



Figure S1 Beta diversity, which was used to estimate the difference in microbiome composition between groups, was visualized by PCoA and NMDS and estimated based on weighted and unweighted UniFrac distance. TT, lung tumor tissues; PT, para-tumor tissues; DN, distal normal lung tissues; BT, bronchial tissues; PCoA, principal coordinate analysis; NMDS, nonmetric multidimensional scaling.