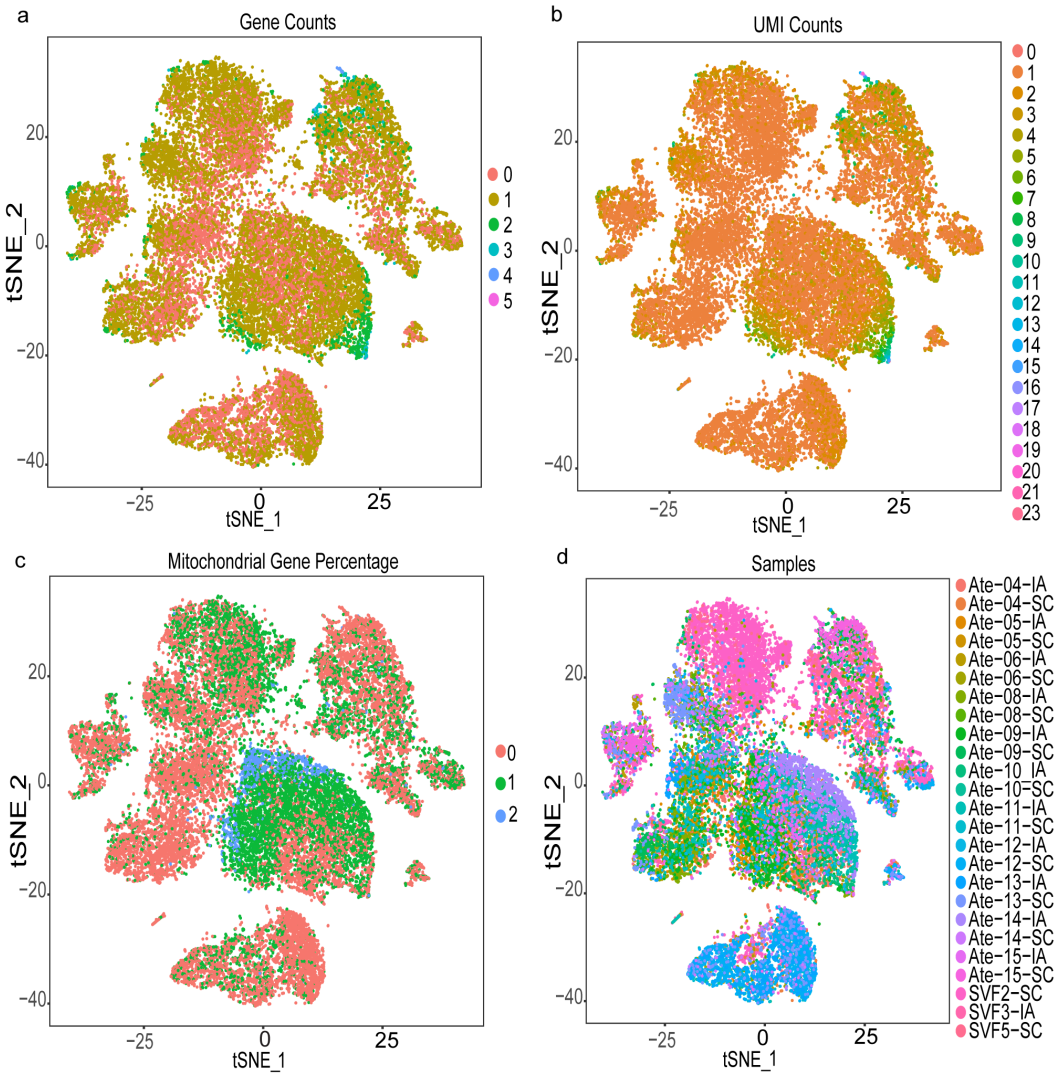
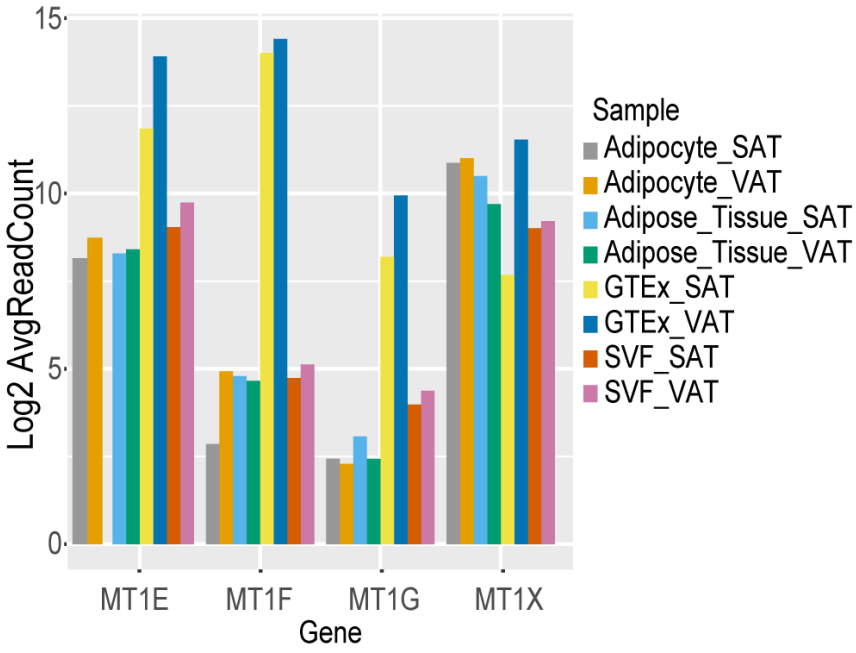
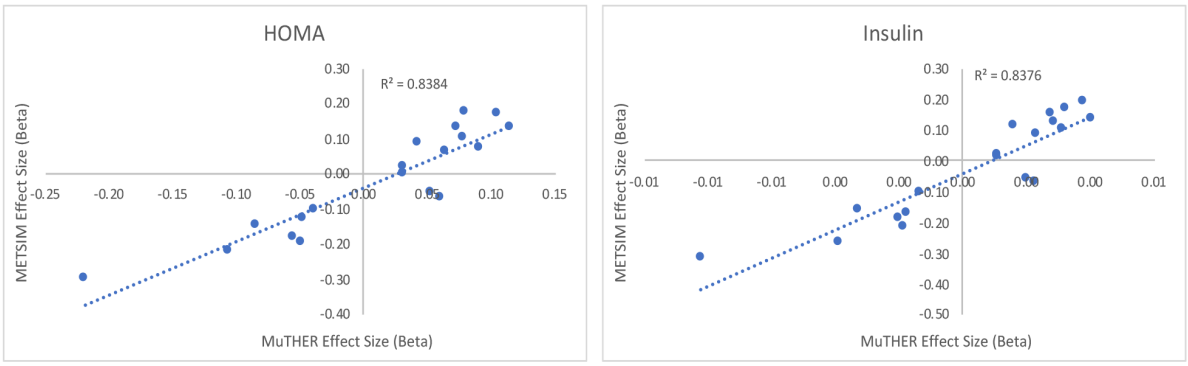


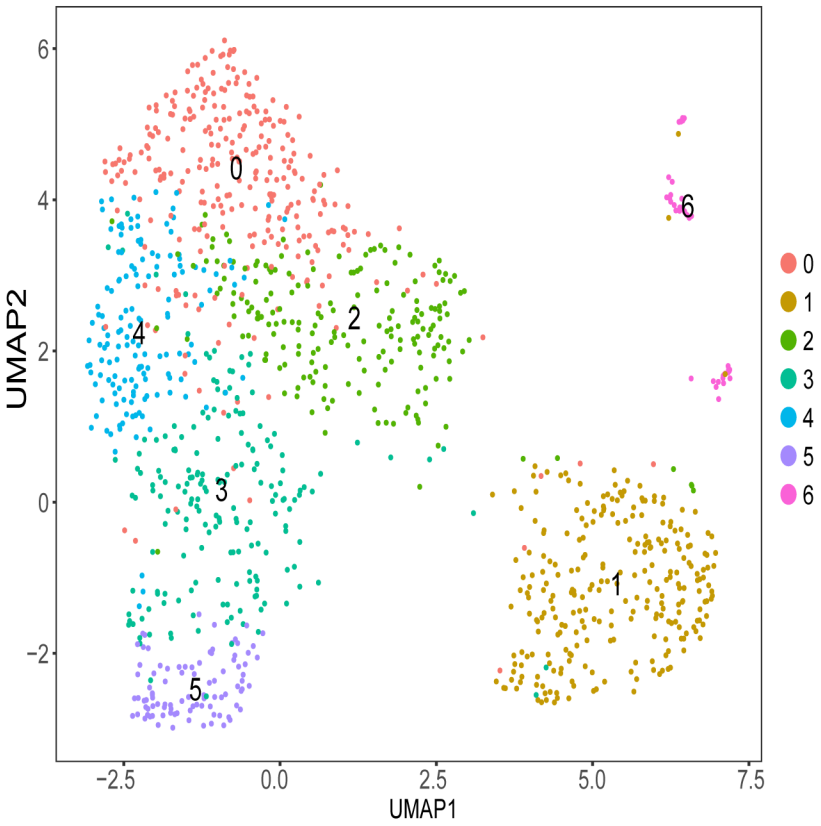
Supplementary Figure 1: UMI, nGene, mitochondrial and sample distribution of SVF clusters from all 25 samples (a) Each cell is colored based on the result obtained by dividing total number of genes expressed by 1000 and then rounding to 0 decimals. (b) Cells are colored based on the result obtained by dividing total number of UMIs expressed by 1000 and then rounding to 0 decimals. (c) cell color shows percentage of mitochondrial gene expression. Group 0 shows cells with mitochondrial gene expression <=5%, group 1 represents 6% to 14% and group 2 represents15% to 24% expression (d) Cells are colored based on the scRNAseq library



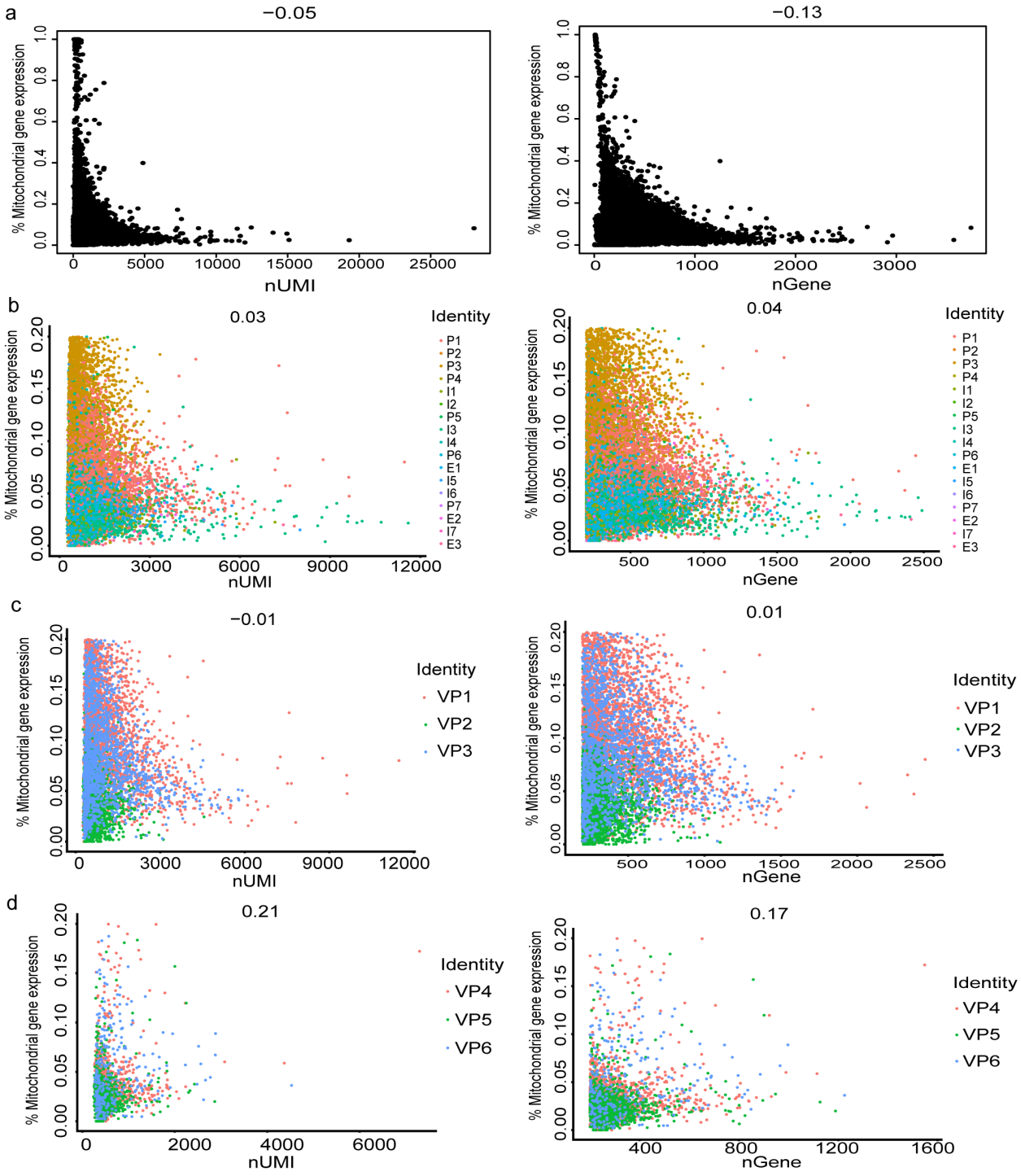
Supplementary Figures 2: Metallothionein gene shows expression in SAT and VAT depots from adipose tissue, adipocyte, SVF and GTEx



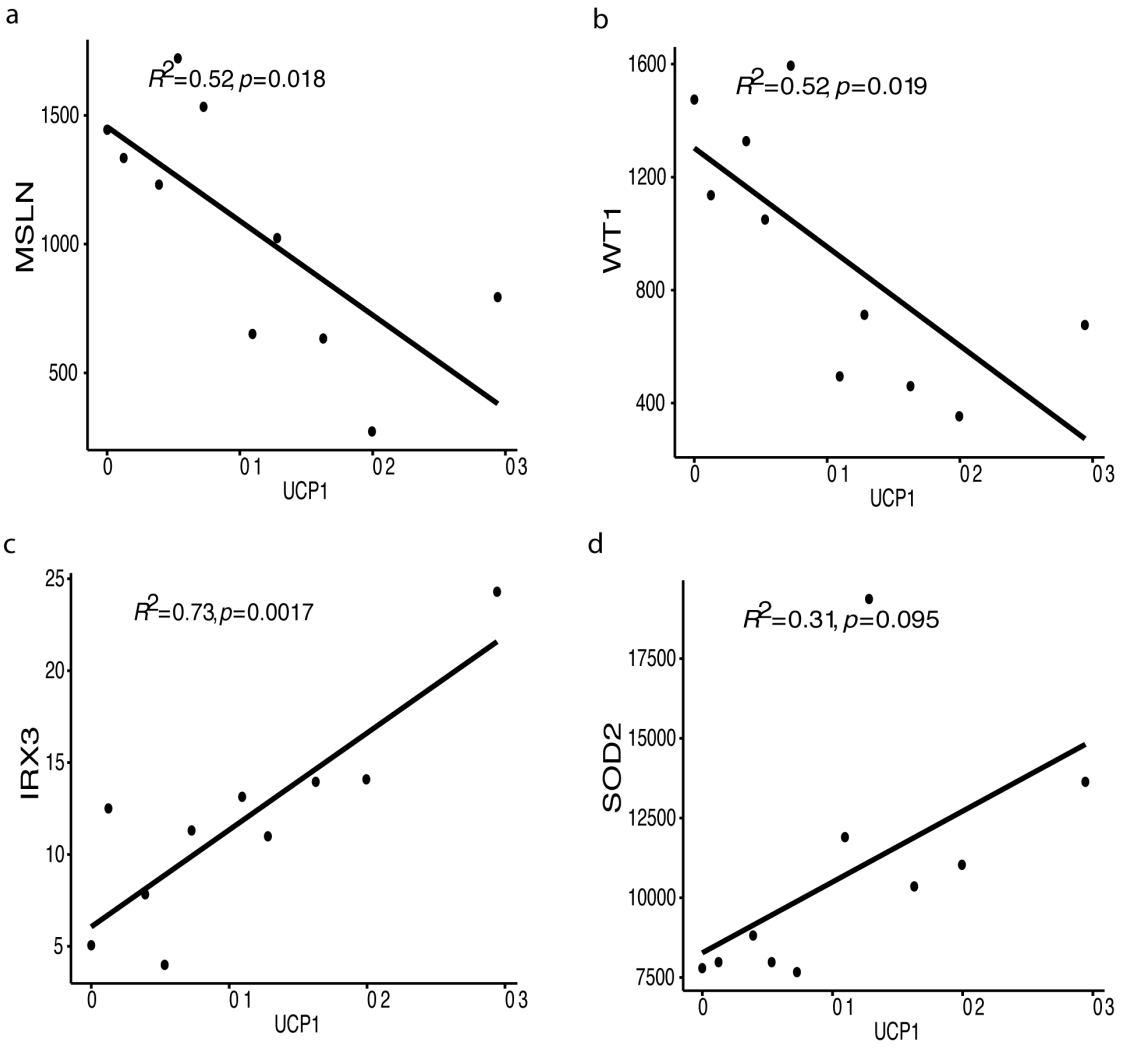
Supplementary Figures 3: T2D associated genes in MuTHER study from SP1 cluster shows strong correlation of effect sizes with METSIM Study



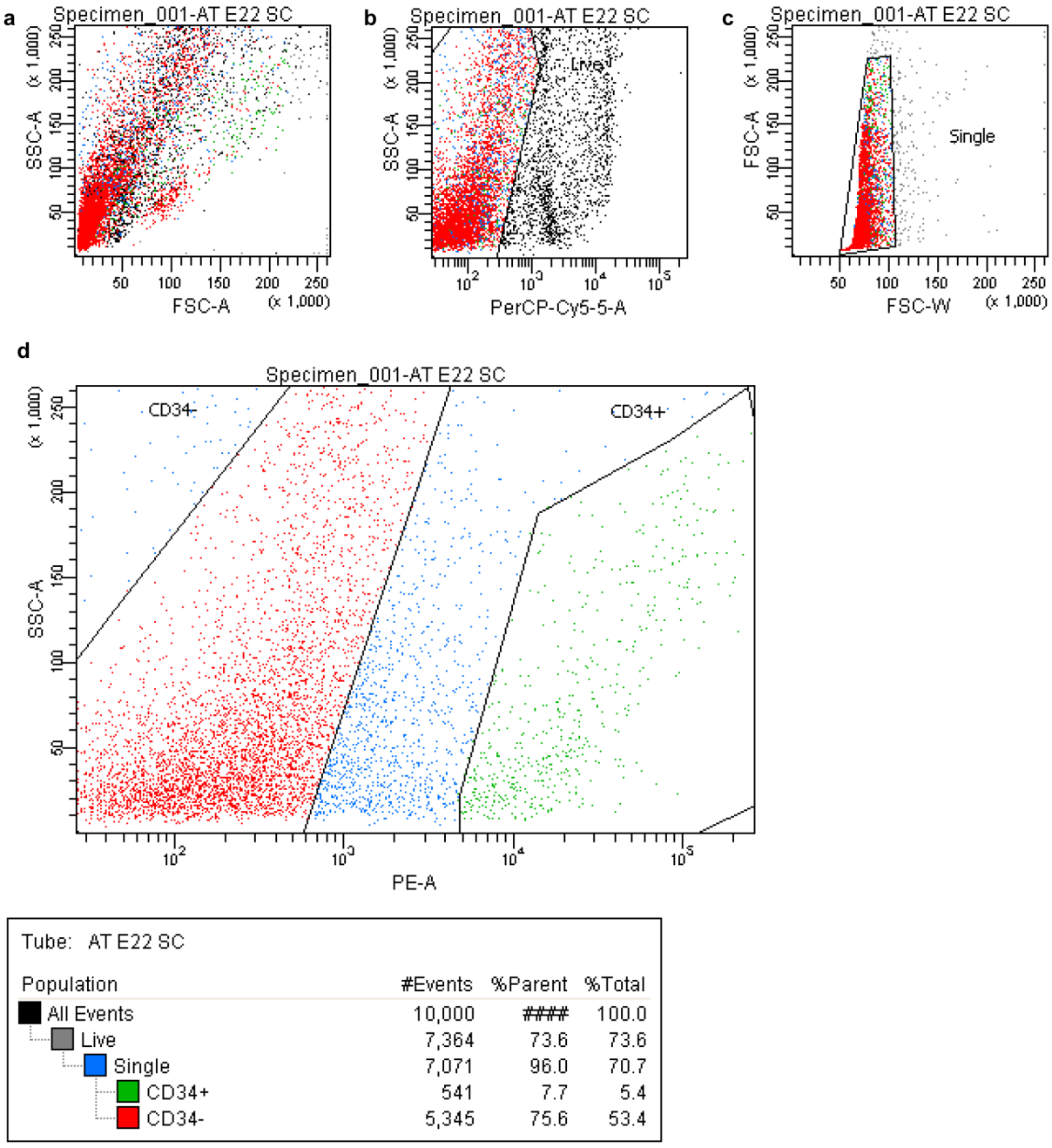
Supplementary Figures 4: Clustering results of CD34 + cell population from SVF of SAT and VAT of 2 individuals.



Supplementary Figures 5: Distribution of mitochondrial gene expression in relation to UMI and Gene distribution in (a) unfiltered initial data (b) All clusters (c) VPM clusters (d) VPC clusters



Supplementary Figure 6: Pearson correlation of *UCP1* with *MSLN* (a), *WT1*(b), *IRX3* (c) and *SOD2* (d) using bulk RNAseq from visceral adipose tissue of 10 individuals.



Supplementary Figure 7: FACS Sorting strategies used for the representative sample included in the study. The cells are filtered for dead cells (b) , the single cells are identified (c) and sorted for CD34+ and CD34- (d)