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Fecal microbiota transplant from highly feed efficient donors shows little effects on age-related changes in feed efficiency-associated fecal microbiota in chickens

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1 **Fecal microbiota transplant from highly feed efficient donors shows little effects on age-**
2 **related changes in feed efficiency-associated fecal microbiota in chickens**

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4 Running title: Fecal transplant and feed efficiency

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6 Sina-Catherine Siegerstetter^a, Renée M. Petri^a, Elizabeth Magowan^b, Peadar G. Lawlor^c,
7 Qendrim Zebeli^a, Niamh E. O'Connell^d, Barbara U. Metzler-Zebeli^a

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9 ^aInstitute of Animal Nutrition and Functional Plant Compounds, Department for Farm
10 Animals and Veterinary Public Health, University of Veterinary Medicine Vienna, Vienna,
11 Austria.

12 ^bAgri-Food and Biosciences Institute, Agriculture Branch, Hillsborough, Northern Ireland,
13 UK.

14 ^cTeagasc, Pig Development Department, Animal & Grassland Research & Innovation Centre,
15 Moorepark, Ireland.

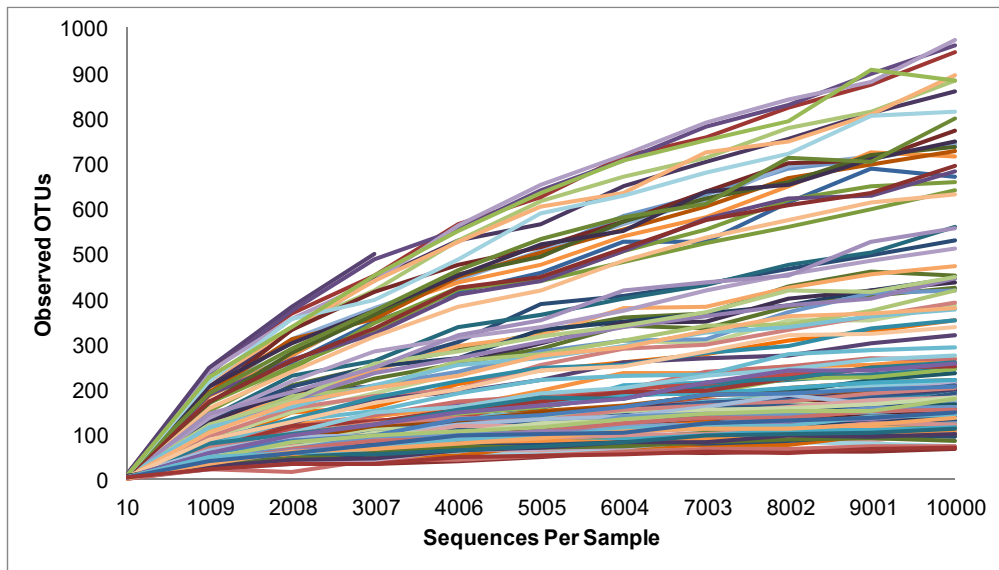
16 ^dInstitute for Global Food Security, Queen's University Belfast, Northern Ireland, UK.

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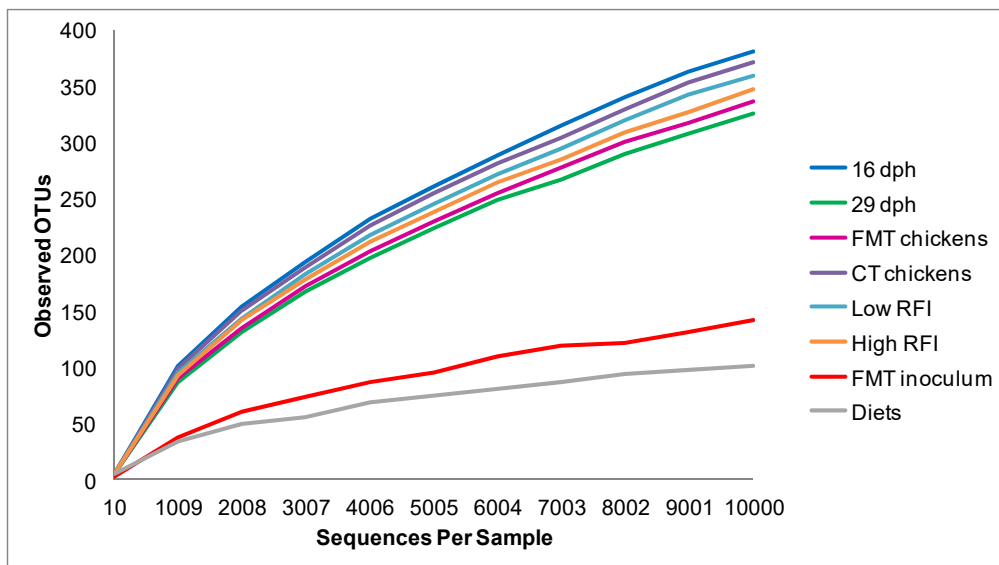
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19 Address correspondence to Barbara U. Metzler-Zebeli, barbara.metzler@vetmeduni.ac.

a



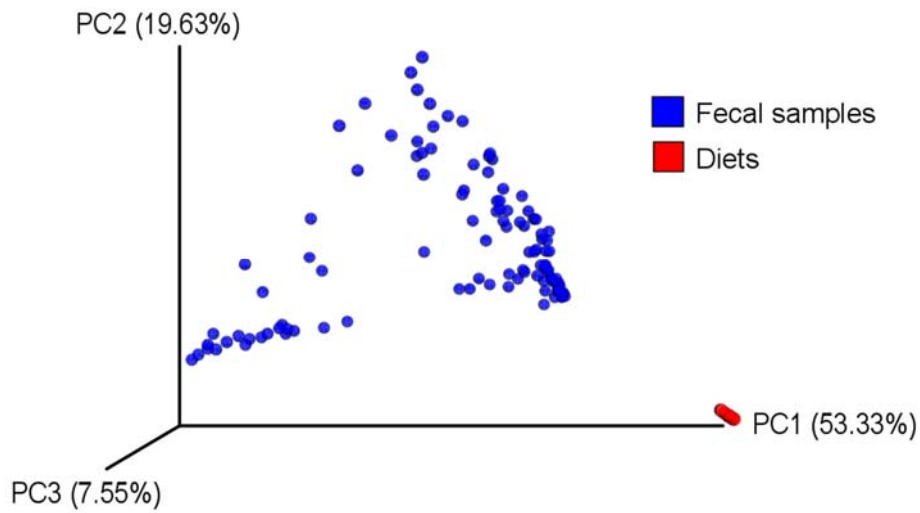
b



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21 **FIG S1** Rarefaction curves showing microbiota diversity based on Observed operational
22 taxonomic units (OTUs): (a) separate for each of the fecal samples ($n = 112$), fecal microbiota
23 transplant (FMT) ($n = 8$) and diet sample ($n = 6$); (b) summarized to day post-hatch (dph),
24 FMT and control (CT) group, residual feed intake (RFI), FMT inoculum and diet sample
25 means. Water samples were not included in the graphs due to their low number of sequencing
26 reads/sample (162 and 180 sequences/sample, respectively).

27



28

29 **FIG S2** Principal coordinate analysis (PCoA) plot of weighted UniFrac analysis of fecal and
30 diet samples. Fecal samples, $n = 111$, diet samples, $n = 6$. Rarefaction depth of 10,000
31 sequences per sample removed 1 sample from the dataset (male, low residual feed intake,
32 control transplant, 16 day post-hatch).

33

34 **TABLE S1** Descriptive statistics for the most abundant bacterial phyla in diet and water
 35 samples

| Item | <i>n</i> | Mean | SE | Minimum | Maximum |
|-----------------------|----------|-------|--------|---------|---------|
| Starter Diet | | | | | |
| <i>Cyanobacteria</i> | 2 | 81.32 | 0.88 | 80.44 | 82.20 |
| <i>Proteobacteria</i> | 2 | 18.39 | 0.88 | 17.51 | 19.27 |
| <i>Firmicutes</i> | 2 | 0.24 | 0.02 | 0.22 | 0.25 |
| Unclassified | 2 | 0.03 | 0.01 | 0.02 | 0.04 |
| <i>Actinobacteria</i> | 2 | 0.02 | 0.004 | 0.01 | 0.02 |
| <i>Tenericutes</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| <i>Spirochaetes</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| <i>TM7</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| Grower Diet | | | | | |
| <i>Cyanobacteria</i> | 2 | 76.22 | 2.81 | 73.42 | 79.03 |
| <i>Proteobacteria</i> | 2 | 23.50 | 2.76 | 20.74 | 26.26 |
| <i>Firmicutes</i> | 2 | 0.21 | 0.01 | 0.20 | 0.22 |
| <i>Actinobacteria</i> | 2 | 0.03 | 0.03 | 0.004 | 0.06 |
| Unclassified | 2 | 0.03 | 0.02 | 0.01 | 0.04 |
| <i>Bacteroidetes</i> | 2 | 0.004 | 0.004 | 0 | 0.008 |
| <i>Tenericutes</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| Finisher Diet | | | | | |
| <i>Cyanobacteria</i> | 2 | 80.02 | 3.06 | 76.96 | 83.07 |
| <i>Proteobacteria</i> | 2 | 19.64 | 3.10 | 16.54 | 22.74 |
| <i>Firmicutes</i> | 2 | 0.27 | 0.05 | 0.22 | 0.32 |
| Unclassified | 2 | 0.03 | 0.01 | 0.02 | 0.04 |
| <i>Actinobacteria</i> | 2 | 0.02 | 0.003 | 0.02 | 0.02 |
| <i>Bacteroidetes</i> | 2 | 0.01 | 0.01 | 0 | 0.03 |
| <i>Spirochaetes</i> | 2 | 0.004 | 0.0001 | 0.004 | 0.004 |
| Water | | | | | |
| <i>Firmicutes</i> | 2 | 77.99 | 4.10 | 73.89 | 82.10 |
| <i>Proteobacteria</i> | 2 | 18.80 | 3.98 | 14.81 | 22.78 |
| <i>Cyanobacteria</i> | 2 | 1.23 | 1.23 | 0 | 2.47 |
| <i>Actinobacteria</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| <i>Tenericutes</i> | 2 | 0.56 | 0.56 | 0 | 1.11 |
| Unclassified | 2 | 0.28 | 0.28 | 0 | 0.56 |
| <i>Bacteroidetes</i> | 2 | 0.28 | 0.28 | 0 | 0.56 |
| <i>Spirochaetes</i> | 2 | 0.28 | 0.28 | 0 | 0.56 |

37 **TABLE S2** Descriptive statistics for the most abundant operational taxonomic units (OTUs)
 38 in diet and water samples

| Item | Taxonomy (Genus) ^a | <i>n</i> | Mean | SE | Minimum | Maximum |
|--------------|--|----------|-------|-------|---------|---------|
| Starter Diet | | | | | | |
| OTU14 | Unclassified <i>Streptophyta</i> | 2 | 31.54 | 6.52 | 25.01 | 38.06 |
| OTU17 | Unclassified <i>Streptophyta</i> | 2 | 23.17 | 3.54 | 19.64 | 26.71 |
| OTU25 | Unclassified <i>Streptophyta</i> | 2 | 14.55 | 2.18 | 12.37 | 16.73 |
| OTU38 | Unclassified mitochondria | 2 | 8.43 | 0.33 | 8.11 | 8.76 |
| OTU57 | Unclassified <i>Streptophyta</i> | 2 | 5.60 | 0.94 | 4.66 | 6.54 |
| OTU61 | Unclassified mitochondria | 2 | 4.45 | 0.26 | 4.19 | 4.71 |
| OTU87 | Unclassified <i>Streptophyta</i> | 2 | 3.30 | 0.68 | 2.62 | 3.98 |
| OTU122 | Unclassified mitochondria | 2 | 1.90 | 0.24 | 1.66 | 2.15 |
| OTU142 | Unclassified <i>Streptophyta</i> | 2 | 1.71 | 0.21 | 1.50 | 1.91 |
| OTU125 | Unclassified mitochondria | 2 | 1.52 | 0.15 | 1.36 | 1.67 |
| OTU375 | Unclassified <i>Streptophyta</i> | 2 | 0.38 | 0.04 | 0.34 | 0.42 |
| OTU381 | <i>Erwinia</i> | 2 | 0.24 | 0.01 | 0.23 | 0.25 |
| OTU557 | Unclassified <i>Streptophyta</i> | 2 | 0.23 | 0.04 | 0.19 | 0.27 |
| OTU508 | Unclassified <i>Streptophyta</i> | 2 | 0.23 | 0.03 | 0.20 | 0.26 |
| OTU53 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.23 | 0.09 | 0.14 | 0.31 |
| OTU643 | <i>Stenotrophomonas</i> | 2 | 0.13 | 0.12 | 0.01 | 0.25 |
| OTU752 | Unclassified mitochondria | 2 | 0.11 | 0.006 | 0.10 | 0.11 |
| OTU621 | <i>Vibrio</i> | 2 | 0.09 | 0.002 | 0.09 | 0.09 |
| OTU1 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.05 | 0.007 | 0.04 | 0.06 |
| OTU2 | <i>Lactobacillus</i> | 2 | 0.02 | 0.007 | 0.02 | 0.03 |
| OTU3 | <i>Turicibacter</i> | 2 | 0.02 | 0.007 | 0.01 | 0.03 |
| OTU5 | <i>Lactobacillus</i> | 2 | 0.01 | 0.002 | 0.008 | 0.01 |
| OTU8 | <i>Lactobacillus</i> | 2 | 0.007 | 0.002 | 0.004 | 0.009 |
| OTU20 | <i>Lactobacillus</i> | 2 | 0.007 | 0.002 | 0.004 | 0.009 |
| OTU127 | <i>Sphingomonas</i> | 2 | 0.006 | 0.003 | 0.003 | 0.008 |
| OTU245 | Unclassified <i>Comamonadaceae</i> | 2 | 0.005 | 0.001 | 0.004 | 0.006 |
| OTU32 | Unclassified <i>Clostridiales</i> | 2 | 0.004 | 0.001 | 0.003 | 0.004 |
| OTU7 | <i>Lactobacillus</i> | 2 | 0.004 | 0.001 | 0.003 | 0.004 |
| OTU4 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.003 | 0.003 | 0 | 0.006 |
| OTU107 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.003 | 0.003 | 0 | 0.006 |
| OTU214 | Unclassified <i>Sinobacteraceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU72 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| OTU105 | Unclassified family 0319-6G20 | 2 | 0.002 | 0.002 | 0 | 0.003 |
| OTU63 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| OTU10 | Unclassified <i>Clostridiales</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| OTU31 | Unclassified <i>Lachnospiraceae</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |

| | | | | | | |
|---------------|--|---|-------|--------|-------|-------|
| OTU15 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| OTU33 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.003 |
| Grower Diet | | | | | | |
| OTU14 | Unclassified <i>Streptophyta</i> | 2 | 29.18 | 2.16 | 27.01 | 31.34 |
| OTU17 | Unclassified <i>Streptophyta</i> | 2 | 21.93 | 0.89 | 21.04 | 22.82 |
| OTU25 | Unclassified <i>Streptophyta</i> | 2 | 13.83 | 0.31 | 13.52 | 14.14 |
| OTU38 | Unclassified mitochondria | 2 | 10.39 | 0.39 | 10.01 | 10.78 |
| OTU61 | Unclassified mitochondria | 2 | 6.70 | 1.95 | 4.75 | 8.64 |
| OTU57 | Unclassified <i>Streptophyta</i> | 2 | 5.52 | 0.16 | 5.36 | 5.67 |
| OTU87 | Unclassified <i>Streptophyta</i> | 2 | 3.22 | 0.11 | 3.12 | 3.33 |
| OTU125 | Unclassified mitochondria | 2 | 2.44 | 0.84 | 1.60 | 3.28 |
| OTU122 | Unclassified mitochondria | 2 | 2.02 | 0.003 | 2.02 | 2.02 |
| OTU142 | Unclassified <i>Streptophyta</i> | 2 | 1.38 | 0.03 | 1.36 | 1.41 |
| OTU381 | <i>Erwinia</i> | 2 | 0.33 | 0.15 | 0.17 | 0.48 |
| OTU375 | Unclassified <i>Streptophyta</i> | 2 | 0.28 | 0.03 | 0.25 | 0.31 |
| OTU508 | Unclassified <i>Streptophyta</i> | 2 | 0.24 | 0.01 | 0.23 | 0.25 |
| OTU752 | Unclassified mitochondria | 2 | 0.14 | 0.02 | 0.12 | 0.16 |
| OTU557 | Unclassified <i>Streptophyta</i> | 2 | 0.12 | 0.01 | 0.11 | 0.13 |
| OTU621 | <i>Vibrio</i> | 2 | 0.10 | 0.02 | 0.08 | 0.12 |
| OTU53 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.09 | 0.01 | 0.08 | 0.10 |
| OTU1 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.07 | 0.004 | 0.06 | 0.07 |
| OTU7 | <i>Lactobacillus</i> | 2 | 0.04 | 0.04 | 0.004 | 0.08 |
| OTU643 | <i>Stenotrophomonas</i> | 2 | 0.03 | 0.02 | 0.009 | 0.06 |
| OTU3 | <i>Turicibacter</i> | 2 | 0.02 | 0.007 | 0.01 | 0.03 |
| OTU26 | Unclassified <i>Clostridiales</i> | 2 | 0.007 | 0.002 | 0.004 | 0.009 |
| OTU127 | <i>Sphingomonas</i> | 2 | 0.006 | 0.002 | 0.004 | 0.008 |
| OTU5 | <i>Lactobacillus</i> | 2 | 0.004 | 0.0002 | 0.004 | 0.004 |
| OTU2 | <i>Lactobacillus</i> | 2 | 0.004 | 0.0002 | 0.004 | 0.004 |
| OTU105 | Unclassified family 0319-6G20 | 2 | 0.004 | 0.004 | 0 | 0.008 |
| OTU110 | <i>Phenylobacterium</i> | 2 | 0.004 | 0.004 | 0 | 0.008 |
| OTU8 | <i>Lactobacillus</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU172 | <i>Slackia</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU20 | <i>Lactobacillus</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU214 | Unclassified <i>Sinobacteraceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU19 | <i>Ruminococcus</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU245 | Unclassified <i>Comamonadaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU29 | Unclassified <i>Clostridiales</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| Finisher Diet | | | | | | |
| OTU14 | Unclassified <i>Streptophyta</i> | 2 | 33.76 | 0.07 | 33.69 | 33.83 |

| | | | | | | |
|--------|---|---|-------|--------|-------|-------|
| OTU17 | Unclassified <i>Streptophyta</i> | 2 | 21.14 | 1.80 | 19.34 | 22.94 |
| OTU25 | Unclassified <i>Streptophyta</i> | 2 | 13.38 | 0.67 | 12.71 | 14.05 |
| OTU38 | Unclassified mitochondria | 2 | 9.39 | 1.05 | 8.35 | 10.44 |
| OTU57 | Unclassified <i>Streptophyta</i> | 2 | 5.85 | 0.16 | 5.70 | 6.01 |
| OTU61 | Unclassified mitochondria | 2 | 4.53 | 0.42 | 4.12 | 4.95 |
| OTU87 | Unclassified <i>Streptophyta</i> | 2 | 2.69 | 0.30 | 2.39 | 2.99 |
| OTU142 | Unclassified <i>Streptophyta</i> | 2 | 1.82 | 0.15 | 1.66 | 1.97 |
| OTU122 | Unclassified mitochondria | 2 | 1.72 | 0.35 | 1.37 | 2.06 |
| OTU125 | Unclassified mitochondria | 2 | 1.66 | 0.14 | 1.52 | 1.79 |
| OTU53 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.54 | 0.46 | 0.07 | 1.00 |
| OTU375 | Unclassified <i>Streptophyta</i> | 2 | 0.39 | 0.002 | 0.39 | 0.39 |
| OTU621 | <i>Vibrio</i> | 2 | 0.28 | 0.26 | 0.02 | 0.54 |
| OTU381 | <i>Erwinia</i> | 2 | 0.22 | 0.04 | 0.19 | 0.26 |
| OTU557 | Unclassified <i>Streptophyta</i> | 2 | 0.22 | 0.03 | 0.19 | 0.25 |
| OTU643 | <i>Stenotrophomonas</i> | 2 | 0.20 | 0.20 | 0.004 | 0.40 |
| OTU508 | Unclassified <i>Streptophyta</i> | 2 | 0.19 | 0.007 | 0.19 | 0.20 |
| OTU752 | Unclassified mitochondria | 2 | 0.10 | 0.002 | 0.10 | 0.11 |
| OTU1 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.04 | 0.009 | 0.03 | 0.05 |
| OTU3 | <i>Turicibacter</i> | 2 | 0.03 | 0.01 | 0.02 | 0.04 |
| OTU9 | Unclassified <i>Clostridiales</i> | 2 | 0.02 | 0.008 | 0.01 | 0.03 |
| OTU2 | <i>Lactobacillus</i> | 2 | 0.01 | 0.005 | 0.004 | 0.02 |
| OTU5 | <i>Lactobacillus</i> | 2 | 0.009 | 0.005 | 0.004 | 0.01 |
| OTU32 | Unclassified <i>Clostridiales</i> | 2 | 0.008 | 0.004 | 0.004 | 0.01 |
| OTU105 | Unclassified family 0319-6G20 | 2 | 0.008 | 0.004 | 0.004 | 0.01 |
| OTU8 | <i>Lactobacillus</i> | 2 | 0.007 | 0.004 | 0.004 | 0.01 |
| OTU31 | Unclassified <i>Lachnospiraceae</i> | 2 | 0.006 | 0.006 | 0 | 0.01 |
| OTU7 | <i>Lactobacillus</i> | 2 | 0.006 | 0.006 | 0 | 0.01 |
| OTU214 | Unclassified <i>Sinobacteraceae</i> | 2 | 0.006 | 0.002 | 0.004 | 0.008 |
| OTU19 | <i>Ruminococcus</i> | 2 | 0.006 | 0.002 | 0.004 | 0.007 |
| OTU127 | <i>Sphingomonas</i> | 2 | 0.005 | 0.005 | 0 | 0.01 |
| OTU26 | Unclassified <i>Clostridiales</i> | 2 | 0.004 | 0.0001 | 0.004 | 0.004 |
| OTU20 | <i>Lactobacillus</i> | 2 | 0.004 | 0.004 | 0 | 0.007 |
| OTU232 | Unclassified family 0319-6G20 | 2 | 0.004 | 0.004 | 0 | 0.007 |
| OTU4 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU63 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU15 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU75 | Unclassified <i>Clostridiales</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU364 | Unclassified <i>Peptostreptococcaceae</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU29 | Unclassified <i>Clostridiales</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU22 | <i>Turicibacter</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |
| OTU411 | Unclassified <i>Clostridiales</i> | 2 | 0.002 | 0.002 | 0 | 0.004 |

Water

| | | | | | | |
|--------|--|---|-------|-------|-------|-------|
| OTU9 | Unclassified <i>Clostridiales</i> | 2 | 14.20 | 14.20 | 0 | 28.40 |
| OTU1 | Unclassified <i>Enterobacteriaceae</i> | 2 | 12.22 | 1.11 | 11.11 | 13.33 |
| OTU32 | Unclassified <i>Clostridiales</i> | 2 | 9.17 | 7.50 | 1.67 | 16.67 |
| OTU11 | Unclassified <i>Clostridiales</i> | 2 | 4.72 | 4.72 | 0.00 | 9.44 |
| OTU5 | <i>Lactobacillus</i> | 2 | 3.73 | 1.27 | 2.47 | 5.00 |
| OTU4 | Unclassified <i>Ruminococcaceae</i> | 2 | 2.90 | 0.43 | 2.47 | 3.33 |
| OTU26 | Unclassified <i>Clostridiales</i> | 2 | 2.81 | 2.19 | 0.62 | 5.00 |
| OTU72 | Unclassified <i>Ruminococcaceae</i> | 2 | 2.59 | 0.74 | 1.85 | 3.33 |
| OTU3 | <i>Turicibacter</i> | 2 | 2.56 | 1.33 | 1.23 | 3.89 |
| OTU8 | <i>Lactobacillus</i> | 2 | 2.28 | 1.05 | 1.23 | 3.33 |
| OTU2 | <i>Lactobacillus</i> | 2 | 1.51 | 0.96 | 0.56 | 2.47 |
| OTU105 | Unclassified family 0319-6G20 | 2 | 1.48 | 0.37 | 1.11 | 1.85 |
| OTU63 | Unclassified <i>Ruminococcaceae</i> | 2 | 1.20 | 0.65 | 0.56 | 1.85 |
| OTU39 | Unclassified <i>Lachnospiraceae</i> | 2 | 1.17 | 0.06 | 1.11 | 1.23 |
| OTU20 | <i>Lactobacillus</i> | 2 | 1.11 | 1.11 | 0 | 2.22 |
| OTU10 | Unclassified <i>Clostridiales</i> | 2 | 1.11 | 1.11 | 0 | 2.22 |
| OTU28 | Unclassified <i>Clostridiales</i> | 2 | 1.11 | 1.11 | 0 | 2.22 |
| OTU251 | Unclassified <i>Clostridiales</i> | 2 | 1.11 | 1.11 | 0 | 2.22 |
| OTU182 | Unclassified <i>Clostridiales</i> | 2 | 0.93 | 0.93 | 0 | 1.85 |
| OTU225 | Unclassified <i>Clostridiales</i> | 2 | 0.93 | 0.93 | 0 | 1.85 |
| OTU79 | <i>Ruminococcus</i> | 2 | 0.90 | 0.34 | 0.56 | 1.23 |
| OTU65 | <i>Ruminococcus</i> | 2 | 0.86 | 0.25 | 0.62 | 1.11 |
| OTU94 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.86 | 0.25 | 0.62 | 1.11 |
| OTU214 | Unclassified <i>Sinobacteraceae</i> | 2 | 0.83 | 0.83 | 0 | 1.67 |
| OTU19 | <i>Ruminococcus</i> | 2 | 0.83 | 0.83 | 0 | 1.67 |
| OTU31 | Unclassified <i>Lachnospiraceae</i> | 2 | 0.83 | 0.83 | 0 | 1.67 |
| OTU245 | Unclassified <i>Comamonadaceae</i> | 2 | 0.83 | 0.83 | 0 | 1.67 |
| OTU15 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.62 | 0.62 | 0 | 1.23 |
| OTU35 | Unclassified <i>Clostridiales</i> | 2 | 0.62 | 0.62 | 0 | 1.23 |
| OTU232 | Unclassified family 0319-6G20 | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU172 | <i>Slackia</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU75 | Unclassified <i>Clostridiales</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU48 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU74 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU342 | <i>Ruminococcus</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU360 | Unclassified <i>Lachnospiraceae</i> | 2 | 0.59 | 0.03 | 0.56 | 0.62 |
| OTU127 | <i>Sphingomonas</i> | 2 | 0.56 | 0.56 | 0 | 1.11 |
| OTU29 | Unclassified <i>Clostridiales</i> | 2 | 0.56 | 0.56 | 0 | 1.11 |
| OTU22 | <i>Turicibacter</i> | 2 | 0.56 | 0.56 | 0 | 1.11 |

| | | | | | | |
|--------|---|---|------|------|---|------|
| OTU165 | Unclassified <i>Lachnospiraceae</i> | 2 | 0.56 | 0.56 | 0 | 1.11 |
| OTU363 | Unclassified <i>RF39</i> | 2 | 0.56 | 0.56 | 0 | 1.11 |
| OTU14 | Unclassified <i>Streptophyta</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU17 | Unclassified <i>Streptophyta</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU25 | Unclassified <i>Streptophyta</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU57 | Unclassified <i>Streptophyta</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU7 | <i>Lactobacillus</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU110 | <i>Phenylobacterium</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU107 | Unclassified <i>Ruminococcaceae</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU364 | Unclassified <i>Peptostreptococcaceae</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU411 | Unclassified <i>Clostridiales</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |
| OTU33 | Unclassified <i>Enterobacteriaceae</i> | 2 | 0.31 | 0.31 | 0 | 0.62 |

39

^aTaxonomic classification based on the 13_8 Greengenes default database in Qiime (version 1.9.1).

40 **TABLE S3** Differences in relative abundance (%) of most abundant operational taxonomic units (OTUs) in feces at 16 and 29 days post-hatch
 41 (dph) in low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)

| Item | Taxonomy (Genus) ^{a,b} | 16 dph | | | | 29 dph | | | | SEM | T ^c | P value | | | |
|-------|---------------------------------|---------|----------|---------|----------|---------|----------|---------|----------|-------|----------------|---------|-------|---------|-----------|
| | | FMT | | CT | | FMT | | CT | | | | FMT | RFI | FMT×RFI | T×FMT×RFI |
| | | Low RFI | High RFI | Low RFI | High RFI | Low RFI | High RFI | Low RFI | High RFI | | | | | | |
| OTU1 | <i>Escherichia/Shigella</i> | 29.79 | 52.21 | 30.47 | 41.94 | 51.47 | 49.59 | 47.33 | 52.14 | 7.638 | 0.032 | 0.619 | 0.105 | 0.850 | 0.401 |
| OTU2 | <i>Lactobacillus</i> | 11.72 | 8.43 | 10.24 | 6.17 | 5.22 | 5.31 | 4.14 | 2.05 | 2.766 | 0.020 | 0.280 | 0.211 | 0.691 | 0.929 |
| OTU3 | <i>Turicibacter</i> | 0.99 | 1.76 | 0.37 | 0.20 | 12.11 | 12.02 | 8.42 | 5.78 | 3.015 | <0.001 | 0.164 | 0.804 | 0.686 | 0.793 |
| OTU7 | <i>Lactobacillus</i> | 4.68 | 5.39 | 7.63 | 8.06 | 0.66 | 0.96 | 1.96 | 0.85 | 1.904 | <0.001 | 0.237 | 0.955 | 0.768 | 0.809 |
| OTU4 | <i>Eubacterium</i> | 5.74 | 2.19 | 3.88 | 6.02 | 0.52 | 1.37 | 1.70 | 1.98 | 1.600 | 0.001 | 0.483 | 0.958 | 0.339 | 0.325 |
| OTU6 | <i>Escherichia/Shigella</i> | 1.71 | 2.96 | 1.79 | 2.37 | 3.15 | 3.01 | 2.85 | 3.19 | 0.435 | 0.007 | 0.628 | 0.114 | 0.881 | 0.430 |
| OTU5 | <i>Lactobacillus</i> | 4.63 | 3.27 | 4.95 | 1.65 | 2.16 | 0.86 | 1.48 | 0.56 | 1.393 | 0.026 | 0.546 | 0.073 | 0.682 | 0.880 |
| OTU8 | <i>Lactobacillus</i> | 3.23 | 2.40 | 3.75 | 1.14 | 1.54 | 0.58 | 1.11 | 0.40 | 1.056 | 0.032 | 0.636 | 0.079 | 0.590 | 0.863 |
| OTU16 | <i>Anaerobacterium</i> | 0.83 | 0.22 | 2.15 | 0.86 | 0.23 | 0.74 | 1.67 | 1.50 | 0.773 | 0.968 | 0.086 | 0.519 | 0.568 | 0.731 |
| OTU15 | <i>Eubacterium</i> | 1.43 | 0.52 | 0.98 | 1.42 | 0.13 | 0.39 | 0.42 | 0.47 | 0.391 | 0.002 | 0.530 | 0.902 | 0.383 | 0.295 |
| OTU22 | <i>Turicibacter</i> | 0.09 | 0.16 | 0.03 | 0.02 | 1.25 | 1.16 | 0.84 | 0.55 | 0.288 | <0.001 | 0.141 | 0.699 | 0.734 | 0.708 |
| OTU26 | <i>Gracilibacter</i> | 0.31 | 0.05 | 0.32 | 0.15 | 0.49 | 0.20 | 0.67 | 1.18 | 0.331 | 0.065 | 0.196 | 0.824 | 0.367 | 0.480 |
| OTU28 | <i>Anaerobacterium</i> | 0.28 | 0.11 | 0.76 | 0.36 | 0.21 | 0.31 | 0.74 | 0.41 | 0.220 | 0.783 | 0.055 | 0.250 | 0.347 | 0.910 |
| OTU13 | <i>Acinetobacter</i> | 0.12 | 0.06 | 0.008 | 0.04 | 0.17 | 1.27 | 0.43 | 0.98 | 0.394 | 0.020 | 0.886 | 0.158 | 0.693 | 0.435 |
| OTU21 | <i>Lactobacillus</i> | 0.64 | 0.40 | 0.69 | 0.21 | 0.32 | 0.13 | 0.22 | 0.08 | 0.196 | 0.048 | 0.574 | 0.051 | 0.703 | 0.868 |
| OTU34 | <i>Turicibacter</i> | 0.03 | 0.04 | 0.006 | 0.007 | 0.66 | 0.37 | 0.60 | 0.58 | 0.137 | <0.001 | 0.789 | 0.409 | 0.474 | 0.712 |
| OTU46 | <i>Lactobacillus</i> | 0.34 | 0.38 | 0.54 | 0.61 | 0.05 | 0.09 | 0.16 | 0.07 | 0.142 | <0.001 | 0.238 | 0.899 | 0.802 | 0.776 |
| OTU33 | <i>Escherichia/Shigella</i> | 0.08 | 0.09 | 0.05 | 0.08 | 0.57 | 0.39 | 0.51 | 0.44 | 0.100 | <0.001 | 0.842 | 0.446 | 0.600 | 0.786 |
| OTU27 | <i>Lactobacillus</i> | 0.52 | 0.34 | 0.40 | 0.27 | 0.19 | 0.22 | 0.16 | 0.08 | 0.117 | 0.014 | 0.262 | 0.270 | 0.835 | 0.851 |
| OTU30 | <i>Lactobacillus</i> | 0.46 | 0.33 | 0.51 | 0.17 | 0.20 | 0.08 | 0.13 | 0.04 | 0.138 | 0.016 | 0.544 | 0.076 | 0.640 | 0.854 |

| | | | | | | | | | | | | | | | |
|--------|-----------------------------|------|------|-------|-------|------|------|------|-------|-------|--------|-------|-------|-------|-------|
| OTU35 | <i>Eisenbergiella</i> | 0.34 | 0.18 | 0.19 | 0.81 | 0.02 | 0.04 | 0.02 | 0.27 | 0.167 | 0.009 | 0.176 | 0.172 | 0.055 | 0.562 |
| OTU58 | <i>Anaerobacterium</i> | 0.17 | 0.04 | 0.50 | 0.15 | 0.05 | 0.18 | 0.39 | 0.32 | 0.174 | 0.873 | 0.090 | 0.444 | 0.439 | 0.687 |
| OTU44 | <i>Turcibacter</i> | 0.04 | 0.07 | 0.01 | 0.007 | 0.52 | 0.49 | 0.36 | 0.25 | 0.123 | <0.001 | 0.164 | 0.736 | 0.745 | 0.794 |
| OTU31 | [<i>Ruminococcus</i>] | 0.60 | 0.12 | 0.26 | 0.33 | 0.06 | 0.05 | 0.07 | 0.09 | 0.126 | 0.003 | 0.840 | 0.310 | 0.132 | 0.241 |
| OTU32 | <i>Saccharofermentans</i> | 0.50 | 0.11 | 0.15 | 0.29 | 0.13 | 0.04 | 0.13 | 0.15 | 0.125 | 0.106 | 0.858 | 0.337 | 0.062 | 0.525 |
| OTU56 | <i>Anaerobacterium</i> | 0.06 | 0.04 | 0.20 | 0.19 | 0.12 | 0.09 | 0.35 | 0.15 | 0.093 | 0.395 | 0.040 | 0.352 | 0.549 | 0.765 |
| OTU42 | <i>Lactobacillus</i> | 0.28 | 0.20 | 0.29 | 0.10 | 0.14 | 0.06 | 0.09 | 0.04 | 0.083 | 0.034 | 0.500 | 0.076 | 0.740 | 0.883 |
| OTU47 | <i>Lactobacillus</i> | 0.27 | 0.10 | 0.31 | 0.10 | 0.11 | 0.11 | 0.08 | 0.03 | 0.077 | 0.045 | 0.724 | 0.049 | 0.693 | 0.469 |
| OTU39 | [<i>Clostridium</i>] | 0.29 | 0.07 | 0.18 | 0.25 | 0.04 | 0.15 | 0.04 | 0.07 | 0.069 | 0.013 | 0.977 | 0.959 | 0.307 | 0.113 |
| OTU43 | <i>Lactobacillus</i> | 0.24 | 0.09 | 0.32 | 0.10 | 0.12 | 0.09 | 0.07 | 0.02 | 0.076 | 0.050 | 0.917 | 0.039 | 0.631 | 0.490 |
| OTU65 | [<i>Clostridium</i>] | 0.09 | 0.06 | 0.04 | 0.14 | 0.07 | 0.15 | 0.17 | 0.29 | 0.068 | 0.097 | 0.153 | 0.153 | 0.325 | 0.633 |
| OTU80 | <i>Acetivibrio</i> | 0.14 | 0.05 | 0.14 | 0.11 | 0.03 | 0.07 | 0.15 | 0.19 | 0.057 | 0.999 | 0.070 | 0.765 | 0.777 | 0.389 |
| OTU81 | <i>Anaerobacterium</i> | 0.24 | 0.01 | 0.13 | 0.07 | 0.17 | 0.05 | 0.13 | 0.06 | 0.088 | 0.910 | 0.787 | 0.050 | 0.320 | 0.952 |
| OTU89 | <i>Hespellia</i> | 0.14 | 0.02 | 0.16 | 0.28 | 0.05 | 0.04 | 0.03 | 0.07 | 0.067 | 0.030 | 0.126 | 0.854 | 0.131 | 0.398 |
| OTU53 | <i>Klebsiella</i> | 0.07 | 0.26 | 0.04 | 0.14 | 0.03 | 0.07 | 0.07 | 0.10 | 0.071 | 0.265 | 0.694 | 0.072 | 0.627 | 0.494 |
| OTU18 | <i>Klebsiella</i> | 0.08 | 0.03 | 0.16 | 0.19 | 0.06 | 0.03 | 0.07 | 0.11 | 0.057 | 0.263 | 0.034 | 0.926 | 0.334 | 0.840 |
| OTU68 | <i>Flintibacter</i> | 0.14 | 0.03 | 0.13 | 0.21 | 0.04 | 0.05 | 0.04 | 0.10 | 0.050 | 0.041 | 0.161 | 0.794 | 0.137 | 0.502 |
| OTU51 | <i>Lactobacillus</i> | 0.19 | 0.06 | 0.17 | 0.05 | 0.11 | 0.06 | 0.05 | 0.03 | 0.057 | 0.233 | 0.457 | 0.043 | 0.838 | 0.779 |
| OTU74 | <i>Eubacterium</i> | 0.19 | 0.08 | 0.11 | 0.17 | 0.02 | 0.05 | 0.05 | 0.06 | 0.052 | 0.004 | 0.753 | 0.956 | 0.391 | 0.405 |
| OTU71 | <i>Lactobacillus</i> | 0.13 | 0.10 | 0.13 | 0.09 | 0.06 | 0.07 | 0.05 | 0.03 | 0.033 | 0.018 | 0.487 | 0.323 | 0.663 | 0.929 |
| OTU95 | <i>Escherichia/Shigella</i> | 0.01 | 0.01 | 0.004 | 0.004 | 0.17 | 0.10 | 0.16 | 0.15 | 0.035 | <0.001 | 0.800 | 0.386 | 0.553 | 0.741 |
| OTU119 | <i>Anaerobacterium</i> | 0.05 | 0.02 | 0.17 | 0.05 | 0.03 | 0.06 | 0.10 | 0.11 | 0.046 | 0.963 | 0.057 | 0.426 | 0.485 | 0.446 |
| OTU96 | <i>Pseudoflavonifractor</i> | 0.11 | 0.03 | 0.08 | 0.13 | 0.02 | 0.03 | 0.04 | 0.11 | 0.036 | 0.096 | 0.145 | 0.590 | 0.081 | 0.432 |
| OTU67 | <i>Lactobacillus</i> | 0.13 | 0.05 | 0.13 | 0.04 | 0.08 | 0.05 | 0.04 | 0.02 | 0.043 | 0.214 | 0.477 | 0.037 | 0.964 | 0.789 |
| OTU84 | <i>Flintibacter</i> | 0.11 | 0.02 | 0.09 | 0.14 | 0.03 | 0.04 | 0.03 | 0.08 | 0.034 | 0.040 | 0.202 | 0.839 | 0.130 | 0.410 |
| OTU129 | <i>Lactobacillus</i> | 0.10 | 0.04 | 0.18 | 0.08 | 0.01 | 0.05 | 0.04 | 0.007 | 0.048 | 0.034 | 0.482 | 0.271 | 0.444 | 0.455 |

| | | | | | | | | | | | | | | | |
|--------|------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|-------|-------|-------|-------|
| OTU107 | <i>Flintibacter</i> | 0.16 | 0.006 | 0.04 | 0.10 | 0.03 | 0.05 | 0.06 | 0.07 | 0.038 | 0.386 | 0.771 | 0.583 | 0.090 | 0.087 |
| OTU103 | <i>Turicibacter</i> | 0.007 | 0.01 | 0.003 | 0.003 | 0.15 | 0.08 | 0.14 | 0.12 | 0.029 | <0.001 | 0.888 | 0.310 | 0.595 | 0.650 |
| OTU113 | <i>Comamonas</i> | 0.13 | 0.26 | 0.02 | 0.09 | 0.001 | 0.003 | 0.003 | 0.006 | 0.050 | 0.001 | 0.055 | 0.168 | 0.729 | 0.133 |
| OTU132 | <i>Lactobacillus</i> | 0.09 | 0.04 | 0.18 | 0.07 | 0.01 | 0.06 | 0.03 | 0.008 | 0.045 | 0.029 | 0.533 | 0.326 | 0.383 | 0.325 |
| OTU93 | <i>Lactobacillus</i> | 0.11 | 0.07 | 0.08 | 0.06 | 0.05 | 0.04 | 0.03 | 0.02 | 0.023 | 0.011 | 0.242 | 0.163 | 0.927 | 0.973 |
| OTU117 | [<i>Clostridium</i>] | 0.15 | 0.002 | 0.04 | 0.08 | 0.03 | 0.04 | 0.06 | 0.05 | 0.035 | 0.346 | 0.988 | 0.334 | 0.102 | 0.070 |
| OTU130 | <i>Anaerobacterium</i> | 0.03 | 0.01 | 0.08 | 0.07 | 0.04 | 0.04 | 0.11 | 0.06 | 0.035 | 0.468 | 0.087 | 0.421 | 0.724 | 0.919 |
| OTU150 | <i>Oscillibacter</i> | 0.13 | 0.01 | 0.13 | 0.08 | 0.02 | 0.02 | 0.03 | 0.03 | 0.048 | 0.063 | 0.506 | 0.239 | 0.596 | 0.621 |
| OTU77 | <i>Oscillibacter</i> | 0.10 | 0.06 | 0.05 | 0.12 | 0.01 | 0.07 | 0.01 | 0.02 | 0.032 | 0.023 | 0.785 | 0.312 | 0.525 | 0.281 |
| OTU98 | <i>Lactobacillus</i> | 0.09 | 0.07 | 0.10 | 0.03 | 0.05 | 0.02 | 0.04 | 0.01 | 0.028 | 0.044 | 0.534 | 0.074 | 0.515 | 0.872 |

42 Data are presented as least-square means and pooled SEM.

43 Low RFI FMT females, $n = 8$ /time point; low RFI FMT males, $n = 7$ /time point; high RFI FMT females, $n = 7$ /time point; high RFI FMT males, $n = 6$ /time point; low RFI CT
44 females, $n = 7$ /time point; low RFI CT males, $n = 7$ /time point; high RFI CT females, $n = 7$ /time point; high RFI CT males, $n = 7$ /time point.

45 ^aTaxonomic classification based on the National Center for Biotechnology Information (NCBI) nucleotide database using Blastn for taxonomic classification and the database
46 limited to the 16S rRNA target (<https://blast.ncbi.nlm.nih.gov/>).

47 ^bSequences not distinguishable between *Escherichia* and *Shigella*.

48 ^cT, time point.

49 **TABLE S4** BLAST search results for selected operational taxonomic units (OTUs)^{a,b}

| OTU | Blast hit (16S NCBI database) | Accession Number | Percent identity |
|-------|---|------------------|------------------|
| OTU1 | <i>Escherichia coli</i> strain JCM 1649 | NR_112558.1 | 100 |
| | <i>Shigella flexneri</i> strain ATCC 29903 | NR_026331.1 | 100 |
| OTU2 | <i>Lactobacillus salivarius</i> strain HO 66 | NR_028725.2 | 99 |
| OTU3 | <i>Turicibacter sanguinis</i> strain MOL361 | NR_028816.1 | 99 |
| OTU4 | <i>Eubacterium desmolans</i> strain ATCC 43058 | NR_044644.2 | 98 |
| OTU5 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 99 |
| OTU6 | <i>Escherichia coli</i> strain JCM 1649 | NR_112558.1 | 99 |
| | <i>Shigella flexneri</i> strain ATCC 29903 | NR_026331.1 | 99 |
| OTU7 | <i>Lactobacillus johnsonii</i> strain CIP 103620 | NR_117574.1 | 99 |
| OTU8 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 99 |
| OTU13 | <i>Acinetobacter bereziniae</i> strain ATCC 17924 | NR_117625.1 | 99 |
| OTU15 | <i>Eubacterium desmolans</i> strain ATCC 43058 | NR_044644.2 | 98 |
| OTU16 | <i>Anaerobacterium chartisolvans</i> strain T-1-35 | NR_125464.1 | 88 |
| OTU18 | <i>Klebsiella variicola</i> strain F2R9 | NR_025635.1 | 99 |
| OTU21 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 99 |
| OTU22 | <i>Turicibacter sanguinis</i> strain MOL361 | NR_028816.1 | 99 |
| OTU24 | <i>Romboutsia timonensis</i> strain DR1 | NR_144740.1 | 99 |
| OTU26 | <i>Gracilibacter thermotolerans</i> strain JW/YJL-S1 | NR_115693.1 | 87 |
| OTU27 | <i>Lactobacillus salivarius</i> strain HO 66 | NR_028725.2 | 99 |
| OTU28 | <i>Anaerobacterium chartisolvans</i> strain T-1-35 | NR_125464.1 | 89 |
| OTU29 | <i>Anaerobacterium chartisolvans</i> strain T-1-35 | NR_125464.1 | 88 |
| OTU30 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 99 |
| OTU31 | [<i>Ruminococcus</i>] <i>torques</i> strain VPI B2-51 | NR_036777.1 | 97 |
| OTU32 | <i>Saccharofermentans acetigenes</i> strain P6 | NR_115340.1 | 87 |
| OTU33 | <i>Escherichia coli</i> strain JCM 1649 | NR_112558.1 | 99 |
| | <i>Shigella flexneri</i> strain ATCC 29903 | NR_026331.1 | 99 |
| OTU34 | <i>Turicibacter sanguinis</i> strain MOL361 | NR_028816.1 | 92 |
| OTU35 | <i>Eisenbergiella massiliensis</i> strain AT11 | NR_144731.1 | 95 |
| OTU39 | [<i>Clostridium</i>] <i>saccharolyticum</i> strain WM1 | NR_102852.1 | 96 |
| OTU42 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 99 |
| OTU43 | <i>Lactobacillus salivarius</i> strain HO 66 | NR_028725.2 | 96 |
| OTU44 | <i>Turicibacter sanguinis</i> strain MOL361 | NR_028816.1 | 99 |
| OTU46 | <i>Lactobacillus johnsonii</i> strain CIP 103620 | NR_117574.1 | 99 |
| OTU47 | <i>Lactobacillus salivarius</i> strain HO 66 | NR_028725.2 | 97 |
| OTU48 | <i>Negativibacillus massiliensis</i> strain Marseille-P3213 | NR_147378.1 | 93 |
| OTU50 | <i>Gracilibacter thermotolerans</i> strain JW/YJL-S1 | NR_115693.1 | 87 |
| OTU51 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 96 |
| OTU52 | [<i>Clostridium</i>] <i>leptum</i> strain DSM 753 | NR_114789.1 | 97 |

| | | | |
|--------|---|-------------|-----|
| OTU53 | <i>Klebsiella oxytoca</i> strain NBRC 102593 | NR_114152.1 | 99 |
| OTU55 | <i>Clostridium disporicum</i> strain DS1 | NR_026491.1 | 100 |
| OTU56 | <i>Anaerobacterium chartisolvens</i> strain T-1-35 | NR_125464.1 | 88 |
| OTU58 | <i>Anaerobacterium chartisolvens</i> strain T-1-35 | NR_125464.1 | 88 |
| OTU60 | [<i>Clostridium</i>] <i>leptum</i> strain DSM 753 | NR_114789.1 | 94 |
| OTU64 | <i>Hespellia stercorisuis</i> strain PC18 | NR_025207.1 | 88 |
| OTU65 | [<i>Clostridium</i>] <i>leptum</i> strain DSM 753 | NR_114789.1 | 92 |
| OTU67 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 97 |
| OTU68 | <i>Flintibacter butyricus</i> strain BLS21 | NR_144611.1 | 98 |
| OTU70 | <i>Negativibacillus massiliensis</i> strain Marseille-P3213 | NR_147378.1 | 93 |
| OTU71 | <i>Lactobacillus salivarius</i> strain HO 66 | NR_028725.2 | 99 |
| OTU74 | <i>Eubacterium desmolans</i> strain ATCC 43058 | NR_044644.2 | 98 |
| OTU75 | <i>Eisenbergiella massiliensis</i> strain AT11 | NR_144731.1 | 95 |
| OTU77 | <i>Oscillibacter ruminantium</i> strain GH1 | NR_118156.1 | 95 |
| OTU79 | [<i>Clostridium</i>] <i>leptum</i> strain DSM 753 | NR_114789.1 | 95 |
| OTU80 | <i>Acetivibrio cellulolyticus</i> strain CD2 | NR_025917.1 | 95 |
| OTU81 | <i>Anaerobacterium chartisolvens</i> strain T-1-35 | NR_125464.1 | 89 |
| OTU83 | <i>Anaerotruncus colihominis</i> strain WAL 14565 | NR_027558.1 | 99 |
| OTU84 | <i>Flintibacter butyricus</i> strain BLS21 | NR_144611.1 | 98 |
| OTU88 | <i>Gracilibacter thermotolerans</i> strain JW/YJL-S1 | NR_115693.1 | 86 |
| OTU89 | <i>Hespellia porcina</i> strain PC80 | NR_025206.1 | 96 |
| OTU93 | <i>Lactobacillus salivarius</i> strain HO 66 | NR_028725.2 | 98 |
| OTU95 | <i>Escherichia coli</i> strain JCM 1649 | NR_112558.1 | 92 |
| | <i>Shigella flexneri</i> strain ATCC 29903 | NR_026331.1 | 92 |
| OTU96 | <i>Pseudoflavonifractor phocaensis</i> strain Marseille-P3064 | NR_147370.1 | 96 |
| OTU97 | <i>Oscillibacter ruminantium</i> strain GH1 | NR_118156.1 | 95 |
| OTU98 | <i>Lactobacillus crispatus</i> strain DSM 20584 | NR_119274.1 | 99 |
| OTU103 | <i>Turicibacter sanguinis</i> strain MOL361 | NR_028816.1 | 91 |
| OTU107 | <i>Flintibacter butyricus</i> strain BLS21 | NR_144611.1 | 94 |
| OTU113 | <i>Comamonas thiooxydans</i> strain S23 | NR_115741.1 | 99 |
| OTU117 | [<i>Clostridium</i>] <i>viride</i> strain T2-7 | NR_026204.1 | 92 |
| OTU119 | <i>Anaerobacterium chartisolvens</i> strain T-1-35 | NR_125464.1 | 87 |
| OTU129 | <i>Lactobacillus johnsonii</i> strain CIP 103620 | NR_117574.1 | 97 |
| OTU130 | <i>Anaerobacterium chartisolvens</i> strain T-1-35 | NR_125464.1 | 88 |
| OTU132 | <i>Lactobacillus johnsonii</i> strain CIP 103620 | NR_117574.1 | 95 |
| OTU150 | <i>Oscillibacter ruminantium</i> strain GH1 | NR_118156.1 | 95 |

50 ^aBLAST search was performed for the most abundant OTUs in the fecal microbiota transplant as well as for the

51 OTUs in feces differently affected by time point, fecal microbiota transplant or residual feed intake.

52 ^bNational Center for Biotechnology Information (NCBI) nucleotide database (<https://blast.ncbi.nlm.nih.gov/>);

53 last accessed 12/10/2017.

54 **TABLE S5** Dietary ingredients and chemical composition of diets (on as-fed basis)

| Item | Starter 1-8 days post-hatch | Grower 9-20 days post-hatch | Finisher 21-30 days post-hatch |
|---|--------------------------------|--------------------------------|-----------------------------------|
| Ingredient (%) | | | |
| Corn | 56.392 | 61.772 | 63.928 |
| Soybean meal | 37.032 | 31.432 | 29.068 |
| Soybean oil | 2.284 | 2.676 | 3.412 |
| Monocalcium phosphate | 1.460 | 1.412 | 1.240 |
| Calcium carbonate | 1.372 | 1.280 | 1.160 |
| DL-Methionine | 0.352 | 0.308 | 0.256 |
| Natrium bicarbonate | 0.204 | 0.212 | 0.136 |
| Lysine-HCL 98 | 0.140 | 0.148 | 0.044 |
| Salt | 0.120 | 0.120 | 0.156 |
| L-Threonine | 0.044 | 0.040 | 0 |
| Premix ¹ | 0.600 | 0.600 | 0.600 |
| Analyzed chemical composition, g/kg dry matter (DM) | | | |
| DM | 882 | 885 | 879 |
| Crude protein | 228 | 207 | 194 |
| Crude fat | 51.1 | 47.5 | 61.0 |
| Crude fiber | 28.0 | 29.0 | 30.1 |
| Crude ash | 52.6 | 50.0 | 46.3 |
| Starch | 356 | 388 | 401 |
| Sugar | 55.0 | 49.9 | 45.4 |
| Calcium | 8.88 | 8.39 | 7.63 |
| Phosphorus | 6.90 | 7.05 | 6.66 |
| ME (MJ/kg) | 12.0 | 12.0 | 12.4 |

55 ¹Provided per kilogram of complete starter diet (Garant - Tiernahrung GmbH, Pöchlarn, Austria): 12,500 IU of
56 vitamin A, 5,000 IU of vitamin D₃, 75.0 mg of vitamin E, 6.0 mg of vitamin K₃, 2.50 mg of vitamin B₁, 7.0 mg
57 of vitamin B₂, 4.50 mg of vitamin B₆, 0.025 mg of vitamin B₁₂, 60.0 mg of nicotinic acid, 15.0 mg of pantothenic
58 acid, 1.0 mg of folic acid, 0.25 mg of biotin, 1,582.065 mg of choline, 400.322 mg of choline chloride, 115.20
59 mg of betaine, 19.98 mg of ethoxyquin, 900.004 FTU of 6Phytase, 0.564 g of β-glucan, 2.428 % of C 18:2,
60 2.804 % of polyenic acid, 30.059 mg of F-Xanto (total). Provided per kilogram of complete grower diet (Garant
61 - Tiernahrung GmbH, Pöchlarn, Austria): 12,500 IU of vitamin A, 5,000 IU of vitamin D₃, 75.0 mg of vitamin E,
62 6.0 mg of vitamin K₃, 2.50 mg of vitamin B₁, 7.0 mg of vitamin B₂, 4.50 mg of vitamin B₆, 0.025 mg of vitamin
63 B₁₂, 60.0 mg of nicotinic acid, 15.0 mg of pantothenic acid, 1.0 mg of folic acid, 0.25 mg of biotin, 1,457.765
64 mg of choline, 400.322 mg of choline chloride, 115.20 mg of betaine, 19.98 mg of ethoxyquin, 900.004 FTU of
65 6Phytase, 0.618 g of β-glucan, 2.692 % of C 18:2, 3.103% of polyenic acid, 30.866 mg of F-Xanto (total).

66 Provided per kilogram of complete finisher diet (Garant - Tiernahrung GmbH, Pöchlarn, Austria): 5,000 IU of
67 vitamin D₃, 75.0 mg of vitamin E, 6.0 mg of vitamin K₃, 2.50 mg of vitamin B₁, 7.0 mg of vitamin B₂, 4.5 mg of
68 vitamin B₆, 0.025 mg of vitamin B₁₂, 60.0 mg of nicotinic acid, 15.0 mg of pantothenic acid, 1.0 mg of folic acid,
69 0.25 mg of biotin, 1,404.717 mg of choline, 400.322 mg of choline chloride, 115.20 mg of betaine, 19.98 mg of
70 ethoxyquin, 900.004 FTU of 6Phytase, 0.639 g of β-glucan, 3.098 % of C 18:2, 3.572 % of polyenic acid, 31.189
71 mg of F-Xanto (total).