FIG S6 The complete *B. breve* genome reconstructed in this study. Metagenomic sequencing of the two selected fecal samples was performed using the Pacific Bioscience Sequel II platform, followed by assembly using Canu v1.8 (1) and deconvolution using BLASTN of the assembly. This complete genome was 2.34M in size (https://doi.org/10.6084/m9.figshare.19709923.v1**, Table S5C**), similar to median *B. breve* genome size of 2.33M reported on NCBI. **A)** KEGG 2013-03-18 release (2) to characterize functional categories of *B. breve* XM1439. **B)** Circular genome display of *B. breve* XM1439, generated by BLAST Ring Image Generator (BRIG) (2011 June vers) (3). **C)** Genome alignment of *B. breve* genome 1439, 1437 using MAUVE (4) using *B. breve* DSM20213 as the reference genome.

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