**ESM Methods**

**Abdominal subcutaneous fat-biopsies:** Biopsies were immediately cleansed from blood, snap-frozen in liquid nitrogen and subsequently stored in -80°C until analyzed. All samples were homogenized, in a HEPES buffer (pH: 7.4) containing 50mmol/l HEPES, 20mmol/l NaF, 2mmol/l NaOV, 5mmol/l EDTA, HALT, 10 μmol/l TSA, 5mmol/l NAM, SDS 5%, and demineralized water using 400μl buffer per 100mg fat tissue in a “Precelley Homogenizer” for 2 x 30s at 5000rpm. Then samples rotated at 37°C for 60min before being centrifuged at 14,000g for 20min. The infranatant was carefully removed and the centrifugation process repeated, until there were no visible traces of fat or sediment in the homogenates.

**WB:** Proteins were visualized and quantified using horseradish peroxidase-conjugated anti-rabbit secondary antibodies, ECL and Image Lab 5.0, Bio-Rad laboratories. Protein levels are expressed as ratio to mean CTR-value at t=30min.

**mRNA:** Primers used were (forward and reverse): G0S2 (5’ CGA GAG CCC AGA GCC GAG ATG 3’ and 5’ AGC ACC ACG CCG AAG AG 3’, 137 bp), ATGL (5’ ACC TCA ATG AAC TTG GCA CC 3’ and 5’ CAA CGC CAC GCA CAT CTA 3’, 122 bp), and CGI-58(5’ TGT CAG CCG GCT TCG AGA TAA G 3’ and 5’ ACC AGT TAG CCA TCC TG CCT CTC 3’, 113 bp)

**Statistical analyses:** When only one measure per day was applied, a repeated measurements mixed model was used, with visit number, visit order and intervention as factors. When unequal standard errors and correlations between the three groups were detected, these were taken into account in the analysis. Model validation was performed by inspection of qq-plots of the residuals and inspection of scatterplots of the predicted versus the fitted values. If residuals were not normally distributed, logarithmic transformation was performed to obtain normality.

Sample size calculation was performed using palmitate-flux-rates as primary outcome and a paired t-test comparing two correlated means as model. We estimated a flux-difference of 80μmol/min, a SDiff. of 60μmol/min, used a 5% significance-level, and power of 90% which resulted in a sample size of n=9.