Profiling taxonomic and functional compositions of selected metagenomes

- Individual metagenomes
  - Taxonomic profiling
    - Profiling with MetaPhyler
    - Determine abundances of all functions (ShotMAP)
  - Functional profiling
    - Search glycerol metabolism gene families
    - Function-taxon association (metaAnnotate)

Comparative analysis of virus and host sequence characteristics

- Make nonredundant list of virus-host pairs from CRISPR mapping
- Calculate virus and host k-mer (dimer and trimer) frequencies
- Calculate overall frequency distance metric for each virus-host pair
- Compare average distance metrics for different sites and hosts

Assembling metagenomes and detecting halobacterial cas genes in metagenomic contigs

- Assemble contigs from Cahuil and combined metagenomes
- Align contigs against several different halobacterial cas operons
- Align contigs against library of cas genes
- Determine how many metagenomes had contigs matching each operon gene
- Determine taxonomic affiliations of best hit genes
- Visualize results as a taxonomic profile