

Figure S1. Comparison of RNA-seq and RT-qPCR data. A Pearson correlation coefficient of 0.71 is observed between the RNA-seq and RT-qPCR data of eight genes.

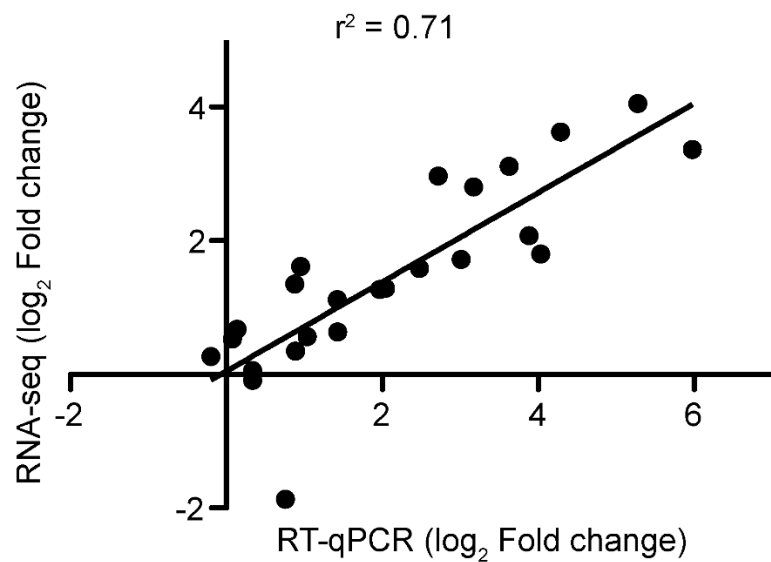


Table S1. Summary of RNA-seq data.

Table S2. The RPKM values of eight differentially expressed genes shown in Fig. 3c.

Table S3. Eighty-four differentially expressed genes identified by RNA-seq.

Table S4. The top five KEGG pathways in which DEGs are enriched.

Table S5. Summary of ChIP-seq data obtained in this study.

Table S6. Summary of 838 high confidence enrichment peaks for PPARD identified by ChIP-seq.

Table S7. The target genes of PPARD identified by ChIP-seq.

Table S8. Primers used in this study.