

Figure S1 Relative abundance of the top 10 gut microbiota among Ebo.PHLF, Enbo.PHLF, Eao.PHLF, Enao.PHLF at the (A) phylum, (B) class and (C) order level.

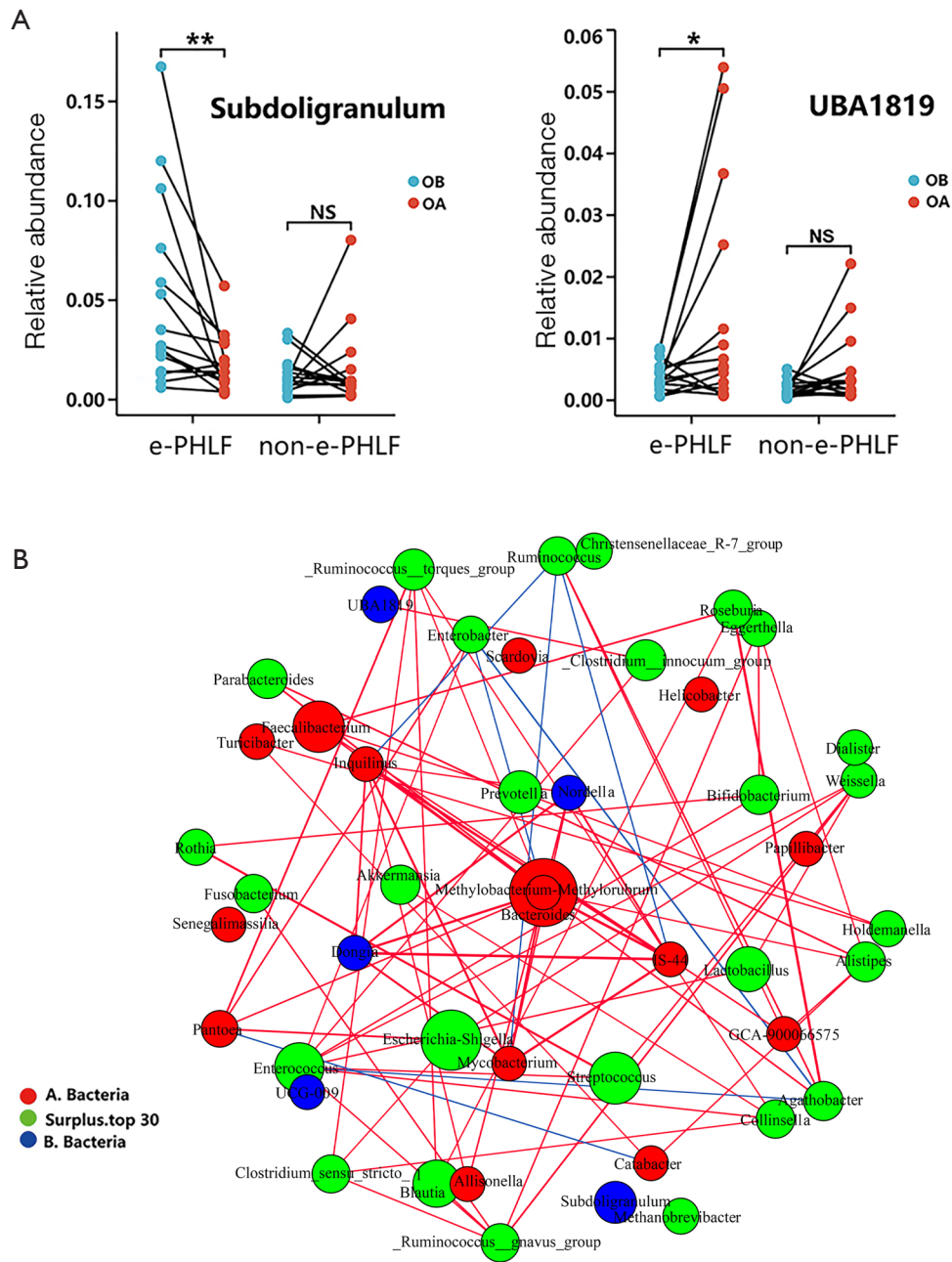


Figure S2 Changes of high abundant species in e-PHLF and non-e-PHLF group before and after surgery, and the symbiotic patterns of differential bacteria and top 30 gut microbes. (A) Comparison between Subdoligranulum and UBA1819 in Eao.PHLF *vs.* Ebo.PHLF (e-PHLF group) and Enao.PHLF *vs.* Enbo.PHLF (non-e-PHLF group). (B) Network analysis revealed the symbiosis pattern of the differential bacteria pre- and post-operatively between the e-PHLF/non-e-PHLF groups and the top 30 gut microbes. A. Bacteria, the differential flora of the PHLF and non-PHLF groups postoperatively; B. Bacteria, the differential flora of the e-PHLF and non-e-PHLF groups preoperatively; Surplus. top 30, the remaining gut microbes after removing some of the differential bacteria in A. Bacteria and B. Bacteria presented in the top 30. *, $P < 0.05$; **, $P < 0.01$. OB, before operation; OA, after operation; NS, not statistically significant. e-PHLF, post-hepatectomy liver failure after extended hepatectomy; non-e-PHLF, post-hepatectomy without liver failure after extended hepatectomy.