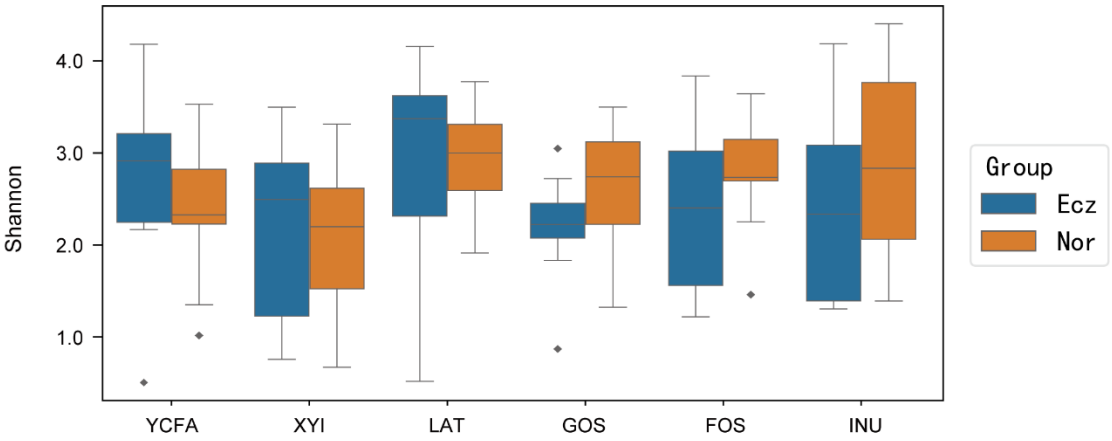
Supplementary information

Supplementary Table S1. The comparison of attribution of network between Ecz and Nor.

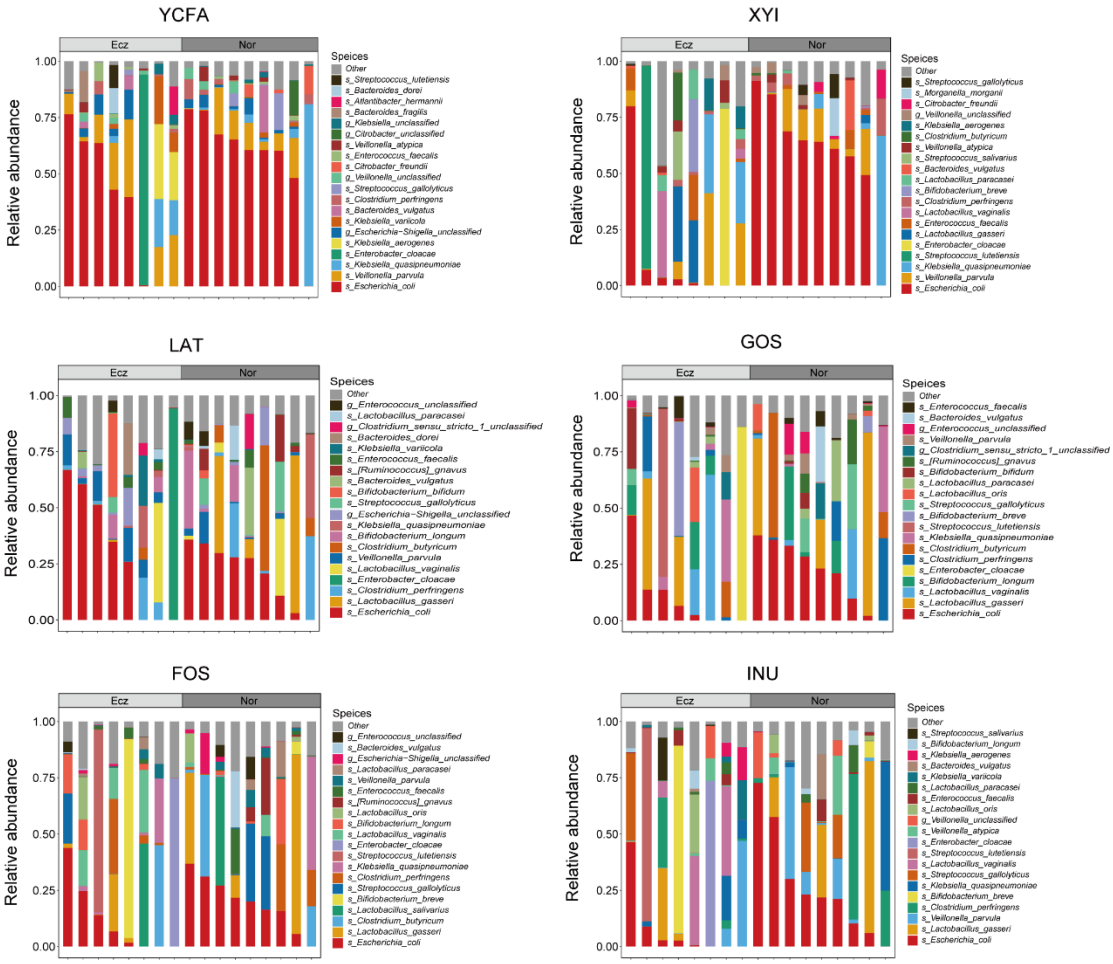
Network index	Group	Feces	YCFA	XYI	LAT	GOS	FOS	INU	p value	q value
Number of nodes	NC	47	41	44	42	38	42	44	0.5117	0.4594
	EC	44	41	39	41	42	42	43		
Number of edges	NC	133	111	118	90	81	100	115	0.3176	0.4419
	EC	87	108	93	79	103	94	116		
Negative edge (negative edge rate) *	NC	65 (49%)	42 (38%)	40 (34%)	40 (44%)	26 (32%)	24 (24%)	44 (38%)	0.0012	0.0047
	EC	24 (28%)	22 (20%)	14 (15%)	11 (14%)	9 (9%)	21 (22%)	23 (20%)		
Average neighbors	NC	5.66	5.42	5.36	4.29	4.46	4.76	5.23	0.3829	0.4419
	EC	3.96	5.27	4.90	4.05	4.91	4.48	5.40		
Characteristic path length	NC	2.64	2.52	3.15	3.06	2.61	3.57	2.83	0.0379	0.1020
	EC	3.60	3.14	2.92	4.29	4.65	3.87	2.87		
Clustering coeffiecient	NC	0.35	0.33	0.57	0.37	0.36	0.58	0.50	0.3339	0.4419
	EC	0.44	0.54	0.51	0.49	0.55	0.57	0.45		
Network density	NC	0.12	0.14	0.13	0.11	0.13	0.12	0.12	0.4814	0.4594
	EC	0.09	0.13	0.13	0.11	0.12	0.11	0.13		
Network heterogeneity	NC	0.43	0.45	0.45	0.38	0.43	0.39	0.48	0.1200	0.2425
	EC	0.47	0.47	0.45	0.53	0.55	0.42	0.44		
Network centralization	NC	0.12	0.12	0.14	0.07	0.11	0.11	0.19	0.9755	0.7882
	EC	0.10	0.15	0.15	0.08	0.13	0.12	0.12		

*** q < 0.05**



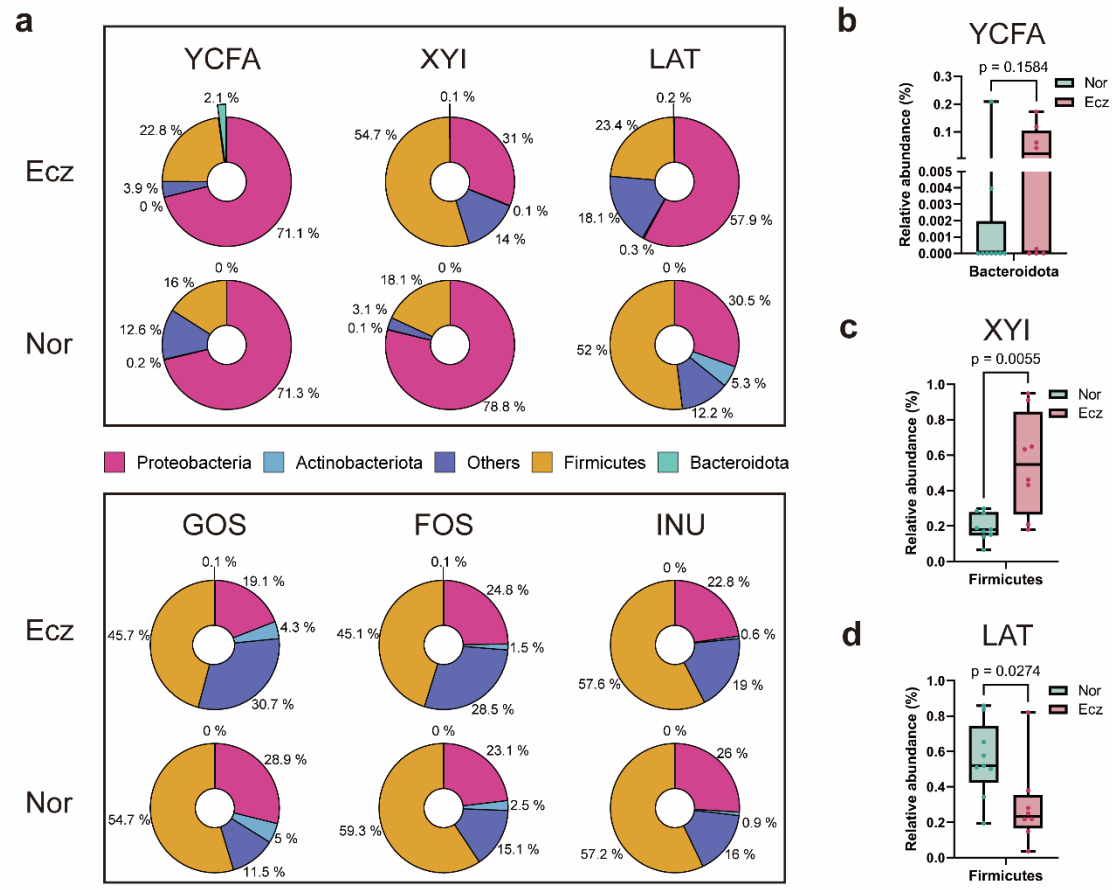
Supplementary Fig. S1 Comparison of α-diversity in fermentation broths' microbiota between Ecz and Nor.

Box plots of the Shannon index of each fermentation broth showed no statistical significance. YCFA: the basic medium without carbon source; the medium containing YCFA and sole carbon source of xylitol (XYI), lactose (LAT), GOS, FOS, and inulin (INU). Data in box plots are presented as medians and interquartile ranges, whiskers: 1.5x interquartile, points: outliers, and statistical analysis was performed using the Mann-Whitney test.



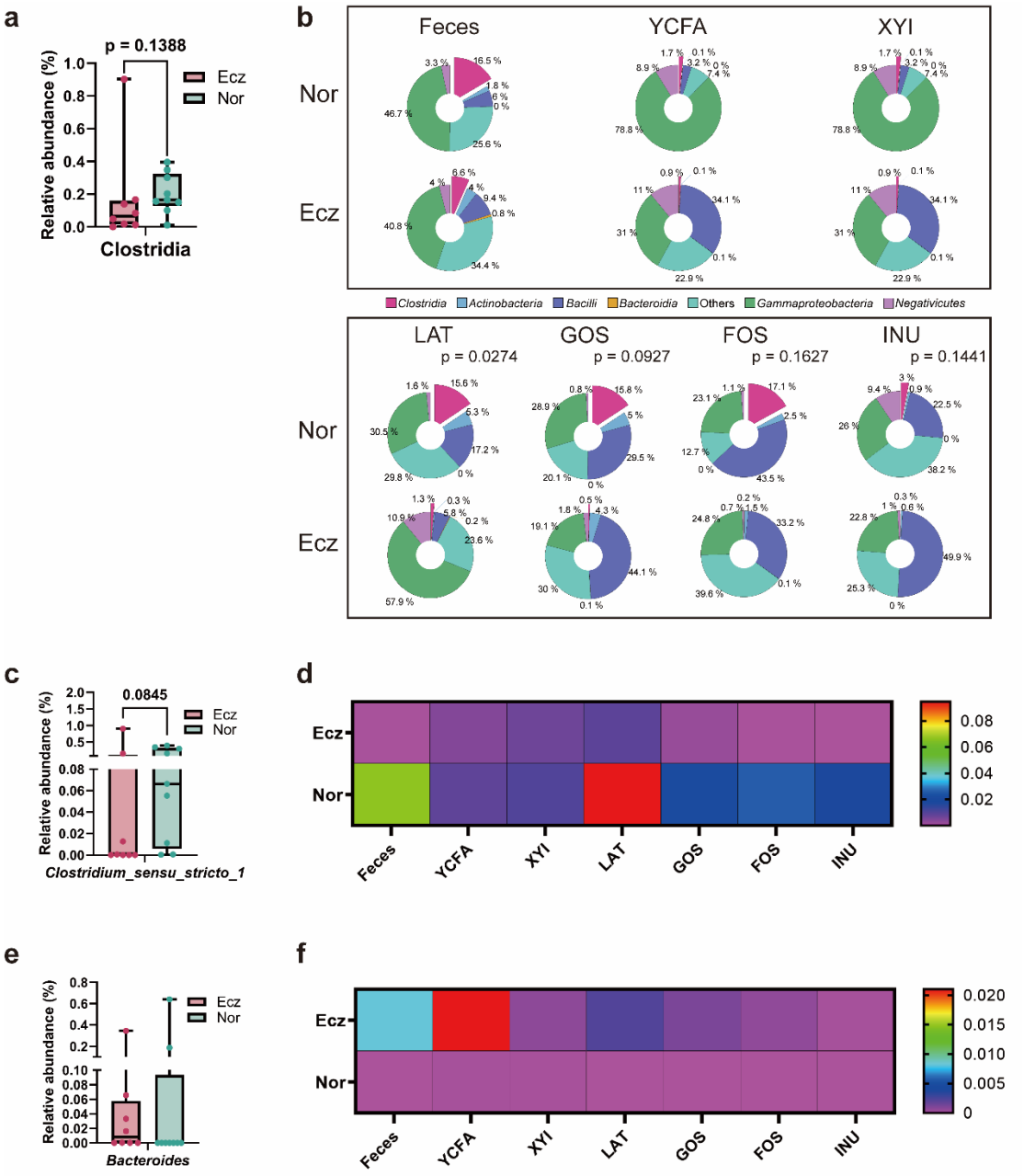
Supplementary Fig. S2 Comparison of top 20 species in fermentation broths' microbiota between Ecz and Nor.

The stacked column chart of top 20 species in each broth. YCFA: the basic medium without carbon source; the medium containing YCFA and sole carbon source of xylitol (XYI), lactose (LAT), galactooligosaccharides (GOS), fructooligosaccharides (FOS), and inulin (INU).



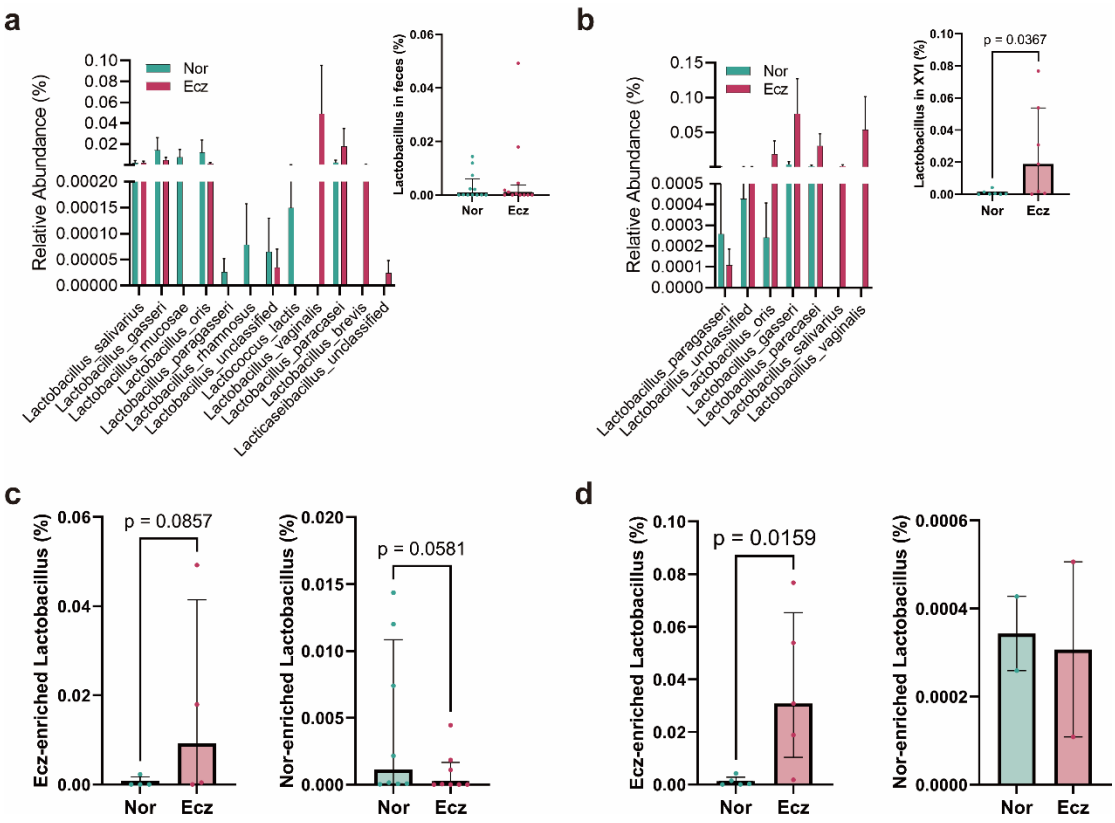
Supplementary Fig. S3 Comparison of relative abundance at phylum level after fermentation.

a: Pie chart at phylum level between Ecz and Nor after fermentations. Bacteroidota are highlighted; b: Box plot of phylum Bacteroidota in YCFA; c: Box plot of phylum Firmicutes in XYI ; d: Box plot of phylum Firmicutes in LAT. YCFA: the basic medium without carbon source; the medium containing YCFA and sole carbon source of xylitol (XYI), lactose (LAT). Data in box plots are presented as: box, medians with interquartile ranges; whiskers: min to max; points: all data. Statistical analysis was performed using Mann-Whitney test and $p < 0.2$ was shown.



Supplementary Fig. S4 Taxa with the same intergroup variation trends between Ecz and Nor in feces and their broths.

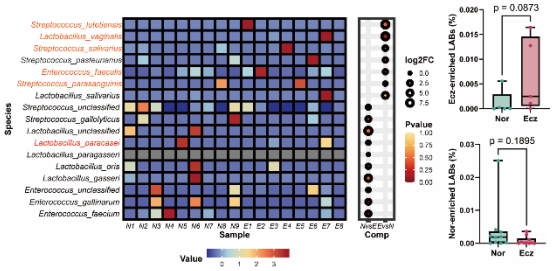
a: Boxplot of class Clostridia in feces; b: Pie chart of class level in feces and broths, Clostridia is highlighted and its statistical difference between two groups was calculated using Mann-Whitney test, and the significant difference was shown in LAT; c: Boxplot of genus *Clostridium_sensu_stricto_1* in feces; d: Heatmap of *Clostridium_sensu_stricto_1* in feces and broths, with an increased trend in Nor group; e: Boxplot of genus *Bacteroides* in feces; f: Heatmap of genus *Bacteroides* in feces and broths, with an increased trend in Ecz group. Data in boxplot are presented as medians with interquartile ranges and analyzed using Mann-Whitney test, and $p < 0.2$ was shown.



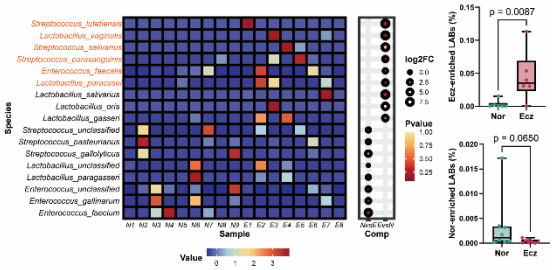
Supplementary Fig. S5 Comparison of relative abundance of *Lactobacillus* in feces and after XYI fermentation.

a: The relative abundance of each species of *Lactobacillus* in feces, of which the sum showed no significant difference between Ecz and Nor (upper right panel); b: The relative abundance of each species of *Lactobacillus* in xylitol (XYI) broth, of which the sum was significantly higher in Ecz compared to Nor (upper right panel); c: Nor-enriched *Lactobacillus* and Ecz-enriched *Lactobacillus* were compared in their total relative abundance between two groups in feces; d: Nor-enriched *Lactobacillus* and Ecz-enriched *Lactobacillus* were compared in their total relative abundance between two groups in XYI broth. Only the top 60 species were analyzed. Data in interleaved bar are presented as mean and SEM. Data in scatter plot with bar are presented as medians with interquartile ranges. Mann-Whitney test was used for statistical analysis, and $p < 0.1$ is shown.

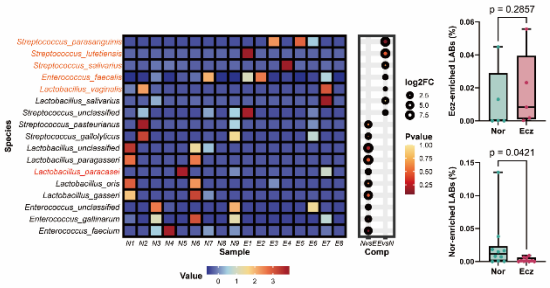
YCFA



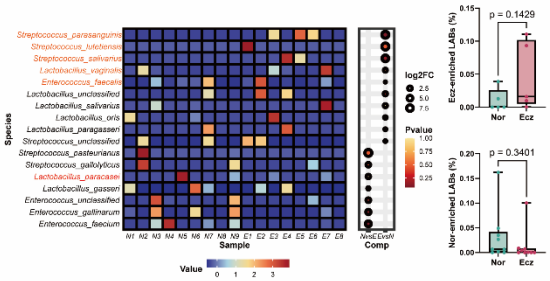
XYI



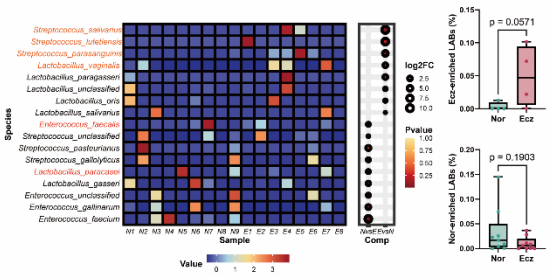
LAT



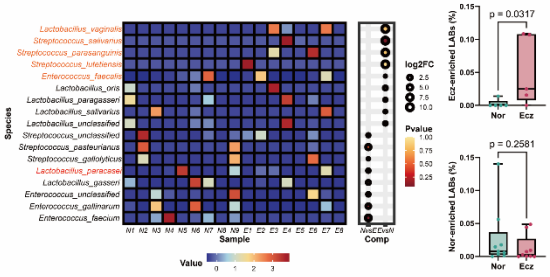
GOS



FOS

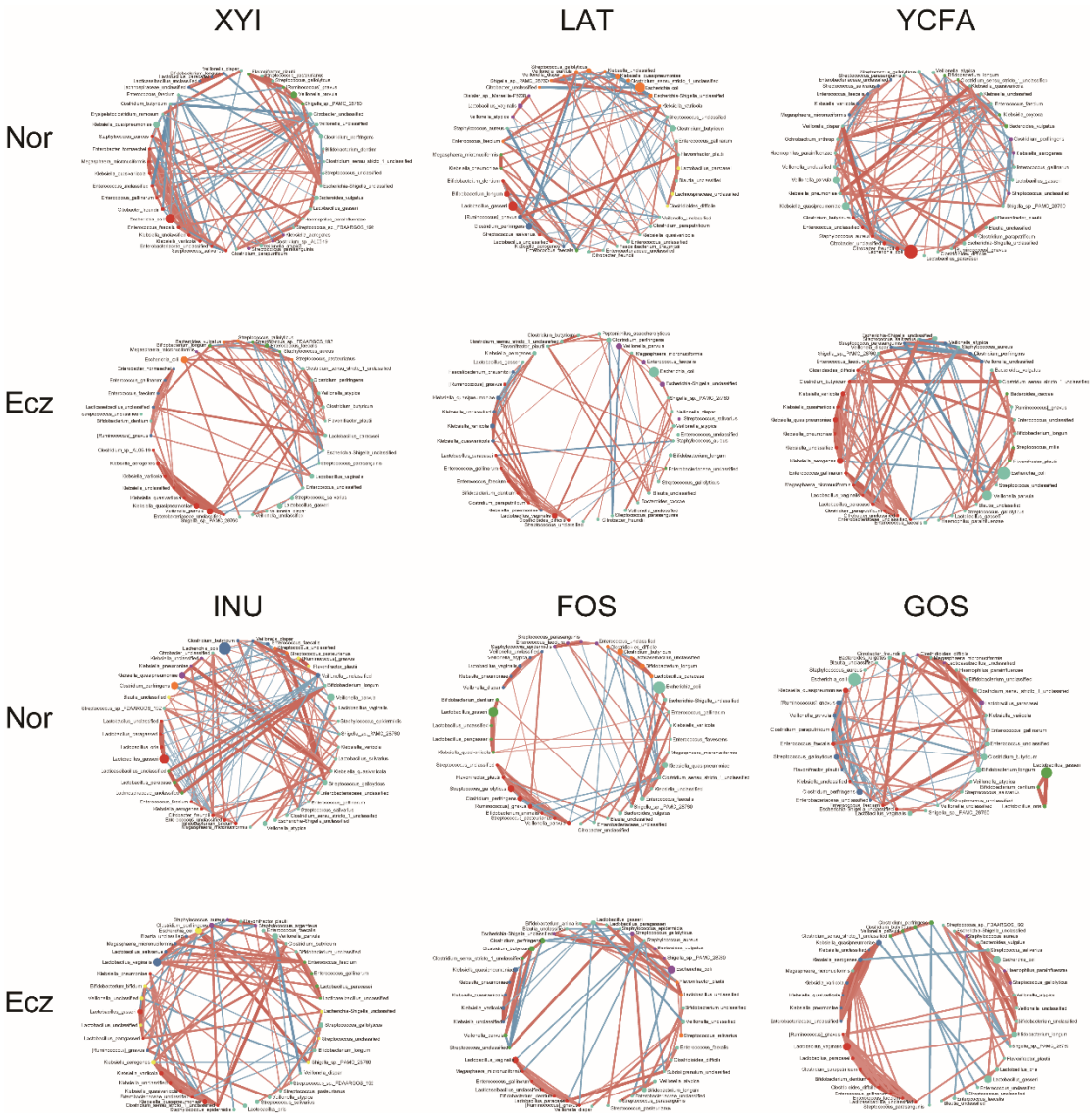


INU



Supplementary Fig. S6 Comparison of LABs in fermentation broths between Ecz and Nor.

Left panel: Heatmap of relative abundance of LABs in each broth. Species belonging to faecal Ecz-enriched LABs are shown in red. **Right upper panel:** Box plot of the total relative abundance of faecal Ecz-enriched LABs which were still divided into the Ecz-enriched cluster (shown in left panel). **Right lower panel:** Box plot of the total relative abundance of Nor-enriched LABs in the left panel. YCFA: the basic medium without carbon source; the medium containing YCFA and sole carbon source of xylitol (XYI), lactose (LAT), galactooligosaccharides (GOS), fructooligosaccharides (FOS), and inulin (INU). Data in box plots are presented as: box, medians with interquartile ranges; whiskers: min to max; points: all data. Mann-Whitney test was used for statistical analysis.



Supplementary Fig. S7 The co-occurrence network diagrams of fermentation broths' microbiota in Nor and Ecz.

The network diagrams were drawn using Cytoscape. The relative abundance of nodes (species) is represented by size, and clusters (modules) are distinguished by color. Red edges indicate positive correlations, while blue edges indicate negative correlations. YCFA: the basic medium without carbon source; the medium containing YCFA and sole carbon source of xylitol (XYI), lactose (LAT), galactooligosaccharides (GOS), fructooligosaccharides (FOS), and inulin (INU).