Supplemental dataset

C:\Users\DELL\Desktop\PCA.tiff

**Figure 1.** Principal component analysis (PCA) on 2.3 million filtered SNPs in minicore population encompassing 206 rice accessions. Five subpopulations were used, *indica* includes *Australica* (AUS) and *indica* (IND), while, *japonica* contains *temperate japonica* (TEJ), *tropical japonica* (TRJ), and aromatic (ARO). Admix represents a mixture of *indica* and *japonica*.

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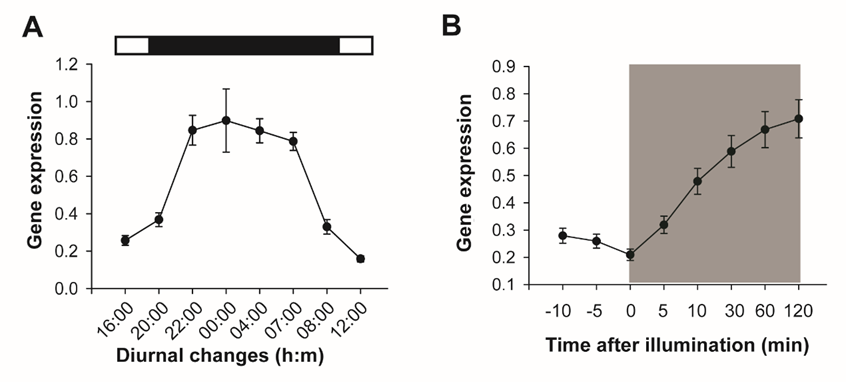
**Figure 2.** Haplotype analysis of *FIP1* (Fip1 motif family protein). (**A**) Pair-wise LD between SNP markers on promoter and coding region of *FIP1* on chromosome 3 (Chr. 3). The LD was indicated as D’ values via Haploview software. Three haplotypes (HapI, HapII and HapIII) harboring three alternative SNPs were identified at different positions of Chr.3. (**B**) Comparison on *R*d among the three haplotypes. A *t*-test was used to estimate the *P-*value among the three haplotypes. The accessions number for each haplotype was indicated in brackets. (**C**) Pie-charts of the three haplotypes. The percentage of each subpopulation counting for the total accessions of each haplotype was displayed. Subpopulation includes admix, ARO, AUS, IND, TEJ, and TRJ.

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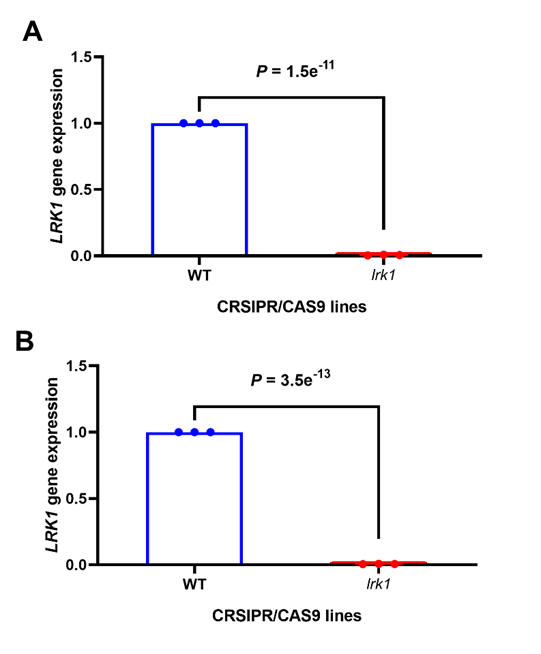
**Figure 3.** Haplotype analysis of *RBC6* (ribosomal protein L6). (**A**) Pair-wise LD between SNP markers on the promoter and coding region of *RBC6* onChr.3. The LD was indicated as D’ values via Haploview software. Two haplotypes (HapI and HapII) harboring three alternative SNPs at different position are shown. (**B**) Comparison on *R*d between hapI and hapII. A *t*-test was applied to evaluate the *P-*value among the two haplotypes. The accessions number for each haplotype was indicated in brackets. (**C**) Pie-charts of the two haplotypes. The percentage of each subpopulation counting for the total accessions of each haplotype was indicated. Subpopulation includes admix, ARO, AUS, IND, TEJ, and TRJ.

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**Figure 4.** Phylogenetic tree of *LRK1* within other species constructed based on the comparison of protein sequences between spices. Protein sequence for each species was downloaded from the NCBI protein database website (https://www.ncbi.nlm.nih.gov/). The nodes are depicted in different colors represent separate clusters. The model plants are highlighted in red and bold font.



**Figure 5.** Light-dependent gene expression of *LRK1*. (**A**) A diurnal evolution of *LRK1* gene expression. White and black bars stand for light (1500 μmol × m-2 × s-1) and dark periods, respectively, in the growth room. (**B**) Response of *LRK1* gene expression to light-dark transition and its evolution during darkness. Grey region represents the dark period after switching from an illumination of 1500 μmol m-2 × s-1. Each data point of the gene expression level (panels A and B) represents the mean of three biological replicates performed on three different leaves obtained from three different plants ± standard error (SE).



**Figure 6.** The expression levels of *LRK1* in WT and CRISPR-CAS9 edited rice lines (*lrk1*). The gene expression of *LRK1* in WT and *LRK1* mutants (*lrk1*) was compared using primer pair 1 (**A**) and primer pair 2 (**B**). The sequences for primer pair 1 are F: CCATGATGGGACCTCTGTGG; R: CATGATCGGCACCAGCCTTT, while for primer 2, they are F: TCCTCGACATCTCCGGCT; R: AGCTGCCCCGAGAGTAGATT, as shown in Table S1. The expression of *LRK1* gene was normalized to 1. The leaf samples in two rice lines were collected at 22:00 in 40-day old plants. Data represent the mean of three biological replicates performed on three different leaves obtained from three different plants ± standard error (SE). The Student’s *t*-test was used to determine the statistical significance of the difference of means between WT and *lrk1*.

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**Figure 7.** Photosynthetic rates assessed in WT and *lrk1* grown under either normal or heat stress conditions. **Panels A and B**, Photosyntheic rates under high light (1500 μmol × m-2 × s-1; *Ahigh*) and low light (100 μmol × m-2 × s-1; *Alow*), respectively, in WT and *lrk1* grown in GR at 25°C. **Panels C and D**, *Ahigh* and*Alow* measured on WT and *lrk1* grown in GR under heat stress condition (35 °C). *Ahigh* and*Alow* were measured during the time lapse of 9:30 am to 11:30 am at the same time during which *R*d was measured for both normal and heat stress conditions. Data was derived from 10 biological replicates for both *Ahigh* and*Alow*. A *t*-test was performed to compare the signifcant differences of *Ahigh* and*Alow* between WT and *lrk1* growth under either normal or heat stress treatment.

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**Figure 8.** Q10 of the leaf *R*d throughout nighttime in WT and *lrk1* mutant. Data was obtained from 60-day old plants grown in GR. Each data point is the average of six meaurments performed on six different plants ± SE.

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