



Fig. S8. Additional changes in species abundance in the expanded meta-analysis. Several *Bacteroides* species (*B. vulgatus*, *B. dorei*, and *B. stercoris*) as well as *Faecalibacterium prausnitzii* were consistently depleted in CRC compared to **a** healthy biopsies and **b** paired normal tissues using Resphera Insight analysis of 16S rRNA gene sequencing data. Random-effects models with 95% CI above or below 0 (red diamonds) were considered statistically significant. Hedge's *g* difference statistic is shown on the X axes. The fixed effects model assumes there exists a single effect size shared by all included studies, while the random effects model allows for variation in the effect size from study to study. Heterogeneity analysis includes estimates of I^2 (percentage of variation reflecting true heterogeneity), τ^2 (random-effects between study variance), and p-value from Cochran's Q test for heterogeneity.