

Supplemental Figure 12

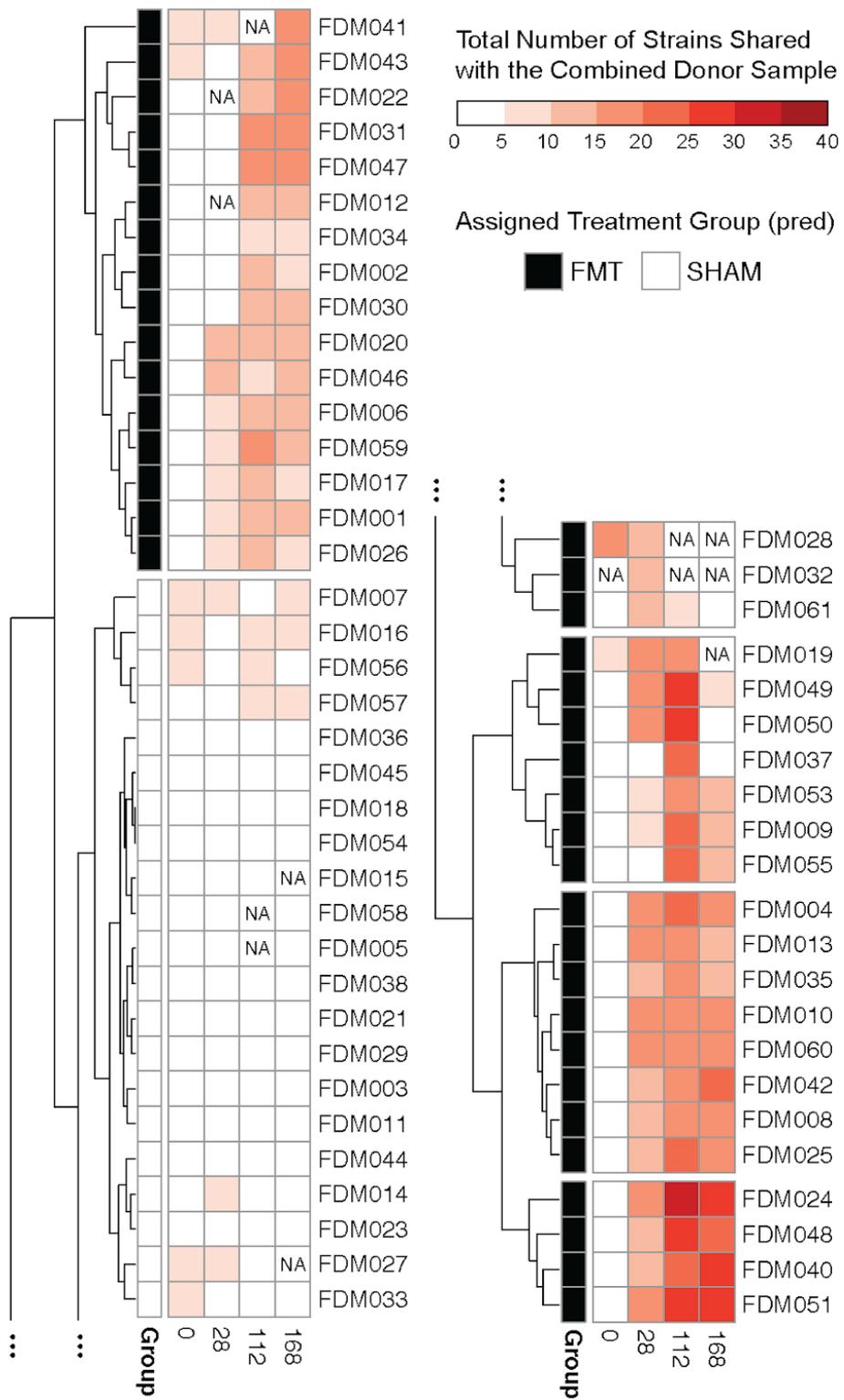


Figure D12. Clustering of all samples from Ng et al. based on shared strain profiles in order to determine the assignment of patients to the FMT or sham treatment groups.

Hierarchical clustering of strain-sharing profiles between a concatenated donor sample (combined from five published donor metagenomes) and each patient from Ng et al. at one pre-FMT (0) and three post-FMT (28, 112, 168) time points highlights 21 patients whose samples share very few (mostly <5) strains with any donor sample. Since treatment assignments were not disclosed by Ng et al., these 21 patients were excluded from the analysis as they most likely belong to the sham treatment group of the study.