Supplemental Figure S2. MIP pooling across multiple targets remains balanced and precise. (A) Boxplot of sequencing libraries for the same set of probes across 5 separate genomic templates overlaid with the fold-change for each probe based on the probe with the fewest reads in each set. (B) a kernel density plot of each dataset based on the fold-change in read depth of each probe (MS = MiSeq-generated data; NS = NextSeq-generated data). (C) A scatterplot of abundance for all strains within each sequenced set versus the standard deviation of the 3 to 4 probes used to calculate that abundance.