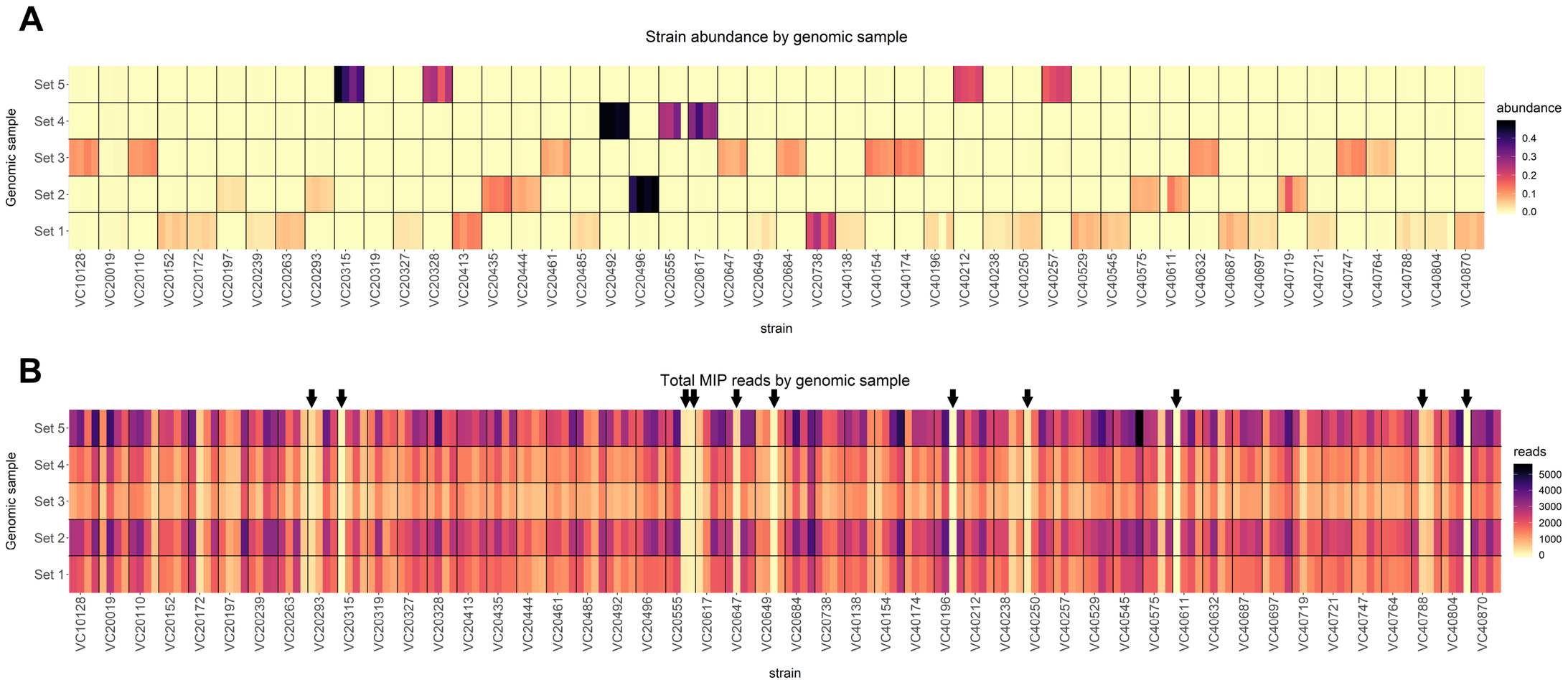

Supplemental Figure S1. MIPs provide sufficient read depth to specific subpopulations of strain abundance in complex compositions of genomic DNA. (A) Strains from non-overlapping sets of mixed genomic samples are identified using a multiplexed pool of MIPs. Strain abundance for each set is indicated 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.