Supporting Information

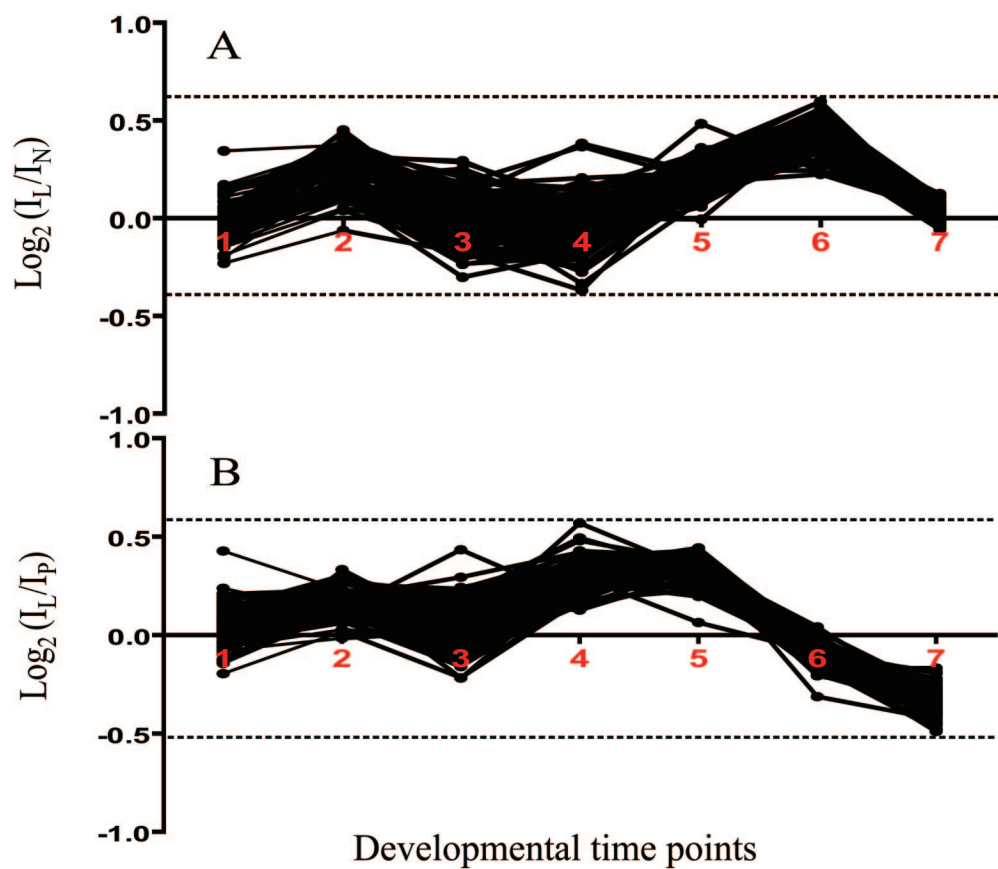## Wei et al. 10.1073/pnas.0902340106

Fig. S1. Expression profile of a polyubiquitin gene (AK062354). All copies of polyubiquitin genes in the array showed an almost identical expression pattern, indicating the reproducibility and homogeneity of the array data. I denote the normalized expression intensity in the array. N, L, and P stand for *93-11*, *LYP9*, and *PA64s*, respectively. Numbers 1–7 denote samples from the following tissues in order: seedling shoot, leaf at tillering stage, flag leaf at booting stage, flag leaf at heading stage, flag leaf at flowering stage, flag leaf at filling stage, and panicle at filling stage.

Fig. S2. Verification of differentially expressed genes (DG) with semiquantitative RT-PCR. Semiquantitative RT-PCR experiments were used to validate DG identified in microarray studies between the hybrid and its parents in the flag leaf at the filling stage. An actin gene was used as a positive control (primer pair: 5′-GTCCCTCACAATTTCCCGC-3′ and 5′-GGTGTCATGGTCGGAATGG-3′). We show the results from 25 PCR experiments; 20 of them agreed with those from the microarray experiments. Those that did not agree with microarray results were tagged by negation sign ¬ in red font. The genes tested are labeled on the top of each panel. H2P, CHP, B2P, CLP, and L2P stand for expression patterns: higher than both parents, close to higher parent, between both parents, close to lower parent, and lower than both parents, respectively. N, L, and P stand for *93-11*, *LYP9*, and *PA64s*, respectively.

Fig. S3. Gene Ontology analysis of all expressed genes in LYP9 hybrid combination along all sample points based on plantGOslim.

Fig. S4. Expression profiles of all expressed ribosomal protein-encoding genes. The normalized expression of commonly shared ribosomal protein genes among all samples were plotted by using Genespring software (Silicon Genetics). Expression profiles of the cytoplasmic ribosomal protein genes (60S/40S; *Upper*) and the plastid ribosomal protein genes (50S/30S; *Lower*). N, L, and P stand for *93-11, LYP9,* and *PA64s*, respectively. Numbers 1–7 denote the 7 samples as in Fig. 2.

Table S1. Number of expressed and enriched genes

Sample	L/N	L/P	Overlap	Total	Enriched
S1	14,280	14,374	14,197	14,457	405
S2	12,478	11,934	11,852	12,560	255
S3	14,250	14,084	13,921	14,413	22
S4	14,196	13,829	13,776	14,249	48
S5	14,592	12,835	11,962	15,465	197
S6	11,721	11,448	10,860	12,309	75
S7	14,102	14,298	13,646	14,754	453
Overlap	7,582	7,332	7,078	-	-
Total	21,871	20,716	20,321	22,266	1,455

N, L, and P stand for *93-11*, *LYP9*, and *PA64s*, respectively. S1–S7 denote the 7 plant samples used in the study: S1, seedling shoot; S2, leaf at tillering stage; S3, flag leaf at booting stage; S4, flag leaf at heading stage; S5, flag leaf at flowering stage; S6, flag leaf at filling stage; and S7, panicle at filling stage.
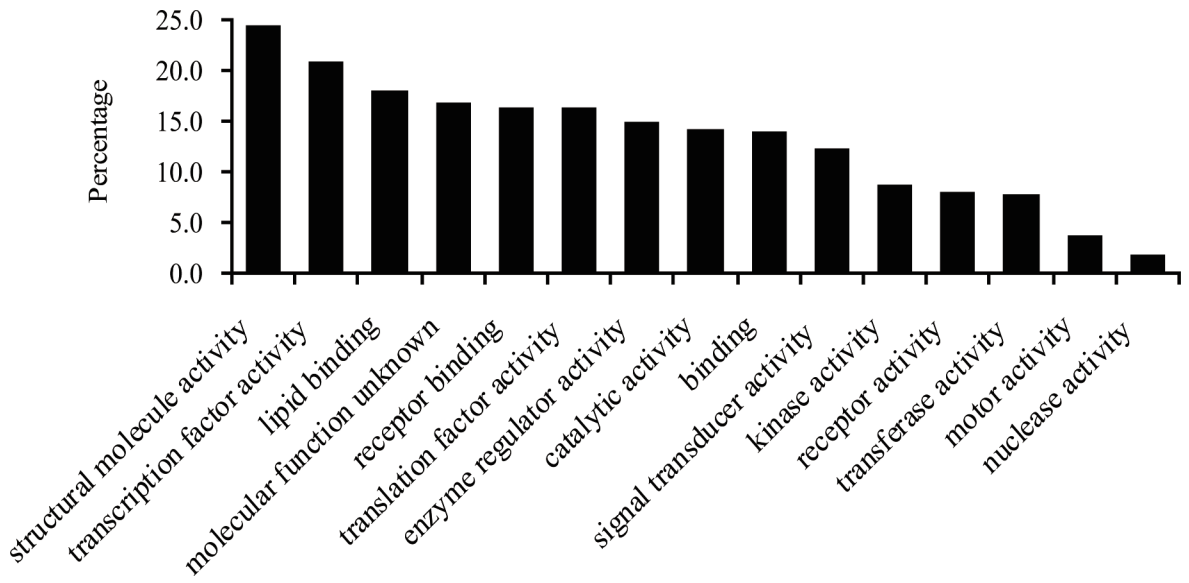
Table S2. Functional classification of DG$_{PP}$ and enrichment on each function category

Functional category	S1	S2	S3	S4	S5	S6	S7
Metabolism							
Amino acid metabolism	10	7	11	7	15*	6	14
Biosynthesis of polyketides and nonribosomal peptides	0	0	0	0	0	1	0
Biosynthesis of secondary metabolites	16	20*	18	21	13	14	12
Carbohydrate metabolism	25	26	34	25	24	22	42*
Energy metabolism	10*	3	10	7	16**	13**	27**
Glycan biosynthesis and metabolism	5	0	4	4	2	2	4
Lipid metabolism	10*	7	10	8	6	6	5
Metabolism of cofactors and vitamins	12	9	23	12	16	9	10
Metabolism of other amino acids	5	2	9*	6	5	6	4
Nucleotide metabolism	3	8	9	3	9	3	5
Xenobiotics biodegradation and metabolism	14	17	26	16	14	10	9
Genetic Information Processing							
DNA metabolism	4	5	12	6	6	2	4
RNA metabolism	18	15	21	12	13	14	33**
Cellular protein metabolism	31	23	49	35	42	37	52*
Environmental Information Processing							
Signal transduction	7	7	13	6	6	11	10
Transport	20	28*	48**	22	20	27	28
Cellular Processes							
Cell motility	0	0	1	2	0	0	2
Cell cycle	5	4	7	5	6	3	6
Cell–cell signaling	0	0	0	0	1	0	0
Cell death	4	4	1	9	6	1	0
Cell growth	0	0	1	0	0	0	0
Other	39*	27	61**	32	39	45**	62**
Unknown	153	177	246	229	176	166	157
Total	305	312	472	389	342	331	383

*Significant enrichment of DG in corresonding function category with $P < 0.05$ as cutoff.
**Significant enrichment of DG in corresonding function category with $P < 0.01$ as cutoff.

Table S3. Functional classification of DG$_{HP}$ and enrichment on each category

Functional category	S1	S2	S3	S4	S5	S6	S7
Metabolism							
Amino acid metabolism	9	19	18	13	26**	23*	42**
Biosynthesis of polyketides and nonribosomal peptides	0	1	0	1	0	2*	1
Biosynthesis of secondary metabolites	15	32**	32	26	27	29*	30
Carbohydrate metabolism	30	49	58	49	60*	52	76*
Energy metabolism	12*	17**	24**	14	21**	37**	64**
Glycan biosynthesis and metabolism	4	0	8	6	3	8	13*
Lipid metabolism	9	11	12	11	12	16*	11
Metabolism of cofactors and vitamins	14	25	32	21	32	23	26
Metabolism of other amino acids	7	10*	9	5	11*	5	9
Nucleotide metabolism	7	9	10	10	13	4	15
Xenobiotics biodegradation and metabolism	14	33	35	27	27	24	21
Genetic Information Processing							
DNA metabolism	10	5	7	4	14	2	3
RNA metabolism	13	24	39	30	36	20	54*
Cellular protein metabolism	32	53	91**	66	68	45	75
Environmental Information Processing							
Signal transduction	4	12	21	20	20*	10	8
Transport	23	50**	74**	49	50*	51**	60
Cellular Processes							
Cell motility	0	1	1	3*	1	0	2
Cell cycle	3	10	6	4	7	4	10
Cell–cell signaling	0	0	2	1	2	1	1
Cell death	6	8	1	8	11	5	3
Cell growth	0	1	1	1	0	0	0
Other	44	51	96**	77**	80**	76**	120**
Unknown	215	285	327	333	261	256	366
Total	376	529	696	627	609	550	794

* and ** separately denote significant enrichment of DG in corresponding function category with $P < 0.05$ and $P < 0.01$ as cutoff, respectively.

Table S4. Percentage of DG$_{HP}$ in QTL-containing genes

No. of genes in QTL	No. of QTLs	No. of DG$_{HP}$	No. of genes	%
≈1–10	2,461	61	518	11.78
≈11–50	236	277	2,756	10.05
≈51–100	324	693	6,951	9.97
≈101–200	649	1,618	17,137	9.44
≈201–500	973	2,568	27,353	9.39
>500	598	2,636	28,152	9.36
Overall	5,241	3,187	36,926	8.63

Other Supporting Information Files

[Dataset S1 (PDF)](#)