**Supplementary Table 1. Hepatic mRNA expression.**

Groups were compared using Student’s t test. Expression was normalized to the geometric mean of *Gapdh*, *β-Actin* and *Cox4i1*. Positive and negative fold changes indicate a respective increase or decrease in mRNA levels.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **SC Group** | | **OP Group** | |
| **Gene Symbol** | **Fold Change** | ***p-value*** | **Fold Change** | ***p-value*** |
| ***Ghr*** | 1.82 | 0.010 | 2.10 | 0.003 |
| ***Insr*** | -0.86 | 0.051 | 1.14 | 0.626 |
| ***Irs-1*** | -0.92 | 0.491 | 1.76 | 0.071 |
| ***Akt3*** | -0.53 | 0.212 | 1.63 | 0.329 |
| ***Pik3ca*** | 1.02 | 0.253 | 2.65 | 0.218 |
| ***Pik3r1*** | 0.94 | 0.466 | 2.52 | 0.670 |
| ***Glut4*** | -1.66 | 0.237 | -0.63 | 0.066 |
| ***Igf-1*** | -0.74 | 0.378 | -1.13 | 0.656 |

**Quantitative real-time PCR**

Total RNA was isolated from liver samples using Trizol (Life Technologies). The quantity and integrity of RNA were determined using a NanoDrop spectrophotometer (NanoDrop Technologies) and an Agilent Bioanalyzer RNA 6000 Nano kit, respectively. RNA integrity number (RIN) ranged from 9.2 to 9.8. Isolated RNA was DNAseI treated (Life Technologies). Single-stranded cDNA was synthesized from 1g of RNA using a Transcriptor First Strand cDNA Synthesis Kit (Roche), according to the manufacturer’s protocol. Real-time PCR analysis was carried out using predesigned PrimeTime qPCR assays (Integrated DNA Technologies) on a Lightcycler 480 (Roche). mRNA levels were normalized to 3 housekeeping genes: *Gapdh, β-Actin* and *Cox4i1* by subtracting the geometric mean Ct of housekeeping genes from the Ct for the gene of interest to produce a ∆Ct value. The ∆Ct for each treatment sample was compared with the mean ∆Ct for vehicle-treated samples using the relative quantification 2-∆∆Ct method to determine fold-change.