Supplementary materials

Supplementary Figure S1. Core species analysis was used to judge whether the sample size is sufficient to evaluate the total core bacterial (A) and fungal (B) species in sputum. X axis: numbers of samples. Y axis: numbers of shared core OTU.

The core species analysis described the changes of core species with the increase of sample size, when the curves reached a plateau, it indicated that the shared core species in sputum did not decrease with increasing samples, therefore, the sample size is enough to detect the core species and for further analysis in present study.







Supplementary Figure S3. No significant differences of the comparisons of top 7 bacterial genera were observed between the baseline and visit 1, between visit 1 and visit 2 using Wilcoxon signed-rank test (corrected p>0.05).



Supplementary Figure S4. No significant differences of the comparisons of top 7 fungal genera were observed between the baseline and visit 1, between visit 1 and visit 2 using Wilcoxon signed-rank test (corrected p>0.05).



Variables	Bacteriome (n=14)	Mycobiome (n=13)	
Age, years, mean \pm SD	41.5 ± 14.75	40.46 ± 14.65	
Male, no. (%)	7 (50)	6 (46.15)	
BMI, kg/m2, mean \pm SD	23.02 ± 2.85	23.93 ± 2.2	
Rhinosinusitis, no. (%)	9 (64.28)	9 (69.23)	
FEV1 (% predicted), mean \pm SD	79.2 ± 24.8	78.97 ± 23.1	
FEV1/FVC (%), mean ± SD	74.38 ± 15.28	74.8 ± 13.74	
ACQ7 score, mean \pm SD	1.05 ± 0.72	1.04 ± 0.75	

Supplementary Table S1. Demographic and clinical characteristics of study subjects.

Supplementary Table S2. PERMANOVA analysis of bacteriome community composition in sputum based on Bray-Curtis distance.

Matrix	SS	MS	F	R2	P value
Bray-Curtis	0.22526	0.11263	0.95272	0.04658	0.492

Supplementary Table S3. PERMANOVA analysis of mycobiome community composition in sputum based on Bray-Curtis distance.

Matrix	SS	MS	F	R2	P value
Bray-Curtis	2.21998	1.10999	3.35345	0.15704	0.001