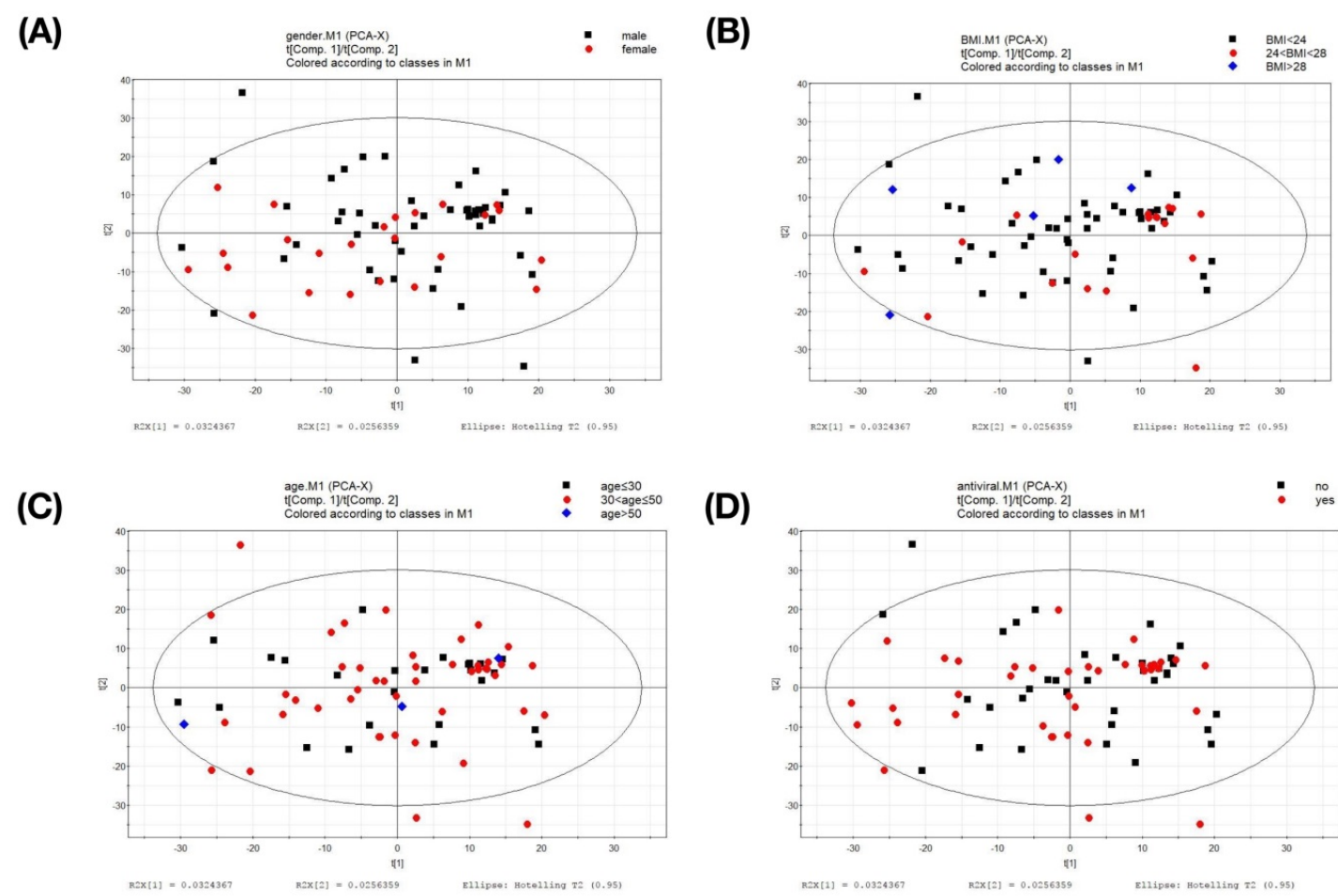


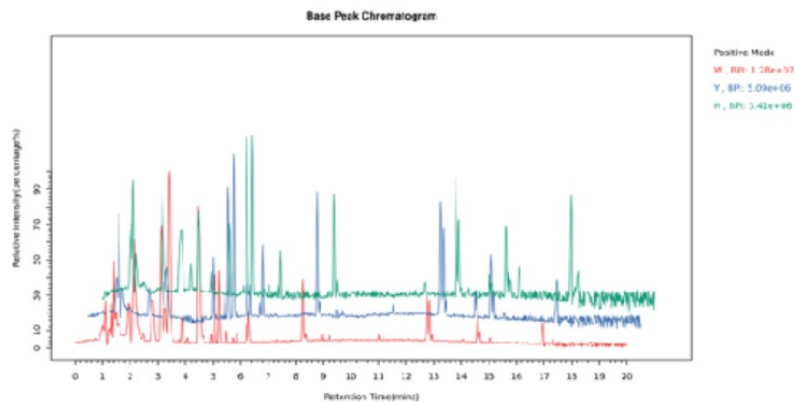
Supplementary Figures



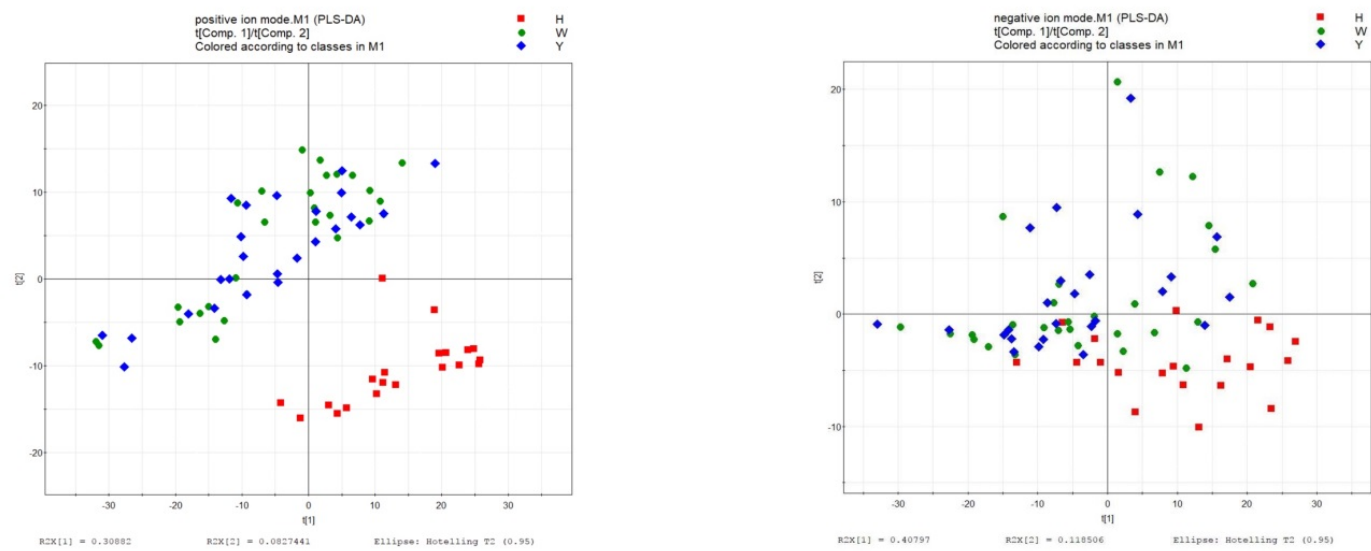
Supplementary Figure 1 Overall compositions of gut microbiota were not significantly affected by (A) gender, (B) BMI, (C) age or (D) antiviral treatment.

Supplementary Figures

(A)

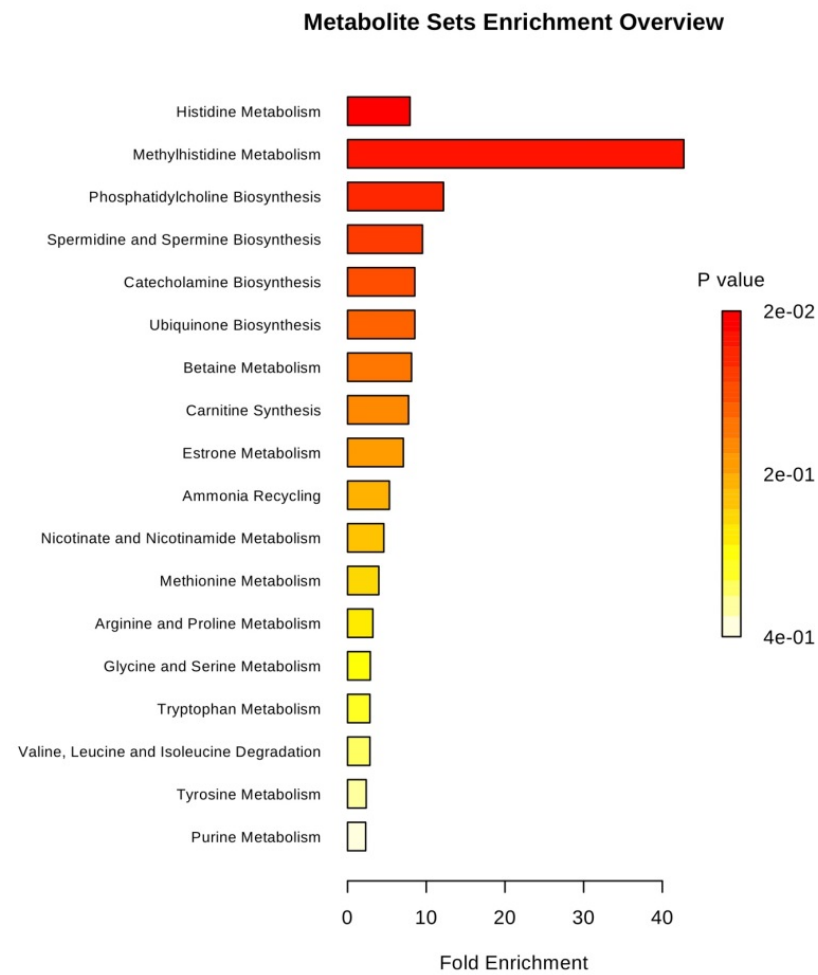


(B)



Supplementary Figure 2 (A)The typical TIC of samples in positive ion mode. **(B)**The metabolites between CHB patients and healthy volunteers were separated by supervised PLS-DA analysis in positive and negative ion mode.

Supplementary Figures



Supplementary Figure 3 Pathway enrichment of differential metabolites between CHB patients and healthy controls .

Supplementary Table 1 Comparison of alpha diversity estimation of the 16S rRNA gene libraries at 97% similarity from the pyrosequencing analysis

Group	The coverage percentage	Richness estimator				Diversity index			
		ACE	95%CI	Chao	95%CI	Shannon	95%CI	Simpson	95%CI
H	0.975	1481.332	1319.699-1672.076	916.922	759.121-1146.586	3.443	3.406-3.480	0.080	0.077-0.083
W	0.972	1714.734	1527.656-1934.046	1030.036	847.537-1293.051	3.485	3.449-3.522	0.076	0.073-0.078
Y	0.972	1765.236	1576.355-1985.516	1039.511	852.266-1310.396	3.385	3.347-3.423	0.088	0.085-0.092

H: Healthy; W: CHB white tongue coating; Y: CHB yellow tongue coating.