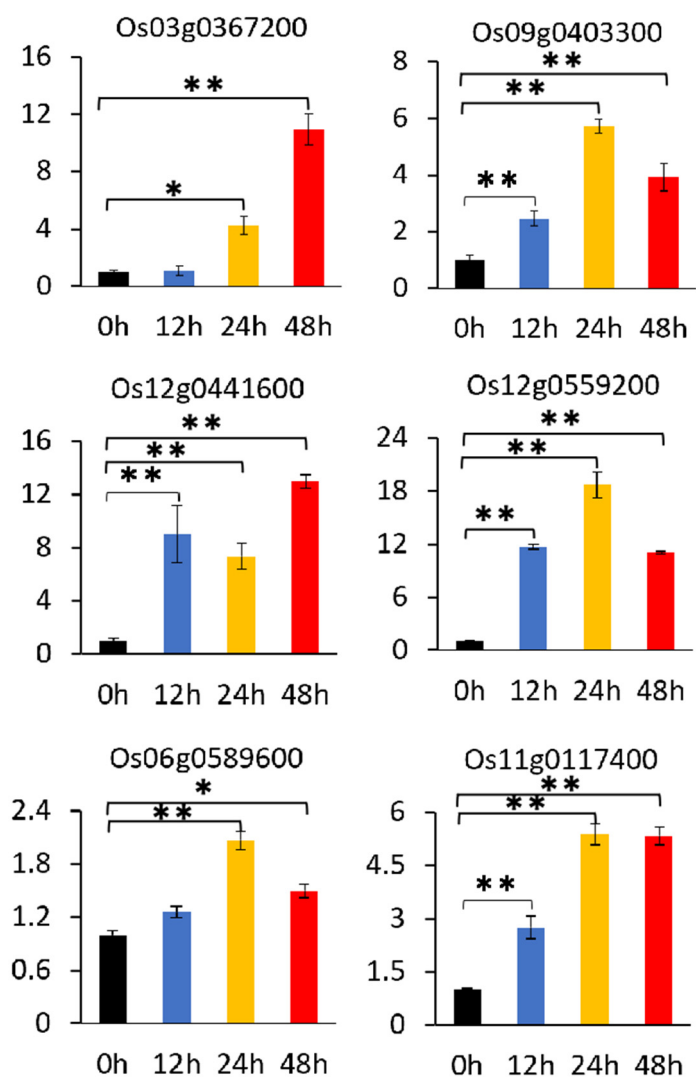
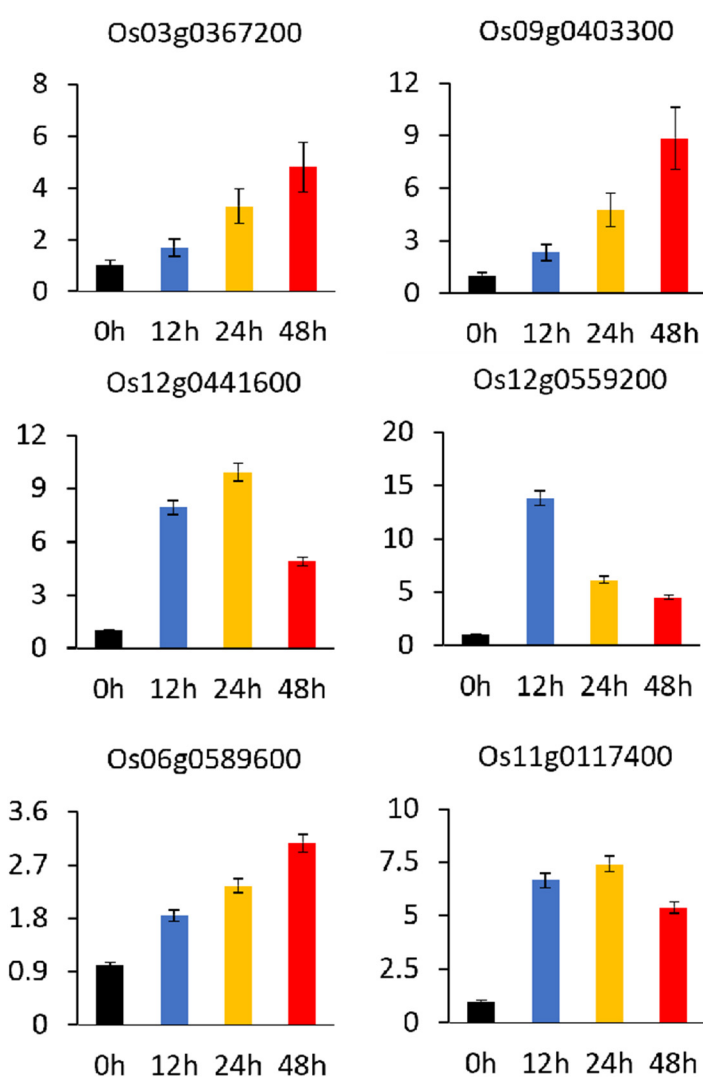
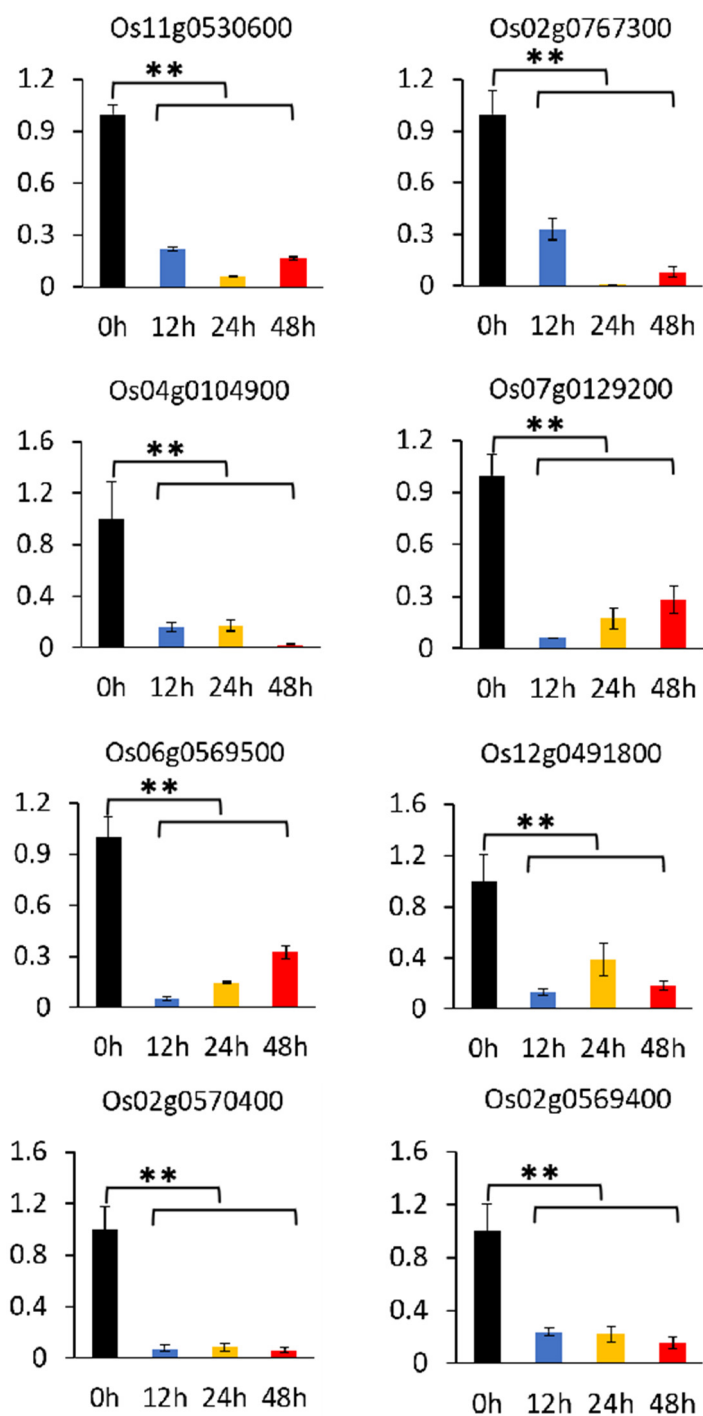


**A****qPCR****B****RNA-Seq**

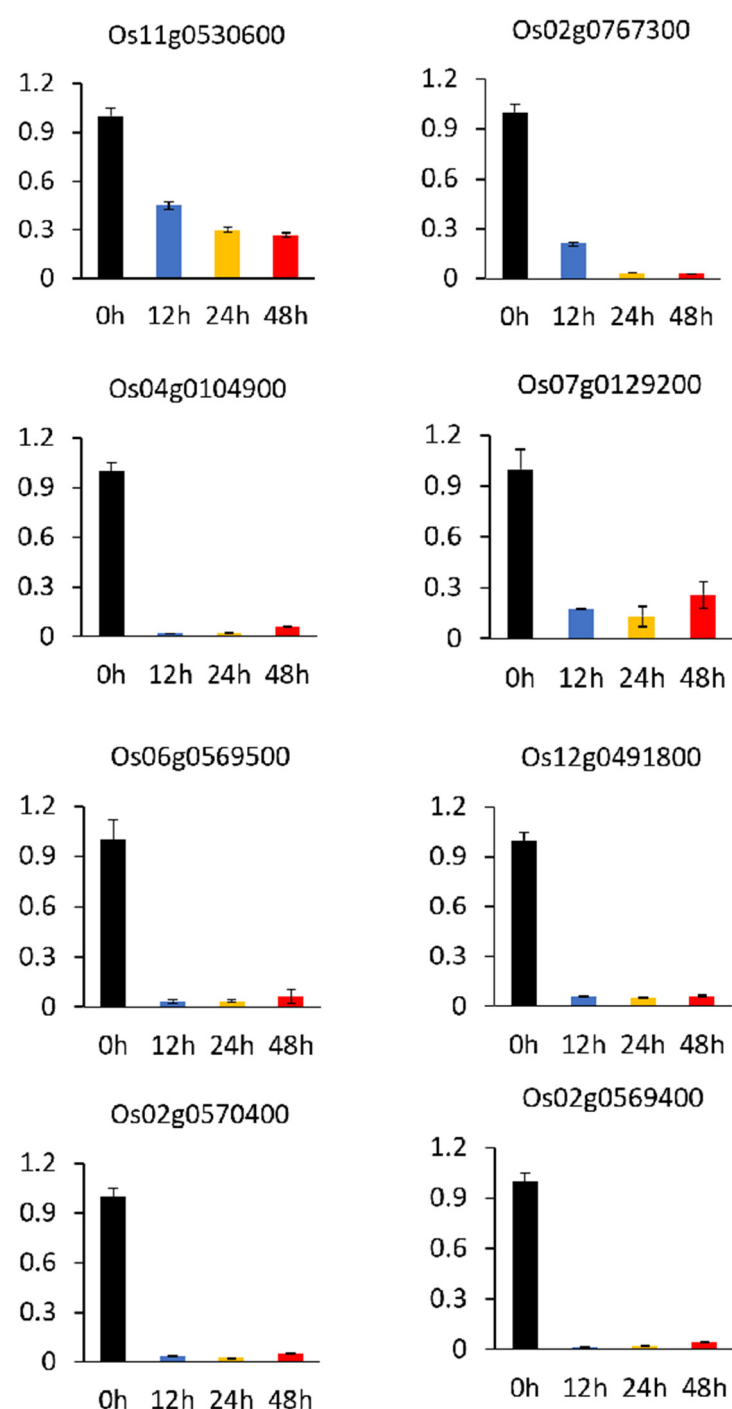
C

qPCR



D

RNA-Seq



**Figure S3.** Validation of the gene expression profiles obtained by RNA-seq using quantitative polymerase chain reaction (qPCR). Fold-changes in transcript abundance obtained by both qPCR and RNA-seq were presented on the same graph for fourteen genes. **(A)** and **(C)** showed the fold-change determined by PCR, **(B)** and **(D)** showed the fold-change in the Fragments Per Kilobase of transcript sequence per Millions mapped reads (FPKM) obtained by RNA-seq. Os11g0530600, Os02g0767300, Os03g0367200, and Os04g0104900 were involved in flavonoid biosynthesis; Os06g0589600, Os07g0129200, and Os11g0117400 were involved in plant-pathogen interaction; Os06g0569500, Os12g0491800, Os02g0570400, and Os02g0569400 were involved in diterpenoid biosynthesis; and other three genes: Os09g0403300, Os12g0441600, and Os12g0559200. \*  $p < 0.05$ , \*\*  $p < 0.01$ .