Supplemental Methods

Quantitative RT-PCR. Isolated islets (100-200) were added to 350-700 μl Lysis/Binding Solution in the RNAqueous Small Scale Phenol-Free Total RNA isolation kit (Ambion, Austin, TX). Trace contaminating DNA was removed with TURBO DNA-free (Ambion, Austin, TX). RNA bioanalysis, quality control and quantity assessment (QC/QA) determined in the Vanderbilt Function Genomics Shared Resource (FGSR) core lab showed a 28S/18S ratio from 1.4 to 2.0 and a RNA integrity number (RIN) from 8.1 to 9.5. Preloaded arrays (Applied Biosystems) of 16 genes were used to determine their expression levels in human and mouse islets. Six out of 16 endogenous genes were stably expressed in islets from both species and 4 of them (*18S/18s, ACTB/Actb, TFRC/Tfrc, TBP/Tbp*) were used in this study. Normalization of genes of interest to multiple endogenous control genes enabled comparison of the mRNA levels between human and mouse islets. mRNA expression during culture at 5 and 11 mM glucose was normalized to *18S/18s* and stable expression of *18S/18s* was confirmed in both glucose concentrations. Relative changes in mRNA expression calculated by the comparative ΔCt method using Applied Biosystems Stepone plus program. Minimum Information for Publication of Quantitative Real-Time PCR Experiments (MIQE) guidelines were followed for qPCR experiments [35].