Supplementary Material

Alterations in the abundance and co-occurrence of *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* in the colonic mucosa of inflammatory bowel disease subjects

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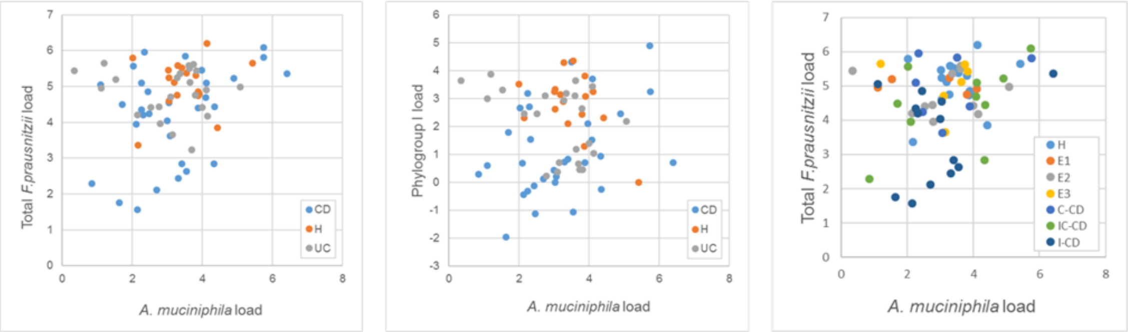
Supplementary Figure



A. Group of subjects

B. Group of subjects

C. Disease location

D. Age of disease onset

E. Age of disease onset

F. Age of disease onset

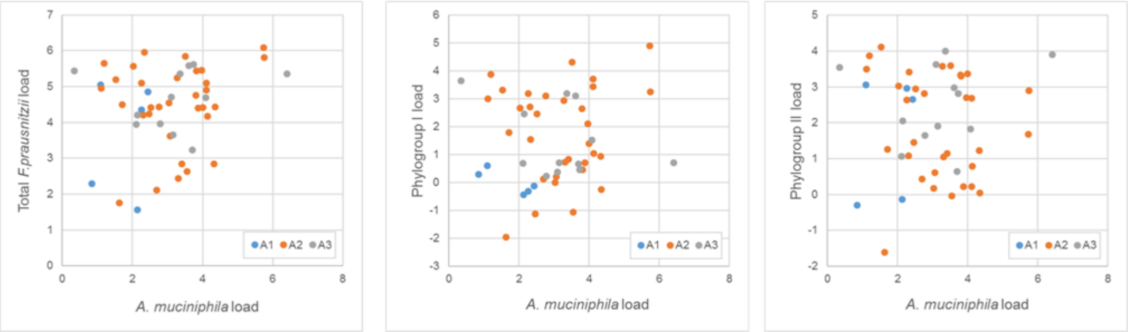


Figure S3. Biplots representing mucosa-associated *F. praunsitzii* and *A.muciniphila* in several groups of subjects (A) Total *F. prausnitzii* and *A muciniphila* load by condition (B) Phylogroup I and *A. muciniphila* by condition. (C) Total *F. prausnitzii* and *A. muciniphila* by inflammatory bowel disease subtype (D to F) Total *F. prausnitzii,* Phylogroup I or Phylogroup II and *A muciniphila* load by age of disease onset, respectively.

H, control subjects; UC, ulcerative colitis; CD, Croh's disease; E1, ulcerative proctitis; E2, ulcerative left-sided colitis; E3, ulcerative pancolitis; IC-CD, ileocolonic CD, I-CD, ileal CD; C-CD, colonic CD.

A. muciniphila load = Log (16S rRNA gene *Akkermansia*/16S rRNA gene million bacteria)

Total *F. prausnitzii* load = Log (16S rRNA gene total *F.prausnitzii*/16S rRNA gene million bacteria)

Phylogroup I load = Log (16S rRNA gene total *F.prausnitzii* phylogroup I/16s rRNA gene million bacteria)

Phylogroup II load = Log (16S rRNA gene total *F.prausnitzii* phylogroup II/16s rRNA gene million bacteria)