Supplementary table 2. Relative abundance of the most representative Genus

|  |  |  |  |
| --- | --- | --- | --- |
|  TaxonomicGenus | Vehicle | DSS | DSS+Oba |
| Relative abundance (%) |
| *Escherichia-Shigella*  | 0.052 ± 0.055 | 41.63 ± 19.41 ## | 9.35 ± 7.04 \*\* |
| *Lactobacillus*  | 13.72 ± 4.42 | 8.67 ± 6.70 | 4.73 ± 5.13 |
| *Bacteroides*  | 3.62 ± 1.86 | 11.99 ± 7.37 | 10.03 ± 8.31 |
| *Lachnospiraceae-* *NK4A136-group* | 10.54 ± 2.18 | 0.56 ± 0.76 | 13.79 ± 9.37 |
| *f-Bacteroidales* *-S24-7-group* | 22.62 ± 8.22 | 0.41 ± 0.64 ### | 0.71 ± 0.53 |
| *Alistipes*  | 14.71 ± 5.14 | 0.14 ± 0.22 ### | 0.41 ± 0.32 |
| *Turicibacter*  | 0.021 ± 0.030 | 0.74 ± 0.57 | 12.05 ± 16.13 |
| *Mucispirillum*  | 0.50 ± 0.35 | 4.25 ± 3.01 # | 7.60 ± 1.39 |
| *f-Lachnospiraceae*  | 5.102 ± 2.79 | 2.05 ± 2.26 | 3.62 ± 1.66 |
| *Romboutsia*  | 0.0067 ± 0.0082 | 0.66 ± 0.42 | 6.38 ± 2.77 |
| *Clostridium-sensu* *-stricto-1* | 0.11 ± 0.060 | 0.34 ± 0.20  | 5.19 ± 5.21 |
| *Parabacteroides* *Citrobacter* | 0.17 ± 0.11 | 4.17 ± 4.65 | 0.27 ± 0.16 |
| *Citrobacter*  | 0.00081 ± 0.016 | 4.18 ± 7.88 | 0.0090 ± 0.018 |
| *Alloprevotella*  | 4.97 ± 8.62 | 0 ± 0 | 0 ± 0 |
| *Ruminiclostridium-9*  | 0.55 ± 0.12 | 0.88 ± 0.88 | 3.33 ± 1.66 |
| *Rikenellaceae-RC9**-gut-group*  | 3.70 ± 1.41 | 0.020 ± 0.025 ## | 0.90 ± 1.22 |
| *Enterococcus*  | 0 ± 0 | 3.15 ± 2.56 # | 0.75 ± 0.89 |
| *Ruminococcaceae**-UCG-014*  | 1.58 ± 0.85 | 0.29 ± 0.35 | 1.80 ± 2.58 |
| *Parasutterella*  | 0.097 ± 0.086 | 0.20 ± 0.18 | 2.50 ± 3.02 |

\*\**p* < 0.01 *vs.* the DSS-treated group; #*p* < 0.05, #*p* < 0.01, ###*p* < 0.001 *vs.* the control group.