



Fig. S9. Prevalence of microbial features in left- vs right-sided tumors from the USA, MAL1, and MAL2 cohorts. All tumors from the three cohorts for which data on biofilms and 16S rRNA gene sequencing were available were included in this analysis. Positive status for *B. fragilis* was defined as an abundance >2% of all microbial sequences, while positive status for human oral microbes from the HOMD database were defined as an abundance >10% of all microbial sequences from the 16S rRNA gene analysis. Data are presented according to tumor side (left panel, left-sided CRC; right panel, right-sided CRC).