***Supplementary table 1. Ventilatory response to the tenth (final) intermittent hypoxia challenge in behaving rats during quiet rest***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| % change from baseline | VEH (n=10) | ABX (n=10) | VEH-FMT (n=10) | ABX-FMT (n=10) | One-way ANOVA |
| *f*R | 75 ± 28 | 61 ± 18 | 51 ± 34 | 67 ± 24 | 0.337 |
| *VT* | 24 ± 8 | 25 ± 8 | 25 ± 13 | 23 ± 10 | 0.931 |
| *VE* | 110 ± 22 | 98 ± 19 | 89 ± 39 | 82 ± 33 | 0.202 |

*f*R*,* respiratory frequency; *VT*, tidal volume; *VE*, minute ventilation; VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA or non-parametric Kruskal-Wallis, where appropriate.

***Supplementary table 2. Ventilation following exposure to acute intermittent hypoxia in behaving rats during quiet rest***

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| % change from baseline | VEH (n=10) | ABX (n=10) | VEH-FMT (n=10) | ABX-FMT (n=9) | One-way ANOVA | VEH vs ABX | VEH-FMT vs ABX-FMT | VEH vs VEH-FMT | ABX vs ABX-FMT | VEH vs ABX-FMT | ABX vs VEH-FMT |
| *fR* | 0 ± 27 | 6 ± 13 | - 6 ± 33 | 4 ± 14 | 0.692 | - | - | - | - | - | - |
| *VT* | -4 ± 13 | 8 ± 16 | -2 ± 12 | -11 ± 8 | **0.029** | 0.364 | 0.804 | 0.999 | **0.02** | 0.999 | 0.64 |
| *VE* | 4 ± 20 | 16 ± 18 | -6 ± 27 | -7 ± 16 | 0.075 | - | - | - | - | - | - |

*fR,* respiratory frequency; *VT*, tidal volume; *VE,* minute ventilation; VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic treated followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA with Bonferroni *post hoc* where appropriate. Each p-value is adjusted to account for multiple comparisons. *p*-values highlight significant differences.

***Supplementary table 3. Cardiorespiratory responsiveness to hypoxic and* hypoxic hypercapnic** ***chemostimulation in urethane anaesthetised rats***

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | ABX (n=8) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA | VEH vs ABX | VEH-FMT vs ABX-FMT | VEH vs VEH-FMT | ABX vs ABX-FMT | VEH vs ABX-FMT | ABX vs VEH-FMT |
| Hypoxia |  |  |  |  |  |  |  |  |  |  |  |
| Δ *fR (brpm)* | 30 ± 15 | 34 ± 11 | 29 ± 21 | 30 ± 24 | 0.824 | - | - | - | - | - | - |
| Δ *VT*(ml 100g-1) | 0.05 ± 0.06 | 0.06 ± 0.03 | 0.08 ± 0.05 | 0.06 ± 0.07 | 0.431 | - | - | - | - | - | - |
| Δ *VE* (ml min-1 100g-1) | 20 ± 10 | 19 ± 7 | 27 ± 12 | 20 ± 16 | 0.443 | - | - | - | - | - | - |
| Δ MAP (mmHg) | -31 ± 10 | -30 ± 16 | -20 ± 12 | -22 ± 17 | 0.228 | - | - | - | - | - | - |
| Δ DBP (mmHg) | -24 ± 7 | -27 ± 12 | -19 ± 10 | -19 ± 11 | 0.221 | - | - | - | - | - | - |
| Δ SBP (mmHg) | -44 ± 17 | -41 ± 16 | -29 ± 18 | -32 ± 24 | 0.299 | - | - | - | - | - | - |
| Δ HR (bpm) | 19 ± 24 | 21 ± 19 | 34 ± 16 | 28 ± 25 | 0.451 | - | - | - | - | - | - |
| Hypoxic Hypercapnia | |  |  |  |  |  |  |  |  |  |  |
| Δ *fR (brpm)* | 31 ± 7 | 36 ± 12 | 29 ± 11 | 33 ± 12 | 0.581 | - | - | - | - | - | - |
| Δ *VT*(ml 100g-1) | 0.17 ± 0.07 | 0.16 ± 0.03 | 0.18 ± 0.07 | 0.17 ± 0.05 | 0.84 | - | - | - | - | - | - |
| Δ *VE*(ml min-1 100g-1) | 31 ± 5 | 31 ± 7 | 38 ± 8 | 33 ± 8 | 0.14 | - | - | - | - | - | - |
| Δ MAP (mmHg) | -20 ± 10 | -18 ± 11 | -2 ± 10 | -10 ± 16 | **0.013** | 0.999 | 0.999 | **0.017** | 0.999 | 0.424 | 0.066 |
| Δ DBP (mmHg) | -16 ± 8 | -16 ± 10 | -6 ± 6 | -10 ± 11 | 0.062 | - | - | - | - | - | - |
| Δ SBP (mmHg) | -30 ± 18 | -19 ± 18 | -12 ± 12 | -17 ± 21 | 0.155 | - | - | - | - | - | - |
| Δ HR (bpm) | 15 ± 14 | 12 ± 15 | 29 ± 12 | 21 ± 12 | 0.052 | - | - | - | - | - | - |

*fR,* respiratory frequency (brpm, breaths per min); *VT*, tidal volume; *VE,* minute ventilation; MAP, mean arterial pressure; DBP, diastolic blood pressure; SBP, systolic blood pressure; HR, heart rate (bpm, beats per min); VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA with Bonferroni *post hoc* where appropriate, or non-parametric Kruskal-Wallis test where appropriate. Data are shown as absolute change from baseline. Each p-value is adjusted to account for multiple comparisons. *p*-values shown in bold highlight significant differences.

***Supplementary table 4. Cardiorespiratory responsiveness to hypercapnic chemostimulation in urethane anaesthetised rats***

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | | ABX (n=8) | | VEH-FMT (n=9) | | ABX-FMT (n=10) | | One-way ANOVA | |
| 5% Carbon Dioxide | | |  | |  | |  | |  | |
| Δ *fR (brpm)* | 14 ± 14 | | 21 ± 19 | | 7 ± 6 | | 10 ± 8 | | 0.131 | |
| Δ *VT*(ml 100g-1) | 0.08 ± 0.12 | | 0.09 ± 0.07 | | 0.1 ± 0.05 | | 0.11 ± 0.02 | | 0.988 | |
| Δ *VE*(ml min-1 100g-1) | 15 ± 3.9 | | 18 ± 5.3 | | 16 ± 6.8 | | 15 ± 6 | | 0.557 | |
| Δ MAP (mmHg) | 10 ± 8 | | 5 ± 5 | | 8 ± 6 | | 5 ± 7 | | 0.634 | |
| Δ DBP (mmHg) | 4 ± 2 | | 4 ± 4 | | 5 ± 3 | | 4 ± 5 | | 0.989 | |
| Δ SBP (mmHg) | 7 ± 6 | | 6 ± 6 | | 7 ± 5 | | 6 ± 9 | | 0.98 | |
| Δ HR (bpm) | -2 ± 9 | | -8 ± 18 | | -2 ± 13 | | -4 ± 9 | | 0.699 | |
| 10% Carbon Dioxide | | | | |  | |  | |  | |
| Δ *fR (brpm)* | 15 ± 20 | | 27 ± 20 | | 6 ± 11 | | 16 ± 12 | | 0.079 | |
| Δ *VT*(ml 100g-1) | 0.25 ± 0.12 | | 0.24 ± 0.08 | | 0.26 ± 0.09 | | 0.28 ± 0.05 | | 0.823 | |
| Δ *VE*(ml min-1 100g-1) | | 32 ± 7.5 | | 38 ± 7.2 | | 32 ± 10.6 | | 36 ± 10.8 | | 0.491 |
| Δ MAP (mmHg) | | 19 ± 9 | | 14 ± 7 | | 13 ± 7 | | 12 ± 8 | | 0.166 |
| Δ DBP (mmHg) | | 12 ± 5 | | 14 ± 7 | | 10 ± 4 | | 9 ± 6 | | 0.163 |
| Δ SBP (mmHg) | | 22 ± 10 | | 16 ± 8 | | 17 ± 8 | | 14 ± 11 | | 0.342 |
| Δ HR (bpm) | | 8 ± 13 | | 3 ± 27 | | 6 ± 26 | | 2 ± 11 | | 0.917 |

*fR,* respiratory frequency (brpm, breaths per min); *VT*, tidal volume; *VE*, minute ventilation; MAP, mean arterial pressure; DBP, diastolic blood pressure; SBP, systolic blood pressure; HR, heart rate (bpm, beats per min); VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA or non-parametric Kruskal-Wallis test, where appropriate. Data are shown as absolute change from baseline.

***Supplementary table 5. Diaphragm EMG activity during baseline and chemostimulation in urethane anaesthetised rats***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | VEH (n=9-10) | ABX (n=8) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA |
| Baseline |  |  |  |  |  |
| Area under the curve (mV.s) | 32 ± 15 | 28 ± 10 | 32 ± 18 | 33 ± 14 | 0.904 |
| Hypoxia |  |  |  |  |  |
| Area under the curve (% change from baseline) | -12 ± 12 | -12 ± 32 | 1 ± 16 | -5 ± 16 | 0.162 |
| 5% Carbon Dioxide | |  |  |  |  |
| Area under the curve (% change from baseline) | 6 ± 7 | 16 ± 14 | 9 ± 10 | 15 ± 10 | 0.138 |
| 10% Carbon Dioxide | |  |  |  |  |
| Area under the curve (% change from baseline) | 29 ± 12 | 21 ± 12 | 24 ± 18 | 20 ± 21 | 0.623 |
| Hypoxic Hypercapnia | |  |  |  |  |
| Area under the curve (% change from baseline) | 6 ± 13 | -6 ± 14 | 13 ± 20 | 9 ± 17 | 0.119 |

VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA or non-parametric Kruskal-Wallis test, where appropriate.

***Supplementary table 6. Cardiorespiratory responses to vagotomy in urethane anaesthetised rats***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | ABX (n=7) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA |
| Baseline |  |  |  |  |  |
| Δ *fR (brpm)* | -42 ± 14 | -46 ± 11 | -37 ± 19 | -40 ± 16 | 0.668 |
| Δ *VT*(ml 100g-1) | 0.17 ± 0.06 | 0.19 ± 0.06 | 0.17 ± 0.1 | 0.18 ± 0.09 | 0.917 |
| Δ *VE* (ml min-1 100g-1) | -7 ± 4 | -6 ± 3 | -3 ± 7 | -5 ± 9 | 0.730 |
| Δ MAP (mmHg) | -1 ± 7 | -6 ± 12 | -1 ± 15 | 2 ± 9 | 0.561 |
| Δ DBP (mmHg) | 2 ± 7 | -3 ± 11 | 1 ± 13 | 3 ± 8 | 0.613 |
| Δ SBP (mmHg) | -0 ± 13 | -8 ± 13 | -2 ± 25 | 1 ± 16 | 0.781 |
| Δ HR (bpm) | 63 ± 26 | 71 ± 31 | 66 ± 35 | 57 ± 32 | 0.707 |

*fR,* respiratory frequency (brpm, breaths per min); *VT*, tidal volume; *VE*, minute ventilation; MAP, mean arterial pressure; DBP, diastolic blood pressure; SBP, systolic blood pressure; HR, heart rate (bpm, beats per min); VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA or non-parametric Kruskal-Wallis test, where appropriate. Data are shown as absolute change from baseline.

***Supplementary table 7. Cardiorespiratory responsiveness to hypoxic and* hypoxic hypercapnic** ***chemostimulation in urethane anaesthetised vagotomised rats***

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | ABX (n=7) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA | VEH vs ABX | VEH-FMT vs ABX-FMT | VEH vs VEH-FMT | ABX vs ABX-FMT | VEH vs ABX-FMT | ABX vs VEH-FMT |
| Hypoxia |  |  |  |  |  |  |  |  |  |  |  |
| Δ *fR (bpm)* | 20 ± 18 | 9 ± 4 | 19 ± 6 | 19 ± 11 | **0.041** | 0.244 | 0.999 | 0.999 | **0.039** | 0.999 | 0.129 |
| Δ *VT* (ml 100g-1) | 0.09 ± 0.05 | 0.12 ± 0.04 | 0.14 ± 0.08 | 0.04 ± 0.08 | **0.015** | 0.999 | **0.013** | 0.849 | 0.139 | 0.417 | 0.999 |
| Δ *VE*(ml min-1 100g-1) | 16.0 ± 5.3 | 12.7 ± 3.8 | 23.0 ± 4.7 | 13.2 ± 10.7 | **0.014** | 0.999 | **0.027** | 0.201 | 0.999 | 0.999 | **0.034** |
| Δ MAP (mmHg) | -23 ± 17 | -18 ± 7 | -27 ± 13 | -29 ± 10 | 0.185 | - | - | - | - | - | - |
| Δ DBP (mmHg) | -19 ± 12 | -17 ± 7 | -25 ± 11 | -26 ± 8 | 0.241 | - | - | - | - | - | - |
| Δ SBP (mmHg) | -30 ± 27 | -23 ± 9 | -33 ± 18 | -34 ± 14 | 0.388 | - | - | - | - | - | - |
| Δ HR (bpm) | 21 ± 6 | 12 ± 14 | 26 ± 7 | 17 ± 12 | **0.037** | 0.391 | 0.243 | 0.999 | 0.999 | 0.999 | **0.042** |
| Hypoxic Hypercapnia | | |  |  |  |  |  |  |  |  |  |
| Δ *fR (brpm)* | 14 ± 12 | 9 ± 17 | 15 ± 7 | 20 ± 4 | 0.294 | - | - | - | - | - | - |
| Δ *VT* (ml 100g-1) | 0.19 ± 0.14 | 0.12 ± 0.15 | 0.23 ± 0.07 | 0.18 ± 0.04 | 0.271 | - | - | - | - | - | - |
| Δ *VE*(ml min-1 100g-1) | 20 ± 15 | 14 ± 18 | 25 ± 5 | 24 ± 4 | 0.255 | - | - | - | - | - | - |
| Δ MAP (mmHg) | -11 ± 20 | -9 ± 22 | -17 ± 15 | -16 ± 11 | 0.729 | - | - | - | - | - | - |
| Δ DBP (mmHg) | -9 ± 16 | -8 ± 18 | -19 ± 6 | -15 ± 8 | 0.296 | - | - | - | - | - | - |
| Δ SBP (mmHg) | -12 ± 29 | -9 ± 22 | -23 ± 16 | -18 ± 12 | 0.338 | - | - | - | - | - | - |
| Δ HR (bpm) | 13 ± 8 | 4 ± 10 | 19 ± 7 | 14 ± 7 | **0.007** | 0.204 | 0.999 | 0.54 | 0.093 | 0.999 | **0.004** |

*fR* respiratory frequency (bpm, breaths per min); *VT,*tidal volume; *VE,* minute ventilation; MAP, mean arterial pressure; DBP, diastolic blood pressure; SBP, systolic blood pressure; HR, heart rate (bpm, beats per min); VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA with Bonferroni *post hoc* where appropriate, or non-parametric Kruskal-Wallis test with Dunn’s multiple comparisons test, where appropriate. Data are shown as absolute change from baseline. Each *p-*value is adjusted to account for multiple comparisons. *p*-values shown in bold highlight significant differences.

***Supplementary table 8. Cardiorespiratory parameter responsiveness to hypercapnic chemostimulation in urethane anaesthetised vagotomised rats***

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | ABX (n=7) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA | VEH vs ABX | VEH-FMT vs ABX-FMT | ABX vs ABX-FMT | VEH vs VEH-FMT | VEH vs ABX-FMT | ABX vs VEH-FMT |
| 5% Carbon Dioxide | |  |  |  |  |  |  |  |  |  |  |
| Δ *fR (brpm)* | 2.5 ± 5.4 | 3.3 ± 3.8 | 1.3 ± 5.5 | 4.5 ± 5.4 | 0.593 | - | - | - | - | - | - |
| Δ *VT* (ml 100g-1) | 0.17 ± 0.17 | 0.12 ± 0.01 | 0.11 ± 0.04 | 0.12 ± 0.04 | 0.505 | - | - | - | - | - | - |
| Δ *VE*(ml min-1 100g-1) | 8.3 ± 4.6 | 9.6 ± 3.1 | 8.1 ± 6.1 | 8.4 ± 5.8 | 0.939 | - | - | - | - | - | - |
| Δ MAP (mmHg) | 6.8 ± 5.4 | 5 ± 6.1 | 13.9 ± 6 | 5.3 ± 9 | 0.059 | - | - | - | - | - | - |
| Δ DBP (mmHg) | 5.8 ± 2.5 | 5.1 ± 5.3 | 9 ± 3.5 | 5 ± 7.2 | 0.389 | - | - | - | - | - | - |
| Δ SBP (mmHg) | 9.1 ± 5.1 | 5.7 ± 8.4 | 15.4 ± 7.4 | 7.8 ± 12.5 | 0.147 | - | - | - | - | - | - |
| Δ HR (bpm) | -8.6 ± 6.1 | -10.2 ± 4.6 | -5.2 ± 7.6 | -10.1 ± 6.5 | 0.201 | - | - | - | - | - | - |
| 10% Carbon Dioxide | | |  |  |  |  |  |  |  |  |  |
| Δ *fR (brpm)* | 2.1 ± 7.4 | 4.6 ± 3.2 | 2.3 ± 5.7 | 5.8 ± 6.6 | 0.502 | - | - | - | - | - | - |
| Δ *VT* (ml 100g-1) | 0.33 ± 0.18 | 0.29 ± 0.04 | 0.26 ± 0.07 | 0.28 ± 0.07 | 0.832 | - | - | - | - | - | - |
| Δ *VE (*ml min-1 100g-1) | 16.7 ± 6.4 | 20.4 ± 2.8 | 18.0 ± 6.6 | 17.6 ± 9.3 | 0.762 | - | - | - | - | - | - |
| Δ MAP (mmHg) | 14.4 ± 8.1 | 11 ± 10.9 | 29.4 ± 10.5 | 18.8 ± 11.8 | **0.006** | 0.999 | 0.205 | 0.798 | **0.022** | 0.999 | **0.008** |
| Δ DBP (mmHg) | 11.4 ± 4.8 | 10.7 ± 10.2 | 21.8 ± 6.3 | 16.6 ± 10.1 | **0.025** | 0.999 | 0.999 | 0.878 | 0.0502 | 0.921 | 0.063 |
| Δ SBP (mmHg) | 19.6 ± 9.3 | 12.6 ± 14.4 | 37.7 ± 14.2 | 26.4 ± 17.5 | **0.007** | 0.999 | 0.546 | 0.328 | 0.051 | 0.999 | **0.008** |
| Δ HR (bpm) | -9.7 ± 7.9 | -10.2 ± 6.2 | -1.7 ± 9.9 | -11 ± 7.9 | 0.072 | - | - | - | - | - | - |

*fR,* respiratory frequency (brpm, breaths per min); *VT*, tidal volume; *VE*, minute ventilation; MAP, mean arterial pressure; DBP, diastolic blood pressure; SBP, systolic blood pressure; HR, heart rate (bpm, beats per min); VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA with Bonferroni *post hoc* or non-parametric Kruskal-Wallis test where appropriate. Data are shown as absolute change from baseline.

***Supplementary table 9. Diaphragm EMG activity and responsiveness to chemostimulation in urethane anaesthetised vagotomised rats***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | ABX (n=7) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA |
| % change from baseline | | | |  |  |
| Normoxia |  |  |  |  |  |
| Area under the curve | 32 ± 12 | 31 ± 15 | 28 ± 13 | 27 ± 10 | 0.788 |
| Hypoxia |  |  |  |  |  |
| Area under the curve | -7 ± 12 | -5 ± 9 | 5 ± 15 | -4 ± 13 | 0.308 |
| 5% Carbon Dioxide | | | | | | | |
| Area under the curve | 1 ± 9 | 0 ± 7 | -1 ± 5 | 6 ± 11 | 0.542 |
| 10% Carbon Dioxide | | | | | | |
| Area under the curve | -3 ± 13 | -7 ± 14 | -12 ± 8 | - 2 ± 8 | 0.176 |
| Hypoxic Hypercapnia | |  |  |  |  |
| Area under the curve | -1 ± 21 | -9 ± 10 | 0 ± 8 | -8 ± 15 | 0.428 |

VEH, autoclaved deionised water; ABX, antibiotic-treated; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic treated followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA or non-parametric Kruskal-Wallis test where appropriate. Responses are expressed as % change from preceding baseline.

***Supplementary table 10. Cerebellar monoamine neurochemistry***

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | VEH (n=10) | ABX (n=8) | VEH-FMT (n=9) | ABX-FMT (n=10) | One-way ANOVA | VEH vs ABX | VEH-FMT vs ABX-FMT | VEH vs VEH-FMT | ABX vs ABX-FMT | VEH vs ABX-FMT | ABX vs VEH-FMT |
| L-DOPA (ng/g) | 213 ± 245 | 2394 ± 1258 | 914 ± 885 | 1479 ± 392 | **0.0001** | **0.0004** | 0.618 | 0.366 | 0.999 | **0.002** | 0.138 |
| DA (ng/g) | 111 ± 29 | 103 ± 74 | 112 ± 29 | 71 ± 32 | 0.114 | - | - | - | - | - | - |
| HVA (ng/g) | 62 ± 48 | 155 ± 69 | 107 ± 56 | 143 ± 34 | **0.002** | **0.007** | 0.796 | 0.358 | 0.999 | **0.007** | 0.507 |
| HVA/DA | 0.59 ± 0.5 | 1.3 ± 0.4 | 1.0 ± 0.7 | 2.3 ± 1.0 | **0.0001** | 0.592 | **0.002** | 0.999 | 0.066 | **0.0001** | 0.999 |
| NA (ng/g) | 89 ± 58 | 222 ± 199 | 343 ± 124 | 128 ± 149 | **0.002** | 0.54 | **0.012** | **0.004** | 0.992 | 0.999 | 0.685 |
| 5-HT (ng/g) | 110 ± 31 | 134 ± 94 | 121 ± 50 | 113 ± 60 | 0.857 | - | - | - | - | - | - |
| 5-HIAA (ng/g) | 171 ± 30 | 193 ± 155 | 166 ± 33 | 146 ± 59 | 0.257 | - | - | - | - | - | - |
| 5-HIAA/5-HT | 1.6 ± 0.3 | 1.7 ± 0.6 | 1.5 ± 0.5 | 1.4 ± 0.2 | 0.355 | - | - | - | - | - | - |

L-DOPA, L-3,4-dihydroxyphenylalaine; DA, dopamine; HVA, homovanillic acid; NA*,* noradrenaline 5-HT, serotonin; 5-HIAA, 5-hydroxyindole acetic acid; VEH, autoclaved deionised water; ABX, antibiotic administration; VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as mean ± SD and were statistically compared using one-way ANOVA with Bonferroni *post hoc* where appropriate, or non-parametric Kruskal-Wallis test with Dunn’s multiple comparison test, where appropriate. Each *p-*value is adjusted to account for multiple comparisons. *p*-values shown in bold highlight significant differences.

***Supplementary table 11. Alpha diversity indices in caecal samples from VEH and VEH-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Alpha diversity | VEH | VEH-FMT | Raw *p*-value | (1/m)\*Q |
| Observed species | 836.5 (90.5) | 891.0 (101.3) | 0.035 | 0.013 |
| Chao1 | 864.9 (84.2) | 918.7 (93.3) | 0.043 | 0.027 |
| Shannon | 6.9 (0.45) | 7.1 (0.27) | 0.063 | 0.053 |
| Simpson | 0.978 (0.01) | 0.982 (0.01) | 0.218 | 0.067 |
| PD whole tree | 43.6 (2.6) | 47.0 (4.3) | 0.004 | 0.007 $ |

VEH, autoclaved deionised water; VEH-FMT, VEH followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. $ indicates an increase in VEH-FMT.

***Supplementary table 12. Alpha diversity indices in caecal samples from VEH and ABX-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Alpha diversity | VEH | ABX-FMT | Raw *p*-value | (1/m)\*Q |
| Observed species | 836.5 (90.5) | 893.0 (116.0) | 0.052 | 0.047 |
| Chao1 | 864.9 (84.2) | 927.3 (114.5) | 0.052 | 0.027 |
| Shannon | 6.9 (0.45) | 7.15 (0.18) | 0.043 | 0.02 |
| Simpson | 0.978 (0.01) | 0.934 (0.01) | 0.123 | 0.06 |
| PD whole tree | 43.6 (2.6) | 45.8 (4.65) | 0.052 | 0.04 |

VEH, autoclaved deionised water; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing.

***Supplementary table 13. Alpha diversity indices in caecal samples from VEH-FMT and ABX-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Alpha diversity | VEH-FMT | ABX-FMT | Raw *p*-value | (i/m)\*Q |
| Observed species | 891.0 (101.3) | 893.0 (116.0) | 0.684 | 0.087 |
| Chao1 | 918.7 (93.3) | 927.3 (114.5) | 0.971 | 0.1 |
| Shannon | 7.1 (0.27) | 7.15 (0.18) | 0.684 | 0.08 |
| Simpson | 0.982 (0.01) | 0.934 (0.01) | 0.739 | 0.093 |
| PD whole tree | 47.0 (4.3) | 45.8 (4.65) | 0.529 | 0.073 |

VEH-FMT, VEH followed by faecal microbiota transfer; ABX-FMT, antibiotic administration followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney U test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing.

***Supplementary table 14. Relative abundance (%) of bacterial PHYLA in caecal samples from VEH and VEH-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phylum | VEH | VEH-FMT | Raw *p*-value | (i/m)\*Q |
| Proteobacteria | 2.55 (2.426) | 7.087 (1.607) | 0.000 | 0.011 $ |
| Bacteroidetes | 29.739 (1.847) | 25.166 (3.665) | 0.000 | 0.004 $ |
| Cyanobacteria | 0.628 (0.726) | 1.396 (0.731) | 0.015 | 0.022 $ |
| Deferribacteres | 0.139 (0.301) | 0.0 (0.002) | 0.000 | 0.007 $ |
| Verrucomicrobia | 0.041 (0.149) | 0.313 (1.67) | 0.105 | 0.044 |
| Firmicutes | 65.518 (2.475) | 64.799 (3.288) | 0.143 | 0.048 |
| Actinobacteria | 0.131 (0.177) | 0.136 (0.139) | 0.481 | 0.074 |
| Saccharibacteria | 0.419 (0.49) | 0.354 (0.207) | 0.529 | 0.529 |
| Tenericutes | 0.360 (0.482) | 0.363 (0.26) | 0.631 | 0.631 |
| No blast hit | 0.085 (0.076) | 0.050 (0.072) | 0.684 | 0.100 |

VEH, autoclaved deionised water; VEH-FMT, VEH followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney U test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. $ indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary table 15. Relative abundance (%) of bacterial PHYLA in caecal samples from VEH and ABX-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phylum | VEH | ABX-FMT | Raw *p-*value | (i/m)\*Q |
| Proteobacteria | 2.55 (2.426) | 7.392 (1.628) | 0.000 | 0.019 & |
| Bacteroidetes | 29.739 (1.847) | 27.723 (7.062) | 0.023 | 0.03 & |
| Cyanobacteria | 0.628 (0.726) | 1.428 (1.335) | 0.015 | 0.026 & |
| Deferribacteres | 0.139 (0.301) | 0 (0.0002) | 0.000 | 0.015 & |
| Verrucomicrobia | 0.041 (0.149) | 0.064 (0.156) | 0.71 | 0.17 |
| Firmicutes | 65.518 (2.475) | 61.676 (8.674) | 0.143 | 0.052 |
| Actinobacteria | 0.131 (0.177) | 0.098 (0.140) | 0.28 | 0.063 |
| Saccharibacteria | 0.419 (0.49) | 0.582 (0.360) | 0.315 | 0.067 |
| Tenericutes | 0.360 (0.482) | 0.569 (1.325) | 0.089 | 0.041 |
| No blast hit | 0.085 (0.076) | 0.081 (0.066) | 0.971 | 0.1 |

VEH, autoclaved deionised water; ABX-FMT, antibiotics followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing.

***Supplementary table 16. Relative abundance (%) of bacterial PHYLA in caecal samples from VEH-FMT and ABX-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Phylum** | **VEH-FMT** | **ABX-FMT** | **Raw *p-*value** | **(i/m)\*Q** |
| **Proteobacteria** | 7.087 (1.607) | 7.392 (1.628) | 0.912 | 0.1 |
| **Bacteroidetes** | 25.166 (3.665) | 27.723 (7.062) | 0.393 | 0.07 |
| **Cyanobacteria** | 1.396 (0.731) | 1.428 (1.335) | 0.853 | 0.096 |
| **Deferribacteres** | 0 (0.002) | 0 (0.0002) | 0.684 | 0.089 |
| **Verrucomicrobia** | 0.313 (1.67) | 0.064 (0.156) | 0.029 | 0.037 ¥ |
| **Firmicutes** | 64.799 (3.288) | 61.676 (8.674) | 0.218 | 0.056 |
| **Actinobacteria** | 0.136 (0.139) | 0.098 (0.140) | 0.684 | 0.085 |
| **Saccharibacteria** | 0.354 (0.207) | 0.582 (0.360) | 0.023 | 0.033 ¥ |
| **Tenericutes** | 0.363 (0.26) | 0.569 (1.325) | 0.218 | 0.059 |
| **No blast** | 0.050 (0.072) | 0.081 (0.066) | 0.634 | 0.1 |

VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotics followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. ¥ indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary 17. Relative abundance (%) of bacterial FAMILIES in caecal samples from VEH and VEH-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Family** | **VEH** | **VEH-FMT** | **Raw *p*-value** | **(i/m) \*Q** |
| **Actinobacteria** |  | | | |
| **Bifidobacteriaceae** *(Bifidobacteriales)* | 0.024 (0.137) | 0.044 (0.584) | 0.631 | 0.073 |
| **Nocardiaceae** *(Corynebacteriales)* | 0.003 (0.004) | 0.0008 (0.002) | 0.123 | 0.03 |
| **Micrococcaceae** *(Micrococcales)* | 0.002 (0.009) | 0.007 (0.011) | 0.315 | 0.046 |
| **Coriobacteriaceae** *(Coriobacteriales)* | 0.091 (0.092) | 0.042 (0.099) | 0.247 | 0.041 |
| **Bacteroidetes** |  | | | |
| **Bacteroidetes VC2.1 Bac22**  *(Uncultured bacterium)* | 0.0 (0.0) | 0.116 (0.081) | 0.000 | 0.001 $ |
| **Bacteroidaceae** *(Bacteroidales)* | 1.656 (1.139) | 1.820 (0.885) | 0.971 | 0.093 |
| **Porphyromonadaceae** *(Bacteroidales)* | 0.387 (0.235) | 0.388 (0.327) | 0.529 | 0.066 |
| **Prevotellaceae** *(Bacteroidales)* | 5.504 (3.486) | 6.082 (3.709) | 0.631 | 0.074 |
| **Rikenellaceae** *(Bacteroidales)* | 3.555 (3.251) | 1.961 (1.097) | 0.089 | 0.025 |
| **S24-7**  *(Bacteroidales)* | 17.898 (3.667) | 14.416 (2.940) | 0.004 | 0.01 $ |
| **Rat ANO60301C** *(Bacteroidales)* | 0.0 (0.003) | 0.0 (0.0004) | 0.393 | 0.057 |
| **Cyanobacteria** |  | | | |
| **Uncultured bacterium** *(Gastranaerophilales)* | 0.627 (0.724) | 0.837 (0.685) | 0.19 | 0.035 |
| **Uncultured organism** *(Gastranaerophilales)* | 0 (0.0006) | 0.491 (0.893) | 0.000 | 0.001 $ |
| **Deferribacteres** |  | | | |
| **Deferribacteraceae** *(Deferribacterales)* | 0.139 (0.301) | 0 (0.002) | 0.000 | 0.002 $ |
| **Firmicutes** |  | | | |
| **Bacillaceae**  *(Bacillales)* | 0.13 (0.279) | 0 (0.0) | 0.000 | 0.003 $ |
| **Streptococcaceae** *(Lactobacillales)* | 0.004 (0.004) | 0.003 (0.005) | 0.912 | 0.091 |
| **Aerococcaceae** *(Lactobacillales)* | 0.006 (0.002) | 0.001 (0.003) | 0.529 | 0.067 |
| **Lactobacillaceae** *(Lactobacillales)* | 2.318 (3.128) | 2.949 (2.691) | 0.481 | 0.063 |
| **Caldicoprobacteraceae** *(Clostridiales)* | 0.015 (0.019) | 0.03 (006) | 0.105 | 0.027 |
| **Christensenellaceae** *(Clostridiales)* | 0.039 (0.089) | 0.058 (0.039) | 0.143 | 0.086 |
| **Clostridiaceae 1** *(Clostridiales)* | 0.117 (0.371) | 0.24 (0.635) | 0.143 | 0.031 |
| **Clostridiales vadinBB60 group** *(Clostridiales)* | 1.746 (1.299) | 3.016 (1.631) | 0.001 | 0.008 $ |
| **Defluviitaleaceae** *(Clostridiales)* | 0.004 (0.008) | 0.004 (0.011) | 0.631 | 0.075 |
| **Eubacteriaceae** *(Clostridiales)* | 0 (0) | 0 (0.001) | 0.315 | 0.047 |
| **Family XIII** *(Clostridiales)* | 0.121 (0.066) | 0.097 (0.028) | 0.190 | 0.036 |
| **Lachnospiraceae** *(Clostridiales)* | 34.595 (7.196) | 35.788 (5.362) | 0.684 | 0.079 |
| **Peptococcaceae** *(Clostridiales)* | 0.431 (0.328) | 0.387 (0.187) | 0.579 | 0.07 |
| **Peptostreptococcaceae** *(Clostridiales)* | 0.676 (1.24) | 0.950 (0.731) | 0.436 | 0.059 |
| **Ruminococcaceae** *(Clostridiales)* | 21.85 (6.573) | 19.23 (4.245) | 0.075 | 0.022 |
| **Erysipelotrichaceae** *(Erysipelotrichales)* | 0.31 (0.23) | 0.391 (0.357) | 0.393 | 0.057 |
| **Proteobacteria** |  | | | |
| **Rhodospirillaceae** *(Rhodospirillales)* | 0.236 (0.38) | 0.446 (0.198) | 0.123 | 0.03 |
| **Mitochondria** *(Rickettsiales)* | 0 (0.001) | 0 (0.0002) | 0.481 | 0.064 |
| **Alcaligenaceae** *(Burkholderiales)* | 0.039 (0.094) | 0.01 (0.011) | 0.005 | 0.011 $ |
| **Burkholderiaceae** *(Burkholderiales)* | 0 (0) | 0 (0.001) | 0.393 | 0.058 |
| **Desulfovibrionaceae** *(Desulfovibrionales)* | 1.84 (2.289) | 2.432 (1.405) | 0.247 | 0.041 |
| **Helicobacteraceae** *(Camplylobacterales)* | 0.002 (0.003) | 4.226 (1.378) | 0.000 | 0.004 $ |
| **Enterobacteriaceae** *(Enterobacteriales)* | 0.004 (0.002) | 0.001 (0.003) | 0.007 | 0.012 $ |
| **Pasteurellaceae** *(Pasteurellales)* | 0.0008 (0.013) | 0.003 (0.006) | 0.971 | 0.093 |
| **Saccharibacteria** |  | | | |
| **Unknown family** *(Unknown order)* | 0.419 (0.490) | 0.354 (0.207) | 0.529 | 0.067 |
| **Tenericutes** |  | | | |
| **Anaeroplasmataceae** *(Anaeroplasmatales)* | 0.083 (0.277) | 0.217 (0.185) | 0.247 | 0.042 |
| **Uncultured Mollicutes** bacterium *(Mollicutes)* | 0 (0.001) | 0 (0.002) | 0.631 | 0.075 |
| **Uncultured bacterium** *(Mollicutes RF9)* | 0.062 (0.033) | 0.078 (0.064) | 0.529 | 0.068 |
| **Uncultured rumen bacteria** *(Mollicutes RF9)* | 0.112 (0.242) | 0.073 (0.079) | 0.971 | 0.094 |
| **Unidentified Mollicutes** *(Mollicutes RF9)* | 0.001 (0.003) | 0.002 (0.003) | 0.353 | 0.051 |
| **Uncultured Bacillales bacterium** *(Mollicutes)* | 0.012 (0.042) | 0.034 (0.100) | 0.218 | 0.04 |
| **Verrucomicrobia** |  |  |  |  |
| **Verrucomicrobiaceae** *(Verrucomicrobiales)* | 0.041 (0.149) | 0.313 (1.167) | 0.105 | 0.028 |

VEH, autoclaved deionised water; VEH-FMT, VEH followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. $ indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary 18. Relative abundance (%) of bacterial FAMILIES in caecal samples from VEH and ABX-FMT rats***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Family** | **VEH** | **ABX-FMT** | **Raw *p*-value** | **(i/m) \*Q** |
| **Actinobacteria** |  | | | |
| **Bifidobacteriaceae** *(Bifidobacteriales)* | 0.024 (0.137) | 0.053 (0.119) | 0.28 | 0.044 |
| **Nocardiaceae** *(Corynebacteriales)* | 0.003 (0.004) | 0.003 (0.004) | 0.739 | 0.082 |
| **Micrococcaceae** *(Micrococcales)* | 0.002 (0.009) | 0.001 (0.004) | 0.436 | 0.06 |
| **Coriobacteriaceae** *(Coriobacteriales)* | 0.091 (0.092) | 0.036 (0.024) | 0.003 | 0.009 & |
| **Bacteroidetes** |  | | | |
| **Bacteroidaceae** *(Bacteroidales)* | 1.656 (1.139) | 2.166 (1.539) | 0.315 | 0.048 |
| **Bacteroidetes VC2.1 Bac22**  *(Uncultured bacterium)* | 0.0 (0.0) | 0.1 (0.062) | 0.000 | 0.004 & |
| **Porphyromonadaceae** *(Bacteroidales)* | 0.387 (0.235) | 0.462 (0.128) | 0.436 | 0.061 |
| **Prevotellaceae** *(Bacteroidales)* | 5.504 (3.486) | 3.306 (3.762) | 0.075 | 0.022 |
| **Rikenellaceae** *(Bacteroidales)* | 3.555 (3.251) | 2.535 (0.804) | 0.315 | 0.08 |
| **S24-7**  *(Bacteroidales)* | 17.898 (3.667) | 17.381 (3.995) | 0.353 | 0.052 |
| **Rat ANO60301C** *(Bacteroidales)* | 0.0 (0.003) | 0.0009 (0.003) | 0.912 | 0.091 |
| **Cyanobacteria** |  | | | |
| Uncultured bacterium *(Gastranaerophilales)* | 0.627 (0.724) | 1.396 (1.062) | 0.035 | 0.029 |
| **Uncultured organism** *(Gastranaerophilales)* | 0 (0.0006) | 0.111 (0.442) | 0.000 | 0.005 & |
| **Deferribacteres** |  | | | |
| **Deferribacteraceae** *(Deferribacterales)* | 0.139 (0.301) | 0.0 (0.0002) | 0.000 | 0.06 & |
| **Firmicutes** |  | | | |
| **Bacillaceae**  *(Bacillales)* | 0.13 (0.279) | 0.0 (0.0) | 0.000 | 0.007 & |
| **Streptococcaceae**  *(Lactobacillales)* | 0.004 (0.004) | 0.001 (0.002) | 0.007 | 0.013 & |
| **Aerococcaceae** *(Lactobacillales)* | 0.006 (0.002) | 0.0 (0.002) | 0.631 | 0.076 |
| **Lactobacillaceae** *(Lactobacillales)* | 2.318 (3.128) | 1.399 (1.76) | 0.19 | 0.036 |
| **Caldicoprobacteraceae** *(Clostridiales)* | 0.015 (0.019) | 0.023 (0.023) | 0.105 | 0.028 |
| **Christensenellaceae** *(Clostridiales)* | 0.039 (0.892) | 0.088 (0.086) | 0.353 | 0.052 |
| **Clostridiaceae 1** *(Clostridiales)* | 0.117 (0.371) | 0.14 (0.469 | 0.436 | 0.062 |
| **Clostridiales vadinBB60 group**  *(Clostridiales)* | 1.746 (1.299) | 3.857 (3.605) | 0.0009 | 0.014 & |
| **Defluviitaleaceae** *(Clostridiales)* | 0.004 (0.008) | 0.008 (0.012) | 0.579 | 0.07 |
| **Eubacteriaceae** *(Clostridiales)* | 0 (0) | 0 (0) | 0.739 | 0.083 |
| **Family XIII** *(Clostridiales)* | 0.121 (0.066) | 0.115 (0.052) | 0.481 | 0.064 |
| **Lachnospiraceae** *(Clostridiales)* | 34.595 (7.196) | 28.987 (10.732) | 0.143 | 0.032 |
| **Peptococcaceae** *(Clostridiales)* | 0.431 (0.328) | 0.425 (0.142) | 0.796 | 0.086 |
| **Peptostreptococcaceae** *(Clostridiales)* | 0.676 (1.244) | 0.351 (0.784) | 0.481 | 0.065 |
| **Ruminococcaceae** *(Clostridiales)* | 21.849 (6.573) | 22.66 (4.94) | 0.912 | 0.092 |
| **Erysipelotrichaceae** *(Erysipelotrichales)* | 0.31 (0.23) | 0.208 (0.238) | 0.796 | 0.087 |
| **Proteobacteria** |  | | | |
| **Rhodospirillaceae** *(Rhodospirillales)* | 0.236 (0.38) | 0.36 (0.243) | 0.247 | 0.043 |
| **Mitochondria** *(Rickettsiales)* | 0 (0.001) | 0 (0.0004) | 0.579 | 0.071 |
| **Alcaligenaceae** *(Burkholderiales)* | 0.039 (0.094) | 0.048 (0.094) | 0.971 | 0.095 |
| **Burkholderiaceae** *(Burkholderiales)* | 0 (0) | 0.0008 (0.003) | 0.052 | 0.021 |
| **Desulfovibrionaceae** *(Desulfovibrionales)* | 1.84 (2.289) | 3.273 (1.256) | 0.023 | 0.014 |
| **Helicobacteraceae** *(Camplylobacterales)* | 0.002 (0.003) | 3.514 (1.354) | 0.000 | 0.007 & |
| **Enterobacteriaceae** *(Enterobacteriales)* | 0.004 (0.002) | 0.002 (0.005) | 0.19 | 0.037 |
| **Pasteurellaceae** *(Pasteurellales)* | 0.0008 (0.013) | 0.002 (0.007) | 1.000 | 0.099 |
| **Saccharibacteria** |  | | | |
| **Unknown family** *(Unknown order)* | 0.419 (0.490) | 0.582 (0.360) | 0.315 | 0.049 |
| **Tenericutes** |  | | | |
| **Anaeroplasmataceae** *(Anaeroplasmatales)* | 0.083 (0.277) | 0.181 (1.059) | 0.19 | 0.038 |
| **Uncultured Moliicutes** bacterium *(Mollicutes)* | 0 (0.001) | 0 (0.0005) | 0.85 | 0.089 |
| **Uncultured bacterium** *(Mollicutes RF9)* | 0.062 (0.033) | 0.095 (0.093) | 0.315 | 0.08 |
| **Uncultured rumen bacteria** *(Mollicutes RF9)* | 0.112 (0.242) | 0.128 (0.321) | 0.579 | 0.072 |
| **Unidentified Mollicutes** *(Mollicutes RF9)* | 0.001 (0.003) | 0.002 (0.002) | 0.28 | 0.045 |
| **Uncultured Bacillales bacterium** *(Mollicutes)* | 0.012 (0.042) | 0.029 (0.071) | 0.19 | 0.05 |
| **Verrucomicrobia** |  |  |  |  |
| **Verrucomicrobiaceae** *(Verrucomicrobiales)* | 0.041 (0.149) | 0.064 (0.156) | 0.739 | 0.083 |

VEH, autoclaved deionised water; ABX-FMT, antibiotics followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. & indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary 19. Relative abundance (%) of bacterial FAMILIES in caecal samples from VEH-FMT and ABX-FMT rats***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Family** | **VEH-FMT** | **ABX-FMT** | **Raw *p*-value** | | | **(i/m)\*Q** |
| **Actinobacteria** |  | | | | | |
| **Bifidobacteriaceae** *(Bifidobacteriales)* | 0.044 (0.584) | 0.053 (0.119) | | 0.796 | 0.088 | |
| **Nocardiaceae** *(Corynebacteriales)* | 0.0008 (0.002) | 0.003 (0.004) | | 0.075 | 0.023 | |
| **Micrococcaceae** *(Micrococcales)* | 0.007 (0.011) | 0.001(0.004) | | 0.035 | 0.019 | |
| **Coriobacteriaceae** *(Coriobacteriales)* | 0.042 (0.099) | 0.036 (0.024) | | 0.315 | 0.051 | |
| **Bacteroidetes** |  | | | | | |
| **Bacteroidetes VC2.1 Bac22**  *(Uncultured bacterium)* | 0.116 (0.081) | 0.1 (0.062) | | 0.853 | 0.09 | |
| **Bacteroidaceae** *(Bacteroidales)* | 1.820 (0.885) | 2.166 (1.539) | | 0.353 | 0.052 | |
| **Porphyromonadaceae** *(Bacteroidales)* | 0.388 (0.327) | 0.462 (0.128) | | 0.971 | 0.096 | |
| **Prevotellaceae** *(Bacteroidales)* | 6.082 (3.709) | 3.306 (3.762) | | 0.247 | 0.043 | |
| **Rikenellaceae** *(Bacteroidales)* | 1.961 (1.097) | 2.535 (0.804) | | 0.353 | 0.054 | |
| **S24-7**  *(Bacteroidales)* | 14.416 (2.940) | 17.381 (3.995) | | 0.043 | 0.02 | |
| **Rat ANO60301C** *(Bacteroidales)* | 0.0 (0.0004) | 0.0009 (0.003) | | 0.143 | 0.033 | |
| **Cyanobacteria** |  | | | | | |
| **Uncultured bacterium** *(Gastranaerophilales)* | 0.837 (0.685) | 1.396 (1.062) | | 0.19 | 0.039 | |
| **Uncultured organism** *(Gastranaerophilales)* | 0.491 (0.893) | 0.111 (0.442) | | 0.089 | 0.026 | |
| **Deferribacteres** |  | | | | | |
| **Deferribacteraceae** *(Deferribacterales)* | 0 (0.002) | 0.0 (0.0002) | | 0.684 | 0.08 | |
| **Firmicutes** |  | | | | | |
| **Bacillaceae**  *(Bacillales)* | 0 (0.0) | 0.0 (0.0) | | 1.00 | 0.099 | |
| **Streptococcaceae** *(Lactobacillales)* | 0.003 (0.005) | 0.001 (0.002) | | 0.003 | 0.009 ¥ | |
| **Aerococcaceae** *(Lactobacillales)* | 0.001 (0.003) | 0.0 (0.002) | | 0.393 | 0.059 | |
| **Lactobacillaceae** *(Lactobacillales)* | 2.949 (2.691) | 1.399 (1.76) | | 0.075 | 0.024 | |
| **Caldicoprobacteraceae** *(Clostridiales)* | 0.03 (006) | 0.023 (0.023) | | 0.796 | 0.088 | |
| **Christensenellaceae** *(Clostridiales)* | 0.058 (0.039) | 0.088 (0.086) | | 0.143 | 0.033 | |
| **Clostridiaceae 1** *(Clostridiales)* | 0.240 (0.635) | 0.14 (0.469) | | 0.353 | 0.055 | |
| **Clostridiales vadinBB60 group**  *(Clostridiales)* | 3.016 (1.631) | 3.857 (3.605) | | 0.971 | 0.096 | |
| **Defluviitaleaceae** *(Clostridiales)* | 0.00 (0.011) | 0.008 (0.012) | | 0.971 | 0.097 | |
| **Eubacteriaceae** *(Clostridiales)* | 0 (0.001) | 0 (0) | | 0.143 | 0.034 | |
| **Family XIII** *(Clostridiales)* | 0.097 (0.028) | 0.115 (0.052) | | 0.28 | 0.046 | |
| **Lachnospiraceae** *(Clostridiales)* | 35.788 (5.362) | 28.987 (10.732) | | 0.029 | 0.017 | |
| **Peptococcaceae** *(Clostridiales)* | 0.387 (0.187) | 0.425 (0.142) | | 0.684 | 0.08 | |
| **Peptostreptococcaceae** *(Clostridiales)* | 0.95 (0.731) | 0.351 (0.784) | | 0.023 | 0.015 | |
| **Ruminococcaceae** *(Clostridiales)* | 19.23 (4.245) | 22.66 (4.94) | | 0.035 | 0.02 | |
| **Erysipelotrichaceae** *(Erysipelotrichales)* | 0.391 (0.357) | 0.208 (0.238) | | 0.436 | 0.062 | |
| **Proteobacteria** |  | | | | | |
| **Rhodospirillaceae** *(Rhodospirillales)* | 0.446 (0.198) | 0.36 (0.243) | | 0.631 | 0.077 | |
| **Mitochondria** *(Rickettsiales)* | 0 (0.0002) | 0 (0.0004) | | 1.000 | 1.00 | |
| **Alcaligenaceae** *(Burkholderiales)* | 0.01 (0.011) | 0.048 (0.094) | | 0.005 | 0.012 ¥ | |
| **Burkholderiaceae** *(Burkholderiales)* | 0 (0.001) | 0.0008 (0.003) | | 0.353 | 0.056 | |
| **Desulfovibrionaceae** *(Desulfovibrionales)* | 2.432 (1.405) | 3.273 (1.256) | | 0.075 | 0.025 | |
| **Helicobacteraceae** *(Camplylobacterales)* | 4.226 (1.378) | 3.514 (1.354) | | 0.105 | 0.029 | |
| **Enterobacteriaceae** *(Enterobacteriales)* | 0.001 (0.003) | 0.002 (0.005) | | 0.631 | 0.078 | |
| **Pasteurellaceae** *(Pasteurellales)* | 0.003 (0.006) | 0.002 (0.007) | | 0.6484 | 0.08 | |
| **Saccharibacteria** |  | | | | | |
| **Unknown family** *(Unknown order)* | 0.354 (0.207) | 0.582 (0.360) | | 0.023 | 0.016 | |
| **Tenericutes** |  | | | | | |
| **Anaeroplasmataceae** *(Anaeroplasmatales)* | 0.217 (0.195) | 0.181 (1.059) | | 0.739 | 0.084 | |
| **Uncultured Mollicutes** bacterium *(Mollicutes)* | 0 (0.002) | 0 (0.0005) | | 0.529 | 0.069 | |
| **Uncultured bacterium** *(Mollicutes RF9)* | 0.078 (0.064) | 0.095 (0.093) | | 0.579 | 0.072 | |
| **Uncultured rumen bacteria** *(Mollicutes RF9)* | 0.073 (0.079) | 0.128 (0.321) | | 0.631 | 0.078 | |
| **Unidentified Mollicutes** *(Mollicutes RF9)* | 0.002 (0.003) | 0.002 (0.002) | | 0.971 | 0.098 | |
| **Uncultured Bacillales bacterium** *(Mollicutes)* | 0.002 (0.003) | 0.029 (0.071) | | 0.739 | 0.085 | |
| **Verrucomicrobia** |  |  | |  |  | |
| **Verrucomicrobiaceae** *(Verrucomicrobiales)* | 0.313 (1.167) | 0.064 (0.156) | | 0.029 | 0.017 | |

VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotics followed by faecal microbial transfer. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. ¥ indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary 20. Relative abundance (%) of bacterial GENERA in the caecal samples from VEH and VEH-FMT rats***

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Genus** | **VEH** | **VEH-FMT** | | **Raw *p*-value** | | **(i/m)\*Q** | | |
| **Bifidobacteriaceae (Bifidobacteriales, Actinobacteria)** | | | | | | | |
| ***Bifidobacterium*** | 0.024 (0.137) | | 0.044 (0.058) | | 0.631 | | 0.07 |
| **Coriobacteriaceae (Coriobacteriales, Actinobacteria)** | | | | | | | |
| ***Uncultured Coriobacteriaceae*** | 0.035 (0.036) | | 0.007 (0.015) | | 0.003 | | 0.005 $ |
| **Uncultured bacterium (Unknown order, Bacteroidetes)** | | | | | | | |
| ***Bacteroidetes VC21 Bac22 uncultured bacterium*** | 0 (0) | | 0.116 (0.081) | | 0.000 | | 0.000 $ |
| **Bacteroidaceae (Bacteroidales, Bacteroidetes)** | | | | | | | |
| ***Bacteroides*** | 1.656 (1.138) | | 1.182 (0.885) | | 0.971 | | 0.094 |
| **Bacteroidales S24-7 group (Bacteroidales, Bacteroidetes)** | | | | | | | |
| ***Uncultured bacterium*** | 17.13 (2.798) | | 14.372 (2.949) | | 0.004 | | 0.006 $ |
| ***unidentified*** | 0.161 (0.933) | | 0.067 (0.059) | | 0.063 | | 0.018 |
| **Porphyromonadaceae (Bacteroidales, Bacteroidetes)** | | | | | | | |
| ***Odoribacter*** | 0.360 (0.212) | | 0.296 (0.289) | | 0.796 | | 0.084 |
| ***Parabacteroides*** | 0.046 (0.042) | | 0.099 (0.07) | | 0.011 | | 0.009 |
| ***Prevotellaceae (Bacteroidales, Bacteroidetes)*** | | | | | | | |
| ***Alloprevotella*** | 1.594 (2.192) | | 0.748 (1.639) | | 0.123 | | 0.026 |
| ***Prevotellaceae NK3B31 group*** | 1.715 (2.18) | | 2.017 (2.704) | | 0.631 | | 0.07 |
| ***Prevotellaceae UCG-001*** | 1.743 (2.486) | | 2.134 (2.167) | | 0.393 | | 0.051 |
| **Rikenellaceae (Bacteroidales, Bacteroidetes)** | | | | | | | |
| ***Alistipes*** | 3.555 (3.252) | | 1.961 (1.097) | | 0.089 | | 0.022 |
| **Uncultured bacterium (Gastranaerophilales, Cyanobacteria)** | | | | | | | |
| ***Uncultured bacterium*** | 0.627 (0.725) | | 0.837 (0.685) | | 0.19 | | 0.032 |
| ***Uncultured organism*** | 0 (0.006) | | 0.491 (0.893) | | 0.000 | | 0.000 $ |
| **Deferribacteraceae (Deferribacterales, Deferribacteres)** | | | | | | | |
| ***Mucispirillum*** | 0.139 (0.301) | | 0 (0.002) | | 0.000 | | 0.001 $ |
| **Bacillaeae (Bacillales, Firmicutes)** | | | | | | | |
| ***Bacillus*** | 0.13 (0.279) | | 0 (0) | | 0.000 | | 0.001 $ |
| **Lactobacillaceae (Lactobacillales, Firmicutes)** | | | | | | | |
| ***Lactobacillus*** | 2.318 (3.128) | | 1.441 (2.691) | | 0.481 | | 0.059 |
| **Caldicoprobacteraceae *(Clostridiales, Firmicutes)*** | | | | | | | |
| ***Caldicoprobacter*** | 0.015 (0.019) | | 0.0297 (0.056) | | 0.105 | | 0.023 |
| **Christensenellaceae (Clostridiales, Firmicutes)** | | | | | | | |
| ***Christensenellaceae R-7 group*** | 0.031 (0.074) | | 0.046 (0.045) | | 0.912 | | 0.091 |
| **Clostridiaceae 1 (Clostridiales, Firmicutes)** | | | | | | | |
| ***Clostridium sensu stricto 1*** | 0.116 (0.371) | | 0.238 (0.065) | | 0.143 | | 0.028 |
| ***Clostridiales vadin BB60 group (Clostridiales, Firmicutes)*** | | | | | | | |
| ***Uncultured clostridiales bacterium*** | 0.004 (0.036) | | 0.045 (0.022) | | 0.029 | | 0.012 |
| ***Uncultured bacterium*** | 1.317 (1.181) | | 2.147 (0.811) | | 0.002 | | 0.004 $ |
| ***Uncultured rumen bacterium*** | 0.058 (0.096) | | 0.021 (0.048) | | 0.19 | | 0.032 |
| ***Unidentified*** | 0.126 (0.341) | | 0.756 (1.352) | | 0.003 | | 0.005 $ |
| **Family XIII (Clostridiales, Firmicutes)** | | | | | | | |
| ***Anaerovorax*** | 0.055 (0.046) | | 0.038 (0.013) | | 0.123 | | 0.027 |
| **Lachnospiraceae (Clostridiales, Firmicutes)** | | | | | | | |
| ***Blautia*** | 0.07 (0.252) | | 0.566 (1.207) | | 0.052 | | 0.016 |
| ***Coprococcus 1*** | 0.125 (0.063) | | 0.127 (0.06) | | 0.631 | | 0.071 |
| ***Coprococcus 2*** | 0.178 (0.462) | | 0.011 (0.207) | | 0.075 | | 0.02 |
| ***Incertae Sedis*** | 1.398 (1.351) | | 0.913 (0.926) | | 0.165 | | 0.03 |
| ***Lachnoclostridium*** | 0.121 (0.07) | | 0.124 (0.040) | | 0.971 | | 0.095 |
| ***Lachnoclostridium 10*** | 0.0 (0) | | 0.133 (0.362) | | 0.000 | | 0.001 $ |
| ***Lachnospiraceae NC2004 group*** | 0.586 (1.377) | | 0.4 (0.391) | | 0.481 | | 0.06 |
| ***Lachnospiraceae NK4A136 group*** | 22.823 (5.829) | | 19.789 (5.348) | | 0.089 | | 0.022 |
| ***Lachnospiraceae NK4B4 group*** | 0.01 (0.116) | | 0.003 (0.016) | | 0.529 | | 0.062 |
| ***Lachnospiraceae UCG-0001*** | 0.168 (0.195) | | 0.303 (0.354) | | 0.075 | | 0.02 |
| ***Lachnospiraceae UCG-0005*** | 0.067 (0.088) | | 0.103 (0.088) | | 0.631 | | 0.071 |
| ***Lachnospiraceae UCG-0006*** | 0.281 (0.218) | | 0.254 (0.268) | | 0.739 | | 0.076 |
| ***Lachnospiraceae UCG-008*** | 0.081 (0.113) | | 0.009 (0.014) | | 0.000 | | 0.001 $ |
| ***Roseburia*** | 0.913 (0.649) | | 1.798 (1.915) | | 0.105 | | 0.024 |
| ***Shuttleworthia*** | 0.024 (0.036) | | 0.015 (0.027) | | 0.912 | | 0.091 |
| ***Tyzzerella*** | 0.207 (0.19) | | 0.117 (0.059) | | 0.007 | | 0.008 $ |
| ***Lachnospiraceae [Eubacterium] oxidoreducens group*** | 0.262 (0.278) | | 0.292 (0.355) | | 0.481 | | 0.06 |
| ***Lachnospiraceae [Eubacterium] ruminantium group*** | 0.185 (0.276) | | 0.035 (0.363) | | 0.739 | | 0.08 |
| ***Lachnospiraceae uncultured*** | 5.073 (4.202) | | 9.821 (5.779) | | 0.005 | | 0.006 $ |
| **Peptococcaceae (Clostridiales, Firmicutes)** | | | | | | | |
| ***Peptococcaceae (uncultured)*** | 0.352 (0.312) | | 0.325 (0.1) | | 0.436 | | 0.055 |
| ***Peptococcus*** | 0.079 (0.029) | | 0.085 (0.083) | | 0.631 | | 0.071 |
| **Peptostreptococcaceae (Clostridiales, Firmicutes)** | | | | | | | |
| ***Intestinibacter*** | 0.092 (0.499) | | 0.046 (0.093) | | 0.853 | | 0.088 |
| ***Peptoclostridium*** | 0.46 (0.906) | | 0.626 (0.767) | | 0.28 | | 0.04 |
| **Ruminococcaceae (Clostridiales, Firmicutes)** | | | | | | | |
| ***Anaerotruncus*** | 0.929 (0.248) | | 0.764 (0.17) | | 0.029 | | 0.012 |
| ***Flavonifractor*** | 0.003 (0.01) | | 0.065 (0.169) | | 0.005 | | 0.007 $ |
| ***Intestinimonas*** | 0.064 (0.04) | | 0.026 (0.015) | | 0.011 | | 0.009 |
| ***Oscillibacter*** | 0.908 (0.281) | | 0.586 (0.175) | | 0.019 | | 0.01 |
| ***Papillibacter*** | 0.071 (0.188) | | 0.161 (0.247) | | 0.247 | | 0.037 |
| ***Ruminoclostridium*** | 0.084 (0.836) | | 0.152 (0.094) | | 0.043 | | 0.015 |
| ***Ruminoclostridium 5*** | 0.343 (0.175) | | 0.407 (0.27) | | 0.218 | | 0.035 |
| ***Ruminoclostridium 6*** | 0.723 (0.781) | | 1.0 (0.9) | | 0.853 | | 0.088 |
| ***Ruminoclostridium 9*** | 3.962 (1.396) | | 2.305 (0.576) | | 0.002 | | 0.005 $ |
| ***Ruminococcaceae NK4A214 group*** | 0.239 (0.146) | | 0.234 (0.094) | | 0.971 | | 0.095 |
| ***Ruminococcaceae UCG-003*** | 1.392 (1.069) | | 1.429 (0.472) | | 0.853 | | 0.089 |
| ***Ruminococcaceae UCG-005*** | 0.324 (0.247) | | 0.417 (0.313) | | 0.393 | | 0.052 |
| ***Ruminococcaceae UCG-009*** | 0.081 (0.043) | | 0.083 (0.029) | | 0.796 | | 0.085 |
| ***Ruminococcaceae UCG-010*** | 0.282 (0.208) | | 0.418 (0.26) | | 0.143 | | 0.029 |
| ***Ruminococcaceae UCG-011*** | 0 (0) | | 0.002 (0.003) | | 0.015 | | 0.01 |
| ***Ruminococcaceae UCG-013*** | 0.067 (0.059) | | 0.204 (0.15) | | 0.001 | | 0.004 $ |
| ***Ruminococcaceae UCG-014*** | 1.134 (0.706) | | 0.945 (0.78) | | 0.739 | | 0.08 |
| ***Ruminococcus 1*** | 2.6 (1.577) | | 2.412 (3.09) | | 0.912 | | 0.092 |
| ***Ruminococcus 2*** | 0.093 (0.114) | | 0.082 (0.045) | | 0.912 | | 0.092 |
| ***[Eubacterium] coprostanoligenes group*** | 1.339 (1.0) | | 0.963 (1.529) | | 0.436 | | 0.056 |
| ***Ruminococcaceae uncultured*** | 7.016 (3.051) | | 5.734 (2.825) | | 0.043 | | 0.015 |
| **Erysipelotrichaceae (Erysipelotrichales, Firmicutes)** | | | | | | | |
| ***Turicibacter*** | 0.206 (0.216) | | 0.297 (0.295) | | 0.393 | | 0.052 |
| ***Erysipelotrichaceae uncultured*** | 0.019 (0.088) | | 0.011 (0.017) | | 0.481 | | 0.061 |
| ***Rhodospirillaceae (Rhodospirillales, Proteobacteria)*** | | | | | | | |
| ***Thalassospira*** | 0.236 (0.415) | | 0.361 (0.186) | | 0.19 | | 0.033 |
| **Alcaligenaceae (Burkholderiales, Proteobacteria)** | | | | | | | |
| ***Parasutterella*** | 0.039 (0.094) | | 0.01 (0.011) | | 0.0005 | | 0.007 $ |
| **Desulfovibrionaceae (Deltaproteobacteria, Proteobacteria)** | | | | | | | |
| ***Bilophila*** | 0.089 (0.327) | | 0.171 (0.128) | | 0.579 | | 0.066 |
| ***Desulfovibrio*** | 1.753 (2.685) | | 2.262 (1.294) | | 0.353 | | 0.048 |
| **Helicobacteraceae (Campylobacterales, Proteobacteria)** | | | | | | | |
| ***Helicobacter*** | 0.002 (0.003) | | 4.226 (1.378) | | 0.000 | | 0.002 $ |
| **Enterobacteriaceae (Enterobacteriales, Proteobacteria)** | | | | | | | |
| ***Enterobacter*** | 0.004 (0.003) | | 0 (0.002) | | 0.004 | | 0.006 $ |
| **Unknown Family (Unknown order, Saccharibacteria)** | | | | | | | |
| ***Candidatus Saccharimonas*** | 0.419 (0.49) | | 0.354 (0.207) | | 0.529 | | 0.063 |
| **Anaeroplasmataceae (Anaeroplasmatales, Tenericutes)** | | | | | | | |
| ***Anaeroplasma*** | 0.083 (0.277) | | 0.217 (0.195) | | 0.247 | | 0.037 |
| **Uncultured bacterium, (Mollicutes RF9, Tenericutes)** | | | | | | | |
| ***Uncultured bacterium*** | 0.062 (0.033) | | 0.078 (0.064) | | 0.529 | | 0.064 |
| **Uncultured rumen bacterium (Mollicutes RF9, Tenericutes)** | | | | | | | |
| ***Uncultured rumen bacterium*** | 0.112 (0.242) | | 0.073 (0.079) | | 0.971 | | 0.096 |
| **Uncultured Bacillales bacterium (NB1-n, Tenericutes)** | | | | | | | |
| ***Uncultured Bacillales bacterium*** | 0.012 (0.042) | | 0.034 (0.1) | | 0.218 | | 0.035 |
| ***Verrucomicrobiaceae (Verrucomicrobiales, Verrucomicrobia)*** | | | | | | | |
| ***Akkermansia*** | 0.041 (0.149) | | 0.313 (1.167) | | 0.105 | | 0.024 |

VEH, autoclaved deionised water; VEH-FMT, VEH followed by faecal microbial transfer. Data in these tables are the top 45% of genera plus genera with raw p < 0.05 and present in > two animals in each group. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. $ indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary 21. Relative abundance (%) of bacterial GENERA in the caecal samples from VEH and ABX-FMT rats***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Genus** | | **VEH** | **ABX-FMT** | | **Raw *p*-value** | **(i/m)\*Q** |
| **Bifidobacteriaceae (Bifidobacteriales, Actinobacteria)** | | | | | |
| ***Bifidobacterium*** | 0.024 (0.137) | 0.052 (0.119) | 0.28 | | 0.04 |
| **Coriobacteriaceae (Coriobacteriales, Actinobacteria)** | | | | | |
| ***Uncultured coriobacteriaceae*** | 0.035 (0.036) | 0.008 (0.011) | 0.000 | | 0.002 & |
| ***Enterorhabdus*** | 0.023 (0.021) | 0.011 (0.01) | 0.011 | | 0.009 |
| **Uncultured bacterium (Unknown order, Bacteroidetes)** | | | | | |
| ***Bacteroidetes VC21 Bac22 uncultured bacterium*** | 0 (0) | 0.1 (0.062) | 0.000 | | 0.002 & |
| **Bacteroidaceae (Bacteroidales, Bacteroidetes)** | | | | | |
| ***Bacteroides*** | 1.656 (1.138) | 2.17 (1.539) | 0.315 | | 0.045 |
| **Bacteroidales S24-7 group (Bacteroidales, Bacteroidetes)** | | | | | |
| ***Uncultured bacterium*** | 17.13 (2.798) | 17.353 (3.996) | 0.631 | | 0.072 |
| ***Unidentified*** | 0.161 (0.933) | 0.0429 (0.177) | 0.043 | | 0.015 |
| **Porphyromonadaceae (Bacteroidales, Bacteroidetes)** | | | | | |
| ***Odoribacter*** | 0.36 (0.212) | 0.296 (0.100) | 0.353 | | 0.048 |
| ***Parabacteroides*** | 0.046 (0.042) | 0.147 (0.129) | 0.023 | | 0.01 |
| ***Prevotellaceae (Bacteroidales, Bacteroidetes)*** | | | | | |
| ***Alloprevotella*** | 1.594 (2.192) | 2.173 (2.118) | 1.000 | | 0.099 |
| ***Prevotellaceae NK3B31 group*** | 1.715 (2.18) | 0.63 (2.525) | 0.143 | | 0.029 |
| ***Prevotellaceae UCG-001*** | 1.743 (2.486) | 1.379 (2.066) | 0.684 | | 0.076 |
| **Rikenellaceae (Bacteroidales, Bacteroidetes)** | | | | | |
| ***Alistipes*** | 3.555 (3.252) | 2.535 (0.804) | 0.315 | | 0.045 |
| **Uncultured bacterium (Gastranaerophilales, Cyanobacteria)** | | | | | |
| ***Uncultured bacterium*** | 0.627 (0.725) | 1.396 (1.062) | 0.035 | | 0.012 |
| ***Uncultured organism*** | 0 (0.0006) | 0.111 (0.442) | 0.000 | | 0.002 $ |
| **Deferribacteraceae (Deferribacterales, Deferribacteres)** | | | | | |
| ***Mucispirillum*** | 0.139 (0.301) | 0 (0.0002) | 0.000 | | 0.003 $ |
| **Bacillaeae (Bacillales, Firmicutes)** | | | | | |
| ***Bacillus*** | 0.13 (0.279) | 0 (0) | 0.000 | | 0.003 $ |
| **Lactobacillaceae (Lactobacillales, Firmicutes)** | | | | | |
| ***Lactobacillus*** | 2.318 (3.128) | 1.399 (1.761) | 0.190 | | 0.033 |
| **Streptococcaceae (Lactobacillales, Firmicutes)** | | | | | |
| ***Streptococcus*** | 0.004 (0.004) | 0.003 (0.005) | 0.007 | | 0.008 $ |
| **Christensenellaceae (Clostridiales, Firmicutes)** | | | | | |
| ***Christensenellaceae R-7 group*** | 0.031 (0.074) | 0.081 (0.082) | 0.393 | | 0.053 |
| **Clostridiaceae 1 (Clostridiales, Firmicutes)** | | | | | |
| ***Clostridium sensu stricto 1*** | 0.116 (0.371) | 0.139 (0.469) | 0.436 | | 0.056 |
| ***Clostridiales vadin BB60 group (Clostridiales, Firmicutes)*** | | | | | |
| ***Uncultured clostridiales bacterium*** | 0.004 (0.036) | 0.031 (0.051) | 0.035 | | 0.013 |
| ***Uncultured bacterium*** | 1.317 (1.181) | 2.927 (2.541) | 0.011 | | 0.01 |
| ***Uncultured rumen bacterium*** | 0.058 (0.096) | 0.077 (0.099) | 0.631 | | 0.072 |
| ***Unidentified*** | 0.126 (0.341) | 0.702 (0.868) | 0.052 | | 0.017 |
| **Family XIII (Clostridiales, Firmicutes)** | | | | | |
| ***Anaerovorax*** | 0.055 (0.046) | 0.053 (0.033) | 0.971 | | 0.096 |
| **Lachnospiraceae (Clostridiales, Firmicutes)** | | | | | |
| ***Blautia*** | 0.07 (0.252) | 0.084 (0.233) | 0.796 | | 0.085 |
| ***Coprococcus 1*** | 0.125 (0.063) | 0.147 (0.138) | 0.481 | | 0.061 |
| ***Coprococcus 2*** | 0.178 (0.462) | 0.155 (0.279) | 0.912 | | 0.092 |
| ***Incertae Sedis*** | 1.398 (1.351) | 0.566 (0.680) | 0.143 | | 0.029 |
| ***Lachnoclostridium*** | 0.121 (0.07) | 0.071 (0.164) | 0.353 | | 0.049 |
| ***Lachnoclostridium 10*** | 0 (0) | 0.128 (0.16) | 0.000 | | 0.003 |
| ***Lachnospiraceae NC2004 group*** | 0.586 (1.377) | 0.07 (0.223) | 0.035 | | 0.013 |
| ***Lachnospiraceae NK4A136 group*** | 22.823 (5.829) | 19.099 (7.826) | 0.052 | | 0.017 |
| ***Lachnospiraceae NK4B4 group*** | 0.01 (0.116) | 0.0008 (0.006) | 0.247 | | 0.037 |
| ***Lachnospiraceae UCG-0001*** | 0.168 (0.195) | 0.193 (0.246) | 0.739 | | 0.081 |
| ***Lachnospiraceae UCG-0005*** | 0.067 (0.088) | 0.063 (0.052) | 0.436 | | 0.056 |
| ***Lachnospiraceae UCG-0006*** | 0.281 (0.218) | 0.346 (0.606) | 0.684 | | 0.076 |
| ***Lachnospiraceae UCG-008*** | 0.081 (0.113) | 0.011 (0.019) | 0.001 | | 0.004 & |
| ***Roseburia*** | 0.913 (0.649) | 0.851 (1.281) | 0.853 | | 0.089 |
| ***Tyzzerella*** | 0.207 (0.19) | 0.177 (0.109) | 0.089 | | 0.022 |
| ***Lachnospiraceae [Eubacterium] oxidoreducens group*** | 0.262 (0.278) | 0.269 (0.465) | 0.631 | | 0.24 |
| ***Lachnospiraceae [Eubacterium] ruminantium group*** | 0.185 (0.276) | 0.043 (0.155) | 0.218 | | 0.1 |
| ***Lachnospiraceae uncultured*** | 5.073 (4.202) | 6.788 (4.27) | 0.28 | | 0.19 |
| ***Natranaerovirga*** | 0.005 (0.007) | 0 (0.0006) | 0.009 | | 0.008 |
| **Peptococcaceae (Clostridiales, Firmicutes)** | | | | | |
| ***Peptococcaceae (uncultured)*** | 0.352 (0.312) | 0.301 (0.104) | 0.631 | | 0.073 |
| ***Peptococcus*** | 0.079 (0.029) | 0.09 (0.04) | 0.165 | | 0.03 |
| **Peptostreptococcaceae (Clostridiales, Firmicutes)** | | | | | |
| ***Intestinibacter*** | 0.092 (0.499) | 0.016 (0.028) | 0.436 | | 0.057 |
| ***Peptoclostridium*** | 0.46 (0.906) | 0.336 (0.434) | 0.796 | | 0.085 |
| **Ruminococcaceae (Clostridiales, Firmicutes)** | | | | | |
| ***Anaerotruncus*** | 0.929 (0.248) | 0.82 (0.202) | 0.165 | | 0.031 |
| ***Intestinimonas*** | 0.064 (0.040) | 0.031 (0.021) | 0.023 | | 0.011 |
| ***Oscillibacter*** | 0.908 (0.281) | 0.701 (0.228) | 0.043 | | 0.015 |
| ***Papillibacter*** | 0.071 (0.188) | 0.151 (0.169) | 0.063 | | 0.019 |
| ***Ruminoclostridium*** | 0.084 (0.836) | 0.112 (0.056) | 0.247 | | 0.038 |
| ***Ruminoclostridium 5*** | 0.343 (0.175) | 0.443 (0.333) | 0.19 | | 0.033 |
| ***Ruminoclostridium 6*** | 0.723 (0.781) | 1.617 (1.084) | 0.123 | | 0.027 |
| ***Ruminoclostridium 9*** | 3.962 (1.396) | 3.133 (2.071) | 0.529 | | 0.064 |
| ***Ruminococcaceae NK4A214 group*** | 0.239 (0.146) | 0.224 (0.204) | 0.436 | | 0.057 |
| ***Ruminococcaceae UCG-002*** | 0.004 (0.006) | 0.008 (0.005) | 0.023 | | 0.010 |
| ***Ruminococcaceae UCG-003*** | 1.392 (1.069) | 1.089 (1.051) | 0.28 | | 0.42 |
| ***Ruminococcaceae UCG-005*** | 0.324 (0.247) | 0.229 (0.172) | 0.247 | | 0.038 |
| ***Ruminococcaceae UCG-009*** | 0.081 (0.043) | 0.092 (0.062) | 0.28 | | 0.42 |
| ***Ruminococcaceae UCG-010*** | 0.282 (0.208) | 0.474 (0.231) | 0.089 | | 0.022 |
| ***Ruminococcaceae UCG-011*** | 0 (0) | 0.001 (0.003) | 0.004 | | 0.006 |
| ***Ruminococcaceae UCG-013*** | 0.067 (0.059) | 0.092 (0.158) | 0.165 | | 0.031 |
| ***Ruminococcaceae UCG-014*** | 1.134 (0.706) | 1.11 (0.57) | 0.912 | | 0.093 |
| ***Ruminococcus 1*** | 2.6 (1.577) | 2.239 (2.498) | 0.971 | | 0.096 |
| ***Ruminococcus 2*** | 0.093 (0.114) | 0.062 (0.109) | 0.579 | | 0.067 |
| ***[Eubacterium] coprostanoligenes group*** | 1.339 (1.0) | 0.841 (0.929) | 0.353 | | 0.049 |
| ***Ruminococcaceae uncultured*** | 7.016 (3.051) | 8.094 (2.842) | 0.436 | | 0.057 |
| **Erysipelotrichaceae (Erysipelotrichales, Firmicutes)** | | | | | |
| ***Allobaculum*** | 0.002 (0.037) | 0.037 (0.083) | 0.063 | | 0.019 |
| ***Turicibacter*** | 0.206 (0.216) | 0.159 (0.229) | 0.739 | | 0.082 |
| ***Erysipelotrichaceae uncultured*** | 0.019 (0.088) | 0.012 (0.006) | 0.393 | | 0.054 |
| ***Rhodospirillaceae (Rhodospirillales, Proteobacteria)*** | | | | | |
| ***Thalassospira*** | 0.236 (0.415) | 0.281 (0.254) | 0.436 | | 0.058 |
| ***Uncultured rhodospirillaceae*** | 0 (0.0343) | 0.002 (0.04) | 0.436 | | 0.058 |
| **Alcaligenaceae (Burkholderiales, Proteobacteria)** | | | | | |
| ***Parasutterella*** | 0.039 (0.094) | 0.048 (0.094) | 0.971 | | 0.097 |
| **Desulfovibrionaceae (Deltaproteobacteria, Proteobacteria)** | | | | | |
| ***Bilophila*** | 0.089 (0.327) | 0.124 (0.08) | 0.631 | | 0.073 |
| ***Desulfovibrio*** | 1.753 (2.685) | 3.152 (1.215) | 0.023 | | 0.011 |
| **Helicobacteraceae (Campylobacterales, Proteobacteria)** | | | | | |
| ***Helicobacter*** | 0.002 (0.003) | 3.515 (1.354) | 0.000 | | 0.003 & |
| **Enterobacteriaceae (Enterobacteriales, Proteobacteria)** | | | | | |
| **Unknown Family (Unknown order, Saccharibacteria)** | | | | | |
| ***Candidatus Saccharimonas*** | 0.419 (0.49) | 0.582 (0.36) | 0.315 | | 0.046 |
| **Anaeroplasmataceae (Anaeroplasmatales, Tenericutes)** | | | | | |
| ***Anaeroplasma*** | 0.083 (0.277) | 0.181 (1.059) | 0.19 | | 0.034 |
| **Uncultured bacterium, (Mollicutes RF9, Tenericutes)** | | | | | |
| ***Uncultured bacterium*** | 0.062 (0.0330 | 0.095 (0.093) | 0.315 | | 0.046 |
| **Uncultured rumen bacterium (Mollicutes RF9, Tenericutes)** | | | | | |
| ***Uncultured rumen bacterium*** | 0.112 (0.242) | 0.128 (0.321) | 0.579 | | 0.067 |
| **Uncultured Bacillales bacterium (NB1-n, Tenericutes)** | | | | | |
| ***Uncultured Bacillales bacterium*** | 0.042 (0.042) | 0.029 (0.071) | 0.19 | | 0.034 |
| ***Verrucomicrobiaceae (Verrucomicrobiales, Verrucomicrobia)*** | | | | | |
| ***Akkermansia*** | 0.041 (0.149) | 0.064 (0.156) | 0.739 | | 0.082 |

VEH, autoclaved deionised water; ABX-FMT, antibiotics followed by faecal microbial transfer. Data in these tables are the top 45% of genera plus genera with raw p < 0.05 and present in > two animals in each group. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. & indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.

***Supplementary 22. Relative abundance (%) of bacterial GENERA in the caecal samples from VEH-FMT and ABX-FMT rats***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Genus** | **VEH-FMT** | **ABX-FMT** | **Raw *p*-value** | **(i/m)\*Q** | |  |
| **Bifidobacteriaceae (Bifidobacteriales, Actinobacteria)** | | | | | |  |
| ***Bifidobacterium*** | 0.044 (0.058) | 0.052 (0.119) | 0.796 | | 0.086 |  |
| **Micrococcaceae (Micrococcales, Actinobacteria)** | | | | | |  |
| ***Rothia*** | 0.008 (0.011) | 0.002 (0.004) | 0.035 | | 0.013 |  |
| **Coriobacteriaceae (Coriobacteriales, Actinobacteria)** | | | | | |  |
| ***Gordonibacter*** | 0.007 (0.012) | 0.003 (0.003) | 0.035 | | 0.013 |  |
| **Uncultured bacterium (Unknown order, Bacteroidetes)** | | | | | |  |
| ***Bacteroidetes VC21 Bac22 uncultured bacterium*** | 0.116 (0.081) | 0.1 (0.062) | 0.853 | | 0.09 |  |
| **Bacteroidaceae (Bacteroidales, Bacteroidetes)** | | | | | |  |
| ***Bacteroides*** | 1.182 (0.885) | 2.17 (1.539) | 0.353 | | 0.05 |  |
| **Bacteroidales S24-7 group (Bacteroidales, Bacteroidetes)** | | | | | |  |
| ***Uncultured bacterium*** | 14.372 (2.949) | 17.353 (3.996) | 0.075 | | 0.021 |  |
| ***Unidentified*** | 0.067 (0.059) | 0.0429 (0.177) | 0.353 | | 0.05 |  |
| **Porphyromonadaceae (Bacteroidales, Bacteroidetes)** | | | | | |  |
| ***Odoribacter*** | 0.296 (0.289) | 0.296 (0.100) | 0.631 | | 0.074 |  |
| ***Parabacteroides*** | 0.099 (0.070) | 0.147 (0.129) | 0.684 | | 0.077 |  |
| ***Prevotellaceae (Bacteroidales, Bacteroidetes)*** | | | | | |  |
| ***Alloprevotella*** | 0.748 (1.639) | 2.173 (2.118) | 0.28 | | 0.043 |  |
| ***Prevotellaceae NK3B31 group*** | 2.017 (2.704) | 0.63 (2.525) | 0.143 | | 0.029 |  |
| ***Prevotellaceae UCG-001*** | 2.134 (2.167) | 1.379 (2.066) | 0.075 | | 0.021 |  |
| **Rikenellaceae (Bacteroidales, Bacteroidetes)** | | | | | |  |
| ***Alistipes*** | 1.961 (1.097) | 2.535 (0.804) | 0.353 | | 0.05 |  |
| **Uncultured bacterium (Gastranaerophilales, Cyanobacteria)** | | | | | |  |
| ***Uncultured bacterium*** | 0.837 (0.685) | 1.396 (1.062) | 0.19 | | 0.034 |  |
| ***Uncultured organism*** | 0.491 (0.893) | 0.111 (0.442) | 0.089 | | 0.023 |  |
| **Lactobacillaceae (Lactobacillales, Firmicutes)** | | | | | |  |
| ***Lactobacillus*** | 1.441 (2.691) | 1.399 (1.761) | 0.075 | | 0.021 |  |
| **Streptococcaceae (Lactobacillales, Firmicutes)** | | | | | |  |
| ***Streptococcus*** | 0.003 (0.005) | 0.001 (0.002) | 0.003 | | 0.005 ¥ |  |
| **Christensenellaceae (Clostridiales, Firmicutes)** | | | | | |  |
| ***Christensenellaceae R-7 group*** | 0.046 (0.045) | 0.081 (0.082) | 0.218 | | 0.036 |  |
| **Clostridiaceae 1 (Clostridiales, Firmicutes)** | | | | | |  |
| ***Clostridium sensu stricto 1*** | 0.238 (0.005) | 0.139 (0.469) | 0.436 | | 0.058 |  |
| ***Clostridiales vadin BB60 group (Clostridiales, Firmicutes)*** | | | | | |  |
| ***Uncultured clostridiales bacterium*** | 0.045 (0.022) | 0.031 (0.051) | 0.579 | | 0.068 |  |
| ***Uncultured bacterium*** | 2.147 (0.811) | 2.927 (2.541) | 0.579 | | 0.068 |  |
| ***Uncultured rumen bacterium*** | 0.021 (0.048) | 0.077 (0.099) | 0.105 | | 0.025 |  |
| ***Unidentified*** | 0.756 (1.352) | 0.702 (0.868) | 0.353 | | 0.05 |  |
| **Family XIII (Clostridiales, Firmicutes)** | | | | | |  |
| ***Anaerovorax*** | 0.038 (0.013) | 0.053 (0.033) | 0.052 | | 0.017 |  |
| **Lachnospiraceae (Clostridiales, Firmicutes)** | | | | | |  |
| ***Blautia*** | 0.566 (1.207) | 0.084 (0.233) | 0.035 | | 0.04 |  |
| ***Coprococcus 1*** | 0.127 (0.06) | 0.147 (0.138) | 0.28 | | 0.043 |  |
| ***Coprococcus 2*** | 0.011 (0.207) | 0.155 (0.279) | 0.075 | | 0.021 |  |
| ***Incertae Sedis*** | 0.913 (0.926) | 0.566 (0.680) | 0.436 | | 0.058 |  |
| ***Lachnoclostridium*** | 0.124 (0.040) | 0.071 (0.164) | 0.218 | | 0.036 |  |
| ***Lachnoclostridium 10*** | 0.313 (0.362) | 0.128 (0.16) | 0.853 | | 0.09 |  |
| ***Lachnospiraceae NC2004 group*** | 0.4 (0.391) | 0.07 (0.223) | 0.052 | | 0.018 |  |
| ***Lachnospiraceae NK4A136 group*** | 19.789 (5.348) | 19.099 (7.826) | 0.631 | | 0.074 |  |
| ***Lachnospiraceae UCG-0001*** | 0.303 (0.354) | 0.193 (0.246) | 0.105 | | 0.025 |  |
| ***Lachnospiraceae UCG-0005*** | 0.103 (0.088) | 0.063 (0.052) | 0.063 | | 0.019 |  |
| ***Lachnospiraceae UCG-0006*** | 0.254 (0.268) | 0.346 (0.606) | 0.739 | | 0.082 |  |
| ***Roseburia*** | 1.798 (1.915) | 0.851 (1.281) | 0.315 | | 0.047 |  |
| ***Tyzzerella*** | 0.117 (0.059) | 0.177 (0.109) | 0.165 | | 0.032 |  |
| ***Lachnospiraceae [Eubacterium] oxidoreducens group*** | 0.292 (0.355) | 0.269 (0.465) | 1.000 | | 0.1 |  |
| ***Lachnospiraceae [Eubacterium] ruminantium group*** | 0.035 (0.363) | 0.043 (0.155) | 0.684 | | 0.078 |  |
| ***Lachnospiraceae [Eubacterium] ventriosum group*** | 0.014 (0.019) | 0.032 (0.046) | 0.035 | | 0.04 |  |
| ***Lachnospiraceae uncultured*** | 9.821 (5.779) | 6.788 (4.27) | 0.123 | | 0.028 |  |
| ***Marvinbryantia*** | 0.002 (0.003) | 0.008 (0.029) | 0.043 | | 0.016 |  |
| **Peptococcaceae (Clostridiales, Firmicutes)** | | | | | |  |
| ***Peptococcaceae (uncultured)*** | 0.325 (0.1) | 0.301 (0.104) | 0.739 | | 0.083 |  |
| ***Peptococcus*** | 0.085 (0.083) | 0.09 (0.04) | 0.631 | | 0.074 |  |
| **Peptostreptococcaceae (Clostridiales, Firmicutes)** | | | | | |  |
| ***Intestinibacter*** | 0.046 (0.093) | 0.016 (0.028) | 0.315 | | 0.047 |  |
| ***Peptoclostridium*** | 0.626 (0.767) | 0.336 (0.434) | 0.007 | | 0.008 ¥ |  |
| **Ruminococcaceae (Clostridiales, Firmicutes)** | | | | | |  |
| ***Anaerotruncus*** | 0.764 (0.170) | 0.82 (0.202) | 0.529 | | 0.065 |  |
| ***Flavonifractor*** | 0.065 (0.169) | 0.018 (0.114) | 0.393 | | 0.054 |  |
| ***Oscillibacter*** | 0.586 (0.175) | 0.701 (0.228) | 0.247 | | 0.039 |  |
| ***Papillibacter*** | 0.161 (0.247) | 0.151 (0.169) | 0.579 | | 0.069 |  |
| ***Ruminoclostridium*** | 0.152 (0.094) | 0.112 (0.056) | 0.105 | | 0.025 |  |
| ***Ruminoclostridium 5*** | 0.407 (0.27) | 0.443 (0.333) | 0.912 | | 0.094 |  |
| ***Ruminoclostridium 6*** | 1.0 (0.9) | 1.617 (1.084) | 0.89 | | 0.023 |  |
| ***Ruminoclostridium 9*** | 2.305 (0.576) | 3.133 (2.071) | 0.035 | | 0.04 |  |
| ***Ruminococcaceae NK4A214 group*** | 0.234 (0.094) | 0.224 (0.204) | 0.579 | | 0.069 |  |
| ***Ruminococcaceae UCG-003*** | 1.429 (0.472) | 1.089 (1.051) | 0.579 | | 0.07 |  |
| ***Ruminococcaceae UCG-005*** | 0.417 (0.313) | 0.229 (0.172) | 0.005 | | 0.007 ¥ |  |
| ***Ruminococcaceae UCG-009*** | 0.083 (0.029) | 0.092 (0.062) | 0.28 | | 0.043 |  |
| ***Ruminococcaceae UCG-010*** | 0.418 (0.26) | 0.474 (0.231) | 0.796 | | 0.086 |  |
| ***Ruminococcaceae UCG-013*** | 0.204 (0.15) | 0.092 (0.158) | 0.043 | | 0.04 |  |
| ***Ruminococcaceae UCG-014*** | 0.945 (0.78) | 1.11 (0.57) | 0.436 | | 0.059 |  |
| ***Ruminococcus 1*** | 2.413 (3.09) | 2.239 (2.498) | 0.971 | | 0.098 |  |
| ***Ruminococcus 2*** | 0.082 (0.045) | 0.062 (0.109) | 0.739 | | 0.083 |  |
| ***[Eubacterium] coprostanoligenes group*** | 0.963 (1.529) | 0.841 (0.929) | 1.000 | | 0.1 |  |
| ***Ruminococcaceae uncultured*** | 5.734 (2.825) | 8.094 (2.842) | 0.009 | | 0.0087 |  |
| **Erysipelotrichaceae (Erysipelotrichales, Firmicutes)** | | | | | |  |
| ***Allobaculum*** | 0.008 (0.003) | 0.037 (0.083) | 0.001 | | 0.004 ¥ |  |
| ***Turicibacter*** | 0.297 (0.295) | 0.159 (0.229) | 0.105 | | 0.026 |  |
| ***Rhodospirillaceae (Rhodospirillales, Proteobacteria)*** | | | | | |  |
| ***Thalassospira*** | 0.361 (0.186) | 0.281 (0.254) | 0.28 | | 0.043 |  |
| ***Uncultured rhodospirillaceae*** | 0.023 (0.054) | 0.002 (0.04) | 0.631 | | 0.075 |  |
| **Alcaligenaceae (Burkholderiales, Proteobacteria)** | | | | | |  |
| ***Parasutterella*** | 0.01 (0.011) | 0.048 (0.094) | 0.005 | | 0.007 ¥ |  |
| **Desulfovibrionaceae (Deltaproteobacteria, Proteobacteria)** | | | | | |  |
| ***Bilophila*** | 0.171 (0.128) | 0.124 (0.08) | 0.353 | | 0.051 |  |
| ***Desulfovibrio*** | 2.262 (1.294) | 3.152 (1.215) | 0.035 | | 0.014 |  |
| **Helicobacteraceae (Campylobacterales, Proteobacteria)** | | | | | |  |
| ***Helicobacter*** | 4.226 (1.378) | 3.515 (1.354) | 0.105 | | 0.026 |  |
| **Enterobacteriaceae (Enterobacteriales, Proteobacteria)** | | | | | |  |
| ***Enterobacter*** | 0 (0.002) | 0.002 (0.004) | 0.28 | | 0.044 |  |
| **Unknown Family (Unknown order, Saccharibacteria** | | | | | |  |
| ***Candidatus Saccharimonas*** | 0.354 (0.207) | 0.582 (0.36) | 0.023 | | 0.011 |  |
| **Anaeroplasmataceae (Anaeroplasmatales, Tenericutes)** | | | | | |  |
| ***Anaeroplasma*** | 0.217 (0.195) | 0.181 (1.059) | 0.739 | | 0.084 |  |
| **Uncultured bacterium, (Mollicutes RF9, Tenericutes)** | | | | | |  |
| ***Uncultured bacterium*** | 0.078 (0.064) | 0.095 (0.093) | 0.579 | | 0.07 |  |
| **Uncultured rumen bacterium (Mollicutes RF9, Tenericutes)** | | | | | |  |
| ***Uncultured rumen bacterium*** | 0.073 (0.079) | 0.128 (0.321) | 0.631 | | 0.075 |  |
| **Uncultured Bacillales bacterium (NB1-n, Tenericutes)** | | | | | |  |
| ***Uncultured Bacillales bacterium*** | 0.034 (0.1) | 0.029 (0.071) | 0.739 | | 0.084 |  |
| ***Verrucomicrobiaceae (Verrucomicrobiales, Verrucomicrobia)*** | | | | | |  |
| ***Akkermansia*** | 0.313 (1.167) | 0.064 (0.156) | 0.029 | | 0.012 |  |
|  |  |  |  | |  |  |

VEH-FMT, VEH followed by faecal microbial transfer; ABX-FMT, antibiotics followed by faecal microbial transfer. Data in these tables are the top 45% of genera plus genera with raw p < 0.05 and present in > two animals in each group. Data are shown as median (IQR) and were statistically compared using unpaired non-parametric Mann-Whitney *U* test and Benjamini-Hochberg adjustment procedure with Q = 0.1 used to correct p values for multiple testing. ¥ indicates an increase or decrease in the relative abundance of bacterial taxa in VEH-FMT.