CD vs HC

UC vs HC

Transcription related proteins

Electron transfer carriers Ascorbate and aldarate metabolism Amino acid related enzymes

Histidine metabolism

Thiamine metabolism

Ribosome Biogenesis Phosphonate and phosphinate metabolism

Valine, leucine and isoleucine biosynthesis

Pantothenate and CoA biosynthesis

C5-Branched dibasic acid metabolism

CD -3 -2 -1 0 1 2 3 LDA Score (log10) UC HC -3 -2 -1 0 1 2 3 LDA Score (log10)

CD vs UC

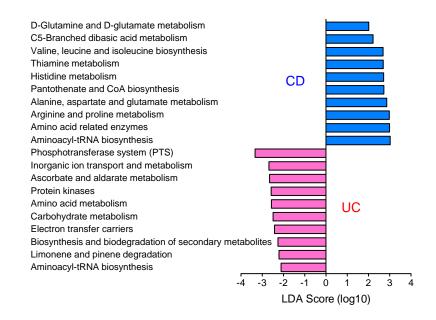


Figure S1. Microbial functional gene pathways in donor stool samples.

The abundance of KEGG metabolic gene pathways was analyzed by PICRUSt based on 16S rRNA sequencing data in Fig. 2. Significantly altered pathway genes in 3 groups (HC-, CD-, and UC donors) were identified by LEfSe analysis. Linear Discriminant Analysis (LDA) score is shown.

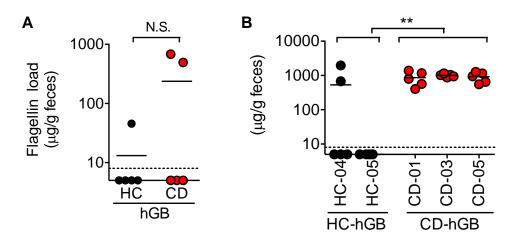


Figure S2. Flagellin production by the microbiota.

(A) Flagellin load in feces from HC- and CD-hGB mice (WT B6). Each dot indicates a different donor described in Fig. 2 (HC-01 - HC-05 and CD-01 - CD05). (B) Flagellin load in IL-10^{-/-}-HC-hGB mice (HC-04 and HC-05) and IL-10^{-/-}-CD-hGB mice (CD-01, -03, -05) mice. Each dot indicates individual mouse. **; P < 0.01, N.S.; Not significant by Mann-Whitney *U*-test. Dots under dotted line indicate flagellin concentration is below the detection limit.

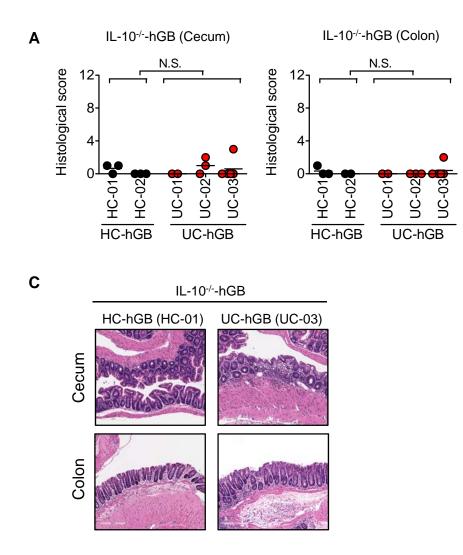


Figure S3. UC-associated microbiota does not promote development of severe colitis in IBD-prone mice.

(A-B) Stool samples were isolated from HC-hGB mice and UC-hGB mice and then inoculated into GF *II10^{-/-}*mice. After 4 weeks of reconstitution, cecum and colonic tissues were harvested. (A) Histological score. Each dot indicates individual mouse. N.S.: Not significant by Mann-Whitney *U*-test. (B) A representative histological image of IL-10^{-/-}HC-hGB (HC-01) and UC-hGB mice (UC-03). Scale bar: 200 μ m.