

Figure S1. The principal component analysis (PCA) of mRNAs (a) and lncRNAs (b). The yellow circles represent RBSDV-infected rice plants. The blue triangles represent the MOCK rice plants.

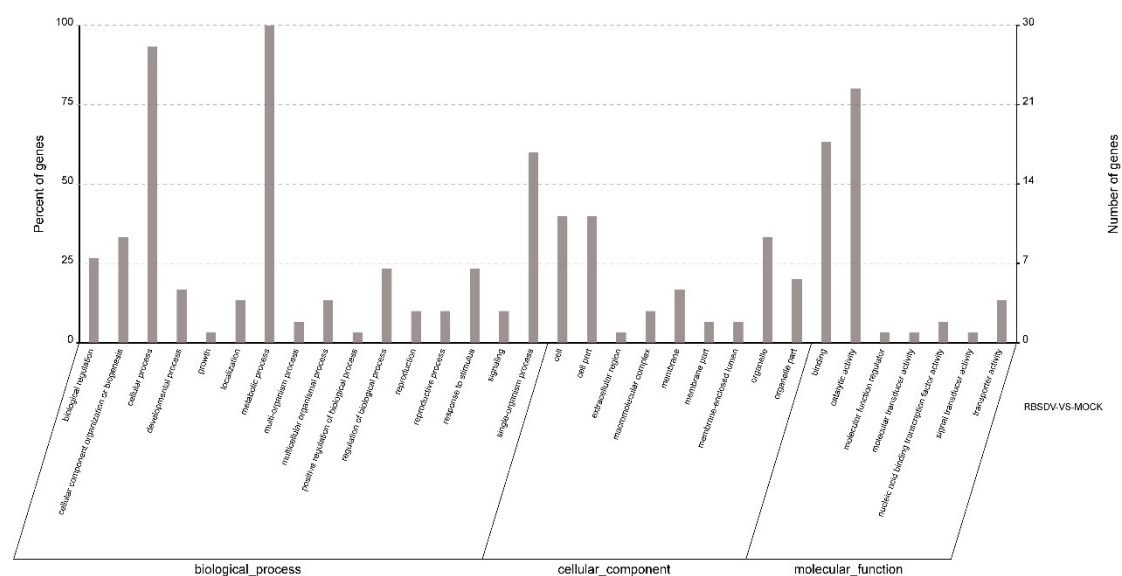


Figure S2. GO enrichment analysis of mRNAs co-located with DElncRNAs identified between the RBSDV-infected and the mock rice plants.

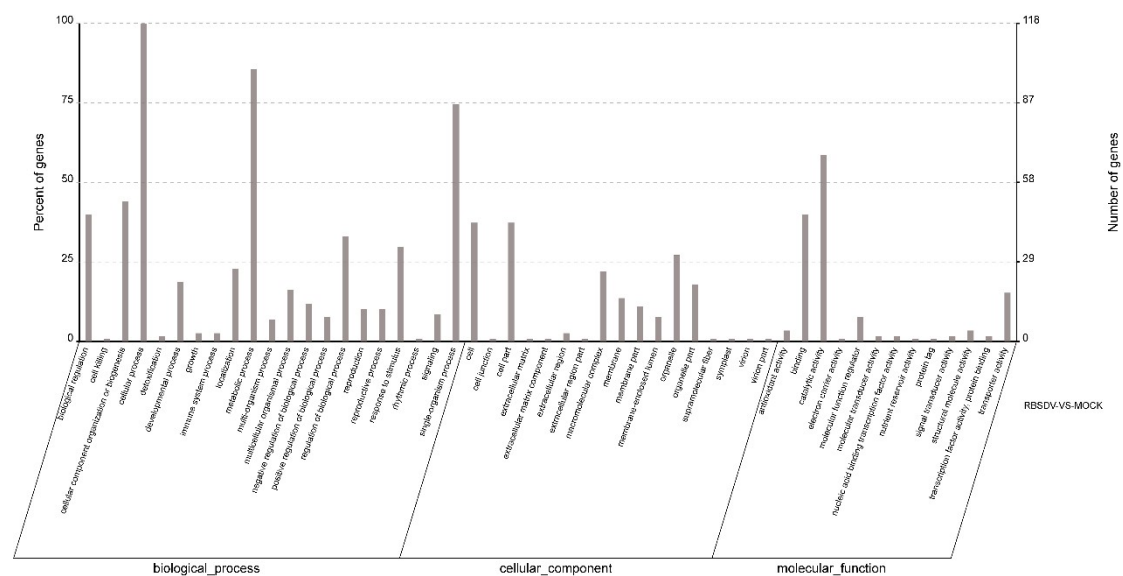


Figure S3. GO enrichment analysis of mRNAs co-expressed with DElncRNAs identified between the RBSDV-infected and the mock rice plants.

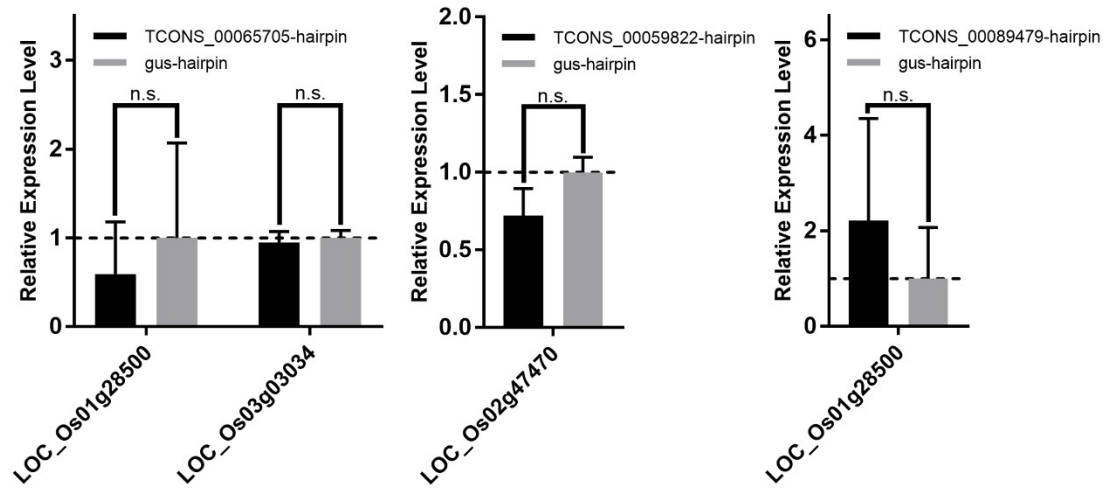


Figure S4. The qRT-PCR data of the mRNAs with no significant changes after silencing lncRNAs. The total RNA of rice callus in Fig. 8 was used for qRT-PCR analyses. *OsUBC* served as an internal reference in relative quantification. The values represent means of the mRNA expression levels \pm standard deviations (SD) relative to the gus-hairpin-expressed callus tissues ($n = 3$ biological replicates). The significant differences between lncRNA-silenced and gus-hairpin-expressed callus tissues were determined by Student's *t*-test.(two-sided, n.s. = not significant)