Data S1: Composition and function of hCom1 and hCom2, related to Figure 1.

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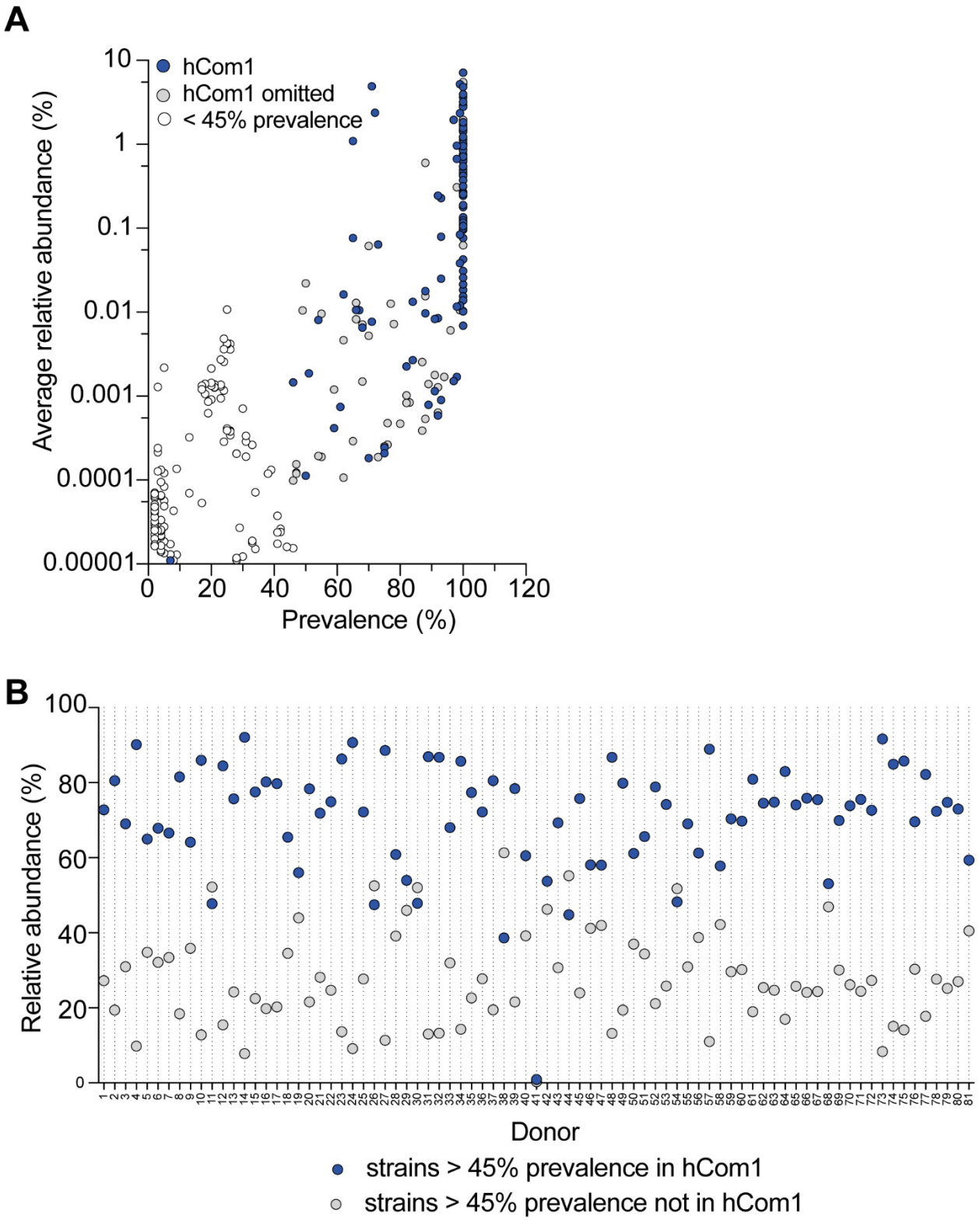
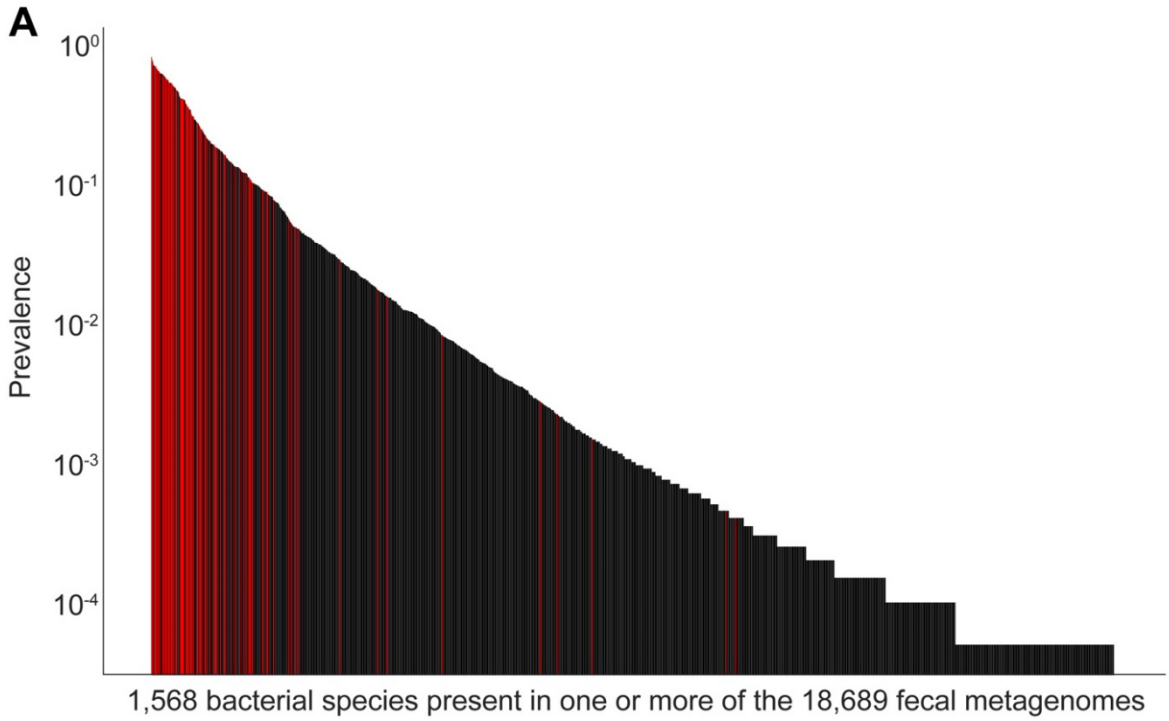
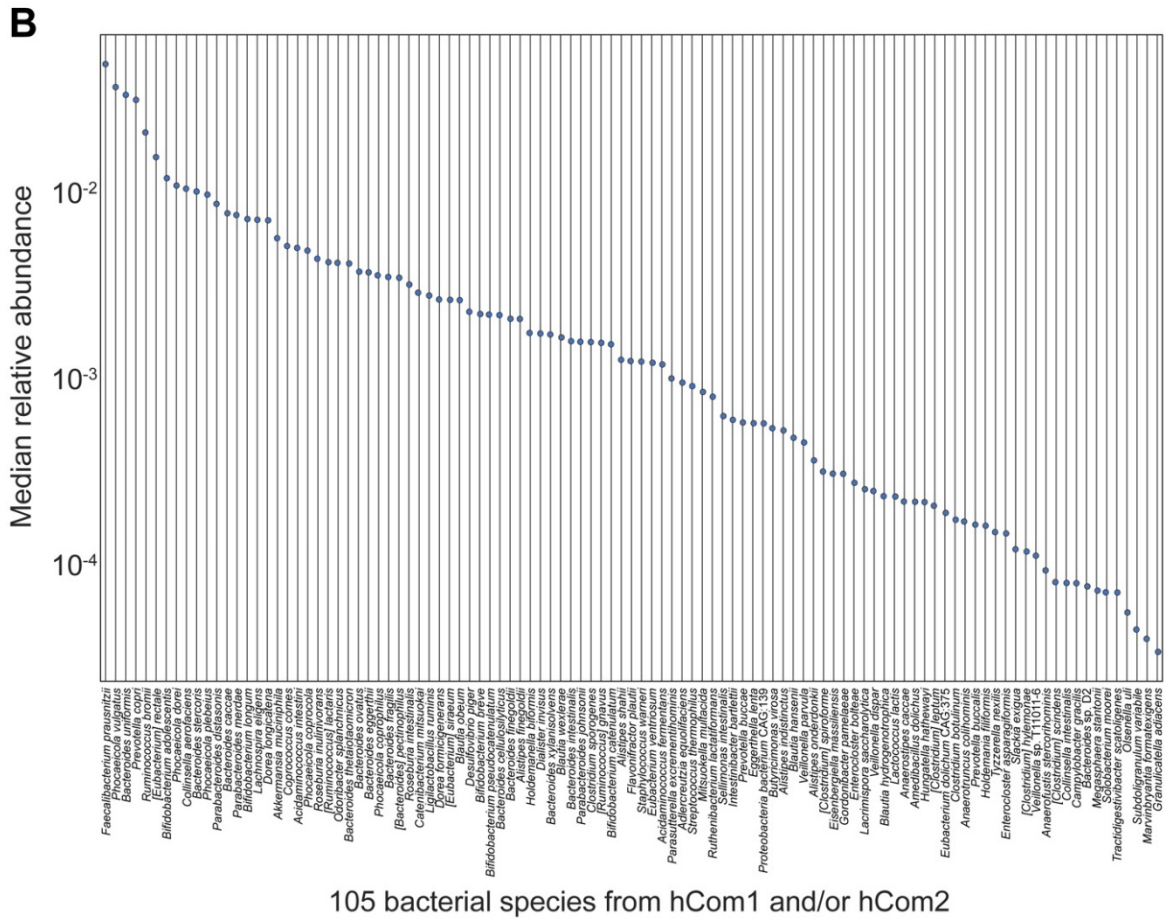
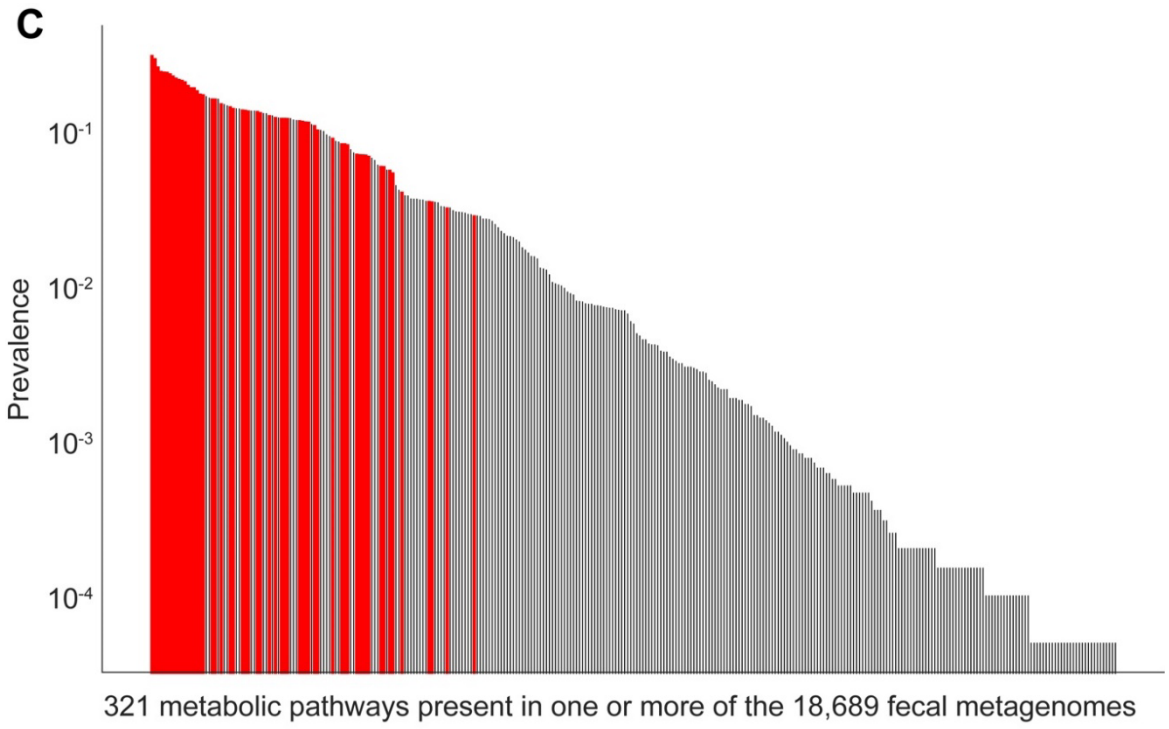


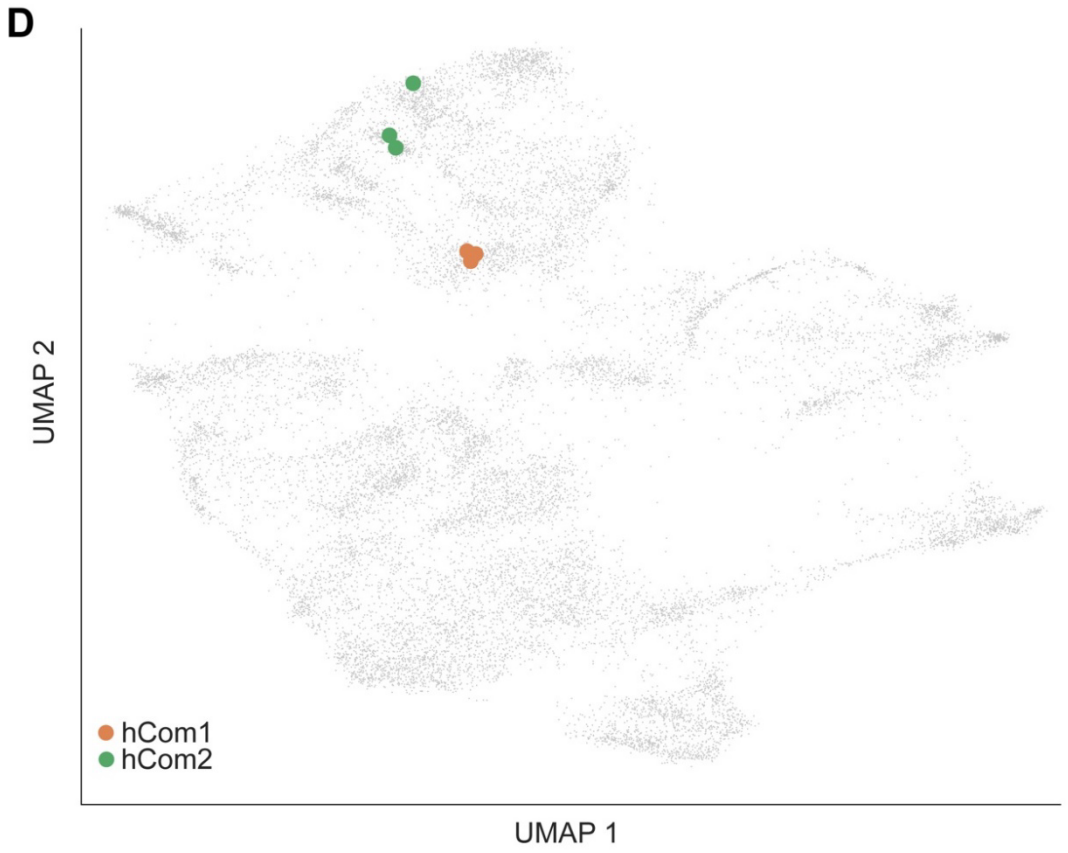
The 104-member community hCom1 is phylogenetically and compositionally reflective of typical Western human gut communities. (**A**) Prevalence versus average relative abundance

of all 522 gut bacterial strains found among the 81 healthy HMP donors. Strains that were present in >45% of donors and included in hCom1 are colored blue and those omitted from hCom1 are colored gray. Strains not considered for inclusion in hCom1 are colored white. (**B**) Donor-specific relative abundance profiles of strains at >45% prevalence across HMP donors. Blue dots represent summed relative abundances of strains included in hCom1 and gray dots represent summed relative abundances of strains omitted from hCom1.


A
Prevalence
10^{0}
10^{-1}
10^{-2}
10^{-3}
10^{-4}
1,568 bacterial species present in one or more of the 18,689 fecal metagenomes


B
Median relative abundance
10^{-2}
10^{-3}
10^{-4}
Faecalibacterium prausnitzii
Phascolarctobacterium faecium
Bacteroides uniformis
Prevotella copri
Ruminococcus bromii
[Eubacterium] eligens
Bifidobacterium adolescentis
Phocaeicola dorei
Collinsella aerofaciens
Bacteroides stercoris
Phocaeicola plebeius
Parabacteroides distasonis
Bacteroides caccae
Parabacteroides merdae
Bifidobacterium longum
Lachnospira eligens
Dorea longicatena
Akkermansia muciniphila
Coprococcus comes
Acidaminococcus intestini
Phocaeicola coprocola
Roseburia inulinivorans
[Ruminococcus] torques
Odoribacter splanchnicus
Bacteroides thetaiotaomicron
Bacteroides ovatus
Bacteroides xylanisolvens
Phocaeicola copriphilus
Bacteroides fragilis
[Bacteroides] pectinophilus
Agathobaculum butyriciproducens
Catenibacterium mitsuokai
Ligilactobacillus ruminis
Romboutsia timonensis
[Eubacterium] siraeum
Blautia obeum
Desulfovibrio piger
Bifidobacterium bifidum
Bifidobacterium pseudocatenulatum
Bacteroides finegoldii
Bacteroides cellulosilyticus
Barnesiella intestinihominis
Alistipes finegoldii
Holdemanella biformis
Dialister invisus
Bacteroides faecis
Blautia wexlerae
Bacteroides intestinalis
Parabacteroides johnsonii
[Clostridium] innocuum
[Ruminococcus] gnavus
Bifidobacterium catenulatum
Alistipes shahii
Flavonifractor plautii
Staphylococcus warneri
Eubacterium ventriosum
Acidaminococcus fermentans
Parasutterella excrementihominis
Adlercreutzia equolifaciens
Streptococcus mutans
Mitsuokella multacida
Ruthenibacterium lactatiformans
Sellimonas intestinalis
Intestinibacter bartlettii
Prevotella buccae
Eggerthella lenta
Proteobacteria bacterium CAG:139
Butyricicoccus pullicaecorum
Alistipes indistinctus
Blautia hansenii
Veillonella parvula
Alistipes onderdonkii
[Clostridium] spiroforme
Eisenbergiella massiliensis
Gordonibacter pamelaeae
Enterocloster bolteae
Lacrimispora saccharolytica
Veillonella dispar
Blautia hydrogenotrophica
Lactococcus lactis
Anaerostipes caccae
Anaerobutyricum soehngenii
Hungatella hathewayi
[Clostridium] leptum
Eubacterium dolichum CAG:375
Clostridium sp. CAG:253
Anaerofustis stercorihominis
[Clostridium] asparagiforme
Collinsella aerofaciens
Campylobacter gracilis
Bacteroides sp. D2
Methanobrevibacter smithii
Solobacterium moorei
Tractidigestivibacter scatoligenes
Olsenella uli
Subdoligranulum unclassified
Marvinbryantia formatexigens
Granulicatella adiacens
105 bacterial species from hCom1 and/or hCom2


C
Prevalence
10^{-1}
10^{-2}
10^{-3}
10^{-4}
321 metabolic pathways present in one or more of the 18,689 fecal metagenomes


D
UMAP 2
UMAP 1
hCom1
hCom2

hCom1 and hCom2 are taxonomically and functionally representative of human gut microbiomes. (**A**) Comparison of hCom1 and hCom2 taxonomy and functionality with fecal metagenomes. Prevalence of the 105 species detected by MetaPhlAn3 in hCom1 and/or hCom2 (red) and the 1,463 species not present in hCom1 or hCom2 (black) in a diverse set of human gut metagenomes. 34/105 species were present in >7,489 (40%) of the samples, and 81/105 species were present in >1,000 samples. (**B**) Relative abundance of hCom1 and hCom2 species in a diverse set of human gut microbiomes. Median relative abundance of all species from hCom1 and hCom2 is shown. Species from hCom1 and hCom2 account for 66% of the aggregate relative abundance on average. (**C,D**) Comparison of the metabolic pathway profile of hCom1, hCom2, and 18,689 gut metagenomes based on the Humann3 pathways list. A pathway was considered to be present if coverage at the community level was >50%. 321 pathways were detected in the 18,689 gut metagenomes. The median gut metagenome contained 59/321 pathways; the hCom1 and hCom2 metagenomes contained an average of 51/321 pathways (red bars).