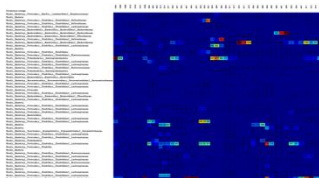


Figure S2

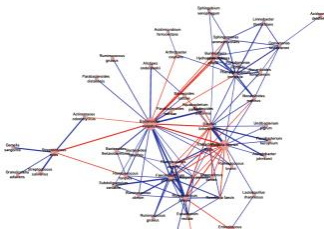
Generate OTU table using 16S sequencing data

Method: reference-based OTU picking against Greengenes database using uclust



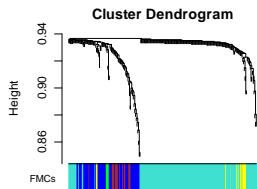
Construct co-occurrence network

Step 1: define co-occurrence correlation using SparCC
Step 2: calculate topological overlap matrix as distance measure



Identify functional microbial communities (FMCs)

Method: hierarchical clustering, Dynamic Tree Cut



Correlate FMCs to external information

Method: correlation between disease states, SNPs, habitats etc.

