



Figure S2. Effect of sequencing depth and amplification cycles on the number of genes detected and the number of genes differentially expressed between blood and adipocytes using TM3'seq. (a,b) Libraries with 1M, 2M, and 3M uniquely mapped RNA-seq reads were amplified for 18 cycles. Two adipocyte and three blood replicates were used. (c,d) Libraries were amplified for 12, 14, and 18 cycles, each sample was down sampled to one million uniquely mapped reads. Each tissue has three technical replicates. The average number of genes detected is shown in (a) and (c). Genes are clustered by abundance: singletons (sing), 2-10 reads, 11-100 reads, and more than 100 reads. Whiskers represent two standard deviations. For some bins, std is too small to be plotted. The number of differentially expressed genes (Bonferroni p-value <0.05) is shown in (b) and (d). The differentially expressed genes identified by each number of cycles are very similar, with the overlap between cycles ranging from 88% to 98%.