

Supplementary File:

Table S1: Fermentation parameters including pH, valerate, and branched chain fatty acid (BCFA) concentrations for the non-substrate control (NSC) and all treatments. Values are given as mean of eight donors including standard deviation.

Treatment	pH	Valerate [mM]	BCFA [mM]	Cell counts [log10(cells/mL)]
NSC	6.63 ± 0.04	0.51 ± 0.38	1.12 ± 0.57	9.12 ± 0.07
FOS	6.11 ± 0.14 ^a	0.35 ± 0.30	0.63 ± 0.30 ^a	9.44 ± 0.11 ^a
2'FL	5.92 ± 0.11 ^{a,b}	0.31 ± 0.31	0.52 ± 0.37 ^a	9.35 ± 0.14 ^{a,b}
3'SL	6.14 ± 0.06 ^a	0.31 ± 0.32	0.67 ± 0.31 ^a	9.46 ± 0.07 ^a
2'FL/DFL	5.93 ± 0.11 ^{a,b}	0.32 ± 0.32	0.52 ± 0.35 ^a	9.36 ± 0.14 ^{a,b}
2'FL/DFL+3'SL	5.95 ± 0.12 ^{a,b}	0.32 ± 0.32	0.52 ± 0.37 ^a	9.35 ± 0.12 ^{a,b}

a: significant effect ($p_{\text{adjusted}} \leq 0.05$) between NSC and treatments; b: significant effect ($p_{\text{adjusted}} \leq 0.05$) between FOS and HMO treatments; NSC: non-substrate control; FOS: fructooligosaccharide; 2'FL: 2'Fucosyllactose; 3'SL: 3'Sialyllactose; DFL: Difucosyllactose

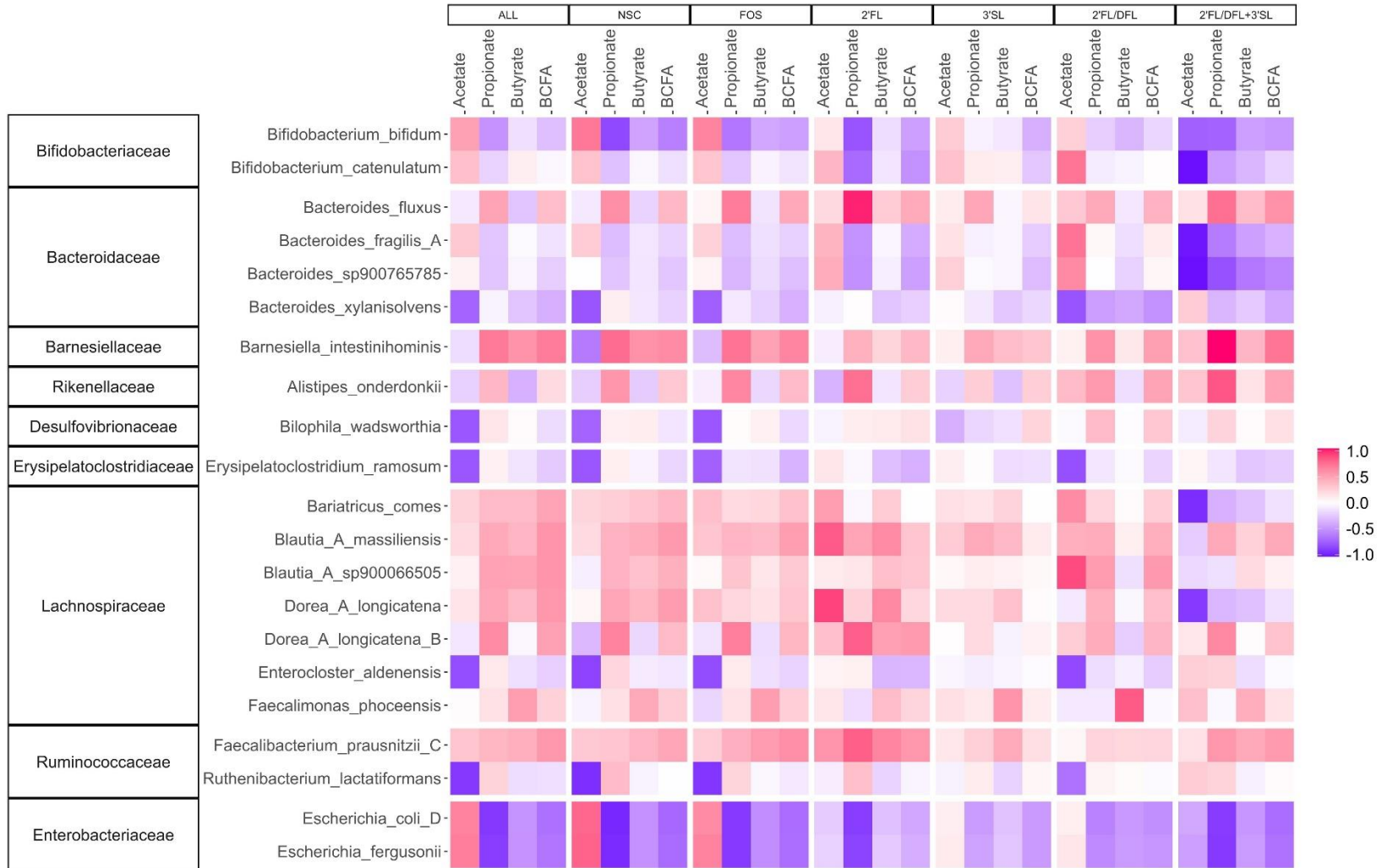


Figure S1: Regularized canonical correlation analysis (rCCA) between bacterial composition and metabolites. Composition is stated at species level including taxa that were significantly ($p_{\text{adjusted}} \leq 0.05$) or consistently affected by any treatment. Bacterial metabolites include acetate, propionate, butyrate and BCFA. Threshold was set to > 0.76 .