










Graphical example of output for different sample population structures

Method	Description	Programs	 Clonal	 Heterogeneous	 Distinct
Consensus SNP calling	The consensus base at each position of the genome defines the strain in that sample. One possible strain detection per sample.	StrainPhlan MIDAS			
Haplotype phasing	Strains are defined as sets of polymorphic bases that co-vary in frequency across samples. Each strain is a distinct genotype. Many possible strain detections per sample.	ConStrain DESMAN			
Characterizing the strain cloud	Distinct strains are not defined. Polymorphic base frequencies, microdiversity, and variations in coverage are calculated for each position along the genome.	inStrain	