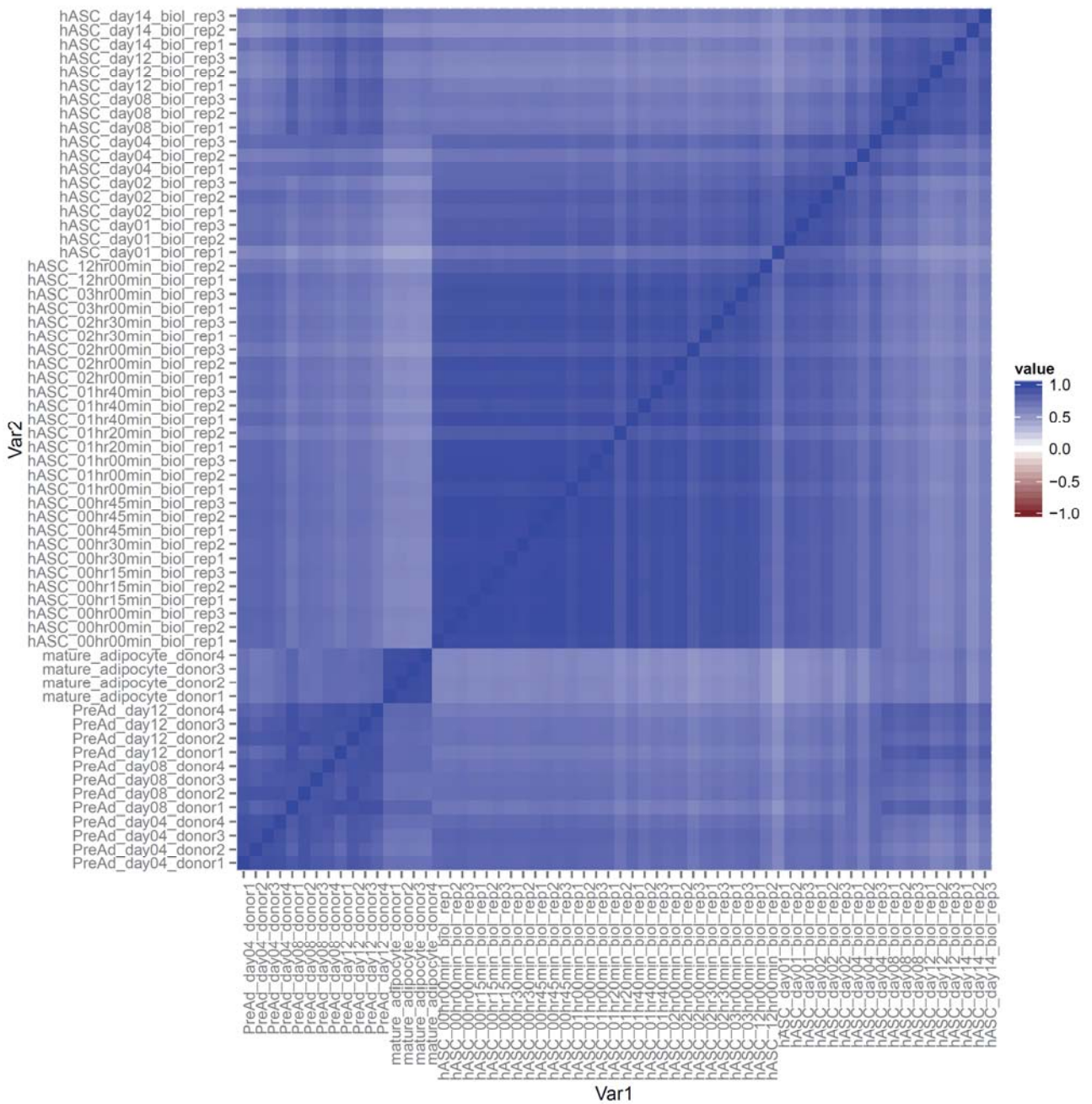


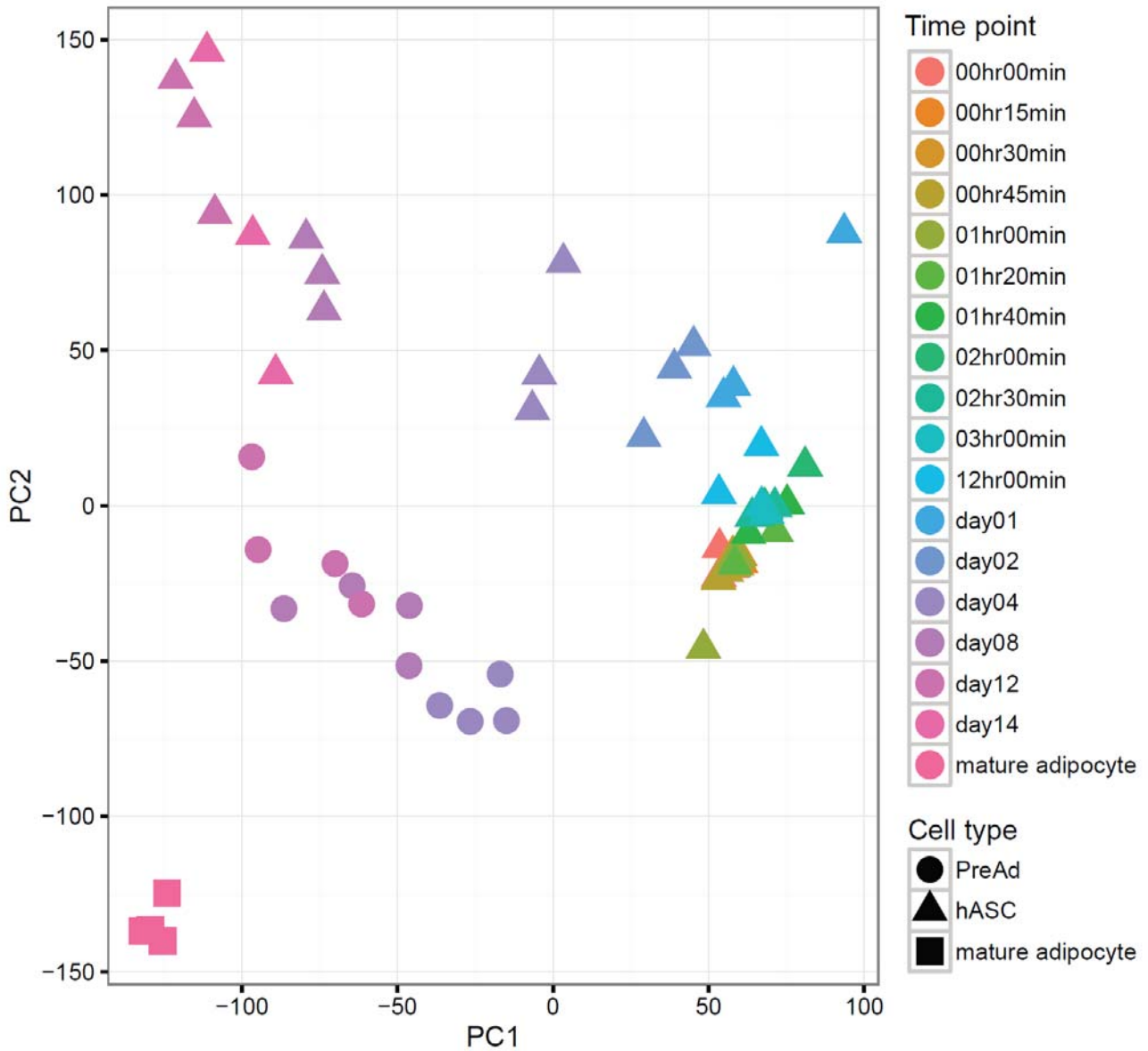
SUPPLEMENTARY DATA

Supplementary Figure S1. Data quality control, between replicate data correlation matrix

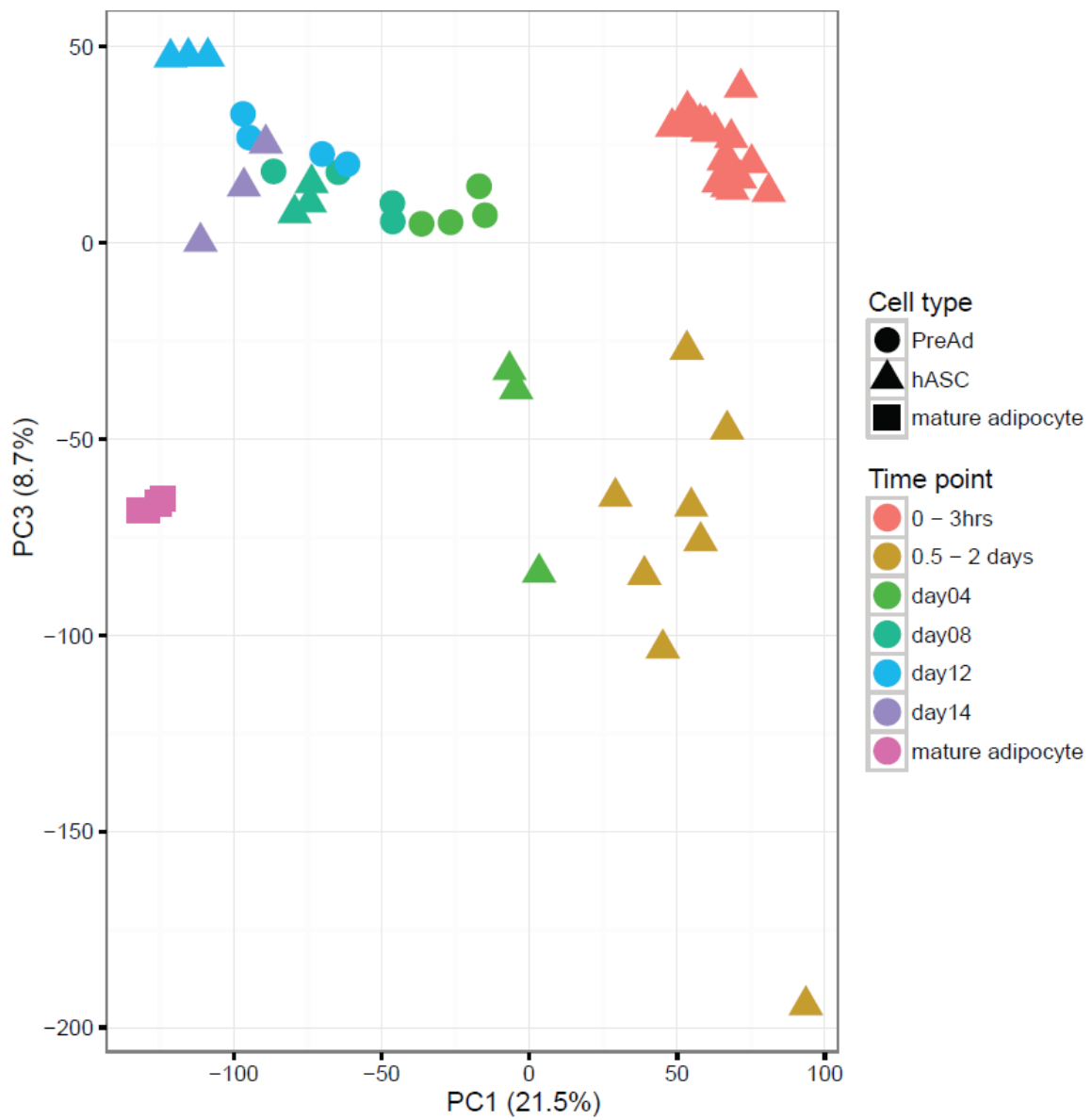


SUPPLEMENTARY DATA

Supplementary Figure S4. A. Detailed version of Figure 1C. Shape represents cell type (circles: PreAd, triangles: hASC, squares: mature adipocytes) and the color scale reflects time from adipogenic induction. **B.** Principal component analysis of promoters with at least 10 TPM expression level in at least one sample. The first and third components capturing the highest variance are plotted.

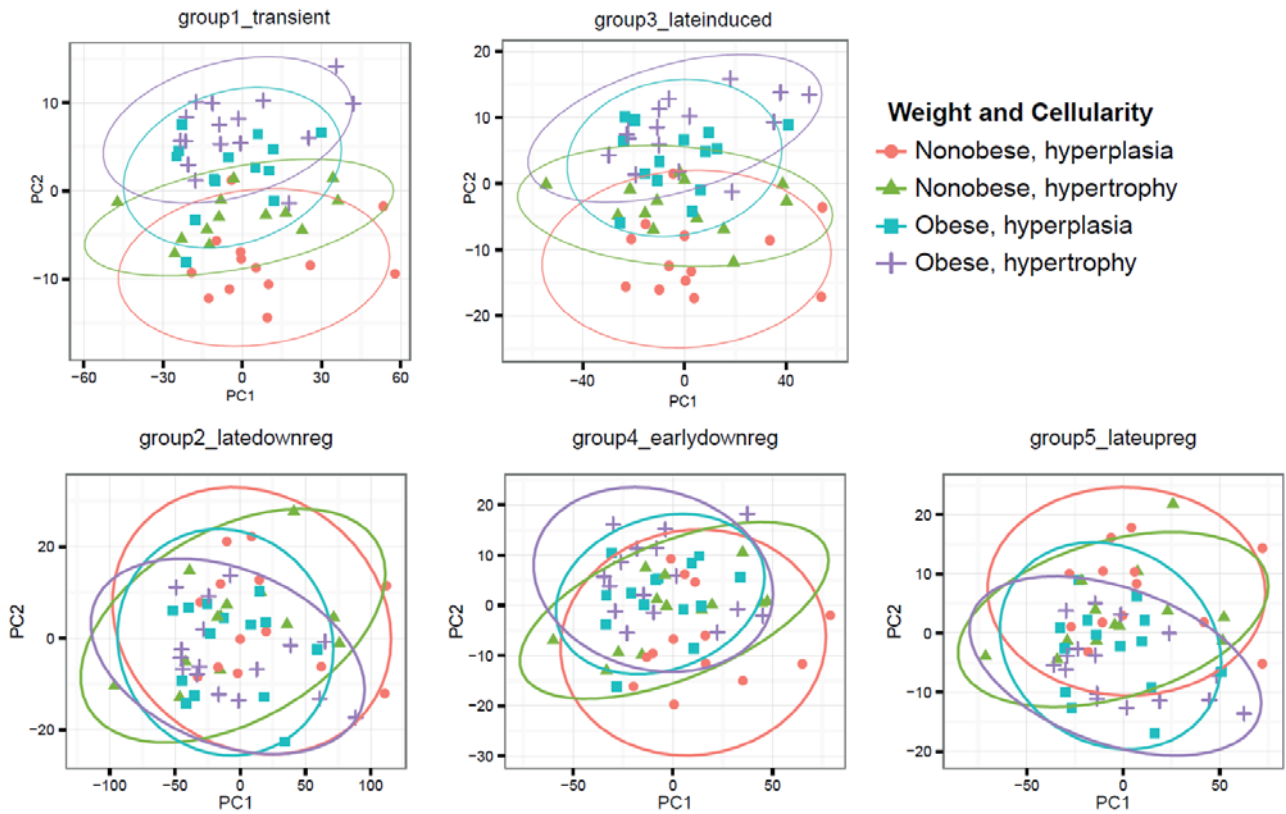


SUPPLEMENTARY DATA



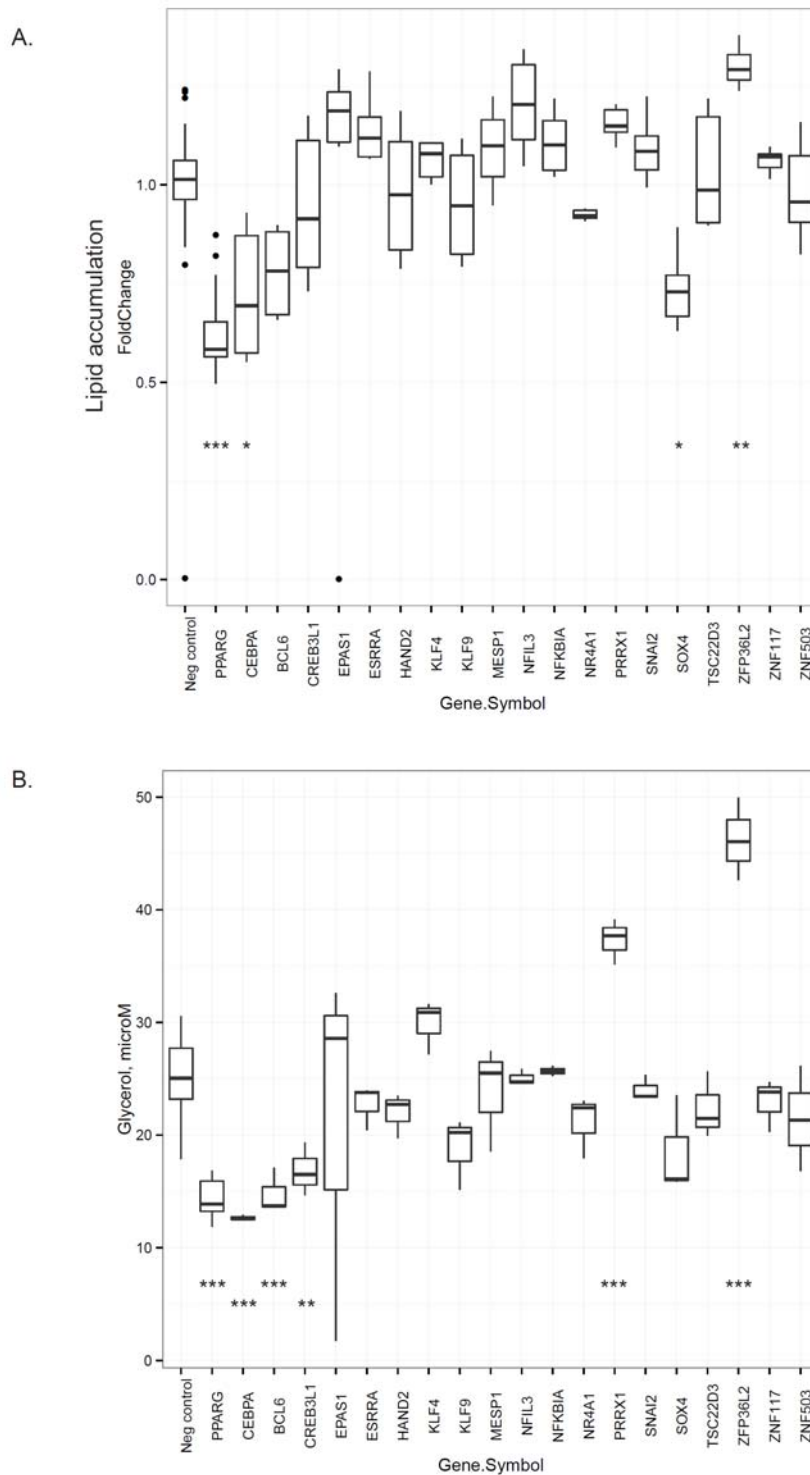
SUPPLEMENTARY DATA

Supplementary Figure S5. Expanded version of figure 5B. Principal component analysis of gene expression of K-means cluster genes' expression in a microarray of WAT from a non-obese/obese cohort of patients. Each subject colored according to weight and adipocyte cellularity status.



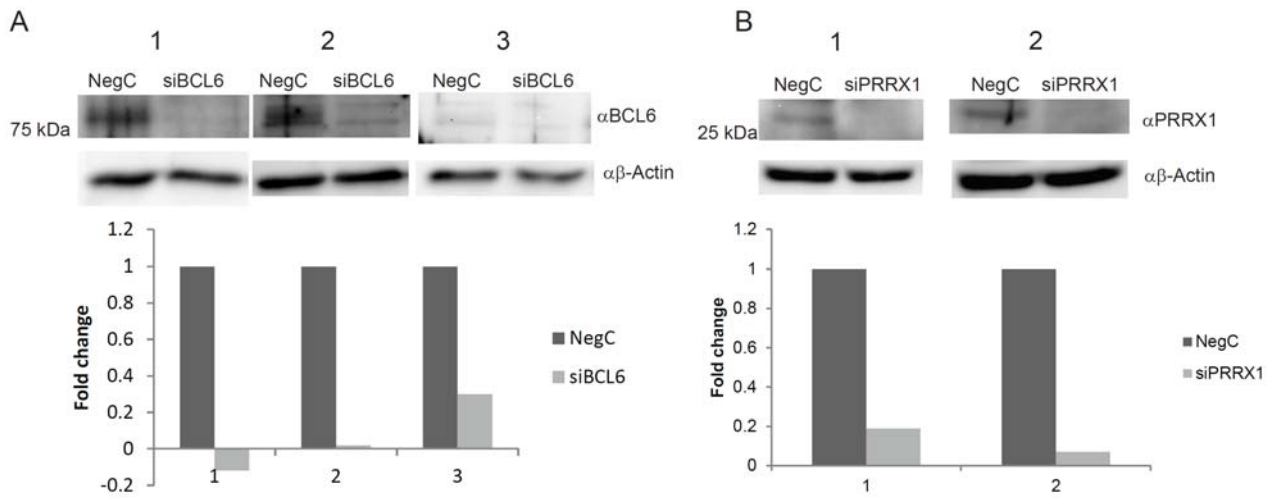
SUPPLEMENTARY DATA

Supplementary Figure S6 A. Boxplot of fold change of lipid accumulation day 9 after adipogenic induction and day 10 after siRNA of indicated transcription factors. **B.** Boxplot of glycerol concentration in culture medium day 9 after adipogenic induction and day 10 after siRNA of indicated transcription factors. Stars correspond to significance according to Bonferroni-corrected Student's t-test p-values. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$



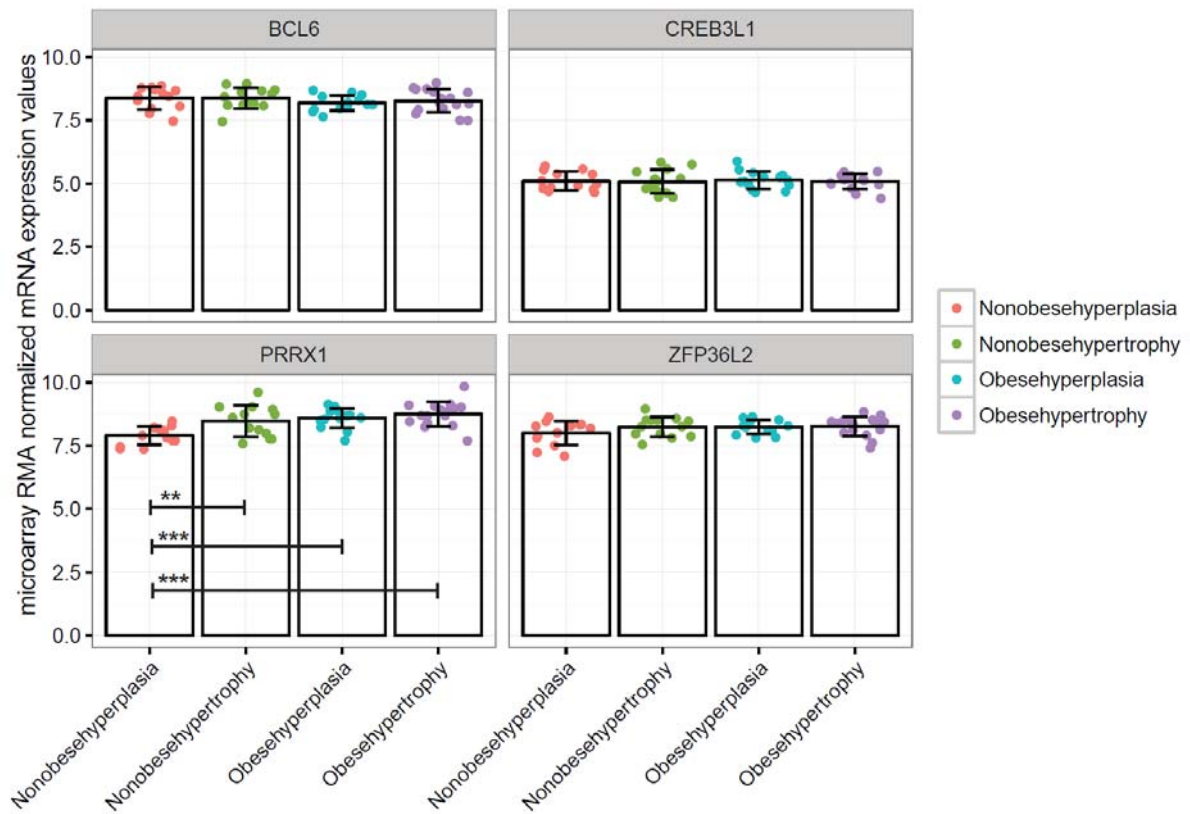
SUPPLEMENTARY DATA

Supplementary Figure S7. Western blot detection and relative quantification of **A.** BCL6 (Santa cruz, N-3, sc-858) and **B.** PRRX1 (Abcam, ab208919). Western bands were quantified using the Quantity One program (BioRad) with local background correction. The bands were normalized by dividing with the corresponding β -Actin western blot signal and the siRNA knock down of PRRX1 or BCL6 signal related to the negative control. Three (BCL6) or two (PRRX1) independent experiments are shown.



SUPPLEMENTARY DATA

Supplementary Figure S8. Expression of *BCL6*, *CREB3L1*, *PRRX1* and *ZFP36L2* mRNA on a microarray from 56 subjects (31) grouped into non-obese hyperplastic, non-obese hypertrophic, obese hyperplastic and obese hypertrophic according to weight status and adipose tissue morphology. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ using ANOVA ($p = 0.0001$) followed by Fisher's PSLD test in StatView.



SUPPLEMENTARY DATA

Supplementary Figure S9. Expression of *BCL6*, *CREB3L1*, *PRRX1* and *ZFP36L2* mRNA at day 4 (A) and day 12 (B) of differentiation when one Dexamethasone (Dexa.), 3-isobutyl-1-methylxanthine (IBMX), Rosiglitazone (Rosig.), Insulin (Ins.) or Triiodothyryne (T3) had been removed from the complete differentiation medium (Full diff.) Each point represents individual measurements, each bar the mean value and each error bar standard deviation. 10 experiments, significance calculated by Student's t-test with Benjamin-Hochberg corrected * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

