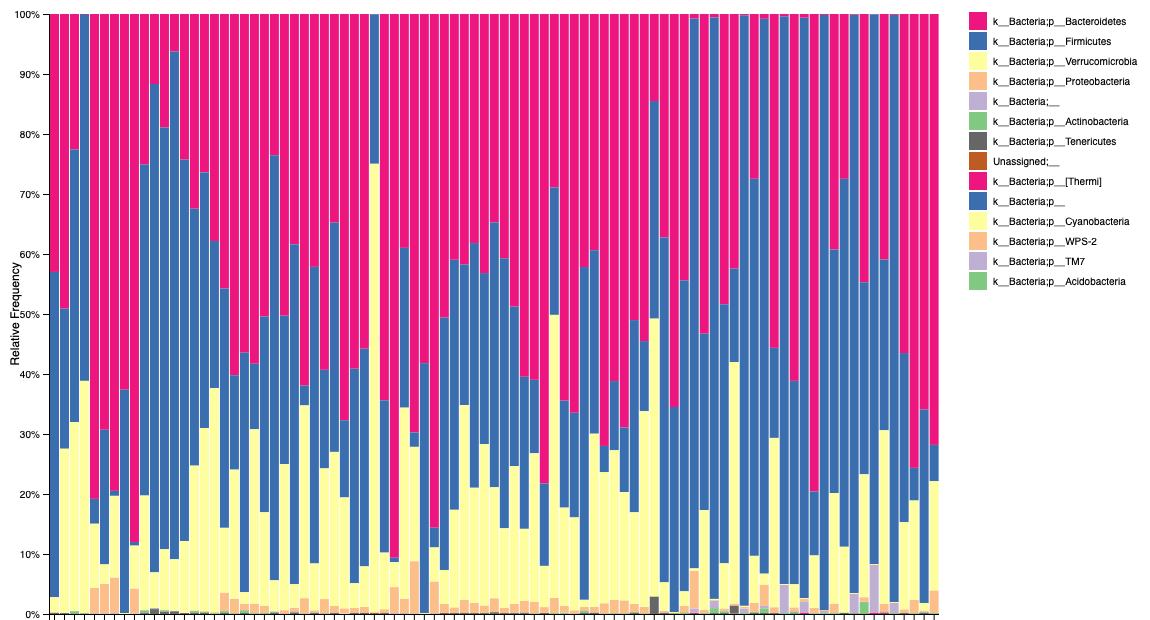
**High Throughput Sequencing**  
**16S rRNA Amplicon Sequencing**

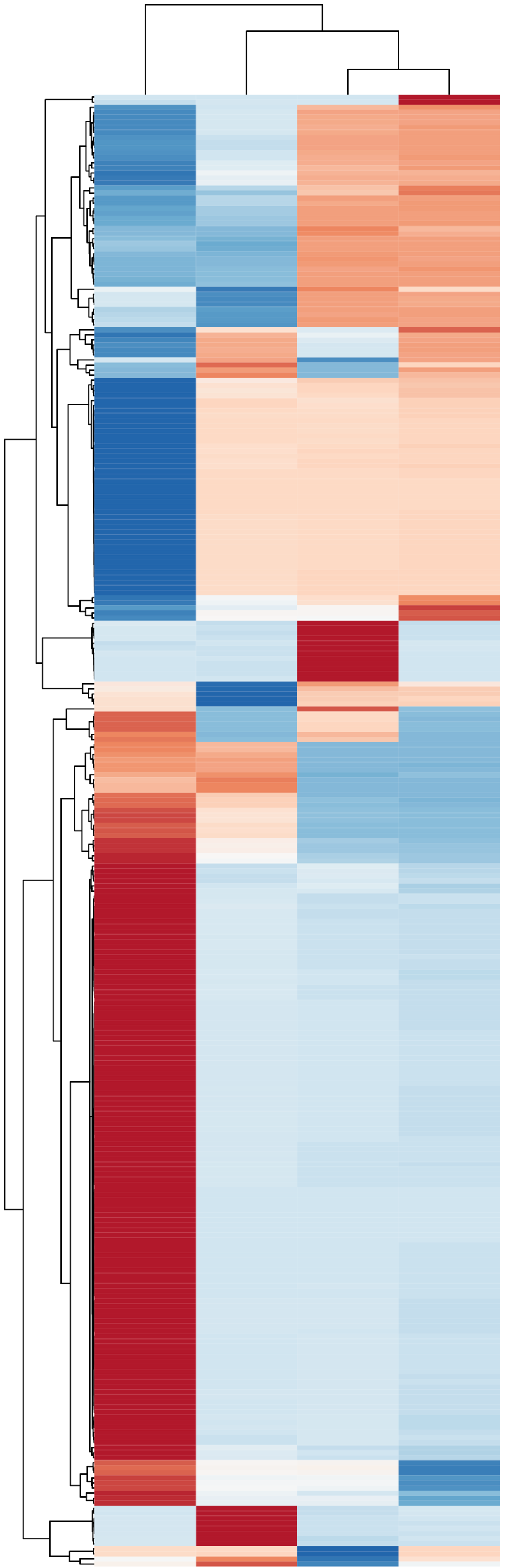
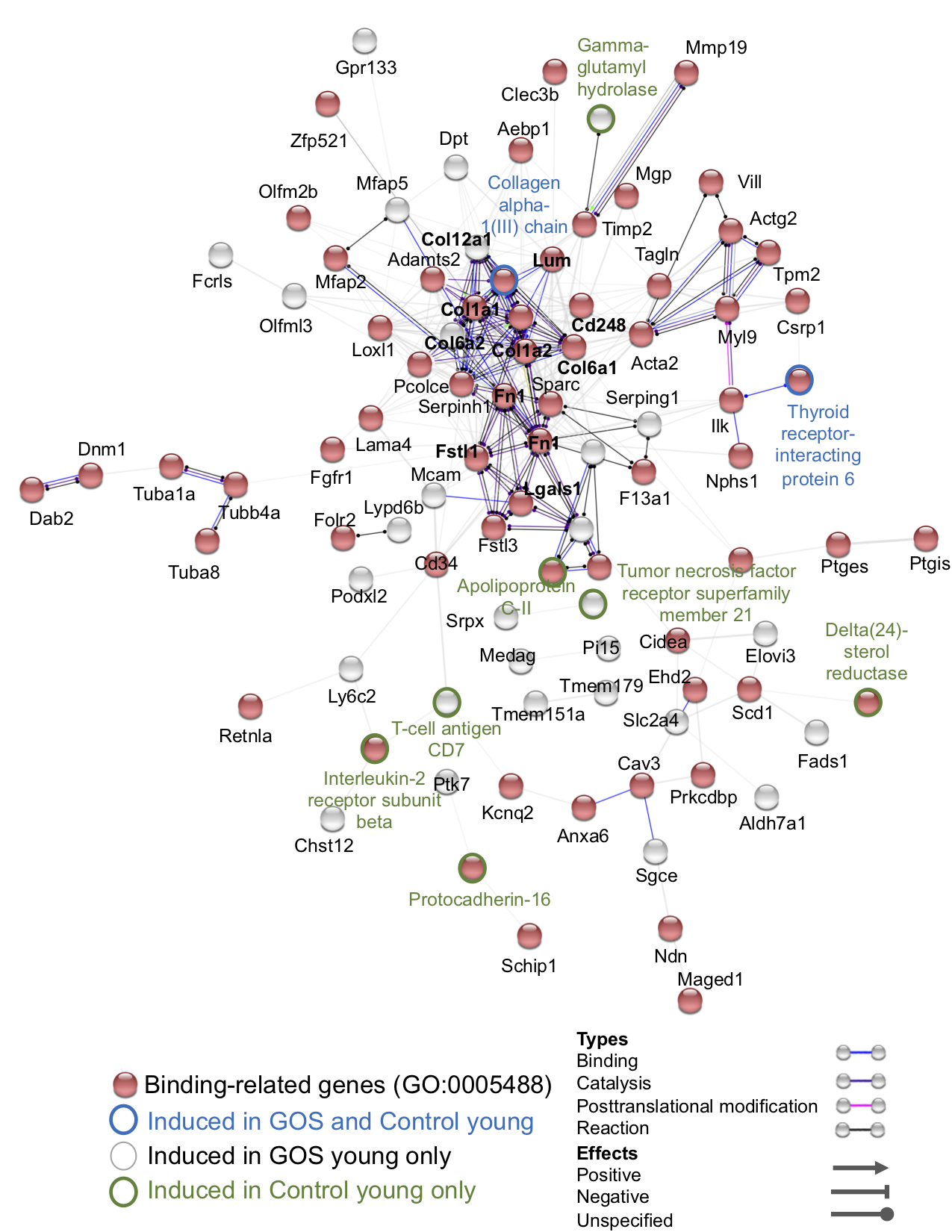
Sequencing of targeted variable regions (V3-V4) in the 16S ribosomal gene allows to determine the bacterial components of microbial complex communities. Data provided include relative abundance of taxa at the genus/species-level, alpha and beta diversity calculations and basic analysis of significantly over or underrepresented groups.

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**Whole Genome Shotgun (WGS) Sequencing**

WGS sequencing generates high depth sequence data (>10M sequences per sample) of entire microbial communities for higher resolution taxonomic characterization compared to 16S rRNA sequencing, providing species/strain-level information and community functional potential (enzymatic pathways and gene families). WGS can also be applied to isolated microbial strains to generate genomic sequencing data.

**RNA Sequencing**

****Total community meta transcriptomics generates sequencing data from genes being actively expressed across community members. RNA sequencing can also be used to target host-specific factors, or to characterize changes in expression of individual bacterial strains in culture.

**Shallow WGS Sequencing**

Whole Genome Shotgun (WGS) sequencing performed at lower sequencing depth (>1M reads per sample) is a cost-effective method to acquire species/strain-level taxonomic characterization of the more abundant members of complex microbial communities. By sequencing at a lower depth, the cost of sequencing is reduced, however this will reduce the ability to accurately assess the identity or potential function of low-abundance community members. This approach is offered as a lower-cost alternative to WGS sequencing while providing higher taxonomic depth than standard 16S rRNA amplicon sequencing.