Figure S1: KEEG analysis of differentially expressed genes in the corpus luteum after LPS (A); treatment or LPS in combination with: GW0724 at a concentration of 1 μmol/L (B); GW0724 at a concentration of 10 μmol/L (C); GSK3787 treatment (D). The color indicates the *p* value of each pathway, while the size of the circle represents gene number in each pathway.
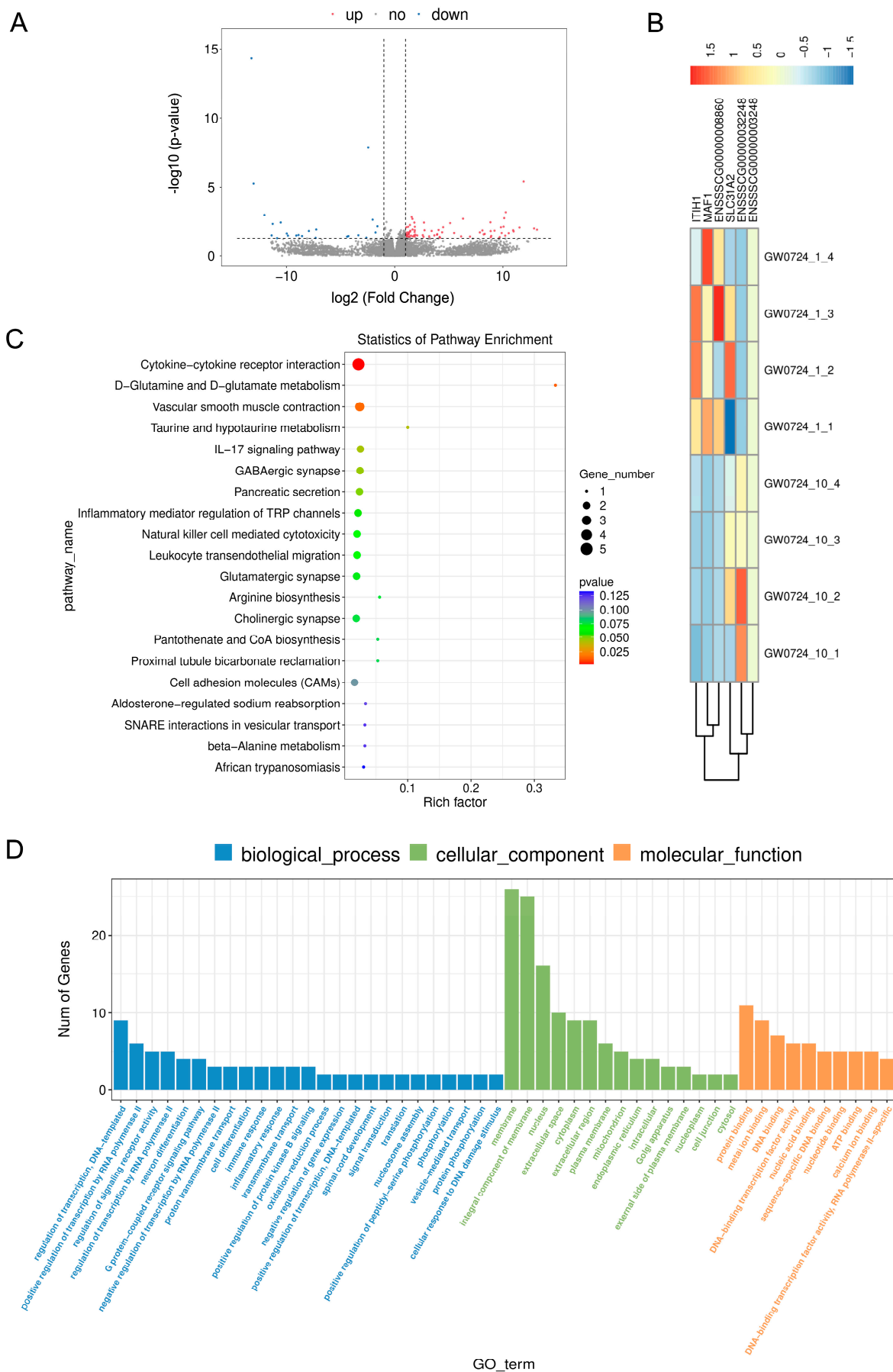
Figure S2: Volcano plots describing the abundance of transcript expression profiles between GW0724 at a concentration of 1 μmol/L and GW0724 at a concentration of 10 μmol/L (A); hierarchical clustering heatmap of differentially expressed genes between GW0724 at a concentration of 1 μmol/L and GW0724 at a concentration of 10 μmol/L (B); KEGG analysis of the differentially expressed genes between GW0724 at a concentration of 1 μmol/L and GW0724 at a concentration of 10 μmol/L (C); GO analysis of the differentially expressed genes between GW0724 at a concentration of 1 μmol/L and GW0724 at a concentration of 10 μmol/L (D).
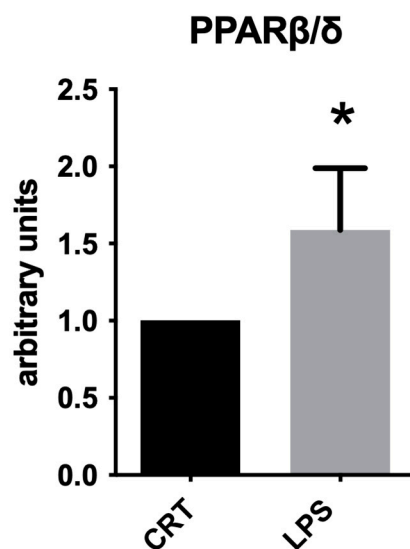
Figure S3: Expression of *PPARβ/δ* mRNA in porcine corpus luteum during mid-luteal phase after LPS treatment. Results were considered statistically significant at $p \leq 0.05$ (*).
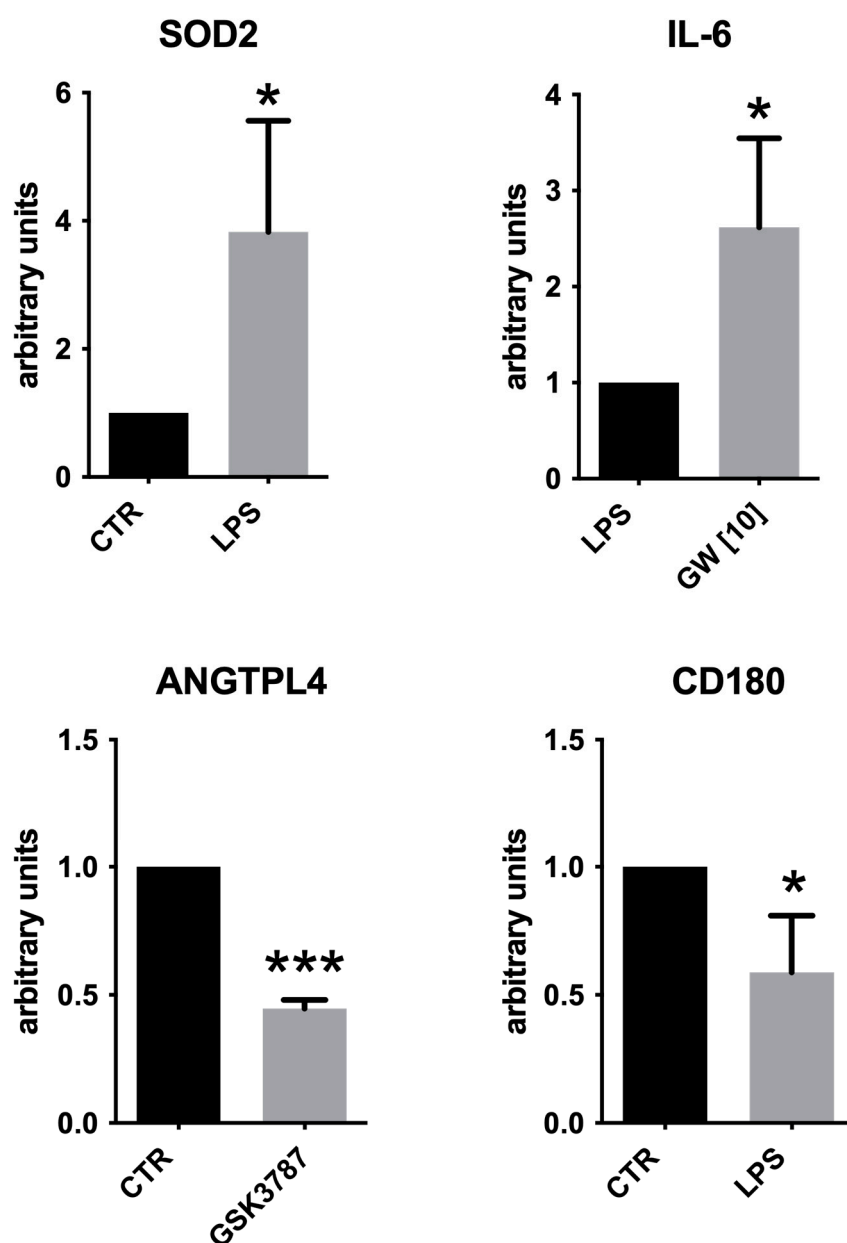

Figure S4: Real-time PCR validation of RNA-Seq results for random differentially expressed genes. Results were considered statistically significant at $p \leq 0.05$ (*), and $p \leq 0.001$ (***).