

**Supplemental Figure 1.** Assessment of sufficient sequencing depth by rarefaction analyses. Individual rarefaction curves for each time-series sample from the Sham (blue) or SNI (red) group.

**Supplemental Table 1.** Differential relative abundance between the SNI group and Sham group for each day at the genus level. indicates significantly higher in relative abundance, whereas indicates significantly lower in relative abundance.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Day | OTU (genus level) | SNI | Sham | p value |
| -1-0 | *Bacteroides* |  |  | 0.040 |
| *Oscillospira* |  |  | 0.026 |
| *Roseburia* |  |  | 0.008 |
| Candidate\_Division\_TM7 |  |  | 0.022 |
| Mollicutes\_unclassified |  |  | 0.034 |
| 1-2 | Ruminococcaceae\_uncultured |  |  | 0.020 |
| Erysipelotrichaceae\_unclassified |  |  | 0.034 |
| *Bacteroides* |  |  | 0.032 |
| Erysipelotrichaceae\_Incertae\_Sedis |  |  | 0.002 |
| *Oscillospira* |  |  | 0.020 |
| Peptococcaceae\_unclassified |  |  | 0.006 |
| *Roseburia* |  |  | 0.004 |
| Mollicutes\_unclassified |  |  | 0.004 |
| 3-5 | Erysipelotrichaceae\_unclassified |  |  | 0.020 |
| Mollicutes\_unclassified |  |  | 0.006 |
| *Turicibacter* |  |  | 0.006 |
| 6-14 | Bacteroidales\_unclassified |  |  | 0.012 |
| *Lactobacillus* |  |  | 0.002 |
| *Bacteroides* |  |  | 0.040 |
| *Allobaculum* |  |  | 0.004 |
| *Akkermansia* |  |  | 0.002 |
| *Bifidobacterium* |  |  | 0.002 |
| *Clostridium* |  |  | 0.010 |
| Mollicutes\_unclassified |  |  | 0.006 |
| Actinobacteria\_unclassified |  |  | 0.008 |
| *Turicibacter* |  |  | 0.002 |
| Peptococcaceae\_unclassified |  |  | 0.010 |

**Supplemental Table 2.1.** The ranks and values of each genus in the Sham group based on betweenness centrality, closeness centrality, and degree centrality.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| OTU | Genus | Degree centrality score | Rank based on degree centralityscore | Closenesscentrality score | Rank based on closenesscentralityscore | Betweeness centrality score  | Rank based on betweenesscentralityscore | Totalrank | Final rank |
| 15 | Erysipelotrichaceae\_unclassified | 30 | 3 | 0.635294 | 2 | 0.070859 | 3 | 8 | 1 |
| 26 | *Oscillospira* | 31 | 2 | 0.606742 | 4 | 0.075661 | 2 | 8 | 1 |
| 13 | *Adlercreutzia* | 32 | 1 | 0.593407 | 5 | 0.060596 | 4 | 10 | 2 |
| 58 | *Turicibacter* | 30 | 4 | 0.613636 | 3 | 0.03778 | 11 | 18 | 3 |
| 33 | *Ruminococcus* | 30 | 5 | 0.514286 | 15 | 0.090011 | 1 | 21 | 4 |
| 23 | *Barnesiella* | 30 | 6 | 0.658537 | 1 | 0.022513 | 20 | 27 | 5 |
| 22 | *Bacteroides* | 27 | 7 | 0.524272 | 14 | 0.051845 | 7 | 28 | 6 |
| 5 | Ruminococcaceae\_unclassified | 26 | 8 | 0.529412 | 13 | 0.050517 | 8 | 29 | 7 |
| 4 | Bacteroidales\_unclassified | 26 | 10 | 0.593407 | 6 | 0.026636 | 16 | 32 | 8 |
| 12 | Mollicutes\_RF9 | 24 | 13 | 0.54 | 9 | 0.037608 | 13 | 35 | 9 |
| 17 | *Lactobacillus* | 20 | 19 | 0.534653 | 12 | 0.051958 | 5 | 36 | 10 |
| 29 | *Parabacteroides* | 26 | 9 | 0.486486 | 21 | 0.04131 | 10 | 40 | 11 |
| 9 | Firmicutes\_unclassified | 22 | 15 | 0.568421 | 8 | 0.021304 | 21 | 44 | 12 |
| 38 | *Parasutterella* | 25 | 11 | 0.495413 | 18 | 0.025906 | 19 | 48 | 13 |
| 10 | Ruminococcaceae\_Incertae\_Sedis | 25 | 12 | 0.461538 | 28 | 0.03788 | 12 | 52 | 14 |
| 59 | Peptococcaceae\_unclassified | 20 | 17 | 0.504673 | 17 | 0.023233 | 18 | 52 | 15 |
| 2 | Bacteroidales\_S24-7 | 24 | 14 | 0.586957 | 7 | 0.010977 | 35 | 56 | 16 |
| 25 | *Allobaculum* | 20 | 16 | 0.534653 | 11 | 0.011336 | 33 | 60 | 17 |
| 16 | Coriobacteriaceae\_;unclassified | 18 | 22 | 0.495413 | 19 | 0.021189 | 22 | 63 | 18 |
| 51 | Clostridium\_unclassified | 16 | 25 | 0.421875 | 35 | 0.056591 | 6 | 66 | 19 |
| 30 | *Mucispirillum* | 16 | 27 | 0.54 | 10 | 0.012288 | 32 | 69 | 20 |
| 27 | Clostridium\_Candidatus\_Arthromitus | 16 | 26 | 0.509434 | 16 | 0.014025 | 28 | 70 | 21 |
| 7 | Ruminococcaceae\_uncultured | 15 | 30 | 0.45 | 29 | 0.026189 | 17 | 76 | 22 |
| 54 | *Desulfovibrio* | 13 | 40 | 0.473684 | 23 | 0.036011 | 14 | 77 | 23 |
| 55 | Mollicutes\_unclassified | 11 | 45 | 0.473684 | 24 | 0.031616 | 15 | 84 | 24 |
| 49 | *Streptococcus* | 13 | 42 | 0.490909 | 20 | 0.016603 | 24 | 86 | 25 |
| 1 | Lachnospiraceae\_unclassified | 18 | 21 | 0.465517 | 26 | 0.009072 | 40 | 87 | 26 |
| 52 | *Escherichia* | 15 | 32 | 0.369863 | 46 | 0.043644 | 9 | 87 | 27 |
| 53 | *Staphylococcus* | 19 | 20 | 0.380282 | 44 | 0.016718 | 23 | 87 | 28 |
| 57 | *Eubacterium* | 17 | 24 | 0.421875 | 36 | 0.013173 | 30 | 90 | 29 |
| 6 | Clostridiales\_unclassified | 15 | 29 | 0.482143 | 22 | 0.007432 | 44 | 95 | 30 |
| 14 | Bacteroidetes\_unclassified | 17 | 23 | 0.415385 | 37 | 0.01002 | 37 | 97 | 31 |
| 45 | Erysipelotrichaceae\_Incertae\_Sedis | 13 | 39 | 0.439024 | 31 | 0.014139 | 27 | 97 | 32 |
| 19 | Clostridiales\_Family\_XIII\_Incertae\_Sedis | 13 | 41 | 0.465517 | 27 | 0.012976 | 31 | 99 | 33 |
| 32 | *Roseburia* | 13 | 38 | 0.421875 | 34 | 0.013423 | 29 | 101 | 34 |
| 34 | Candidate\_division\_TM7 | 15 | 31 | 0.312139 | 49 | 0.015425 | 26 | 106 | 35 |
| 28 | *Akkermansia* | 14 | 34 | 0.409091 | 38 | 0.0103 | 36 | 108 | 37 |
| 31 | *Hydrogenoanaerobacterium* | 15 | 28 | 0.397059 | 39 | 0.008491 | 41 | 108 | 38 |
| 21 | *Acetanaerobacterium* | 12 | 43 | 0.394161 | 41 | 0.017137 | 25 | 109 | 40 |
| 11 | Lachnospiraceae\_uncultured | 14 | 33 | 0.388489 | 43 | 0.011192 | 34 | 110 | 41 |
| 48 | *Bifidobacterium* | 14 | 35 | 0.439024 | 32 | 0.007303 | 45 | 112 | 42 |
| 24 | *Coprobacillus* | 11 | 47 | 0.473684 | 25 | 0.00496 | 46 | 118 | 44 |
| 40 | Porphyromonadaceae\_unclassified | 13 | 37 | 0.377622 | 45 | 0.009755 | 38 | 120 | 45 |
| 50 | Clostridia\_unclassified | 11 | 46 | 0.425197 | 33 | 0.007948 | 42 | 121 | 47 |
| 8 | Lachnospiraceae\_Incertae\_Sedis | 9 | 48 | 0.442623 | 30 | 0.004331 | 47 | 125 | 48 |
| 47 | *Olsenella* | 20 | 18 | 0 | 54 | 0 | 54 | 126 | 49 |
| 20 | *Oscillibacter* | 13 | 36 | 0.348387 | 47 | 0.002927 | 50 | 133 | 50 |
| 35 | *Lachnospira* | 12 | 44 | 0.278351 | 51 | 0.009703 | 39 | 134 | 51 |
| 44 | *Acinetobacter* | 8 | 50 | 0.325301 | 48 | 0.007594 | 43 | 141 | 52 |
| 3 | Bacteria\_unclassified | 6 | 53 | 0.394161 | 40 | 0.003004 | 49 | 142 | 53 |
| 18 | *Moryella* | 7 | 52 | 0.391304 | 42 | 0.003227 | 48 | 142 | 54 |
| 56 | Actinobacteria\_unclassified | 8 | 51 | 0.301676 | 50 | 0.000426 | 52 | 153 | 55 |
| 42 | *Weissella* | 8 | 49 | 0 | 53 | 0 | 53 | 155 | 56 |
| 37 | *Enterococcus* | 5 | 54 | 0.27551 | 52 | 0.001054 | 51 | 157 | 57 |
| 41 | *Alcaligenes* | 1 | 55 | 0 | 55 | 0 | 55 | 165 | 58 |

 **Supplemental Table 2.2.** The ranks and values of each genus in the SNI group based on betweenness centrality, closeness centrality, and degree centrality.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| OTU | Genus | Degree centrality score | Rank based on degree centralityscore | Closeness centralityscore  | Rank based on closeness centralityscore | Betweeness centrality score | Rank based on betweeness centrality score | Total Rank | Final rank |
| 53 | *Staphylococcus* | 30 | 2 | 0.574713 | 3 | 0.115747 | 1 | 6 | 1 |
| 7 | Ruminococcaceae\_uncultured | 32 | 1 | 0.543478 | 7 | 0.10805 | 2 | 10 | 2 |
| 58 | *Turicibacter* | 25 | 5 | 0.549451 | 6 | 0.082056 | 3 | 14 | 3 |
| 33 | *Ruminococcus* | 26 | 4 | 0.609756 | 2 | 0.045515 | 10 | 16 | 4 |
| 30 | *Mucispirillum* | 22 | 7 | 0.555556 | 5 | 0.059444 | 5 | 17 | 5 |
| 4 | Bacteroidales\_unclassified | 30 | 3 | 0.666667 | 1 | 0.025343 | 22 | 26 | 6 |
| 9 | Firmicutes\_unclassified | 19 | 11 | 0.505051 | 11 | 0.039362 | 11 | 33 | 7 |
| 5 | Ruminococcaceae\_unclassified | 21 | 8 | 0.462963 | 21 | 0.054642 | 7 | 36 | 8 |
| 23 | *Barnesiella* | 16 | 19 | 0.510204 | 10 | 0.05149 | 9 | 38 | 9 |
| 1 | Lachnospiraceae\_unclassified | 23 | 6 | 0.568182 | 4 | 0.014449 | 30 | 40 | 10 |
| 29 | *Parabacteroides* | 18 | 14 | 0.485437 | 14 | 0.033292 | 12 | 40 | 11 |
| 20 | *Oscillibacter* | 20 | 9 | 0.434783 | 29 | 0.054735 | 6 | 44 | 12 |
| 22 | *Bacteroides* | 15 | 20 | 0.49505 | 12 | 0.029306 | 15 | 47 | 13 |
| 51 | Clostridium\_unclassified | 20 | 10 | 0.485437 | 15 | 0.023442 | 24 | 49 | 14 |
| 34 | Candidate\_division\_TM7 | 15 | 23 | 0.471698 | 20 | 0.053482 | 8 | 51 | 15 |
| 11 | Lachnospiraceae\_uncultured | 18 | 12 | 0.471698 | 19 | 0.026233 | 21 | 52 | 16 |
| 49 | *Streptococcus* | 15 | 24 | 0.454545 | 24 | 0.067679 | 4 | 52 | 17 |
| 14 | Bacteroidetes\_unclassified | 18 | 16 | 0.515464 | 9 | 0.021133 | 28 | 53 | 18 |
| 31 | *Hydrogenoanaerobacterium* | 18 | 13 | 0.458716 | 22 | 0.030498 | 18 | 53 | 19 |
| 10 | Ruminococcaceae\_Incertae\_Sedis | 18 | 15 | 0.490196 | 13 | 0.01472 | 26 | 54 | 20 |
| 2 | Bacteroidales\_S24-7 | 17 | 17 | 0.537634 | 8 | 0.011255 | 33 | 58 | 21 |
| 54 | *Desulfovibrio* | 13 | 31 | 0.485437 | 16 | 0.030957 | 14 | 61 | 22 |
| 32 | *Roseburia* | 15 | 21 | 0.431034 | 31 | 0.032031 | 13 | 65 | 23 |
| 48 | *Bifidobacterium* | 15 | 25 | 0.485437 | 18 | 0.023676 | 23 | 66 | 24 |
| 45 | Erysipelotrichaceae\_Incertae\_Sedis | 16 | 18 | 0.45045 | 25 | 0.02297 | 25 | 68 | 25 |
| 26 | *Oscillospira* | 15 | 22 | 0.446429 | 27 | 0.026324 | 20 | 69 | 26 |
| 21 | *Acetanaerobacterium* | 14 | 29 | 0.485437 | 17 | 0.019491 | 27 | 73 | 27 |
| 15 | Erysipelotrichaceae\_unclassified | 13 | 30 | 0.446429 | 28 | 0.031567 | 17 | 75 | 28 |
| 38 | *Parasutterella* | 14 | 28 | 0.458716 | 23 | 0.014173 | 32 | 83 | 29 |
| 25 | *Allobaculum* | 12 | 34 | 0.396825 | 39 | 0.029213 | 16 | 89 | 30 |
| 3 | Bacteria\_unclassified | 14 | 26 | 0.42735 | 34 | 0.005155 | 38 | 98 | 31 |
| 19 | Clostridiales\_Family\_XIII\_Incertae\_Sedis | 12 | 32 | 0.42735 | 35 | 0.011934 | 31 | 98 | 32 |
| 28 | *Akkermansia* | 12 | 33 | 0.420168 | 36 | 0.014698 | 29 | 98 | 33 |
| 55 | Mollicutes\_unclassified | 10 | 37 | 0.446429 | 26 | 0.008011 | 35 | 98 | 34 |
| 17 | *Lactobacillus* | 11 | 35 | 0.431034 | 32 | 0.005056 | 40 | 107 | 35 |
| 56 | Actinobacteria\_unclassified | 8 | 46 | 0.35461 | 44 | 0.027212 | 19 | 109 | 36 |
| 27 | Clostridium\_Candidatus\_Arthromitus | 9 | 38 | 0.434783 | 30 | 0.004413 | 44 | 112 | 37 |
| 6 | Clostridiales\_unclassified | 14 | 27 | 0.316456 | 48 | 0.00444 | 43 | 118 | 38 |
| 35 | *Lachnospira* | 8 | 45 | 0.393701 | 40 | 0.010638 | 34 | 119 | 39 |
| 12 | Mollicutes\_RF9 | 9 | 40 | 0.37037 | 41 | 0.005965 | 39 | 120 | 40 |
| 18 | *Moryella* | 9 | 41 | 0.406504 | 37 | 0.004616 | 42 | 120 | 41 |
| 57 | *Eubacterium* | 9 | 39 | 0.396825 | 38 | 0.004203 | 45 | 122 | 42 |
| 59 | Peptococcaceae\_unclassified | 10 | 36 | 0.359712 | 42 | 0.003707 | 46 | 124 | 43 |
| 24 | *Coprobacillus* | 8 | 44 | 0.328947 | 46 | 0.006675 | 36 | 126 | 44 |
| 16 | Coriobacteriaceae\_unclassified | 8 | 43 | 0.357143 | 43 | 0.004853 | 41 | 127 | 45 |
| 50 | Clostridia\_unclassified | 7 | 47 | 0.431034 | 33 | 0.001446 | 50 | 130 | 46 |
| 52 | *Escherichia* | 6 | 48 | 0.324675 | 47 | 0.006617 | 37 | 132 | 47 |
| 13 | *Adlercreutzia* | 8 | 42 | 0.263158 | 50 | 0.001897 | 48 | 140 | 48 |
| 44 | *Acinetobacter* | 4 | 50 | 0.342466 | 45 | 0.001468 | 49 | 144 | 49 |
| 8 | Lachnospiraceae\_Incertae\_Sedis | 5 | 49 | 0.314465 | 49 | 0.002069 | 47 | 145 | 50 |
| 40 | Porphyromonadaceae\_unclassified | 2 | 51 | 0 | 51 | 0 | 51 | 153 | 51 |