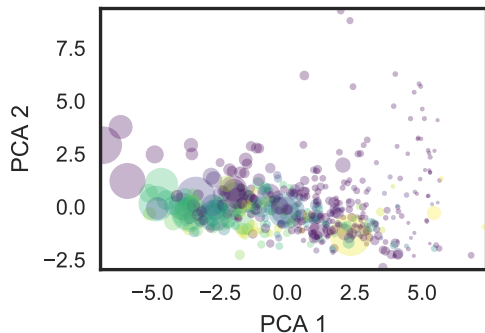
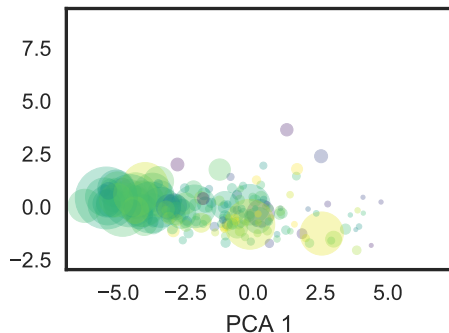


a SAG Contigs with < 5% aligned to MAG

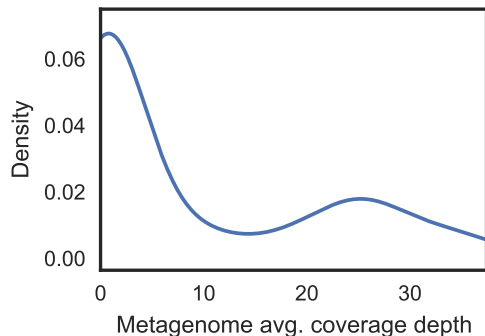


b SAG Contigs with > 5% aligned to MAG

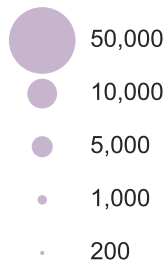


Metagenome avg. coverage depth
PCA 2

c



Contig lengths



d

