

Supplementary materials

Table S1: Significant relative abundance taxa in in gut microbiome composition in naïve mice subjected to FMT from mice exposed to RA and IH and treated with VSL3

| Taxon | Relative Abundance (Mean \pm SD) | | | | ANCOM | ALDEx2 | |
|--|------------------------------------|--------------------|-------------------|--------------------|---------|----------|----------|
| | RA FMT | RA FMT PRO | IH FMT | IH FMT PRO | W score | glm.ep | glm.eBH |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Dubosiella; s__uncultured_bacterium | 3.75% \pm 1.23% | 0.44% \pm 0.27% | 1.77% \pm 0.89% | 15.05% \pm 5.65% | | 6.96E-09 | 4.05E-06 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales | 0.59% \pm 0.17% | 0.91% \pm 0.26% | 0.69% \pm 0.05% | 0.32% \pm 0.02% | | 8.86E-08 | 2.11E-05 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 0.08% \pm 0.03% | 0.15% \pm 0.04% | 0.41% \pm 0.04% | 0.26% \pm 0.07% | | 8.94E-08 | 2.24E-05 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales | 0.72% \pm 0.29% | 0.19% \pm 0.05% | 0.07% \pm 0.04% | 0.16% \pm 0.07% | | 5.72E-07 | 1.13E-04 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 0.41% \pm 0.16% | 0.33% \pm 0.02% | 0.00% \pm 0.00% | 0.00% \pm 0.00% | 1700 | 1.25E-06 | 1.67E-04 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Lactococcus; s__Lactococcus_lactis | 0.00% \pm 0.00% | 0.11% \pm 0.10% | 0.00% \pm 0.00% | 0.26% \pm 0.30% | 1591 | 7.52E-06 | 5.09E-04 |
| d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Sutterellaceae; g__Parasutterella; s__uncultured_organism | 0.25% \pm 0.13% | 1.00% \pm 0.17% | 0.11% \pm 0.10% | 0.16% \pm 0.04% | | 4.14E-06 | 5.30E-04 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_organism | 0.67% \pm 0.36% | 0.01% \pm 0.01% | 0.26% \pm 0.09% | 0.17% \pm 0.09% | 1623 | 7.93E-06 | 6.13E-04 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 19.29% \pm 4.36% | 17.86% \pm 4.95% | 8.05% \pm 1.08% | 6.76% \pm 3.20% | | 4.97E-06 | 6.58E-04 |
| d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Bifidobacteriales; f__Bifidobacteriaceae; g__Bifidobacterium; s__Bifidobacterium_animalis | 0.00% \pm 0.00% | 0.13% \pm 0.06% | 0.00% \pm 0.00% | 0.15% \pm 0.09% | 1631 | 2.05E-05 | 1.09E-03 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 0.35% \pm 0.11% | 0.30% \pm 0.05% | 0.11% \pm 0.03% | 0.36% \pm 0.13% | | 2.28E-05 | 1.83E-03 |
| d__Bacteria; p__Firmicutes; c__Bacilli; | 0.65% \pm | 0.04% \pm | 0.16% \pm | 2.40% \pm | | 5.17E-05 | 2.93E-03 |

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|---|------------------|------------------|-------------------|------------------|------|----------|----------|
| o__Erysipelotrichales; f__Erysipelotrichaceae; g__Dubosiella; s__uncultured_bacterium | 0.22% | 0.06% | 0.08% | 0.89% | | | |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 0.42% ± 0.13% | 0.12% ± 0.02% | 0.30% ± 0.10% | 0.41% ± 0.21% | | 5.08E-05 | 3.52E-03 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium | 0.24% ± 0.14% | 0.66% ± 0.19% | 0.19% ± 0.09% | 0.55% ± 0.10% | | 6.14E-05 | 4.14E-03 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus | 5.89% ± 2.04% | 1.99% ± 0.41% | 10.49% ± 8.26% | 2.20% ± 0.45% | | 6.79E-05 | 4.72E-03 |
| d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Atopobiaceae; g__Coriobacteriaceae_UCG-002; s__uncultured_bacterium | 0.13% ± 0.09% | 0.21% ± 0.15% | 0.07% ± 0.02% | 0.69% ± 0.31% | | 1.22E-04 | 6.89E-03 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales | 0.45% ± 0.27% | 0.83% ± 0.22% | 0.05% ± 0.05% | 1.92% ± 0.89% | | 2.62E-04 | 9.45E-03 |
| d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Eggerthellaceae; g__Enterorhabdus | 0.10% ± 0.05% | 0.05% ± 0.02% | 0.17% ± 0.04% | 0.19% ± 0.02% | | 2.33E-04 | 9.79E-03 |
| d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__uncultured; g__uncultured; s__Azospirillum_sp. | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.11% ± 0.05% | 1577 | 5.48E-04 | 1.21E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.13% ± 0.12% | 0.00% ± 0.00% | 1557 | 5.36E-04 | 1.27E-02 |
| d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Sutterellaceae; g__Parasutterella; s__uncultured_bacterium | 0.70% ± 0.22% | 0.43% ± 0.09% | 0.97% ± 0.18% | 1.15% ± 0.22% | | 3.64E-04 | 1.47E-02 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__RF39; f__RF39; g__RF39 | 0.01% ± 0.00% | 0.00% ± 0.00% | 0.02% ± 0.01% | 0.05% ± 0.05% | | 7.27E-04 | 1.51E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridia_UCG-014; f__Clostridia_UCG-014; g__Clostridia_UCG-014 | 0.00% ± 0.01% | 0.01% ± 0.02% | 0.17% ± 0.08% | 0.03% ± 0.02% | | 5.52E-04 | 1.60E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridia_UCG-014; f__Clostridia_UCG-014; g__Clostridia_UCG-014 | 0.01% ± 0.02% | 0.19% ± 0.13% | 0.18% ± 0.07% | 0.02% ± 0.03% | | 6.09E-04 | 1.67E-02 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 0.21% ± 0.13% | 0.08% ± 0.02% | 0.08% ± 0.02% | 0.03% ± 0.02% | | 5.29E-04 | 1.73E-02 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 1.20% ± 0.28% | 2.24% ± 0.93% | 2.72% ± 0.96% | 3.39% ± 0.56% | | 5.48E-04 | 1.98E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; | 0.00% ± | 0.01% ± | 0.04% ± | 0.03% ± | | 1.28E-03 | 2.05E-02 |

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| o__Clostridiales; f__Clostridiaceae; g__Clostridium_sensu_stricto_1 | 0.00% | 0.01% | 0.01% | 0.01% | | | |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__Oscillospiraceae; g__uncultured; s__uncultured_Clostridiales | 0.19% ± 0.10% | 0.24% ± 0.11% | 0.33% ± 0.09% | 0.73% ± 0.30% | | 7.03E-04 | 2.27E-02 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Lleibacterium; s__Lleibacterium_valens | 28.57% ± 5.19% | 28.77% ± 13.01% | 39.26% ± 7.85% | 16.60% ± 5.86% | | 6.82E-04 | 2.35E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__Oscillospiraceae; g__Colidextribacter | 0.06% ± 0.03% | 0.00% ± 0.00% | 0.03% ± 0.04% | 0.05% ± 0.03% | | 1.64E-03 | 2.66E-02 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium | 0.04% ± 0.02% | 0.22% ± 0.14% | 0.43% ± 0.33% | 0.32% ± 0.16% | | 8.68E-04 | 2.68E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridia_UCG-014; f__Clostridia_UCG-014; g__Clostridia_UCG-014 | 0.00% ± 0.00% | 0.03% ± 0.02% | 0.15% ± 0.05% | 0.01% ± 0.01% | | 1.70E-03 | 2.99E-02 |
| d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium | 1.61% ± 0.66% | 1.11% ± 0.10% | 2.83% ± 1.25% | 3.75% ± 0.78% | | 1.06E-03 | 3.14E-02 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelatoclostridiaceae; g__Erysipelatoclostridium; s__unidentified | 0.09% ± 0.06% | 0.07% ± 0.02% | 0.00% ± 0.01% | 0.00% ± 0.00% | | 2.08E-03 | 3.31E-02 |
| d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Eggerthellaceae; g__Enterorhabdus; s__uncultured_bacterium | 0.05% ± 0.03% | 0.15% ± 0.01% | 0.04% ± 0.03% | 0.05% ± 0.01% | | 1.45E-03 | 3.44E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.03% ± 0.01% | | 2.58E-03 | 3.78E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae | 0.10% ± 0.08% | 0.00% ± 0.00% | 0.03% ± 0.03% | 0.00% ± 0.00% | | 3.20E-03 | 3.80E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__UCG-010; g__UCG-010; s__unidentified | 0.04% ± 0.02% | 0.09% ± 0.03% | 0.01% ± 0.01% | 0.00% ± 0.00% | | 3.93E-03 | 3.84E-02 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Faecalibaculum; s__uncultured_bacterium | 0.14% ± 0.04% | 0.62% ± 0.36% | 0.30% ± 0.15% | 0.14% ± 0.01% | | 1.60E-03 | 3.91E-02 |
| d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus_danieliae | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.03% ± 0.01% | 0.00% ± 0.00% | | 2.39E-03 | 4.16E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__[Eubacterium]_coprostanoligenes_group; g__[Eubacterium]_coprostanoligenes_group; s__uncultured_bacterium | 0.00% ± 0.00% | 0.00% ± 0.00% | 0.06% ± 0.05% | 0.01% ± 0.01% | | 3.15E-03 | 4.34E-02 |
| d__Bacteria; p__Firmicutes; c__Clostridia; | 0.04% ± | 0.33% ± | 0.05% ± | 0.00% ± | | 2.80E-03 | 4.66E-02 |

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| o__Oscillospirales; f__Ruminococcaceae; g__Incertae_Sedis; s__uncultured_bacterium | 0.05% | 0.12% | 0.06% | 0.00% | | | |
| d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptococcales; f__Peptococcaceae; g__uncultured; s__unidentified | 0.04% ± 0.05% | 0.00% ± 0.00% | 0.03% ± 0.02% | 0.07% ± 0.03% | | 5.07E-03 | 4.76E-02 |
| d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Eggerthellaceae; g__Gordonibacter; s__uncultured_bacterium | 0.13% ± 0.08% | 0.19% ± 0.04% | 0.08% ± 0.05% | 0.05% ± 0.01% | | 2.54E-03 | 4.91E-02 |