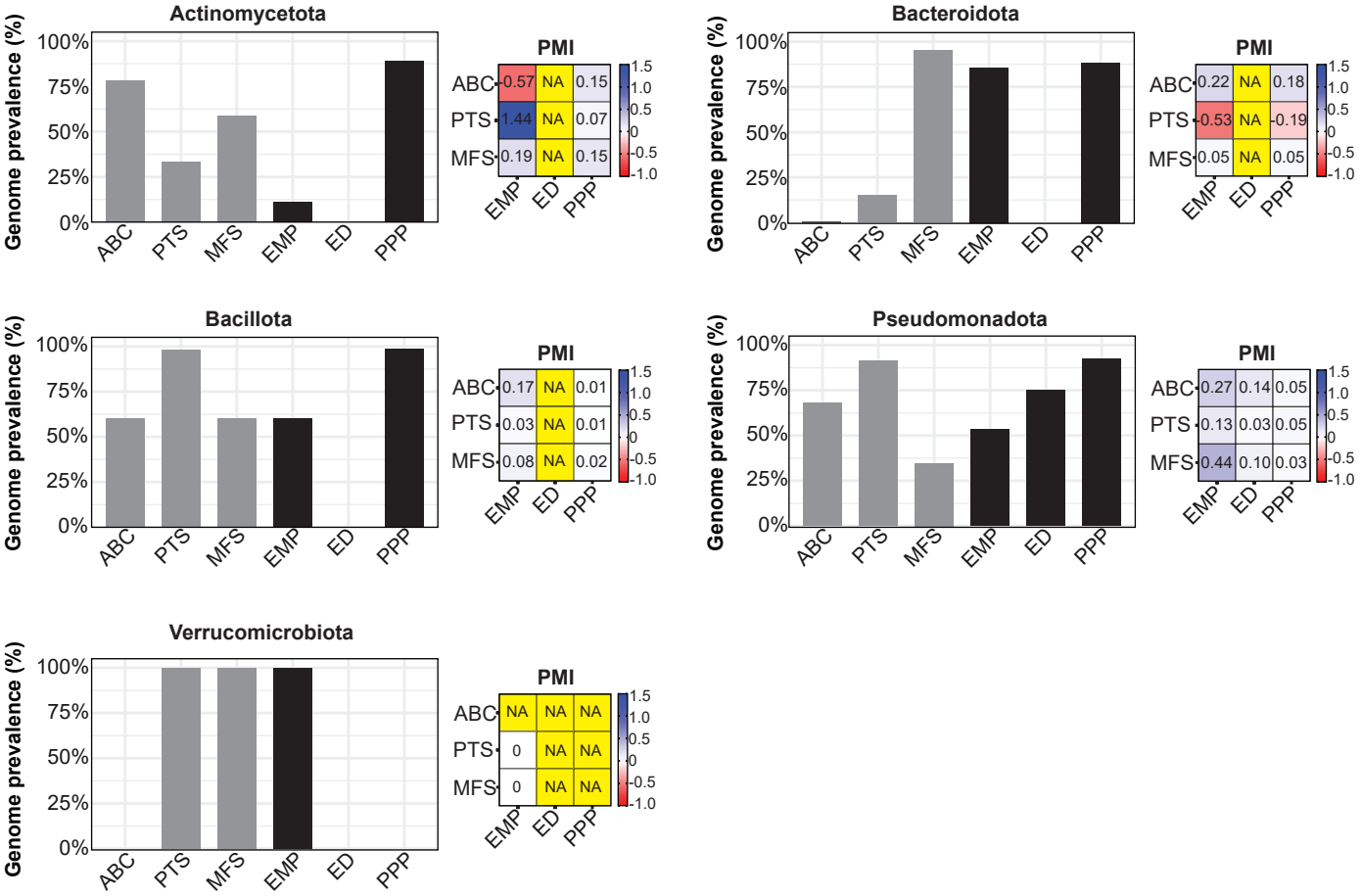
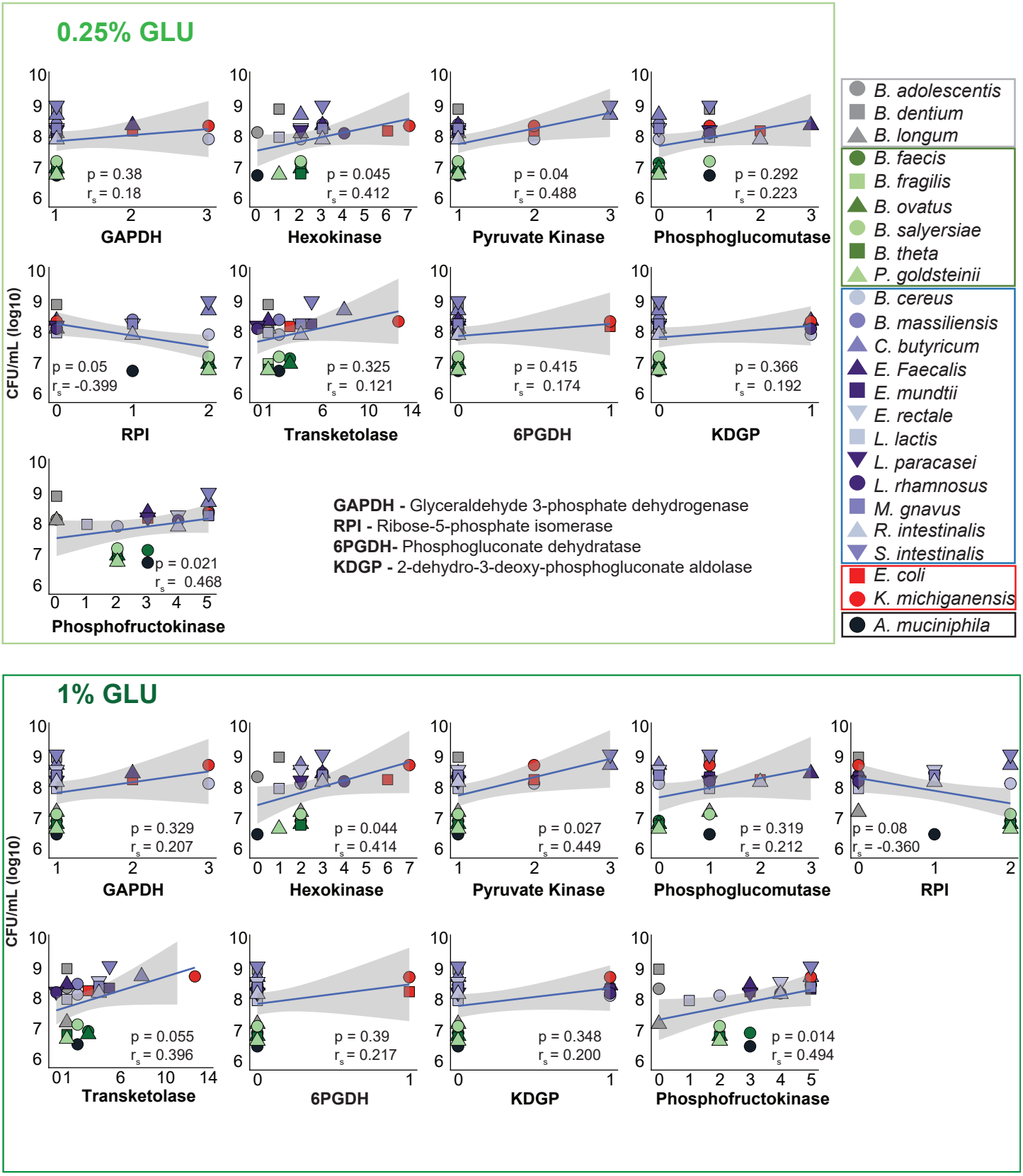


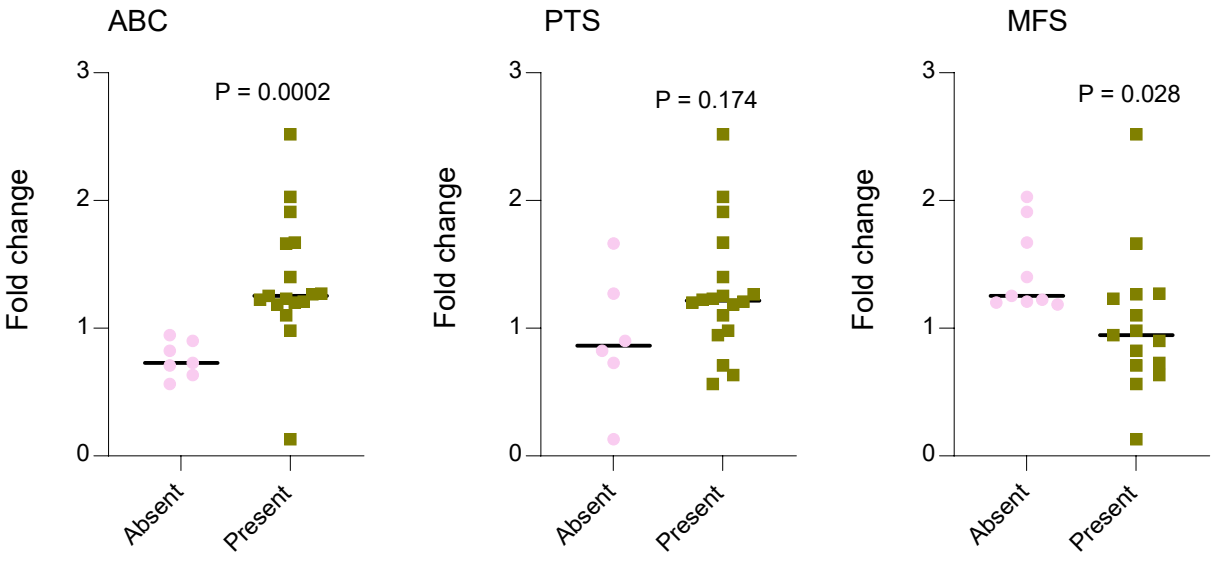
Extended Data Fig. 1. Sugar metabolism gene profiles reveal intra-phyla functional diversity in gut bacteria

Bar plots show the genome prevalence of sugar transporter types (ABC, PTS, MFS) and glycolytic pathways (EMP, ED, PPP) across bacterial phyla, highlighting functional differences within phyla. Heatmaps illustrate pairwise mutual information (PMI) between transporter and pathway features, capturing phylum-specific patterns. “NA” indicates missing PMI values due to the absence of one or both features.



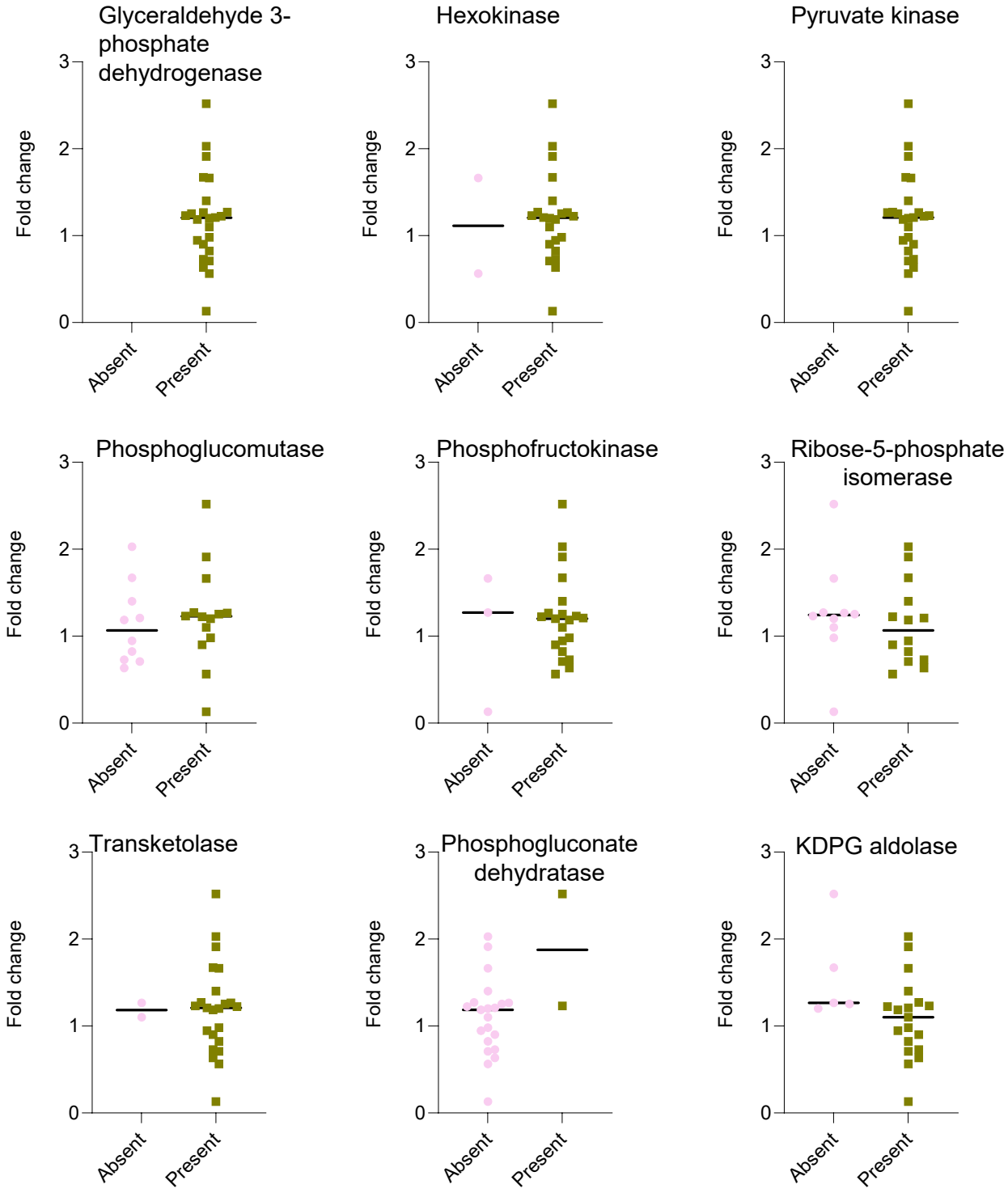
Extended Data Fig. 2. Growth correlates poorly with glycolytic gene profiles across EMP, PPP, and ED pathways

Spearman correlation (r_s) analysis of the colony-forming units (CFUs) and genes involved in glycolytic pathways for 24 bacterial strains. Bacteria were cultured in BHI-NG medium supplemented with either 0.25% or 1% GLU, and samples were collected 24 hours post-inoculation. Each dot represents mean CFU of the indicated species from two independent experiments (n = 6). *P*-values are derived from Spearman correlation. Blue lines show linear regression fits; shaded areas indicate 95% confidence intervals.



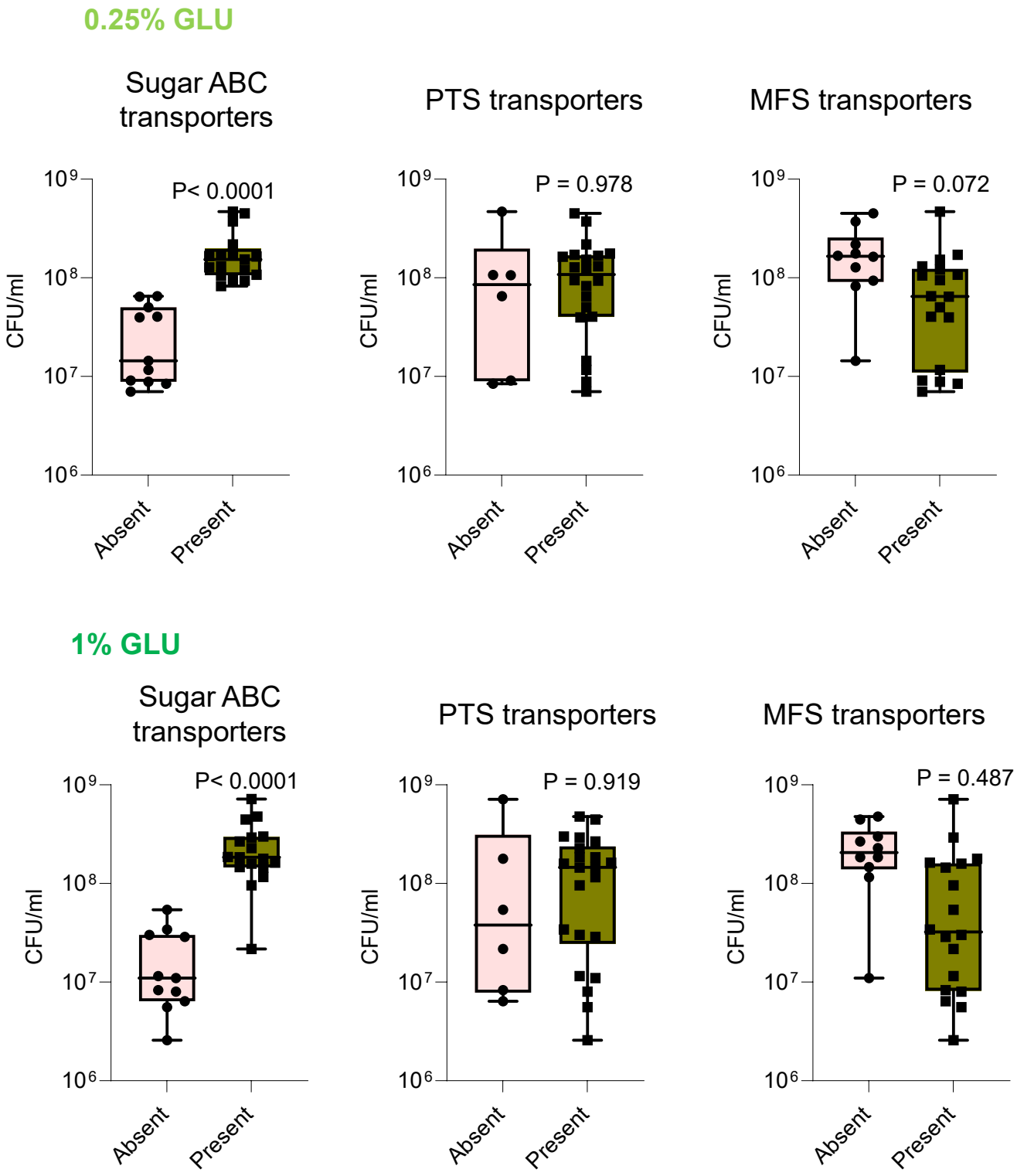
Extended Data Fig. 3 . Sugar transporter presence distinguishes bacterial growth responses to glucose

Analysis of bacterial growth differences (fold change) based on the presence or absence of sugar transporters. Each data point represents the mean fold change in colony-forming units (CFUs) between 1% and 0.25% glucose (GLU) conditions at 24 hours for an individual strain, derived from two independent experiments (n = 6). Bacteria were cultured in BHI-NG medium supplemented with either 0.25% or 1% GLU, and samples were collected 24 hours post-inoculation. Statistical analysis was performed using an unpaired t-test with Welch's correction, $p < 0.05$ was considered statistically significant.



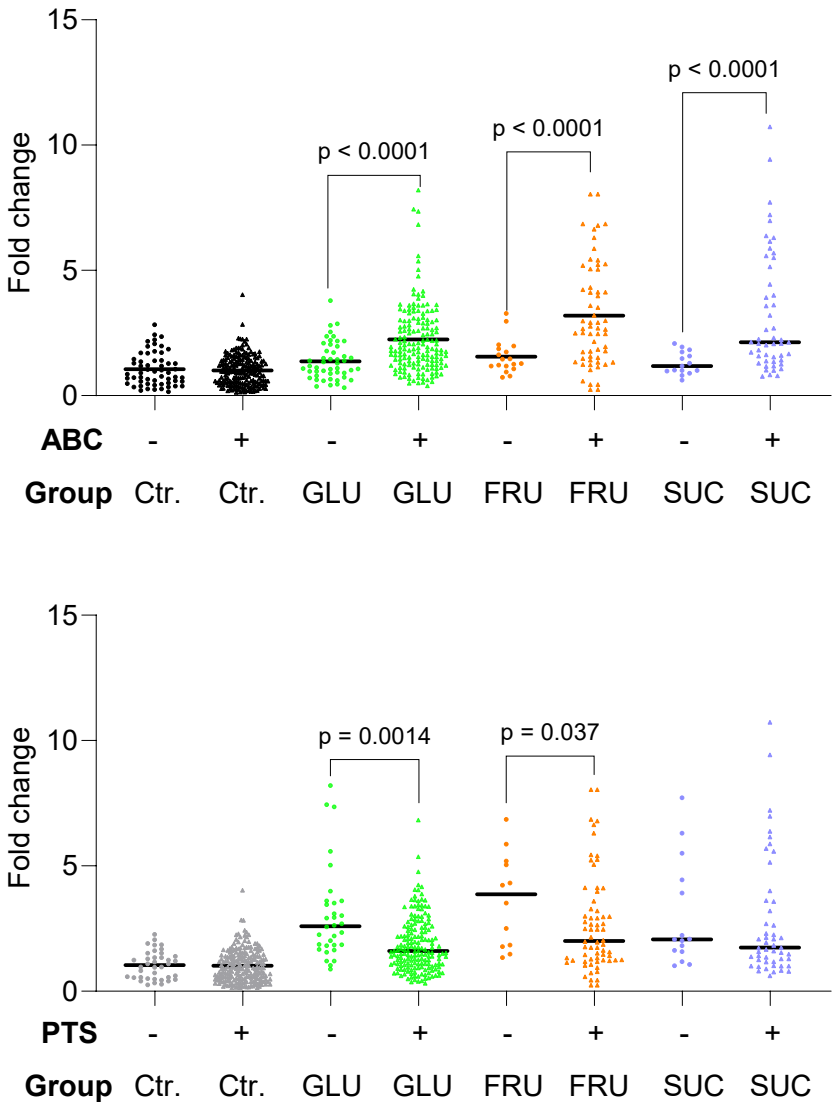
Extended Data Fig. 4 . Bacterial growth responses to glucose are not determined by glycolytic enzyme presence

Analysis of bacterial growth differences (fold change) based on the presence or absence of enzymes involved in glycolytic pathways. Each data point represents the mean fold change in colony-forming units (CFUs) between 1% and 0.25% glucose (GLU) conditions at 24 hours for an individual strain, derived from two independent experiments (n = 6). Bacteria were cultured in BHI-NG medium supplemented with either 0.25% or 1% GLU, and samples were collected 24 hours post-inoculation. Statistical analysis was performed using an unpaired t-test with Welch's correction, $p < 0.05$ was considered statistically significant. No significant differences were observed.



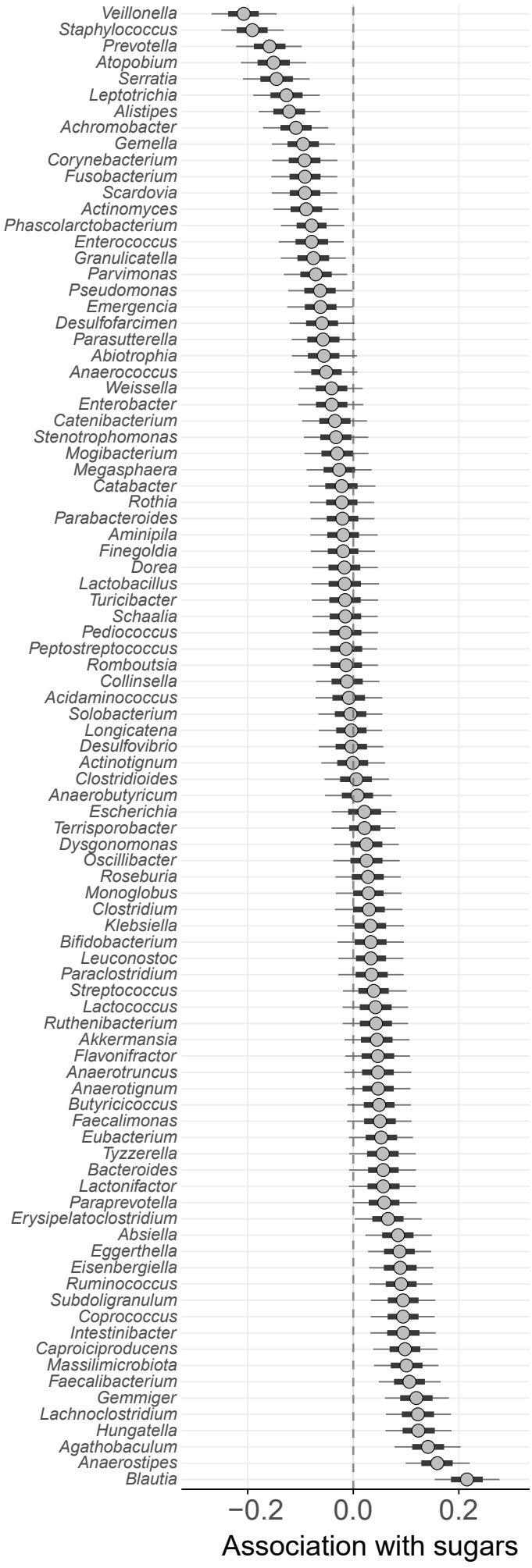
Extended Data Fig. 5 . Strains encoding sugar ABC transporters show superior growth under varying glucose levels

Bar plots illustrating differences in growth among bacteria from Figures 1f and 2e, when categorized by the presence or absence of the indicated transporters. Each dot represents the average CFU of an individual species from two independent experiments (n = 6). Bacteria were cultured in BHI-NG medium supplemented with 0.25% or 1% glucose (GLU) and harvested at 24 hours post inoculation. Statistical analysis was performed using unpaired *t*-test with Welch's correction. $p < 0.05$ was considered statistically significant.



Extended Data Fig. 6. Transporter-specific growth responses of gut bacteria to dietary glucose, fructose, and sucrose *in vivo*

Fold change from fecal samples of C57BL/6 mice colonized with OMM[15] species, with *ad libido* access to regular drinking water (control, Ctr.), or drinking water supplemented with 10% glucose (GLU), 10% fructose (FRU), and 10% sucrose (SUC) water, categorized by the presence (+) or absence (–) of ABC or PTS transporters. Each dot represents the mean fold change (from day 0 to day 14) for an individual bacterial species. Data were combined from 3 independent experiments (n = 10 control female mice, n = 9 control male mice, n = 7 10% GLU female mice, n = 9 10% GLU male mice, n = 3 10% FRU female mice, n = 3 10% FRU male mice, n = 3 10% SUC female mice, and n = 2 10% SUC male mice). Statistical analysis was performed using an unpaired t-test with Welch's correction. $P < 0.05$ is considered statistically significant.



Extended Data Fig. 7. Bayesian inference of sugar intake effects on gut microbial genera in HCT patients.

Genus–sugar associations are shown for all genera included in the HCT patient microbiome analysis. Bayesian linear regressions were performed between prior 2-day sugar intake and the relative abundance of each genus (n = 1009 samples, N = 158 patients, including all 91 genera). Posterior means for the effect of sugar are plotted with 66% and 95% credible intervals.