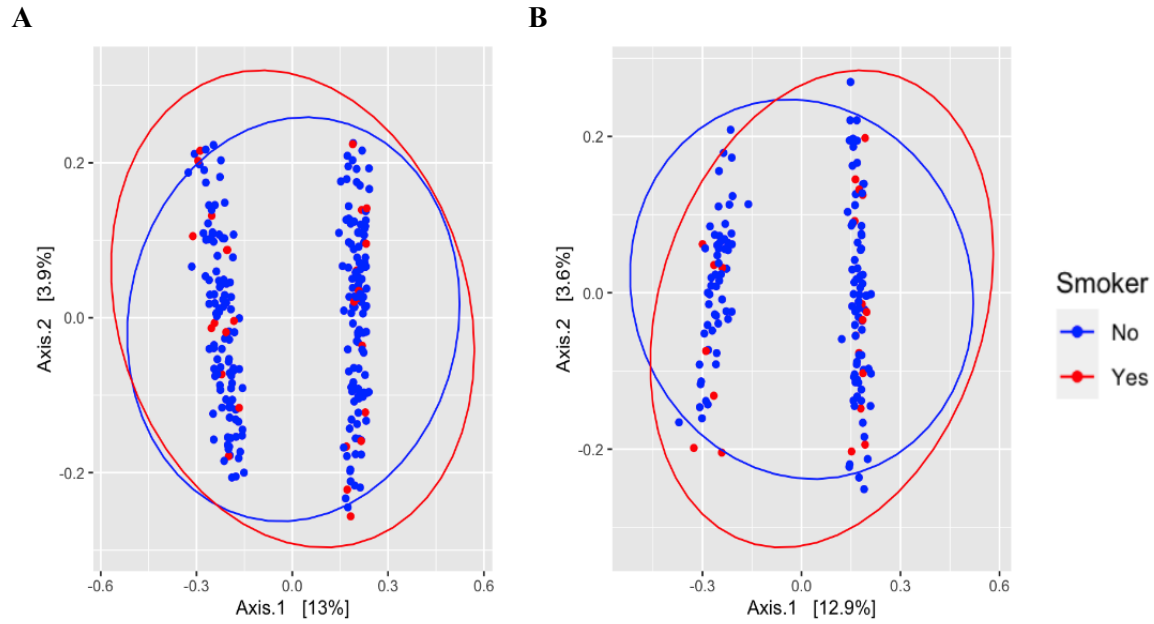


## SUPPLEMENTARY FIGURE



**FIG. S1 Possible confounding variables between cardiometabolic status and smoking.** Comparing microbial diversity between smokers and non-smokers based on their cardiometabolic statuses using the unweighted UniFrac beta diversity metric. **(A)** Healthy cardiometabolic status. **(B)** Abnormal cardiometabolic status.

## SUPPLEMENTARY TABLE

**TABLE. S1 Shared and Unique Differentially Abundant Bacterial species from the Healthy and Abnormal Cardiometabolic Status Groups.** Identifying shared and unique ASVs with Log<sub>2</sub> fold change > 2 following DESeq2 analysis.

Shared Species					
Phylum	Class	Order	Family	Genus	Species
p_Verrucomicrobiota	c_Verrucomicrobiae	o_Verrucomicrobiales	f_Akkermansiaceae	g_Akkermansia	NA
p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	NA	NA	NA
p_Actinobacteriota	c_Coriobacteriia	o_Coriobacteriales	f_Eggerthellaceae	g_Enterorhabdus	s_uncultured_bacterium
p_Actinobacteriota	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Libanicoccus	NA
p_Actinobacteriota	c_Coriobacteriia	o_Coriobacteriales	f_Eggerthellaceae	g_Slackia	s_Slackia_piriformis
p_Firmicutes	c_Negativicutes	o_Veillonellales-Selenomonadales	f_Veillonellaceae	g_Dialister	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Enterococcaceae	g_Enterococcus	NA

p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__Bacteroides_stercoris
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	NA
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	s__uncultured_bacterium
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	s__Prevotellaceae_bacterium
p__Firmicutes	c__Clostridia	o__Peptostreptococcales-Tissierellales	f__Anaerovoracaceae	g__Family_XIII_AD3011_group	s__metagenome
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Butyricoccaceae	g__UCG-009	s__uncultured_bacterium
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__UCG-002	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Butyricoccaceae	g__Butyricoccus	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__Ruminococcus	s__Clostridiaceae_bacterium
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__[Eubacterium]_coprostanoligenes_group	g__[Eubacterium]_coprostanoligenes_group	s__gut_metagenome
p__Firmicutes	c__Clostridia	o__Clostridia_UCG-014	f__Clostridia_UCG-014	g__Clostridia_UCG-014	NA

p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_UCG-001	NA
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Anaerostipes	NA
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_NK4A136_group	NA
<b>Healthy Cardiometabolic Status Unique Bacterial Species</b>					
Phylum	Class	Order	Family	Genus	Species
p_Desulfobacterota	c_Desulfovibrionia	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Desulfovibrio	s_metagenome
p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Escherichia-Shigella	NA
p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	NA	NA

p__Proteobacteria	c__Gammaproteobacteria	o__Pasteurales	f__Pasteurellaceae	g__Haemophilus	NA
p__Cyanobacteria	c__Vampirivibrionia	o__Gastranaerophilales	f__Gastranaerophilales	g__Gastranaerophilales	s__uncultured_bacterium
p__Actinobacteriota	c__Actinobacteria	o__Bifidobacteriales	f__Bifidobacteriaceae	g__Bifidobacterium	s__Bifidobacterium_bifidum
p__Actinobacteriota	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Gordonibacter	s__Gordonibacter_pamelaeae
p__Actinobacteriota	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__Atopobium	NA
p__Firmicutes	c__Clostridia	o__Christensenellales	f__Christensenellaceae	g__Christensenellaceae_R-7_group	NA
p__Firmicutes	c__Bacilli	o__Erysipelotrichales	f__Erysipelatoclostridiaceae	g__Catenibacterium	s__uncultured_bacterium
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__Bacteroides_eggerthii
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__Bacteroides_thetaiotaomicron
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__Bacteroides_sp.
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__Alistipes_inops

p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	NA
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	s__gut_metagenome
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	NA
p__Firmicutes	c__Clostridia	o__Peptostreptococcales-Tissierellales	f__Peptostreptococcaceae	g__Intestinibacter	NA
p__Firmicutes	c__Clostridia	o__Christensenellales	f__Christensenellaceae	g__Christensenellaceae_R-7_group	NA
p__Firmicutes	c__Clostridia	o__Clostridiales	f__Clostridiaceae	g__Clostridium_sensu_stricto_1	s__metagenome
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__UCG-010	g__UCG-010	s__metagenome
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Butyricoccaceae	g__Butyricoccus	s__Butyricoccus_sp.
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__NK4A214_group	s__metagenome
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__UCG-005	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__CAG-352	s__uncultured_bacterium

p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_uncultured	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_[Ruminococcus]_torques_group	NA
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_[Eubacterium]_hallii_group	NA
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium

p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_human_gut
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_gut_metagenome
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_FCS020_group	s_uncultured_organism
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_UCG-003	s_uncultured_bacterium
<b>Abnormal Cardiometabolic Status Unique Bacterial Species</b>					
Phylum	Class	Order	Family	Genus	Species
p_Verrucomicrobiota	c_Verrucomicrobiae	o_Verrucomicrobiales	f_Akkermansiaceae	g_Akkermansia	s_Akkermansia_muciniphila
p_Desulfobacterota	c_Desulfovibrionia	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Desulfovibrio	s_Desulfovibrio_fairfieldensis
p_Desulfobacterota	c_Desulfovibrionia	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Desulfovibrio	s_Desulfovibrio_piger
p_Cyanobacteria	c_Vampirivibrionia	o_Gastranaerophilales	f_Gastranaerophilales	g_Gastranaerophilales	NA
p_Actinobacteriota	c_Actinobacteria	o_Actinomycetales	f_Actinomycetaceae	g_Actinomyces	NA
p_Actinobacteriota	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Libanicoccus	s_uncultured_bacterium



p_Firmicutes	c_Negativicutes	o_Acidaminococcales	f_Acidaminococcaceae	g_Phascalactobacterium	s_Phascalactobacterium_faecium
p_Firmicutes	c_Negativicutes	o_Veillonellales-Selenomonadales	f_Veillonellaceae	g_Dialister	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Streptococcus	NA
p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Lactococcus	s_Lactococcus_garvieae
p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Leuconostocaceae	g>Weissella	NA

p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__Bacteroides_fragilis
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__Bacteroides_ovatus
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__Alistipes_shahii
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__Alistipes_finegoldii
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__Alistipes_indistinctus
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Barnesiellaceae	g__Barnesiella	NA
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Muribaculaceae	g__Muribaculaceae	s__uncultured_Porphyromonadaceae
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Tannerellaceae	g__Parabacteroides	s__uncultured_bacterium
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__uncultured	g__uncultured	s__gut_metagenome
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Alloprevotella	s__uncultured_organism
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Paraprevotella	s__uncultured_bacterium

p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	s__Prevotella_buccalis
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	s__Prevotellaceae_bacterium
p__Bacteroidota	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	NA
p__Firmicutes	c__Clostridia	o__Peptococcales	f__Peptococcaceae	g__Peptococcus	s__uncultured_bacterium
p__Firmicutes	c__Clostridia	o__Clostridia_vadinBB60_group	f__Clostridia_vadinBB60_group	g__Clostridia_vadinBB60_group	s__metagenome
p__Firmicutes	c__Clostridia	o__Clostridiales	f__Clostridiaceae	g__Clostridium_sensu_stricto_1	s__Clostridium_perfringens
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__UCG-002	s__uncultured_rumen
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__UCG-010	g__UCG-010	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__UCG-002	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__UCG-002	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__UCG-005	s__uncultured_organism

p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Oscillospiraceae	g__NK4A214_group	s__metagenome
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__[Eubacterium]_siraeum_group	s__[Eubacterium]_siraeum
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__[Eubacterium]_siraeum_group	s__[Eubacterium]_siraeum
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__Subdoligranulum	s__uncultured_bacterium
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__Subdoligranulum	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__Subdoligranulum	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__Ruminococcaceae	g__Ruminococcus	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__[Eubacterium]_coprostanoligenes_group	g__[Eubacterium]_coprostanoligenes_group	NA
p__Firmicutes	c__Clostridia	o__Oscillospirales	f__[Eubacterium]_coprostanoligenes_group	g__[Eubacterium]_coprostanoligenes_group	s__gut_metagenome
p__Firmicutes	c__Clostridia	o__Clostridia_UCG-014	f__Clostridia_UCG-014	g__Clostridia_UCG-014	NA
p__Firmicutes	c__Clostridia	o__Clostridia_UCG-014	f__Clostridia_UCG-014	g__Clostridia_UCG-014	NA

p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_gut_metagenome
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_gut_metagenome
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	NA
p_Firmicutes	c_Clostridia	o_Clostridia_UCG-014	f_Clostridia_UCG-014	g_Clostridia_UCG-014	s_gut_metagenome
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Roseburia	s_Roseburia_hominis
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Roseburia	NA
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Dorea	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Coprococcus	s_Lachnospiraceae_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_[Ruminococcus]_torques_group	s_Ruminococcus_lactaris

p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_CAG-56	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Butyrvibrio	s_Butyrvibrio_crossotus
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_[Eubacterium]_xylanophilum_group	NA
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_Lachnospiraceae
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_gut_metagenome
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_gut_metagenome
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_gut_metagenome
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_gut_metagenome
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_organism

p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	NA
p_Firmicutes	c_Bacilli	o_RF39	f_RF39	g_RF39	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_ND3007_group	s_metagenome
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_NK4A136_group	s_gut_metagenome
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_NK3A20_group	s_uncultured_bacterium
p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Blautia	NA