

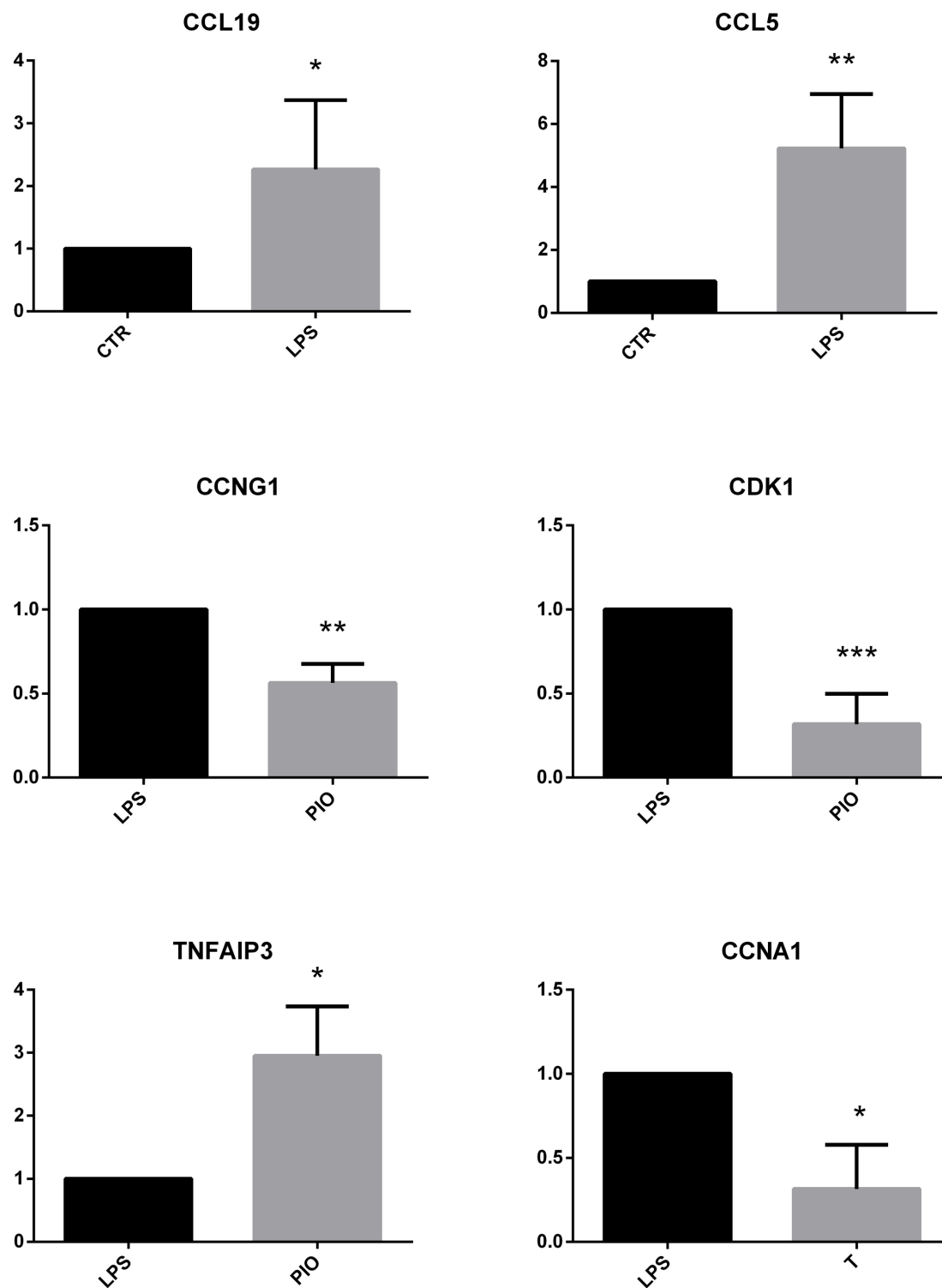
Supplementary information to

PPAR γ regulates the expression of genes involved in DNA damage repair in inflamed endometrium – transcriptome analysis

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Supplementary Figure 1

Real-time PCR validation of RNA-seq results for random DEGs. Validation was performed for *CCL5*, *CCL19*, *CDK1*, *CCNA1*, *CCNG1* and *TNFAIP3*.

Gene	Forward	Reverse	bp
<i>CCL5</i>	ACACCACACCCTGCTGTTTT	TCTTCTCTGGGTTGGCACAC	150
<i>CCL19</i>	TTCGAGCCTTTCGCTACCTG	AGTCTCTTGATGATGCGCTCC	130
<i>CDK1</i>	TGCTTATGCAAGACTCCAGGT	TCCCTTGCAGGATTTGGTACA	141
<i>CCNA1</i>	GCTGAAATGAGATACCGGCCT	AGTCCACCAGAATCGTTCGC	85
<i>CCNG1</i>	TGGATTGTTTCTGGGCGTACT	TCAGGATTGTGGAGAAAGGCT	147
<i>GAPDH</i>	ACATCATCCCTGCTTCTACCG	CCAGTGAGCTTCCCGTTGAG	76
<i>TNFAIP3</i>	GTGACCCTGAAGGACAGTGG	CGAATCTTCCTCGCTCTCTGT	70
<i>ACTB</i>	ACATCAAGGAGAAGCTCTGCTACG	GAGGGGCGATGATCTTGATCTTCA	366

Supplementary Table S 7

Primers used in Real-time PCR validation of DEGs.

Supplementary materials

Supplementary Table S 1

Summary of the sequencing depth and mapping reads according to the porcine reference genome.

Supplementary Table S 2

The paired-end bases mapped to the coding, UTR, intronic and intergenic regions in ENSEMBL pig genome.

Supplementary Table S 3

Differentially expressed genes identified in the porcine endometrium after LPS and PPAR γ ligands treatment.

Supplementary Table S 4

Results of Gene Ontology enrichment analysis of DEGs significantly modulated by subclinical LPS and PPAR γ ligands in porcine endometrium.

Supplementary Table S 5

Differentially long non-coding RNAs induced by LPS and PPAR γ ligands treatment.

Supplementary Table S 6

Differentially alternative splicing events after LPS and PPAR γ ligands treatment.