Supplementary data
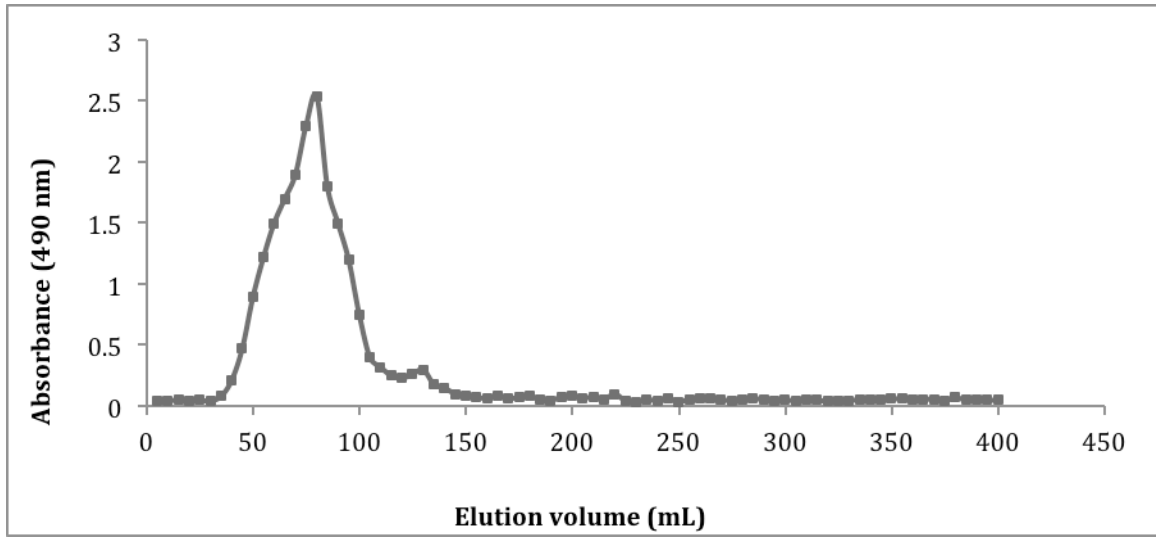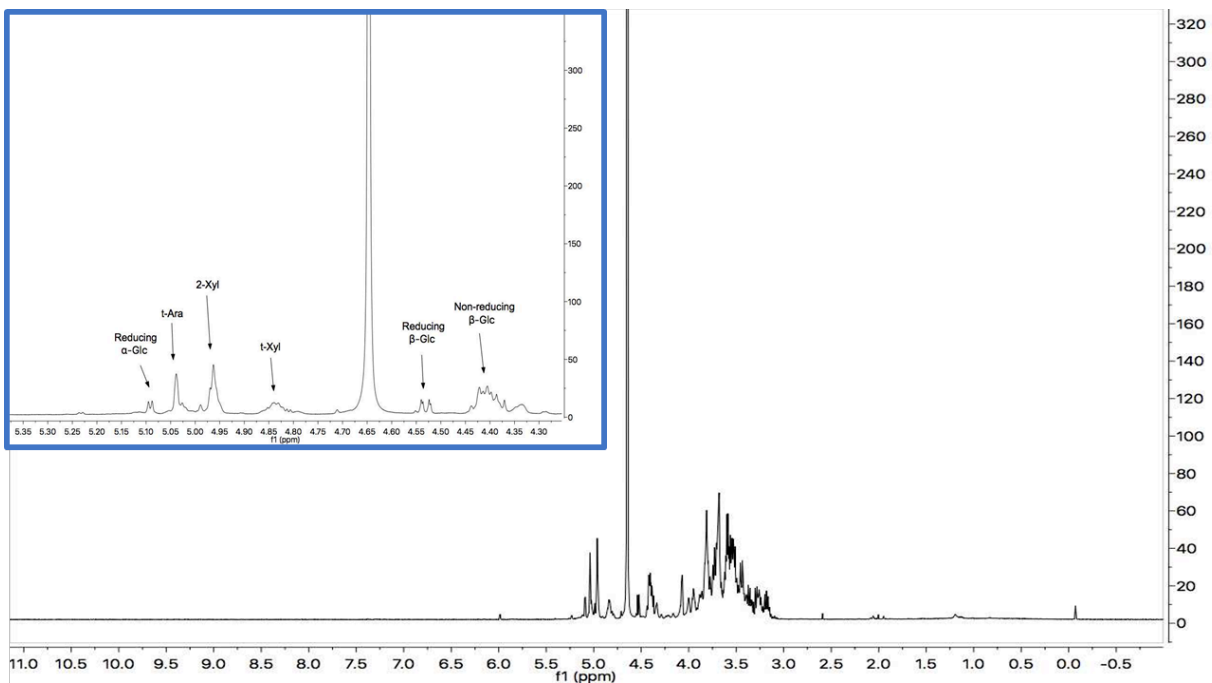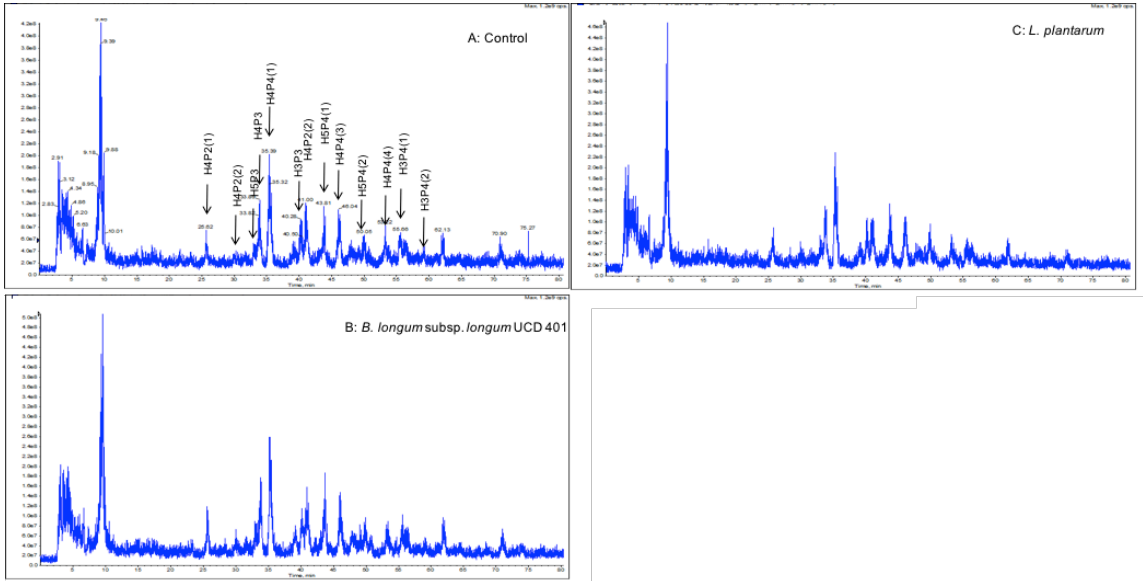

Fig. S1. Elution profile of cranberry xyloglucans on a sephacryl S-100 HR 16/60 column, eluted with deionized water.

**Fig. S2.** ^{1}H NMR spectra of cranberry xyloglucan (500 MHz, D$_2$O). The inset blue box shows an expanded anomeric region of the ^{1}H NMR spectrum.

Fig. S3. LC-MS analysis of xyloglucans (A) before fermentation and remaining post-fermentation by (B) *B. longum* subsp. *longum* UCD 401 and (C) *Lactobacillus plantarum* ATCC BAA-793. Shown in the upper left section are the full scan MS of the blank control along with the corresponding xyloglucan structures between DP=6-9.
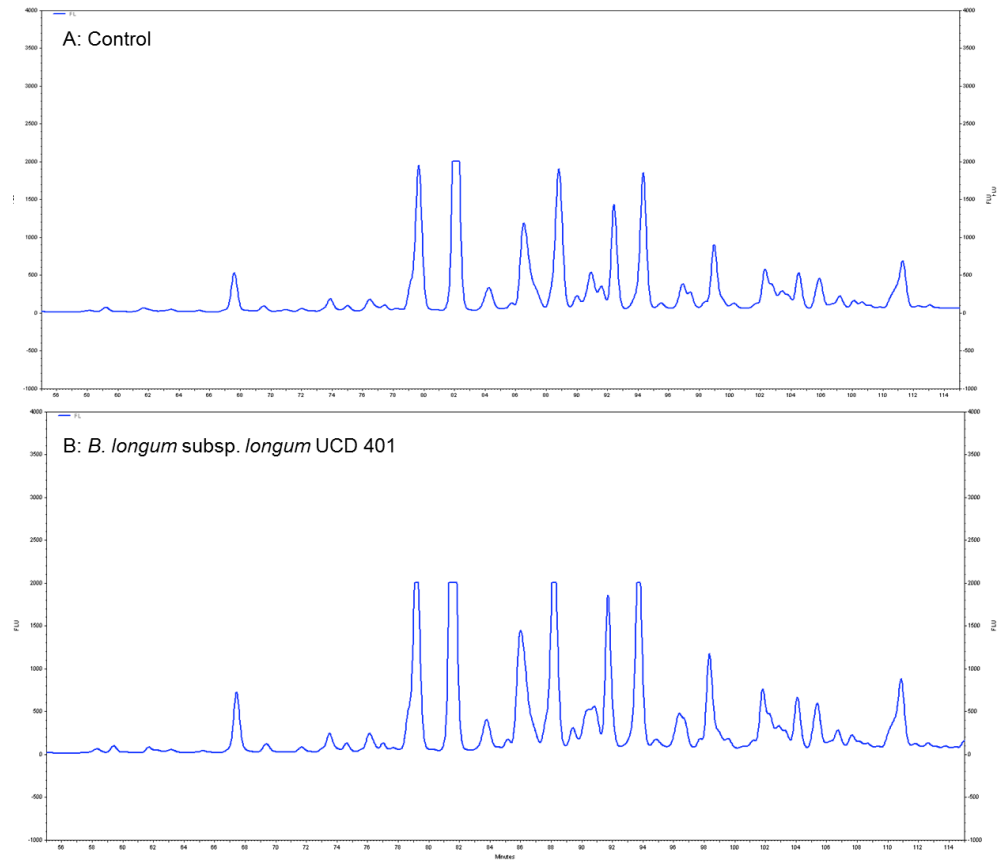
**Fig. S4**. FL-HPLC chromatograms of xyloglucans (A) before fermentation (control) and remaining post fermentation by (B) *B. longum* subsp. *longum* UCD 401.
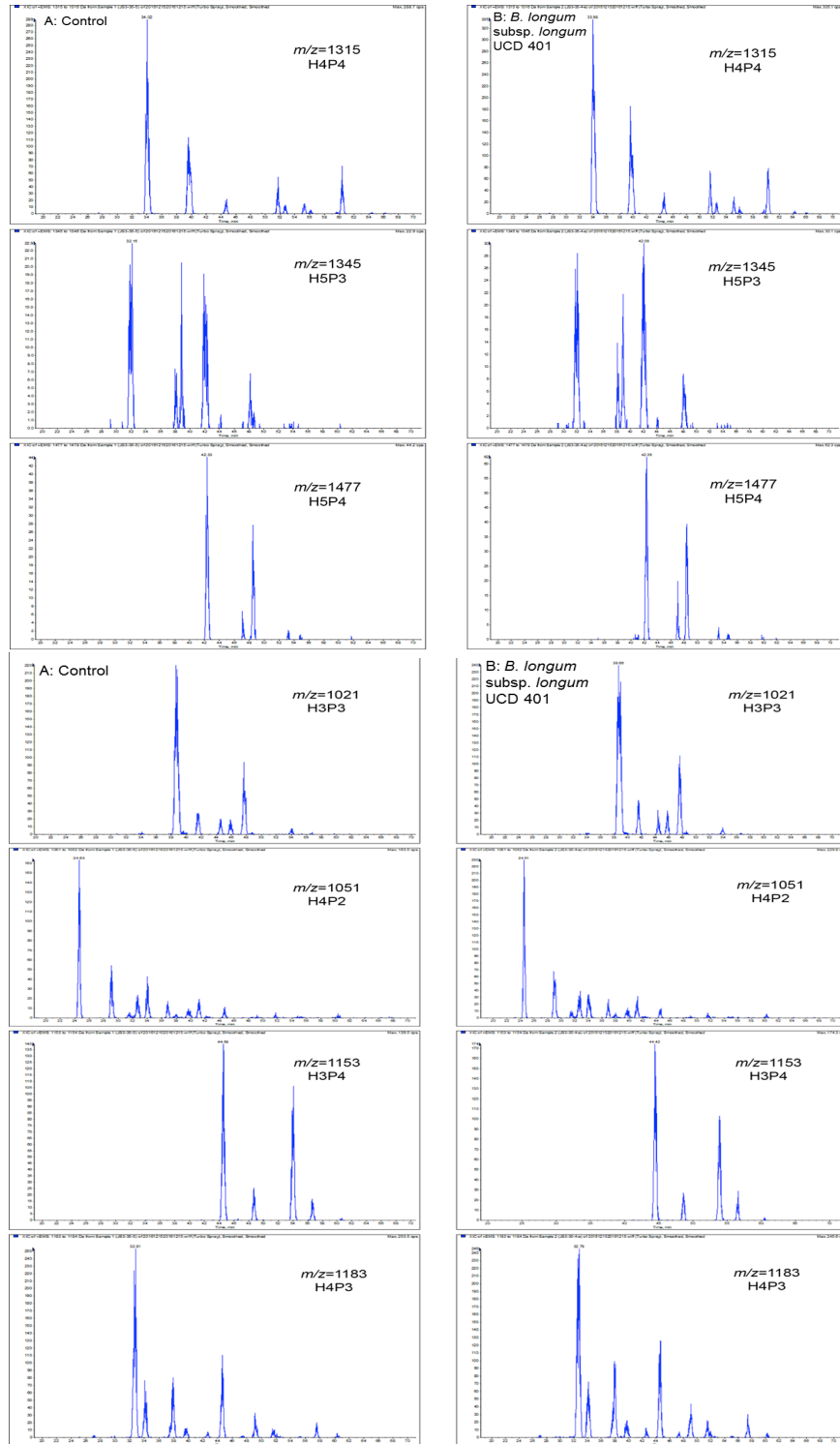
Fig. S5. LC-MS analysis for specific xyloglucan structures by *B. longum* subsp. *longum* UCD 401 fermentation. The extracted ion chromatograms (EIC) of xyloglucans (A) before incubation (control) and (B) after incubation with *B. longum* subsp. *longum* UCD 401.
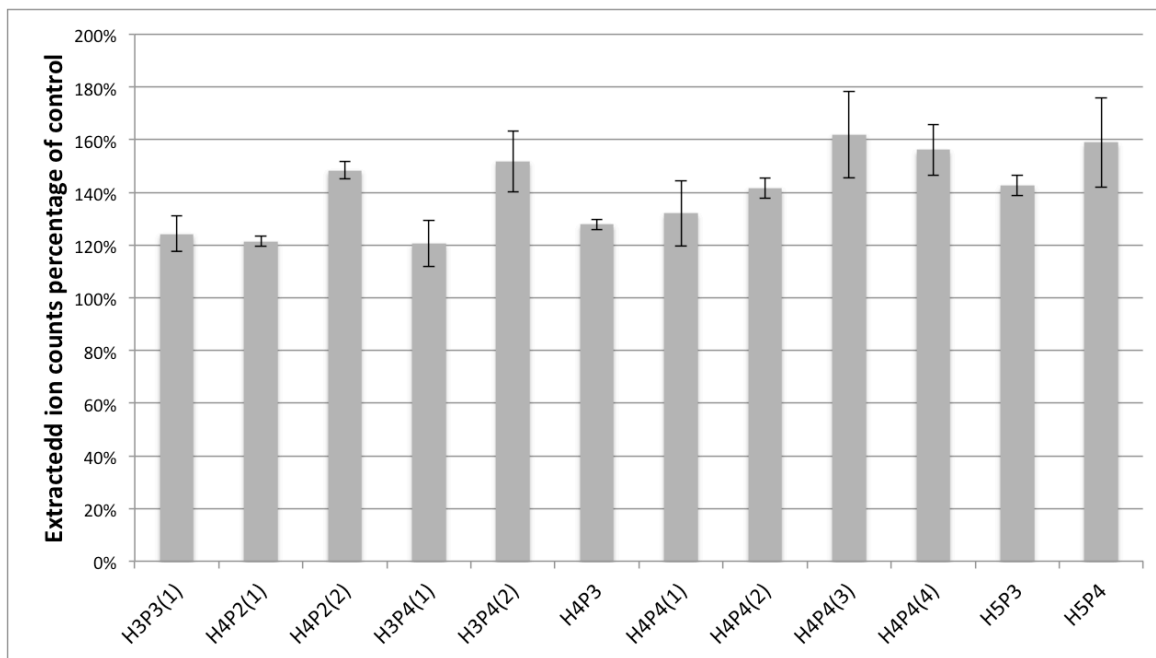
Fig. S6. Abundance of xyloglucan glycoprofiles LC-MS analysis of *B. longum* subsp. *longum* UCD 401 grown on a medium supplemented with 2 % (w/v) cranberry xyloglucans. The quantity of xyloglucans is represented as the percentage of extracted ion counts compared to control (t=0) (see Fig. S5 and Table S1 for full scan MS and detailed structure of xyloglucans)
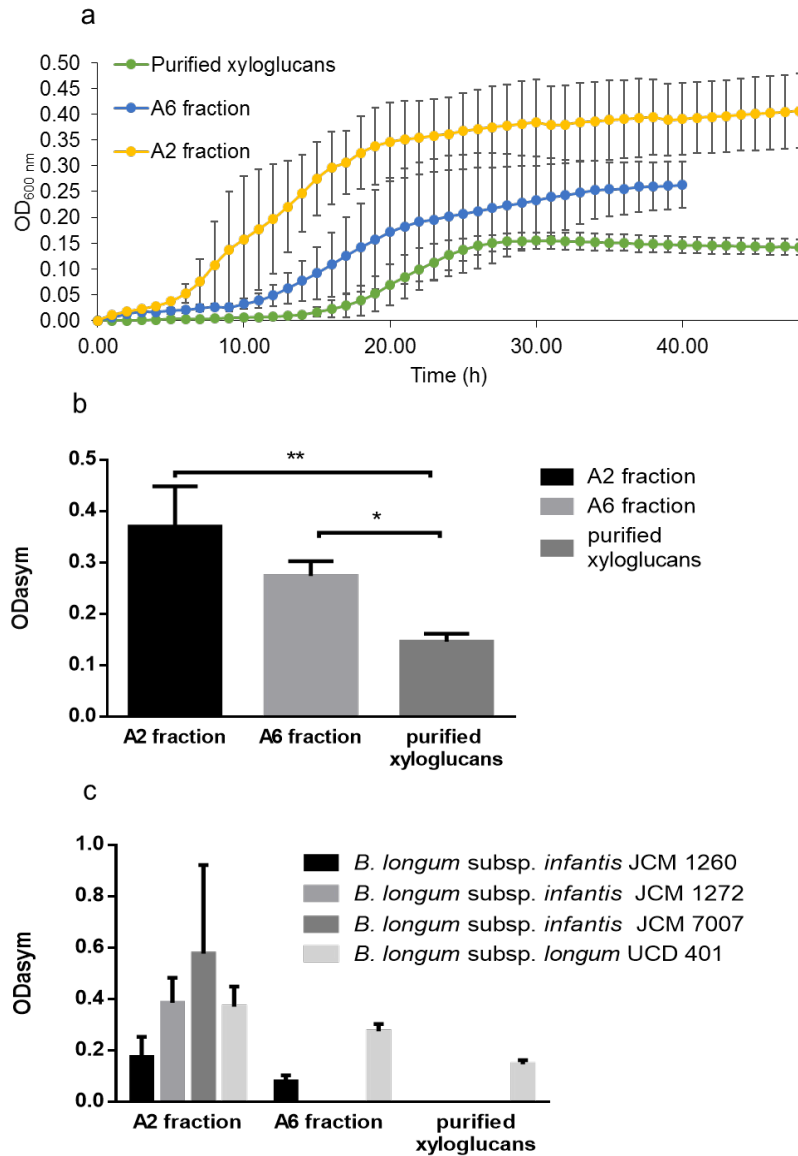
Fig. S7. Comparison of utilization of different xyloglucan fractions. (a) the growth curve of *B. longum* subsp. *longum* UCD 401 on modified MRS containing 2% (w/v) A2 fraction (yellow), A6 fraction (blue), purified xyloglucans (green). (b) Asymptotic OD (OD600 nm at the stationary level) of *B. longum* subsp. *longum* UCD 401 on A2 and A6 fractions and purified xyloglucans. (c) Asymptotic OD (OD600 nm at the stationary level) of *B. longum* subsp. *infantis* JCM 1260, *B. longum* subsp. *infantis* JCM 1272, *B. longum* subsp. *infantis* JCM 7007 and *B. longum* subsp. *longum* UCD 401 on A2 and A6 fractions and purified xyloglucans
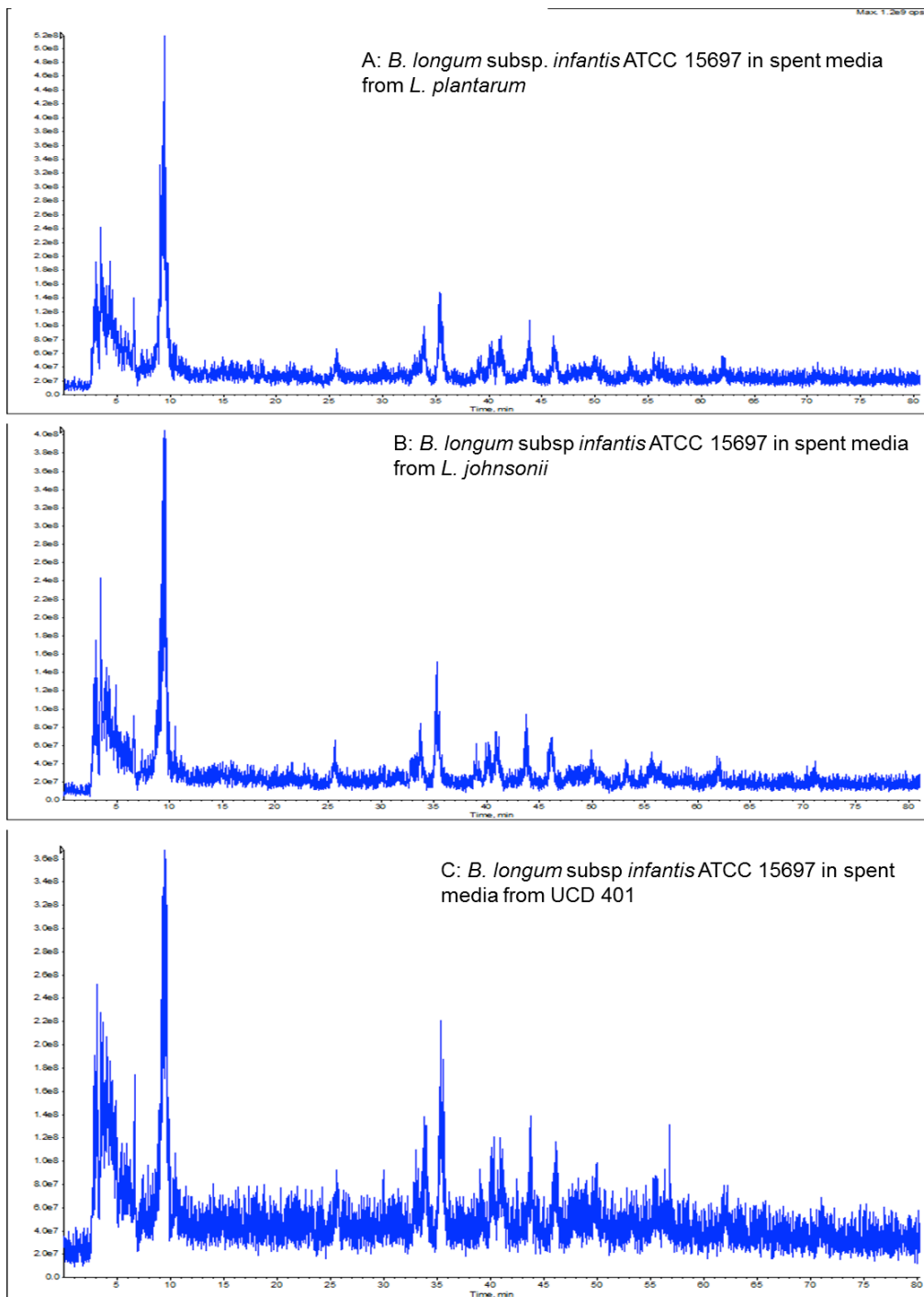
Fig. S8. LC-MS analysis of xyloglucans remaining after syntropic interactions of *B. longum* subsp. *infantis* ATCC 15697 between (A) *Lactobacillus plantarum* ATCC BAA-793, (B) *Lactobacillus plantarum* ATCC BAA-793 and (C) *B. longum* subsp. *longum* UCD 401 (see Fig. S5 for full scan MS and detailed structure of xyloglucans remaining after fermentation of three strains)
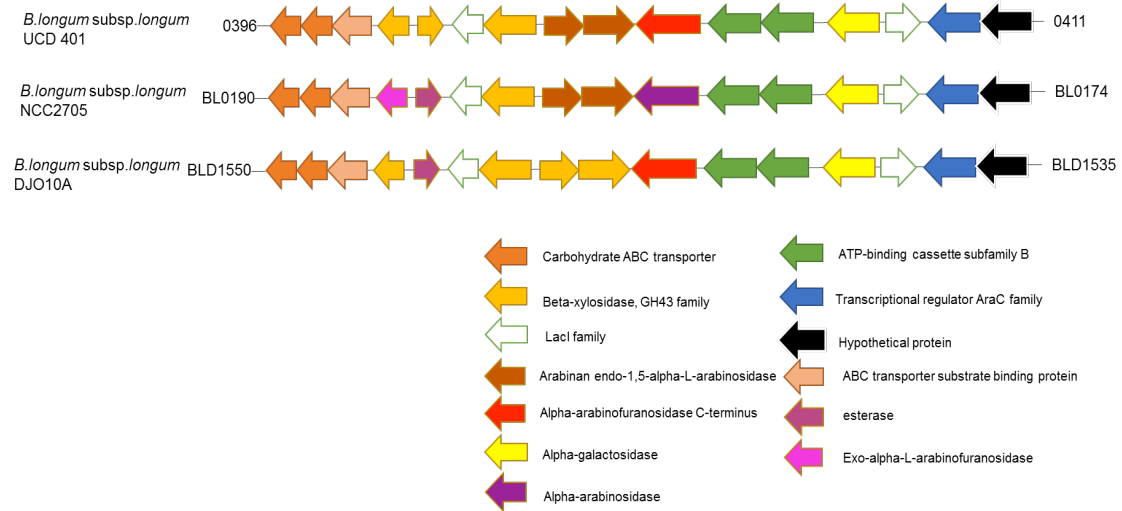
Fig. S9. Genomic regions putatively linked with xyloglucan/arabinoxylose utilization in *B. longum* strains. Gene orthologous annotations for *B. longum* subsp. *longum* UCD 401 were obtained from genomic sequence available as draft in the Joint Genome Institute Integrated Microbiome Genomes and Microbiome platform (IMG). Genes are represented by arrows and are colored according to predicted function (not depicted according to scale).
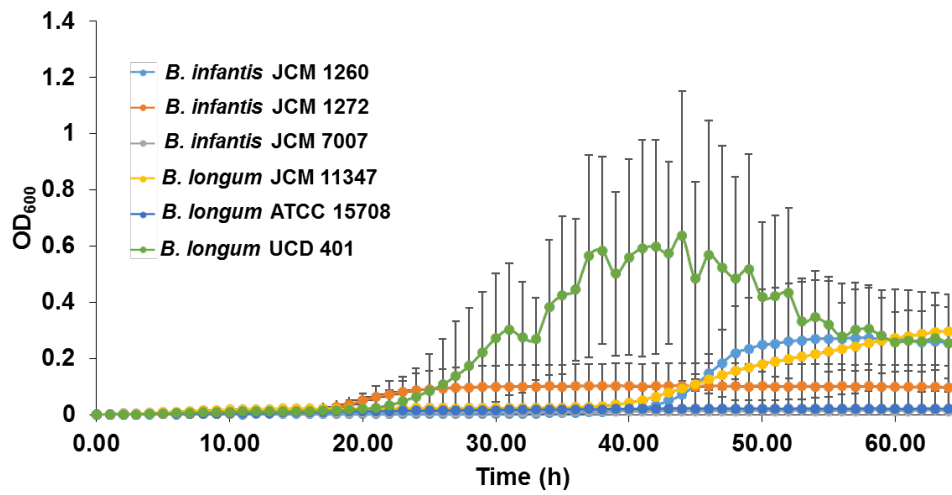
Fig. S10. Growth curves of *B. longum* subsp. *infantis* JCM 1260, *B. longum* subsp. *infantis* JCM 1272, *B. longum* subsp. *infantis* JCM 7007, *B. longum* subsp. *longum* JCM 11347, *B. longum* subsp. *longum* ATCC 15708, *B. longum* subsp. *longum* UCD 401 on modified MRS containing 2 % (w/v) arabinose with triplicates.

Table S1. MALDI-TOF Mass Spectrometry of cranberry xyloglucans with sodium adduct ions, composition and tentative assignments[a]

[M+Na]$^+$	Composition	Assigned structure
923	H_3P_3	SXG, XSG
953	H_4P_2	SGGG
1055	H_3P_4	SSG, GSS
1085	H_4P_3	GSXG
1217	H_4P_4	SSGG
1247	H_5P_3	SXGGG
1379	H_5P_4	SSGGG

[a]H: hexose, P: pentose, G: β-D-glucopyranosyl (β-D-Glc*p*), X: β-D-Glc*p* substituted at O-6 position with α-D-xylopyranosyl (α-D-Xyl*p*), S: X substituted at O-2 position of α-D-xyl*p* with α-D-arabinofuranosyl (α-D-Ara*f*).