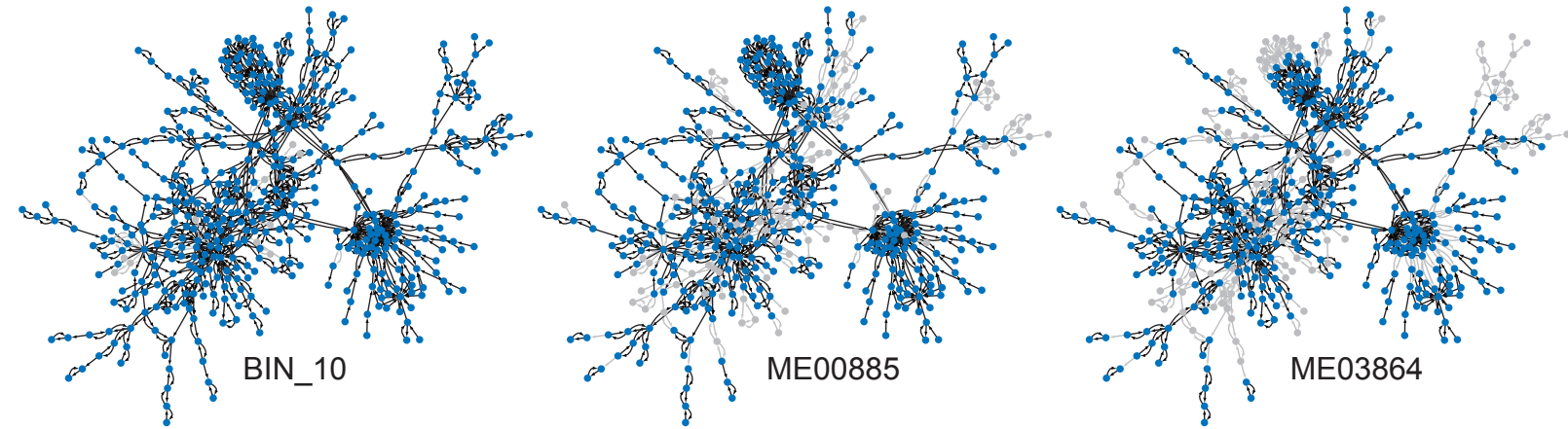
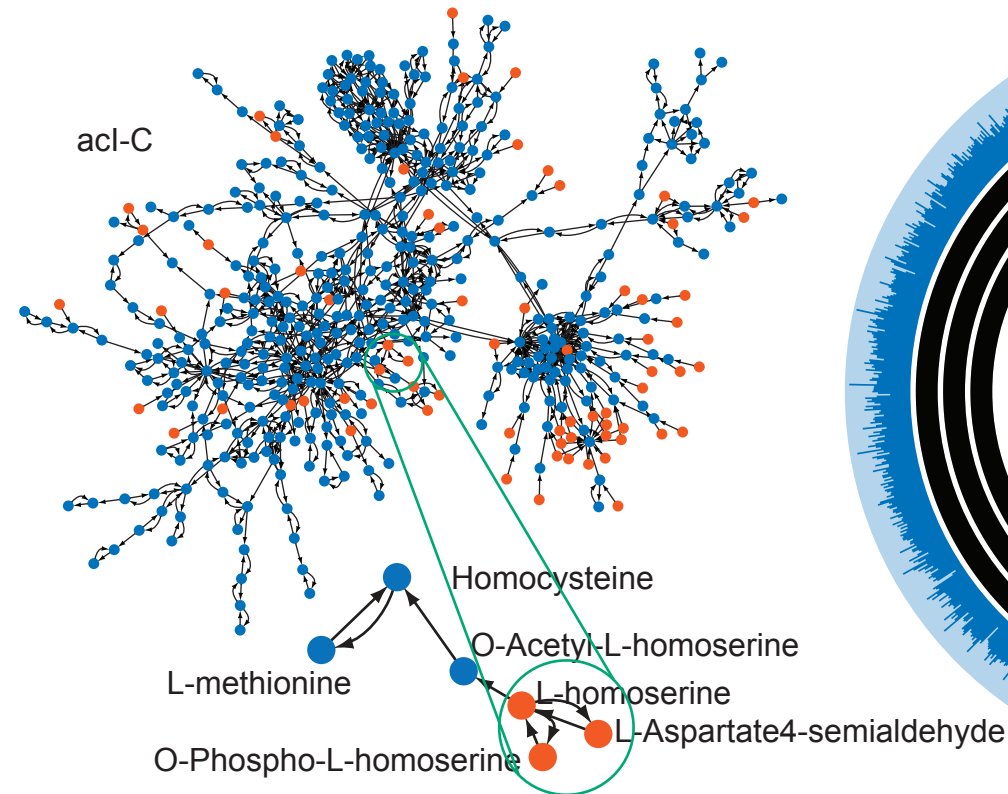


A) Annotate microbial contigs using KBase and build a metabolic network reconstruction from the annotations. Convert reconstruction to a metabolic network graph. Metabolites are represented as nodes, and reactions as directed edges.



B) Create a composite network graph for each clade. Compute seed compounds for the composite graph.



C) Map metatranscriptomic reads to individual genomes. Identify orthologous gene clusters, and count unique mapped reads. Normalize.

