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CORRECTION
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# Corrigendum: Sialyllactose and Galactooligosaccharides Promote Epithelial Barrier Functioning and Distinctly Modulate Microbiota Composition and Short Chain Fatty Acid Production *In Vitro*

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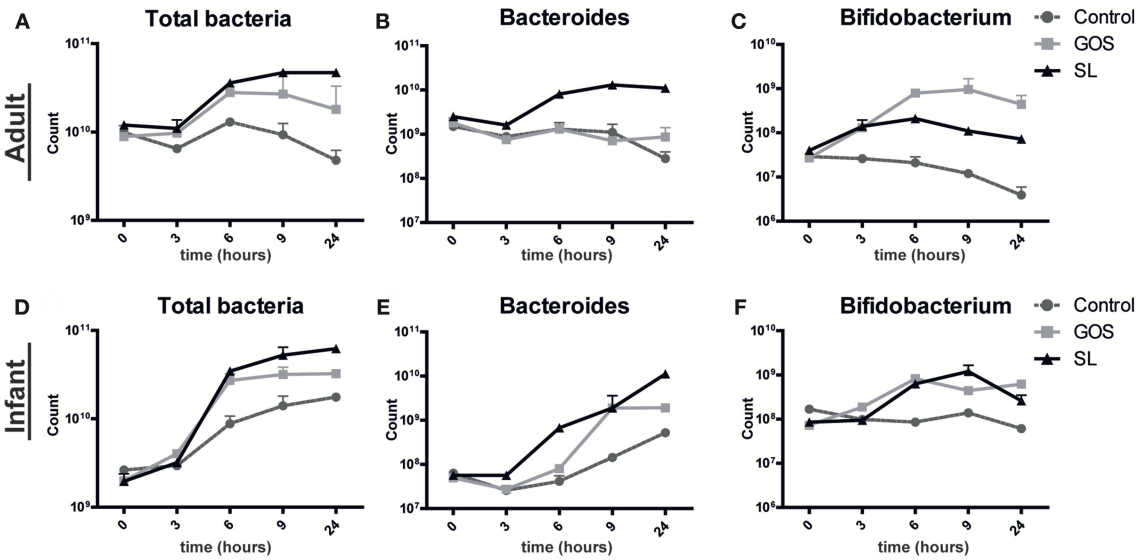
## A Corrigendum on

**Sialyllactose and Galactooligosaccharides Promote Epithelial Barrier Functioning and Distinctly Modulate Microbiota Composition and Short Chain Fatty Acid Production *In Vitro*** *by Perdijk, O., van Baarlen, P., Fernandez-Gutierrez, M. M., van den Brink, E., Schuren, F. H. J., Brugman, S., et al. (2019). Front. Immunol. 10:94. doi: 10.3389/fimmu.2019.00094*

In the original article, there was a mistake in **Figure 3** as published. **Figure 3C** and **Figure 3F** were mistakenly swapped. The corrected **Figure 3** appears below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.




**G** **Adult**

| strain | Control | | GOS | | SL | |
|---|---|---|---|---|---|---|
| Bacteroides fragilis | 6 | 13 | 37 | 13 | 134 | 111 |
| Bacteroides ovatus | 201 | 173 | 144 | 87 | 107 | 104 |
| Bacteroides vulgatus | 115 | 135 | 129 | 193 | 179 | 218 |
| Bacteroides prevotella group | 35 | 20 | 40 | 49 | 99 | 65 |
| Bacteroides theiatomicron | 10 | 10 | 10 | 4 | 2 | 2 |
| | | | | | | |
| Bifidobacterium adolescentis / B. angulatum | 4 | 9 | 87 | 18 | 8 | 6 |
| Bifidobacterium angulatum | 1 | 1 | 39 | 12 | 1 | 1 |
| Bifidobacterium bifidum | 3 | 4 | 40 | 45 | 6 | 7 |
| Bifidobacterium breve | 1 | 1 | 5 | 15 | 1 | 1 |
| Bifidobacterium catenulatum group | 3 | 4 | 67 | 11 | 4 | 3 |
| Bifidobacterium infantis | 1 | 1 | 13 | 46 | 2 | 2 |
| Bifidobacterium longum | 2 | 2 | 14 | 74 | 2 | 2 |
| Bifidobacterium group 02 | 4 | 6 | 100 | 40 | 4 | 4 |
| Bifidobacteriaceae | 6 | 11 | 123 | 72 | 13 | 13 |
| | | | | | | |
| Collinsella aerofaciens | 3 | 45 | 89 | 86 | 173 | 215 |
| Eubacterium halii | 1 | 3 | 39 | 6 | 20 | 33 |
| Faecalibacterium prausnitzii | 1 | 4 | 4 | 3 | 52 | 86 |
| Ruminococcus albus | 6 | 41 | 73 | 12 | 131 | 97 |
| Ruminococcus obeum | 2 | 2 | 2 | 3 | 10 | 19 |
| Ruminococcus productus | 1 | 1 | 1 | 1 | 26 | 25 |

**H** **Infant**

| strain | Control | | GOS | | SL | |
|---|---|---|---|---|---|---|
| Bacteroides distasonis | 4 | 8 | 16 | 9 | 29 | 26 |
| Bacteroides fragilis | 18 | 36 | 104 | 146 | 144 | 242 |
| Bacteroides ovatus | 27 | 25 | 106 | 150 | 111 | 201 |
| Bacteroides prevotella group | 11 | 16 | 29 | 52 | 50 | 142 |
| Bacteroides thetaiotaomicron | 31 | 52 | 92 | 81 | 137 | 232 |
| Bacteroides vulgatus | 11 | 20 | 66 | 37 | 127 | 240 |
| Bacteriodes species | 28 | 62 | 75 | 110 | 114 | 220 |
| Bacteroides group | 8 | 17 | 26 | 35 | 70 | 83 |
| | | | | | | |
| Bifidobacterium catenulatum | 9 | 9 | 59 | 32 | 42 | 38 |
| Bifidobacterium catenulatum group | 7 | 11 | 10 | 26 | 15 | 43 |
| Bifidobacterium species | 77 | 45 | 110 | 212 | 168 | 167 |
| Bifidobacterium group 02 | 5 | 7 | 9 | 13 | 15 | 33 |
| | | | | | | |
| Clostridium butyricum | 1 | 1 | 21 | 22 | 35 | 19 |
| Prevotella group 03 | 8 | 4 | 28 | 2 | 55 | 13 |
| Ruminococcus albus | 19 | 6 | 20 | 1 | 90 | 6 |
| Streptococcus agalactiae | 2 | 2 | 11 | 30 | 1 | 1 |
| Streptococcus anginosus | 1 | 1 | 4 | 9 | 2 | 1 |
| Streptococcus bovis | 4 | 2 | 59 | 80 | 3 | 6 |
| Veillonella species | 4 | 8 | 59 | 1 | 78 | 5 |

**FIGURE 3 |** SL and GOS differentially modulate microbiota composition. Batch cultures of adult and infant pooled fecal samples cultured in growth medium were supplemented with or without SL or GOS in duplo. Fecal samples were collected at the start of the batch culture and after 3, 6, 9, and 24 h. Microbiota composition on genus level **(A–F)** and on species level **(G,H)** was determined by qPCR and chip analysis, respectively. Bacterial numbers were shown as mean ± SEM of two independent batch cultures. Raw fluorescence data are shown for both individual runs for chip analysis.