Supplementary table S1-20: oral microbial table
Supplementary table S21-37: gut microbial table
Supplementary table S38-40: lipid molecule table
Supplementary table S41: correlation analysis table

Supplementary table S1. Clinical data of all confirmed patients (77 from Henan and 74 from Hangzhou) and healthy controls (n=150).

Supplementary table S2. The detailed values of oral microbial diversity index and observed OTUs in the discovery cohort (100 healthy controls and 48 CP).

Supplementary table S3. The abundance and composition at the genus and phylum level of each sample in the discovery cohort (100 healthy controls and 48 CP).

Supplementary table S4. The different degree of genus and phylum level (p value) between the healthy controls (n=100) and CP (n=48) in the discovery cohort.

Supplementary table S5. The relative abundance and distribution of the key 45 OTUs in the discovery cohort (100 healthy controls and 48 CP).

Supplementary table S6. The corresponding LDA value and p value of the biomarkers in the discovery cohort (100 healthy controls and 48 CP).

Supplementary table S7. By random forest classifier model, the corresponding output value of each optimal microbial marker in the discovery cohort, and the corresponding POD value for each sample in the discovery cohort (100 healthy controls and 48 CP).

Supplementary table S8. By random forest classifier model, the corresponding output value of each optimal microbial marker in the validation cohort, and the corresponding POD value for each sample in validation cohort (50 healthy controls and 24 CP).

Supplementary table S9. By random forest classifier model, the corresponding output value of each optimal microbial marker in the independent diagnosis cohort, and the corresponding POD value of each sample in the independent diagnosis cohort (74 CP from Hangzhou, china).

Supplementary table S10. By random forest classifier model, the corresponding output value of each optimal microbial marker, and the corresponding POD value of each sample in the SP (n=37) and HC (n=50) groups.

Supplementary table S11. The levels of Ig-G antibody in CP (n=6), SP (tongue coating, n=37; fecal, n=23), and HC (tongue coating, n=22; fecal, n=18).

Supplementary table S12. The detailed values of oral microbial diversity index and observed OTUs among CP (n=72), SP (n=37), and HC (n=150) groups.

Supplementary table S13. The abundance and composition at the genus level and phylum level of each sample among CP (n=72), SP (n=37), and HC (n=150) groups.

Supplementary table S14. The relative abundance and distribution of the key 84 OTUs among CP (n=72), SP (n=37), and HC (n=150) groups.

Supplementary table S15. The abundance and composition at the genus level of each sample among CP (n=72), SP (n=37), CPR (n=22), and SPR (n=37) groups.

Supplementary table S16. The detailed values of oral microbial diversity index and observed OTUs among CP (n=72), CPR (n=22), and HC (n=150) groups.

Supplementary table S17. The abundance and composition at the genus and phylum level of each sample among CP (n=72), CPR (n=22), and HC (n=150) groups.

Supplementary table S18. The different degree of genus and phylum level (p value) among the CP (n=72), CPR (n=22), and HC (n=150) groups.

Supplementary table S19. The relative abundance and distribution of the key 90 OTUs among the CP (n=72), CPR (n=22), and HC (n=150) groups.

Supplementary table S20. The corresponding LDA value and p value of the biomarkers among the CP (n=72), CPR (n=22), and HC (n=150) groups.

Supplementary table S21. The detailed values of gut microbial diversity index and observed OTUs in the discovery cohort (48 healthy controls and 24 CP).

Supplementary table S22. The abundance and composition at the genus and phylum level of each sample in the discovery cohort (48 healthy controls and 24 CP).

Supplementary table S23. The different degree of genus and phylum level (p value) between the healthy controls (n=48) and CP (n=24) in the discovery cohort.

Supplementary table S24. The relative abundance and distribution of the key 40 OTUs in the discovery cohort (48 healthy controls and 24 CP).

Supplementary table S25. The corresponding LDA value and p value of the biomakers in the discovery cohort (48 healthy controls and 24 CP).

Supplementary table S26. By random forest classifier model, the corresponding output value of each optimal microbial marker in the discovery cohort, and the corresponding POD value for each sample in the discovery cohort (48 healthy controls and 24 CP).

Supplementary table S27. By random forest classifier model, the corresponding output value of each optimal microbial marker in the validation cohort, and the corresponding POD value for each sample in validation cohort (24 healthy controls and 12 CP).

Supplementary table S28. By random forest classifier model, the corresponding output value of each optimal microbial marker, and the corresponding POD value of each sample in the SP (n=23) and HC (n=24) groups.

Supplementary table S29. The detailed values of gut microbial diversity index and observed OTUs among CP (n=36), SP (n=23), and HC (n=72) groups.

Supplementary table S30. The abundance and composition at the genus and phylum level of each sample among CP (n=36), SP (n=23), and HC (n=72) groups.

Supplementary table S31. The relative abundance and distribution of the key 51 OTUs among CP (n=36), SP (n=23), and HC (n=72) groups.

Supplementary table S32. The abundance and composition at the genus level of each sample among CP (n=36), SP (n=23), CPR (n=18), and SPR (n=23) groups.

Supplementary table S33. The detailed values of gut microbial diversity index and observed OTUs among CP (n=36), CPR (n=18), and HC (n=72) groups.

Supplementary table S34. The abundance and composition at the genus and phylum level of each sample among CP (n=36), CPR (n=18), and HC (n=72) groups.

Supplementary table S35. The different degree of genus and phylum level (p value) among the CP (n=36), CPR (n=18), and HC (n=72) groups.

Supplementary table S36. The relative abundance and distribution of the key 76 OTUs among CP (n=36), CPR (n=18), and HC (n=72) groups.

Supplementary table S37. The corresponding LDA value and p value of the biomakers among CP (n=36), CPR (n=18), and HC (n=72) groups.

Supplementary table S38. Number of lipid subclass and corresponding lipid molecules.

Supplementary table S39. The average abundance and composition at the subclass level in CP (n=73), CPR (n=22) groups, and in SP (n=30), SPR (n=30) groups.

Supplementary table S40. The relative abundance and distribution of the key 169 lipid molecule in CP (n=73), CPR (n=22) groups, and in SP (n=30), SPR (n=30) groups.

Supplementary table S41. The p value between oral OTUs and gut OTUs of CP (n=11) and HC (n=18) obtained by spearman correlation analysis； the p value among oral OTUs, gut OTUs, and lipid molecules of CP (n=37) and CPR (n=18) obtained by spearman correlation analysis; the p value between oral OTUs and clinical indicators of CP (n=48) and HC (n=100) obtained by spearman correlation analysis; the p value between gut OTUs and clinical indicators of CP (n=24) and HC (n=48) obtained by spearman correlation analysis.