Alteration of Gut Microbiome in Lung Cancer Patients

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ABSTRACT Lung cancer is the leading cause of cancer death. Better understanding of factors and pathways involved in lung cancer is needed to improve diagnose and treatment strategies. Recent studies have provided insights into the possible correlation between intestinal dysbiosis and cancer development. Although the immunological relationship between gut and lung had been suggested by many researches, however, to date, no study had investigated the characterization of gut microbiome in treatment naïve lung cancer patients, whether it is distinct from that of health individuals and contribute to the onset and development of lung cancer remain unclear. In this study, we investigated whether gut microbiome of lung cancer patients (LC, n=28) is altered compare with that of matched healthy individuals (HC, n=19) by high throughout sequencing of the V3-V4 regions of 16S rDNA in their fecal samples. We also identified microbiota signatures specific for different histological types of lung cancer, including SSC, ADC, and SCLC. The gut microbiome of lung cancer patients is characterized by decreased relative abundance of *Prevotella*, and increased bacteria groups such as *Actinomyces*, and *Streptococcus*, etc. We also detected a mild structural shift in gut microbiome between ADC and SCLC patients. Our results showed that the gut microbiome of lung cancer patients altered significantly compared with healthy individuals. However, the association between microbial dysbiosis and lung cancer is not clearly understood, future studies involving larger cohorts and metagenomics, or metabolomics, may elucidate the correlations between gut microbiota and lung cancer development.

IMPORTANCE This is the first report to show the alteration of gut microbiome in

lung cancer patients. Our results showed that the gut microbiome of lung cancer patients altered significantly compared with healthy individuals.

KEYWORDS: lung cancer, gut microbiome, dysbiosis, *Prevotella*

INTRODUCTION

Lung cancer is the leading cause of cancer death (1). There are estimated 1.82 million new cases of lung cancer globally, which constitutes nearly 13% of all newly diagnosed cancer cases annually (2). More than one-third of lung cancer worldwide occurring in China, where 733,000 new cases of lung cancer are diagnosed, and about 591,000 Chinese people died from it each year (3-4). Better understanding of factors and pathways involved in lung cancer is urgently needed to improve treatment strategies.

As a heterogeneous disease, many factors are involved in the onset and development of lung cancer. Although smoking is considered as an important factor, only 10–15% of smokers develop cancer (5), which highlights other influences, such as the involvement of microbial communities. Recent studies showed that changes in the lung microbiome may be relevant for progression and exacerbations in lung cancer (6,7). By comparison of microbiome in bronchoalveolar lavage fluid of patients with lung cancer with benign mass like lesions, Lee *et al.* found that the genera *Veillonella* and *Megasphaera* are more abundant in lung cancer patients, which may serve as potential biomarkers for the disease detection/classification (8). A recent research, in which surgical lung tissue samples were used, concluded that the microbiota of the lung cancer is unique, with the genus *Thermus* more abundant in tissue from advanced stage (IIIB, IV) patients, while *Legionella* is higher in patients who develop metastases (9). These studies provide insights into the possible correlation between microbiota and lung cancer development.

However, lung microbiota doesn't seem to be the only microbial factor contributing to the development of lung cancer. The influence of gut microbiota on lung immunity has been vastly explored and several studies have linked changes in the gut microbiome with lung diseases (10,11). For example, gut flora is responsible for inducing lung inflammatory reaction against bacterial challenge and enhancing neutrophils infiltration through TLR4 in mice (12,13). Antibiotic treatment can cause overgrowth of particular fungal species in the gut and promote allergic airway inflammation via fungi-induced prostaglandin E2 (14). Conversely, the lung microbiota also influences the gut microbiota through the blood stream. Acute lung injury (ALI) can disrupt the lung microbiota, induces a transient translocation of bacteria into blood and causes an acute increase of bacterial load in cecum (15). These studies emphasized the important role of gut-lung axis in development of diseases (16). However, to date, no study had investigated the characterization of gut microbiome in treatment naïve lung cancer patients, whether it is distinct from that of health individuals and contribute to the onset and development of lung cancer remain unclear.

In this study, we investigated whether gut microbiome of lung cancer patients (LC, n=28) is altered compare with that of matched healthy individuals (HC, n=19) by high throughout sequencing of the V3-V4 regions of 16S rDNA in their fecal samples. We also identified microbiota signatures specific for different histological types of lung cancer, including SSC, ADC, and SCLC.

RESULTS

Characteristics of participants. A total of 50 participants enrolled in the Department of Medical Oncology, The Second Affiliated Hospital of Dalian Medical University (Dalian, China). Participants were excluded after fecal sample collection because of antibiotic use, received chemotherapy, or combined with other diseases such as diabetes mellitus (Fig. 1). Finally, a total of 28 LC patients were remained, they were mainly males (83%) with a median age of 65 years old (Table 1) and with an average smoking index of 606.79±127.1. 19 healthy controls (HC) were included for age and gender matching, with an average smoking index of 350.00±72.1 ($P > 0.05$ compared with LC group) (details in Table 1). More than 64% of the enrolled LC patients were smokers, with a high smoking index about 606.79±127.1. Among them, 28.57% (8/28) of the patients were diagnosed as SCLC, and 71.43% (20/28) were NSCLC. Among the NSCLC patients, 21.43% (6/28) were diagnosed as squamous cell carcinoma and 50.00% (14/28) were adenocarcinoma.

The overall structure of gut microbiome in LC patients. By sequencing of the 16S ribosomal RNA gene, we found that The HC and LC groups share about 2368 same Operational Taxonomic Units (OTUs), but there are 372 OTUs were obtained specifically in the HC group, and 202 were obtained specifically in the LC group (Fig. 2A). We observed significant decrease in alpha diversity of gut microbiota in LC group, which expressed by the ACE and Chao1 index (Fig. 2B and C). Whereas the Shannon diversity index and the Simpson index did not show significant differences between two groups (Fig. S1). Changes in the relative abundance of gut microbes in LC patients were observed not only on the phylum level, but also on the levels of

order, class, and family (Fig. S4). At genus level, significant decreased abundance of *Prevotella* and elevated abundance of *Bacteroides*, and *Ruminococcus* etc. were detected in LC patients (Fig. 2D).

The beta diversity metrics from the control and LC individuals also showed strong grouping pattern. Although significant inter-individual variation exists among patients and the healthy controls, the fecal microbiota of the two groups still separated clearly according to community composition using Principal component analysis (PCA, Fig. S3), and unweighted/weighted UniFrac Principal coordinates analysis (PCoA) (Fig. 2E). These differences were also observed by the two-dimensional Nonmetric Multidimensional Scaling (NMDS) based on unweighted/weighted UniFrac (Fig. 2F). Most of the samples from each group clustered together as evaluated by Hierarchical clustering based on Weighted UniFrac by the method of Unweighted pair-group method with arithmetic means (UPGMA, Fig. S4). Especially, when analyzed by the method of Partial Least Squares Discriminant Analysis (PLSDA), we observed a significant separation between the LC patients and HCs (Fig. 2G).

Altered microbiota composition in LC patients. The alteration of gut microbiome in LC patients was further proved by the LEfSe approach, which identified the key phylotypes responsible for the difference between the two groups. *Actinobacteria*, *Bacilli*, *Ruminococcus*, *Streptococcus*, and *Mycobacteriaceae*, etc, which were most abundant in the LC group, and *Prevotella*, *Bacteroidetes*, and *Dialister*, which were most abundant in the HCs, were the dominant phylotypes that

contributed to the difference between the intestinal microbiota of LC patients and HCs (Fig. 3A and B). The significantly elevated relative abundance of *Actinomyceae*, *Streptococcus*, and *Ruminococcus*, and decreased abundance of *Prevotellaceae* were observed in the gut microbiome of most of the LC patients, which suggested a highly consistence among different individuals (Fig. S5).

Using the method of Metastats, we found a significant decrease in the abundance of *Bacteroidetes* (phylum), *Bacteroidia* (class), *Bacteroidales* (order) and elevated abundance of *Firmicutes* (phylum), *Bacilli* (class), *Actinomycetales* (order), *Bacillales* (order), *Lactobacillales* (order) in gut of the LC patients (Fig. S6). On the family level, significant elevation of the relative abundance of *Streptococcaceae*, *Actinomycetaceae*, decreased abundance of the *Prevotellaceae* and *Veillomellaceae* were observed in gut of LC patients compared with HCs (Fig. 4A). These changes may mainly due to the changing of genus such as the *Streptococcus*, *Actimomyces*, and *Prevotella* etc (Fig. 4B). In addition, we also detected elevation of genera such as *Ruminococcus*, *Rothia*, *Bacillus*, *Peptostreptococcus*, *Mycoacterium*, etc, and decreased abundance of *Dialister* in gut of LC patients, which are consistent with LEfSe analysis results.

Comparison of gut microbiome in LC patients with specific histological types. We further performed a detailed comparison of the gut microbiome in lung cancer patients according to different histological types, including adenocarcinoma (Group A, n=14), squamous cell carcinoma (Group B, n=6), and SCLC (Group C, n=8). Only the index of alpha diversity (ACE) in SCLC patients is significantly lower than control (Fig. 5A). Other groups showed no significant differences compared either with HC

or other groups, although the average indexes of each of the specific histological type are obviously lower than that of the HCs (Fig. 5A and Fig. S7). The beta diversity analysis by PCoA and NMDS showed no obvious separation between groups (Fig. 5B and C). When analyzed by the method of PLSDA, we observed a mild separation between group A and C, which suggested that the gut microbiome of SCLC patients may differ from that of LC patients with adenocarcinoma (Fig. 5D). The taxonomy-based comparison at the genus level showed that, *Bifidobacterium*, *Clostridium*, and *Prevotella*, etc, are the dominant phylotypes in group A, but were significantly reduced in the other two groups. In group B, the dominant genera including *Ruminococcus*, *Lachnospira*, and *Lactobacillus*, etc, which are less abundant in group A and C. in addition, the genera of *Streptococcus*, *Anaerotruncus*, and *Bacillus*, etc are more abundant in group C when compared with group A and B (Fig. S8).

DISCUSSION

Alterations of the gut microbiome influence the incidence and progression of not only gastric carcinogenesis (17), but also extra-intestinal cancers, such as breast and hepatocellular carcinoma, presumably through inflammatory and metabolic circuitries (18). Meanwhile, gut microbiota was also found contribute to the acute lung injury (19), the exacerbation of chronic obstructive pulmonary disease (COPD) (20), and the development of asthma (21), which highlighted its important role in affecting the respiratory system. Actually the hypothesis of “gut–lung” axis has been raised 20

183 years ago, when study found that gut-derived injurious factors can reach to the lung
184 and systemic circulation via the intestinal lymphatics (22). Gut flora was found to be
185 responsible for inducing lung inflammation against bacteria in mice and enhancing
186 neutrophils infiltration through activation of tool like receptor 4 (TLR4) (23). Such
187 immune transmission from gut to lung has been proved by many studies. One
188 viewpoint supports that exacerbation of chronic lung diseases occur as an
189 uncontrolled and inappropriate inflammatory response to bacteria colonizing damaged
190 airways due to an ineffective Peyer's patch-derived T lymphocyte response (24).
191 These studies above strongly suggested a possible correlation between intestinal
192 dysbiosis and the development of lung cancer. However, to our knowledge, no study
193 has explored this possibility yet.

194 Although based on a small number of cases, we found a statistically significant
195 decrease of alpha diversity in gut microbiota of lung cancer patients, compared with
196 that of the healthy controls, which was consist with previous discovery that
197 non-malignant lung tissues have higher microbiota alpha diversity than the paired
198 tumors (10). The decline in both the bacterial diversity and richness was found in gut
199 of patients with chronic inflammation such as inflammatory bowel disease (IBD) and
200 colonrectal cancer, especially in patients with conventional adenoma (25). Reduced
201 respiratory microbiome was also shown associated with greater emphysema and
202 increased immune cell infiltration in COPD patients (26). These observations seem in
203 line with the hygiene hypothesis that diverse microbes play an essential role in
204 establishing the immune networks of a host, while in patients with various

non-communicable inflammatory diseases, such as asthma, these regulatory networks seemed to be underrepresented and poorly developed (27).

Alterations of the gut microbial structure in lung cancer patients were characterized by the significant decrease of *Bacteroidetes* (phylum), *Bacteroidia* (Class), *Bacteroidales* (Order), and increase of *Firmicutes* (phylum), *Bacilli* (Class), *Actinomycetales*, and *Bacillales* (Order), which were mainly contributed by the reduction of bacteria genera such as *Prevotella* and *Dialister*, and the increase in *Ruminococcus*, *Streptococcus*, *Rothia*, *Bacillus*, *Actinomyces*, *Peptostreptococcus*, *etc.* These changes are not consistent with previous studies in sliva, bronchoalveolar lavage fluid, or lung tissues in patients with lung cancer, except that the genus of *Streptococcus* was previously found increased in lower airway of LC patients (28). But interestingly, they are highly agreed with the observations in patients with colon cancer that the class of *Bacilli*, genera of *Streptococcus*, *Actinomyces*, *Peptostreptococcus*, and etc are enriched (29). Importantly, we found a significantly increased ratio of *Bacteroides*/*Prevotella*, which was also proved in patients with colorectal cancer when compared with normal individuals (25). Taken together, these results indicate a state of dysbiosis in the gut microbiome of patients with lung cancer.

As the major genus that was found significantly reduced in LC patients' gut, *Prevotella* had drawn many of our attentions. *Prevotella* strains are classically considered commensal bacteria due to the extensive presence in the healthy human body and the rare involvement in infections. *Prevotella* can stimulate epithelial cells to produce cytokines such as IL-8, IL-6 and CCL20, which can promote mucosal

Th17 immune responses and neutrophil recruitment (30). Increased *Prevotella* abundance is associated with augmented Th17-mediated mucosal inflammation, which is in line with the marked capacity of *Prevotella* in driving Th17 immune responses through activation of TLR2 (30). These studies suggested an immune-stimulating activity of this genus. Congruously, *Prevotella* abundance was found reduced within the lung microbiota of patients with asthma and COPD (31), which further highlighted its important role in affecting lung cancer development.

On the other side, the increasing of certain bacteria in LC patients suggested a deleterious role of them in the development of cancer. Species of *Streptococcus* are found to increase in patients with LC. Compared to healthy controls, the NSCLC patients presented significantly higher frequencies of Th1 and Th17 cells reacting to *S. salivarius* and *S. agalactiae*, in the PB, LC, and GI tract (32). The order of *Actinomycetales* had been as potential colorectal cancer driver bacteria (25). Among them, the filamentous Gram-positive anaerobic genus *Actinomyces*, was found to cause *Actinomycosis*, which is a rare and slowly progressive infectious disease that can affect a variety of organ systems including the lung (33). *Actinomyces* was also found significantly associated with the carcinoma-in-adenoma group (34). Besides, *Peptostreptococcus* species, *P. stomatis* was confirming known to be associated with CRC (35). *P. anaerobius*, which is increased in human colon tumors compared with nontumor tissues, can enhance AOM-induced tumorigenesis in mice by activating TLR2/4-ROS-cholesterol axis (36). In addition, species of *Atopobium*, *A. parvalum* was found positively correlates with pediatric IBD disease severity (37).

However, the effects of these bacteria on lung cancer development are still unclear, which deserves in-deep study.

In addition, we compared the gut microbiome of lung cancer patients according to different histological types based on collected samples, including SSC, ADC, and SCLC. Although the alpha diversity among groups showed no difference, we detected an obvious separation of beta diversity between patients with ADC and SCLC. Given the limited number of study cases, further large scale studies on the characterization of gut microbiome in LC patients with different histological types are necessary.

Conclusions. In conclusion, this is the first report to show the alteration of gut microbiome in lung cancer patients. Our results showed that the gut microbiome of lung cancer patients altered significantly compared with healthy individuals. However, the association between microbial dysbiosis and lung cancer is not clearly understood, future studies involving larger cohorts and metagenomics, or metabolomics, may elucidate the correlations between gut microbiota and lung cancer development.

MATERIALS AND METHODS

Study subjects and sample collection. The recruitment of participants and the process of sample collection are depicted in Fig. 1. Fifty patients (age, 50 – 75 years) were ultimately recruited from the Second Affiliated Hospital of Dalian Medical University, Dalian, China, from September 2015 to July 2016. Fecal samples were collected in Stool Collection Tubes, which were pre-filled with Stool DNA Stabilizer for collection (Stratec, Germany), then frozen and stored at -80 °C for further use. All

subjects were examined clinically before sampling and were subsequently divided into three groups: SCLC (n=17), AC (n=18), SCC (n=15). The samples of the healthy controls (HC, n = 30) were collected during routine physical examination at the First Affiliated Hospital of Dalian Medical University, Dalian, China.

The participants with the following diseases were excluded: cardiovascular disease, diabetes mellitus, liver cirrhosis, irritable bowel syndrome, inflammatory bowel disease, infections with known active bacteria, fungi, or virus. Those who abused drug or alcohol in the last year, or used antibiotics, probiotics, prebiotics, or synbiotics in the month, or received chemotherapy before collection of the fecal sample were also excluded.

DNA extraction, polymerase chain reaction (PCR) and pyrosequencing. The microbial genome was extracted using E.Z.N.A. ® Stool DNA kit (Omega Bio-tek, Inc.) according to the manufacturer's instructions. A Nanodrop 2000 Spectrophotometer was used to evaluate the purity and concentration of isolated DNA. The polymerase chain reaction (PCR) to amplify the V3-V4 region of bacterial 16S ribosomal RNA gene was performed as described previously. After amplicons extraction, samples were purified using AXYGEN gel extraction kit (Qiagen) and quantified by Quant-iT PicoGreen dsDNA Assay Kit on Microplate reader (BioTek，FLx800). Sequencing and data analysis were subsequently performed on an Illumina MiSeq platform by Personal Biotechnology Co., Ltd. (Shanghai, China). The taxa classification and statistical analysis were conducted as described in previous studies.

Statistics and analysis. Illumina MiSeq sequences obtained after quality control

293 analysis were used in the present analysis, which were uploaded to QIIME
294 (Quantitative Insights Into Microbial Ecology, v1.8.0) for further study. The
295 operational taxonomy units (OTUs) of representative sequences at a similarity cutoff
296 of 97% and their relative abundance (α-diversity) were used to calculate ACE and
297 Chao1 index by UCLUST. The abundance and diversity of the OTUs (β-diversity)
298 were examined using principal component analysis (PCA), Principal coordinates
299 analysis (PCoA) and nonmetric multidimensional scaling (NMDS) with weighted and
300 unweighted UniFrac analysis in R software. The statistical significance of the
301 separation among groups was assessed by the linear discriminant analysis effect size
302 (LEfSe) method based on linear discriminant analysis scores exploited by Curtis
303 Huttenhower (http://huttenhower.sph.harvard.edu/galaxy/), which used the
304 nonparametric factorial Kruskal–Wallis and Wilcoxon rank sum test to identify key
305 OTUs for separating different treatment groups at a significance level of 0.05.
306 Metastats analysis was performed based on the raw count data matrix to find out the
307 taxa statistically different between HC and LC samples.

308 For the analyses of clinical data, the non-parametric *t*-test between HC and LC
309 groups was performed with the assistance of GraphPad Prism 6 (Graph Pad Software,
310 La Jolla, CA, USA). Results were considered to be statistically significant with $P <$
311 0.05. The taxa classification and statistical analysis were conducted as described in
312 previous studies (38).

313 **Ethics statement.** This study protocol was approved by the Ethics Committee of
314 the Second Affiliated Hospital of Dalian Medical University, Dalian, China. After

315 receiving a written description of the aim of this study, all participants gave written
316 informed consent prior to enrollment.
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318

SUPPLEMENTARY MATERIAL

Supplementary Figure legends

FIG S1, Comparison of the Shannon **(A)** and Simpson **(B)** index of gut microbiome in HC and LC groups.

FIG S2, The gut bacterial composition in different groups at Phylum, Class, Order, and Family levels.

FIG S3, Principal component analysis of gut microbiome in HC and LC groups. PC1 and PC2 account for 73.08% of the variation.

FIG S4, Hierarchical clustering based on Weighted UniFrac by the method of UPGMA. Number of samples: HC, 2-20, LC, 62-98

FIG S5, The relative abundance of the most differentially abundant bacterial taxons identified by LEfSe in each samples of different among groups.

FIG S6, The specific bacterial Phyla, Classes, and Orders that are significantly changed in LC patients compared with HCs detected by the MetaStat method.

FIG S7, Alpha diversity of gut microbiota in LC patients with specific histological types. **(A)** Venn diagram of shared and independent bacterial OTUs in different groups. **(B)** ACE, **(C)** Chao1, **(D)** Shannon, **(E)** Simpson.

FIG S8, The taxonomy-based comparison among groups at the genus level showed by heat map.

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CONFLICTS OF INTERSTS

The authors declare no competing interest.

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488 **TABLE 1** Characteristics of the study population

Variables	Healthy controls	Patients with lung cancer	*p*-value
Sample size	n=19	n=28	
Age	57.21±1.706	61.50±1.345	0.0525
Gender (F/M)	3/19	6/28	0.6385
BMI(kg/m^2)	24.57±1.427	25.95±1.025	0.0831
Smoking index	350.00 ± 72.1	606.79 ±127.1	0.0845
Final diagnosis			
		SCLC 8 (28.57%)	
		Extensive/limited stage 5/3	
		NSCLC 20 (71.43%)	
		Squamous cell carcinoma 6 (21.43%)	
		Stage IIA/IIB/IIIA/IIIB/IV 1/1/1/1/2	
		Adenocarcinoma 14 (50.00%)	
		Stage IIA/IIIA/IIIB/IV 2/2/1/9	

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FIGURE LEGEND

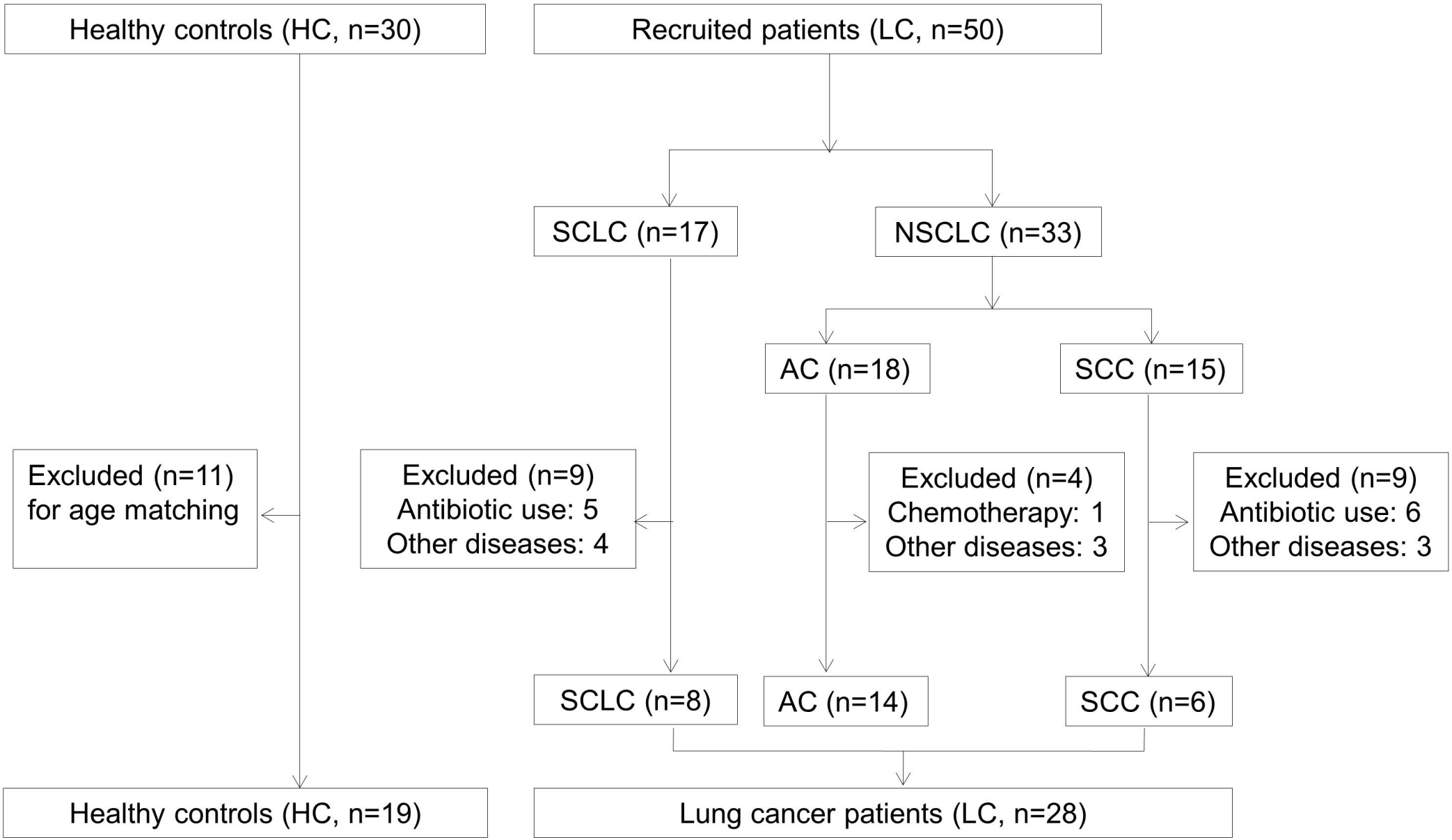
FIG 1 The recruitment of participants and the process of sample collection.

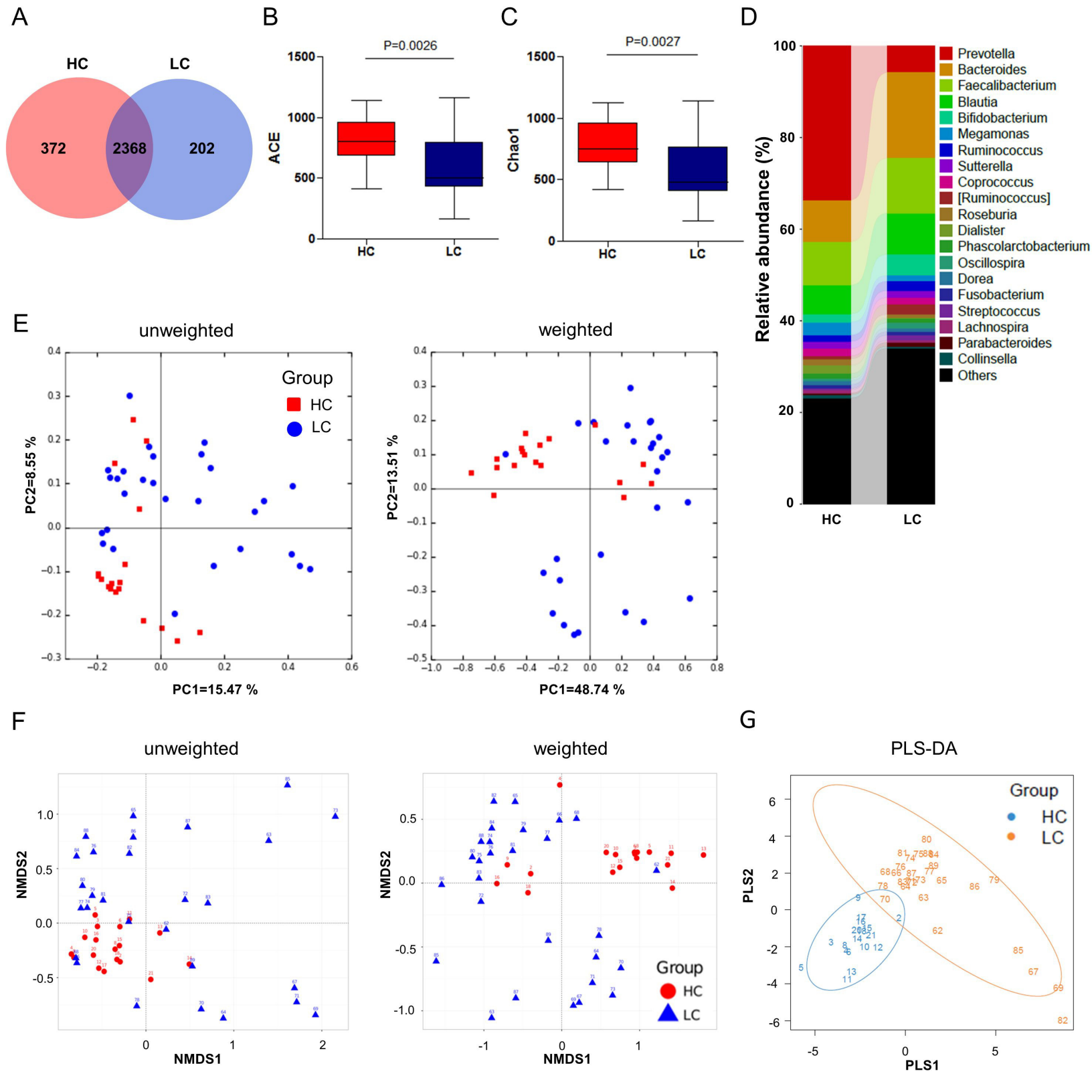
FIG 2 The intestinal bacterial composition in HCs and LC patients. **(A)** Venn diagram of shared and independent bacterial OTUs in HC and LC groups. **(B)** Comparison of the ACE and Chao1 index of HC and LC groups. **(C)** The bacterial composition in different groups at Genus level. **(D)** Principal Coordinate Analysis (PCoA) based on weighted Unifrac distances among different samples. **(E)** NMDS based on weighted Unifrac distances among different samples. **(F)** PLS-DA of the gut microbiome in HC and LC patients.

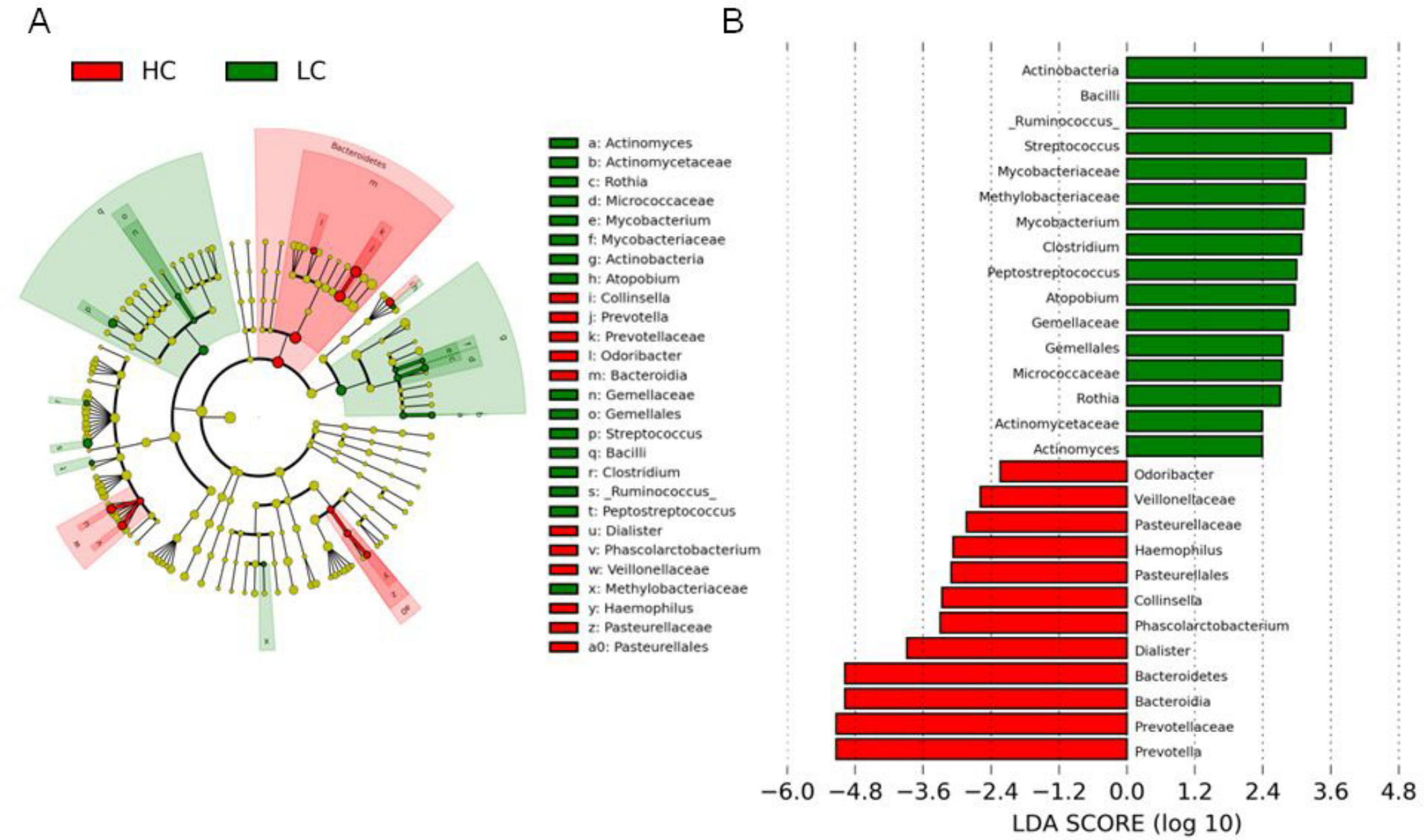
FIG 3 LEfSe analysis of gut microbiota in HC and LC groups. **(A)** LEfSe identified the most differentially abundant bacterial taxons among groups. Group-specific enriched taxa are indicated with a positive LDA score bar with different colors. Only taxa meeting an LDA significant threshold >2 are shown. **(B)** Taxonomic cladogram obtained from LEfSe analysis of 16S rDNA sequences. The brightness of each dot is proportional to its effect size.

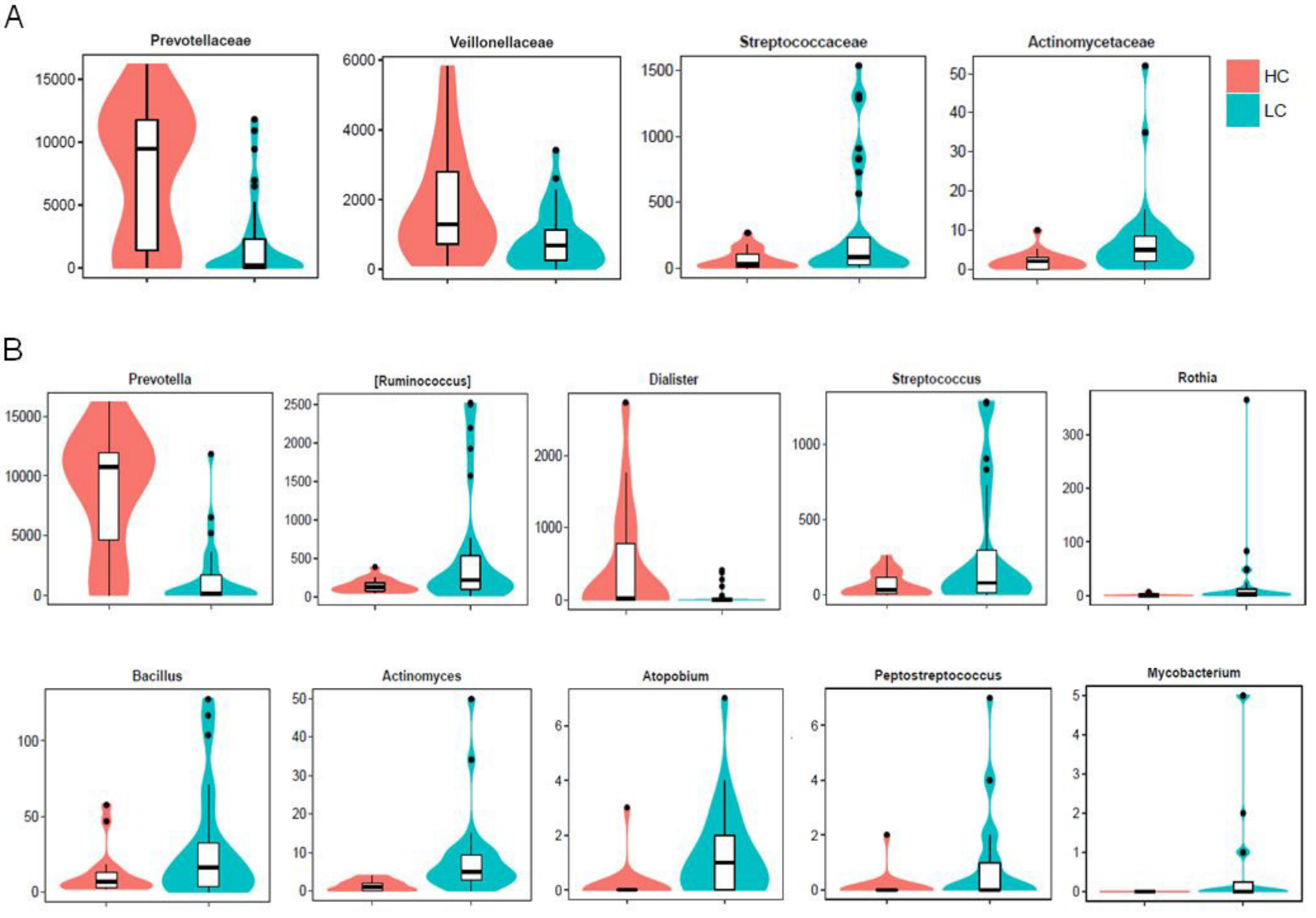
FIG 4 The specific bacterial groups that are significantly changed in LC patients compared with HCs detected by the MetaStat method. **(A)** Families, **(B)** Genera.

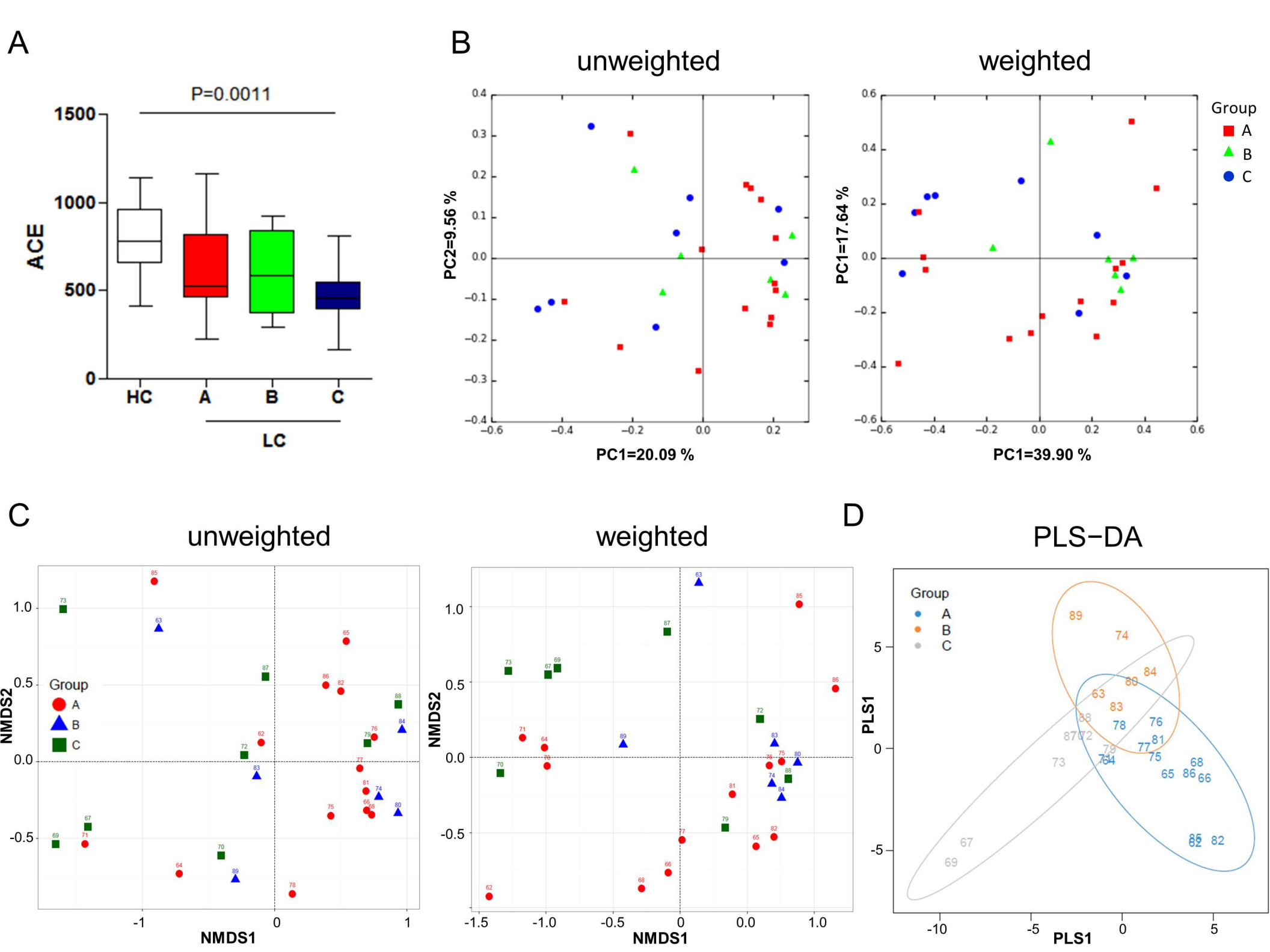
FIG 5 Comparison of gut microbiome in LC patients with specific histological types. **(A)** Comparison of the ACE index of different groups. **(B)** PCoA based on unweighted and weighted Unifrac distances among different samples. **(C)** NMDS based on unweighted and weighted Unifrac distances among different samples. **(D)** PLS-DA of the gut microbiome in LC patients with specific histological types.


Healthy controls (HC, n=30)
Recruited patients (LC, n=50)
SCLC (n=17)
NSCLC (n=33)
AC (n=18)
SCC (n=15)
Excluded (n=11)
for age matching
Excluded (n=9)
Antibiotic use: 5
Other diseases: 4
Excluded (n=4)
Chemotherapy: 1
Other diseases: 3
Excluded (n=9)
Antibiotic use: 6
Other diseases: 3
SCLC (n=8)
AC (n=14)
SCC (n=6)
Healthy controls (HC, n=19)
Lung cancer patients (LC, n=28)


A
HC
LC
372
2368
202
B
P=0.0026
ACE
1500
1000
500
0
HC
LC
C
P=0.0027
Chao1
1500
1000
500
0
HC
LC
D
Relative abundance (%)
100
80
60
40
20
0
HC
LC
Prevotella
Bacteroides
Faecalibacterium
Blautia
Bifidobacterium
Megamonas
Ruminococcus
Sutterella
Coprococcus
[Ruminococcus]
Roseburia
Dialister
Phascolarctobacterium
Oscillospira
Dorea
Fusobacterium
Streptococcus
Lachnospira
Parabacteroides
Collinsella
Others
E
unweighted
Group
HC
LC
PC2=8.55 %
PC1=15.47 %
weighted
PC2=13.51 %
PC1=48.74 %
F
unweighted
NMDS2
NMDS1
weighted
Group
HC
LC
NMDS2
NMDS1
G
PLS-DA
Group
HC
LC
PLS2
PLS1


A
HC
LC
Bacteroidetes
a: Actinomyces
b: Actinomycetaceae
c: Rothia
d: Micrococcaceae
e: Mycobacterium
f: Mycobacteriaceae
g: Actinobacteria
h: Atopobium
i: Collinsella
j: Prevotella
k: Prevotellaceae
l: Odoribacter
m: Bacteroidia
n: Gemellaceae
o: Gemellales
p: Streptococcus
q: Bacilli
r: Clostridium
s: _Ruminococcus_
t: Peptostreptococcus
u: Dialister
v: Phascolarctobacterium
w: Veillonellaceae
x: Methylobacteriaceae
y: Haemophilus
z: Pasteurellaceae
a0: Pasteurellales
B
Actinobacteria
Bacilli
Ruminococcus
Streptococcus
Mycobacteriaceae
Methylobacteriaceae
Mycobacterium
Clostridium
Peptostreptococcus
Atopobium
Gemellaceae
Gemellales
Micrococcaceae
Rothia
Actinomycetaceae
Actinomyces
Odoribacter
Veillonellaceae
Pasteurellaceae
Haemophilus
Pasteurellales
Collinsella
Phascolarctobacterium
Dialister
Bacteroidetes
Bacteroidia
Prevotellaceae
Prevotella
−6.0 −4.8 −3.6 −2.4 −1.2 0.0 1.2 2.4 3.6 4.8
LDA SCORE (log 10)


A
Prevotellaceae
Veillonellaceae
Streptococcaceae
Actinomycetaceae
HC
LC
B
Prevotella
[Ruminococcus]
Dialister
Streptococcus
Rothia
Bacillus
Actinomyces
Atopobium
Peptostreptococcus
Mycobacterium


A
P=0.0011
ACE
1500
1000
500
0
HC
A
B
C
LC
B
unweighted
weighted
PC2=9.56 %
PC1=20.09 %
PC1=17.64 %
PC1=39.90 %
Group
A
B
C
C
unweighted
weighted
NMDS2
NMDS1
Group
A
B
C
D
PLS−DA
PLS1
PLS1
Group
A
B
C