



Supplementary Figure 3. Sequencing metrics for various stages of the computational pipeline

The total number of reads in each sequencing library from raw demultiplexed reads through the stages of quality control/trimming, human depletion, deduplication, and negative depletion (A). The distribution of the percentage of reads retained after each incremental step for all samples (C). Comparison of human abundance for each subject between routine, hybrid capture (HC), methylated DNA depletion (MDD), and hybrid capture plus methylated DNA depletion (HC+MDD) on DNA samples (B). Comparison for RNA (D).