

Figure S1 Between-groups comparison of alpha diversity by using Shannon and Simpson indices (A) and (C) group ao and group bo; (B) and (D) Comparison of subgroups between Group A and Group B.

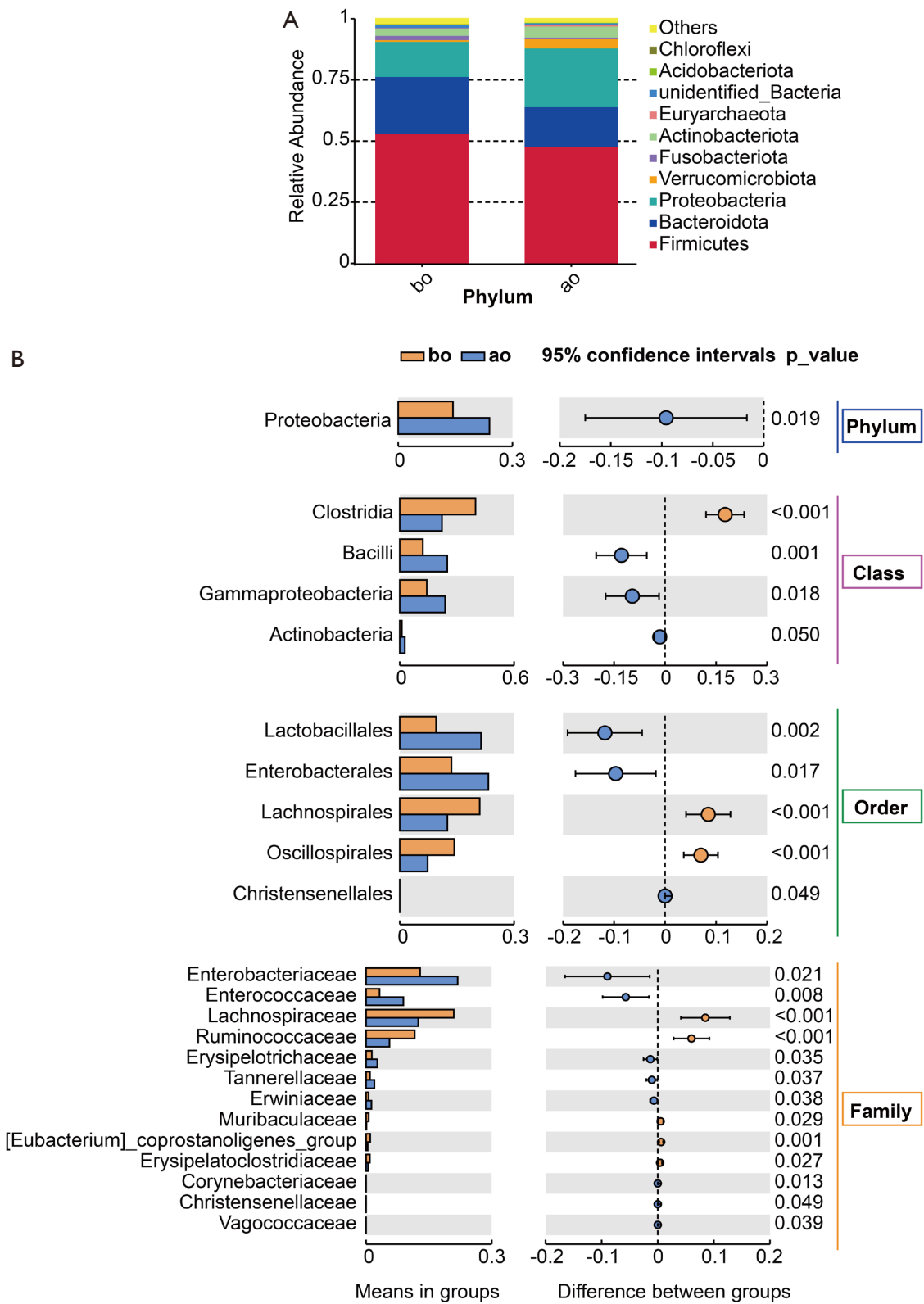


Figure S2 Group ao vs. group bo. (A) Relative abundance is shown for the top 10 at phylum; (B) gut microbiota revealed striking differences at phylum, class, order, family levels.

Table S1 Results of differential screening of fecal metabolites

Compared Samples	Num. of Total Ident.	Num. of Total Sig.	Num. of Sig.Up	Num. of Sig.down
ao.PHLF. vs. bo.PHLF_neg	859	156	20	136
ao.PHLF. vs. bo.PHLF_pos	1802	430	54	376

Compared Samples: Sample Pairs Compared: the former Versus the latter. Num of Total Ident: Results of Total Metabolite Identification. Num of Total Sig: Total Number of Significantly Different Metabolites. Num of Sig Up: Total Number of Significantly Upregulated Metabolites. Num of Sig down: Total Number of Significantly Downregulated Metabolites.

Table S2 Results of differential screening of serum metabolites

Compared Samples	Num. of Total Ident.	Num. of Total Sig.	Num. of Sig.Up	Num. of Sig.down
ao.PHLF. vs. bo.PHLF_neg	431	160	45	115
ao.PHLF. vs. bo.PHLF_pos	765	201	92	109

Compared Samples: Sample Pairs Compared: the former Versus the latter. Num of Total Ident: Results of Total Metabolite Identification. Num of Total Sig: Total Number of Significantly Different Metabolites. Num of Sig Up: Total Number of Significantly Upregulated Metabolites. Num of Sig down: Total Number of Significantly Downregulated Metabolites.

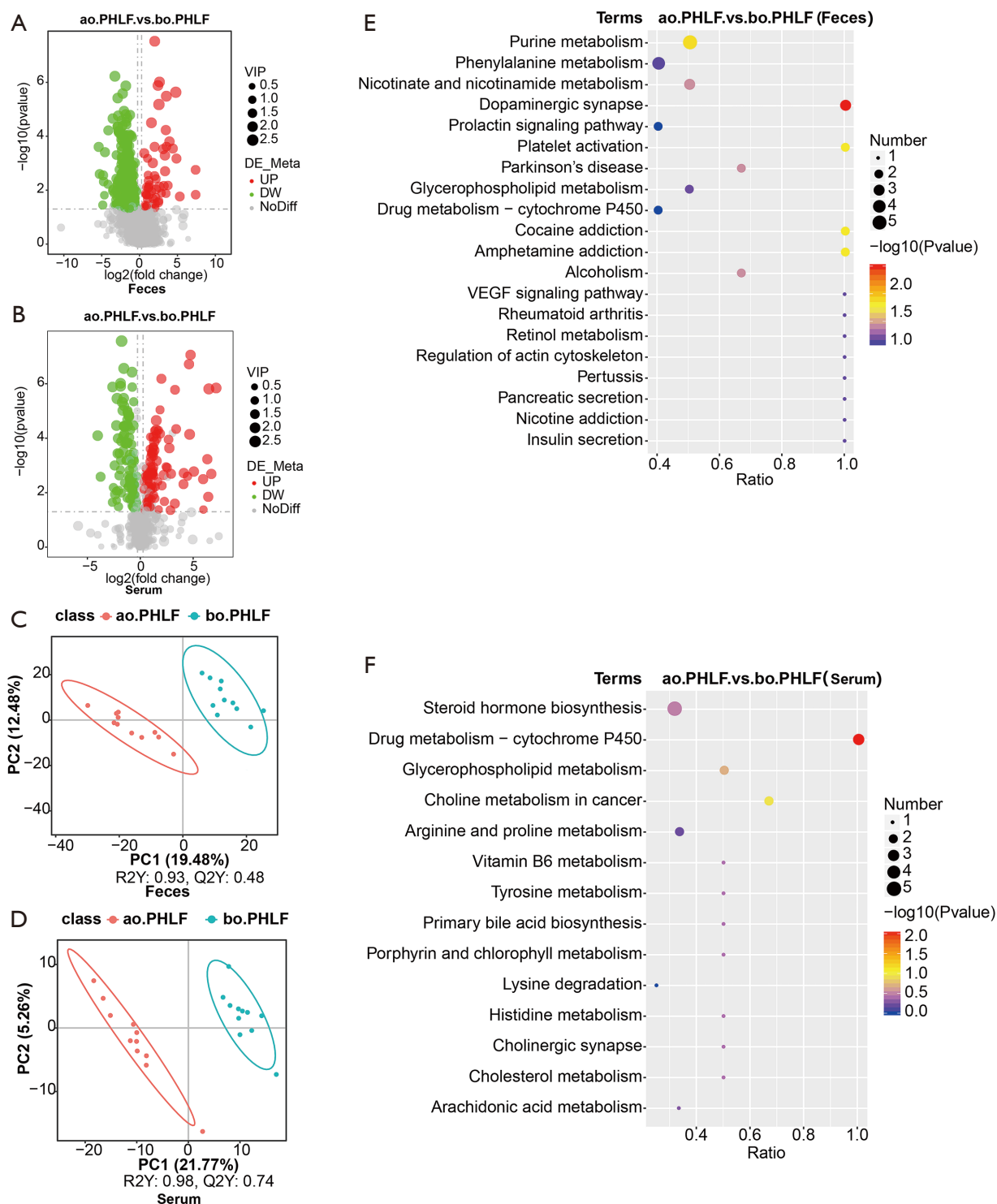


Figure S3 Comparative metabolomics analysis determined the change in fecal and serum metabolites in ao.PHLF from bo.PHLF. The metabolites were identified in PIM. Volcano plot showed the number of dysregulated metabolites in (A) fecal and (B) serum. Partial least square discriminant analysis (PLS-DA) of fecal and serum metabolites profiles in (C) fecal and (D) serum. KEGG enrichment scatter plot showed the alteration in metabolisms and biological processes in (E) fecal and (F) serum, annotated pathways were sorted by the values of $-\log_{10}$ (P value).