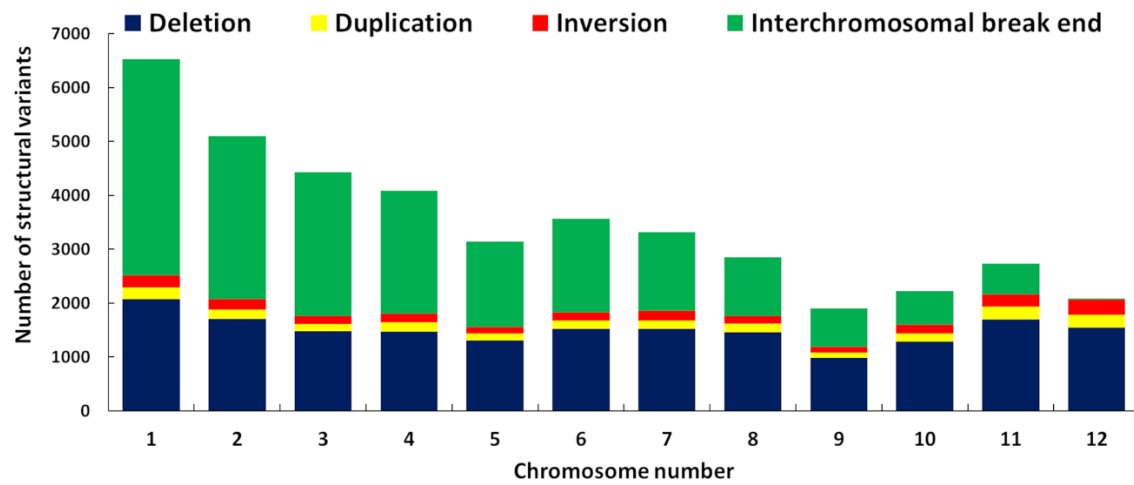
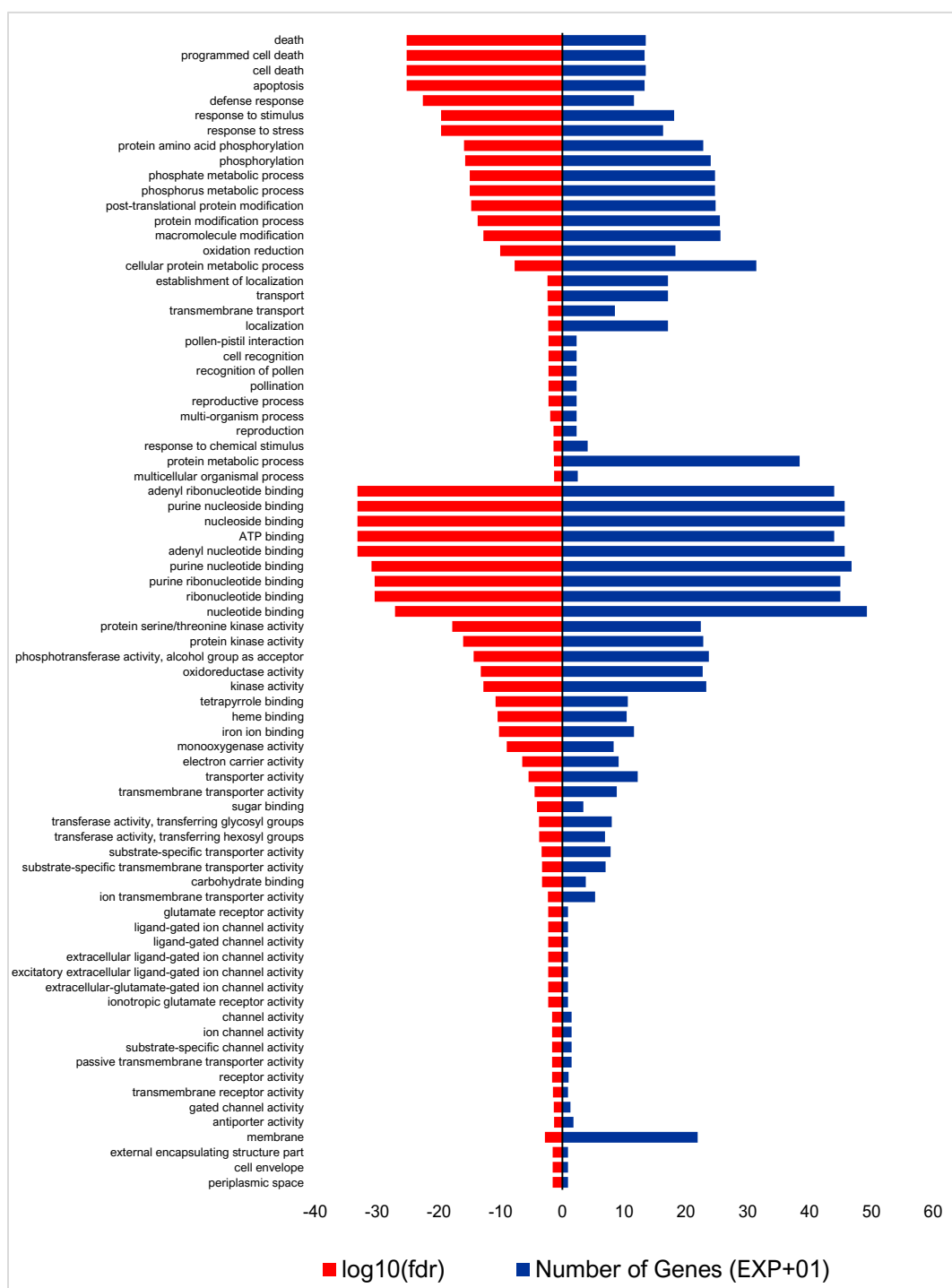


**Figure S1.** Unique SNP and InDels with high impact identified in PSRR-1 through comparison with 3K-Rice genome data set.

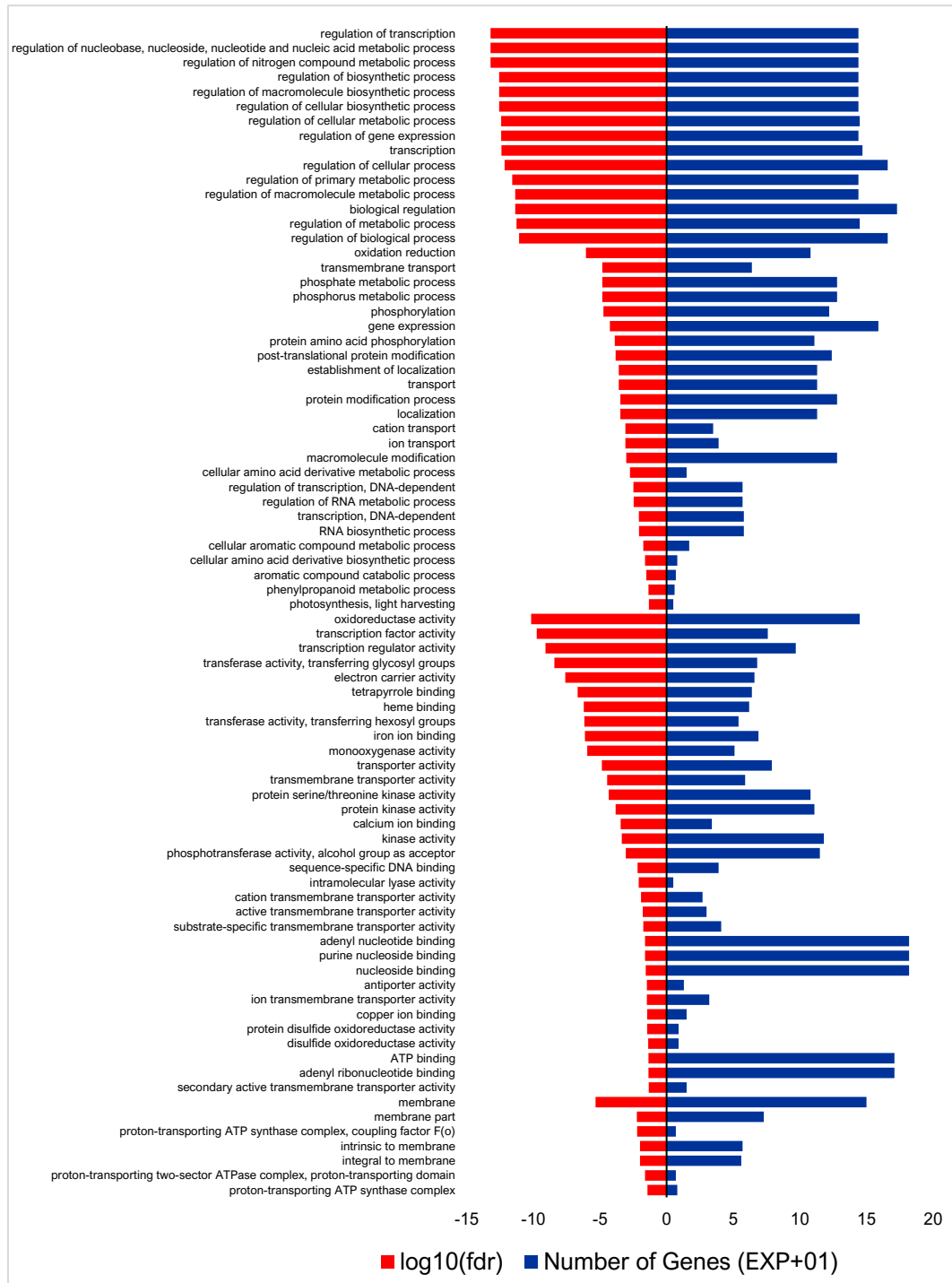


**Figure S2.** Types of structural variants identified in PSRR-1 through comparison with 3K-Rice genome data set and their distribution in rice genome

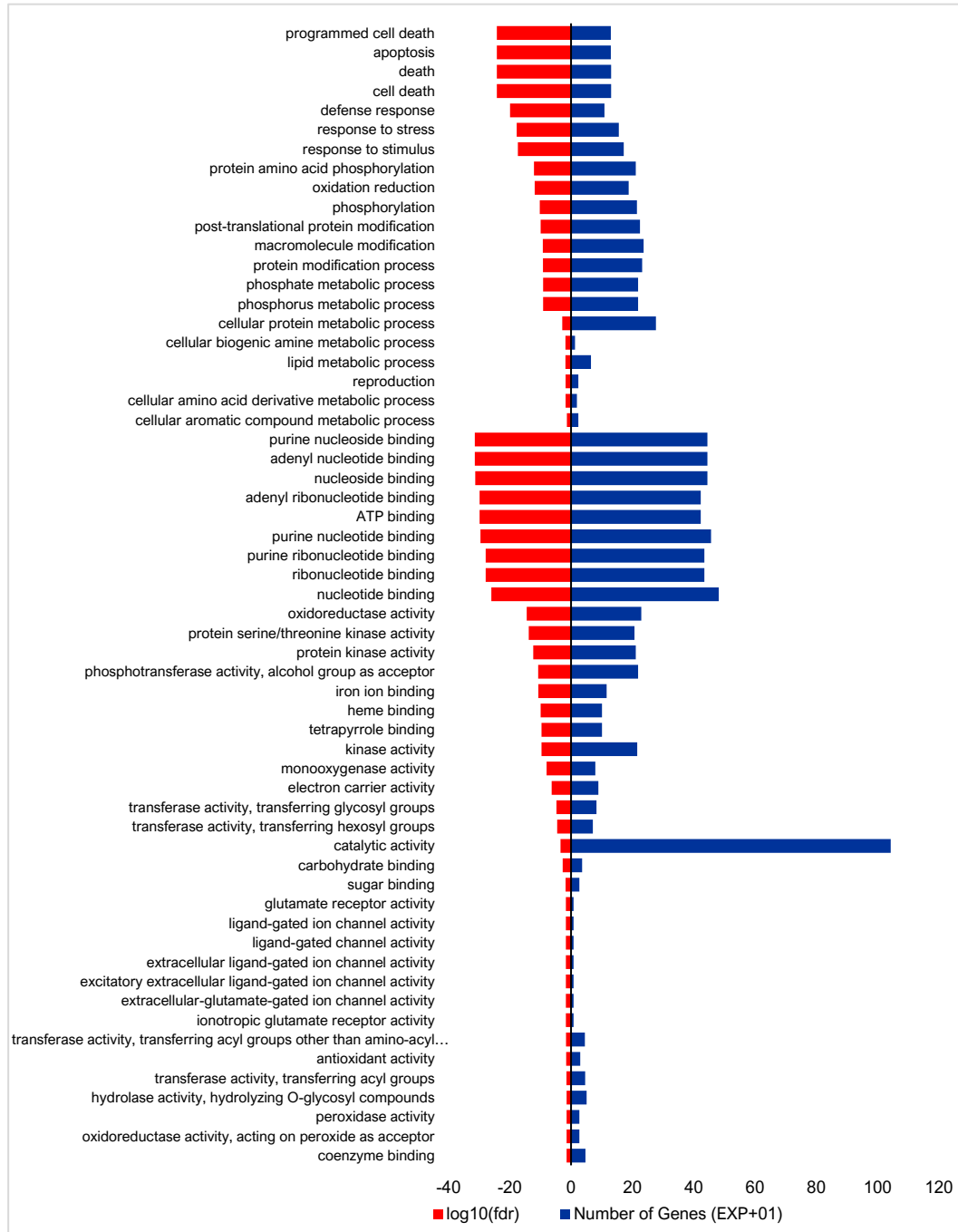
A



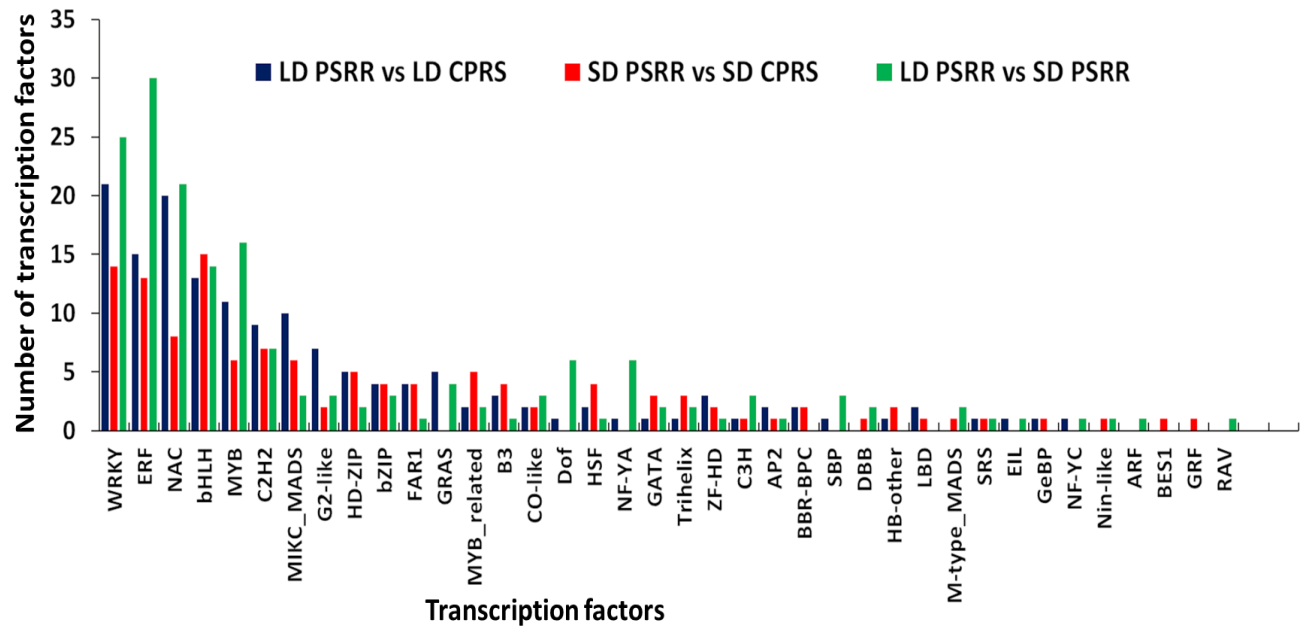
**B**



C



**Figure S3.** Gene ontology of differentially expressed genes between PSRR-1 and Cypress under different daylength conditions. (A) Long day PSRR-1 vs long day Cypress, (B) long day PSRR-1 vs short day PSRR-1, and (C) short day PSRR-1 vs short day Cypress.



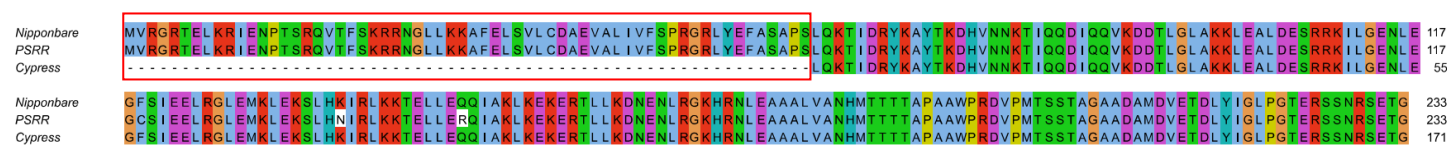
**Figure S4.** List of transcription factor families and their frequencies represented among the differentially expressed genes under different daylength conditions. (A) Long-day PSRR-1 vs long-day Cypress, (B) long-day PSRR-1 vs short-day PSRR-1, and (C) short-day PSRR-1 vs short-day Cypress.

[illegible]



**Figure S5.** Nucleotide sequence alignment of *OsMADS56* (LOC\_Os10g39130) in Nipponbare, Cypress, PSRR-1. The sequences of *OsMADS56* were aligned with MUSCLE using Jalview (version 2.11.1.4). Numbers on the right side of the sequences are base pair coordinates in reference to Nipponbare. Dark blue shade indicates differences in nucleotide sequence in all three samples while light blue signifies variation in one sample. Dash represents gaps in the sequence. Red box highlights the 1008 bp deletion in Cypress.





**Figure S6.** Protein sequence alignment of *OsMADS56* (LOC\_Os10g39130.1) in Nipponbare, Cypress, PSRR-1. The sequences of *OsMADS56* were aligned with MUSCLE using Jalview (version 2.11.1.4). Color shade signifies amino acid profile used in ClustalX alignments. Dash symbolizes gaps in the sequence. Red box highlights absence of start codon due to the 1008 bp deletion involving the CDS region in Cypress.