# Supplemental figures

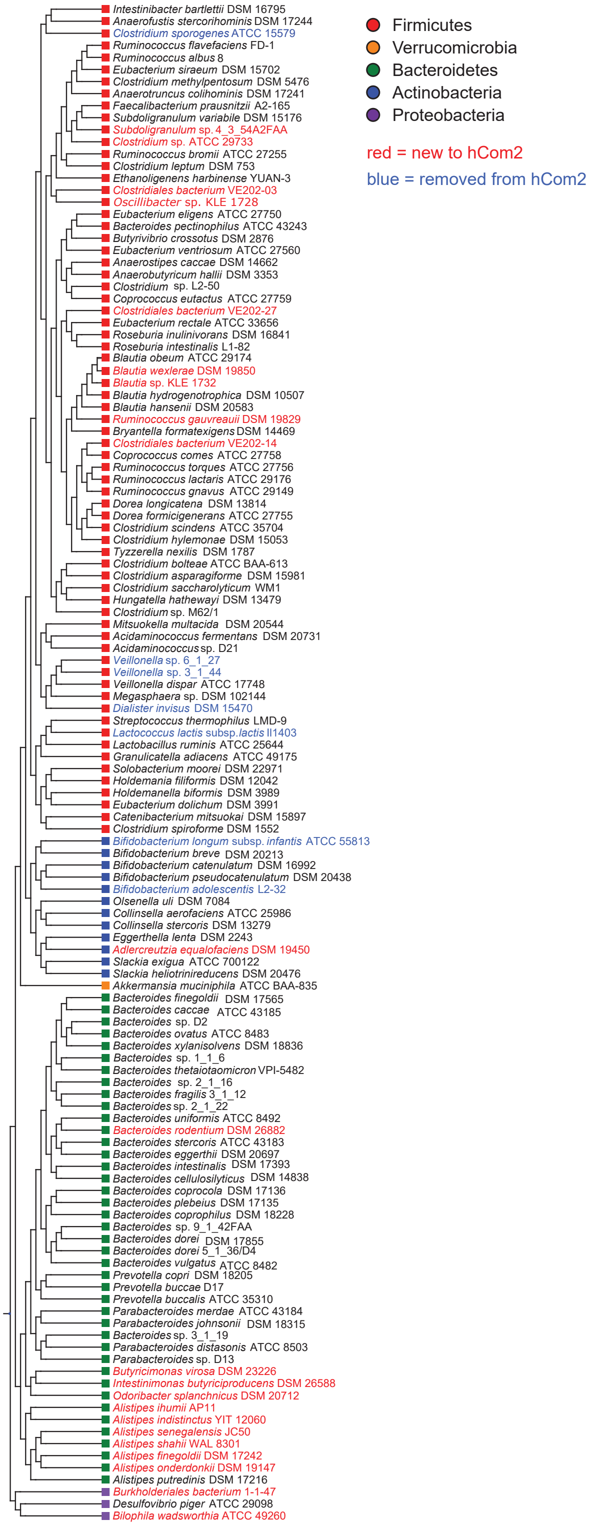

**Figure S1. Phylogenetic tree of strains from hCom1 and hCom2, related to Figures 4 and 5**

Strains in black are present in hCom1 and hCom2. Strains in red are only in hCom2, and strains in blue are only in hCom1.

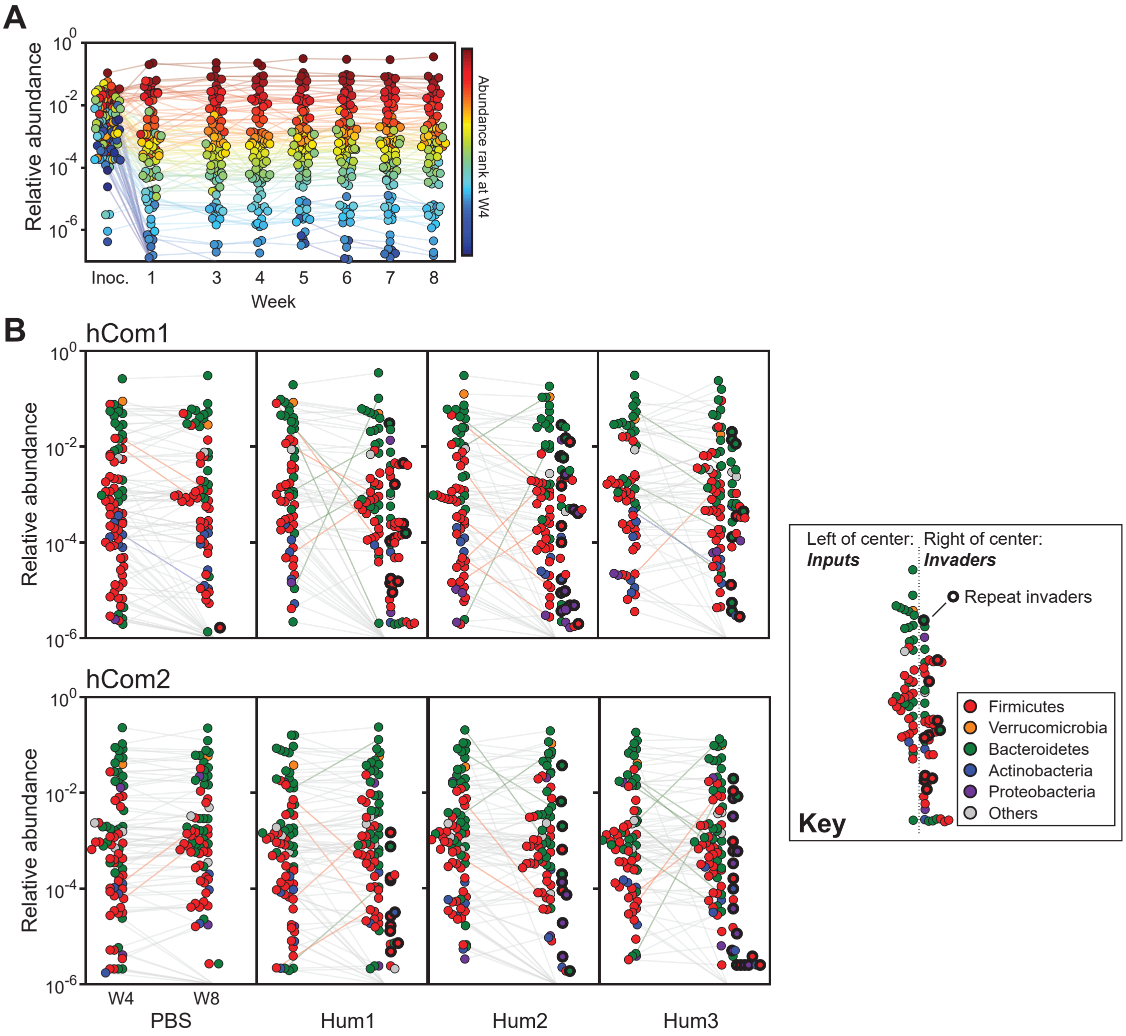

**Figure S2. Stability and invading strains from the first and second fecal challenge experiments, related to Figures 4 and 5**

(A) Average relative abundances of MIDAS bins for hCom2-colonized mice over all 8 weeks of the experiment duration.

(B) Microbiome compositions in hCom1- and hCom2-colonized mice. Week-4 and week-8 species distributions are shown for each group. Week 8 distributions are split into two groups: on the left are input species and on the right are invading species, as depicted in the right inset. Invading species from weeks 5–8 that are common to all three groups are outlined in bold (Table S4).

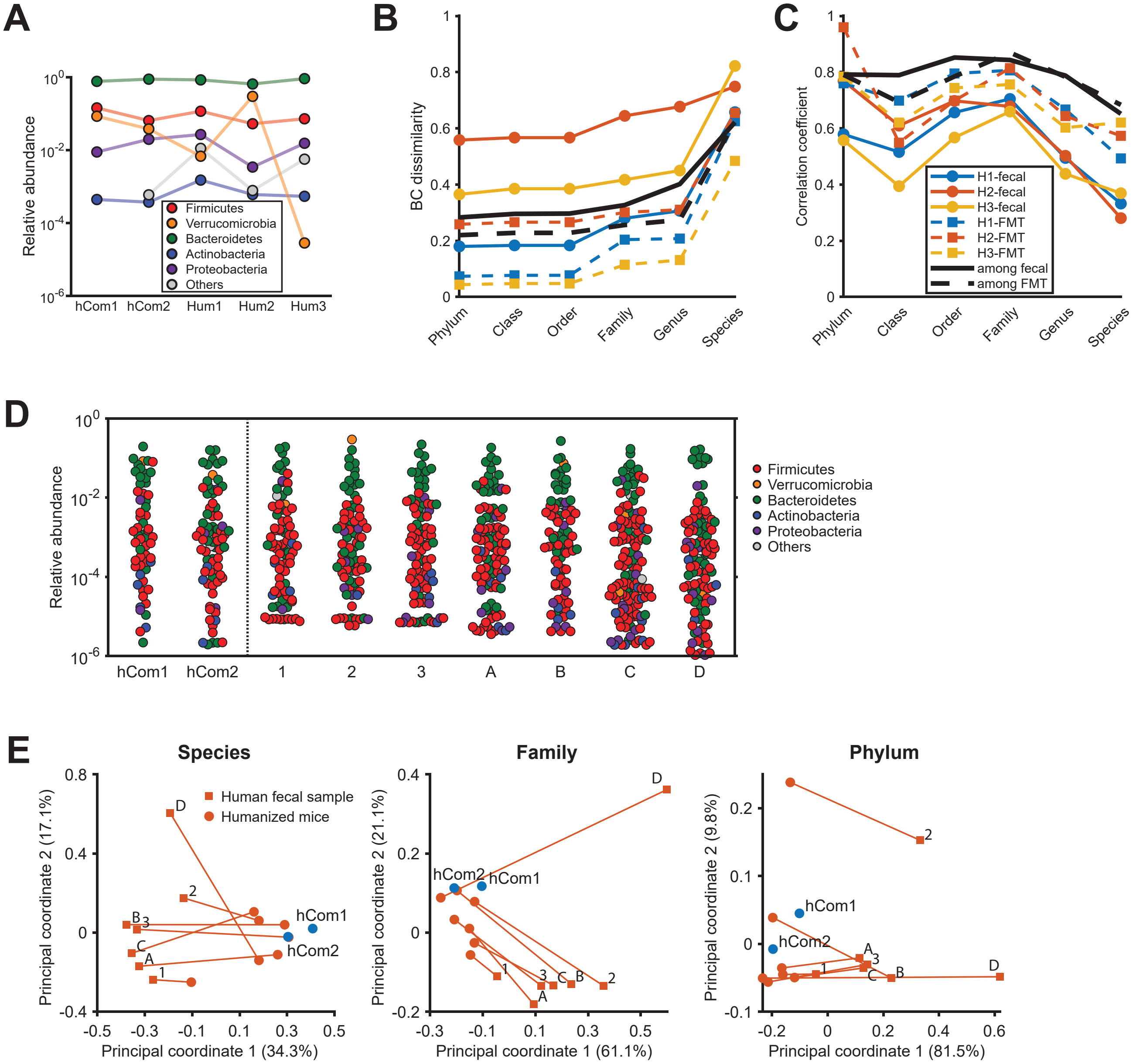

**Figure S3. The architecture of hCom2 more closely resembles that of a human fecal consortium than hCom1, related to Figures 4 and 5**

(A) Phylum-level relative abundances from mice colonized with hCom1, hCom2, or healthy human fecal samples Hum1–3 (n = 5 mice per group).

(B and C) Bray-Curtis (BC) dissimilarities (B) and correlation coefficients (C) at each taxonomic level between fecal pellets from germ-free mice colonized with hCom2; human fecal samples Hum1, Hum2, and Hum3 (H1-fecal, H2-fecal, and H3-fecal, respectively); and fecal pellets from germ-free mice colonized by Hum1, Hum2, and Hum3 at week 4 (H1-FMT, H2-FMT, and H3-FMT, respectively). The average similarity among the fecal or humanized fecal samples is shown as bold or dashed black lines, respectively.

(D) Composition as determined by MIDAS of hCom1-colonized mice; hCom2-colonized mice; the three original samples from Hum1-FMT, Hum2-FMT, and Hum3-FMT (labeled 1–3); and four additional humanized mouse samples from human fecal samples unrelated to Hum1–3 (labeled A–D).

(E) Principal coordinate analysis of BC dissimilarity at the species, family, and phylum levels. Each circle denotes a human fecal sample and is connected by a line to a square that represents the corresponding sample from humanized mice at week 4.