**Supplemental Table 2**. Changes within SCFA producers based on study group, analyzed at the genus level.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Difference Between Groups (%)** | **Absolute Change (Fiber)** | **Absolute Change (No Fiber)** | **Order** | **Family** | **Genus** |
| **+1.16** | +0.72 | -0.44 | Clostridiales | Ruminococcaceae | Faecalibacterium |
| **+0.49** | +0.35 | -0.14 | Bacteroidales | Marinifilaceae | Odoribacter |
| **+0.44** | -0.02 | -0.46 | Clostridiales | Ruminococcaceae | Flavonifractor |
| **+0.28** | +0.14 | -0.14 | Clostridiales | Ruminococcaceae | Oscillibacter |
| **+0.11** | +0.00 | -0.11 | Clostridiales | Eubacteriaceae | Eubacterium |
| **-0.03** | +0.03 | +0.06 | Clostridiales | Ruminococcaceae | Butyricicoccus |
| **-0.17** | -0.17 | +0.00 | Clostridiales | Lachnospiraceae | Roseburia |
| **-0.33** | +0.29 | +0.62 | Clostridiales | Lachnospiraceae | Anaerostipes |
| **-2.70** | -2.74 | -0.04 | Bacteroidales | Rikenellaceae | Alistipes |

Differences between groups are expressed as the mean relative abundance (%) for Day 3 minus the mean relative abundance for Day 0 (i.e., as absolute changes in proportions rather than as within-individual changes as in Figure 2).