Online Supplement

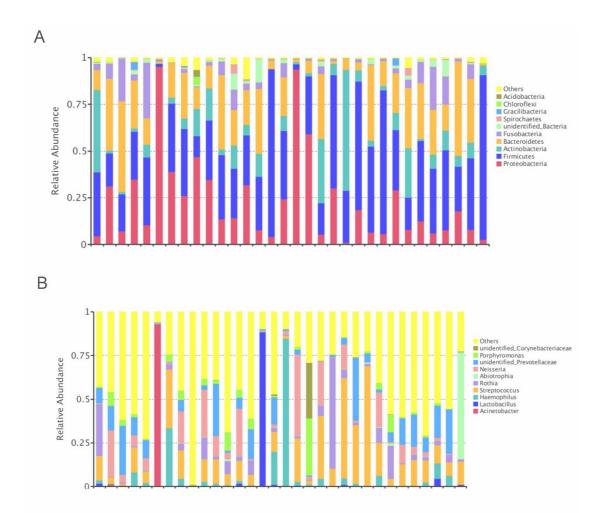
Respiratory Microbiome Profiles Associated With Distinct Inflammatory Phenotype and Clinical Indexes in Chronic Obstructive Pulmonary Disease

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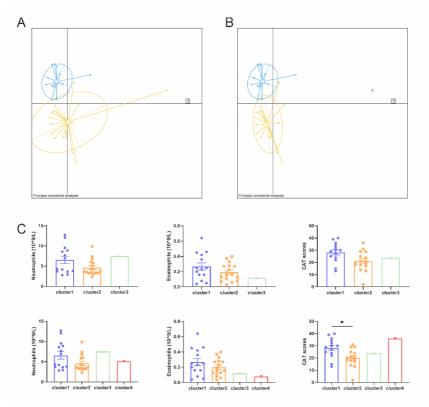
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Supplementary Figure 1 Composition of the respiratory bacterial community in 32 patients (A) Microbiome profiles of all stable samples at the phylum level. (B) Microbiome profiles of patients with COPD at the genus level.

COPD, chronic obstructive pulmonary disease



Supplementary Figure 2 Participant clustering and characteristics. (A-B) Two-dimensional (2D) principal coordinate analysis (PCoA) plot for 3 and 4 cluster. (C) Comparison of blood inflammatory phenotypes and CAT scores in clusters. CAT: COPD Assessment Test; COPD, chronic obstructive pulmonary disease

	Prevotella	Fusobacterium	Bacteroides
BMI	0.610	0.461	0.075
Smoking index	0.995	0.925	0.425
Number of	0.1.4.4	0.000	0.010
exacerbations	0.144	0.309	0.018
FEV_1 %pred (
%)	0.917	0.845	0.910
CAT score	0.555	0.045	0.143
mMRC score	0.780	0.617	0.916
Blood	0.001	0.700	0.75(
neutrophils	0.901	0.799	0.776
Blood	0.000	0.500	0.400
eosinophils	0.686	0.598	0.492

Supplementary Table 1 Correlation analysis between the dominant genera in each cluster and

clinical index

Abbreviations: BMI, body mass index; COPD, chronic obstructive pulmonary disease;

FEV1%pred, predicted percentage of forced expiratory volume in 1 s; CAT, COPD

Assessment Test; mMRC score, Modified British Medical Research Council