

Table S1. Relative abundance (%) of faecal microbiota genera of mice during the 15- and 30-day intervention period

| Phylum | Genus | CG1 | | CG2 | | | TG1 | | TG2 | | |
|-----------------------------------|---|----------|-----------|----------|----------|-----------|----------|-----------|----------|----------|-----------|
| | | At start | On Day 15 | At start | On Day15 | On Day 30 | At start | On Day 15 | At start | On Day15 | On Day 30 |
| <i>Bacteroidota</i> | <i>Muribaculaceae</i> | 33.9 | 34.7 | 4.4 | 6.9 | 34.0 | 49.4 | 6.9 | 6.0 | 5.9 | 37.2 |
| | <i>Alistipes</i> | 19.6 | 1.0 | 18.5 | 12.3 | 13.0 | 13.4 | 20.7 | 11.0 | 9.8 | 0.9 |
| | <i>Prevotellaceae_UCG-1</i> | 2.0 | 1.0 | 0.0 | 1.2 | 1.8 | 1.8 | 4.7 | 0.0 | 2.9 | 1.4 |
| | <i>Bacteroides</i> | 0.0 | 6.4 | 1.8 | 8.9 | 7.3 | 9.9 | 9.0 | 15.0 | 13.5 | 0.6 |
| | <i>Muribaculum</i> | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.3 | 0.0 | 0.0 |
| <i>Bacillota</i> | <i>Bacillus</i> | 4.0 | 0.0 | 0.0 | 0.0 | 0.7 | 1.4 | 0.0 | 0.9 | 0.0 | 0.0 |
| | <i>Lachnospiraceae_A2</i> | 3.4 | 2.3 | 5.6 | 5.5 | 2.4 | 0.0 | 0.0 | 3.4 | 0.0 | 1.2 |
| | <i>Lactobacillus</i> | 2.9 | 0.6 | 1.2 | 1.2 | 0.6 | 1.4 | 1.8 | 0.7 | 1.2 | 1.2 |
| | <i>RF39</i> | 2.6 | 0.9 | 0.0 | 0.0 | 0.0 | 0.0 | 2.4 | 0.0 | 0.0 | 1.0 |
| | <i>Lachnospiraceae_NK4A136_group</i> | 2.3 | 23.9 | 32.1 | 24.1 | 1.1 | 2.8 | 2.2 | 29.3 | 25.7 | 22.9 |
| | <i>Oscillibacter</i> | 1.7 | 1.0 | 0.0 | 1.3 | 0.9 | 1.3 | 1.2 | 1.7 | 1.5 | 1.1 |
| | <i>Clostridiales_vadin_BB6_group</i> | 1.4 | 1.2 | 1.9 | 0.9 | 1.0 | 0.0 | 1.7 | 0.0 | 1.4 | 0.8 |
| | <i>Lachnospiraceae_UCG-1</i> | 1.1 | 1.4 | 1.6 | 1.7 | 0.9 | 2.0 | 2.1 | 0.0 | 0.0 | 0.7 |
| | <i>Colidextribacter</i> | 1.1 | 1.0 | 1.3 | 0.9 | 0.8 | 0.0 | 1.0 | 1.1 | 1.3 | 0.7 |
| | <i>Streptococcus</i> | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| | <i>Clostridia_UCG-14</i> | 0.0 | 3.7 | 4.4 | 2.3 | 4.4 | 2.8 | 4.1 | 2.8 | 1.1 | 0.0 |
| | <i>Roseburia</i> | 0.0 | 3.4 | 3.5 | 2.7 | 0.0 | 0.6 | 3.2 | 0.9 | 7.9 | 5.6 |
| | <i>Marvinbryantia</i> | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| | <i>Staphylococcus</i> | 0.0 | 0.0 | 0.9 | 0.0 | 0.0 | 0.0 | 2.4 | 0.0 | 0.0 | 0.0 |
| | <i>[Eubacterium]_xylanophilum_group</i> | 0.0 | 0.0 | 0.7 | 0.7 | 0.3 | 0.0 | 0.0 | 0.5 | 0.6 | 1.0 |
| | <i>Lachnospiraceae_UCG-6</i> | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 | 1.1 |
| <i>Actinomycetota</i> | <i>Kocuria</i> | 0.9 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| | <i>Micrococcus</i> | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| | <i>Adlercreutzia</i> | 0.0 | 0.5 | 0.0 | 4.4 | 4.7 | 0.7 | 0.7 | 6.2 | 0.7 | 3.7 |
| | <i>Bifidobacterium</i> | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| <i>Candidatus Patescibacteria</i> | <i>Candidatus Saccharimonas</i> | 2.9 | 7.8 | 2.3 | 12.7 | 15.7 | 0.6 | 17.6 | 6.9 | 11.0 | 7.9 |
| <i>Thermodesulfobacteriota</i> | <i>Desulfovibrio</i> | 1.5 | 0.8 | 1.8 | 1.4 | 0.8 | 1.1 | 1.2 | 1.6 | 1.4 | 0.6 |
| <i>Deferribacterota</i> | <i>Mucispirillum</i> | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 | 0.0 |

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|-----------------------|-----------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <i>Mycoplasmata</i> | <i>Anaeroplasmata</i> | 2.0 | 0.8 | 2.2 | 0.7 | 0.8 | 1.6 | 3.2 | 1.1 | 0.9 | 0.9 |
| <i>Pseudomonadota</i> | <i>Pseudomonas</i> | 0.0 | 0.0 | 1.9 | 0.0 | 2.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 |
| <i>Streptophyta</i> | <i>Incertae sedis</i> | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.6 | 0.0 |

CG – control group, TG – test group.