



Supplemental Figure 1: Human Microbiome Project mock community sequence similarity

ASVs/OTUs output by each sequence processing method on the Human Microbiome Project mock community were compared to the expected sequences from the mock community using BLASTN. Sequences were then binned together based on their difference in sequence identity to the expected sequences. ALL sequences with identity below 75% were binned together. A) DADA2; B) Deblur; C) UNOISE3; D) Open reference 97% OTU clustering