamnolacturonate lyase family protein.
76	Os07g0498400	CI197845	6.98	11.19	1.27	Protein kinase domain containing protein.
77	Os06g0459300	AK109467	6.96	11.17	1.27	Allergen V5/tpx-1 related family protein.
78	Os04g0517900	CI431602	8.88	13.09	1.27	(No Hit)
79	Os04g0517900	CI431602	9.31	13.50	1.26	(No Hit)
80	Os11g0253300	X80876	12.65	16.80	1.25	Peptidase C1A, papain family protein.
81	Os09g0123800	AK069466	6.93	10.98	1.25	Conserved hypothetical protein.
82	Os09g0518200	AK064395	7.33	11.43	1.24	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
83	Os04g0324100	CI401469	9.43	13.53	1.23	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
84	Os03g0159700	AK071242	5.78	9.87	1.23	P60C protein.
85	Os02g0551000	AK070492	6.84	9.72	1.23	Conserved hypothetical protein.
86	Os08g0161800	AK059496	3.92	8.00	1.23	Cholinephosphate cytidyltransferase.
87	Os01g0142300	AK072289	5.75	9.82	1.22	Glycosyl transferase, group 1 domain containing protein.
88	Os02g0658100	AK059231	5.42	9.49	1.22	Conserved hypothetical protein.
89	Os01g0389700	AK078158	6.07	10.11	1.22	Protein of unknown function DUF679 family protein.
90	Os08g0556900	AK099308	4.40	8.44	1.22	Cysteine proteinase (EC 3.4.22.1).
91	Os01g0142300	AK060202	5.36	9.40	1.22	Glycosyl transferase, group 1 domain containing protein.
92	Os03g0644400	AB022783	9.83	13.84	1.21	Amino acid permease.
93	Os01g0784800	AK062055	6.82	12.63	1.21	Minor allergen.
94	Os03g0644400	AK062055	9.88	13.88	1.20	Amino acid permease.
95	Os08g0556900	AK105612	4.37	8.36	1.20	Cysteine proteinase (EC 3.4.22.1).
96	Os08g0280100	AK072150	4.82	8.81	1.20	Phytase.
97	Os08g0470200	AK059496	13.08	17.04	1.20	Carbonic anhydrase, eukaryotic family protein.
98	Os11g0156200	AK100124	3.74	7.71	1.20	Peptidase S28 family protein.
99	Os01g0297700	AK106554	13.84	17.80	1.19	Protein of unknown function DUF6 domain containing protein.
100	Os01g0784800	AK104580	10.27	14.21	1.19	Minor allergen.
101	Os02g0120500	AK108176	4.43	8.36	1.19	Basic helix-loop-helix dimerization region bHLH domain containing protein.
102	Os04g0533100	AK107680	7.21	11.14	1.18	AP2 domain containing protein RAP2.4 (Fragment).
103	Os12g0568500	CI549138	5.65	9.56	1.18	Metallothionein-like protein type 1.
104	Os08g0556900	AK072235	4.24	8.13	1.17	Cysteine proteinase (EC 3.4.22.1).
105	Os02g0732000	AK108499	6.72	10.81	1.17	Universal stress protein (Usp) family protein.
106	Os04g0103900	CI348974	6.93	8.61	1.17	Actin-binding FH2 domain containing protein.
107	Os03g0644400	AK067118	9.15	13.00	1.16	Amino acid permease.
108	Os08g0695400	AK071198	9.59	13.45	1.16	Haem peroxidase, plant/fungal/bacterial family protein.
109	Os09g0485100	AK107051	8.85	12.68	1.15	Calcium-binding EF-hand domain containing protein.
110	Os11g0249600	AK070268	3.98	7.52	1.15	Polysaccharide C (Fragment).
111	Os02g0765600	M24286	13.63	17.46	1.15	RAMy1A
112	Os02g0740400	AK111360	6.74	10.56	1.15	Lipolytic enzyme, G-D-S-L family protein.
113	Os03g0327800	CI362055	8.42	12.22	1.14	NAC-domain containing protein 29 (ANAC029) (NAC-LIKE, ACTIVATED BY AP3/P1) protein (NAP).
114	Os12g0244400	AK070261	4.03	7.63	1.14	Amino acid polyphosphate transporter DUF791 family protein.
115	Os01g1097000	AK072035	7.05	10.85	1.14	Uncharacterized Cys-rich domain containing protein.
116	Os01g0801500	AK060529	6.63	10.41	1.14	Beta-1,3-glucanase precursor.
117	Os10g1097000	AK120107	7.22	10.98	1.13	Uncharacterized Cys-rich domain containing protein.
118	Os02g0115900	AK065743	13.42	17.17	1.13	Endosperm luminal binding protein.
119	Os02g0765600	AK101744	13.39	17.14	1.13	RAMy1A
120	Os02g0115900	AK119653	13.71	17.45	1.13	Endosperm luminal binding protein.
121	Os11g0197000	AK069501	6.58	10.32	1.13	Uncharacterized Cys-rich domain containing protein.
122	Os02g0771400	Os02g0771400	4.53	8.27	1.12	Putative tyrosine phosphatase family protein.
123	Os04g0412400	AK111482	7.06	10.79	1.12	Hypothetical protein.
124	Os03g0238600	AK070684	9.69	13.41	1.12	Purple acid phosphatase.
125	Os06g0695300	CI548521	4.84	8.56	1.12	Haem peroxidase, plant/fungal/bacterial family protein.
126	Os02g0115900	AK063006	13.23	16.95	1.12	Endosperm luminal binding protein.
127	Os02g0115900	AF008825	13.42	17.13	1.12	Endosperm luminal binding protein.
128	Os09g0297900	AK107955	4.25	7.96	1.12	Conserved hypothetical protein.
129	Os05g0527300	AK069288	9.85	13.53	1.11	Hypothetical protein.
130	Os03g0180100	AK103226	5.41	9.09	1.11	Conserved hypothetical protein.
131	Os07g0103900	AK109450	6.31	8.99	1.11	Concanavalin A-like lectin/glucanase domain containing protein.
132	Os01g0801500	AK099192	6.45	10.12	1.10	Beta-1,3-glucanase precursor.
133	Os04g0634400	AK099573	5.11	8.77	1.10	CE1_I mismatch endonuclease.
134	Os06g0359900	CI515333	9.47	13.12	1.10	Myo_DNA-binding domain containing protein.
135	Os01g0330400	Os01g0330400	9.27	12.91	1.10	K ⁺ potassium transporter family protein.
136	Os12g0191500	AK061040	5.23	8.88	1.10	Peroxidase 43 precursor (EC 1.11.1.7) (Aterox P43).
137	Os06g0647200	Os06g0647200	5.79	9.43	1.10	Response regulator receiver domain containing protein.
138	Os12g0534900	AY364310	4.30	7.94	1.10	Rac GTPase activating protein 1.
139	Os03g0406100	CI226571	7.71	8.35	1.10	SFX_N-terminal domain containing protein.
140	Os01g0699900	AK067766	4.33	7.96	1.09	AWPM-19-like family protein.
141	Os03g0250000	AK121051	10.63	14.25	1.09	Conserved hypothetical protein.
142	Os03g0150500	AK106694	10.77	14.39	1.09	Phosphate transporter 6.
143	Os12g0660000	AK065451	6.94	10.56	1.09	HCO ₃ ⁻ transporter domain containing protein.
144	Os12g0637000	CI495215	3.61	7.23	1.09	Purple acid phosphatase precursor (EC 3.1.3.2).
145	Os04g0445000	AK105506	11.54	15.13	1.08	Potassium channel SKOR (Stelar K ⁺) outward rectifying channel).
146	Os12g0418000	AK104877	13.24	16.83	1.08	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2).
147	Os12g0664500	CI226286	8.27	11.94	1.07	(No Hit)
148	Os05g0576800	AK070644	9.00	12.55	1.07	MAP kinase homolog.
149	Os01g0734800	AK102415	4.99	8.53	1.07	UDP

159	Oo5g0376100	CI228796	8.33	11.82	1.05	(No Hit)
160	Oo5g0734800	AK061830	6.15	9.63	1.05	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
161	Oo5g0382200	AK070711	6.08	11.20	1.05	Calcium-binding protein precursor (Calreticulin).
162	Oo5g0905000	CI228796	8.32	11.79	1.05	(No Hit)
163	Oo5g0636400	AK061848	5.37	8.84	1.04	CEL1 mismatch endonuclease.
164	Oo5g0125500	AK072127	4.59	8.05	1.04	Oligopeptide transporter OPT superfamily protein.
165	Oo1g0133600	AK105318	4.55	7.12	1.04	Zn-finger, DHHC type domain containing protein.
166	Oo5g0161800	AK120381	4.78	8.22	1.04	Cholinephosphate cytidyltransferase.
167	Oo5g0248600	AK073611	11.62	15.06	1.03	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho- D-glycerate hydro-lyase 2).
168	Oo5g0145900	AK120297	7.44	10.86	1.03	PGPD14.
169	Oo5g0249900	AK111100	6.08	9.49	1.03	Expansin EXP5A.
170	Oo5g0128100	AK106990	6.37	9.78	1.03	Calysin family protein.
171	Oo5g0272000	AK061307	11.19	14.58	1.02	Peptidase A1, pepsin family protein.
172	Oo5g0276500	M81143	14.18	17.57	1.02	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B).
173	Oo5g0254500	AK064485	9.29	12.67	1.02	Glycerophosphoryl diester phosphodiesterase family protein.
174	Oo5g0559900	AK105318	4.55	7.12	1.02	Beta-expansin precursor.
175	Oo5g0766900	AY224473	13.61	16.98	1.02	Serine carboxypeptidase II chains A and B (EC 3.4.16.6) (Carboxypeptidase D) (CPDW-II) (CP-WII).
176	Oo5g0136100	CI144901	8.22	11.59	1.01	Conserved hypothetical protein.
177	Oo5g0142200	AK058916	5.24	8.61	1.01	Beta-ketolacyl reductase GLB8.
178	Oo5g0470200	AK069039	13.83	17.18	1.01	Carbonic anhydrase, eukaryotic family protein.
179	Oo5g0308500	AK099525	5.48	8.82	1.01	Phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein.
180	Oo5g0659700	CI396619	6.01	9.35	1.00	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
181	Oo5g0414100	AK100586	5.57	8.90	1.00	Hypothetical protein.
182	Oo5g0241300	AK100233	10.06	13.37	1.00	Conserved hypothetical protein.
183	Oo5g0208900	AK100323	11.11	14.40	0.99	SPX, N-terminal domain containing protein.
184	Oo5g0550500	AK064698	4.16	7.45	0.99	Pectinacetylase.
185	Oo5g0205900	AK111887	11.37	14.66	0.99	Calcineurin B-like protein 3.
186	Oo5g0476000	AK073549	4.41	8.69	0.99	Hypothetical protein.
187	Oo5g0308500	AK061542	5.95	9.23	0.99	Phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein.
188	Oo5g0327600	X95402	9.96	13.23	0.99	Ricin B-related lectin domain containing protein.
189	Oo5g0618700	AK101305	3.89	7.16	0.98	Protein rich protein.
190	Oo5g0654900	CI273254	6.19	9.45	0.98	(No Hit)
191	Oo5g0671200	AF077760	4.85	8.11	0.98	MADS-box protein SPW1.
192	Oo5g0162600	CI517494	6.61	9.86	0.98	(No Hit)
193	Oo5g0466300	AK102696	4.82	8.07	0.98	GRAM domain containing protein.
194	Oo5g0248600	AK105318	4.53	7.87	0.98	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho- D-glycerate hydro-lyase 2).
195	Oo5g0125500	AF393848	4.55	7.79	0.97	Oligopeptide transporter OPT superfamily protein.
196	Oo5g0131200	Oo5g0131200	6.52	9.75	0.97	Zinc finger DHHC domain containing protein 7 (Sertoli cell gene with a zinc finger domain protein).
197	Oo5g0671200	AK069317	4.81	8.04	0.97	MADS-box protein SPW1.
198	Oo5g0665500	AK102613	7.36	10.58	0.97	Alpha-beta hydrolase family protein.
199	Oo5g0378700	AK108178	8.42	11.82	0.96	Uncharacterized plant-specific domain containing protein.
200	Oo5g0511500	AK070722	6.73	9.92	0.96	NBS-LRR protein (Fragment).
201	Oo5g0799500	AK109346	9.15	12.33	0.96	Methyladenine glycosylase family protein.
202	Oo5g0586000	CI252201	8.75	11.94	0.96	Protein of unknown function DUF581 family protein.
203	Oo5g0516200	AK101629	6.56	9.10	0.96	UDP-glucose 6-dehydrogenase (EC 1.1.2.2) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH).
204	Oo5g0689200	AK073453	8.48	11.66	0.96	Mg2+-transporter protein, CorA-like family protein.
205	Oo5g0566000	AY339063	6.74	9.92	0.96	HCO3--transporter domain containing protein.
206	Oo5g0308500	AK062083	5.09	8.25	0.95	Phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein.
207	Oo5g0220700	Oo5g0220700	7.59	10.79	0.95	Protein kinase domain containing protein.
208	Oo5g0257100	AK105219	5.65	8.80	0.95	Plant metallothionein, family 15 protein.
209	Oo5g0332900	AK103073	6.86	10.01	0.95	Protein kinase domain containing protein.
210	Oo5g0470200	AK102642	5.25	8.40	0.95	Pectate lyase (Fragment).
211	Oo5g0476000	AK064071	15.11	18.26	0.95	Ramyase.
212	Oo5g0368700	AK119706	5.03	8.17	0.95	Ribosome-inactivating protein family protein.
213	Oo5g0293900	AK105200	8.96	12.09	0.94	Conserved hypothetical protein.
214	Oo5g0655400	D26538	9.69	12.81	0.94	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
215	Oo5g0655400	AK104751	7.08	10.37	0.94	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
216	Oo5g0109700	AK059364	6.95	10.06	0.94	Uncharacterized Cys-rich domain containing protein.
217	Oo5g0655400	AB011368	4.85	11.55	0.94	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
218	Oo5g0476500	AK110990	6.84	9.95	0.93	Conserved hypothetical protein.
219	Oo5g0498000	AK061431	5.86	7.66	0.93	Epoxide hydrolase family protein.
220	Oo5g0206500	CI546463	4.74	7.82	0.93	Protein kinase domain containing protein.
221	Oo5g0655400	AK059150	8.92	12.00	0.93	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
222	Oo5g0213300	CI241132	8.16	11.24	0.93	(No Hit)
223	Oo5g0238600	AK104751	7.08	10.37	0.92	Purple acid phosphatase.
224	Oo5g0109400	AK105266	6.60	9.65	0.92	Extensin-like protein.
225	Oo5g0238600	AK119619	10.60	13.64	0.91	Purple acid phosphatase.
226	Oo5g0238600	AK104621	10.93	13.96	0.91	Purple acid phosphatase.
227	Oo5g0272000	AK072228	12.47	15.49	0.91	Peptidase A1, pepsin family protein.
228	Oo5g0514900	AK070288	5.07	11.09	0.91	Glycoside hydrolase, family 28 protein.
229	Oo5g0615000	AK064014	10.25	13.27	0.91	Hypothetical protein.
230	Oo5g0220300	ALU95433	4.88	7.89	0.91	Phi-1 protein.
231	Oo5g0689600	AK063053	6.56	9.16	0.90	Nicotianamine synthase 9 (EC 2.5.1.43) (S-adenosyl-L-methionine-S-adenosyl-L-methionine-S-adenosyl-methionine 3-amino-3- carboxypropyltransferase 9).
232	Oo5g0261300	AK066386	7.16	10.16	0.90	Sterol desaturase family protein.
233	Oo5g0689600	AB023819	9.36	12.36	0.90	Nicotianamine synthase 9 (EC 2.5.1.43) (S-adenosyl-L-methionine-S-adenosyl-L-methionine-S-adenosyl-methionine 3-amino-3- carboxypropyltransferase 9).
234	Oo5g0216700	AK101556	14.78	17.77	0.90	Multi antimicrobial extrusion protein MatE family protein.
235	Oo5g0704000	Oo5g0704000	4.53	7.52	0.90	Hypothetical protein.
236	Oo5g0117400	CI094948	9.18	6.88	0.90	Peptidase S10, serine carboxypeptidase family protein.
237	Oo5g0357400	D10417	12.93	15.90	0.90	RAMYB
238	Oo5g0272000	AK061628	12.33	15.31	0.90	Peptidase A1, pepsin family protein.
239	Oo5g0608300	AK111353	5.83	8.80	0.89	Auxin responsive SAUR protein family protein.
240	Oo5g0368700	AK064673	4.69	7.66	0.89	Ribosome-inactivating protein family protein.
241	Oo5g0368500	AK071046	9.92	12.89	0.89	Glutamine amidotransferase class-I domain containing protein.
242	Oo5g0272000	AK099781	11.94	14.90	0.89	Peptidase A1, pepsin family protein.
243	Oo5g0126200	AK059608	7.98	10.95	0.89	Bifunctional nuclease.
244	Oo5g0216500	AK101781	7.63	10.58	0.89	Pyruvate kinase family protein.
245	Oo5g0143200	AK105996	5.09	8.04	0.89	Pectinesterase family protein.
246	Oo5g0206500	AK061447	7.02	9.96	0.89	Conserved hypothetical protein.
247	Oo5g0153800	Oo5g0153800	10.60	13.54	0.89	Esterase/lipase/thioesterase domain containing protein.
248	Oo5g0445300	AK052479	8.26	11.17	0.89	Plant invertase/pectin methyltransferase inhibitor domain containing protein.
249	Oo5g0143200	AK073604	4.84	7.78	0.88	Pectinesterase family protein.
250	Oo5g0373100	AK107517	3.97	6.91	0.88	Conserved hypothetical protein.
251	Oo5g0265400	CI259458	6.69	9.62	0.88	Zn-finger, RING domain containing protein.
252	Oo5g0483200	AK063628	5.99	9.91	0.88	Conserved hypothetical protein.
253	Oo5g02061300	AK070784	7.63	10.55	0.88	Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT).
254	Oo5g0151500	AK105865	7.14	10.06	0.88	Glycosyl transferase, family 29 protein.
255	Oo5g0404900	AK107531	6.45	9.37	0.88	Conserved hypothetical protein.
256	Oo5g0589700	AK063053	6.57	7.28	0.88	Dual-specific kinase DSK1.
257	Oo5g0135300	AK104961	10.05	12.96	0.88	Cyclin-like F-box domain containing protein.
258	Oo5g0489600	AK068039	7.20	10.10	0.87	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
259	Oo5g05041400	AK124887	11.11	14.02	0.87	(No Hit)
260	Oo5g0797800	AK059364	5.33	8.23	0.87	AUX/IAA protein family protein.
261	Oo5g02114200	AK103982	13.99	16.89	0.87	Serine carboxypeptidase III precursor (EC 3.4.16.5).
262	Oo5g06560500	AK101389	13.88	16.77	0.87	Peptidase S10, serine carboxypeptidase family protein.
263	Oo5g0457000	Oo5g0457000	4.46	7.35	0.87	Hypothetical protein.
264	Oo5g01064100	AK081502	9.29	12.18	0.87	(No Hit)
265	Oo5g0133300	AK072221	9.45	12.44	0.87	Cyclin-like F-box domain containing protein.
266	Oo5g0132400	AK106795	4.72	7.61	0.87	Conserved hypothetical protein.
267	Oo5g0114200	AK073508	13.95	16.83	0.87	Serine carboxypeptidase III precursor (EC 3.4.16.5).
268	Oo5g0157500	AK058389	6.83	9.71	0.87	Glycosyl transferase, family 29 protein.
269	Oo5g0116100	AK081502	9.28	12.17	0.87	(No Hit)
270	Oo5g02114200	AK061078	14.02	16.89	0.87	Serine carboxypeptidase III precursor (EC 3.4.16.5).
271	Oo5g0173300	AK066358	6.69	9.56	0.86	Dehydration-responsive protein RD22 precursor.
272	Oo5g0173300	AK106043	6.89	9.75	0.86	Dehydration-responsive protein RD22 precursor.
273	Oo5g0613900	AK066906	6.30	11.16	0.86	Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT).
274	Oo5g0206500	AK068742	6.86	9.73	0.86	Conserved hypothetical protein.
275	Oo5g0199200	AK068268	14.50	17.36	0.86	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI).
276	Oo5g0199200	AK059538	14.29	17.13	0.86	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI).
277	Oo5g0172700	AK052056	6.78	9.59	0.85	MADS-box protein SPW1.
278	Oo5g0555900	AK100959	4.25	7.08	0.85	Beta-expansin precursor.
279	Oo5g0908600	CI394003	6.89	9.71	0.85	Amino acid/polyamine transporter II family protein.
280	Oo5g0652300	AK063136	9.02	11.84	0.85	Hypothetical protein.
281	Oo5g0172300	AK052056	6.78	9.59	0.85	Dehydration-responsive protein RD22 precursor.
282	Oo5g02048500	Oo5g02048500	4.12	6.93	0.85	Zn-finger, CCHC type domain containing protein.
283	Oo5g0795300	AK064239	5.13	7.94	0.84	Extensin protein-like.
284	Oo5g0117100	AK059932	7.83	10.63	0.84	Alpha-beta hydrolase fold domain containing protein.
285	Oo5g01653000	AK070479	8.36	11.17	0.84	Palmitoyl protein thioesterase family protein.
286	Oo5g0199200	AB039278	14.33	17.12	0.84	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI).
287	Oo5g0526200	AK071877	10.75	13.54	0.84	OCL3 protein.
288	Oo5g0606400	AK068670	4.77	7.53	0.83	Conserved hypothetical protein.
289	Oo5g0565700	AK111333	5.54	8.30	0.83	Alpha-beta hydrolase family protein.
290	Oo5g0202000	AK056393	5.45	8.21	0.83	Pathogenicity protein PATH531-like protein.
291	Oo5g0390800	CI453222	4.70	7.45	0.83	(No Hit)
292	Oo5g0265200	AY339378	12.05	14.81	0.83	Ethylene responsive element binding factor3 (OsERF3).
293	Oo5g0176700	AK070672	12.10	15.05	0.83	Conserved hypothetical protein.
294	Oo5g0617200	AK073063	1.15	6.90	0.83	Ribonucleoside-5-phosphate reductase small chain (EC 1.17.1.1) (Ribonucleotide reductase R2 subunit).
295	Oo5g01068900	AK099469	7.08	9.83	0.83	Proteinase inhibitor 19, subtilisin propeptide domain containing protein.
296	Oo5g0478000	AK111029	5.84	8.59	0.83	Zn-finger, RING domain containing protein.
297	Oo5g0269300	AK111655	5.03	7.76	0.82	Protein kinase domain containing protein.
298	Oo5g0106500	CI319331	9.86	12.67	0.82	Nuclein-like domain containing protein.
299	Oo5g0206500	CI138873	7.12	9.85	0.82	Zn-finger, Dof type domain containing protein.
300	Oo5g020694100	CI279422	6.12	8.84	0.82	Cyclin-like F-box domain containing protein.
301	Oo5g0174500	AY062182	5.81	8.53	0.82	HAP3.
302	Oo5g05917600	AK069458	5.72	8.44	0.82	L-asparaginase (EC 3.5.1.1) (L-asparagine amidohydrolase).
303	Oo5g06560500	AK119519	12.49	15.21	0.82	Peptidase S10, serine carboxypeptidase family protein.
304	Oo5g0530700	AK060014	10.41	13.13	0.82	Conserved hypothetical protein.
305	Oo5g0785800	AB071806	5.			

319	Os05g0209600	AY580163	12.37	15.05	0.81	Lipolytic enzyme, G-D-S-L family protein.
320	Os02g0252400	AK107294	13.27	15.95	0.81	Zn-finger, Dof type domain containing protein.
321	Os05g0434800	C1293793	13.56	15.95	0.81	Protein of unknown function DUF1218 family protein.
322	Os06g0593100	AK071175	10.95	13.63	0.81	UDP-galactose/UDP-glucose transporter.
323	Os05g0310500	AK059697	13.37	16.05	0.81	Cathepsin B (Fragment).
324	Os02g0681100	AK100594	5.19	7.86	0.80	Protein of unknown function DUF604 family protein.
325	Os12g0218700	AK121982	0.16	0.53	0.80	Cystinosis homolg.
326	Os11g0216000	AK060466	6.40	9.07	0.80	Pyruvate kinase family protein.
327	Os01g0886600	AK070098	7.71	10.38	0.80	CLP protease regulatory subunit CLPX precursor.
328	Os10g0236100	C1158157	11.50	14.16	0.80	Sucrose-phosphate synthase (EC 2.4.1.14).
329	Os06g0161900	AK032301	6.21	8.89	0.80	Actin-crosslinking proteins family protein.
330	Os01g0357200	AK009419	10.21	12.88	0.80	Conserved hypothetical protein.
331	Os09g0494600	AK107667	9.99	12.65	0.80	Protein of unknown function DUF599 family protein.
332	Os01g0580200	AK103045	7.94	10.59	0.80	Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-galactosidase) (Exo-1-4)-beta-D-galactanase).
333	Os07g0605400	AK103128	4.92	7.57	0.80	Conserved hypothetical protein.
334	Os04g0504000	AK121982	0.16	0.53	0.80	Adenosine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT).
335	Os03g0196400	CI428136	8.45	11.09	0.79	Protein of unknown function DUF588 family protein.
336	Os08g0142500	CI476796	4.07	6.70	0.79	(No HI)
337	Os08g0200600	AK105596	7.77	10.40	0.79	No apical meristem (NAM) protein domain containing protein.
338	Os01g0294300	AK105670	7.70	10.33	0.79	Extensin-like protein.
339	Os09g0473900	CI016216	6.62	9.24	0.79	Viral coat and capsid protein family protein.
340	Os03g0769500	AK107501	8.37	10.99	0.79	Calcium-binding EF-hand domain containing protein.
341	Os08g0517400	CI483079	7.57	10.18	0.79	(No HI)
342	Os03g0250200	AK068940	4.62	7.23	0.79	Pathogenicity protein PATH531-like protein.
343	Os01g0292200	AK061640	12.34	14.95	0.79	CBL-interacting protein kinase 1.
344	Os02g0740500	AU094334	13.85	16.46	0.78	Conserved hypothetical protein.
345	Os04g0456700	AK085178	9.50	12.11	0.78	Lipoxygenase, LH2 domain containing protein.
346	Os10g0502100	AK114333	11.43	14.04	0.78	Conserved hypothetical protein.
347	Os01g0892400	CI197373	10.03	12.63	0.78	Pectinacetylase family protein.
348	Os10g0390900	Os10g0390900	8.76	11.36	0.78	Synaptotagmin, N-terminal domain containing protein.
349	Os08g0451700	AK102108	7.05	9.64	0.78	Conserved hypothetical protein.
350	Os05g0155500	AK082718	9.45	12.04	0.78	ApocB-1 binding protein 2.
351	Os05g0516400	AK110196	5.15	7.74	0.78	Pistil-specific extensin-like protein family protein.
352	Os01g0292200	AK068440	12.32	14.91	0.78	CBL-interacting protein kinase 1.
353	Os12g0236400	D10334	10.27	12.86	0.78	Adenylyl kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
354	Os01g0699900	AK087910	7.90	10.49	0.78	Protein kinase 3.
355	Os04g0556000	AK063759	7.37	9.95	0.78	Copper-translocating P-type ATPase family protein.
356	Os05g0132100	AK069689	6.98	9.56	0.78	AMP-dependent synthetase and ligase domain containing protein.
357	Os10g0415200	AK068567	6.96	9.54	0.78	Exocyst complex subunit Sec15-like family protein.
358	Os03g0114400	AK108730	6.27	10.85	0.78	AAK-ATPase, central region domain containing protein.
359	Os05g0378000	Os05g0378000	11.67	14.26	0.77	Luminal binding protein 2 precursor (BIP2) (Heat shock protein 70 homolog 2) (B70) (B-70).
360	Os12g0566000	AK100510	4.67	7.24	0.77	HCO ₃ -transporter domain containing protein.
361	Os08g0200600	AK120197	7.64	10.21	0.77	No apical meristem (NAM) protein domain containing protein.
362	Os08g0770800	AK108200	4.10	6.67	0.77	Ctr copper transporter family protein.
363	Os01g0154000	AK074017	9.39	12.96	0.77	Protein kinase 5, domain containing protein.
364	Os01g0688900	AK062271	6.88	9.44	0.77	Proteinase inhibitor I9, subtilisin propeptide domain containing protein.
365	Os01g0763600	AK081563	10.16	12.72	0.77	Glycerophosphoryl diester phosphodiesterase family protein.
366	Os04g0364800	CI423611	11.36	13.92	0.77	Barwin-related endoglucanase domain containing protein.
367	Os03g0290200	AK085209	3.89	6.45	0.77	Senescence-associated protein 5.
368	Os09g0526700	AK073610	9.50	12.06	0.77	UDP-Glucose 4-epimerase (EC 5.1.3.2).
369	Os04g0684800	AK058755	10.22	12.77	0.77	Ubiquitin-conjugating enzymes domain containing protein.
370	Os12g0129300	AK062739	7.92	10.47	0.77	Arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II.
371	Os03g0263700	AK108717	9.45	12.03	0.77	UDP-Glucose 4-epimerase (EC 5.1.3.2).
372	Os06g0208200	CI512834	4.55	7.09	0.76	(No HI)
373	Os04g0605500	AK120057	8.27	10.81	0.76	Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca ²⁺ -ATPase isoform 8).
374	Os01g0283300	AK104803	7.89	10.43	0.76	Hypothetical protein.
375	Os01g0561600	AK084944	4.45	6.97	0.76	Tyrosine P450 family protein.
376	Os10g0500000	AK066334	4.32	6.84	0.76	Plant protein of unknown function DUF828 family protein.
377	Os03g0212800	AY129294	5.50	8.02	0.76	Beta-glucosidase.
378	Os02g0136400	CI863965	4.25	6.76	0.76	Conserved hypothetical protein.
379	Os12g0562000	AK120617	9.20	11.72	0.76	Hypothetical protein.
380	Os01g0244400	CI475611	4.85	7.35	0.75	(No HI)
381	Os02g0710900	AK100997	11.54	14.04	0.75	Heat shock protein Hsp70 family protein.
382	Os04g0223900	CI103951	5.31	7.81	0.75	Conserved hypothetical protein.
383	Os05g0165800	AK083754	4.15	7.75	0.75	Adenylyl-CoA O-methyltransferase 5 (EC 2.1.1.104) (Trans-cofeyl-CoA 3-O-methyltransferase 5) (CCoAMT-5) (CCoAMT-5).
384	Os01g0878400	AK073884	11.34	13.84	0.75	Amino acid/polyamine transporter II family protein.
385	Os12g0236400	AK069870	11.10	13.60	0.75	Adenylyl kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
386	Os06g0164400	CI556798	9.02	11.52	0.75	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
387	Os04g0257400	AK059949	8.73	11.23	0.75	Conserved hypothetical protein.
388	Os01g0283300	AK106177	7.56	10.44	0.75	Hypothetical protein.
389	Os04g0527400	AK060860	9.18	11.68	0.75	Conserved hypothetical protein.
390	Os05g0110800	AK104935	9.73	12.22	0.75	Conserved hypothetical protein.
391	Os04g0556000	AK072299	12.01	14.50	0.75	Copper-translocating P-type ATPase family protein.
392	Os01g0892400	AK064882	9.36	11.85	0.75	Pectinacetylase family protein.
393	Os01g0707500	AK100208	8.06	10.55	0.75	Transcription factor.
394	Os12g0236400	AK059754	11.06	13.55	0.75	Adenylyl kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
395	Os07g0643400	AK108437	4.35	6.83	0.75	Esterase/phosphatase domain containing protein.
396	Os02g0441000	AK108717	9.45	12.03	0.75	Hypothetical protein.
397	Os08g0451700	AK101935	6.30	8.78	0.75	Conserved hypothetical protein.
398	Os11g0241700	AK068339	11.81	14.29	0.75	Protein of unknown function DUF538 family protein.
399	Os03g0316000	AK103709	7.17	9.65	0.75	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
400	Os05g0439900	AK085271	4.45	6.94	0.75	TGF-beta receptor, type III extracellular region family protein.
401	Os07g0681300	CI162141	7.23	9.70	0.74	Cytochrome P450 family protein.
402	Os02g0572600	AK102182	10.69	13.16	0.74	Protein kinase PKN/PRK1, effector domain containing protein.
403	Os08g0494900	CI424647	7.09	9.56	0.74	(No HI)
404	Os01g0236400	D1012429	10.49	12.95	0.74	Adenylyl kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
405	Os10g0415200	AK070924	8.68	11.15	0.74	Exocyst complex subunit Sec15-like family protein.
406	Os10g0494000	AK071373	11.91	14.37	0.74	Protein of unknown function DUF789 family protein.
407	Os10g0494000	AK108057	11.70	14.16	0.74	Protein of unknown function DUF789 family protein.
408	Os01g0763600	AK085209	3.89	6.45	0.74	Glycerophosphoryl diester phosphodiesterase family protein.
409	Os10g0500000	AK059709	4.37	6.82	0.74	Plant protein of unknown function DUF828 family protein.
410	Os01g0283300	AK104498	8.23	10.69	0.74	Hypothetical protein.
411	Os01g0963600	AK069804	7.32	9.77	0.74	ABA/WDS induced protein family protein.
412	Os07g0245100	AK100716	9.33	11.79	0.74	Nitrogen fixation protein.
413	Os04g0491700	AK069132	11.02	13.47	0.74	General substrate transporter family protein.
414	Os04g0410400	AK108077	7.21	9.66	0.74	Root cap family protein.
415	Os01g0283300	AK068117	7.67	10.12	0.74	Hypothetical protein.
416	Os05g0324700	AK063581	8.43	10.87	0.74	Hypothetical protein.
417	Os05g0574300	AU097673	10.89	13.32	0.73	Histone H2B.2.
418	Os07g0666200	CI027348	9.35	11.78	0.73	Histone H3.
419	Os08g0428900	AK120080	7.82	10.25	0.73	Phosphatidylinositol-4-phosphate 5-kinase family protein.
420	Os07g0913300	AK108437	4.35	6.83	0.73	TGF-beta receptor, type III extracellular region family protein.
421	Os01g0892400	AK064882	9.36	11.85	0.73	Conserved hypothetical protein.
422	Os08g0517300	AK107181	6.05	8.47	0.73	Conserved hypothetical protein.
423	Os04g0196200	CI443816	4.50	6.91	0.73	O-methyltransferase, family 2 domain containing protein.
424	Os05g0110800	AK067749	8.97	11.38	0.73	Conserved hypothetical protein.
425	Os03g0793300	AK059754	11.06	13.55	0.73	Zn-finger, A20-like domain containing protein.
426	Os01g0693300	AK101201	9.60	12.01	0.73	Lipid phosphate phosphatase 2 (EC 3.1.3.-) (ALPPT2) (Phosphatidic acid phosphatase 2) (APAP2) (Prenyl diphosphate phosphatase).
427	Os04g0412300	AK110902	4.71	7.12	0.73	Glycoside hydrolase, family 17 protein.
428	Os06g0216300	AJ557138	12.37	14.79	0.73	Oxo-phytyldioic acid reductase (12-oxophytyldioic acid reductase).
429	Os01g0425000	AK108531	6.10	8.52	0.73	Conserved hypothetical protein.
430	Os06g0216300	AB040743	12.19	14.59	0.72	Oxo-phytyldioic acid reductase (12-oxophytyldioic acid reductase).
431	Os12g0562000	AY072714	13.17	15.58	0.72	Hypothetical protein.
432	Os03g0712700	AK121196	8.88	8.28	0.72	Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM2).
433	Os04g0588900	AK111623	9.17	8.66	0.72	Protein of unknown function DUF8 domain containing protein.
434	Os06g0216200	AU092237	13.22	15.61	0.72	Oxo-phytyldioic acid reductase.
435	Os07g0188000	AK100285	8.07	10.46	0.72	Argonaute protein.
436	Os06g0216300	AK103057	12.61	15.00	0.72	Oxo-phytyldioic acid reductase (12-oxophytyldioic acid reductase).
437	Os09g0526700	AB097461	10.11	11.51	0.72	UDP-Glucose 4-epimerase (EC 5.1.3.2).
438	Os11g0117900	CI425334	9.30	11.69	0.72	(No HI)
439	Os03g0279700	AK111338	10.31	12.70	0.72	ZPT2-12.
440	Os02g0211000	Os02g0211000	4.73	7.12	0.72	Viral coat and capsid protein family protein.
441	Os05g0516400	AK058264	6.46	8.84	0.72	Pistil-specific extensin-like protein family protein.
442	Os08g0494900	CI412756	6.82	9.20	0.72	(No HI)
443	Os07g0556300	AK109557	7.80	10.18	0.72	Octosapeptide/Phox/Berm1p domain containing protein.
444	Os05g0310500	AK101093	14.83	17.20	0.71	Cathepsin B (Fragment).
445	Os08g0405000	AK058761	11.13	13.50	0.71	MIR domain containing protein.
446	Os03g0213100	AK073633	9.90	12.26	0.71	Protein transport protein SecE1 alpha subunit.
447	Os03g0205800	Os03g0205800	11.65	14.01	0.71	GCN5-related N-acetyltransferase domain containing protein.
448	Os06g0216300	AJ557139	10.61	12.98	0.71	Oxo-phytyldioic acid reductase (12-oxophytyldioic acid reductase).
449	Os03g0212800	AK119546	4.48	6.84	0.71	Beta-glucosidase.
450	Os07g0681300	CI428967	6.64	9.01	0.71	Harpin-induced 1 domain containing protein.
451	Os11g0249400	Os11g0249400	8.58	10.95	0.71	Glycoside hydrolase, family 28 protein.
452	Os02g0594800	AK121953	8.21	10.67	0.71	No apical meristem (NAM) protein domain containing protein.
453	Os06g0210300	CI088249	5.22	7.57	0.71	(No HI)
454	Os01g0270900	AK121603	7.34	9.68	0.71	Peptidase A1, pepsin family protein.
455	Os06g0212900	AK104048	4.41	6.76	0.71	Heat shock protein Hsp70 family protein.
456	Os07g0604700	CI447910	13.18	15.52	0.70	B12D family protein.
457	Os02g0491900	Os02g0491900	8.10	10.44	0.70	Peptidase aspartic family protein.
458	Os01g0189200	AK105873	9.77	12.11	0.70	Protein of unknown function DUF8 domain containing protein.
459	Os02g0603600	AK110833	9.08	11.42	0.70	MYC1.
460	Os03g0131200	AK062174	12.38	14.71	0.70	Catalase isozyme 2 (EC 1.11.1.6).
461	Os02g0588900	AK100542	10.86	13.19	0.70	Glycerophosphoryl diester phosphodiesterase family protein.
462	Os02g0652000	AK108207	6.90	9.24	0.70	PRF5-like protein.
463	Os03g0749500	AK073110	10.30	12.63	0.70	Exo-beta-gl

479	Oso4g0412300	AK121151	6.81	9.10	0.69	Glycoside hydrolase, family 17 protein.
480	Oso4g0588700	AK063488	5.70	7.99	0.69	Zn-finger, RING domain containing protein.
481	Oso6g0559000	AK080786	9.06	12.25	0.69	Heat shock protein DnaJ family protein.
482	Oso7g0530700	AK096533	10.02	12.31	0.69	Conserved hypothetical protein.
483	Oso3g0402000	Oso3g0402000	5.30	7.59	0.69	Plant disease resistance response protein family protein.
484	Oso6g0175500	AK058599	9.58	11.86	0.69	Epsin, N-terminal domain containing protein.
485	Oo1g0165500	CI045454	7.31	9.58	0.68	(No Hit)
486	Oso3g0131200	AK066378	12.32	14.59	0.68	Catalase isozyme 2 (EC 1.11.1.6).
487	Oso9g0287000	AK106057	4.92	7.18	0.68	Pathogenesis-related transcriptional factor and ERF domain containing protein.
488	Oso6g0250600	CI355861	8.49	10.75	0.68	EAG/ELKERG potassium channel family protein.
489	Oso1g0679900	AK072323	9.18	11.45	0.68	YTH domain protein 2 (High-glucose-regulated protein 8) (NY-REN-2 antigen) (CLL-associated antigen KW-14). Splice isoform 2.
490	Oso1g0168100	AK103697	7.46	9.72	0.68	Ca ²⁺ -dependent nuclease.
491	Oso1g0544600	AK105882	8.49	10.74	0.68	Zn-finger, RING domain containing protein.
492	Oso6g0175500	AK100481	10.17	12.42	0.68	Epsin, N-terminal domain containing protein.
493	Oso7g0246200	AK104826	14.37	16.62	0.68	Calreticulin (Fragment).
494	Oso2g0114400	CI138490	9.71	11.95	0.67	Phosphotriester acyltransferase family protein.
495	Oso5g0310500	AK100225	13.89	16.13	0.68	Cathepsin B (Fragment).
496	Oso3g0575200	AK066919	9.00	11.25	0.68	K ⁺ potassium transporter family protein.
497	Oso3g0131200	AS020502	12.63	14.87	0.68	Catalase isozyme 2 (EC 1.11.1.6).
498	Oso7g0246200	AK063441	14.13	16.37	0.67	Calreticulin (Fragment).
499	Oso6g0106800	AK105782	11.04	13.28	0.67	Conserved hypothetical protein.
500	Oso6g0208700	AY669072	12.05	14.29	0.67	Putative tyrosine phosphatase family protein.
501	Oso3g0131200	AY339372	12.75	14.99	0.67	Catalase isozyme 2 (EC 1.11.1.6).
502	Oso6g0156600	AK121377	12.85	14.99	0.67	Major facilitator superfamily protein.
503	Oso4g0655000	AK067259	8.66	10.89	0.67	Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca ²⁺ -ATPase isoform 8).
504	Oso7g0246200	AK099348	14.10	16.33	0.67	Calreticulin (Fragment).
505	Oso6g0208700	AB021259	13.90	16.13	0.67	Calreticulin (Fragment).
506	Oso1g0679900	AK121381	10.16	12.39	0.67	YTH domain protein 2 (High-glucose-regulated protein 8) (NY-REN-2 antigen) (CLL-associated antigen KW-14). Splice isoform 2.
507	Oso1g0175600	AK072421	6.81	9.04	0.67	HCO ₃ ⁻ -transporter domain containing protein.
508	Oso1g0869900	AB125305	12.29	14.51	0.67	Protein kinase 3.
509	Oso7g0246200	AK104328	14.21	16.43	0.67	Calreticulin (Fragment).
510	Oso4g0497200	CI043990	10.26	12.38	0.67	Celastrolase protein/Celastrolase homolog OR16sep) (Endo-1,4-beta-D- glucanase KORRIGAN) (EC 3.2.1.4).
511	Oso1g0901800	AK070266	8.05	10.26	0.67	Protein of unknown function DUF212 family protein.
512	Oso3g0199100	AK068890	10.91	13.13	0.67	Protein of unknown function DUF677 family protein.
513	Oso3g0281800	AK090717	12.29	14.50	0.67	Hypothetical protein.
514	Oso7g0246200	AK063441	14.13	16.37	0.67	SKP1 component family protein.
515	Oo1g0117900	CI433221	8.68	10.89	0.67	(No Hit)
516	Oso6g0501900	AK106229	10.99	13.20	0.67	Cytochrome P450 family protein.
517	Oso6g0208700	AK068860	12.31	14.53	0.67	Putative tyrosine phosphatase family protein.
518	Oso1g0707500	AK100119	8.36	11.57	0.67	Transcription factor.
519	Oso2g0783000	AK430899	8.86	11.07	0.67	Uncharacterized Cys-rich domain containing protein.
520	Oso2g0720900	AK068691	8.81	11.02	0.66	Peptidase A1, pepsin family protein.
521	Oso1g0582000	Oso1g0582000	7.51	9.72	0.66	Cytochrome P450 family protein.
522	Oso1g0582000	AK071898	5.24	7.45	0.66	NPH3 domain containing protein.
523	Oso3g0348900	AK068540	10.65	12.85	0.66	CHY zinc finger domain containing protein.
524	Oso4g0652700	AK059436	7.76	9.96	0.66	Nuclease I.
525	Oso7g0584200	AK102803	7.78	9.98	0.66	NPH3 domain containing protein.
526	Oso5g0446500	AK099953	9.96	12.16	0.66	Hypothetical protein.
527	Oso3g0849200	AK072278	14.80	16.99	0.66	Phyrase.
528	Oso6g0156600	AK063143	11.24	13.42	0.66	Major facilitator superfamily protein.
529	Oso1g0679900	AK100018	8.54	10.72	0.66	YTH domain protein 2 (High-glucose-regulated protein 8) (NY-REN-2 antigen) (CLL-associated antigen KW-14). Splice isoform 2.
530	Oso2g0121200	AK086210	8.10	10.29	0.66	Conserved hypothetical protein.
531	Oso1g0493000	AK090983	11.03	13.21	0.66	AMP-dependent synthetase and ligase domain containing protein.
532	Oso2g0399000	Oso2g0399000	6.09	8.27	0.65	WD40-like domain containing protein.
533	Oso5g0310500	AK064820	14.09	16.26	0.65	Cathepsin B (Fragment).
534	Oso6g0140700	AY208984	9.50	11.67	0.65	Homeobox-leucine zipper protein HAT14 (HD-ZIP protein 14).
535	Oso1g0865300	CI043990	10.26	12.38	0.65	Conserved hypothetical protein.
536	Oso2g0731400	CI043585	11.48	13.65	0.65	Plastocyanin-like domain containing protein.
537	Oso1g0191300	AK061716	6.39	8.56	0.65	No apical meristem (NAM) protein domain containing protein.
538	Oso2g0653400	CI248859	10.93	13.10	0.65	Transferase family protein.
539	Oso2g0708000	AK100119	8.36	11.57	0.65	Conserved hypothetical protein.
540	Oso3g0810300	AK106765	11.22	13.38	0.65	NUDX1 hydrolase domain containing protein.
541	Oso1g0439300	AK068470	8.48	10.64	0.65	Hypothetical protein.
542	Oso4g0415000	AK108862	9.40	11.56	0.65	Conserved hypothetical protein.
543	Oso5g0272800	AK100119	8.36	11.57	0.65	Conserved hypothetical protein.
544	Oso3g0128800	AK066570	6.36	8.51	0.65	Conserved hypothetical protein.
545	Oso6g0554300	AK103962	7.17	9.32	0.65	Hypothetical protein.
546	Oso5g0489200	AK069135	11.29	13.44	0.65	Plant lipid transferase/storage/hyacinth-alpha amylase inhibitor domain containing protein.
547	Oso3g0121200	AK100119	8.36	11.57	0.65	Peroxidase 1.
548	Oso1g0389900	CI516365	9.94	12.09	0.65	Eukaryotic peptide chain release factor subunit 1-3 (eRF1-3) (Eukaryotic release factor 1-3) (Omnipotent suppressor protein 1 homolog 3) (SUP1 homolog 3).
549	Oso7g0296000	AK121178	10.19	12.33	0.64	Conserved hypothetical protein.
550	Oso4g0672000	AK107505	7.52	9.65	0.64	Leucine-rich repeat, plant specific; containing protein.
551	Oso3g0128800	AK073682	11.34	13.47	0.64	Conserved hypothetical protein.
552	Oso3g0348900	AK073680	11.34	13.47	0.64	CHY zinc finger domain containing protein.
553	Oso6g0708400	CI363475	6.72	8.85	0.64	Cyclophilin.
554	Oso5g0556600	AU082976	10.28	12.40	0.64	Conserved hypothetical protein.
555	Oso6g0140700	AF145726	9.38	11.51	0.64	Homeobox-leucine zipper protein HAT14 (HD-ZIP protein 14).
556	Oso1g0469000	AK069087	8.37	10.50	0.64	TPR-like domain containing protein.
557	Oso1g0762900	CI476984	11.07	13.19	0.64	Conserved hypothetical protein.
558	Oso1g0146200	CI533713	7.94	10.06	0.64	(No Hit)
559	Oso3g0327600	AK069815	7.52	9.64	0.64	Ricin B-related lectin domain containing protein.
560	Oso2g0718000	Oso2g0718000	8.10	10.32	0.64	Conserved hypothetical protein.
561	Oso3g0121200	AK073847	6.35	8.47	0.64	Peroxidase 1.
562	Oso2g0719700	AK119930	8.53	10.64	0.64	IQ calmodulin-binding region domain containing protein.
563	Oso4g0530200	AK105586	7.75	9.87	0.64	Conserved hypothetical protein.
564	Oso2g0589500	AK100119	8.10	10.32	0.64	Conserved hypothetical protein.
565	Oso5g0132100	AK060660	10.76	12.87	0.63	AMP-dependent synthetase and ligase domain containing protein.
566	Oso1g0161500	AK064192	6.28	8.38	0.63	Hypothetical protein.
567	Oso4g0684800	AK068799	9.34	11.44	0.63	Ubiquitin-conjugating enzymes domain containing protein.
568	Oso2g0497600	AK106189	7.17	9.27	0.63	Conserved hypothetical protein.
569	Oso3g0692700	AK058266	11.45	13.54	0.63	Protein of unknown function DUF538 family protein.
570	Oso1g0629600	AK071156	13.42	15.51	0.63	Peptidase S10, serine carboxypeptidase family protein.
571	Oso1g0191300	AK068231	6.48	8.56	0.63	No apical meristem (NAM) protein domain containing protein.
572	Oso6g0140700	AK105150	8.46	10.53	0.63	Homeobox-leucine zipper protein HAT14 (HD-ZIP protein 14).
573	Oso1g0201200	AK069456	10.01	12.11	0.63	Peroxidase (EC 1.11.1.7).
574	Oso3g0310800	AK099476	10.92	13.01	0.63	Parvalbumin family protein.
575	Oso4g0410600	AK121649	8.30	10.39	0.63	Purple acid phosphatase.
576	Oso1g0162600	AK072168	7.95	10.04	0.63	Giantella homologue (Fragment).
577	Oso3g0151500	AK109181	8.57	10.65	0.63	Hypothetical protein.
578	Oso6g0143100	AK061597	12.03	14.12	0.63	Hypothetical protein.
579	Oso7g0883200	AK068606	9.74	11.82	0.63	NAC-domain containing protein 19 (ANAC019) (ANAC) (Abscisic-acid- responsive NAC).
580	Oso9g0451500	AK062254	12.54	14.62	0.63	Thioredoxin-related domain containing protein.
581	Oso1g0805600	CI061414	12.97	15.05	0.63	Acyl-CoA oxidase.
582	Oso3g0575200	AJ427973	10.66	12.73	0.62	K ⁺ potassium transporter family protein.
583	Oso5g0468900	CI533281	6.86	8.93	0.62	(No Hit)
584	Oso1g0113000	AK058635	13.49	15.56	0.62	NADPH-dependent coenzyme reductase (EC 1.1.1.247).
585	Oso3g0310800	AK059603	10.73	12.81	0.62	Parvalbumin family protein.
586	Oso2g0637000	Oso2g0637000	14.55	16.62	0.62	Barwin-related endoglycanase domain containing protein.
587	Oso2g0689200	AK072660	10.65	12.72	0.62	Protein of unknown function DUF250 domain containing protein.
588	Oso1g0894600	AK073332	7.31	9.38	0.62	Zn-finger, RING domain containing protein.
589	Oso3g0785900	AK103358	10.06	12.12	0.62	Glutathione S-transferase GST 19 (EC 2.5.1.18).
590	Oso7g0452100	CI536997	8.87	10.94	0.62	Alpha-galactosidase (EC 3.2.1.22) (Fragment).
591	Oso3g0213100	AK062070	11.94	14.01	0.62	Protein transport protein Sec61 alpha subunit.
592	Oso2g0314600	AK068924	9.22	11.27	0.62	Peptidase A1, pepsin family protein.
593	Oso1g0802300	CI408253	7.98	9.14	0.62	Pectinacylase family protein.
594	Oso1g0803200	U54702	11.43	13.48	0.62	Cysteine proteinase inhibitor-1 (Oryzacystatin-I).
595	Oso1g0694600	CI546906	13.53	15.58	0.62	Hypothetical protein.
596	Oso1g0146200	CI533713	7.54	9.59	0.62	(No Hit)
597	Oso1g0803200	AK061870	10.49	12.54	0.62	Cysteine proteinase inhibitor-1 (Oryzacystatin-I).
598	Oso6g0675600	AK063648	9.15	11.20	0.62	GRAB2 protein.
599	Oso1g0509100	AK069166	9.31	11.35	0.62	Conserved hypothetical protein.
600	Oso3g0205700	AK103674	7.38	9.42	0.62	Photoreceptor-interacting protein-like.
601	Oso3g0762500	AK103002	10.37	12.34	0.61	Conserved hypothetical protein.
602	Oso7g0492000	AK121796	10.37	12.41	0.61	Nucleoside diphosphate kinase I (EC 2.7.4.6) (NDK 1) (NDP kinase 1) (NDPK 1).
603	Oso2g0542400	AK065397	8.45	10.48	0.61	Conserved hypothetical protein.
604	Oso3g0643300	AK099445	12.45	14.47	0.61	Ornithine aminotransferase (EC 2.6.1.13).
605	Oso4g0421000	AK061161	12.90	14.88	0.61	Calnexin (Fragment).
606	Oso2g0689200	AK071254	10.80	12.81	0.61	Protein of unknown function DUF250 domain containing protein.
607	Oso7g0659400	AU091627	8.84	10.86	0.61	HAD-superfamily hydrolase, subfamily IA, variant 1 protein.
608	Oso6g0106800	AK122178	10.17	12.18	0.61	Conserved hypothetical protein.
609	Oso9g0385700	AK065210	12.84	14.86	0.61	Zn-finger, AN1-like domain containing protein.
610	Oso3g0106800	AK105911	10.22	12.23	0.61	Conserved hypothetical protein.
611	Oso5g0556300	CI354452	10.83	12.84	0.61	Protein of unknown function DUF1298 domain containing protein.
612	Oso3g0643300	AK108010	10.35	12.35	0.60	Ornithine aminotransferase (EC 2.6.1.13).
613	Oso4g0421000	AK061161	12.90	14.89	0.60	Calnexin (Fragment).
614	Oso1g0770700	Oso1g0770700	11.33	13.33	0.60	Copper transporter 1.
615	Oso2g0274900	AK073967	12.55	14.54	0.60	General substrate transporter family protein.

* The log₂ ratio of the GA-induced signal intensity change in WT seeds.

Table S10. List of categorized under Down-group3.

Probe#	ID	Accession	WT±GA*	gid1±GA*	slr1±GA*	gid2±GA*	gamyb±GA*	Annotation
1	Os03g0244200	AK105771	-0.69	-0.01	0.00	0.24	-0.33	Thaumatococcus-like protein.
2	Os03g0244200	AK101837	-0.70	-0.01	0.00	0.24	-0.32	Thaumatococcus-like protein.
3	Os05g0560200	CI026016	-0.71	-0.06	-0.05	-0.11	-0.67	Hypothetical protein.
4	Os10g0474800	Os10g0474800	-0.71	-0.01	-0.05	-0.05	-0.69	Conserved hypothetical protein.
5	Os03g0305200	AK108450	-0.72	-0.03	0.10	0.20	-0.60	Hypothetical protein.
6	Os08g0127900	AF051153	-0.72	-0.22	0.04	-0.26	-1.03	Globulin 1 (Fragment).
7	Os04g0422600	AK099964	-0.72	-0.10	-0.13	-0.39	-0.59	Protein of unknown function DUF6 domain containing protein.
8	Os09g0323500	AK071737	-0.72	-0.13	-0.06	-0.13	-0.91	Protein of unknown function DUF833 family protein.
9	Os01g0363300	AK060356	-0.73	-0.05	0.09	0.03	-0.51	Protein of unknown function DUF588 family protein.
10	Os01g0679500	CI135763	-0.73	-0.03	0.19	-0.10	-0.74	Peptidase A1, pepsin family protein.
11	Os11g0294400	AK062429	-0.74	0.06	-0.02	-0.21	-0.57	WW/Rsp5/WWP domain containing protein.
12	Os01g0363300	AK059622	-0.76	-0.04	0.13	0.04	-0.64	Protein of unknown function DUF588 family protein.
13	Os12g0466200	CI557936	-0.77	-0.05	0.15	0.11	-0.44	Hypothetical protein.
14	Os02g0693700	AK106518	-0.78	0.06	-0.07	-0.20	-0.95	MDR-like p-glycoprotein.
15	Os01g0391100	AK108533	-0.78	-0.12	0.07	-0.11	-1.59	ABC transporter related domain containing protein.
16	Os02g0693700	AK103774	-0.78	0.06	-0.06	-0.20	-0.97	MDR-like p-glycoprotein.
17	Os06g0648500	AK106895	-0.79	-0.01	-0.10	-0.24	-0.51	Hypothetical protein.
18	Os05g0316800	AK110613	-0.83	0.07	0.09	-0.04	-0.52	Ethylene-responsive element binding protein.
19	Os10g0554200	AK068409	-0.83	-0.03	-0.10	0.09	-0.67	Nitrate transporter.
20	Os12g0599800	AK111139	-0.83	0.02	-0.09	0.19	-1.13	Hypothetical protein.
21	Os03g0793700	AF051154	-0.86	-0.10	0.06	-0.30	-0.63	Globulin 2 (Fragment).
22	Os03g0161400	CI259418	-0.87	0.01	0.00	-0.09	-0.64	IQ calmodulin-binding region domain containing protein.
23	Os02g0743400	AK102343	-0.89	0.01	0.10	0.02	-0.91	Auxin transport protein REH1.
24	Os09g0412400	AK073672	-0.90	0.00	0.12	0.13	-0.50	Conserved hypothetical protein.
25	Os10g0475000	CI161649	-1.01	0.01	-0.03	-0.09	-0.67	Conserved hypothetical protein.
26	Os04g0526600	AK106723	-1.04	0.07	-0.01	-0.15	-0.63	Alpha-amylase/subtilisin inhibitor (RASI).
27	Os03g0164300	AK070845	-1.05	-0.03	-0.09	-0.21	-0.78	Conserved hypothetical protein.
28	Os01g0124400	AK099279	-1.07	-0.15	-0.10	-0.42	-1.10	Proteinase inhibitor I12, Bowman-Birk family protein.
29	Os01g0124400	AK064050	-1.08	-0.15	-0.12	-0.43	-1.17	Proteinase inhibitor I12, Bowman-Birk family protein.
30	Os09g0369500	AK105322	-1.11	0.04	-0.12	-0.21	-0.69	Conserved hypothetical protein.
31	Os03g0404500	AK061614	-1.14	-0.06	-0.16	-0.35	-1.07	Non-protein coding transcript, unclassifiable transcript.
32	Os02g0743400	AF056027	-1.15	0.03	0.10	0.00	-1.04	Auxin transport protein REH1.
33	Os02g0743400	AK099634	-1.17	0.04	0.10	0.01	-0.87	Auxin transport protein REH1.
34	Os01g0391100	AK063499	-1.17	0.04	-0.04	-0.13	-1.26	ABC transporter related domain containing protein.
35	Os03g0118800	AK071039	-1.19	0.03	0.08	-0.22	-0.88	HMG-CoA synthase.
36	Os03g0404500	AK098956	-1.19	-0.06	-0.18	-0.34	-1.23	Non-protein coding transcript, unclassifiable transcript.
37	Os10g0360700	CI015964	-1.20	-0.12	0.08	-0.04	-1.13	Conserved hypothetical protein.
38	Os03g0406900	CI447475	-1.21	-0.02	0.06	-0.20	-0.75	Protein of unknown function family protein.
39	Os08g0544400	AK107688	-1.24	0.02	-0.05	-0.30	-0.85	ABC transporter related domain containing protein.
40	Os10g0431900	AK106265	-1.25	-0.05	0.05	-0.35	-0.98	Avr9/Cf-9 rapidly elicited protein 264.
41	Os10g0431900	AK072305	-1.25	-0.05	-0.01	-0.35	-1.30	Avr9/Cf-9 rapidly elicited protein 264.
42	Os10g0579800	AK121847	-1.26	-0.01	0.07	-0.09	-0.65	TGF-beta receptor, type I/II extracellular region family protein.
43	Os02g0511600	AK111241	-1.27	0.15	-0.11	-0.38	-1.05	Conserved hypothetical protein.
44	Os01g0686300	AK109457	-1.28	-0.01	0.00	0.19	-1.26	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
45	Os04g0233400	AK119661	-1.29	-0.22	-0.05	-0.05	-0.76	MipE.
46	Os12g0599700	AK108003	-1.34	0.02	-0.04	0.04	-1.29	Hypothetical protein.
47	Os04g0631100	AK121883	-1.36	0.03	-0.05	-0.44	-0.98	General substrate transporter family protein.
48	Os02g0629200	AK061782	-1.36	-0.19	0.07	0.42	-0.92	Plasma membrane integral protein ZmPIP2-3.
49	Os03g0322900	CI387122	-1.37	-0.04	0.01	-0.28	-0.80	Late embryogenesis abundant protein repeat containing protein.
50	Os09g0369500	AK105479	-1.37	0.02	-0.16	-0.29	-0.84	Conserved hypothetical protein.
51	Os02g0629200	AK120386	-1.37	-0.20	0.00	0.42	-0.93	Plasma membrane integral protein ZmPIP2-3.
52	Os08g0127900	AK119657	-1.42	-0.28	0.06	-0.48	-1.33	Globulin 1 (Fragment).
53	Os08g0127900	AK105316	-1.46	-0.30	0.07	-0.50	-1.48	Globulin 1 (Fragment).
54	Os01g0159000	AK070330	-1.47	-0.06	0.36	-0.03	-0.82	Hypothetical protein.
55	Os01g0159000	AK106273	-1.48	-0.06	0.34	0.01	-0.86	Hypothetical protein.
56	Os06g0697000	AK105513	-1.51	-0.24	0.13	-0.38	-0.93	Xyloglucan endotransglucosylase/hydrolase protein A precursor
57	Os12g0134700	CI136652	-1.66	0.01	-0.29	-0.30	-1.14	(No Hit)

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S11. List of probes categorized under Down-group4.

Probe#	ID	Accession	WT±GA*	<i>gid1</i> ±GA*	<i>slr1</i> ±GA*	<i>gid2</i> ±GA*	<i>gamyb</i> ±GA*	Annotation
1	<i>Os12g0550800</i>	AK098944	-0.85	-0.66	0.04	0.42	-0.87	Hypothetical protein.
2	<i>Os12g0550800</i>	AK102550	-0.87	-0.67	-0.05	0.43	-0.89	Hypothetical protein.
3	<i>Os01g0313600</i>	Cl434821	-0.97	-0.71	0.00	0.44	-1.17	(No Hit)

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S12. List of probes categorized under Down-group5.

Probe#	ID	Accession	WT±GA*	<i>gid1</i> ±GA*	<i>slr1</i> ±GA*	<i>gid2</i> ±GA*	<i>gamyb</i> ±GA*	Annotation
1	<i>Os01g0106400</i>	AY071920	-0.75	0.43	0.15	-0.71	-0.85	Isoflavone reductase-like protein.
2	<i>Os04g0206500</i>	AK110892	-0.76	0.05	0.14	-0.56	-1.14	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
3	<i>Os01g0106400</i>	AK102701	-0.77	0.42	0.18	-0.72	-0.83	Isoflavone reductase-like protein.
4	<i>Os01g0106400</i>	AK109339	-0.77	0.44	0.13	-0.71	-0.86	Isoflavone reductase-like protein.
5	<i>Os12g0630200</i>	CI025931	-0.85	0.06	-0.07	-0.98	-0.92	Antifungal protein R (Fragment).
6	<i>Os09g0272600</i>	AK063844	-1.31	0.10	-0.07	-0.97	-1.40	Conserved hypothetical protein.
7	<i>Os09g0457400</i>	AK099330	-1.43	0.06	-0.20	-1.07	-1.87	RAmy3A
8	<i>Os09g0457400</i>	AK099392	-1.43	0.06	-0.17	-1.06	-1.92	RAmy3A
9	<i>Os09g0457400</i>	AK063988	-1.55	0.07	-0.21	-1.10	-1.83	RAmy3A

* The log₁₀ ratio of the GA-induced signal intensity change.

Probe#	ID	Accession	WT±GA*	gid1±GA*	slr1±GA*	gid2±GA*	gamyb±GA*	Annotation
1	Os01g0794400	AK122041	-0.70	-0.05	0.07	-0.28	-0.32	Thioredoxin domain 2 containing protein.
2	Os07g0442900	AK073296	-0.71	-0.15	0.09	-0.34	-0.38	Plant integral membrane protein family protein.
3	Os02g0783700	AK120371	-0.72	-0.03	0.00	-0.34	-0.33	Lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme.
4	Os09g0109600	AK063582	-0.74	-0.09	-0.01	-0.39	-0.47	Conserved hypothetical protein.
5	Os11g0594000	CI552411	-0.76	0.07	0.03	-0.27	-0.27	General substrate transporter family protein.
6	Os12g0156200	AY333186	-0.78	0.08	0.08	-0.31	-0.27	DNA-binding factor of bZIP class.
7	Os04g0104900	AK069960	-0.78	-0.04	-0.14	-0.68	-0.34	Caffeic acid 3-O-methyltransferase (EC 2.1.1.68)
8	Os11g0620300	AK107901	-0.80	0.02	0.03	-0.26	-0.42	Nonspecific lipid-transfer protein 2 (LTP 2).
9	Os12g0555200	AK099157	-0.80	-0.10	-0.15	-0.65	-0.35	Probenazole-inducible protein PBZ1.
10	Os11g0599200	AK100744	-0.80	0.29	-0.34	-0.50	-0.67	Hypothetical protein.
11	Os12g0555200	AK070762	-0.81	-0.11	-0.15	-0.66	-0.45	Probenazole-inducible protein PBZ1.
12	Os01g0138800	AK106157	-0.83	0.13	0.15	-0.50	-0.56	Conserved hypothetical protein.
13	Os04g0402500	AU101423	-0.88	0.10	-0.10	-0.22	-0.42	Zn-finger, RING domain containing protein.
14	Os06g0486800	AB019533	-0.89	-0.01	0.11	-0.37	-0.38	Formate dehydrogenase, mitochondrial precursor
15	Os03g0165900	AK063721	-0.90	0.44	0.08	-0.50	-0.19	MSS-like protein (Fragment).
16	Os03g0618300	AK073307	-0.91	0.21	0.33	-0.53	-0.58	Isopenicillin N synthase family protein.
17	Os03g0745700	CI257891	-0.92	0.04	-0.01	-0.38	-0.33	ATMRK1.
18	Os03g0793700	U45320	-0.93	-0.10	0.05	-0.33	-0.49	Globulin 2 (Fragment).
19	Os03g0165900	AK102116	-0.93	0.45	0.19	-0.53	-0.29	MSS-like protein (Fragment).
20	Os08g0406400	AK062031	-0.94	0.05	0.00	-0.54	-0.42	Sulfate transporter (Fragment).
21	Os01g0816100	AK073848	-1.02	0.11	0.10	-0.40	-0.38	NAC-domain containing protein 2 (ANAC002).
22	Os01g0816100	AB028183	-1.03	0.11	0.12	-0.40	-0.25	NAC-domain containing protein 2 (ANAC002).
23	Os04g0179700	AK119327	-1.06	-0.01	-0.58	-0.53	-0.82	Terpene synthase.
24	Os03g0809200	AK102250	-1.11	0.00	0.09	-0.50	-0.37	DNA-binding protein (Fragment).
25	Os04g0179700	AY347880	-1.13	0.00	-0.51	-0.58	-0.75	Terpene synthase.
26	Os08g0441500	AK072872	-1.15	-0.06	-0.48	-0.60	-1.03	Cinnamoyl-CoA reductase.
27	Os03g0277600	AK061425	-1.15	-0.04	-0.36	-0.78	-0.54	Protein of unknown function DUF26 domain containing protein.
28	Os04g0444300	AK102641	-1.16	0.03	0.26	-0.32	-0.61	Conserved hypothetical protein.
29	Os08g0441500	AK105870	-1.16	-0.06	-0.53	-0.58	-0.58	Cinnamoyl-CoA reductase.
30	Os08g0441500	AK105802	-1.22	-0.06	-0.52	-0.61	-0.92	Cinnamoyl-CoA reductase.
31	Os05g0247100	AK065866	-1.37	0.02	-0.14	-1.07	-0.63	Glycoside hydrolase, family 18 protein.
32	Os01g0595600	AK066814	-1.52	0.07	-0.25	-0.61	-0.66	Alpha/beta hydrolase fold domain containing protein.

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S14. Primers used for this study.

Primer name	Forward primer	Reverse primer	Used for
<i>RAmy1A</i> (Os02g0765600)	CAGGGGTACGCATACATCCT	GATCACCTTGCCATCGATCT	Expression analysis (<i>RAmy</i>)
<i>RAmy1B</i> (Os01g0357400)	TGGCGAACAAACACTTCTTG	CCTAGCTTGCCATAAGCAG	Expression analysis (<i>RAmy</i>)
<i>RAmy1C</i> (Os02g0765400)	GGTGGAGAGGCACAATTAGC	TAAAACCATGCATGCAAACG	Expression analysis (<i>RAmy</i>)
<i>RAmy2A</i> (Os06g0713800)	GCGATATGATGCTTGTGTGC	CATGGTTTATCGATCCCACA	Expression analysis (<i>RAmy</i>)
<i>RAmy3A</i> (Os09g0457400)	GTTCCGACTGGAACCTCAAGC	GAGTTATGTTGCCACAGTCT	Expression analysis (<i>RAmy</i>)
<i>RAmy3B</i> (Os09g0457600)	GAAAATCCTTGCTGCTGAGG	CCCTGCAGGAACTCTGAGAC	Expression analysis (<i>RAmy</i>)
<i>RAmy3C</i> (Os09g0457800)	CGAGATATGGAGCAACATGC	TGTTGTGCGATGAAGGTGAC	Expression analysis (<i>RAmy</i>)
<i>RAmy3D</i> (Os08g0473900)	GTCGACGAGAAGGTCATGGT	CCTTCTCCAGACGCTGTAG	Expression analysis (<i>RAmy</i>)
<i>RAmy3E</i> (Os08g0473600)	CGGGTGGTACAACCTTCTGC	AGGCACTCGACGTTCTTGTC	Expression analysis (<i>RAmy</i>)
<i>Os02g0740400</i>	TGATGAGGCTGAAAGTGACG	ATATGCACGGACCGATGAAG	Expression analysis (<i>gid1</i>)
<i>Os12g0550800</i>	CGAGTCAACTCCATTCAGCA	TTAACACACAGCTCAGCATCG	Expression analysis (<i>gid1</i>)
<i>Os01g0313600</i>	AAGCATCACGCATAGTGTCTG	ATCGCAGGGACAACCTTCTTG	Expression analysis (<i>gid1</i>)
<i>Os01g0126100</i>	ATGAGGACAACGCCATGATT	TCTGTTGAGGGATCCCATT	Expression analysis (<i>slr1</i>)
<i>Os11g0241700</i>	TGGCGAAACTCATCTTCTCTC	GAACCTCTGCAGCATGTCCG	Expression analysis (<i>slr1</i>)
<i>Os01g0800500</i>	GGCAGTCCAGGACCAATTTA	CGCGTACACAGCCTGATAGT	Expression analysis (<i>slr1</i>)
<i>Os07g0600000</i>	AGGGCAAAAACCATGATGAC	ACGCCGTTGATACAGGAAAG	Expression analysis (<i>slr1</i>)
<i>Os04g0538400</i>	ATGCGGTGTGACGCAGAAAT	CCCCCTGATTATTCCAGTT	Expression analysis (<i>slr1</i>)
<i>Os12g0131900</i>	GTGGTGTTCATCACGCAGAC	CATAGGATCTCGCCACGAAG	Expression analysis (<i>slr1</i>)
<i>Os02g0766900</i>	CTCTTCTGGCAGGTGATGG	TGTCTCGTGAATTGGCAAAC	Expression analysis (<i>slr1</i>)
<i>Os03g0369100</i>	TGGAGCCTAGGGCAATAAATAG	TTTTCCCAATTTTGCACTCC	Expression analysis (<i>slr1</i>)
<i>Os05g0589700</i>	CAAGGCCTGCAGTGTGTGTA	TCCCAACACATGAGATCCA	Expression analysis (<i>slr1</i>)
<i>Os04g0179700</i>	TTCTACTCTCAGGCCGATGG	TCCGATACCGTAGGAAAAC	Expression analysis (<i>slr1</i>)
<i>Os04g0179100</i>	AACCTAAAAGGGCGTTGGACT	ACCAAAGCTCGAGTTGACG	Expression analysis (<i>slr1</i>)
<i>Os08g0441500</i>	TGTACGAGACGGTGAAGTGC	GGCTTCAGACCAGACAAACC	Expression analysis (<i>slr1</i>)
<i>Os04g0227500</i>	GTGACTCTGGTCCCCTACTG	ATACTGTTTTGCGCCAAGC	Expression analysis (<i>gid2</i>)
<i>Os04g0324100</i>	GAACCTGCCCGGTACAAGAGGA	GACTCGGTCAAGGTTGGTGT	Expression analysis (<i>gid2</i>)
<i>Os05g0527300</i>	TTCTGTTTAGGGGACCATGC	ACAATTGGAGAGGCTGGATG	Expression analysis (<i>gid2</i>)
<i>Os12g0566000</i>	CTCAACAGTCCAATGGCTTC	TGACCTCGATAGGCAGCAG	Expression analysis (<i>gid2</i>)
<i>Os03g0279700</i>	ACGCTACCCGAGAAAGTCAAC	CGAAAGGGAAAAGGACAACC	Expression analysis (<i>gid2</i>)
<i>Os01g0106400</i>	GAAGCTGGAGAGGGTGTACG	TTCAGAGGAGCCTGTTGAGG	Expression analysis (<i>gid2</i>)
<i>Os12g0630200</i>	ACAGTACGCCAAAGGATGAT	CGCATGCATGGTAAATGGTAG	Expression analysis (<i>gid2</i>)
<i>Os10g0517500</i>	CATGTCCGTCGGGTACAAC	AAATCGGATCGTCGCTAATG	Expression analysis (<i>gid2</i>)
<i>Os03g0277600</i>	TACACGCCGTTTCAACAACAT	CGCAGTATTGACCGAACCTT	Expression analysis (<i>gid2</i>)
<i>Os08g0327700</i>	GCCAGTACCAGTATCTCATTC	TCCACAACATGATACCACTTC	Expression analysis (<i>gid2</i>)
<i>Os11g0582400</i>	CTAGGGTTTTCCATGGTTCGAT	TGGCCATCTATCTCCTGCTC	Expression analysis (<i>gid2</i>)
<i>Os04g0364800</i>	CCTACCCGACGTACACTTGC	TCCGTGTTGCTGTGGTACAT	Expression analysis (<i>gamyb</i>)
<i>Os02g0693700</i>	AGGCGCTCGTGTCTACTAC	GAACCACCCGATCTCGTTC	Expression analysis (<i>gamyb</i>)
<i>Os01g0124400</i>	AAGAAGAAGCCGTGGAAGTG	TAGACGCTCGATGCAGATGAG	Expression analysis (<i>gamyb</i>)
<i>Os10g0431900</i>	GCCTGAGAAGAAGGGAGAGG	CTACCCCTTGCTGCACACTC	Expression analysis (<i>gamyb</i>)
<i>Os09g0272600</i>	GACTTAGGCCGATGATCCAG	GCGAGATCGTTGAAACACAA	Expression analysis (<i>gamyb</i>)
<i>Os03g0118800</i>	TGCCTCCAGGCACCTACTAC	CTATGCCGTTGGCTTATTGC	Expression analysis (<i>gamyb</i>)
<i>Os08g0544400</i>	GGTGTACGGCTCATGTTCT	TGAAGTAGCGGTCCTGGATG	Expression analysis (<i>gamyb</i>)
<i>Os04g0631100</i>	GCAACCGGAGACAAAATTGAT	GGAACAGAGCAACACAGCAA	Expression analysis (<i>gamyb</i>)
<i>Os03g0322900</i>	GAGGCGACCAAGAACAAGC	TCACGCCGTCCTTGAACCT	Expression analysis (<i>gamyb</i>)
<i>Os01g0159000</i>	GGATGCAAAACGTGAACAATG	TGCTCCTCATCTCCATCTCC	Expression analysis (<i>gamyb</i>)
<i>Os11g0138300</i>	AGAGAAGGCCACAAGGGAAC	GGGCAAAAACAACCAAAATCAC	Expression analysis (<i>gamyb</i>)
<i>Os01g0146200</i>	TGTTCCGATCCCCTGGTAAG	TGACCAAAACAGCAAACATC	Expression analysis (Up1 gene)
<i>Os02g0115900</i>	TCACGATCACGAACGAGAAG	GTAGGTCTCGAGCTGGTTGC	Expression analysis (Up1 gene)
<i>Os10g0544600</i>	ATTTCCGCGTAGGTGAGATG	ACGAACCTGCATCCACCATT	Expression analysis (Up2 gene)
<i>Os03g0623100</i>	ATCCGTTGTCACGTATGCTG	AAGAACGACCATCCAAAAG	Expression analysis (Dw1 gene)
<i>Os11g0671000</i>	TGGTCCGATCTCTGTCCAG	GACACGTACCGGCTCTCTGTC	Expression analysis (Dw1 gene)
<i>Os11g0444700</i>	TAGCGATCAGATTGCGAACC	CCCAGCAACAACAGTACATGC	Expression analysis (Dw2 gene)
<i>Os01g0773700</i>	GTAACATGGTGGTTGTGAACG	TCTTGTAAAGTTGCCAGATGC	Expression analysis (Dw2 gene)
<i>Os02g0743400</i>	TTGGAAGGGAGTCAAACGAG	AACCGAACCGTTTCTGTGAC	Expression analysis (Dw3 gene)
<i>Os11g0599200</i>	TCAGGGAGATGATGGTAGGG	ACACACCGTACAGCCATCAA	Expression analysis (Dw6 gene)
<i>Os01g0595600</i>	AGCTAGCCACTTGCCACTTC	CGTACATGACGCCAAAACA	Expression analysis (Dw6 gene)

Underlines indicate the enzyme site used for cloning into the indicated vector.

Table S2. List of GA down-regulated probes.

Probe#	ID	Accession	WT-GA	WT+GA	WT±GA	Annotation
1	Os05g0215700	AK119724	12.35	10.09	-0.68	Hypothetical protein.
2	Os12g0541700	AK103420	12.52	10.25	-0.68	RALF.
3	Os07g0951400	AF210325	10.75	8.47	-0.68	Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRTase), Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMPDecase)].
4	Os01g0951400	AB037418	10.75	8.47	-0.68	Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRTase), Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMPDecase)].
5	Os02g0530600	AK105277	10.94	8.66	-0.69	Poly(ADP-ribose) polymerase, catalytic region domain containing protein.
6	Os03g0675600	AK062614	14.29	12.01	-0.69	Phytosulfoxines 3 precursor [Contains: Phytosulfoxine-alpha (PSK-alpha) (Phytosulfoxine- α); Phytosulfoxine-beta (PSK-beta) (Phytosulfoxine- β)].
7	Os06g0503400	AK073583	15.13	12.84	-0.69	Reticulon family protein.
8	Os03g0244200	AK105771	15.90	13.60	-0.69	Thaumatin-like protein.
9	Os01g0135700	AK062711	11.53	9.23	-0.69	Flagellar calcium-binding protein (cattiglin) family protein.
10	Os06g0485600	AK073111	11.81	9.50	-0.70	Phi-1 protein.
11	Os01g0644200	AY549310	12.71	10.40	-0.70	Conserved hypothetical protein.
12	Os03g0244200	AK101837	15.81	13.49	-0.70	Thaumatin-like protein.
13	Os07g0561800	AK108426	13.37	11.04	-0.70	Hypothetical protein.
14	Os12g0604700	AK072382	9.45	7.12	-0.70	LSTK-1-like kinase.
15	Os03g0159600	AK106743	10.97	8.64	-0.70	Rab28 protein.
16	Os03g0134100	AK119903	12.75	10.45	-0.70	Conserved hypothetical protein.
17	Os09g0533900	AK100445	10.22	7.89	-0.70	Endo-beta-1,4-galactanase (EC 3.2.1.4) (Fragment).
18	Os05g0552100	AK101673	12.41	10.07	-0.70	Conserved hypothetical protein.
19	Os01g0794400	AK122041	10.19	7.85	-0.70	Thioredoxin domain 2 containing protein.
20	Os02g0216300	AK060081	11.23	8.89	-0.71	Conserved hypothetical protein.
21	Os05g0494000	AK099695	10.91	8.57	-0.71	Cytochrome P450 98A1 (EC 1.14.-.-).
22	Os09g0533900	AK067774	10.03	7.69	-0.71	Endo-beta-1,4-galactanase (EC 3.2.1.4) (Fragment).
23	Os01g0951500	CH10336	9.60	7.25	-0.71	(No Hit)
24	Os12g0604700	AK101826	9.70	7.35	-0.71	LSTK-1-like kinase.
25	Os05g0560200	CI026016	12.10	9.75	-0.71	Hypothetical protein.
26	Os06g0565600	AK068985	11.69	9.34	-0.71	4-coumarate-CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) (Clone 4CL14) (Fragment).
27	Os02g0530600	AK102681	11.14	8.79	-0.71	Poly(ADP-ribose) polymerase, catalytic region domain containing protein.
28	Os08g0468100	AK101662	10.14	7.78	-0.71	Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
29	Os03g0133100	AK063668	11.03	8.67	-0.71	Hypothetical protein.
30	Os07g0442900	AK073296	11.04	8.68	-0.71	Plant integral membrane protein family protein.
31	Os12g0605800	AF251074	9.64	7.27	-0.71	Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit)
32	Os10g0474800	Os10g0474800	11.62	9.25	-0.71	Conserved hypothetical protein.
33	Os04g0413900	AK100104	12.15	9.77	-0.71	Conserved hypothetical protein.
34	Os05g0133100	AK068407	8.84	6.46	-0.72	Pil protein.
35	Os09g0439000	AK063243	9.30	6.92	-0.72	Conserved hypothetical protein.
36	Os08g0547100	AK108374	9.89	7.51	-0.72	Glucosamine/galactosamine-6-phosphate isomerase domain containing protein.
37	Os06g0699400	AK071376	9.19	6.81	-0.72	MAP kinase 2.
38	Os03g0305200	AK108450	9.18	6.80	-0.72	Hypothetical protein.
39	Os02g0831000	CI122953	9.07	6.69	-0.72	(No Hit)
40	Os04g0646000	AK070318	11.44	9.05	-0.72	Shikimate kinase.
41	Os01g0727500	AK101236	13.41	11.02	-0.72	Protein of unknown function DUF584 family protein.
42	Os05g0127900	AF051153	12.52	10.12	-0.72	Globulin 1 (Fragment).
43	Os05g0144100	AK069280	11.76	9.36	-0.72	WD40-like domain containing protein.
44	Os04g0422600	AK099664	9.92	7.52	-0.72	Protein of unknown function DUF6 domain containing protein.
45	Os04g0402700	AK058995	13.62	11.22	-0.72	Hypothetical protein.
46	Os09g0323500	AK071737	10.53	8.12	-0.72	Protein of unknown function DUF833 family protein.
47	Os03g0134100	AK064199	12.35	9.95	-0.72	Conserved hypothetical protein.
48	Os02g0783700	AK1020371	10.67	8.26	-0.72	Lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme.
49	Os02g0622200	AK105687	14.32	11.91	-0.73	Phospho-2-dehydro-3-deoxyheptanate aldolase 1, chloroplast precursor (EC 2.5.1.54) (Phospho-2-keto-3-deoxyheptanate aldolase 1) (DAHPSynthetase 1)
50	Os02g0203300	Os02g0203300	9.19	6.78	-0.73	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
51	Os06g0557100	AK119892	8.84	6.43	-0.73	Protein kinase domain containing protein.
52	Os04g0565200	AK111866	8.56	6.15	-0.73	Cis-zeatin O-glucosyltransferase.
53	Os03g0133100	AK119903	10.85	8.43	-0.73	Hypothetical protein.
54	Os01g0880300	AK101982	8.85	6.43	-0.73	Phosphatase family protein.
55	Os09g0505500	CI122953	9.26	6.84	-0.73	(No Hit)
56	Os03g0412900	Os03g0412900	9.10	6.68	-0.73	Conserved hypothetical protein.
57	Os07g0622200	AB122058	14.62	12.19	-0.73	Phospho-2-dehydro-3-deoxyheptanate aldolase 1, chloroplast precursor (EC 2.5.1.54) (Phospho-2-keto-3-deoxyheptanate aldolase 1) (DAHPSynthetase 1)
58	Os07g0638300	AK060356	11.49	9.06	-0.73	Protein of unknown function DUF588 family protein.
59	Os01g0679500	AK133763	10.86	8.43	-0.73	Peptidase A1, pepsin family protein.
60	Os06g0486600	AK101753	11.34	8.91	-0.73	Formate dehydrogenase, mitochondrial precursor (EC 1.2.1.2) (NAD-dependent formate dehydrogenase) (FDH).
61	Os03g0693900	AK061572	8.93	6.49	-0.73	Beta-1,3-galactanase-like protein.
62	Os08g0468100	AK121810	10.59	8.15	-0.73	Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
63	Os07g0666600	AK068545	8.28	5.84	-0.73	Conserved hypothetical protein.
64	Os02g0216300	AK070589	10.32	7.87	-0.74	Conserved hypothetical protein.
65	Os11g0181200	AK063747	12.26	9.81	-0.74	Hypothetical protein.
66	Os07g0622200	AK063747	12.26	9.81	-0.74	Phospho-2-dehydro-3-deoxyheptanate aldolase 1, chloroplast precursor (EC 2.5.1.54) (Phospho-2-keto-3-deoxyheptanate aldolase 1) (DAHPSynthetase 1)
67	Os10g0506900	AK067420	10.32	7.87	-0.74	Hypothetical protein.
68	Os03g0425300	AK120530	8.84	6.39	-0.74	Dialcylglycerol kinase, catalytic region domain containing protein.
69	Os04g0460300	AK106202	10.63	8.17	-0.74	Amino acid/polyamine transporter II family protein.
70	Os03g0817900	AK071479	9.72	7.26	-0.74	Protein of unknown function DUF231 domain containing protein.
71	Os06g0486600	AK065872	11.74	9.29	-0.74	Formate dehydrogenase, mitochondrial precursor (EC 1.2.1.2) (NAD-dependent formate dehydrogenase) (FDH).
72	Os04g0406000	AK067948	11.34	8.91	-0.74	Shikimate kinase.
73	Os01g0112000	AK106123	10.23	7.77	-0.74	Conserved hypothetical protein.
74	Os03g0183300	AK119553	14.60	12.13	-0.74	Pathogenesis-related transcriptional factor and ERF domain containing protein.
75	Os03g0219400	AK100702	9.06	6.60	-0.74	Glycoside hydrolase, family 20 protein.
76	Os03g0255100	AK061989	8.64	6.17	-0.74	Beta-galactosidase (EC 3.2.1.23).
77	Os11g0294400	AK062429	10.41	7.94	-0.74	WW/Rsp5/WWP domain containing protein.
78	Os09g0243500	AK109419	11.08	8.61	-0.74	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
79	Os09g0109600	AK063582	11.94	9.47	-0.74	Conserved hypothetical protein.
80	Os05g0133100	AK099152	8.76	6.28	-0.75	Pil protein.
81	Os10g0567400	AK067730	7.94	5.47	-0.75	Rieske [2Fe-2S] region domain containing protein.
82	Os02g0216300	AK061737	10.28	7.80	-0.75	Conserved hypothetical protein.
83	Os03g0219400	AK121985	8.79	6.30	-0.75	Glycoside hydrolase, family 20 protein.
84	Os02g0216300	AK104214	10.38	7.89	-0.75	Conserved hypothetical protein.
85	Os04g0520700	AK065832	10.78	8.29	-0.75	Protein of unknown function DUF584 family protein.
86	Os02g0466400	AK071209	10.95	8.45	-0.75	Inositol phosphate kinase.
87	Os03g0183300	AK105922	14.65	12.15	-0.75	Pathogenesis-related transcriptional factor and ERF domain containing protein.
88	Os08g0243500	AK099083	10.80	8.30	-0.75	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
89	Os01g0106400	AY071920	10.95	8.45	-0.75	Isoflavone reductase-like protein.
90	Os02g0574500	AK065365	10.20	7.70	-0.75	Conserved hypothetical protein.
91	Os02g0633000	AK093220	11.84	9.33	-0.76	Protein of unknown function DUF588 family protein.
92	Os12g0552500	AK068459	13.08	10.56	-0.76	Universal stress protein (Usp) family protein.
93	Os05g0349800	AK119674	13.87	11.36	-0.76	Embryonic abundant protein 1.
94	Os02g0522300	AK068634	10.93	8.41	-0.76	Hypothetical protein.
95	Os03g0183300	AK106163	14.82	12.30	-0.76	Pathogenesis-related transcriptional factor and ERF domain containing protein.
96	Os03g0139000	AK102177	10.15	7.64	-0.76	Protein kinase domain containing protein.
97	Os02g0633000	AK101538	11.84	9.33	-0.76	Cosin, N-terminal domain containing protein.
98	Os02g0575500	AK099974	7.71	5.19	-0.76	ABC transporter-like.
99	Os12g0517300	Os12g0517300	7.50	4.98	-0.76	Conserved hypothetical protein.
100	Os11g0552500	CI275181	7.66	5.14	-0.76	(No Hit)
101	Os09g0528200	AK059755	9.80	7.27	-0.76	Homeodomain leucine zipper protein (Fragment).
102	Os03g0139000	AK105632	10.54	8.01	-0.76	Protein kinase domain containing protein.
103	Os11g0594000	CI552514	11.81	7.78	-0.76	General substrate transporter family protein.
104	Os01g0142800	AK105664	11.87	9.34	-0.76	Peptide transporter.
105	Os05g0179300	AK100028	9.43	6.90	-0.76	Transferase family protein.
106	Os05g0557200	AK062090	13.00	10.46	-0.76	ARM repeat fold domain containing protein.
107	Os04g0206500	AK110892	8.50	5.97	-0.76	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
108	Os08g0344600	AK059591	11.13	8.60	-0.76	Phosphate/phosphoenolpyruvate translocator.
109	Os05g0205000	AK062320	10.33	7.80	-0.76	Multifunctional transport intrinsic membrane protein 2.
110	Os05g0557200	AK102111	13.01	10.47	-0.76	ARM repeat fold domain containing protein.
111	Os10g0360100	AK106326	8.48	5.94	-0.76	Sugar transporter protein.
112	Os01g0773700	AK060476	8.49	5.95	-0.76	Photosystem II reaction center W protein (PSII 1.6 kDa protein) (Fragment).
113	Os02g0574500	AK103980	10.53	7.99	-0.76	Conserved hypothetical protein.
114	Os02g0104500	AK120063	8.85	6.31	-0.77	DNA-binding protein DF1.
115	Os01g0511100	AK070914	15.70	13.16	-0.77	Universal stress protein (Usp) family protein.
116	Os01g0106400	AK102701	10.87	8.32	-0.77	Isoflavone reductase-like protein.
117	Os12g0230500	CI211517	11.40	8.85	-0.77	(No Hit)
118	Os08g0465800	AF358767	13.76	11.21	-0.77	Glutamate decarboxylase (EC 4.1.1.15).
119	Os02g0574500	AK059863	10.69	8.14	-0.77	Conserved hypothetical protein.
120	Os04g0244800	AK121488	14.86	12.11	-0.77	Heavy metal transport/detoxification protein domain containing protein.
121	Os01g0106400	AK104214	10.85	8.30	-0.77	Isoflavone reductase-like protein.
122	Os02g0600200	AK058978	9.57	7.07	-0.77	IQ calmodulin-binding region domain containing protein.
123	Os12g0607000	AK065892	13.55	10.99	-0.77	Homocysteine S-methyltransferase 2 (EC 2.1.1.10) (S-methylmethionine:homocysteine methyltransferase 2) (SMM:Hcy S-methyltransferase 2) (ZmHMT-2).
124	Os12g0541300	CH402228	11.69	9.13	-0.77	Respiratory burst oxidase homology.
125	Os03g0287000	CI032353	12.62	10.06	-0.77	(No Hit)
126	Os02g0301100	AK100174	15.26	12.70	-0.77	MNS and saliva related transmembrane protein family protein.
127	Os03g0139000	AK108065	9.50	6.94	-0.77	CSS domain containing protein.
128	Os12g0607000	AK103294	11.60	9.04	-0.78	Homocysteine S-methyltransferase 2 (EC 2.1.1.10) (S-methylmethionine:homocysteine methyltransferase 2) (SMM:Hcy S-methyltransferase 2) (ZmHMT-2).
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144	Os04g0104900	AK069960	8.08	5.49	-0.78	Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
145	Os04g0623500	AK068638	14.40	11.81	-0.78	(S)-2-hydroxy-acid oxidase, peroxisomal (EC 1.1.3.15) (Glycolate oxidase) (GOX) (Short chain alpha-hydroxy acid oxidase).
146	Os02g0693700	AK106518	13.18	10.59	-0.78	MDR-like p-glycoprotein.
147	Os01g0391100	AK106533	10.58	6.08	-0.78	ABC transporter related domain containing protein.
148	Os04g0679600	AK109942	7.67	5.06	-0.78	CBS domain containing protein.
149	Os07g0503300	AK105785	8.78	6.17	-0.78	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
150	Os04g0690900	Cl064179	8.84	6.23	-0.78	(No Hit)
151	Os09g0528200	AF145730	10.07	7.46	-0.78	Homeodomain leucine zipper protein (Fragment).
152	Os02g0693700	AK103774	13.16	10.56	-0.78	MDR-like p-glycoprotein.
153	Os08g0446800	AK068619	7.93	7.93	-0.79	Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
154	Os03g0305400	AK071397	12.58	9.97	-0.79	Universal stress protein (Usp) family protein.
155	Os05g0420200	AK067880	8.32	5.71	-0.79	Protein of unknown function DUF179 family protein.
156	Os08g0425800	AK101198	12.02	9.41	-0.79	Conserved hypothetical protein.
157	Os04g0638700	AK062886	7.92	5.30	-0.79	Conserved hypothetical protein.
158	Os01g0658900	U42208	9.59	6.97	-0.79	G-box binding factor 1.
159	Os01g0654400	Cl049497	15.64	13.02	-0.79	Conserved hypothetical protein.
160	Os11g0475500	AK102516	9.65	7.03	-0.79	Hypothetical protein.
161	Os05g0426000	AK063475	15.98	13.36	-0.79	MNS3 and saliva related transmembrane protein family protein.
162	Os03g0429800	AK065099	13.12	10.49	-0.79	Xanthine dehydrogenase 1 (EC 1.1.1.204).
163	Os01g0658900	AK121925	9.71	7.08	-0.79	G-box binding factor 1.
164	Os11g0442500	Cl064179	9.34	6.70	-0.79	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
165	Os06g0646500	AK106895	8.49	5.85	-0.79	Hypothetical protein.
166	Os01g0738400	AK110681	8.59	5.75	-0.79	Zinc finger transcription factor.
167	Os01g0154000	AK108752	8.66	6.01	-0.80	Hypothetical protein.
168	Os01g0256500	AK069098	16.54	13.90	-0.80	Zn-induced protein.
169	Os07g0601000	AK067272	9.53	6.88	-0.80	NADPH HC toxin reductase (Fragment).
170	Os02g0526700	Cl042177	8.07	5.42	-0.80	Conserved hypothetical protein.
171	Os11g0626300	AK107901	12.37	9.72	-0.80	Non-specific lipid-transfer protein 2 (LTP 2).
172	Os08g0344600	AK068619	11.16	8.50	-0.80	Phosphate/phosphoenolpyruvate translocator.
173	Os12g0555200	AK099157	8.78	6.12	-0.80	Probenazole-inducible protein PBZ1.
174	Os07g0561800	AK111334	8.29	5.63	-0.80	Hypothetical protein.
175	Os01g0173000	Cl284943	10.23	7.57	-0.80	Putative thiol-disulfide oxidoreductase DCC family protein.
176	Os11g0599200	AK100744	11.60	8.94	-0.80	Hypothetical protein.
177	Os10g0567400	AF284781	9.57	6.91	-0.80	Rieske [2Fe-2S] region domain containing protein.
178	Os03g0425300	AK058684	10.84	8.17	-0.80	Diacylglycerol kinase, catalytic region domain containing protein.
179	Os06g0681200	AK107980	10.47	7.80	-0.80	Plastocyanin-like domain containing protein.
180	Os03g0280400	AK063845	11.05	8.38	-0.80	Uncharacterized plant-specific domain O1589 containing protein.
181	Os12g0555200	AK070762	9.29	6.62	-0.81	Probenazole-inducible protein PBZ1.
182	Os01g0140100	AK068990	10.62	7.94	-0.81	Peptidase A1, pepsin family protein.
183	Os07g0180000	AK103199	11.62	8.93	-0.81	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.
184	Os11g0119400	AK111119	8.69	6.01	-0.81	Alpha/beta-hydrolase fold domain containing protein.
185	Os06g0706400	AK064899	11.23	8.54	-0.81	Peptide transporter PTR2-B (Histidine transporting protein).
186	Os02g0581100	Cl430502	7.46	4.77	-0.81	Conserved hypothetical protein.
187	Os01g0142800	AK058745	12.74	10.04	-0.81	Peptide transporter.
188	Os10g0360100	AK121279	13.06	10.36	-0.81	Sugar transporter protein.
189	Os10g0462600	AK068108	10.47	7.76	-0.81	Hypothetical protein.
190	Os09g0436000	Cl399152	9.21	6.50	-0.82	Conserved hypothetical protein.
191	Os05g0496000	AK101499	11.47	8.76	-0.82	Conserved hypothetical protein.
192	Os03g0268400	AK121972	12.37	9.66	-0.82	Mannose-1-phosphate guanylyltransferase (EC 2.7.1.13) (ATP-mannose-1-phosphate guanylyltransferase) (GDP-mannose pyrophosphorylase) (NDP-mannose pyrophosphorylase).
193	Os04g0480700	AK121175	9.89	7.17	-0.82	Cytochrome P450 71A1 (EC 1.14.-.-) (CYP71A1) (ARP-2).
194	Os05g0563600	AK058836	9.58	6.87	-0.82	Beta-ig-H3/fasciilin domain containing protein.
195	Os08g0444400	Cl428563	11.47	8.75	-0.82	(No Hit)
196	Os06g0109000	AK068089	7.00	4.27	-0.82	Phosphoglycerate/bisphosphoglycerate mutase family protein.
197	Os01g0658900	AY60984	8.07	5.34	-0.82	G-box binding factor 1.
198	Os02g0533800	AK121139	15.15	12.42	-0.82	Conserved hypothetical protein.
199	Os10g0567400	AK065124	9.33	6.60	-0.82	Rieske [2Fe-2S] region domain containing protein.
200	Os11g0213000	Cl066566	9.50	6.75	-0.83	Protein kinase domain containing protein.
201	Os05g0215700	AK107771	13.25	10.50	-0.83	Hypothetical protein.
202	Os01g0138800	AK106157	7.66	4.91	-0.83	Conserved hypothetical protein.
203	Os03g0153000	Cl850393	14.00	11.25	-0.83	Major lipid transfer/storage/trypsin-alpha amylase inhibitor domain containing protein.
204	Os06g0221300	AK108233	13.07	10.32	-0.83	Dehydration stress-induced protein.
205	Os04g0179200	AK106087	8.89	6.14	-0.83	Stern sesquiolaricresinol dehydrogenase (Fragment).
206	Os10g0567400	AK071899	9.37	6.62	-0.83	Rieske [2Fe-2S] region domain containing protein.
207	Os02g0725900	AJ300218	9.74	6.99	-0.83	Transcription factor CBF/NF-Y/archaeal histone domain containing protein.
208	Os12g0600100	AK063550	8.65	5.89	-0.83	TPR-like domain containing protein.
209	Os05g0216900	AK110513	9.95	7.19	-0.83	Cysteine-responsive element binding protein.
210	Os10g0567400	AB021310	9.80	7.04	-0.83	Rieske [2Fe-2S] region domain containing protein.
211	Os02g0744900	AK061968	7.65	4.89	-0.83	Geranylgeranyl hydrogenase.
212	Os10g0554200	AK068409	7.86	5.09	-0.83	Nitrate transporter.
213	Os04g0690900	Cl443257	9.41	6.64	-0.83	(No Hit)
214	Os08g0453200	AK067942	11.07	8.30	-0.83	Conserved hypothetical protein.
215	Os12g0599000	AK111193	7.00	4.44	-0.83	Hypothetical protein.
216	Os03g0231600	AK105963	10.09	7.31	-0.84	Branched-chain-amino-acid aminotransferase 3, chloroplast precursor (EC 2.6.1.42) (Abtcat-3).
217	Os09g0394300	AK105580	9.36	6.58	-0.84	Glycoside hydrolase, family 9 protein.
218	Os03g0669300	AK120903	11.42	8.62	-0.84	Beta-1,3-glucanase-like protein.
219	Os08g0425800	AK061339	13.37	10.58	-0.84	Conserved hypothetical protein.
220	Os02g0206100	AK066593	7.43	4.63	-0.84	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
221	Os11g0299000	AK108421	10.79	7.64	-0.84	Hypothetical protein.
222	Os01g0256500	AY072712	17.15	14.34	-0.84	Zn-induced protein.
223	Os04g0562100	AK060598	9.01	6.20	-0.84	Amino acid/polyamine transporter II family protein.
224	Os03g0154000	AK103088	11.81	9.00	-0.84	Aromatic-ring hydroxylase family protein.
225	Os04g0658200	Cl452886	9.52	6.72	-0.85	(No Hit)
226	Os12g0550800	AK098944	7.45	4.64	-0.85	Hypothetical protein.
227	Os11g0428000	Cl215293	12.12	7.70	-0.85	Conserved hypothetical protein.
228	Os03g0758300	AK067626	7.68	4.86	-0.85	Cyclic nucleotide-gated ion channel 2 (ACNCGC2) (Cyclic nucleotide- and calmodulin-regulated ion channel 2) (DEFENSE NO DEATH 1).
229	Os04g0659100	X14246	8.53	5.72	-0.85	Glutamine synthetase shoot isozyme, chloroplast precursor (EC 6.3.1.2) (Glutamate-ammonia ligase) (Clone lambda-GS31).
230	Os02g0522300	AK068116	7.07	4.25	-0.85	Hypothetical protein.
231	Os03g0287800	Os03g0287800	9.99	7.17	-0.85	Glycosyl transferase, family 43 protein.
232	Os01g0256500	AK119698	17.01	14.19	-0.85	Zn-induced protein.
233	Os04g0497700	AK121024	7.68	4.86	-0.85	CONSTANS-like protein.
234	Os05g0520000	AK068587	8.37	5.55	-0.85	TPR-like domain containing protein.
235	Os10g0564500	AK103690	11.67	8.85	-0.85	Protein kinase domain containing protein.
236	Os04g0659100	AK065491	8.85	6.02	-0.85	Glutamine synthetase shoot isozyme, chloroplast precursor (EC 6.3.1.2) (Glutamate-ammonia ligase) (Clone lambda-GS31).
237	Os12g0630200	Cl025931	14.58	11.75	-0.85	Antifungal protein R (Fragment).
238	Os02g0681000	AK103328	10.79	7.96	-0.85	MscS Mechanosensitive ion channel family protein.
239	Os01g0256500	AF022734	17.02	14.19	-0.85	Zn-induced protein.
240	Os02g0652000	AK063448	10.12	7.29	-0.85	Major facilitator superfamily protein.
241	Os08g0465800	AB050600	14.33	11.49	-0.85	Glutamate decarboxylase (EC 4.1.1.15).
242	Os01g0256500	U46138	17.19	14.35	-0.86	Zn-induced protein.
243	Os04g0504700	AK068596	9.87	7.03	-0.86	Conserved hypothetical protein.
244	Os03g0793700	AF051154	13.20	10.36	-0.86	Globulin 2 (Fragment).
245	Os04g0269600	AK100640	13.17	10.33	-0.86	Copper amine oxidase family protein.
246	Os01g0256500	AK069399	7.50	4.68	-0.86	Cationic amino acid transporter (Fragment).
247	Os08g0465800	AY428025	14.11	11.26	-0.86	Glutamate decarboxylase (EC 4.1.1.15).
248	Os12g0175400	AK063027	7.00	4.15	-0.86	Conserved hypothetical protein.
249	Os03g0586500	AK068097	10.41	7.56	-0.86	Conserved hypothetical protein.
250	Os02g0219900	AK060915	8.03	5.17	-0.86	Protein of unknown function DUF588 family protein.
251	Os12g0752000	Os12g0752000	12.72	9.86	-0.86	Conserved hypothetical protein.
252	Os05g0314700	AK111406	7.06	4.20	-0.86	Hypothetical protein.
253	Os12g0242500	Cl523984	8.35	5.49	-0.86	(No Hit)
254	Os10g0506900	AK100756	9.39	6.53	-0.86	Hypothetical protein.
255	Os08g0465800	AK061977	14.89	12.02	-0.86	Glutamate decarboxylase (EC 4.1.1.15).
256	Os04g0269600	AK068662	13.28	10.41	-0.86	Copper amine oxidase family protein.
257	Os10g0564500	AB125304	11.85	8.98	-0.86	Protein kinase domain containing protein.
258	Os03g0572000	AK111362	10.78	7.90	-0.86	Non-protein coding transcript, unclassifiable transcript.
259	Os09g0423500	AK120024	8.64	5.77	-0.86	Peptidase A1, pepsin family protein.
260	Os01g0138900	AK058378	11.79	8.92	-0.86	Mandelate racemase/muconate lactonizing enzyme family protein.
261	Os03g0374600	AK110542	10.36	7.49	-0.87	Glycoside hydrolase, family 17 protein.
262	Os04g0659100	AK099252	9.05	6.17	-0.87	Glutamine synthetase shoot isozyme, chloroplast precursor (EC 6.3.1.2) (Glutamate-ammonia ligase) (Clone lambda-GS31).
263	Os04g0269600	AK060758	13.44	10.56	-0.87	Copper amine oxidase family protein.
264	Os10g0564500	AK069399	7.50	4.68	-0.87	Protein kinase domain containing protein.
265	Os03g0161400	Cl259418	8.07	5.18	-0.87	IQ calmodulin-binding region domain containing protein.
266	Os12g0550800	AK102550	7.52	4.63	-0.87	Hypothetical protein.
267	Os04g0691900	AK068257	9.69	6.79	-0.87	Phosphatidylinositol-4-phosphate 5-kinase family protein.
268	Os03g0586500	AK059901	10.78	7.88	-0.87	Conserved hypothetical protein.
269	Os02g0219900	AK104393	8.05	5.15	-0.87	Protein of unknown function DUF588 family protein.
270	Os07g0638100	AK107804	7.09	4.16	-0.88	TOB1, C-terminal domain containing protein.
271	Os01g0643900	AK108288	8.84	5.73	-0.88	Oleosin family protein.
272	Os04g0402500	AU101423	10.99	8.08	-0.88	Zn-finger, RING domain containing protein.
273	Os12g0147200	AK063680	15.24	12.33	-0.88	Hypothetical protein.
274	Os01g0240900	Os01g0240900	12.27	9.35	-0.88	Peptidase C1A, papain family protein.
275	Os11g0444700	AK104816	14.23	11.31	-0.88	Octicosapeptide/Phox/Bem1p domain containing protein.
276	Os05g0553300	AK107804	7.09	4.16	-0.88	Conserved hypothetical protein.
277	Os03g0286900	AK070972	13.51	10.38	-0.88	Low-temperature induced protein LtO1.2.
278	Os07g0663700	AK070585	9.94	7.00	-0.88	Short-chain dehydrogenase/reductase SDR family protein.
279	Os05g0560000	AF093635	10.10	7.16	-0.88	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex 1 11 kDa protein) (GOSS protein).
280	Os02g0626200	AK121303	7.04	4.10	-0.88	Non-protein coding transcript, unclassifiable transcript.
281	Os01g0124200	AK104110	15.61	12.67	-0.88	Bowman Birks trypsin inhibitor.
282	Os07g0592100	AK107947	10.50	7.56	-0.88	Short-chain dehydrogenase/reductase SDR family protein.
283	Os10g0564500	AK069399	7.50	4.68	-0.89	TPR-like domain containing protein.
284	Os06g0486800	AB019533	13.44	10.50	-0.89	Formate dehydrogenase, mitochondrial precursor (EC 1.2.1.2) (NAD-dependent formate dehydrogenase) (FDH).
285	Os01g0124200	AK067257	15.28	12.34	-0.89	Bowman Birks trypsin inhibitor.
286	Os03g0189600	AK066331	11.04	8.10	-0.89	Alcohol dehydrogenase.
287	Os01g0728700	AK108000	12.28	9.33	-0.89	Conserved hypothetical protein.
288	Os11g0586800	Cl218813	8.05	5.09	-0.89	Protein of unknown function DUF231 domain containing protein.

289	Os03g0829200	AK108175	8.82	5.87	-0.89	Soluble epoxide hydrolase.
290	Os03g0766800	AK120228	9.99	7.03	-0.89	Conserved hypothetical protein.
291	Os01g0239700	AK067723	9.48	6.52	-0.89	Leucine-rich receptor-like protein kinase.
292	Os01g0849000	AK070587	7.31	4.35	-0.89	Conserved hypothetical protein.
293	Os08g0385000	AK107755	11.47	8.51	-0.89	Conserved hypothetical protein.
294	Os02g0626400	AK061959	10.47	7.52	-0.89	Phenylalanine ammonia-lyase (EC 4.3.1.5).
295	Os02g0743400	AK102343	11.26	8.30	-0.89	Auxin transport protein REH1.
296	Os03g0747500	AK108009	9.46	6.49	-0.90	Seed maturation protein domain containing protein.
297	Os09g0509700	AK120589	9.24	6.26	-0.90	HD1.
298	Os02g0219900	AK064866	8.00	5.03	-0.90	Protein of unknown function DUF588 family protein.
299	Os11g0444700	AK068452	14.65	11.67	-0.90	Octicosapeptide/Phox/Bem1p domain containing protein.
300	Os12g0512100	AK121039	10.07	7.09	-0.90	General substrate transporter family protein.
301	Os01g0908200	AK067269	11.98	9.00	-0.90	BTB/POZ domain containing protein.
302	Os06g0270900	AK073079	15.57	12.58	-0.90	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
303	Os03g0806600	AK070959	9.79	6.80	-0.90	Conserved hypothetical protein.
304	Os10g0517500	AK105292	10.79	7.73	-0.90	Cys/Met metabolism: pyridoxal-phosphate-dependent enzymes family protein.
305	Os03g0165800	AK063721	7.80	4.81	-0.90	MSS-like protein (Fragment).
306	Os01g0239700	AK070058	9.42	6.43	-0.90	Leucine-rich receptor-like protein kinase.
307	Os09g0412400	AK073672	11.71	8.72	-0.90	Conserved hypothetical protein.
308	Os12g0265800	AK108847	9.68	6.69	-0.90	Non-protein coding transcript, unclassifiable transcript.
309	Os01g0276300	AK108165	12.96	9.97	-0.90	Group 3 late embryogenesis abundant protein (Fragment).
310	Os01g0124200	AK104367	15.76	12.77	-0.90	Bowman bark trypsin inhibitor.
311	Os04g0658200	CM52886	9.47	6.47	-0.90	(No Hit)
312	Os08g0465800	AK121088	12.85	9.85	-0.90	Glutamate decarboxylase (EC 4.1.1.15).
313	Os03g0192700	AK103501	14.09	11.09	-0.90	Myo-inositol-1-phosphate synthase.
314	Os10g0567400	AK062219	8.97	5.97	-0.90	Rieske [2Fe-2S] region domain containing protein.
315	Os02g0759900	AK059854	9.12	6.12	-0.90	Conserved hypothetical protein.
316	Os07g0198700	AK073755	11.50	8.49	-0.90	Exostosin-like family protein.
317	Os10g0517500	AK105295	11.41	8.40	-0.90	Cys/Met metabolism: pyridoxal-phosphate-dependent enzymes family protein.
318	Os11g0417800	CH48419	7.53	4.52	-0.90	(No Hit)
319	Os03g0140700	AK070000	11.78	8.77	-0.91	TPR-like domain containing protein.
320	Os03g0192700	AK058750	13.77	10.76	-0.91	Myo-inositol-1-phosphate synthase.
321	Os06g0272700	CI136777	8.08	5.07	-0.91	(No Hit)
322	Os04g0476600	AK105486	8.92	5.91	-0.91	C2 domain containing protein.
323	Os11g0417800	AK55290	7.41	4.39	-0.91	(No Hit)
324	Os02g0582800	AK107707	7.51	4.49	-0.91	Protein of unknown function DUF581 family protein.
325	Os01g0239700	AK122130	10.24	7.22	-0.91	Leucine-rich receptor-like protein kinase.
326	Os01g0749000	AK107290	9.17	6.15	-0.91	Protein of unknown function DUF1264 family protein.
327	Os04g0635700	AK098916	9.14	6.11	-0.91	Conserved hypothetical protein.
328	Os07g0557500	AK100765	12.33	9.31	-0.91	Cation/proton exchanger 1a.
329	Os04g0699000	AK059100	12.91	9.90	-0.91	IQ calmodulin-binding region domain containing protein.
330	Os03g0618300	AK073307	12.03	9.00	-0.91	Isopenicillin N synthase family protein.
331	Os08g0428200	AJ311051	11.29	8.26	-0.91	Typical P-type R2R3 Myb protein (Fragment).
332	Os03g0192700	AB012107	14.45	11.41	-0.91	Myo-inositol-1-phosphate synthase.
333	Os03g0822000	AF247164	16.44	13.40	-0.91	Alpha-expansin OsEXPA7.
334	Os03g0822000	AK101784	16.47	13.42	-0.92	Alpha-expansin OsEXPA7.
335	Os04g0699000	AK059100	12.91	9.90	-0.92	IQ calmodulin-binding region domain containing protein.
336	Os02g0219900	AK098194	8.36	5.32	-0.92	Protein of unknown function DUF588 family protein.
337	Os01g0773700	AK119161	9.26	6.21	-0.92	Photosystem II reaction center W protein (PSII 6.1 kDa protein) (Fragment).
338	Os02g0828200	AK071199	9.60	6.55	-0.92	TPR-like domain containing protein.
339	Os03g0157300	AK063160	9.69	6.64	-0.92	Uncharacterized Cys-rich domain containing protein.
340	Os04g0178300	AK100631	9.11	6.06	-0.92	Copaly diphosphate synthase (Fragment).
341	Os01g0305900	Os0103900	10.09	7.04	-0.92	Typical A-type R2R3 Myb protein (Fragment).
342	Os03g0145700	CI257891	10.09	7.04	-0.92	ATMKR1.
343	Os06g0270900	AK120296	15.54	12.48	-0.92	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
344	Os07g0663700	AK104614	9.95	6.89	-0.92	Short-chain dehydrogenase/reductase SDR family protein.
345	Os07g0171100	AJ417523	8.43	5.35	-0.92	TPR-like domain containing protein.
346	Os03g0249700	AK121219	9.83	6.75	-0.93	Hypothetical protein.
347	Os06g0270900	AB044537	15.25	12.18	-0.93	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
348	Os06g0270900	CI318193	11.07	7.99	-0.93	CONSTANS-like protein COp6.
349	Os01g0844300	AK105246	9.01	5.93	-0.93	Peptidylprolyl isomerase.
350	Os03g0793700	U45320	14.84	11.76	-0.93	Globulin 2 (Fragment).
351	Os06g0270900	AK061794	15.64	12.55	-0.93	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
352	Os06g0699400	AJ512642	12.02	8.92	-0.93	MAP kinase 2.
353	Os07g0633400	AK108988	11.32	8.22	-0.93	CBS domain containing protein.
354	Os11g0620300	AJ704707	12.92	9.80	-0.93	Lipid-specific lipid transfer protein 2 (LTP 2).
355	Os08g0394000	CI443895	9.97	6.88	-0.93	Hypothetical protein.
356	Os06g0699400	AJ251330	12.40	9.30	-0.93	MAP kinase 2.
357	Os03g0165900	AK102116	8.39	5.29	-0.93	MSS-like protein (Fragment).
358	Os06g0642500	AK067059	6.89	3.78	-0.94	Cytochrome P450 71A1 (EC 1.14.-.-) (CYPLXIA1) (ARP-2).
359	Os04g0527900	AK108116	12.25	9.14	-0.94	Tonoplast intrinsic protein (Putative beta-tonoplast intrinsic protein).
360	Os04g0137100	AK069347	10.99	7.90	-0.94	CBS domain containing protein.
361	Os06g0246500	AK105105	11.69	8.58	-0.94	Pyruvate dehydrogenase E1 alpha subunit (EC 1.2.4.1).
362	Os08g0406400	AK062031	8.78	5.67	-0.94	Sulfate transporter (Fragment).
363	Os08g0102700	AK061430	10.27	7.15	-0.94	Harpin-induced 1 domain containing protein.
364	Os06g0270900	AF162665	15.67	12.55	-0.94	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
365	Os03g0198600	AY554034	10.14	7.02	-0.94	Homeodomain leucine zipper protein CPHB-7.
366	Os04g0873700	AK069241	12.21	9.09	-0.94	Conserved hypothetical protein.
367	Os06g0270900	AK099248	15.28	12.16	-0.94	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
368	Os09g0452200	AK106042	7.75	4.61	-0.95	LysM-domain GPI-anchored protein 1 precursor. Splice isoform 2.
369	Os03g0198600	AK073446	10.71	7.56	-0.95	Homeodomain leucine zipper protein CPHB-7.
370	Os05g0560000	AK060254	9.06	5.91	-0.95	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) (GOSS protein).
371	Os05g0475400	AK060423	9.95	6.81	-0.95	Alanine glyoxylate aminotransferase-like protein (Fragment).
372	Os11g0182200	AK095861	11.72	8.67	-0.95	Transferase family protein.
373	Os02g0458800	AK072353	8.68	5.53	-0.95	Cytochrome b-245, heavy chain family protein.
374	Os08g0102700	AK067526	9.74	6.59	-0.95	Harpin-induced 1 domain containing protein.
375	Os05g0151200	CI409979	13.54	10.39	-0.95	(No Hit)
376	Os06g0553100	CI480869	12.92	9.77	-0.95	Heat shock transcription factor 29 (Fragment).
377	Os08g0102700	AK104488	9.42	6.26	-0.95	Harpin-induced 1 domain containing protein.
378	Os03g0157300	AK103362	10.14	6.98	-0.95	Uncharacterized Cys-rich domain containing protein.
379	Os10g0429300	CI429411	10.04	6.95	-0.95	Receptor-like protein kinase.
380	Os08g0102700	AK072003	9.79	6.63	-0.95	Harpin-induced 1 domain containing protein.
381	Os03g0429800	AK103000	11.71	8.54	-0.95	Xanthine dehydrogenase 1 (EC 1.1.1.204).
382	Os05g0560000	AK061603	9.53	6.35	-0.95	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) (GOSS protein).
383	Os10g0510400	AK100601	11.28	8.10	-0.96	Putative methyltransferase DUF248 family protein.
384	Os07g0541200	CI373246	8.12	4.94	-0.96	Protein kinase family protein.
385	Os07g0158800	AK064542	10.77	7.59	-0.96	Thiazole biosynthetic enzyme 1, chloroplast precursor.
386	Os07g0171100	AK066475	8.28	5.09	-0.96	TPR-like domain containing protein.
387	Os05g0151200	CI409979	13.08	9.90	-0.96	(No Hit)
388	Os10g0510400	AK073237	11.39	8.20	-0.96	Putative methyltransferase DUF248 family protein.
389	Os11g0240600	AK061589	10.31	7.12	-0.96	Esterase/lipase/thioesterase domain containing protein.
390	Os11g0240600	AK120858	10.35	7.15	-0.96	Esterase/lipase/thioesterase domain containing protein.
391	Os09g0467400	AK068819	13.06	8.85	-0.96	Protein of unknown function DUF250 domain containing protein.
392	Os07g0134000	AK108110	9.87	6.67	-0.96	Amino acid permease 6.
393	Os03g0343900	AK105813	7.93	4.73	-0.96	Photosystem II protein PsbX family protein.
394	Os05g0205100	AK111332	7.57	4.35	-0.97	NLI interacting factor domain containing protein.
395	Os01g0290700	AK058263	12.74	9.52	-0.97	MDR-like p-glycoprotein.
396	Os01g0929200	CI085053	9.53	6.31	-0.97	Protein kinase domain containing protein.
397	Os11g0182200	AK060223	12.91	9.69	-0.97	Transferase family protein.
398	Os11g0605100	AK065824	8.90	5.68	-0.97	Disease resistance protein family protein.
399	Os03g0797400	AK072595	15.73	12.51	-0.97	Tryptophan synthase, alpha chain domain containing protein.
400	Os02g0626100	AK060724	16.02	12.80	-0.97	Phenylalanine ammonia-lyase (EC 4.3.1.5).
401	Os02g0626100	AK102817	16.14	12.91	-0.97	Phenylalanine ammonia-lyase (EC 4.3.1.5).
402	Os07g0601100	AK062499	10.02	6.79	-0.97	NADPH HC toxin reductase (Fragment).
403	Os01g0313600	CI434821	9.76	6.53	-0.97	(No Hit)
404	Os03g0737000	AK061742	14.86	11.64	-0.97	CBS domain containing protein.
405	Os06g0638500	CI069341	10.18	6.95	-0.97	Protein kinase domain containing protein.
406	Os08g0102700	AK061780	9.49	6.27	-0.97	Harpin-induced 1 domain containing protein.
407	Os07g0171100	AK062132	8.15	4.92	-0.97	TPR-like domain containing protein.
408	Os04g0497700	AK059443	8.39	5.15	-0.97	CONSTANS-like protein.
409	Os08g0102700	AK098293	9.95	6.66	-0.97	Harpin-induced 1 domain containing protein.
410	Os02g0570400	AK068310	7.76	4.52	-0.97	Terpene synthase, metal-binding domain containing protein.
411	Os02g0626100	AK067923	16.04	12.81	-0.98	Phenylalanine ammonia-lyase (EC 4.3.1.5).
412	Os09g0511900	AK066336	7.79	4.55	-0.98	Glycoside hydrolase, family 1 protein.
413	Os02g0626100	AK058306	16.14	12.90	-0.98	Phenylalanine ammonia-lyase (EC 4.3.1.5).
414	Os05g0171900	AK069814	15.24	11.99	-0.98	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.
415	Os04g0653600	AK068179	10.18	6.92	-0.98	AP2/EREBP transcription factor BABY BOOM1.
416	Os05g0296000	AB110170	13.02	9.85	-0.98	Thiazole biosynthetic enzyme 1, chloroplast precursor.
417	Os07g0171100	AF227978	8.32	5.05	-0.98	TPR-like domain containing protein.
418	Os11g0182200	AK104889	12.41	9.13	-0.99	Transferase family protein.
419	Os03g0429800	AK073276	11.97	8.69	-0.99	Xanthine dehydrogenase 1 (EC 1.1.1.204).
420	Os07g0614000	AK069163	11.66	8.38	-0.99	Strictosidine synthase family protein.
421	Os01g0852200	AK102621	9.36	6.06	-0.99	Major facilitator superfamily protein.
422	Os02g0302400	CI232219	10.06	6.76	-0.99	1-aminocyclopropane-1-carboxylate synthase family protein.
423	Os03g0663800	AK105347	8.13	4.83	-0.99	Globulin 1 (Fragment).
424	Os05g0171900	AK119669	15.75	12.45	-0.99	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.
425	Os05g0171900	AK119584	15.76	12.45	-0.99	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.
426	Os12g0147800	AK059860	10.21	6.90	-0.99	Phytosulfokines 5 precursor (Secretory protein SH27A) [Contains: Phytosulfokine-alpha (PSK-alpha) (Phytosulfokine-a); Phytosulfokine-beta (PSK-beta) (Phytosulfokine-b)].
427	Os04g0526600	AY166458	14.33	11.02	-1.00	Alpha-amylase/subtilisin inhibitor (RA5).
428	Os01g0959000	AK101121	12.30	8.99	-1.00	Protein of unknown function DUF221 domain containing protein.
429	Os01g0642100	AK063793	8.86	5.55	-1.00	Non-protein coding transcript, uncharacterized transcript.
430	Os05g0113300	AK106443	8.55	5.24	-1.00	Conserved hypothetical protein.
431	Os08g0102700	AK061546	10.03	6.71	-1.00	Harpin-induced 1 domain containing protein.
432	Os01g0865100	AK071410	12.35	9.03	-1.00	Uricase (Fragment).
433	Os04g0546500	U25970	14.05	10.72	-1.00	Oleosin Zm-1 (Oleosin 16 kDa) (Lipid body-associated major protein) (Lipid body-associated protein L3).

434	Os12g0156200	U04297	9.76	6.42	-1.00	DNA-binding factor of bZIP class.
435	Os01g0773700	AK060438	10.58	7.24	-1.01	Photosystem II reaction center W protein (PSII 6.1 kDa protein) (Fragment).
436	Os09g0365100	AK121161	8.81	5.46	-1.01	Non-protein coding transcript, unclassifiable transcript.
437	Os05g0355400	AK063864	10.72	7.37	-1.01	Conserved hypothetical protein.
438	Os01g0852200	AK063954	9.86	6.49	-1.01	Major facilitator superfamily protein.
439	Os03g0452000	CI420549	11.14	7.77	-1.01	(No Hit)
440	Os10g0475000	CI161649	12.89	9.52	-1.01	Conserved hypothetical protein.
441	Os01g0557500	AB112656	12.24	8.87	-1.02	Cation/proton exchanger 1a.
442	Os07g0134000	AK058572	10.13	6.75	-1.02	Amino acid permease 6.
443	Os10g0549000	AK078877	10.54	7.17	-1.02	Cytochrome P450 family protein.
444	Os01g0816100	AK073848	11.88	8.50	-1.02	NAC-domain containing protein 2 (ANAC002).
445	Os05g0110100	CI121142	9.67	6.28	-1.02	Conserved hypothetical protein.
446	Os12g0134900	CI387037	11.67	8.28	-1.02	Cytochrome P450 family protein.
447	Os05g0500200	CI436216	7.79	4.40	-1.02	Hypothetical protein.
448	Os03g0822000	AK063455	7.85	4.45	-1.02	Alpha-expansin OsEXPA7.
449	Os02g0187800	AK052904	12.96	9.55	-1.03	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
450	Os06g0467000	AK061867	13.41	10.00	-1.03	Protein of unknown function DUF250 domain containing protein.
451	Os02g0657000	AY346094	7.72	4.31	-1.03	AP2 domain-containing protein Rap211.
452	Os09g0437500	AK099618	8.52	5.09	-1.03	Dormancyauxin associated family protein.
453	Os02g0187800	AB122054	12.90	9.47	-1.03	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
454	Os07g0816100	AB028183	12.41	8.97	-1.03	NAC-domain containing protein 2 (ANAC002).
455	Os02g0187800	AK071789	11.99	8.55	-1.03	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
456	Os01g0832500	AK105604	10.61	7.17	-1.04	Glycoside transferase, six-hairpin domain containing protein.
457	Os03g0305600	AK063714	13.31	9.87	-1.04	Mitochondrial import inner membrane translocase, subunit Tim17/22 family protein.
458	Os10g0492600	AB114828	15.63	12.19	-1.04	Tonoplast membrane integral protein ZmTIP3-1.
459	Os09g0320100	CI124328	10.64	7.19	-1.04	(No Hit)
460	Os04g0526600	AK106723	14.96	11.51	-1.04	Alpha-amylase/subtilisin inhibitor (RASI).
461	Os05g0572700	AK108969	11.74	8.28	-1.04	Protein phosphatase 2C.
462	Os04g0583200	AK073181	9.23	5.77	-1.04	Conserved hypothetical protein.
463	Os08g0105800	AK067200	9.12	5.65	-1.04	E-class P450, group I family protein.
464	Os07g0134000	AK103862	11.65	8.18	-1.04	Amino acid permease 6.
465	Os10g0492600	AK111931	15.88	12.41	-1.04	Tonoplast membrane integral protein ZmTIP3-1.
466	Os02g0824500	AK111296	10.53	7.06	-1.05	Remorin.
467	Os03g0409100	AK073459	11.72	8.24	-1.05	Ankyrin repeat containing protein.
468	Os06g0492500	CI124328	10.22	6.75	-1.05	(No Hit)
469	Os03g0164300	AK070845	11.01	7.52	-1.05	Conserved hypothetical protein.
470	Os08g0473900	AK073487	14.97	11.48	-1.05	RAMy3D
471	Os03g0699000	U43931	15.19	11.69	-1.05	Oleocin family protein.
472	Os02g0569900	AK105913	9.20	5.70	-1.05	Cytochrome P450 family protein.
473	Os07g0766000	Os01g0766000	12.06	8.56	-1.05	Multi antimicrobial extrusion protein MatE family protein.
474	Os03g0824500	AK071422	12.62	9.15	-1.05	Short-chain dehydrogenase/reductase SDR family protein.
475	Os01g0532300	CI542224	7.85	4.34	-1.06	Conserved hypothetical protein.
476	Os02g0187800	AK105011	12.98	9.47	-1.06	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
477	Os06g0321600	CI430143	12.83	9.31	-1.06	(No Hit)
478	Os08g0473900	M24287	15.13	11.60	-1.06	RAMy3D
479	Os04g0179700	AK119327	10.07	6.54	-1.06	Terpene synthase.
480	Os03g0111300	AK062506	17.65	14.12	-1.06	Non-specific lipid transfer protein 2 (nslTP2) (7 kDa lipid transfer protein).
481	Os12g0147800	AF063633	12.81	9.28	-1.06	Proteinase 5 precursor (Secretory protein SH2TA) [Contains: Phytosulfokine-alpha (PSK-alpha) (Phytosulfokine-a), Phytosulfokine- beta (PSK-beta) (Phytosulfokine-b)].
482	Os01g0124400	AK098929	13.33	9.78	-1.07	Proteinase inhibitor I12, Bowman-Birk family protein.
483	Os01g0849600	AK108159	12.47	8.92	-1.07	Universal stress protein (Usp) family protein.
484	Os12g0147800	AK101186	13.19	9.64	-1.07	Phytosulfokines 5 precursor (Secretory protein SH2TA) [Contains: Phytosulfokine-alpha (PSK-alpha) (Phytosulfokine-a), Phytosulfokine- beta (PSK-beta) (Phytosulfokine-b)].
485	Os06g0324400	AK063726	14.22	10.67	-1.07	Late embryogenesis abundant (LEA) group 1 family protein.
486	Os05g0525900	AK059594	16.04	12.48	-1.07	Zn-finger transcription factor.
487	Os02g0442000	CI124328	10.82	7.25	-1.07	(No Hit)
488	Os01g0124400	AK064050	13.03	9.46	-1.08	Proteinase inhibitor I12, Bowman-Birk family protein.
489	Os02g0821500	Os02g0821500	9.92	6.34	-1.08	Multi antimicrobial extrusion protein MatE family protein.
490	Os01g0935600	AK061490	9.90	6.33	-1.08	Glycoside transferase, six-hairpin domain containing protein.
491	Os03g0758300	AK060339	9.33	5.76	-1.08	Cyclic nucleotide-gated ion channel 2 (ACNCGC2) (Cyclic nucleotide-and calmodulin-regulated ion channel 2) (DEFENSE NO DEATH 1).
492	Os07g0433200	AK063453	12.69	9.12	-1.08	(No Hit)
493	Os06g0437800	AK065169	8.98	5.40	-1.08	Dormancyauxin associated family protein.
494	Os07g0134000	AK120257	12.34	8.75	-1.08	Amino acid permease 6.
495	Os06g0306600	AK106075	7.72	4.13	-1.08	Esterase/lipase/thioesterase domain containing protein.
496	Os08g0473900	AK119761	15.06	11.46	-1.08	RAMy3D
497	Os08g0473900	AK119561	16.03	12.44	-1.08	RAMy3D
498	Os11g0533700	CI076279	14.83	11.23	-1.08	(No Hit)
499	Os03g0409100	AK063455	12.32	8.72	-1.08	Ankyrin repeat containing protein.
500	Os02g0185400	CI448460	10.39	6.78	-1.09	E-class P450, group I family protein.
501	Os04g0559700	AK104736	13.25	9.64	-1.09	HvPIP1;5 protein.
502	Os10g0437500	AK071152	13.30	9.68	-1.09	Universal stress protein (Usp) family protein.
503	Os04g0390700	AK107261	13.01	9.39	-1.09	Short-chain dehydrogenase/reductase SDR family protein.
504	Os04g0559700	AK065188	13.15	9.54	-1.09	HvPIP1;5 protein.
505	Os04g0141300	CI076279	14.51	10.89	-1.09	(No Hit)
506	Os04g0559700	AK098849	13.33	9.71	-1.09	HvPIP1;5 protein.
507	Os12g0612600	CI076279	14.55	10.92	-1.09	(No Hit)
508	Os03g0153900	AK106420	8.11	4.48	-1.09	Aromatic-ring hydroxylase family protein.
509	Os01g0711500	CI076279	14.92	11.28	-1.09	Calceinein B (Fragment).
510	Os01g0158900	AK108324	12.33	8.69	-1.10	SNF4.
511	Os10g0576000	AK061355	13.04	9.40	-1.10	TPR-like domain containing protein.
512	Os10g0576600	AK104496	13.06	9.40	-1.10	TPR-like domain containing protein.
513	Os02g0177600	AK070083	10.76	7.09	-1.10	4-coumarate-CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1).
514	Os04g0179100	CI027926	9.77	6.10	-1.11	Glucose/ribitol dehydrogenase family protein.
515	Os07g0269000	CI251879	13.31	9.63	-1.11	(No Hit)
516	Os02g0626400	AK120127	15.07	11.39	-1.11	Phenylalanine ammonia-lyase (EC 4.3.1.5).
517	Os06g0305000	AK111040	11.61	7.34	-1.11	Steroid nuclear receptor, ligand-binding domain containing protein.
518	Os01g0859300	AK070998	14.29	10.60	-1.11	ABA response element binding factor.
519	Os08g0273600	CI488276	13.01	9.32	-1.11	(No Hit)
520	Os02g0626400	AK065208	14.93	11.23	-1.11	Phenylalanine ammonia-lyase (EC 4.3.1.5).
521	Os03g0809200	AK102250	9.39	5.69	-1.11	DNA-binding protein (Fragment).
522	Os09g0369500	AK105322	8.44	4.74	-1.11	Conserved hypothetical protein.
523	Os01g0192000	AK100770	13.21	9.50	-1.12	Zn-finger, C-x8-C-x5-C-x3-H type domain containing protein.
524	Os03g0183200	AK108889	8.53	4.87	-1.12	Conserved hypothetical protein.
525	Os02g0644000	AY062178	15.93	12.21	-1.12	C13 endopeptidase NP1 (Fragment).
526	Os04g0510900	AK063625	13.80	10.08	-1.12	Embryo-specific protein 1 (ATS1).
527	Os01g0192000	AK073660	13.30	9.58	-1.12	Zn-finger, C-x8-C-x5-C-x3-H type domain containing protein.
528	Os02g0644000	AB081464	16.05	12.32	-1.12	C13 endopeptidase NP1 (Fragment).
529	Os07g0529600	AK089918	13.44	9.70	-1.13	Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
530	Os06g0484500	AK105604	10.61	7.17	-1.13	Hypothetical protein.
531	Os01g0644200	AK063634	12.00	8.26	-1.13	Conserved hypothetical protein.
532	Os08g0320900	AK107815	11.32	7.57	-1.13	Conserved hypothetical protein.
533	Os05g0474600	AK066733	11.65	7.90	-1.13	Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).
534	Os06g0110200	AK107973	15.57	11.82	-1.13	Late embryogenesis abundant (LEA) group 1 family protein.
535	Os05g0470100	CI076113	10.76	7.01	-1.13	(No Hit)
536	Os03g0411900	CI256174	11.59	7.83	-1.13	Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
537	Os07g0529600	AK064916	13.03	9.27	-1.13	Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
538	Os12g0148700	AK071332	8.92	5.15	-1.13	Hypothetical protein.
539	Os04g0179700	AY347880	10.29	6.52	-1.13	Terpene synthase.
540	Os08g0273600	CI451276	13.42	9.65	-1.13	(No Hit)
541	Os05g0474600	AK102864	11.54	7.77	-1.13	Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).
542	Os03g0277500	AK063650	16.83	13.05	-1.14	Glyoxalase/biomecryn resistance protein/dioxygenase domain containing protein.
543	Os02g0509600	AK111075	10.25	6.47	-1.14	Conserved hypothetical protein.
544	Os03g0404500	AK061614	7.96	4.19	-1.14	Non-protein coding transcript, unclassifiable transcript.
545	Os10g0576600	AK104125	16.02	12.24	-1.14	TPR-like domain containing protein.
546	Os02g0140800	CI228187	11.07	7.29	-1.14	Conserved hypothetical protein.
547	Os04g0653600	AK059064	10.03	6.24	-1.14	AP2/EREBP transcription factor BABY BOOM1.
548	Os06g0512900	AK107748	12.93	9.14	-1.14	Hypothetical protein.
549	Os09g0325700	AK063334	12.80	9.01	-1.14	Protein phosphatase 2C (EC 3.1.3.16) (PP2C).
550	Os06g0983000	AK071637	11.94	8.15	-1.14	Protein phosphatase 2C family protein.
551	Os09g0396900	AK071589	11.27	7.47	-1.14	Protein of unknown function DUF125 family protein.
552	Os02g0809500	AK100684	9.13	5.33	-1.14	Conserved hypothetical protein.
553	Os10g0576600	AK099195	16.34	12.53	-1.15	TPR-like domain containing protein.
554	Os08g0441500	AK072872	11.84	8.03	-1.15	Cinnamoyl-CoA reductase.
555	Os02g0644000	AK101360	15.40	11.59	-1.15	C13 endopeptidase NP1 (Fragment).
556	Os04g0178300	AK121319	9.12	5.31	-1.15	Copaly diphosphate synthetase (Fragment).
557	Os03g0561000	CI404894	14.20	10.37	-1.15	(No Hit)
558	Os02g0743400	AF056027	12.84	9.01	-1.15	Auxin transport protein REH1.
559	Os02g0644000	AK070079	15.29	11.47	-1.15	C13 endopeptidase NP1 (Fragment).
560	Os03g0277600	AK061425	12.36	8.53	-1.15	Protein of unknown function DUF26 domain containing protein.
561	Os02g0570000	AK103800	5.29	2.99	-1.15	AP2 domain-containing protein Rap211.
562	Os08g0505900	AK120908	8.82	4.99	-1.16	DNA-damage-repair/tolerance protein DRT100 precursor.
563	Os04g0444300	AK102641	9.17	5.32	-1.16	Conserved hypothetical protein.
564	Os01g0388000	AK069778	8.92	5.08	-1.16	Cytochrome P450 family protein.
565	Os08g0441500	AK105870	11.51	7.65	-1.16	Cinnamoyl-CoA reductase.
566	Os04g0178300	AY530101	9.55	5.69	-1.16	Copaly diphosphate synthetase (Fragment).
567	Os05g0576000	AK103170	10.67	6.80	-1.16	Esterase/lipase/thioesterase domain containing protein.
568	Os02g0252700	AK103494	13.27	9.39	-1.17	Conserved hypothetical protein.
569	Os02g0743400	AK099634	12.46	8.58	-1.17	Auxin transport protein REH1.
570	Os01g0391100	AK063499	8.87	4.98	-1.17	ABC transporter related domain containing protein.
571	Os03g0197300	AK102651	16.85	12.96	-1.17	RmlC-like cupin family protein.
572	Os06g0147100	AK120518	12.96	9.05	-1.18	Conserved hypothetical protein.
573	Os08g0505900	AK063670	8.94	5.03	-1.18	DNA-damage-repair/tolerance protein DRT100 precursor.
574	Os07g0480900	AK063422	16.24	12.33	-1.18	Cysteine protease (Fragment).
575	Os03g0118800	AK071039	13.52	9.58	-1.19	HMG-CoA synthase.
576	Os09g0482300	AY688675	15.20	11.26	-1.19	Conserved hypothetical protein.
577	Os06g0147100	AK119696	13.07	9.13	-1.19	Conserved hypothetical protein.
578	Os05g0381400	AK102039	13.73	9.79	-1.19	ABA induced plasma membrane protein PM 19.

579	Os03g0404500	AK098956	8.69	4.74	-1.19	Non-protein coding transcript, unclassifiable transcript.
580	Os09g0127700	AK107885	12.87	8.92	-1.19	Conserved hypothetical protein.
581	Os12g0506700	Cl275400	13.79	9.84	-1.19	VMP3 protein.
582	Os05g0468900	Cl459446	13.73	9.74	-1.20	Cold-regulated protein.
583	Os10g0360700	Cl015964	8.67	4.68	-1.20	Conserved hypothetical protein.
584	Os03g0153500	Os03g0153500	11.39	7.37	-1.21	Aromatic-ring hydroxylase family protein.
585	Os03g0793700	U45321	15.51	11.49	-1.21	Globulin 2 (Fragment).
586	Os03g0406900	Cl447475	10.50	6.48	-1.21	Protein of unknown function family protein.
587	Os05g0110100	AK098779	9.76	5.72	-1.22	Conserved hypothetical protein.
588	Os08g0415500	AK105302	12.19	8.15	-1.22	Cinnamoyl-CoA reductase.
589	Os04g0231800	AK068417	15.32	11.27	-1.22	Protein of unknown function DUF1165 family protein.
590	Os02g0570400	AB089272	9.22	5.16	-1.22	Terpene synthase, metal-binding domain containing protein.
591	Os05g0140800	AK110652	14.37	10.31	-1.22	Glucose/ribitol dehydrogenase family protein.
592	Os04g0589900	AK063682	15.52	11.45	-1.22	Late embryogenesis abundant (LEA) group 1 family protein.
593	Os07g0190000	AK100909	8.49	4.41	-1.23	1-deoxy-D-xylulose 5-phosphate synthase 2 precursor.
594	Os04g0239400	AK061312	8.20	4.11	-1.23	MipE.
595	Os03g0168100	AK121575	12.02	7.92	-1.23	Late embryogenesis abundant protein repeat containing protein.
596	Os05g0367900	Cl483366	9.54	5.45	-1.23	Harpin-induced 1 domain containing protein.
597	Os04g0390800	AK108276	14.88	10.76	-1.24	Short-chain dehydrogenase/reductase SDR family protein.
598	Os08g0544400	AK107688	14.20	10.07	-1.24	ABC transporter related domain containing protein.
599	Os10g0431900	AK106265	12.23	8.08	-1.25	Avr9/Cf-9 rapidly elicited protein 264.
600	Os10g0431900	AK072305	12.25	8.09	-1.25	Avr9/Cf-9 rapidly elicited protein 264.
601	Os06g0650700	AK107786	13.96	9.79	-1.26	Non-protein coding transcript, unclassifiable transcript.
602	Os09g0479800	AK108585	11.68	7.50	-1.26	Phosphofruktokinase family protein.
603	Os10g0579800	AK121847	11.54	7.36	-1.26	TGF-beta receptor, type III extracellular region family protein.
604	Os03g0808300	AK109389	13.90	9.72	-1.26	Remorin, C-terminal region domain containing protein.
605	Os02g0511600	AK111241	8.70	4.49	-1.27	Conserved hypothetical protein.
606	Os05g0249300	Cl476617	13.72	9.49	-1.27	(No Hit)
607	Os10g0564100	AK107224	11.75	7.52	-1.27	Conserved hypothetical protein.
608	Os03g0189600	AK061930	13.01	8.77	-1.28	Alcohol dehydrogenase.
609	Os12g0530300	AK107694	11.56	7.31	-1.28	Non-protein coding transcript, unclassifiable transcript.
610	Os04g0233400	AK061491	8.56	4.31	-1.28	MipE.
611	Os08g0417000	AK104072	11.25	7.00	-1.28	2OG-Fe(II) oxygenase domain containing protein.
612	Os05g0569500	AF048992	13.87	9.61	-1.28	Protein of unknown function DUF1264 family protein.
613	Os01g0686200	AK109457	9.78	5.52	-1.28	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
614	Os01g0743500	AY444338	13.28	8.99	-1.29	NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME).
615	Os08g0467500	AK064041	13.39	9.11	-1.29	Abscisic acid and stress inducible (A22) gene.
616	Os04g0233400	AK119661	8.85	4.56	-1.29	MipE.
617	Os01g0743500	AK073858	12.68	8.39	-1.29	NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME).
618	Os05g0569500	AK073481	13.96	9.66	-1.29	Protein of unknown function DUF1264 family protein.
619	Os08g0417000	AK068735	10.97	6.67	-1.30	2OG-Fe(II) oxygenase domain containing protein.
620	Os08g0467500	AK100937	13.81	9.50	-1.30	Abscisic acid and stress inducible (A22) gene.
621	Os05g0542500	AK063984	10.71	6.38	-1.30	Group 3 LEA (Type I) protein.
622	Os09g0452200	AK059479	8.69	4.36	-1.30	LysM-domain GPI-anchored protein 1 precursor. Splice isoform 2.
623	Os09g0272600	AK063844	10.95	6.58	-1.31	Conserved hypothetical protein.
624	Os02g0115700	AK061923	10.93	6.55	-1.32	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
625	Os10g0422000	Cl144686	11.96	7.59	-1.32	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
626	Os09g0482600	Cl255075	15.12	10.72	-1.32	Heat shock protein 82.
627	Os03g0580300	Cl455551	10.49	6.08	-1.33	(No Hit)
628	Os04g0610600	AK073109	12.55	8.14	-1.33	Cor14b protein precursor.
629	Os07g0298900	AK064565	10.23	5.80	-1.33	Heavy metal transport/detoxification protein domain containing protein.
630	Os02g0115700	AK065094	11.20	6.77	-1.34	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
631	Os12g0599100	AK108003	9.88	5.42	-1.34	Hypothetical protein.
632	Os02g0571100	AK070796	9.16	4.68	-1.35	Terpene synthase, metal-binding domain containing protein.
633	Os10g0528100	AK108376	11.51	7.03	-1.35	Glutathione S-transferase GST 42 (EC 2.5.1.18) (Fragment).
634	Os02g0115700	AK099231	11.27	6.77	-1.35	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
635	Os05g0122700	Cl441278	13.06	8.56	-1.35	Small hydrophobic protein 2.
636	Os02g0115700	X61626	11.34	6.84	-1.36	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
637	Os03g0381500	AK108125	12.85	8.34	-1.36	Hypothetical protein.
638	Os04g0631100	AK121886	14.77	10.25	-1.36	General substrate transporter family protein.
639	Os02g0629200	AK061782	9.43	4.91	-1.36	Plasma membrane integral protein ZmPIP2-3.
640	Os02g0115700	AK099923	11.47	6.94	-1.36	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
641	Os04g0233400	AK102155	8.68	4.14	-1.37	MipE.
642	Os03g0322900	Cl387122	14.95	10.41	-1.37	Late embryogenesis abundant protein repeat containing protein.
643	Os09g0369500	AK105479	15.52	10.98	-1.37	Conserved hypothetical protein.
644	Os05g0241500	AK065866	14.36	8.06	-1.37	Glycoside hydrolase, family 18 protein.
645	Os02g0115700	AK071061	10.74	6.18	-1.37	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
646	Os02g0629200	AK120386	9.65	5.09	-1.37	Plasma membrane integral protein ZmPIP2-3.
647	Os04g0352200	AK103395	9.49	4.88	-1.39	Conserved hypothetical protein.
648	Os08g0127900	U25968	15.96	11.34	-1.39	Globulin 1 (Fragment).
649	Os03g0157700	AK102075	12.48	7.81	-1.41	Protein of unknown function DUF639 family protein.
650	Os05g0542500	AK106990	16.87	12.18	-1.41	Group 3 LEA (Type I) protein.
651	Os05g0355400	AK070138	10.14	5.45	-1.41	Conserved hypothetical protein.
652	Os03g0157700	AK106245	12.61	7.92	-1.41	Protein of unknown function DUF639 family protein.
653	Os05g0542500	AK119713	16.96	12.25	-1.42	Group 3 LEA (Type I) protein.
654	Os08g0127900	AK119657	15.82	11.10	-1.42	Globulin 1 (Fragment).
655	Os03g0623100	AK063716	11.86	6.94	-1.42	Conserved hypothetical protein.
656	Os09g0242000	AK119722	14.81	10.07	-1.42	Oleosin Zm-1 (Oleosin 16 kDa) (Lipid body-associated major protein) (Lipid body-associated protein L3).
657	Os09g0457400	AK098330	14.23	9.48	-1.43	RAmy3A.
658	Os05g0542500	U57641	17.02	12.27	-1.43	Group 3 LEA (Type I) protein.
659	Os09g0457400	AK099392	14.45	9.69	-1.43	RAmy3A.
660	Os01g0213500	Cl426147	11.61	6.83	-1.44	Conserved hypothetical protein.
661	Os06g0572400	AK070273	12.71	7.92	-1.44	CD9/CD37/CD63 antigen family protein.
662	Os08g0327700	AK107930	16.75	11.71	-1.45	Late embryogenesis abundant (LEA) group 1 family protein.
663	Os06g0561000	AK068862	12.75	7.90	-1.46	Myo-inositol oxygenase.
664	Os06g0561000	AK103977	12.58	7.73	-1.46	Myo-inositol oxygenase.
665	Os01g0702500	X57327	16.79	11.93	-1.46	Dehydrin RAB25.
666	Os08g0127900	AK105316	16.18	11.32	-1.46	Globulin 1 (Fragment).
667	Os01g0159000	AK070330	13.84	8.97	-1.47	Hypothetical protein.
668	Os09g0324000	AK107774	15.30	10.39	-1.48	Oleosin Zm-1 (Oleosin 16 kDa) (Lipid body-associated major protein) (Lipid body-associated protein L3).
669	Os01g0159000	AK108273	11.49	6.57	-1.48	Hypothetical protein.
670	Os11g0671000	AF467730	15.20	10.23	-1.50	Dormancy-associated protein.
671	Os04g0313300	AK121730	11.95	6.96	-1.50	Conserved hypothetical protein.
672	Os11g0671000	AK060981	15.40	10.40	-1.51	Dormancy-associated protein.
673	Os06g0697000	AK105513	13.39	8.38	-1.51	Xyloglucan endotransglucosylase/hydrolase A precursor (EC 2.4.1.207) (VxXTH1).
674	Os01g0702500	AK063691	16.75	11.71	-1.52	Dehydrin RAB25.
675	Os01g0596500	AK068814	12.14	7.10	-1.52	Alpha/beta hydrolase fold domain containing protein.
676	Os02g0250600	Cl479812	15.29	10.23	-1.53	Late embryogenesis abundant protein repeat containing protein.
677	Os07g0422100	U57639	13.63	8.55	-1.53	AWPM-19-like family protein.
678	Os03g0336100	AK105307	16.36	11.25	-1.54	RmlC-like cupin family protein.
679	Os01g0702500	AY333185	13.82	8.70	-1.54	Dehydrin RAB25.
680	Os12g0464400	AK121922	13.70	8.57	-1.55	Short-chain dehydrogenase/reductase SDR family protein.
681	Os07g0422100	AK063592	13.40	8.26	-1.55	AWPM-19-like family protein.
682	Os09g0457400	AK063988	12.67	7.52	-1.55	RAmy3A.
683	Os10g0505900	AK062588	14.46	9.28	-1.56	Conserved hypothetical protein.
684	Os04g0386700	Cl061748	14.86	9.68	-1.56	Conserved hypothetical protein.
685	Os11g0671000	AK119708	16.02	10.80	-1.57	Dormancy-associated protein.
686	Os11g0451700	Cl050356	15.82	10.57	-1.58	Dehydrin 9.
687	Os01g0705200	AK064074	15.92	10.66	-1.58	Late embryogenesis abundant protein repeat containing protein.
688	Os01g0705200	AK073837	16.04	10.77	-1.58	Late embryogenesis abundant protein repeat containing protein.
689	Os01g0705200	D26536	16.04	10.77	-1.59	Late embryogenesis abundant protein repeat containing protein.
690	Os07g0638300	AK102982	17.89	12.48	-1.63	Peroxisomal protein 2 (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
691	Os04g0434400	AK063725	13.97	8.49	-1.65	Hypothetical protein.
692	Os12g0134700	Cl136652	13.87	8.37	-1.66	(No Hit)
693	Os11g0138100	AK103307	11.80	6.28	-1.66	E-class P450, group 1 family protein.
694	Os07g0638300	AK101401	17.95	12.28	-1.71	Peroxisomal protein 2 (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
695	Os07g0638300	D63917	18.00	12.31	-1.71	Peroxisomal protein 2 (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
696	Os03g0793700	AY098743	14.33	8.57	-1.73	Globulin 2 (Fragment).
697	Os07g0638300	AY336994	17.85	12.06	-1.74	Peroxisomal protein 2 (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
698	Os11g0582400	AF516927	17.29	11.38	-1.78	Hypothetical protein.
699	Os11g0582400	U25969	16.98	10.93	-1.82	Hypothetical protein.
700	Os11g0582400	AK073083	16.94	10.89	-1.82	Hypothetical protein.
701	Os06g0623200	AK107469	11.74	5.68	-1.82	Cinnamoyl-CoA reductase (EC 1.2.1.44).
702	Os11g0582400	AK108352	17.20	11.02	-1.86	Hypothetical protein.
703	Os03g0793700	AK121667	16.18	9.79	-1.92	Globulin 2 (Fragment).
704	Os11g0582400	AF049348	13.63	6.92	-2.02	Hypothetical protein.

* The log₂ ratio of the GA-induced signal intensity change in WT seeds.

Table S3. List of probes up- or down-regulated by GA by more than 3-folds in *slr1*.

Probe#	ID	Accession	WT \pm GA*	<i>slr1</i> \pm GA*	Annotation
1	<i>Os01g0126100</i>	AK106990	1.03	0.76	Calycin family protein.
2	<i>Os11g0241700</i>	AK068339	0.75	0.59	Protein of unknown function DUF538 family protein.
3	<i>Os08g0473600</i>	AK106526	2.24	-0.49	RAmy3E
4	<i>Os08g0473600</i>	AK103413	2.22	-0.50	RAmy3E
5	<i>Os02g0765400</i>	M81144	2.15	-0.73	RAmy1C
6	<i>Os01g0800500</i>	AK066643	2.09	-0.58	Metallophosphoesterase domain containing protein.
7	<i>Os07g0600000</i>	AK105907	1.98	-0.50	Hypothetical protein.
8	<i>Os04g0538400</i>	AK108230	1.98	-0.54	Nodulin 21 (N-21).
9	<i>Os08g0473600</i>	AK064300	1.75	-0.48	RAmy3E
10	<i>Os12g0131900</i>	Os12g0131900	1.65	-0.60	MYST1 protein (Fragment).
11	<i>Os02g0766900</i>	Os02g0766900	1.28	-0.67	Glycoside hydrolase, family 5 protein.
12	<i>Os03g0369100</i>	AK111061	1.06	-0.55	Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor domain containing protein.
13	<i>Os05g0589700</i>	AK068031	0.88	-0.49	Dual-specific kinase DSK1.
14	<i>Os04g0179700</i>	AK119327	-1.06	-0.58	Terpene synthase.
15	<i>Os04g0179100</i>	Cl027926	-1.11	-0.58	Glucose/ribitol dehydrogenase family protein.
16	<i>Os04g0179700</i>	AY347880	-1.13	-0.51	Terpene synthase.
17	<i>Os08g0441500</i>	AK105870	-1.16	-0.53	Cinnamoyl-CoA reductase.
18	<i>Os08g0441500</i>	AK105802	-1.22	-0.52	Cinnamoyl-CoA reductase.

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S4. List of probes up- or down-regulated by GA by more than 3-folds in *gid2*.

Probe#	ID	Accession	WT ± GA*	<i>gid2</i> ± GA*	Annotation
1	Os09g0457600	Cl048168	2.51	0.70	RAmy3B
2	Os08g0473600	AK106526	2.24	0.80	RAmy3E
3	Os08g0473600	AK103413	2.22	0.79	RAmy3E
4	Os02g0765400	M81144	2.15	0.51	RAmy1C
5	Os08g0473600	AK064300	1.75	0.75	RAmy3E
6	Os04g0227500	AK104227	1.75	0.53	DSBA oxidoreductase family protein.
7	Os04g0227500	AK060052	1.74	0.52	DSBA oxidoreductase family protein.
8	Os04g0227500	AK059943	1.71	0.50	DSBA oxidoreductase family protein.
9	Os09g0457800	AK101358	1.52	0.55	RAmy3C
10	Os04g0517900	Cl431602	1.27	0.51	(No Hit)
11	Os04g0517900	Cl431602	1.26	0.51	(No Hit)
12	Os04g0324100	Cl401469	1.23	0.56	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
13	Os05g0527300	AK069268	1.11	0.62	Hypothetical protein.
14	Os12g0566000	AK060451	1.09	0.56	HCO3-transporter domain containing protein.
15	Os12g0566000	AK070617	1.07	0.55	HCO3-transporter domain containing protein.
16	Os12g0566000	AY339063	0.96	0.50	HCO3-transporter domain containing protein.
17	Os08g0473600	AK064071	0.95	0.52	RAmy3E
18	Os01g0868900	AK099469	0.83	0.48	Proteinase inhibitor I9, subtilisin propeptide domain containing protein.
19	Os03g0279700	AK111338	0.72	0.52	ZPT2-12.
20	Os03g0131200	AK062174	0.70	0.50	Catalase isozyme 2 (EC 1.11.1.6).
21	Os03g0131200	AK066378	0.68	0.48	Catalase isozyme 2 (EC 1.11.1.6).
22	Os03g0131200	AB020502	0.68	0.48	Catalase isozyme 2 (EC 1.11.1.6).
23	Os09g0433000	AK063243	-0.72	-0.53	Conserved hypothetical protein.
24	Os07g0622200	AK105687	-0.73	-0.52	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (EC 2.5.1.54)
25	Os07g0622200	AB122058	-0.73	-0.52	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (EC 2.5.1.54)
26	Os07g0622200	AK069968	-0.74	-0.52	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (EC 2.5.1.54)
27	Os01g0106400	AY071920	-0.75	-0.71	Isoflavone reductase-like protein.
28	Os04g0206500	AK110892	-0.76	-0.56	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
29	Os01g0106400	AK102701	-0.77	-0.72	Isoflavone reductase-like protein.
30	Os01g0106400	AK109339	-0.77	-0.71	Isoflavone reductase-like protein.
31	Os07g0503300	AK106005	-0.77	-0.56	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
32	Os04g0104900	AK069960	-0.78	-0.68	Caffeic acid 3-O-methyltransferase(COMT) (CAOMT).
33	Os07g0503300	AK105785	-0.78	-0.56	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
34	Os12g0555200	AK099157	-0.80	-0.65	Probenazole-inducible protein PBZ1.
35	Os11g0599200	AK100744	-0.80	-0.50	Hypothetical protein.
36	Os06g0681200	AK107980	-0.80	-0.61	Plastocyanin-like domain containing protein.
37	Os12g0555200	AK070762	-0.81	-0.66	Probenazole-inducible protein PBZ1.
38	Os05g0563600	AK058836	-0.82	-0.53	Beta-Ig-H3/fasciclin domain containing protein.
39	Os11g0213000	Cl066566	-0.83	-0.56	Protein kinase domain containing protein.
40	Os01g0138800	AK106157	-0.83	-0.50	Conserved hypothetical protein.
41	Os03g0103300	Cl385032	-0.83	-0.64	Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor domain containing protein.
42	Os04g0179200	AK106087	-0.83	-0.62	Stem secoisolariciresinol dehydrogenase (Fragment).
43	Os03g0758300	AK067626	-0.85	-0.60	Cyclic nucleotide-gated ion channel 2 (AtCNGC2)
44	Os12g0630200	Cl025931	-0.85	-0.98	Antifungal protein R (Fragment).
45	Os12g0175400	AK063027	-0.86	-0.67	Conserved hypothetical protein.
46	Os02g0626200	AK121303	-0.88	-0.56	Non-protein coding transcript, unclassifiable transcript.
47	Os10g0517500	AK105942	-0.90	-0.72	Cys/Met metabolism pyridoxal-phosphate-dependent enzymes family protein.
48	Os03g0165900	AK063721	-0.90	-0.50	MS5-like protein (Fragment).
49	Os10g0517500	AK100465	-0.90	-0.77	Cys/Met metabolism pyridoxal-phosphate-dependent enzymes family protein.
50	Os02g0592800	AK107707	-0.91	-0.48	Protein of unknown function DUF581 family protein.

51	Os03g0618300	AK073307	-0.91	-0.53	Isopenicillin N synthase family protein.
52	Os04g0178300	AK100631	-0.92	-0.51	Copalyl diphosphate synthetase (Fragment).
53	Os03g0165900	AK102116	-0.93	-0.53	MS5-like protein (Fragment).
54	Os08g0406400	AK062031	-0.94	-0.54	Sulfate transporter (Fragment).
55	Os05g0475400	AK060423	-0.95	-0.64	Alanine:glyoxylate aminotransferase-like protein (Fragment).
56	Os10g0342300	Cl429411	-0.95	-0.49	Receptor-like protein kinase.
57	Os02g0626100	AK060724	-0.97	-0.56	Phenylalanine ammonia-lyase (EC 4.3.1.5).
58	Os02g0626100	AK102817	-0.97	-0.56	Phenylalanine ammonia-lyase (EC 4.3.1.5).
59	Os02g0626100	AK067923	-0.98	-0.57	Phenylalanine ammonia-lyase (EC 4.3.1.5).
60	Os02g0626100	AK058306	-0.98	-0.55	Phenylalanine ammonia-lyase (EC 4.3.1.5).
61	Os10g0512400	AK067847	-1.02	-0.57	Cytochrome P450 family protein.
62	Os02g0187800	AK059804	-1.03	-0.65	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
63	Os02g0187800	AB122054	-1.03	-0.66	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
64	Os02g0187800	AK071794	-1.03	-0.65	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
65	Os03g0305600	AK063714	-1.04	-0.49	Mitochondrial import inner membrane translocase, subunit Tim17/22 family protein.
66	Os02g0187800	AK105011	-1.06	-0.66	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Brown-midrib 1 protein).
67	Os04g0179700	AK119327	-1.06	-0.53	Terpene synthase.
68	Os03g0758300	AK060339	-1.08	-0.65	Cyclic nucleotide-gated ion channel 2 (AtCNGC2)
69	Os08g0473900	AK119561	-1.08	-0.49	Alpha-amylase type B (Fragment).
70	Os02g0177600	AK070083	-1.10	-0.50	4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1).
71	Os04g0179100	Cl027926	-1.11	-0.64	Glucose/ribitol dehydrogenase family protein.
72	Os03g0809200	AK102250	-1.11	-0.50	DNA-binding protein (Fragment).
73	Os01g0644200	AK063634	-1.13	-0.51	Conserved hypothetical protein.
74	Os04g0179700	AY347880	-1.13	-0.58	Terpene synthase.
75	Os08g0441500	AK072872	-1.15	-0.60	Cinnamoyl-CoA reductase.
76	Os04g0178300	AK121319	-1.15	-0.62	Copalyl diphosphate synthetase (Fragment).
77	Os03g0277600	AK061425	-1.15	-0.78	Protein of unknown function DUF26 domain containing protein.
78	Os08g0441500	AK105870	-1.16	-0.58	Cinnamoyl-CoA reductase.
79	Os04g0178300	AY530101	-1.16	-0.59	Copalyl diphosphate synthetase (Fragment).
80	Os08g0441500	AK105802	-1.22	-0.61	Cinnamoyl-CoA reductase.
81	Os02g0570400	AB089272	-1.22	-0.64	Terpene synthase, metal-binding domain containing protein.
82	Os07g0190000	AK100909	-1.23	-0.55	1-deoxy-D-xylulose 5-phosphate synthase 2 precursor.
83	Os09g0272600	AK063844	-1.31	-0.97	Conserved hypothetical protein.
84	Os05g0247100	AK065866	-1.37	-1.07	Glycoside hydrolase, family 18 protein.
85	Os08g0127900	U25968	-1.39	-0.49	Globulin 1 (Fragment).
86	Os08g0127900	AK119657	-1.42	-0.48	Globulin 1 (Fragment).
87	Os09g0457400	AK099330	-1.43	-1.07	Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
88	Os09g0457400	AK099392	-1.43	-1.06	Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
89	Os08g0327700	AK107930	-1.45	-0.69	Late embryogenesis abundant (LEA) group 1 family protein.
90	Os06g0561000	AK068862	-1.46	-0.68	Myo-inositol oxygenase.
91	Os06g0561000	AK103977	-1.46	-0.68	Myo-inositol oxygenase.
92	Os08g0127900	AK105316	-1.46	-0.50	Globulin 1 (Fragment).
93	Os01g0595600	AK066814	-1.52	-0.61	Alpha/beta hydrolase fold domain containing protein.
94	Os09g0457400	AK063988	-1.55	-1.10	Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
95	Os11g0451700	Cl050356	-1.58	-0.63	Dehydrin 9.
96	Os11g0582400	AF516927	-1.78	-0.94	Hypothetical protein.
97	Os11g0582400	U25969	-1.82	-0.92	Hypothetical protein.
98	Os11g0582400	AK073083	-1.82	-0.91	Hypothetical protein.
99	Os11g0582400	AK108352	-1.86	-0.96	Hypothetical protein.
100	Os11g0582400	AF049348	-2.02	-0.86	Hypothetical protein.

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S5. List of probes up- or down-regulated by GA by more than 3-folds in *gamyb*.

Probe#	ID	Accession	WT \pm GA*	<i>gamyb</i> \pm GA*	Annotation
1	Os08g0473600	AK103413	2.22	0.49	RAmy3E
2	Os01g0800500	AK066643	2.09	0.49	Metallophosphoesterase domain containing protein.
3	Os02g0740400	AK099325	1.89	0.73	Lipolytic enzyme, G-D-S-L family protein.
4	Os04g0227500	AK059943	1.71	0.74	DSBA oxidoreductase family protein.
5	Os12g0131900	Os12g0131900	1.65	0.48	MYST1 protein (Fragment).
6	Os02g0659900	CI436459	1.65	0.53	(No Hit)
7	Os03g0327700	AK120305	1.64	0.49	Hypothetical protein.
8	Os05g0574100	AK106699	1.32	0.49	Lipase, class 3 family protein.
9	Os02g0656100	AK058231	1.22	0.50	Conserved hypothetical protein.
10	Os01g0142300	AK060202	1.22	0.48	Glycosyl transferase, group 1 domain containing protein.
11	Os03g0644400	AB022783	1.21	0.50	Amino acid permease.
12	Os02g0740400	AK111360	1.15	0.67	Lipolytic enzyme, G-D-S-L family protein.
13	Os02g0115900	AF006825	1.12	0.51	Endosperm luminal binding protein.
14	Os05g0527300	AK069268	1.11	0.50	Hypothetical protein.
15	Os05g0376100	CI228796	1.05	0.49	(No Hit)
16	Os03g0248600	AK073611	1.03	0.48	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2)
17	Os04g0445300	AK063073	0.89	0.51	Plant invertase/pectin methylesterase inhibitor domain containing protein.
18	Os11g0564100	AU081502	0.87	0.48	(No Hit)
19	Os01g0733500	AK059056	0.85	0.49	Dehydration-responsive protein RD22 precursor.
20	Os07g0296000	AK073416	0.81	0.48	Conserved hypothetical protein.
21	Os03g0279700	AK111338	0.72	0.49	ZPT2-12.
22	Os07g0531500	CI426967	0.71	0.49	Harpin-induced 1 domain containing protein.
23	Os06g0210300	CI268249	0.71	0.49	(No Hit)
24	Os03g0131200	AK062174	0.70	0.50	Catalase isozyme 2 (EC 1.11.1.6).
25	Os07g0457600	Os07g0457600	0.70	0.49	Disease resistance protein family protein.
26	Os03g0131200	AB020502	0.68	0.49	Catalase isozyme 2 (EC 1.11.1.6).
27	Os03g0131200	AY339372	0.67	0.49	Catalase isozyme 2 (EC 1.11.1.6).
28	Os04g0415000	AK108662	0.65	0.50	Conserved hypothetical protein.
29	Os04g0364800	CI423611	0.77	-0.99	Barwin-related endoglucanase domain containing protein.
30	Os02g0652000	AK108827	0.70	-0.70	PREG-like protein.
31	Os12g0455000	AK111239	0.70	-0.48	Conserved hypothetical protein.
32	Os05g0560200	CI026016	-0.71	-0.67	Hypothetical protein.
33	Os10g0474800	Os10g0474800	-0.71	-0.69	Conserved hypothetical protein.
34	Os03g0305200	AK108450	-0.72	-0.60	Hypothetical protein.
35	Os08g0127900	AF051153	-0.72	-1.03	Globulin 1 (Fragment).
36	Os04g0422600	AK099964	-0.72	-0.59	Protein of unknown function DUF6 domain containing protein.
37	Os09g0323500	AK071737	-0.72	-0.91	Protein of unknown function DUF833 family protein.
38	Os01g0363300	AK060356	-0.73	-0.51	Protein of unknown function DUF588 family protein.
39	Os01g0679500	CI135763	-0.73	-0.74	Peptidase A1, pepsin family protein.
40	Os11g0294400	AK062429	-0.74	-0.57	WW/Rsp5/WWP domain containing protein.
41	Os01g0106400	AY071920	-0.75	-0.85	Isoflavone reductase-like protein.
42	Os01g0363300	AK059622	-0.76	-0.64	Protein of unknown function DUF588 family protein.
43	Os04g0206500	AK110892	-0.76	-1.14	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
44	Os01g0106400	AK102701	-0.77	-0.83	Isoflavone reductase-like protein.
45	Os01g0106400	AK109339	-0.77	-0.86	Isoflavone reductase-like protein.
46	Os02g0693700	AK106518	-0.78	-0.95	MDR-like p-glycoprotein.
47	Os01g0391100	AK108533	-0.78	-1.59	ABC transporter related domain containing protein.
48	Os02g0693700	AK103774	-0.78	-0.97	MDR-like p-glycoprotein.
49	Os06g0648500	AK106895	-0.79	-0.51	Hypothetical protein.
50	Os11g0599200	AK100744	-0.80	-0.67	Hypothetical protein.
51	Os01g0138800	AK106157	-0.83	-0.56	Conserved hypothetical protein.
52	Os05g0316800	AK110613	-0.83	-0.52	Ethylene-responsive element binding protein.
53	Os10g0554200	AK068409	-0.83	-0.67	Nitrate transporter.
54	Os12g0599800	AK111139	-0.83	-1.13	Hypothetical protein.
55	Os12g0550800	AK098944	-0.85	-0.87	Hypothetical protein.
56	Os12g0630200	CI025931	-0.85	-0.92	Antifungal protein R (Fragment).
57	Os03g0793700	AF051154	-0.86	-0.63	Globulin 2 (Fragment).
58	Os03g0161400	CI259418	-0.87	-0.64	IQ calmodulin-binding region domain containing protein.
59	Os12g0550800	AK102550	-0.87	-0.89	Hypothetical protein.
60	Os02g0743400	AK102343	-0.89	-0.91	Auxin transport protein REH1.
61	Os09g0412400	AK073672	-0.90	-0.50	Conserved hypothetical protein.
62	Os03g0618300	AK073307	-0.91	-0.58	Isopenicillin N synthase family protein.
63	Os03g0793700	U45320	-0.93	-0.49	Globulin 2 (Fragment).
64	Os01g0313600	CI434821	-0.97	-1.17	(No Hit)
65	Os10g0475000	CI161649	-1.01	-0.67	Conserved hypothetical protein.
66	Os04g0526600	AK106723	-1.04	-0.63	Alpha-amylase/subtilisin inhibitor (RASI).
67	Os03g0164300	AK070845	-1.05	-0.78	Conserved hypothetical protein.
68	Os04g0179700	AK119327	-1.06	-0.82	Terpene synthase.
69	Os01g0124400	AK099279	-1.07	-1.10	Proteinase inhibitor I12, Bowman-Birk family protein.
70	Os01g0124400	AK064050	-1.08	-1.17	Proteinase inhibitor I12, Bowman-Birk family protein.
71	Os09g0369500	AK105322	-1.11	-0.69	Conserved hypothetical protein.
72	Os01g0192000	AK100770	-1.12	-0.51	Zn-finger, C-x8-C-x5-C-x3-H type domain containing protein.

73	Os04g0179700	AY347880	-1.13	-0.75	Terpene synthase.
74	Os03g0404500	AK061614	-1.14	-1.07	Non-protein coding transcript, unclassifiable transcript.
75	Os08g0441500	AK072872	-1.15	-1.03	Cinnamoyl-CoA reductase.
76	Os02g0743400	AF056027	-1.15	-1.04	Auxin transport protein REH1.
77	Os03g0277600	AK061425	-1.15	-0.54	Protein of unknown function DUF26 domain containing protein.
78	Os04g0444300	AK102641	-1.16	-0.61	Conserved hypothetical protein.
79	Os08g0441500	AK105870	-1.16	-0.58	Cinnamoyl-CoA reductase.
80	Os02g0743400	AK099634	-1.17	-0.87	Auxin transport protein REH1.
81	Os01g0391100	AK063499	-1.17	-1.26	ABC transporter related domain containing protein.
82	Os03g0118800	AK071039	-1.19	-0.88	HMG-CoA synthase.
83	Os03g0404500	AK098956	-1.19	-1.23	Non-protein coding transcript, unclassifiable transcript.
84	Os10g0360700	CI015964	-1.20	-1.13	Conserved hypothetical protein.
85	Os03g0153500	Os03g0153500	-1.21	-0.52	Aromatic-ring hydroxylase family protein.
86	Os03g0406900	CI447475	-1.21	-0.75	Protein of unknown function family protein.
87	Os08g0441500	AK105802	-1.22	-0.92	Cinnamoyl-CoA reductase.
88	Os04g0233400	AK061312	-1.23	-0.54	MipE.
89	Os08g0544400	AK107688	-1.24	-0.85	ABC transporter related domain containing protein.
90	Os10g0431900	AK106265	-1.25	-0.98	Avr9/Cf-9 rapidly elicited protein 264.
91	Os10g0431900	AK072305	-1.25	-1.30	Avr9/Cf-9 rapidly elicited protein 264.
92	Os10g0579800	AK121847	-1.26	-0.65	TGF-beta receptor, type I/II extracellular region family protein.
93	Os02g0511600	AK111241	-1.27	-1.05	Conserved hypothetical protein.
94	Os04g0233400	AK061491	-1.28	-0.58	MipE.
95	Os01g0686300	AK109457	-1.28	-1.26	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
96	Os04g0233400	AK119661	-1.29	-0.76	MipE.
97	Os09g0272600	AK063844	-1.31	-1.40	Conserved hypothetical protein.
98	Os12g0599700	AK108003	-1.34	-1.29	Hypothetical protein.
99	Os04g0631100	AK121883	-1.36	-0.98	General substrate transporter family protein.
100	Os02g0629200	AK061782	-1.36	-0.92	Plasma membrane integral protein ZmPIP2-3.
101	Os04g0233400	AK102155	-1.37	-0.57	MipE.
102	Os03g0322900	CI387122	-1.37	-0.80	Late embryogenesis abundant protein repeat containing protein.
103	Os09g0369500	AK105479	-1.37	-0.84	Conserved hypothetical protein.
104	Os05g0247100	AK065866	-1.37	-0.63	Glycoside hydrolase, family 18 protein.
105	Os02g0629200	AK120386	-1.37	-0.93	Plasma membrane integral protein ZmPIP2-3.
106	Os08g0127900	U25968	-1.39	-0.51	Globulin 1 (Fragment).
107	Os08g0127900	AK119657	-1.42	-1.33	Globulin 1 (Fragment).
108	Os09g0457400	AK099330	-1.43	-1.87	RAmy3A
109	Os09g0457400	AK099392	-1.43	-1.92	RAmy3A
110	Os06g0572400	AK070273	-1.44	-0.61	CD9/CD37/CD63 antigen family protein.
111	Os08g0127900	AK105316	-1.46	-1.48	Globulin 1 (Fragment).
112	Os01g0159000	AK070330	-1.47	-0.82	Hypothetical protein.
113	Os01g0159000	AK106273	-1.48	-0.86	Hypothetical protein.
114	Os06g0697000	AK105513	-1.51	-0.93	Xyloglucan endotransglucosylase/hydrolase protein A precursor
115	Os01g0595600	AK066814	-1.52	-0.66	Alpha/beta hydrolase fold domain containing protein.
116	Os07g0422100	U57639	-1.53	-0.54	AWPM-19-like family protein.
117	Os07g0422100	AK063592	-1.55	-0.53	AWPM-19-like family protein.
118	Os09g0457400	AK063988	-1.55	-1.83	RAmy3A
119	Os12g0134700	CI136652	-1.66	-1.14	(No Hit)
120	Os11g0138300	AK103307	-1.66	-0.81	E-class P450, group I family protein.
121	Os03g0793700	AY098743	-1.73	-0.66	Globulin 2 (Fragment).
122	Os07g0503300	AK106005	-0.77	0.48	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
123	Os01g0154000	AK108752	-0.80	0.49	Hypothetical protein.

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S6. List of probes categorized under Up-group1.

Probe#	ID	Accession	WT±GA*	gid1±GA*	sir1±GA*	gid2±GA*	gamyb±GA*	Annotation
1	Os09g0457600	CI048168	2.51	-1.02	0.70	-0.39	0.27	RAMy3B
2	Os08g0473600	AK106526	2.24	-0.44	0.80	-0.49	0.30	RAMy3E
3	Os08g0473600	AK103413	2.22	-0.45	0.79	-0.50	0.49	RAMy3E
4	Os02g0785400	M81144	2.15	-0.27	0.51	-0.73	0.12	RAMy1C
5	Os01g0800500	AK066643	2.09	-0.42	0.21	-0.58	0.49	Metallophosphoesterase domain containing protein.
6	Os07g0600000	AK105907	1.98	-0.18	0.06	-0.50	0.31	Hypothetical protein.
7	Os04g0538400	AK108230	1.98	-0.07	0.28	-0.54	0.32	Nodulin 21 (N-21).
8	Os02g0740400	AK070261	1.90	-0.59	0.30	-0.30	0.45	Lipolytic enzyme, G-D-S-L family protein.
9	Os02g0740400	AK099325	1.89	-0.59	0.30	-0.30	0.73	Lipolytic enzyme, G-D-S-L family protein.
10	Os01g0842500	AK066513	1.86	-0.03	0.06	-0.32	0.26	Laccase (EC 1.10.3.2).
11	Os07g0357400	AK036498	1.85	-0.02	0.03	-0.33	0.44	RAMy1B
12	Os04g0441700	AK072763	1.82	-0.05	-0.03	0.06	0.29	Conserved hypothetical protein.
13	Os08g0473600	AK064300	1.75	-0.44	0.75	-0.48	0.47	RAMy3E
14	Os04g0227500	AK104227	1.75	-0.13	0.53	-0.22	0.29	DSBA oxidoreductase family protein.
15	Os04g0227500	AK060052	1.74	-0.13	0.52	-0.22	0.23	DSBA oxidoreductase family protein.
16	Os04g0227500	AK059943	1.71	-0.13	0.50	-0.25	0.74	DSBA oxidoreductase family protein.
17	Os03g0248500	CI557828	1.68	-0.02	0.10	0.26	0.01	(No Hit)
18	Os03g0248500	CI557828	1.67	-0.02	0.08	0.22	0.31	(No Hit)
19	Os05g0298700	AK108917	1.65	-0.20	0.17	-0.45	0.39	Xylan endohydrolase isoenzyme X-I (EC 3.2.1.8).
20	Os12g0131900	Os12g0131900	1.65	-0.24	0.19	-0.60	0.48	MYST1 protein (Fragment).
21	Os02g0659900	CI436459	1.65	0.02	0.07	-0.13	0.53	(No Hit)
22	Os03g0327700	AK120305	1.64	0.01	0.05	-0.12	0.49	Hypothetical protein.
23	Os04g0515900	AK062955	1.63	-0.20	0.30	-0.07	0.23	NAM / CUC2-like protein.
24	Os05g0523300	AK071192	1.61	-0.18	0.36	-0.22	0.48	AUX/IAA protein family protein.
25	Os01g0134800	AK063402	1.60	-0.10	0.32	-0.16	0.22	(1,4)-beta-xylan endohydrolase, isoenzyme X-II (EC 3.2.1.8) (Fragment).
26	Os01g0166500	AK122083	1.60	0.00	0.06	-0.22	0.26	Conserved hypothetical protein.
27	Os05g0514000	CI260287	1.59	-0.19	0.24	-0.18	0.14	Lipase, class 3 family protein.
28	Os01g0323200	AK107372	1.57	-0.13	0.07	-0.12	0.34	Beta-glucosidase
29	Os02g0721100	AK108167	1.55	-0.02	0.09	-0.43	0.47	Ubiquitin-conjugating enzyme E2-17 kDa 11 (EC 6.3.2.19) (Ubiquitin- protein ligase 11) (Ubiquitin carrier protein 11).
30	Os06g0143100	AK121057	1.54	-0.10	0.36	-0.30	0.39	Hypothetical protein.
31	Os04g0521100	CI561264	1.54	-0.03	-0.08	-0.33	0.21	Plasma membrane intrinsic protein (Aquaporin).
32	Os03g0102700	AF261275	1.53	-0.13	0.21	-0.33	0.17	Beta-expansin precursor.
33	Os09g0457800	AK101358	1.52	-0.47	0.55	-0.16	0.25	RAMy3C
34	Os01g0878900	AK104652	1.52	-0.16	0.14	-0.27	-0.21	4,5-DOPA dioxygenase extradiol.
35	Os02g0282200	CI537771	1.50	-0.08	0.12	-0.45	0.26	HAD-superfamily subfamily IB hydrolase, hypothetical 1 protein.
36	Os01g0878900	AK104655	1.50	-0.16	0.17	-0.26	0.21	4,5-DOPA dioxygenase extradiol.
37	Os01g0878900	AK060927	1.49	-0.14	0.16	-0.22	-0.24	4,5-DOPA dioxygenase extradiol.
38	Os02g0655500	AK109040	1.49	-0.04	0.10	-0.24	0.09	Protein kinase domain containing protein.
39	Os03g0159100	AK065635	1.49	-0.10	0.24	-0.32	0.38	Protein kinase APK1B (EC 2.7.1.-).
40	Os01g0720400	AK061237	1.49	-0.32	0.18	0.09	0.33	HAD-superfamily subfamily IB hydrolase, hypothetical 1 protein.
41	Os01g0878900	AK104601	1.49	-0.15	0.17	-0.19	-0.20	4,5-DOPA dioxygenase extradiol.
42	Os01g0878900	AK104432	1.48	-0.15	0.17	-0.30	-0.18	4,5-DOPA dioxygenase extradiol.
43	Os03g0196500	CI200378	1.48	-0.08	0.06	-0.19	0.22	Cyclin-like F-box domain containing protein.
44	Os01g0166500	AK101697	1.47	-0.07	0.09	-0.22	0.24	Conserved hypothetical protein.
45	Os01g0878900	AK104462	1.46	-0.16	0.15	-0.27	-0.21	4,5-DOPA dioxygenase extradiol.
46	Os11g0139400	AK107562	1.44	-0.16	0.43	-0.17	0.18	Conserved hypothetical protein.
47	Os09g0479900	CI269495	1.42	-0.15	0.27	-0.18	0.04	Peptidase S8 and S53, subtilisin, kexin, sedolisin domain containing protein.
48	Os01g0772100	CI463833	1.39	-0.12	0.34	-0.19	0.23	LOB domain protein 30.
49	Os03g0858800	AK109467	1.38	-0.03	0.17	-0.01	0.40	Multi antimicrobial extrusion protein MatE family protein.
50	Os01g0212400	AK066468	1.37	-0.03	0.15	0.03	0.21	Calcium-binding EF-hand domain containing protein.
51	Os01g0731100	AK106037	1.35	-0.06	0.19	-0.19	0.40	Conserved hypothetical protein.
52	Os08g0280100	AK119420	1.35	-0.02	-0.07	-0.37	0.43	Phytase
53	Os03g0475100	AK105839	1.32	-0.05	0.35	-0.35	0.05	Esterase/lipase/thioesterase domain containing protein.
54	Os05g0574100	AK106699	1.32	-0.38	0.36	-0.36	0.49	Lipase, class 3 family protein.
55	Os11g0255300	AK071495	1.32	-0.27	0.46	-0.09	0.38	Peptidase C1A, papain family protein.
56	Os12g0463300	CI405888	1.31	0.01	0.08	-0.20	0.26	(No Hit)
57	Os08g0124600	CI405888	1.31	0.03	0.09	-0.13	0.26	(No Hit)
58	Os08g0459300	AK060409	1.31	-0.02	0.08	-0.09	0.40	Allergen V5/Tpx-1 related family protein.
59	Os02g0481400	CI405888	1.31	0.02	0.09	-0.14	0.30	(No Hit)
60	Os05g0570700	CI386359	1.30	0.01	0.09	-0.17	0.37	(No Hit)
61	Os04g0280700	CI386359	1.30	0.02	0.09	-0.15	0.29	(No Hit)
62	Os08g0289400	CI405888	1.30	0.04	0.09	-0.19	0.24	Zn-finger, CCHC-type domain containing protein.
63	Os02g0120500	AK119580	1.29	-0.16	0.04	-0.15	0.26	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
64	Os01g0731100	AK109409	1.29	-0.04	0.15	-0.20	0.24	Conserved hypothetical protein.
65	Os02g0577500	CI405888	1.29	0.01	0.08	-0.14	0.32	(No Hit)
66	Os01g0731100	AK061471	1.29	-0.05	0.20	-0.24	0.30	Conserved hypothetical protein.
67	Os02g0766900	Os02g0766900	1.28	-0.16	0.09	-0.67	0.43	Glycoside hydrolase, family 5 protein.
68	Os03g0102700	AK061423	1.28	-0.04	0.11	-0.17	0.43	Beta-expansin precursor.
69	Os07g0164200	CI405888	1.28	0.02	0.10	-0.14	0.29	(No Hit)
70	Os09g0518200	AK121725	1.27	0.17	0.23	-0.14	0.23	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
71	Os06g0151900	AK058759	1.27	-0.04	0.02	0.47	0.39	Hypothetical protein.
72	Os03g0854900	CI386359	1.27	0.02	0.09	-0.15	0.30	(No Hit)
73	Os11g0107400	AK065945	1.27	-0.09	0.36	-0.23	0.24	Nodulin-like domain containing protein.
74	Os01g0281600	AK062646	1.27	-0.15	0.25	-0.28	0.46	Plastocyanin-like domain containing protein.
75	Os11g0134100	Os11g0134100	1.27	-0.07	0.08	-0.37	0.46	Rhamnogalacturonate lyase family protein.
76	Os07g0494400	CI197948	1.27	-0.04	0.22	-0.33	0.17	Protein kinase domain containing protein.
77	Os09g0459300	AK101358	1.27	-0.01	0.14	-0.09	0.42	Allergen V5/Tpx-1 related family protein.
78	Os04g0517900	CI431602	1.27	-0.19	0.51	0.07	0.28	(No Hit)
79	Os04g0517900	CI431602	1.26	-0.20	0.51	0.06	0.36	(No Hit)
80	Os11g0255300	X80876	1.25	-0.25	0.47	-0.09	0.16	Peptidase C1A, papain family protein.
81	Os09g0129500	AK099466	1.25	0.00	0.16	-0.28	0.33	Conserved hypothetical protein.
82	Os09g0518200	AK064395	1.24	0.15	0.18	-0.13	0.24	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
83	Os04g0324100	CI401469	1.23	0.12	0.56	-0.24	0.31	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
84	Os03g0158700	AK071242	1.23	-0.08	0.16	-0.14	0.33	P69C protein.
85	Os02g0656100	AK073462	1.23	-0.11	0.19	-0.21	0.43	Conserved hypothetical protein.
86	Os03g0158700	AK059796	1.23	0.00	0.21	-0.13	0.32	Cholinephosphatase cytidyltransferase.
87	Os01g0142300	AK072289	1.22	-0.01	0.10	-0.05	0.31	Glycosyl transferase, group 1 domain containing protein.
88	Os02g0656100	AK058231	1.22	-0.11	0.20	-0.15	0.50	Conserved hypothetical protein.
89	Os01g0388700	AK071508	1.22	-0.22	0.41	-0.05	0.21	Protein of unknown function DUF679 family protein.
90	Os08g0556900	AK099308	1.22	-0.44	-0.03	0.10	-0.19	Cysteine proteinase (EC 3.4.22.-).
91	Os01g0142300	AK060202	1.22	-0.03	0.11	-0.10	0.48	Glycosyl transferase, group 1 domain containing protein.
92	Os03g0644400	AB022783	1.21	-0.11	0.29	-0.27	0.50	Amino acid permease.
93	Os01g0784800	AK059820	1.21	-0.19	0.14	-0.14	0.13	Minor allergen.
94	Os03g0644400	AK062005	1.20	-0.11	0.30	-0.27	0.47	Amino acid permease.
95	Os08g0556900	AK105612	1.20	-0.45	-0.01	-0.21	-0.16	Cysteine proteinase (EC 3.4.22.-).
96	Os08g0280100	AK072150	1.20	-0.06	0.01	-0.11	0.28	Phytase.
97	Os08g0470200	AK059773	1.20	-0.10	0.14	-0.12	0.37	Carbonic anhydrase, eukaryotic family protein.
98	Os11g0156200	AK100124	1.20	-0.01	0.05	-0.06	0.04	Peptidase S28 family protein.
99	Os01g0297700	AK106554	1.19	-0.18	0.23	0.05	0.16	Protein of unknown function DUF6 domain containing protein.
100	Os01g0784800	AK104580	1.19	-0.19	0.05	-0.13	0.30	Minor allergen.
101	Os02g0120500	AK106761	1.19	-0.14	0.00	0.02	0.44	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
102	Os04g0529100	AK107680	1.18	-0.34	0.43	-0.02	0.23	AP2 domain containing protein RAP2.4 (Fragment).
103	Os12g0568500	CI549138	1.18	-0.16	0.10	-0.33	0.02	Metallothionein-like protein type 1.
104	Os08g0556900	AK072235	1.17	-0.44	-0.02	-0.17	-0.16	Cysteine proteinase (EC 3.4.22.-).
105	Os02g0773200	AK108499	1.17	0.03	0.15	-0.01	0.21	Universal stress protein (Usp) family protein.
106	Os04g0100300	CI346974	1.17	-0.04	0.08	-0.13	0.22	Actin-binding FH2 domain containing protein.
107	Os03g0644400	AK067118	1.16	-0.10	0.29	-0.25	0.30	Amino acid permease.
108	Os06g095400	AK073198	1.16	-0.35	0.22	-0.05	0.26	Haem peroxidase, plant/fungal/bacterial family protein.
109	Os09g0483100	AK107051	1.15	-0.26	0.26	-0.18	0.20	Calcium-binding EF-hand domain containing protein.
110	Os11g0249600	AK065749	1.15	-0.07	0.04	-0.12	0.14	Polygalacturonase C (Fragment).
111	Os02g0765600	M24286	1.15	-0.30	0.46	-0.13	0.45	RAMy1A
112	Os02g0740400	AK113660	1.15	-0.19	0.14	-0.09	0.67	Lipolytic enzyme, G-D-S-L family protein.
113	Os03g0327800	CI362055	1.14	-0.22	0.10	-0.14	0.03	NAC-domain containing protein 29 (ANAC029) (NAC2) (NAC-LIKE, ACTIVATED BY AP3/PI protein) (NAP).
114	Os12g0244400	AK070297	1.14	-0.04	0.05	-0.03	-0.06	Amino acid/polyamine transporter II family protein.
115	Os11g0109700	AK072035	1.14	-0.02	0.10	-0.01	0.20	Uncharacterized Cys-rich domain containing protein.
116	Os01g0801500	AK060529	1.14	-0.04	0.03	-0.28	0.25	Beta-1,3-glucanase precursor.
117	Os11g0109700	AK120107	1.13	-0.03	0.10	-0.01	0.19	Uncharacterized Cys-rich domain containing protein.
118	Os02g0115900	AK065749	1.13	-0.14	0.04	-0.19	0.25	Endosperm luminal binding protein.
119	Os02g0765600	AK101744	1.13	-0.29	0.44	-0.15	0.23	RAMy1A
120	Os02g0115900	AK119653	1.13	-0.12	0.04	-0.18	0.14	Endosperm luminal binding protein.
121	Os11g0109700	AK065601	1.13	-0.03	0.08	-0.04	0.30	Uncharacterized Cys-rich domain containing protein.
122	Os02g0771400	Os02g0771400	1.12	-0.03	-0.01	-0.16	0.17	Putative tyrosine phosphatase family protein.
123	Os04g0124000	AK111482	1.12	-0.07	0.10	-0.21	0.22	Hypothetical protein.
124	Os03g0238600	AK070684	1.12	-0.02				

137	Os06g0647200	Os06g0647200	1.10	-0.11	0.10	-0.19	-0.10	Response regulator receiver domain containing protein.
138	Os2g0533400	AY364310	1.10	-0.03	0.00	-0.19	0.35	Rac GTPase activating protein 1.
139	Os03g0406100	C1226571	1.10	-0.03	0.00	-0.09	0.22	SPX, N-terminal domain containing protein.
140	Os01g0699900	AK067766	1.09	-0.07	-0.02	-0.26	0.35	AWP/M-19-like family protein.
141	Os01g0254800	AK121241	1.09	-0.01	0.18	-0.13	0.47	Conserved hypothetical protein.
142	Os03g0150500	AK106894	1.09	-0.20	0.34	-0.06	0.37	Phosphate transporter 6.
143	Os12g0566000	AK060451	1.09	-0.12	0.56	-0.15	0.09	HCO3-transporter domain containing protein.
144	Os12g0637000	CI495215	1.09	-0.01	0.03	-0.13	0.06	Purple acid phosphatase precursor (EC 3.1.3.2).
145	Os04g0445000	AK105506	1.08	-0.12	0.45	0.00	0.46	Potassium channel SKOR (Stellar K+) outward rectifying channel).
146	Os03g0248600	AK104877	1.08	-0.01	0.22	0.01	0.26	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho- D-glycerate hydro-lyase 2).
147	Os12g0564500	CI228796	1.07	-0.08	0.08	0.00	0.22	(No Hit)
148	Os05g0578800	AK070644	1.07	-0.17	0.25	-0.09	0.30	MAP kinase homologue.
149	Os01g0734800	AK102415	1.05	-0.01	0.15	-0.25	-0.02	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
150	Os02g0163800	CI228796	1.07	-0.09	0.03	-0.03	0.45	Peptidase aspartic family protein.
151	Os12g0566000	AK070617	1.07	-0.13	0.55	-0.13	0.19	HCO3-transporter domain containing protein.
152	Os01g0788800	AK061235	1.07	-0.03	0.10	-0.22	0.33	Conserved hypothetical protein.
153	Os05g0376700	CI228796	1.06	-0.07	0.05	-0.03	0.23	Zn-finger, CCHC type domain containing protein.
154	Os12g0288500	CI228796	1.06	-0.07	0.03	-0.03	0.46	(No Hit)
155	Os03g0369100	AK111061	1.06	-0.05	0.13	-0.55	0.16	Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor domain containing protein.
156	Os01g0361700	CI513118	1.06	-0.21	0.21	-0.10	0.48	Phospholipid/glycerol acyltransferase family protein.
157	Os03g0252000	AK061420	1.05	-0.01	0.17	-0.13	0.39	Conserved hypothetical protein.
158	Os03g0246100	AK106861	1.05	0.01	0.24	-0.19	0.41	Glycoside hydrolase, family 17 protein.
159	Os05g0376100	CI228796	1.05	-0.09	0.04	-0.04	0.49	(No Hit)
160	Os01g0734800	AK061830	1.05	0.30	-0.13	-0.05	0.27	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
161	Os03g0832200	AK070712	1.05	-0.14	-0.10	-0.30	0.33	Calcium-binding protein precursor (Calreticulin).
162	Os09g0500800	CI228796	1.05	-0.08	0.05	-0.04	0.46	(No Hit)
163	Os04g0636400	AK061848	1.04	-0.08	0.08	-0.09	0.33	CEL I mismatch endonuclease.
164	Os04g0125500	AK072127	1.04	-0.10	0.20	-0.12	0.33	Oligopeptide transporter OPT superfamily protein.
165	Os11g0131800	Os11g0131800	1.01	-0.18	0.11	-0.18	0.01	Zn-finger, DHHC type domain containing protein.
166	Os01g0161800	AK120881	1.04	0.03	0.22	-0.19	0.16	Cholinephosphate cytidyltransferase.
167	Os03g0248600	AK073611	1.03	0.00	0.22	0.01	0.48	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho- D-glycerate hydro-lyase 2).
168	Os03g0145900	AK120297	1.03	-0.20	0.31	-0.05	0.28	PGPD14.
169	Os01g0248900	AK111100	1.03	-0.24	0.27	-0.25	0.10	Expansin EXPA5.
170	Os02g0720900	AK061307	1.02	-0.05	0.32	-0.06	0.14	Peptidase A1, pepsin family protein.
171	Os02g0765300	M81143	1.02	-0.27	0.36	-0.13	0.44	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (isozyme 1B).
172	Os02g0514500	AK064485	1.02	0.05	0.18	-0.05	0.29	Glycerophosphoryl diester phosphodiesterase family protein.
173	Os10g0355900	AK105318	1.02	-0.10	-0.07	-0.08	0.00	Beta-expansin precursor.
174	Os10g0569300	CI224473	1.02	-0.14	0.22	-0.05	0.40	Serine carboxypeptidase II chains A and B (EC 3.4.16.6) (Carboxypeptidase D) (CPDW-II) (CP-WII).
175	Os12g0136100	CI144901	1.01	-0.16	0.37	-0.20	0.42	Conserved hypothetical protein.
176	Os11g0432600	AK059916	1.01	-0.05	0.16	-0.32	0.34	Beta-ketoacyl reductase GL8B.
177	Os08g0470200	AK060039	1.01	-0.10	0.12	-0.10	0.21	Carbonic anhydrase, eukaryotic family protein.
178	Os03g0850700	AK099525	1.01	-0.10	0.11	-0.20	0.44	Phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein.
179	Os06g0590700	CI396619	1.00	-0.09	0.09	-0.10	0.11	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
180	Os03g0414100	AK100586	1.00	-0.03	0.12	-0.08	0.14	Hypothetical protein.
181	Os08g0241300	AK108203	1.00	-0.08	0.22	-0.12	0.34	Conserved hypothetical protein.
182	Os02g0809800	AK073760	0.99	-0.11	0.22	-0.02	0.44	SPX, N-terminal domain containing protein.
183	Os10g0550500	AK064698	0.99	-0.02	0.04	-0.08	0.07	Pectinacetylesterase.
184	Os12g0597000	AK111887	0.99	-0.08	0.28	-0.02	0.23	Calcineurin B-like protein 3.
185	Os05g0476000	AK073548	0.99	-0.05	0.09	-0.21	-0.05	Hypothetical protein.
186	Os03g0850700	AK061542	0.99	-0.12	0.12	-0.24	0.38	Phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein.
187	Os03g0327600	X95402	0.99	-0.03	0.12	-0.11	0.39	Ricin B-related lectin domain containing protein.
188	Os06g0168700	AK101305	0.98	0.02	0.08	-0.06	0.18	Prolin rich protein.
189	Os06g0634800	CI275354	0.98	-0.12	0.23	-0.23	-0.15	(No Hit)
190	Os05g0712700	AF077760	0.98	-0.01	0.06	-0.15	0.35	MADS-box protein SPW1.
191	Os10g0162200	CI517494	0.98	-0.32	0.16	-0.25	-0.29	(No Hit)
192	Os09g0466300	AK102696	0.98	-0.05	-0.03	-0.21	-0.03	GRAM domain containing protein.
193	Os03g0248600	AK099342	0.98	0.00	0.21	0.01	0.43	Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho- D-glycerate hydro-lyase 2).
194	Os06g0125500	AF393848	0.97	-0.10	0.17	-0.20	0.19	Oligopeptide transporter OPT superfamily protein.
195	Os12g0131200	Os12g0131200	0.97	-0.17	0.12	0.06	-0.14	Zinc finger DHHC domain containing protein 7 (Sertoli cell gene with a zinc finger domain protein).
196	Os06g0712700	AK069317	0.97	0.00	0.00	-0.17	0.30	MADS-box protein SPW1.
197	Os07g0685500	AK078883	0.97	-0.31	0.42	-0.17	0.42	Alpha/beta hydrolase family protein.
198	Os08g0617800	AK106178	0.96	-0.25	0.22	-0.13	0.19	Nicotianamine plant-specific domain containing protein.
199	Os12g0511500	AK070722	0.96	-0.06	0.32	0.01	-0.10	UBS-RLR protein (Fragment).
200	Os01g0798500	AK109346	0.96	0.07	0.10	-0.07	0.20	Methyladenine glycosylase family protein.
201	Os04g0586000	CI252201	0.96	-0.04	0.33	0.12	0.23	Protein of unknown function DUF581 family protein.
202	Os04g0581600	AK101692	0.96	-0.05	0.43	-0.04	0.13	UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH).
203	Os01g0869200	AK073453	0.96	-0.21	0.34	-0.14	-0.13	Mg2+ transporter protein, Cora-like family protein.
204	Os12g0566000	AY339063	0.96	-0.12	0.50	-0.22	0.10	HCO3-transporter domain containing protein.
205	Os03g0850700	AK062083	0.95	-0.09	0.11	-0.19	0.27	Phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein.
206	Os03g0292700	Os03g0292700	0.95	-0.14	0.29	0.17	0.00	Protein kinase domain containing protein.
207	Os12g0511500	AK105219	0.95	-0.23	0.02	-0.34	-0.24	Plant metallothionein, family 15 protein.
208	Os03g0332900	AK103073	0.95	-0.03	0.18	-0.20	0.11	Protein kinase domain containing protein.
209	Os04g0137100	CI126462	0.95	-0.04	0.14	-0.12	0.26	Pectate lyase (Fragment).
210	Os08g0473600	AK064071	0.95	-0.36	0.52	-0.44	0.30	RAMy3E
211	Os03g0687700	AK119706	0.95	-0.16	0.01	-0.15	0.08	Ribosome-inactivating protein family protein.
212	Os08g0293900	AK105200	0.94	0.02	0.01	-0.01	0.45	Conserved hypothetical protein.
213	Os03g0655400	D26538	0.94	-0.23	0.15	-0.09	0.22	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
214	Os03g0655400	AF010584	0.94	-0.23	0.15	-0.10	0.15	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
215	Os11g0101300	AK069389	0.94	-0.07	0.07	-0.07	0.19	Ubiquitin-like Cys-rich domain containing protein.
216	Os03g0655400	AB011368	0.94	-0.22	0.14	-0.11	0.34	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
217	Os10g0476500	AK110990	0.93	-0.09	0.10	-0.12	0.22	Conserved hypothetical protein.
218	Os10g0498000	AK071470	0.93	-0.01	0.18	-0.23	0.38	Epoxide hydrolase.
219	Os02g0665800	CI546463	0.93	0.00	0.03	-0.09	-0.01	Protein kinase domain containing protein.
220	Os03g0655400	AK059150	0.93	-0.22	0.15	-0.10	0.29	CAS15 (Cold acclimation responsive protein BudCAR4) (Cold acclimation responsive protein BudCAR6).
221	Os05g0215300	CI234132	0.93	0.09	0.09	-0.05	0.28	(No Hit)
222	Os03g0238600	AK104751	0.92	-0.01	0.09	-0.09	0.13	Purple acid phosphatase.
223	Os01g0594300	AK105268	0.92	-0.24	0.12	0.12	0.22	Extensin-like protein.
224	Os03g0238600	AK119619	0.91	-0.01	0.08	-0.08	0.17	Purple acid phosphatase.
225	Os03g0238600	AK104621	0.91	-0.02	0.08	-0.09	0.03	Purple acid phosphatase.
226	Os02g0720900	AK072228	0.91	0.02	0.28	0.09	0.33	Peptidase A1, pepsin family protein.
227	Os03g0124900	AK070284	0.91	-0.15	0.36	-0.17	0.25	Glycoside hydrolase, family 28 protein.
228	Os04g0615000	AK064014	0.91	-0.07	0.14	-0.11	-0.04	Hypothetical protein.
229	Os06g0220300	AU095433	0.91	-0.16	0.19	-0.15	0.03	Phi-1 protein.
230	Os07g0689600	AK078556	0.90	0.04	0.01	0.01	0.16	Nicotianamine synthase 9 (EC 2.5.1.43) (S-adenosyl-L-methionine:S-adenosyl-L-methionine:S-adenosyl-methionine 3-amino-3- carboxypropyltransferase 9).
231	Os03g0689600	AK069389	0.89	-0.14	0.09	0.08	0.30	Ubiquitin-like F-box domain containing protein.
232	Os07g0689600	AB023819	0.90	0.03	0.01	0.02	0.17	Nicotianamine synthase 9 (EC 2.5.1.43) (S-adenosyl-L-methionine:S-adenosyl-L-methionine:S-adenosyl-methionine 3-amino-3- carboxypropyltransferase 9).
233	Os03g0216700	AK101556	0.90	-0.13	0.36	0.03	0.22	Multi antimicrobial extension protein MatE family protein.
234	Os11g0700400	Os11g0700400	0.90	-0.03	0.10	-0.01	0.17	Hypothetical protein.
235	Os04g0176400	CI096496	0.90	-0.01	0.04	-0.18	0.10	Peptidase S10, serine carboxypeptidase family protein.
236	Os01g0357400	D10417	0.90	-0.26	0.34	-0.12	0.08	RAMy1B
237	Os02g0720900	AK061628	0.90	0.04	0.28	0.10	0.37	Peptidase A1, pepsin family protein.
238	Os04g0608300	AK111353	0.89	-0.01	-0.01	-0.17	0.44	Auxin responsive SAUR protein family protein.
239	Os03g0689600	AK069389	0.89	-0.14	0.02	0.17	0.11	Ribosome-inactivating protein family protein.
240	Os03g0685300	AK071046	0.89	-0.01	0.20	-0.02	0.36	Glutamine amidotransferase class-I domain containing protein.
241	Os02g0720900	AK099781	0.89	0.03	0.30	0.10	0.28	Peptidase A1, pepsin family protein.
242	Os01g0128200	AK059608	0.89	-0.18	0.16	0.05	0.18	Bifunctional nuclease.
243	Os11g0216000	AK101789	0.89	0.07	0.02	0.03	-0.08	Pyruvate kinase family protein.
244	Os01g0743200	AK105996	0.89	-0.03	0.03	-0.16	0.18	Pectinesterase family protein.
245	Os02g0661900	AK061447	0.89	-0.10	0.19	-0.07	0.32	Conserved hypothetical protein.
246	Os07g0153800	Os07g0153800	0.89	-0.21	0.26	-0.12	-0.32	Esterase/lipase/thioesterase domain containing protein.
247	Os04g0493000	AK063073	0.89	-0.04	0.29	-0.21	0.51	Plant invertase/pectin methyltransferase inhibitor domain containing protein.
248	Os01g0743200	AK073604	0.88	-0.05	0.02	-0.09	0.16	Pectinesterase family protein.
249	Os03g0373100	AK107517	0.88	-0.04	0.03	-0.11	0.24	Conserved hypothetical protein.
250	Os02g0524500	CI250458	0.88	0.04	0.23	-0.16	-0.02	Zn-finger, RING domain containing protein.
251	Os04g0483200	AK069389	0.88	-0.09	0.18	-0.17	0.39	Conserved hypothetical protein.
252	Os02g0613900	AK070784	0.88	0.02	0.35	-0.12	0.05	Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT).
253	Os12g0151500	AK105865	0.88	0.04	0.17	-0.08	0.14	Glycosyl transferase, family 29 protein.
254	Os04g0404900	AK107531	0.88	-0.21	0.21	-0.07	0.17	Conserved hypothetical protein.
255	Os05g0589700	AK069389	0.88	-0.07	0.10	-0.49	0.27	Dual-specific kinase DSK1.
256	Os10g0135300	AK104301	0.88	-0.04	0.18	-0.11	0.04	Cyclin-like F-box domain containing protein.
257	Os04g0489							

275	Os11g0199200	AK059538	0.86	-0.05	0.11	-0.05	0.33	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI).
276	Os06g0712700	AB003323	0.85	0.01	0.02	-0.11	0.25	MADS-box protein SPW1.
277	Os10g0555900	AK100959	0.85	-0.08	-0.06	-0.02	0.00	Beta-expansin precursor.
278	Os07g0909600	CJ394303	0.85	-0.03	0.38	-0.02	0.14	Amino acid/polyamine transporter II family protein.
279	Os01g0653400	AK068670	0.85	-0.34	0.43	0.00	0.42	Hypothetical protein.
280	Os01g0733500	AK059056	0.85	-0.19	0.18	-0.36	0.49	Dehydration-responsive protein RD22 precursor.
281	Os08g0248500	Os08g0248500	0.85	0.00	0.06	-0.07	0.17	Zn-finger, CCHC type domain containing protein.
282	Os03g0795300	AK064239	0.84	-0.04	0.02	0.04	-0.04	Extensin protein-like.
283	Os12g0117100	AK059932	0.84	-0.10	0.32	0.00	0.15	Alpha/beta hydrolase fold domain containing protein.
284	Os10g0563000	AK072479	0.84	0.04	-0.21	-0.19	0.37	Palmitoyl protein thioesterase family protein.
285	Os10g0199200	AB039278	0.84	-0.04	0.10	-0.06	0.32	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI).
286	Os09g0562600	AK071877	0.84	-0.36	0.42	-0.13	0.33	OCL3 protein.
287	Os01g0653400	AK068670	0.83	-0.14	0.27	0.00	0.08	Conserved hypothetical protein.
288	Os07g0565700	AK111937	0.83	0.00	0.06	-0.07	0.19	Alpha/beta hydrolase family protein.
289	Os03g0250200	AK058393	0.83	0.00	0.19	0.00	0.25	Pathogenicity protein PATH531-like protein.
290	Os09g0390800	CJ453322	0.83	-0.13	0.17	-0.28	0.10	(No Hit)
291	Os02g0655200	AY339378	0.83	-0.05	0.11	-0.08	0.21	Ethylene responsive element binding factor3 (OsERF3).
292	Os01g0767600	AK070672	0.83	-0.03	0.18	0.02	0.29	Conserved hypothetical protein.
293	Os06g0127900	AK073063	0.83	-0.02	0.00	-0.09	0.24	Ribonucleoside-diphosphate reductase small chain (EC 1.17.4.1) (Ribonucleotide reductase R2 subunit).
294	Os01g0868900	AK099469	0.83	-0.26	0.48	-0.20	0.26	Proteinase inhibitor I9, subtilisin propeptide domain containing protein.
295	Os05g0479000	AK111029	0.83	-0.08	0.19	-0.06	0.14	Zn-finger, RING domain containing protein.
296	Os03g0269300	AK111855	0.82	-0.10	0.15	-0.12	0.26	Protein kinase domain containing protein.
297	Os12g0106500	CJ139357	0.82	-0.01	0.08	0.00	0.20	Nodulin-like domain containing protein.
298	Os06g0284500	CJ138873	0.82	-0.11	0.33	-0.06	0.01	Zn-finger, Dof type domain containing protein.
299	Os02g0694100	CJ279422	0.82	-0.04	0.21	-0.11	0.34	Cyclin-like F-box domain containing protein.
300	Os08g0174500	AY062182	0.82	-0.31	0.39	-0.09	0.31	HAP3.
301	Os03g0597600	AK069458	0.82	0.08	0.15	0.11	0.28	L-asparaginase (EC 3.5.1.1) (L-asparagine amidohydrolase).
302	Os08g0605000	AK119519	0.82	-0.12	0.28	0.04	0.02	Peptidase S10, serine carboxypeptidase family protein.
303	Os03g0533000	AK068114	0.82	-0.09	0.22	-0.01	0.16	Conserved hypothetical protein.
304	Os03g0785800	AB071806	0.82	-0.04	0.03	-0.20	0.11	Transcription factor PGR8 (Fragment).
305	Os05g0209600	AK100289	0.82	-0.07	-0.01	-0.17	0.42	Lipolytic enzyme, G-D-S-L family protein.
306	Os04g0619300	AK065137	0.81	-0.07	0.07	-0.15	0.16	Cyclin-like F-box domain containing protein.
307	Os01g0292200	AK065588	0.81	-0.17	0.34	-0.12	0.22	CBL-interacting protein kinase 1.
308	Os05g0209600	AK059511	0.81	-0.07	-0.01	-0.17	0.45	Lipolytic enzyme, G-D-S-L family protein.
309	Os06g0208200	CJ251401	0.81	-0.08	0.01	-0.15	0.25	(No Hit)
310	Os04g0619300	AK061943	0.81	-0.08	0.08	-0.15	0.20	Cyclin-like F-box domain containing protein.
311	Os03g0360300	CJ201609	0.81	-0.25	0.12	0.03	0.27	(No Hit)
312	Os06g0591900	AK069274	0.81	-0.07	0.06	0.17	0.20	UDP-galactose/UDP-glucose transporter.
313	Os07g0565700	AK112115	0.81	0.00	0.05	-0.09	0.24	Alpha/beta hydrolase family protein.
314	Os10g0555900	AF261271	0.81	-0.08	-0.08	-0.11	-0.07	Beta-expansin precursor.
315	Os01g0868900	AK099470	0.81	-0.28	0.47	-0.15	0.22	Proteinase inhibitor I9, subtilisin propeptide domain containing protein.
316	Os02g0252400	AB028131	0.81	-0.05	0.28	-0.05	0.07	Zn-finger, Dof type domain containing protein.
317	Os07g0296000	AK073416	0.81	-0.27	0.27	0.05	0.48	Conserved hypothetical protein.
318	Os05g0209600	AY580163	0.81	-0.07	-0.02	-0.17	0.34	Lipolytic enzyme, G-D-S-L family protein.
319	Os02g0252400	AK107294	0.81	-0.04	0.27	-0.05	0.06	Zn-finger, Dof type domain containing protein.
320	Os03g0439800	CJ293977	0.81	-0.05	0.30	0.05	-0.16	Protein of unknown function DUF1218 family protein.
321	Os05g0593100	AK071175	0.81	-0.07	0.06	-0.16	0.28	UDP-galactose/UDP-glucose transporter.
322	Os05g0310500	AK059697	0.81	0.01	0.12	0.03	0.26	Cathepsin B (Fragment).
323	Os02g0681100	AK100584	0.80	0.03	0.08	0.06	0.20	Protein of unknown function DUF604 family protein.
324	Os12g0278700	AK071421	0.80	0.18	-0.08	0.08	-0.10	Cytosin homolog.
325	Os11g0216000	AK060466	0.80	0.02	-0.04	0.07	0.07	Pyruvate kinase family protein.
326	Os01g0868600	AK070098	0.80	-0.08	0.09	-0.04	0.17	CLP protease regulatory subunit CLPX precursor.
327	Os11g0236100	CJ158157	0.80	-0.18	0.28	-0.26	0.14	Sucrose-phosphate synthase (EC 2.4.1.14).
328	Os09g0161900	AK106234	0.80	-0.05	0.14	0.00	0.29	Actin-crosslinking proteins family protein.
329	Os01g0357200	AK099419	0.80	0.02	0.27	-0.04	0.09	Conserved hypothetical protein.
330	Os09g0494600	AK107667	0.80	-0.14	0.20	0.11	0.16	Protein of unknown function DUF599 family protein.
331	Os01g0580200	AK103045	0.80	-0.06	0.10	-0.01	0.14	Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-galactosidase) (Exo-(1->4)-beta-D-galactanase).
332	Os07g0605400	AK103128	0.80	-0.11	0.26	-0.03	0.35	Conserved hypothetical protein.
333	Os04g0504000	AK121982	0.79	0.00	0.29	-0.10	-0.11	Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT).
334	Os03g0196400	CJ428136	0.79	0.02	0.35	-0.10	-0.17	Protein of unknown function DUF588 family protein.
335	Os08g0142500	CJ476796	0.79	-0.01	0.14	-0.03	0.02	(No Hit)
336	Os05g0209600	AK069274	0.79	-0.07	0.30	0.05	-0.16	No apical meristem (NAM) protein domain containing protein.
337	Os01g0594300	AK105670	0.79	-0.20	0.11	0.20	0.12	Extensin-like protein.
338	Os09g0473900	CJ016216	0.79	0.01	-0.07	-0.07	0.15	Viral coat and capsid protein family protein.
339	Os03g0769500	AK107501	0.79	-0.14	0.29	-0.30	-0.21	Calcium-binding EF-hand domain containing protein.
340	Os08g0517400	CJ483079	0.79	-0.06	0.01	0.06	0.28	(No Hit)
341	Os03g0250200	AK068940	0.79	-0.02	0.18	-0.05	0.25	Pathogenicity protein PATH531-like protein.
342	Os01g0292200	AK061640	0.79	-0.15	0.33	-0.13	0.25	CBL-interacting protein kinase 1.
343	Os02g0740500	AJ094334	0.78	-0.06	0.07	-0.08	0.41	Conserved hypothetical protein.
344	Os03g0176700	AK061759	0.78	-0.26	0.21	-0.09	-0.10	Lipoxygenase, L42 domain containing protein.
345	Os10g0502100	AK063028	0.78	-0.01	0.22	-0.06	-0.01	Conserved hypothetical protein.
346	Os01g0892400	CJ191737	0.78	-0.09	0.29	-0.10	-0.15	Pectinacetyltransferase family protein.
347	Os10g0390900	Os10g0390900	0.78	-0.15	0.28	0.03	0.25	Synaptotagmin, N-terminal domain containing protein.
348	Os08g0451700	AK102108	0.78	-0.20	0.06	-0.16	0.27	Conserved hypothetical protein.
349	Os05g0156500	AK062718	0.78	-0.09	0.08	-0.10	0.30	Apobec-1 binding protein 2.
350	Os05g0516400	AK110196	0.78	-0.10	0.15	-0.04	0.34	Pistil-specific extensin-like protein family protein.
351	Os01g0292200	AK068440	0.78	-0.14	0.33	-0.13	0.27	CBL-interacting protein kinase 1.
352	Os12g0236400	D10334	0.78	-0.02	0.16	-0.05	0.23	Adenylate kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
353	Os01g0868900	AK070098	0.78	-0.03	0.27	-0.07	0.09	Protein kinase 3.
354	Os04g0556000	AK063759	0.78	-0.02	0.05	-0.09	0.16	Copper-translocating P-type ATPase family protein.
355	Os05g0132100	AK069689	0.78	-0.05	0.09	-0.09	0.08	AMP-dependent synthetase and ligase domain containing protein.
356	Os10g0415200	AK068567	0.78	0.01	0.15	-0.13	0.24	Exocyst complex subunit Sec15-like family protein.
357	Os03g0114400	AK108730	0.78	-0.03	0.05	-0.28	-0.26	AAAATPase, central region domain containing protein.
358	Os05g0367800	Os05g0367800	0.77	-0.13	0.01	-0.06	-0.08	Luminal binding protein 2 precursor (BiP2) (Heat shock protein 70 homolog 2) (B70) (B70).
359	Os12g0566000	AK100510	0.77	-0.08	0.34	0.02	0.26	HCO3-transporter domain containing protein.
360	Os08g0230600	AK120197	0.77	-0.21	0.36	0.15	0.10	No apical meristem (NAM) protein domain containing protein.
361	Os01g0770800	AK109200	0.77	0.00	0.05	-0.11	0.47	Cir copper transporter family protein.
362	Os06g0150400	AK067407	0.77	-0.06	0.09	-0.12	0.22	Saposin B domain containing protein.
363	Os01g0868900	AK062271	0.77	-0.25	0.46	-0.13	0.23	Proteinase inhibitor I9, subtilisin propeptide domain containing protein.
364	Os01g0763600	AK061563	0.77	-0.03	0.15	-0.05	0.41	Glycerophosphoryl diester phosphodiesterase family protein.
365	Os08g0260600	AK108529	0.77	-0.09	0.03	-0.10	0.01	Senescence-associated protein 5.
366	Os09g0526700	AK073610	0.77	-0.10	0.16	0.04	-0.11	UDP-Glucose 4-epimerase (EC 5.1.3.2).
367	Os04g0684800	AK058755	0.77	-0.05	0.39	0.04	0.42	Ubiquitin-conjugating enzymes domain containing protein.
368	Os12g0129300	AK062739	0.77	-0.09	0.22	-0.06	0.26	Arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II.
369	Os05g0564900	AK104677	0.77	-0.11	0.16	0.05	0.03	UDP-Glucose 4-epimerase (EC 5.1.3.2).
370	Os06g0208200	CJ152834	0.76	-0.10	0.04	-0.13	0.19	(No Hit)
371	Os04g0605500	AK120057	0.76	-0.11	-0.01	-0.08	0.26	Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 8).
372	Os01g0283300	AK104803	0.76	-0.15	0.31	-0.15	0.28	Hypothetical protein.
373	Os01g0561600	AK069494	0.76	-0.07	-0.42	-0.39	0.00	Cytochrome P450 family protein.
374	Os10g0560000	AK066334	0.76	0.06	0.15	0.02	0.34	Plant protein of unknown function DUF828 family protein.
375	Os03g0212800	AY129294	0.76	-0.26	0.26	0.00	0.15	Beta-glucosidase.
376	Os02g0136400	CB838965	0.76	0.03	-0.02	0.05	0.11	Conserved hypothetical protein.
377	Os12g0564900	AK126607	0.75	-0.21	0.16	-0.03	0.29	Hypothetical protein.
378	Os10g0244400	CJ475611	0.75	-0.05	0.03	0.03	0.03	(No Hit)
379	Os02g0710900	AK100997	0.75	-0.06	0.07	-0.10	0.21	Heat shock protein Hsp70 family protein.
380	Os04g0223900	CJ103951	0.75	0.01	0.10	-0.04	0.36	Conserved hypothetical protein.
381	Os06g0165800	AK065744	0.75	-0.06	0.04	-0.10	-0.03	Caffeoyl-CoA O-methyltransferase 5 (EC 2.1.1.104) (Trans-caffeoyl-CoA 3-O-methyltransferase 5) (CCoAMT-5) (CCoAMT-5).
382	Os01g0878400	AK073884	0.75	-0.01	0.18	0.04	-0.08	Amino acid/polyamine transporter II family protein.
383	Os12g0236400	AK069870	0.75	-0.01	0.17	-0.04	0.33	Adenylate kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
384	Os08g0164400	CJ566798	0.75	-0.03	0.16	-0.04	0.12	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
385	Os04g0527400	AK066591	0.75	-0.03	0.07	0.10	0.22	Conserved hypothetical protein.
386	Os01g0283300	AK106177	0.75	-0.15	0.32	-0.15	0.26	Hypothetical protein.
387	Os04g0527400	AK060660	0.75	-0.03	0.07	0.07	0.23	Conserved hypothetical protein.
388	Os05g0110800	AK104935	0.75	-0.22	0.31	0.01	0.09	Conserved hypothetical protein.
389	Os04g0556000	AK072990	0.75	0.00	0.12	-0.08	0.01	Copper-translocating P-type ATPase family protein.
390	Os01g0892600	AK064882	0.75	-0.09	0.28	-0.09	0.04	Pectinacetyltransferase family protein.
391	Os01g0707500	AK100208	0.75	-0.09	0.33	0.13	0.15	Transcription factor.
392	Os12g0236400	AK059754	0.75	-0.02	0.17	-0.06	0.32	Adenylate kinase A (EC 2.7.4.3) (ATP-AMP transphosphorylase).
393	Os07g0964900	AK109437	0.75	-0.01	0.05	-0.14	0.47	Esterase/lipase/thioesterase domain containing protein.
394	Os02g0441000	AK108073	0.75	0.03	0.05	-0.04	0.27	Conserved hypothetical protein.
395	Os08g0451700	AK101935	0.75	-0.18	0.06	-0.13	0.18	Conserved hypothetical protein.
396	Os03g0311600	AK103709	0.75	0.0				

413	Oso5g0324700	AK063581	0.74	-0.10	-0.18	0.11	0.09	Hypothetical protein.
414	Oso5g0574300	AU097673	0.73	-0.10	0.26	-0.02	0.45	Histone H2B.2.
415	Oso1g0866200	C1027348	0.73	0.06	-0.01	0.06	0.37	Histone H3.
416	Oso5g0422900	AK120080	0.73	0.00	0.12	-0.08	0.22	Phosphatidylinositol-4-phosphate 5-kinase family protein.
417	Oso1g0911300	AJ557138	0.73	-0.10	0.36	-0.05	-0.03	TGF-beta receptor, type III extracellular region family protein.
418	Oso1g0636900	AK067056	0.73	0.00	0.14	-0.22	0.16	Conserved hypothetical protein.
419	Oso8g0517300	AK107181	0.73	-0.03	0.02	0.17	0.34	Conserved hypothetical protein.
420	Oso4g0196200	C1443816	0.73	-0.04	0.36	0.07	0.06	O-methyltransferase, family 2 domain containing protein.
421	Oso5g0110800	AK067749	0.73	-0.22	0.31	-0.01	0.05	Conserved hypothetical protein.
422	Oso3g0793000	AK108205	0.73	-0.04	0.10	-0.02	0.25	Zn-finger, A20-like domain containing protein.
423	Oso1g0693300	AK101201	0.73	0.04	-0.11	-0.15	-0.38	Lipid phosphate phosphatase 2 (EC 3.1.3.-) (ATLPP2) (Phosphatidic acid phosphatase 2) (ATPAP2) (Prenyl diphosphate phosphatase).
424	Oso4g0412300	AK110902	0.73	-0.05	0.05	-0.17	0.24	Glycoside hydrolase, family 17 protein.
425	Oso5g0216300	AJ557138	0.73	-0.10	0.36	-0.05	-0.03	Oxo-phytydienic acid reductase (12-oxophytodienoic acid reductase).
426	Oso7g0425000	AK108531	0.73	0.04	0.17	-0.08	0.28	Conserved hypothetical protein.
427	Oso6g0216300	AB040743	0.72	0.19	-0.08	0.13	0.15	Oxo-phytydienic acid reductase (12-oxophytodienoic acid reductase).
428	Oso12g0562000	AY072714	0.72	-0.20	0.14	-0.04	0.46	Hypothetical protein.
429	Oso3g0712700	AK121196	0.72	-0.05	0.17	-0.15	0.28	Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2).
430	Oso4g0598800	AK111623	0.72	-0.03	0.30	-0.17	-0.46	Wall-associated kinase-like protein.
431	Oso6g0216200	AU092237	0.72	0.18	-0.08	0.10	-0.04	Oxo-phytydienic acid reductase.
432	Oso7g0186000	AK100285	0.72	-0.06	0.08	-0.04	0.14	Argonate protein.
433	Oso5g0216300	AK103067	0.72	0.19	-0.10	0.12	0.06	Oxo-phytydienic acid reductase (12-oxophytodienoic acid reductase).
434	Oso5g0526700	AB097460	0.72	-0.12	0.15	0.02	0.27	UDP-Glucose 4-epimerase (EC 5.1.3.2).
435	Oso1g0117900	C1425334	0.72	-0.11	0.33	0.07	-0.28	(No Hit)
436	Oso3g0279700	AK111338	0.72	-0.15	0.52	0.33	0.49	ZPT2-12.
437	Oso2g0211000	Oso2g0211000	0.72	-0.02	0.01	-0.09	0.08	Viral coat and capsid protein family protein.
438	Oso5g0516400	AK068854	0.72	-0.06	0.10	-0.09	0.13	Pistill-specific extensin-like protein family protein.
439	Oso8g0499400	C1412756	0.72	-0.06	0.13	-0.11	-0.04	(No Hit)
440	Oso7g0556300	AK109557	0.72	-0.06	0.14	-0.04	0.13	Octicosapeptide/Phox/Bem1p domain containing protein.
441	Oso5g0316300	AK103067	0.71	0.00	0.16	0.03	0.28	Cathepsin B (Fragment).
442	Oso6g0440500	AK058761	0.71	-0.05	0.08	-0.08	0.24	MIR domain containing protein.
443	Oso3g0213100	AK073633	0.71	-0.11	0.18	-0.04	0.31	Protein transport protein Sec61 alpha subunit.
444	Oso3g0205800	Oso3g0205800	0.71	-0.01	0.25	0.17	0.25	GCN5-related N-acetyltransferase domain containing protein.
445	Oso6g0216300	AJ557138	0.71	0.20	-0.10	0.13	-0.07	Oxo-phytydienic acid reductase (12-oxophytodienoic acid reductase).
446	Oso3g0212800	AK119546	0.71	0.04	-0.02	-0.16	0.23	Beta-glucosidase.
447	Oso7g0531500	C1426967	0.71	-0.03	0.20	0.14	0.49	Harpin-induced 1 domain containing protein.
448	Oso11g0249400	Oso11g0249400	0.71	-0.17	0.29	-0.10	0.24	Glycoside hydrolase, family 28 protein.
449	Oso2g0594900	AK112513	0.71	0.02	-0.01	-0.05	-0.02	No apical meristem (NAM) protein domain containing protein.
450	Oso2g0210300	C1269249	0.71	-0.30	0.12	0.12	0.49	(No Hit)
451	Oso2g0270200	AK121603	0.71	-0.07	0.46	-0.03	0.19	Peptidase A1, pepsin family protein.
452	Oso6g0212900	AK104048	0.71	-0.01	0.07	-0.11	0.29	Heat shock protein Hsp70 family protein.
453	Oso7g0604700	C1447910	0.70	-0.08	0.20	0.23	0.15	B12D family protein.
454	Oso2g0491900	Oso2g0491900	0.70	-0.04	0.02	0.06	0.16	Peptidase aspartic family protein.
455	Oso1g0199500	C150873	0.70	-0.19	0.02	-0.09	-0.05	Protein of unknown function DUF6 domain containing protein.
456	Oso2g0603600	AK110833	0.70	-0.13	0.40	0.09	0.07	MYC1.
457	Oso3g0131200	AK062174	0.70	-0.15	0.50	0.23	0.50	Catalase isozyme 2 (EC 1.11.1.6).
458	Oso1g0589500	AK103067	0.70	-0.13	0.17	0.03	0.12	Glycerophosphoryl diester phosphodiesterase family protein.
459	Oso3g0749500	AK073110	0.70	-0.16	0.02	-0.16	-0.19	Exo-beta-glucanase.
460	Oso12g0455000	AK111239	0.70	-0.31	0.22	-0.09	-0.48	Conserved hypothetical protein.
461	Oso7g0298200	C1404454	0.70	-0.13	0.12	0.10	0.30	(No Hit)
462	Oso8g0501200	C1404454	0.70	-0.13	0.11	0.10	0.28	(No Hit)
463	Oso3g0691400	AK071319	0.70	-0.07	0.18	-0.18	0.10	Thioesterase superfamily domain containing protein.
464	Oso8g0187500	AK120496	0.70	0.00	0.39	0.02	-0.07	Roc1.
465	Oso6g0166800	AK073364	0.70	-0.07	0.43	-0.05	0.26	Conserved hypothetical protein.
466	Oso7g0457600	Oso7g0457600	0.70	-0.10	0.13	-0.05	0.49	Disease resistance protein family protein.
467	Oso2g0731600	AK058271	0.70	-0.20	0.18	-0.01	0.06	Thioredoxin-related domain containing protein.
468	Oso4g0605500	AK120495	0.70	-0.11	0.03	-0.10	0.10	Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 8).
469	Oso1g0407200	AK101309	0.70	-0.03	0.24	0.08	0.30	Protein of unknown function DUF962 family protein.
470	Oso4g0586500	AK106447	0.69	-0.24	0.13	0.01	0.18	Conserved hypothetical protein.
471	Oso6g0124100	C1404454	0.69	-0.12	0.11	0.08	0.31	(No Hit)
472	Oso8g0187500	AB077993	0.69	-0.01	0.38	-0.01	-0.15	Roc1.
473	Oso3g0270800	Oso3g0270800	0.69	-0.07	0.09	-0.23	0.00	Conserved hypothetical protein.
474	Oso4g0413100	AK121196	0.69	-0.06	0.37	0.14	0.47	Glycoside hydrolase, family 17 protein.
475	Oso4g0586700	AK063488	0.69	0.00	0.08	-0.06	0.01	Zn-finger, RING domain containing protein.
476	Oso6g0650900	AK107961	0.69	-0.15	0.04	-0.16	-0.03	Heat shock protein DnaJ family protein.
477	Oso7g0530700	AK099533	0.69	-0.08	0.25	-0.02	-0.02	Conserved hypothetical protein.
478	Oso3g0400200	Oso3g0400200	0.69	-0.02	-0.01	-0.13	0.11	Plant disease resistance response protein family protein.
479	Oso6g0175500	AK058599	0.69	0.01	0.04	-0.08	-0.05	Epsin, N-terminal domain containing protein.
480	Oso1g0108500	C1404454	0.68	-0.13	0.10	0.11	0.41	(No Hit)
481	Oso3g0131200	AK066378	0.68	-0.14	0.48	0.23	0.40	Catalase isozyme 2 (EC 1.11.1.6).
482	Oso5g0256900	C155255	0.68	-0.06	0.46	0.09	0.25	EYH/ELK/ERCs potassium channel family protein.
483	Oso1g0679900	AK120262	0.68	-0.04	0.00	0.00	0.26	YTH domain protein 2 (High-glucose-regulated protein 8) (NY-REN-2 antigen) (CLL-associated antigen KW-14). Splice isoform 2.
484	Oso1g0166100	AK103697	0.68	-0.01	0.08	0.05	0.20	Ca(2+)-dependent nuclease.
485	Oso6g0175500	AK100481	0.68	0.02	0.04	-0.05	-0.12	Epsin, N-terminal domain containing protein.
486	Oso7g0246200	AK104826	0.68	-0.06	0.09	-0.06	0.36	Calreticulin (Fragment).
487	Oso2g0114400	C138049	0.68	-0.07	0.32	-0.01	0.14	Phospholipid/glycerol acyltransferase family protein.
488	Oso5g0310500	AK100225	0.68	0.00	0.14	0.02	0.27	Cathepsin B (Fragment).
489	Oso3g0575200	AK066919	0.68	-0.09	0.30	-0.16	-0.12	K+ potassium transporter family protein.
490	Oso3g0131200	AB020502	0.68	-0.14	0.48	0.22	0.49	Catalase isozyme 2 (EC 1.11.1.6).
491	Oso7g0246200	AK063488	0.67	-0.06	0.07	-0.06	0.36	Calreticulin (Fragment).
492	Oso6g0106800	AK105782	0.67	-0.07	0.43	-0.05	0.03	Conserved hypothetical protein.
493	Oso6g0208700	AY669072	0.67	-0.03	0.13	-0.04	0.30	Putative tyrosine phosphatase family protein.
494	Oso3g0131200	AY339372	0.67	-0.14	0.47	0.23	0.49	Catalase isozyme 2 (EC 1.11.1.6).
495	Oso8g0156600	AK121377	0.67	-0.08	0.26	0.09	0.39	Major facilitator superfamily protein.
496	Oso4g0605500	AK067259	0.67	-0.10	0.01	-0.08	0.12	Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 8).
497	Oso7g0246200	AK099348	0.67	-0.08	0.09	-0.08	0.29	Calreticulin (Fragment).
498	Oso7g0246200	AB021259	0.67	-0.06	0.10	-0.06	0.33	Calreticulin (Fragment).
499	Oso1g0679900	AK121361	0.67	-0.04	0.10	0.00	0.23	YTH domain protein 2 (High-glucose-regulated protein 8) (NY-REN-2 antigen) (CLL-associated antigen KW-14). Splice isoform 2.
500	Oso1g0175500	AK072421	0.67	0.00	0.13	-0.04	0.24	HCO3-transporter domain containing protein.
501	Oso1g0869900	AB125305	0.67	0.01	0.01	-0.07	0.16	Protein kinase 3.
502	Oso7g0246200	AK104328	0.67	-0.06	0.09	-0.06	0.38	Calreticulin (Fragment).
503	Oso4g0497200	C1043990	0.67	-0.02	0.06	0.02	0.26	Cellulase precursor (Cellulase homolog OR16pep) (Endo-1,4-beta-D- glucanase KORRIGAN) (EC 3.2.1.4).
504	Oso1g0901800	AK070266	0.67	0.06	0.24	0.01	0.20	Protein of unknown function DUF212 family protein.
505	Oso3g0199100	AK069890	0.67	-0.10	0.21	-0.04	0.12	Protein of unknown function DUF677 family protein.
506	Oso3g0261800	AK060177	0.67	-0.02	0.14	-0.07	-0.16	Hypothetical protein.
507	Oso7g0679900	AK073278	0.67	-0.03	0.11	-0.03	0.36	KRP1 component family protein.
508	Oso1g0117900	C1433221	0.67	-0.12	0.32	0.03	-0.37	(No Hit)
509	Oso6g0501900	AK106229	0.67	-0.11	0.14	-0.11	-0.06	Cytochrome P450 family protein.
510	Oso6g0208700	AK065860	0.67	-0.02	0.13	-0.04	0.37	Putative tyrosine phosphatase family protein.
511	Oso1g0707500	AK106119	0.67	-0.13	0.37	0.13	0.22	Transcription factor.
512	Oso2g0763000	C1436098	0.67	0.02	0.30	0.01	0.07	Uncharacterized Cys-rich domain containing protein.
513	Oso2g0720900	AK069691	0.66	-0.02	0.43	-0.05	0.40	Peptidase A1, pepsin family protein.
514	Oso12g0582000	Oso12g0582000	0.66	0.02	0.24	-0.25	0.32	Cytochrome P450 family protein.
515	Oso12g0582000	AK071918	0.66	-0.01	0.10	-0.11	0.05	NPH3 domain containing protein.
516	Oso3g0348900	AK059950	0.66	-0.03	0.28	0.06	0.32	CHY zinc finger domain containing protein.
517	Oso4g0652700	AK059436	0.66	-0.03	0.00	0.03	-0.18	Nuclease 1.
518	Oso7g0584200	AK102803	0.66	-0.16	0.16	0.15	0.00	NPH3 domain containing protein.
519	Oso5g0446500	AK099953	0.66	-0.05	0.17	-0.11	0.17	Hypothetical protein.
520	Oso3g0848200	AK072278	0.66	-0.16	0.25	0.03	0.44	Phytase.
521	Oso8g0156600	AK063143	0.66	-0.11	0.24	0.09	0.17	Major facilitator superfamily protein.
522	Oso7g0679900	AK100018	0.66	-0.04	0.08	0.00	0.25	YTH domain protein 2 (High-glucose-regulated protein 8) (NY-REN-2 antigen) (CLL-associated antigen KW-14). Splice isoform 2.
523	Oso2g0741700	AK069210	0.66	-0.03	0.08	-0.08	0.24	Conserved hypothetical protein.
524	Oso2g0132100	AK059083	0.66	-0.02	0.15	-0.07	0.02	AMP-dependent synthetase and ligase domain containing protein.
525	Oso2g0539900	Oso2g0539900	0.65	-0.10	-0.01	-0.03	-0.15	WD40-like domain containing protein.
526	Oso5g0310500	AK064820	0.65	0.00	0.14	0.02	0.33	Cathepsin B (Fragment).
527	Oso6g0140700	AY206864	0.65	-0.09	0.31	0.07	0.01	Homeobox-leucine zipper protein HAT14 (HD-ZIP protein 14).
528	Oso1g0895300	AK073544	0.65	-0.14	0.18	0.19	0.30	Conserved hypothetical protein.
529	Oso2g0731400	C1043585	0.65	-0.06	0.19	-0.11	0.05	Plastocyanin-like domain containing protein.
530	Oso1g0191300	AK061716	0.65	-0.08	0.13	-0.05	0.19	No apical meristem (NAM) protein domain containing protein.
531	Oso2g0653400	C145659	0.65	0.03	0.10	0.03	-0.01	Transferase family protein.
532	Oso3g0708000	AK109110	0.65	0.02	-0.01	0.01	0.04	Conserved hypothetical protein.
533	Oso3g0810300	AK106765	0.65	-0.18	0.33	-0.03	-0.02	NUDX hydrolase domain containing protein.
534	Oso11g0439300	AK068470	0.65	-0.04	0.13	0.02	0.12	Hypothetical protein.
535	Oso4g0415000	AK108662	0.65	-0.06	0.01	-0.01	0.50	

551	Os02g0771800	Os02g0771800	0.64	-0.15	0.27	0.08	0.17	Conserved hypothetical protein.
552	Os02g0719700	AK119930	0.64	0.01	0.07	-0.04	0.01	IQ calmodulin-binding region domain containing protein.
553	Os04g0530200	AK105586	0.64	-0.04	-0.07	-0.04	0.07	Conserved hypothetical protein.
554	Os02g0588500	AK100170	0.64	-0.12	0.16	0.04	-0.20	Glycerophosphoryl diester phosphodiesterase family protein.
555	Os05g0132100	AK060660	0.63	-0.04	0.12	-0.03	0.14	AMP-dependent synthetase and ligase domain containing protein.
556	Os12g0161500	AK064192	0.63	-0.07	0.01	-0.14	-0.11	Hypothetical protein.
557	Os04g0684800	AK066799	0.63	-0.01	0.33	0.04	0.37	Ubiquitin-conjugating enzymes domain containing protein.
558	Os02g0497600	AK106982	0.63	0.10	-0.10	0.12	0.33	Conserved hypothetical protein.
559	Os03g0692700	AK058266	0.63	-0.14	0.21	-0.08	0.25	Protein of unknown function DUF538 family protein.
560	Os01g0191300	AK066231	0.63	-0.06	0.14	-0.05	0.23	No apical meristem (NAM) protein domain containing protein.
561	Os06g0140700	AK105150	0.63	-0.07	0.31	0.07	0.01	Homeobox-leucine zipper protein HAT14 (HD-ZIP protein 14).
562	Os12g0112000	AK069456	0.63	-0.08	0.06	-0.26	-0.10	Peroxidase (EC 1.11.1.7).
563	Os03g0310800	AK039476	0.63	0.15	-0.18	0.07	-0.03	Parvalbumin family protein.
564	Os04g0410600	AK121649	0.63	-0.23	0.17	-0.17	0.04	Purple acid phosphatase.
565	Os06g0143100	AK061597	0.63	-0.07	0.24	-0.22	0.27	Hypothetical protein.
566	Os07g0683200	AK068606	0.63	0.04	0.13	0.05	0.07	NAC-domain containing protein 19 (ANAC019) (ANAC) (Abscisic-acid- responsive NAC).
567	Os09g0451500	AK062254	0.63	-0.10	0.07	-0.15	0.13	Thioredoxin-related domain containing protein.
568	Os11g0605500	Cl061414	0.63	-0.12	0.15	-0.07	0.16	Acyl-CoA oxidase.
569	Os03g0575200	AJ427973	0.62	-0.10	0.30	-0.15	-0.37	K ⁺ potassium transporter family protein.
570	Os09g0468900	ClS33281	0.62	0.04	0.06	-0.10	0.17	(No Hit)
571	Os10g0113000	AK059636	0.62	0.04	0.03	-0.04	-0.12	NADPH-dependent codeinone reductase (EC 1.1.1.247).
572	Os03g0310800	AK058663	0.62	0.14	-0.20	0.06	-0.18	Parvalbumin family protein.
573	Os02g0637000	Os02g0637000	0.62	-0.08	0.09	-0.15	-0.08	Barwin-related endoglucanase domain containing protein.
574	Os02g0689200	AK072660	0.62	0.01	0.01	0.00	0.10	Protein of unknown function DUF250 domain containing protein.
575	Os01g0894600	AK073332	0.62	-0.07	0.18	0.01	0.03	Zn-finger, RING domain containing protein.
576	Os03g0785900	AK103358	0.62	0.12	-0.11	0.26	0.16	Glutathione S-transferase GST 19 (EC 2.5.1.18).
577	Os07g0452100	ClS35697	0.62	-0.08	0.22	-0.16	0.12	Alpha-galactosidase (EC 3.2.1.22) (Fragment).
578	Os03g0213100	AK062070	0.62	-0.05	0.12	-0.08	0.11	Protein transport protein Sec61 alpha subunit.
579	Os02g0314800	AK068924	0.62	-0.05	0.00	0.05	0.14	Peptidase A1, pepsin family protein.
580	Os01g0892500	ClA06253	0.62	-0.30	0.37	-0.15	-0.04	Pectinacetyltransferase family protein.
581	Os01g0803200	US4702	0.62	-0.12	0.03	-0.05	-0.08	Cysteine proteinase inhibitor-I (Oryzacystatin-I).
582	Os01g0146200	ClS33713	0.62	-0.15	0.17	-0.08	0.36	(No Hit)
583	Os01g0803200	AK061770	0.62	-0.12	0.04	-0.04	-0.06	Cysteine proteinase inhibitor-I (Oryzacystatin-I).
584	Os06g0675600	AK063648	0.62	-0.06	0.12	-0.02	-0.06	GRAB2 protein.
585	Os10g0509100	AK069166	0.62	-0.16	0.09	-0.09	-0.01	Conserved hypothetical protein.
586	Os03g0205700	AK103674	0.62	0.01	0.21	-0.04	0.18	Photoreceptor-interacting protein-like.
587	Os03g0762500	AK103002	0.61	-0.10	0.08	0.10	0.18	Conserved hypothetical protein.
588	Os01g0492000	AK121796	0.61	-0.05	0.05	0.05	0.08	Nucleoside diphosphate kinase I (EC 2.7.4.6) (NDK I) (NDP kinase I) (NDPK I).
589	Os02g0542400	AK065397	0.61	-0.07	0.01	0.06	0.07	Conserved hypothetical protein.
590	Os03g0643300	AK099445	0.61	-0.01	0.10	0.01	0.32	Ornithine aminotransferase (EC 2.6.1.13).
591	Os04g0402100	AK061185	0.61	-0.08	0.04	-0.05	-0.01	Calnexin (Fragment).
592	Os02g0689200	AK071254	0.61	0.01	0.01	0.01	-0.09	Protein of unknown function DUF250 domain containing protein.
593	Os07g0659400	AU091627	0.61	-0.05	0.06	0.02	0.26	HAD-superfamily hydrolase, subfamily IA, variant 1 protein.
594	Os06g0106800	AK122178	0.61	-0.06	0.33	-0.06	0.15	Conserved hypothetical protein.
595	Os09g0385700	AK065210	0.61	0.04	0.05	0.01	0.08	Zn-finger, AN1-like domain containing protein.
596	Os06g0106800	AK105911	0.61	-0.07	0.34	-0.05	0.15	Conserved hypothetical protein.
597	Os05g0556300	ClS54452	0.61	-0.05	0.14	-0.23	-0.13	Protein of unknown function DUF1298 domain containing protein.
598	Os03g0643300	AK108010	0.60	0.04	0.22	-0.04	0.46	Ornithine aminotransferase (EC 2.6.1.13).
599	Os04g0402100	AK069118	0.60	-0.08	0.03	-0.03	0.01	Calnexin (Fragment).
600	Os01g0770700	Os01g0770700	0.60	-0.07	0.01	0.01	0.26	Copper transporter 1.
601	Os02g0274900	AK073967	0.60	0.02	0.08	0.01	0.05	General substrate transporter family protein.

* The log₂ ratio of the GA-induced signal intensity change.

Table S7. List of probes categorized under Up-group2.

Probe#	ID	Accession	WT±GA*	gid1±GA*	slr1±GA*	gid2±GA*	gamyb±GA*	Annotation
1	<i>Os01g0126100</i>	AK106990	1.03	-0.25	0.76	0.34	-0.01	Calycin family protein.
2	<i>Os04g0364800</i>	Cl423611	0.77	-0.07	-0.16	0.09	-0.99	Barwin-related endoglucanase domain containing protein.
3	<i>Os11g0241700</i>	AK068339	0.75	-0.14	0.59	0.16	0.18	Protein of unknown function DUF538 family protein.
4	<i>Os02g0652000</i>	AK108827	0.70	-0.02	0.08	0.06	-0.70	PREG-like protein.
5	<i>Os10g0544600</i>	AK061763	0.69	0.02	0.43	0.07	-0.11	Zn-finger, RING domain containing protein.
6	<i>Os09g0287000</i>	AK106057	0.68	-0.07	0.41	0.18	0.32	Pathogenesis-related transcriptional factor and ERF domain containing protein.
7	<i>Os10g0544600</i>	AK105882	0.68	0.02	0.40	0.06	-0.18	Zn-finger, RING domain containing protein.
8	<i>Os03g0121200</i>	AK103660	0.65	-0.22	0.22	0.22	-0.17	Peroxidase 1.
9	<i>Os04g0677200</i>	AK107505	0.64	0.01	0.06	0.18	-0.21	Leucine-rich repeat, plant specific containing protein.
10	<i>Os03g0121200</i>	AK073847	0.64	-0.21	0.18	0.22	-0.20	Peroxidase 1.
11	<i>Os01g0629600</i>	AK071156	0.63	0.03	-0.04	0.14	-0.37	Peptidase S10, serine carboxypeptidase family protein.
12	<i>Os01g0182600</i>	AK072166	0.63	-0.14	0.37	0.04	0.31	Gigantea homologue (Fragment).
13	<i>Os03g0151500</i>	AK109181	0.63	0.24	0.39	0.23	0.06	Hypothetical protein.
14	<i>Os01g0694600</i>	CI546906	0.62	0.01	-0.03	0.07	-0.35	Hypothetical protein.

* The log₁₀ ratio of the GA-induced signal intensity change.

Table S8. List of probes categorized under Down-group1.

Probe#	ID	Accession	WTGGA*	gdfTsGA*	grrTsGA*	gq2sGA*	gamyTsGA*	Annotation
0	Os20521570	AK111714	-0.68	-0.15	0.00	-0.15	0.00	Hypothetical protein.
2	Os12a0541700	AK103420	-0.68	-0.05	0.06	-0.38	-0.26	RALF.
3	Os01g0951400	AF210325	-0.68	0.05	0.13	-0.22	0.01	Uridine 5'-monophosphate synthase
4	Os01g0951400	AB037418	-0.68	0.06	0.12	-0.21	0.00	Uridine 5'-monophosphate synthase
5	Os02g0330900	AK105277	-0.69	0.02	0.09	-0.22	-0.46	Poly(ADP-ribose) polymerase, catalytic region domain containing protein.
6	Os03g0675600	AK062614	-0.69	0.10	0.00	0.06	0.35	Phytosulfokines 3 precursor [Contains: Phytosulfokine-alpha
7	Os06g0503400	AK073583	-0.69	0.01	0.07	-0.11	0.32	Retinulin family protein.
8	Os01g0135700	AK065281	-0.69	0.01	0.07	-0.12	-0.38	FasII-like calcium-binding protein (callicain) family protein.
9	Os08g0485000	AK073011	-0.70	0.02	-0.04	-0.05	0.24	Pha-1 protein.
10	Os01g0644200	AY549310	-0.70	-0.09	0.08	-0.33	0.31	Conserved hypothetical protein.
11	Os12g0604700	AK072382	-0.70	-0.04	-0.03	-0.16	-0.22	LSTK-1-like kinase.
12	Os03g0159400	AK106743	-0.70	0.01	0.07	-0.29	0.07	Rat29 protein.
13	Os03g0734100	AK119903	-0.70	-0.06	0.07	-0.40	0.26	Conserved hypothetical protein.
14	Os09g0339000	AK100449	-0.70	0.01	0.07	-0.33	-0.05	Endo-beta-1,4-glucanase (EC 3.2.1.4) (Fragment).
15	Os05g0521000	AK101673	-0.70	0.01	0.07	-0.31	-0.17	Conserved hypothetical protein.
16	Os02g0216300	AK060081	-0.71	0.00	0.06	-0.11	0.28	Conserved hypothetical protein.
17	Os05g0494000	AK099655	-0.71	0.03	0.07	-0.26	0.47	Cytochrome P450 98A1 (EC 1.14.14.1).
18	Os09g0339000	AK087774	-0.71	0.01	0.05	-0.32	-0.04	Endo-beta-1,4-glucanase (EC 3.2.1.4) (Fragment).
19	Os01g0951500	AK141836	-0.71	0.03	0.00	-0.11	0.07	(No Hit)
20	Os12g0604700	AK101826	-0.71	-0.04	0.01	-0.15	-0.27	LSTK-1-like kinase.
21	Os06g0503400	AK069885	-0.71	-0.04	0.03	-0.25	0.06	4-coumarate-CoA ligase 1
22	Os02g0330900	AK102681	-0.71	-0.06	0.01	-0.45	-0.16	Poly(ADP-ribose) polymerase, catalytic region domain containing protein.
23	Os06g0468100	AK101662	-0.71	0.01	0.04	0.03	0.07	Nitrate reductase (NADH) 1 (EC 1.7.1.1) (NR1).
24	Os03g0133100	AK063608	-0.71	-0.19	0.12	-0.30	-0.18	Hypothetical protein.
25	Os12g0604700	AF251074	-0.71	-0.02	0.07	-0.21	-0.14	Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
26	Os04g0413900	AK101018	-0.71	0.01	0.09	-0.05	0.13	Conserved hypothetical protein.
27	Os05g0133100	AK068407	-0.72	0.03	0.03	-0.08	-0.01	Pili protein.
28	Os09g0433000	AK063243	-0.72	0.11	0.07	-0.53	0.46	Conserved hypothetical protein.
29	Os08g0547100	AK109374	-0.72	0.02	0.14	-0.20	-0.15	Glucosaminylglucosamine-6-phosphate isomerase domain containing protein.
30	Os06g0894000	AK071916	-0.72	-0.01	0.06	-0.07	0.16	MAP kinase 2.
31	Os04g0640600	AK070318	-0.72	-0.02	0.03	-0.32	0.23	Shikimate kinase.
32	Os01g0727500	AK107206	-0.72	0.08	-0.04	-0.32	0.10	Protein of unknown function DUF584 family protein.
33	Os05g0135700	AK065281	-0.72	0.01	0.07	-0.12	-0.19	WD40-like domain containing protein.
34	Os04g0427000	AK058995	-0.72	0.05	-0.01	-0.05	-0.15	Hypothetical protein.
35	Os03g0734100	AK064199	-0.72	-0.06	0.08	-0.40	0.02	Conserved hypothetical protein.
36	Os07g0622200	AK105687	-0.72	0.07	0.01	-0.52	0.22	Phospho-2-dehydro-3-deoxyheptanoate aldolase 1, chloroplast precursor
37	Os02g0216300	AK1020300	-0.73	-0.02	0.18	-0.16	0.02	UDP-glucuronosyl(UDP)-glucosyltransferase family protein.
38	Os04g0562500	AK118666	-0.73	0.01	-0.09	-0.38	0.25	Cis-zeatin O-glucosyltransferase.
39	Os03g0133100	AK119680	-0.73	-0.20	0.13	-0.29	-0.25	Hypothetical protein.
40	Os03g0133100	AK102681	-0.73	0.01	0.09	-0.17	0.02	Conserved hypothetical protein.
41	Os07g0622200	AB122058	-0.73	0.08	0.00	-0.52	0.21	Phospho-2-dehydro-3-deoxyheptanoate aldolase 1, chloroplast precursor
42	Os06g0468100	AK104788	-0.73	-0.02	0.12	-0.35	-0.14	Formate dehydrogenase, mitochondrial precursor
43	Os08g0468100	AK121810	-0.73	0.00	0.03	0.02	0.03	Nitrate reductase (NADH) 1 (EC 1.7.1.1) (NR1).
44	Os02g0216300	AK101662	-0.74	0.01	0.04	0.03	0.11	Conserved hypothetical protein.
45	Os11g0181200	AK063747	-0.74	-0.21	0.02	-0.21	0.43	Hypothetical protein.
46	Os07g0622200	AK099688	-0.74	0.07	0.00	-0.52	0.16	Phospho-2-dehydro-3-deoxyheptanoate aldolase 1, chloroplast precursor (EC 2.5.1.54) (Phospho-2-keto-3-deoxyheptanoate aldolase 1) (DAPH synthetase 1) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1).
47	Os02g0216300	AK101662	-0.74	0.01	0.04	0.03	0.11	Diacetylhydrolase, catalytic region domain containing protein.
48	Os04g0460300	AK106202	-0.74	0.03	0.06	-0.04	0.10	Amino acid/polyamine transporter II family protein.
49	Os03g0817900	AK071479	-0.74	-0.06	0.06	-0.41	0.19	Protein of unknown function DUF231 domain containing protein.
50	Os06g0468100	AK065872	-0.74	-0.02	0.12	-0.36	-0.07	Formate dehydrogenase, mitochondrial precursor (EC 1.2.1.2) (NAD- dependent formate dehydrogenase) (FDH).
51	Os04g0427000	AK067948	-0.74	0.01	0.02	-0.34	0.03	Shikimate kinase.
52	Os01g0112000	AK103623	-0.74	0.01	0.15	-0.23	-0.02	Conserved hypothetical protein.
53	Os03g0183300	AK119553	-0.74	0.06	0.21	-0.26	0.27	Pathogenesis-related transcriptional factor and ERF domain containing protein.
54	Os03g0219400	AK109202	-0.74	0.07	0.01	-0.14	0.04	Glyoxalase hydrolase, family 20 protein.
55	Os03g0255100	AK061989	-0.74	-0.16	-0.06	-0.10	0.07	Beta-galactosidase (EC 3.2.1.23).
56	Os08g0243500	AK068915	-0.74	0.06	0.08	-0.39	-0.04	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
57	Os05g0133100	AK069152	-0.75	0.03	0.03	-0.08	0.07	Pili protein.
58	Os01g0567400	AK067730	-0.75	0.01	0.02	-0.24	0.11	Rieske [2Fe-2S] region domain containing protein.
59	Os02g0216300	AK061737	-0.75	-0.01	0.08	-0.12	0.12	Conserved hypothetical protein.
60	Os03g0219400	AK121985	-0.75	0.01	0.03	-0.12	-0.08	Glycoside hydrolase, family 20 protein.
61	Os02g0216300	AK104214	-0.75	0.01	0.08	-0.13	0.39	Conserved hypothetical protein.
62	Os04g0460300	AK069352	-0.75	0.07	-0.01	-0.19	-0.00	Protein of unknown function DUF484 family protein.
63	Os02g0246400	AK071209	-0.75	0.01	0.05	-0.28	-0.15	Inositol phosphate kinase.
64	Os03g0183300	AK105922	-0.75	0.06	0.21	-0.26	0.24	Pathogenesis-related transcriptional factor and ERF domain containing protein.
65	Os08g0243500	AK069152	-0.75	0.06	0.08	-0.39	-0.08	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
66	Os02g0257400	AK065365	-0.75	0.05	-0.08	-0.12	0.17	Conserved hypothetical protein.
67	Os12g0604700	AK066459	-0.76	0.02	0.15	-0.15	-0.12	Universal stress protein (Usp) family protein.
68	Os05g0349800	AK119674	-0.76	-0.20	0.07	-0.23	0.32	Embryonic abundant protein 1.
69	Os03g0183300	AK109202	-0.76	0.08	0.20	-0.27	0.20	Pathogenesis-related transcriptional factor and ERF domain containing protein.
70	Os03g0133000	AK102717	-0.76	-0.01	0.02	-0.27	-0.19	Protein kinase domain containing protein.
71	Os02g0803300	AK101538	-0.76	0.07	0.08	-0.30	0.16	Epsin, N-terminal domain containing protein.
72	Os02g0575500	AK059144	-0.76	0.06	0.03	-0.08	0.10	ABC transporter-like.
73	Os12a0517300	Os12a0517300	-0.76	-0.17	-0.10	-0.21	0.28	Conserved hypothetical protein.
74	Os09g0528200	AK059755	-0.76	0.05	-0.11	-0.28	0.21	Homeodomain leucine zipper protein (Fragment).
75	Os03g0133000	AK105632	-0.76	-0.01	0.02	-0.26	-0.11	Protein kinase domain containing protein.
76	Os01g0142800	AK105664	-0.76	0.06	0.07	-0.37	0.12	Peptide transporter.
77	Os05g0179300	AK100028	-0.76	0.05	0.10	-0.32	-0.02	Transferase family protein.
78	Os05g0557200	AK062090	-0.76	-0.03	0.09	-0.13	-0.13	ARM repeat fold domain containing protein.
79	Os08g0344600	AK069591	-0.76	0.01	0.04	-0.10	0.12	Phosphate phosphoenolpyruvate translocator.
80	Os05g0205000	AK062320	-0.76	-0.04	0.00	-0.09	-0.14	Multifunctional transport intrinsic membrane protein 2.
81	Os05g0557200	AK102111	-0.76	0.03	0.09	-0.13	-0.13	ARM repeat fold domain containing protein.
82	Os10g0391000	AK106326	-0.76	0.03	0.08	0.00	0.05	Sugar transporter domain containing protein.
83	Os01g0173100	AK061949	-0.76	0.07	0.04	-0.05	0.22	Phosphoserine II reaction center W protein (PSII 6 kDa protein) (Fragment).
84	Os02g0257400	AK103980	-0.76	0.04	-0.02	-0.13	0.14	Conserved hypothetical protein.
85	Os02g0104500	AK120063	-0.77	0.02	0.12	-0.10	0.09	DNA-binding protein DF1.
86	Os07g0109100	AK071914	-0.77	0.00	0.10	-0.22	-0.25	Universal stress protein (Usp) family protein.
87	Os12a0230500	CI211517	-0.77	-0.04	0.02	-0.28	0.34	(No Hit)
88	Os08g0468100	AF358767	-0.77	0.00	0.07	-0.12	0.01	Glutamate decarboxylase (EC 4.1.1.15).
89	Os02g0257400	AK059863	-0.77	0.04	-0.02	-0.13	0.14	Conserved hypothetical protein.
90	Os04g0427000	AK121488	-0.77	0.05	0.08	-0.22	0.11	Heavy metal transport/detoxification protein domain containing protein.
91	Os02g0602000	AK058978	-0.77	-0.06	0.08	-0.23	-0.15	IQ calmodulin-binding region domain containing protein.
92	Os12a0607000	AK065892	-0.77	-0.06	0.08	-0.04	-0.01	Homocysteine S-methyltransferase 2 (EC 2.1.1.10) (S-methylmethionine:homocysteine methyltransferase 2) (SMH-Hcy S-methyltransferase 2) (ZmHMT-2).
93	Os12g0541300	CI481968	-0.77	0.07	0.07	-0.08	-0.20	Respiratory burst oxidase homolog.
94	Os03g0287000	CI032353	-0.77	0.00	0.03	-0.22	-0.14	(No Hit)
95	Os02g0301100	AK100174	-0.77	0.02	0.20	0.00	0.00	MN3 and saliv related transmembrane protein family protein.
96	Os12a0607000	AK103293	-0.77	-0.07	0.07	-0.06	0.10	Homocysteine S-methyltransferase 2 (EC 2.1.1.10) (S-methylmethionine:homocysteine methyltransferase 2) (SMH-Hcy S-methyltransferase 2) (ZmHMT-2).
97	Os01g01503300	AK103599	-0.77	0.10	0.03	-0.56	0.46	UDP-glucuronosyl(UDP)-glucosyltransferase family protein.
98	Os01g0298900	AK061588	-0.77	-0.02	0.07	-0.14	0.30	Cationic amino acid transporter (Fragment).
99	Os04g0387800	AK063862	-0.77	0.01	0.11	-0.06	0.02	Conserved hypothetical protein.
100	Os04g0623500	AK069221	-0.78	-0.03	0.00	-0.46	0.20	(S)-2-hydroxyacid oxidase, peroxisomal (EC 1.1.3.15) (Glycolate oxidase) (GOX) (Short chain alpha-hydroxy acid oxidase).
101	Os10g0439800	Os10g0439800	-0.78	0.03	0.07	-0.29	0.03	Cytochrome P450 family protein.
102	Os09g0528200	AK103160	-0.78	0.04	-0.07	-0.29	0.32	Homeodomain leucine zipper protein (Fragment).
103	Os09g0482000	AJ077506	-0.78	-0.14	-0.01	-0.18	0.02	Conserved hypothetical protein.
104	Os05g0349800	AK063877	-0.78	0.20	0.07	-0.17	0.04	Embryonic abundant protein 1.
105	Os03g0249800	AK067814	-0.78	-0.02	0.09	-0.26	0.00	Xanthine dehydrogenase 1 (EC 1.1.1.204).
106	Os01g0142800	AK102216	-0.78	0.04	0.05	-0.36	0.23	Peptide transporter.
107	Os04g0623500	AK069638	-0.78	-0.01	0.11	-0.46	0.17	(S)-2-hydroxyacid oxidase, peroxisomal (EC 1.1.3.15) (Glycolate oxidase) (GOX) (Short chain alpha-hydroxy acid oxidase).
108	Os04g0279000	AK105842	-0.78	0.08	0.08	-0.18	-	

168	Osl020564500	AK103690	-0.85	-0.03	-0.06	-0.26	0.02	Protein kinase domain containing protein.
169	Osl040695100	AK065491	-0.85	0.00	-0.04	-0.44	0.00	Glutamine synthetase shoot isozyme, chloroplast precursor (EC 6.3.1.2) (Glutamate--ammonia ligase) (Clone lambda-GS31).
170	Osl020610100	AK065488	-0.85	0.02	-0.02	0.04	0.08	Msx3 Mechanosensitive ion channel family protein.
171	Osl020565500	AF022734	-0.85	-0.12	0.01	-0.04	0.32	Zn-induced protein.
172	Osl020662800	AK063448	-0.85	0.04	0.01	-0.15	0.10	Major facilitator superfamily protein.
173	Osl020645800	AK050300	-0.85	0.00	-0.08	-0.13	0.02	Glutamate decarboxylase (EC 4.1.1.15).
174	Osl020565500	U46138	-0.86	-0.11	0.03	-0.04	0.35	Zn-induced protein.
175	Osl020565500	AK068596	-0.86	-0.05	-0.07	-0.02	0.04	Conserved hypothetical protein.
176	Osl040269600	AK100640	-0.86	0.00	-0.02	-0.37	-0.05	Copper amine oxidase family protein.
177	Osl020239900	AK060994	-0.86	0.08	-0.11	0.22	0.38	Cationic amino acid transporter (Fragment).
178	Osl020645800	U428025	-0.86	0.02	0.08	-0.13	-0.11	Glutamate decarboxylase (EC 4.1.1.15).
179	Osl120175400	AK063027	-0.86	0.04	-0.06	-0.67	-0.14	Conserved hypothetical protein.
180	Osl020662800	AK060907	-0.86	-0.01	-0.01	-0.16	0.02	Conserved hypothetical protein.
181	Osl020211900	AK060915	-0.86	-0.09	-0.02	-0.06	-0.03	Protein of unknown function DUF588 family protein.
182	Osl120275200	Osl120275200	-0.86	-0.08	0.07	-0.01	-0.12	Conserved hypothetical protein.
183	Osl050231700	AK111406	-0.86	-0.18	0.08	-0.19	0.17	Hypothetical protein.
184	Osl120242500	Osl023994	-0.86	0.51	-0.13	-0.14	0.23	(No Hit)
185	Osl020645800	AK061977	-0.86	0.00	0.08	-0.13	-0.01	Glutamate decarboxylase (EC 4.1.1.15).
186	Osl040269600	AK066862	-0.86	0.00	-0.04	-0.37	0.03	Copper amine oxidase family protein.
187	Osl100564500	AB125304	-0.86	-0.03	-0.06	-0.26	0.03	Protein kinase domain containing protein.
188	Osl0203357200	AK111362	-0.86	0.02	0.09	-0.05	0.10	Non-protein coding transcript, unclassifiable transcript.
189	Osl090242300	AK120024	-0.86	0.08	0.01	-0.31	0.19	Peptidase A1, pepsin family protein.
190	Osl020374600	AK110542	-0.87	0.07	0.12	-0.33	0.06	Glycoside hydrolase, family 17 protein.
191	Osl040269600	AK069252	-0.87	0.03	-0.03	-0.47	0.03	Glutamine synthetase shoot isozyme, chloroplast precursor (EC 6.3.1.2) (Glutamate--ammonia ligase) (Clone lambda-GS31).
192	Osl040269600	AK060758	-0.87	0.00	-0.02	-0.37	0.03	Copper amine oxidase family protein.
193	Osl020564500	D88399	-0.87	-0.04	-0.06	-0.26	0.03	Protein kinase domain containing protein.
194	Osl040695100	AK068257	-0.87	-0.04	-0.02	-0.27	-0.01	Phosphatidylinositol-4-phosphate 5-kinase family protein.
195	Osl020565500	AK060901	-0.87	0.02	0.17	-0.01	0.09	Conserved hypothetical protein.
196	Osl020211900	AK104393	-0.87	-0.07	0.01	-0.07	-0.01	Protein of unknown function DUF588 family protein.
197	Osl070663800	AK100429	-0.88	-0.13	0.03	-0.19	0.05	ToB1_C-terminal domain containing protein.
198	Osl010549000	AK060908	-0.88	0.01	-0.13	-0.16	0.20	Cleasin family protein.
199	Osl120174200	AK063680	-0.88	0.01	-0.01	-0.19	-0.02	Hypothetical protein.
200	Osl020420900	AK010240900	-0.88	-0.07	-0.09	-0.21	-0.20	Peptidase C1A, papain family protein.
201	Osl030289900	AK0710872	-0.88	0.00	0.02	-0.25	-0.22	Low-temperature induced protein H101.2.
202	Osl070663700	AK060908	-0.88	0.12	-0.10	-0.42	0.02	Short-chain dehydrogenase/reductase SDR family protein.
203	Osl050560000	AF093635	-0.88	0.01	0.09	-0.08	-0.18	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) (GOSS protein).
204	Osl020662800	AK121303	-0.88	0.02	-0.09	-0.56	0.08	Non-protein coding transcript, unclassifiable transcript.
205	Osl020142000	AK060910	-0.88	-0.03	-0.05	-0.35	0.19	Bowman Birk trypsin inhibitor.
206	Osl020592100	AK107947	-0.88	-0.03	0.04	-0.21	-0.02	Short-chain dehydrogenase/reductase SDR family protein.
207	Osl020124200	AK067257	-0.89	-0.05	-0.36	-0.34	0.09	Bowman Birk trypsin inhibitor.
208	Osl030218900	AK066331	-0.89	0.01	0.01	-0.30	0.23	Alcohol dehydrogenase.
209	Osl010728700	AK100700	-0.89	0.03	0.02	-0.33	0.42	Conserved hypothetical protein.
210	Osl110586800	CI218813	-0.89	-0.04	0.02	-0.28	-0.28	Protein of unknown function DUF231 domain containing protein.
211	Osl030289900	AK108175	-0.89	0.04	-0.04	-0.31	-0.13	Soluble epoxide hydrolase.
212	Osl020662800	AK121303	-0.89	0.02	-0.09	-0.56	0.08	Conserved hypothetical protein.
213	Osl020645800	AK070587	-0.89	0.02	-0.02	-0.20	-0.24	Conserved hypothetical protein.
214	Osl020383000	AK107755	-0.89	0.00	0.05	-0.19	0.12	Conserved hypothetical protein.
215	Osl020629400	AK061959	-0.89	0.03	0.02	-0.37	0.03	Phenylalanine ammonia-lyase (EC 4.3.1.5).
216	Osl020374600	AK110542	-0.90	-0.01	-0.03	-0.23	-0.05	Seed maturation protein domain containing protein.
217	Osl090509700	AK120589	-0.90	-0.08	-0.04	-0.09	0.14	Hd1.
218	Osl020211900	AK104206	-0.90	-0.06	-0.02	-0.07	0.09	Protein of unknown function DUF588 family protein.
219	Osl120512100	AK121039	-0.90	-0.07	0.01	-0.45	-0.04	General substrate transporter family protein.
220	Osl010209200	AK067269	-0.90	0.04	-0.04	-0.27	-0.02	BTB/POZ domain containing protein.
221	Osl060207900	AK073079	-0.90	-0.01	0.16	-0.13	-0.15	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
222	Osl030289900	AK070959	-0.90	0.07	-0.01	-0.39	0.21	Conserved hypothetical protein.
223	Osl020517500	AK108484	-0.90	-0.05	-0.02	-0.22	0.00	Cytoplasmic malonate pyruvate-dependent phosphatase family protein.
224	Osl120258500	AK108847	-0.90	-0.05	-0.02	-0.20	0.22	Non-protein coding transcript, unclassifiable transcript.
225	Osl020276300	AK108165	-0.90	-0.02	0.01	-0.18	0.22	Group 3 late embryogenesis abundant protein (Fragment).
226	Osl020124200	AK104387	-0.90	-0.05	-0.35	-0.35	0.22	Bowman Birk trypsin inhibitor.
227	Osl020645800	AK101989	-0.90	0.09	-0.14	-0.09	-0.14	Glutamate decarboxylase (EC 4.1.1.15).
228	Osl030192700	AK103501	-0.90	-0.03	0.13	-0.38	-0.03	Myo-inositol-1-phosphate synthase.
229	Osl100564500	AK062219	-0.90	0.01	0.21	-0.24	-0.02	Rieske [2Fe-2S] region domain containing protein.
230	Osl020759900	AK050854	-0.90	-0.05	-0.16	-0.23	0.16	Conserved hypothetical protein.
231	Osl0702188700	AK073755	-0.90	-0.07	0.02	-0.29	-0.08	Exostosin-like family protein.
232	Osl100517500	AK100465	-0.90	0.07	0.10	-0.77	-0.02	Cys/Met metabolism pyridoxal-phosphate-dependent enzymes family protein.
233	Osl110417800	CA48419	-0.90	-0.22	0.03	-0.27	0.01	(No Hit)
234	Osl020142000	AK073000	-0.91	0.09	0.15	-0.15	0.19	TPK-like domain containing protein.
235	Osl030192700	AK058750	-0.91	-0.03	0.12	-0.38	-0.03	Myo-inositol-1-phosphate synthase.
236	Osl0602072700	CI136777	-0.91	-0.03	-0.06	-0.28	-0.32	(No Hit)
237	Osl040269600	AK069252	-0.91	0.02	0.06	-0.17	0.14	C2 domain containing protein.
238	Osl110417800	CI455200	-0.91	-0.22	-0.04	-0.27	-0.01	(No Hit)
239	Osl020592800	AK107707	-0.91	-0.14	-0.01	-0.48	0.06	Protein of unknown function DUF581 family protein.
240	Osl020174900	AK107290	-0.91	-0.01	0.14	-0.45	0.23	Protein of unknown function DUF1264 family protein.
241	Osl100557500	AK100765	-0.91	-0.05	0.12	0.04	-0.15	Cation/proton exchanger 1a.
242	Osl040269600	AK100392	-0.91	0.01	0.06	-0.13	-0.20	IQ calmodulin-binding region domain containing protein.
243	Osl020428200	AJ311051	-0.91	0.02	0.03	-0.20	-0.13	Typical P-type Rf23 Mvb protein (Fragment).
244	Osl030192700	AK103501	-0.91	-0.04	-0.39	0.05	0.05	Myo-inositol-1-phosphate synthase.
245	Osl030289900	AF247164	-0.91	0.04	0.01	-0.38	0.10	Alpha-expansin OsEPA7.
246	Osl030282000	AK101784	-0.92	0.05	0.02	-0.38	0.15	Alpha-expansin OsEPA7.
247	Osl040269600	AK059100	-0.92	0.01	0.06	-0.13	-0.20	IQ calmodulin-binding region domain containing protein.
248	Osl020211900	AK060914	-0.92	0.00	-0.08	-0.07	0.05	Protein of unknown function DUF588 family protein.
249	Osl020282000	AK071199	-0.92	0.00	0.02	-0.12	-0.11	TPK-like domain containing protein.
250	Osl030192700	AK063160	-0.92	0.01	0.05	-0.15	-0.04	Uncharacterized Cys-rich domain containing protein.
251	Osl040269600	AK100631	-0.92	0.14	-0.21	-0.51	-0.21	Copylipid diphosphate synthase (Fragment).
252	Osl010335900	Osl010335900	-0.92	0.00	-0.01	-0.21	-0.07	Typical A-type Rf23 Mvb protein (Fragment).
253	Osl060207900	AK120296	-0.92	0.00	0.15	-0.14	-0.19	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
254	Osl070663700	AK104614	-0.92	-0.14	-0.17	-0.43	-0.03	Short-chain dehydrogenase/reductase SDR family protein.
255	Osl070171100	AJ417522	-0.92	0.04	-0.15	-0.07	-0.17	TPK-like domain containing protein.
256	Osl030249700	AK121219	-0.93	-0.18	-0.19	-0.14	-0.17	Hypothetical protein.
257	Osl060207900	AB044537	-0.93	-0.01	0.15	-0.13	-0.19	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
258	Osl060269600	CI311619	-0.93	0.06	0.05	-0.19	-0.21	CONSTANS-like protein C06.
259	Osl010384400	AK105246	-0.93	0.01	0.14	-0.29	0.22	Peptidylglyoxyl isomerase.
260	Osl060207900	AK061794	-0.93	0.00	0.15	-0.13	-0.13	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
261	Osl060269600	AJ512642	-0.93	0.01	0.08	-0.08	0.10	MAP kinase 2.
262	Osl020534000	AK106988	-0.93	0.04	0.07	-0.15	0.05	CBS domain containing protein.
263	Osl110620300	AJ074770	-0.93	0.02	0.05	-0.28	-0.35	Nonspecific lipid-transfer protein 2 (LTP2).
264	Osl060269600	AJ251330	-0.93	0.01	0.06	-0.07	0.10	MAP kinase 2.
265	Osl040269600	AK108116	-0.94	-0.03	0.09	-0.19	0.02	Tonoplast intrinsic protein (Putative beta-tonoplast intrinsic protein).
266	Osl040185700	AK068434	-0.94	0.00	0.04	-0.06	-0.15	CBS domain containing protein.
267	Osl060246500	AK105105	-0.94	-0.06	0.01	-0.25	0.09	Pyruvate dehydrogenase E1 alpha subunit (EC 1.2.4.1).
268	Osl0208102700	AK061430	-0.94	-0.01	0.04	-0.07	0.04	Harpin-induced 1 domain containing protein.
269	Osl060227900	AF162655	-0.94	0.00	0.15	-0.13	-0.14	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
270	Osl060227900	AK099248	-0.94	0.00	0.14	-0.14	-0.19	RF2 (EC 1.2.1.3) (T cytoplasm male sterility restorer factor 2).
271	Osl090242300	AK106942	-0.95	0.03	0.23	-0.20	-0.21	LysM-domain GPI-anchored protein 1 precursor. Splice isoform 2.
272	Osl050560000	AK080294	-0.95	0.02	0.01	-0.08	-0.20	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) (GOSS protein).
273	Osl050475400	AK060913	-0.95	0.09	-0.13	-0.04	-0.04	Alanine aminotransferase-like protein (Fragment).
274	Osl11021200	AK099589	-0.95	0.08	0.09	-0.08	0.14	Transferase family protein.
275	Osl050465800	AK072353	-0.95	-0.02	0.00	-0.34	0.06	Cytochrome b-245, heavy chain family protein.
276	Osl020102700	AK065526	-0.95	-0.01	0.04	-0.06	-0.10	Harpin-induced 1 domain containing protein.
277	Osl050151200	CI409979	-0.95	-0.01	-0.06	-0.25	0.00	(No Hit)
278	Osl060553100	CI480869	-0.95	0.09	0.02	-0.23	-0.11	Heat shock transcription factor 29 (Fragment).
279	Osl0208102700	AK104488	-0.95	-0.01	0.09	-0.07	0.03	Harpin-induced 1 domain containing protein.
280	Osl030151200	AK103362	-0.95	0.01	0.03	-0.15	-0.10	Uncharacterized Cys-rich domain containing protein.
281	Osl100342300	AK129411	-0.95	0.06	-0.14	-0.49	0.03	Receptor-like protein kinase.
282	Osl0208102700	AK072003	-0.95	0.00	0.04	-0.07	-0.02	Harpin-induced 1 domain containing protein.
283	Osl030246500	AK1002000	-0.95	0.02	-0.30	0.06	0.06	Xanthine dehydrogenase 2 (EC 1.1.1.204).
284	Osl050560000	AK061603	-0.96	0.02	0.05	-0.08	-0.21	Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) (GOSS protein).
285	Osl07020541200	CI379248	-0.96	-0.03	-0.21	-0.35	0.01	Protein kinase family protein.
286	Osl0702188700	AK106452	-0.96	-0.03	0.03	-0.26	0.17	Arabidopsis protein of unknown function DUF266 family protein.
287	Osl070171100	AK104614	-0.96	0.05	0.01	-0.38	-0.14	TPK-like domain containing protein.
288	Osl050151200	CI409979	-0.96	-0.01	-0.07	-0.25	-0.02	(No Hit)
289	Osl110240600	AK061589	-0.96	0.11	-0.06	0.04	-0.04	Esterase/lipase/thioesterase domain containing protein.
290	Osl100246500	AK120858	-0.96					

337	Os10g0512400	AK067847	-1.02	0.09	0.00	-0.57	-0.05	Cytochrome P450 family protein.
338	Os09g0114100	AK121142	-1.02	-0.08	0.04	-0.13	-0.22	Conserved hypothetical protein.
339	Os12g0134900	C1387037	-1.02	0.01	0.00	-0.21	0.14	Cytochrome P450 family protein.
340	Os05g0502000	CI436216	-1.02	0.05	-0.06	-0.25	0.17	Hypothetical protein.
341	Os03g0822000	AK063455	-1.02	0.02	-0.07	-0.36	0.06	Alpha-expansin OsEXPAT.
342	Os02g0187800	AK058294	-1.03	0.11	0.10	-0.10	0.35	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.105) (CAD) (Brown-midrib 1 protein).
343	Os09g0467400	AK061667	-1.03	0.07	0.03	-0.13	-0.07	Protein of unknown function DUF255 domain containing protein.
344	Os02g0657000	AY346094	-1.03	0.03	0.10	-0.20	-0.13	AP2 domain-containing protein Rap211.
345	Os09g0437500	AK059818	-1.03	-0.15	-0.13	-0.10	0.14	Dormancy-associated protein.
346	Os02g0187800	AK121142	-1.03	0.11	0.11	-0.68	0.48	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.105) (CAD) (Brown-midrib 1 protein).
347	Os02g0187800	AK071794	-1.03	0.12	0.10	-0.65	0.38	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.105) (CAD) (Brown-midrib 1 protein).
348	Os01g0935600	AK105604	-1.04	-0.05	-0.05	-0.36	-0.17	Glycoside transferase, six-hairpin domain containing protein.
349	Os03g0305600	AK082314	-1.04	-0.07	-0.07	-0.49	-0.28	Mitochondrial import inner membrane translocase, subunit Tim17/22 family protein.
350	Os10g0452600	AB114828	-1.04	-0.11	-0.08	-0.29	-0.10	Tonoplast membrane integral protein ZmTIP3-1.
351	Os09g0320100	CI124328	-1.04	-0.08	0.02	-0.20	0.04	(No Hit)
352	Os05g0572700	AK108969	-1.04	0.02	-0.13	-0.32	0.26	Protein phosphatase 2C.
353	Os06g0105800	AK067200	-1.04	0.03	0.00	-0.18	-0.05	E-class P450, group 1 family protein.
354	Os07g0134000	AK103862	-1.04	0.05	0.01	-0.22	0.27	Amino acid permease 6.
355	Os10g0492600	AK111931	-1.04	-0.11	-0.07	-0.30	-0.12	Tonoplast membrane integral protein ZmTIP3-1.
356	Os05g0284500	AK111286	-1.05	0.00	0.02	-0.19	-0.13	Remorin.
357	Os06g0462000	CI124329	-1.05	0.07	0.03	-0.20	0.13	(No Hit)
358	Os08g0473900	AK073487	-1.05	-0.32	0.30	-0.45	-0.27	RAmy3D
359	Os03g0699000	U43931	-1.05	-0.01	0.11	-0.36	0.46	Oleosin family protein.
360	Os02g0659000	AK105913	-1.05	-0.15	-0.18	-0.46	-0.35	Cytochrome P450 family protein.
361	Os10g0766000	Os10g0766000	-1.05	0.03	-0.14	-0.29	-0.25	Multi antimicrobial extension protein MatE family protein.
362	Os03g0842900	AK107425	-1.05	-0.12	0.04	-0.29	0.18	Short-chain dehydrogenase/reductase SDR family protein.
363	Os01g0532300	CI542224	-1.06	-0.15	-0.06	-0.20	0.35	Conserved hypothetical protein.
364	Os02g0187800	AK121142	-1.06	0.11	0.10	-0.66	0.38	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.105) (CAD) (Brown-midrib 1 protein).
365	Os06g0321600	CI430143	-1.06	-0.15	0.09	-0.20	0.06	(No Hit)
366	Os08g0473900	M24287	-1.06	-0.33	0.30	-0.46	-0.20	RAmy3D
367	Os02g0153000	AK062566	-1.06	-0.10	0.07	-0.25	0.05	Non-specific lipid-transfer protein 2 (nLTP2) (7 kDa lipid transfer protein).
368	Os12g0147000	AF068333	-1.06	0.08	-0.04	-0.25	0.43	Phytosulfokines 5 precursor (Secretory protein SH27A) [Contains: Phytosulfokine-alpha (PSK-alpha) (Phytosulfokine-a), Phytosulfokine-beta (PSK-beta) (Phytosulfokine-b)].
369	Os01g0849600	AK108159	-1.07	-0.11	0.12	-0.30	-0.33	Universal stress protein (Usp) family protein.
370	Os12g0147000	AK101186	-1.07	0.08	-0.05	-0.27	0.38	Phytosulfokines 5 precursor (Secretory protein SH27A) [Contains: Phytosulfokine-alpha (PSK-alpha) (Phytosulfokine-a), Phytosulfokine-beta (PSK-beta) (Phytosulfokine-b)].
371	Os06g0324400	AK106501	-1.07	0.02	0.02	-0.24	0.37	Late embryogenesis abundant (LEA) group 1 family protein.
372	Os05g0525900	AK108249	-1.07	0.00	0.05	-0.04	0.03	Zn-finger transcription factor.
373	Os02g0442000	CI124328	-1.07	-0.07	0.01	-0.20	0.07	(No Hit)
374	Os02g0215200	Os02g0215200	-1.07	-0.06	-0.14	-0.02	-0.31	Multi-antimicrobial extension protein MatE family protein.
375	Os10g0935600	AK061490	-1.08	-0.05	0.02	-0.37	-0.21	Glycoside transferase, six-hairpin domain containing protein.
376	Os03g0758300	AK060339	-1.08	-0.07	0.08	-0.65	0.09	Cyclic nucleotide-gated ion channel 2 (AICNGC2) (Cyclic nucleotide-and calmodulin-regulated ion channel 2) (DEFENSE NO DEATH 1).
377	Os07g0433200	CI430143	-1.08	-0.16	0.10	-0.20	0.06	(No Hit)
378	Os09g0437500	AK105913	-1.08	-0.16	-0.13	-0.11	0.22	Dormancy-associated family protein.
379	Os07g0134000	AK120257	-1.08	0.04	0.00	-0.21	0.40	Amino acid permease 6.
380	Os08g0473900	AK119761	-1.08	-0.32	0.31	-0.46	-0.36	RAmy3D
381	Os08g0473900	AK119561	-1.08	-0.33	0.29	-0.49	-0.28	RAmy3D
382	Os11g0533700	CI076279	-1.08	-0.03	0.09	-0.31	0.18	(No Hit)
383	Os04g0559700	AK104736	-1.09	0.04	0.03	-0.39	0.10	HvPIP1-5 protein.
384	Os10g0437500	AK107152	-1.09	0.03	0.09	-0.10	-0.10	Universal stress protein (Usp) family protein.
385	Os04g0390700	AK107628	-1.09	0.03	0.07	-0.21	0.03	Short-chain dehydrogenase/reductase SDR family protein.
386	Os04g0559700	AK065188	-1.09	0.04	0.04	-0.39	0.10	HvPIP1-5 protein.
387	Os04g0141300	CI076279	-1.09	-0.03	0.09	-0.31	0.21	(No Hit)
388	Os04g0559700	AK092869	-1.09	0.04	0.03	-0.39	0.10	HvPIP1-5 protein.
389	Os12g0134000	AK076279	-1.09	0.03	0.09	-0.31	0.24	(No Hit)
390	Os03g0153900	AK106420	-1.09	-0.01	0.06	-0.35	-0.05	Aromatic-ring hydroxylase family protein.
391	Os01g0171500	CI076279	-1.09	-0.03	0.09	-0.31	0.20	Calceinurin B (Fragment).
392	Os02g0153900	AK106420	-1.10	-0.04	0.07	-0.37	0.21	SNF4.
393	Os10g0576600	AK061555	-1.10	0.01	0.14	-0.02	-0.19	TPR-like domain containing protein.
394	Os10g0576600	AK104486	-1.10	0.01	0.14	-0.02	-0.19	TPR-like domain containing protein.
395	Os02g0171600	AK070083	-1.10	0.00	-0.05	-0.50	0.19	4-coumarate-CoA ligase 1 (EC 6.2.1.12) (ACL 1) (4-coumaroyl-CoA synthase 1).
396	Os04g0171600	AK072928	-1.11	0.04	-0.06	-0.64	-0.24	Glucosyltransferase family protein.
397	Os07g0269000	CI251879	-1.11	-0.16	0.09	-0.20	0.18	(No Hit)
398	Os02g0626400	CI120127	-1.11	0.01	0.01	-0.42	0.22	Phenylalanine ammonia-lyase (EC 4.3.1.5).
399	Os11g0420100	AK108249	-1.11	0.04	0.09	-0.21	0.08	Steroid nuclear receptor ligand-binding domain containing protein.
400	Os01g0859300	AK070998	-1.11	0.06	0.09	-0.17	0.34	ABA response element binding factor.
401	Os08g0273600	CI488276	-1.11	-0.15	0.08	-0.21	0.23	(No Hit)
402	Os02g0629400	AK085208	-1.11	0.01	0.00	-0.42	0.20	Phenylalanine ammonia-lyase (EC 4.3.1.5).
403	Os03g0163200	AK106987	-1.12	-0.08	0.06	-0.34	-0.12	Conserved hypothetical protein.
404	Os02g0644000	AY062178	-1.12	-0.02	0.06	-0.04	0.03	C13 endopeptidase NP1 (Fragment).
405	Os04g0510900	AK063625	-1.12	-0.02	0.03	-0.26	0.30	Embryo-specific protein 1 (ATS1).
406	Os02g0644000	AY062178	-1.12	-0.02	0.05	-0.05	0.06	C13 endopeptidase NP1 (Fragment).
407	Os06g0484500	AK108194	-1.13	0.06	-0.11	-0.27	-0.16	Hypothetical protein.
408	Os01g0644200	AK063634	-1.13	-0.13	0.13	-0.51	0.24	Conserved hypothetical protein.
409	Os08g0329900	AK107815	-1.13	-0.22	-0.07	-0.28	-0.20	Conserved hypothetical protein.
410	Os05g0474900	AK061963	-1.13	-0.23	-0.13	-0.37	0.53	Aldose reductase (EC 1.1.1.21) (AR) (Aldohydro reductase).
411	Os06g0110200	AK107973	-1.13	-0.15	0.05	-0.04	0.15	Late embryogenesis abundant (LEA) group 1 family protein.
412	Os05g0470100	CI278113	-1.13	0.02	0.06	-0.30	0.16	(No Hit)
413	Os03g0411300	CI256714	-1.13	-0.03	0.20	-0.21	0.21	Calcium-binding EF-hand domain containing protein.
414	Os12g0147000	AK107332	-1.13	0.01	0.11	-0.28	-0.20	Hypothetical protein.
415	Os08g0273600	CI451276	-1.13	-0.15	0.09	-0.20	0.48	(No Hit)
416	Os05g0474600	AK102864	-1.13	-0.24	0.04	-0.37	0.18	Aldose reductase (EC 1.1.1.21) (AR) (Aldohydro reductase).
417	Os03g0277500	AK063630	-1.14	0.03	0.04	-0.19	0.06	Glycosyltransferase family protein.
418	Os02g0596900	AK111075	-1.14	0.04	0.05	-0.21	0.15	Conserved hypothetical protein.
419	Os10g0576600	AK104125	-1.14	0.03	0.08	0.00	-0.19	TPR-like domain containing protein.
420	Os03g0140000	CI223237	-1.14	0.07	-0.14	-0.21	0.16	Conserved hypothetical protein.
421	Os04g0559700	AK059064	-1.14	0.02	0.08	-0.33	0.16	AP2/EERF transcription factor BABY BOOM1.
422	Os06g0651200	AK107748	-1.14	-0.04	0.11	-0.17	0.10	Hypothetical protein.
423	Os09g0327000	AK063334	-1.14	0.14	0.05	-0.34	0.38	Protein phosphatase 2C (EC 3.1.3.16) (PP2C).
424	Os06g0698300	AK071637	-1.14	0.00	0.05	-0.30	0.01	Protein phosphatase 2C family protein.
425	Os09g0399900	AK071589	-1.14	0.03	0.11	-0.25	-0.42	Protein of unknown function DUF125 family protein.
426	Os02g0809500	AK100684	-1.14	-0.05	0.05	-0.40	-0.12	Conserved hypothetical protein.
427	Os10g0576600	AK081955	-1.15	0.02	0.08	-0.01	-0.08	TPR-like domain containing protein.
428	Os02g0644000	AY062178	-1.15	-0.02	0.06	-0.06	0.02	C13 endopeptidase NP1 (Fragment).
429	Os04g0178300	AK121319	-1.15	-0.18	-0.39	-0.62	-0.13	Coagul/diphosphate synthetase (Fragment).
430	Os03g0681000	CI404894	-1.15	-0.16	0.07	-0.21	0.29	(No Hit)
431	Os02g0644000	AY062178	-1.15	-0.01	0.08	-0.05	0.05	C13 endopeptidase NP1 (Fragment).
432	Os02g0657000	AK108830	-1.15	0.05	-0.01	-0.19	-0.12	AP2 domain-containing protein Rap211.
433	Os01g0388000	AK069778	-1.16	0.05	-0.04	-0.28	0.10	Cytochrome P450 family protein.
434	Os04g0178300	AK153101	-1.16	-0.17	-0.40	-0.59	-0.21	Coagul/diphosphate synthetase (Fragment).
435	Os05g0557900	AK103110	-1.16	0.08	-0.03	-0.41	-0.31	Esterase/lipase/esterase domain containing protein.
436	Os02g0252700	AK103494	-1.17	-0.16	0.01	-0.41	-0.22	Conserved hypothetical protein.
437	Os03g0197300	AK102651	-1.17	-0.05	0.07	-0.31	0.25	RmlC-like cupin family protein.
438	Os07g0489900	AK083422	-1.18	-0.08	0.12	-0.30	0.10	Cysteine protease (Fragment).
439	Os09g0482300	AY688675	-1.19	-0.06	-0.07	-0.22	0.14	Conserved hypothetical protein.
440	Os05g0381400	AK102039	-1.19	-0.10	0.15	-0.39	0.18	ABA induced plasma membrane protein PM 19.
441	Os10g0127700	AK107885	-1.19	-0.03	0.06	-0.23	0.22	Conserved hypothetical protein.
442	Os12g0134000	AK127540	-1.19	0.02	0.08	-0.04	-0.10	VMP5 protein.
443	Os05g0468800	CI459446	-1.20	-0.02	0.08	-0.23	0.31	Cold-regulated protein.
444	Os03g0153500	Os03g0153500	-1.21	0.00	0.02	-0.35	-0.52	Aromatic-ring hydroxylase family protein.
445	Os03g0793700	U43521	-1.21	-0.11	0.07	-0.38	-0.41	Globulin 2 (Fragment).
446	Os05g0110100	AK099779	-1.22	-0.06	0.03	-0.15	-0.26	Conserved hypothetical protein.
447	Os04g0231800	AK068417	-1.22	-0.17	0.08	-0.21	0.17	Protein of unknown function DUF1165 family protein.
448	Os02g0570400	AB089272	-1.22	-0.05	-0.41	-0.64	-0.04	Terpene synthase, metal-binding domain containing protein.
449	Os05g0140900	AK118552	-1.22	-0.16	0.06	-0.32	-0.03	Glucosyltransferase family protein.
450	Os04g0589800	AK063682	-1.22	-0.05	-0.04	-0.20	0.18	Late embryogenesis abundant (LEA) group 1 family protein.
451	Os07g0190000	AK109009	-1.23	-0.11	-0.32	-0.55	-0.04	1-deoxy-D-xylulose 5-phosphate synthase 2 precursor.
452	Os03g0161000	CI128125	-1.23	0.01	0.14	-0.29	0.24	Late embryogenesis abundant protein repeat containing protein.
453	Os05g0381700	CI483366	-1.23	-0.18	0.00	-0.30	-0.27	Harpin-induced 1 domain containing protein.
454	Os04g0390800	AK108276	-1.24	-0.03	0.01	-0.17	0.31	Short-chain dehydrogenase/reductase SDR family protein.
455	Os06g0650700	AK107886	-1.26	-0.08	-0.07	-0.32	0.13	Non-protein coding transcript, unclassifiable transcript.
456	Os08g0473900	AK119565	-1.26	0.01	-0.07	-0.14	-0.01	Phosphotransferase family protein.
457	Os03g0808300	AK109389	-1.26	0.02	0.04	-0.23	0.35	Remorin, C-terminal region domain containing protein.
458	Os05g0249300	CI476617	-1.27	-0.16	0.08	-0.21	0.30	

506	Ox070422100	U57639	-1.53	-0.10	-0.07	-0.29	-0.54	AWPM-19-like family protein.
507	Ox090336100	AK105307	-1.54	-0.08	-0.15	-0.40	0.23	RrmC-like cupin family protein.
508	Ox010702500	AK333185	-1.54	-0.12	0.00	-0.23	-0.02	Dehydrin RA425.
509	Ox120464400	AK121922	-1.55	-0.04	-0.02	-0.15	-0.02	Short-chain dehydrogenase/reductase SDR family protein.
510	Ox070422100	AK063592	-1.55	-0.11	-0.04	-0.28	-0.53	AWPM-19-like family protein.
511	Ox100505900	AK062588	-1.56	-0.05	0.07	-0.32	0.03	Conserved hypothetical protein.
512	Ox040386700	CI061748	-1.56	-0.02	0.10	-0.28	0.01	Conserved hypothetical protein.
513	Ox1100671000	AK119708	-1.57	-0.04	0.12	-0.02	0.20	Dormancy-associated protein.
514	Ox1100451700	CI050356	-1.58	-0.10	0.14	-0.63	-0.20	Dehydrin 9.
515	Ox010702500	AK064074	-1.58	-0.03	0.08	-0.29	-0.07	Late embryogenesis abundant protein repeat containing protein.
516	Ox010702500	AK073837	-1.58	-0.03	0.08	-0.26	0.01	Late embryogenesis abundant protein repeat containing protein.
517	Ox010702500	D26536	-1.59	-0.03	0.08	-0.28	0.01	Late embryogenesis abundant protein repeat containing protein.
518	Ox070638300	AK102962	-1.63	0.00	0.04	-0.27	0.29	Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
519	Ox040434400	AK063725	-1.65	0.00	0.16	-0.22	0.01	Hypothetical protein.
520	Ox070638300	AK101401	-1.71	0.00	0.04	-0.27	0.28	Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
521	Ox070638300	D63917	-1.71	0.00	0.04	-0.27	0.30	Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
522	Ox060793700	AY068743	-1.73	-0.09	0.09	-0.43	-0.66	Globulin 2 (Fragment).
523	Ox070638300	AY336994	-1.74	0.00	0.04	-0.27	0.31	Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2)
524	Ox1100582400	AF516927	-1.78	-0.21	-0.12	-0.94	0.29	Hypothetical protein.
525	Ox1100582400	U25969	-1.82	-0.22	-0.11	-0.92	0.16	Hypothetical protein.
526	Ox1100582400	AK073083	-1.82	-0.23	-0.11	-0.91	0.22	Hypothetical protein.
527	Ox060602300	AK107469	-1.82	-0.22	-0.07	-0.20	0.18	Cinnamoyl-CoA reductase (EC 1.2.1.44).
528	Ox1100582400	AK108352	-1.86	-0.22	-0.11	-0.96	0.22	Hypothetical protein.
529	Ox060793700	AK121667	-1.92	-0.13	0.07	-0.45	-0.37	Globulin 2 (Fragment).
530	Ox1100582400	AF049348	-2.02	-0.21	0.03	-0.86	-0.09	Hypothetical protein.

* The log₂ ratio of the GA-induced signal intensity change.

Table S9. List of probes categorized under Down-group2.

Probe#	ID	Accession	WT±GA*	gid1±GA*	slr1±GA*	gid2±GA*	gamyb±GA*	Annotation
1	Os07g0561800	AK108426	-0.70	0.04	0.20	0.13	-0.10	Hypothetical protein.
2	Os02g0831000	Cl122953	-0.72	-0.07	0.10	0.04	-0.15	(No Hit)
3	Os06g0557100	AK119892	-0.73	-0.07	-0.07	-0.02	-0.20	Protein kinase domain containing protein.
4	Os01g0880300	AK101962	-0.73	-0.03	-0.15	0.09	-0.11	Pectinesterase family protein.
5	Os09g0505500	Cl122953	-0.73	-0.08	0.12	0.04	-0.07	(No Hit)
6	Os03g0669300	AK061572	-0.73	0.00	-0.05	-0.10	-0.31	Beta-1,3-glucanase-like protein.
7	Os07g0666600	AK068545	-0.73	-0.16	-0.17	-0.19	-0.35	Conserved hypothetical protein.
8	Os10g0506900	AK067420	-0.74	-0.17	0.11	0.12	-0.06	Hypothetical protein.
9	Os02g0522300	AK068634	-0.76	-0.12	0.10	0.14	-0.28	Hypothetical protein.
10	Os11g0552500	Cl275181	-0.76	0.01	-0.09	0.00	-0.33	(No Hit)
11	Os03g0737000	AK100865	-0.77	-0.01	0.08	0.22	-0.24	CBS domain containing protein.
12	Os10g0506900	AK064891	-0.77	-0.16	0.14	0.12	0.03	Hypothetical protein.
13	Os03g0826900	AK099709	-0.78	-0.12	0.01	-0.07	-0.26	Conserved hypothetical protein.
14	Os01g0704300	AK068954	-0.78	0.00	-0.04	-0.08	-0.24	Galactose oxidase, central domain containing protein.
15	Os04g0690900	Cl064179	-0.78	-0.02	-0.05	0.18	-0.18	(No Hit)
16	Os03g0305400	AK071397	-0.79	-0.04	0.18	0.16	0.00	Universal stress protein (Usp) family protein.
17	Os11g0475500	AK102516	-0.79	-0.06	0.10	-0.05	-0.22	Hypothetical protein.
18	Os11g0442500	Cl064179	-0.79	-0.02	-0.03	0.18	-0.16	Basic helix-loop-helix dimerisation region bHLH domain containing protein.
19	Os07g0601000	AK067272	-0.80	-0.04	0.20	0.07	0.17	NADPH HC toxin reductase (Fragment).
20	Os07g0561800	AK111334	-0.80	0.02	-0.03	0.13	-0.05	Hypothetical protein.
21	Os09g0436000	Cl399152	-0.82	-0.04	0.10	0.03	-0.28	Conserved hypothetical protein.
22	Os04g0480700	AK121175	-0.82	0.05	0.20	0.00	-0.18	Cytochrome P450 71A1 (EC 1.14.--) (CYPLXXIA1) (ARP-2).
23	Os02g0533800	AK121139	-0.82	-0.04	0.26	0.01	-0.17	Conserved hypothetical protein.
24	Os02g0725900	AJ300218	-0.83	-0.19	-0.25	-0.01	-0.21	Transcription factor CBF/NF-Y/archaeal histone domain containing protein.
25	Os04g0690900	Cl443257	-0.83	-0.02	-0.03	0.18	-0.20	(No Hit)
26	Os03g0669300	AK120903	-0.84	0.00	-0.05	-0.10	-0.37	Beta-1,3-glucanase-like protein.
27	Os11g0429900	Cl215581	-0.84	-0.05	0.08	0.04	-0.35	Hypothetical protein.
28	Os04g0658200	Cl452886	-0.85	0.06	-0.04	-0.11	-0.29	(No Hit)
29	Os11g0429800	Cl215581	-0.85	-0.04	0.07	0.04	-0.37	Conserved hypothetical protein.
30	Os02g0522300	AK068116	-0.85	-0.06	-0.08	0.04	-0.27	Hypothetical protein.
31	Os10g0506900	AK100756	-0.86	-0.07	0.07	0.09	-0.28	Hypothetical protein.
32	Os01g0138900	AK058378	-0.86	-0.04	-0.05	-0.16	-0.42	Mandelate racemase/muconate lactonizing enzyme family protein.
33	Os11g0444700	AK104816	-0.88	-0.07	0.09	0.10	0.02	Octicosapeptide/Phox/Bem1p domain containing protein.
34	Os05g0553300	AK107804	-0.88	-0.18	0.05	0.02	-0.17	Conserved hypothetical protein.
35	Os10g0576600	AK060369	-0.89	0.02	0.00	0.03	-0.34	TPR-like domain containing protein.
36	Os01g0239700	AK067723	-0.89	0.06	-0.04	-0.01	-0.34	Leucine-rich receptor-like protein kinase.
37	Os11g0444700	AK066452	-0.90	-0.07	0.10	0.10	0.02	Octicosapeptide/Phox/Bem1p domain containing protein.
38	Os01g0239700	AK070058	-0.90	0.05	-0.01	-0.01	-0.37	Leucine-rich receptor-like protein kinase.
39	Os04g0658200	Cl452886	-0.90	0.07	-0.02	-0.11	-0.27	(No Hit)
40	Os01g0239700	AK122130	-0.91	0.07	-0.03	-0.02	-0.35	Leucine-rich receptor-like protein kinase.
41	Os04g0635700	AK098916	-0.91	-0.05	0.09	0.14	-0.10	Conserved hypothetical protein.
42	Os01g0773700	AK119161	-0.92	-0.08	0.00	0.06	0.04	Photosystem II reaction center W protein (PSII 6.1 kDa protein) (Fragment).
43	Os08g0394000	Cl443895	-0.93	-0.12	0.03	-0.12	-0.41	Hypothetical protein.
44	Os06g0642500	AK067059	-0.94	-0.07	-0.01	0.22	-0.24	Cytochrome P450 71A1 (EC 1.14.--) (CYPLXXIA1) (ARP-2).
45	Os03g0198600	AY554034	-0.94	0.01	0.06	0.16	-0.34	Homeodomain leucine zipper protein CPHB-7.
46	Os04g0587500	AK060241	-0.94	-0.07	-0.08	-0.09	-0.36	Conserved hypothetical protein.
47	Os03g0198600	AK073446	-0.95	0.01	0.07	0.17	-0.32	Homeodomain leucine zipper protein CPHB-7.
48	Os10g0510400	AK100601	-0.96	0.03	0.06	0.03	-0.28	Putative methyltransferase DUF248 family protein.
49	Os10g0510400	AK073237	-0.96	0.03	0.08	0.03	-0.27	Putative methyltransferase DUF248 family protein.
50	Os05g0205100	AK111332	-0.97	-0.15	-0.22	0.27	-0.30	NLI interacting factor domain containing protein.
51	Os11g0605100	AK065824	-0.97	-0.13	0.16	0.10	-0.20	Disease resistance protein family protein.
52	Os04g0526600	AY166458	-1.00	0.06	-0.01	-0.10	-0.43	Alpha-amylase/subtilisin inhibitor (RASI).
53	Os01g0773700	AK060438	-1.01	-0.09	0.02	0.07	0.01	Photosystem II reaction center W protein (PSII 6.1 kDa protein) (Fragment).
54	Os04g0583200	AK073181	-1.04	-0.04	-0.10	-0.13	-0.41	Conserved hypothetical protein.
55	Os03g0409100	AK073459	-1.05	-0.03	0.24	0.08	-0.44	Ankyrin repeat containing protein.
56	Os06g0306600	AK106075	-1.08	-0.05	-0.03	0.10	-0.15	Esterase/lipase/thioesterase domain containing protein.
57	Os03g0409100	AK105845	-1.08	-0.02	0.28	0.09	-0.33	Ankyrin repeat containing protein.
58	Os02g0185400	Cl448460	-1.09	-0.03	0.17	0.04	-0.31	E-class P450, group I family protein.
59	Os01g0192000	AK100770	-1.12	0.10	0.04	0.04	-0.51	Zn-finger, C-x8-C-x5-C-x3-H type domain containing protein.
60	Os01g0192000	AK073660	-1.12	0.10	0.04	0.03	-0.39	Zn-finger, C-x8-C-x5-C-x3-H type domain containing protein.
61	Os07g0529600	AK099918	-1.13	-0.06	0.12	0.04	-0.29	Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
62	Os07g0529600	AK064916	-1.13	-0.06	0.11	0.04	-0.31	Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
63	Os08g0505900	AK120908	-1.16	-0.01	-0.16	0.17	-0.20	DNA-damage-repair/tolerance protein DRT100 precursor.
64	Os06g0147100	AK120518	-1.18	-0.08	0.08	0.03	-0.40	Conserved hypothetical protein.
65	Os08g0505900	AK060670	-1.18	0.00	-0.10	0.17	-0.29	DNA-damage-repair/tolerance protein DRT100 precursor.
66	Os06g0147100	AK119696	-1.19	-0.08	0.09	0.03	-0.36	Conserved hypothetical protein.
67	Os04g0233400	AK061312	-1.23	-0.24	0.05	-0.06	-0.54	MipE.
68	Os04g0233400	AK061491	-1.28	-0.23	-0.01	-0.06	-0.58	MipE.
69	Os03g0580300	Cl455551	-1.33	-0.11	0.06	0.15	-0.37	(No Hit)
70	Os02g0115700	AK065094	-1.34	-0.24	0.07	0.18	0.07	Catalase isozyme A (EC 1.11.1.6) (CAT-A).
71	Os04g0233400	AK102155	-1.37	-0.23	-0.03	-0.05	-0.57	MipE.
72	Os06g0572400	AK070273	-1.44	0.06	-0.03	0.01	-0.61	CD9/CD37/CD63 antigen family protein.
73	Os11g0138300	AK103307	-1.66	0.07	-0.03	-0.35	-0.81	E-class P450, group I family protein.

* The log₁₀ ratio of the GA-induced signal intensity change.