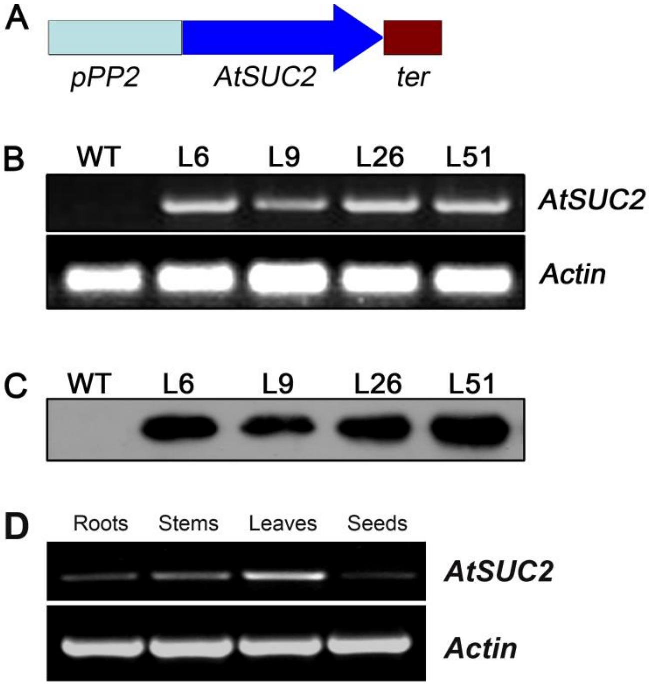
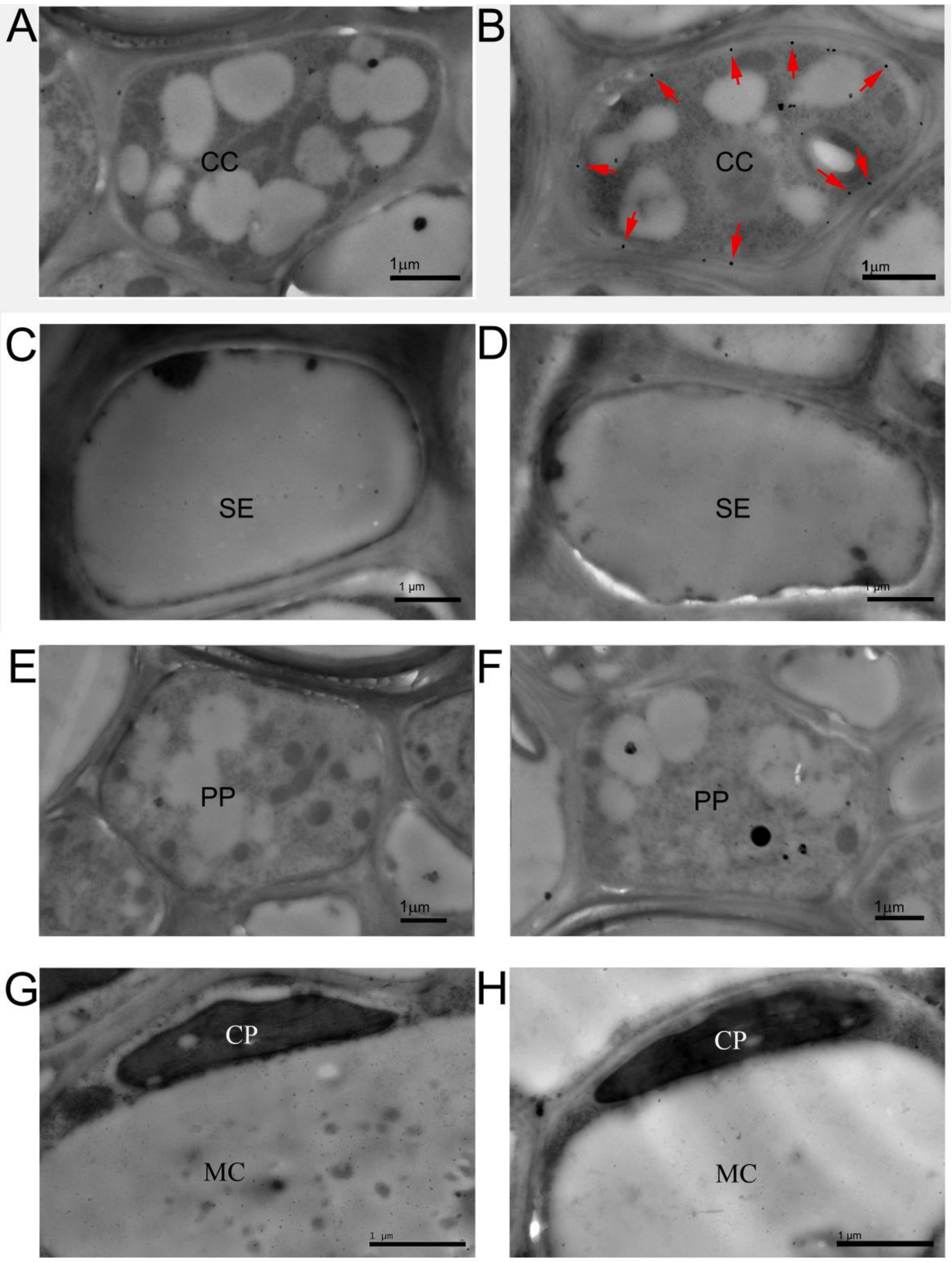


Supplemental Figure S1. Characterization of *pPP2*::*AtSUC2* rice plants.

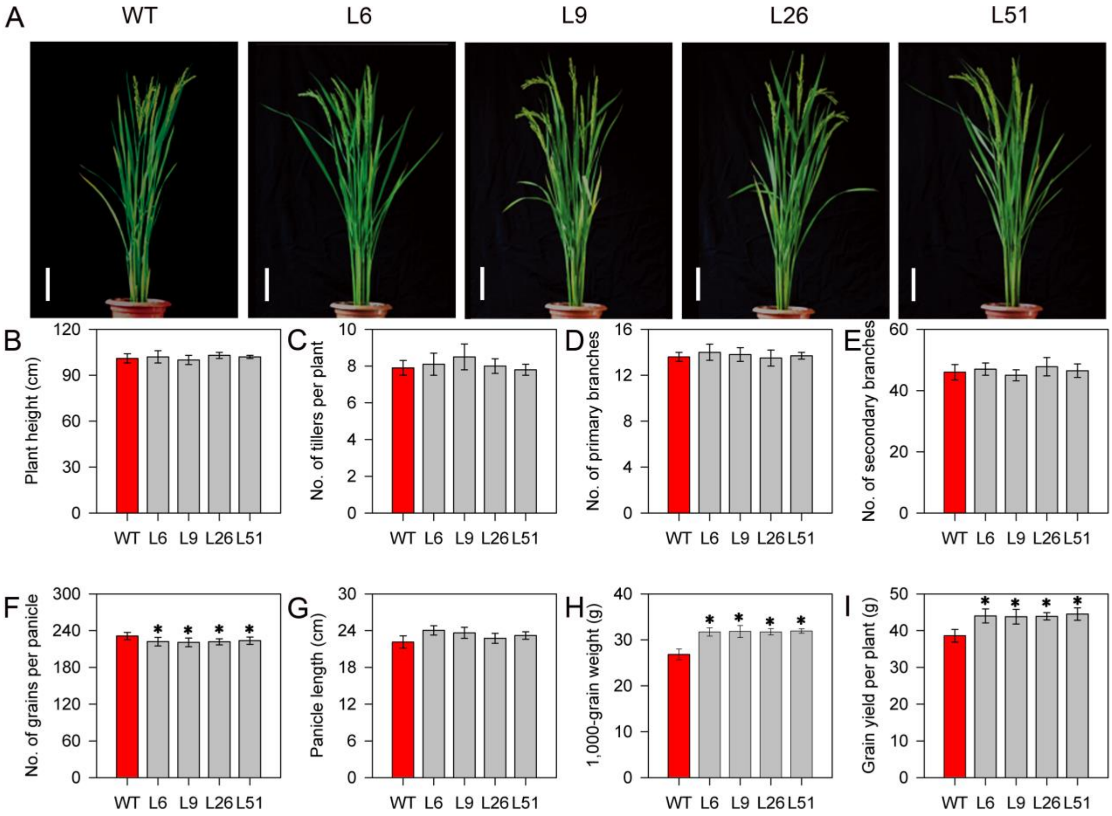
(**A**) Schematic map of the construct used in *AtSUC2*-overexpressing. (**B**) RT-PCR analyses in flag leaves of wild-type (WT) and transgenic plants on the 10th d after fertilization. RT-PCR was performed with specific primers for *Arabidopsis* SUC2 and actin-specific primers. (**C)** Immunoblot analysis of AtSUC2 protein on the basis of equal total leaf proteins (15 μg) in flag leaves of wild-type (WT) and transgenic plants 10 days after fertilization. **(D)** RT-PCR analyses in flag leaves, roots, stems, flowers, and seeds of transgenic plants (line 51) on the 10th d after fertilization. RT-PCR was performed with specific primers for *Arabidopsis* SUC2 and actin-specific primers.



Supplemental Figure S2. Localization of AtSUC2 in leaves of wild-type (WT) and *pPP2*::*AtSUC2* rice plants (line 51).

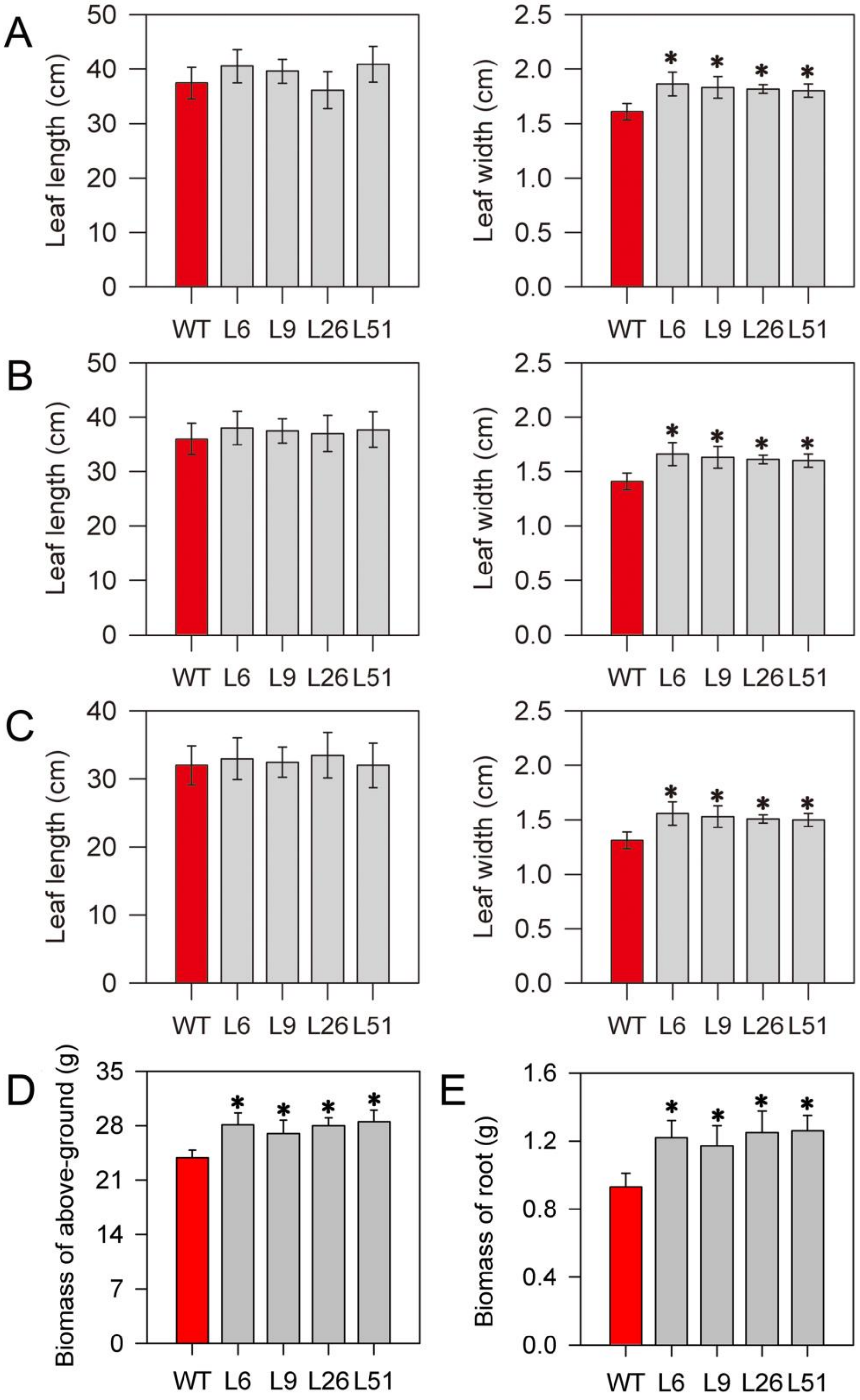
AtSUC2 was localized by immunogold labeling and transmission electron microscopy. Arrows indicate gold particles conjugated to an anti-AtSUC2 polyclonal antibody. Bars = 1 μm. SE, the sieve element; CC, the companion cell; PP, the phloem parenchyma cell; CP, the chloroplast. (**A**) Detection of AtSUC2 in companion cells in WT leaves. (**B**) Detection of AtSUC2 in companion cells in L51 leaves. (**C**) Detection of AtSUC2 in sieve element cells in WT leaves. (**D**) Detection of AtSUC2 in sieve element cells in L51 leaves. (**E**) Detection of AtSUC2 in phloem parenchyma cells in

WT leaves. (**F**) Detection of AtSUC2 in phloem parenchyma cells in L51 leaves. (**G**) Detection of AtSUC2 in mesophyll cells in WT leaves. (**H**) Detection of AtSUC2 in mesophyll cells in L51 leaves.



Supplemental Figure S3. Phenotype and grain yield of wild-type (WT) and *pPP2*::*AtSUC2* rice plants.

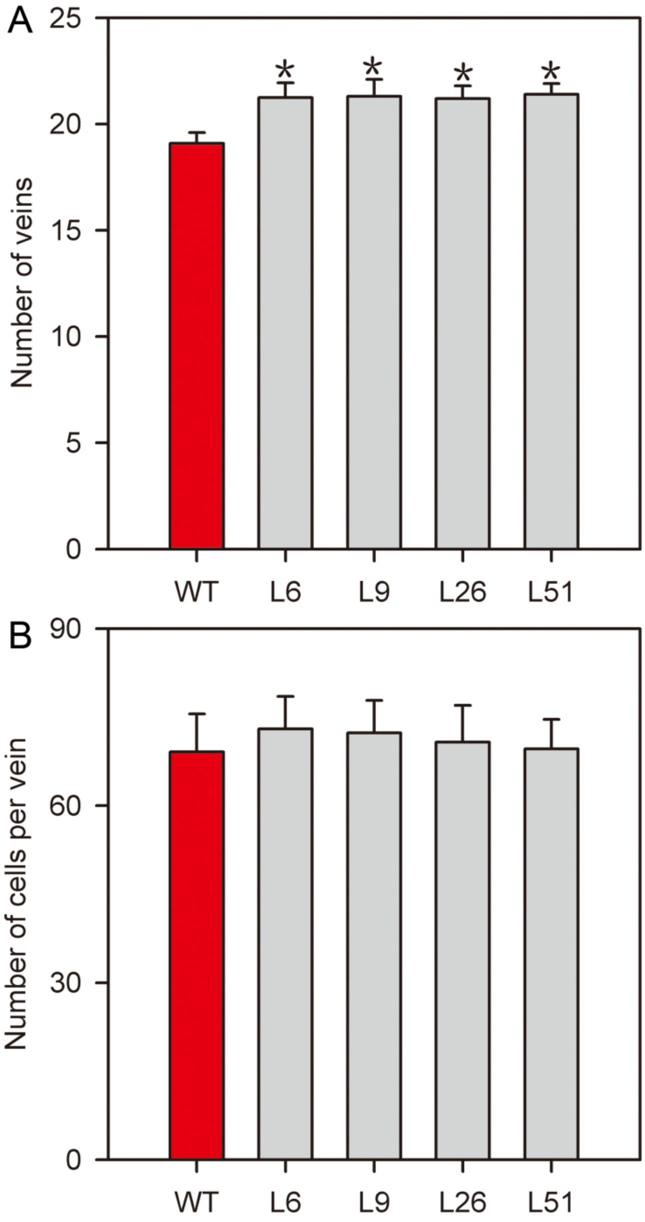
All data are given as mean ± SD. Asterisks indicate significant difference from the wild-type (** $P < 0.05$, ** $P < 0.01$). A Student's *t*-test was used to generate the *P* values. (**A**) Mature plant appearance. Bars = 10 cm. (**B**) Plant height (n = 60). (C) Number of tillers per plants (n = 60). (**D**) Number of primary branches (n = 60). (**E**) Number of secondary branches (n = 60). (**F**) Number of grains per panicle (n = 60). (**G**) Panicle length (n = 60). (**H**) 1000-grain weight (n = 60). (**I**) Grain yield per plant (n = 60).



Supplemental Figure S4. Leaf length and width and biomass of wild-type (WT) *pPP2*::*AtSUC2* rice plants.

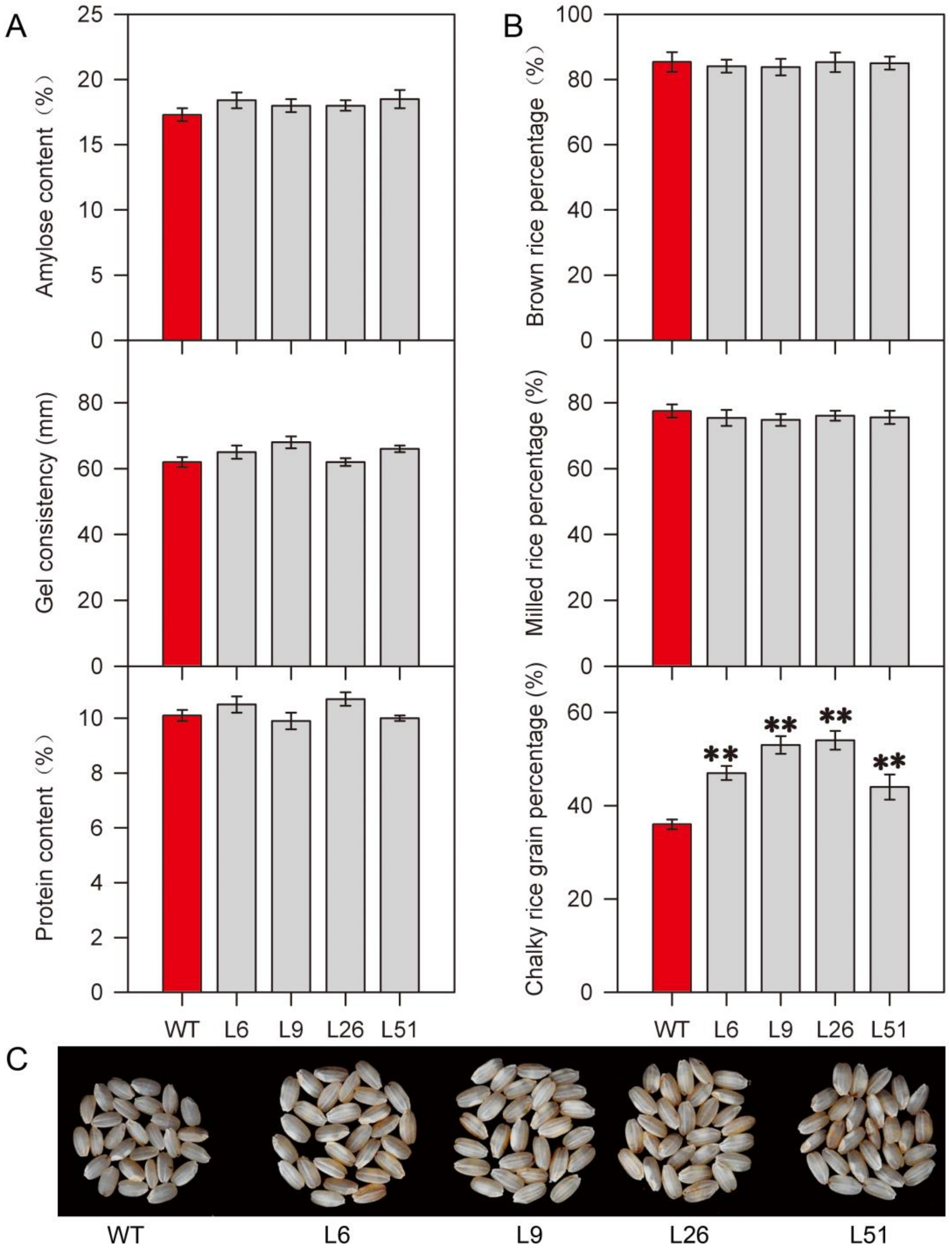
All data are given as mean ± SD. Asterisks indicate significant difference from the wild-type (* $P < 0.05$). A Student's *t*-test was used to generate the *P* values.

(**A**) Flag leaf length and width (n = 60). (**B**) Top second leaf length and width (n = 60). (**C**) Top third leaf length and width (n = 60). (**D**) Biomass of above-ground (n = 60). (**E**) Biomass of roots (n = 60).



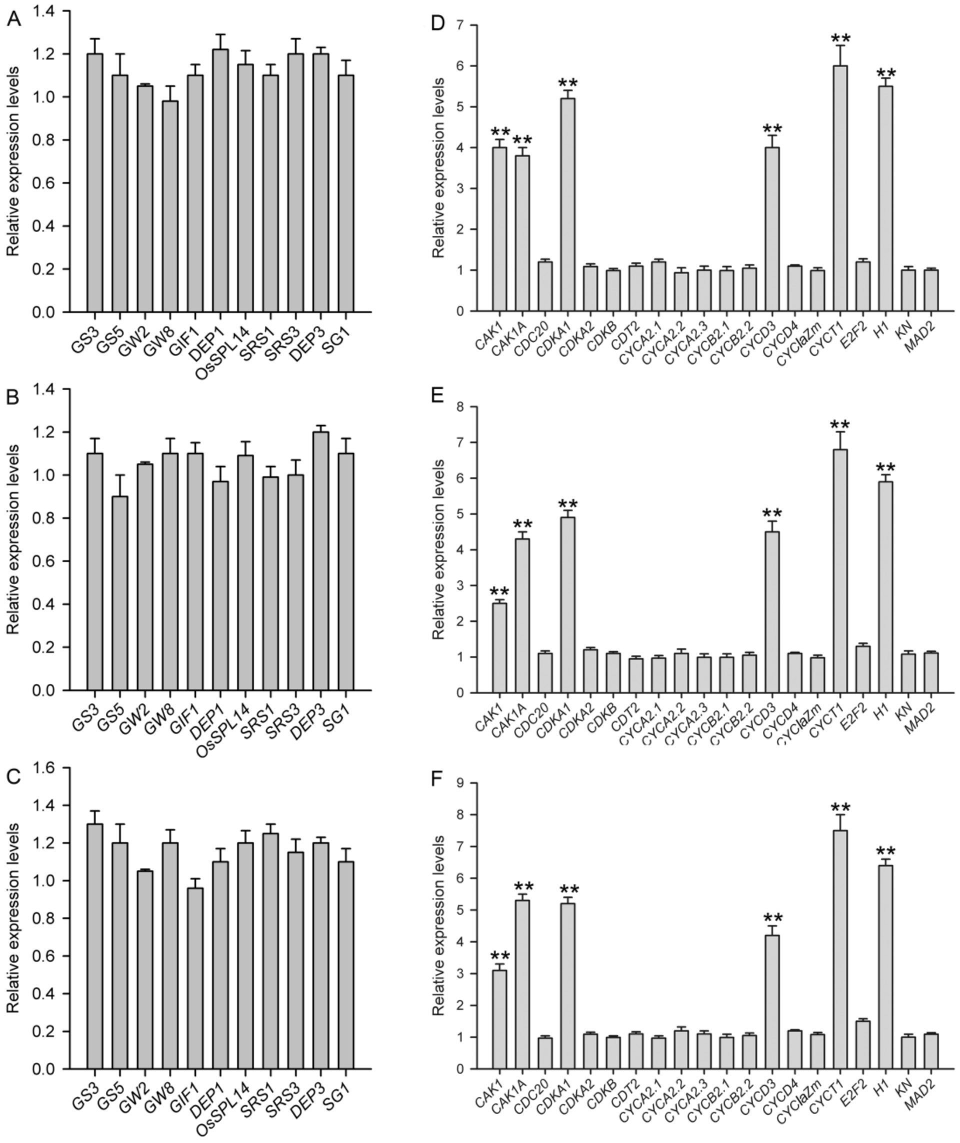
Supplemental Figure S5. Histological analyses of flag leaves on the 10th day after fertilization in wild-type (WT) and *pPP2*::*AtSUC2* rice plants.

All data are given as mean ± SD. Asterisks indicate significant difference from the wild-type (* $P < 0.05$). A Student's *t*-test was used to generate the *P* values. (**A**) Number of veins at cross-section of the middle of flag leaves in WT and transgenic plants (n=5). (**B**) Average number of upper epidermal cells per vein at cross-section of the middle of flag leaves in WT and transgenic plants (n=5).



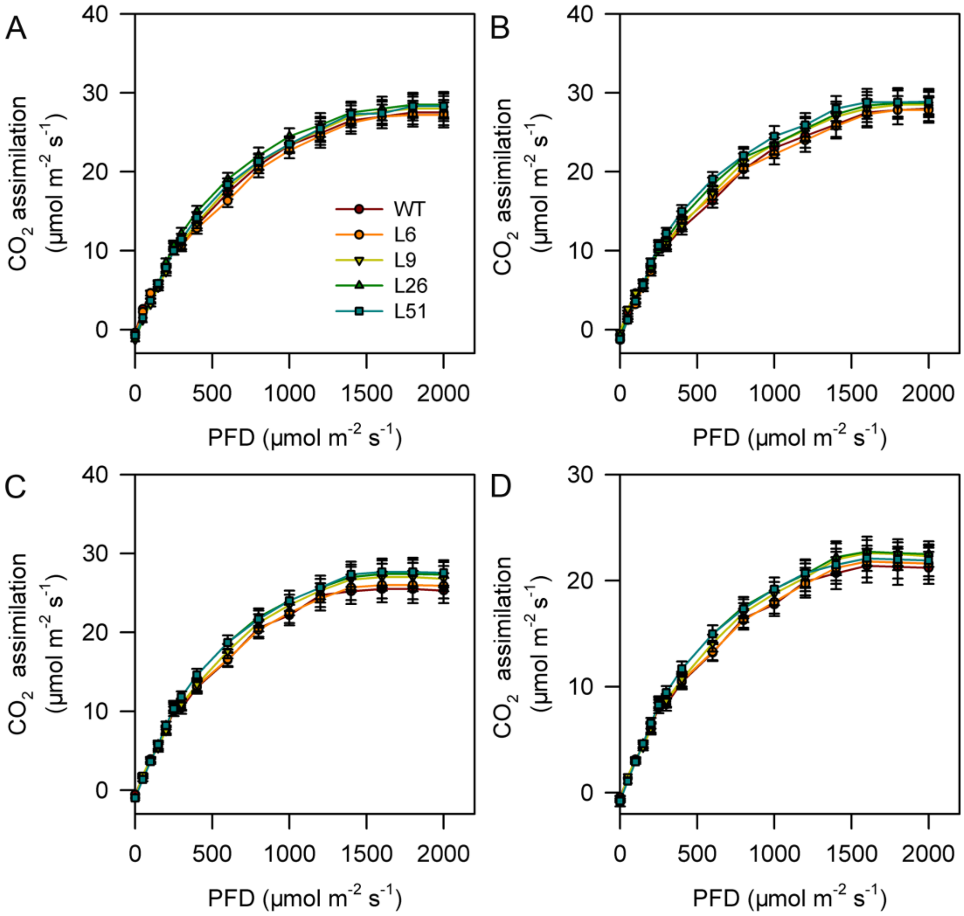
Supplemental Figure S6. Comparisons of grain quality traits between wild-type (WT) *pPP2*::*AtSUC2* rice plants.

All data are given as mean ± SD. Asterisks indicate significant difference from the wild-type (** $P < 0.01$). A Student's *t*-test was used to generate the *P* values. (**A**) Three physicochemical traits of rice grains: amylose content, gel consistency, and protein content (n = 6). (**B**) Milling quality trait and appearance quality trait: brown rice percentage, miller rice percentage, and chalky rice percentage (n = 6). (**C**) Appearance of head milled rice.



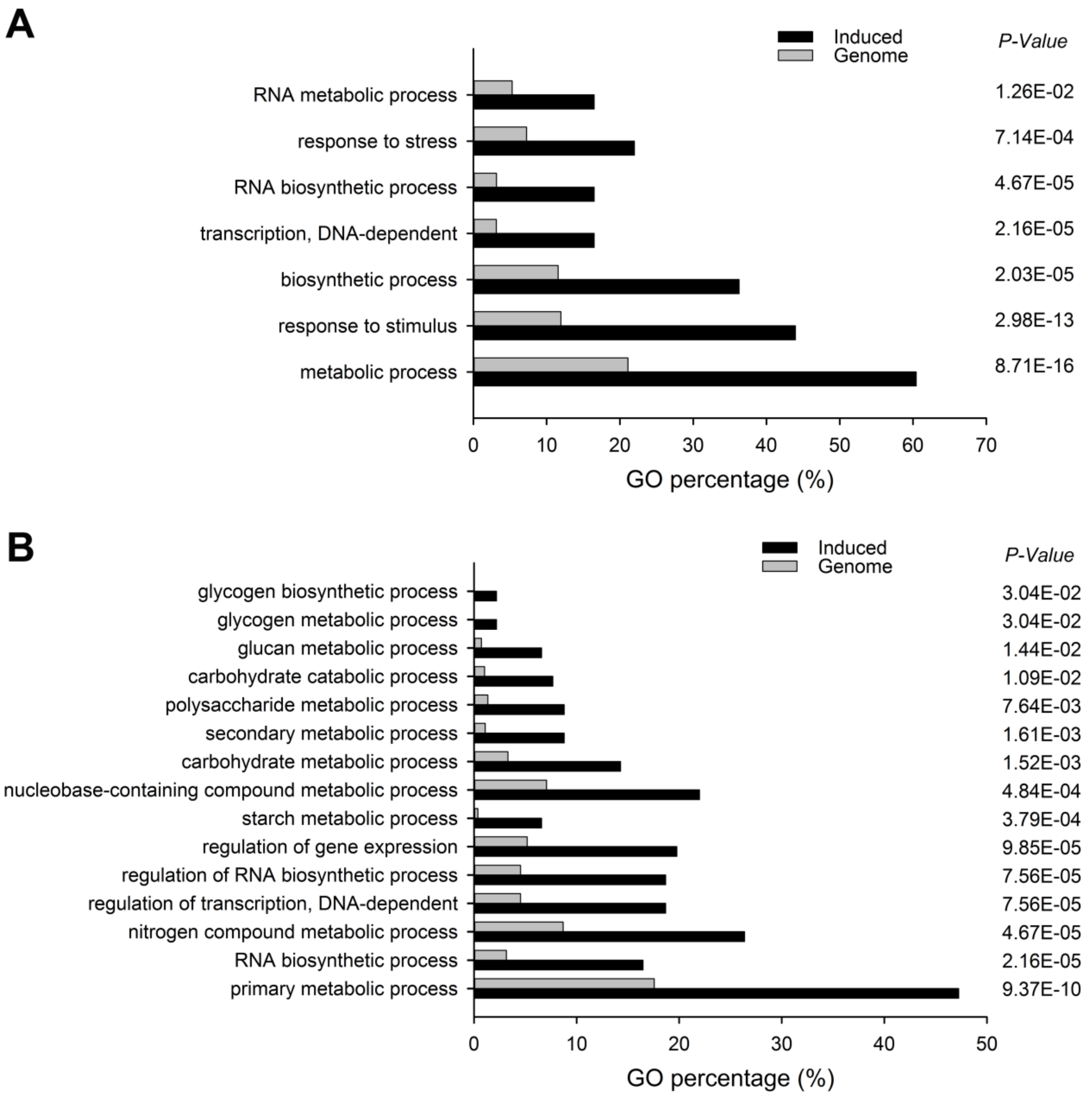
Supplemental Figure S7. Comparisons of transcripts of genes determining for grain size and genes involved in cell cycle between wild-type (WT) and *pPP2*::*AtSUC2* rice plants.

The analysis of relative expression ratio was determined by qRT-PCR using young panicles during the inflorescence development. The data were expressed relative to the level of transcripts in WT. All data are given as mean ± SD (n = 5). Asterisks indicate significant difference from the wild-type (* $P < 0.05$, **$P < 0.01$). A Student's *t*-test was used to generate the *P* values. (**A, D**) Young panicle (<0.2 cm in length). (**B, E**) Panicle of length 3 cm. (**C, F**) Panicle of length 6 cm.



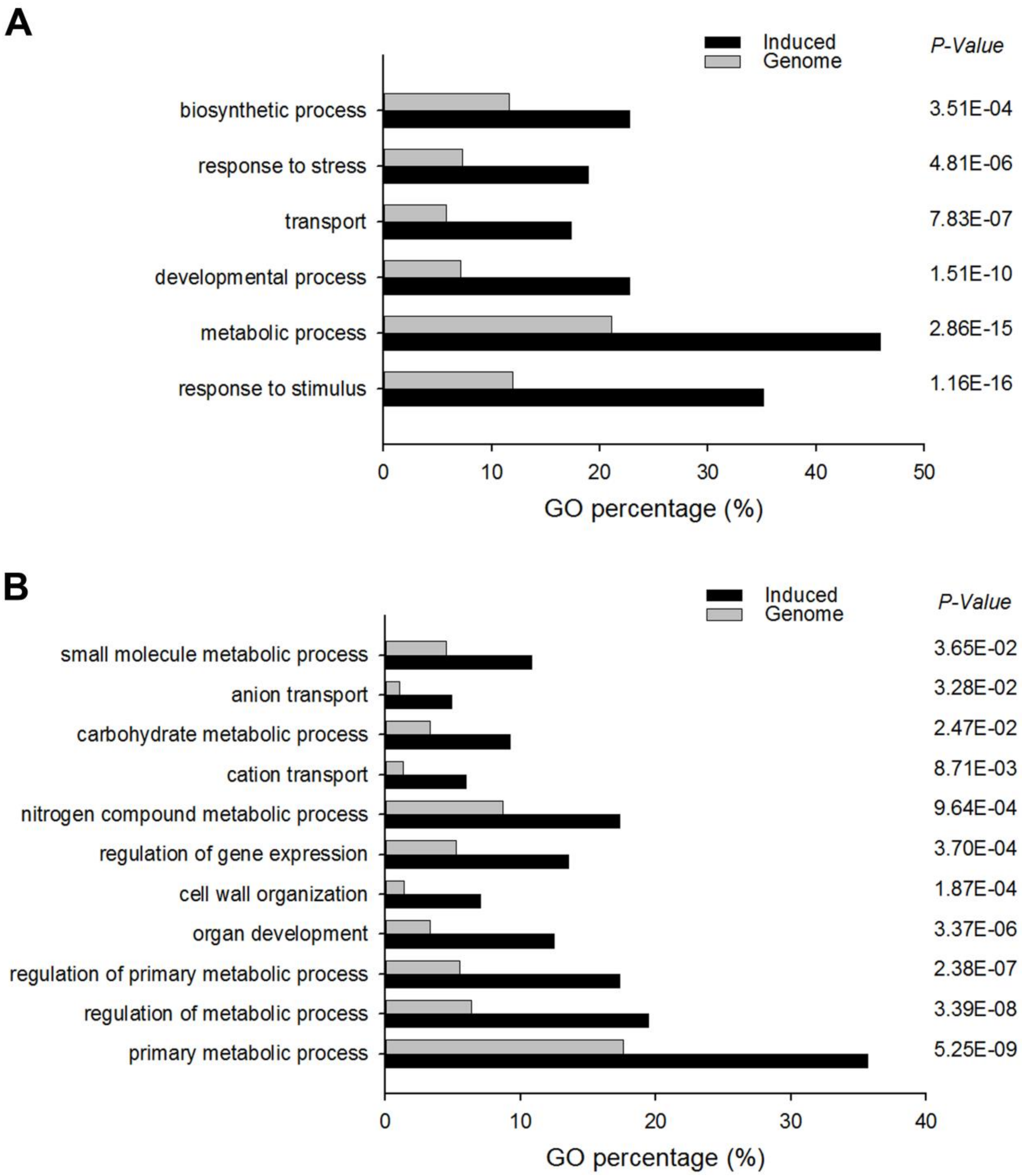
Supplemental Figure S8. CO_2 assimilation in leaves of wild-type (WT) and *pPP2*::*AtSUC2* rice plants.

All data are given as mean ± SD (n =10). Significant differences from the WT are based on Student's *t*-test and indicated by * if $P < 0.05$ or ** if $P < 0.01$. (**A**) Tillering stage. (**B**) 0 day after fertilization. (**C**) The 10th day after fertilization. (**D**) The 20th day after fertilization.



Supplemental Figure S9. Global analysis of gene expression profiles in flag leaves of *pPP2*::*AtSUC2* rice plants (line 51).

(A) Expression profiles of genes up-regulated in flag leaves of Line 51 based on the Gene Ontology (GO) annotation (biological process) in TAIR. **(B)** Analysis of genes induced in flag leaves of line 51 by specific GO terms. The flag leaves on the 10th day after fertilization were used for the microarray analysis. *P*-values in A and B were calculated by Fisher's test to compare the percentage distribution of GO annotation from genes induced by overexpressed *AtSUC2* and the whole genome.



Supplemental Figure S10. Global analysis of gene expression profiles in developing seeds of *pPP2*::*AtSUC2* rice plants (line 51).

(A) Expression profiles of genes up-regulated in developing seeds of Line 51 based on the Gene Ontology (GO) annotation (biological process) in TAIR. **(B)** Analysis of genes induced in developing seeds of line 51 by specific GO terms. The developing seeds on the 10th day after fertilization were used for the microarray analysis. *P*-values in A and B were calculated by Fisher's test to compare the percentage distribution of GO annotation from genes induced by overexpressed *AtSUC2* and the whole genome.

Supplemental Table S1. Genes found to be significantly up-regulated (≥1.5, A) or down-regulated (≤1.5, B) in flag leaves of *pPP2*::*AtSUC2* rice plants (line 51) on the 10th day after fertilization in a microarray analysis. Data were mean from three biological replicates

A (Up-regulated 117 genes)			
Locus	**Fold change**	***P*-Value**	**Description**
Os01g0108500	115.97	3.54E-07	Conserved hypothetical protein
Os01g0288700	4.61	9.05E-03	Hypothetical gene
Os01g0384800	2.35	3.93E-02	Conserved hypothetical protein
Os01g0385000	8.09	3.31E-02	Malic acid transport protein
Os01g0385400	6.48	3.73E-02	malic acid transport protein
Os01g0567200	161.56	5.57E-05	Conserved hypothetical protein
Os01g0602200	2.06	1.84E-04	Cytochrome P450
Os01g0606900	2.06	4.28E-04	Heat shock protein DnaJ
Os01g0633100	1.86	5.05E-05	ADP glucose pyrophosphorylase large subunit 2 (AGPL2)
Os01g0687400	2.28	1.20E-03	Similar to chitinase
Os01g0704100	1.64	3.80E-03	Nitrate transporter 2.3(OsNRT2.3)
Os01g0723700	2.21	7.34E-04	Transcriptional factor B3 family protein
Os01g0845900	255.04	2.45E-04	Unknown
Os01g0866400	1.60	2.49E-03	Cytosolic fructose-1,6-bisphosphatase 1 (cyFBP1)
Os02g0117700	1.96	2.42E-04	UDP-glucose pyrophosphorylase 2 (UGP2)
Os02g0132300	2.05	1.92E-02	Similar to erythrocyte membrane protein PFEMP3
Os02g0185400	17.20	7.40E-03	Cytochrome P450 family protein
Os02g0207900	3.80	4.39E-03	Alpha/beta hydrolase
Os02g0211100	2.70	7.24E-04	Hypothetical protein
Os02g0252400	8.42	7.51E-03	Rice prolamin box binding factor
Os02g0441000	2.97	2.04E-02	Conserved hypothetical protein
Os02g0579600	2.93	2.02E-02	Transcription factor MADS27
Os02g0620500	1.67	2.80E-04	Ammonium transporter 1.2 (OsAMT1.2)

Os02g0629300	3.09	9.41E-05	Conserved hypothetical protein
Os02g0631200	1.57	1.85E-03	Photosystem II oxygen evolving complex protein PsbQ
Os02g0805300	1.57	2.81E-02	Auxin-responsive protein IAA12
Os02g0814600	2.48	5.00E-03	EF-HAND 1 domain containing protein
Os02g0830200	2.97	5.80E-03	Oligopeptidase A (OsRR3)
Os03g0106500	5.02	2.50E-04	Expansin-B1 (Beta-expansin-1, OsEXPB1)
Os03g0106900	15.39	4.33E-07	Beta-expansin precursor (Beta-expansin 1)
Os03g0115800	11943.03	1.76E-07	Conserved hypothetical protein
Os03g0170900	3.32	9.43E-03	Sucrose transporter 1 (OsSUT1)
Os03g0412400	5.31	1.12E-03	Conserved hypothetical protein
Os03g0429900	147.51	7.79E-07	Nucleic acid-binding, OB-fold domain containing protein
Os03g0640000	2.13	1.00E-02	Patatin family protein
Os03g0847700	3.32	1.39E-04	Conserved hypothetical protein
Os04g0223500	2.66	1.93E-03	Dimethylaniline monooxygenase
Os04g0510000	755.71	4.80E-07	Conserved hypothetical protein
Os04g0526300	2.19	1.05E-02	Sulfotransferase family protein
Os04g0565200	2.47	3.69E-02	Similar to Cis-zeatin O-glucosyltransferase 1
Os04g0599300	3.42	4.78E-02	Basic helix-loop-helix dimerisation region bHLH domain containing protein
Os04g0604000	2.43	3.65E-02	Similar to Actin filament bundling protein P-115-ABP
Os04g0640300	2.26	1.26E-02	Conserved hypothetical protein
Os04g0677300	5.62	3.59E-03	Harpin-induced 1 domain containing protein
Os05g0100100	3.68	4.86E-04	Conserved hypothetical protein
Os05g0108900	2.26	1.60E-02	Cytochrome b5
Os05g0112900	2.27	9.28E-04	Pentatricopeptide repeat domain containing protein
Os05g0124700	65.42	4.49E-04	Deoxynucleoside kinase family protein
Os05g0164400	5.24	4.41E-03	Fructose-2, 6-bisphosphatase
Os05g0196200	2.27	1.99E-02	Pollen-specific protein
Os05g0211800	2.79	4.57E-02	Hypothetical conserved gene
Os05g0270500	85.90	4.36E-05	Similar to predicted protein

Os05g0296200	2.60	4.04E-03	Conserved hypothetical protein
Os05g0296800	10.47	1.66E-03	Small heat shock protein
Os05g0417400	9.31	6.16E-05	Universal stress protein family protein
Os05g0515500	5.72	6.64E-04	Auxin response factor 14
Os05g0571200	4.20	1.29E-02	Similar to WRKY transcription factor 19
Os05g0588800	2.12	9.36E-04	Similar to Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia lipolytica
Os06g0133000	3.06	1.78E-04	Granule-bound starch synthase I, chloroplast precursor
Os06g0200800	4.22	9.33E-03	Conserved hypothetical protein
Os06g0261300	4.38	3.36E-04	Conserved hypothetical protein
Os06g0265100	465.62	1.10E-07	Asparagine synthetase
Os06g0276300	2.02	1.52E-02	NB-ARC domain containing protein
Os06g0517000	2.29	2.02E-04	Hypothetical gene
Os06g0521400	2.07	4.54E-03	Haem peroxidase
Os06g0566600	3.07	8.94E-05	Hypothetical protein
Os06g0595900	2.28	2.95E-03	Transcription elongation factor S-II
Os06g0633800	1.54	2.33E-02	Amino acid transporter-like 5 (OsATL5)
Os06g0635500	2.91	4.70E-03	Hypothetical conserved gene
Os06g0675600	3.14	3.94E-02	Similar to GRAB2 protein
Os06g0695100	3.05	3.35E-04	Conserved hypothetical protein
Os06g0726400	1.53	5.56E-03	Branching enzyme I (BEI)
Os07g0122000	2.93	3.16E-02	Protein of unknown function DUF1719
Os07g0146700	3.55	1.44E-03	Conserved hypothetical protein
Os07g0489200	5.34	1.57E-03	UDP-glucuronosyl/UDP-glucosyltransferase family protein
Os07g0490100	16.85	4.55E-05	UDP-glucuronosyl/UDP-glucosyltransferase family protein
Os07g0539100	6.93	7.70E-04	Glycoside hydrolase, family 17 protein
Os07g0543300	2.20	7.41E-03	Beta-amylase
Os07g0563100	3.12	1.49E-03	Hypothetical protein
Os07g0580700	7.40	1.63E-03	Integrin alpha chain

Os07g0603700	3.23	4.19E-02	Similar to cytochrome P-450
Os07g0617200	3.16	3.53E-04	Ethylene response factor
Os07g0622500	2.43	4.03E-02	Similar to mutator-like transposase
Os07g0641400	3.07	2.51E-03	Calcium/calmodulin-dependent serine/threonine-protein kinase
Os08g0124700	2.28	1.05E-02	Resistance protein candidate
Os08g0246800	4.30	5.89E-04	Conserved hypothetical protein
Os08g0315200	3.21	5.38E-03	Retrotransposon gag protein family protein
Os08g0540400	3.89	3.71E-02	Similar to calcium-dependent protein kinase
Os09g0122500	6.94	2.83E-02	Unknown
Os09g0452400	3.33	1.87E-02	Peptidase A1 domain containing protein
Os10g0107100	59.88	1.35E-05	Nucleic acid-binding, OB-fold domain containing protein
Os10g0113000	2.02	6.31E-03	Chalcone reductase
Os10g0114300	11.74	5.67E-04	Similar to NADPH-dependent codeinone reductase
Os10g0200000	2.21	9.17E-04	Protein kinase
Os10g0318200	3.46	1.02E-03	Hypothetical protein
Os10g0340100	35.67	6.31E-04	Hypothetical conserved gene
Os10g0348900	2.12	7.96E-03	Conserved hypothetical protein
Os10g0419400	2.66	1.37E-03	Similar to SIPL
Os10g0463000	3.28	5.36E-04	Conserved hypothetical protein
Os10g0522500	2.39	4.02E-03	Similar to predicted protein
Os10g0525400	8.81	2.40E-02	Glutathione S-transferase
Os11g0102200	3.72	4.38E-03	Similar to non-phototrophic hypocotyl 1a
Os11g0173500	2.23	3.06E-06	Hypothetical conserved gene
Os11g0224300	181.04	3.07E-06	Integrase
Os11g0245100	6.87	1.48E-02	Similar to glutathione S-transferase 2
Os11g0282700	13.26	2.91E-04	Homeodomain-like containing protein
Os11g0491600	12.63	1.69E-04	WRKY transcription factor
Os12g0101800	4.11	9.43E-05	Non-phototrophic hypocotyl 1a
Os12g0156100	5.74	8.44E-03	Similar to NAC-domain containing protein 90 (ANAC090)

Os12g0169300	11.82	2.57E-04	Conserved hypothetical protein
Os12g0248600	3.65	4.75E-02	Hypothetical protein
Os12g0543800	12.04	7.82E-05	Conserved hypothetical protein
Os12g0547600	3.18	6.60E-03	Calmodulin binding protein-like family protein
Os12g0555000	5.13	5.28E-03	Lipase (root specific rice PR10，RSOsPR10)
Os12g0555300	2.83	5.64E-03	Pathogenesis-related protein
Os12g0555500	2.99	4.88E-04	Probenazole-inducible protein PBZ1
Os12g0571000	2.27	3.52E-03	Metallothionein-like protein type 1
B (Down-regulated 94 genes)			
Os01g0212100	0.310	7.69E-05	Similar to predicted protein
Os01g0246400	0.068	1.53E-02	Similar to low molecular mass early light-inducible protein HV90
Os01g0595900	0.462	1.94E-04	Cyclin-like F-box domain containing protein
Os01g0659900	0.428	3.71E-02	Cyclin-like F-box domain containing protein
Os01g0720400	0.495	3.11E-02	HAD-superfamily subfamily IB hydrolase
Os01g0830500	0.259	2.59E-03	2OG-Fe(II) oxygenase domain containing protein
Os01g0909500	0.436	1.73E-04	Similar to cDNA clone: J013116D08
Os01g0953500	0.446	1.47E-02	C2 calcium-dependent membrane targeting domain containing protein
Os02g0103500	0.481	4.75E-02	Similar to nodulin protein
Os02g0139500	0.093	4.04E-03	Similar to cycloartenol synthase
Os02g0145200	0.325	1.05E-03	Conserved hypothetical protein
Os02g0172800	0.210	2.13E-03	Similar to Zinc-binding protein
Os02g0202200	0.444	1.67E-02	SPX, N-terminal domain containing protein
Os02g0492900	0.083	4.34E-02	Similar to ankyrin-like protein
Os02g0628900	0.223	5.63E-03	Hypothetical conserved gene
Os02g0635600	0.385	1.42E-05	Tyrosine protein kinase domain containing protein
Os02g0709000	0.278	2.96E-03	Exonuclease domain containing protein
Os02g0807300	0.481	5.84E-03	Conserved hypothetical protein
Os02g0828200	0.426	3.12E-03	TPR-like domain containing protein

Os03g0103200	0.149	6.38E-03	Similar to physical impedance induced protein
Os03g0183000	0.458	1.36E-02	Similar to AP2 domain containing protein RAP2.6
Os03g0233000	0.191	2.62E-03	Protein of unknown function DUF607 family protein
Os03g0267500	0.451	3.33E-04	Fructose-1,6-bisphosphatase
Os03g0579800	0.431	4.31E-04	Hypothetical protein
Os03g0679800	0.299	1.38E-02	Similar to TPR domain containing protein
Os04g0115200	0.469	1.53E-02	Conserved hypothetical protein
Os04g0172100	0.471	2.67E-03	Hypothetical protein
Os04g0266400	0.491	6.26E-05	Similar to OSIGBa0139I12.2 protein
Os04g0357200	0.103	2.69E-02	Non-protein coding transcript
Os04g0462400	0.287	1.20E-02	Similar to lysine/histidine transporter
Os04g0472300	0.402	3.57E-02	Hypothetical conserved gene
Os04g0493400	0.315	4.85E-02	Similar to Chitinase
Os04g0494100	0.304	4.26E-02	Similar to Chitinase
Os04g0528400	0.327	1.32E-04	ABC transporter
Os04g0555300	0.417	7.72E-03	Major facilitator superfamily protein
Os04g0568600	0.424	3.67E-02	Similar to 6-phospho-3-hexuloisomerase
Os05g0131000	0.456	3.74E-02	Protein of unknown function DUF247
Os05g0151200	0.320	4.30E-02	TspO/MBR-related protein family protein
Os05g0155000	0.466	9.71E-03	Similar to protein MFP-b
Os05g0197900	0.413	3.83E-02	Protein of unknown function DUF247
Os05g0256100	0.309	1.51E-03	Serine/threonine protein kinase
Os05g0360400	0.347	4.75E-02	Zinc finger, RING/FYVE/PHD-type domain containing protein
Os05g0382400	0.482	3.92E-02	Conserved hypothetical protein
Os05g0418800	0.414	6.78E-03	Similar to CUC2
Os05g0563300	0.499	2.09E-03	Conserved hypothetical protein
Os05g0571700	0.423	1.50E-05	Cyclin-like F-box domain containing protein
Os06g0112100	0.386	2.64E-03	Nucleoside phosphorylase
Os06g0141200	0.262	1.27E-02	RNA-binding protein

Os06g0141300	0.336	4.93E-04	Unknown
Os06g0147000	0.498	4.26E-02	Conserved hypothetical protein
Os06g0226500	0.385	1.87E-02	Brassinosteroid upregulated1
Os06g0304600	0.487	4.12E-03	Aspartic proteinase nepenthesin-2
Os06g0317200	0.424	2.11E-02	Glycine-rich protein
Os06g0358800	0.276	2.88E-02	Ribonuclease III domain containing protein
Os06g0360300	0.317	7.04E-03	NAD(P)-binding domain containing protein
Os06g0363900	0.172	4.40E-04	Similar to Stable protein 1
Os06g0367500	0.246	3.68E-02	B-cell receptor-associated 31-like domain containing protein
Os06g0488200	0.232	4.81E-05	Myosin heavy chain
Os06g0579400	0.410	3.36E-02	Non-protein coding transcript
Os06g0713400	0.462	1.15E-03	Cyclin-like F-box domain containing protein
Os07g0100600	0.339	1.76E-03	Peptide transporter 1 (OsPTR1)
Os07g0100800	0.342	9.58E-04	Similar to amino acid permease
Os07g0106700	0.300	2.22E-02	Similar to aminotransferase-like protein
Os07g0151700	0.341	2.83E-03	Conserved hypothetical protein
Os07g0232800	0.492	1.19E-02	Similar to Zinc transporter protein ZIP1
Os07g0301000	0.210	2.13E-03	Similar to stable protein 1
Os07g0435900	0.016	4.20E-06	SET domain containing protein
Os07g0456400	0.149	3.40E-05	LUC7 related family protein
Os07g0525100	0.349	1.34E-03	Protein of unknown function DUF6 domain containing protein
Os07g0527000	0.490	1.18E-03	Similar to nodulin-like protein
Os08g0100300	0.020	9.81E-04	Non-protein coding transcript
Os08g0148600	0.441	1.93E-03	Similar to glycosyltransferase QUASIMODO1
Os08g0189600	0.374	1.82E-02	*Oryza sativa* germin-like protein 8-7
Os08g0234400	0.176	1.84E-03	Hypothetical gene
Os08g0327700	0.238	3.75E-02	Late embryogenesis abundant (LEA) group 1 family protein
Os08g0419100	0.489	4.30E-03	Conserved hypothetical protein
Os08g0507400	0.449	1.81E-02	Cytochrome P450 family protein

Os09g0339600	0.238	1.43E-03	Hypothetical conserved gene
Os09g0415300	0.143	8.14E-05	Hypothetical conserved gene
Os09g0438100	0.363	2.31E-02	Conserved hypothetical protein
Os09g0544000	0.362	2.36E-02	Transferase family protein
Os10g0159300	0.214	4.82E-03	Conserved hypothetical protein
Os10g0170600	0.319	2.29E-03	HAT family dimerization domain containing protein
Os10g0368100	0.258	7.51E-03	Similar to glutathione S-transferase GSTU35
Os10g0427300	0.398	2.08E-02	Conserved hypothetical protein
Os10g0513200	0.470	3.11E-02	Similar to aquaporin NIP3-1
Os10g0529600	0.406	3.01E-03	Conserved hypothetical protein
Os10g0530400	0.459	2.31E-02	Unknown
Os11g0236100	0.364	1.48E-02	Similar to Sucrose-phosphate synthase
Os11g0278300	0.499	3.96E-02	Hypothetical conserved gene
Os11g0428500	0.401	1.27E-04	Conserved hypothetical protein
Os12g0129700	0.430	4.71E-03	Cyclin-like F-box domain containing protein
Os12g0406000	0.140	1.69E-04	Hypothetical conserved gene
Os12g0553600	0.403	9.03E-05	Hypothetical conserved gene

Supplemental Table S2. Genes found to be significantly up-regulated (≥1.5, A) or down-regulated (≤1.5, B) in developing seeds of *pPP2*::*AtSUC2* rice plants (line 51) on the 10th day after fertilization in a microarray analysis. Data were mean from three biological replicates

A (Up-regulated 204 genes)			
Locus	**Fold change**	***P*-Value**	**Description**
Os01g0108500	75.03	2.01E-06	Conserved hypothetical protein
Os01g0139000	2.33	2.42E-02	Reticulon family protein
Os01g0168800	2.12	3.13E-02	Alpha/beta hydrolase fold-1 domain containing protein
Os01g0171000	2.13	1.30E-02	Similar to leucine-rich repeat receptor-like kinase
Os01g0214600	2.11	2.21E-02	Lipase, GDSL domain containing protein
Os01g0253500	2.15	3.26E-02	Conserved hypothetical protein
Os01g0266400	2.28	5.65E-03	Conserved hypothetical protein
Os01g0541800	3.20	1.36E-02	MtN3 and saliva related transmembrane protein family protein
Os01g0566500	5.43	3.39E-02	Similar to dioxygenase RAMOSUS1
Os01g0567200	78.12	1.05E-05	Conserved hypothetical protein
Os01g0611000	2.67	1.10E-02	Hypothetical conserved gene
Os01g0652300	2.89	2.97E-02	Lipase-like protein
Os01g0683700	2.43	3.99E-03	Protein of unknown function DUF599 family protein
Os01g0723700	2.13	3.87E-02	Transcriptional factor B3 family protein
Os01g0750300	2.17	2.35E-02	Unknown
Os01g0805600	4.54	1.51E-04	Cyclins in embryo and endosperm development, CycB1;1
Os01g0806400	2.37	4.32E-02	Protein of unknown function DUF617
Os01g0813800	2.88	2.29E-02	Glycoside hydrolase, family 1 protein
Os01g0850700	11.04	7.32E-03	Similar to laccase-7
Os01g0889900	2.92	1.34E-02	Serine/threonine protein kinase-related domain containing protein
Os01g0927000	3.39	6.90E-03	Similar to SET domain-containing protein SET118
Os01g0930400	4.87	2.13E-02	Potassium transporter 5
Os01g0946500	3.87	2.93E-02	Glucan endo-1,3-beta-glucosidase GV
Os02g0123800	4.39	3.80E-02	Unknown

Os02g0213100	2.91	8.08E-03	Conserved hypothetical protein
Os02g0216200	60.31	1.62E-05	Hypothetical protein
Os02g0232900	4.66	2.07E-02	Aquaporin NIP1-1
Os02g0234700	2.03	1.74E-02	Conserved hypothetical protein
Os02g0246900	2.32	3.32E-02	Conserved hypothetical protein
Os02g0252400	11.15	6.89E-04	Rice prolamin box binding factor
Os02g0253800	57.77	1.24E-05	Hypothetical protein
Os02g0278700	4.31	2.29E-03	Similar to kaurene synthase A
Os02g0511400	4.38	7.06E-04	Glucose/ribitol dehydrogenase family protein
Os02g0613900	3.80	5.41E-03	Similar to Adenine phosphoribosyltransferase 2
Os02g0648300	2.61	7.05E-03	DNA-binding domain containing protein
Os02g0671800	4.36	3.61E-02	Hypothetical protein
Os02g0695200	11.46	4.71E-05	Similar to P-type R2R3 Myb protein
Os02g0777400	2.29	2.38E-02	Similar to ERECTA-like kinase 1
Os03g0103300	3.26	3.03E-03	QLTG-3-1 protein
Os03g0115700	11.68	2.15E-02	Short-chain dehydrogenase/reductase SDR family protein
Os03g0115800	296.57	3.30E-04	Conserved hypothetical protein
Os03g0128000	2.88	9.97E-03	Hypothetical protein
Os03g0141100	25.43	9.32E-03	Conserved hypothetical protein
Os03g0168300	4.64	6.22E-03	Conserved hypothetical protein
Os03g0170600	2.45	1.89E-02	Similar to homeobox-leucine zipper protein HOX21
Os03g0270900	2.57	4.72E-02	Hypothetical conserved gene
Os03g0287400	3.43	9.51E-03	Similar to LOB domain protein 4
Os03g0303100	3.46	3.70E-02	Protein of unknown function DUF1645 family protein
Os03g0338700	2.90	2.81E-02	Hypothetical conserved gene
Os03g0370400	5.77	2.42E-02	Protein of unknown function DUF679 family protein
Os03g0429900	444.37	2.60E-07	Nucleic acid-binding, OB-fold domain containing protein
Os03g0582000	2.24	4.94E-02	Glutamate formiminotransferase
Os03g0629800	547.00	2.05E-07	Conserved hypothetical protein

Os03g0637900	2.01	8.59E-03	Conserved hypothetical protein
Os03g0646100	2.42	8.49E-03	Similar to plastid division protein ftsZ1 precursor
Os03g0663800	1.60	4.27E-03	Globulin1
Os03g0673000	2.28	1.50E-02	Similar to knotted1-type homeobox protein OSH10
Os03g0773700	2.74	4.83E-02	Similar to receptor-like protein kinase 2
Os03g0793800	6.09	2.19E-02	Lipid transfer protein
Os03g0861400	2.67	2.60E-02	Hypothetical conserved gene
Os04g0175600	2.56	7.64E-03	O-methyltransferase
Os04g0175900	3.28	1.14E-03	Winged helix repressor DNA-binding domain containing protein
Os04g0208500	5.17	1.58E-03	Cyclin-like F-box domain containing protein
Os04g0209300	2.61	2.96E-02	Glutathione-conjugate transporter
Os04g0219800	2.68	1.49E-02	Hypothetical protein
Os04g0223500	10.74	3.50E-04	Dimethylaniline monooxygenase
Os04g0223600	200.72	4.10E-06	Hypothetical gene
Os04g0249600	4.13	3.97E-04	senescence-associated protein DIN1
Os04g0295100	2.14	1.58E-03	Similar to predicted protein
Os04g0397900	111.49	1.50E-05	Conserved hypothetical protein
Os04g0401000	4.63	1.17E-03	Heavy metal transport
Os04g0412300	2.47	3.70E-03	Similar to H0717B12.10 protein
Os04g0422300	365.77	2.39E-06	Protein of unknown function DUF6
Os04g0422700	3.88	1.64E-02	Conserved hypothetical protein
Os04g0436900	2.15	8.04E-03	Hypothetical protein
Os04g0442300	2.71	3.93E-02	A-type response regulator 1
Os04g0447800	6.15	3.03E-03	Glutamate decarboxylase
Os04g0478000	2.12	1.91E-04	Conserved hypothetical protein
Os04g0482300	3.95	2.80E-03	BTB domain containing protein
Os04g0496300	10.11	2.13E-02	Conserved hypothetical protein
Os04g0510000	251.14	2.37E-04	Conserved hypothetical protein
Os04g0526300	6.38	4.17E-03	Sulfotransferase family protein

Os04g0581100	5.86	4.26E-02	2OG-Fe(II) oxygenase domain containing protein
Os04g0585900	3.57	2.48E-02	Protein of unknown function DUF581 family protein
Os04g0587500	2.53	4.41E-02	HAT dimerisation domain containing protein
Os04g0604000	2.34	1.73E-02	Actin filament bundling protein
Os04g0621800	2.10	8.28E-03	Conserved hypothetical protein
Os04g0677300	3.42	2.85E-03	Harpin-induced 1 domain containing protein
Os04g0678700	2.02	2.14E-04	NADPH-protochlorophyllide oxidoreductase
Os04g0689400	2.94	7.79E-03	Protein kinase
Os05g0100100	6.01	1.14E-03	Conserved hypothetical protein
Os05g0112900	2.00	2.54E-02	Pentatricopeptide repeat domain containing protein
Os05g0119700	2.11	3.20E-02	Hypothetical protein
Os05g0124700	39.15	2.40E-05	Deoxynucleoside kinase family protein
Os05g0143000	6.79	3.06E-03	Conserved hypothetical protein
Os05g0164400	3.48	2.04E-03	Harpin-induced 1 domain containing protein
Os05g0231700	2.21	1.26E-03	Tonoplast intrinsic protein (OsTIP4;1)
Os05g0263300	7.40	4.93E-03	Unknown
Os05g0270500	1300.97	7.97E-07	Predicted protein
Os05g0296200	40.03	2.39E-06	Conserved hypothetical protein
Os05g0296800	5.75	1.19E-02	Hypothetical protein
Os05g0307100	2.37	1.34E-02	Hypothetical protein
Os05g0417400	7.79	1.91E-03	Universal stress protein family protein
Os05g0424000	1.67	9.27E-04	Amino acid transporter (OsAAP7)
Os05g0429900	2.02	5.71E-03	Similar to MybHv5
Os05g0453700	3.59	4.34E-02	Similar to USP family protein
Os05g0477600	2.39	3.42E-04	Alpha-expansin (OsEXPA4)
Os05g0507000	6.25	1.56E-02	Conserved hypothetical protein
Os05g0515500	3.69	7.63E-04	Similar to O-methyltransferase ZRP4
Os05g0557100	2.50	4.41E-02	Peptidase A1 domain containing protein
Os05g0566800	2.05	1.02E-02	Cold acclimation protein COR413-TM1

Os05g0580000	2.10	5.78E-04	ADP glucose pyrophosphorylase large subunit 1 (AGPL1)
Os05g0588800	2.35	1.83E-02	Similar to Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia lipolytica
Os06g0141200	2.23	4.46E-02	RNA-binding protein
Os06g0163900	8.70	5.07E-04	NB-ARC domain containing protein
Os06g0200800	3.94	1.71E-02	Conserved hypothetical protein
Os06g0212900	2.01	1.93E-02	Heat shock protein Hsp70 family protein
Os06g0234200	2.18	2.79E-04	Rac-like GTP-binding protein
Os06g0261300	3.79	1.35E-03	Conserved hypothetical protein
Os06g0294200	2.44	1.50E-03	Conserved hypothetical protein
Os06g0306600	2.14	2.56E-02	Alpha/beta hydrolase fold-3 domain containing protein
Os06g0329900	2.20	1.52E-02	SAM dependent carboxyl methyltransferase family protein. [Os06t0329900-01]
Os06g0561000	2.57	6.02E-03	Myo-inositol oxygenase
Os06g0602400	19.19	7.51E-03	DEAD-box RNA helicase DEAD3
Os06g0697000	5.31	2.90E-02	Xyloglucan endotransglycosylase
Os06g0726400	1.57	6.39E-03	Branching enzyme I (BEI)
Os07g0110000	5.74	1.47E-04	Hypothetical protein
Os07g0115300	2.05	3.13E-02	Peroxidase 2
Os07g0132100	5.51	8.98E-03	Similar to lectin-like receptor kinase 7
Os07g0137000	3.68	2.12E-04	Myb transcription factor
Os07g0146800	8.84	2.99E-03	Hypothetical conserved gene
Os07g0147600	2.56	4.39E-05	Protein kinase
Os07g0160100	2.27	6.63E-04	YABBY protein (OsYAB1)
Os07g0241600	2.14	2.25E-02	Hypothetical conserved gene
Os07g0457200	23.57	2.74E-03	Hypothetical conserved gene
Os07g0520300	4.75	2.01E-02	Cytochrome P450 family protein
Os07g0558900	3.39	1.41E-02	Unknown
Os07g0592100	2.36	4.87E-03	Similar to Alcohol dehydrogenase-like protein
Os07g0607400	10.80	1.40E-02	Pectin lyase fold/virulence factor domain containing protein
Os07g0622400	2.53	7.63E-04	Conserved hypothetical protein

Os07g0641400	2.39	8.59E-03	Hypothetical protein
Os07g0647900	3.09	4.79E-04	DEAD-like helicase
Os08g0113700	2.21	1.59E-03	Conserved hypothetical protein
Os08g0189600	2.88	4.93E-02	*Oryza sativa* germin-like protein 8-7
Os08g0193600	2.47	3.76E-03	Hypothetical conserved gene
Os08g0193900	2.06	1.83E-02	Cyclin-like F-box domain containing protein
Os08g0213100	4.79	1.29E-02	Hypothetical conserved gene
Os08g0240000	27.20	8.21E-04	Similar to STF-1
Os08g0246800	2.13	2.22E-02	Conserved hypothetical protein
Os08g0389700	2.27	2.21E-02	Protein of unknown function DUF81 family protein
Os08g0410900	123.14	6.14E-06	Hypothetical gene
Os08g0439300	3.99	4.73E-02	Conserved hypothetical protein
Os08g0457100	2.25	3.86E-02	Conserved hypothetical protein
Os08g0495800	2.68	9.64E-04	Similar to alkaline alpha galactosidase 3
Os08g0497300	2.11	1.86E-03	alpha-tocopherol transport family protein
Os08g0499300	3.28	3.58E-03	WRKY transcription factor 30
Os08g0502400	4.47	1.27E-02	FAS1 domain domain containing protein
Os08g0527900	3.20	3.43E-02	Peptidase
Os09g0298200	1.81	2.98E-03	ADP glucose pyrophosphorylase small subunit 1 (AGPS1)
Os09g0339600	2.10	5.08E-03	Unknown
Os09g0391500	5.85	2.60E-02	Hypothetical gene
Os09g0412400	2.48	4.25E-02	Conserved hypothetical protein
Os09g0418500	2.19	4.15E-02	Similar to PnC401 homologue
Os09g0491900	8.59	4.49E-02	Unknown
Os09g0501600	2.12	3.23E-02	Similar to MYC1
Os10g0107100	163.83	6.21E-05	OB-fold domain containing protein
Os10g0111700	3.99	4.42E-03	Similar to POT family protein, expressed
Os10g0133500	3.91	7.98E-04	Transferase
Os10g0157400	2.02	1.60E-02	Serine/threonine protein kinase domain containing protein

Os10g0328100	4.01	1.02E-04	Expressed protein
Os10g0429400	2.40	2.93E-04	Similar to BTB/POZ domain containing protein, expressed
Os10g0432200	2.55	3.34E-02	Similar to 68 kDa protein HP68
Os10g0450900	2.18	1.43E-03	Glycine-rich cell wall structural protein
Os10g0479500	2.02	7.89E-03	Lysine decarboxylase-like protein
Os10g0522500	2.58	3.70E-03	Similar to predicted protein
Os10g0555900	7.35	1.38E-03	Beta-expansin-3 (OsEXPB3)
Os10g0567900	14.60	5.73E-03	HAT dimerisation domain containing protein
Os11g0125900	2.24	4.06E-02	ATP-diphosphohydrolase
Os11g0196400	6.86	2.96E-04	Non-protein coding transcript
Os11g0208000	3.59	3.14E-04	Cyclin-like F-box domain containing protein
Os11g0224300	322.40	1.10E-06	Integrase, catalytic core domain containing protein
Os11g0282700	14.60	9.47E-04	Homeodomain-like containing protein
Os11g0286800	3.07	5.60E-04	Cycloartenol synthase
Os11g0289700	4.70	3.80E-03	Unknown
Os11g0422000	77.02	1.31E-06	Conserved hypothetical protein
Os11g0513000	3.62	9.54E-03	Hypothetical conserved gene
Os11g0516800	2.01	5.23E-03	Conserved hypothetical protein
Os11g0517400	2.46	1.91E-02	Hypothetical protein
Os11g0518600	2.82	2.02E-02	Hypothetical protein
Os11g0576700	3.55	1.17E-02	ABC transporter
Os11g0593100	3.98	1.40E-02	Protein of unknown function DUF295 family protein
Os12g0113600	50.62	4.85E-04	Hypothetical protein
Os12g0117900	2.42	6.60E-03	Hypothetical conserved gene
Os12g0123500	2.03	2.78E-02	ATP-diphosphatase
Os12g0228500	3.43	4.54E-02	Conserved hypothetical protein
Os12g0236800	22.31	2.79E-04	Hypothetical conserved gene
Os12g0286200	3.26	4.21E-03	Conserved hypothetical protein
Os12g0454600	2.03	2.48E-02	Cupredoxin domain containing protein

Os12g0454800	3.11	2.21E-02	CHASE domain receptor-like serine/threonine kinase
Os12g0508400	2.81	1.46E-02	Hypothetical protein
Os12g0514100	2.57	4.98E-03	Ribosome associated membrane RAMP4 family protein
Os12g0539800	39.45	1.95E-04	Unknown
Os12g0554100	3.31	7.34E-03	Protein of unknown function DUF231
B (Down-regulated 129 genes)			
Os01g0101800	0.357	2.12E-03	Conserved hypothetical protein
Os01g0146200	0.456	1.14E-03	Conserved hypothetical protein
Os01g0162300	0.411	2.02E-02	Leucine-rich repeat, plant specific containing protein
Os01g0175600	0.356	1.50E-02	Bicarbonate transporter
Os01g0253900	0.390	2.15E-03	Lipase
Os01g0275900	0.478	2.83E-02	Hypothetical conserved gene
Os01g0339500	0.215	3.31E-03	Conserved hypothetical protein
Os01g0391100	0.349	1.28E-02	Hypothetical gene
Os01g0511800	0.414	4.49E-02	Conserved hypothetical protein
Os01g0512400	0.460	1.91E-03	Conserved hypothetical protein
Os01g0516400	0.347	3.90E-02	Stress-responsive protein
Os01g0603200	0.487	1.23E-02	Conserved hypothetical protein
Os01g0632000	0.436	3.35E-02	Conserved hypothetical protein
Os01g0733100	0.341	4.05E-02	Hypothetical conserved gene
Os01g0872900	0.398	2.56E-03	Protein of unknown function DUF635 family protein
Os01g0873000	0.366	4.19E-03	Hypothetical conserved gene
Os01g0909500	0.457	4.79E-03	Unknown
Os01g0974600	0.463	7.08E-03	Similar to RNA-binding glycine rich protein (RGP-2)
Os02g0129000	0.138	3.57E-03	Hypothetical conserved gene
Os02g0139500	0.240	9.93E-04	Similar to cycloartenol synthase
Os02g0202200	0.328	7.29E-04	Rice SPX domain gene (OsSPX1)
Os02g0203200	0.460	1.88E-02	Conserved hypothetical protein

Os02g0261900	0.496	2.30E-02	Unknown
Os02g0597300	0.364	1.37E-02	Hypothetical protein
Os02g0635600	0.452	1.80E-03	Tyrosine protein kinase domain containing protein
Os02g0669700	0.455	2.34E-02	Nucleotide-binding, alpha-beta plait domain containing protein
Os02g0670700	0.357	3.46E-02	Hypothetical conserved gene
Os02g0694600	0.328	1.46E-03	Hypothetical conserved gene
Os02g0770800	0.222	2.18E-02	Nitrate reductase
Os02g0806900	0.260	8.16E-04	Pyridoxal phosphate-dependent transferase
Os02g0807100	0.219	1.04E-02	Hypothetical gene
Os02g0807300	0.260	1.47E-03	Conserved hypothetical protein
Os03g0111600	0.422	2.19E-02	Protein of unknown function DUF1618 domain containing protein
Os03g0150800	0.418	9.37E-05	Phosphate transporter (OsPht1;2; OsPT2)
Os03g0197200	0.390	4.50E-02	Sorbitol transporter
Os03g0306700	0.248	2.70E-03	bZIP transcription factor
Os03g0365200	0.473	2.05E-02	Conserved hypothetical protein
Os03g0579800	0.295	2.74E-03	Hypothetical protein
Os03g0582900	0.124	2.23E-02	Non-protein coding transcript
Os03g0598500	0.427	7.97E-03	Conserved hypothetical protein
Os03g0727000	0.448	4.57E-02	Similar to homeobox protein OSH1
Os04g0116200	0.045	2.24E-02	Protein of unknown function DUF827
Os04g0118800	0.450	5.80E-03	NB-ARC domain containing protein
Os04g0168300	0.240	2.18E-02	Hypothetical protein
Os04g0186400	0.408	9.38E-03	Phosphate transporter (OsPht1;4; OsPT4)
Os04g0208200	0.197	3.58E-02	Cysteine proteinase
Os04g0286500	0.476	7.03E-03	Hypothetical conserved gene
Os04g0337300	0.499	8.43E-04	Hypothetical protein
Os04g0377400	0.427	4.60E-03	Conserved hypothetical protein
Os04g0394100	0.405	6.27E-03	Glycerophosphoryl diester phosphodisterase
Os04g0398600	0.369	3.56E-02	Similar to pectin-glucuronyltransferase

Os04g0513700	0.361	4.12E-02	Hypothetical conserved gene
Os04g0528400	0.375	4.92E-04	ABC transporter
Os04g0574800	0.390	2.13E-02	Similar to dihydrodipicolinate synthase 1
Os05g0155000	0.420	8.27E-04	Similar to protein MFP-b
Os05g0163700	0.484	2.62E-02	Acyl-coenzyme A oxidase 4
Os05g0241100	0.332	3.13E-04	Leucyl-tRNA synthetase
Os05g0268500	0.332	4.30E-02	Similar to serine carboxypeptidase II chains A and B
Os05g0269500	0.413	6.43E-03	Generative cell specific-1, HAP2-GCS1 domain containing protein
Os05g0384600	0.492	8.59E-03	Similar to ATPase
Os05g0436000	0.425	2.94E-02	Unknown
Os05g0521300	0.435	4.80E-02	Similar to histidine-containing phosphotransfer protein 4
Os05g0531200	0.425	8.86E-03	Pollen Ole e 1 allergen and extensin domain containing protein
Os05g0571300	0.326	3.61E-02	Hypothetical protein
Os05g0571700	0.362	2.52E-04	Cyclin-like F-box domain containing protein
Os06g0182100	0.414	3.89E-04	Hypothetical conserved gene
Os06g0206700	0.323	7.10E-03	Similar to kinesin-related protein
Os06g0273400	0.433	1.52E-02	Conserved hypothetical protein
Os06g0363900	0.047	5.04E-05	Similar to stable protein 1
Os06g0367500	0.159	3.50E-02	B-cell receptor-associated 31-like domain containing protein
Os06g0472000	0.483	1.39E-02	Methionine sulphoxide reductase B domain containing protein
Os06g0488200	0.461	1.27E-02	Similar to myosin heavy chain
Os06g0553200	0.350	4.67E-02	Conserved hypothetical protein
Os06g0579200	0.029	1.12E-02	Unknown
Os06g0597900	0.481	2.55E-02	SOUL haem-binding protein domain containing protein
Os06g0678700	0.484	4.09E-02	Hypothetical conserved gene
Os06g0711200	0.470	6.12E-03	Conserved hypothetical protein
Os07g0100600	0.334	1.77E-03	Peptide transporter
Os07g0168800	0.357	1.34E-02	Zinc finger, AN1-type domain containing protein
Os07g0200500	0.467	6.76E-03	Similar to OSIGBa0126B18.3 protein

Os07g0215500	0.434	3.81E-02	Allergenic protein
Os07g0291400	0.314	4.42E-02	Similar to acrosin precursor
Os07g0301000	0.045	4.15E-05	Similar to stable protein 1
Os07g0414200	0.311	3.57E-02	Methyltransferase, METTL2
Os07g0435900	0.029	2.48E-05	SET domain containing protein
Os07g0456400	0.060	1.67E-05	LUC7 related family protein
Os07g0513200	0.468	1.57E-02	Pentatricopeptide repeat domain containing protein
Os07g0538700	0.393	3.80E-02	Hypothetical conserved gene
Os07g0539300	0.421	3.29E-03	Glycoside hydrolase, family 17 protein
Os07g0565800	0.494	8.13E-03	Conserved hypothetical protein
Os07g0658300	0.451	3.24E-03	Pleckstrin homology-type domain containing protein
Os08g0100300	0.012	2.84E-04	Non-protein coding transcript
Os08g0127800	0.492	1.31E-02	Conserved hypothetical protein
Os08g0141800	0.385	4.14E-02	Hypothetical conserved gene
Os08g0244500	0.400	7.44E-03	Glycoside hydrolase, family 17 protein
Os08g0290700	0.255	3.31E-02	Winged helix repressor DNA-binding domain containing protein
Os08g0367300	0.192	2.94E-04	Hypothetical conserved gene
Os08g0440300	0.483	2.27E-02	Ribonuclease CAF1 family protein
Os08g0528200	0.491	3.07E-02	Conserved hypothetical protein
Os08g0532600	0.498	4.79E-03	Similar to peroxidase
Os08g0561000	0.469	7.03E-03	Homeodomain-like containing protein
Os09g0129600	0.242	4.57E-02	Recombinase, conserved site domain containing protein
Os09g0269900	0.424	3.87E-02	Conserved hypothetical protein
Os09g0286800	0.180	3.79E-02	Unknown
Os09g0423800	0.450	1.05E-02	Similar to AP2-1 protein
Os10g0128400	0.263	6.09E-03	Conserved hypothetical protein
Os10g0149200	0.434	3.91E-02	Protein of unknown function DUF1210 family protein
Os10g0170600	0.160	2.13E-03	HAT family dimerisation domain containing protein
Os10g0343500	0.094	1.55E-04	Hypothetical conserved gene

Os10g0450400	0.475	2.42E-03	Protein of unknown function DUF594 family protein
Os10g0515100	0.389	1.01E-02	Conserved hypothetical protein
Os10g0529600	0.413	1.51E-02	Conserved hypothetical protein
Os11g0102900	0.393	8.26E-03	Unknown
Os11g0117200	0.356	4.73E-02	Hypothetical conserved gene
Os11g0294400	0.453	1.45E-02	WW/Rsp5/WWP domain containing protein
Os11g0428500	0.370	6.48E-04	Conserved hypothetical protein
Os11g0461000	0.380	3.23E-02	Unknown
Os11g0470200	0.393	4.22E-02	Protein kinase, expressed
Os11g0547300	0.211	3.16E-02	Hypothetical conserved gene
Os11g0625000	0.275	1.14E-02	Expressed protein
Os11g0674300	0.299	2.33E-02	Hypothetical conserved gene
Os12g0129700	0.221	2.08E-02	Cyclin-like F-box domain containing protein
Os12g0152200	0.493	2.97E-03	Cyclin-like F-box domain containing protein
Os12g0199000	0.182	5.10E-03	Hypothetical conserved gene
Os12g0244800	0.445	2.03E-02	Hypothetical protein
Os12g0472500	0.411	6.67E-03	Glutelin family protein
Os12g0614900	0.396	2.48E-02	Hypothetical gene
Os12g0634200	0.305	4.42E-02	Hypothetical conserved gene

Supplemental Table S3. Statistical analyses of microarray and qRT-PCR data for genes in flag leaves of *pPP2*::*AtSUC2* rice plants (line 51) on the 10th day after fertilization

Gene	Accession Number	Microarray		qRT-PCR	
		Expression	p-Value	Expression	p-Value
Carbohydrate transport and metabolism					
Fructose-2, 6-bisphosphatase	Os05g0164400	5.24**	4.40E-03	7.89**	6.35E-03
Malic acid transport protein	Os01g0385400	6.48**	3.73E-02	16.49**	1.06E-03
Beta-amylase	Os07g0543300	2.20**	7.41E-03	5.60**	7.09E-04
Fructose-1,6-bisphosphatase	Os03g0267500	0.45**	3.33E-02	0.23**	4.90E-03
ADP glucose pyrophosphorylase large subunit 2 (*AGPL2*)	Os01g0633100	1.85**	5.05E-02	2.15**	4.57E-03
Granule-bound starch synthase I (*GBSSI*)	Os06g0133000	3.06**	1.78E-02	1.73**	3.34E-03
Branching enzyme I (*BEI*)	Os06g0726400	1.52**	5.56E-03	1.61**	7.56E-04
UDP-glucose pyrophosphorylase 2 (*UGP2*)	Os02g0117700	1.96**	2.42E-02	2.55**	3.66E-03
Cytosolic fructose-1,6-bisphosphatase 1 (*cyFBP1*)	Os01g0866400	1.59**	2.49E-02	1.67**	4.73E-04
Sucrose transporter 1 (*OsSUT1*)	Os03g0170900	3.32**	9.43E-03	2.50**	3.57E-05
Amino acid transport and metabolism					
Glutathione S-transferase	Os10g0525400	8.80**	2.40-02	32.65**	8.67E-05
Oligopeptidase A (*OsRR3*)	Os02g0830200	2.97**	5.80E-02	16.30**	1.24E-04
Asparagine synthetase	Os06g0265100	465.61**	1.10E-07	123.90**	4.53E-04
Aspartic proteinase nepenthesin-2	Os06g0304600	0.49**	4.11E-02	0.35**	9.27E-05
Amino acid transporter-like 5 (*OsATL5*)	Os06g0633800	1.53**	2.33E-02	2.71**	5.53E-03
Peptide transporter 1 (*OsPTR1*)	Os07g0100600	0.33**	1.76E-03	0.25**	3.23E-04
Nitrate transporter 2.3a (*OsNRT2.3a*)	Os01g0704100	1.63**	3.80E-02	1.73**	3.45E-03
Ammonium transporter 1.2 (*OsAMT1.2*)	Os02g0620500	1.67**	2.80E-01	1.82**	2.30E-02

Lipid transport and metabolism					
Lipase (*OsPR10*)	Os12g0555000	5.13**	5.28E-03	10.77**	6.54E-03
O-methyltransferase	Os05g0515500	5.71**	6.64E-04	20.34**	5.33E-05
Inorganic transport and metabolism					
Major facilitator superfamily protein	Os04g0555300	0.43**	7.72E-03	0.30**	4.56E-04
ABC transporter	Os04g0528400	0.33**	1.32E-04	0.47**	2.35E-03
Transcription					
A-type response regulator gene (*OsRR3*)	Os02g0830200	2.97**	5.80E-02	3.40**	2.18E-03
Rice prolamin box binding factor	Os02g0252400	8.42**	7.51E-03	7.89**	1.96E-04
WRKY transcription factor	Os11g0491600	12.63**	1.69E-04	15.70**	3.88E-04
Transcriptional factor B3 family protein	Os01g0723700	2.21**	7.34E-04	3.20**	4.35E-03
Transcription elongation factor S-II	Os06g0595900	2.28**	2.94E-03	4.08**	8.06E-04
WRKY transcription factor 19	Os05g0571200	4.20**	1.29E-02	3.80**	1.16E-03
Basic helix-loop-helix dimerization region bHLH domain containing protein	Os04g0599300	3.42**	4.77E-02	13.50**	1.32E-03
Energy production and conversion					
Photosystem II oxygen evolving complex protein PsbQ	Os02g0631200	1.57**	1.85E-02	5.90**	3.20E-04
Similar to Low molecular mass early light-inducible protein HV90	Os01g0246400	0.06**	1.53E-02	0.43**	6.45E-03
Signal transduction mechanisms					
Brassinosteroid up-regulated 1 (*BU1*)	Os06g0226500	0.39**	1.87E-01	0.45**	3.45E-03

Auxin-responsive protein (*IAA12*)	Os02g0805300	1.57**	0.028131	4.70**	2.10E-03
Auxin response factor 14	Os05g0515500	5.72**	6.64E-04	14.32**	1.23E-04
Ethylene response factor	Os07g0617200	3.16**	3.53E-04	3.90**	4.50E-04
A-type response regulator 3, cytokinin signalling	Os02g0830200	2.97**	5.8E-03	6.45**	3.22E-04
Calmodulin binding protein-like family protein	Os12g0547600	3.18**	6.60E-03	10.34	3.45E-04
Defense mechanisms					
Small heat shock protein	Os05g0296800	10.47**	0.001661	45.67**	2.34E-03
Universal stress protein family protein	Os05g0417400	9.31**	6.16E-05	17.32**	6.45E-06
Calcium/calmodulin-dependent serine/threonine-protein kinase	Os07g0641400	3.07**	9.50E-02	6.02**	3.23E-04
Calcium-dependent protein kinase	Os08g0540400	3.89**	3.71E-02	6.89**	2.12E-03
Universal stress protein	Os05g0417400	9.30**	6.16E-05	19.47**	7.17E-06
Heat shock protein DnaJ	Os01g0606900	2.05**	4.28E-02	5.28**	3.45E-03
Resistance protein candidate	Os08g0124700	2.28**	1.05E-02	6.23**	2.34E-04
Pathogenesis-related protein	Os12g0555300	2.83**	5.64E-03	4.23**	3.98E-04
Cell wall/membrane/envelope biogenesis					
Expansin-B1 (*OsEXPB1*)	Os03g0106500	5.02**	2.50E-04	13.56**	3.45E-04
Secondary metabolites biosynthesis, transport, and catabolism					
Cis-zeatin O-glucosyltransferase 1	Os04g0565200	2.47**	3.69E-02	4.36**	6.45E-04
Chalcone reductase	Os10g0113000	2.02**	6.30E-03	4.23**	5.43E-04
Chitinase	Os01g0687400	2.28**	1.20E-02	7.39**	3.45E-04
Cytochrome P450	Os01g0602200	2.06**	1.84E-02	9.34**	2.39E-03
Cytochrome b5	Os05g0108900	2.25**	1.60E-01	3.38**	1.29E-03

C4-dicarboxylate transporter/malic acid transport protein	Os01g0385400	6.47**	3.73E-03	13.32**	4.56E-04
Nucleotide transport and metabolism					
Deoxynucleoside kinase	Os05g0124700	65.42**	4.49E-04	134.45**	5.89E-05
NADPH-dependent codeinone reductase	Os10g0114300	11.73**	5.67E-04	23.69**	7.45E-04
Nucleoside phosphorylase	Os06g0112100	0.39**	2.64E-03	0.35**	3.45E-03
RNA-binding protein	Os06g0141200	0.26**	1.27E-02	0.12**	3.20E-04
General function prediction only					
Similar to stable protein 1	Os06g0363900	0.17**	4.40E-04	0.24**	1.22E-03
Conserved hypothetical protein	Os04g0510000	755.71**	4.80E-07	568.98**	5.76E-07
Probenazole-inducible protein	Os12g0555000	5.13**	5.28E-03	7.32**	3.08E-05
Myosin heavy chain	Os06g0488200	0.23**	4.81E-05	0.67**	5.76E-04
Pollen-specific protein	Os05g0196200	2.26**	1.99E-02	3.49**	2.30E-04
Nonphototrophic hypocotyl 1a	Os12g0101800	4.10**	9.43E-05	9.87**	9.78E-06
Similar to SIPL	Os10g0419400	2.66**	1.37E-03	6.32**	3.49E-05
Integrase	Os11g0224300	181.04**	3.07E-06	172.12**	3.45E-07
Alpha/beta hydrolase	Os02g0207900	3.80**	4.39E-02	5.87**	7.83E-04
Serine/threonine protein kinase	Os05g0256100	0.32**	1.51E-03	0.25**	2.45E-06
Glycine-rich protein	Os06g0317200	0.42**	2.10E-02	0.34**	7.56E-04
Late embryogenesis abundant (LEA) group 1 family protein	Os08g0327700	0.24**	3.75E-02	0.25**	3.87E-04
Haem peroxidase	Os06g0521400	2.06**	4.54E-02	4.37**	3.98E-05
Cell cycle control, cell division, and chromosome partitioning					
Cyclin-like F-box domain containing protein	Os06g0713400	0.41**	1.14E-02	0.33**	1.23E-04

Cyclin-like F-box domain containing protein	Os01g0595900	0.47**	1.93E-02	0.23**	3.98E-03

Supplemental Table S4. Statistical analyses of microarray and qRT-PCR data for genes in developing seeds of *pPP2*::*AtSUC2* rice plants (line 51) on the 10th day after fertilization

Gene	Accession Number	Microarray		qRT-PCR	
		Expression	p-Value	Expression	p-Value
Carbohydrate transport and metabolism					
Ribosome associated membrane RAMP4 family protein	Os12g0514100	2.57**	4.98E-01	3.20**	5.72E-03
Glutathione-conjugate transporter	Os04g0209300	2.61**	2.96E-02	2.56**	3.65E-03
Tonoplast intrinsic protein (*OsTIP4;1*)	Os05g0231700	2.21**	1.26E-01	2.45**	2.13E-02
Sorbitol transporter	Os03g0197200	0.39**	4.50E-02	0.25**	5.33E-03
Branching enzyme I (*BEI*)	Os06g0726400	1.57**	6.39E-02	1.92**	3.56E-02
ADP glucose pyrophosphorylase large subunit 1 (*AGPL1*)	Os05g0580000	2.09**	5.78E-02	2.57**	3.45E-04
ADP glucose pyrophosphorylase small subunit 1 (*AGPS1*)	Os09g0298200	1.81**	2.98E-02	1.93**	1.23E-04
Amino acid transport and metabolism					
Pleckstrin homology-type domain containing protein	Os07g0658300	0.33**	4.30E-02	0.25**	2.32-03
Nitrate reductase [NAD(P)H] (EC 1.7.1.2)	Os02g0770800	0.22**	2.18E-02	0.36**	3.12E-03
Peptidase (Ubiquitin carboxyl-terminal hydrolase)	Os08g0527900	3.20**	3.43E-02	3.00**	4.58E-03
Lysine decarboxylase-like protein	Os10g0479500	2.02**	7.89E-03	4.67**	3.20E-03
Glutamate decarboxylase	Os04g0447800	6.15**	3.03E-03	10.45**	4.50E-04
Glutamate formiminotransferase	Os03g0582000	2.24**	4.94E-02	3.21**	5.65E-04
Amino acid transporter (*OsAAP7*)	Os05g0424000	1.66**	9.27E-02	1.99**	3.66E-03
Globulin1	Os03g0663800	1.60**	4.27E-02	1.92**	5.76E-03
Lipid transport and metabolism					
Lipase	Os01g0253900	0.39**	2.15E-03	0.22**	4.50E-04

Lipase-like protein	Os01g0652300	2.89**	2.97E-02	5.67**	3.22E-04
Lipid transfer protein	Os03g0793800	6.09**	2.19E-02	8.98**	3.45E-04
alpha-tocopherol transport family protein	Os08g0497300	2.11**	1.86E-02	5.33**	9.53E-04
Acyl-coenzyme A oxidase	Os05g0163700	0.49**	2.62E-02	0.33**	1.23E-03
Inorganic transport and metabolism					
Potassium transporter (OsHAK5)	Os01g0930400	4.87**	2.13E-02	5.66**	3.40E-03
Phosphate transporter (*OsPht1;2; OsPT2*)	Os03g0150800	0.42**	9.37E-05	0.33**	2.38E-04
Phosphate transporter (*OsPht1;4; OsPT4*)	Os04g0186400	0.41**	9.38E-03	0.54**	3.23E-03
ABC transporter	Os11g0576700	3.55**	1.17E-02	4.50**	2.39E-03
Heavy metal transporter (*Pyricularia oryzae* resistance-21, *pi21*)	Os04g0401000	4.63**	1.17E-02	3.78**	9.25E-04
ABC transporter	Os04g0528400	0.38**	4.92E-04	0.45**	2.23E-05
Bicarbonate transporter	Os01g0175600	0.36**	1.50E-02	0.56**	8.67E-04
Secondary metabolites biosynthesis, transport, and catabolism					
O-methyltransferase	Os04g0175600	2.56**	7.64E-03	4.34**	2.56-03
Protochlorophyllide reductase	Os04g0678700	2.02**	2.14E-02	5.39**	9.12E-03
Squalene cyclase domain containing protein	Os11g0286800	2.10**	4.40E-03	4.32**	4.88E-03
Cytochrome P450	Os07g0520300	4.75**	2.01E-02	8.43**	2.30E-03
Xyloglucan endotransglycosylase	Os06g0697000	5.31**	2.90E-02	8.90**	4.98E-04
Cycloartenol synthase	Os11g0286800	3.07**	5.60E-04	6.56**	5.65E-04
Glycoside hydrolase	Os08g0244500	0.40**	7.44E-03	0.33**	8.66E-03
Kaurene synthase A	Os02g0278700	4.31**	2.29E-02	4.89**	5.45E-03
Sulfotransferase	Os04g0526300	6.38**	4.17E-03	9.76**	7.12E-03
Dimethylaniline monooxygenase	Os04g0223500	10.74**	3.50E-04	15.87**	3.12E-03

NADPH: protochlorophyllide oxidoreductase A (*OsPORA*)	Os04g0678700	2.02**	2.14E-01	5.96**	5.67E-03
Cell cycle control, cell division, and chromosome partitioning					
Cyclin-D5-1 (*CYCD5.1*)	Os03g0617500	2.38**	2.22E-01	4.72**	2.30E-03
Cyclins in embryo and endosperm development (*CycB1;1*)	Os01g0805600	4.54**	1.50E-01	10.23**	3.40E-04
Cyclin-like F-box domain containing protein	Os08g0193900	2.06**	1.82E-02	1.89**	1.02E-03
Cyclin-like F-box domain containing protein	Os04g0208500	5.17**	1.58E-02	7.23**	2.30E-04
Cyclin-like F-box domain containing protein	Os12g0129700	0.22**	2.08E-02	0.23**	3.45E-03
Transcription					
A-type response regulator 1 (*OsRR1*)	Os04g0442300	2.71**	3.93E-01	4.50**	4.21E-03
YABBY protein (*OsYAB1*)	Os07g0160100	2.27**	6.63E-04	3.77**	2.30E-03
Rice prolamin box binding factor (*RPBF*)	Os02g0252400	11.15**	6.89E-02	20.89**	4.20E-04
Transcriptional factor B3 family protein	Os01g0723700	2.13**	3.87E-02	3.31**	3.25E-04
WRKY transcription factor 30	Os08g0499300	3.28**	3.58E-03	5.34**	3.22E-03
bZIP transcription factor	Os03g0306700	0.25**	2.70E-02	0.45**	2.30E-03
Myb transcription factor	Os07g0137000	3.68**	2.12E-02	4.24**	4.23E-03
Defense mechanisms					
Senescence-associated protein DIN1	Os04g0249600	4.13**	3.97E-04	7.20**	6.32-03
Peroxidase 2	Os07g0115300	2.05**	3.13E-02	4.32**	2.13E-03
Heat shock protein Hsp70 family protein	Os06g0212900	2.01**	1.93E-02	2.08**	4.78E-03
Cold acclimation protein COR413-TM1	Os05g0566800	2.05**	1.02E-02	4.76**	3.67E-03
Stress-responsive protein	Os01g0516400	0.35**	3.9E-02	0.32**	9.50E-04
Universal stress protein	Os05g0417400	7.79**	1.91E-02	9.87**	2.65E-04

Nucleotide transport and metabolism					
Leucyl-tRNA synthetase	Os05g0241100	0.33**	3.13E-04	0.33**	7.56E-04
ATP-diphosphohydrolase	Os11g0125900	2.24**	4.06E-02	3.45**	3.66E-03
Deoxynucleoside kinase family protein	Os05g0124700	39.15**	2.40E-05	78.03**	4.73E-04
ATP-diphosphatase	Os12g0123500	2.03**	2.78E-02	4.32**	3.57E-05
Adenine phosphoribosyltransferase	Os02g0613900	3.80**	5.41E-03	4.56**	3.20E-04
Cell wall/membrane/envelope biogenesis					
Glycine-rich cell wall structural protein	Os10g0450900	2.18**	1.43E-02	3.78**	6.45E-03
Beta-expansin-3 (*OsEXPB3*)	Os10g0555900	8.94**	4.13E-02	16.09**	9.53E-04
Alpha-expansin (*OsEXPA4*)	Os05g0477600	2.39**	3.42E-02	4.50**	8.67E-04
Actin filament bundling protein	Os04g0604000	2.34**	1.72E-02	2.20**	3.45E-03
General function prediction only					
Laccase-7	Os01g0850700	11.03**	7,.32E-03	16.78**	7.56E-04
Protein kinase	Os11g0470200	0.4**	4.22E-02	0.43**	3.66E-03
Protein kinase	Os07g0147600	2.56**	4.39E-05	3.45**	4.73E-04
BTB domain containing protein	Os04g0482300	3.95**	2.80E-03	9.76**	3.57E-05
Protein kinase	Os04g0689400	2.94**	7.80E-03	4.09**	9.56E-04
Major QTL controlling low-temperature germinability in rice (*qLTG3-1*)	Os03g0103300	3.26**	3.03E-01	6.65**	4.66E-03
Similar to USP family protein	Os05g0453700	3.59**	4.34E-02	7.88**	3.20E-04
Rac-like GTP-binding protein	Os06g0234200	2.18**	2.79E-04	3.45**	6.45E-03
Hypothetical protein	Os12g0113600	50.61**	4.85E-04	78.56**	4.53E-04
Reticulon family protein	Os01g0139000	2.33**	2.42E-02	2.09**	3.45E-03

Hypothetical protein	Os05g0296800	5.74**	1.19E-02	9.84**	2.10E-03
Protein of unknown function DUF6	Os04g0422300	365.77**	2.39E-06	200.78**	1.23E-04
NB-ARC domain containing protein	Os06g0163900	8.70**	5.07E-04	7.89**	4.50E-04
DNA-binding domain containing protein	Os02g0648300	2.61**	7.05E-03	4.98**	3.22E-04
FAS1 domain containing protein	Os08g0502400	4.47**	1.27E-02	7.76**	3.45E-04
Replication, recombination, and repair					
RNA-binding protein	Os06g0141200	2.23**	4.46E-02	3.45**	9.27E-05
Homeobox-leucine zipper protein	Os03g0170600	2.45**	1.89E-02	6.76**	5.53E-03
DEAD-box RNA helicase DEAD3	Os06g0602400	19.19**	7.51E-03	45.37**	3.23E-04
DEAD-like helicase	Os07g0647900	3.09**	4.79E-04	6.37**	3.45E-03
Signal transduction mechanisms					
A-type response regulator 1, cytokinin signalling	Os04g0442300	2.71**	3.92E-02	4.34**	2.30E-02
Rice SPX domain gene (*OsSPX1*)	Os02g0202200	0.33**	7.29E-04	0.23**	6.54E-03
Energy production and conversion					
Glycoside hydrolase	Os01g0813800	2.88**	2.29E-02	4.55**	5.33E-05
Glucose/ribitol dehydrogenase	Os02g0511400	4.38**	7.06E-04	5.67**	6.35E-03
Alcohol dehydrogenase-like protein	Os07g0592100	2.36**	4.87E-03	4.66**	1.06E-03
Glucose-1-phosphate adenylyltransferase	Os09g0298200	2.02**	1.75E-02	1.99**	7.09E-04
Glucan endo-1,3-beta-glucosidase GV	Os01g0946500	3.87**	2.93E-02	3.98**	4.90E-03
Transferase	Os10g0133500	3.91**	7.98E-04	6..54**	4.57E-03
Myo-inositol oxygenase	Os06g0561000	2.57**	6.02E-03	5.43**	3.34E-03

Supplemental Table S5. Primer sequences used for PCR and quantitative real-time RT-PCR

Gene	Accession Number	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
Genes used to create transgenic plants			
AtSUC2-vector	At1G22710	TGCCATGGATATGGTCAGCCATCCA	CGGGTAACCCTGCTAAAATTCAATG
AtSUC2-RT-PCR	At1G22710	GCGAGCCATA GCGATATTCG	GTAAGATCCCGCAGCGTAAC
Actin 1	Os03g0718100	CCCTCCTGAAAGGAAGTACAGTGT	GTCCGAAGAATTAGAAGCATTTCC
Genes involved in starch biosynthesis			
BEI	Os06g0726400	GGCATTGCACTCCAAAAGAT	GCTCCAGTTGTTGCCTTCTC
BEIIa	Os02g0528200	GCCAATGCCAGGAAGATGA	GCGCAACATAGGATGGGTTT
BEIIb	Os02g0528200	ATGCTAGAGTTTGACCGC	AGTGTGATGGATCCTGCC
APGL1	Os05g0580000	CATCAAGGACGGGAAGGTCA	ACTTCACTCGGGGCAGCTTA
APGL2	Os01g0633100	CTGAGGAAGAGGTGCTTTGG	TCTTTCGGGAGGATTGTGTC
APGL3	Os03g0735000	GACCATTTGCGGCAGGAATA	TGGAACAACCAATACCCCAGA
AGPL4	Os07g0243200	TCCCTTCTGGTTTGTTGCATTT	CCAAAACGTTCTTGCCATGC
AGPS1	Os09g0298200	AGAATGCTCGTATTGGAGAAAATG	GGCAGCATGGAATAAACCAC
AGPS2a	Os08g0345800	AGTAGTGGGACTCCGGTCCT	ATGCCACCTTTTTCACCAAG
AGPS2b	Os08g0345800	AACAATCGAAGCGCGAGAAA	GCCTGTAGTTGGCACCCAGA
SSI	Os06g0160700	TCATGGATGTGAAGGAGCAA	TGGCAGTGAACCACAAACAT
SSIIa	Os06g0229800	GATCGACCAGGATGACGATT	GGGTAAAGCACCTGCAACAT
SSIIb	Os02g0744700	CGGAACTACAAGGAGAGCTGGA	GTGCCGCCGTCTCAGCAG
SSIIc	Os10g0437600	CGTGGCCCATTAGATGACTT	CAGTAAGCAAACGGTCAGCA
SSIIIa	Os08g0191500	GCCTGCCCTGGACTACATTG	GCAAACATATGTACACGGTTCTGG
SSIIIb	Os04g0624600	ATTCCGCTCGCAAGAACTGA	CAACCGCAGGATAACGGAAA
SSIVa	Os01g0720600	GGGAGCGGCTCAAACATAAA	CCGTGCACTGACTGCAAAAT
SSIVb	Os05g0533600	GAGCTGCTCCTGCTCAAGAT	ACACAATTGCACCCTTGACA
GBSSI	Os06g0133000	TCCGAGAGGTTCAGGTCATC	TCCGAGAGGTTCAGGTCATC

GBSSII	Os07g0412100	AAACGGGCTCTGAAGCAGTA	CTCCTCCCACTTCTTTGCAG
ISA2	Os05g0395300	TAGAGGTCCTCTTGGAGG	AATCAGCTTCTGAGTCACCG
ISA3	Os09g0468700	ACAGCTTGAGACACTGGGTTGAG	GCATCAAGAGGACAACCATCTG
Susy1	Os06g0194900	AATGGTATCCTCCGCAAGTG	GGCTTGCATTTCCCTCATAA
Susy2	Os03g0401300	GCTGAAGGACAGGAACAAGC	CACCACAGACAACCACAAGG
Susy3	Os07g0616800	CATGTACCCCCTGCTCAACT	GTCAGCTGTAATGCCTGCAA
PPDKB	Os05g0405000	CATGCACTGTTCGAGGAGAA	GGGAAATGGCTCTCCCTTAG
PGla	Os09g0465600	TCAGCATGCCTACATTCAGC	TGCAACATCCCGAACAAATA
PGlb	Os06g0256500	GTTGCACGAAGCATCAAAGA	ATGTTTCGCAACAGCATCAG
Amy3B	Os09g0457500	TCCTTATCGCCTTGCTCTGT	GAAGCGTCCAGGTCGTAGAG
Amy3C	Os09g0457800	CTGGCTCCACACAGAACTCA	CGTAGACATCTCCGTCAGCA
Amy3D	Os08g0473900	GTCGACGAGAAGGTCATGGT	CCTTCTCCCAGACGCTGTAG
Amy3E	Os08g0473600	ACAAGGTCATGCAGGGCTAC	GTTCCTTGACCGGATTTCAG
Genes involved in sucrose biosynthesis			
SPP	Os01g0376700	TTGATGTTAAAATAAT	ATGACACCATGTACACCAG
UGP1	Os01g0264100	ATGTCGTCGGAGGCGCGGG	CGGCGGCGGAGGAGGAGCG
UGP2	Os02g0117700	AGGAGCATGTGGAATGGGCA	TGGTCCGGTGCATCCCAT
SPS1	Os01g0702900	CGGCGTGCAGGTGGATCTCG	TGCTTCACGCACCGCAG
SPS2	Os02g0184400	ATGTGGTTGAACTTGCTAAA	GATATGGCCAAGTGCACC
SPS6	Os06g0634800	TCTTCAGCGGCCTCCTCCGC	GCGCCGACTCCGACGAC
cyFBP1	Os01g0866400	ATGGATCACGAGGCGGACG	TTGTTGACGGCGGAGGCGAC
PFPα	Os02g0714200	GTGGAAGTGATGGTCTTCTC	CAATGATTACTAAAGCATCC
PPase	Os01g0866500	GAGCGAGGCGGACGGAGGCG	GTGTCGAGGTCGTGCCAGG
Genes involved in production of storage protein			
GluA1	Os01g0762500	CATTTGAGCCAATTCGGAGT	GGCCTGATTGTTGGAACTGT

GluA2	Os10g0400200	GCAAGAGCAGGAACAAGGAC	CCTCATGGTGCAAAAGGTCT
GluA3	Os03g0427300	TGAAAACCAACCCTGACTCC	ACTCATCTCCCCTGTTGTGC
GluB1	Os02g0249800	GCCAAAGTCAGAGCCAAAAG	GAACCAATGTGCAACACCAG
GluB4	Os02g0242600	GCGACCAGAAGGCTACAAAG	TTGCTTGTTGATCGTTGCTC
Globulin1	Os03g0663800	ATCGAGAACGGCGAGAAGT	GGACGGAGATGGTATGGAGA
Globulin2	Os03g0793700	CGACGAGGTGTTCTACGTCA	GTGTTGGCGGAGTAGACGAT
11s-Globulin	Os05g0116000	CACCAAACCCGATCTTCAGT	CGGAACAGCTTCTCCATCTC
19kD-Globulin	Os08g0498400	GCCAGTAATTGCAGGGGATA	AGGTCACCACCAACGTAAGC
10kD-Prolamin	Os03g0766100	TGCAGTATTTCCCACCAACA	ACATGAACATGGCTGTGGAG
13kD-Prolamin	Os07g0219400	CACAGCGCAGTTTGATGTTT	GCTTGCCGCAATGCTATACT
17kD-Prolamin	Os06g0507001	TTTGATGCTTGCACCTATGG	GCAGCTGCTCAGTTTTAGCC
RA16	Os07g0214600	AGGTAGTGATCTCGGCGTTG	CCGATTCCTGGCTGACATAG
RA17	Os03g0791200	TTCTCGGTATTGCTCCTCGT	CTTATTCCTGGCCGACATTG
RA5B	Os07g0215500	TGGCTTCCAACAAGGTAGTG	ACCTGGTCTTGGTGGTGGTA
RAG2	Os07g0214300	AGGTAGTGTTCTCGGCGTTG	GTACATCGGGTAGCCCATTC
RG21	Os02g0268100	TGGCGACCATAGCTTTCTCT	GGGTTGTGCCATGGATTTAC
AlaAT	Os10g0390500	CCATTTCTCGAGCAACAACA	ATTTGCAGGGTATCCGTCAC
PDI	Os11g0199200	ACCAGGGCAAGAACATTCAG	TTGCGTCTTCTGGTGACTTG
Genes involved in regulating grain size			
GS3	Os03g0407400	ACGATTTCATCGGAGAAGCGAAG	CAGCAGCAGATCCAGGAGAG
GS5	Os05g0158500	CATTCCATGCAAATGCCAGTGGAC	CAGCCCTGCTTTGATGAGCTTG
GW2	Os02g0244100	CAGCAGCGCATTCCCAGTTTTC	GTGGTCAGCCGAGCACTCTC
GW8	Os08g0531600	AGGAGTTTGATGAGGCCAAG	GCGTGTAGTATGGGCTCTCC
GIF1	Os04g0413500	CTCAGTGTCA CGTGACCTCA	GAACTGCGTCGCGTTGATGC
DEP1	Os09g0441900	GCGAGATCACGTTCCTCAAG	TGCAGTTTGGCTTACAGCAT

OsSPL14	Os08g0509600	CAGCTACCACATGAAGTC	CTACAGAGACCAATCCATC
SRS1/DEP2	Os07g0616000	GAGGTGGAGC AATGTAAGTG	CATGATGTAACTGCATGCTT
SRS-3	Os05g0154700	GCAACAGCAACAACGGCCGAC	TGTGTGCTGCTATGAGAGCCTCC
DEP3	Os06g0677000	GCTCTCCGGG AACCCCGATG	TTCTTGAACACCGACTCCGG
SG1	Os09g0459200	CCCAGATGGATCTTGGAGGT	GGCAGACAGCAAGCTGAAAG
Genes involved in cell cycle			
CAK1	Os06g0171700	GACGGTCAGATTAGACGCAAGA	TCCAAAGGATGTCCACA
CAK1A	Os06g0334400	GACCGACAAGGGTTTCAGCAT	CCAGCATGTTCAGGAAGATACAAT
CDC20	Os04g0599800	TCGAATCACCTGTTTGTTGGC	TGGAGACAATCCAACGCAAAG
CDKA1	Os03g0118400	GGTTTGGACCTTCTCTCTAAAATGC	AGAGCCTGTCTAGCTGTGATCCTT
CDKA2	Os02g0123100	CGAGATTTGAAGCCCCAGAA	TCCGCGAGCTTCAATGAGTT
CDKB	Os08g0512600	AAGTTTGGCCAGGAGTGAGCA	TCAAGAGCATCAGCGTCGAGA
CDT2	Os03g0699100	AACCGCACCAAACACTGGAA	GCAATTCACCATCTGCACTGG
CYCA2.1	Os12g0581800	AGGTTGTCAAGATGGAGAGCGA	CGCTTTTTGTCTTCCTGGCA
CYCA2.2	Os12g0502300	AGGTTGTCAAGATGGAGAGCGA	CGCTTTTTGTCTTCCTGGCA
CYCA2.3	Os01g0233500	GTTTCGGTTGACGAGACGATGT	CGCTGCAAGGAACCTAGAACTG
CYCB2.1	Os04g0563700	AAGTTTGGCCAGGAGTGAGCA	TCAAGAGCATCAGCGTCGAGA
CYCB2.2	Os06g0726800	CTCAAGGCTGCACAATCTGACA	GCATTGACGGCTGGAATTTG
CYCD3	Os11g0706801	CCTTCCACACTGACGGTACAGT	TGCCGCTGCCAAATAGACA
CYCD4	Os09g0466100	GCCATGGAGTTGATACATCCAA	CCAGTAGGGCTCCGTGGAAT
CYCIaZm	Os01g0805600	CACTCTCAAGCACCACACTGGA	ACAACCCTCAGCTTGCTCTCAG
CYCT1	Os02g0438200	GCATTTGTTGCAGCTCAAG	TCACCACTTCGCTGACTTATTG
E2F2	Os12g0158800	TGTTGGTGGCTGCCGATAT	CGCCAGGTGCACCCTTT
H1	Os04g0253000	GCAAGGCACCTGCAGCTT	AGGCAGCCTTTGTACAGATCCT
KN	Os03g0736500	CACCAGCTTCAAGAGATCGTGA	CCGGAATTGAGACACAACTGC

MAD2	Os04g0486500	GAGCCATGCATATTCGACGTG	GGTGTCGAAGGAATGCAGCTT
Genes involved in C and N transports			
OsSUT1	Os03g0170900	TCATCCCTCAGGTGGTCATCG	CTTGGAGATCTTGGGCAGCAG
OsSUT2	Os12g0641400	GGCGGCCT AGCGGCGGCG	CGAAGGCGTGCGGGATGC
OsSUT3	Os10g0404500	CCGTCGACAT GGAGCTCGA	AACGTACGGGGTGAGGAGA
OsSUT4	Os02g0827200	CGCCGGCGGT GGCGGCCTCA	CGTGAGGAGCGAGAGCTGA
OsSUT5	Os02g0576600	CTAGTGCGAAACTCCATCAAA	AAAATATTTGGGTTTCCTGAGAT
OsSWEET11	Os08g0535200	GACGTTCTTG CAGGTGTACA	TAGCGGACGATGTAGGCGGC
OsSWEET14	Os11g0508600	TTCCCAACG TGCTGGGCTT CT	GCACCTCGCGGGTCTTGACG
OsTPT1	Os01g0239200	ACAACATGGGCGAGGATCAT	CAATCTTACCACCGCAATATGC
OsTPT2	Os05g0241200	TAGTTGGGTAGCTGCTTTGATCGA	AAATGGGATGATGGAGGCTTTG
OsMT	Os04g0602400	GCTGCCAGGCAGGAAGCT	GGTTCCAGTTTCACCACGACA
OspGlcT	Os01g0133400	GGTTCCAGTTTCACCACGACA	CGGTGGCATACTGGCATCTA
OsGPT1	Os08g0187800	GCAAGCACTGAGGCCAATTTTG	AAGGAACAAGAAACGAGCAACATAGAC
OsGPT2-1	LOC_Os07g34010	ACTCGGTGCTCGGGATGTAAC	AGAAGAAACATTGGCAGCTACAC
OsGPT2-2	LOC_Os07g33960	ACTCGGTGCTCGGGATGTAAC	AGAAGAAACATTGGCAGCTACAC
OsGPT2-3	Os07g0523400	GGATTGAAGAAGACTCGATGCGA	GGCTTGAATAATGCCATCTTGG
OsBT1-1	Os02g0202400	CTGGAATCGGATGAAACTCGTGTA	TCAGCAGAAATCAGTTATTGGACATG
OsBT1-2	Os05g0171300	TGATTGTGCATGGGTGTGATG	AACAGAGGAAATCGAATCCTACG
OsBT1-3	Os06g0602700	TTGCTAGCGTCGGTCTCAAAG	GCAATGATCAGCGAACGGAA
OsAAP7	Os05g0424000	ATCAAGCGGGCGAACTGCT	TGCACGACGCCGAGGCCG
OsAAP8	Os01g0882800	GTCGCTGGGGTGGGCCATCG	GCTCAGGTTGGCGTTCAC
OsAAP11	Os11g0195600	CGGGCGGGCG CGGCGGATGG	CCATCCGCCGCGCCCG
OsLHT1	Os08g0127100	GCTGTGGCAGATGGTGGAGA	TTCTCGCCGAACGCGTGC
OsATL5	Os06g0633800	CAGCAGCGAATCGCCGAATG	CCCGGAAAATGAAGCTCCAT

OsATL6	Os02g0191300	GGAATTGGGAATGGATCACC	ACTGACCGGAGAAAGAAGC
OsCAT4	Os03g0654400	TGGATGGCGGCGGCGAGGTT	GATCGCGACCAGCGCCGG
OsCAT11	Os12g0623500	TCGAGGAAGGCGGCGCGATG	CAATCGCGACGAGCTGCGT
OsPTR1	Os07g0100600	GGAGGCGACGACGACTGAC	GCCAGGCGCTCGCAGCACTC
OsPTR7	Os01g0142600	GTACACATCTCACCGGT A	GAAGCGTCAAATCCAAAACG
OsNRT2.3	Os01g0704100	ATGGAGGCTAAGCCGGTG	ACCACGCCATGTGGAAGGA
OsAMT1.1	Os04g0509600	AAGATGGCGACGTGCGCGGC	CATGGCGAACACGAGGTACG
OsAMT1.2	Os02g0620500	GCGGCCAACTACATCTGCAA	GCGAACACGAGGTAGGCCG
OsAMT1.3	Os02g0620600	GACGTCGGCCGTGGACTCGA	CGTCGAGCACGTTGGAAGC