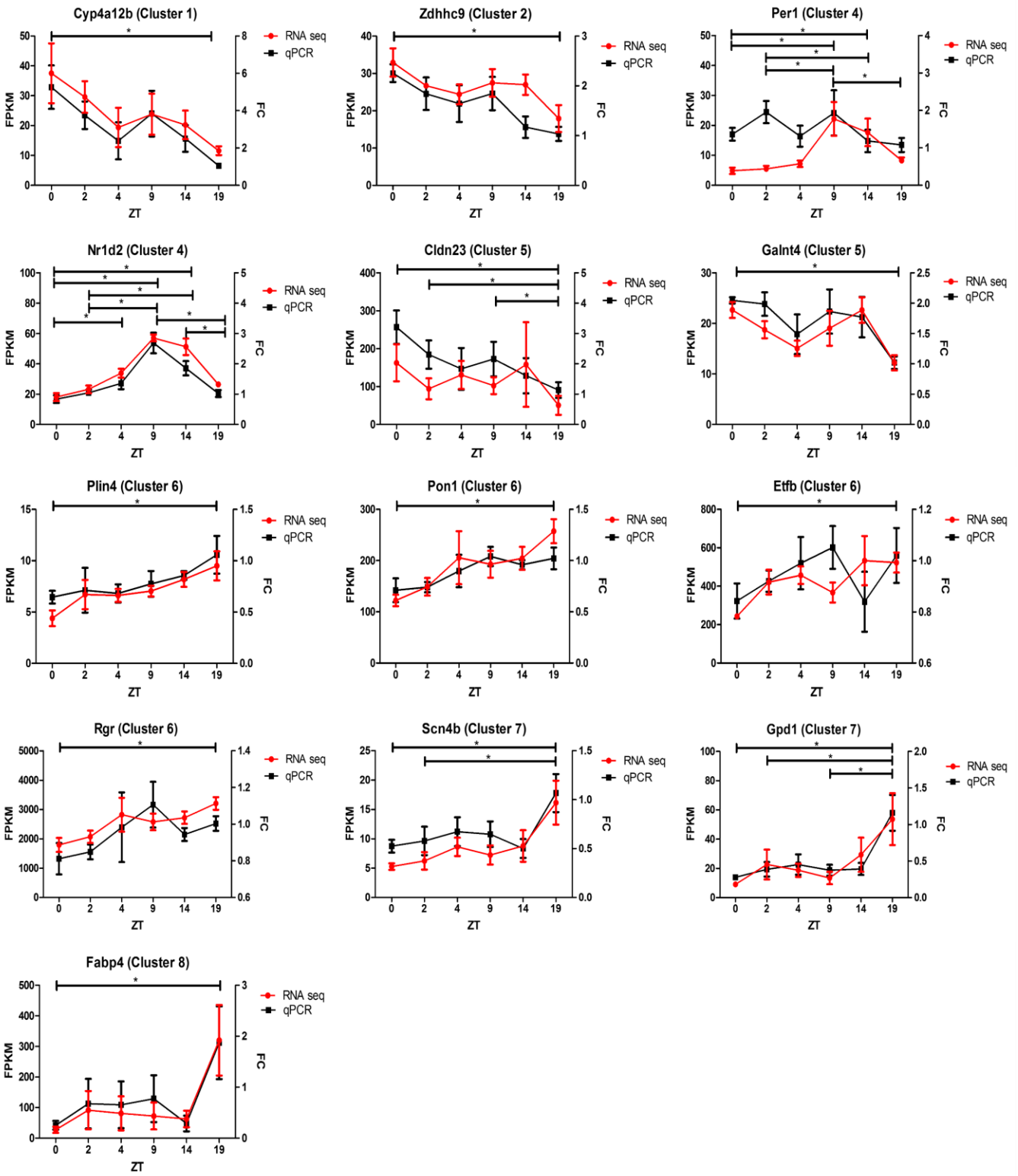

Figure S1. Validation of RNA-seq data using quantitative RT-PCR analyses. To check the validity of our RNA-seq data, 13 differentially expressed genes were selected derived

representing 7 of the 8 identified clusters and subsequently analyzed using qRT-PCR. *Gusb* expression was used as housekeeping gene. Relative expression levels (fold change, FC) were compared with RNA-sequencing data (fragments per kilobase mapped, FPKM). *, $P<0.05$ by RNA-seq analysis.