Comparative transcriptome analysis reveals molecular response to salinity stress of salt-tolerant and sensitive genotypes of *indica* rice at seedling stage

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Supplementary Figures

Figure S1. The growth vigor of these two genotypes in the absence of salinity. The leaf four rows were tolerant Xian156 seedlings, while right four rows were sensitive IR28 seedlings.

Figure S2. The saturation curve of all sequencing data from 18 RNA library indicated that sequencing depth was enough for transcriptome assembly and expression detection.

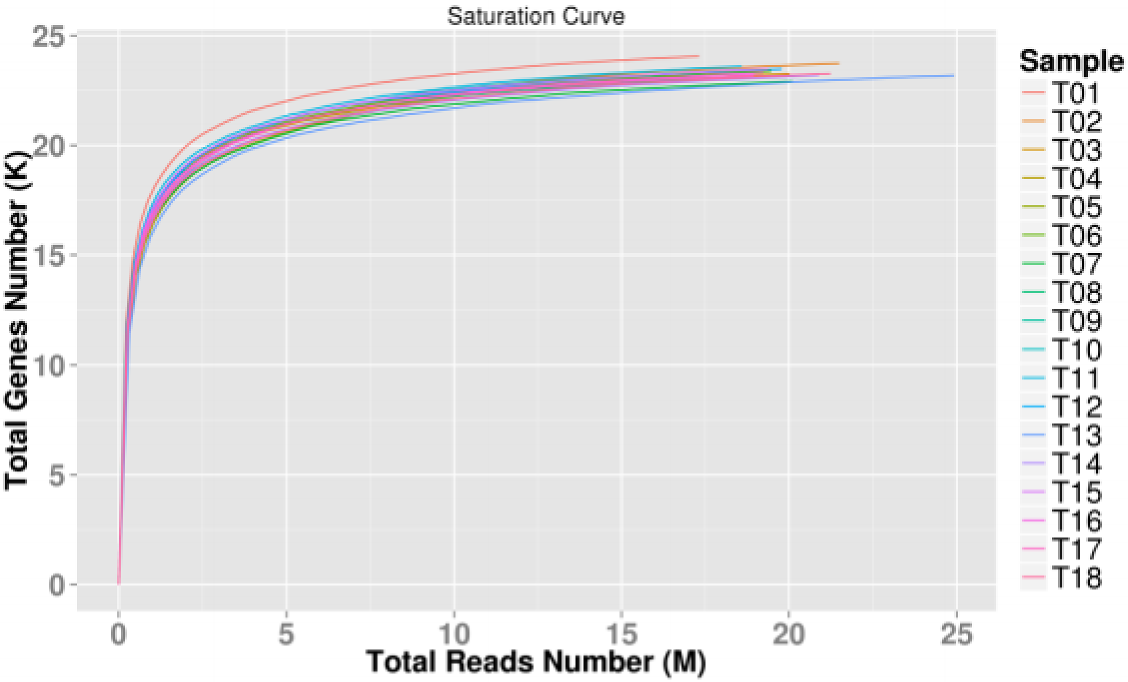


Figure S3. Venn diagram of lncRNAs predicted by CPC, CNCI, CPAT and Pfam pipelines.

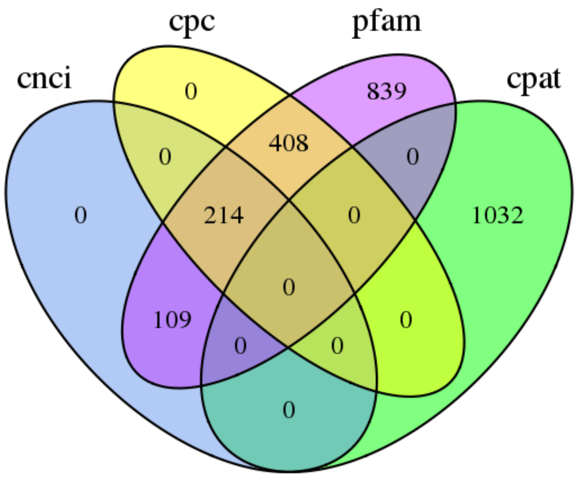


Figure S4. After comparing with proteins in NCBI NR database, homologs of most newly identified genes were also found in other monocots, such as *Oryza brachyantha*, *Zea mays*, *Oryza sativa* and *Setariz italic*.

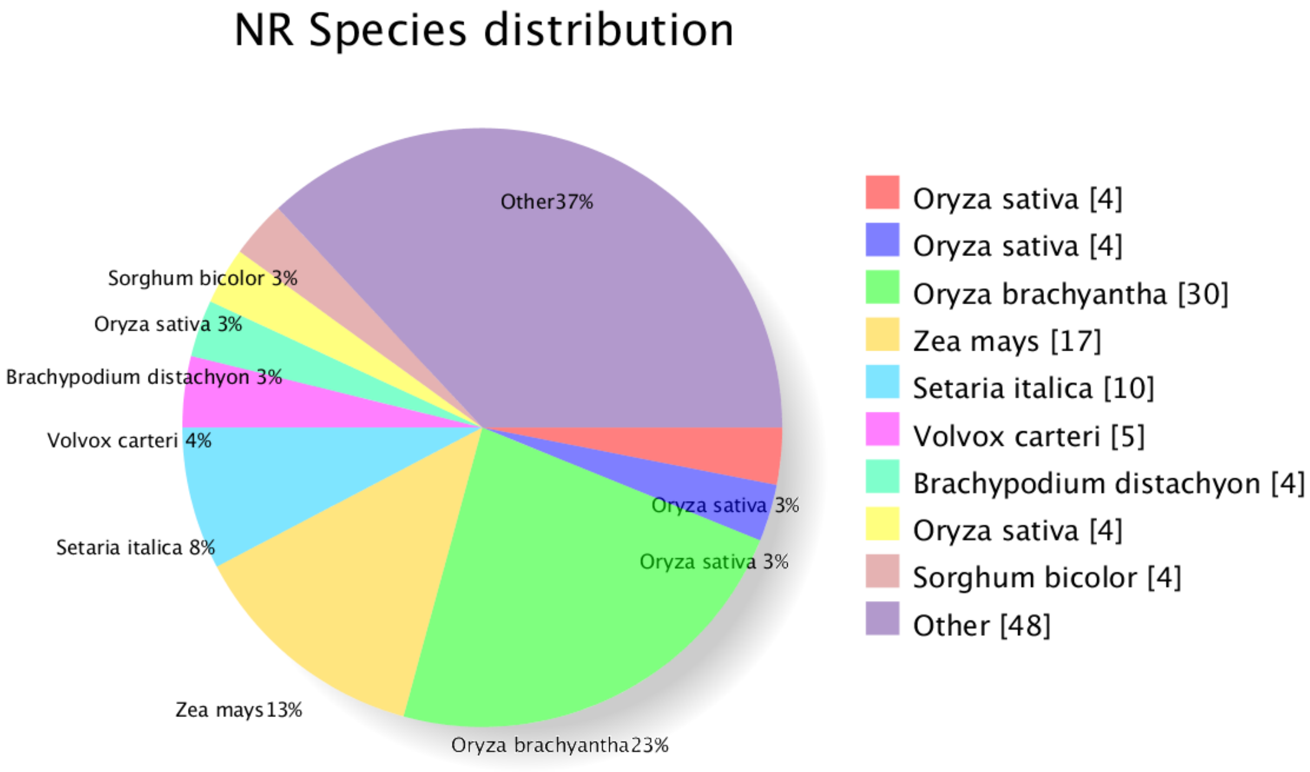
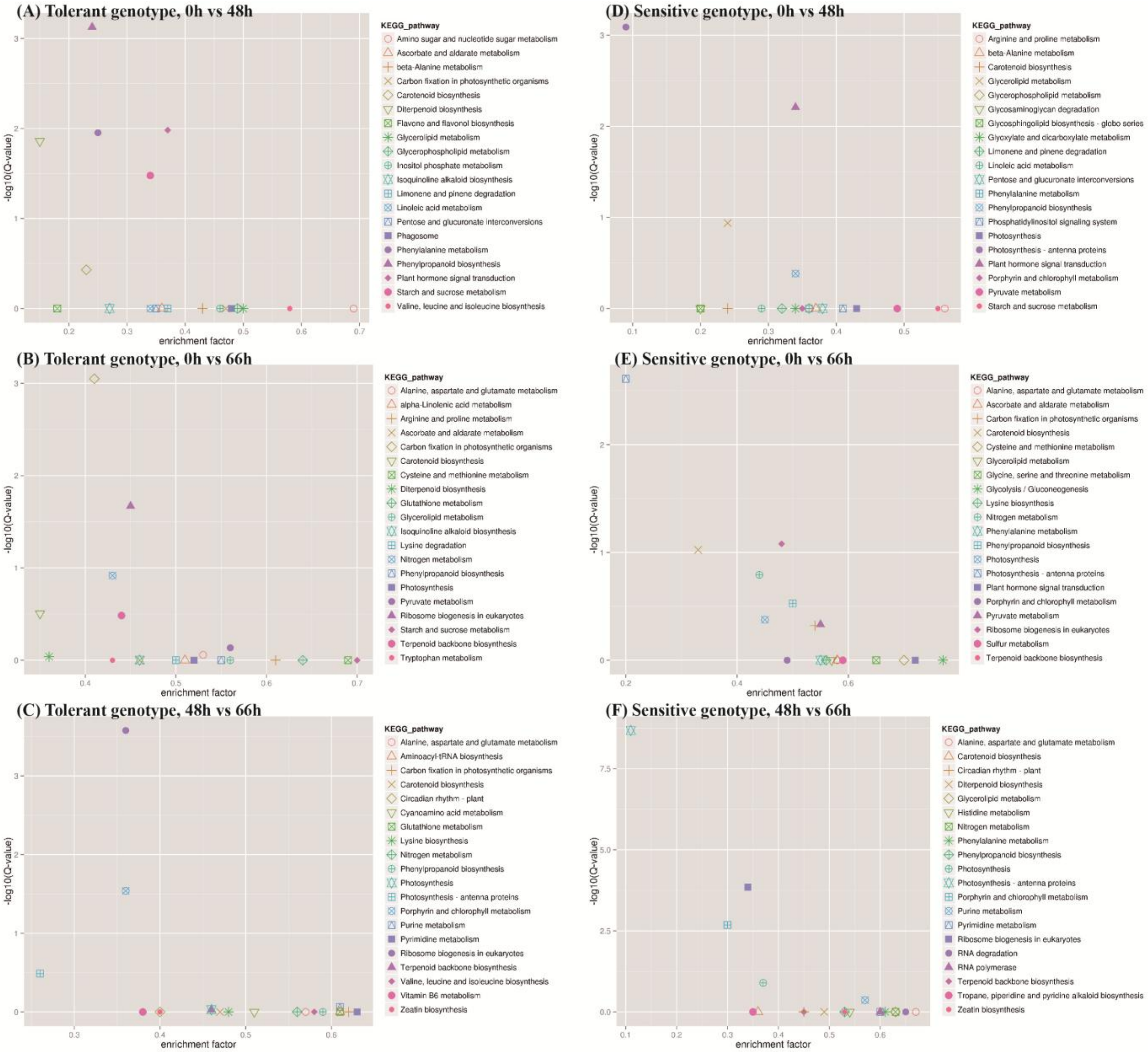


Figure S5. The KEGG enrichment of DEGs between different time-points.



(A) Tolerant genotype, 0h vs 48h

(B) Tolerant genotype, 0h vs 66h

(C) Tolerant genotype, 48h vs 66h

(D) Sensitive genotype, 0h vs 48h

(E) Sensitive genotype, 0h vs 66h

(F) Sensitive genotype, 48h vs 66h