

Supplement

Figure legend

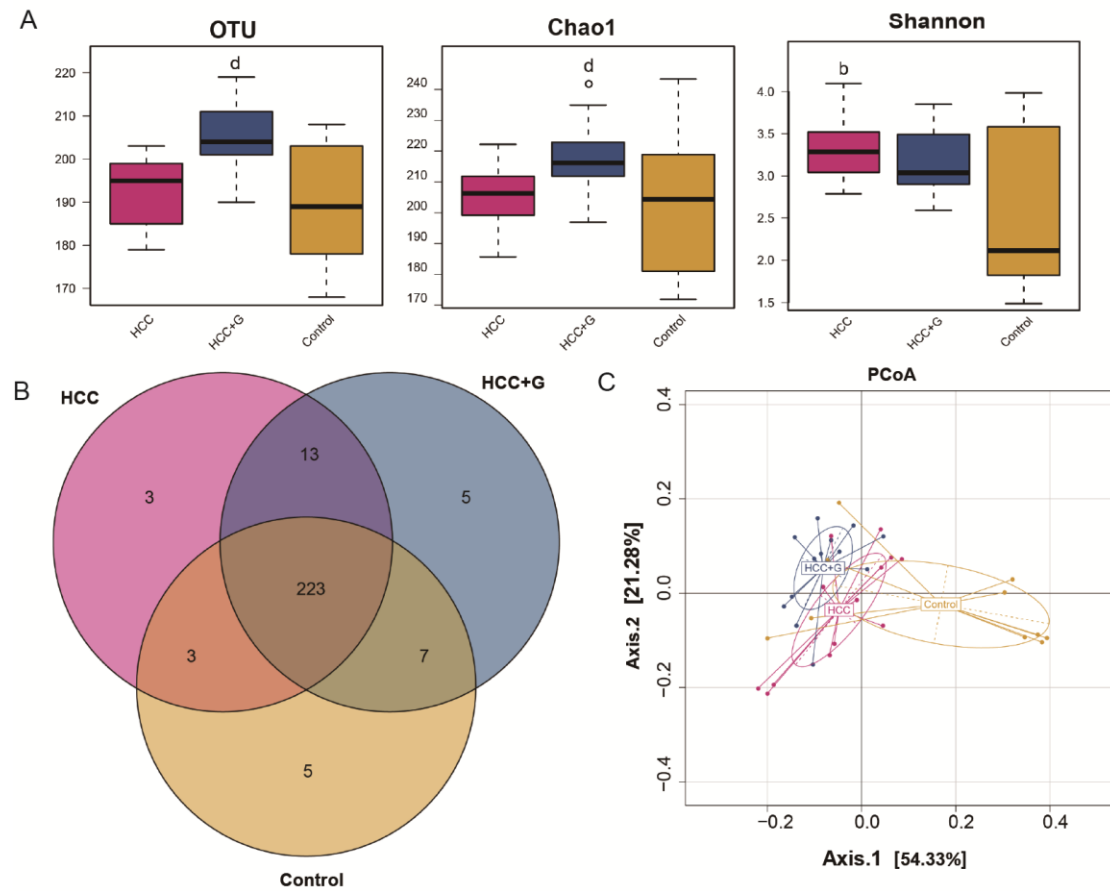


Figure S1 Granulocyte-macrophage colony-stimulating factor alleviated the intestinal dysbiosis induced by the hepatocellular carcinoma. A: Diversity index (OTU, Chao1 and Shannon), Data are presented as the means \pm SE and analyzed by one-way ANOVA with post hoc Tukey's test. ^a $P < 0.05$ and ^b $P < 0.01$ hepatocellular carcinoma (HCC) vs Control; ^c $P < 0.05$ and ^d $P < 0.01$ HCC + G vs HCC; B: Venn diagram between three groups; C: PCoA plot of the microbiota based on weighted UniFrac metric. GMCSF: Granulocyte-macrophage colony-stimulating factor; HCC: hepatocellular carcinoma.

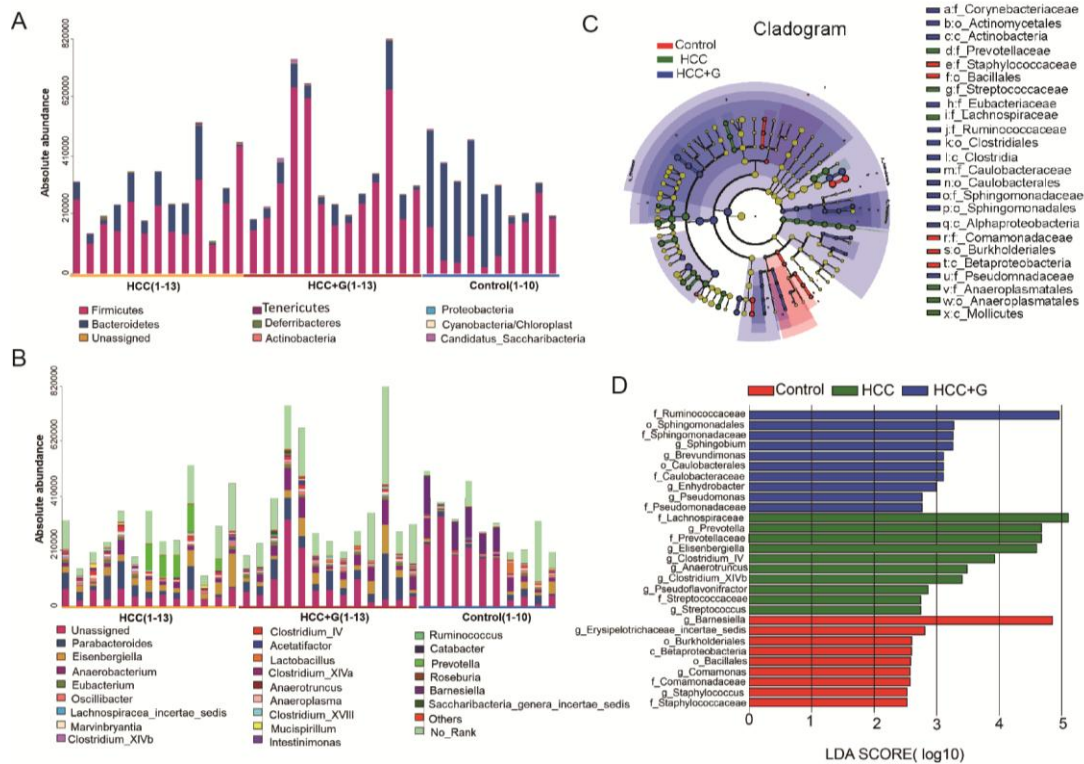


Figure S2. Granulocyte-macrophage colony-stimulating factor alleviated the intestinal dysbiosis induced by hepatocellular carcinoma. A, B: Most abundant taxa at the phylum (A), and genus (B) level; C: LefSe cladogram representing taxon enrichment in the Control, hepatocellular carcinoma (HCC) and HCC + granulocyte-macrophage colony-stimulating factor groups. Rings from the inside going outwards represented taxonomic levels from phylum to genus levels. Sizes of circles indicate the relative abundance of each taxon; (D) Discriminative biomarkers with an LDA score > 2 . GMCSF: Granulocyte-macrophage colony-stimulating factor; HCC: hepatocellular carcinoma.

Table**Table S1. Specific primer sequences for quantitative PCR**

Gene	forward sequence (5'-3')	reverse sequence (5'-3')
ZO1	GCCGCTAAGAGCACAGCAA	GCCGCTAAGAGCACAGCAA
IL-1 β	GAAATGCCACCTTTTGACAG TG	TGGATGCTCTCATCAGGAC AG
IL-4	GGTCTCAACCCCCAGCTAGT	GCCGATGATCTCTCTCAAGT GAT
IL-10	CTTACTGACTGGCATGAGGA TCA	GCAGCTCTAGGAGCATGTG G
GMCSF	CTCAGAAATGTTTGACCTCC AG	TGACAAGCAGAAAGTCCTT CAG
TGF β	CTTCAATACGTCAGACATTC GGG	GTAACGCCAGGAATTGTTG CTA
Claudin -1	TGCCCCAGTGGAAGATTTAC T	CTTTGCGAAACGCAGGACA T
CD14	ACTTCTCAGATCCGAAGCCA G	CCGCCGTACAATTCCACAT
TLR4	ATGGCATGGCTTACACCACC	GAGGCCAATTTGTCTCCAC A
GAPDH	GGCATCCTGGGCTACACTGA	GTGGTCGTTGAGGGC AATG

GMCSF: Granulocyte-macrophage colony-stimulating factor.