Supplementary Table 3. The species contributing to the difference of gut microbiome between control fermentation at T14, T24, and T36, and the gut microbiome at T0. Bacterial species are presented when the contribution is more than 1%.

| **Taxon** | **Mean T0** | **Mean Control T14** | **Contrib. % Control T14** | **Mean Control T24** | **Contrib. % Control T24** | **Mean Control T36** | **Contrib. % Control T36** |
|---|---|---|---|---|---|---|---|
| *Escherichia_coli* | 0,304 | 0,887 | 48,74 | 0,746 | 38,87 | 0,613 | 29,84 |
| *Bifidobacterium_bifidum* | 0,167 | 0,00557 | 13,45 | 0,00489 | 14,21 | 0,00457 | 15,61 |
| *Bacteroides_dorei* | 0,0342 | 0,0204 | 1,171 | 0,135 | 8,86 | 0,1921 | 15,22 |
| *Bifidobacterium_longum*_subsp,_*longum* | 0,1599 | 0,0208 | 11,62 | 0,0175 | 12,52 | 0,0168 | 13,79 |
| *Bifidobacterium_unidentified* | 0,124 | 0,0215 | 8,553 | 0,0227 | 8,9 | 0,0277 | 9,272 |
| *Enterococcus_faecalis* | 0,0021 | 0,0142 | 1,009 | 0,008 | 0,5186 | 0,0131 | 1,062 |
| *Bacteroides_ovatus*_V975 | 0,000941 | 0,000941 | 0,0218 | 0,0169 | 1,402 | 0,0284 | 2,648 |

Supplementary Table 4. The species contributing to the difference of gut microbiome between GOS/inulin fermentation at T14, T24, and T36, and the gut microbiome at T0. Bacterial species are presented when the contribution is more than 1%.

| **Taxon** | **Mean T0** | **Mean GOS/inulin T14** | **Contrib. % GOS/inulin T14** | **Mean GOS/inulin T24** | **Contrib. % GOS/inulin T24** | **Mean GOS/inulin T36** | **Contrib. % GOS/inulin T36** |
|---|---|---|---|---|---|---|---|
| *Escherichia_coli* | 0,304 | 0,716 | 46,43 | 0,607 | 43,07 | 0,549 | 33,46 |
| *Bifidobacterium_bifidum* | 0,167 | 0,0094 | 17,68 | 0,00885 | 22,35 | 0,00996 | 21,36 |
| *Bifidobacterium_longum*_subsp,_*longum* | 0,1599 | 0,0587 | 11,39 | 0,1448 | 2,151 | 0,2089 | 6,684 |
| *Bifidobacterium_unidentified* | 0,124 | 0,1512 | 3,07 | 0,165 | 5,867 | 0,1919 | 9,279 |
| *Bacteroides_dorei* | 0,0342 | 0,0087 | 2,867 | 0,00985 | 3,448 | 0,00518 | 3,956 |

Supplementary Table 5. The species contributing to the difference of gut microbiome between 3-FL fermentation at T14, T24, and T36, and the gut microbiome at T0. Bacterial species are presented when the contribution is more than 1%.

| **Taxon** | **Mean T0** | **Mean 3-FL T14** | **Contrib. % 3-FL T14** | **Mean 3-FL T24** | **Contrib. % 3-FL T24** | **Mean 3-FL T36** | **Contrib. % 3-FL T36** |
|---|---|---|---|---|---|---|---|
| *Escherichia_coli* | 0,304 | 0,759 | 46,41 | 0,706 | 38,08 | 0,611 | 32,72 |
| *Bifidobacterium_bifidum* | 0,167 | 0,00264 | 16,72 | 0,000538 | 15,7 | 0,00141 | 17,56 |
| *Bifidobacterium_longum*_subsp,_*longum* | 0,1599 | 0,0713 | 9,036 | 0,0589 | 9,554 | 0,0621 | 10,4 |
| *Bifidobacterium_unidentified* | 0,124 | 0,0769 | 4,791 | 0,0277 | 9,099 | 0,0351 | 9,442 |
| *Enterococcus_faecalis* | 0,0021 | 0,0357 | 3,431 | 0,037 | 3,295 | 0,0629 | 6,465 |
| *Bacteroides_dorei* | 0,0342 | 0,0177 | 1,683 | 0,122 | 8,328 | 0,1286 | 10,04 |

Supplementary Table 6. The species contributing to the difference of gut microbiome between LNT2 fermentation at T14, T24, and T36, and the gut microbiome at T0. Bacterial species are presented when the contribution is more than 1%.

| **Taxon** | **Mean T0** | **Mean LNT2 T14** | **Contrib. % LNT2 T14** | **Mean LNT2 T24** | **Contrib. % LNT2 T24** | **Mean LNT2 T36** | **Contrib. % LNT2 T36** |
|---|---|---|---|---|---|---|---|
| *Escherichia_coli* | 0,304 | 0,729 | 49,1 | 0,7 | 48,34 | 0,597 | 44,39 |
| *Bifidobacterium_bifidum* | 0,167 | 0,00364 | 18,79 | 0,0051 | 19,67 | 0,00887 | 23,84 |
| *Bifidobacterium_longum*_subsp,_*longum* | 0,1599 | 0,0982 | 7,12 | 0,0851 | 9,121 | 0,0995 | 9,132 |
| *Bacteroides_dorei* | 0,0342 | 0,00864 | 2,945 | 0,0117 | 2,744 | 0,00156 | 4,931 |
| *Bifidobacterium_unidentified* | 0,124 | 0,1102 | 1,662 | 0.117 | 0.8893 | 0,0764 | 7,181 |
| *Enterococcus_faecalis* | 0,0021 | 0,00698 | 0,5626 | 0,0101 | 0,975 | 0,00633 | 0,6395 |