

Supplementary material

2.4.2 Effect of anthocyanin concentration in the juice on the functional predictions of the gut microbiota

The gut microbiota of the -31% CJ-treated mice, nucleotides, amino acid, menaquinol biosynthesis (e.g., guanosine ribonucleotides de novo biosynthesis, superpathway of L-lysine, L-threonine and L-methionine biosynthesis I) pathways were more abundant compared to the 26% CJ-treated mice (Figure S1a). In parallel, aromatic compound, amino acid degradation (e.g., toluene degradation), organic acid, amino acid fermentation (pyruvate fermentation) and short chain fatty acid (SCFA) biosynthesis (acetate and butanoate) pathways were more represented in the gut microbiota of the 26% CJ-treated mice compared to the -31% CJ-treated mice (Figure S1a). Comparably, sugar degradation (e.g., glucose and glucose-1-phosphate degradation), nucleotides and amino acid biosynthesis (e.g., guanosine deoxyribonucleotides de novo biosynthesis II) and generation of precursor metabolites and energy (pentose phosphate pathways) pathways were more abundant in the gut microbiota of the -31% CJ-treated mice compared to the -19% CJ-treated mice (Figure S1b). In contrast, aromatic compound (e.g., catechol degradation I), sugar and fatty acid degradation (e.g., fatty acid β -oxidation I) and fermentation (e.g., pyruvate fermentation to butanoate) pathways were enriched in the gut microbiota of the -19% CJ-treated mice compared to the -31% CJ-treated mice, (Figure S1b).

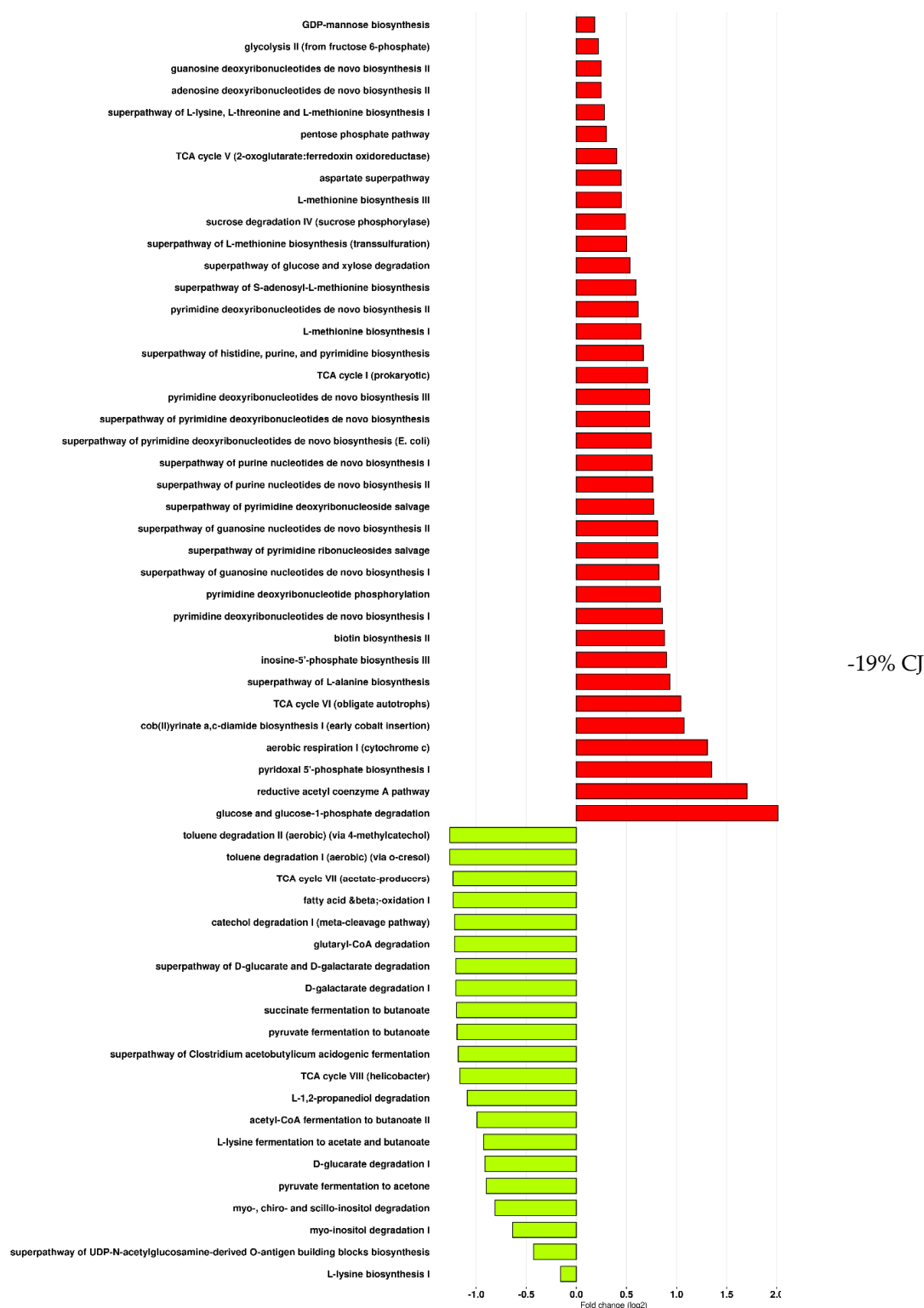
-31% CJ

(most impoverished juice)

vs



(a)



(b)

Figure S1. Administration of cranberry juices (CJs) with different anthocyanin concentrations is associated with changes in the gut microbial functional pathways of mice in comparison with the most anthocyanin-

impoverished CJ. The differential abundance analysis was calculated in order to explore microbial pathways that more strongly discriminated between the gut microbiota of mice treated with (a) -31% CJ (red) and 26% CJ (blue), (b) -31% CJ (red) and -19% CJ (green).

Function of sugar degradation pathway was more represented in the 26% CJ-treated mice compared to the -19% group (Figure S2b). Pathways associated to alcohol and peptidoglycan biosynthesis were more abundant in the 44% CJ-treated mice compared to the 26% group (Figure S2a).

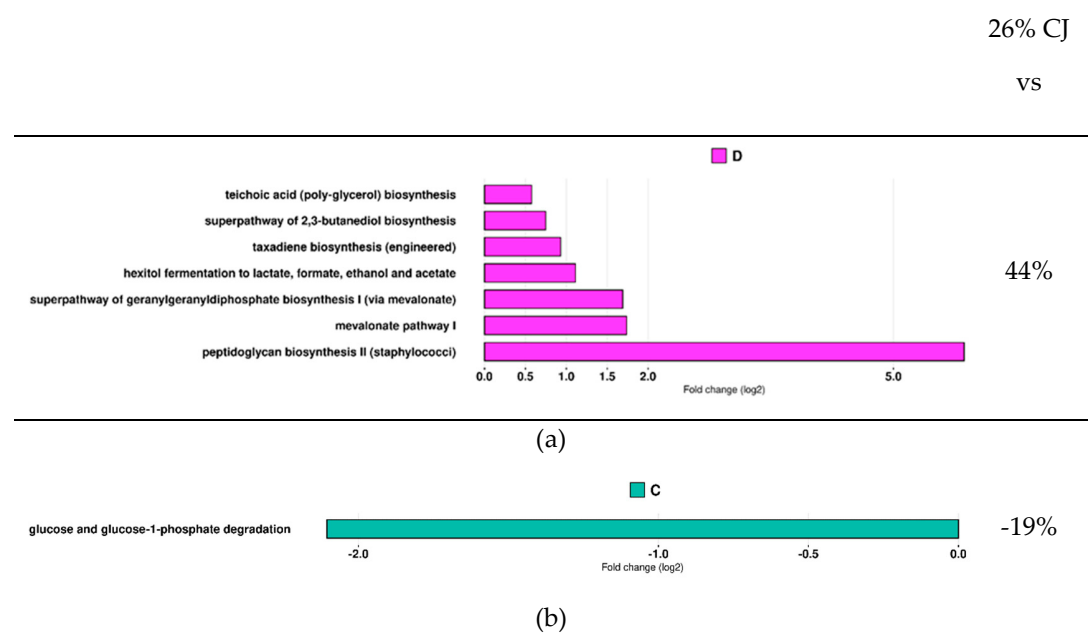


Figure S2. Administration of cranberry juices (CJs) with different anthocyanin concentrations is associated with changes in the gut microbial pathways in comparison with the 26% CJ. The differential abundance analysis was calculated in order to explore the microbial pathways that more strongly discriminated between the gut microbiota of mice treated with (a) 26% CJ (blue) and 44% CJ (pink), (b) 26% CJ (blue) and -19% CJ (green).