Title: Different metabolic features of Bacteroides fragilis growing in the presence of glucose and exopolysaccharides of bifidobacteria as fermentable carbohydrates

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Figure S1. Relative expression levels of different genes in cultures of *B. fragilis* grown in the presence of bifidobacterial EPS fractions with respect to the cultures in glucose. Glutamate dehydrogenase (*gdhB*), pyruvate phosphate dikinase (*ppdK*), methyl-malonyl CoA mutase (*mutB*), acetolactate synthetase (*ilvB*), membrane protein OmpA (*ompA*), transketolase (*tktB*), phosphoenolpyruvate carboxykinase (*pckA*), malate dehydrogenase (*mdh*) and pyruvate carboxylase (*pyc*) genes. Grey bars, changes in gene expression levels in the presence of EPS E44 with respect to glucose. Black bars, changes in gene expression levels in the presence of EPS R1 with respect to glucose.