Supplemental material

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Gut

Fig. S1 The characterization and comparison of oral microbial community and gene function between CP and HC groups. (A) A shannon-wiener curve between the number of sequences and the null diversity in CP and HC. As estimated by simpson index (B), oral microbial diversity was significantly decreased in CP (n=48) compared with that in the HC (n=100) (all $p < 0.001$). (C) A Venn diagram displaying the overlaps between groups showed that 1392 of the total number of 2407 OTUs were shared in both groups, while 685 of 2407 OTUs were unique to CP group. (D) The PCoA analysis using unweighted unifrac showed the oral taxonomic composition was significantly different between CP and HC. (E) 6 phylum were significantly decreased, while 2 phylum were significantly increased in CP group versus HCs (all $P<0.05$). *, $p < 0.05$, **, $p < 0.01$, ***, $p < 0.001$. (F) Average compositions and relative abundance of the bacterial community in CP and HC groups at the phylum level; CP, confirmed patients; HCs, healthy controls. (G) Based on the LDA selection, 8 genera were significantly enriched, while 21 genera were significantly reduced in CP compared with HC ($p<0.05$, LDA > 2). (H) Importance distribution map of the selected microbial markers in the model. (I) Eight microbial markers were selected as the optimal markers set by the random forest model. NMDS, non-metric multi-dimensional scaling; CV Error, the cross-validation error. Center line, median; box limits, upper and lower quartiles; circle or square symbol, mean; error bars, 95% CI.

Fig. S2 The characterization and comparison of oral microbial community among CP, SP, CPR, and HC groups. (A) As estimated by the simpson index, showed that oral microbial diversity of CP (n=72) and SP (n=37) was similar (p>0.05), but significantly decreased versus the healthy controls (n=150) (p<0.001). (B) The PCoA analysis showed the oral microbial communities in CP group and SP were similar, but significantly different from HC. (C) A Venn diagram displaying the overlaps among groups showed that 1244 of the total number of 2952 OTUs were shared in CP, SP, and HC groups, while 1280 of the 2184 OTUs were shared between CP and SP. (D) Average

compositions and relative abundance of the oral bacterial community in CP, SP, and HC groups at the phylum level. As estimated by the simpson index (E), showed that oral microbial diversity in CPR (n=22) group was similar with CP (n=72) (all p>0.05), but significantly decreased versus HC (n=150) (all p<0.001). (F) The PCoA analysis showed the oral microbial communities in CPR group were different from the CP and HC group. (G) A Venn diagram displaying the overlaps among groups showed that 941 of the total number of 2832 OTUs were shared in CP, CPR, and HC groups, 985 of the 1012 OTUs in CPR were shared with HCs, and 953 OTUs were shared with CP group. (H) Average compositions and relative abundance of the bacterial community in CP, CPR, and HC groups at the phylum level; (I) phylum of *Candidate_division_TM7* were gradually increased among CP, CPR, and HC groups ($p < 0.001$). (J) Average compositions and relative abundance of the bacterial community in three groups at the genus level. *, $p < 0.05$, **, $p < 0.01$, ***, $p < 0.001$. (K) Based on the LDA selection, 5 genera were significantly enriched in CP, 11 genera were significantly enriched in CPR, and 15 genera were significantly enriched in HCs ($p<0.05$, LDA > 2). Center line, median; box limits, upper and lower quartiles; circle or square symbol, mean; error bars, 95% CI.

Fig. S3 The characterization and comparison of gut microbial community and gene function between CP and HC groups. (A) A shannon-wiener curve between the number of sequences and the null diversity in CP and HC. As estimated by the simpson index (B), gut microbial diversity was significantly decreased in CP (n=24) compared with that in the HC (n=48) (p<0.001). (C) A Venn diagram displaying the overlaps between groups showed that 634 of the total number of 1704 OTUs were shared in both groups, while 1003 of 1704 OTUs were unique to CP group. (D) The NMDS analysis using unweighted unifrac showed the gut taxonomic composition was significantly different between CP and HC. (E) 3 phylum were significantly decreased, while 3 phylum were significantly increased in CP group versus HCs (all *p* < 0.05). *, $p < 0.05$, **, $p < 0.01$, ***, $p < 0.001$. (F) Average compositions and

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relative abundance of the bacterial community in CP and HC groups at the phylum level. (G) Based on the LDA selection, 17 genera were significantly enriched, while 25 genera were significantly reduced in CP compared with HC (all $p < 0.05$, LDA > 2.5). (H) Importance distribution map of the selected microbial markers in the model. (I) Seven microbial markers were selected as the optimal markers set by the random forest model. Center line, median; box limits, upper and lower quartiles; circle or square symbol, mean; error bars, 95% CI.

Fig. S4 The characterization and comparison of oral microbial community among CP, SP, CPR, and HC groups. (A) As estimated by the simpson index, showed that gut microbial diversity of CP (n=36) and SP (n=23) was similar ($p > 0.05$), but significantly decreased versus the HCs (n=72) ($p < 0.001$). (B) The NMDS analysis showed the gut microbial communities in CP group and SP were similar, but significantly different from HC. (C) A Venn diagram displaying the overlaps among groups showed that 715 of the total number of 2175 OTUs were shared in CP, SP, and HC groups, while 722 of the 1421 OTUs were shared between CP and SP. (D) Average compositions and relative abundance of the gut bacterial community in CP, SP, and HC groups at the phylum level. As estimated by the simpson index (E) showed that fecal microbial diversity in CPR (n=18) was similar with CP (n=36) (all $p > 0.05$), but significantly decreased versus HC (n=72) (all $p < 0.001$). (F) The NMDS analysis showed the gut microbial communities in CPR group were different from the CP and HC group. (G) A Venn diagram displaying the overlaps among groups showed that 595 of the total number of 2190 OTUs were shared in CP, CPR, and HC groups, 769 of the 816 OTUs in CPR were shared with HCs, and 615 OTUs of 816 OTUs were shared with CP group. (H) Average compositions and relative abundance of the bacterial community in CP, CPR, and HC groups at the phylum level; (I) phylum of *Bacteria_unclassified* were gradually increased ($p < 0.001$), while 2 phylum were gradually decreased among ($p < 0.01$) among CP, CPR, and HC groups. (J) Average compositions and relative abundance of the bacterial community in three groups at the

genus level. *, $p < 0.05$, **, $p < 0.01$, ***, $p < 0.001$. (K) Based on the LDA selection, 15 genera were significantly enriched in CP, 10 genera were significantly enriched in CPR, and 17 genera were significantly enriched in HCs ($p<0.05$, LDA > 2). Center line, median; box limits, upper and lower quartiles; circle or square symbol, mean; error bars, 95% CI.

Fig. S5 The characterization of lipid molecules between SP and SPR, and linkage among oral, gut distinctive microbiome and 7 clinical index between CP and HC. The base peak chromatogram of QC samples in positive (A) and negative (B) ion mode. The PCA analysis (C) and the CV plot (D) for QC samples showed that the quality of the data is qualified. (E) Average compositions and relative abundance of the bacterial community in SP (n=30), and SPR (n=30) groups at the sub class level. (F) PCA analysis showed that the lipid distribution in SP (n=30) group were different from the SPR (n=30). (G) 20 enriched pathways with the most significant differences between the SP (n=30) and SPR (n=30) groups were identified based on KEGG. (H) Heatmap showing the partial Spearman's correlation coefficients among 68 distinctive oral OTUs and 7 clinical indicators between CP (n=48) and HC (n=100). (I) Heatmap showing the partial Spearman's correlation coefficients among 104 distinctive gut OTUs and 7 clinical indicators between CP (n=24) and HCs (n=48). QC, quality control; DG, diglyceride; LPC, lyso-phosphatidylcholine; SM, sphingomyelin; TG, triglyceride; WBC, white blood cell; NEUT, neutrophil; LYMPH, lymphocyte; PLT, platelet; ALT, alanine aminotransferase; AST, aspartate aminotransferase; CREA, creatinine.

Fig. S6 The distribution of lipid molecules for each individual. (A) Heatmap for relative abundances of differential lipid molecules for each sample in CP (n=73) and CPR (n=22) groups. The results showed 47 lipid molecules were enriched in the CP

group, while 122 lipid molecules were enriched in the CPR group. (B) Heatmap for

relative abundances of differential lipid molecules for each sample in SP (n=30) and

SPR (n=30) groups. The results showed 107 lipid molecules were enriched in the SP

group, while 159 lipid molecules were enriched in the SPR group.