

SUPPLEMENTARY MATERIALS

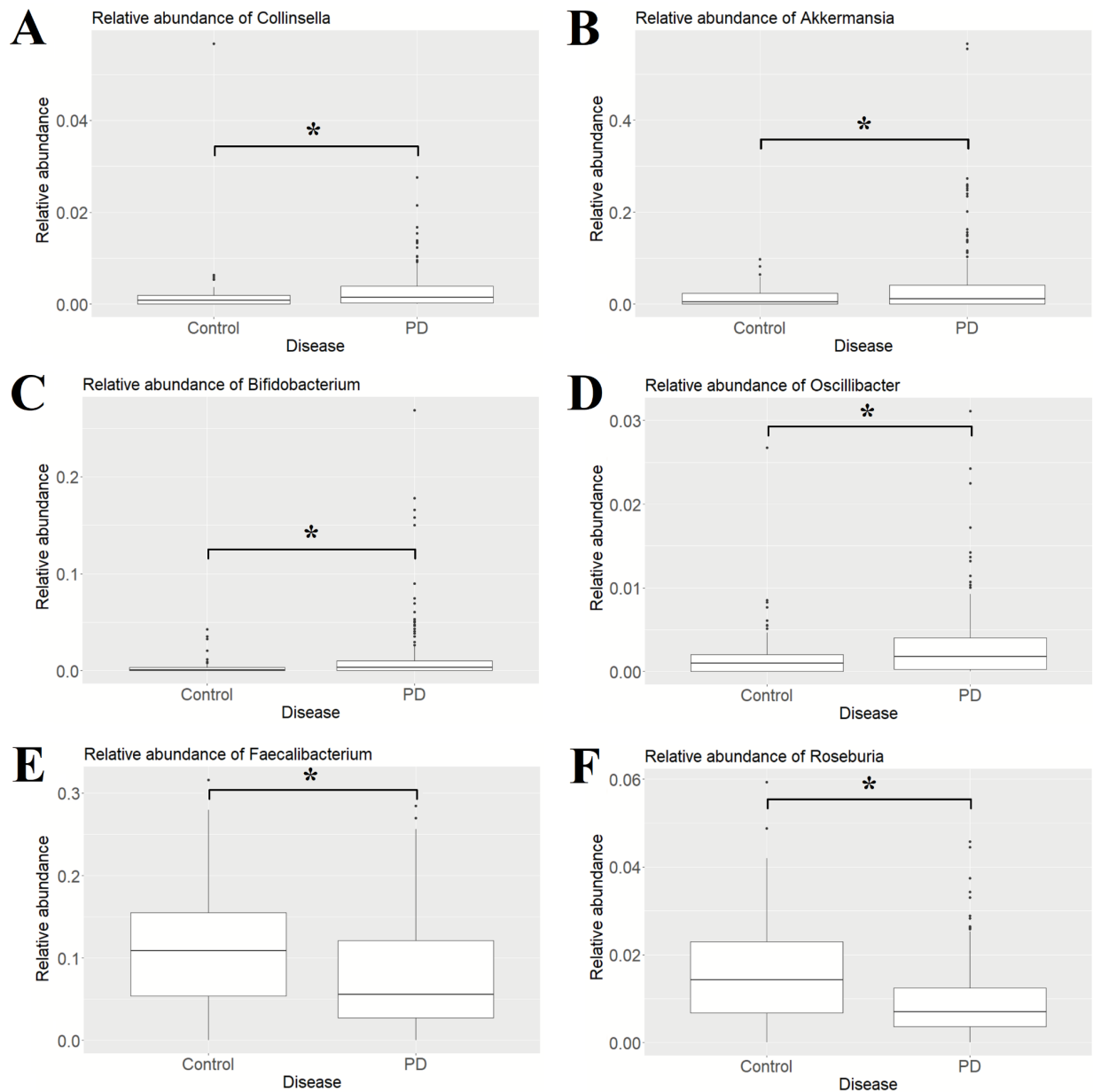


Figure S1. Relative abundances of differentially abundant genera in the PD gut microbiome compared to the non-PD microbiome. Relative abundances of (A) *Collinsella*, (B) *Akkermansia*, (C) *Bifidobacterium*, (D) *Oscillibacter*, (E) *Faecalibacterium*, and (F) *Roseburia*. Asterisk denotes $p_{\text{adj}} < 0.05$.

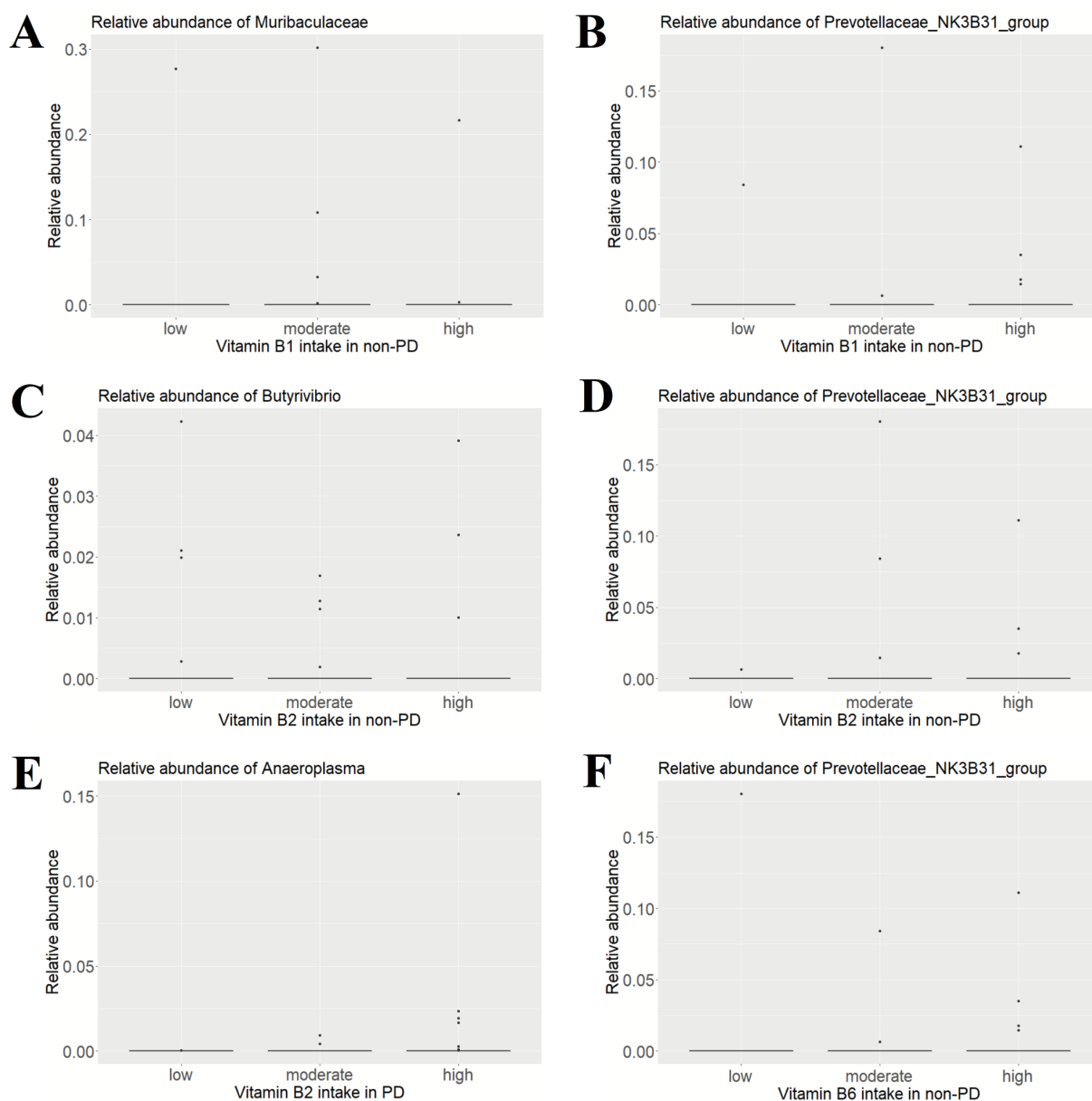


Figure S2. In the non-PD gut microbiome, genera *Muribaculaceae* (differentially abundant by B1 intake), *Butyrivibrio* (differentially abundant by B2 intake) and *Prevotellaceae NK3B31 group* (differentially abundant by B1, B2, and B6 intake) are present in very few samples. In the PD gut microbiome, the genus *Anaeroplasma* (differentially abundant by B2 intake) is present in very few samples. Abundance of genus relative to all genera in the gut microbiome: (A) *Muribaculaceae* and (B) *Prevotellaceae NK3B31 group* by vitamin B1 intake in non-PD; (C) *Butyrivibrio* and (D) *Prevotellaceae NK3B31 group* by vitamin B2 intake in non-PD; (E) *Anaeroplasma* by vitamin B2 intake in PD; and (F) *Prevotellaceae NK3B31 group* by vitamin B6 intake in non-PD.

Table S1. Certain phyla and genera are missing from the PD gut microbiome dataset.

Taxonomic classification of the PD and non-PD gut microbiome was performed via a naïve Bayes machine-learning classifier that was pre-trained to sort taxa in the SILVA 138 99% identity reference set. Taxa only found in the non-PD gut microbiome are listed and sorted in alphabetical order. Abbreviations: d__ = domain, p__ = phylum, c__ = class, o__ = order, f__ = family, g__ = genus.

Taxa missing from the PD gut microbiome
Phyla
d__Eukaryota.p__Incertae_Sedis
p__Elusimicrobiota
Genera
d__Eukaryota.p__Heterokonta.c__Blastocystae.o__Blastocystida.f__Blastocystidae.g__Blastocystis
p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Atopobium
p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__gir-aah93h0.g__gir-aah93h0
p__Campilobacterota.c__Campylobacteria.o__Campylobacterales.f__Helicobacteraceae.g__Helicobacter
p__Elusimicrobiota.c__Elusimicrobia.o__Elusimicrobiales.f__Elusimicrobiaceae.g__Elusimicrobium
p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__uncultured
p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae.g__Granulicatella
p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Shuttleworthia
p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Papillibacter
p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae.g__Anaerovibrio
p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Leptotrichiaceae.g__Leptotrichia
p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacteriales.f__Morganellaceae.g__Morganella
p__Spirochaetota.c__Spirochaetia.o__Spirochaetales.f__Spirochaetaceae.g__Treponema
p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__uncultured

Table S2. Certain phyla and genera are unique to the PD gut microbiome dataset.

Taxonomic classification of the PD and non-PD gut microbiome was performed via a naïve Bayes machine-learning classifier that was pre-trained to sort taxa in the SILVA 138 99% identity reference set. Taxa only found in the PD gut microbiome are listed and sorted in alphabetical order. Abbreviations: p__ = phylum, c__ = class, o__ = order, f__ = family, g__ = genus.

Taxa unique to the PD gut microbiome

Genera

p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae.g__Mobiluncus

p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae.g__Scardovia

p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Libanicoccus

p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Olsenella

p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__Raoultibacter

p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Denitrobacterium

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__uncultured

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__CAG.873

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_UCG.003

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__dgA.11_gut_group

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenella

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenellaceae

p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Erysipelotrichaceae_UCG.006

p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Pediococcus

p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae.g__Gemella

p__Firmicutes.c__Clostridia.o__Caldicoprobales.f__Caldicoprobacteraceae.g__Caldicoprobacter

p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenella

p__Firmicutes.c__Clostridia.o__Clostridia.f__Hungateiclostridiaceae.g__uncultured

p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostignum

p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Catenibacillus

p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Cellulosilyticum

p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Epulopiscium

p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_NK3A20_group

p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Oribacterium

p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Pygmaibacter

p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Anaerovorax

p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__uncultured

p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Peptostreptococcus

p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcales.Tissierellales.g__Murdochiella

p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcales.Tissierellales.g__Peptoniphilus

p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae.g__uncultured

p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Sporomusaceae.g__Anaerosporomusa

p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Anaeroglobus

p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__uncultured

p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Leptotrichiaceae.g__Sneathia

p__Proteobacteria.c__Gammaproteobacteria.o__Aeromonadales.f__Succinivibrionaceae.g__Succinivibrio

p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacteriales.f__Enterobacteriaceae.g__Cronobacter

p__Proteobacteria.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.g__Actinobacillus

p__Spirochaetota.c__Brachyspirae.o__Brachyspirales.f__Brachyspiraceae.g__Brachyspira
