

Supplemental Figure S1. MIPs provide sufficient read depth to specific subpopulations of strain abundance in complex compositions of genomic DNA. (A) Strains from non-overlapping sets of mixed genomic samples are identified using a multiplexed pool of MIPs. Strain abundance for each set is indicated by the heatmap legend with each strain subdivided into four abundance estimations calculated from MIP sequencing data. (B) A heatmap of total reads per MIP per set broken down by specific strain and MIP with black arrows indicating probes with total reads below 20% of the mean read depth across the set.

VC20738-

VC40138

VC40154

VC40174

VC40196

VC40212

VC40238

VC40257

VC40250

VC40545-

VC40529

VC40575-

VC40611

VC40632

VC40719-

VC40721

VC40764

VC40747

VC40788

VC40804

VC40697

VC40687

VC40870-

VC20315-

VC20293

VC20152

VC20172

VC20239-

VC20263

VC20319-

VC20327

VC20413-

VC20435

VC20444

VC20461

VC20485-

VC20492

VC20496-

VC20555

VC20617

VC20647

VC20649

VC20684

strain