**Supplementary Table S1.** *Primer sets to quantify mRNA of selected genes by quantitative PCR analysis.*

|  |  |
| --- | --- |
| **Gene1** | **Primer sequence** |
| SCD1 | F 5’-GGCGTTCCAGAATGACGTTT-3’ |
|  | R 5’-AAAGCCACGTCGGGAATTG -3’ |
| ACC | F 5’-CATCTTGTCCGAAACGTCGAT-3’ |
|  | R 5’-CCCTTCGAACATACACCTCCA-3’ |
| FAS | F 5’-ACCTCGTGAAGGCTGTGACTCA-3’ |
|  | R 5’-TGAGTCGAGGCCAAGGTCTGAA-3’ |
| 18S | F 5’-AGAAACGGCTACCACATCCAA-3’ |
|  | R 5’-GGGTCGGGAGTGGGTAATTT-3’ |
| ACTB | F 5’-GCCCTGAGGCTCTCTTCCA-3’ |
|  | R 5’-CGGATGTCGACGTCACACTT-3’ |
| MRPL39 | F 5’-TTGGTCAGAGCCCCAGAAGT-3’ |
|  | R 5’-AGGTTCTCTTTTGTTGGCATCC-3’  |
| SREBP-1 | F 5’-GGTTTCCAGAGGGACCTGAGT-3’ |
|  | R 5’-TGGCCCCTGCCATCAGT-3’ |
| INSIG-1 | F 5’-GCATCGACAGTCACCTTGGA-3’ |
|  | R 5’-TGTCAAGGAGAGCTGAACGTTATT-3’ |
| PPARα | F 5’-GGATGTCCCATAACGCGATT-3’ |
|  | R 5’-GGTCATGCTCACACGTAAGGATT-3’ |
| PPARδ | F 5’-TGTGGCAGCCTCAATATGGA-3’ |
|  | R 5’-GACGGAAGAAGCCCTTGCA-3’ |

1 SCD1 = stearoyl-coA desaturase 1; ACC = acetyl coA carboxylase; FAS = fatty acid synthase; 18S = 18S ribosomal RNA; ACTB = *β*-actin; MRPL39 = mitochondrial ribosomal protein L39; SREBP-1 = sterol regulatory element binding protein 1; INSIG-1 = insulin induced gene 1; PPARα = peroxisome proliferator-activated receptor alpha; PPARδ = peroxisome proliferator-activated receptor delta.

**Supplementary Table S2.** *Primers sets to establish the expression profile of PPARG in various bovine cell models by PCR analysis.*

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene1** | **Accession number** | **Primer sequence** | **Amplicon size** |
| PPARy1 &PPARy2 | JN641299 &NM\_181024.2 | F 5’-AAGAGCCTTCCAACTCCCTCAT-3’R 5’-AGGACCCCATCCTTATTCATCA-3’ | 721 bp |
| PPARy2 only | NM\_181024.2 | F 5’-CGTGCTGTGATGGGTGAAAC-3’R 5’-TGGGAGAAGGAAGATGCTGT-3’ | 1568 bp |

1Through alternative splicing PPARG is expressed in at least two forms: PPARy1 = Peroxisome proliferator-activated receptor gamma isoform 1; PPARy2 = Peroxisome proliferator-activated receptor gamma isoform 2

**Supplementary Figure S1.** PCR analysis of the expression pattern of *PPARG* in different bovine cell systems. Native mammary, fat body and liver tissues were collected via biopsy. Total RNA was converted to cDNA in the presence (+RT) or absence (-RT) of reverse transcriptase. Subsequently, using gene specific primers, fragmental cDNAs of both isoforms of bovine PPARy (i.e. 1 and 2; upper panel) or PPARy2 only (lower panel) were amplified by PCR and subjected to agarose gel electrophoresis. Of note: the blot demonstrated a cDNA fragment corresponding to the expected PPARy cDNA fragment size (721 bp, upper panel; 1569 bp, lower panel) in native fat body tissue, but not MAC-T cells. The same MAC-T cDNA samples were used to quantify mRNA levels of lipogenic genes as indicated in **Table 1**. The identity of the amplified cDNA fragments were confirmed by sequencing. PTC = positive template control (i.e. pGEMT plasmid containing the full length cDNA sequence of bovine PPARy2). NTC = no template control (i.e. empty pGEMT plasmid). Blot is representative for three independent experiments.

