



- [3] p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium
- [6] p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides
- [7] p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides
- [8] p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella
- [9] p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__
- [10] p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__
- [27] p__Firmicutes;c__Clostridia;o__Clostridiales;f__;g__
- [32] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;Other
- [33] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__
- [35] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia
- [36] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Coproccoccus
- [37] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea
- [38] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnobacterium
- [39] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospira
- [40] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Roseburia
- [41] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Ruminococcus]
- [45] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__
- [47] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Oscillospira
- [48] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus
- [50] p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Dialister
- [62] p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__[Coprobacillaceae];g__
- [69] p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Sutterella
- [80] p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobiaceae;g__Akkermansia

Supplemental Fig.S1. The taxonomic composition at genus level of gut microbiome determined by 16S rRNA analysis of stool samples collected from healthy volunteers. Top 7 genera of *Coproccoccus* (#36, p_Firmicutes, f_Lachnospiraceae), *Bacteroides* (#6, p_Bacteroidetes, f_Bacteroidaceae), *Roseburia* (#40, p_Firmicutes, f_Lachnospiraceae), *Prevotella* (#8, p_Bacteroidetes, f_Prevotellaceae), non-identifies genus of f_Lachnospiraceae (#32, p_Firmicutes), non-identifies genus of f_Coprobacillaceae (#62, p_Firmicutes), *Blautia* (#35, p_Firmicutes, f_Lachnospiraceae).