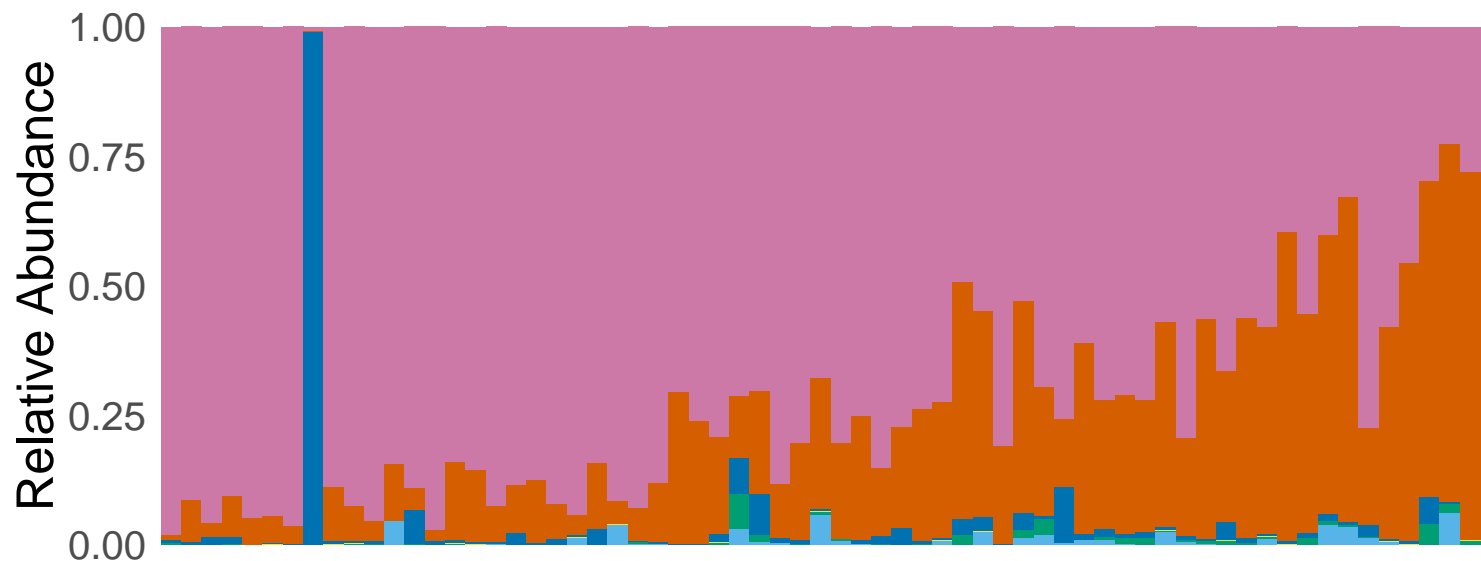


Web Figure 1 – Phylum-level relative abundance of the eight most abundant phyla in matched 16S rRNA (16S) and metagenomic shotgun (MGX) sequencing samples from the Human Microbiome Project. 16S samples are shown in Panel A and MGX samples are shown in Panel B; samples are ordered in both plots by abundance of Bacteroidetes in 16S samples. Notably, the figure illustrates the Bacteroidetes/Firmicutes gradient with reasonable agreement between the 16S and MGX samples.

A



B



Bacteroidetes Firmicutes Proteobacteria Tenericutes
Actinobacteria Verrucomicrobia Fusobacteria Spirochaetes