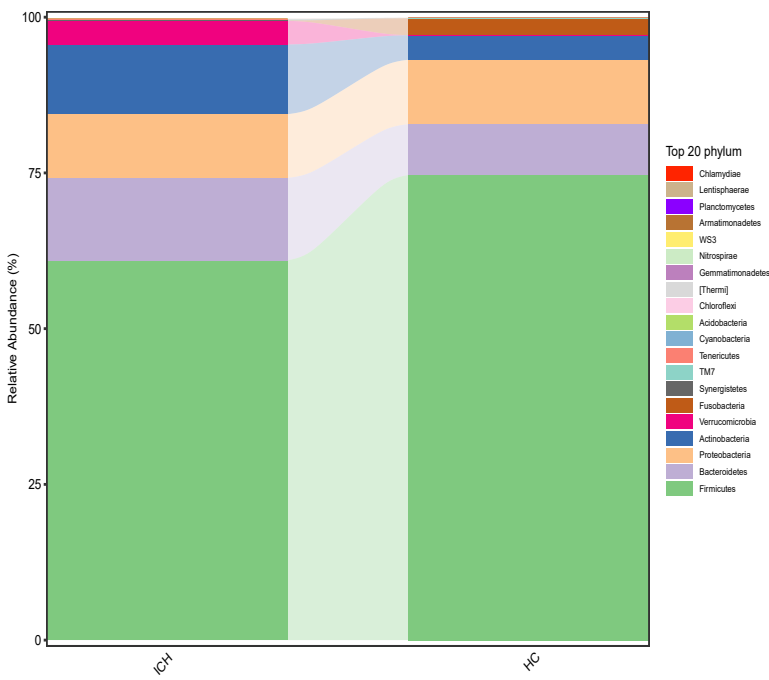


Figure S1

A



B

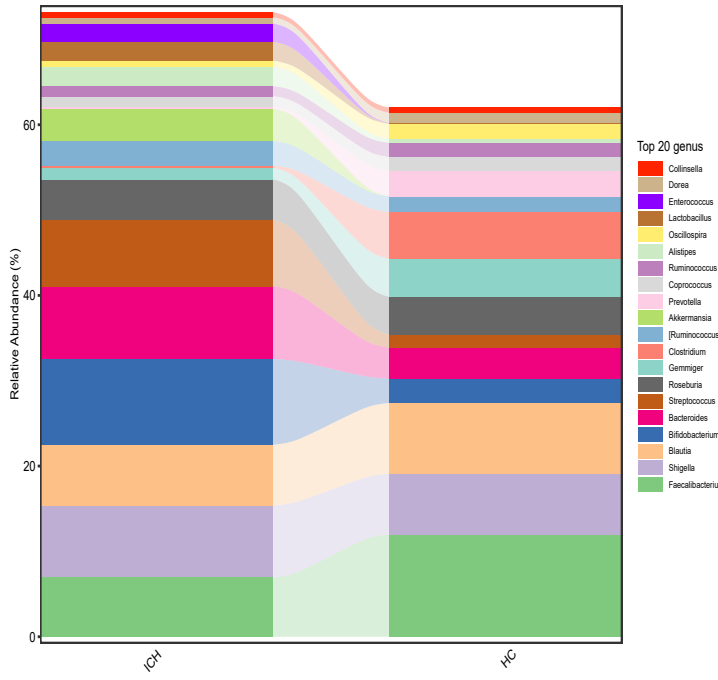
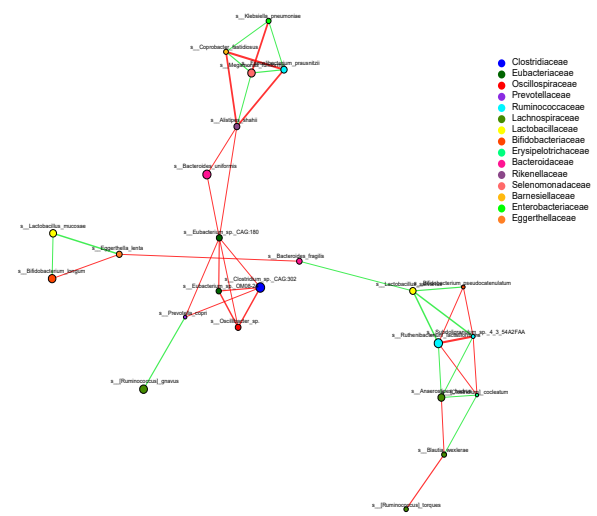


Figure S2

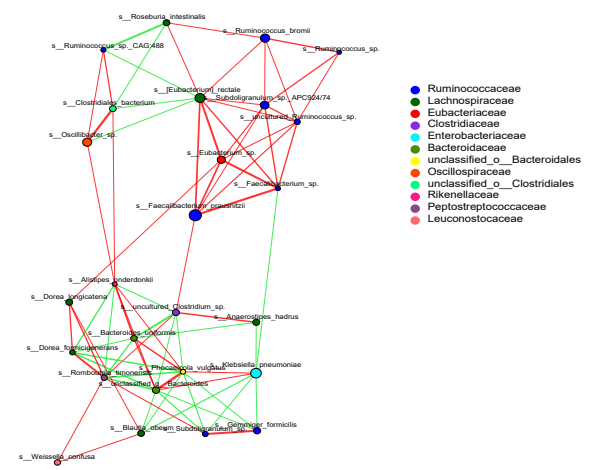


Figure S3

A



B



C

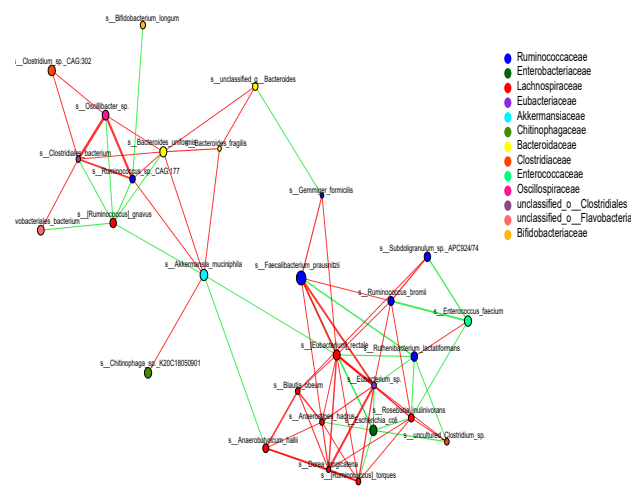


Figure S4

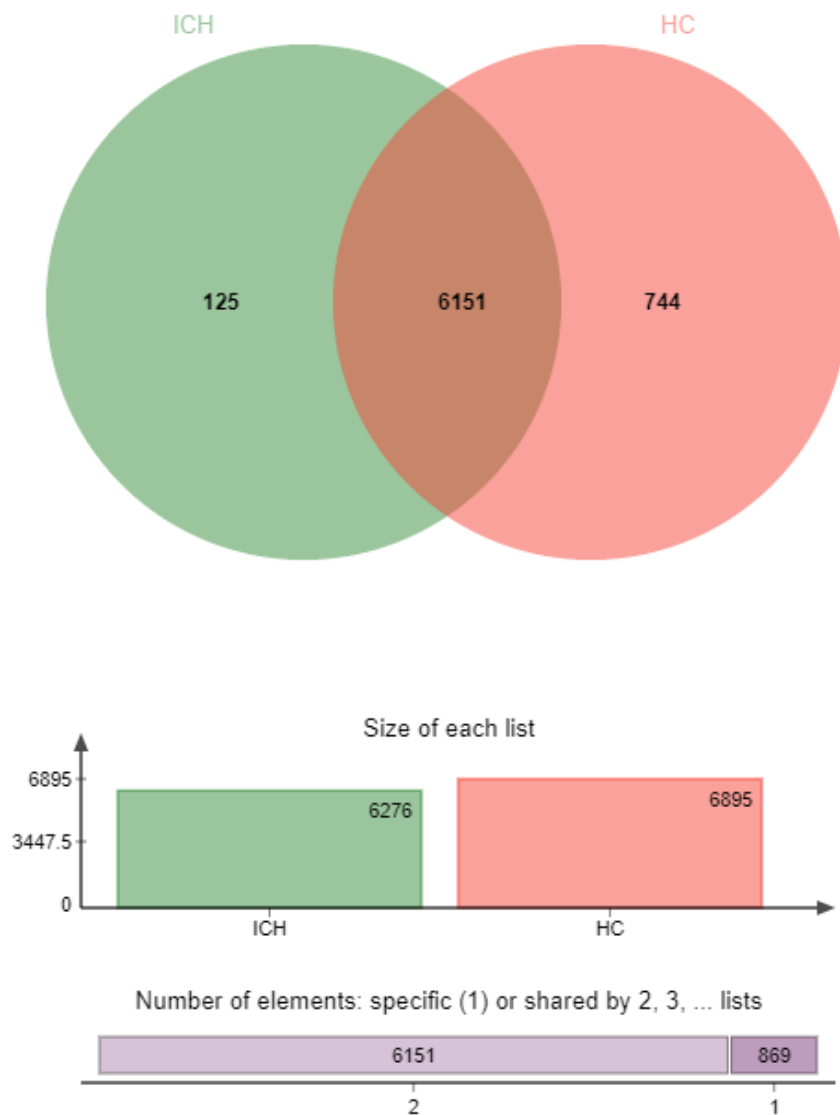


Figure S5

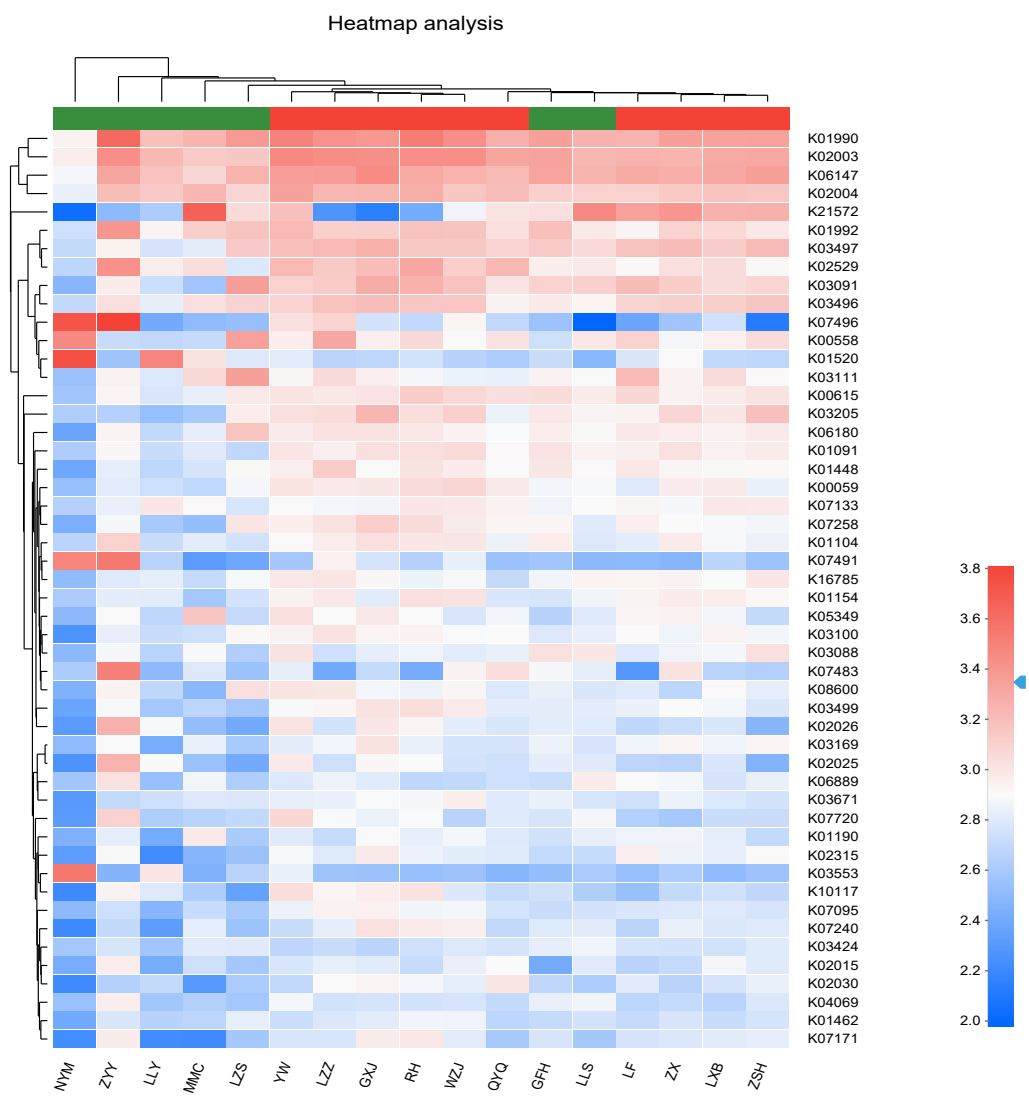


Figure S6

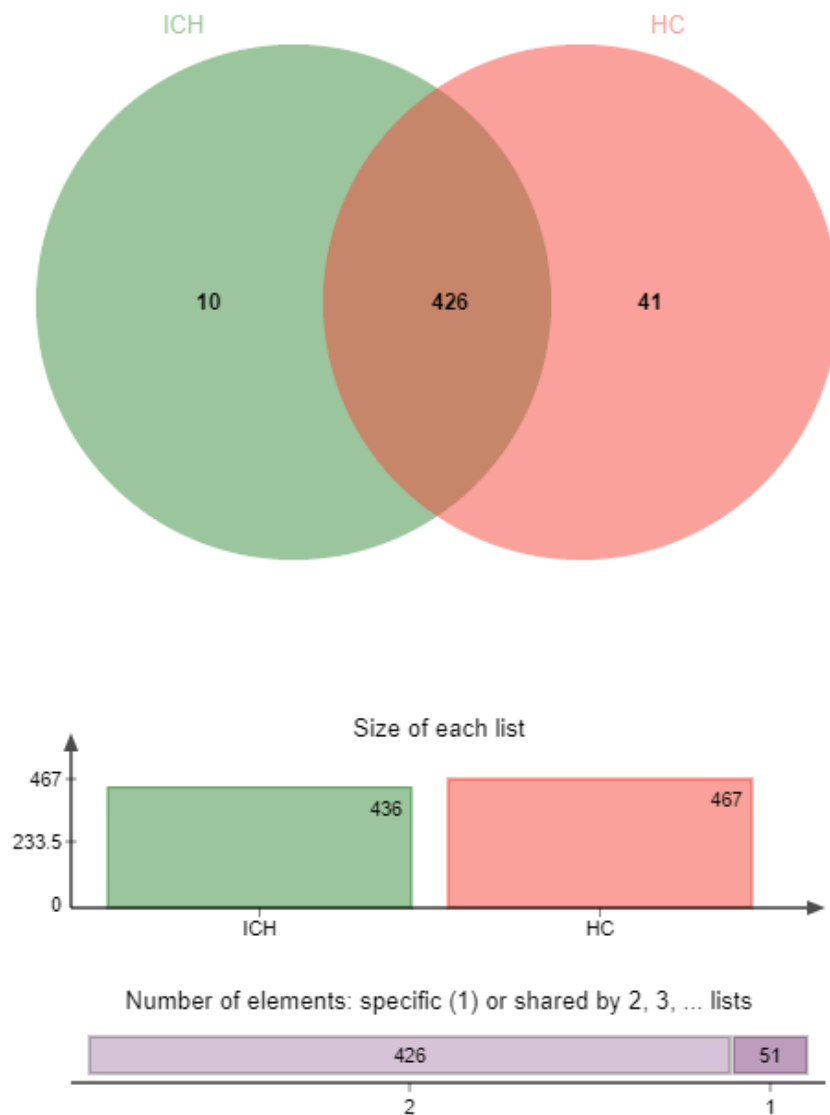
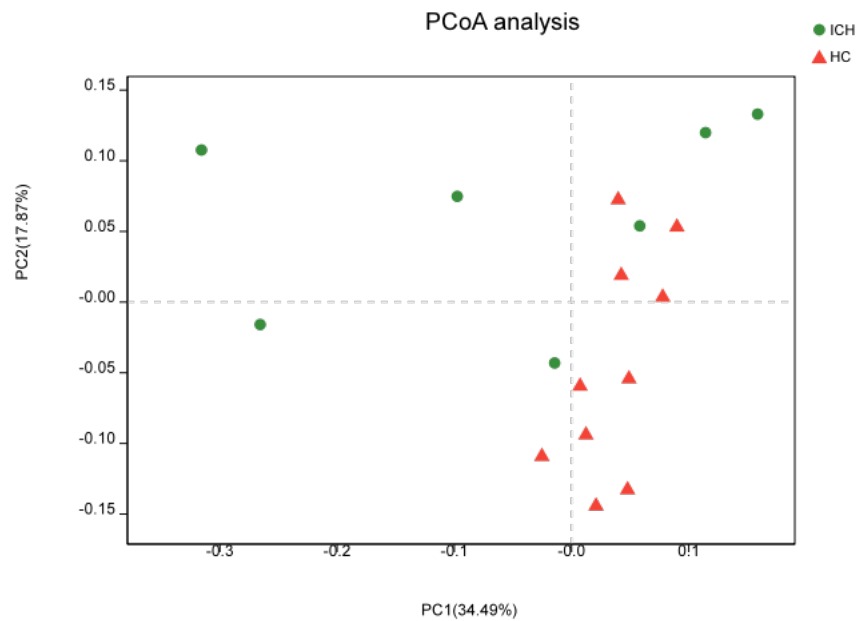


Figure S7



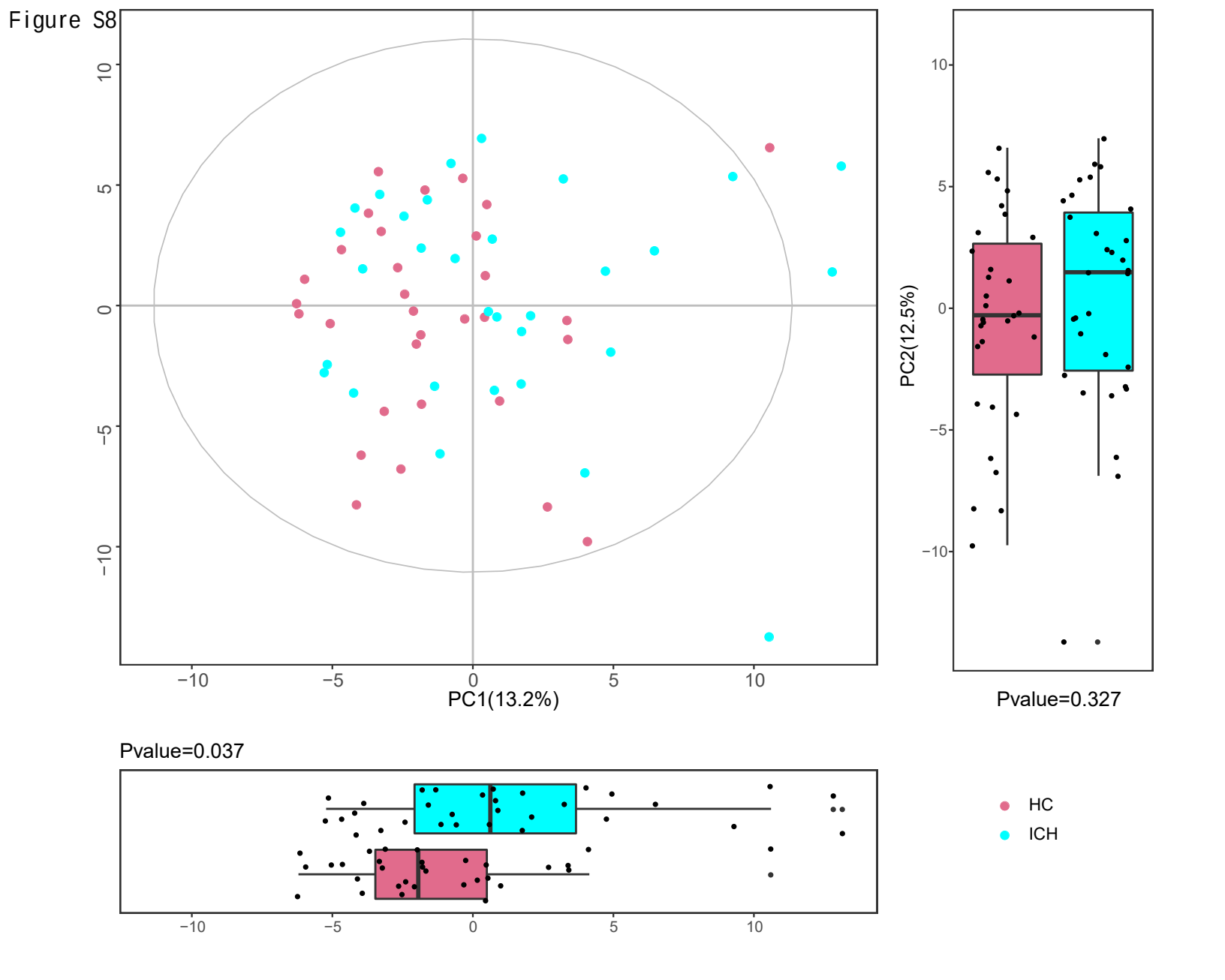


Figure S9

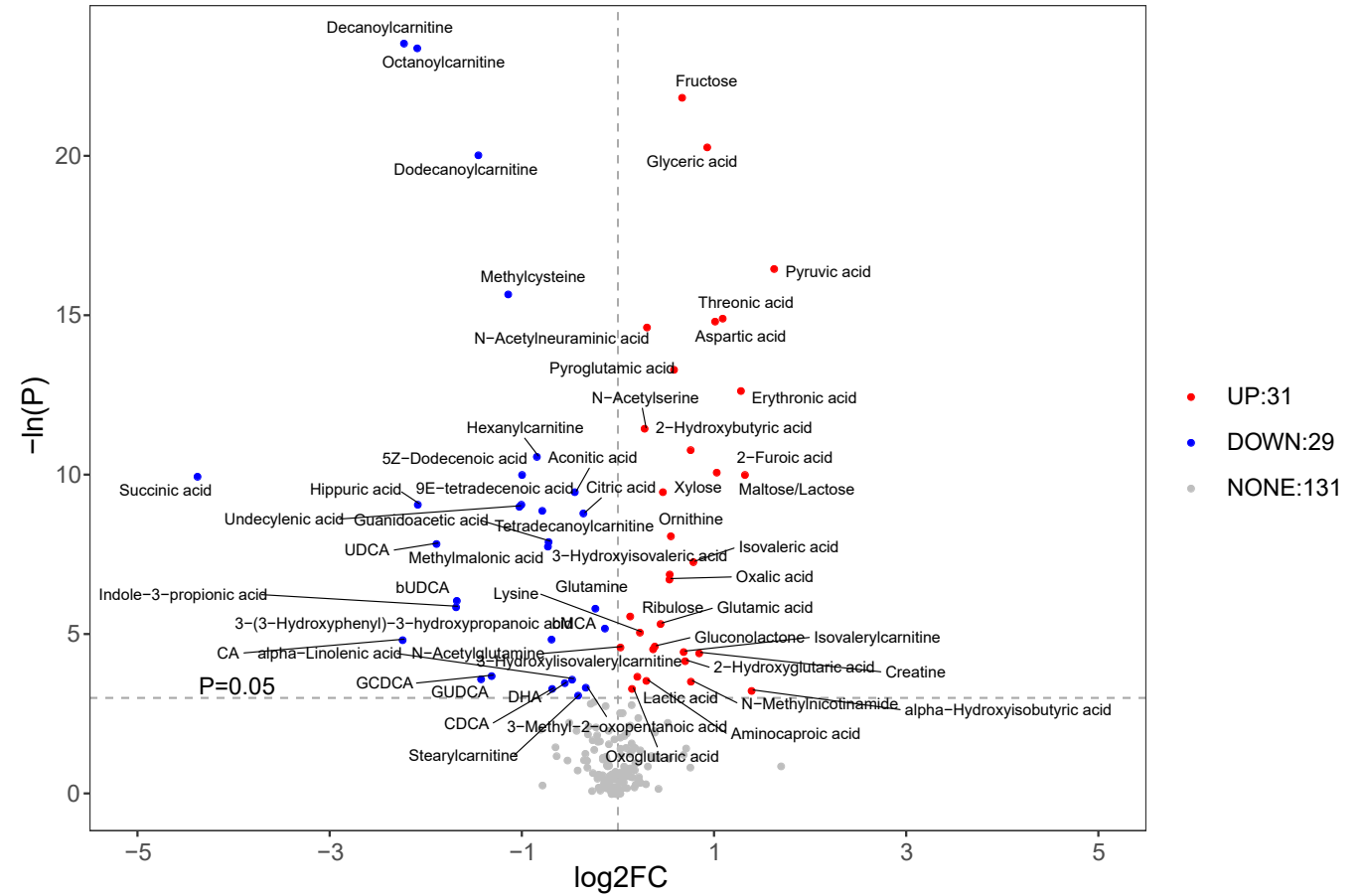


Figure S10

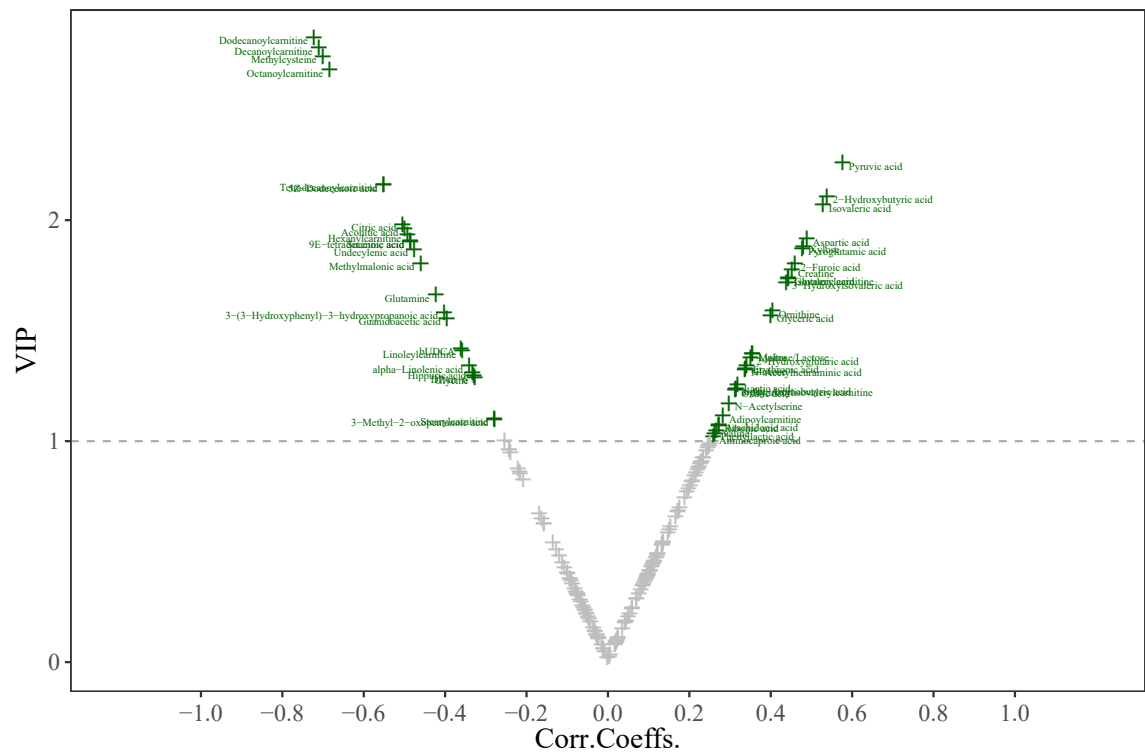


Figure S1. Microbial composition of ICH and HC groups

(A)Phyla level; (B)Genus level.

Figure S2. Varying distribution of microbiota correlated with the ICH and HC groups

Figure S3. Microbial correlation network

(A)Microbial correlation network among the first 30 species in ICH; (B) Microbial correlation network among the first 30 species in HCs; (C) Microbial correlation network among the first 30 species in all subjects, including ICH and HC.

Figure S4. The shared and unique function KOs of ICH and HC

Figure S5. Heat map of top 50 most abundant KOs

Figure S6. The shared and unique CAZy enzyme genes of ICH and HC

Figure S7. PCoA based on Bray–Curtis difference index shows functional (CAZy enzyme) (β) diversity between samples

Figure S8. PCA based on the relative abundance of serum metabolites showing grouped discrimination

Figure S9. Volcano plot showing the differentially accumulated [$\log_2$ (FC) on X-axis] and significantly changed [$-\ln(p)$ on Y-axis] serum metabolites of ICH and HC

Figure S10. V plot showing differentially accumulated serum metabolites of ICH and HC from the OPLS-DA models