



Figure S1. Comparison of mapping parameters between NEB and TM3'seq libraries. The amount of reads trimmed out (for details on trimming parameters see Materials and Methods), uniquely mapped, and assigned to genes is shown. (a) Comparison between (blue) NEB and (red) TM3'seq libraries. (b) Comparison between TM3'seq libraries amplified using 12 (green), 15 (light blue), and 18 (dark blue) PCR cycles. There are six individual data points per group, three blood samples, and three adipocyte samples.