Supplementary Figures

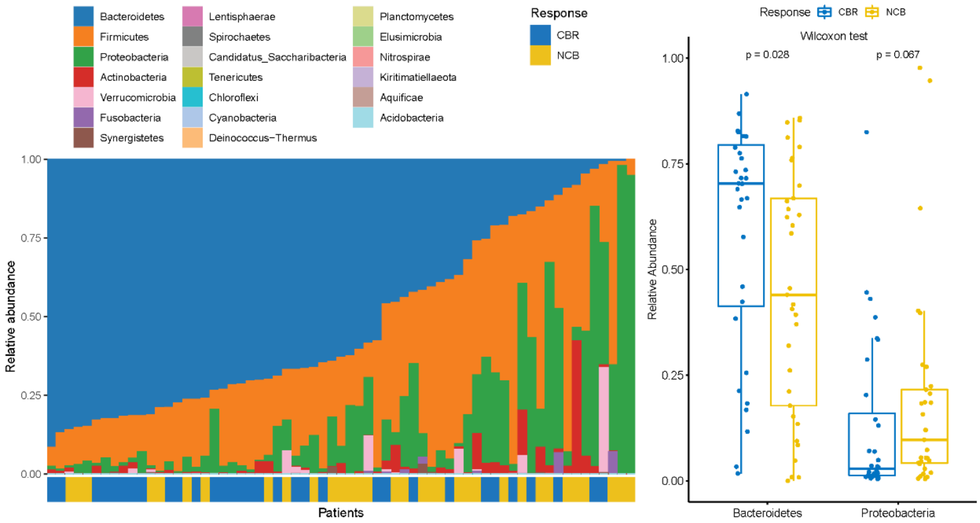

Figure S1 Gut microbiome composition at the phylum level in 65 patients with hepatobiliary cancers (ordered by the most abundant taxa, Bacteroidetes phylum). CBR, clinical benefit response; NCB, non-clinical benefit.

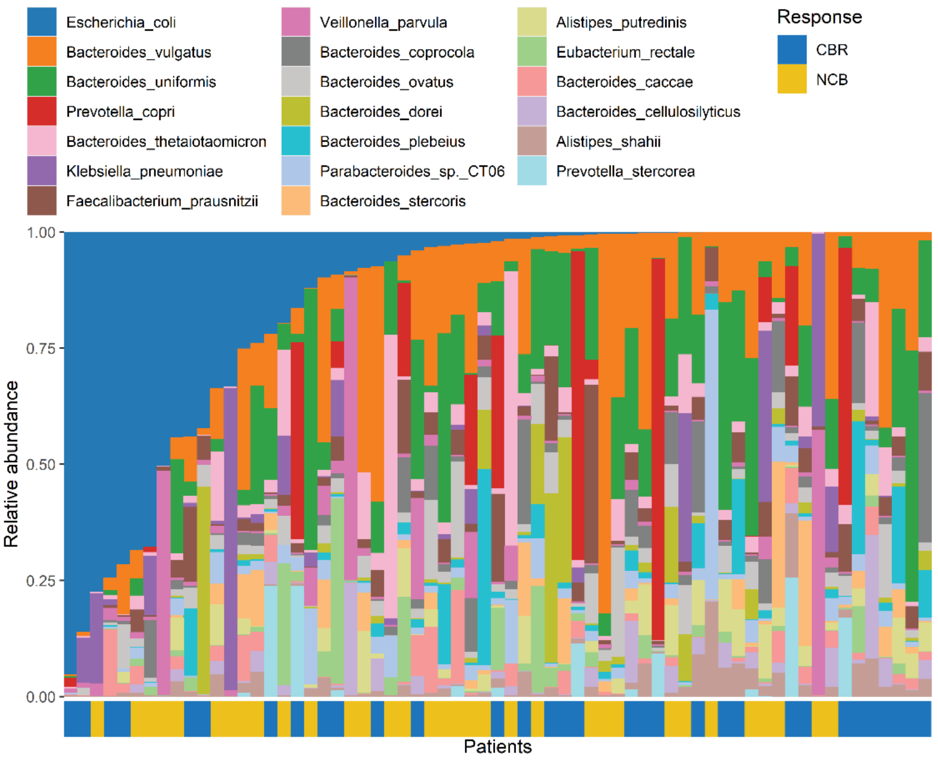

Figure S2 Gut microbiome composition at the specie level in 65 patients with hepatobiliary cancers. CBR, clinical benefit response; NCB, non-clinical benefit.

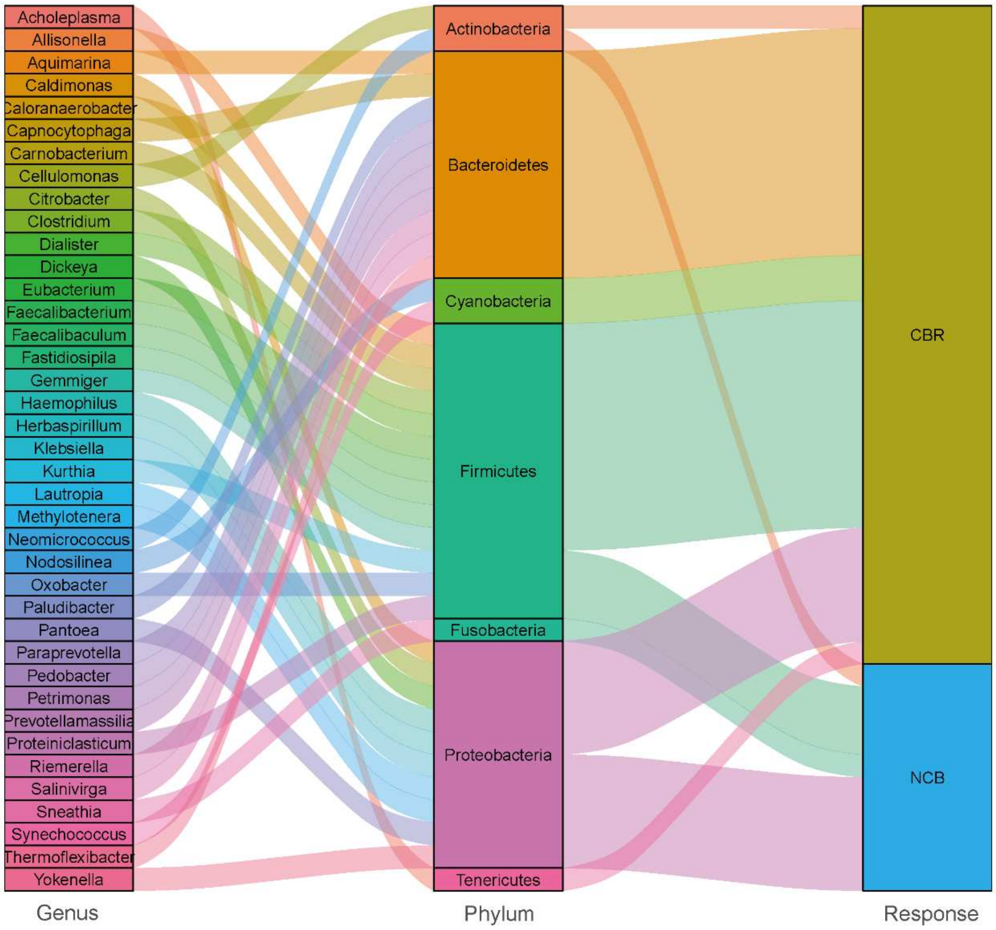

Figure S3 Statistically different genera between the CBR group and NCB group. CBR, clinical benefit response; NCB, non-clinical benefit.

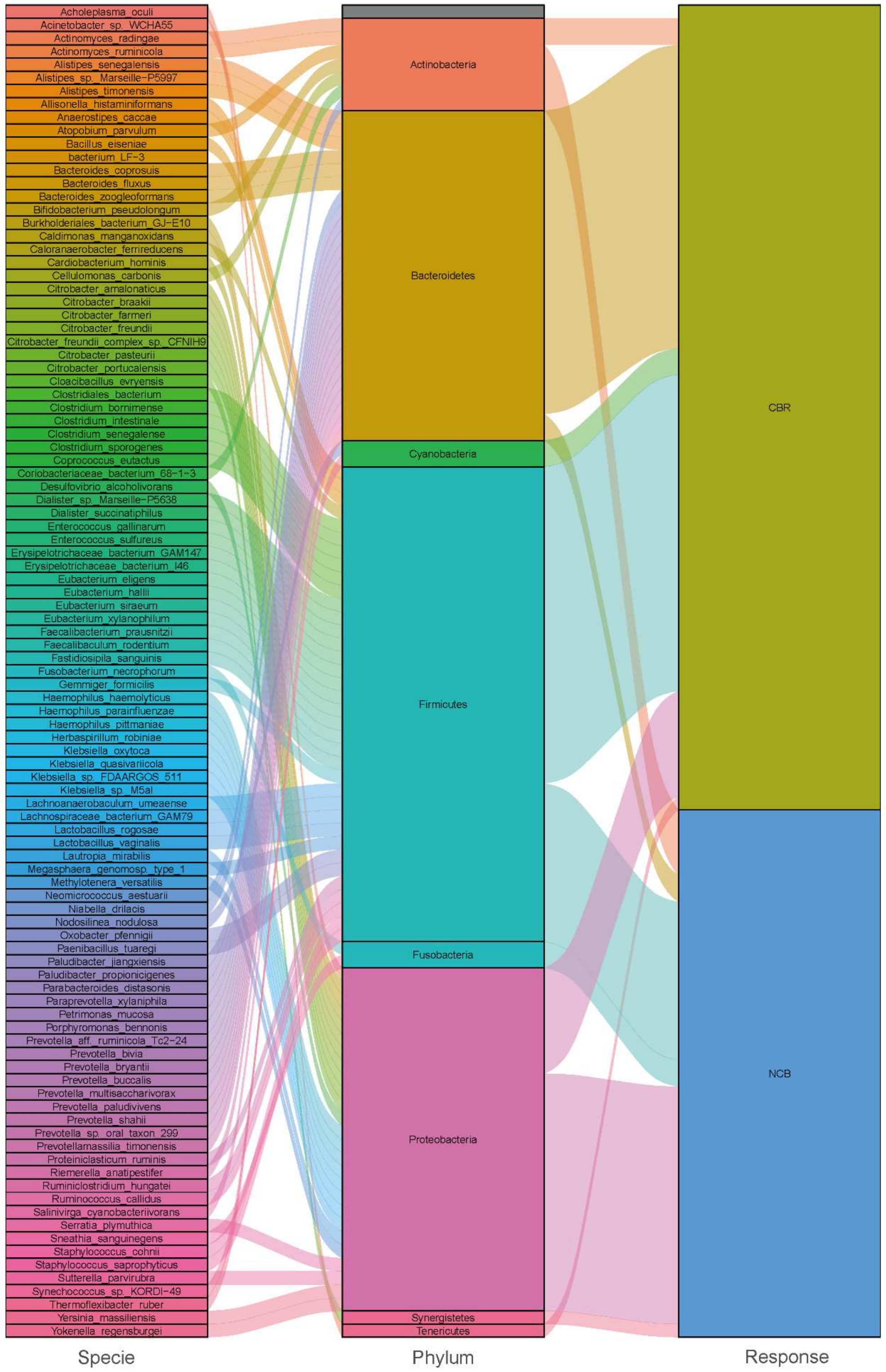

Figure S4 Statistically different species between the CBR group and NCB group. CBR, clinical benefit response; NCB, non-clinical benefit.

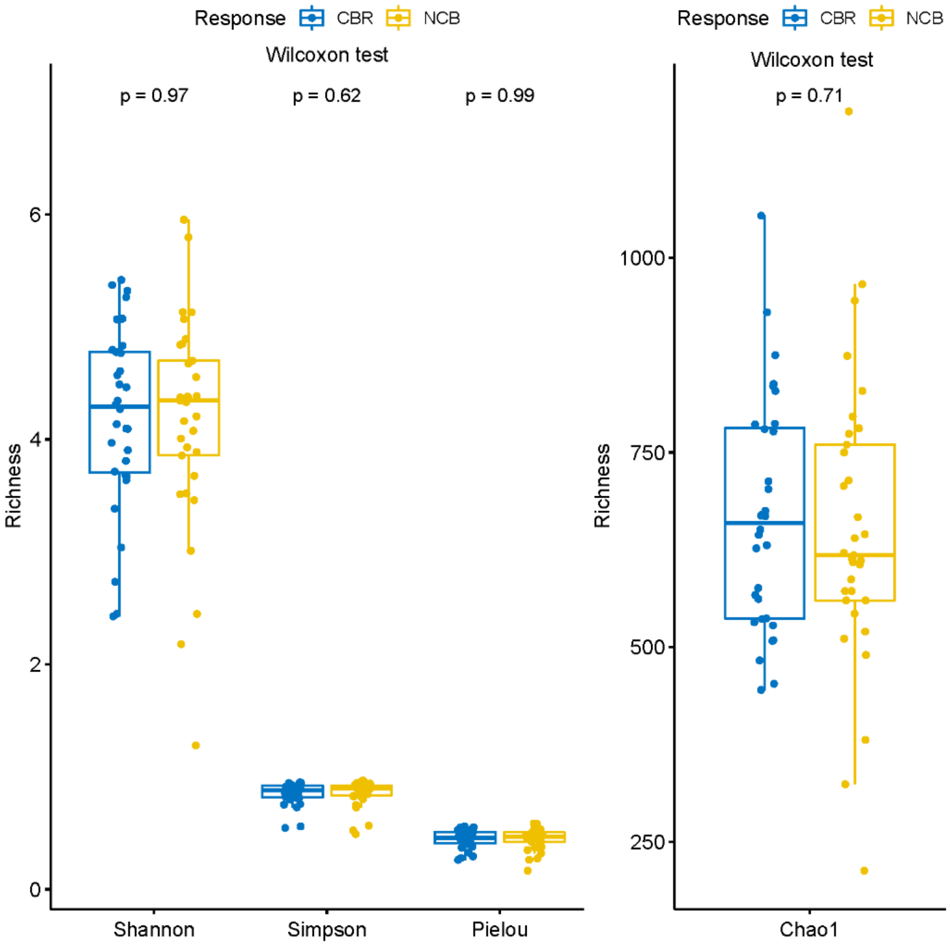

Figure S5 Gut microbiome alpha diversity comparison between the CBR group and NCB group (Wilcoxon test). CBR, clinical benefit response; NCB, non-clinical benefit.

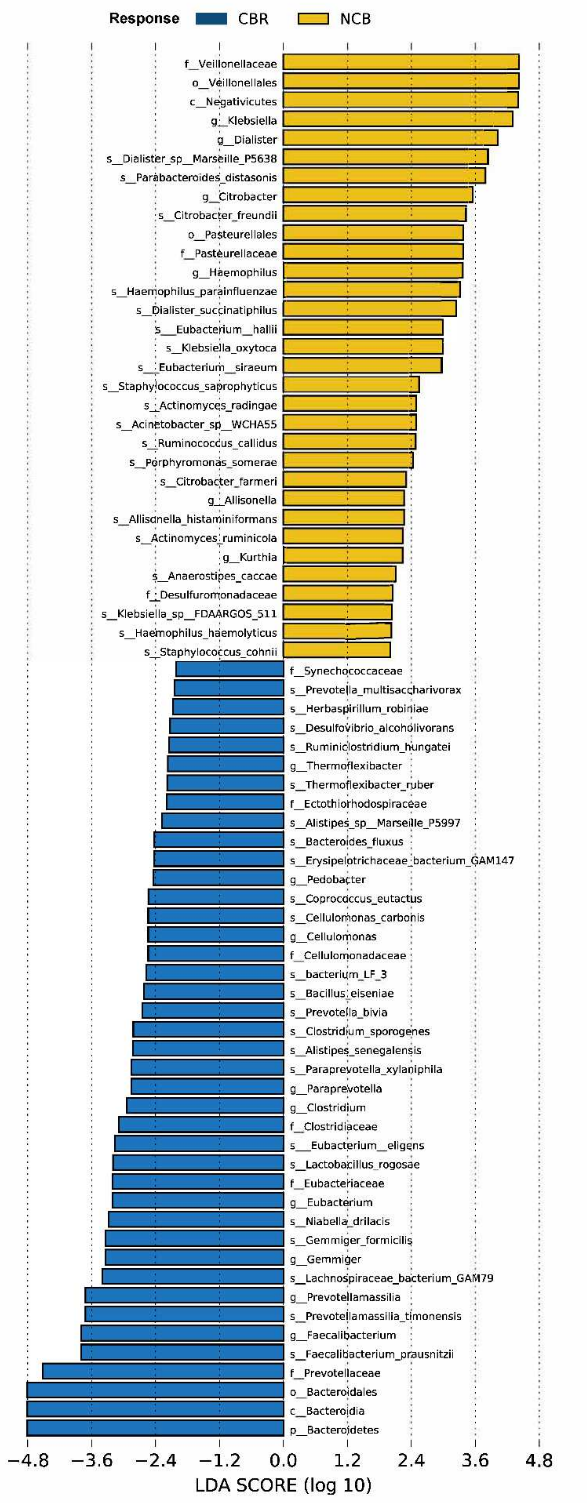

Figure S6 Significantly differentially enriched taxa in the CBR group and NCB group identified by LEfSe (LDA>2, p<0.05). CBR, clinical benefit response; NCB, non-clinical benefit; LDA, linear discriminant analysis; LEfSe, linear discriminant analysis effect size.

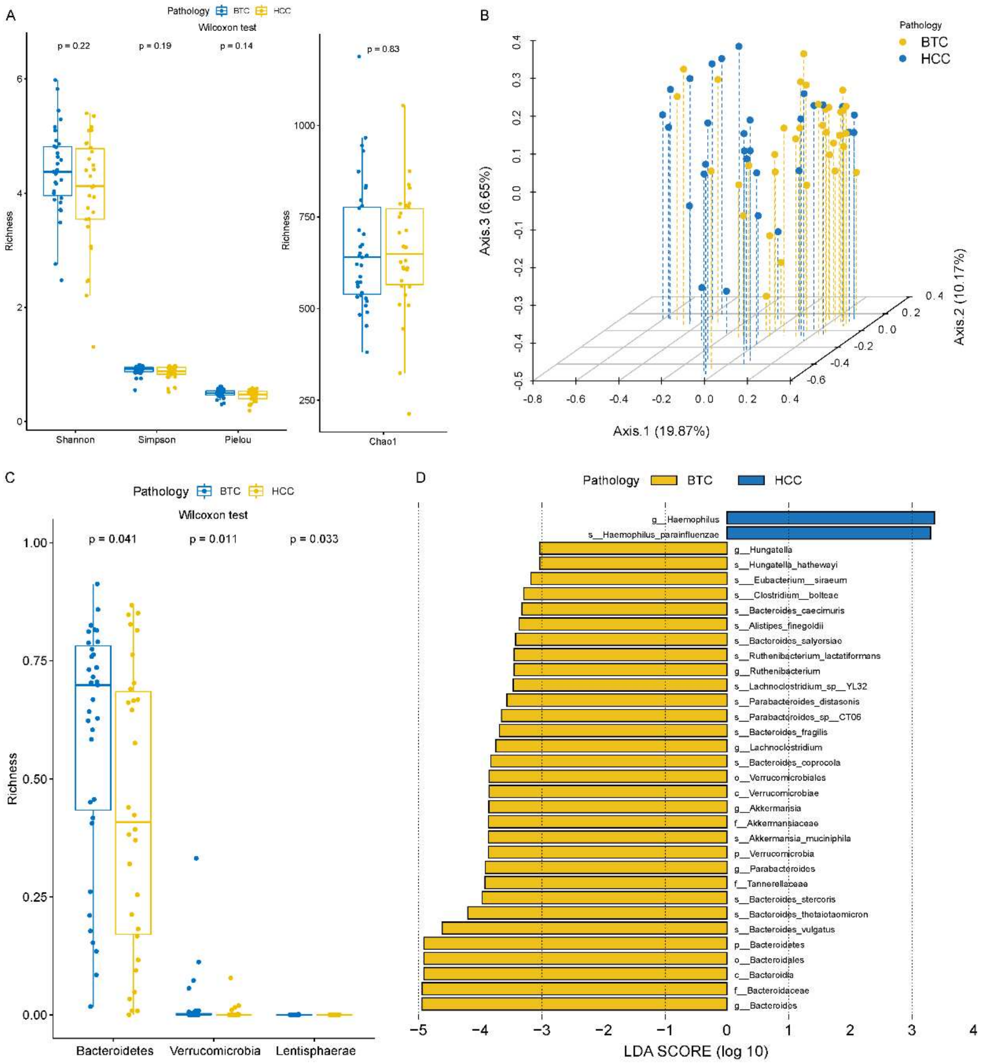

Figure S7 (**A**) Gut microbiome alpha diversity comparison between the HCC subgroup and BTC subgroup (Wilcoxon test). (**B**) PCoA showed the beta diversity evaluated by Bray-Curtis distance between the HCC subgroup and BTC subgroup. (**C**) Significantly different phylum between the HCC subgroup and BTC subgroup (Wilcoxon test). (**D**) Significantly differentially enriched taxa in patients with HCC and BTC identified by LEfSe of the 30 patients with HCC (LDA>3, p<0.05). HCC, hepatocellular carcinoma; BTC, biliary tract cancer; PCoA, principal coordinate analysis; LEfSe, linear discriminant analysis effect size; LDA, linear discriminant analysis.

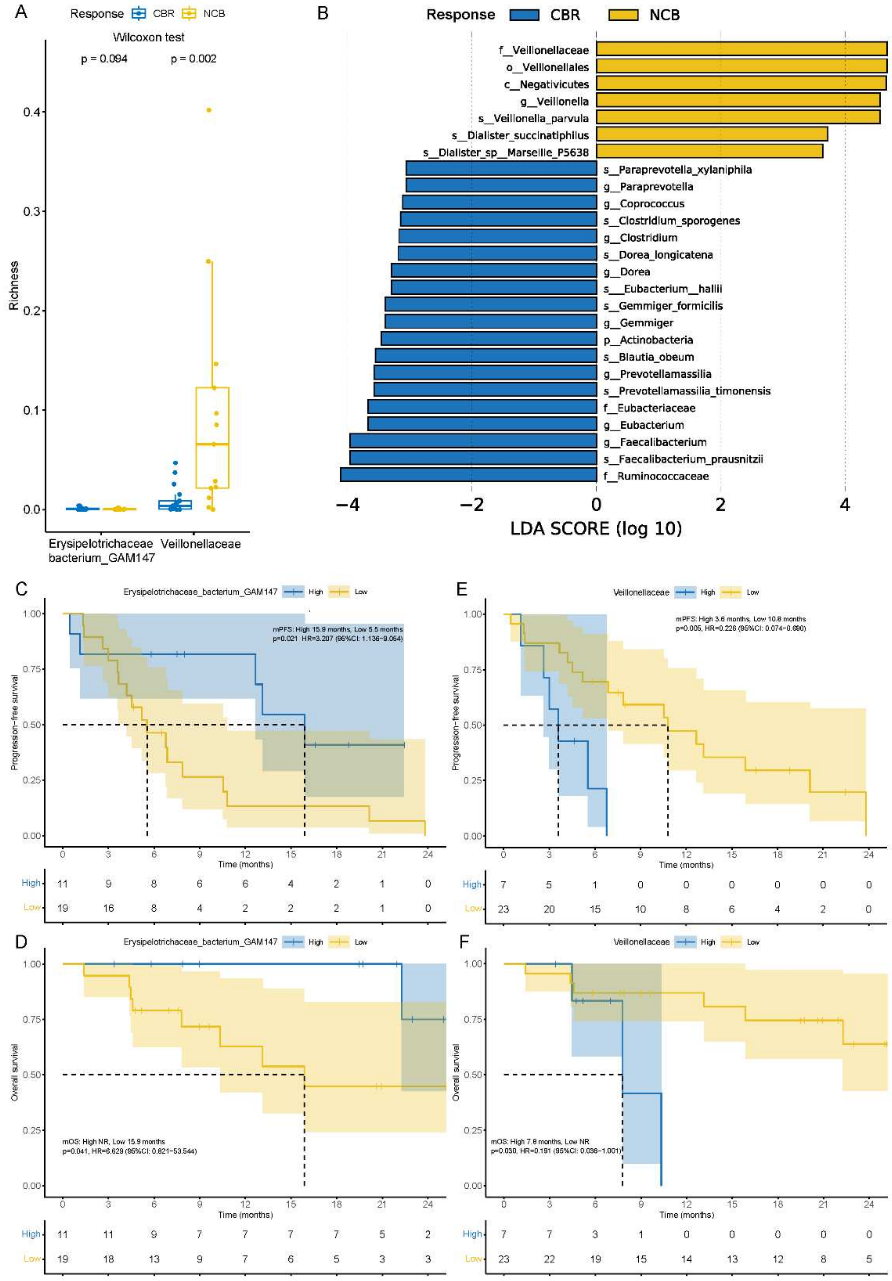

Figure S8 (**A**) Relative abundance comparison of Erysipelotrichaceae bacterium-GAM147 and Veillonellaceae family in the CBR group and NCB group among the 30 HCC patients (Wilcoxon test). (**B**) Significantly differentially enriched taxa in the CBR group and NCB group among the 30 HCC patients identified by LEfSe (LDA>3, p<0.05). The Kaplan-Meier method with log-rank test estimates the median progression-free survival and median overall survival for the 30 HCC patients with higher or lower abundance of (**C-D**) Erysipelotrichaceae bacterium-GAM147 and (**E-F**) Veillonellaceae family. CBR, clinical benefit response; NCB, non-clinical benefit; HCC, hepatocellular carcinoma; LEfSe, linear discriminant analysis effect size; LDA, linear discriminant analysis; mPFS, median progression-free survival; mOS, median overall survival.

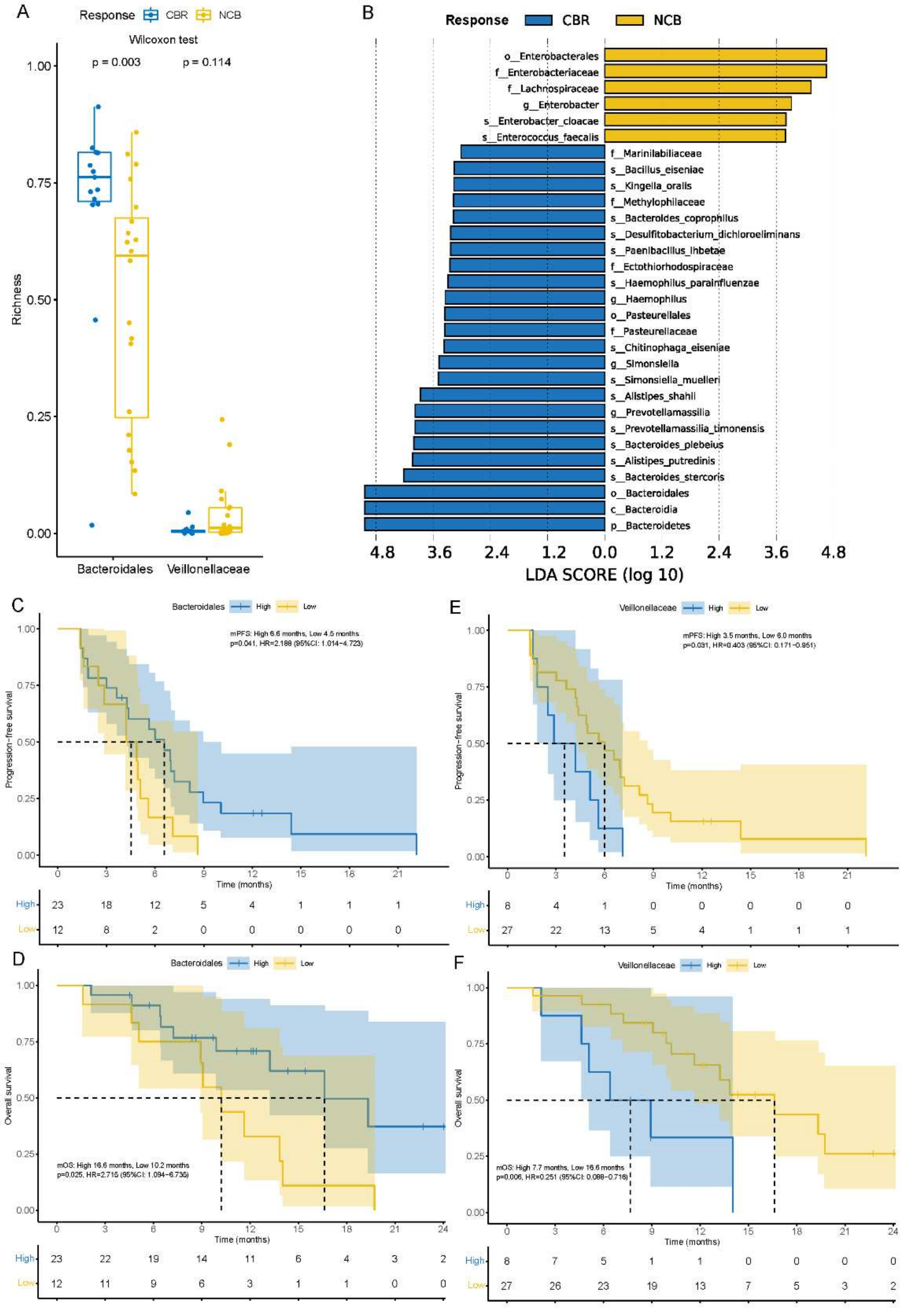

Figure S9 (**A**) Relative abundance comparison of Bacteroidales order and Veillonellaceae family in the CBR group and NCB group among the 35 BTC patients (Wilcoxon test). (**B**) Significantly differentially enriched taxa in the CBR group and NCB group among the 35 BTC patients identified by LEfSe (LDA>3, p<0.05). The Kaplan-Meier method with log-rank test estimates the median progression-free survival and median overall survival for the 35 BTC patients with higher or lower abundance of (**C-D**) Bacteroidales order and (**E-F**) Veillonellaceae family. CBR, clinical benefit response; NCB, non-clinical benefit; BTC, biliary tract cancer; LEfSe, linear discriminant analysis effect size; LDA, linear discriminant analysis; mPFS, median progression-free survival; mOS, median overall survival.

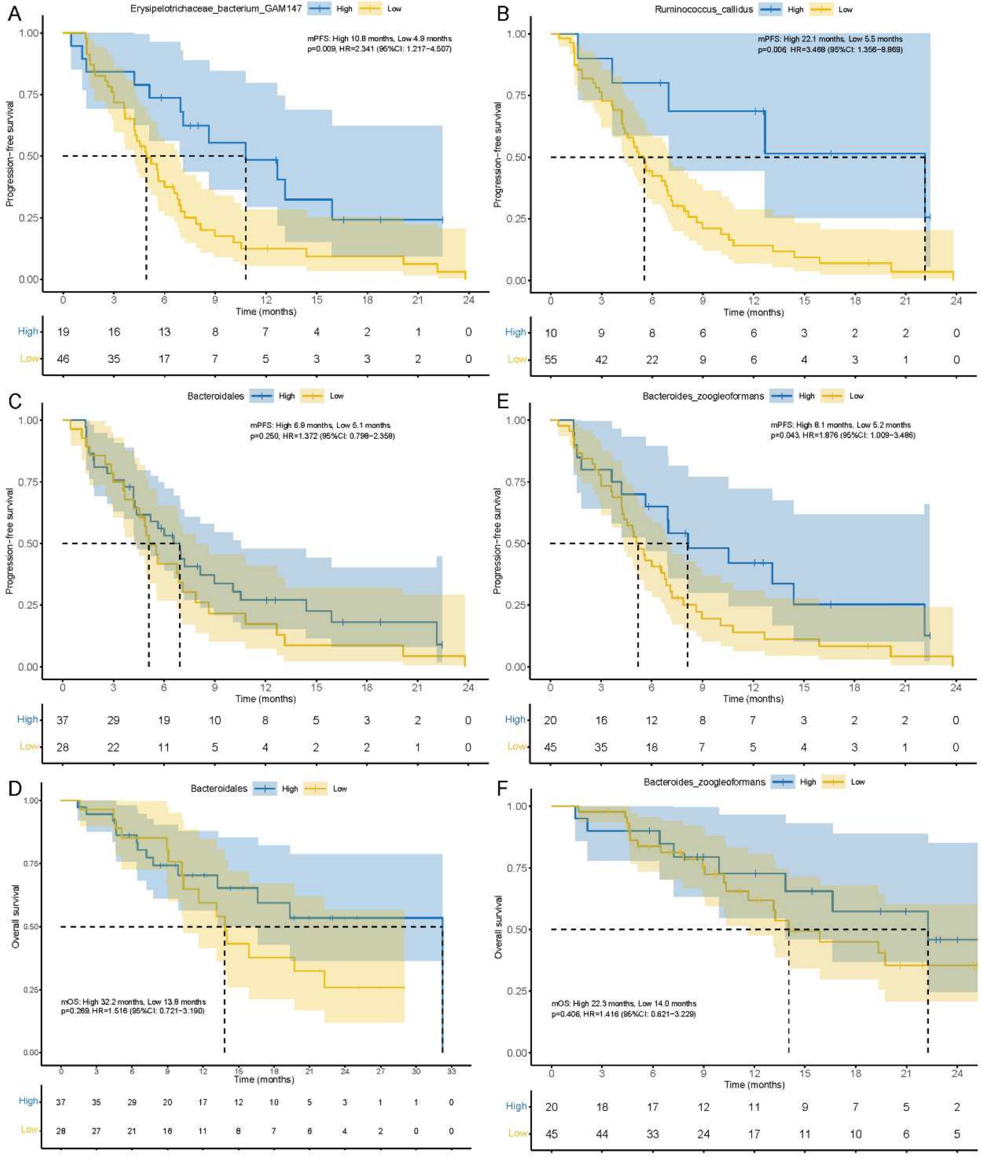

Figure S10 The Kaplan-Meier method with log-rank test estimates the median progression-free survival and overall survival for all 65 patients with higher or lower abundance of (**A**) Erysipelotrichaceae bacterium-GAM147, (**B**) Ruminococcus callidus, (**C-D**) Bacteroidales order and (**E-F**) Bacteroides zoogleoformans. mPFS, median progression-free survival; mOS, median overall survival.

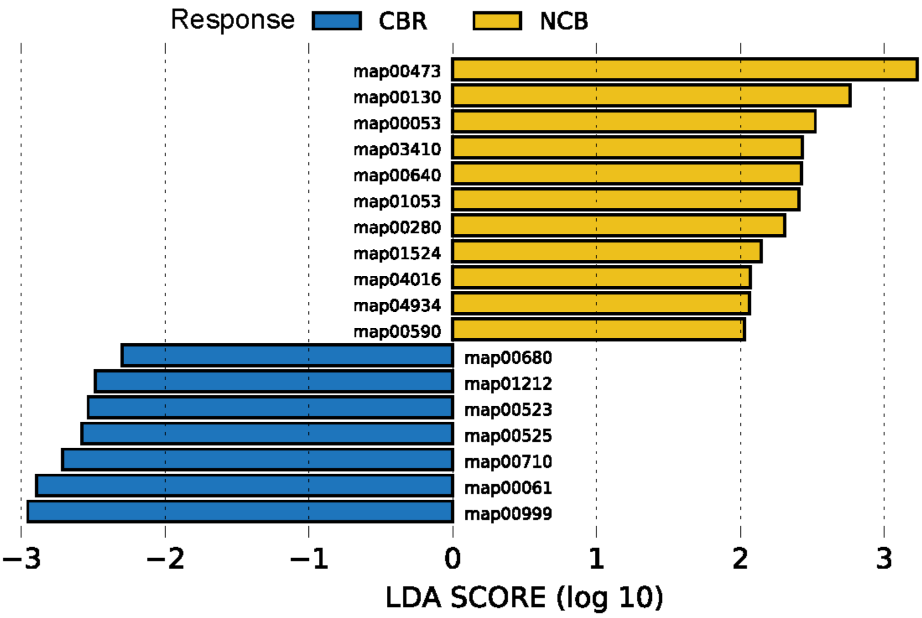

Figure S11 Significantly different KEGG pathways enriched in the CBR group and NCB group identified by LEfSe (LDA>2, p<0.05). KEGG, Kyoto Encyclopedia of Genes and Genomes; CBR, clinical benefit response; NCB, non-clinical benefit; LEfSe, linear discriminant analysis effect size; LDA, linear discriminant analysis.

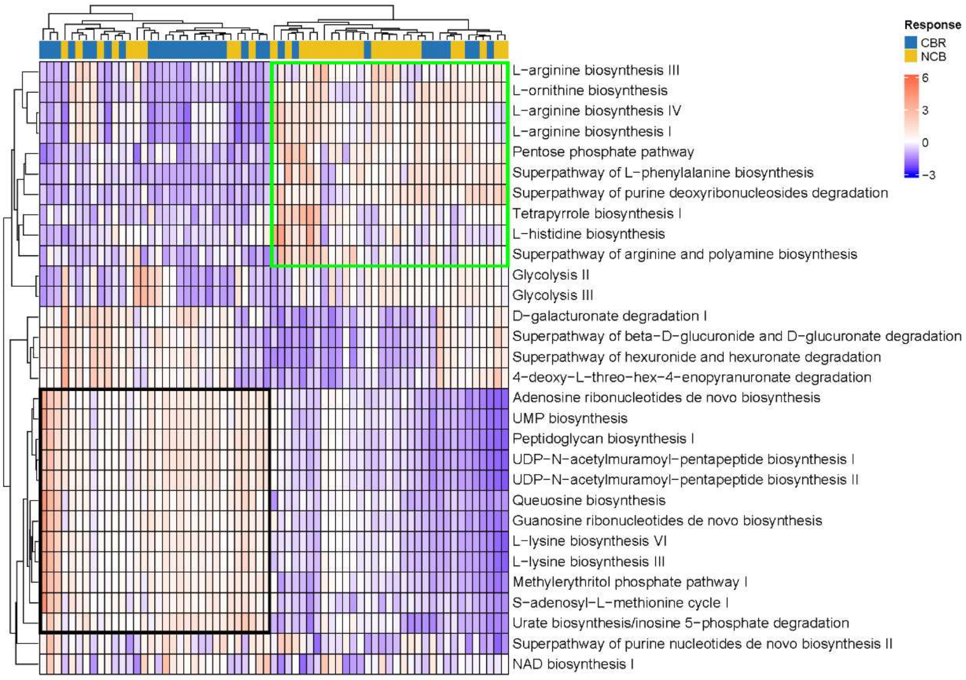

Figure S12 MetaCyc hierarchy of pathway classifications showed different metabolic pathways enriched in the CBR group and NCB group. CBR, clinical benefit response; NCB, non-clinical benefit.