

Electronic Supplementary Information†

Title: RNA-sequencing *Oryza sativa* transcriptome in response to herbicide isoproturon and characterization of genes involved in IPU detoxification

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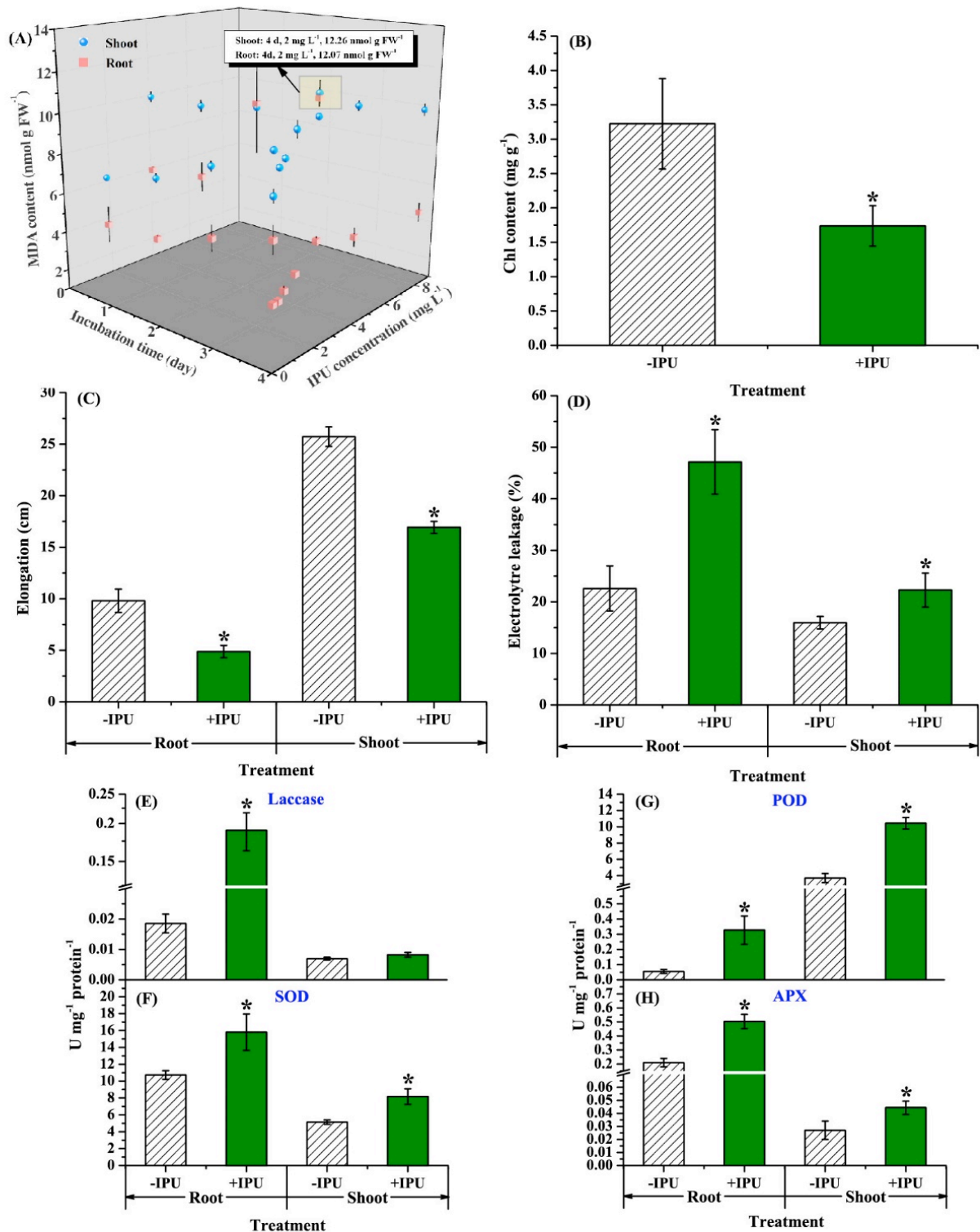
EIC Figs. S1–7 (Pages 2–11);

EIC Tables S1–11 (Pages 12–92);

EIC Data S1—Materials and methods (Pages 93–97);

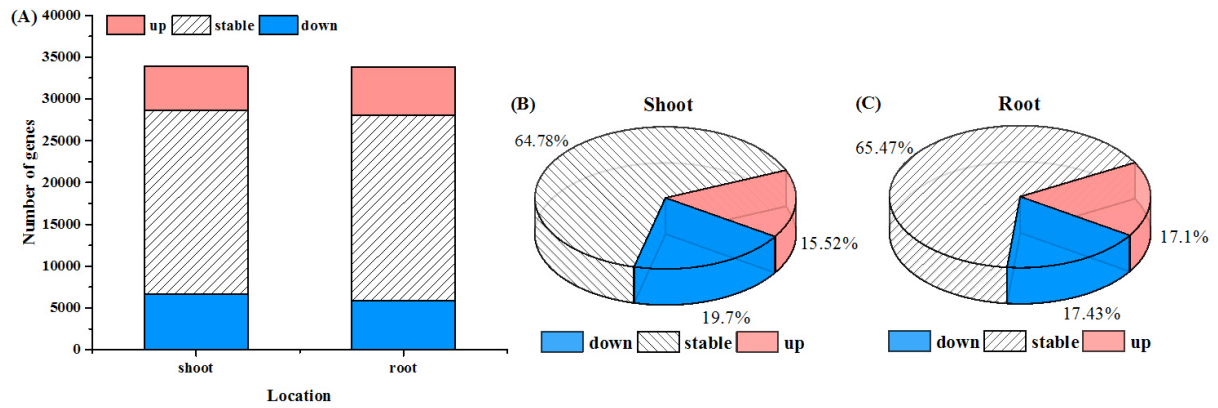
EIC Data S2—Results and discussion (Pages 97–102).

† Electronic supplementary information (ESI) available. See online.

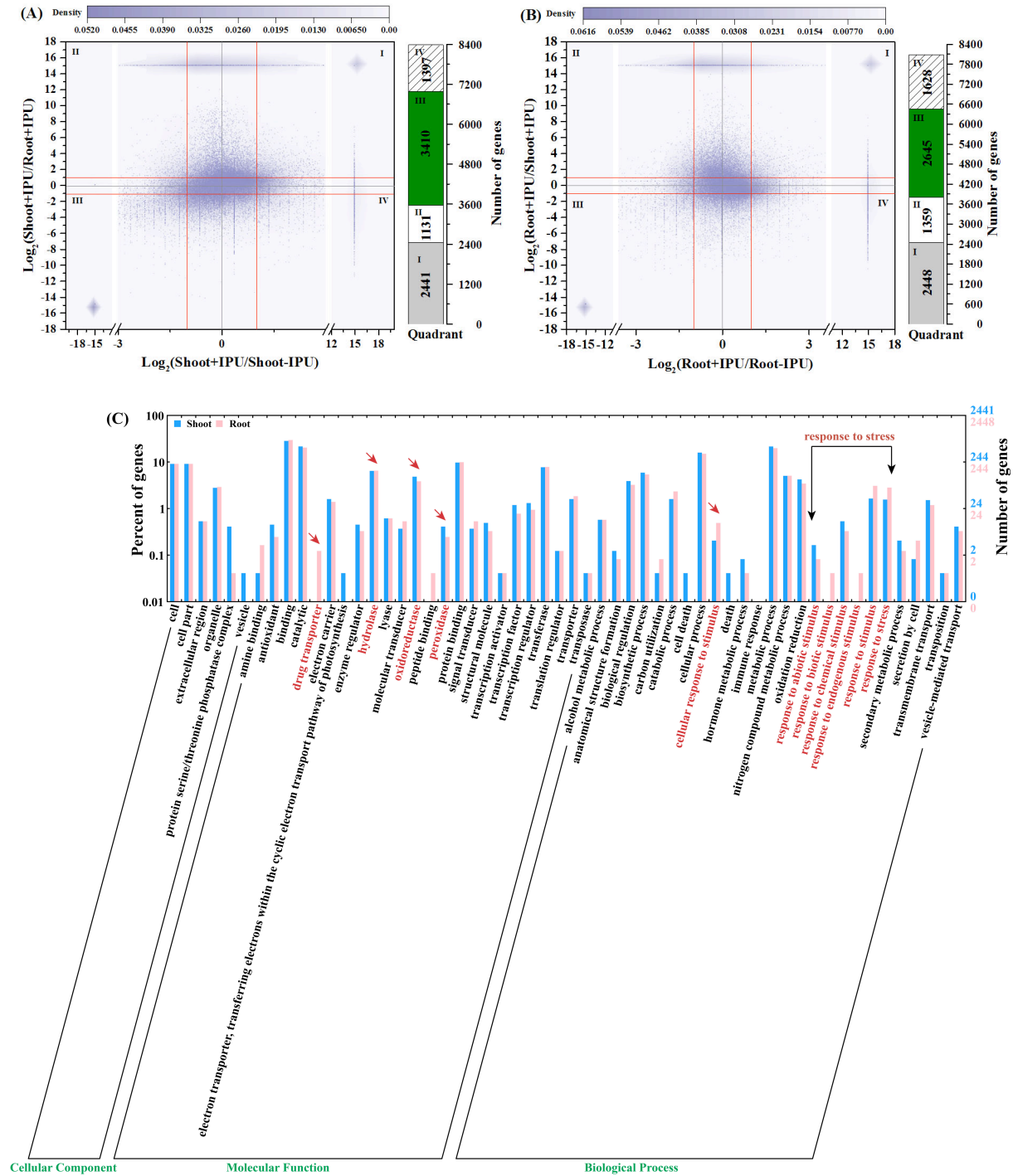


ESI Fig. S1 Effect of isoproturon on the content of MDA (A) and chlorophyll (B), elongation (C), electrolyte leakage (D), and laccase (E), SOD (F), POD (G) and APX (H) activities of rice. Rice seedlings for MDA test were exposed to 0, 2, 4, 6, 8 mg L⁻¹ IPU for 1, 2, 3, 4 d. For

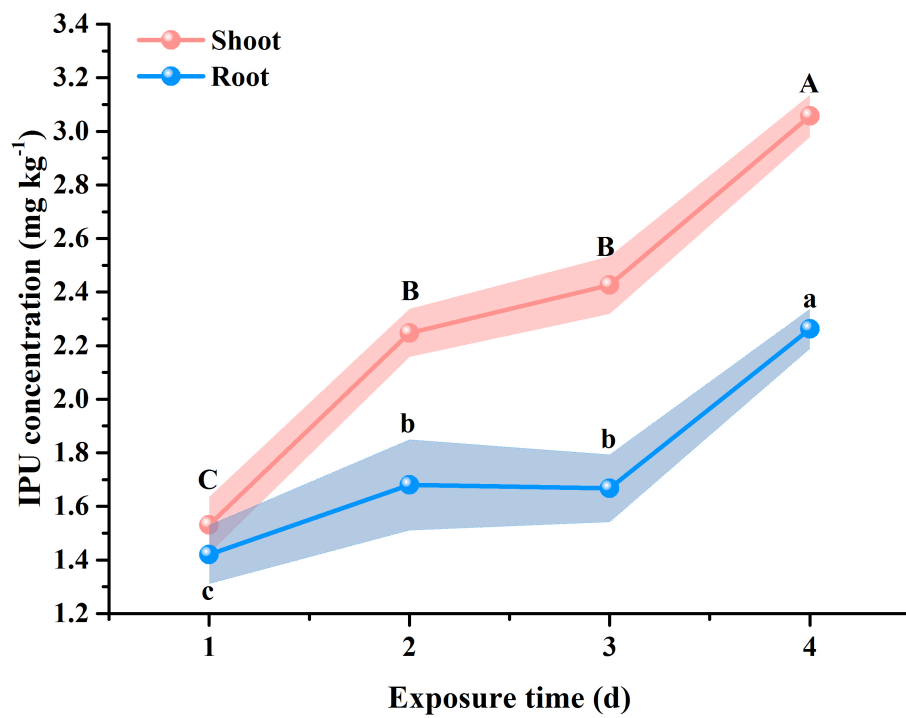
the rest experiments, rice seedlings were exposed to 0 and 2 mg L⁻¹ IPU for 4 d. Values are the means \pm SD ($n=3$). Asterisks indicate significant differences between the treatments and the control ($p < 0.05$).



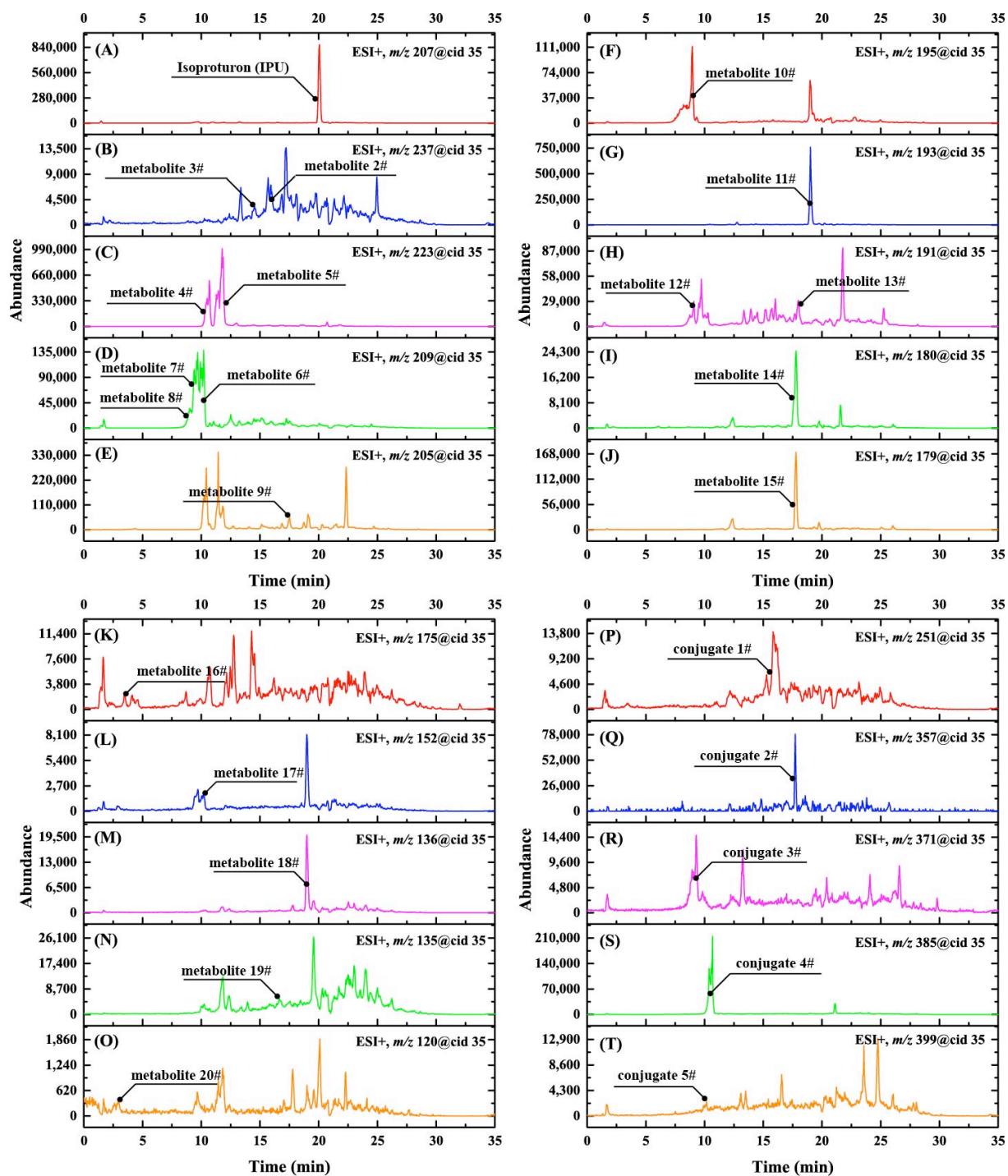
ESI Fig. S2 Number and percentage of genes regulated or with a stable expression after IPU application compared to control. (A) Number of genes up-regulated, down-regulated or with a stable expression in shoot and root of IPU-treated rice seedlings compared to the control. (B, C) The percentage of genes up-regulated, down-regulated or with a stable expression in shoot and root of IPU-treated rice seedlings compared to the control.



ESI Fig. S3 2D density plot of gene expression analysis and Gene Ontology (GO) term enrichment analyses of DEGs which are both induced by IPU and up-regulation in s in shoot and root of *Oryza sativa*. The gene-normalized signal intensities are shown in the density plot using a Log_2Ratio .



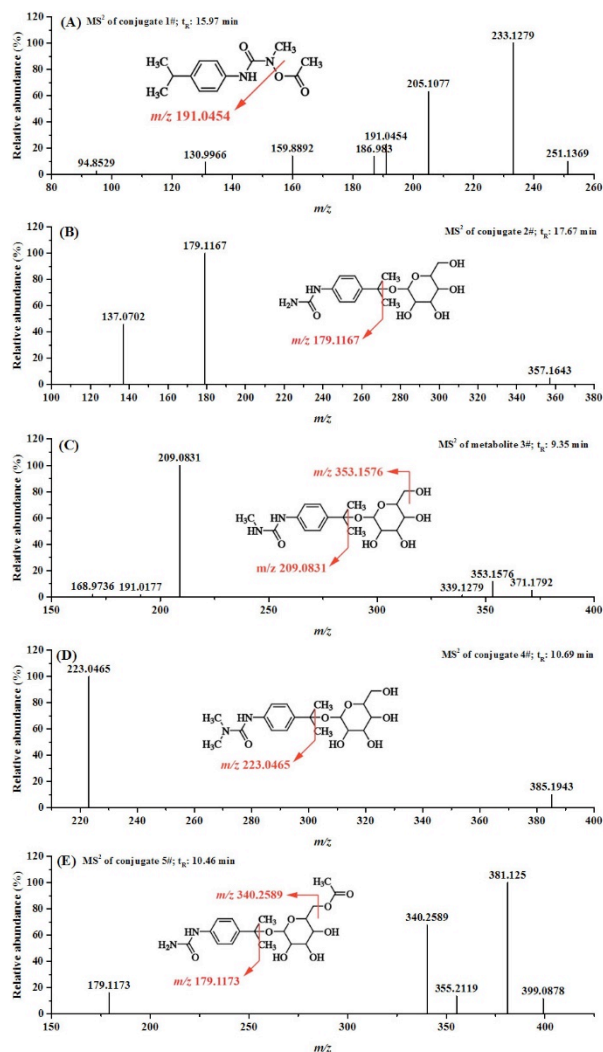
ESI Fig. S4 IPU content in shoot and root of rice exposed to 2 mg L⁻¹ for 1, 2, 3 and 4 d.



ESI Fig. S5 Extracted ion chromatograms of isotreturon (IPU) and its metabolites and conjugates in rice from UHPLC LTQ Orbitrap XL analysis. (A) Extracted ion chromatogram of m/z 207.1479 (IPU). The metabolites as follow: (B) the peak of metabolite 2# (m/z 237.1575) at 15.71 min and metabolite 3# (m/z 237.1212) at 14.49 min; (C) the peak of

metabolite 4# (m/z 223.1423) at 10.66 min and metabolite 5# (m/z 223.1423) at 11.69 min; (D) the peak of metabolite 6# (m/z 209.1276) at 10.18 min, metabolite 7# (m/z 209.1276) at 9.65 min and metabolite 8# (m/z 209.1276) at 9.40 min; (E) the peak of metabolite 9# (m/z 205.1323) at 17.35 min; (F) the peak of metabolite 10# (m/z 195.1140) at 7.94 min; (G) the peak of metabolite 11# (m/z 193.1335) at 18.96 min; (H) the peak of metabolite 12# (m/z 191.1172) at 8.63 min and metabolite 13# (m/z 191.1172) at 17.88 min; (I) the peak of metabolite 14# (m/z 180.1371) at 17.59 min; (J) the peak of metabolite 15# (m/z 179.1167) at 17.78 min; (K) the peak of metabolite 16# (m/z 175.0856) at 3.15 min; (L) the peak of metabolite 17# (m/z 152.1061) at 10.23 min; (M) the peak of metabolite 18# (m/z 136.1111) at 18.84 min; (N) the peak of metabolite 19# (m/z 135.0794) at 16.66 min; (O) the peak of metabolite 20# (m/z 120.0802) at 2.74 min. The conjugates as follow: (P) the peak of conjugate 1# (m/z 251.1369) at 15.97 min; (Q) the peak of conjugate 2# (m/z 357.1643) at 15.97 min; (R) the peak of conjugate 3# (m/z 371.1792) at 9.35 min; (S) the peak of conjugate 4# (m/z 385.1943) at 10.69 min; (T) the peak of conjugate 5# (m/z 399.1730) at 10.46 min.

Supplementary Figure S6. MS² spectra of IPU and its metabolites in rice from UHPLC LTQ Orbitrap XL analysis. The ion data were obtained from (A) IPU with precursor ion *m/z* 207.1479, (B) metabolite 2# with precursor ion *m/z* 237.1575, (C) metabolite 3# with precursor ion *m/z* 237.1212, (D) metabolite 4# with precursor ion *m/z* 223.1423, (E) metabolite 5# with precursor ion *m/z* 223.1423, (F) metabolite 6# with precursor ion *m/z* 209.1276, (G) metabolite 7# with precursor ion *m/z* 209.1276, (H) metabolite 8# with precursor ion *m/z* 209.1276, (I) metabolite 9# with precursor ion *m/z* 205.1323, (J) metabolite 10# with precursor ion *m/z* 195.1140, (K) metabolite 11# with precursor ion *m/z* 193.1326, (L) metabolite 12# with precursor ion *m/z* 191.1172, (M) metabolite 13# with precursor ion *m/z* 191.1172, (N) metabolite 14# with precursor ion *m/z* 180.1371, (O) metabolite 15# with precursor ion *m/z* 179.1167, (P) metabolite 11# with precursor ion *m/z* 175.0856, (Q) metabolite 17# with precursor ion *m/z* 152.1061, (R) metabolite 18# with precursor ion *m/z* 136.1111, (S) metabolite 19# with precursor ion *m/z* 135.0794, and (T) metabolite 20# with precursor ion *m/z* 120.0802 of degradation products.



Supplementary Figure S7. MS² spectra of conjugates of IPU in rice from UHPLC LTQ Qorbitrap XL analysis. The ion data were obtained from (A) conjugate 1# with precursor ion m/z 251.1369, (B) conjugate 2# with m/z precursor ion 357.1643, (C) conjugate 3# with precursor ion m/z 371.1792, (D) conjugate 4# with precursor ion m/z 385.1943, and (E) conjugate 5# with precursor ion m/z 399.1730 of conjugates.

ESI Table S1.

Results from transcriptome analysis with reference genome of *Oryza sativa* cDNA using Solexa RNA paired-end sequencing

Sample	Raw Data		Valid Data			Valid Ratio (Base)
	Read	Base	Read	Base	Average length	
Shoot+IPU	26113896	2611389600	25735956	2562496108	99.56	98.12%
Shoot-IPU	29482952	2948295200	29038570	2891052202	99.55	98.05%
Root+IPU	22209562	2220956200	21758504	2162612328	99.39	97.37%
Root-IPU	24517652	2451765200	23983926	2380447568	99.25	97.09%

ESI Table S2.

Reads number based on the RNA-Seq data in four libraries of rice exposed to IPU.

Libraries name	Clean reads ^a	Aligned ratio ^b
Shoot+IPU	12867978	94.25%
Shoot-IPU	14519285	94.45%
Root+IPU	10879252	77.34%
Root-IPU	11991963	72.36%

^aClean reads which are filtered from dirty raw reads are mapped to reference sequences using soap2.21.

Mismatches no more than 2 bases are allowed in the alignment. Mapped reads are the sum of perfect match reads and less than 2 bp mismatch reads.

^bNumbers enclosed in parenthesis represent the percent of reads in each library.

ESI Table S3.

Primer sequences used for real-time PCR analyses.

Gene symbol	Primer sequence		Amplicon length (bp)	E(%)
		(5'-3')		
Os08t0547300	S	GTGATGTGGTCGGTGTTCCGG	20	98.7
	A	TCTTCTTGAGGTCAAAGGGTGC	22	
Os08t0152400	S	TGACCGTGATGGAGCCGTTC	20	101.3
	A	GCTGAGGAAGTTGCCGAGGA	20	
Os04t0206700	S	GCCGAAGGAGGCAGATTAC	19	96.8
	A	ACGCCAAGCAAGGTGAAGT	19	
Os10t0555100	S	CCAGCCTTCTATGGATGTCTTC	22	98.6
	A	GCGATATGTCCCGTTGAGC	19	
Os12t0123200	S	GGCTCCCTGTCGTATGTGATTC	22	100.8
	A	TGTCCAGAGGCAGCAGATGTT	21	
Os07t0168300	S	AGTCCCAGGTCATCGTCCAGT	21	91.7
	A	CGCCGTGTAGAACGACCTGTT	21	
Os09t0344500	S	GGCTCCCAGTAACAACAACATC	22	94.3
	A	TACCTTTCCTCCAGCATCCC	20	
Os05t0102000	S	GTGGTTGAGCCTATGCTTGGAC	22	99.7
	A	GGTCGTTGTTGTGGCGGTAG	20	
Os03t0273200	S	TGCCTCGCATTGCTTCTCC	19	99.3
	A	GTGCCAGTGGATGGTAATGTTG	22	
Os01t0850700	S	AATGGTGGAGCCGGAATGT	19	98.8
	A	TGAAGAAGAGGTGCGTGTTGAGT	23	
Os01t0770500	S	GACCCATCGACTGGAAGAAC	20	93.3
	A	TCAAAGTGACCGAAGTAGCG	20	
Os09t0472100	S	GCGTTGGCAGGAAGGTTAGG	20	102.5
	A	ACCGTCAGCGTGTTTCATCAG	20	

S and A represent sense and antisense;

E, amplification efficiency.

ESI Table S4.

Recoveries, RSD and detection limit of IPU in plant tissues.

Sample	Added concentration (mg kg ⁻¹)	Recovery (%)			Average recovery (%)	RSD (%)	IDL pg injected	MDL (mg kg ⁻¹)	MQL (mg kg ⁻¹)
		1	2	3					
Shoot	0.5	95.7	101.3	92.2	96.4	4.76			
	1.0	107.7	104.5	108.2	106.8	1.88		0.0114	0.0380
	5.0	106.9	105.7	101.4	104.7	2.76			
Root	0.5	104.3	91.0	96.5	97.3	6.87	57.5		
	1.0	99.0	102.9	102.3	101.4	2.07		0.00371	0.0124
	5.0	89.8	93.4	90.2	91.1	2.17			

RSD, relative standard deviation;

IDL, instrumental detection limits;

MDL, method detection limits;

MQL, method quantification limits.

ESI Table S5. Top 200 annotated genes most up-regulation in shoots and roots in the presence of IPU and absence of IPU.

Rank overall	Gene ID	Shoot			R	FDR	Annotation
		FPKM		Log ₂ Ratio			
		Control	IPU				
1	Os01t0729900-03	0.00	896.87	Inf	up	9.25E-14	Conserved hypothetical protein.
2	Os08t0473900-03	0.00	779.79	Inf	up	2.11E-13	Similar to Alpha amylase isozyme 3D.
3	Os01t0283100-02	0.00	475.15	Inf	up	2.83E-11	Similar to Ferripyochelin-binding protein-like.
4	Os07t0179700-00	0.00	362.61	Inf	up	8.77E-10	Hypothetical conserved gene.
5	Os01t0186400-01	0.00	331.92	Inf	up	2.76E-09	Hypothetical conserved gene.
6	Os04t0488700-02	0.00	325.10	Inf	up	3.37E-09	Similar to protein kinase KIPK.
7	Os07t0204900-02	0.00	302.37	Inf	up	8.48E-09	Similar to Zeta-carotene desaturase.
8	Os04t0394200-03	0.00	251.22	Inf	up	6.89E-08	Similar to 2-oxoglutarate dehydrogenase E2 subunit.
9	Os12t0504900-00	0.00	242.12	Inf	up	9.68E-08	Glucoamylase, putative domain containing protein.
10	Os02t0775600-02	0.00	229.62	Inf	up	1.89E-07	Zinc finger, C2H2-like domain containing protein.
11	Os11t0704600-02	0.00	214.84	Inf	up	4.05E-07	Similar to Beta-1,3 glucanase precursor (EC 3.2.1.39).
12	Os06t0129900-02	0.00	205.75	Inf	up	6.32E-07	Similar to cytochrome P450.
13	Os04t0440100-02	0.00	201.20	Inf	up	8.19E-07	Similar to H0525C06.10 protein.
14	Os02t0783700-01	0.00	178.47	Inf	up	2.81E-06	Similar to Lysine ketoglutarate reductase/saccharopine dehydrogenase.
15	Os03t0729200-03	0.00	173.92	Inf	up	3.59E-06	Similar to predicted protein.
16	Os03t0165300-02	0.00	158.00	Inf	up	9.07E-06	Homeobox domain containing protein.
17	Os01t0621900-04	0.00	152.32	Inf	up	1.23E-05	Hypothetical conserved gene.
18	Os03t0758300-02	0.00	143.23	Inf	up	2.21E-05	Similar to Cyclic nucleotide-gated ion channel 2 (Fragment).
19	Os09t0323100-02	0.00	128.45	Inf	up	6.06E-05	Zinc finger, RING/FYVE/PHD-type domain containing protein.
20	Os03t0748000-02	0.00	125.04	Inf	up	7.48E-05	Similar to YT521-B-like family protein, expressed.
21	Os06t0655500-02	0.00	125.04	Inf	up	7.48E-05	Hypothetical conserved gene.
22	Os05t0411300-02	0.00	123.90	Inf	up	8.08E-05	Similar to DNA binding protein.
23	Os06t0126000-05	0.00	118.22	Inf	up	1.29E-04	Hypothetical conserved gene.

24	Os10t0503700-02	0.00	115.95	Inf	up	1.49E-04	Similar to ATP-dependent RNA helicase dhh1.
25	Os06t0663400-02	0.00	111.40	Inf	up	2.11E-04	Serine/threonine protein kinase-like protein.
26	Os11t0113700-02	0.00	110.26	Inf	up	2.30E-04	Serine/threonine protein kinase, Microbe-associated molecular pattern-induced defense signaling pathway
27	Os08t0473800-01	0.00	101.17	Inf	up	4.69E-04	Similar to Alpha-amylase isozyme 3D precursor (EC 3.2.1.1).
28	Os12t0113500-02	0.00	97.76	Inf	up	6.27E-04	Serine/threonine protein kinase, Microbe-associated molecular pattern-induced defense signaling pathway
29	Os08t0110800-02	0.00	95.48	Inf	up	7.40E-04	Hypothetical conserved gene.
30	Os09t0490200-02	0.00	95.48	Inf	up	7.40E-04	Similar to EIL3.
31	Os04t0670800-02	0.00	94.35	Inf	up	8.14E-04	UBX domain containing protein.
32	Os06t0335500-02	0.00	92.07	Inf	up	9.77E-04	Similar to Auxin-responsive protein IAA21.
33	Os04t0414100-02	0.00	89.80	Inf	up	1.19E-03	Similar to OSIGBa0137L20.4 protein.
34	Os02t0326000-01	0.00	88.66	Inf	up	1.31E-03	Protein of unknown function DUF2232, membrane domain containing protein.
35	Os01t0754500-02	0.00	87.53	Inf	up	1.44E-03	Hypothetical conserved gene.
36	Os01t0654100-03	0.00	86.39	Inf	up	1.58E-03	Similar to CTP synthase.
37	Os04t0441900-03	0.00	85.25	Inf	up	1.73E-03	Similar to predicted protein.
38	Os12t0459300-02	0.00	85.25	Inf	up	1.73E-03	Hypothetical gene.
39	Os08t0517001-00	0.00	84.12	Inf	up	1.89E-03	Hypothetical protein.
40	Os08t0556000-02	0.00	84.12	Inf	up	1.89E-03	Similar to predicted protein.
41	Os09t0459800-04	0.00	81.84	Inf	up	2.28E-03	Similar to predicted protein.
42	Os12t0439700-00	0.00	81.84	Inf	up	2.28E-03	Similar to RER1A protein.
43	Os10t0575200-03	0.00	79.57	Inf	up	2.77E-03	Similar to GRV2 (KATAMARI2)%3B binding / heat shock protein binding.
44	Os01t0958000-02	0.00	78.43	Inf	up	3.07E-03	Similar to Cyclin-dependent kinase C-2.
45	Os07t0681500-02	0.00	78.43	Inf	up	3.07E-03	Similar to predicted protein.
46	Os07t0467600-02	0.00	77.30	Inf	up	3.34E-03	Similar to predicted protein.
47	Os04t0571800-02	0.00	76.16	Inf	up	3.65E-03	Zinc finger, RING/FYVE/PHD-type domain containing protein.
48	Os09t0135800-02	0.00	76.16	Inf	up	3.65E-03	Armadillo-like helical domain containing protein.
49	Os03t0227800-01	0.00	75.02	Inf	up	3.97E-03	Conserved hypothetical protein.
50	Os08t0422000-02	0.00	73.89	Inf	up	4.31E-03	Similar to CM0545.530.nc protein (Fragment).
51	Os07t0204900-03	0.00	72.75	Inf	up	4.77E-03	Similar to Zeta-carotene desaturase.

52	Os11t0637700-02	0.00	72.75	Inf	up	4.77E-03	Nucleotide-binding, alpha-beta plait domain containing protein.
53	Os01t0936100-02	0.00	71.61	Inf	up	5.21E-03	Similar to protein kinase family protein.
54	Os03t0441500-02	0.00	71.61	Inf	up	5.21E-03	Similar to ABC transporter.
55	Os11t0240600-02	0.00	71.61	Inf	up	5.21E-03	Similar to gibberellin receptor GID1L2.
56	Os06t0639100-03	0.00	70.48	Inf	up	5.82E-03	Similar to protein binding / zinc ion binding.
57	Os05t0132100-03	0.00	69.34	Inf	up	6.34E-03	Similar to cDNA clone:001-200-C01, full insert sequence.
58	Os06t0167100-02	0.00	69.34	Inf	up	6.34E-03	Similar to AP-1 complex subunit gamma-1.
59	Os09t0308900-03	0.00	69.34	Inf	up	6.34E-03	Similar to lipid phosphate phosphatase 3.
60	Os06t0535300-02	0.00	67.07	Inf	up	7.87E-03	Hypothetical conserved gene.
61	Os07t0484300-02	0.00	67.07	Inf	up	7.87E-03	Similar to protein binding protein.
62	Os04t0650800-02	0.00	65.93	Inf	up	8.67E-03	Similar to H0212B02.14 protein.
63	Os05t0494100-02	0.00	65.93	Inf	up	8.67E-03	Similar to dr1-associated corepressor.
64	Os05t0283000-01	0.00	57.97	Inf	up	1.77E-02	Conserved hypothetical protein.
65	Os06t0142650-00	0.00	57.97	Inf	up	1.77E-02	Similar to Avr9/Cf-9 rapidly elicited protein 11 (Fragment).
66	Os03t0374100-03	0.00	56.84	Inf	up	1.97E-02	Hepatocellular carcinoma-associated antigen 59 family protein.
67	Os03t0360750-00	0.00	55.70	Inf	up	2.19E-02	Hypothetical protein.
68	Os03t0696300-02	0.00	54.56	Inf	up	2.39E-02	Similar to nuclear transcription factor Y subunit A-1.
69	Os01t0654100-02	0.00	53.43	Inf	up	2.63E-02	CTP synthase domain containing protein.
70	Os04t0107900-04	0.00	52.29	Inf	up	2.90E-02	Similar to Heat shock protein 82.
71	Os08t0132600-02	0.00	52.29	Inf	up	2.90E-02	Conserved hypothetical protein.
72	Os08t0435750-00	0.00	52.29	Inf	up	2.90E-02	Non-protein coding transcript.
73	Os11t0210300-02	0.00	52.29	Inf	up	2.90E-02	Similar to Alcohol dehydrogenase 1.
74	Os01t0709500-03	0.00	51.15	Inf	up	3.17E-02	Similar to Serine/threonine-protein kinase PBS1 (EC 2.7.1.37)
75	Os03t0245700-03	0.00	51.15	Inf	up	3.17E-02	Similar to senescence-associated protein 15.
76	Os04t0660400-03	0.00	50.02	Inf	up	3.57E-02	Similar to Amylogenin%3B reversibly glycosylatable polypeptide (Amylogenin).
77	Os01t0917400-03	0.88	672.94	9.58	up	5.94E-12	Hypothetical conserved gene.
78	Os06t0172901-00	0.88	650.20	9.53	up	7.78E-12	Hypothetical protein.
79	Os04t0530500-02	3.52	1595.96	8.83	up	2.63E-13	Zinc finger, RING/FYVE/PHD-type domain containing protein.

80	Os03t0648400-03	6.16	2761.10	8.81	up	3.75E-13	Similar to DnaJ protein homolog (DNAJ-1).
81	Os04t0555300-02	0.88	294.41	8.39	up	6.67E-08	Similar to Glycerol 3-phosphate permease.
82	Os12t0566700-02	0.88	222.80	7.98	up	1.46E-06	Similar to GDSL-like Lipase/Acylhydrolase family protein, expressed.
83	Os12t0583900-03	0.88	209.16	7.89	up	2.81E-06	Similar to PDE135 (PIGMENT DEFECTIVE EMBRYO 135)%3B transmembrane transporter.
84	Os07t0573800-03	3.52	802.53	7.83	up	2.83E-11	FMN-binding split barrel domain containing protein.
85	Os12t0420200-02	1.76	334.20	7.57	up	6.32E-08	Similar to CRB%3B binding / catalytic/ coenzyme binding.
86	Os05t0583100-02	0.88	162.55	7.53	up	3.22E-05	Similar to transposon protein.
87	Os03t0249700-02	3.52	635.43	7.50	up	3.30E-10	Conserved hypothetical protein.
88	Os08t0473900-02	139.00	24912.38	7.49	up	2.02E-05	Similar to Alpha amylase isozyme 3D.
89	Os02t0586900-02	2.64	422.86	7.32	up	1.15E-08	Similar to Glycine rich protein (Fragment).
90	Os01t0663800-02	0.88	131.86	7.23	up	2.23E-04	Hypothetical conserved gene.
91	Os12t0550800-02	0.88	128.45	7.19	up	2.79E-04	Conserved hypothetical protein.
92	Os12t0605800-03	1.76	251.22	7.16	up	1.42E-06	Similar to Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial.
93	Os01t0667200-02	0.88	98.89	6.81	up	2.25E-03	Similar to Glyoxalase II.
94	Os06t0193000-02	0.88	90.94	6.69	up	3.96E-03	Similar to ubiquitin-conjugating enzyme E2 J2.
95	Os10t0503500-03	0.88	90.94	6.69	up	3.96E-03	Similar to Malic enzyme.
96	Os08t0473900-01	47.50	4677.61	6.62	up	2.01E-08	Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
97	Os12t0277500-04	2.64	253.49	6.59	up	3.40E-06	Similar to RuBisCO large subunit-binding protein subunit alpha, chloroplastic (Fragment).
98	Os03t0826900-01	27.30	2479.19	6.51	up	1.90E-09	Conserved hypothetical protein.
99	Os10t0360100-01	2.64	223.93	6.41	up	1.18E-05	Similar to Sugar transporter protein.
100	Os03t0576900-05	1.76	139.82	6.31	up	3.92E-04	Similar to cDNA clone:001-047-G03, full insert sequence.
101	Os06t0194900-04	7.04	553.58	6.30	up	2.83E-08	Similar to Sucrose synthase 2.
102	Os01t0229200-03	0.88	61.38	6.12	up	3.79E-02	Hypothetical conserved gene.
103	Os11t0126900-01	0.88	61.38	6.12	up	3.79E-02	NAC-domain protein, Drought tolerance
104	Os08t0190100-01	4.40	292.14	6.05	up	3.61E-06	Germin-like protein 8-11, Disease resistance
105	Os05t0581800-03	0.88	55.70	5.98	up	6.05E-02	Hypothetical conserved gene.
106	Os08t0363200-01	0.88	55.70	5.98	up	6.05E-02	Conserved hypothetical protein.
107	Os10t0580900-02	1.76	102.30	5.86	up	4.27E-03	Conserved hypothetical protein.

108	Os06t0103300-02	5.28	304.64	5.85	up	4.38E-06	Similar to Homogentisate 1,2-dioxygenase.
109	Os12t0437800-01	169.00	9422.28	5.80	up	1.17E-05	Similar to MPI.
110	Os12t0550800-01	11.40	628.61	5.78	up	8.24E-08	Hypothetical conserved gene.
111	Os09t0243200-01	43.10	2182.50	5.66	up	6.32E-08	Zinc finger, RING/FYVE/PHD-type domain containing protein.
112	Os01t0729900-04	8.80	439.91	5.64	up	8.43E-07	Similar to predicted protein.
113	Os01t0159000-01	39.60	1946.07	5.62	up	6.32E-08	Similar to cDNA clone:J023049H21, full insert sequence.
114	Os07t0496200-03	1.76	86.39	5.62	up	1.28E-02	Similar to Malic enzyme.
115	Os04t0570800-01	6.16	294.41	5.58	up	1.15E-05	Protein of unknown function DUF248, methyltransferase putative family protein.
116	Os02t0483500-01	11.40	496.75	5.44	up	8.90E-07	Transferase family protein.
117	Os08t0518100-02	2.64	113.67	5.43	up	4.19E-03	Hypothetical conserved gene.
118	Os01t0793800-01	16.70	716.13	5.42	up	2.20E-07	Conserved hypothetical protein.
119	Os12t0467700-02	1.76	73.89	5.39	up	3.02E-02	Similar to ATPase 2.
120	Os12t0468000-02	1.76	73.89	5.39	up	3.02E-02	Similar to ATPase 2.
121	Os06t0559500-02	2.64	107.99	5.35	up	5.91E-03	Similar to Acid phosphatase (EC 3.1.3.2) 1 allozyme 1.
122	Os12t0277500-03	5.28	214.84	5.35	up	1.44E-04	Similar to RuBisCO large subunit-binding protein subunit alpha, chloroplastic (Fragment).
123	Os07t0529000-01	144.00	5654.05	5.29	up	9.58E-06	Similar to Isocitrate lyase (Fragment).
124	Os03t0178200-02	1.76	68.20	5.28	up	4.63E-02	Protein of unknown function YGGT family protein.
125	Os02t0546600-01	1.76	67.07	5.25	up	5.04E-02	Similar to AP2 domain containing protein RAP2.2 (Fragment).
126	Os05t0151400-02	4.40	155.73	5.15	up	1.38E-03	Similar to TOC159 (PLASMID PROTEIN IMPORT 2).
127	Os02t0514500-01	15.80	556.99	5.14	up	1.70E-06	Similar to Glycerophosphoryl diester phosphodesterase (Fragment).
128	Os04t0636900-01	2.64	89.80	5.09	up	1.92E-02	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.
129	Os04t0679400-03	15.00	489.93	5.03	up	4.15E-06	Similar to H0801D08.15 protein.
130	Os01t0839900-01	10.60	341.02	5.01	up	2.51E-05	Thaumatococcus, pathogenesis-related family protein.
131	Os03t0751100-02	1.76	56.84	5.01	up	1.08E-01	Similar to Glutathione transporter.
132	Os06t0114650-01	1.76	54.56	4.95	up	1.29E-01	Similar to predicted protein.
133	Os03t0656800-02	3.52	106.85	4.92	up	1.13E-02	Similar to 3-glucanase.
134	Os04t0486950-01	268.00	8145.74	4.92	up	1.47E-04	Similar to Malate synthase.
135	Os08t0189600-01	4.40	128.45	4.87	up	5.39E-03	Germin-like protein 8-7, Disease resistance

136	Os02t0719800-01	1.76	51.15	4.86	up	1.66E-01	Similar to AML1.
137	Os03t0291500-01	640.00	18061.36	4.82	up	3.38E-03	Similar to Asparagine synthetase.
138	Os05t0223200-01	17.60	489.93	4.80	up	1.03E-05	Similar to Glycine-rich RNA-binding protein GRP2A.
139	Os05t0588900-01	5.28	145.50	4.78	up	3.68E-03	Similar to mitochondrial chaperone BCS1.
140	Os08t0189900-01	17.60	478.56	4.77	up	1.23E-05	Germin-like protein 8-10, Disease resistance
141	Os08t0230600-01	12.30	328.51	4.74	up	7.48E-05	LIM, zinc-binding domain containing protein.
142	Os03t0727800-01	9.68	258.04	4.74	up	2.55E-04	Cyclin-like F-box domain containing protein.
143	Os01t0934000-02	2.64	68.20	4.69	up	7.94E-02	WD40 repeat-like domain containing protein.
144	Os10t0447400-01	2.64	67.07	4.67	up	8.64E-02	Conserved hypothetical protein.
145	Os04t0175400-01	40.50	1024.19	4.66	up	3.61E-06	Conserved hypothetical protein.
146	Os03t0136900-02	5.28	128.45	4.60	up	8.61E-03	Similar to Aconitate hydratase 2, mitochondrial.
147	Os01t0703000-01	5.28	127.31	4.59	up	9.08E-03	Similar to Poly(A) polymerase gamma (EC 2.7.7.19)
148	Os04t0688300-01	187.00	4467.31	4.58	up	7.04E-05	Haem peroxidase, plant/fungal/bacterial family protein.
149	Os06t0172800-00	568.00	13289.41	4.55	up	2.59E-03	Similar to alkaline alpha galactosidase 2.
150	Os10t0370600-01	2.64	60.25	4.51	up	1.39E-01	Hypothetical protein.
151	Os11t0205300-00	5.28	114.81	4.44	up	1.77E-02	Non-protein coding transcript.
152	Os02t0611200-03	22.90	496.75	4.44	up	3.84E-05	Similar to S-adenosylmethionine decarboxylase 2.
153	Os04t0461100-02	6.16	131.86	4.42	up	1.09E-02	Similar to H0219H12.12 protein.
154	Os08t0158400-00	2.64	55.70	4.40	up	1.93E-01	Similar to Berberine bridge enzyme-like protein.
155	Os09t0515200-02	7.04	145.50	4.37	up	8.13E-03	Beta 7 subunit of 20S proteasome.
156	Os01t0770500-02	2.64	54.56	4.37	up	2.08E-01	Similar to ABC transporter ATP-binding protein.
157	Os01t0827800-00	2.64	54.56	4.37	up	2.08E-01	Similar to AT-rich element binding factor 3.
158	Os03t0663500-00	2.64	54.56	4.37	up	2.08E-01	Similar to Osmotin precursor.
159	Os12t0583700-00	41.30	844.58	4.35	up	1.69E-05	Zinc finger, C2H2-type domain containing protein.
160	Os02t0214500-01	2.64	53.43	4.34	up	2.23E-01	No apical meristem (NAM) protein domain containing protein.
161	Os01t0138800-01	25.50	505.84	4.31	up	6.21E-05	Peptidase C26 domain containing protein.
162	Os07t0551400-02	13.20	261.45	4.31	up	8.53E-04	Similar to USP family protein.
163	Os02t0514326-00	2.64	52.29	4.31	up	2.37E-01	Hypothetical protein.

164	Os02t0771500-01	4.40	86.39	4.30	up	5.84E-02	Conserved hypothetical protein.
165	Os03t0133100-01	42.20	812.76	4.27	up	2.59E-05	Conserved hypothetical protein.
166	Os03t0255100-02	16.70	319.42	4.26	up	4.29E-04	Similar to Beta-galactosidase.
167	Os05t0475400-01	514.00	9675.77	4.24	up	2.67E-03	Similar to Alanine:glyoxylate aminotransferase-like protein (Fragment).
168	Os08t0507100-00	5.28	98.89	4.23	up	4.07E-02	Cytochrome P450 family protein.
169	Os05t0372100-05	6.16	114.81	4.22	up	2.51E-02	Similar to protein kinase family protein.
170	Os06t0594300-01	4.40	81.84	4.22	up	7.65E-02	Hypothetical protein.
171	Os10t0431900-02	3.52	63.66	4.18	up	1.66E-01	Serine/threonine protein kinase-related domain containing protein.
172	Os12t0255850-01	3.52	63.66	4.18	up	1.66E-01	Conserved hypothetical protein.
173	Os02t0168200-01	6.16	109.13	4.15	up	3.29E-02	Similar to Transfactor-like protein.
174	Os01t0594300-01	10.60	186.42	4.14	up	5.06E-03	Similar to leucine-rich repeat family protein / extensin family protein.
175	Os02t0285800-02	10.60	186.42	4.14	up	5.06E-03	Similar to predicted protein.
176	Os05t0475475-00	79.20	1367.48	4.11	up	4.78E-05	Hypothetical gene.
177	Os05t0473000-01	16.70	276.22	4.05	up	1.52E-03	Streptomyces cyclase/dehydrase family protein.
178	Os05t0455200-02	3.52	57.97	4.04	up	2.35E-01	Similar to QSH-1.
179	Os02t0192001-00	7.92	127.31	4.01	up	2.55E-02	Conserved hypothetical protein.
180	Os11t0149200-00	6.16	98.89	4.01	up	5.73E-02	Conserved hypothetical protein.
181	Os03t0770851-00	5.28	81.84	3.95	up	1.07E-01	Hypothetical protein.
182	Os07t0608300-02	15.00	228.48	3.93	up	4.11E-03	Alpha/beta hydrolase fold-1 domain containing protein.
183	Os02t0482400-01	5.28	79.57	3.91	up	1.22E-01	Similar to Ornithine decarboxylase (EC 4.1.1.17) (ODC).
184	Os05t0125600-02	3.52	52.29	3.89	up	3.35E-01	Non-protein coding transcript.
185	Os08t0476050-01	3.52	52.29	3.89	up	3.35E-01	Hypothetical conserved gene.
186	Os05t0145100-01	4.40	64.79	3.88	up	2.16E-01	Conserved hypothetical protein.
187	Os06t0561000-01	2020.00	29658.19	3.88	up	1.13E-01	Similar to Myo-inositol oxygenase.
188	Os02t0514150-00	3.52	51.15	3.86	up	3.62E-01	Hypothetical conserved gene.
189	Os04t0108101-00	5.28	76.16	3.85	up	1.50E-01	Hypothetical protein.
190	Os07t0561800-01	5.28	76.16	3.85	up	1.50E-01	Similar to carbohydrate transporter/ sugar porter.
191	Os01t0884350-00	8.80	125.04	3.83	up	3.71E-02	Hypothetical protein.

192	Os01t0327100-02	7.04	98.89	3.81	up	7.66E-02	Similar to Peroxidase 8.
193	Os05t0171900-01	1000.00	13988.49	3.81	up	2.19E-02	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.
194	Os03t0708800-03	7.04	97.76	3.80	up	8.07E-02	Hypothetical conserved gene.
195	Os06t0703900-02	4.40	60.25	3.78	up	2.76E-01	Homeodomain-like containing protein.
196	Os05t0222200-02	13.20	179.60	3.77	up	1.42E-02	ABC transporter-like domain containing protein.
197	Os10t0565200-00	18.50	243.26	3.72	up	5.91E-03	Hypothetical conserved gene.
198	Os06t0152200-02	10.60	136.41	3.69	up	3.71E-02	Zinc-finger protein R2931.
199	Os10t0456800-01	662.00	8470.85	3.68	up	1.07E-02	Similar to PGPD14 protein.
200	Os10t0492600-01	38.70	493.34	3.67	up	8.92E-04	Similar to Tonoplast membrane integral protein ZmTIP3-1.

Rank Overall	Gene ID	Root		Log ₂ Ratio	R ^a	FDR	Annotation
		FPKM					
		Control	IPU				
1	Os01t0142800-03	0	205	Inf	up	2.93E-09	Similar to Peptide transporter.
2	Os01t0148700-02	0	95	Inf	up	5.58E-05	Protein of unknown function DUF1677, Oryza sativa family protein.
3	Os01t0550300-01	0	51	Inf	up	1.11E-02	Similar to Gda-1 protein.
4	Os01t0686800-01	0	165	Inf	up	7.11E-08	Protein containing the WD-40 repeat, Innate immunity
5	Os01t0730300-03	0	59	Inf	up	3.96E-03	Similar to predicted protein.
6	Os01t0800300-03	0	52	Inf	up	9.70E-03	Immunoglobulin/major histocompatibility complex, conserved site domain containing protein.
7	Os02t0768600-01	0	56	Inf	up	5.76E-03	Similar to Chloroplast inorganic pyrophosphatase (EC 3.6.1.1).
8	Os02t0822000-03	0	70	Inf	up	1.04E-03	Hypothetical conserved gene.
9	Os03t0269000-02	0	72	Inf	up	8.34E-04	Short chain alcohol dehydrogenase-like.
10	Os03t0289200-02	0	71	Inf	up	9.44E-04	Similar to protein YIP1.
11	Os03t0669300-03	0	109	Inf	up	1.23E-05	Glycoside hydrolase, family 17 protein.
12	Os03t0713400-03	0	66	Inf	up	1.67E-03	Similar to NADH-ubiquinone oxidoreductase 75 kDa subunit.
13	Os03t0796600-02	0	84	Inf	up	1.92E-04	Non-protein coding transcript.
14	Os03t0797700-02	0	67	Inf	up	1.48E-03	rRNA-processing protein EFG1 domain containing protein.
15	Os03t0821900-02	0	60	Inf	up	3.48E-03	Similar to Protein kinase APK1B.
16	Os03t0851800-02	0	54	Inf	up	7.49E-03	Similar to Pantoate--beta-alanine ligase.

17	Os04t0129500-03	0	88	Inf	up	1.24E-04	Similar to OSIGBa0131J24.5 protein.
18	Os04t0401700-02	0	250	Inf	up	1.15E-10	Similar to Isoform 2 of Potassium transporter 1.
19	Os04t0504800-03	0	65	Inf	up	1.87E-03	Similar to polyadenylate-binding protein 2.
20	Os04t0573200-02	0	191	Inf	up	8.69E-09	Similar to OSIGBa0147H17.7 protein.
21	Os04t0678250-00	0	79	Inf	up	3.55E-04	Hypothetical protein.
22	Os04t0693000-02	0	106	Inf	up	1.71E-05	Similar to dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDasubunit.
23	Os05t0149800-02	0	139	Inf	up	6.48E-07	Similar to Discordia 1.
24	Os05t0411300-03	0	60	Inf	up	3.48E-03	Similar to DNA binding protein.
25	Os05t0455600-02	0	179	Inf	up	2.22E-08	Prenylated rab acceptor PRA1 family protein.
26	Os06t0573600-03	0	147	Inf	up	3.30E-07	Similar to Beta-galactosidase.
27	Os07t0100500-02	0	52	Inf	up	9.70E-03	Conserved hypothetical protein.
28	Os07t0170100-02	0	335	Inf	up	4.61E-13	Similar to Branched chain alpha-keto acid dehydrogenase E1 beta subunit.
29	Os07t0516500-04	0	52	Inf	up	9.70E-03	Hypothetical conserved gene.
30	Os07t0566200-02	0	124	Inf	up	2.76E-06	Similar to catalytic/ protein phosphatase type 2C.
31	Os08t0224100-03	0	67	Inf	up	1.48E-03	Similar to Serine/threonine protein kinase.
32	Os08t0518100-02	0	72	Inf	up	8.34E-04	Hypothetical conserved gene.
33	Os08t0532200-03	0	60	Inf	up	3.48E-03	Similar to Glutamate-1-semialdehyde aminotransferase (GSA- AT).
34	Os09t0459800-02	0	69	Inf	up	1.15E-03	Similar to ARP protein.
35	Os09t0497400-02	0	136	Inf	up	8.31E-07	Similar to Protein pob.
36	Os09t0567400-02	0	76	Inf	up	5.06E-04	Similar to Histidine-containing phosphotransfer protein.
37	Os11t0210500-02	0	316	Inf	up	1.33E-12	Similar to Alcohol dehydrogenase.
38	Os11t0472000-02	0	78	Inf	up	3.96E-04	Hypothetical conserved gene.
39	Os11t0702700-02	0	84	Inf	up	1.92E-04	Homeodomain-like containing protein.
40	Os12t0515400-02	0	94	Inf	up	6.26E-05	Similar to plastidic 2-oxoglutarate/malate transporter.
41	Os03t0784900-02	2	532	8.06	up	3.11E-15	Glycolipid transfer protein, GLTP domain containing protein.
42	Os03t0158500-04	2	438	7.77	up	1.99E-13	Similar to YT521-B-like family protein, expressed.
43	Os03t0151800-03	1	189	7.56	up	7.11E-08	Hypothetical conserved gene.
44	Os03t0437600-02	2	259	7.02	up	2.50E-09	Similar to Hydrolase.

45	Os11t0384789-02	2	259	7.02	up	2.50E-09	Similar to Hydrolase.
46	Os08t0416900-02	1	106	6.73	up	9.62E-05	Similar to dnaJ domain containing protein.
47	Os05t0372100-04	1	88	6.46	up	6.45E-04	Similar to protein kinase family protein.
48	Os01t0754200-02	1	78	6.29	up	1.85E-03	Similar to ATGSL05 (GLUCAN SYNTHASE-LIKE 5)%3B 1,3-beta-glucan synthase/ transferase.
49	Os05t0169100-02	8	595	6.22	up	3.51E-13	Similar to 60S ribosomal protein L10-2.
50	Os04t0449950-00	1	70	6.13	up	4.53E-03	Non-protein coding transcript.
51	Os02t0288200-02	1	66	6.04	up	7.02E-03	Hypothetical conserved gene.
52	Os08t0224200-02	1	64	6.00	up	9.03E-03	Similar to H0702G05.3 protein.
53	Os05t0594100-02	3	190	5.98	up	8.22E-07	Similar to GDA2 protein.
54	Os10t0571200-02	1	63	5.98	up	9.93E-03	Similar to Pyruvate kinase.
55	Os10t0412100-02	1	59	5.88	up	1.58E-02	Similar to Endonuclease/Exonuclease/phosphatase family protein, expressed.
56	Os01t0936100-02	1	55	5.78	up	2.45E-02	Similar to protein kinase family protein.
57	Os07t0639800-02	6	326	5.76	up	3.61E-09	Similar to Eukaryotic translation initiation factor 6 (Fragment).
58	Os03t0802300-02	1	54	5.75	up	2.74E-02	Conserved hypothetical protein.
59	Os08t0155400-03	2	107	5.74	up	3.02E-04	Similar to cDNA clone:J023045B01, full insert sequence.
60	Os01t0645200-03	2	95	5.57	up	9.91E-04	Bile acid:sodium symporter domain containing protein.
61	Os07t0424400-03	10	449	5.49	up	3.34E-10	Similar to cDNA clone:J023086F23, full insert sequence.
62	Os03t0165300-02	2	88	5.46	up	1.91E-03	Homeobox domain containing protein.
63	Os07t0600700-02	2	76	5.25	up	6.54E-03	X8 domain containing protein.
64	Os03t0271200-02	2	67	5.07	up	1.68E-02	Similar to Protein TOC75, chloroplastic.
65	Os04t0630600-00	2	64	5.00	up	2.25E-02	Similar to H0323C08.16 protein.
66	Os08t0556900-02	8	254	4.99	up	7.91E-07	Similar to Vignain.
67	Os04t0555300-02	8	239	4.90	up	1.94E-06	Similar to Glycerol 3-phosphate permease.
68	Os07t0682400-03	10	257	4.68	up	2.31E-06	Nucleotide-binding, alpha-beta plait domain containing protein.
69	Os06t0189600-03	3	76	4.66	up	1.44E-02	Protein of unknown function DUF1677, Oryza sativa family protein.
70	Os07t0498300-02	7	171	4.61	up	8.43E-05	Similar to cDNA clone:001-022-F09, full insert sequence.
71	Os06t0639100-03	3	72	4.58	up	2.08E-02	Similar to protein binding / zinc ion binding.
72	Os05t0372100-05	6	128	4.42	up	1.12E-03	Similar to protein kinase family protein.

73	Os02t0104200-02	6	127	4.40	up	1.17E-03	Conserved hypothetical protein.
74	Os01t0598600-03	3	53	4.14	up	1.26E-01	Similar to predicted protein.
75	Os05t0461300-02	27	454	4.07	up	5.15E-07	Similar to RAB8C.
76	Os07t0568300-02	9	143	3.99	up	1.74E-03	Similar to ZF protein (Fragment).
77	Os02t0215200-03	4	57	3.83	up	1.42E-01	Similar to Histone deacetylase.
78	Os01t0814400-02	5	71	3.83	up	6.87E-02	Conserved hypothetical protein.
79	Os08t0473900-01	13	182	3.81	up	7.88E-04	Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
80	Os05t0102800-01	7	91	3.70	up	3.20E-02	Similar to AML1.
81	Os09t0484300-03	7	85	3.60	up	5.27E-02	Similar to Polyubiquitin-like protein.
82	Os03t0283600-02	6	72	3.58	up	9.59E-02	Similar to CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase.
83	Os04t0488800-00	7	82	3.55	up	6.49E-02	Conserved hypothetical protein.
84	Os02t0586000-01	318	3556	3.48	up	1.35E-07	Quinonprotein alcohol dehydrogenase-like domain containing protein.
85	Os07t0568600-02	11	123	3.48	up	1.48E-02	Similar to calcium-dependent protein kinase, isoform AK1.
86	Os08t0135800-01	5	55	3.46	up	2.44E-01	Zinc finger, CCCH-type domain containing protein.
87	Os03t0130350-00	8	87	3.44	up	6.42E-02	Similar to predicted protein.
88	Os01t0719100-03	5	52	3.38	up	3.08E-01	Hypothetical gene.
89	Os12t0277000-02	6	62	3.37	up	2.02E-01	Hypothetical conserved gene.
90	Os04t0650700-01	7	71	3.34	up	1.43E-01	Similar to OSIGBa0113E10.3 protein.
91	Os04t0458200-02	19	189	3.31	up	3.48E-03	Similar to cDNA clone:J033037C08, full insert sequence.
92	Os01t0975300-02	13	127	3.29	up	2.14E-02	Similar to Myb factor protein.
93	Os03t0376900-02	13	125	3.27	up	2.43E-02	Nucleotide-binding, alpha-beta plait domain containing protein.
94	Os06t0559400-02	39	370	3.25	up	1.74E-04	Conserved hypothetical protein.
95	Os10t0504650-00	7	65	3.22	up	2.21E-01	Similar to nonspecific lipid-transfer protein.
96	Os05t0571000-02	6	54	3.17	up	3.59E-01	Similar to SPA1 (SUPPRESSOR OF PHYA-105 1)%3B protein binding / signal transducer.
97	Os02t0817800-02	9	77	3.10	up	1.70E-01	Similar to Telomere binding protein-1.
98	Os07t0501900-03	9	77	3.10	up	1.70E-01	Similar to zinc finger family protein.
99	Os04t0650700-02	786	6491	3.05	up	9.26E-06	Similar to OSIGBa0113E10.3 protein.
100	Os09t0504700-03	10	81	3.02	up	1.70E-01	Zinc finger, RING/FYVE/PHD-type domain containing protein.

101	Os11t0525200-02	10	78	2.96	up	2.04E-01	Similar to Cytochrome P450 51 (EC 1.14.13.70) (CYPLI)
102	Os04t0650800-02	32	241	2.91	up	5.75E-03	Similar to H0212B02.14 protein.
103	Os02t0247600-01	15	112	2.90	up	8.70E-02	Conserved hypothetical protein.
104	Os01t0760300-01	14	103	2.88	up	1.15E-01	Similar to Pollen-specific kinase partner protein.
105	Os11t0135000-01	10	73	2.87	up	2.75E-01	Similar to Major facilitator superfamily antiporter.
106	Os04t0628100-01	8	58	2.86	up	4.40E-01	Similar to Polyubiquitin.
107	Os09t0490200-01	10	72	2.85	up	2.94E-01	Similar to Ethylene signal transcription factor.
108	Os01t0773100-02	8	57	2.83	up	4.66E-01	Similar to F20D22.3 protein.
109	Os10t0561900-03	116	825	2.83	up	1.33E-04	Similar to Protein-tyrosine phosphatase mitochondrial 1.
110	Os02t0644000-01	9	64	2.83	up	3.85E-01	Similar to C13 endopeptidase NP1 (Fragment).
111	Os08t0503600-01	12	83	2.79	up	2.32E-01	Hypothetical protein.
112	Os04t0614600-02	11	76	2.79	up	2.86E-01	Similar to OSIGBa0126B18.7 protein.
113	Os06t0131001-00	24	165	2.78	up	3.60E-02	Conserved hypothetical protein.
114	Os02t0435000-02	8	54	2.75	up	5.72E-01	Translocation protein Sec62 family protein.
115	Os08t0484500-02	21	139	2.73	up	7.26E-02	Similar to Phospho-2-dehydro-3-deoxyheptonate aldolase 2.
116	Os08t0102700-05	10	65	2.70	up	4.34E-01	Harpin-induced 1 domain containing protein.
117	Os02t0832600-01	24	154	2.68	up	6.14E-02	Similar to PRLI-interacting factor A (Fragment).
118	Os04t0652700-02	17	109	2.68	up	1.52E-01	Similar to nuclease PA3.
119	Os09t0508401-00	9	56	2.64	up	6.12E-01	Non-protein coding transcript.
120	Os01t0872700-01	11	68	2.63	up	4.42E-01	Zinc finger, CCHC-type domain containing protein.
121	Os09t0565700-01	11	68	2.63	up	4.42E-01	Prephenate dehydratase domain containing protein.
122	Os05t0481500-01	12	74	2.62	up	3.88E-01	K Homology domain containing protein.
123	Os02t0789400-01	14	86	2.62	up	2.92E-01	Similar to 9G8-like SR protein (RSZp22 splicing factor).
124	Os02t0585650-01	484	2885	2.58	up	2.33E-04	Hypothetical gene.
125	Os01t0172400-03	132	782	2.57	up	9.28E-04	Phospholipase D alpha 1 precursor (EC 3.1.4.4)
126	Os02t0779200-02	88	518	2.56	up	2.40E-03	Similar to Subtilisin protease (Fragment).
127	Os02t0783650-01	18	104	2.53	up	2.29E-01	Hypothetical gene.
128	Os12t0503000-05	14	79	2.50	up	4.14E-01	Similar to Allantoin permease.

129	Os04t0479100-02	16	90	2.49	up	3.31E-01	Similar to OSIGBa0116M22.10 protein.
130	Os03t0656850-00	21	117	2.48	up	2.00E-01	Conserved hypothetical protein.
131	Os08t0485600-01	11	60	2.45	up	6.70E-01	Methyl-CpG DNA binding domain containing protein.
132	Os03t0432100-01	19	103	2.44	up	2.80E-01	Similar to Pyruvate, phosphate dikinase 2.
133	Os09t0557900-01	26	140	2.43	up	1.51E-01	Similar to Protein phosphatase 2C gamma isoform (EC 3.1.3.16)
134	Os08t0425500-01	33	177	2.42	up	8.78E-02	Endonuclease/exonuclease/phosphatase domain containing protein.
135	Os03t0187350-01	12	64	2.42	up	6.49E-01	Conserved hypothetical protein.
136	Os08t0189850-01	12	64	2.42	up	6.49E-01	Germin-like protein 8-9, Disease resistance
137	Os04t0516600-01	69	366	2.41	up	1.35E-02	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 domain containing protein.
138	Os03t0159900-02	10	52	2.38	up	8.70E-01	Hypothetical conserved gene.
139	Os04t0173300-02	48	249	2.38	up	4.35E-02	Similar to Transmembrane protein 115.
140	Os05t0405000-02	499	2568	2.36	up	1.15E-03	Similar to Isoform 2 of Pyruvate, phosphate dikinase 1, chloroplastic.
141	Os02t0784801-00	10	51	2.35	up	9.09E-01	Non-protein coding transcript.
142	Os02t0473200-02	16	81	2.34	up	5.06E-01	Similar to OSIGBa0137O04.7 protein.
143	Os10t0341700-02	23	116	2.33	up	2.75E-01	Cellulose synthase-like H1.
144	Os02t0245000-02	59	296	2.33	up	3.26E-02	Similar to predicted protein.
145	Os04t0306800-01	13	65	2.32	up	7.05E-01	RNA recognition motif, RNP-1 domain containing protein.
146	Os04t0390000-01	27	135	2.32	up	2.09E-01	Similar to OSIGBa0096P03.7 protein.
147	Os04t0636900-01	12	60	2.32	up	7.76E-01	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.
148	Os03t0794900-02	50	246	2.30	up	6.01E-02	Similar to Proline-rich protein (Fragment).
149	Os09t0352400-02	15	73	2.28	up	6.37E-01	Similar to predicted protein.
150	Os03t0233000-01	511	2485	2.28	up	2.04E-03	Protein of unknown function DUF607 family protein.
151	Os07t0665100-01	34	165	2.28	up	1.55E-01	Hypothetical protein.
152	Os06t0651600-02	11	53	2.27	up	9.35E-01	Similar to protein phosphatase type-2C.
153	Os02t0730000-02	345	1662	2.27	up	2.53E-03	Mitochondrial aldehyde dehydrogenase ALDH2a.
154	Os01t0622700-01	23	109	2.24	up	3.70E-01	Similar to Protein ABIL1.
155	Os11t0216900-01	22	102	2.21	up	4.24E-01	Similar to IDI2.
156	Os10t0548200-03	16	74	2.21	up	6.79E-01	Hypothetical conserved gene.

157	Os02t0796500-02	38	174	2.20	up	1.75E-01	B-type response regulator, Cytokinin signaling
158	Os01t0748900-02	26	119	2.19	up	3.47E-01	Membrane attack complex component/perforin/complement C9 family protein.
159	Os06t0704600-01	39	178	2.19	up	1.70E-01	Similar to Delta-aminolevulinic acid dehydratase (Fragment).
160	Os02t0274900-03	13	59	2.18	up	9.09E-01	Similar to metabolite transport protein csbC.
161	Os01t0871200-01	113	510	2.17	up	1.96E-02	Zinc finger, C2H2-type domain containing protein.
162	Os01t0831300-01	14	63	2.17	up	8.64E-01	Similar to Ammonium transporter.
163	Os11t0307550-00	18	81	2.17	up	6.48E-01	Conserved hypothetical protein.
164	Os11t0456300-02	14	63	2.17	up	8.64E-01	Similar to SKP1-like protein 1A.
165	Os06t0132100-03	120	537	2.16	up	1.92E-02	Transmembrane receptor, eukaryota domain containing protein.
166	Os06t0724100-01	44	195	2.15	up	1.59E-01	Zinc finger, RING/FYVE/PHD-type domain containing protein.
167	Os04t0670200-02	566	2504	2.15	up	5.30E-03	Granulin domain containing protein.
168	Os03t0198300-02	23	101	2.13	up	5.03E-01	Heat shock protein DnaJ, N-terminal domain containing protein.
169	Os12t0605800-01	61	267	2.13	up	8.84E-02	Similar to 3-methylcrotonyl CoA carboxylase biotin-containing subunit (Fragment).
170	Os03t0826900-01	534	2307	2.11	up	6.59E-03	Conserved hypothetical protein.
171	Os03t0636600-01	16	69	2.11	up	8.36E-01	Hypothetical conserved gene.
172	Os08t0221300-00	20	86	2.10	up	6.59E-01	Conserved hypothetical protein.
173	Os01t0283300-01	17	73	2.10	up	7.98E-01	Conserved hypothetical protein.
174	Os01t0655400-01	17	73	2.10	up	7.98E-01	Conserved hypothetical protein.
175	Os01t0172400-01	46	196	2.09	up	1.82E-01	Similar to Phospholipase D alpha 1.
176	Os02t0783625-00	84	356	2.08	up	6.04E-02	Similar to Lysine ketoglutarate reductase/saccharopine dehydrogenase.
177	Os01t0259200-01	17	72	2.08	up	8.25E-01	Similar to serine/threonine protein kinase PBS1.
178	Os04t0481100-01	17	72	2.08	up	8.25E-01	Similar to H0510A06.3 protein.
179	Os07t0570500-01	13	55	2.08	up	1.00E+00	Similar to predicted protein.
180	Os02t0297600-02	53	222	2.07	up	1.58E-01	Protein of unknown function DUF707 family protein.
181	Os06t0103300-02	78	326	2.06	up	7.61E-02	Similar to Homogentisate 1,2-dioxygenase.
182	Os10t0160100-02	24	100	2.06	up	5.79E-01	Glycoside hydrolase, family 17 protein.
183	Os11t0701700-02	30	125	2.06	up	4.14E-01	Hypothetical gene.
184	Os04t0275950-01	19	79	2.06	up	7.63E-01	Conserved hypothetical protein.

185	Os06t0182500-01	15	62	2.05	up	9.87E-01	Zinc finger, LIM-type domain containing protein.
186	Os11t0704600-02	23	95	2.05	up	6.30E-01	Similar to Beta-1,3 glucanase precursor (EC 3.2.1.39).
187	Os01t0265800-02	92	378	2.04	up	6.46E-02	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.
188	Os04t0688300-01	415	1705	2.04	up	1.15E-02	Haem peroxidase, plant/fungal/bacterial family protein.
189	Os03t0429800-01	19	78	2.04	up	8.04E-01	Similar to Xanthine dehydrogenase 1 (EC 1.1.1.204).
190	Os02t0794700-02	31	127	2.03	up	4.25E-01	Similar to Leucine aminopeptidase (Cytosol aminopeptidase) (Fragment).
191	Os04t0468600-06	23	94	2.03	up	6.56E-01	Similar to cDNA clone:006-303-A07, full insert sequence.
192	Os08t0152400-00	78	317	2.02	up	9.45E-02	Similar to P450.
193	Os01t0209000-02	16	65	2.02	up	9.65E-01	Alg9-like mannosyltransferase family protein.
194	Os08t0465800-02	32	130	2.02	up	4.21E-01	Similar to Glutamate decarboxylase.
195	Os06t0194900-02	947	3834	2.02	up	1.39E-02	Sucrose synthase 2 (EC 2.4.1.13).
196	Os05t0438600-01	255	1031	2.02	up	1.86E-02	Fructose-1,6-bisphosphatase class 1/Sedoheptulose-1,7-bisphosphatase domain containing protein.
197	Os01t0760600-03	160	640	2.00	up	3.36E-02	Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A).
198	Os03t0644400-01	27	108	2.00	up	5.78E-01	Amino acid permease.
199	Os07t0664600-01	42	167	1.99	up	3.14E-01	Glucose/ribitol dehydrogenase family protein.
200	Os04t0439100-02	67	266	1.99	up	1.43E-01	T-complex 11 family protein.

This calculation is based on the expressed tag frequency;

The mean of FPKM values are more than 10;

Inf and -Inf indicate positive infinity and negative infinity, respectively;

R, regulation.

ESI Table S6. Top 200 annotated genes most down-regulation in shoots and roots in the presence of IPU and absence of IPU. This calculation is based on the expressed tag frequency. The mean of FPKM values are more than 10. Inf and -Inf indicate positive infinity and negative infinity, respectively. R, regulation.

Rank overall	Gene ID	Shoot					Annotation
		FPKM		Log ₂ Ratio	R	FDR	
		Control	IPU				
1	Os01t0121800-02	31.70	0.00	-Inf	down	7.59E-03	Similar to xylosyltransferase 1.
2	Os01t0206700-02	106.00	0.00	-Inf	down	4.36E-06	Similar to cDNA clone:J013031K24, full insert sequence.
3	Os01t0229200-04	50.10	0.00	-Inf	down	8.94E-04	Hypothetical conserved gene.
4	Os01t0236700-02	95.90	0.00	-Inf	down	9.97E-06	Hypothetical conserved gene.
5	Os01t0290000-02	283.00	0.00	-Inf	down	9.01E-11	Similar to Cyprosin precursor (EC 3.4.23.-) (Fragment).
6	Os01t0290000-03	159.00	0.00	-Inf	down	8.17E-08	Similar to Cyprosin precursor (EC 3.4.23.-) (Fragment).
7	Os01t0579600-03	46.60	0.00	-Inf	down	1.32E-03	Similar to Calcineurin B-like protein 9.
8	Os01t0580100-02	27.30	0.00	-Inf	down	1.30E-02	Similar to Dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase-like protein.
9	Os01t0617900-03	605.00	0.00	-Inf	down	3.75E-15	Similar to oxygen-evolving complex-related.
10	Os01t0686800-01	51.90	0.00	-Inf	down	7.37E-04	Protein containing the WD-40 repeat, Innate immunity
11	Os01t0698300-02	30.80	0.00	-Inf	down	8.45E-03	Similar to transposon protein.
12	Os01t0707500-02	93.30	0.00	-Inf	down	1.26E-05	Similar to Transcription factor LAX PANICLE.
13	Os01t0718300-03	32.50	0.00	-Inf	down	6.82E-03	Similar to Brassinosteroid-insensitive 1.
14	Os01t0723800-02	121.00	0.00	-Inf	down	1.22E-06	Hypothetical conserved gene.
15	Os01t0736900-02	483.00	0.00	-Inf	down	7.14E-14	Similar to seed maturation protein.
16	Os01t0750300-03	56.30	0.00	-Inf	down	4.59E-04	Similar to cDNA clone:J023093O20, full insert sequence.
17	Os01t0752800-02	72.10	0.00	-Inf	down	9.06E-05	Non-protein coding transcript.
18	Os01t0772600-03	67.70	0.00	-Inf	down	1.40E-04	Similar to ATP binding protein.
19	Os01t0781700-00	26.40	0.00	-Inf	down	1.45E-02	Similar to Blast resistance protein Pi37.

20	Os01t0871800-01	22.00	0.00	-Inf	down	2.55E-02	TGF-beta receptor, type I/II extracellular region family protein.
21	Os01t0872100-01	78.30	0.00	-Inf	down	4.99E-05	TGF-beta receptor, type I/II extracellular region family protein.
22	Os01t0919600-02	442.00	0.00	-Inf	down	2.38E-13	Similar to predicted protein.
23	Os01t0934500-01	20.20	0.00	-Inf	down	3.21E-02	Hypothetical protein.
24	Os01t0945300-02	42.20	0.00	-Inf	down	2.18E-03	Amino acid/polyamine transporter I family protein.
25	Os01t0960400-02	36.90	0.00	-Inf	down	4.03E-03	Similar to predicted protein.
26	Os01t0967800-02	87.10	0.00	-Inf	down	2.19E-05	Hypothetical conserved gene.
27	Os02t0115600-02	47.50	0.00	-Inf	down	1.20E-03	Nucleic acid-binding, OB-fold-like domain containing protein.
28	Os02t0120800-02	38.70	0.00	-Inf	down	3.27E-03	Similar to Small GTP-binding protein (Fragment).
29	Os02t0194700-02	430.00	0.00	-Inf	down	3.39E-13	Similar to Lipoxygenase.
30	Os02t0218200-02	52.80	0.00	-Inf	down	6.70E-04	Similar to APM1 (AMINOPEPTIDASE M1).
31	Os02t0255000-03	71.30	0.00	-Inf	down	9.89E-05	Similar to Cyclic nucleotide-gated ion channel 1.
32	Os02t0288200-02	62.50	0.00	-Inf	down	2.41E-04	Hypothetical conserved gene.
33	Os02t0294100-02	21.10	0.00	-Inf	down	2.86E-02	Cyclin-like F-box domain containing protein.
34	Os02t0501350-01	20.20	0.00	-Inf	down	3.21E-02	Conserved hypothetical protein.
35	Os02t0519300-02	20.20	0.00	-Inf	down	3.21E-02	Similar to H0112G12.10 protein.
36	Os02t0525900-03	74.80	0.00	-Inf	down	7.00E-05	Similar to H0502B11.5 protein.
37	Os02t0613900-02	21.10	0.00	-Inf	down	2.86E-02	Similar to adenine phosphoribosyltransferase 2.
38	Os02t0614600-02	104.00	0.00	-Inf	down	5.05E-06	Hypothetical conserved gene.
39	Os02t0615800-02	109.00	0.00	-Inf	down	3.25E-06	Hypothetical conserved gene.
40	Os02t0623500-02	41.30	0.00	-Inf	down	2.41E-03	Similar to Lysyl-tRNA synthetase.
41	Os02t0657850-00	36.90	0.00	-Inf	down	4.03E-03	Conserved hypothetical protein.
42	Os02t0674233-00	85.30	0.00	-Inf	down	2.58E-05	Hypothetical conserved gene.
43	Os02t0696650-00	20.20	0.00	-Inf	down	3.21E-02	Hypothetical gene.
44	Os02t0714000-03	24.60	0.00	-Inf	down	1.81E-02	Hypothetical gene.
45	Os02t0714600-02	173.00	0.00	-Inf	down	3.29E-08	Ribose-phosphate pyrophosphokinase 4 (EC 2.7.6.1).
46	Os02t0725200-02	144.00	0.00	-Inf	down	2.25E-07	Similar to Ribulose-1,5-bisphosphate carboxylase.
47	Os02t0745700-02	58.10	0.00	-Inf	down	3.81E-04	Similar to protein SUR2.
48	Os02t0752000-02	27.30	0.00	-Inf	down	1.30E-02	Similar to predicted protein.
49	Os02t0759800-02	145.00	0.00	-Inf	down	2.12E-07	Similar to pre-mRNA-splicing factor prp45.

50	Os02t0778200-02	53.70	0.00	-Inf	down	6.09E-04	Similar to predicted protein.
51	Os02t0778300-02	24.60	0.00	-Inf	down	1.81E-02	Similar to predicted protein.
52	Os02t0819600-02	69.50	0.00	-Inf	down	1.18E-04	Serine/threonine protein kinase-related domain containing protein.
53	Os02t0823500-00	32.50	0.00	-Inf	down	6.82E-03	Non-protein coding transcript.
54	Os02t0829600-01	42.20	0.00	-Inf	down	2.18E-03	Zinc finger, RING/FYVE/PHD-type domain containing protein.
55	Os03t0114300-02	76.50	0.00	-Inf	down	5.91E-05	Similar to ATP binding protein.
56	Os03t0119500-02	34.30	0.00	-Inf	down	5.52E-03	Similar to cDNA clone:J023020014, full insert sequence.
57	Os03t0130500-02	44.00	0.00	-Inf	down	1.78E-03	Similar to ESTs AU031435(E61570).
58	Os03t0142800-02	66.00	0.00	-Inf	down	1.68E-04	Hypothetical conserved gene.
59	Os03t0143700-02	36.90	0.00	-Inf	down	4.03E-03	Hypothetical conserved gene.
60	Os03t0152800-03	23.80	0.00	-Inf	down	2.03E-02	Similar to predicted protein.
61	Os03t0166800-02	174.00	0.00	-Inf	down	3.12E-08	Similar to Endonuclease/Exonuclease/phosphatase family protein, expressed.
62	Os03t0170200-02	38.70	0.00	-Inf	down	3.27E-03	Conserved hypothetical protein.
63	Os03t0174600-02	35.20	0.00	-Inf	down	4.97E-03	Similar to tRNA methyltransferase.
64	Os03t0191100-03	60.70	0.00	-Inf	down	2.89E-04	Mitochondrial carrier protein domain containing protein.
65	Os03t0197125-00	25.50	0.00	-Inf	down	1.62E-02	Hypothetical gene.
66	Os03t0204366-00	30.80	0.00	-Inf	down	8.45E-03	Conserved hypothetical protein.
67	Os03t0220300-02	58.10	0.00	-Inf	down	3.81E-04	Hypothetical conserved gene.
68	Os03t0241600-02	70.40	0.00	-Inf	down	1.08E-04	Serine/threonine protein kinase-related domain containing protein.
69	Os03t0253600-01	22.90	0.00	-Inf	down	2.27E-02	Conserved hypothetical protein.
70	Os03t0254700-02	81.80	0.00	-Inf	down	3.57E-05	Similar to predicted protein.
71	Os03t0257900-03	25.50	0.00	-Inf	down	1.62E-02	Similar to Lectin-like receptor kinase 7%3B2.
72	Os03t0262150-01	24.60	0.00	-Inf	down	1.81E-02	Hypothetical gene.
73	Os03t0266800-02	50.10	0.00	-Inf	down	8.94E-04	Similar to BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1.
74	Os03t0271200-02	74.80	0.00	-Inf	down	7.00E-05	Similar to Protein TOC75, chloroplastic.
75	Os03t0278000-03	45.70	0.00	-Inf	down	1.46E-03	Similar to D-TDP-glucose dehydratase.
76	Os03t0283600-02	224.00	0.00	-Inf	down	1.68E-09	Similar to CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase.
77	Os03t0285166-00	33.40	0.00	-Inf	down	6.13E-03	Non-protein coding transcript.
78	Os03t0287600-00	22.90	0.00	-Inf	down	2.27E-02	Conserved hypothetical protein.
79	Os03t0289200-02	109.00	0.00	-Inf	down	3.25E-06	Similar to protein YIP1.

80	Os03t0355600-02	88.00	0.00	-Inf	down	2.02E-05	Similar to predicted protein.
81	Os03t0363900-02	31.70	0.00	-Inf	down	7.59E-03	Zinc finger, DHHC-type domain containing protein.
82	Os03t0375300-02	28.20	0.00	-Inf	down	1.17E-02	Similar to cationic amino acid transporter.
83	Os03t0401300-03	86.20	0.00	-Inf	down	2.38E-05	Similar to Sucrose synthase metabolism (Fragment).
84	Os03t0429800-04	75.70	0.00	-Inf	down	6.43E-05	Similar to Aldehyde oxidase and xanthine dehydrogenase.
85	Os03t0582000-01	66.00	0.00	-Inf	down	1.68E-04	Similar to Glutamate formiminotransferase.
86	Os03t0640800-03	22.00	0.00	-Inf	down	2.55E-02	Similar to cDNA clone:J033124M18, full insert sequence.
87	Os03t0686201-01	21.10	0.00	-Inf	down	2.86E-02	Hypothetical gene.
88	Os03t0711400-02	88.00	0.00	-Inf	down	2.02E-05	Similar to cDNA clone:J023075G08, full insert sequence.
89	Os03t0800000-01	29.90	0.00	-Inf	down	9.41E-03	Similar to Nitrate and chloride transporter.
90	Os03t0802300-03	34.30	0.00	-Inf	down	5.52E-03	Hypothetical conserved gene.
91	Os03t0806700-02	84.50	0.00	-Inf	down	2.79E-05	Protein of unknown function DUF868, plant family protein.
92	Os03t0810600-02	29.00	0.00	-Inf	down	1.05E-02	Similar to ATP/GTP/Ca ⁺⁺ binding protein.
93	Os03t0821900-02	74.80	0.00	-Inf	down	7.00E-05	Similar to Protein kinase APK1B.
94	Os03t0832800-01	26.40	0.00	-Inf	down	1.45E-02	Similar to glycerol-3-phosphate acyltransferase 1.
95	Os03t0832800-03	49.30	0.00	-Inf	down	9.85E-04	Similar to glycerol-3-phosphate acyltransferase 1.
96	Os03t0856400-02	110.00	0.00	-Inf	down	3.03E-06	Similar to Protein kinase AKINbetagamma-2.
97	Os04t0118400-03	53.70	0.00	-Inf	down	6.09E-04	Similar to H0613H07.5 protein.
98	Os04t0390000-04	311.00	0.00	-Inf	down	2.71E-11	Similar to OSIGBa0096P03.7 protein.
99	Os04t0422000-02	280.00	0.00	-Inf	down	1.06E-10	PAP fibrillin family protein.
100	Os04t0442300-02	133.00	0.00	-Inf	down	5.12E-07	A-type response regulator, Cytokinin signaling
101	Os04t0448800-02	20.20	0.00	-Inf	down	3.21E-02	Similar to Mitochondrial phosphate transporter (Fragment).
102	Os04t0459500-01	22.00	0.00	-Inf	down	2.55E-02	Similar to H0219H12.1 protein.
103	Os04t0462900-06	52.80	0.00	-Inf	down	6.70E-04	Similar to prohibitin2.
104	Os04t0477025-00	22.00	0.00	-Inf	down	2.55E-02	Hypothetical gene.
105	Os04t0485700-01	39.60	0.00	-Inf	down	2.95E-03	Similar to Exonuclease.
106	Os04t0488600-03	73.90	0.00	-Inf	down	7.63E-05	Similar to predicted protein.
107	Os04t0605300-02	102.00	0.00	-Inf	down	5.86E-06	Leucine-rich repeat, typical subtype containing protein.
108	Os04t0613800-03	45.70	0.00	-Inf	down	1.46E-03	Hypothetical conserved gene.
109	Os04t0640700-02	44.00	0.00	-Inf	down	1.78E-03	Similar to OSIGBa0138H21-OSIGBa0138E01.14 protein.

110	Os04t0641000-02	22.00	0.00	-Inf	down	2.55E-02	Similar to DNA-directed RNA polymerase.
111	Os04t0650000-03	39.60	0.00	-Inf	down	2.95E-03	Similar to cDNA clone:J013002H09, full insert sequence.
112	Os04t0682800-02	53.70	0.00	-Inf	down	6.09E-04	Similar to H0124B04.17 protein.
113	Os04t0684000-01	26.40	0.00	-Inf	down	1.45E-02	Hypothetical protein.
114	Os05t0143500-03	32.50	0.00	-Inf	down	6.82E-03	Similar to Kinase (Fragment).
115	Os05t0147400-02	22.00	0.00	-Inf	down	2.55E-02	Similar to T-complex protein 1 subunit zeta.
116	Os05t0150900-03	22.90	0.00	-Inf	down	2.27E-02	Similar to Histidyl-tRNA synthetase (Fragment).
117	Os05t0179800-02	36.90	0.00	-Inf	down	4.03E-03	Similar to early fruit mRNA.
118	Os05t0230600-02	42.20	0.00	-Inf	down	2.18E-03	Similar to predicted protein.
119	Os05t0285900-02	20.20	0.00	-Inf	down	3.21E-02	Conserved hypothetical protein.
120	Os05t0289400-02	46.60	0.00	-Inf	down	1.32E-03	Hypothetical conserved gene.
121	Os05t0349700-03	47.50	0.00	-Inf	down	1.20E-03	Similar to Chlorophyll synthase.
122	Os05t0393400-01	27.30	0.00	-Inf	down	1.30E-02	Similar to PAC (Fragment).
123	Os05t0405900-03	21.10	0.00	-Inf	down	2.86E-02	Conserved hypothetical protein.
124	Os05t0468750-00	44.00	0.00	-Inf	down	1.78E-03	Hypothetical gene.
125	Os05t0474600-02	36.10	0.00	-Inf	down	4.47E-03	Similar to predicted protein.
126	Os05t0499800-01	28.20	0.00	-Inf	down	1.17E-02	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
127	Os05t0515400-02	55.40	0.00	-Inf	down	5.04E-04	Similar to Auxin response factor 14.
128	Os05t0519400-02	52.80	0.00	-Inf	down	6.70E-04	Similar to predicted protein.
129	Os05t0545000-02	190.00	0.00	-Inf	down	1.18E-08	Similar to Phosphatidylinositol transfer-like protein III.
130	Os05t0559900-02	33.40	0.00	-Inf	down	6.13E-03	Similar to SKIP interacting protein 25.
131	Os05t0571000-02	144.00	0.00	-Inf	down	2.25E-07	Similar to SPA1 signal transducer.
132	Os05t0591900-02	132.00	0.00	-Inf	down	5.46E-07	Non-protein coding transcript.
133	Os06t0113900-06	66.90	0.00	-Inf	down	1.53E-04	Hypothetical conserved gene.
134	Os06t0136600-02	42.20	0.00	-Inf	down	2.18E-03	Similar to Enolase.
135	Os06t0227200-03	193.00	0.00	-Inf	down	1.01E-08	Hypothetical conserved gene.
136	Os06t0258900-02	29.90	0.00	-Inf	down	9.41E-03	Similar to predicted protein.
137	Os06t0275800-03	150.00	0.00	-Inf	down	1.47E-07	Amino acid transporter, transmembrane domain containing protein.
138	Os06t0474800-01	65.10	0.00	-Inf	down	1.83E-04	Similar to 3Fe-4S ferredoxin.
139	Os06t0498500-02	29.90	0.00	-Inf	down	9.41E-03	CCAAT-binding factor domain containing protein.

140	Os06t0559500-03	119.00	0.00	-Inf	down	1.49E-06	Similar to Acid phosphatase (EC 3.1.3.2) 1 allozyme 1.
141	Os06t0563300-01	106.00	0.00	-Inf	down	4.05E-06	Similar to Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit Bbeta isoform.
142	Os06t0573600-03	237.00	0.00	-Inf	down	8.75E-10	Similar to Beta-galactosidase.
143	Os06t0652000-02	33.40	0.00	-Inf	down	6.13E-03	Similar to DNA-directed RNA polymerase.
144	Os06t0664200-02	50.10	0.00	-Inf	down	8.94E-04	Hypothetical gene.
145	Os06t0704400-03	55.40	0.00	-Inf	down	5.04E-04	Similar to cDNA clone:001-132-E04, full insert sequence.
146	Os06t0707400-02	39.60	0.00	-Inf	down	2.95E-03	Similar to NBS-LRR disease resistance protein homologue.
147	Os06t0716700-03	118.00	0.00	-Inf	down	1.60E-06	Similar to Heat shock protein 90.
148	Os06t0730900-02	31.70	0.00	-Inf	down	7.59E-03	Peptidase A22B, signal peptide peptidase domain containing protein.
149	Os07t0134000-04	56.30	0.00	-Inf	down	4.59E-04	Similar to Amino acid permease 6.
150	Os07t0161000-02	30.80	0.00	-Inf	down	8.45E-03	Hypothetical conserved gene.
151	Os07t0190900-02	32.50	0.00	-Inf	down	6.82E-03	Hypothetical conserved gene.
152	Os07t0220600-01	34.30	0.00	-Inf	down	5.52E-03	Hypothetical conserved gene.
153	Os07t0270900-02	36.90	0.00	-Inf	down	4.03E-03	Mak16 protein family protein.
154	Os07t0295400-02	28.20	0.00	-Inf	down	1.17E-02	Conserved hypothetical protein.
155	Os07t0445600-02	22.00	0.00	-Inf	down	2.55E-02	Conserved hypothetical protein.
156	Os07t0452700-02	51.00	0.00	-Inf	down	8.11E-04	Conserved hypothetical protein.
157	Os07t0481000-02	73.90	0.00	-Inf	down	7.63E-05	Similar to MYND finger family protein.
158	Os07t0516500-04	123.00	0.00	-Inf	down	1.06E-06	Hypothetical conserved gene.
159	Os07t0533900-00	24.60	0.00	-Inf	down	1.81E-02	Conserved hypothetical protein.
160	Os07t0541200-00	20.20	0.00	-Inf	down	3.21E-02	Similar to receptor-like serine-threonine protein kinase.
161	Os07t0567050-00	20.20	0.00	-Inf	down	3.21E-02	Non-protein coding transcript.
162	Os07t0592200-03	28.20	0.00	-Inf	down	1.17E-02	Similar to predicted protein.
163	Os07t0683900-02	169.00	0.00	-Inf	down	4.36E-08	Similar to Osr40g2 protein (Fragment).
164	Os08t0111200-02	20.20	0.00	-Inf	down	3.21E-02	Similar to predicted protein.
165	Os08t0130500-02	89.70	0.00	-Inf	down	1.72E-05	Similar to 60S acidic ribosomal protein p0.
166	Os08t0192300-00	20.20	0.00	-Inf	down	3.21E-02	Conserved hypothetical protein.
167	Os08t0263300-01	37.80	0.00	-Inf	down	3.63E-03	Similar to cDNA clone:J013108L16, full insert sequence.
168	Os08t0344600-02	149.00	0.00	-Inf	down	1.66E-07	Similar to Phosphoenolpyruvate/phosphate translocator.
169	Os08t0377400-02	36.10	0.00	-Inf	down	4.47E-03	Exonuclease domain containing protein.

170	Os08t0396700-02	22.90	0.00	-Inf	down	2.27E-02	NB-ARC domain containing protein.
171	Os08t0416900-02	50.10	0.00	-Inf	down	8.94E-04	Similar to dnaJ domain containing protein.
172	Os08t0451201-00	93.30	0.00	-Inf	down	1.26E-05	Conserved hypothetical protein.
173	Os08t0451400-03	73.90	0.00	-Inf	down	7.63E-05	Similar to ARID/BRIGHT DNA-binding domain-containing protein.
174	Os08t0526150-00	26.40	0.00	-Inf	down	1.45E-02	Hypothetical protein.
175	Os09t0115400-03	121.00	0.00	-Inf	down	1.30E-06	Hypothetical conserved gene.
176	Os09t0115400-04	203.00	0.00	-Inf	down	5.45E-09	Hypothetical conserved gene.
177	Os09t0130800-04	61.60	0.00	-Inf	down	2.63E-04	Similar to predicted protein.
178	Os09t0284200-02	23.80	0.00	-Inf	down	2.03E-02	Similar to Serine/threonine protein phosphatase.
179	Os09t0372400-01	24.60	0.00	-Inf	down	1.81E-02	Similar to cDNA clone:J033042L23, full insert sequence.
180	Os09t0408966-00	22.00	0.00	-Inf	down	2.55E-02	Hypothetical protein.
181	Os09t0434900-02	55.40	0.00	-Inf	down	5.04E-04	Zinc finger, RING-type domain containing protein.
182	Os09t0501650-00	41.30	0.00	-Inf	down	2.41E-03	Hypothetical protein.
183	Os09t0509350-00	29.90	0.00	-Inf	down	9.41E-03	Hypothetical protein.
184	Os09t0530350-00	25.50	0.00	-Inf	down	1.62E-02	Hypothetical protein.
185	Os09t0541050-00	95.00	0.00	-Inf	down	1.08E-05	Hypothetical protein.
186	Os09t0567400-02	34.30	0.00	-Inf	down	5.52E-03	Similar to Histidine-containing phosphotransfer protein.
187	Os10t0109600-02	22.00	0.00	-Inf	down	2.55E-02	Peroxidase (EC 1.11.1.7).
188	Os10t0110800-02	38.70	0.00	-Inf	down	3.27E-03	Similar to cDNA clone:J023063N08, full insert sequence.
189	Os10t0130500-01	49.30	0.00	-Inf	down	9.85E-04	Hypothetical protein.
190	Os10t0167700-02	35.20	0.00	-Inf	down	4.97E-03	Conserved hypothetical protein.
191	Os10t0180000-02	31.70	0.00	-Inf	down	7.59E-03	Similar to secondary cell wall-related glycosyltransferase family 47.
192	Os10t0206800-02	98.50	0.00	-Inf	down	7.93E-06	Similar to predicted protein.
193	Os10t0317900-03	202.00	0.00	-Inf	down	5.73E-09	Non-protein coding transcript.
194	Os10t0381800-02	20.20	0.00	-Inf	down	3.21E-02	Zinc finger, SWIM-type domain containing protein.
195	Os10t0397200-02	161.00	0.00	-Inf	down	7.28E-08	Similar to predicted protein.
196	Os10t0473400-03	196.00	0.00	-Inf	down	8.19E-09	Similar to catalytic.
197	Os10t0476000-02	74.80	0.00	-Inf	down	7.00E-05	Similar to Adaptin ear-binding coat-associated protein 2.
198	Os10t0480200-03	29.90	0.00	-Inf	down	9.41E-03	Similar to Homeobox-leucine zipper protein HOX9.
199	Os10t0495300-02	190.00	0.00	-Inf	down	1.18E-08	Similar to ALG2-interacting protein X.

200	Os10t0502566-00	32.50	0.00	-Inf	down	6.82E-03	Non-protein coding transcript.
Rank overall	Gene ID	Root					Annoation
		FPKM		Log ₂ Ratio	R	FDR	
		Control	IPU				
1	Os08t0314800-03	391	1	-8.61	down	6.02E-17	Hypothetical conserved gene.
2	Os03t0749300-04	357	1	-8.48	down	4.32E-16	Similar to Cell wall beta-glucosidase.
3	Os03t0405500-02	320	1	-8.32	down	4.35E-15	Hypothetical conserved gene.
4	Os07t0645400-02	246	1	-7.94	down	7.93E-13	Similar to NADH-ubiquinone oxidoreductase 51 kDa subunit.
5	Os12t0566000-03	186	1	-7.54	down	1.10E-10	Similar to Boron transporter.
6	Os03t0805400-03	137	1	-7.10	down	1.12E-08	Similar to phosphoric ester hydrolase.
7	Os04t0439100-03	137	1	-7.10	down	1.12E-08	Similar to H0525C06.4 protein.
8	Os09t0557900-02	254	2	-6.99	down	2.55E-12	Similar to Protein phosphatase 2C gamma isoform (EC 3.1.3.16)
9	Os11t0199200-02	232	2	-6.86	down	1.33E-11	Similar to Protein disulfide isomerase.
10	Os03t0751100-02	275	3	-6.52	down	2.48E-12	Similar to Glutathione transporter.
11	Os04t0556300-02	81	1	-6.34	down	6.00E-06	Similar to Glutathione peroxidase.
12	Os09t0322000-03	70	1	-6.13	down	2.45E-05	Similar to sugar transport protein 14.
13	Os02t0759800-02	127	2	-5.99	down	1.34E-07	Similar to pre-mRNA-splicing factor prp45.
14	Os09t0381400-02	171	3	-5.83	down	7.55E-09	Similar to cysteine protease.
15	Os07t0195100-02	157	3	-5.71	down	2.60E-08	Similar to Ras-related protein ARA-3.
16	Os01t0326000-02	49	1	-5.61	down	4.32E-04	Similar to Class III peroxidase 13.
17	Os08t0345700-02	223	5	-5.48	down	9.79E-10	Similar to Fructose-6-phosphate 1-phosphotransferase (Fragment).
18	Os05t0282900-01	81	2	-5.34	down	2.08E-05	Conserved hypothetical protein.
19	Os03t0136900-02	155	4	-5.28	down	8.79E-08	Similar to Aconitate hydratase 2, mitochondrial.
20	Os11t0414000-02	115	3	-5.26	down	1.41E-06	Similar to predicted protein.
21	Os09t0482300-01	38	1	-5.25	down	2.17E-03	Late embryogenesis abundant protein, LEA-18 domain containing protein.
22	Os09t0482550-01	38	1	-5.25	down	2.17E-03	Late embryogenesis abundant protein, LEA-18 domain containing protein.
23	Os05t0107600-01	37	1	-5.21	down	2.52E-03	ABC transporter-like domain containing protein.
24	Os08t0536100-04	37	1	-5.21	down	2.52E-03	Hypothetical conserved gene.
25	Os11t0244100-00	37	1	-5.21	down	2.52E-03	Transferase family protein.

26	Os01t0842200-02	110	3	-5.20	down	2.35E-06	Similar to SCARECROW-like protein.
27	Os02t0702500-02	36	1	-5.17	down	2.93E-03	Similar to B0403H10-OSIGBa0105A11.22 protein.
28	Os09t0560700-02	35	1	-5.13	down	3.41E-03	Molybdenum cofactor sulfuryase, C-terminal domain containing protein.
29	Os12t0109700-01	34	1	-5.09	down	3.98E-03	Protein of unknown function DUF2985 domain containing protein.
30	Os02t0680400-02	32	1	-5.00	down	5.40E-03	Similar to CAAX prenyl protease 1 homolog.
31	Os07t0583600-03	64	2	-5.00	down	1.67E-04	Similar to Chitin-inducible gibberellin-responsive protein 2.
32	Os02t0580966-00	31	1	-4.95	down	6.30E-03	Hypothetical protein.
33	Os03t0239300-03	213	7	-4.93	down	1.12E-08	Zinc finger, C2H2-type domain containing protein.
34	Os02t0577700-00	30	1	-4.91	down	7.36E-03	Similar to H0815C01.4 protein.
35	Os06t0705600-00	29	1	-4.86	down	8.60E-03	Oligopeptide transporter domain containing protein.
36	Os08t0113100-02	768	27	-4.83	down	6.15E-14	Similar to cDNA clone:J023041C07, full insert sequence.
37	Os03t0826600-02	169	6	-4.82	down	1.50E-07	Similar to Hydrolase, acting on ester bonds.
38	Os02t0595100-02	56	2	-4.81	down	4.68E-04	Similar to N-acetylglucosaminyltransferase III.
39	Os03t0702000-03	28	1	-4.81	down	1.01E-02	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
40	Os05t0401100-02	28	1	-4.81	down	1.01E-02	Protein of unknown function DUF477 family protein.
41	Os09t0114500-02	56	2	-4.81	down	4.68E-04	Similar to Kinesin-like protein.
42	Os09t0284200-02	27	1	-4.75	down	1.18E-02	Similar to Serine/threonine protein phosphatase.
43	Os01t0119000-02	106	4	-4.73	down	8.68E-06	Glycosyltransferase AER61, uncharacterized domain containing protein.
44	Os04t0560100-02	26	1	-4.70	down	1.38E-02	Conserved hypothetical protein.
45	Os08t0274700-02	260	10	-4.70	down	3.85E-09	Similar to TTN10.
46	Os09t0435100-01	26	1	-4.70	down	1.38E-02	Hypothetical gene.
47	Os06t0319366-00	307	12	-4.68	down	8.27E-10	Hypothetical genes.
48	Os04t0562000-01	25	1	-4.64	down	1.62E-02	Zinc finger, DHHC-type domain containing protein.
49	Os07t0176200-02	25	1	-4.64	down	1.62E-02	Similar to Transcription factor CPP.
50	Os01t0729900-04	73	3	-4.60	down	1.36E-04	Similar to predicted protein.
51	Os01t0236700-02	24	1	-4.58	down	1.90E-02	Hypothetical conserved gene.
52	Os05t0162200-01	24	1	-4.58	down	1.90E-02	Conserved hypothetical protein.
53	Os07t0501900-01	24	1	-4.58	down	1.90E-02	Similar to predicted protein.
54	Os12t0182200-02	24	1	-4.58	down	1.90E-02	Similar to Dihydrolipoyllysine-residue acetyltransferase
55	Os12t0431850-00	24	1	-4.58	down	1.90E-02	Hypothetical protein.

56	Os03t0268900-01	23	1	-4.52	down	2.23E-02	Similar to tropinone reductase.
57	Os12t0102500-02	23	1	-4.52	down	2.23E-02	Serine/threonine protein kinase-related domain containing protein.
58	Os06t0146500-00	22	1	-4.46	down	2.62E-02	Hypothetical conserved gene.
59	Os07t0121500-00	22	1	-4.46	down	2.62E-02	Hypothetical conserved gene.
60	Os07t0168600-02	149	7	-4.41	down	1.55E-06	Similar to 3-glucanase.
61	Os02t0217250-00	21	1	-4.39	down	3.09E-02	Hypothetical protein.
62	Os03t0744100-01	21	1	-4.39	down	3.09E-02	Similar to SKIP interacting protein 16.
63	Os08t0532500-02	21	1	-4.39	down	3.09E-02	Conserved hypothetical protein.
64	Os03t0170900-02	20	1	-4.32	down	3.64E-02	Similar to Sucrose transporter.
65	Os03t0183800-02	20	1	-4.32	down	3.64E-02	Similar to Leucine-rich repeat transmembrane protein kinase 1 (Fragment).
66	Os04t0605300-02	20	1	-4.32	down	3.64E-02	Leucine-rich repeat, typical subtype containing protein.
67	Os05t0102800-04	20	1	-4.32	down	3.64E-02	Similar to AML6.
68	Os10t0555900-01	40	2	-4.32	down	4.00E-03	Similar to Beta-expansin.
69	Os02t0830100-03	39	2	-4.29	down	4.59E-03	Similar to predicted protein.
70	Os10t0534500-02	390	20	-4.29	down	7.54E-10	Similar to Resistance protein candidate (Fragment).
71	Os01t0253100-02	58	3	-4.27	down	8.19E-04	Hypothetical conserved gene.
72	Os09t0279500-03	19	1	-4.25	down	4.30E-02	Similar to Plastid-specific 30S ribosomal protein 2, chloroplast precursor (PSRP- 2).
73	Os11t0457300-01	19	1	-4.25	down	4.30E-02	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
74	Os02t0451900-01	37	2	-4.21	down	6.07E-03	Conserved hypothetical protein.
75	Os08t0234000-02	37	2	-4.21	down	6.07E-03	Similar to 60S ribosomal protein L7-2.
76	Os12t0221600-01	145	8	-4.18	down	3.97E-06	Conserved hypothetical protein.
77	Os02t0217600-01	70	4	-4.13	down	4.02E-04	Similar to Isoform 2 of Serine/threonine-protein phosphatase PP2A-3 catalytic subunit.
78	Os04t0412300-02	35	2	-4.13	down	8.02E-03	Glycoside hydrolase, family 17 protein.
79	Os05t0177900-00	35	2	-4.13	down	8.02E-03	Conserved hypothetical protein.
80	Os05t0385400-01	35	2	-4.13	down	8.02E-03	Conserved hypothetical protein.
81	Os06t0694200-01	35	2	-4.13	down	8.02E-03	Esterase, SGNH hydrolase-type domain containing protein.
82	Os09t0412700-01	87	5	-4.12	down	1.24E-04	Conserved hypothetical protein.
83	Os01t0172400-04	86	5	-4.10	down	1.37E-04	Similar to Phospholipase D alpha 1.
84	Os01t0101900-00	85	5	-4.09	down	1.52E-04	Similar to OSIGBa0075F02.3 protein.
85	Os01t0971800-00	68	4	-4.09	down	5.04E-04	Similar to Two-component response regulator ARR11.

86	Os03t0264400-02	34	2	-4.09	down	9.23E-03	Similar to Anthranilate synthase component I family protein, expressed.
87	Os02t0820400-02	101	6	-4.07	down	5.75E-05	Transferase family protein.
88	Os07t0529600-01	2646	158	-4.07	down	4.34E-13	Similar to Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
89	Os04t0233400-02	1811	109	-4.05	down	8.65E-13	Similar to cDNA clone:006-302-B10, full insert sequence.
90	Os01t0296200-00	111	7	-3.99	down	4.06E-05	Similar to polygalacturonase.
91	Os03t0819600-02	346	22	-3.98	down	1.23E-08	Chalcone isomerase (EC 5.5.1.6).
92	Os04t0530500-02	1141	73	-3.97	down	9.19E-12	Zinc finger, RING/FYVE/PHD-type domain containing protein.
93	Os02t0569900-01	31	2	-3.95	down	1.41E-02	Cytochrome P450 family protein.
94	Os05t0429500-01	31	2	-3.95	down	1.41E-02	Similar to dienelactone hydrolase family protein.
95	Os06t0683000-03	31	2	-3.95	down	1.41E-02	Hypothetical conserved gene.
96	Os04t0178300-02	92	6	-3.94	down	1.37E-04	Similar to Syn-copalyl diphosphate synthase.
97	Os01t0871900-00	60	4	-3.91	down	1.26E-03	Similar to POT family protein.
98	Os04t0616600-01	30	2	-3.91	down	1.63E-02	Serine/threonine protein kinase-related domain containing protein.
99	Os09t0326900-02	224	15	-3.90	down	4.91E-07	Similar to BRI1-KD interacting protein 107 (Fragment).
100	Os08t0534350-00	44	3	-3.87	down	4.71E-03	Similar to cation cation antiporter.
101	Os01t0282866-00	29	2	-3.86	down	1.87E-02	Hypothetical protein.
102	Os01t0740400-01	29	2	-3.86	down	1.87E-02	Protein of unknown function DUF1005 family protein.
103	Os08t0380100-02	86	6	-3.84	down	2.48E-04	Similar to Polygalacturonase isoenzyme 1 beta subunit (Fragment).
104	Os02t0552200-00	28	2	-3.81	down	2.16E-02	Conserved hypothetical protein.
105	Os09t0452800-01	126	9	-3.81	down	3.20E-05	Peptidase A1 domain containing protein.
106	Os02t0200900-04	353	26	-3.76	down	3.65E-08	Similar to F-box family member.
107	Os03t0324300-02	705	52	-3.76	down	4.89E-10	Similar to ETHYLENE-INSENSITIVE3-like 1 protein.
108	Os11t0100800-01	40	3	-3.74	down	7.86E-03	Similar to Exo70 exocyst complex subunit family protein.
109	Os06t0606599-00	53	4	-3.73	down	2.84E-03	Hypothetical protein.
110	Os05t0474700-01	26	2	-3.70	down	2.88E-02	Conserved hypothetical protein.
111	Os07t0569166-01	65	5	-3.70	down	1.27E-03	Conserved hypothetical protein.
112	Os08t0476300-02	39	3	-3.70	down	8.95E-03	Glucose/ribitol dehydrogenase family protein.
113	Os09t0505700-01	26	2	-3.70	down	2.88E-02	Aldolase-type TIM barrel domain containing protein.
114	Os10t0569600-00	26	2	-3.70	down	2.88E-02	Similar to RIR1b protein precursor.
115	Os05t0208500-01	62	5	-3.63	down	1.77E-03	Hypothetical protein.

116	Os01f0871800-01	37	3	-3.62	down	1.16E-02	TGF-beta receptor, type I/II extracellular region family protein.
117	Os02t0120100-02	74	6	-3.62	down	8.31E-04	Similar to ATP binding protein.
118	Os05t0239151-00	49	4	-3.61	down	4.56E-03	Hypothetical protein.
119	Os02t0727300-03	48	4	-3.58	down	5.14E-03	Similar to ubiquitin-protein ligase.
120	Os02t0799300-02	24	2	-3.58	down	3.85E-02	Similar to predicted protein.
121	Os06t0490200-03	24	2	-3.58	down	3.85E-02	Conserved hypothetical protein.
122	Os02t0569400-02	35	3	-3.54	down	1.50E-02	Similar to Cyt-P450 monooxygenase.
123	Os10t0476700-03	35	3	-3.54	down	1.50E-02	Esterase, SGNH hydrolase-type, subgroup domain containing protein.
124	Os07t0181000-02	58	5	-3.54	down	2.75E-03	Similar to Pyruvate kinase.
125	Os01t0974200-03	23	2	-3.52	down	4.45E-02	Conserved hypothetical protein.
126	Os03t0273200-01	23	2	-3.52	down	4.45E-02	Similar to Laccase (EC 1.10.3.2).
127	Os03t0410300-02	23	2	-3.52	down	4.45E-02	Protein of unknown function DUF1313 family protein.
128	Os03t0301700-01	80	7	-3.51	down	7.43E-04	Similar to Calmodulin-binding protein phosphatase.
129	Os02t0114200-02	194	17	-3.51	down	6.91E-06	Similar to Serine carboxypeptidase 3.
130	Os03t0274000-02	125	11	-3.51	down	8.53E-05	Similar to oxysterol-binding protein.
131	Os06t0111500-02	305	27	-3.50	down	4.38E-07	Similar to 6-phosphogluconate dehydrogenase, decarboxylating.
132	Os03t0334800-02	177	16	-3.47	down	1.43E-05	Similar to Lung seven transmembrane receptor family protein, expressed.
133	Os01t0882800-01	22	2	-3.46	down	5.16E-02	Similar to Amino acid carrier (Fragment).
134	Os02t0238500-01	22	2	-3.46	down	5.16E-02	Similar to scramblase family protein.
135	Os02t0255200-02	44	4	-3.46	down	8.28E-03	Similar to 40S ribosomal protein S15a.
136	Os03t0679100-01	22	2	-3.46	down	5.16E-02	Vacuolar protein sorting-associated protein 26 family protein.
137	Os07t0660466-00	22	2	-3.46	down	5.16E-02	Hypothetical protein.
138	Os09t0558300-02	22	2	-3.46	down	5.16E-02	Similar to cyclic nucleotide-gated ion channel 14.
139	Os12t0104900-00	22	2	-3.46	down	5.16E-02	EF-HAND 2 domain containing protein.
140	Os12t0621300-01	22	2	-3.46	down	5.16E-02	Hypothetical conserved gene.
141	Os03t0442800-01	32	3	-3.42	down	2.23E-02	Hypothetical gene.
142	Os07t0152900-04	32	3	-3.42	down	2.23E-02	Similar to Glycolate oxidase (EC 1.1.3.15) (Fragment).
143	Os02t0640800-01	21	2	-3.39	down	5.97E-02	Similar to Carbonyl reductase 1.
144	Os02t0699850-01	21	2	-3.39	down	5.97E-02	Hypothetical gene.
145	Os10t0109750-00	21	2	-3.39	down	5.97E-02	Hypothetical protein.

146	Os12t0635700-01	52	5	-3.38	down	5.35E-03	Similar to GNS1/SUR4 membrane protein.
147	Os01t0653350-00	31	3	-3.37	down	2.54E-02	Similar to WD-40 repeat family protein (Fragment).
148	Os01t0121100-01	101	10	-3.34	down	4.02E-04	Similar to SLL2.
149	Os04t0497400-01	20	2	-3.32	down	6.93E-02	Similar to 6,7-dimethyl-8-ribityllumazine synthase (Fragment).
150	Os05t0556650-00	20	2	-3.32	down	6.93E-02	Hypothetical gene.
151	Os07t0123400-01	20	2	-3.32	down	6.93E-02	Similar to ternary complex factor MIP1.
152	Os07t0152101-01	20	2	-3.32	down	6.93E-02	Hypothetical gene.
153	Os08t0427300-02	30	3	-3.32	down	2.89E-02	Similar to Myrosinase (Fragment).
154	Os09t0555500-01	50	5	-3.32	down	6.70E-03	Similar to Chloroplast phytoene synthase 3.
155	Os11t0474500-00	20	2	-3.32	down	6.93E-02	NB-ARC domain containing protein.
156	Os01t0186900-01	49	5	-3.29	down	7.50E-03	Similar to cDNA clone:001-117-G12, full insert sequence.
157	Os02t0771666-00	68	7	-3.28	down	2.42E-03	Hypothetical gene.
158	Os03t0300600-03	136	14	-3.28	down	1.17E-04	Similar to Chaperone protein dnaJ.
159	Os01t0901550-00	29	3	-3.27	down	3.30E-02	Hypothetical gene.
160	Os04t0137100-00	29	3	-3.27	down	3.30E-02	Similar to OSIGBa0147B06.7 protein.
161	Os01t0290000-04	19	2	-3.25	down	8.04E-02	Similar to retrotransposon protein SINE subclass.
162	Os01t0821800-03	19	2	-3.25	down	8.04E-02	Nucleic acid-binding, OB-fold-like domain containing protein.
163	Os03t0383800-03	38	4	-3.25	down	1.71E-02	Nucleotide-binding, alpha-beta plait domain containing protein.
164	Os11t0547000-01	57	6	-3.25	down	4.88E-03	Similar to FKF1.
165	Os01t0174700-03	47	5	-3.23	down	9.40E-03	Similar to predicted protein.
166	Os11t0489250-00	312	34	-3.20	down	2.00E-06	Similar to Cytochrome P450 family protein, expressed.
167	Os01t0191200-01	27	3	-3.17	down	4.30E-02	Similar to Acid phosphatase.
168	Os01t0276066-00	18	2	-3.17	down	9.34E-02	Non-protein coding transcript.
169	Os03t0656000-00	18	2	-3.17	down	9.34E-02	Hypothetical conserved gene.
170	Os04t0437600-02	18	2	-3.17	down	9.34E-02	Similar to H0315A08.7 protein.
171	Os04t0448800-02	18	2	-3.17	down	9.34E-02	Similar to Mitochondrial phosphate transporter (Fragment).
172	Os05t0121850-01	18	2	-3.17	down	9.34E-02	Hypothetical gene.
173	Os08t0278600-01	27	3	-3.17	down	4.30E-02	Similar to complex 1 protein containing protein.
174	Os09t0493800-02	27	3	-3.17	down	4.30E-02	Similar to Chaperone protein dnaJ 10 (AtJ10) (AtDjC10).
175	Os03t0181100-01	209	24	-3.12	down	2.46E-05	Tify domain containing protein.

176	Os05t0535700-02	52	6	-3.12	down	8.30E-03	Conserved hypothetical protein.
177	Os07t0538250-00	26	3	-3.12	down	4.91E-02	Hypothetical protein.
178	Os10t0416100-02	26	3	-3.12	down	4.91E-02	Similar to Chitinase (Fragment).
179	Os04t0533300-02	69	8	-3.11	down	3.28E-03	Similar to remorin.
180	Os12t0617400-01	77	9	-3.10	down	2.26E-03	Viviparous-14.
181	Os05t0142200-00	34	4	-3.09	down	2.78E-02	Conserved hypothetical protein.
182	Os03t0806700-02	211	25	-3.08	down	2.87E-05	Protein of unknown function DUF868, plant family protein.
183	Os01t0667550-00	25	3	-3.06	down	5.61E-02	Hypothetical gene.
184	Os01t0834200-03	25	3	-3.06	down	5.61E-02	Similar to T-cell immune regulator 1 transcript variant 3 (Fragment).
185	Os04t0380200-01	50	6	-3.06	down	1.03E-02	Conserved hypothetical protein.
186	Os01t0600900-03	83	10	-3.05	down	1.89E-03	Similar to Chlorophyll a-b binding protein 2, chloroplastic.
187	Os03t0282900-02	114	14	-3.03	down	5.83E-04	Conserved hypothetical protein.
188	Os02t0467600-01	32	4	-3.00	down	3.55E-02	Similar to Cinnamate 4-hydroxylase CYP73.
189	Os04t0499100-01	32	4	-3.00	down	3.55E-02	Biopterin transport-related protein BT1 family protein.
190	Os04t0501600-02	24	3	-3.00	down	6.40E-02	Similar to H0311C03.6 protein.
191	Os06t0228200-03	24	3	-3.00	down	6.40E-02	Similar to NOD26-like membrane integral protein.
192	Os07t0529600-02	96	12	-3.00	down	1.24E-03	Similar to Pathogen-induced defense-responsive protein 8.
193	Os12t0221400-01	32	4	-3.00	down	3.55E-02	Similar to cDNA clone:001-112-B09, full insert sequence.
194	Os03t0321900-01	63	8	-2.98	down	5.83E-03	Similar to tRNA-specific adenosine deaminase.
195	Os02t0817800-01	47	6	-2.97	down	1.42E-02	Similar to Telomere binding protein-1.
196	Os05t0316100-01	47	6	-2.97	down	1.42E-02	Zinc/iron permease family protein.
197	Os06t0709100-02	94	12	-2.97	down	1.46E-03	Cyclin-like F-box domain containing protein.
198	Os07t0618400-02	39	5	-2.96	down	2.33E-02	Similar to Leucine-rich repeat transmembrane protein kinase 1 (Fragment).
199	Os12t0165000-02	39	5	-2.96	down	2.33E-02	Similar to predicted protein.
200	Os09t0483150-00	31	4	-2.95	down	4.02E-02	Hypothetical gene.

ESI Table S7. Forty most abundant genes in the four libraries of *Oryza sativa* based on the expressed tag frequency. The order of other three libraries is subject to the order Shoot+IPU, Shoot-IPU, Root+IPU and Root-IPU, respectively. Red regions indicate the up-regulation. Blue regions indicate the down-regulation.

Rank overall	Gene ID	Shoot+IPU	Signature abundance					Description
		Up	Shoot-IPU	Log ₂ Ratio _{shoot}	Root+IPU	Root-IPU	Log ₂ Ratio _{root}	
1	Os11t0703900-01	107000	47000	1.19	141387	162259	-0.20	Heat shock protein 70.
2	Os01t0256500-02	85500	38700	1.14	304017	216413	0.49	Similar to ZnI.
3	Os02t0161900-01	52000	13500	1.94	71434	47584	0.59	Similar to polyubiquitin containing 7 ubiquitin monomers.
4	Os05t0375400-01	46400	16400	1.5	36186	19473	0.89	Beta-glucanase precursor.
5	Os03t0146100-01	46400	18700	1.31	67463	51536	0.39	Tonoplast intrinsic protein (Tonoplast water channel).
6	Os02t0465900-01	40500	11100	1.87	21290	15834	0.43	ChaC-like protein family protein.
7	Os04t0667800-01	34800	15200	1.19	32084	26911	0.25	Ubiquitin-conjugating enzyme.
8	Os04t0679400-04	33700	4880	2.79	14138	8220	0.78	Similar to H0801D08.15 protein.
9	Os06t0336200-01	32200	14000	1.2	16013	16267	-0.02	Delta-tonoplast intrinsic protein.
10	Os05t0176700-01	31900	8180	1.96	17729	10955	0.69	Conserved hypothetical protein.
11	Os06t0612800-01	31300	12000	1.39	51759	41822	0.31	Similar to PVPR3 protein.
12	Os06t0561000-01	29700	2020	3.88	10873	3384	1.68	Similar to Myo-inositol oxygenase.
13	Os08t0473900-02	24900	139	7.49	0	23	-Inf	Similar to Alpha amylase isozyme 3D.
14	Os02t0606200-01	24200	11400	1.09	15749	8808	0.84	Zinc finger, B-box domain containing protein.
15	Os12t0428000-01	23700	2900	3.03	12300	8043	0.61	Similar to senescence-associated protein DIN1.
16	Os05t0344200-01	21200	7930	1.42	10719	8994	0.25	Conserved hypothetical protein.
17	Os09t0482400-01	20100	6710	1.58	9621	9287	0.05	Similar to Heat shock protein 81-3.
18	Os05t0489600-01	19800	8940	1.14	21473	17218	0.32	Similar to ADP-ribosylation factor 1.
19	Os09t0482100-01	19100	5550	1.78	9781	10249	-0.07	Similar to Heat shock protein 82.
20	Os04t0598000-01	18700	4870	1.94	5581	4381	0.35	Similar to OSJNba0093F12.14 protein.
21	Os03t0291500-01	18100	640	4.82	2231	2083	0.10	Similar to Asparagine synthetase.
22	Os03t0701200-01	18000	2360	2.93	5470	2309	1.24	Similar to Sugar-starvation induced protein.
23	Os03t0342900-02	17900	7770	1.2	8564	6217	0.46	Dormancyauxin associated family protein.

24	Os05t0489600-03	17600	8420	1.06	20671	15749	0.39	Similar to ADP-ribosylation factor 1.
25	Os04t0555300-01	16600	6350	1.39	5276	3973	0.41	Similar to glycerol 3-phosphate permease.
26	Os03t0231600-01	15800	1790	3.14	7266	2421	1.59	Similar to Branched-chain-amino-acid aminotransferase 3.
27	Os01t0681600-02	15000	4310	1.8	10595	7067	0.58	Spliceosome associated protein 61(SAP 61).
28	Os05t0129300-02	14800	5900	1.33	12490	8004	0.64	Basic/leucine zipper protein.
29	Os09t0553900-01	14500	6260	1.21	61	52	0.23	Conserved hypothetical protein.
30	Os05t0171900-01	14000	1000	3.81	4584	1743	1.40	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.
31	Os03t0266300-03	13300	1920	2.79	9988	4018	1.31	Class I low-molecular-weight heat shock protein 17.9.
32	Os06t0172800-00	13300	568	4.55	6254	2545	1.30	Similar to alkaline alpha galactosidase 2.
33	Os02t0670900-02	13300	3080	2.11	2460	1661	0.57	Similar to amino acid transport protein.
34	Os01t0332100-01	13200	5670	1.22	211	136	0.63	Similar to Neutral invertase-like protein.
35	Os04t0583200-01	12800	1330	3.26	13391	7199	0.90	Conserved hypothetical protein.
36	Os07t0663800-01	12600	5110	1.3	3372	2430	0.47	Similar to Oxidoreductase, short chain dehydrogenase/reductase family protein.
37	Os07t0559700-00	12400	2250	2.46	1505	861	0.81	Similar to Monosaccharide transporter 3.
38	Os01t0916400-01	12200	2610	2.23	1848	859	1.11	Similar to Selenium binding protein.
39	Os11t0106700-02	11800	5540	1.1	91	122	-0.42	Similar to Ferritin 1, chloroplast precursor(ZmFer1).
40	Os01t0188400-01	11300	4910	1.2	8049	4489	0.84	NADP-dependent malic enzyme, chloroplast precursor(NADP-ME).

Rank overall	Gene ID	Shoot-IPU		Signature abundance				Description
		Down	Shoot+IPU	Log ₂ Ratio _{shoot}	Root+IPU	Root-IPU	Log ₂ Ratio _{root}	
1	Os01t0102900-01	32900	7220	-2.19	643	1498	-1.22	Light regulated Lir1 family protein.
2	Os11t0167800-01	26700	9540	-1.48	10420	24654	-1.24	Similar to Anth (Pollen-specific desiccation-associated LLA23 protein).
3	Os02t0121300-01	24700	11300	-1.12	16228	29999	-0.89	Cyclophilin 2.
4	Os07t0529600-01	24500	123	-7.64	158	2646	-4.07	Similar to Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
5	Os01t0303000-02	24300	7950	-1.61	39	151	-1.95	Similar to CP12.
6	Os01t0357100-02	17900	8680	-1.05	4490	4331	0.05	Similar to Ferredoxin-nitrite reductase.
7	Os10t0330000-01	12500	4210	-1.57	9589	11058	-0.21	Conserved hypothetical protein.
8	Os08t0468100-01	11600	5800	-1	312	655	-1.07	Similar to Nitrate reductase.
9	Os11t0147800-01	10900	5400	-1.01	3472	3299	0.07	Similar to Wali7 protein.
10	Os02t0115700-01	8270	2780	-1.57	725	1138	-0.65	Catalase isozyme A (CAT-A).

11	Os12t0115500-01	7910	3520	-1.17	25	5	2.32	Similar to nonspecific lipid-transfer protein 3.
12	Os11t0644700-01	7790	1290	-2.6	191	328	-0.78	Plant disease resistance response protein family protein.
13	Os09t0541000-01	7580	1280	-2.56	30	9	1.74	Similar to Aquaporin 2.
14	Os11t0645400-01	7230	1730	-2.06	258	475	-0.88	Plant disease resistance response protein family protein.
15	Os08t0139700-01	5800	2310	-1.33	4	0	Inf	Similar to terpene synthase 6.
16	Os01t0123900-01	5490	1990	-1.46	5	5	0.00	Similar to Bowman-Birk type proteinase inhibitor (EBI).
17	Os04t0650700-02	5340	634	-3.07	6491	786	3.05	Similar to OSIGBa0113E10.3 protein.
18	Os12t0515800-01	5170	2330	-1.15	1	0	Inf	Hypothetical conserved gene.
19	Os08t0468100-03	4460	2120	-1.07	290	554	-0.93	Similar to Nitrate reductase.
20	Os02t0194700-01	3960	647	-2.61	3	2	0.58	Similar to Lipoxygenase 2.3, chloroplast precursor (LOX2:Hv:3).
21	Os07t0631900-01	3800	1740	-1.12	61	133	-1.12	Nucleotide-binding, alpha-beta plait domain containing protein.
22	Os03t0197100-01	3520	1550	-1.18	112	168	-0.58	Similar to Sugar transporter protein.
23	Os01t0191200-02	3190	382	-3.06	198	138	0.52	Similar to Acid phosphatase.
24	Os11t0209000-01	3180	1430	-1.15	7	0	Inf	Glycine rich family protein.
25	Os03t0388900-01	2970	1260	-1.24	48	80	-0.74	Peptidase C14, caspase catalytic domain containing protein.
26	Os02t0704000-01	2730	259	-3.4	7	14	-1.00	Carotenoid oxygenase family protein.
27	Os02t0308800-01	2610	799	-1.71	0	0	0.00	FAS1 domain domain containing protein.
28	Os06t0705100-02	2580	11.4	-7.83	0	1	-Inf	Similar to Thylakoid lumenal 13.3 kDa protein (P16.5).
29	Os05t0231700-01	2530	658	-1.94	342	696	-1.03	Similar to Tonoplast intrinsic protein.
30	Os09t0530000-01	2500	1050	-1.26	7	7	0.00	Rhodanese-like domain containing protein.
31	Os03t0757900-01	2340	1070	-1.13	1305	1947	-0.58	Similar to UDP-Glc dehydrogenase(UDPGDH).
32	Os11t0267000-03	2330	562	-2.05	110	76	0.53	GUN4-like domain containing protein.
33	Os04t0678700-01	2290	641	-1.84	1	2	-1.00	Similar to NADPH- protochlorophyllide oxidoreductase (POR).
34	Os08t0162800-01	2270	1100	-1.04	1074	1990	-0.89	Similar to Acyl-CoA-binding protein.
35	Os03t0843800-00	2160	447	-2.28	1	0	Inf	Methyl chloride transferase.
36	Os08t0139100-01	2150	522	-2.04	88	103	-0.23	Similar to DAG protein, chloroplast precursor.
37	Os07t0142900-01	2040	471	-2.12	1	1	0.00	Aldo/keto reductase family protein.
38	Os10t0529300-01	2020	975	-1.05	637	633	0.01	Similar to Tau class GST protein 3.
39	Os04t0439100-02	2010	980	-1.03	266	67	1.99	T-complex 11 family protein.
40	Os07t0413800-04	2010	690	-1.54	4	2	1.00	Similar to predicted protein.

Rank overall	Gene ID	Root+IPU		Signature abundance				Description
		Up	Root-IPU	Log ₂ Ratio _{root}	Shoot+IPU	Shoot-IPU	Log ₂ Ratio _{shoot}	
1	Os03t0305100-01	37244	16418	1.18	10800	2870	1.91	Similar to AMP-binding protein.
2	Os03t0826800-01	22837	9550	1.26	6190	518	3.58	Conserved hypothetical protein.
3	Os04t0468600-02	17591	7327	1.26	22.7	35.2	-0.63	Heavy metal transport/detoxification protein.
4	Os03t0734000-01	16438	7452	1.14	0	0.88	-Inf	Pentatricopeptide repeat containing protein.
5	Os06t0561000-01	10873	3384	1.68	29700	2020	3.88	Similar to Myo-inositol oxygenase.
6	Os03t0266300-03	9988	4018	1.31	13300	1920	2.79	Class I low-molecular-weight heat shock protein 17.9.
7	Os07t0638100-01	9548	4705	1.02	1590	525	1.60	Six-bladed beta-propeller, TolB-like domain containing protein.
8	Os02t0689900-01	8533	3598	1.25	2010	513	1.97	TGF-beta receptor, type I/II extracellular region family protein.
9	Os03t0231600-01	7266	2421	1.59	15800	1790	3.14	Similar to Branched-chain-amino-acid aminotransferase 3.
10	Os01t0975300-01	7249	3481	1.06	800	499	0.68	Similar to Myb factor protein.
11	Os10t0456800-01	6840	2374	1.53	8470	662	3.68	Similar to PGPD14 protein.
12	Os04t0650700-02	6491	786	3.05	634	5340	-3.07	Similar to OSIGBa0113E10.3 protein.
13	Os06t0172800-00	6254	2545	1.30	13300	568	4.55	Similar to alkaline alpha galactosidase 2.
14	Os02t0541325-00	5998	2428	1.30	7690	1380	2.48	Similar to Serine decarboxylase.
15	Os04t0482300-01	5793	2591	1.16	8340	846	3.30	Kelch related domain containing protein.
16	Os03t0701200-01	5470	2309	1.24	18000	2360	2.93	Similar to Sugar-starvation induced protein.
17	Os02t0586900-02	5311	1420	1.90	423	2.64	7.32	Similar to Glycine rich protein.
18	Os05t0171900-01	4584	1743	1.40	14000	1000	3.81	Glyoxalase/bleomycin resistance protein.
19	Os06t0573600-01	4508	1317	1.78	4370	3310	0.40	Similar to Beta-galactosidase precursor (Lactase).
20	Os02t0533800-01	4409	1818	1.28	2790	984	1.50	Similar to ATPase inhibitor.
21	Os01t0916100-01	4233	1982	1.09	60.2	30.8	0.97	Similar to loricrin.
22	Os01t0138800-01	4073	1278	1.67	506	25.5	4.31	Peptidase C26 domain containing protein.
23	Os06t0194900-02	3834	947	2.02	1820	1180	0.63	Sucrose synthase 2 (EC 2.4.1.13).
24	Os02t0586000-01	3556	318	3.48	0	0	0.00	Quinonprotein alcohol dehydrogenase-like domain containing protein.
25	Os03t0255500-01	3484	986	1.82	3080	2000	0.62	Similar to Phosphoenolpyruvate carboxykinase 4.
26	Os06t0612800-02	3326	1103	1.59	987	585	0.75	Similar to cDNA clone:006-301-C11, full insert sequence.
27	Os10t0493600-01	3281	1277	1.36	5070	1980	1.36	Alpha-galactosidase precursor.
28	Os04t0659300-01	3147	854	1.88	4060	347	3.55	Protein of unknown function DUF26 domain containing protein.

29	Os02t0585650-01	2885	484	2.58	0	0	0.00	Hypothetical gene.
30	Os01t0194300-01	2752	1239	1.15	627	203	1.63	Similar to NPR1.
31	Os03t0583800-01	2719	1297	1.07	12800	12300	0.05	Mpv17/PMP22 family protein.
32	Os03t0364400-02	2666	979	1.45	1420	272	2.39	Similar to Phytosulfokine receptor-like protein.
33	Os01t0850700-02	2635	1027	1.36	11200	5140	1.12	Cupredoxin domain containing protein.
34	Os05t0405000-02	2568	499	2.36	3900	1080	1.85	Similar to Isoform 2 of Pyruvate, phosphate dikinase 1, chloroplastic.
35	Os04t0670200-02	2504	566	2.15	767	304	1.34	Granulin domain containing protein.
36	Os03t0233000-01	2485	511	2.28	27.3	7.04	1.95	Protein of unknown function DUF607 family protein.
37	Os03t0826900-01	2307	534	2.11	2480	27.3	6.51	Conserved hypothetical protein.
38	Os07t0638400-01	2203	964	1.19	54.6	7.92	2.78	Similar to 1-Cys peroxiredoxin.
39	Os10t0493600-03	2109	950	1.15	1880	1110	0.76	Similar to Alpha-galactosidase.
40	Os03t0351800-01	2028	999	1.02	1640	1100	0.57	Zinc finger, RING/FYVE/PHD-type domain containing protein.

Rank overall	Gene ID	Root-IPU		Signature abundance				Description
		Down	Root+IPU	Log ₂ Ratio _{root}	Shoot+IPU	Shoot-IPU	Log ₂ Ratio _{shoot}	
1	Os11t0167800-01	24654	10420	-1.24	9540	26700	-1.48	Similar to Pollen-specific desiccation-associated LLA23 protein.
2	Os05t0160300-01	9747	4260	-1.19	971	1020	-0.07	Bifunctional inhibitor/plant lipid transfer protein.
3	Os02t0669100-01	7048	2944	-1.26	9180	6010	0.61	Dehydrin family protein.
4	Os11t0428800-01	5215	1657	-1.65	0	0	0.00	Cupredoxin domain containing protein.
5	Os12t0555000-01	3837	1680	-1.19	11.4	15.8	-0.48	Similar to Probenazole-inducible protein PBZ1.
6	Os02t0716500-01	3763	1846	-1.03	25800	15500	0.74	Similar to Delta-12 fatty acid desaturase.
7	Os03t0332533-01	3557	1582	-1.17	7.96	8.8	-0.15	Similar to Plant acid phosphatase family protein.
8	Os04t0403900-00	3328	1663	-1.00	1300	2370	-0.86	Similar to H0502B11.1 protein.
9	Os11t0247300-02	2963	719	-2.04	795	679	0.23	Similar to Alpha-tubulin.
10	Os07t0529600-01	2646	158	-4.07	123	24500	-7.64	Similar to Thiazole biosynthetic enzyme 1-1, chloroplast precursor.
11	Os03t0401300-03	2627	1044	-1.33	0	86.2	-Inf	Similar to Sucrose synthase metabolism.
12	Os07t0175600-01	2490	1144	-1.12	101	70.4	0.52	Plant lipid transfer protein and hydrophobic protein.
13	Os08t0157500-02	2349	353	-2.73	641	1050	-0.72	Similar to Quercetin 3-O-methyltransferase 1.
14	Os04t0188500-01	2240	1012	-1.15	0	0	0.00	Conserved hypothetical protein.
15	Os11t0507200-00	2189	951	-1.20	21.6	29.9	-0.47	Similar to transferase.
16	Os04t0507950-01	2151	979	-1.14	2.27	6.16	-1.44	Hypothetical conserved gene.

17	Os08t0519100-02	2103	898	-1.23	0	0	0.00	Hypothetical conserved gene.
18	Os03t0279200-01	2084	966	-1.11	259	370	-0.52	Similar to Histone H2A.
19	Os10t0569400-01	1930	927	-1.06	14.8	164	-3.47	RIR1a protein precursor.
20	Os04t0233400-02	1811	109	-4.05	957	735	0.38	Similar to cDNA clone:006-302-B10, full insert sequence.
21	Os01t0916600-01	1773	683	-1.38	33	647	-4.29	RNA recognition motif, glycine rich protein domain containing protein.
22	Os02t0653200-01	1675	715	-1.23	12.5	17.6	-0.49	Cupredoxin domain containing protein.
23	Os01t0559900-01	1578	746	-1.08	899	1460	-0.70	Non-protein coding transcript.
24	Os01t0974200-02	1567	780	-1.01	806	1300	-0.69	Metallothionein-like protein.
25	Os01t0975900-02	1538	485	-1.66	184	662	-1.84	Similar to Tonoplast membrane integral protein ZmTIP1-2.
26	Os01t0102900-01	1498	643	-1.22	7220	32900	-2.19	Light regulated Lir1 family protein.
27	Os07t0174400-00	1437	657	-1.13	0	7.04	-Inf	Similar to Non-specific lipid-transfer protein.
28	Os03t0242300-01	1431	294	-2.28	580	1020	-0.81	Hypothetical protein.
29	Os11t0211800-01	1387	606	-1.19	30.7	193	-2.65	Similar to Specific abundant protein-like protein 1.
30	Os08t0249000-01	1372	385	-1.83	348	594	-0.77	Zinc finger, B-box domain containing protein.
31	Os11t0180000-01	1339	574	-1.22	53.4	79.2	-0.57	Plant disease resistance response protein family protein.
32	Os09t0482200-01	1338	460	-1.54	306	364	-0.25	Peptidase A1 domain containing protein.
33	Os09t0482500-01	1338	460	-1.54	306	364	-0.25	Peptidase A1 domain containing protein.
34	Os05t0207300-01	1334	649	-1.04	347	508	-0.55	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.
35	Os01t0962600-01	1240	572	-1.12	78.4	159	-1.02	Similar to 40S ribosomal protein S10-1.
36	Os03t0155300-00	1239	472	-1.39	0	0	0.00	Similar to Alpha-expansin precursor.
37	Os08t0524400-00	1225	609	-1.01	18.2	15.8	0.20	Protein of unknown function DUF568.
38	Os01t0756900-01	1224	552	-1.15	26.1	43.1	-0.72	Hypothetical protein.
39	Os01t0797600-01	1209	477	-1.34	2920	2670	0.13	AP2/ERF family protein.
40	Os02t0716500-04	1184	426	-1.47	6320	4270	0.57	Similar to Delta-12 fatty acid desaturase.

ESI Table S8.

Significantly enriched gene ontology (GO) terms in shoot/root-IPU and shoot/root+IPU libraries of rice. GO terms including three ontologies: biological process, cellular component and molecular function with corrected *P*-value < 0.01, indicate significantly enriched in differentially expressed genes (DEGs).

GO_term	Cluster frequency	Genome frequency of use	Corrected <i>P</i> -value
	Shoot+IPU vs Shoot-IPU		
Biological process	DEGs(1016)	Genes(20886)	
oxidation-reduction process	11.52%(117,66↑,51↓)	7.83%(1636)	8.88E-06
carbohydrate metabolic process	4.82%(49,37↑,12↓)	2.88%(602)	1.67E-04
transmembrane transport	4.53%(46,21↑,25↓)	3.16%(660)	5.92E-03
signal transduction	1.77%(18,10↑,?8↓)	0.88%(184)	1.64E-03
response to stress	1.38%(14,13↑,1↓)	0.44%(92)	3.55E-05
cellulose biosynthetic process	0.79%(8,4↑,4↓)	0.29%(60)	2.33E-03
amino acid transmembrane transport	0.69%(7,3↑,4↓)	0.16%(34)	1.79E-04
thiamine biosynthetic process	0.49%(5,0↑,5↓)	0.04%(8)	3.36E-07
cellular glucan metabolic process	0.39%(4,3↑,1↓)	0.13%(27)	8.91E-03
protein refolding	0.39%(4,2↑,2↓)	0.07%(15)	5.38E-04
1,3-beta-D-glucan biosynthetic process	0.30%(3,1↑,2↓)	0.08%(16)	6.33E-03
response to wounding	0.30%(3,3↑,0↓)	0.05%(10)	9.23E-04
glutamate biosynthetic process	0.20%(2,1↑,1↓)	0.02%(4)	4.42E-04
glutamine metabolic process	0.20%(2,1↑,1↓)	0.04%(9)	7.73E-03
mannose metabolic process	0.20%(2,0↑,2↓)	0.03%(7)	3.47E-03
methionine biosynthetic process	0.20%(2,0↑,2↓)	0.04%(8)	5.35E-03
response to water	0.20%(2,2↑,0↓)	0.03%(7)	3.47E-03
sphingolipid metabolic process	0.20%(2,0↑,2↓)	0.04%(9)	7.73E-03
acyl-CoA metabolic process	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
asparagine biosynthetic process	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
bacteriochlorophyll biosynthetic process	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
cellular homeostasis	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
ceramide metabolic process	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
fatty-acyl-CoA biosynthetic process	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
glyoxylate cycle	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
heme oxidation	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
inositol catabolic process	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
lysyl-tRNA aminoacylation	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
nitrate assimilation	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
pathogenesis	0.10%(1,0↑,1↓)	0.00%(1)	0.00E+00
proline catabolic process	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
pyrimidine base catabolic process	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
RNA splicing	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
tRNA wobble uridine modification	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
tyrosine metabolic process	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03

vesicle docking	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
Cellular component	DEGs(1016)	Genes(20886)	
membrane	8.46%(86,35↑,51↓)	6.66%(1390)	9.06E-03
1,3-beta-D-glucan synthase complex	0.30%(3,1↑,2↓)	0.08%(16)	6.33E-03
COPI vesicle coat	0.30%(3,1↑,2↓)	0.07%(15)	4.94E-03
protein phosphatase type 2A complex	0.30%(3,2↑,1↓)	0.09%(18)	9.86E-03
microtubule associated complex	0.20%(2,2↑,0↓)	0.04%(8)	5.35E-03
phosphopyruvate hydratase complex	0.20%(2,0↑,2↓)	0.04%(8)	5.35E-03
Golgi apparatus	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
Golgi apparatus part	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
molybdopterin synthase complex	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
transcription factor TFIIE complex	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
Molecular function	DEGs(1016)	Genes(20886)	
catalytic activity	11.42%(116,80↑,36↓)	8.12%(1696)	6.83E-05
oxidoreductase activity	5.91%(60,39↑,21↓)	4.20%(878)	3.28E-03
hydrolase activity, hydrolyzing O-glycosyl compounds	3.25%(33,25↑,8↓)	1.72%(360)	1.79E-04
cation binding	3.05%(31,24↑,7↓)	1.38%(289)	1.31E-05
metal ion binding	2.95%(30,14↑,16↓)	1.54%(321)	2.30E-04
flavin adenine dinucleotide binding	1.48%(15,11↑,4↓)	0.79%(166)	7.13E-03
magnesium ion binding	1.38%(14,7↑,7↓)	0.70%(146)	5.06E-03
nutrient reservoir activity	0.79%(8,8↑,0↓)	0.35%(73)	8.74E-03
amino acid transmembrane transporter activity	0.69%(7,3↑,4↓)	0.16%(34)	1.79E-04
cellulose synthase (UDP-forming) activity	0.69%(7,3↑,4↓)	0.27%(56)	5.44E-03
ligase activity	0.59%(6,5↑,1↓)	0.17%(36)	1.53E-03
serine-type endopeptidase inhibitor activity	0.59%(6,5↑,1↓)	0.22%(46)	6.42E-03
lipoxygenase activity	0.49%(5,1↑,4↓)	0.09%(18)	1.46E-04
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0.49%(5,1↑,4↓)	0.11%(24)	8.25E-04
thiamine pyrophosphate binding	0.49%(5,4↑,1↓)	0.08%(17)	1.02E-04
transaminase activity	0.49%(5,4↑,1↓)	0.15%(32)	3.99E-03
xyloglucan:xyloglucosyl transferase activity	0.39%(4,3↑,1↓)	0.13%(27)	8.91E-03
1,3-beta-D-glucan synthase activity	0.30%(3,1↑,2↓)	0.08%(16)	6.33E-03
acyl-CoA dehydrogenase activity	0.30%(3,3↑,0↓)	0.05%(11)	1.40E-03
antioxidant activity	0.30%(3,3↑,0↓)	0.08%(16)	6.33E-03
oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor	0.30%(3,3↑,0↓)	0.07%(15)	4.94E-03

oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor	0.30%(3,2↑,1↓)	0.02%(5)	2.68E-05
oxoglutarate dehydrogenase (succinyl-transferring) activity	0.30%(3,2↑,1↓)	0.03%(6)	7.72E-05
potassium ion binding	0.30%(3,2↑,1↓)	0.09%(18)	9.86E-03
protein phosphatase type 2A regulator activity	0.30%(3,2↑,1↓)	0.09%(18)	9.86E-03
pyruvate kinase activity	0.30%(3,2↑,1↓)	0.09%(18)	9.86E-03
transcription cofactor activity	0.30%(3,2↑,1↓)	0.07%(15)	4.94E-03
3-deoxy-7-phosphoheptulonate synthase activity	0.20%(2,1↑,1↓)	0.03%(6)	2.05E-03
biotin carboxylase activity	0.20%(2,2↑,0↓)	0.01%(3)	1.15E-04
CTP synthase activity	0.20%(2,2↑,0↓)	0.04%(9)	7.73E-03
diphosphate-fructose-6-phosphate 1-phosphotransferase activity	0.20%(2,1↑,1↓)	0.03%(6)	2.05E-03
folic acid binding	0.20%(2,0↑,2↓)	0.02%(4)	4.42E-04
glucose-6-phosphate dehydrogenase activity	0.20%(2,0↑,2↓)	0.04%(9)	7.73E-03
glucosylceramidase activity	0.20%(2,0↑,2↓)	0.03%(7)	3.47E-03
mannosidase activity	0.20%(2,0↑,2↓)	0.03%(7)	3.47E-03
phosphopyruvate hydratase activity	0.20%(2,0↑,2↓)	0.04%(8)	5.35E-03
phosphotransferase activity, for other substituted phosphate groups	0.20%(2,0↑,2↓)	0.04%(9)	7.73E-03
shikimate kinase activity	0.20%(2,2↑,0↓)	0.04%(8)	5.35E-03
4-hydroxyphenylpyruvate dioxygenase activity	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
acyl-CoA thioesterase activity	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
adenosylhomocysteinase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
aldehyde-lyase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
anthranilate synthase activity	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
asparagine synthase (glutamine-hydrolyzing) activity	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
carotene 7,8-desaturase activity	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
dihydrolipoyllysine-residue (2-methylpropanoyl)transferase activity	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
formate-tetrahydrofolate ligase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
gamma-glutamyltransferase activity	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
glutamate-1-semialdehyde 2,1-aminomutase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
glycerol kinase activity	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
glycerone kinase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03

heme oxygenase (decyclizing) activity	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
homogentisate 1,2-dioxygenase activity	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
inositol oxygenase activity	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
ion channel inhibitor activity	0.10%(1,0↑,1↓)	0.00%(1)	0.00E+00
isocitrate lyase activity	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
isopentenyl-diphosphate delta-isomerase activity	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
L-lactate dehydrogenase activity	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
lysine-tRNA ligase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
malate dehydrogenase (NADP+) activity	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
malate synthase activity	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
oxidoreductase activity, acting on other nitrogenous compounds as donors, with NAD or NADP as acceptor	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
peroxiredoxin activity	0.10%(1,1↑,0↓)	0.01%(3)	6.86E-03
phosphoribosyl-AMP cyclohydrolase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
phosphoribosyl-ATP diphosphatase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
phosphoribosylformylglycinamide synthase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
proline dehydrogenase activity	0.10%(1,1↑,0↓)	0.00%(1)	0.00E+00
protein methyltransferase activity	0.10%(1,0↑,1↓)	0.01%(3)	6.86E-03
protochlorophyllide reductase activity	0.10%(1,0↑,1↓)	0.00%(1)	0.00E+00
pyruvate, phosphate dikinase activity	0.10%(1,1↑,0↓)	0.01%(2)	2.36E-03
S-methyl-5-thioribose kinase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03
sulfurtransferase activity	0.10%(1,0↑,1↓)	0.01%(2)	2.36E-03

Root+IPU vs Root-IPU

Biological process	DEGs(867)	Genes(20886)	Corrected <i>P</i> -value
oxidation-reduction process	10.61%(92,46↑,46↓)	7.83%(1636)	1.17E-03
metabolic process	8.42%(73,47↑,26↓)	6.33%(1323)	5.43E-03
carbohydrate metabolic process	4.73%(41,20↑,21↓)	2.88%(602)	7.55E-04
lipid transport	1.38%(12,2↑,10↓)	0.52%(108)	5.36E-04
cellulose biosynthetic process	1.27%(11,3↑,8↓)	0.29%(60)	5.40E-06
oligopeptide transport	1.27%(11,7↑,4↓)	0.48%(101)	9.73E-04
glycolysis	1.04%(9,2↑,7↓)	0.37%(77)	1.27E-03
phosphorylation	0.69%(6,4↑,2↓)	0.15%(32)	2.81E-04
amine metabolic process	0.58%(5,1↑,4↓)	0.10%(21)	1.60E-04
transcription initiation from RNA polymerase II promoter	0.46%(4,2↑,2↓)	0.09%(19)	8.71E-04
phosphatidylcholine metabolic process	0.35%(3,3↑,0↓)	0.05%(11)	7.70E-04

tetrapyrrole biosynthetic process	0.35%(3,3↑,0↓)	0.04%(9)	3.14E-04
thiamine biosynthetic process	0.35%(3,0↑,3↓)	0.04%(8)	1.81E-04
cellular biosynthetic process	0.23%(2,1↑,1↓)	0.04%(9)	4.96E-03
gluconeogenesis	0.23%(2,2↑,0↓)	0.04%(8)	3.41E-03
glutamine metabolic process	0.23%(2,2↑,0↓)	0.04%(9)	4.96E-03
glycolipid transport	0.23%(2,1↑,1↓)	0.04%(8)	3.41E-03
hexose metabolic process	0.23%(2,1↑,1↓)	0.03%(6)	1.30E-03
mature ribosome assembly	0.23%(2,1↑,1↓)	0.01%(3)	7.13E-05
nitrate assimilation	0.23%(2,0↑,2↓)	0.01%(3)	7.13E-05
nuclear mRNA splicing, via spliceosome	0.23%(2,1↑,1↓)	0.05%(10)	6.87E-03
chromosome organization	0.12%(1,1↑,0↓)	0.02%(4)	9.77E-03
deoxyribonucleoside diphosphate metabolic process	0.12%(1,0↑,1↓)	0.01%(2)	1.72E-03
fatty-acyl-CoA biosynthetic process	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
glyoxylate cycle	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
heme oxidation	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
inositol catabolic process	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
molybdopterin cofactor biosynthetic process	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
negative regulation of apoptosis	0.12%(1,0↑,1↓)	0.01%(2)	1.72E-03
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
pantothenate biosynthetic process	0.12%(1,1↑,0↓)	0.02%(4)	9.77E-03
pathogenesis	0.12%(1,0↑,1↓)	0.00%(1)	0.00E+00
prolyl-tRNA aminoacylation	0.12%(1,0↑,1↓)	0.02%(4)	9.77E-03
pyrimidine base catabolic process	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
transcription termination, DNA-dependent	0.12%(1,1↑,0↓)	0.01%(3)	5.02E-03
tyrosine metabolic process	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
Cellular component	DEGs(867)	Genes(20886)	
membrane	9.69%(84,39↑,45↓)	6.66%(1390)	2.07E-04
clathrin adaptor complex	0.35%(3,1↑,2↓)	0.10%(20)	8.39E-03
intrinsic to endoplasmic reticulum membrane	0.35%(3,1↑,2↓)	0.09%(19)	6.94E-03
outer membrane	0.23%(2,2↑,0↓)	0.05%(10)	6.87E-03
transcription factor TFIIE complex	0.23%(2,1↑,1↓)	0.01%(3)	7.13E-05
eukaryotic translation initiation factor 3 complex	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
Golgi apparatus	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
Golgi apparatus part	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
signal recognition particle receptor complex	0.12%(1,0↑,1↓)	0.01%(2)	1.72E-03
Molecular function	DEGs(867)	Genes(20886)	
catalytic activity	12.69%(110,67↑,43↓)	8.12%(1696)	9.44E-07

cation binding	2.31%(20,10↑,10↓)	1.38%(289)	9.52E-03
pyridoxal phosphate binding	1.85%(16,13↑,3↓)	0.76%(159)	3.39E-04
flavin adenine dinucleotide binding	1.73%(15,9↑,6↓)	0.79%(166)	1.53E-03
copper ion binding	1.61%(14,3↑,11↓)	0.69%(145)	1.04E-03
cellulose synthase (UDP-forming) activity	1.27%(11,3↑,8↓)	0.27%(56)	2.51E-06
kinase activity	0.81%(7,6↑,1↓)	0.20%(41)	2.41E-04
potassium ion binding	0.81%(7,2↑,5↓)	0.09%(18)	2.58E-07
pyruvate kinase activity	0.81%(7,2↑,5↓)	0.09%(18)	2.58E-07
transaminase activity	0.81%(7,6↑,1↓)	0.15%(32)	3.69E-05
lipid binding	0.69%(6,1↑,5↓)	0.15%(31)	2.27E-04
cofactor binding	0.58%(5,4↑,1↓)	0.18%(37)	3.89E-03
primary amine oxidase activity	0.58%(5,1↑,4↓)	0.06%(13)	6.72E-06
quinone binding	0.58%(5,1↑,4↓)	0.13%(28)	8.65E-04
oxidoreductase activity, acting on the CH-CH group of donors	0.46%(4,3↑,1↓)	0.13%(27)	4.59E-03
acyl-CoA dehydrogenase activity	0.35%(3,3↑,0↓)	0.05%(11)	7.70E-04
molybdenum ion binding	0.35%(3,0↑,3↓)	0.06%(12)	1.12E-03
oxidoreductase activity, acting on NADH or NADPH	0.35%(3,1↑,2↓)	0.07%(14)	2.11E-03
phospholipase D activity	0.35%(3,3↑,0↓)	0.05%(11)	7.70E-04
protein-disulfide reductase activity	0.35%(3,1↑,2↓)	0.05%(10)	5.07E-04
sucrose synthase activity	0.35%(3,2↑,1↓)	0.06%(13)	1.56E-03
alpha-amylase activity	0.23%(2,1↑,1↓)	0.05%(10)	6.87E-03
dolichyl-diphosphooligosaccharide-protein glycotransferase activity	0.23%(2,1↑,1↓)	0.03%(7)	2.20E-03
glycolipid binding	0.23%(2,1↑,1↓)	0.04%(8)	3.41E-03
glycolipid transporter activity	0.23%(2,1↑,1↓)	0.04%(8)	3.41E-03
guanyl nucleotide binding	0.23%(2,0↑,2↓)	0.05%(10)	6.87E-03
hydrogen-translocating pyrophosphatase activity	0.23%(2,2↑,0↓)	0.04%(9)	4.96E-03
oxidoreductase activity, acting on other nitrogenous compounds as donors, with NAD or NADP as acceptor	0.23%(2,0↑,2↓)	0.01%(3)	7.13E-05
peptide-methionine-(S)-S-oxide reductase activity	0.23%(2,1↑,1↓)	0.02%(5)	6.69E-04
phosphoenolpyruvate carboxykinase activity	0.23%(2,2↑,0↓)	0.02%(4)	2.76E-04
phosphoenolpyruvate carboxykinase (ATP) activity	0.23%(2,2↑,0↓)	0.02%(4)	2.76E-04
phosphoribulokinase activity	0.23%(2,2↑,0↓)	0.02%(4)	2.76E-04
purine nucleotide binding	0.23%(2,2↑,0↓)	0.02%(4)	2.76E-04
ribosome binding	0.23%(2,1↑,1↓)	0.04%(8)	3.41E-03
transcription coactivator activity	0.23%(2,0↑,2↓)	0.02%(4)	2.76E-04

3-dehydroquinate dehydratase activity	0.12%(1,0↑,1↓)	0.02%(4)	9.77E-03
4-hydroxyphenylpyruvate dioxygenase activity	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
5'-3' exoribonuclease activity	0.12%(1,1↑,0↓)	0.01%(3)	5.02E-03
adenosylhomocysteinase activity	0.12%(1,0↑,1↓)	0.01%(2)	1.72E-03
aldehyde-lyase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
aminomethyltransferase activity	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
anthranilate synthase activity	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
biotin carboxylase activity	0.12%(1,1↑,0↓)	0.01%(3)	5.02E-03
CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
dihydrolipoyllysine-residue (2-methylpropanoyl)transferase activity	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
dihydroxy-acid dehydratase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
ferredoxin-NAD(P) reductase activity	0.12%(1,0↑,1↓)	0.02%(4)	9.77E-03
folic acid binding	0.12%(1,1↑,0↓)	0.02%(4)	9.77E-03
glutamate-1-semialdehyde 2,1-aminomutase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
glutamyl-tRNA reductase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
heme oxygenase (decyclizing) activity	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
homogentisate 1,2-dioxygenase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides	0.12%(1,1↑,0↓)	0.02%(4)	9.77E-03
hydroxymethylglutaryl-CoA lyase activity	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
inositol oxygenase activity	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
ion channel inhibitor activity	0.12%(1,0↑,1↓)	0.00%(1)	0.00E+00
malate synthase activity	0.12%(1,1↑,0↓)	0.00%(1)	0.00E+00
mevalonate kinase activity	0.12%(1,1↑,0↓)	0.01%(3)	5.02E-03
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	0.12%(1,1↑,0↓)	0.01%(3)	5.02E-03
oxo-acid-lyase activity	0.12%(1,0↑,1↓)	0.02%(4)	9.77E-03
pantoate-beta-alanine ligase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
peroxiredoxin activity	0.12%(1,1↑,0↓)	0.01%(3)	5.02E-03
phosphoglycerate dehydrogenase activity	0.12%(1,1↑,0↓)	0.02%(4)	9.77E-03
phosphomethylpyrimidine kinase activity	0.12%(1,0↑,1↓)	0.00%(1)	0.00E+00
porphobilinogen synthase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
proline-tRNA ligase activity	0.12%(1,0↑,1↓)	0.02%(4)	9.77E-03
pyruvate, phosphate dikinase activity	0.12%(1,1↑,0↓)	0.01%(2)	1.72E-03
ribonucleoside-diphosphate reductase activity	0.12%(1,0↑,1↓)	0.02%(4)	9.77E-03
ribulose-phosphate 3-epimerase activity	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03

selenium binding	0.12%(1,1↑,0↓)	0.02%(4)	9.77E-03
shikimate 3-dehydrogenase (NADP+) activity	0.12%(1,0↑,1↓)	0.01%(3)	5.02E-03
signal recognition particle binding	0.12%(1,0↑,1↓)	0.01%(2)	1.72E-03
thiamine-phosphate diphosphorylase activity	0.12%(1,0↑,1↓)	0.00%(1)	0.00E+00

ESI Table S9.

Significant pathway enrichment analysis in KEGG in each pair of rice libraries. Pathways with *P*-value < 0.05 indicate significantly enriched in differentially expressed genes (DEGs).

Pathway	DEGs(107)	Genes(2048)	<i>P</i> -value	Pathway_ID
Shoot+IPU vs Shoot-IPU				
Protein processing in endoplasmic reticulum	16(14.95%,10↑,6↓)	182(8.89%)	0.011266	osa04141
Circadian rhythm - plant	6(5.61%,0↑,6↓)	25(1.22%)	0.000192	osa04712
Phosphatidylinositol sigling system	3(2.80%,3↑,0↓)	23(1.12%)	0.028911	osa04070
Alanine, aspartate and glutamate metabolism	2(1.87%,2↑,0↓)	5(0.24%)	0.001285	osa00250
Caffeine metabolism	2(1.87%,1↑,1↓)	2(0.10%)	0	osa00232
Cutin, suberine and wax biosynthesis	2(1.87%,2↑,0↓)	13(0.63%)	0.027028	osa00073
Fatty acid elongation	2(1.87%,2↑,0↓)	10(0.49%)	0.012715	osa00062
Fructose and mannose metabolism	2(1.87%,1↑,1↓)	6(0.29%)	0.002472	osa00051
Galactose metabolism	2(1.87%,2↑,0↓)	8(0.39%)	0.006407	osa00052
Inositol phosphate metabolism	2(1.87%,2↑,0↓)	16(0.78%)	0.047242	osa00562
Thiamine metabolism	2(1.87%,0↑,2↓)	4(0.20%)	0.000534	osa00730
Butanoate metabolism	1(0.93%,1↑,0↓)	3(0.15%)	0.007839	osa00650
Cysteine and methionine metabolism	1(0.93%,1↑,0↓)	7(0.34%)	0.047808	osa00270
Other glycan degradation	1(0.93%,0↑,1↓)	6(0.29%)	0.035338	osa00511
Sulfur metabolism	1(0.93%,1↑,0↓)	6(0.29%)	0.035338	osa00920
Ubiquinone and other terpenoid-quinone biosynthesis	1(0.93%,1↑,0↓)	5(0.24%)	0.024382	osa00130
Pathway	DEGs(142)	Genes(2048)	<i>P</i> _value	Pathway_ID
Root+IPU vs Root-IPU				
Ubiquitin mediated proteolysis	7(4.93%,5↑,2↓)	54(2.64%)	0.029886	osa04120
Diterpenoid biosynthesis	4(2.82%,1↑,3↓)	17(0.83%)	0.004679	osa00904
Biosynthesis of amino acids	3(2.11%,2↑,1↓)	18(0.88%)	0.031586	osa01230
Cysteine and methionine metabolism	3(2.11%,2↑,1↓)	7(0.34%)	0.000658	osa00270
Fructose and mannose metabolism	3(2.11%,1↑,2↓)	6(0.29%)	0.000298	osa00051
Photosynthesis - anten proteins	3(2.11%,1↑,2↓)	14(0.68%)	0.012829	osa00196
Sphingolipid metabolism	3(2.11%,2↑,1↓)	13(0.63%)	0.009676	osa00600
Alanine, aspartate and glutamate metabolism	2(1.41%,2↑,0↓)	5(0.24%)	0.002944	osa00250
Galactose metabolism	2(1.41%,2↑,0↓)	8(0.39%)	0.014113	osa00052
Sulfur metabolism	2(1.41%,2↑,0↓)	6(0.29%)	0.005589	osa00920
2-Oxocarboxylic acid metabolism	1(0.70%,0↑,1↓)	4(0.20%)	0.026108	osa01210
Arachidonic acid metabolism	1(0.70%,1↑,0↓)	4(0.20%)	0.026108	osa00590
Biosynthesis of unsaturated fatty acids	1(0.70%,0↑,1↓)	4(0.20%)	0.026108	osa01040
Butanoate metabolism	1(0.70%,1↑,0↓)	3(0.15%)	0.013674	osa00650
Caffeine metabolism	1(0.70%,1↑,0↓)	2(0.10%)	0.004776	osa00232
Degradation of aromatic compounds	1(0.70%,0↑,1↓)	1(0.05%)	0	osa01220
Fatty acid biosynthesis	1(0.70%,0↑,1↓)	5(0.24%)	0.041551	osa00061
Flavonoid biosynthesis	1(0.70%,0↑,1↓)	3(0.15%)	0.013674	osa00941
Glycosphingolipid biosynthesis - globo series	1(0.70%,1↑,0↓)	2(0.10%)	0.004776	osa00603

One carbon pool by folate	1(0.70%,0↑,1↓)	2(0.10%)	0.004776	osa00670
Taurine and hypotaurine metabolism	1(0.70%,1↑,0↓)	4(0.20%)	0.026108	osa00430
Thiamine metabolism	1(0.70%,0↑,1↓)	4(0.20%)	0.026108	osa00730
Valine, leucine and isoleucine biosynthesis	1(0.70%,0↑,1↓)	4(0.20%)	0.026108	osa00290

ESI Table S10. The expression of IPU-associated genes encoding detoxification enzymes family, antioxidase family, transporters family and transcription factors family. Detoxification enzymes family include P450 family, oxidoreductase family, monooxygenase family, glucosyltransferase (GTs) family, glutathione S-transferase (GST) family, methyltransferase family, hydrolase family, acyltransferase family and S/TPK family. Antioxidase family include laccase family, monodehydroascorbate reductase family, superoxide dismutase (SOD) family, peroxidase (POD) family, ascorbate peroxidase (APX) family and catalase (CAT) family. Transporters family include MATE family, ABC transporters family, amino acid family, (oligo) peptide family, sugar family, monosaccharide transporters family and multidrug resistance protein (MRP) family. Red boxes indicate $\text{Log}_2(\text{IPU}/\text{CK}) \geq 1$, and blue boxes indicate $\text{Log}_2(\text{IPU}/\text{CK}) \leq -1$. Inf and -Inf indicate positive infinity and negative infinity, respectively. \uparrow , the number of up-regulated genes; \downarrow , the number of down-regulated genes. Red regions indicate the up-regulation. Blue regions indicate the down-regulation.

Gene both in shoot and root			Gene only in shoot		Gene only in root	
Gene ID	$\text{Log}_2(\text{IPU}/\text{CK})$		Gene ID	$\text{Log}_2(\text{IPU}/\text{CK})$	Gene ID	$\text{Log}_2(\text{IPU}/\text{CK})$
	Shoot	Root		Shoot		Root
Metabolic enzymes						
Cytochrome P450	17 \uparrow , 12 \downarrow	16 \uparrow , 11 \downarrow		7 \uparrow , 14 \downarrow		9 \uparrow , 17 \downarrow
Os02t0571900-01	Inf	-Inf	Os08t0243500-02	Inf	Os01t0627900-01	-Inf
Os01t0728300-01	0.057	4.000	Os08t0507100-00	4.230	Os02t0570700-01	-Inf
Os11t0525200-02	-1.740	2.963	Os02t0186200-00	2.780	Os07t0418500-02	-Inf
Os10t0166600-01	0.032	2.322	Os02t0185400-01	2.600	Os08t0105400-00	-Inf
Os08t0152400-00	0.647	2.023	Os01t0602500-01	1.680	Os01t0377250-00	Inf
Os11t0143200-01	1.030	2.000	Os10t0144700-00	1.120	Os03t0603100-00	Inf
Os08t0547300-01	1.920	1.841	Os05t0515200-01	1.110	Os01t0628000-01	2.193
Os01t0543600-01	-0.215	1.784	Os06t0680700-01	0.989	Os05t0181200-01	1.826
Os03t0760300-01	-0.002	1.766	Os02t0173100-01	0.955	Os07t0418500-01	1.392
Os02t0173100-02	0.012	1.700	Os10t0514400-01	0.785	Os01t0627800-01	1.379
Os08t0507702-01	1.350	1.218	Os01t0627933-00	0.692	Os11t0483000-00	1.111
Os03t0248200-01	-0.166	1.138	Os01t0227700-01	0.656	Os01t0388101-00	1.100
Os07t0217600-01	-0.023	1.138	Os05t0211100-01	0.267	Os03t0417700-01	1.098
Os03t0594900-01	0.065	1.119	Os06t0642500-02	-0.021	Os02t0569400-01	0.743
Os06t0642500-01	-0.450	1.115	Os08t0105800-01	-0.224	Os05t0382500-01	0.568
Os01t0197100-00	-0.272	1.062	Os10t0378100-01	-0.250	Os10t0514901-00	0.509
Os07t0518100-01	-0.853	1.034	Os03t0140100-02	-0.385	Os02t0221900-02	0.415
Os03t0760200-01	1.210	0.888	Os07t0681300-00	-0.396	Os12t0443000-00	0.415
Os09t0528700-00	-3.950	0.871	Os01t0349800-01	-0.467	Os03t0594100-01	0.396
Os05t0405600-01	0.703	0.813	Os02t0570500-01	-0.475	Os09t0403300-00	0.348
Os04t0480700-01	1.410	0.807	Os11t0289700-01	-0.521	Os07t0635200-00	0.320
Os01t0627500-01	-0.043	0.804	Os11t0465200-02	-0.654	Os06t0565100-00	0.255
Os01t0544200-01	-0.904	0.663	Os06t0267400-00	-0.694	Os10t0171500-02	0.220
Os02t0185200-01	-0.092	0.650	Os10t0525000-02	-0.759	Os10t0167250-00	0.186
Os12t0139300-01	0.470	0.640	Os02t0323600-01	-0.893	Os06t0641200-00	0.175
Os10t0524700-00	0.846	0.615	Os02t0278400-01	-0.917	Os07t0520300-01	0.147
Os08t0508000-01	2.320	0.600	Os08t0262500-01	-0.953	Os09t0447500-01	0.125

Os10t0317900-01	-0.327	0.597	Os04t0407900-01	-1.080	Os06t0641500-00	0.000
Os08t0243500-01	-0.103	0.554	Os06t0640100-00	-1.080	Os10t0165300-01	0.000
Os03t0370900-01	0.601	0.531	Os10t0164500-00	-1.110	Os06t0500700-01	-0.005
Os09t0530300-01	0.249	0.503	Os10t0196000-01	-1.320	Os05t0482400-01	-0.060
Os01t0804400-01	-0.424	0.493	Os02t0278400-02	-1.370	Os04t0570000-00	-0.067
Os07t0635300-01	-0.130	0.493	Os02t0504000-01	-1.560	Os10t0167200-00	-0.110
Os10t0515200-01	0.565	0.476	Os09t0264400-01	-1.600	Os06t0191800-01	-0.131
Os09t0558900-01	0.104	0.437	Os03t0140100-01	-1.860	Os02t0666500-01	-0.234
Os01t0627400-01	-1.130	0.425	Os03t0248300-01	-2.000	Os06t0146700-01	-0.263
Os10t0139700-01	1.020	0.355	Os11t0635500-01	-2.020	Os01t0854800-01	-0.266
Os12t0582700-01	Inf	0.323	Os03t0658800-01	-2.260	Os03t0760000-01	-0.363
Os06t0639800-01	-0.681	0.322	Os03t0658800-03	-2.440	Os05t0415800-01	-0.370
Os10t0513900-01	0.370	0.302	Os08t0152300-00	-2.470	Os07t0647200-00	-0.377
Os06t0570100-01	-0.411	0.300	Os04t0171800-01	-2.880	Os01t0803900-01	-0.390
Os05t0424300-01	-0.574	0.294			Os12t0512800-01	-0.515
Os08t0465700-01	-0.096	0.230			Os06t0600400-01	-0.569
Os01t0700900-01	-0.460	0.209			Os12t0134900-01	-0.585
Os04t0653400-01	-0.343	0.208			Os02t0529800-00	-0.608
Os01t0211200-00	0.274	0.199			Os10t0439924-01	-0.637
Os10t0320100-01	-0.790	0.193			Os10t0403000-00	-0.737
Os12t0119000-01	-0.467	0.193			Os12t0118900-01	-0.737
Os03t0850200-00	-0.121	0.193			Os06t0613600-01	-0.745
Os02t0185300-01	0.824	0.193			Os01t0377000-01	-0.756
Os06t0129900-02	Inf	0.188			Os04t0178400-01	-1.000
Os06t0328900-01	0.483	0.145			Os09t0530275-00	-1.059
Os01t0628700-01	1.090	0.145			Os01t0627600-01	-1.101
Os07t0635500-01	1.230	0.132			Os06t0349700-00	-1.248
Os07t0635700-00	-0.820	0.126			Os05t0372300-01	-1.263
Os06t0102100-01	-0.332	0.126			Os02t0569000-01	-1.515
Os07t0644600-01	0.378	0.102			Os02t0184700-00	-1.663
Os02t0108800-01	-2.630	0.102			Os12t0582000-00	-1.700
Os06t0599200-01	2.280	0.049			Os01t0561600-01	-1.729
Os09t0441400-01	0.374	0.043			Os10t0515900-01	-1.907
Os06t0129900-01	-1.280	0.031			Os04t0180400-01	-2.115
Os06t0204100-00	0.613	0.024			Os06t0642600-00	-3.000
Os01t0804900-01	1.550	0.004			Os02t0569400-02	-3.544
Os02t0817900-01	-0.394	0.000				
Os06t0294600-02	0.333	-0.015				
Os05t0494000-01	0.500	-0.024				
Os06t0641800-00	-0.789	-0.038				
Os01t0951500-01	0.230	-0.039				
Os03t0760500-01	-1.410	-0.042				
Os01t0388000-01	-0.987	-0.061				
Os02t0184900-01	0.207	-0.067				
Os01t0211600-01	0.387	-0.109				

Os10t0512400-01	-1.730	-0.135				
Os02t0204700-00	-0.587	-0.151				
Os03t0367101-00	0.592	-0.151				
Os08t0472800-01	0.449	-0.175				
Os01t0183600-01	0.614	-0.184				
Os03t0370900-02	-0.863	-0.222				
Os06t0501900-01	-0.746	-0.226				
Os02t0221900-01	-0.085	-0.259				
Os02t0173100-03	-3.270	-0.263				
Os01t0858350-01	-0.511	-0.265				
Os05t0200400-01	0.718	-0.268				
Os01t0227400-01	-0.752	-0.280				
Os03t0140200-01	-0.536	-0.287				
Os05t0320700-02	0.025	-0.331				
Os09t0457100-01	0.838	-0.348				
Os12t0150200-01	2.290	-0.363				
Os02t0186900-01	-0.399	-0.387				
Os04t0469800-01	-0.338	-0.389				
Os03t0650200-00	0.540	-0.399				
Os11t0525200-01	0.183	-0.406				
Os03t0227700-01	-0.696	-0.412				
Os05t0405500-01	0.208	-0.443				
Os04t0101400-01	-0.891	-0.577				
Os03t0223100-02	-1.580	-0.585				
Os12t0582666-00	-0.103	-0.585				
Os09t0447300-01	0.282	-0.608				
Os01t0227500-01	-0.789	-0.637				
Os05t0445100-01	0.625	-0.645				
Os05t0101600-01	-0.279	-0.678				
Os01t0602400-01	0.707	-0.678				
Os03t0367200-01	0.858	-0.705				
Os02t0503900-01	0.713	-0.774				
Os10t0486100-00	0.104	-0.829				
Os04t0560100-01	0.296	-0.848				
Os11t0151400-01	1.500	-0.921				
Os03t0332100-00	-0.676	-1.000				
Os03t0134500-00	-0.071	-1.093				
Os12t0268000-01	0.682	-1.117				
Os07t0518500-02	-1.680	-1.131				
Os03t0602300-01	-0.239	-1.280				
Os02t0186800-00	-4.630	-1.451				
Os06t0640800-00	-0.422	-1.503				
Os10t0525000-01	0.343	-2.000				
Os11t0489250-00	-1.660	-3.198				
Os02t0569900-01	2.220	-3.954				

Oxidoreductase	6 ↑, 3 ↓	5 ↑, 8 ↓		1 ↑, 5 ↓		0 ↑, 4 ↓
Os07t0675000-03	Inf	3.858	Os10t0558700-01	2.830	Os07t0664150-00	-Inf
Os03t0774200-02	2.400	0.160	Os03t0784000-03	0.985	Os10t0558400-00	0.126
Os03t0713400-03	2.000	Inf	Os08t0379400-03	0.659	Os01t0316100-00	0.000
Os07t0663800-01	1.300	0.473	Os10t0558750-01	0.604	Os11t0255500-01	-0.153
Os10t0516300-01	1.090	0.962	Os11t0287100-00	0.370	Os09t0514100-02	-0.170
Os10t0536400-01	1.050	0.215	Os08t0379400-02	0.245	Os12t0260500-01	-0.481
Os01t0120600-01	0.613	0.531	Os01t0777700-00	0.209	Os07t0663900-00	-0.931
Os01t0830100-01	0.590	0.510	Os08t0379400-01	0.091	Os07t0592100-01	-1.000
Os03t0122300-02	0.511	-0.900	Os05t0538900-01	-0.009	Os09t0445600-01	-1.037
Os09t0567366-02	0.501	Inf	Os04t0668800-01	-0.186	Os07t0663700-01	-1.766
Os03t0690500-00	0.479	0.376	Os10t0475100-00	-0.230		
Os08t0485400-01	0.386	-0.263	Os02t0320800-01	-0.322		
Os03t0101600-01	0.378	0.366	Os02t0280700-01	-0.333		
Os02t0150300-01	0.317	0.091	Os01t0126200-01	-0.488		
Os03t0713400-01	0.294	-0.112	Os05t0411200-01	-0.835		
Os01t0720300-00	0.286	-0.134	Os09t0567366-03	-0.839		
Os05t0533700-01	0.263	0.412	Os01t0274100-00	-0.910		
Os01t0809900-01	0.240	0.329	Os10t0113900-01	-1.050		
Os09t0524500-01	0.218	-0.111	Os04t0473025-00	-1.220		
Os09t0567366-01	0.156	0.090	Os04t0678700-01	-1.840		
Os09t0514100-01	0.147	0.000	Os10t0559200-01	-2.250		
Os10t0576000-01	0.136	-0.340	Os10t0558700-03	-2.540		
Os07t0585800-01	0.123	0.057				
Os05t0313500-01	0.081	0.391				
Os06t0214900-01	0.076	0.234				
Os01t0723400-01	0.071	0.559				
Os08t0391700-00	0.070	-1.184				
Os03t0313000-01	0.012	-0.089				
Os03t0129900-01	0.009	-0.509				
Os09t0503100-01	0.005	-0.382				
Os02t0235900-01	0.003	-0.042				
Os10t0474100-00	-0.015	0.325				
Os07t0564500-01	-0.045	-1.229				
Os10t0403700-00	-0.047	-0.051				
Os10t0474900-00	-0.066	0.474				
Os04t0372700-01	-0.096	-1.000				
Os01t0227100-02	-0.105	Inf				
Os07t0645400-02	-0.120	-7.943				
Os01t0173000-01	-0.132	-0.170				
Os01t0328700-01	-0.140	0.020				
Os05t0552500-02	-0.151	0.464				
Os09t0500200-01	-0.153	-0.355				
Os10t0561100-01	-0.154	-1.170				
Os11t0645200-01	-0.188	-0.402				

Os05t0401500-01	-0.222	0.056				
Os08t0431500-01	-0.270	-0.244				
Os07t0155100-01	-0.303	-0.585				
Os10t0579300-01	-0.305	-0.404				
Os01t0727400-01	-0.308	0.459				
Os10t0558900-01	-0.346	-1.415				
Os02t0621800-01	-0.357	-0.185				
Os12t0534000-01	-0.361	-0.074				
Os03t0774200-01	-0.401	-0.129				
Os03t0713400-02	-0.496	-1.366				
Os06t0286310-01	-0.509	-0.464				
Os08t0151800-01	-0.597	-0.331				
Os01t0558800-01	-0.612	0.848				
Os03t0341300-01	-0.636	-0.637				
Os07t0664000-00	-0.668	-0.048				
Os04t0227500-01	-0.712	-0.453				
Os01t0273800-01	-0.725	-0.280				
Os08t0390200-01	-0.742	-1.807				
Os06t0181400-01	-0.888	-0.874				
Os01t0901700-01	-0.893	1.663				
Os05t0363600-01	-0.893	-0.287				
Os01t0370000-01	-1.120	0.498				
Os01t0190000-01	-1.230	-0.462				
Os06t0178700-01	-2.220	0.263				
Monoxygenase	2 ↑ , 6 ↓	3 ↑ , 5 ↓		1 ↑ , 1 ↓		5 ↑ , 6 ↓
Os04t0128900-01	1.280	0.018	Os01t0645400-01	3.690	Os09t0441600-00	
Os06t0203200-01	1.200	0.848	Os07t0291750-00	0.785	Os01t0627600-01	-1.101
Os02t0471300-01	0.817	0.415	Os11t0287100-00	0.370	Os03t0231700-02	-1.178
Os09t0549300-00	0.723	-0.585	Os09t0441700-00	0.129	Os01t0700500-01	-1.322
Os06t0698785-01	0.653	1.023	Os02t0561500-00	-0.331	Os07t0112000-00	-1.485
Os03t0231800-03	0.119	0.318	Os12t0512000-01	-0.708	Os02t0569400-02	-3.544
Os03t0231800-02	0.084	0.026	Os01t0274100-00	-0.910	Os09t0441625-00	Inf
Os10t0553800-01	0.020	0.524	Os07t0111900-00	-1.050	Os01t0728300-01	4.000
Os07t0437000-01	-0.293	-0.032			Os01t0627800-01	1.379
Os01t0680900-01	-0.363	-0.205			Os01t0388101-00	1.100
Os04t0223500-01	-0.455	-2.550			Os03t0182000-00	1.000
Os08t0547900-01	-0.636	-1.606			Os10t0317900-01	0.597
Os10t0317900-02	-0.652	-1.208			Os01t0627400-01	0.425
Os02t0503100-00	-0.800	-0.684			Os02t0221900-02	0.415
Os03t0231700-01	-0.805	-0.240			Os02t0580600-01	0.379
Os01t0645400-02	-0.853	1.322			Os01t0700900-01	0.209
Os01t0901700-01	-0.893	1.663			Os10t0320100-01	0.193
Os04t0223901-00	-0.999	-1.766			Os03t0162000-01	0.160
Os06t0528700-01	-1.090	-0.485			Os01t0224700-01	0.000
Os06t0649700-00	-1.440	0.119			Os01t0388000-01	-0.061

Os04t0423100-00	-2.110	-1.152			Os01t0732700-01	-0.372
Os10t0554300-00	-2.700	-0.415			Os12t0512800-01	-0.515
Os09t0548400-01	-3.020	-0.310			Os01t0602400-01	-0.678
Os07t0111700-01	-4.970	0.153				
GTs	22 ↑ , 23 ↓	11 ↑ , 13 ↓		4 ↑ , 6 ↓		2 ↑ , 8 ↓
Os10t0180000-02	-Inf	-Inf	Os04t0271700-01	3.430	Os05t0301500-03	-Inf
Os05t0499800-01	-Inf	-1.551	Os04t0271700-02	1.250	Os08t0446550-00	2.087
Os10t0437000-03	Inf	-4.170	Os01t0805500-00	1.090	Os04t0319800-01	1.141
Os04t0693000-02	5.230	Inf	Os04t0272200-01	1.010	Os04t0206600-01	0.807
Os09t0518200-01	2.180	0.429	Os10t0331600-00	0.881	Os03t0702000-01	0.652
Os04t0206700-01	2.070	0.556	Os01t0734600-01	0.608	Os02t0242900-00	0.531
Os02t0206400-00	2.010	-0.710	Os04t0197500-00	0.540	Os04t0130433-00	0.290
Os05t0526900-01	1.950	0.611	Os05t0177500-01	0.498	Os06t0283100-00	0.238
Os07t0503300-02	1.950	0.035	Os07t0490100-02	0.370	Os07t0486700-00	0.197
Os01t0176200-01	1.950	-0.585	Os01t0686200-01	0.343	Os03t0824600-00	0.170
Os03t0757000-01	1.940	0.326	Os04t0272700-04	0.339	Os07t0672700-00	0.070
Os10t0555100-01	1.830	-0.289	Os01t0919400-00	0.334	Os05t0527100-00	0.009
Os02t0203300-00	1.820	0.645	Os11t0444000-01	0.026	Os07t0202000-00	0.000
Os03t0841600-01	1.780	0.507	Os04t0565400-01	-0.077	Os09t0480400-01	0.000
Os02t0755900-01	1.410	0.056	Os09t0119600-01	-0.155	Os03t0804900-00	-0.050
Os01t0805400-01	1.390	0.579	Os07t0503500-01	-0.432	Os05t0527000-01	-0.058
Os07t0503300-01	1.370	0.831	Os07t0503500-02	-0.524	Os01t0686300-01	-0.142
Os01t0734800-02	1.370	-0.222	Os01t0516700-01	-0.713	Os01t0620800-01	-0.303
Os01t0119000-02	1.330	-4.728	Os02t0207400-00	-0.785	Os03t0643800-00	-0.415
Os07t0657400-01	1.310	0.624	Os07t0489200-01	-0.928	Os06t0282400-00	-0.447
Os01t0176200-02	1.200	0.459	Os01t0735300-01	-1.080	Os03t0702500-01	-0.485
Os11t0599200-01	1.120	0.405	Os07t0490100-01	-1.110	Os01t0597800-01	-0.544
Os10t0178500-01	1.030	1.170	Os11t0457000-00	-1.190	Os01t0175850-00	-0.667
Os02t0330200-01	1.020	0.046	Os05t0527800-01	-1.250	Os02t0242100-01	-0.712
Os07t0241800-01	0.977	0.366	Os05t0527900-01	-1.310	Os04t0529700-01	-0.759
Os09t0518400-00	0.955	-Inf	Os01t0880200-02	-2.760	Os06t0706850-00	-0.788
Os04t0556500-01	0.913	-0.238			Os06t0212300-00	-0.878
Os03t0567600-02	0.784	0.649			Os04t0565200-01	-0.893
Os03t0757100-00	0.765	-0.485			Os05t0493600-00	-0.893
Os09t0518000-00	0.727	-0.415			Os07t0241600-00	-1.000
Os06t0593200-01	0.705	-0.474			Os04t0319700-00	-1.222
Os02t0755600-01	0.689	0.690			Os01t0736300-01	-1.322
Os01t0906000-01	0.669	-0.943			Os08t0168700-00	-2.115
Os03t0300000-02	0.663	-0.040			Os06t0590700-01	-3.170
Os02t0688500-01	0.661	-0.395			Os10t0162980-01	-3.459
Os03t0757500-01	0.659	-0.120			Os03t0702000-03	-4.807
Os02t0135500-02	0.640	0.099				
Os01t0956200-01	0.617	0.224				
Os01t0867600-01	0.610	0.476				
Os04t0525200-01	0.573	-0.222				

Os04t0320700-02	0.543	-0.356				
Os07t0201800-00	0.540	-1.819				
Os04t0320700-01	0.511	0.272				
Os04t0324100-01	0.491	0.213				
Os03t0757600-01	0.477	0.613				
Os05t0391600-01	0.417	0.117				
Os07t0510400-02	0.404	-0.059				
Os02t0188000-01	0.373	0.181				
Os11t0145200-01	0.358	0.796				
Os04t0556400-01	0.307	-1.280				
Os03t0401300-01	0.302	0.043				
Os06t0593800-01	0.273	0.845				
Os06t0289200-01	0.257	0.208				
Os01t0179600-01	0.256	0.366				
Os11t0202500-00	0.244	-0.392				
Os07t0510400-01	0.242	-0.554				
Os05t0499600-01	0.235	-0.140				
Os03t0567600-01	0.201	0.181				
Os07t0489300-01	0.155	1.433				
Os09t0531900-01	0.152	-0.078				
Os02t0490500-01	0.136	0.036				
Os10t0437000-01	0.129	0.031				
Os11t0441500-01	0.115	0.337				
Os01t0638000-01	0.107	0.193				
Os05t0526800-01	0.071	0.355				
Os06t0343600-01	0.071	0.206				
Os02t0210800-01	0.048	0.515				
Os06t0282000-01	0.016	-0.457				
Os07t0419500-01	0.009	0.404				
Os04t0131900-01	0.005	0.241				
Os01t0172000-01	-0.001	-0.017				
Os01t0498300-01	-0.029	0.322				
Os09t0517900-01	-0.047	-0.220				
Os02t0755500-01	-0.090	1.138				
Os02t0664200-01	-0.126	0.152				
Os04t0525100-01	-0.136	0.251				
Os07t0100300-02	-0.146	0.290				
Os07t0201500-00	-0.166	0.531				
Os08t0327100-01	-0.173	0.382				
Os02t0327700-01	-0.193	0.182				
Os04t0506000-01	-0.210	-0.387				
Os06t0220500-01	-0.215	0.939				
Os05t0215300-01	-0.270	-0.255				
Os11t0461200-01	-0.276	0.252				
Os02t0206700-01	-0.284	-0.042				

Os06t0288300-01	-0.287	-0.138				
Os07t0240600-01	-0.289	0.534				
Os07t0241500-01	-0.308	0.547				
Os05t0500200-01	-0.317	0.022				
Os07t0510500-01	-0.334	0.047				
Os02t0329800-01	-0.351	-0.247				
Os06t0707200-01	-0.371	0.113				
Os06t0712500-01	-0.372	-0.481				
Os02t0206100-01	-0.389	2.070				
Os04t0206700-02	-0.421	-0.306				
Os04t0196600-01	-0.447	-0.239				
Os06t0470000-01	-0.451	0.058				
Os11t0128000-01	-0.484	0.138				
Os10t0492200-01	-0.496	-0.132				
Os01t0119000-01	-0.531	1.085				
Os04t0451200-01	-0.532	0.231				
Os01t0697100-01	-0.560	0.158				
Os06t0707000-00	-0.569	-0.354				
Os06t0289900-01	-0.576	0.322				
Os07t0241700-00	-0.630	-1.193				
Os01t0119100-00	-0.648	-0.183				
Os01t0926700-00	-0.688	-0.532				
Os02t0589400-01	-0.701	-0.044				
Os07t0502900-00	-0.723	0.107				
Os02t0206100-02	-0.754	1.492				
Os02t0243300-01	-0.764	-0.126				
Os07t0660500-00	-0.800	1.487				
Os03t0684500-01	-0.800	1.115				
Os07t0201300-00	-0.823	0.749				
Os02t0331200-01	-0.840	-0.161				
Os03t0757200-01	-0.882	0.154				
Os10t0122000-00	-0.942	0.181				
Os06t0192100-00	-1.050	-2.170				
Os04t0271700-03	-1.110	1.000				
Os01t0176000-01	-1.140	0.291				
Os05t0552700-01	-1.160	2.000				
Os06t0475400-01	-1.210	0.140				
Os07t0148200-01	-1.250	-0.204				
Os07t0503900-01	-1.290	-0.244				
Os04t0503700-01	-1.380	-0.848				
Os01t0734800-01	-1.490	0.353				
Os01t0865400-01	-1.580	-0.324				
Os05t0499800-02	-1.640	-0.993				
Os02t0490500-02	-1.720	-0.368				
Os04t0272700-02	-1.750	0.049				

Os11t0457300-01	-2.020	-4.248				
Os01t0638600-00	-2.380	-1.371				
Os02t0331200-02	-2.730	-0.301				
Os03t0567600-03	-3.390	-0.135				
Os09t0482900-01	-3.420	-1.363				
Os02t0135500-01	-4.060	-Inf				
Os01t0735900-01	-4.920	0.468				
Os05t0500000-00	-6.900	0.037				
Methyltransferase	8 ↑ , 28 ↓	11 ↑ , 17 ↓		2 ↑ , 6 ↓		2 ↑ , 2 ↓
Os10t0578600-01	Inf	-Inf	Os02t0725200-02	-Inf	Os08t0498600-01	2.700
Os11t0557700-02	-3.630	1.363	Os05t0102000-01	2.030	Os04t0104900-01	1.222
Os04t0570800-01	5.580	0.058	Os09t0344500-01	1.070	Os09t0445100-00	0.737
Os11t0557700-01	1.820	-0.823	Os02t0804300-02	0.692	Os07t0640000-01	0.387
Os06t0152400-01	1.690	1.170	Os10t0181600-01	0.664	Os11t0305400-00	0.199
Os07t0206700-02	1.450	2.000	Os06t0242900-01	0.592	Os04t0176200-00	0.034
Os04t0645500-01	1.080	-0.244	Os01t0712600-00	0.370	Os11t0259700-01	0.000
Os09t0307800-02	1.020	2.503	Os05t0324200-01	0.370	Os01t0225500-00	-0.170
Os11t0256900-01	1.020	1.402	Os03t0685100-01	0.318	Os02t0120300-01	-0.290
Os01t0828300-01	0.998	-0.138	Os05t0324100-01	0.080	Os10t0104900-01	-0.290
Os09t0474400-00	0.884	-0.931	Os07t0464200-00	0.055	Os08t0113400-01	-0.807
Os03t0824200-01	0.822	0.342	Os09t0411650-01	-0.058	Os06t0474300-01	-1.000
Os01t0846600-01	0.755	-1.059	Os03t0729700-01	-0.145	Os10t0422200-02	-1.222
Os06t0646000-02	0.729	1.379	Os03t0775000-00	-0.307		
Os04t0481400-01	0.717	0.723	Os07t0179300-00	-0.367		
Os05t0564100-01	0.661	0.415	Os02t0137600-01	-0.415		
Os06t0153900-01	0.661	0.415	Os01t0193600-01	-0.800		
Os05t0497600-01	0.660	0.148	Os12t0441600-00	-0.852		
Os04t0319600-01	0.567	0.534	Os05t0515500-01	-0.853		
Os01t0716500-01	0.537	-0.245	Os05t0497675-01	-0.903		
Os01t0535900-01	0.535	0.095	Os10t0357800-01	-0.916		
Os08t0517600-02	0.529	0.881	Os06t0314600-01	-1.050		
Os04t0481300-01	0.479	-0.322	Os07t0463600-00	-1.220		
Os04t0175600-01	0.473	-0.128	Os01t0920300-02	-1.530		
Os12t0612500-01	0.465	-0.241	Os07t0462800-00	-1.920		
Os02t0593900-01	0.438	-0.327	Os10t0118000-01	-2.720		
Os10t0392500-00	0.419	1.354				
Os12t0203100-01	0.396	-0.415				
Os02t0612100-01	0.370	0.314				
Os07t0667400-01	0.370	-0.130				
Os06t0244000-01	0.341	0.604				
Os07t0414200-01	0.321	0.415				
Os03t0738400-03	0.274	-0.092				
Os05t0224900-01	0.246	0.290				
Os02t0672600-01	0.242	0.114				
Os06t0646000-01	0.219	0.363				

Os03t0110800-01	0.213	0.419				
Os01t0883900-01	0.198	0.387				
Os08t0557000-01	0.153	0.138				
Os06t0101100-01	0.138	-0.585				
Os01t0874900-01	0.131	-0.095				
Os12t0607000-02	0.083	-0.242				
Os05t0224800-01	0.048	1.147				
Os03t0738400-01	0.015	0.447				
Os02t0761900-02	0.012	0.107				
Os06t0128100-01	-0.009	-0.394				
Os02t0675700-01	-0.010	-0.352				
Os03t0379100-01	-0.035	-0.101				
Os02t0761900-01	-0.049	0.162				
Os08t0154000-01	-0.054	0.485				
Os07t0656800-01	-0.061	0.105				
Os08t0498400-02	-0.064	-2.256				
Os06t0152300-01	-0.068	-0.231				
Os07t0206700-01	-0.082	-0.017				
Os06t0138600-01	-0.090	-0.248				
Os02t0121200-01	-0.092	0.274				
Os06t0140100-01	-0.107	0.052				
Os11t0260100-00	-0.116	0.181				
Os02t0744100-01	-0.125	-0.160				
Os08t0506500-00	-0.129	0.222				
Os02t0755000-01	-0.131	-0.285				
Os04t0602900-02	-0.137	-2.032				
Os01t0772150-00	-0.145	-0.237				
Os07t0692401-00	-0.159	0.285				
Os06t0236900-01	-0.161	-0.067				
Os07t0247100-01	-0.172	0.447				
Os05t0105000-01	-0.211	-0.123				
Os04t0606900-01	-0.215	0.848				
Os04t0677066-00	-0.215	0.059				
Os02t0701600-01	-0.218	0.146				
Os02t0823400-01	-0.234	0.186				
Os07t0671700-01	-0.241	0.489				
Os10t0489100-01	-0.242	0.507				
Os03t0775200-01	-0.259	-0.031				
Os08t0498400-01	-0.263	-0.525				
Os12t0607000-01	-0.291	-1.392				
Os10t0510400-02	-0.295	-0.853				
Os12t0409000-01	-0.301	0.020				
Os04t0623800-01	-0.329	0.012				
Os05t0429000-01	-0.367	0.573				
Os01t0883900-02	-0.367	-0.692				

Os11t0455800-02	-0.369	-1.000				
Os02t0290400-01	-0.375	0.146				
Os03t0243800-00	-0.408	0.363				
Os01t0920300-01	-0.415	-0.193				
Os04t0507800-01	-0.419	1.254				
Os06t0105500-01	-0.427	0.100				
Os02t0804300-01	-0.478	0.118				
Os06t0132400-01	-0.483	-1.700				
Os08t0119500-01	-0.510	-1.263				
Os09t0518900-01	-0.513	-0.794				
Os08t0411200-01	-0.517	0.807				
Os02t0725600-01	-0.523	-0.528				
Os01t0722800-00	-0.537	0.256				
Os02t0750500-01	-0.574	-0.700				
Os11t0455800-01	-0.575	-0.163				
Os07t0297300-00	-0.589	-0.273				
Os03t0780900-01	-0.590	-0.188				
Os03t0147700-01	-0.592	2.379				
Os06t0103900-01	-0.630	-0.337				
Os10t0569300-01	-0.652	0.429				
Os08t0157500-01	-0.664	-0.237				
Os09t0415700-01	-0.667	-0.807				
Os10t0510400-01	-0.685	-0.096				
Os05t0567400-01	-0.708	-0.046				
Os08t0157500-02	-0.717	-2.734				
Os06t0153900-02	-0.730	3.059				
Os03t0786700-01	-0.800	0.030				
Os12t0613200-02	-0.806	0.485				
Os08t0498100-01	-0.823	-0.485				
Os03t0822300-01	-0.893	-0.617				
Os02t0556400-01	-0.903	-0.704				
Os09t0481400-01	-0.930	-0.075				
Os03t0174600-02	-Inf	-1.222				
Os05t0378800-02	-1.010	-0.093				
Os03t0136200-01	-1.010	-0.323				
Os01t0701700-01	-1.090	-1.823				
Os03t0221200-01	-1.100	-0.571				
Os06t0165800-01	-1.100	-1.027				
Os01t0742000-01	-1.190	-1.170				
Os07t0569500-01	-1.220	0.294				
Os06t0162600-01	-1.230	-0.044				
Os05t0141400-01	-1.270	0.534				
Os03t0833200-01	-1.370	-0.807				
Os01t0631200-01	-1.390	-0.406				
Os02t0139200-01	-1.410	-0.300				

Os07t0164000-01	-1.480	-0.585				
Os05t0515600-01	-1.630	-1.280				
Os06t0142800-01	-1.730	-1.093				
Os04t0379300-01	-1.760	0.796				
Os09t0359900-01	-1.800	-0.222				
Os01t0695100-01	-1.840	-0.078				
Os04t0570800-02	-2.010	0.180				
Os10t0578600-02	-2.220	-2.459				
Os09t0359800-01	-2.410	-0.471				
Os10t0522000-01	-2.420	-0.313				
Os05t0548900-01	-2.890	-1.072				
Os03t0355800-02	-3.060	-0.700				
Os03t0566600-01	-3.090	0.392				
Os06t0329900-01	-3.810	0.190				
GST	2 ↑, 4 ↓	0 ↑, 2 ↓		1 ↑, 2 ↓		0 ↑, 1 ↓
Os10t0525800-00	-Inf	-1.222	Os10t0528300-01	1.140	Os06t0227500-00	0.848
Os10t0529400-01	1.510	-0.460	Os10t0529800-00	0.660	Os01t0692100-01	0.784
Os03t0135100-01	1.090	0.147	Os11t0588300-02	0.408	Os02t0564000-01	0.481
Os01t0369700-01	0.543	-0.822	Os11t0588300-01	-0.249	Os08t0550500-01	0.363
Os01t0764000-01	0.494	0.030	Os04t0270100-03	-0.367	Os06t0168000-01	0.315
Os01t0369700-03	0.460	0.182	Os10t0527800-01	-0.515	Os01t0949800-01	0.254
Os07t0468100-01	0.297	0.000	Os10t0528900-01	-0.844	Os10t0530600-01	0.222
Os03t0134900-01	0.080	0.108	Os10t0529300-01	-1.050	Os11t0245100-01	0.218
Os03t0135300-01	0.077	-0.267	Os10t0525400-03	-2.250	Os02t0814800-01	0.206
Os10t0531400-01	0.047	0.799			Os10t0527601-00	0.206
Os05t0412800-01	0.007	-0.457			Os03t0595600-00	0.115
Os01t0949750-00	-0.059	-0.011			Os10t0530200-01	-0.030
Os12t0210200-01	-0.061	-0.234			Os01t0949700-01	-0.032
Os10t0543800-00	-0.116	-0.065			Os04t0435500-01	-0.239
Os03t0135200-01	-0.133	-0.152			Os10t0528400-01	-0.255
Os10t0528100-01	-0.151	-0.286			Os10t0481300-01	-0.503
Os12t0210300-01	-0.272	0.318			Os02t0319300-01	-0.529
Os10t0368100-01	-0.273	0.807			Os01t0558100-01	-0.807
Os10t0525400-01	-0.351	0.000			Os01t0950000-01	-0.883
Os01t0764000-03	-0.369	-0.189			Os10t0528200-01	-1.531
Os07t0468100-02	-0.469	-0.415				
Os09t0467200-01	-0.566	-0.301				
Os01t0692000-01	-0.952	0.737				
Os10t0530900-01	-1.160	-0.957				
Os12t0123200-01	-1.770	-1.000				
Os07t0168300-01	-2.290	-0.727				
Hydrolase	3 ↑, 2 ↓	1 ↑, 3 ↓		16 ↑, 11 ↓		6 ↑, 9 ↓
Os03t0805400-03	Inf	-7.098	Os01t0215700-01	-3.500	Os01t0595600-01	0.988
Os05t0429500-01	-2.590	-3.954	Os01t0276500-02	-1.900	Os01t0636400-01	-1.934
Os06t0214800-01	-1.670	-0.994	Os02t0655600-01	2.230	Os01t0934700-01	-2.585

Os08t0473900-01	6.620	3.807	Os02t0816100-02	-2.060	Os03t0437600-02	7.017
Os11t0700900-01	Inf	-2.524	Os03t0258200-01	2.230	Os03t0669300-03	Inf
			Os03t0722500-02	-3.250	Os03t0826600-02	-4.816
			Os04t0513900-01	1.680	Os03t0829200-01	1.611
			Os05t0406100-01	-1.760	Os04t0412300-02	-4.129
			Os05t0429500-02	-2.480	Os05t0571100-02	-Inf
			Os05t0517500-02	-4.750	Os06t0694200-01	-4.129
			Os05t0542200-01	2.540	Os07t0162600-02	0.991
			Os05t0542200-02	2.180	Os08t0110000-01	-2.423
			Os06t0179000-01	-1.630	Os08t0475100-01	-1.581
			Os06t0184300-03	2.490	Os10t0160100-01	-2.313
			Os06t0306600-01	1.780	Os10t0160100-02	2.059
			Os07t0539100-02	3.120	Os10t0476700-03	-3.544
			Os07t0565700-02	Inf	Os10t0493600-01	1.361
			Os07t0608300-02	3.930	Os11t0384789-02	7.017
			Os08t0445700-01	1.430		
			Os08t0473800-01	Inf		
			Os09t0511600-03	2.160		
			Os11t0132600-01	-Inf		
			Os11t0239500-01	2.350		
			Os11t0439600-01	-1.600		
			Os11t0702200-01	Inf		
			Os11t0704600-03	-4.090		
			Os12t0566700-02	7.980		
Acyltransferase	0 ↑ , 1 ↓	0 ↑ , 1 ↓		1 ↑ , 4 ↓		
Os03t0232800-02	-2.230	-Inf	Os02t0114400-00	1.550		
			Os02t0590200-01	-1.520		
			Os02t0590400-03	-4.480		
			Os03t0832800-01	-Inf		
			Os03t0832800-03	-Inf		
S/TPK	21 ↑ , 24 ↓	22 ↑ , 7 ↓		1 ↑ , 9 ↓		0 ↑ , 3 ↓
Os01t0138400-01	0.562	0.792	Os10t0561500-01	-0.537	Os04t0634000-01	0.949
Os01t0170300-01	-0.837	-0.243	Os10t0548700-01	-2.690	Os11t0133500-00	0.881
Os01t0223900-01	-0.045	-0.450	Os10t0531700-00	-0.910	Os11t0664000-01	0.459
Os01t0224000-00	2.100	0.830	Os09t0482640-01	-0.548	Os12t0614600-01	0.279
Os01t0259200-01	0.040	2.082	Os07t0494800-01	-0.800	Os07t0686800-01	0.247
Os01t0267800-00	0.107	1.032	Os04t0649700-01	0.884	Os10t0342300-01	0.000
Os01t0292200-01	-0.777	0.432	Os03t0841100-01	0.054	Os12t0125300-01	0.000
Os01t0514700-01	1.140	-0.495	Os03t0828800-01	-0.133	Os11t0225000-01	-0.126
Os01t0587400-01	-1.910	0.040	Os03t0424200-01	-0.268	Os12t0608500-01	-0.181
Os01t0602800-01	-0.513	-0.209	Os03t0268200-01	-1.700	Os08t0376600-01	-0.309
Os01t0607900-01	-0.142	-0.417	Os02t0218400-01	-1.370	Os06t0575400-01	-0.459
Os01t0621600-01	-0.534	-0.155	Os02t0111600-01	-1.020	Os11t0691650-00	-0.778
Os01t0670100-01	-0.215	-0.607	Os01t0927500-01	-3.630	Os08t0117700-01	-1.000
Os01t0699100-01	0.488	-0.826	Os01t0824600-01	0.477	Os01t0784200-00	-1.087

Os01t0699400-01	1.390	-0.173	Os01t0784700-00	-1.540	Os12t0102500-02	-4.524
Os01t0699500-01	0.355	-0.453	Os01t0783800-01	-1.090		
Os01t0699600-01	0.215	-0.578	Os01t0581400-01	-1.130		
Os01t0748600-02	0.626	1.092	Os01t0206700-03	1.000		
Os01t0889900-01	-0.231	0.000	Os01t0206700-01	-1.400		
Os01t0927500-02	-0.215	-0.893				
Os01t0929200-01	-0.282	-0.617				
Os02t0120100-01	2.880	1.881				
Os02t0153700-01	0.007	-0.206				
Os02t0161000-01	0.169	0.138				
Os02t0174200-01	0.608	0.098				
Os02t0190500-01	-0.853	0.000				
Os02t0193600-01	0.855	-0.392				
Os02t0655800-01	0.307	0.303				
Os02t0655800-02	-1.810	-1.426				
Os02t0681700-01	-0.618	0.154				
Os02t0767400-01	0.884	-0.129				
Os02t0819600-01	0.760	0.154				
Os02t0819600-02	-Inf	-0.121				
Os03t0113000-01	-0.159	-0.583				
Os03t0113000-02	-1.490	-0.325				
Os03t0114300-01	0.464	1.372				
Os03t0122000-01	0.723	-0.107				
Os03t0127700-02	-0.367	-0.346				
Os03t0130900-01	-0.546	0.693				
Os03t0130900-02	-0.258	-0.541				
Os03t0221700-02	-0.857	-0.219				
Os03t0225100-02	0.197	-0.194				
Os03t0227900-00	0.794	-0.381				
Os03t0241600-01	-0.838	0.429				
Os03t0241600-02	-Inf	-1.044				
Os03t0281466-01	-0.167	0.246				
Os03t0289100-01	0.537	0.391				
Os03t0295600-01	-2.370	1.585				
Os03t0295600-02	0.440	-0.512				
Os03t0319400-01	-0.200	-1.379				
Os03t0339900-01	-3.410	1.125				
Os03t0407900-01	-0.532	0.537				
Os03t0556600-01	-1.370	-0.214				
Os03t0634400-01	-2.600	-0.320				
Os03t0711300-01	0.723	-0.710				
Os03t0764300-01	0.020	0.220				
Os03t0825300-02	0.107	2.263				
Os03t0825300-03	-0.215	-0.801				
Os03t0838100-01	0.428	-0.109				

Os03t0838100-02	-0.370	-0.504				
Os03t0838100-04	-1.190	1.562				
Os03t0839900-01	-0.060	0.744				
Os03t0839900-02	-0.730	-0.464				
Os04t0103500-01	0.626	1.000				
Os04t0103700-01	0.955	1.000				
Os04t0368000-01	-1.950	-0.285				
Os04t0463000-01	0.767	-0.036				
Os04t0472500-00	-0.505	-0.497				
Os04t0487200-01	0.277	0.056				
Os04t0540900-01	-0.664	-0.658				
Os04t0584100-01	1.950	-0.166				
Os04t0599000-02	-0.013	-0.126				
Os04t0616600-01	-2.220	-3.907				
Os04t0649700-02	-1.740	-0.415				
Os05t0127300-01	0.531	-0.427				
Os05t0136200-01	1.030	1.322				
Os05t0136200-02	1.530	0.350				
Os05t0165900-01	-0.396	3.459				
Os05t0166300-01	0.463	0.000				
Os05t0169600-01	0.955	-0.492				
Os05t0440800-01	-0.232	0.632				
Os05t0466900-01	0.048	-0.497				
Os05t0480000-01	0.392	0.541				
Os05t0480400-01	0.037	0.428				
Os05t0498900-01	0.312	0.926				
Os05t0519200-02	0.401	0.446				
Os05t0530500-02	0.314	0.347				
Os05t0545300-01	2.620	-0.322				
Os05t0545400-01	0.961	0.000				
Os05t0550800-01	-0.215	-0.250				
Os05t0588300-01	-0.420	-0.042				
Os06t0181200-01	0.460	0.233				
Os06t0202900-01	-0.032	-0.155				
Os06t0486400-01	-0.266	0.399				
Os06t0494100-01	0.429	0.254				
Os06t0509100-01	0.547	0.848				
Os06t0557100-01	0.103	0.337				
Os06t0557100-02	0.842	-1.784				
Os06t0574200-01	0.511	0.403				
Os06t0602500-01	-0.515	1.459				
Os06t0667000-01	-0.161	-0.257				
Os06t0690200-01	0.200	0.251				
Os06t0714900-01	-0.734	-1.070				
Os06t0714900-02	2.510	1.057				

Os06t0717200-01	-0.291	0.113				
Os07t0134600-01	0.141	-0.016				
Os07t0150700-01	-0.045	-0.038				
Os07t0409900-01	-0.215	-0.585				
Os07t0471000-01	0.143	0.922				
Os07t0472400-01	-0.952	-0.678				
Os07t0534700-01	-2.220	0.765				
Os07t0537500-01	1.470	0.381				
Os07t0538200-01	2.380	0.271				
Os07t0538200-02	1.500	0.249				
Os07t0540100-01	0.045	0.358				
Os07t0553633-01	-1.130	1.222				
Os07t0678600-01	0.514	-0.105				
Os08t0138700-01	-2.130	-0.181				
Os08t0200500-01	-0.293	-1.000				
Os08t0224100-03	-1.070	Inf				
Os08t0249100-01	-1.630	-0.070				
Os08t0276400-01	-0.070	-0.148				
Os08t0453800-00	-Inf	0.107				
Os08t0484600-01	1.510	0.454				
Os08t0491200-01	0.337	-0.303				
Os08t0506400-01	-0.952	-0.500				
Os08t0564700-01	-0.816	-0.015				
Os09t0237600-01	-1.590	0.110				
Os09t0372800-01	1.170	0.878				
Os09t0372800-02	-3.320	0.049				
Os09t0400500-01	-0.157	-0.413				
Os09t0454900-01	1.170	0.437				
Os09t0544300-01	0.362	0.524				
Os09t0562600-01	-0.424	-0.585				
Os09t0566550-01	0.023	1.720				
Os09t0570000-01	-0.408	0.138				
Os10t0100500-01	-0.083	0.096				
Os10t0101000-01	-0.039	0.085				
Os10t0112700-01	-0.408	0.308				
Os10t0153900-01	0.785	3.585				
Os10t0180800-01	2.050	1.170				
Os10t0431900-01	-1.480	0.267				
Os10t0431900-02	4.180	-0.282				
Os10t0468500-01	1.430	-0.022				
Os10t0497600-01	0.218	0.401				
Os10t0497600-02	0.029	-0.152				
Os10t0516200-00	-1.670	-0.198				
Os10t0518800-01	0.205	0.315				
Os10t0580300-01	0.215	0.383				

Os11t0113700-01	3.330	1.136				
Os11t0113700-02	Inf	1.628				
Os11t0150700-00	0.665	-1.459				
Os11t0233800-01	-0.367	0.000				
Os12t0102500-01	0.007	1.300				
Os12t0113500-02	Inf	0.856				
Os12t0235700-00	-3.240	-0.037				
Os12t0424700-00	-0.355	0.280				
Os12t0527700-01	0.296	0.688				
Os12t0632900-01	-0.786	0.205				
Gene both in shoot and root			Gene only in shoot		Gene only in root	
Gene ID	Log ₂ (IPU/CK)		Gene ID	Log ₂ (IPU/CK)	Gene ID	Log ₂ (IPU/CK)
	Shoot	Root		Shoot		Root
Antioxidase						
Laccase	2 ↑, 2 ↓	1 ↑, 3 ↓		2 ↑, 1 ↓		0 ↑, 2 ↓
Os01t0850700-01	1.290	1.379	Os03t0273200-02	Inf	Os01t0850550-00	0.654
Os12t0257600-00	1.240	-1.000	Os05t0458500-00	1.590	Os12t0259800-00	0.203
Os01t0827300-01	0.370	-0.403	Os11t0641800-01	-1.340	Os01t0850800-00	-0.080
Os01t0842500-01	0.200	-0.732			Os01t0634500-00	-0.181
Os05t0458600-01	-0.361	-0.363			Os11t0108700-00	-0.585
Os03t0273200-01	-0.478	-3.524			Os03t0297900-00	-0.646
Os01t0842400-01	-1.730	-0.485			Os11t0696900-01	-1.000
Os11t0708100-01	-2.220	-1.064			Os12t0108000-01	-1.830
Monodehydroascorbate reductase	1 ↑, 0 ↓					
Os02t0707100-02	1.660	0.547				
Os02t0707100-01	-0.178	0.206				
Os08t0557600-01	0.534	0.004				
Os09t0567300-01	-0.253	-0.070				
Os02t0707000-00	0.370	-0.913				
SOD	1 ↑, 0 ↓					0 ↑, 0 ↓
Os01t0284500-01	1.870	-0.341			Os12t0613250-00	0.300
Os07t0665200-01	0.381	0.144				
Os04t0573200-01	0.376	-0.965				
Os03t0219200-01	0.360	0.195				
Os03t0351500-01	0.058	0.046				
Os06t0143000-01	-0.021	0.861				
Os08t0561700-01	-0.142	-0.152				
Os05t0323900-01	-0.191	-0.127				
Os06t0115400-01	-0.320	-0.181				
Os01t0249200-01	-0.760	-0.660				
Os04t0573200-03	-2.090	-0.075				
Peroxidase	15 ↑, 18 ↓	2 ↑, 9 ↓		3 ↑, 4 ↓		3 ↑, 8 ↓
Os04t0688300-01	4.580	2.039	Os03t0121200-03	Inf	Os06t0521900-00	-Inf
Os09t0538600-01	0.581	1.322	Os04t0688500-01	2.810	Os06t0547100-00	1.585

Os10t0109600-02	-Inf	-0.668	Os11t0210100-01	1.260	Os01t0901800-01	1.263
Os01t0270300-01	-Inf	-1.142	Os04t0498700-01	0.659	Os06t0695200-00	1.059
Os11t0112400-01	4.180	-1.100	Os07t0156200-00	0.543	Os01t0787000-02	0.907
Os01t0327100-02	3.810	-0.293	Os04t0498700-02	0.522	Os06t0490400-00	0.755
Os02t0240100-01	3.050	-0.327	Os11t0661600-01	0.370	Os02t0161800-01	0.652
Os06t0695400-01	2.540	-0.778	Os07t0677400-00	0.242	Os03t0368300-01	0.621
Os06t0695500-01	2.360	0.088	Os01t0326100-01	0.177	Os09t0323700-00	0.533
Os04t0688600-01	1.820	0.191	Os02t0240300-01	-0.191	Os04t0651000-01	0.450
Os06t0547400-01	1.810	-0.118	Os04t0602100-01	-0.315	Os07t0104500-01	0.438
Os05t0134400-01	1.780	-0.280	Os01t0378100-01	-0.505	Os05t0135400-01	0.235
Os05t0162000-01	1.760	0.567	Os12t0530100-01	-0.609	Os06t0546500-01	0.215
Os10t0109300-01	1.480	-0.744	Os04t0683850-00	-0.642	Os05t0134700-02	0.115
Os07t0677600-01	1.450	0.972	Os08t0522400-01	-1.400	Os01t0205900-01	0.043
Os10t0566800-01	1.220	0.248	Os07t0157600-00	-2.050	Os04t0688200-01	0.000
Os04t0688100-02	1.180	0.121	Os02t0553200-02	-2.520	Os09t0323900-00	0.000
Os07t0694300-01	1.000	0.225	Os03t0339300-02	-4.390	Os04t0423800-01	-0.194
Os09t0507500-01	0.852	-0.179			Os07t0499500-01	-0.237
Os04t0688100-01	0.797	0.297			Os01t0327000-01	-0.256
Os01t0963000-01	0.789	-0.692			Os04t0656800-01	-0.260
Os10t0109600-01	0.779	0.074			Os05t0134800-00	-0.272
Os03t0805400-01	0.777	0.626			Os03t0121300-01	-0.308
Os03t0121200-01	0.740	-0.124			Os03t0234500-01	-0.322
Os10t0109300-02	0.728	0.614			Os03t0369000-01	-0.335
Os08t0127500-01	0.541	-0.189			Os07t0677300-01	-0.349
Os03t0285700-01	0.494	-0.085			Os01t0294500-00	-0.349
Os01t0270300-02	0.419	-0.060			Os11t0112200-01	-0.354
Os01t0172600-01	0.394	0.301			Os05t0135000-01	-0.423
Os04t0465100-01	0.386	0.050			Os03t0563600-01	-0.508
Os02t0664000-01	0.300	0.060			Os05t0135200-01	-0.515
Os02t0833900-03	0.298	-0.054			Os07t0638600-00	-0.519
Os06t0185900-01	0.282	-0.285			Os10t0536600-00	-0.600
Os04t0556300-01	0.261	0.151			Os04t0689000-01	-0.642
Os08t0532700-01	0.244	-0.354			Os01t0263000-00	-0.692
Os02t0236800-02	0.237	0.239			Os06t0695300-01	-0.737
Os03t0288700-01	0.225	0.100			Os07t0639000-01	-0.749
Os01t0326300-01	0.220	0.229			Os07t0156467-00	-0.773
Os12t0178100-01	0.187	-0.027			Os07t0157000-00	-0.807
Os01t0327400-01	0.145	-0.716			Os05t0134700-01	-0.856
Os07t0104100-01	0.140	-0.697			Os03t0368000-00	-0.866
Os06t0521500-02	0.129	-0.216			Os07t0639400-01	-0.880
Os03t0358100-01	0.118	0.199			Os03t0369600-00	-0.931
Os02t0704500-01	0.112	0.194			Os03t0339400-01	-1.280
Os07t0677100-01	0.107	0.096			Os07t0531400-01	-1.322
Os01t0327100-01	0.105	-0.677			Os08t0302000-01	-1.449
Os07t0626700-01	0.080	-1.858			Os01t0205900-02	-2.385

Os05t0499400-01	0.066	-0.495			Os06t0681600-02	-2.459
Os01t0263300-01	0.058	-0.177			Os01t0326000-02	-5.615
Os06t0521500-01	0.048	0.101			Os04t0556300-02	-6.340
Os05t0134400-02	0.005	-0.218				
Os05t0548800-01	-0.005	0.072				
Os06t0625500-01	-0.034	-0.619				
Os01t0901800-02	-0.061	0.473				
Os01t0543100-01	-0.063	-0.475				
Os06t0306300-01	-0.098	-0.654				
Os04t0223300-00	-0.099	-0.142				
Os02t0236800-01	-0.101	-0.311				
Os06t0625500-03	-0.112	-0.215				
Os05t0499400-02	-0.119	-1.485				
Os08t0549100-01	-0.123	0.314				
Os07t0677200-01	-0.137	-0.573				
Os07t0115300-01	-0.144	0.180				
Os02t0553200-01	-0.196	-0.263				
Os06t0681600-01	-0.208	-0.587				
Os07t0694700-01	-0.258	-0.155				
Os03t0762400-01	-0.264	-0.142				
Os04t0486900-01	-0.272	0.044				
Os06t0274800-01	-0.282	-0.993				
Os01t0962700-01	-0.286	-0.097				
Os02t0236600-01	-0.306	0.101				
Os03t0121200-02	-0.408	-1.115				
Os12t0112000-01	-0.453	-1.787				
Os08t0532600-01	-0.505	0.459				
Os07t0677200-02	-0.505	-1.286				
Os01t0294700-01	-0.508	-0.450				
Os02t0192700-02	-0.549	-2.322				
Os03t0368900-01	-0.560	-0.100				
Os11t0284900-01	-0.584	-0.055				
Os05t0135500-01	-0.659	-0.663				
Os09t0471100-01	-0.685	0.771				
Os02t0661800-01	-0.694	0.524				
Os02t0833900-02	-0.886	-0.064				
Os05t0499300-01	-0.952	-0.417				
Os03t0235000-01	-0.984	-0.896				
Os01t0787000-01	-1.010	-0.527				
Os09t0308900-01	-1.050	0.507				
Os07t0676900-01	-1.060	-0.409				
Os12t0178200-01	-1.080	0.000				
Os03t0234900-01	-1.340	-0.040				
Os12t0191500-01	-1.350	-1.078				
Os01t0326000-01	-1.400	-0.248				

Os08t0113000-01	-1.500	-0.642				
Os06t0522300-01	-1.540	-0.597				
Os03t0762300-01	-1.620	-0.206				
Os04t0434800-02	-1.630	-0.361				
Os03t0805400-02	-1.950	0.000				
Os04t0434800-01	-2.030	0.555				
Os10t0536700-01	-2.440	-0.467				
Os01t0963000-04	-5.490	-0.363				
Os03t0762300-02	-6.230	0.140				
Ascorbate peroxidase	3 ↓	1 ↑		2 ↑, 0 ↓		
Os09t0538600-01	0.581	1.322	Os04t0602100-01	-0.315		
Os03t0285700-01	0.494	-0.085	Os08t0522400-01	-1.400		
Os04t0223300-00	-0.099	-0.142	Os02t0553200-02	-2.520		
Os08t0549100-01	-0.123	0.314				
Os02t0553200-01	-0.196	-0.263				
Os07t0694700-01	-0.258	-0.155				
Os12t0178200-01	-1.080	0.000				
Os04t0434800-02	-1.630	-0.361				
Os04t0434800-01	-2.030	0.555				
Catalase	0 ↑, 3 ↓	1 ↑, 2 ↓		0 ↑, 0 ↓		
Os06t0727200-02	0.352	0.558	Os03t0131200-01	-0.098		
Os06t0727200-01	0.316	0.448				
Os03t0131200-02	-0.009	1.807				
Os02t0115700-03	-1.460	-Inf				
Os02t0115700-01	-1.570	-0.650				
Os02t0115700-02	-7.300	-Inf				
Gene both in shoot and root			Gene only in shoot		Gene only in root	
Gene ID	Log ₂ (IPU/CK)		Gene ID	Log ₂ (IPU/CK)	Gene ID	Log ₂ (IPU/CK)
	Shoot	Root				
Transporter						
MATE	0 ↑, 0 ↓	3 ↑, 3 ↓		0 ↑, 1 ↓		0 ↑, 1 ↓
Os03t0858800-01	0.687	-0.116	Os09t0524300-00	0.604	Os10t0344900-01	0.737
Os10t0345100-01	0.641	1.060	Os11t0126100-01	-0.913	Os09t0468000-01	-0.303
Os07t0516600-01	0.474	-0.789	Os11t0129200-00	-2.460	Os06t0495500-01	-1.348
Os08t0480000-01	0.399	-0.472				
Os03t0216700-01	0.345	-1.080				
Os03t0839200-01	0.333	-0.065				
Os07t0502200-01	0.327	0.215				
Os02t0273800-02	0.263	0.137				
Os02t0273800-01	0.263	-0.316				
Os03t0572900-01	0.209	0.488				
Os01t0504500-02	0.169	-0.682				
Os03t0626700-01	0.145	-0.429				
Os06t0707100-01	0.078	-0.325				

Os10t0206800-01	0.037	0.593				
Os01t0684900-01	0.033	0.194				
Os03t0570800-01	-0.058	-1.860				
Os04t0571600-01	-0.360	0.537				
Os08t0550200-01	-0.369	-1.820				
Os10t0190900-01	-0.374	-0.527				
Os06t0494400-01	-0.401	0.329				
Os10t0195000-01	-0.657	2.110				
Os02t0676400-00	-0.800	3.540				
Os12t0126000-01	-0.807	-0.913				
Monosaccharide transporter	2 ↑, 0 ↓	1 ↑, 1 ↓				1 ↑, 1 ↓
Os07t0559700-00	2.460	0.806			Os06t0141100-00	3.700
Os07t0106200-03	1.270	-0.208			Os02t0574000-01	-0.986
Os02t0573500-01	0.536	0.464				
Os09t0268300-02	0.266	1.222				
Os04t0452700-01	-0.052	0.902				
Os03t0594400-01	-0.065	-0.056				
Os04t0453200-01	-0.087	0.427				
Os04t0454200-01	-0.117	-1.182				
Os07t0131600-01	-0.320	-0.075				
Os04t0453400-02	-1.400	-0.809				
ABC transporter	4 ↑, 6 ↓	8 ↑, 7 ↓		4 ↑, 5 ↓		2 ↑, 0 ↓
Os03t0441500-02	Inf	-Inf	Os01t0218700-02	Inf	Os05t0137200-03	Inf
Os11t0587600-01	-Inf	0.251	Os01t0786000-01	Inf	Os06t0126100-01	1.807
Os01t0770500-02	4.370	3.322	Os05t0222200-02	3.770	Os04t0528400-01	0.585
Os09t0472100-01	1.600	0.259	Os01t0902100-00	1.140	Os06t0589300-01	0.171
Os05t0384600-01	1.180	0.000	Os04t0209200-01	0.998	Os04t0588700-01	0.095
Os03t0281900-01	0.955	-1.049	Os10t0494300-01	0.855	Os01t0393400-00	0.000
Os03t0142800-01	0.807	0.556	Os03t0157400-02	0.785	Os08t0398300-01	-0.219
Os08t0564300-01	0.757	2.678	Os01t0977901-00	0.633	Os12t0239900-01	-0.263
Os06t0128300-01	0.738	-0.597	Os11t0416900-01	0.377	Os01t0533900-02	-0.344
Os02t0528900-01	0.732	0.619	Os02t0318500-00	0.225	Os01t0696600-01	-0.848
Os08t0564100-01	0.636	0.016	Os01t0695800-01	0.177	Os01t0615500-00	-0.954
Os04t0194500-01	0.554	0.848	Os01t0724500-01	0.048		
Os06t0554800-01	0.494	0.474	Os07t0464600-01	-0.033		
Os01t0356400-01	0.478	0.318	Os04t0528300-01	-0.296		
Os12t0267800-01	0.474	0.458	Os07t0191600-02	-0.308		
Os03t0859500-01	0.469	0.630	Os09t0125900-01	-0.402		
Os01t0173900-01	0.337	0.363	Os07t0288700-02	-0.641		
Os03t0280000-01	0.310	0.724	Os05t0222200-01	-0.661		
Os08t0384500-01	0.259	0.567	Os01t0534700-00	-0.952		
Os01t0121700-01	0.238	0.436	Os03t0157400-01	-0.974		
Os02t0575500-01	0.174	0.441	Os02t0318600-00	-1.100		
Os01t0609900-02	0.129	-0.246	Os06t0731200-01	-1.130		

Os09t0392400-02	0.080	-3.585	Os12t0411700-01	-1.470		
Os07t0522500-01	0.035	-0.386	Os04t0528400-02	-1.700		
Os01t0218700-01	0.029	4.087	Os01t0695700-00	-2.220		
Os08t0167000-01	0.011	0.010				
Os01t0966100-01	-0.017	0.379				
Os02t0826500-01	-0.026	0.356				
Os08t0398000-01	-0.067	0.173				
Os03t0332700-01	-0.080	0.035				
Os04t0620066-00	-0.100	1.214				
Os05t0107600-01	-0.259	-5.209				
Os11t0490800-01	-0.355	-0.280				
Os03t0441500-01	-0.375	0.585				
Os09t0332700-01	-0.377	1.433				
Os10t0442950-00	-0.405	1.027				
Os03t0181750-00	-0.438	-0.807				
Os01t0770500-01	-0.514	-2.807				
Os02t0318450-00	-0.566	Inf				
Os03t0670100-01	-0.860	0.170				
Os05t0137100-01	-1.110	-0.363				
Os01t0976100-01	-1.140	0.737				
Os08t0564300-05	-1.400	-Inf				
Os01t0836600-01	-1.630	-1.666				
Os06t0128300-03	-6.770	5.209				
(Oligo)peptide transporter	5 ↑ , 5 ↓	6 ↑ , 4 ↓		1 ↑ , 1 ↓		1 ↑ , 2 ↓
Os03t0719900-01	4.690	4.459	Os07t0603800-02	2.050	Os08t0486933-00	1.138
Os01t0142800-03	3.340	Inf	Os02t0116400-01	-0.075	Os05t0411100-00	-0.129
Os04t0524500-01	1.640	1.426	Os12t0638200-01	-0.128	Os01t0902700-01	-0.286
Os02t0695900-01	1.390	0.271	Os07t0100600-01	-1.530	Os01t0960900-00	-1.524
Os02t0695800-01	1.320	0.332			Os06t0706100-00	-1.759
Os06t0125500-02	0.950	2.907				
Os04t0491200-00	0.785	0.411				
Os04t0524600-01	0.381	0.254				
Os10t0470700-01	0.331	0.580				
Os01t0142800-01	0.307	0.052				
Os11t0235200-01	0.209	0.256				
Os03t0719900-02	0.154	0.988				
Os06t0125500-01	0.080	-2.170				
Os03t0235300-01	0.048	1.503				
Os08t0527733-00	-0.045	0.000				
Os10t0469900-02	-0.047	Inf				
Os03t0719900-04	-0.065	0.142				
Os04t0390600-01	-0.150	0.346				
Os06t0706400-01	-0.253	0.637				
Os12t0638300-01	-0.340	-1.293				

Os05t0338900-00	-0.474	-0.496				
Os02t0580900-02	-0.581	0.720				
Os05t0431700-01	-0.600	-0.731				
Os06t0125400-00	-0.864	-0.562				
Os03t0235700-01	-0.889	-0.312				
Os01t0872500-02	-0.934	0.646				
Os01t0871600-01	-1.060	-0.421				
Os05t0410900-02	-1.240	-0.397				
Os06t0705600-00	-2.050	-4.858				
Os06t0127700-01	-2.150	-1.222				
Os01t0872500-01	-3.330	-0.633				
Amino acid transporter	2 ↑ , 1 ↓			0 ↑ , 2 ↓		1 ↑ , 7 ↓
Os01t0825800-02	2.830	0.612	Os01t0945300-02	-Inf	Os01t0878700-03	-Inf
Os02t0655700-01	1.140	0.149	Os04t0542800-01	-0.210	Os12t0485600-01	1.585
Os04t0435100-01	0.291	0.225	Os01t0945300-01	-4.300	Os01t0856500-02	0.907
Os03t0576900-01	-0.402	-0.500			Os02t0788800-01	0.846
Os06t0539400-01	-0.623	-0.987			Os12t0623500-01	0.718
Os10t0437100-01	-0.677	-0.755			Os03t0817200-01	0.714
Os02t0700500-01	-1.050	-0.541			Os02t0101000-01	0.645
					Os06t0275800-01	0.610
					Os04t0460300-01	0.599
					Os10t0415100-01	0.591
					Os01t0945200-00	0.531
					Os07t0231400-01	0.522
					Os08t0127100-02	0.508
					Os01t0856500-01	0.492
					Os06t0633800-01	0.483
					Os08t0127100-01	0.423
					Os03t0641200-00	0.382
					Os01t0945100-00	0.344
					Os01t0825800-01	0.276
					Os02t0191300-01	0.228
					Os04t0470700-01	0.219
					Os01t0878700-02	0.197
					Os12t0623500-02	0.118
					Os05t0586500-01	0.089
					Os06t0644700-01	0.079
					Os06t0633800-02	0.054
					Os10t0415100-02	-0.062
					Os01t0209800-02	-0.067
					Os12t0181600-01	-0.132
					Os06t0275800-02	-0.206
					Os01t0597600-01	-0.300
					Os01t0209800-01	-0.322

					Os01t0857400-01	-0.382
					Os11t0169200-00	-0.437
					Os02t0788800-02	-0.487
					Os06t0228500-01	-0.600
					Os03t0654400-01	-0.678
					Os04t0543600-01	-0.766
					Os01t0908600-01	-0.807
					Os03t0654400-02	-1.000
					Os01t0878400-01	-1.047
					Os06t0275800-03	-1.170
					Os01t0617650-00	-1.222
					Os04t0562100-01	-1.467
					Os03t0375900-01	-1.763
Sugar transporter	9 ↑ , 7 ↓	4 ↑ , 3 ↓		2 ↑ , 0 ↓		1 ↑ , 0 ↓
Os10t0539900-04	-Inf	-0.491	Os11t0620400-01	Inf	Os06t0141100-00	3.700
Os10t0360100-01	6.410	1.212	Os04t0511400-01	4.120	Os07t0206600-01	0.349
Os07t0561800-01	3.850	0.000	Os07t0561800-02	0.633	Os11t0643800-01	-0.358
Os07t0559700-00	2.460	0.806	Os09t0268300-02	0.266	Os11t0594000-01	-0.907
Os07t0106200-02	2.260	0.410	Os03t0363600-01	0.107	Os02t0574000-01	-0.986
Os12t0512100-01	1.640	0.902	Os03t0101300-02	-1.140		
Os05t0169700-00	1.590	0.000				
Os02t0672400-02	1.400	0.415				
Os07t0106200-03	1.270	-0.208				
Os03t0218400-01	1.010	-0.707				
Os02t0832100-00	0.829	-0.072				
Os04t0491700-01	0.817	0.906				
Os07t0151200-00	0.655	0.271				
Os02t0573500-01	0.536	0.464				
Os01t0133400-01	0.528	0.547				
Os08t0410500-01	0.467	0.777				
Os09t0268300-02	0.266	1.222				
Os07t0131250-00	0.094	-1.000				
Os03t0363500-02	-0.003	0.585				
Os04t0452700-01	-0.052	0.902				
Os03t0594400-01	-0.065	-0.056				
Os04t0453200-01	-0.087	0.427				
Os04t0454200-01	-0.117	-1.182				
Os10t0579200-01	-0.121	0.245				
Os02t0604300-01	-0.225	0.159				
Os04t0490600-01	-0.225	0.000				
Os06t0523400-01	-0.246	-0.898				
Os11t0620400-02	-0.265	0.405				
Os01t0898900-01	-0.300	-0.152				
Os07t0131600-01	-0.320	-0.075				
Os03t0101300-01	-0.341	-0.152				

Os04t0529800-01	-0.352	-0.206				
Os07t0573700-01	-0.367	-0.093				
Os02t0573300-01	-0.738	0.030				
Os02t0672400-01	-0.893	1.054				
Os03t0197100-01	-1.180	-0.585				
Os04t0453400-02	-1.400	-0.809				
Os02t0110400-01	-1.420	0.027				
Os10t0539900-02	-1.440	0.082				
Os02t0574100-01	-2.760	1.132				
Os02t0229400-02	-3.900	-1.939				
MRP	0 ↑ , 1 ↓	1 ↑ , 0 ↓		0 ↑ , 0 ↓		
Os01t0533900-01	-Inf	0.152	Os05t0196100-01	-0.751		
Os05t0196100-02	0.909	0.405				
Os06t0158900-00	-0.453	1.000				
Gene both in shoot and root			Gene only in shoot		Gene only in root	
Gene ID	Log ₂ (IPU/CK)		Gene ID	Log ₂ (IPU/CK)	Gene ID	Log ₂ (IPU/CK)
	Shoot	Root				
Transcription factors						
NAC family	5 ↑ , 3 ↓	7 ↑ , 2 ↓		0 ↑ , 0 ↓		7 ↑ , 3 ↓
Os11t0126900-01	6.120	0.452	Os07t0566500-01	-0.478	Os11t0127000-01	-Inf
Os07t0683200-01	1.790	1.015			Os05t0194500-01	2.322
Os03t0815100-01	1.310	-0.144			Os01t0191300-03	2.000
Os08t0200600-01	1.150	-0.438			Os06t0560300-00	1.807
Os01t0816100-01	1.030	0.097			Os06t0101800-01	1.322
Os03t0327800-01	0.993	0.616			Os01t0888300-01	1.195
Os05t0194500-01	0.557	2.322			Os06t0104200-01	1.115
Os03t0133000-01	0.480	0.343			Os07t0683200-01	1.015
Os06t0104200-01	0.463	1.115			Os01t0261200-02	0.789
Os02t0822400-02	0.119	0.042			Os11t0126900-01	0.452
Os01t0888300-01	0.053	1.195			Os01t0191300-01	0.441
Os11t0184900-02	0.046	0.249			Os03t0119966-01	0.263
Os07t0225300-01	-0.017	-1.136			Os02t0810900-01	0.210
Os01t0261200-02	-0.033	0.789			Os01t0816100-01	0.097
Os06t0101800-01	-0.045	1.322			Os03t0815100-01	-0.144
Os01t0191300-01	-0.325	0.441			Os12t0156100-01	-0.144
Os02t0810900-01	-0.518	0.210			Os06t0530400-01	-0.241
Os06t0560300-00	-0.718	1.807			Os08t0200600-01	-0.438
Os01t0191300-03	-1.040	2.000			Os07t0225300-01	-1.136
Os12t0156100-01	-1.220	-0.144			Os02t0810900-02	-2.598
Os03t0777000-01	-1.630	-1.000				
WRKY family	6 ↑ , 6 ↓	3 ↑ , 7 ↓		2 ↑ , 3 ↓		2 ↑ , 0 ↓
Os06t0649000-02	-Inf	-1.399	Os07t0416100-01	3.370	Os02t0265200-02	Inf
Os09t0417800-01	2.940	0.049	Os05t0322900-03	2.500	Os11t0117500-01	2.170
Os03t0321800-01	2.830	-0.202	Os11t0685700-00	0.080	Os02t0698800-01	0.829
Os01t0186000-01	2.600	-0.100	Os04t0545000-01	-0.308	Os11t0686250-00	0.585

Os07t0680400-01	1.750	0.201	Os01t0842801-00	-0.367	Os11t0686400-00	0.485
Os12t0597700-01	1.380	0.506	Os08t0499300-01	-0.667	Os05t0478800-00	0.222
Os11t0490900-01	1.340	0.455	Os03t0855100-01	-0.815	Os01t0289732-01	0.211
Os09t0417600-02	0.939	-1.177	Os12t0102300-01	-1.010	Os01t0972800-01	0.000
Os03t0321700-01	0.794	-0.403	Os02t0462800-01	-1.050	Os03t0758950-00	0.000
Os01t0750100-02	0.751	0.889	Os11t0117600-00	-2.050	Os02t0770500-00	-0.033
Os09t0481700-01	0.689	0.546			Os05t0567200-00	-0.134
Os05t0343400-01	0.686	0.243			Os05t0478400-00	-0.302
Os01t0584900-01	0.659	-0.807			Os03t0798500-00	-0.341
Os12t0507300-00	0.657	0.234			Os12t0116700-01	-0.363
Os08t0235800-00	0.647	-0.225			Os03t0335200-01	-0.483
Os01t0289600-00	0.616	0.696			Os06t0158100-00	-0.531
Os08t0276200-01	0.601	0.392			Os01t0714800-01	-0.710
Os12t0102350-01	0.582	1.032				
Os01t0246700-01	0.556	-0.427				
Os03t0444900-00	0.519	0.472				
Os01t0734000-01	0.501	-0.218				
Os05t0183100-01	0.491	-0.426				
Os05t0565900-00	0.440	0.737				
Os01t0626400-01	0.437	-0.559				
Os02t0181300-01	0.435	-0.244				
Os01t0826400-01	0.417	-0.589				
Os06t0649000-01	0.370	-1.186				
Os12t0116400-00	0.370	-1.355				
Os12t0597700-02	0.343	0.822				
Os03t0758000-01	0.338	0.508				
Os01t0750100-01	0.338	0.241				
Os06t0146250-00	0.337	0.474				
Os01t0665750-01	0.267	0.615				
Os01t0624700-01	0.244	0.360				
Os03t0321800-02	0.232	-0.676				
Os07t0583700-01	0.203	0.292				
Os09t0481700-02	0.173	-0.519				
Os01t0750100-03	0.122	-0.025				
Os05t0537100-00	0.106	-0.636				
Os01t0665500-00	0.092	0.559				
Os01t0730700-01	0.007	0.072				
Os01t0201250-00	0.004	-0.336				
Os09t0334500-01	-0.005	0.053				
Os07t0596900-00	-0.080	-0.383				
Os04t0287400-01	-0.182	0.221				
Os08t0326900-01	-0.215	0.158				
Os05t0474800-01	-0.227	-0.452				
Os11t0116900-01	-0.276	0.184				
Os01t0185900-01	-0.282	0.382				

Os05t0137500-00	-0.316	0.334				
Os05t0571200-01	-0.367	-0.241				
Os02t0265200-01	-0.373	0.412				
Os09t0417600-01	-0.478	0.120				
Os07t0111400-00	-0.630	-1.057				
Os05t0322900-01	-0.636	-0.315				
Os04t0605100-01	-0.698	-0.223				
Os01t0656400-00	-0.718	1.322				
Os05t0322900-02	-0.746	-0.374				
Os05t0583000-01	-0.832	-1.926				
Os05t0129800-01	-1.060	1.000				
Os01t0182700-01	-1.120	-0.263				
Os08t0386200-01	-1.120	-0.414				
Os01t0821600-01	-1.220	-0.177				
Os04t0471700-00	-1.570	-2.170				
Myb family	0 ↑ , 5 ↓	0 ↑ , 1 ↓		8 ↑ , 9 ↓		10 ↑ , 4 ↓
Os03t0241100-03	0.269	0.569	Os01t0812000-01	Inf	Os02t0695200-02	-Inf
Os07t0438800-01	0.204	0.681	Os10t0561400-03	Inf	Os06t0507300-01	-Inf
Os01t0589300-01	0.112	0.462	Os09t0532900-01	3.540	Os05t0140100-03	Inf
Os03t0241100-01	0.012	0.642	Os01t0128000-01	2.860	Os01t0975300-02	3.288
Os05t0442400-01	-0.078	0.485	Os01t0722300-01	2.320	Os07t0647600-01	2.000
Os01t0812000-02	-0.123	0.300	Os02t0759800-01	1.360	Os04t0593200-01	1.766
Os04t0243400-01	-0.129	0.305	Os11t0700500-01	1.220	Os04t0110300-02	1.585
Os03t0329900-01	-0.137	0.220	Os07t0558100-00	1.210	Os06t0171900-02	1.509
Os11t0183700-01	-0.141	0.213	Os10t0561400-02	0.986	Os08t0157600-01	1.356
Os03t0654600-01	-0.246	0.469	Os04t0110300-02	0.984	Os06t0605600-01	1.100
Os03t0771100-01	-0.268	0.194	Os02t0260700-01	0.977	Os01t0975300-01	1.058
Os01t0176700-01	-0.403	-0.206	Os08t0428200-01	0.955	Os01t0841500-01	1.000
Os03t0847600-01	-0.434	0.429	Os11t0684000-01	0.923	Os12t0567300-00	0.982
Os09t0532900-04	-0.436	0.307	Os08t0151000-00	0.872	Os03t0371800-00	0.874
Os05t0195700-02	-0.460	-0.010	Os02t0241200-00	0.846	Os02t0776700-02	0.856
Os03t0847600-02	-0.480	0.394	Os02t0104500-01	0.745	Os07t0484700-01	0.807
Os02t0618400-02	-0.488	-0.415	Os05t0429900-01	0.735	Os02t0271900-01	0.807
Os12t0586300-00	-0.531	-0.386	Os05t0553400-01	0.692	Os12t0207200-01	0.807
Os05t0543600-01	-0.901	-0.415	Os01t0975300-01	0.682	Os11t0106100-00	0.778
Os01t0274800-01	-1.370	0.181	Os12t0613300-02	0.677	Os05t0114700-02	0.763
Os01t0285300-01	-1.620	-0.890	Os08t0144000-01	0.662	Os12t0175400-01	0.742
Os07t0432800-01	-1.630	-1.874	Os07t0688200-01	0.659	Os09t0248900-01	0.710
Os04t0594100-01	-1.780	-0.170	Os11t0128500-01	0.653	Os07t0438800-01	0.681
Os11t0632200-01	-1.950	-0.280	Os09t0299200-01	0.625	Os03t0142600-00	0.678
			Os07t0497500-00	0.611	Os03t0241100-03	0.569
			Os05t0114700-02	0.592	Os01t0589300-01	0.462
			Os05t0140100-02	0.545	Os05t0195700-01	0.368
			Os03t0371800-00	0.522	Os04t0243400-01	0.305
			Os12t0564100-01	0.512	Os01t0812000-02	0.300

			Os01t0187900-01	0.501	Os06t0112700-00	0.276
			Os03t0315400-01	0.477	Os03t0329900-01	0.220
			Os02t0187700-00	0.453	Os11t0183700-01	0.213
			Os08t0435700-00	0.434	Os04t0463600-01	0.196
			Os02t0260700-02	0.389	Os03t0771100-01	0.194
			Os04t0480300-01	0.370	Os01t0274800-01	0.181
			Os08t0151300-01	0.370	Os06t0221000-00	0.181
			Os07t0484700-01	0.348	Os02t0641900-01	0.152
			Os12t0125000-01	0.331	Os03t0252900-00	0.120
			Os06t0637500-02	0.309	Os05t0459000-01	0.000
			Os10t0408700-02	0.305	Os05t0195700-02	-0.010
			Os07t0647600-01	0.249	Os02t0700600-01	-0.064
			Os01t0708000-00	0.205	Os09t0106700-01	-0.138
			Os06t0507400-01	0.202	Os09t0431300-00	-0.149
			Os10t0408700-01	0.185	Os04t0594100-01	-0.170
			Os02t0776700-01	0.167	Os01t0176700-01	-0.206
			Os06t0303700-00	0.147	Os11t0632200-01	-0.280
			Os03t0773100-01	0.135	Os08t0548000-01	-0.290
			Os12t0613300-01	0.130	Os12t0586300-00	-0.386
			Os06t0171900-02	0.115	Os02t0618400-02	-0.415
			Os01t0702700-01	0.110	Os05t0543600-01	-0.415
			Os04t0463600-01	0.107	Os09t0538400-01	-0.473
			Os01t0841500-01	0.099	Os01t0285300-01	-0.890
			Os08t0157600-01	0.021	Os07t0432800-01	-1.874
			Os12t0175400-01	0.007	Os08t0486300-00	-2.269
			Os10t0561400-01	0.007		
			Os02t0700600-01	0.004		
			Os07t0629000-01	0.004		
			Os09t0106700-01	-0.043		
			Os04t0532800-01	-0.085		
			Os07t0627300-01	-0.098		
			Os01t0874300-01	-0.114		
			Os08t0437300-00	-0.129		
			Os11t0207600-00	-0.133		
			Os01t0850400-01	-0.133		
			Os09t0401000-01	-0.145		
			Os06t0258000-01	-0.178		
			Os11t0558200-01	-0.179		
			Os03t0720800-01	-0.310		
			Os12t0567300-00	-0.361		
			Os01t0127450-00	-0.367		
			Os08t0151300-02	-0.367		
			Os09t0538400-01	-0.374		
			Os02t0271900-01	-0.388		
			Os01t0305900-01	-0.581		

			Os02t0174000-00	-0.630		
			Os01t0298400-01	-0.630		
			Os11t0180900-00	-0.712		
			Os09t0248900-01	-0.765		
			Os06t0605600-01	-0.768		
			Os05t0206200-01	-0.978		
			Os01t0663051-00	-1.160		
			Os12t0207200-01	-1.290		
			Os02t0696900-00	-1.410		
			Os02t0776700-02	-1.480		
			Os02t0732600-01	-1.540		
			Os05t0195700-01	-1.670		
			Os05t0567600-00	-2.920		
			Os02t0695200-01	-3.440		
			Os05t0140100-03	-5.740		

ESI Table S11. The predicted promoters of up-regulated IPU-associated genes under IPU exposure

Gene ID	Predicted Promoters ^a												Log ₂ Ratio ^b		Annotation
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	Shoot	Root	
P450 (26)															
Os01t0388101-00	0	15	0	1	5	0	0	0	0	3	0	0	0.00	1.10	Similar to Phytochrome P450.
Os01t0602500-01	0	17	0	1	6	1	0	0	0	8	0	0	1.68	0.00	Cytochrome P450 domain containing protein.
Os01t0627800-01	2	23	0	5	8	0	0	0	0	8	2	2	0.00	1.38	Similar to Cytochrome P450 monooxygenase.
Os01t0628000-01	0	18	0	9	4	0	0	0	0	6	0	0	0.00	2.19	Similar to Phytochrome P450-like protein.
Os01t0628700-01	1	36	0	1	7	3	0	1	2	4	0	1	1.09	0.14	Cytochrome P450 family protein.
Os01t0728300-01	4	21	0	0	5	0	0	1	0	5	0	1	0.06	4.00	Cytochrome P450 family protein.
Os01t0804900-01	2	12	0	10	4	0	0	0	0	1	0	0	1.55	0.00	Cytochrome P450 family protein.
Os02t0173100-02	1	20	0	6	3	2	0	0	0	8	0	0	0.01	1.70	Cytochrome P450 family protein.
Os02t0185400-01	0	23	0	1	6	3	0	0	2	9	0	0	2.60	0.00	Cytochrome P450 family protein.
Os02t0186200-00	4	6	0	2	11	1	0	0	0	1	0	0	2.78	0.00	Cytochrome P450 domain containing protein.
Os03t0417700-01(<i>GL3.2</i>)	2	7	1	0	5	2	1	0	0	4	0	0	0.00	1.10	Cytochrome P450 family protein.
Os03t0594900-01	3	12	0	10	18	2	0	2	0	1	0	2	0.06	1.12	Cytochrome P450 family protein.
Os03t0760200-01 (<i>CYP81A6</i>)	1	15	0	15	10	1	0	0	0	6	1	1	1.21	0.89	Cytochrome P450.
Os04t0480700-01	3	28	0	0	11	0	0	0	0	7	0	0	1.41	0.81	Similar to Cytochrome P450.
Os05t0181200-01	1	23	0	1	5	0	0	0	0	10	0	0	0.00	1.83	Similar to Cytochrome P450.
Os05t0515200-01	1	16	0	2	11	0	0	0	0	5	0	1	1.11	0.00	Cytochrome P450 family protein.
Os06t0599200-01	1	25	0	7	2	0	0	0	2	6	0	0	2.28	0.05	Similar to Cytochrome P450.
Os07t0418500-01	1	21	0	10	8	0	0	2	2	9	0	2	0.00	1.39	Similar to Cytochrome P450 monooxygenase CYP72A5.
Os07t0635500-01	2	18	1	0	3	0	1	0	2	9	0	0	1.23	0.13	Cytochrome P450 family protein.
Os08t0152400-00	3	22	0	13	6	0	0	0	0	5	0	0	0.65	2.02	Similar to cytochrome P450.
Os08t0507100-00	4	16	0	5	7	2	0	0	0	4	0	0	4.23	0.00	Similar to Cytochrome P450 CYP71K14.
Os08t0507702-01	0	12	0	2	9	0	0	1	0	6	1	3	1.35	1.22	Cytochrome P450 family protein.
Os08t0508000-01	0	10	0	2	7	0	0	0	0	2	0	0	2.32	0.60	Cytochrome P450 family protein.
Os10t0139700-01	3	22	0	3	5	0	0	0	0	6	1	1	1.02	0.36	Cytochrome P450 family protein.

Os10t0144700-00	1	17	0	1	15	2	0	0	0	5	0	0	1.12	0.00	Cytochrome P450 family protein.	
Os10t0166600-01	0	20	0	0	7	1	0	0	0	4	0	0	0.03	2.32	Similar to P450.	
Monoxygenases (5)																
Os01t0645400-01 (<i>OsYUCCA1</i>)	1	11	1	0	4	1	1	0	0	5	0	0	3.69	0.00	Flavin monooxygenase-like enzyme, Auxin biosynthesis.	
Os03t0182000-00	2	21	0	0	7	0	0	0	2	12	0	0	0.00	1.00	Similar to Flavin-dependent monooxygenase 1.	
Os04t0128900-01 (<i>OsYUCCA7</i>)	4	13	0	0	10	0	0	0	2	4	0	0	1.28	0.02	Flavin monooxygenase-like enzyme, Auxin biosynthesis	
Os06t0203200-01	1	25	0	0	7	0	0	0	0	3	0	0	1.20	0.85	Flavin-containing monooxygenase FMO family protein.	
Os06t0698785-01	1	10	0	0	11	1	0	0	0	4	0	0	0.65	1.02	Similar to Choline monooxygenase.	
Oxidoreductase (4)																
Os03t0713400-03	2	18	0	2	14	0	0	0	4	6	0	0	2.00	Inf	Similar to NADH-ubiquinone oxidoreductase 75 kDa subunit.	
Os03t0774200-02	2	18	0	0	8	4	0	0	2	8	0	0	2.40	0.16	Similar to NADH-ubiquinone oxidoreductase subunit 8.	
Os07t0663800-01	0	26	0	5	5	1	0	0	0	6	0	0	1.30	0.47	Similar to Oxidoreductase.	
Os07t0675000-03	1	12	0	0	11	1	0	0	0	4	0	0	Inf	3.86	Acyl-CoA dehydrogenase/ oxidoreductase.	
GTs (5)																
Os02t0203300-00	2	18	0	1	6	2	0	0	0	2	0	0	1.82	0.64	Similar to UDP-glycosyltransferase UGT75E3.	
Os02t0330200-01	1	19	0	5	7	1	0	0	0	4	0	0	1.02	0.05	Glycosyltransferase AER61.	
Os04t0693000-02	1	28	0	0	7	1	0	0	0	7	0	0	5.23	Inf	Similar to dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit.	
Os07t0657400-01	2	26	0	0	10	2	0	0	2	6	0	0	1.31	0.62	Glycosyltransferase AER61.	
Os08t0446550-00	2	20	0	8	8	3	0	0	2	4	0	0	0.00	2.09	Glycosyltransferase AER61.	
GST (1)																
Os03t0135100-01	2	13	0	0	8	0	0	0	0	1	0	0	1.09	0.15	Glutathione S-transferase GSTF15.	
MTs (7)																
Os04t0104900-01	4	24	0	2	9	1	0	0	0	7	0	0	0.00	1.02	Similar to 0-methyltransferase (EC 2.1.1.6).	
Os05t0102000-01	3	11	0	1	6	2	0	0	0	4	0	0	2.03	0.00	SAM dependent carboxyl methyltransferase family protein.	
Os06t0152400-01	1	26	0	1	8	1	0	0	0	10	0	0	1.69	1.00	Hexaprenyldihydroxybenzoate methyltransferase.	
Os06t0646000-02	1	16	0	0	10	2	0	0	0	2	0	0	0.73	1.45	Methyltransferase type 11 domain containing protein.	
Os07t0206700-02	0	6	0	0	4	1	0	0	0	1	0	0	1.45	1.82	Similar to Cycloartenol-C-24-methyltransferase 1.	
Os07t0206700-02	0	6	0	0	4	1	0	0	0	1	0	0	1.45	1.82	Similar to Cycloartenol-C-24-methyltransferase 1.	

Os09t0344500-01	6	12	0	0	3	0	0	0	0	2	0	0	1.07	0.00	Similar to <i>O</i> -methyltransferase ZRP4 (EC 2.1.1.-) (OMT).	
ABC transporters (9)																
Os01t0218700-01	2	28	0	0	12	0	0	0	0	7	0	0	0.03	4.09	ABC transporter integral membrane type 1.	
Os01t0770500-02	0	11	0	1	7	0	0	0	0	2	0	0	4.37	3.32	Similar to ABC transporter ATP-binding protein.	
Os01t0770500-02	0	11	0	1	7	0	0	0	0	2	0	0	4.37	3.32	Similar to ABC transporter ATP-binding protein.	
Os01t0902100-00	4	14	0	2	9	2	0	0	2	3	0	0	1.14	0.00	Similar to MRP-like ABC transporter.	
Os05t0222200-02	3	15	0	4	12	2	0	0	0	7	0	0	3.77	0.00	ABC transporter-like domain containing protein.	
Os05t0384600-01	0	28	0	0	11	2	0	0	0	8	0	0	1.18	0.00	ABC transporter-like domain containing protein.	
Os06t0126100-01	3	19	0	1	7	0	0	0	0	7	0	0	0.00	1.81	ABC transporter, conserved site domain containing protein.	
Os08t0564300-01	2	23	0	1	7	2	0	1	0	11	0	1	0.76	2.68	ABC transporter-like domain containing protein.	
Os09t0472100-01	2	22	0	3	8	0	0	0	2	9	0	0	1.60	0.26	Similar to ABC transporter.	

^a 12 promoters were predicted as follows:

- I. *TATCCAOSAMY*, TATCCA element found in alpha-amylase promoters of rice (*O.s.*) at positions ca.90 to 150bp upstream of the transcription start sites, and are binding sites of *OsMYBS1*, *OsMYBS2* and *OsMYBS3* which mediate sugar and hormone regulation of alpha-amylase gene expression;
- II. *WRKY71OS* has a core of TGAC-containing W-box of binding site of rice WRKY24/71/72, transcriptional repressors of the gibberellin signaling pathway;
- III. *ABREMOTIFAOSOSEM*, motif A ABRE-like sequence found in rice, is essential for activation by VP1 and important for regulation by abscisic acid (ABA);
- IV. *GCCCCORE*, Core of GCC-box found in many pathogen-responsive genes, has been shown to function as ethylene-responsive element and appears to play important roles in regulating jasmonate-responsive and defense-related gene expression;
- V. *MYBCORE* has a binding site for all animal MYB and some plant MYB proteins that are responsive to abiotic stress;
- VI. *MYBPLANT* has a plant MYB binding site, which consensus sequence related to box P in promoters of phenylpropanoid biosynthetic genes such as PAL;
- VII. *ACGTABREMOTIFAOSOSEM*, ABRE motif A found in the promoter of the rice, is required for ABA-responsiveness and VP1;
- VIII. *EMBPITAEM* has an ng site of trans-acting factor EMBP-1 and a binding site of ABFs whose expression is induced by ABA and various stress treatment;
- IX. *RYREPEATVFLEB4* is RY repeat motif which is found in rice;
- X. *WBOXATNPRI*, W-box found in promoter of *Arabidopsis thaliana* NPR1 gene recognized specifically by salicylic acid (SA)-induced WRKY DNA binding proteins;
- XI. *ABREA2HVAI* is an ABA responsive element which has stress response in barely;
- XII. ABREATCONSENSUS AB is A-responsive elements (ABREs) found in the promoter of ABA and/or stress-regulated genes;

Red boxes indicate the max values in each column;

^b Ratio, fold-change values.

EIC Data S1—Materials and methods

Enzymatic activities assays

Assay of laccase activity. Activities of laccase were determined according to the methods of Carine et al. (2009) with some modification.¹ Laccase activity was assayed by adding 5 mL of modified universal buffer (MUB) solution pH 2.0 and 200 μ L of a 0.01 M ABTS solution to the mixture. The mixture was incubated at 30 °C for 5 min. It was then centrifuged at 11,300 \times g at 4 °C for 2 min and the oxidation rate of ABTS to ABTS⁺⁺ released in the supernatant was measured at 420 nm ($\epsilon = 18,460 \text{ M}^{-1} \text{ cm}^{-1}$). Laccase activity was expressed in units defined as μmol of ABTS⁺⁺ formed from ABTS min^{-1} (U) and g^{-1} of crude protein (U g^{-1} protein). Enzyme assays were carried out simultaneously as controls: (1) without ABTS, (2) without crude enzyme extract added to the reaction mixture.

Assay of POD activity. POD activity was analyzed based on guaiacol oxidation using hydrogenperoxide. The reaction mixture contained 2.5 mL of 100 mM HAc-NaAc buffer (pH 5.4), 0.1 mL of 1 percent H_2O_2 , 0.5 mL of 0.5% (w/v) guaiacol and 50 mL enzyme extract. The increase in absorbance at 470 nm was recorded.²

Assay of SOD activity. SOD activity was determined by measuring its inhibition of the photo chemical reduction of NBT. Three milliliters of reaction mixture contained 50 mM phosphate buffer (pH 7.8), 0.01 mM EDTA, 10 mM methionine, 0.6 mM riboflavin, 1.13 mM NBT and 10–60 mL enzyme extract. The increased absorbance was measured at 560 nm. One

unit of SOD was defined as the amount of enzyme causing half-maximal inhibition of the NBT reduction under the condition described previously.³

Assay of APX activity. APX activity was measured by the decrease in absorbance at 290 nm. The reaction mixture contained 50 mM Hepes-NaOH (pH 7.6), 0.25 mM ascorbate and 0.1 mM H₂O₂.⁴ To test whether “unspecific peroxidases” act as APX, samples were incubated for 10 min with 50 μM *p*-chloromercuribenzoate,^{5,6} which has been reported to inhibit APX preferentially.⁷

CPR extraction and activity assay. Shoot and root tissues (approximately 15 g) were ground to powder in liquid nitrogen and extracted with 1.5 volumes of 100 mM potassium phosphate buffer (pH 7.5) containing 250 mM sucrose, 40 mM ascorbate acid, 5 mM DTT and 1 mM EDTA. The crude homogenized tissues were filtered through several layers of chilled cheesecloth and centrifuged at 12,000×*g* for 15 min. The supernatant was transferred and centrifuged at 100,000×*g* for 90 min (Beckman ultracentrifuge Optima XE-100). Finally, the pellet was resuspended in 100 mM potassium phosphate buffer (pH 7.5), containing 20% (*v/v*) glycerol and 10 mM mercaptoethanol. The microsomal sample was stored at -70 °C prior to use. The protein content of microsomes was measured by the method of Bradford with bovine serum albumin (BSA) as a standard.⁸

NADPH-cytochrome P450 reductase (CPR) activity was conducted by the method of Tan et al. (2015).⁹ The 200 μL reaction mixture contained 100 mM potassium phosphate buffer (pH 7.5), 5 mg mL⁻¹ cytochrome *c* and microsomal suspension (0.5~1 mg mL⁻¹ protein). 10 μL of

10 mM NADPH was last added to start the reaction. The increase of absorbance at 550 nm was recorded for 5 min at 25 °C using a microplate reader (Molecular Devices SpectraMax M5). The control reaction mixture contained the same components except for potassium phosphate buffer replace the microsomal suspension. The enzyme activity was expressed as $\text{nmol min}^{-1} \text{mg}^{-1}$ protein using a millimolar extinction coefficient of 21.1 cm^{-1} .

Assay of GTs activity. The *O*-GTs, *N*-GTs and total GTs activity was assayed based on methods of Lu et al., (2015) with slightly modifications.¹⁰ The rate of decrease in the *p*-nitrophenol, 2, 4-dichloroaniline and isoproturon (IPU) concentration was assayed for the measurement of the *O*-GTs, *N*-GTs and total GTs activity with HPLC analysis in the reaction mixture, respectively. The assay mix (250 μL) contained 100 μL of the enzymatic extraction, 2 mM UDP-glucose and 0.04 mM *p*-nitrophenol or 0.02 mM 2, 4-dichloroaniline or 0.02 mM IPU. The reaction was carried out at 30 °C for 2 h, and were terminated by addition of 250 μL methanol and chilling to -20 °C for 0.5 h. The centrifuged supernatant was filtered through a 0.2 mm PTEF membrane (Iwaki Co. Ltd., Japan) prior to analysis using HPLC. One unit of the *O*-GTs, *N*-GTs and total GTs activity corresponded to the amount of enzyme activity that consumes 1 μmol of *p*-nitrophenol, 2, 4-dichloroaniline and IPU per minute under standard assay conditions, respectively.

Analysis of *p*-nitrophenol, 2, 4-dichloroaniline and IPU were performed using a Waters HPLC system (HPLC, Waters 515; Waters Technologies Co. Ltd., USA, <http://www.waters.com>) with ultraviolet (UV) detection at a wavelength of 317 nm, 245 nm and 241 nm, respectively. The operating conditions were: Hypersil reversed phase C_8 column

(Thermo, 250 mm×4.6 mm i.d.); mobile phase, methanol: water (3:2; v/v) for the analysis of *p*-nitrophenol and methanol: water (3:1, v/v) for the analysis of 2, 4-dichloroaniline and IPU; flow rate, 0.6 mL min⁻¹; injection volume, 20 μL; temperature, 25 °C. Under the conditions, the retention time of *p*-nitrophenol, 2, 4-dichloroaniline and IPU were 6.32 min, 13.89 min and 16.77 min.

Assay of *O*-MT activity. The *O*-MT activity was assayed according to the methods of was assayed based on methods of Proestos et al., (2006) with some modifications.¹¹ The rate of increase the product concentration (4-hydroxy-3-methoxy benzoic) was assayed for the measurement of the *O*-MT activity with HPLC analysis in the reaction mixture (500 μL) that contained 200 μL of the enzymatic extraction, 1 mM MgCl₂, 1 mM S-adenosyl-L-methionine (SAM) and 2 mM 3, 4-dihydroxybenzoic acid. The reaction was homogenized, incubated for 90 min at 37 °C and stopped by 500 μL methanol. The centrifuged supernatant was filtered through a 0.2 mm PTEF membrane (Iwaki Co. Ltd., Japan) prior to analysis using HPLC. Analysis of 4-hydroxy-3-methoxy benzoic was performed with ultraviolet (UV) detection at a wavelength of 256 nm. The analytical column was reversed-phase C₁₈ (Thermo, 250 mm × 4.6 mm). The mobile phase consisted of acetonitrile and water (20:80, v/v). The flow-rate was 0.6 mL min⁻¹. The injection volume was 20 μL. Under the conditions, the retention time of 4-hydroxy-3-methoxy benzoic was 32.11 min. One unit of the *O*-MT activity corresponded to the amount of enzyme activity that consumes 1 μmol of 4-hydroxy-3-methoxy benzoic per minute under standard assay conditions

Assay of glutathione *S*-transferase (GST) activity. GST activity was followed by the method of Yin et al., (2008) with some modification.¹² The reaction mixture consisted of 3mL 100mM sodium phosphate buffer (pH 6.5) containing 1mM GSH, 75 μ L of 40mM 1-chloro-2,4-dinitro-benzene (CDNB), and 150 μ L enzyme extract. The change in absorbance was recorded at 340 nm.

EIC Data S2—Results and discussion

Analysis of IPU residues and derivatives in rice tissues

The extract MS² spectra of the molecular ion of m/z 207.1479 occurred at the retention time of 20.22 min (ESI Fig. S5A). Fragmentation of IPU led to two product ions at m/z 164.8821 and 134.0373. The most abundant product ion at m/z 164.8821 was generated by the loss of isopropyl group (42 Da). The product ions at m/z 134.0373 was 31 Da less than m/z 164.8821, indicating the loss of $-N(CH_3)_2$ group (ESI Fig. S6A). These characteristic product ions above were important for identification of IPU-metabolites.

The MS/MS spectra recorded from the m/z 237.1575 precursor ions at 15.71 min produced ions at m/z 219.1227, m/z 205.0577, and m/z 160, respectively (ESI Figs. S5B and S6B). The main fragment ion of m/z 205.0577 was confirmed by loss of methoxy group, and subsequently it lost an isopropyl to form m/z 164.9981. Thus, metabolite 2# was identified as 2-methoxyl-IPU in shoot alone (ESI Fig. S6B). A functional group isomer of metabolite 2# (m/z 237.1212) was identified as 2-methylehanoic-IPU at 14.49 min in shoot and root of rice (ESI Fig. 5B),

according to the fragment ion of m/z 219.0644 which was generated by a loss of $-OH$ group (ESI Fig. 6C).

Hydroxylation of IPU was detected at m/z 223.1423 including three isomers. The peak of first isomer (1-OH-isopropyl-IPU) and second isomers (2-OH-isopropyl-IPU) was at 10.66 min, because they are structural isomers which eliminate $-OH$ and $-N(CH_3)_2$ groups to yield the product ions of m/z 205.0757 and m/z 159.9032 (ESI Fig. S5C). The mass spectrum of third isomer (metabolite 4#) peaked at 10.66 min was produced by loss of 15 Da (methyl group) from metabolite 2# (ESI Fig. S6E). Its main product ion was m/z 164.9033, which were produced by the cleavage of amido bond. Thus, metabolite 2# was identified as 2-methylehanoic-demethyl-IPU (ESI Fig. S6E).

Likewise, three isomers of m/z 209.1276 were detected at 9.40, 9.65 and 10.18 min, respectively (ESI Fig. S5D). The first isomer (metabolite 6#) was confirmed by the $N-OH$ substitution for the $N-CH_3$ of IPU. Two main fragment ions at m/z 191.0083 and m/z 166.9824 were created after loss of hydroxyl and isopropyl groups (ESI Fig. S6F). With the structural mode, the IPU-derivative is $N-OH$ -demethyl-IPU. Due to the absence of m/z 166.9824 in the second isomer (metabolite 7#), we deduced that the $-OH$ group was linked to isopropyl group, and identified metabolite 7# as 1-OH-didemthyl-IPU or 2-OH-didemthyl-IPU. The third isomer which had a solemn fragment ion of m/z 135.9044, was defined as 2-methoxyl-didemthyl-IPU (ESI Fig. S6H).

Isopropenyl-IPU (metabolite 9#) was eluted at 17.35 min with protonated molecular ion $[M+H]^+$ of m/z 205.1323 in the full-scan MS (ESI Fig. S5E). In the MS^2 spectrum, it had the typical and most abundant fragment ion at m/z 159.9131 (loss of $-N(CH_3)_2$ group) (ESI Fig.

S6I).

Metabolite 10# peaked at 7.94 min had a protonated molecular ion $[M+H]^+$ at m/z 195.1128 (ESI Fig. S5F). The MS/MS spectra gave prominent ions at m/z 176.9940 and 151.0396, which were produced by the loss of $-OH$ and the cleavage of amido linkage, respectively (ESI Fig. S6E). Thus, we tentatively elucidated metabolite 10# (1-OH-didemethyl-IPU or 2-OH-didemethyl-IPU) to be formed by *N*-dealkylation of metabolite 7#.

Metabolite 11# eluted at 18.96 min with a protonated molecular ion $[M+H]^+$ at m/z 193.1335 was 14 Da less than its parent IPU and formed by a loss of methyl group (ESI Fig. S5G). The corresponding fragment ions at m/z 150.9291 were generated by loss of the isopropyl group and m/z 135.9277 through cleaving of amino C–N bond (ESI Fig. S6K). Thus, metabolite 11# could be characterized as *N*-dealkylation products of parent IPU.

From the accurate mass value of $[M+H]^+$ ion (m/z 191.1179), we found two isomers at 8.63 and 17.88 min (ESI Fig. S5H). The MS² spectra of one isomer (metabolite 12#) gave prominent ions at m/z 160.0135 and m/z 145.9161, which were produced by the loss of $-N=CH_2$ and further loss of $-CH_3$, respectively (ESI Fig. S6L). Hence, metabolite 12# was identified as methyleneimido-IPU. The other isomer can be determined that the new compound metabolite 13# was the *N*-demethylated metabolite 13# (ESI Fig. S6M), according to its fragments at m/z 134 which was yielded by loss of $-N(CH_3)_2$ and $=CH_2$ groups.

For m/z 180.1383, which peaked at 17.59 min, the fragment ion of m/z 149.0315 and m/z 106.8587 from loss of $-NH-CH_3$ and 2-methoxy-isopropyl groups, respectively, indicated that metabolite 14# was likely identified as 4-(1-methoxy-2-methyl-2-propanyl)-*N*-methylaniline (ESI Figs. S5I and S6N).

The molecular ion at m/z 179.1167 (metabolite 15#) was eluted at 17.78 min (ESI Fig. S5J). The MS² spectra showed that elimination of C₃H₇ group led to occurrence of fragment ions at m/z 136.9184, from which metabolite 11# was defined as didesmethyl-IPU (ESI Fig. S6O). Subsequently, metabolite 11# loss –CONH₂ group to form 4-isopropylphenol (metabolite 18#) at 18.84 min whose fragment ions was m/z 93.7707 (ESI Figs. S5M and S6R). Moreover, the amino group of metabolite 18# was substituted by hydroxyl group, which generated 4-isopropylaniline (metabolite 19#) at 16.66 min (ESI Figs. S5N and S6S).

For m/z 175.0856, which peaked at 3.15 min, the fragment ion of m/z 145.1216 from the loss of –N=CH₂ group indicated that the double bond occurred on the –N(CH)₃. So the metabolite 16# was defined as isopropenyl-demethyl-methyleneimido-IPU (ESI Figs. S5K and S6P). After the cleavage of amido linkage, 4-vinylaniline (metabolite 20#) was formed with the fragment ions of m/z 103.0033 and 93.0137 (ESI Figs. S5O and S6T).

Based on the fragment ions of m/z 121.0020 and m/z 105.8634 which was generated by loss of –CH₃OH and further loss of –NH₂, the metabolite 17# was identified as 1-(4-aminophenyl)-2-propanol or 2-(4-aminophenyl)-2-propanol from metabolite 10# via the cleavage of amido linkage (ESI Figs. S5L and S6Q).

Compared to the controls and IPU treatment, five new peaks linked to one IPU-conjugate and four glucosylated IPU derivatives were identified. The peak at 15.97min was detected by MS and revealed a glucosylated IPU-derivative (conjuagte1#, m/z 251.1390) with [M+H]⁺ ions at m/z 233.1279 and m/z 205.1077(ESI Figs. S5P and S7A), which could be attributed to the loss of a hydroxyl group and carboxyl group. With the mass spectrum, a structure like *N*-acetyloxy-monodemethyl-IPU.

According to the fragment ions of m/z 179.1167 and m/z 137.0702, the parent ion of m/z 357.1643 at 17.67 min was assigned to 2-OH-didemethyl-IPU-*O*-glucoside (conjugate 2#), a sugar ring linked to metabolite 10# by the *O*-glycosidic bond (ESI Figs. S5Q and S7B). The other conjugates were formed by glycosylation and yielded a similar fragment ion. Two major IPU-derived conjugates (m/z 371.1792 and m/z 385.1943) eluted at 9.35 and 10.69 min were detected by MS/MS analysis (ESI Figs. S5R and S7C). There were fragment ions at m/z 223.0465 and m/z 209.0831, indicating that metabolites 4# (m/z 223.1423) and 7# (m/z 209.1276) were the reasonable sugar (162 Da) receptors (ESI Figs. S6W and S7D). Thus, the two compounds with 2-OH-monodemethyl-IPU-*O*-glucoside and 2-OH-IPU-*O*-glucoside were assigned conjugates 3# and 4#, respectively.

A small peak (t_R = 10.46 min) at m/z 399.1730 was detected (ESI Fig. S5T) with fragment ions at m/z 381.1250, m/z 340.2589 and m/z 179.1173. Ion of m/z 381.1250 was attributed to the dehydroxylated form of its precursor. Elimination of $-\text{CH}_3\text{COO}$ from m/z 399.1730 resulted in the formation of m/z 340.2589 ion. Further loss of sugar ring led to the formation of m/z 179.1173 fragment ion, suggesting that the IPU-derived degradation product was conjugated to metabolite 10# (ESI Fig. S7E). Thus, the metabolite was identified as 2-OH-didemethyl-IPU-*O*-acetylglucoside. Overall, all the IPU-derivatives were summarized in Table 1.

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