

TABLE S1 Key Medications: ACS vs. Control

Medication class	ACS group (n = 15)	Control group (n = 15)
Antiplatelet agents	15	0
Anticoagulants	15	0
ACEi/ARB	11	0
Beta-blockers	11	0
Statins	13	0
Diuretics	4	0
Vasopressors	3	0
Other non-cardiovascular medications	0	2

Antiplatelet agents include aspirin, clopidogrel, ticagrelor, and tirofiban. Anticoagulants include low-molecular-weight heparin, unfractionated heparin, factor Xa inhibitors, and non-vitamin K antagonist oral anticoagulants. Statins include atorvastatin and rosuvastatin.

Angiotensin-converting enzyme inhibitors, ACEi; angiotensin receptor blockers, ARB.

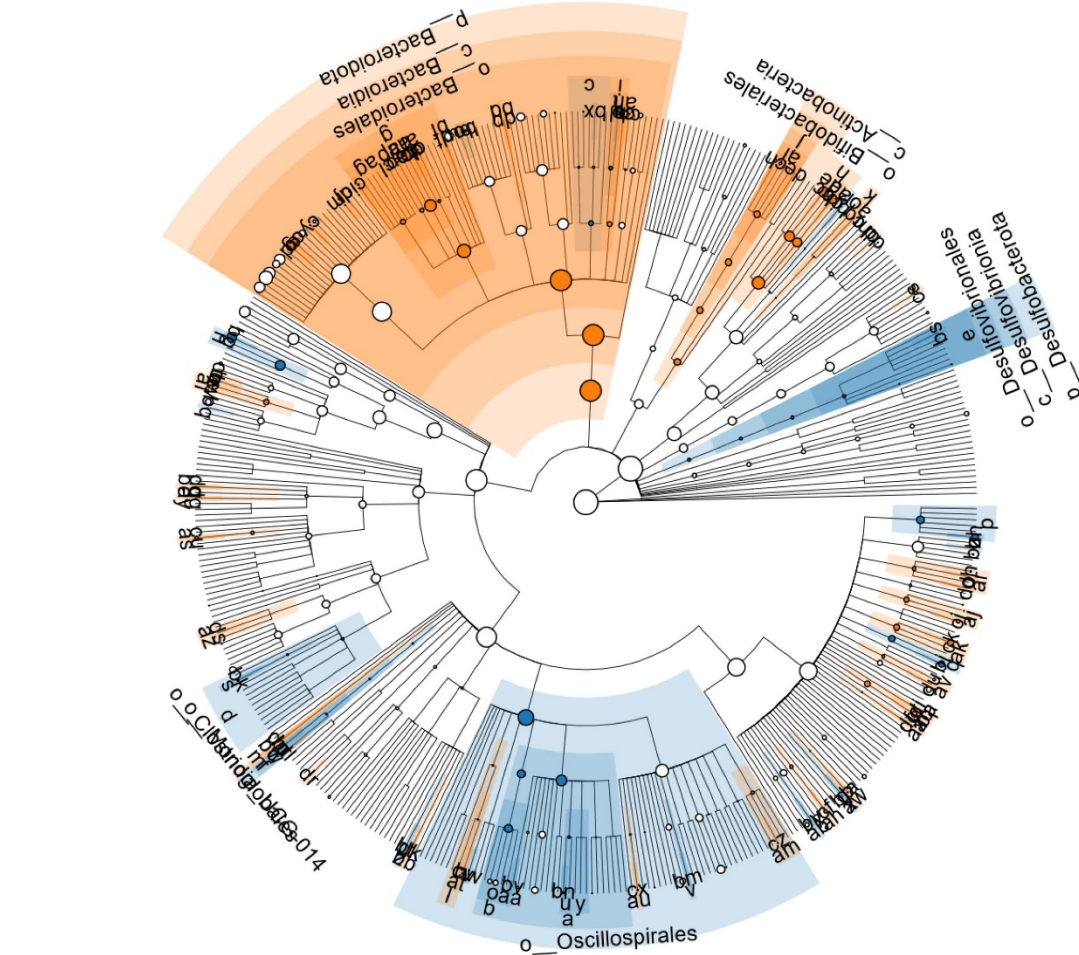


Figure S1. LefSe analysis of the differences in the relative abundances of microbiota between the ACS and control groups.

Blue and orange indicate the significantly enriched microbiota in the ACS and control groups, respectively. The circles of cladogram from inside to outside represent the phylum, class, order, family, genus, and species.

AMI
Control

a: f__Oscillospiraceae	s: g__Ligilactobacillus	ak: g__Anaerostipes	bu: s__Alistipes_sp.	cm: s__Bacteroides_coprocola	de: s__Bifidobacterium_bifidum
b: f__[Eubacterium]_coprostanoligenes_group	t: g__Muribaculaceae	al: g__Paraprevotella	bv: s__Family_Oscillospiraceae_sp.	cn: s__Genus_Coproacter_sp.	df: s__Genus_[Eubacterium]_elgens_group_sp.
c: f__Marinifilaceae	u: g__Oscillibacter	am: g__Ruminococcus	bw: s__Genus_UCG-010_sp.	co: s__Genus_CAG-873_sp.	dg: s__Genus_Erysipelotrichaceae_UCG-003_sp.
d: f__Lactobacillaceae	v: g__UBA1819	an: g__CAG-873	bx: s__Butyricimonas_virosa	cp: s__Genus_Prevotellaceae_NK3B31_group_sp.	dh: s__Coprococcus_unidentified
e: f__Desulfotribionaceae	w: g__Clostridia_UCG-014	ao: g__Haemophilus	by: s__Genus_Eisenbergiella_sp.	cq: s__Genus_Haemophilus_sp.	di: s__Genus_[Eubacterium]_ruminantium_group_sp.
f: f__Clostridia_UCG-014	x: g__Hungateella	ap: g__Prevotellaceae_NK3B31_group	bz: s__Blautia_sp.	cr: s__Genus_[Eubacterium]_hallii_group_sp.	dj: s__Bacteroides_clarus
g: f__Prevotellaceae	y: g__Colidextribacter	aq: g__[Eubacterium]_hallii_group	ca: s__Genus_Prevotella_9_sp.	cs: s__Fusobacterium_varium	dk: s__Genus_Romboutsia_sp.
h: f__Enterobacteriaceae	z: g__Peptoclostridium	ar: g__Coprococcus	cb: s__Genus_Escherichia-Shigella_sp.	ct: s__Genus_Paraprevotella_sp.	dl: s__Genus_Clostridia_UCG-014_sp.
i: f__Muribaculaceae	aa: g__Family_Oscillospiraceae_sp.	as: g__Holdemania	cc: s__Genus_Klebsiella_sp.	cu: s__Genus_Holdemania_sp.	dm: s__Sutterella_wadsworthensis
j: f__Bifidobacteriaceae	ab: g__Eisenbergiella	at: g__Butyricoccus	cd: s__Bacteroides_plebeius	cv: s__Genus_Butyricoccus_sp.	dn: s__Genus_Monoglobus_sp.
k: f__Pasteurellaceae	ac: g__Prevotella_9	au: g__CAG-352	ce: s__Genus_Veillonella_sp.	cw: s__Veillonella_atypica	do: s__Coprococcus_eutactus
l: f__Butyricoccaceae	ad: g__Escherichia-Shigella	av: g__Agathobacter	cf: s__Genus_Fusicatenibacter_sp.	cx: s__Genus_CAG-352_sp.	dp: s__Genus_Rikenellaceae_RC9_gut_group_sp.
m: f__Monoglobaceae	ae: g__Klebsiella	aw: g__Lachnospira	cg: s__Bacteroides_ovatus	cy: s__Bacteroides_intestinalis	dq: s__Genus_Catenibacterium_sp.
n: g__Megamonas	af: g__Veillonella	ax: g__[Eubacterium]_elgens_group	ch: s__Genus_Bifidobacterium_sp.	cz: s__Ruminococcus_bicirculans	dr: s__Clostridium_perfringens
o: g__[Eubacterium]_coprostanoligenes_group	ag: g__Prevotella	ay: g__Erysipelotrichaceae_UCG-003	ci: s__Prevotella_stercorea	da: s__Genus_Lachnospira_sp.	ds: s__Lactococcus_garvieae
p: g__Lachnospiraceae	ah: g__Fusicatenibacter	az: g__Lactococcus	cj: s__Genus_Roseburia_sp.	db: s__Genus_Dialister_sp.	dt: s__Family_Prevotellaceae_sp.
q: g__[Ruminococcus]_torques_group	ai: g__Bifidobacterium_piger	ba: g__[Eubacterium]_ruminantium_group	ck: s__Desulfovibrio_piger	dc: s__Paraprevotella_xylaniphila	du: s__Eubacterium_ramulus
r: g__Succinivibrio	aj: g__Roseburia	bb: g__Romboutsia	bt: s__Genus_Peptoclostridium_sp.	dd: s__Sutterella_gut_metagenome	