

(A)

(B)

Figure S1. Heat map of the percentage shared microbial community structure in the top 10 at the phylum, family, and genus level on goat kids and lambs, respectively. (A) Four groups. (B) Each sample of four groups. All data are converted by $-\log_{10}$. The left side represents DL versus DG, the right represents HL versus HG. * $p < 0.05$; ** $p < 0.01$.

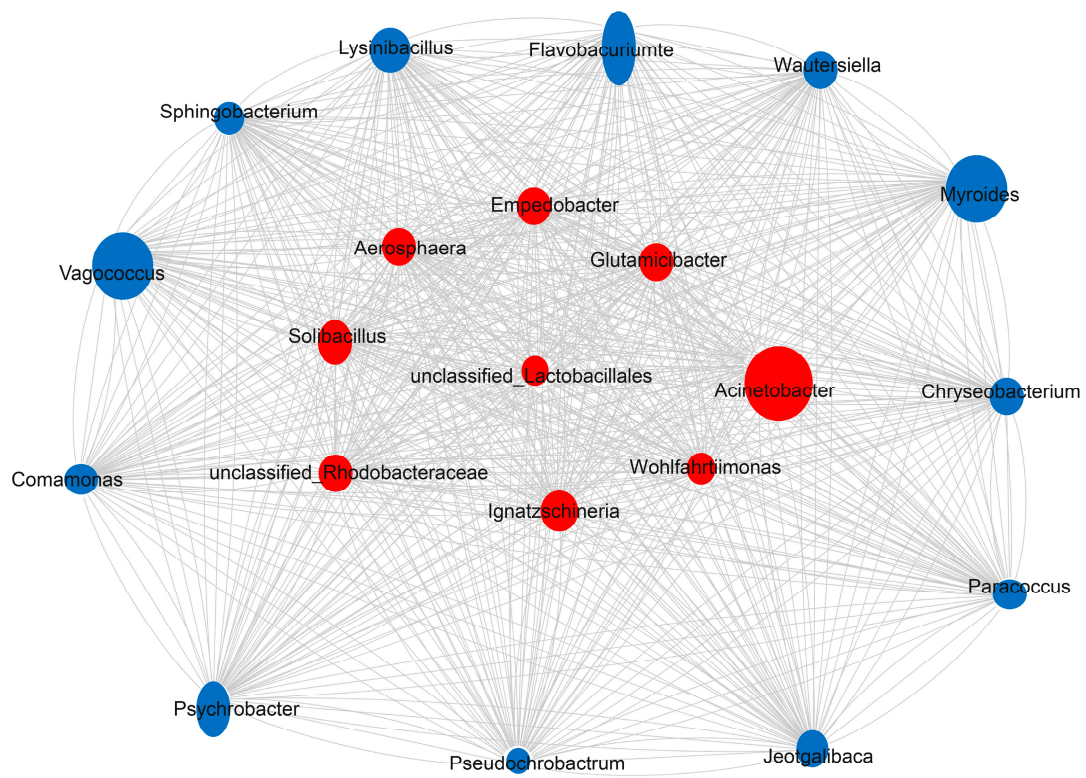


Figure S2. TC-microbial interaction network and hub microbiota in the MEGreen module.