



Fig. S7. Associations of specific species with clinical tumor stage. The percent abundance of sequences from *B. fragilis* (top left), *F. nucleatum* (top right), *F. nucleatum* + other HOMD (bottom left), and *B. fragilis*, *F. nucleatum*, + other HOMD (bottom right) compared to the total number of sequences from 16S rRNA gene sequencing are presented according to clinical tumor stage status for studies in which tumor stage information was available.