



Figure 1. Community analysis of fecal microbiome data.

(A) Study population overview. Grey bands between the bar plots represent the samples which have matching body sites. (B) Bray-Curtis distance-based redundancy analysis (dbRDA) of PDAC, CP and control fecal microbiome data in ES cohort. PDAC samples are shown as red colored circles, CP patients as green and controls as blue. Richness, exponential Shannon (exp(Shannon)) and inverse Simpson (inv(Simpson)) diversity measures are also visualized with arrows similarly like tested metadata variables. The distance of meta-variable from the center represents the confounding effect size (see Methods). (C) Wilcoxon test results of ES fecal microbiome data to test enriched taxa between PDAC and control cases (see Methods). Y-axis is \log_{10} (FDR corrected p-values), x-axis is generalized fold change and dot size represents the relative abundance of given species/strains. Red dots represent significantly differentially abundant species/strains in either group, while black dots show non-significant species after FDR correction. Green and brown-coloured species are selected in metagenomic model-1 as predictors of PDAC. ES: Spanish