SI Appendix

Title:

Integrated analysis of phenome, genome and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase

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SI Materials and Methods

Hybrid combinations and populations

The hybrid rice (*Oryza sativa* L.) cultivar Liang-you-pei 9 (LYP9), a two-line hybrid that was developed by crossing 93-11 with Peiai64S (PA64S), and its parental lines were used in this study. Another 13 commercial hybrid rice combinations, plus their parents (Fig. 2, *SI Appendix*, Dataset S1), were also studied to analyze heterotic performance with respect to yield-related traits. A population containing 219 recombinant inbred lines (RILs, F_{10} generation) was developed by single seed descent from a cross between 93-11 and PA64S, and these 219 RILs were then backcrossed to the maternal parent PA64S to obtain 219 BC_1 lines (RILBC) (1). All materials are maintained at the China National Hybrid Rice R&D Center. Both RILs and RILBCs were used to map QTLs associated with heterosis for yield traits. In addition, a set of 361 hybrid combinations were collected from the market to genotype the *RH8* locus (*SI Appendix*, Dataset S5). Young inflorescences (<1 mm, 1-2 mm, 2-3 mm and 3-4 mm, 7-10 cm) were collected in the morning using a dissecting microscope and frozen in liquid nitrogen immediately after harvest. Leaves of six-week old seedlings were also collected and kept at -80^{o}C for use.

Plant growth and phenotyping

All plants were grown in randomized block designs with at least three biological replicates using standard agricultural management practices in Changsha (28°12'N, 112°58'E， long-day conditions) and in Sanya (18°15'N, 109°30'E, short-day conditions), China. A total of 300 plants in a 16 m^2 plot were characterized for each sample. Plant height (PH), heading date (HD), effective panicle number (EPN), spikelet per panicle (SPP), seed setting rate (SSR), kilo-grain weight (KGW), field yield (FY), and yield per pot (YPP) were surveyed in the field of Changsha, China, for four summers (2008, 2010, 2011, and 2014) for the RIL and RILBC populations

and for six summers (2010-2015) in Changsha and one winter (2011) in Sanya for LYP9 and its parents. The values for high-parent heterosis (HPH), mid-parent hetosis (MPH), and paternal parent heterosis (PPH) were calculated using the formulas "100*(F1-HP)/HP", "100*(F1-MP)/MP", and "100*(F1-PP)/PP", respectively. Significant phenotypic differences between genotypes were statistically analyzed using Student's t test ($P<0.05$).

Cluster analysis of heterosis performance

In order to uncover heterosis traits that are shared by other combinations, the heterosis performance of 13 rice hybrids plus LYP9 were characterized for four summers (2011-2014) in Changsha, China (Fig. 2; *SI Appendix* Dataset S1). The averages of two to four years for each type of heterosis were used to perform cluster analysis with the Vegan package in R by Bray-Curtis distance based on the heterosis performance for yield-related traits (http://cran.r-project.org/, http://vegan.r-forge.r-project.org/). In the cluster tree, the percent heterosis for each component trait was classified by the depth of two colors, green and red, which represented negative and positive heterosis, respectively.

RNA isolation and mRNA-seq library construction

Young inflorescences and leaves were ground to a fine powder in liquid nitrogen, and the total RNA was isolated using Trizol reagent (Invitrogen). We harvested the rice samples once in the morning (around 8:00-10:00 am) from the paddy field in Changsha, China. Total RNA from each sample was used to isolate poly (A) mRNA and to prepare a directional SOLiD RNA-Seq library according to the manufacturer's protocol. Library quality control and quantification were performed with a Bioanalyzer Chip DNA 1000 series II (Agilent). cDNA in the range 150–200 bp was selected with Novex precast gel products (Invitrogen, Cat. no. NP0322BOX). The cDNA was amplified with 15 cycles of PCR and purified using the PureLink PCR Micro Kit (Invitrogen, Cat. no. K310250). The cDNA library was sequenced on an

AB SOLiD 4.0 sequencer according to the manufacturer's instructions (Thermofisher Scientific).

Read mapping and gene expression quantification

The rice (*Oryza sativa* subsp. *japonica*) genome sequences and annotated gene structure information were downloaded from the Rice Genome Annotation Project website (http://rice.plantbiology.msu.edu, TIGR Version 6.1) (2). The exon-exon junction references were constructed as follows: first, we joined all possible pairs of non-redundant exons that belong to the same gene such that the genomic order of the exons was retained; then we constructed a junction sequence that consists of the last 49 bp of the 5' exon and the first 49 bp of the 3' exon, and the redundant sequences were removed from the resulting set of 98-bp exon junction sequences. All sequence reads were mapped to the rice genome and the in-house-built junction sequences using AB's SOLiD Corona_lite_v4.2 software available at http://waprna.big.ac.cn (3). We used a recursive strategy to improve the usable sequence read information, in which the 50-mer reads were first mapped to the genome and junction reference with a tolerance of 5 mismatches. The reads that failed to be mapped were progressively trimmed, removing five bases at one time from the 3' end. After this, the reads were mapped to the genome again until a match was found (unless the read had been trimmed by 25 bases) (4). All mapping was carried out in color-space, reads mapping to multiple genomic locations were discarded. All of the uniquely mapped reads were used for calculating the gene's RPKM values (reads per kilobase of exon per million mapped sequenced reads), which is used for defining gene expression level. The normalized gene expression value was used to calculate the Pearson correlation coefficient between any two replicated samples, and it was applied to assess the technological and biological replication (5). We calculated read coverage along the annotated transcript units based on the uniquely mapped reads. The length of each cDNA was divided into 100 equal segments (bins) for all annotated cDNAs, and the mean number of the read coverage for each segment of each individual cDNA was

calculated. The median values for each bin for all cDNAs were plotted against the segment number.

By calculating the read coverage for the annotated introns and exons in the rice genome of each sample, an empirical cutoff value (about 5% of genes contained >N reads per kb intron) was arbitrarily determined and used as a cutoff for detection of gene expression in each mRNA-Seq sample (6). Sequenced reads were randomly selected and the expressed gene number was calculated to evaluate the sequencing saturation.

Differentially expressed gene identification and classification

We identified differentially expressed genes (DEGs) from different varieties and samples using an R package called DEGseq (7). For each gene, the P-value and Q-value were computed, and the significance threshold to control the false discovery rate at a given value was calculated. The fold changes were also estimated between the F_1 hybrid and its parental lines (F, 93-11 and M, PA64S) based on the following formula: FC (Fold-Change)=F_1/[(F+M)/2]. The DEGs were classified into five major expression patterns based on gene expression level and three different tests using DEGseq (7). Moreover, each gene was classified based on the expression level of the F_1 hybrid versus both parental lines; tests 1 and 2 were used to estimate whether the expression level of the considered gene in the F_1 hybrid significantly differs from that of the LP and/or the HP, whereas test 3 compares HP and LP. The five patterns are OHP (over-higher parents, $F_1 > LP \geq HP$, all the three tests are 'yes'), BLP (below-lower parents, $F_1 < LP \leq HP$, all the three tests are 'yes'), OMP (over mid-parents, $LP<F_1<HP$ or $LP<F_1=HP$, tests 1 and 3 are 'yes'), BMP (below mid-parents, $LP<F_1<HP$ or $LP=F_1<HP$, tests 2 and 3 are 'yes'), and MPV (similar to mid-parents). Non-additively expressed genes were identified by comparing their expression levels in the hybrid to the mid-parent value (MPV).

To associate cellular functions with the set of differentially expressed genes, we used an in-house-built pipeline to do KEGG pathway annotation (3), and Fisher's exact test was applied to test for enrichment of functional categories.

Genomic variation identification

Genomic variations between 93-11 and PA64S were identified as follows: (1) the known variations were directly downloaded from the RGKbase database (http://rgkbase.big.ac.cn/RGKbase/Ni.php) (8); (2) the resequencing reads from 93-11 and PA64S were aligned to the TIGR ver6.1 genome sequence, and the sequence variations were called using GATK software (9); (3) eSNPs were called from transcriptome sequences using in-house-built methods for each sample. To be confident of the base calls, for each variety, we focused our analysis on high quality sites (average quality score >=15) that were covered by at least four uniquely mapped reads and two non-redundant reads. A SNP locus was included for further analysis only if nearly homozygous (the major allele frequency >0.85). We quantified the allelic imbalance within a sample as the major allele frequency (MAF) of the gene. MAE, PAE, and BAE expression patterns were classified according to the expression levels of the two alleles; when only one allele was expressed, it was categorized as MAE, when the allele expression was biased to one parent by more than 2-fold, it was categorized as PAE, and when two alleles were expressed equally, it was categorized as BAE.

Genome Resequencing and QTL mapping

The genomic DNAs of LYP9 RILs together with their parents (93-11 and PA64S) were isolated using the cetyl-trimethyl ammonium bromide (CTAB) method with minor modifications (10). Sequencing libraries were constructed from these samples and sequenced on the Illumina HiSeq2500 according to the manufacturer's instructions. The sequencing reads were aligned to the *indica* reference genome (93-11, http://rice.genomics.org.cn) using BWA software (11). Identification of

polymorphic sites including SNPs and InDels between the RILs and the parents was performed with GATK software (9). The co-segregating SNP and/or InDel markers were combined into Bins, which were then used to construct the genetic map of the RIL population using HighMap software (12). Briefly, based on the sequence variations between 93-11 and PA64s and the variant sequences among the RILs, 780,717 loci were randomly selected for genetic map construction. The loci that co-segregated with each other were anchored into the same block, called a Bin. A total of 2,972 Bins were used for construction of the final map with HighMap software (*SI Appendix,* Fig. S7). The RIL map consists of 12 linkage groups that correspond to the 12 rice chromosomes, each with 248 Bins on average. The 12 linkage groups range from 81.8 cM to 228.7 cM in length, with a total genetic distance of 1,573.1 cM and average neighboring Bin distance of 0.3 cM. The Spearman coefficient for each chromosome was at least 0.9975, very close to 1.0, indicating full collinearity between the genetic map and the rice genome.

The QTLs for each trait were detected by QTLMap6 software (http://www.kyazma.nl/index.php/mc.MapQTL). The LOD threshold was set to 2.5, and the 99% confidence interval for QTLs was determined by subtracting 2.0 LOD from the peak value, and the maximum interval length was not larger than 10 cM (13, 14). The mapped QTLs from the RIL populations were named *qSPPx* for spikelets (the x indicates the chromosome number), *qPHx* for plant height, *qHDx* for heading date, *qEPx* for effective panicle number, *qSSRx* for seed setting rate, and *qKGWx* for grain weight. Correspondently, the QTLs detected in the RILBCs were thus named *qhSPPx* for spikelets (h is the abbreviation of heterosis, and x indicates the chromosome number), *qhPHx* for PH, *qhHDx* for HD, *qhEPx* for EPN, *qhSSRx* for SSR, and *qhKGWx* for GW. Through conjoint analysis of QTLs detected in both the RI and the BC populations, the additive effects (ADD), the dominance effects (DOM), and the degree of dominance (DOM/ADD) of each heterosis QTL were calculated. The loci with absolute values of DOM/ADD <0.2 were considered to have no significant dominance, 0.2-0.8 showed partial dominance, 0.8-1.2 showed complete

dominance, and 1.2 or more showed over-dominance (15). For the loci detected only in the RILBC1 population, the performance of the related heterozygosis genotype should differ significantly from its parents. When the effect was similar to over-dominance (the value of DOM was larger than that of ADD) but without additive effects, it was then regarded as "Superdominance" in this paper. Although the degree of dominance of QTLs detected only in the RIL population can also be estimated, it is omitted for further analyses due to the absence of phenotypic value of heterozygote. For a single heterozygous locus, the contribution to heterosis, higher parent heterosis (HPH), middle parent heterosis (MPH) or low parents heterosis (LPH) could be determined statistically by comparing the performance of the heterozygote with the higher parent value (HPV), the middle parent value (MPV), and the lower parent value (LPV).

Genotyping analysis of *RH8* and *Ghd7*

The coding regions of *RH8/DHT8/Ghd8/LHD1* (LOC_Os08g07740) and *Ghd7* (LOC_Os07g15770) in the parental lines of the 14 phenotyped hybrid combinations were amplified from genomic DNA using Trans Start Fast Pfu DNA polymerase (TransGen Biotech) for sequencing. Sequence contigs were assembled with the program SEQUENCHER 4.1.2. InDel and CAPS markers based on the *RH8* truncated allele haplotype (ZS97A/TFA/FYA/J23A/V20A) and the +322bp SNP allele haplotype (MH63/R527/MY46/JY207/FH838), were designed to identify these types in hybrid populations. An InDel Marker was applied to genotyping *Ghd7* in hybrid populations, of which *Ghd7* loci such as in 'Zhenshan97' were completely deleted and no PCR products were amplified. Table S6 (*SI Appendix*) provides a list of all primers used for polymerase chain reaction (PCR) amplification and DNA sequencing.

SI References

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SI Figures

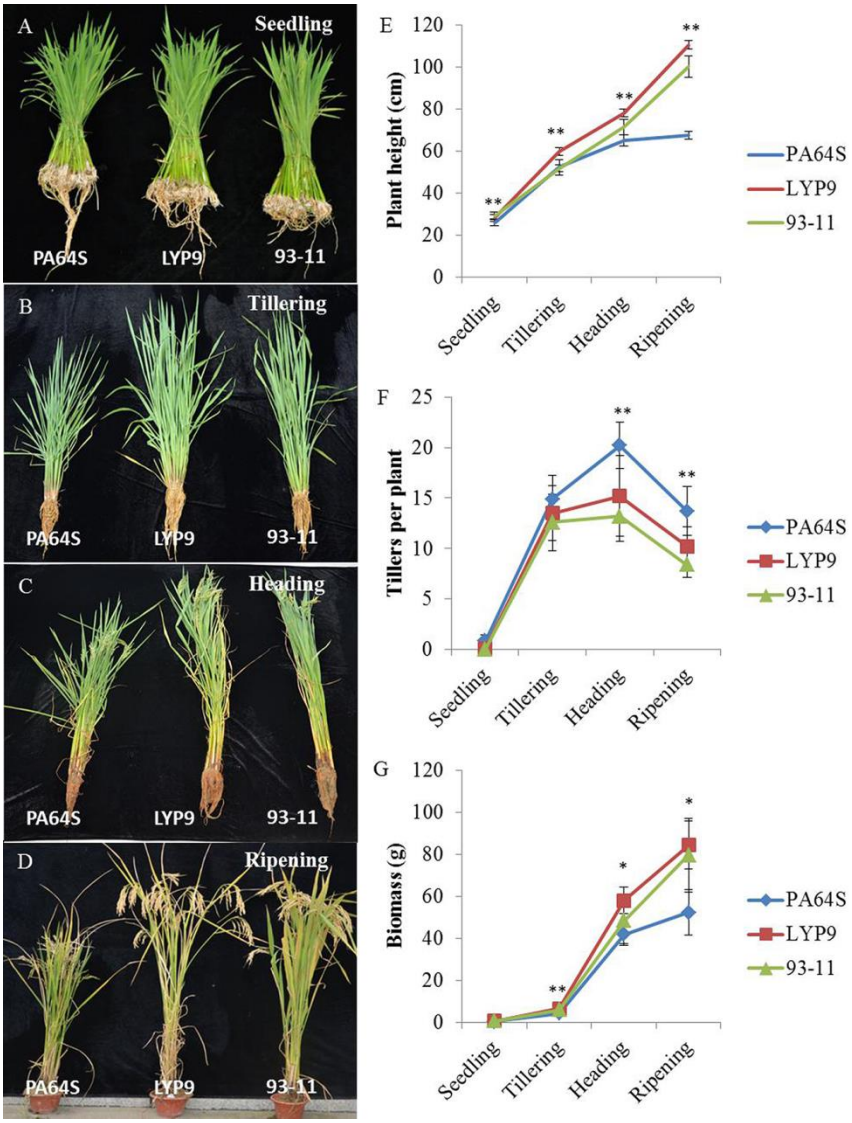

Fig. S1 Vegetative growth of LYP9 and its parents at the 20 day-old-seedling, tillering, heading, and maturity stages.

(**A**), 20-day old seeding; (**B**) tillering stage; (**C**), heading stage, (**D**) maturity stage; (**E-G**), comparisons of tiller number (**E**), plant height (**F**), and biomass (**G**) at four developmental stages. '*' and '**' represent significant differences (5% or 1%, respectively) between LYP9 and the higher parent.

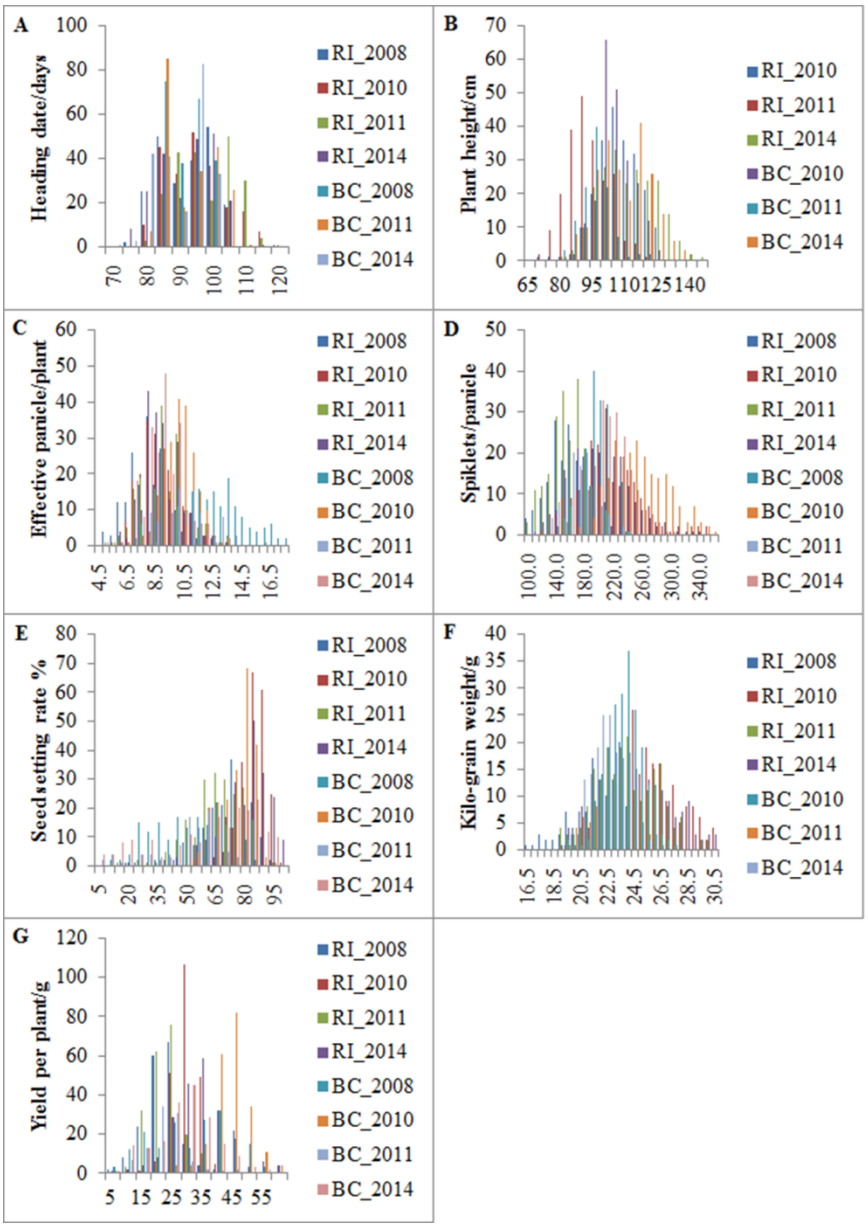

Fig.S2 The frequency of yield-related traits of RILs population and its PA64S-backcrossed population in four years.

(**A**) Heading date; (**B**) Plant height; (**C**) Effective panicles per plant; (**D**) Spikilets per panicle; (**E**) Seed setting rate; (**F**) Kilo-grain weight; (**G**) Yield per plant.

RI: recombinant inbred line (RIL) population; and BC: backcross population, the F1 population of backcrossing to PA64S.

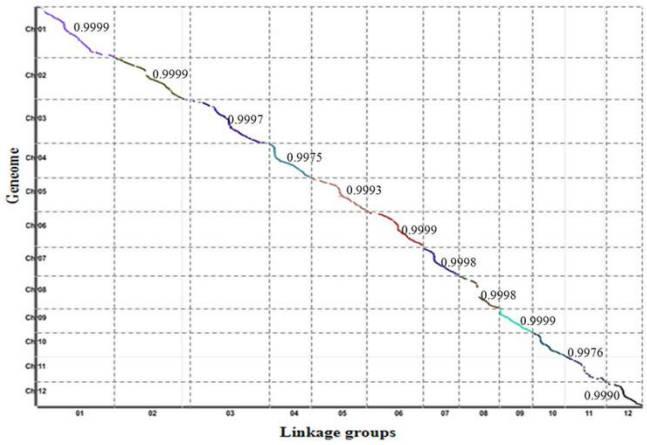

Fig. S3 Collinearity between the Bin map derived from the LYP9 RIL population and the reference genome (cv. Nipponbare)

The horizontal and the vertical axes represent the genetic positions of the 12 linkage groups from the LYP9 RIL population map and the physical positions of the 12 rice chromosomes, respectively. The scattered points represent the Bin markers used in QTL mapping. The data for each chromosome and linkage group pair is the value of Spearman correlation coefficient, which indicates good collinearity when it is close to 1.

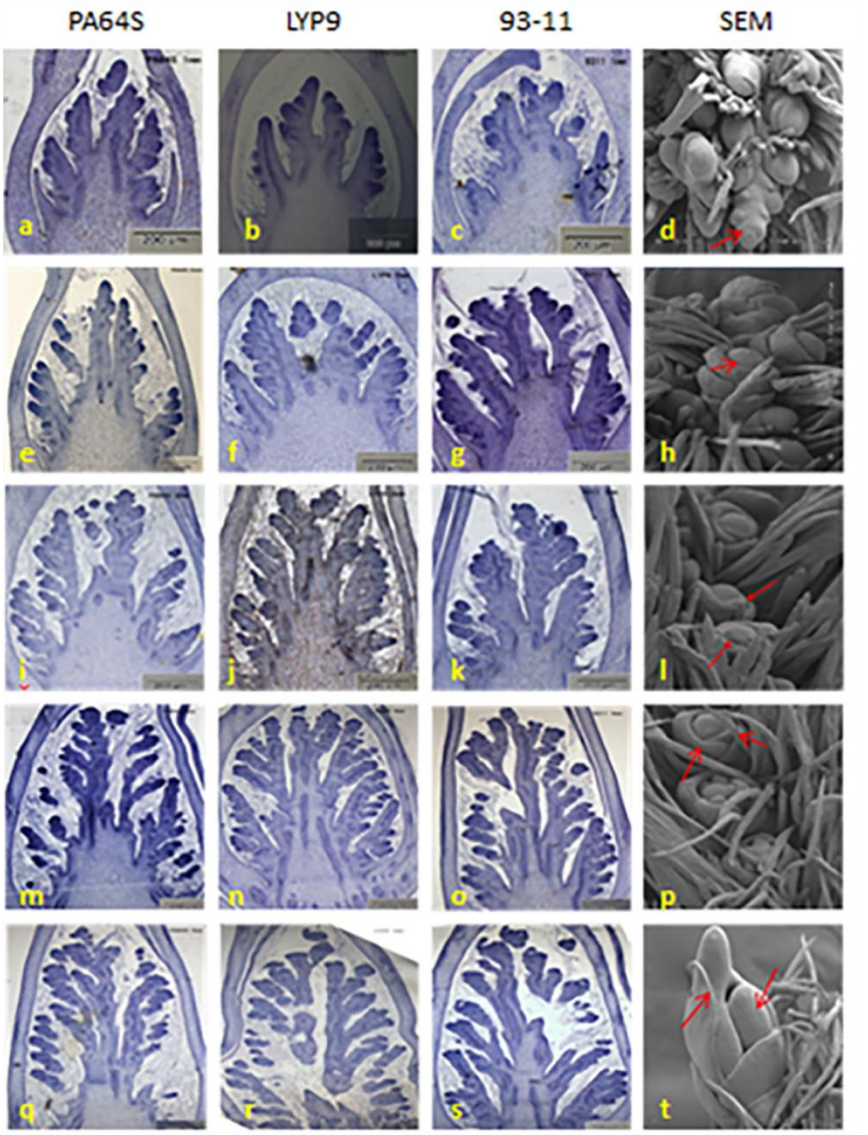

Fig. S4 Comparative microanatomy of the development of the young inflorescence in LYP9 and its parental lines, PA64S and 93-11.

(a-d) Histological examination of the rice inflorescence at <1 mm. The panicle at this stage is of key importance for primary branch formation, but the secondary branch number has not yet been determined. **(e-h)** The panicle at 1-2 mm in length. The uppermost primary branch has elongated, and the secondary branch primordia have initiated. Thus, at this stage, the number of primary branches has been determined. Organ primordia of the terminal flower have emerged; however, no stamen primordia were observed. Tertiary branch primordia were not observed in the lowest secondary branches. **(i-l)** The panicle at 2-3 mm in length. The secondary branch number has

been determined. Tertiary branch primordia (or spikelet primordia) have formed in the lowest secondary branches, and stamen primordia formation has initiated. The number of secondary branches has been determined by this stage. **(m-p)** The panicle at 3-4 mm in length. The palea and lemma in the terminal flower of the uppermost primary branch are obviously elongated but are not closed. Thus, the number of spikelets has been determined by this stage. **(q-t)** The panicle at 4-5 mm in length. The stamen primordia are clearly observed and the lemma and palea are closed. No more spikelets have formed at this stage.

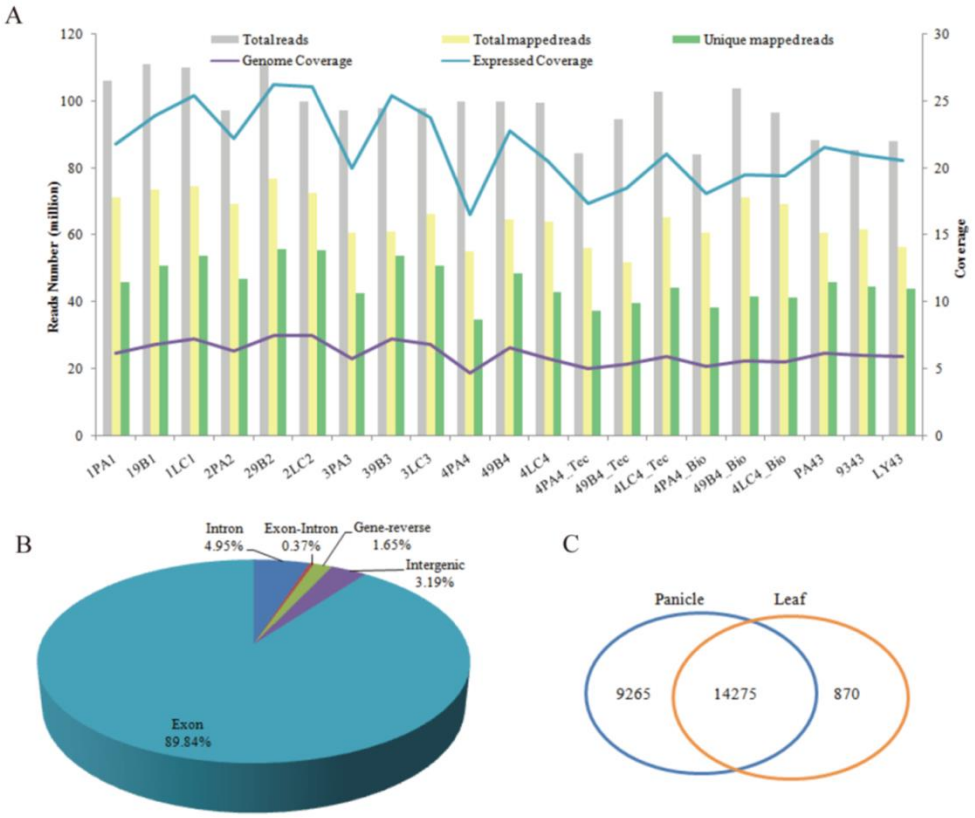

Fig. S5 Comparative RNA-seq analysis of the super-hybrid rice LYP9 and its parental lines 93-11 and PA64S.

(**A**) Number of sequence reads, total mapped reads, uniquely mapped reads, and genome coverage and expressed transcript coverage for each sequenced sample. (**B**) Genomic distribution of sequence reads among annotated rice genomic features. (**C**) Venn diagram showing the overlap of expressed genes between panicle and leaf.

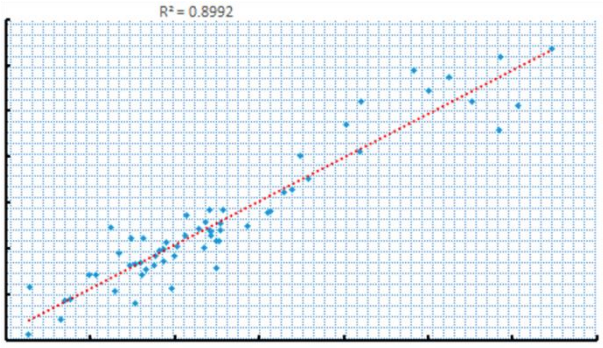

Fig. S6 Validating the RNA-seq data using qRT-PCR.

qRT-PCR validation was performed by comparing the log2 ratio of RPKM by RNA-seq and the log2 ratio of relative expression of 30 genes calculated by qRT-PCR. The Pearson Correlation Coefficient was calculated.

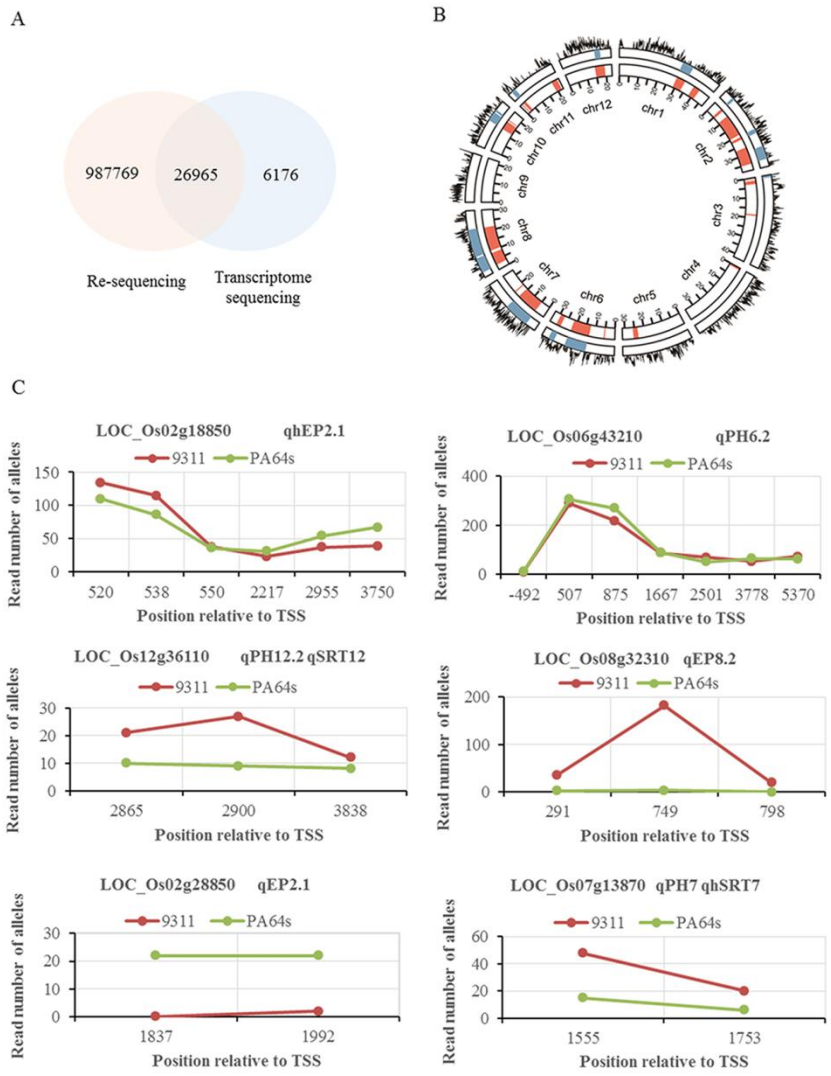

Fig. S7. Genomic variation between the two parental genomes 93-11 and PA64S.

(**A**) Veen diagram of identified single nucleotide variation by re-sequencing and transcriptome sequencing. (**B**) Density distribution of identified SNPs along whole genome plotted by 50kb sliding window and 10kb step length. (**C**) Example of allelic expression pattern in F1 hybrid.

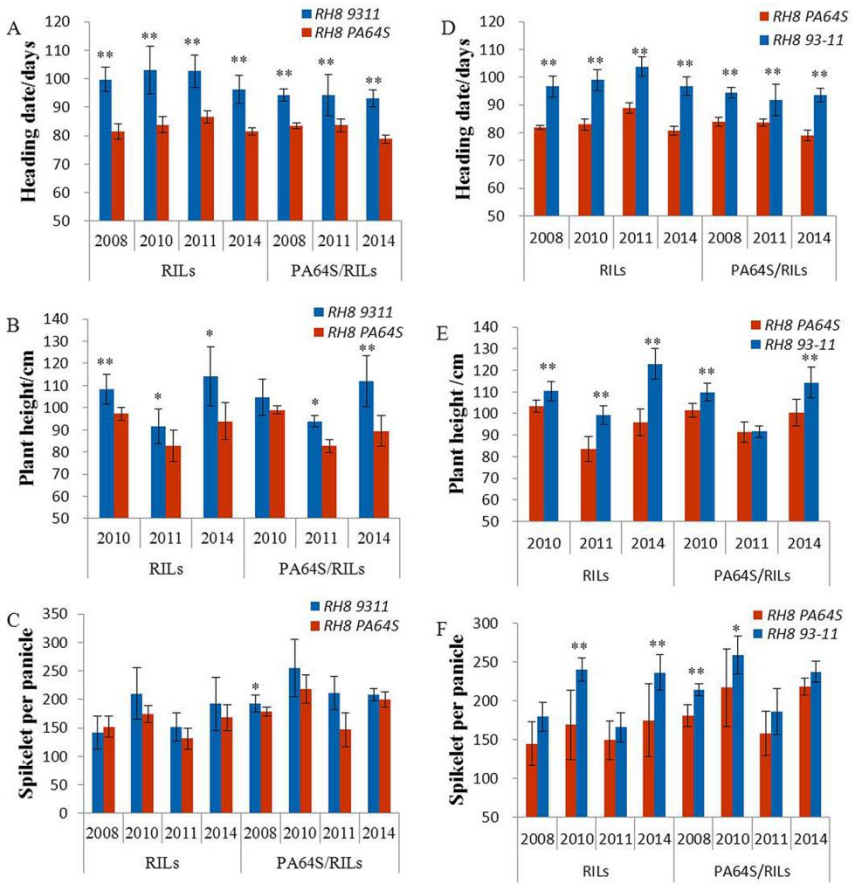

Fig. S8 Heterosis of *RH8* for heading date, plant height, and spikelets per panicle in the lines with genomes closing to PA64S or 93-11 (>65%).

(**A-C**) Comparison of the 93-11 and PA64S alleles of *RH8* in the RILs with genomes close to PA64S (>65%) in the RIL and BC populations for the traits heading date (**A**), plant height (**B**), and spikelet number per panicle (**C**); (**D-F**) Comparison of the 93-11 and PA64S alleles of *RH8* in the RILs with genomes close to 93-11 (>65%) in the RIL and BC populations for heading date (**D**), plant height (**E**), and spikelet number per panicle (**F**). '*' and '**' represent significant differences at P<0.05 or 0.01, respectively, as determined by Student's *t* test.

SI Tables

Table S1. Statistics of differentially expressed genes (DEGs) for each developmental period.

Table S2. Classification of differentially expressed genes (DEGs) between the F_1 hybrids and their parental lines for each developmental stage based on gene expression levels.

Table S3. Seventeen genes that overlapped with the QTL peak signals.

Table S4. Allelic combinations of *RH8* in a set of 361 commercial rice hybrids

Table S5 Genotypes of *Ghd7* in 14 hybrid combinations

Table S6. List of oligonucleotide primers used for PCR amplification and DNA sequencing.

Table S1. Statistics of differentially expressed genes (DEGs) in each developmental period

	P1	P2	P3	P4	Leaf
Total ExpGene #	16633	16382	16252	16919	15145
Total DEG (P<0.001)	10558	11566	11648	11205	10821
Total DEG %	63.48%	70.60%	71.67%	66.23%	71.45%
Common DEGs		**6133**			10821
93-11 vs PA64s	8667	9280	8146	9385	8200
93-11 vs LYP9	5588	6738	7804	5895	6192
PA64s vs LYP9	6664	7438	7734	7336	7659
F1>MPV[a] #	4872	6039	5089	5219	6151
F1>MPV & F1>HP #	1880	2731	2973	1941	3609
F1<MPV #	5653	5499	6536	5954	4640
F1<MPV # & F1<LP	1883	1863	3806	2029	1919
F1=MPV #	33	28	22	32	30
F1>MPV (Ratio>2) #	31	21	14	19	117
F1<MPV (Ratio<0.5) #	65	71	203	73	161
TE-related DEG #	242	260	253	252	204
TF DEG #	739	791	773	762	646
TF DEG %	7.0%	6.8%	6.6%	6.8%	6.0%
TF Gene (F1>MPV)#	315	445	302	398	371
Common TF DEGs #		**454**			646

Note: [a] MPV(mid-parent value) = (Fa+Mo)/2

P1: panicles of lengths of 0-1 mm; P2: panicles of lengths of 1-2 mm ; P3: panicles of lengths of 2-3 mm ; P4: panicles of lengths of 3-4 mm.

Table S2 Classification of differentially expressed genes (DEGs) between F1 hybrid to their parental lines in each developmental period stage according to gene expression levels

Pattern[a]	Expression Pattern[b]	Criteria			Total number of genes					Number of nonadditive genes[c]				
		LP≠F1	HP≠F1	HP≠LP	P1	P2	P3	P4_B	Leaf	P1	P2	P3	P4_B	Leaf
OHP	F1>HP(F)>LP(M)	Y	Y	Y	99	152	345	160	392	99	152	345	160	392
	F1>HP(F)=LP(M)	Y	Y	N	349	587	907	282	948	349	587	907	282	948
	F1>HP(M)>LP(F)	Y	Y	Y	78	138	248	80	186	78	138	248	80	186
	Sum				526	877	1500	522	1526	526	877	1500	522	1526
	(Sum/Total) %				5.0%	7.6%	12.9%	4.7%	14.1%	16.3%	20.0%	23.9%	14.3%	29.1%
BLP	F1<LP(F)<HP(M)	Y	Y	Y	107	140	392	131	300	107	140	392	131	300
	F1<LP(F)=HP(M)	Y	Y	N	253	307	1044	343	344	253	307	1044	343	344
	F1<LP(M)<HP(F)	Y	Y	Y	44	89	384	101	124	44	89	384	101	124
	Sum				404	536	1820	575	768	404	536	1820	575	768
	(Sum/Total) %				3.8%	4.6%	15.6%	5.1%	7.1%	12.5%	12.2%	29.0%	15.8%	14.6%
OMP	LP<F1<HP	Y	Y	Y	873	1068	620	1010	743	139	249	163	152	173
	LP<F1=HP	Y	N	Y	2308	2724	1941	2531	2541	655	978	758	835	1043
	Sum				3181	3792	2561	3541	3284	794	1227	921	987	1216
	(Sum/Total) %				30.1%	32.8%	22.0%	31.6%	30.3%	24.6%	27.9%	14.7%	27.1%	23.2%
BMP	LP<F1<HP	Y	Y	Y	1426	1506	1053	1465	1128	285	348	276	330	370
	LP=F1<HP	N	Y	Y	2423	2322	2319	2564	1880	815	931	1105	841	892
	Sum				3849	3828	3372	4029	3008	1100	1279	1381	1171	1262
	(Sum/Total) %				36.5%	33.1%	28.9%	36.0%	27.8%	34.1%	29.1%	22.0%	32.1%	24.0%
~MPV	Ambiguous	vary	vary	vary	2598	2533	2395	2538	2235	400	476	644	392	476
	(Sum/Total) %				24.6%	21.9%	20.6%	22.7%	20.7%	12.4%	10.8%	10.3%	10.7%	9.1%
	Total				10558	11566	11648	11205	10821	3224	4395	6266	3647	5248

Note:[a] DEGs were classified into four major patterns based on gene expression level and three different tests,OHP (over-higher parents), BLP (below-lower parents), OMP (over mid-parents), BMP (below mid-parents). [b]Higher parent (HP),lower parent (LP). [C] non-additive genes were determined by comparing F1 hybrid expression levels to the mid-parent value(MPV)

Table S3 Seventeen genes that overlapped with the QTL peak signals

#QTL	Year	Chr	QTL_Etart	QTL End	Peak Start	Peak End	TIGR_ID
qhEP2.2	2010	2	20613225	22499562	21755525	21762095	LOC_Os02g33680,LOC_Os02g51760,LOC_Os02g51780
qhEP8.2	2010	8	9754078	21997809	19921005	20043742	LOC_Os08g30480
qhKGW10.1	2010	10	12128159	15282602	14181169	14207577	LOC_Os10g30280
qhKGW10.2	2010	10	16794050	17672567	17147467	17215965	LOC_Os10g34350,LOC_Os10g34380,LOC_Os10g34370,LOC_Os10g34390
qhKGW11.2	2011	11	1846187	3781250	2746754	2751892	LOC_Os11g06070
qhPH12.22	2014	12	17596664	18220616	17657805	17810221	LOC_Os12g36170,LOC_Os12g36180,LOC_Os12g36194,LOC_Os12g36210
qhPH6.1	2010	6	12804716	22214277	20900333	20920306	LOC_Os06g34660
qhPH6.2	2014	6	27781841	28314807	28051291	28111018	LOC_Os06g44050
qhSPP1	2008	1	28596855	33584095	30229665	30642682	LOC_Os01g47350,LOC_Os01g47360,LOC_Os01g47450,LOC_Os01g47560 LOC_Os01g47600,LOC_Os01g47620,LOC_Os01g47650,LOC_Os01g47660, LOC_Os01g47680,LOC_Os01g47710,LOC_Os01g47730,LOC_Os01g47760
qhSPP2.1	2014	2	4090670	5284201	4669122	4710089	LOC_Os02g07690,LOC_Os02g07700
qhSPP2.2	2014	2	28795776	34712318	33718984	33764990	LOC_Os02g51790
qhSRT12	2014	12	16952661	18139431	17248402	17328731	LOC_Os12g35620,LOC_Os12g35640,LOC_Os12g35670
qSRT3	2014	3	215235	1089464	250176	666664	LOC_Os03g01008,LOC_Os03g01014,LOC_Os03g01090,LOC_Os03g01100, LOC_Os03g01120,LOC_Os03g01160,LOC_Os03g01170,LOC_Os03g01180, LOC_Os03g01190,LOC_Os03g01200,LOC_Os03g01216,LOC_Os03g01240, LOC_Os03g01300,LOC_Os03g01530,LOC_Os03g01550,LOC_Os03g01600, LOC_Os03g01670
qSRT7	2014	7	4850103	14586562	6956507	6978106	LOC_Os07g12250
qSRT8	2014	8	4015325	6161423	4846573	4898619	LOC_Os08g08000

Table S4. Allelic combinations of RH8 in a set of 361 commercial rice hybrids

Hybrid type	Cultivar No.	Cultivar name	~1kb deletion: 0; no ~1kb deletion:1	1bp deletion:0; hybrid: H, no 1 bp deletion: 1	both non-functional: 0；hybrid: H（two conditions：0 and1, 1 and H）；both functional: 1
2-line	14CSH18	Cliangyou 1102	1	0	0
2-line	14CSH319	Cliangyou 34156	1	0	0
2-line	14CSH369	Cliangyou 386	1	0	0
2-line	14CSH286	Cliangyou 396	1	0	0
2-line	14CSH372	Cliangyou 4418	0	0	0
2-line	14CSH324	Cliangyou 513	1	0	0
2-line	14CSH403	Cliangyou 755	1	0	0
2-line	14CSH316	Cliangyouhongmi R01	1	0	0
2-line	14CSH425	Yliangyou 2010	0	0	0
2-line	14CSH414	Yliangyou 2108	1	0	0
2-line	14CSH391	Yliangyou 488	1	0	0
2-line	14CSH416	Yliangyou 51	1	0	0
2-line	14CSH402	Yliangyou 527	1	0	0
2-line	14CSH126	Yliangyou 5845	?	0	0
2-line	14CSH386	Yliangyou 696	1	0	0
2-line	14CSH98	Yliangyou 8188	0	0	0
2-line	14CSH235	Yliangyou 9918	1	0	0
2-line	14CSH394	Aoliangyou 200	0	0	0
2-line	14CSH400	Aoliangyou 28	0	0	0
2-line	14CSH389	Aoliangyou 69	0	0	0
2-line	14CSH395	Aoliangyou 76	0	0	0
2-line	14CSH399	Aolongyou 282	0	0	0
2-line	14CSH113	Aoyou 83	0	0	0
2-line	14CSH396	Baliangyou 18	0	0	0
2-line	14CSH220	Fengliangyou 6#	1	0	0
2-line	14CSH89	Huayou 230	1	0	0
2-line	14CSH100	Liangyou 1259	1	0	0
2-line	14CSH77	Liangyou 15	1	0	0
2-line	14CSH93	Liangyou 1586	1	0	0
2-line	14CSH112	Liangyou 2111	1	0	0
2-line	14CSH96	Liangyou 2161	1	0	0
2-line	14CSH116	Liangyou 2186	1	0	0
2-line	14CSH259	Liangyou 266	1	0	0

2-line	14CSH32	Liangyouhang 2#	1	0	0
2-line	14CSH162	Longliangyou 340	1	0	0
2-line	14CSH73	Longping 602	1	0	0
2-line	14CSH313	Luliangyou 4026	0	0	0
2-line	14CSH46	Luliangyou 98	1	0	0
2-line	14CSH301	Luliangyou 996	0	0	0
2-line	14CSH114	Mingliangyou 527	1	0	0
2-line	14CSH330	Tanliangyou 215	1	0	0
2-line	14CSH404	Changliangyou 173	1	0	0
2-line	14CSH241	Zhuliangyou 06	1	0	0
2-line	14CSH72	Zhuliangyou 08	1	0	0
2-line	14CSH410	Zhuliangyou 10	1	0	0
2-line	14CSH413	Zhuliangyou 120	1	0	0
2-line	14CSH388	Zhuliangyou 173	1	0	0
2-line	14CSH336	Zhuliangyou 189	1	0	0
2-line	14CSH45	Zhuliangyou 1#	1	0	0
2-line	14CSH306	Zhuliangyou 211	1	0	0
2-line	14CSH294	Zhuliangyou 4024	0	0	0
2-line	14CSH48	Zhuliangyou 538	0	0	0
2-line	14CSH243	Zhuliangyou 611	1	0	0
2-line	14CSH370	Zhuliangyou 729	1	0	0
2-line	14CSH308	Zhuliangyou 819	1	0	0
2-line	14CSH346	Zhuliangyou 90	1	0	0
2-line	14CSH16	Zhunliangyou 199	1	0	0
2-line	14CSH148	Zhunliangyou 608	1	0	0
2-line	14CSH405	Nliangyou 2#	1	1	1
2-line	14CSH175	Yliangyou 689	1	1	1
2-line	14CSH172	Guangliangyouai 93	1	1	1
2-line	14CSH163	Hualiangyou 1206	1	1	1
2-line	14CSH245	Huiliangyou 1813	1	1	1
2-line	14CSH246	Huiliangyou 6#	1	1	1
2-line	14CSH189	Liangyou 036	1	1	1
2-line	14CSH160	Liangyou 3905	1	1	1
2-line	14CSH255	Shenliangyou 3059	1	1	1
2-line	14CSH325	Shenliangyou 871	1	1	1
2-line	14CSH39	Shuangliangyou 1#	1	1	1
2-line	14CSH177	Tianliangyou 616	1	1	1
2-line	14CSH227	Wandao153 (2 Line)	1	1	1
2-line	14CSH401	Xiangliangyou 2#	1	1	1
2-line	14CSH176	Yanliangyou 2208	1	1	1
2-line	14CSH339	Cliangyou 4488	1	H	H
2-line	14CSH335	Cliangyou 7#	1	H	H
2-line	14CSH292	Cliangyouhuazhan	1	H	H
2-line	14CSH329	Nliangyou 1#	1	H	H
2-line	14CSH312	Tliangyou 272	1	H	H

2-line	14CSH382	Yliangyou 143	1	H	H
2-line	14CSH4	Yliangyou 16#	1	H	H
2-line	14CSH19	Yliangyou 19	1	H	H
2-line	14CSH340	Yliangyou 1998	1	H	H
2-line	14CSH201	Yliangyou 1#	1	H	H
2-line	14CSH236	Yliangyou 29	1	H	H
2-line	14CSH161	Yliangyou 2#	1	H	H
2-line	14CSH411	Yliangyou 302	1	H	H
2-line	14CSH285	Yliangyou 3218	1	H	H
2-line	14CSH277	Yliangyou 3399	1	H	H
2-line	14CSH233	Yliangyou 372	1	H	H
2-line	14CSH49	Yliangyou 5813	1	H	H
2-line	14CSH56	Yliangyou 5967	1	H	H
2-line	14CSH30	Yliangyou 599	1	H	H
2-line	14CSH338	Yliangyou 6#	1	H	H
2-line	14CSH217	Yliangyou 837	1	H	H
2-line	14CSH234	Yliangyou 900	1	H	H
2-line	14CSH190	Fengliangyou 1#	1	H	H
2-line	14CSH351	Guang8you 199	1	H	H
2-line	14CSH256	Guangliangyou 1128	1	H	H
2-line	14CSH55	Heliangyou 114	1	H	H
2-line	14CSH311	Hualiangyou 164	1	H	H
2-line	14CSH244	Huiliangyou 996	0	1	H
2-line	14CSH284	Keliangyou 529	1	H	H
2-line	14CSH260	Kiangyou 3219	1	H	H
2-line	14CSH28	Liangyou 616	1	H	H
2-line	14CSH170	Liangyou 6326	1	H	H
2-line	14CSH409	Lingliangyou 102	0	1	H
2-line	14CSH248	Lingliangyou 942	1	H	H
2-line	14CSH263	Peiliangyou 981	1	H	H
2-line	14CSH254	Shenliangyou 1#	1	H	H
2-line	14CSH307	Shenliangyou 5814	1	H	H
2-line	14CSH224	Shenliangyou 829	1	H	H
2-line	14CSH58	Shenliangyou 862	1	H	H
2-line	14CSH57	Shenliangyou 865	1	H	H
2-line	14CSH326	Tanliangyou 921	1	H	H
2-line	14CSH331	Wangliangyou 5511	1	H	H
2-line	14CSH169	Xiangliangyou 396	1	H	H
2-line	14CSH5	Xinliangyou 223	1	H	H
2-line	14CSH168	Xinliangyou 6#	1	H	H
2-line	14CSH297	Yangliangyou 6#	1	H	H
2-line	14CSH250	Zhongliangyou 189	1	H	H
2-line	14CSH305	Zhuliangyou 02	1	H	H
2-line	14CSH242	Zhuliangyou 168	1	H	H

2-line	14CSH47	Zhuliangyou 6108	1	H	H
2-line	14CSH251	Zhunliangyou 1141	0	1	H
3-line	14CSH270	1you 899	0	0	0
3-line	14CSH133	Ⅱyou 162	0	0	0
3-line	14CSH65	Ⅱyou 1733	0	0	0
3-line	14CSH24	Ⅱyou 183	0	0	0
3-line	14CSH273	Ⅱyou 28	0	0	0
3-line	14CSH134	Ⅱyou 310	0	0	0
3-line	14CSH333	Ⅱyou 372	0	?	0
3-line	14CSH88	Ⅱyou 549	0	0	0
3-line	14CSH272	Ⅱyou 598	0	0	0
3-line	14CSH193	Ⅱyou 602	0	0	0
3-line	14CSH95	Ⅱyou 6078	0	?	0
3-line	14CSH125	Ⅱyou 629	0	?	0
3-line	14CSH25	Ⅱyou 673	0	0	0
3-line	14CSH92	Ⅱyou 838	0	0	0
3-line	14CSH38	Ⅱyou 936	0	0	0
3-line	14CSH271	ⅡyouH 505	0	0	0
3-line	14CSH42	Ⅱyouhang 2#	0	0	0
3-line	14CSH76	B6you 4761	0	?	0
3-line	14CSH121	Byou 827	1	0	0
3-line	14CSH131	Dyou 20	0	0	0
3-line	14CSH257	Fyou 498	1	0	0
3-line	14CSH102	Fyou 993	1	0	0
3-line	14CSH204	Gyou 217	1	0	0
3-line	14CSH293	H37you 207	1	0	0
3-line	14CSH322	Hyou 159	1	0	0
3-line	14CSH13	Hyou 518	1	0	0
3-line	14CSH207	Kyou 40	1	0	0
3-line	14CSH226	Kyou 88	0	0	0
3-line	14CSH109	Nyou 69	0	0	0
3-line	14CSH192	Q you 5#	0	0	0
3-line	14CSH188	Q2 you 3#	0	?	0
3-line	14CSH194	Qxiang 101	1	0	0
3-line	14CSH87	Qyou 108	0	0	0
3-line	14CSH198	Qyou 18	0	0	0
3-line	14CSH221	Qyou 1#	0	0	0
3-line	14CSH225	Qyou 4108	0	0	0
3-line	14CSH223	Qyou 6#	0	0	0
3-line	14CSH222	Tyou 111	0	0	0
3-line	14CSH393	Tyou 15	0	0	0
3-line	14CSH295	Tyou 180	0	0	0
3-line	14CSH63	Tyou 463	0	0	0
3-line	14CSH321	Tyou 535	0	0	0
3-line	14CSH318	TyouH 505	0	0	0

3-line	14CSH212	Changyou 10#	0	0	0
3-line	14CSH33	Changyou 964	0	0	0
3-line	14CSH200	Chuanfeng 6#	0	0	0
3-line	14CSH107	Chuanjiangyou 527	0	?	0
3-line	14CSH123	Chuannong2you 498	1	0	0
3-line	14CSH94	Chuannongyou 527	1	0	0
3-line	14CSH184	Chuannongyou 528	0	0	0
3-line	14CSH15	Chuanxiangyou 1101	1	0	0
3-line	14CSH239	Chuanxiangyou 506	0	0	0
3-line	14CSH44	Chuanyou 673	1	0	0
3-line	14CSH363	Dexiang 4103	1	0	0
3-line	14CSH82	Deyou 4727	1	0	0
3-line	14CSH431	Fengyou 191	1	0	0
3-line	14CSH105	Fengyou 22	0	?	0
3-line	14CSH360	Fengyou 2#	0	0	0
3-line	14CSH423	Fengyou 9#	0	?	0
3-line	14CSH104	Fengyouxiangzhan	0	0	0
3-line	14CSH429	Fengyuanyou 299	0	0	0
3-line	14CSH110	Fuyou 8217	0	0	0
3-line	14CSH191	Gangyou 188	1	0	0
3-line	14CSH75	Gangyou 22	0	0	0
3-line	14CSH101	Gangyou 301	1	0	0
3-line	14CSH209	Gangyou 36	0	0	0
3-line	14CSH132	Gangyou 364	1	0	0
3-line	14CSH197	Gangyou 48	1	0	0
3-line	14CSH208	Gangyou 527	1	0	0
3-line	14CSH182	Gangyou 618	1	0	0
3-line	14CSH91	Gangyou 725	1	0	0
3-line	14CSH185	Gangyou 88	1	0	0
3-line	14CSH211	Gangyou 881	1	0	0
3-line	14CSH206	Gangyou 900	1	0	0
3-line	14CSH195	Gangyou 94-11	1	0	0
3-line	14CSH117	Guofeng 1 #	0	0	0
3-line	14CSH315	Heyou 1#	0	0	0
3-line	14CSH268	Hongliangyou 166	0	0	0
3-line	14CSH180	Hongyou 2009	1	0	0
3-line	14CSH60	Huyou 196	0	0	0
3-line	14CSH203	Huaxiang 4016	1	0	0
3-line	14CSH381	Jianyou 8#	0	0	0
3-line	14CSH337	Jiefengyou 1#	0	0	0
3-line	14CSH29	Jinnong2you 3#	1	0	0
3-line	14CSH390	Jinyou 117	0	0	0
3-line	14CSH36	Jinyou 1398	0	0	0
3-line	14CSH332	Jinyou 212	0	?	0
3-line	14CSH334	Jinyou 268	0	0	0

3-line	14CSH249	Jinyou 402	0	?	0
3-line	14CSH323	Jinyou 433	0	0	0
3-line	14CSH320	Jinyou 463	0	0	0
3-line	14CSH353	Jinyou 59	0	?	0
3-line	14CSH103	Jinyougui 99	0	0	0
3-line	14CSH397	Jinyouhuai 340	0	0	0
3-line	14CSH280	Kexiangyou 56	0	0	0
3-line	14CSH279	Keyou 21	0	0	0
3-line	14CSH216	Liangxiang 1#（Neixiang6you 498）	1	0	0
3-line	14CSH420	Longxiangyou 3117	0	0	0
3-line	14CSH428	Longxiangyou 3208	1	0	0
3-line	14CSH426	Longxiangyou 7#	0	0	0
3-line	14CSH85	Luyou 578	1	0	0
3-line	14CSH357	Luyou 9803	0	0	0
3-line	14CSH90	Mianyou 725	0	0	0
3-line	14CSH218	Nei2you 111	1	0	0
3-line	14CSH408	Nei5you 263	1	0	0
3-line	14CSH124	Nei5you 39	1	0	0
3-line	14CSH213	Nei5youH 25	1	0	0
3-line	14CSH362	Nei5youyuxiang 1#	1	0	0
3-line	14CSH274	Neiwuyou 8105	1	0	0
3-line	14CSH219	Neixiang 8518	1	0	0
3-line	14CSH119	Neixiangyou 9#	1	0	0
3-line	14CSH210	Neixiangyou 1#	1	0	0
3-line	14CSH289	Nongxiangyou 204	1	0	0
3-line	14CSH253	Qianyou 1#	0	0	0
3-line	14CSH64	Rongyou 1506	0	0	0
3-line	14CSH70	Rongyou 225	0	?	0
3-line	14CSH359	Rongyou 390	0	0	0
3-line	14CSH67	Rongyou 608	0	0	0
3-line	14CSH97	Rong18you 662	1	0	0
3-line	14CSH214	Rongyou 357	0	0	0
3-line	14CSH35	Shanyou 016	0	0	0
3-line	14CSH78	Shanyou 63	0	0	0
3-line	14CSH62	Shanyou 736	0	0	0
3-line	14CSH51	Shanyou 963	0	0	0
3-line	14CSH317	Shangyou 518	1	0	0
3-line	14CSH2	Shenyou 957	0	0	0
3-line	14CSH27	Shenyou 9775	0	0	0
3-line	14CSH377	Shengtaiyou 018	1	0	0
3-line	14CSH376	Shengtaiyou 722	1	0	0
3-line	14CSH269	Shengyou 99-98	1	0	0
3-line	14CSH345	Shuofeng 2#	1	0	0
3-line	14CSH354	Taiyou 390	0	0	0

3-line	14CSH74	Tengyou 527	1	0	0
3-line	14CSH68	Tianfengyou 101	0	0	0
3-line	14CSH52	Tianfengyou 6418	0	0	0
3-line	14CSH50	Tianfengyou T025	0	?	0
3-line	14CSH199	Tianlongyou 827	1	0	0
3-line	14CSH352	Tianyou 122	0	0	0
3-line	14CSH361	Tianyou 2168	0	0	0
3-line	14CSH365	Tianyou 290	0	?	0
3-line	14CSH41	Tianyou 673	0	0	0
3-line	14CSH240	Tianyou 8012	0	0	0
3-line	14CSH366	Tianyou 998	0	0	0
3-line	14CSH281	Tianyouxiang 99	0	0	0
3-line	14CSH265	Weiyou 46	0	0	0
3-line	14CSH264	Weiyou 462	0	0	0
3-line	14CSH266	Weiyou 535	0	0	0
3-line	14CSH3	Weiyou 644	0	0	0
3-line	14CSH275	Weiyou 8#	0	?	0
3-line	14CSH136	Wenfu 7#	1	0	0
3-line	14CSH328	Wufengyou 569	0	0	0
3-line	14CSH53	Wuyou 156	0	0	0
3-line	14CSH355	Wuyou 369	0	?	0
3-line	14CSH368	Wuyou 613	0	?	0
3-line	14CSH205	Xiyou 17	0	0	0
3-line	14CSH278	Xiangfeiyou 8118	0	0	0
3-line	14CSH309	Xiangfengyou 9#	0	0	0
3-line	14CSH298	Xiangyou 616	0	0	0
3-line	14CSH11	Xiangyou 66	0	0	0
3-line	14CSH276	Xiangyou 66	0	0	0
3-line	14CSH252	Xieyou 1429	1	0	0
3-line	14CSH367	Xieyou 716	0	0	0
3-line	14CSH415	Xinxiangyou 111	0	0	0
3-line	14CSH374	Xinyou 9113	1	0	0
3-line	14CSH142	Yixiang 1979	1	0	0
3-line	14CSH137	Yixiang 481	1	0	0
3-line	14CSH143	Yixiang 725	1	0	0
3-line	14CSH215	Yixiangyou 2115	1	0	0
3-line	14CSH81	Yiyou 2815	1	0	0
3-line	14CSH86	Yiyou 591	1	0	0
3-line	14CSH34	Yiyou 673	1	0	0
3-line	14CSH54	YouI 2009	0	0	0
3-line	14CSH66	YouI 608	0	0	0
3-line	14CSH69	YouI 651	0	0	0
3-line	14CSH202	Yuyou 528	1	0	0
3-line	14CSH111	Yuyou 7109	0	0	0
3-line	14CSH120	Yuyou 388	1	0	0

3-line	14CSH130	Yuanyou 409	0	?	0
3-line	14CSH375	Yueyou 360	1	0	0
3-line	14CSH387	Yueyou 518	1	0	0
3-line	14CSH384	Zhongyou 117	0	0	0
3-line	14CSH108	Zhongyou 18	1	0	0
3-line	14CSH187	Zhongyou 6761	1	0	0
3-line	14CSH407	Zhongyou 9806	0	0	0
3-line	14CSH181	Zhongfeng 2# (3 line)	0	0	0
3-line	14CSH71	Kyou 451	1	1	1
3-line	14CSH22	Jiayou 5#	1	1	1
3-line	14CSH59	Jiangke 736	1	1	1
3-line	14CSH167	Qiyou 1068	1	1	1
3-line	14CSH150	Xieyou 80	1	1	1
3-line	14CSH149	Yueyou 938	1	1	1
3-line	14CSH159	Zheyou 18	1	1	1
3-line	14CSH267	Dqibaoyou 1#	1	H	H
3-line	14CSH283	Bingyou 3218	1	H	H
3-line	14CSH282	Bingyou 3399	1	H	H
3-line	14CSH291	Caiyouhuazhan	0	1	H
3-line	14CSH424	Fengyouhuazhan	1	H	H
3-line	14CSH232	Guyou 16	1	H	H
3-line	14CSH231	Guyou 169	0	1	H
3-line	14CSH230	Guyou 3139	1	H	H
3-line	14CSH228	Guyou 3301	1	H	H
3-line	14CSH229	Guyou 527	1	H	H
3-line	14CSH40	Guyou 964	1	H	H
3-line	14CSH14	Huaxiangyou 69	1	H	H
3-line	14CSH406	Huayou 322	0	1	H
3-line	14CSH356	Jinyou 163	0	1	H
3-line	14CSH310	Jinyou 284	0	1	H
3-line	14CSH427	Longxiangyouhuazhan	0	1	H
3-line	14CSH171	Lvfeng 20	1	H	H
3-line	14CSH165	Qianyou 930	0	1	H
3-line	14CSH364	Qingyou 109	0	1	H
3-line	14CSH43	Shanyou 70	0	1	H
3-line	14CSH430	Shenyou 9520	0	1	H
3-line	14CSH122	Shenyou 9734	0	1	H
3-line	14CSH378	Shengtaiyou 9712	1	H	H
3-line	14CSH379	Tanyuanyou 0845	1	H	H
3-line	14CSH37	Teyou 009	1	H	H
3-line	14CSH237	Teyou 107	1	H	H
3-line	14CSH31	Teyou 175	1	H	H
3-line	14CSH26	Teyouhang 2#	1	H	H
3-line	14CSH61	Tianfengyou 316	0	1	H
3-line	14CSH304	Tianyouhuazhan	0	1	H

3-line	14CSH262	Wuyouhuazhan	0	1	H
3-line	14CSH261	Xinlongyou 1#	1	H	H
3-line	14CSH341	Xingyou 1#	0	1	H
3-line	14CSH155	Yongyou 15	0	1	H
3-line	14CSH327	Yueyou 27	1	H	H
3-line	14CSH299	Yueyou 712	1	H	H
3-line	14CSH373	Yueyou 9264	1	H	H
3-line	14CSH300	Zaofengyouhuazhan	1	H	H
2-line	14CSH115	Ejingza 1#	1	1	1
3-line	14CSH79	Yunyou 948	1	0	0
3-line	14CSH147	Chunyou 84	1	1	1
3-line	14CSH157	Yongyou 12	1	1	1
3-line	14CSH173	Yongyou 17	1	1	1
3-line	14CSH156	Yongyou 538	1	1	1
3-line	14CSH158	Yongyou 9#	1	1	1

Table S5 Genotypes of *Ghd7* in 14 hybrid combinations

Hybrids	Maternal parents	Paternal parents	*Ghd7*		Two or three line hybrid rice
			M	P	
Z1007	Zi100A	RB207-1	-	++	3-line
YY1	Y58S	93-11	-	++	2-line
PA64S/JSD	PA64S	Jusuidao	+	++	2-line
LY1128	P88S	HR1128	-	++	2-line
YY2	Y58S	Yuanhui2	-	++	2-line
Ⅱ Y838	Ⅱ-32A	Fuhui838	-	++	3-line
FY299	FengyuanA	Xianghui299	-	++	3-line
LYP9	PA64S	93-11	+	++	2-line
LY0293	P88S	0293	-	++	2-line
YTA/93-11	YuetaiA	93-11	+	++	3-line
V46	V20A	Miyang46	-	++	3-line
SY63	Zhenshan97A	Minghui63	-	++	3-line
JY207	Jin23A	Xianhui207	-	++	3-line
PA64S/R527	PA64S	Shuhui527	+	++	2-line

++: functional allele similar to $Ghd7^{93\text{-}11}$

+: weakly functional allele identical to $Ghd7^{Nipponbare}$

-: nonfunctional allele

Table S6. List of primers used for PCR and sequencing

	Forward primer	Reverse primer	Product size (bp)
RH8cds	GTCCTTATGTTTGCTTTGTGTCCG	AATATATGTTTTCCCCAATGTGCC	1335
RH8Seq-1	ACTCGCATCTCCTCACCTCCTTTC	_	_
RH8Seq-2	TATTTTTCTTCAATTTTAAACCATAC	_	_
RH8indel	TCCGCATCGATACCGTCTTCCC	TCAACCACCTCCGTTGCCTCCT	1440
RH8caps (Digested with *Tsp*R1)	CACCACTCCATCCTCAACTCCC	TGTTTTCCCCAATGTGCCAAGC	1240

Other Supporting Information Files

Dataset S1 (XLSX)

Dataset S2 (XLSX)

Dataset S3 (XLSX)

Dataset S4 (XLSX)

Dataset S5 (XLSX)

Dataset S1. Phenotypic data for LYP9 and its parents for the years 2010-2015.

Dataset S2. QTL information on yield-related traits detected in the RIL and RILBC1 populations.

Dataset S3. Overview of the mRNA sequencing and mapping results.

Techniques and biological replicates are also included. All of the sequence reads from each sample were mapped onto the genome and junction sequences of *O. sativa japonica* (TIGR Ver 6.1), and only uniquely-mapped reads were used for further expression abundance quantification.

Dataset S4. Flowering-, circadian rhythm-, and panicle branching-related non-additively expressed genes.

Dataset S5. Enriched pathways of the DEGs that overlapped with QTL regions.