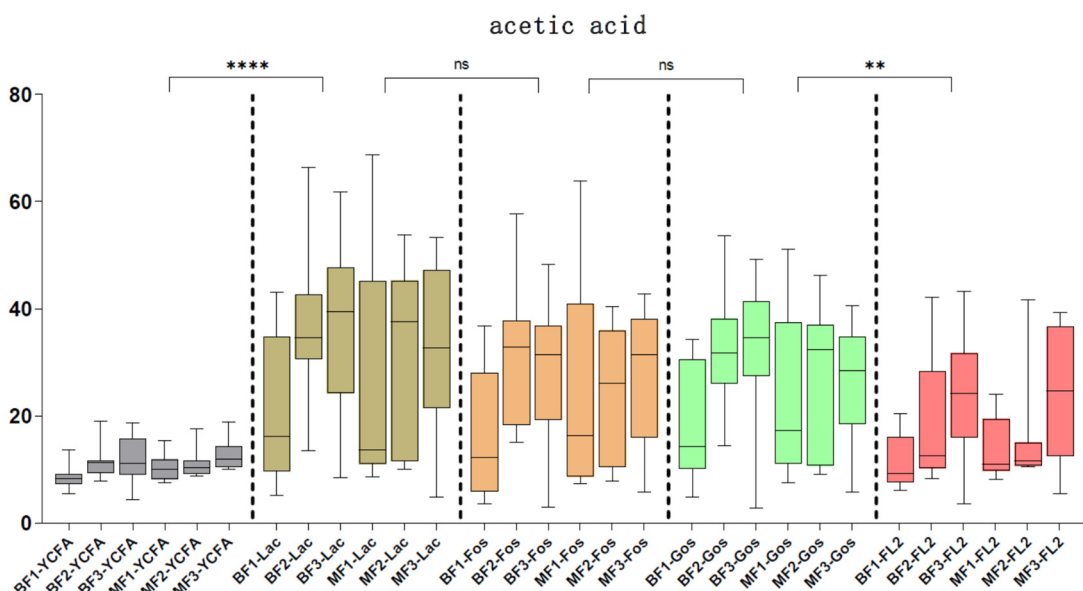
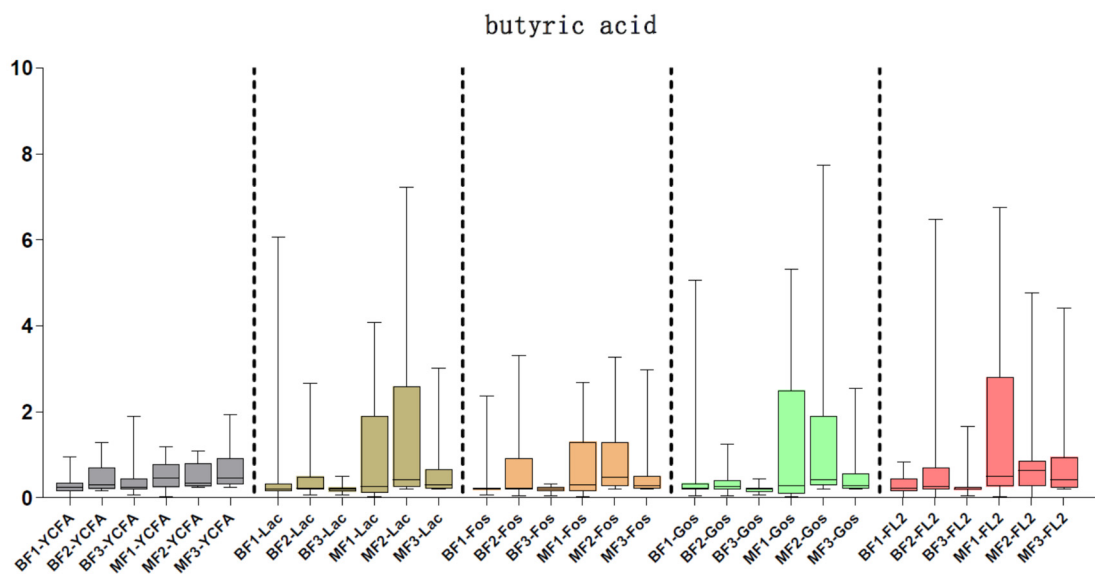
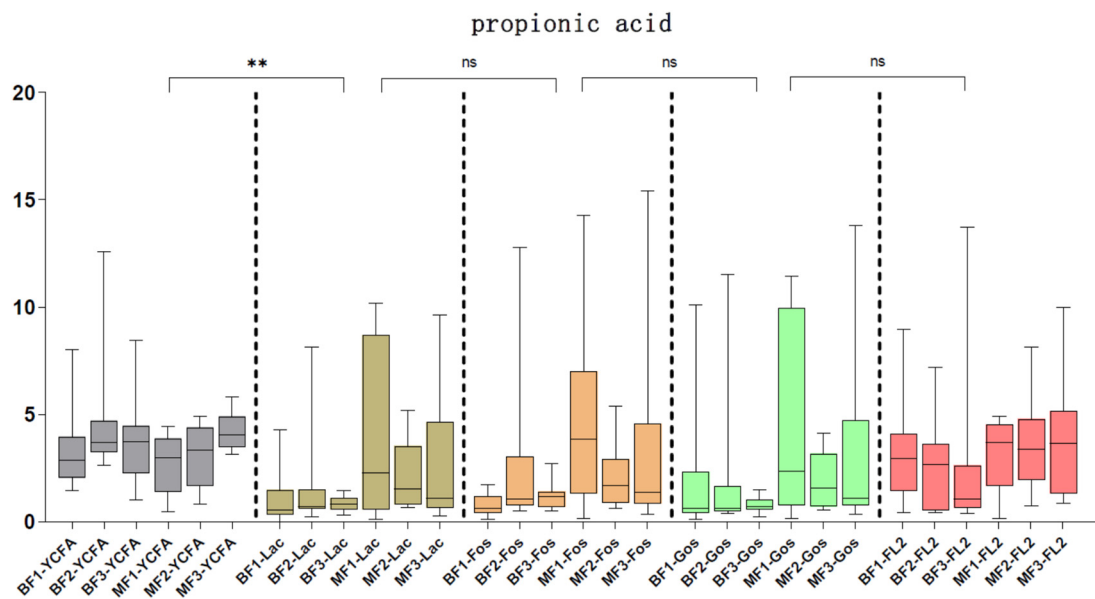
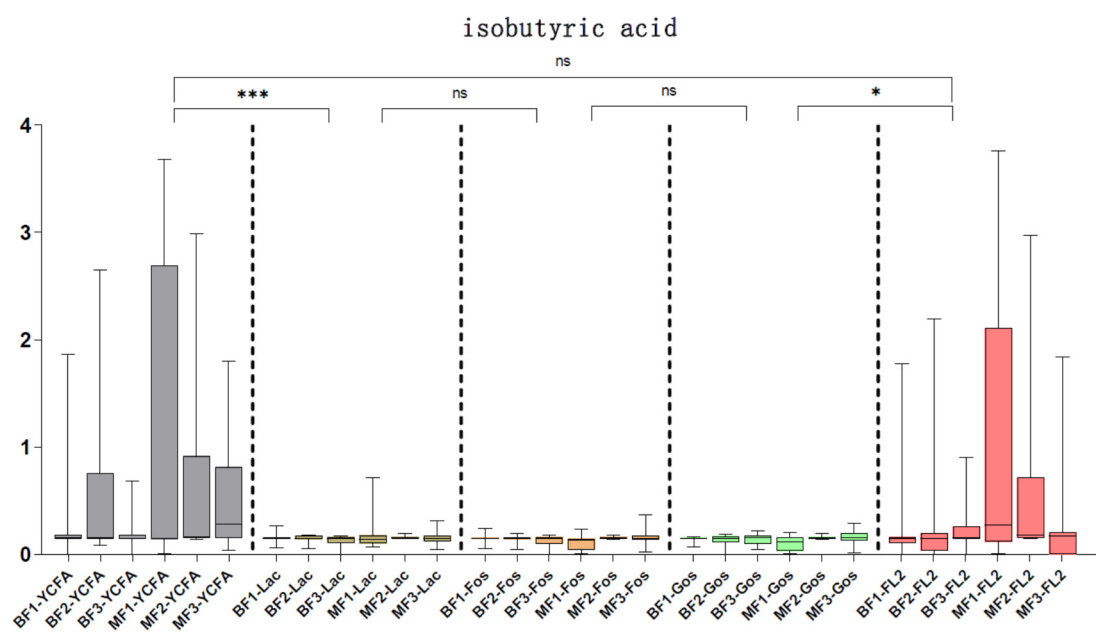
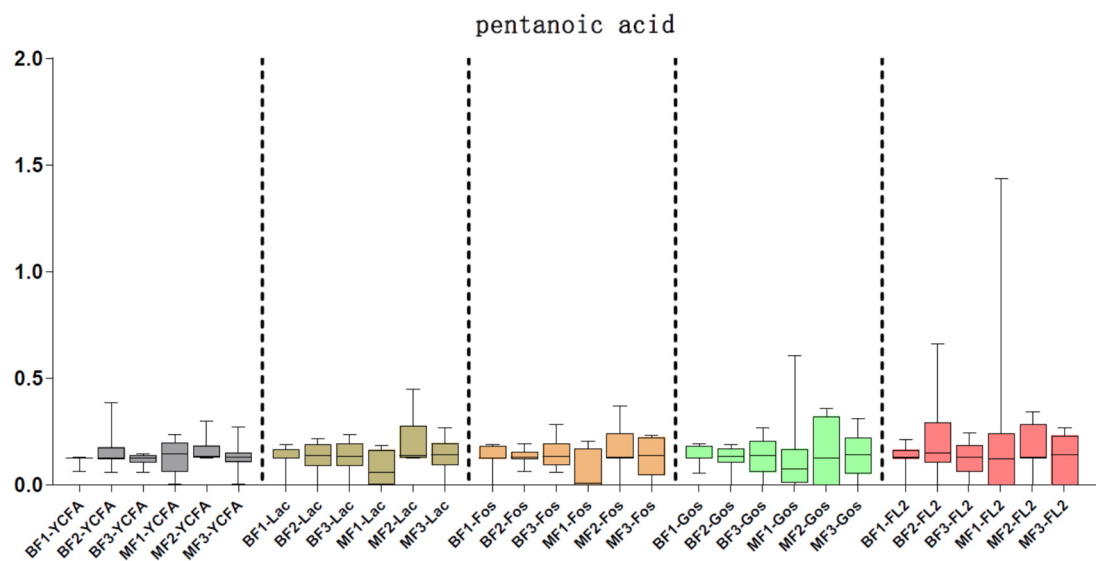


Figure S1. Comparison of *in vitro* simulated fermented fecal ammonia levels in infants and toddlers fed differently and at different growth stages







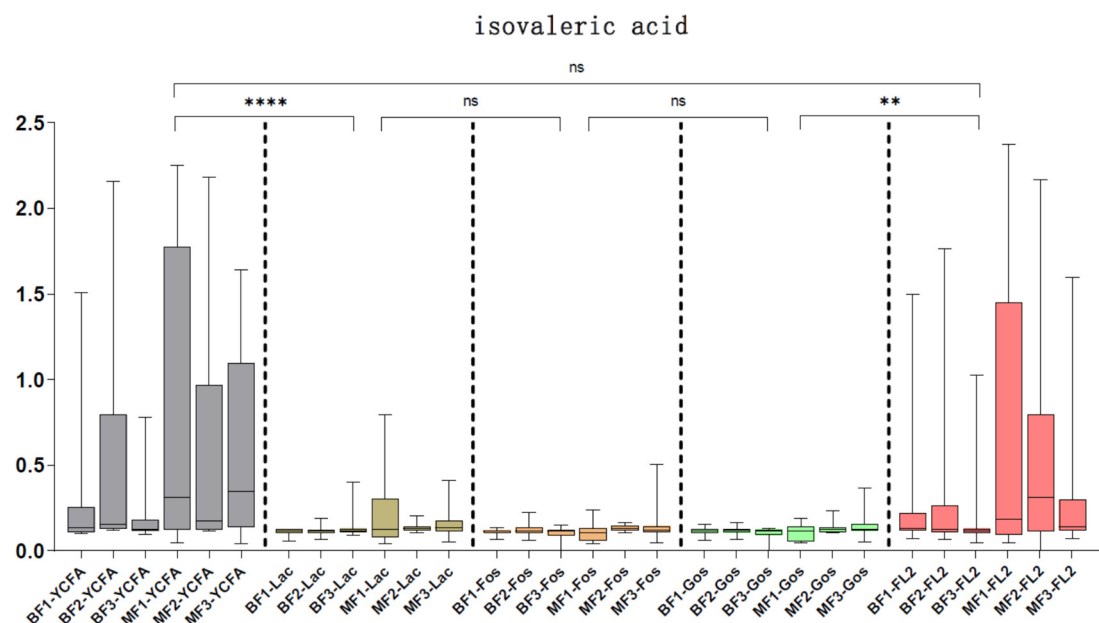


Figure S2. Comparison of *in vitro* simulated fermentation of SCFA production by fecal bacteria from infants and toddlers fed differently and at different growth stages

Data were expressed as the mean \pm SEM. Differences are considered significant at $P < 0.05$ (*), $P < 0.01$ (**), $P < 0.001$ (***) and $P < 0.0001$ (****)

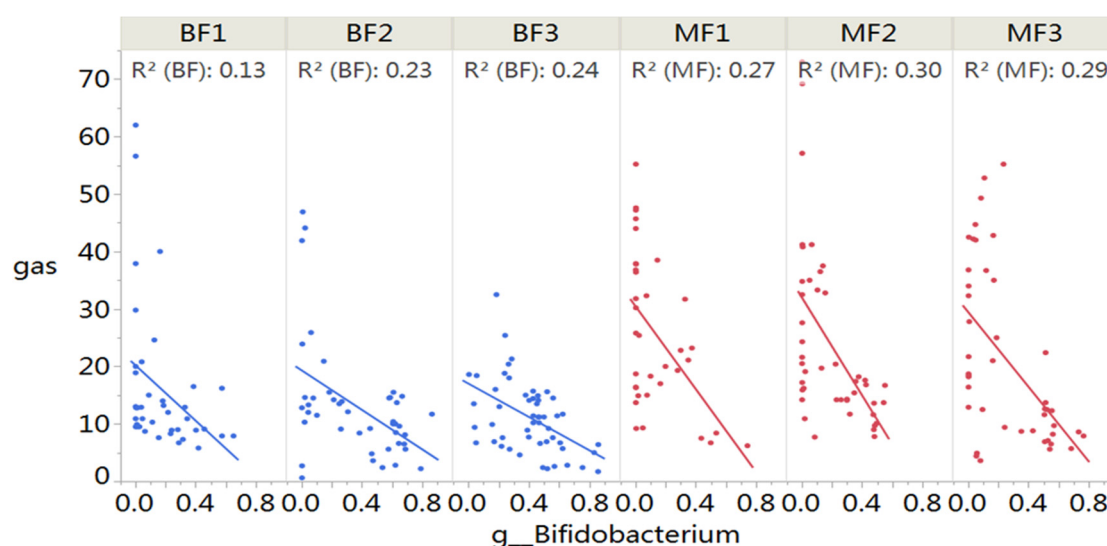


Figure S3 Correlation analysis between *in vitro* fermentation gas production and abundance of *Bifidobacterium* spp. in infants and toddlers fed differently and at different growth stages

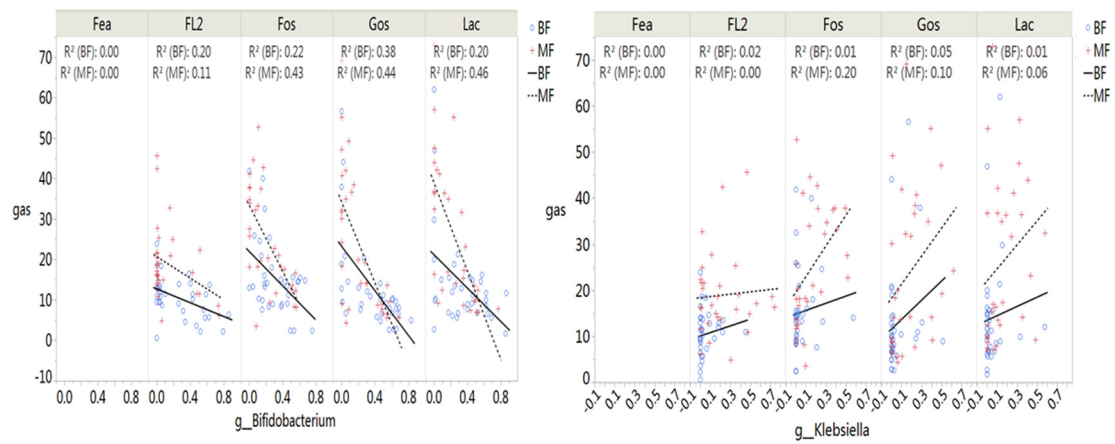


Figure S4 Correlation analysis between fermentation gas production and abundance of *Bifidobacterium* and *Klebsiella* in fecal bacteria and carbon sources in media from different feeding methods

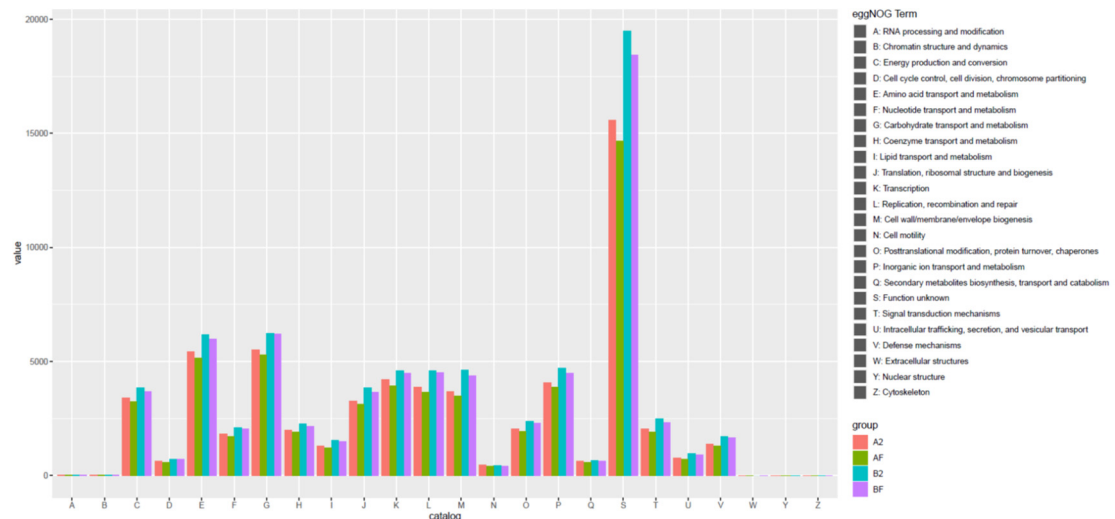


Figure S5. Analysis of differences in functional gene enrichment in fecal bacteria from different feeding methods grown on media with different carbon sources (2'-FL and FOS). A2 represent the fermentation of intestinal flora from MF in the medium containing the carbon source of 2'-FL; AF represent the fermentation of intestinal flora from MF in the medium containing the carbon source of FOS; B2 represent the fermentation of intestinal flora from BF in the medium containing the carbon source of 2'-FL; BF represent the fermentation of intestinal flora from BF in the medium containing the carbon source of FOS.

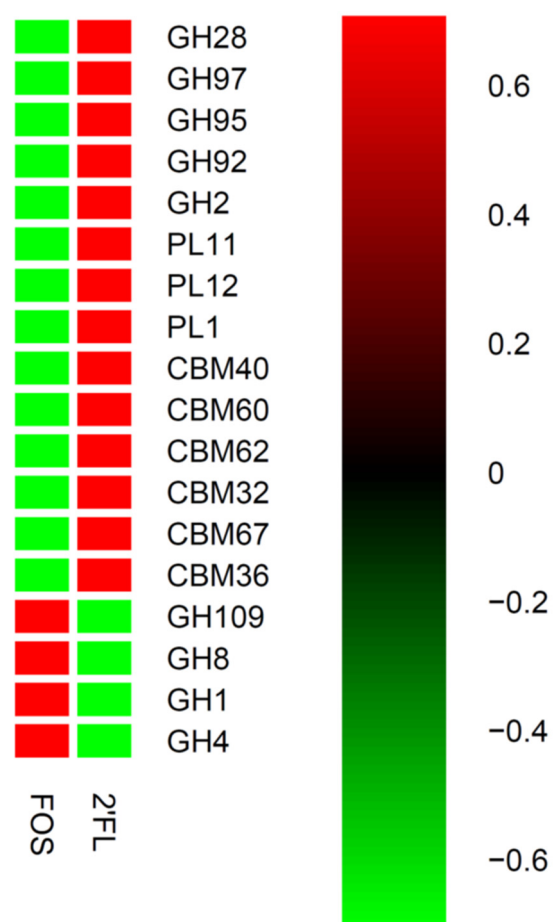


Figure S6. The heat map of the CAZY families showing the enrichment of genes related to oligosaccharide metabolism in infant fecal bacteria cultured in medium with two different carbon sources (2'-FL and FOS).

Table S1. The results of transcriptome analysis

Group	log2FoldChange	pvalue	padj	gene_name	gene_biotype	gene_description
Kpn vs 2FL Kpn	-4.21	2.10E-02	1.00E+00	SERF1A	protein_coding	small EDRK-rich factor 1A [Source:HGNC Symbol;Acc:HGNC:10755]
Kpn vs 2FL Kpn	-4.26	2.56E-02	1.00E+00	MARK2P17	processed_pseudogene	microtubule affinity regulating kinase 2 pseudogene 17 [Source:HGNC Symbol;Acc:HGNC:50318]
CK vs Kpn	5.707077	0.0098251	1	MARK2P17	processed_pseudogene	microtubule affinity regulating kinase 2 pseudogene 17 [Source:HGNC Symbol;Acc:HGNC:50318]
CK vs Kpn	4.193578	0.0160419	0.933202	SERF1A	protein_coding	small EDRK-rich factor 1A [Source:HGNC Symbol;Acc:HGNC:10755]
Cp vs 2FL Cp	0.80	3.24E-04	1.00E+00	TRIB3	protein_coding	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:HGNC:16228]
Cp vs 2FL Cp	1.01	1.16E-02	1.00E+00	ADM2	protein_coding	adrenomedullin 2 [Source:HGNC Symbol;Acc:HGNC:28898]
Cp vs 2FL Cp	0.48	1.43E-02	1.00E+00	PCK2	protein_coding	phosphoenolpyruvate carboxykinase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:8725]
CK vs Cp	-2.7753	0.0061879	0.999979	ADM2	protein_coding	adrenomedullin 2 [Source:HGNC Symbol;Acc:HGNC:28898]

CK vs Cp	-2.37877	0.0157859	0.999979	TRIB3	protein_coding	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:HGNC:16228]
CK vs Cp	-1.50417	0.0346799	0.999979	PCK2	protein_coding	phosphoenolpyruvate carboxykinase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:8725]