SM Table 1. Bacterial taxa affected by iron treatment

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Bacterial taxa | Percent abundance of bacterial group [mean ± SD] for the different treatments | | | | | | | | *P*- Value for factorial ANOVA | | | Correlations of  bacterial taxa with histology scores | |
| WT Fe ade,  sham-inj. | TNFΔARE  Fe ade, sham-inj. | WT Fe def, sham-inj. | | TNFΔARE  Fe def, sham-inj. | WT Fe def, iron-inj. | TNFΔARE  Fe def,  iron-inj. | | Fe ade, sham-inj.  vs  Fe def, sham-inj. | Fe ade, sham-inj.  vs  Fe def,  iron-inj. | Fe def,  sham-inj.  vs  Fe def,  iron-inj. |
| R | *P-value* |
| Family level |  |  |  | |  |  |  | |  |  |  |  |  |
| Bifidobacteriaceae | 0.04 ± 0.05 | 0.03 ± 0.03 | 4.41 ± 5.27 | | 3.95 ± 2.43 | 3.41 ± 4.76 | 3.52 ± 3.18 | | **0.0029** | **0.0116** | > 0.01 | -0.6339 | 0.0112 |
| Rikenellaceae | 1.92 ± 2.39 | 3.69 ± 4.54 | 0.27 ± 0.15 | | 0.32 ± 0.10 | 0.82 ± 0.65 | 0.40 ± 0.11 | | **0.0061** | **0.0337** | > 0.01 | 0.5486 | 0.0343 |
| Unclassified Desulfovibrionales | 0.11 ± 0.03 | 0.11 ± 0.08 | 0.49 ± 0.34 | | 1.11 ± 0.87 | 1.12 ± 1.47 | 1.19 ± 0.98 | | **0.0157** | **0.0025** | > 0.01 | -0.5826 | 0.0227 |
| Bacteroidaceae | 4.02 ± 2.56 | 5.36 ± 3.27 | 0.87 ± 0.69 | | 0.24 ± 0.09 | 3.55 ± 1.93 | 0.84 ± 0.47 | | **< 0.0001** | **0.0048** | **0.0083** | 0.7734 | **0.0007** |
| Desulfovibrionaceae | 3.87 ± 1.37 | 2.49 ± 1.27 | 0.79 ± 0.53 | | 1.03 ± 1.01 | 1.63 ± 0.41 | 0.87 ± 0.37 | | **< 0.0001** | **0.0001** | > 0.01 | 0.7306 | **0.0020** |
| Lactobacillaceae | 1.17 ± 2.21 | 1.55 ± 2.00 | 2.98 ± 3.06 | | 4.49 ± 2.14 | 0.33 ± 0.53 | 0.73 ± 0.56 | | **0.0270** | > 0.01 | **0.0047** | -0.1917 | 0.4937 |
| Erysipelotrichaceae | 6.68 ± 7.64 | 12.04 ± 9.94 | 17.04 ± 14 18 | | 27.51 ± 9.57 | 19.61 ± 7.07 | 29.02 ± 4.01 | | **0.0093** | **0.0019** | > 0.01 | -0.7491 | **0.0013** |
| Lachnospiraceae | 40.09 ± 8.82 | 24.67 ± 7.96 | 22.02 ± 11.89 | | 15.34 ± 5.88 | 24.21 ± 5.60 | 17.75 ± 4.87 | | **0.0022** | **0.0167** | > 0.01 | 0.5632 | 0.0288 |
| Succinivibrionaceae | 0.75 ± 0.30 | 0.56 ± 0.31 | 1.73 ± 1.13 | | 1.56 ± 0.40 | 1.00 ± 0.69 | 1.61 ± 0.51 | | **0.0032** | **0.0438** | > 0.01 | -0.8440 | **< 0.0001** |
| Genus level |  |  |  | |  |  |  | |  |  |  |  |  |
| Unclassified Prevotellaceae | 1.88 ± 0.96 | 1.87 ± 1.12 | 2.99 ± 1.53 | | 3.44 ± 0.66 | 2.79 ± 1.15 | 3.56 ± 0.50 | | **0.0147** | **0.0160** | > 0.01 | -0.7947 | **0.0004** |
| *Bifidobacterium* | 0.01 ± 0.01 | 0.02 ± 0.01 | 3.86 ± 4.62 | | 3.31 ± 2.81 | 2.76 ± 3.89 | 2.77 ± 2.43 | | **0.0022** | **0.0120** | > 0.01 | -0.6373 | 0.0106 |
| *Lactobacillus* | 1.16 ± 2.19 | 1.50 ± 1.93 | 2.91 ± 3.00 | | 4.40 ± 2.14 | 0.32 ± 0.54 | 0.71 ± 0.54 | | **0.0277** | **0.0044** | > 0.01 | -0.1917 | 0.4937 |
| *Clostridum* | 0.08 ± 0.05 | 0.11 ± 0.11 | 0.21 ± 0.12 | | 0.28 ± 0.07 | 0.21 ± 0.13 | 0.30 ± 0.11 | | **0.0052** | **0.0037** | > 0.01 | -0.7128 | **0.0029** |
| *Succinivibrio* | 0.72 ± 0.30 | 0.54 ± 0.29 | 1.71 ± 1.11 | | 1.50 ± 0.39 | 0.92 ± 0.56 | 1.53 ± 0.47 | | **0.0021** | **0.0487** | > 0.01 | -0.8495 | **< 0.0001** |
| Unclassified Erysipelotrichaceae | 2.30 ± 2.78 | 3.56 ± 2.68 | 5.12 ± 4.01 | | 9.93 ± 3.70 | 8.05 ± 3.48 | 12.32 ± 1.35 | | **0.0067** | **< 0.0001** | > 0.01 | -0.8349 | **0.0001** |
| *Turicibacter* | 0.18 ± 0.13 | 0.17 ± 0.08 | 0.36 ± 0.14 | | 0.51 ± 0.16 | 0.27 ± 0.19 | 0.50 ± 0.18 | | **0.0022** | **0.0162** | > 0.01 | -0.7656 | **0.0009** |
| *Bacteroides* | 4.02 ± 2.56 | 5.36 ± 3.27 | 0.87 ± 0.69 | | 0.24 ± 0.09 | 3.54 ± 1.93 | 0.84 ± 0.47 | | **< 0.0001** | **0.0047** | **0.0085** | 0.7734 | **0.0007** |
| *Dorea\** | 2.59 ± 1.39 | 0.14 ± 0.13 | 0.32 ± 0.26 | | 0.42 ± 0.33 | 0.17 ± 0.17 | 0.22 ± 0.24 | | > 0.01 | **0.0046** | > 0.01 | -0.3674 | 0.1780 |
| *Lachnospiraceae Insertae Sedis* | 7.19 ± 2.68 | 2.95 ± 0.65 | 2.82 ± 1.53 | | 2.12 ± 0.35 | 3.28 ± 1.16 | 2.38 ± 0.47 | | **0.0005** | **0.0043** | > 0.01 | 0.5458 | 0.0353 |
| *Desulfovibrio* | 2.19 ± 1.11 | 1.69 ± 0.84 | 0.30 ± 0.22 | 0.44 ± 0.56 | | 0.66 ± 0.32 | | 0.37 ± 0.26 | **< 0.0001** | **< 0.0001** | > 0.01 | 0.0747 | **0.0014** |

\*These bacterial groups showed statistically significant interactions between iron treatment and genotype.

SM Table 2. OTUs affected by iron treatment

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Highest match in RDP database (type strain) | Sequence similarity score  to closest type strain1 | Percent abundance of bacterial group [mean ± SD] for the different treatments | | | | | | *P-values* | | | Correlation parameters of  bacterial taxa with histology scores | |
| WT Fe ade,  sham-inj. | TNFΔARE  Fe ade, sham-inj. | WT Fe def, sham-inj. | TNFΔARE  Fe def, sham-inj. | WT Fe def, iron-inj. | TNFΔARE  Fe def,  iron-inj. | Fe ade, sham-inj.  vs  Fe def, sham-inj. | Fe ade, sham-inj.  vs  Fe def,  iron-inj. | Fe def,  sham-inj.  vs  Fe def,  iron-inj. | *R* | *P-value* |
| Allobaculum stercoricanis (T) DSM 13633 | 0.484 | 1.301 ± 1.364 | 1.344 ± 1.206 | 2.258 ± 1.162 | 4.448 ± 2.770 | 5.255 ± 3.333 | 8.807 ± 1.545 | **0.0327** | **< 0.0001** | **0.0149** | -0.7288 | **0.0021** |
| Lactobacillus johnsonii (T); ATCC 33200 (T). | 0.969 | 1.045 ± 2.284 | 1.482 ± 2.016 | 2.934 ± 3.348 | 4.061 ± 2.348 | 0.012 ± 0.028 | 0.658 ± 0.711 | > 0.01 | > 0.01 | **0.0070** | -0.1469 | 0.6013 |
| Desulfovibrio desulfuricans subsp. desulfuricans (T); ATCC29577 | 0.726 | 3.673 ± 0.606 | 2.851 ± 0.509 | 0.729 ± 0.940 | 1.152 ± 0.734 | 1.152 ± 0.734 | 0.606 ± 0.422 | **< 0.0001** | **< 0.0001** | > 0.01 | 0.7430 | **0.0015** |
| Clostridium oroticum (T); M59109\* | 0.805 | 5.447 ± 3.306 | 0.050 ± 0.069 | 0.375 ± 0.316 | 0.347 ± 0.428 | 0.012 ± 0.017 | 0.136 ± 0.234 | **0.0277** | **0.0005** | > 0.01 | -0.3498 | 0.2013 |
| Clostridium xylanolyticum (T); ATCC 4963\* | 0.813 | 4.545 ± 3.624 | 1.209 ± 0.745 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.000 ± 0.000 | **0.0008** | **0.0008** | > 0.01 | 0.8509 | **< 0.0001** |
| Bacteroides dorei (T); JCM 13471 | 0.729 | 1.143 ± 0.602 | 2.039 ± 1.695 | 0.220 ± 0.226 | 0.016 ± 0.022 | 1.047 ± 0.949 | 0.177 ± 0.190 | **0.0018** | **0.0395** | > 0.01 | 0.6888 | **0.0045** |
| Succinivibrio dextrinosolvens (T); DSM 3072 | 0.805 | 0.184 ± 0.110 | 0.245 ± 0.161 | 0.698 ± 0.444 | 0.566 ± 0.201 | 0.389 ± 0.221 | 0.723 ± 0.371 | **0.0070** | **0.0290** | > 0.01 | -0.6690 | **0.0064** |
| Bacteroides dorei (T); JCM 13471 | 0.760 | 0.844 ± 0.379 | 1.374 ± 1.293 | 0.158 ± 0.170 | 0.014 ± 0.019 | 0.741 ± 0.780 | 0.126 ± 0.127 | **< 0.0001** | **0.0129** | > 0.01 | 0.6483 | **0.0090** |
| Clostridium orbiscindens (T); DSM 6740 | 0.685 | 0.333 ± 0.307 | 0.160 ± 0.250 | 0.869 ± 1.016 | 0.760 ± 0.355 | 0.081 ± 0.052 | 0.035 ± 0.064 | **0.0318** | > 0.01 | **0.0039** | -0.3047 | 0.2695 |
| Clostridium orbiscindens (T); DSM 6740\* | 0.662 | 1.059 ± 0.366 | 0.421 ± 0.275 | 0.207 ± 0.197 | 0.769 ± 0.142 | 0.420 ± 0.199 | 0.308 ± 0.188 | **< 0.0001** | **0.0002** | > 0.01 | 0.6086 | 0.0161 |
| Succinivibrio dextrinosolvens (T); DSM 3072 | 0.812 | 0.187 ± 0.182 | 0.123 ± 0.103 | 0.438 ± 0.319 | 0.460 ± 0.165 | 0.244 ± 0.165 | 0.387 ± 0.093 | **0.0044** | > 0.01 | > 0.01 | -0.7974 | **0.0004** |
| Parabacteroides distasonis (T); M86695 | 0.598 | 0.114 ± 0.097 | 0.062 ± 0.071 | 0.171 ± 0.160 | 0.454 ± 0.269 | 0.397 ± 0.298 | 0.629 ± 0.265 | > 0.01 | **0.0005** | > 0.01 | -0.7494 | **0.0013** |
| Marinilabilia salmonicolor (T); M62422 | 0.536 | 0.079 ± 0.123 | 0.035 ± 0.058 | 0.368 ± 0.228 | 0.380 ± 0.178 | 0.426 ± 0.415 | 0.391 ± 0.102 | **0.0015** | **0.0029** | > 0.01 | -0.8171 | **0.0002** |
| Desulfovibrio desulfuricans subsp. desulfuricans (T); ATCC29577 | 0.606 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.231 ± 0.190 | 0.346 ± 0.423 | 0.538 ± 0.780 | 0.622 ± 0.624 | **0.0056** | **0.0001** | > 0.01 | -0.5154 | 0.0493 |
| Turicibacter sanguinis (T); AF349724 | 0.894 | 0.158 ± 0.157 | 0.120 ± 0.063 | 0.284 ± 0.100 | 0.384 ± 0.123 | 0.207 ± 0.167 | 0.412 ± 0.132 | **0.0065** | **0.0242** | > 0.01 | 0.7572 | **0.0011** |
| Bacteroides eggerthii (T); L16485\* | 0.712 | 0.448 ± 0.701 | 0.430 ± 0.402 | 0.030 ± 0.034 | 0.009 ± 0.012 | 0.848 ± 0.369 | 0.020 ± 0.032 | **0.0021** | > 0.01 | **0.0064** | 0.7715 | **0.0008** |
| Allobaculum stercoricanis (T); type strain: DSM 13633\* | 0.515 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.024 ± 0.023 | 0.030 ± 0.042 | 0.000 ± 0.000 | 1.452 ± 1.632 | > 0.01 | **0.0036** | **0.0250** | -0.3288 | 0.2314 |
| Bacteroides capillosus (T); ATCC 29799 | 0.614 | 0.041 ± 0.065 | 0.160 ± 0.066 | 0.117 ± 0.154 | 0.303 ± 0.157 | 0.399 ± 0.497 | 0.495 ± 0.213 | > 0.01 | **0.0060** | > 0.01 | -0.5932 | 0.0198 |
| Clostridium oroticum (T); M59109 | 0.760 | 1.572 ± 0.881 | 0.027 ± 0.060 | 0.116 ± 0.085 | 0.076 ± 0.037 | 0.019 ± 0.031 | 0.072 ± 0.103 | **0.0283** | **0.0010** | > 0.01 | -0.4056 | 0.1336 |
| Allobaculum stercoricanis (T); DSM 13633 (T).\* | 0.494 | 0.146 ± 0.192 | 0.050 ± 0.064 | 0.181 ± 0.158 | 0.237 ± 0.118 | 0.222 ± 0.100 | 0.566 ± 0.163 | > 0.01 | **0.0002** | > 0.01 | -0.7037 | **0.0034** |
| Clostridium lituseburense (T); M59107\* | 0.885 | 0.107 ± 0.083 | 0.085 ± 0.061 | 0.156 ± 0.090 | 0.481 ± 0.154 | 0.249 ± 0.163 | 0.215 ± 0.112 | **0.0013** | **0.0206** | > 0.01 | -0.6560 | **0.0079** |
| Allobaculum stercoricanis (T); DSM 13633 (T). | 0.491 | 0.052 ± 0.088 | 0.066 ± 0.053 | 0.150 ± 0.068 | 0.268 ± 0.158 | 0.261 ± 0.219 | 0.513 ± 0.233 | **0.0176** | **0.0004** | > 0.01 | -0.6645 | **0.0069** |
| Bacteroides dorei (T); JCM 13471 | 0.697 | 0.287 ± 0.164 | 0.813 ± 0.755 | 0.077 ± 0.094 | 0.000 ± 0.000 | 0.329 ± 0.288 | 0.058 ± 0.079 | **0.0001** | **0.0215** | > 0.01 | 0.6406 | 0.0101 |
| Clostridium oroticum (T); M59109\* | 0.746 | 1.231 ± 0.748 | 0.014 ± 0.019 | 0.124 ± 0.129 | 0.064 ± 0.058 | 0.005 ± 0.012 | 0.046 ± 0.067 | **0.0025** | **0.0007** | > 0.01 | -0.3527 | 0.1973 |
| Allobaculum stercoricanis (T); DSM 13633 (T). | 0.486 | 0.077 ± 0.100 | 0.132 ± 0.136 | 0.183 ± 0.159 | 0.181 ± 0.108 | 0.258 ± 0.150 | 0.421 ± 0.181 | > 0.01 | **0.0038** | > 0.01 | -0.4793 | 0.0706 |
| Allobaculum stercoricanis (T); type strain: DSM 13633 | 0.480 | 0.076 ± 0.142 | 0.079 ± 0.081 | 0.080 ± 0.096 | 0.272 ± 0.096 | 0.264 ± 0.213 | 0.487 ± 0.078 | > 0.01 | **0.0009** | **0.0245** | -0.6624 | **0.0071** |
| Allobaculum stercoricanis (T); DSM 13633 (T) | 0.471 | 0.057 ± 0.127 | 0.060 ± 0.055 | 0.105 ± 0.061 | 0.168 ± 0.052 | 0.292 ± 0.073 | 0.519 ± 0.219 | **0.0102** | **< 0.0001** | **0.0008** | -0.6052 | 0.0168 |
| Allobaculum stercoricanis (T); type strain: DSM 13633 | 0.482 | 0.087 ± 0.142 | 0.067 ± 0.042 | 0.093 ± 0.093 | 0.229 ± 0.081 | 0.343 ± 0.347 | 0.375 ± 0.169 | > 0.01 | **0.0016** | > 0.01 | -0.7068 | **0.0032** |
| Clostridium lituseburense (T); M59107 | 0.888 | 0.022 ± 0.033 | 0.178 ± 0.092 | 0.121 ± 0.034 | 0.268 ± 0.205 | 0.259 ± 0.188 | 0.258 ± 0.201 | > 0.01 | **0.0098** | > 0.01 | -0.3000 | 0.2773 |
| Desulfitobacterium metallireducens (T); AF297871 | 0.443 | 0.545 ± 0.274 | 0.170 ± 0.128 | 0.159 ± 0.147 | 0.029 ± 0.029 | 0.119 ± 0.110 | 0.125 ± 0.091 | **0.0030** | > 0.01 | > 0.01 | 0.4450 | 0.0965 |
| Allobaculum stercoricanis (T); DSM 13633 (T). | 0.487 | 0.044 ± 0.071 | 0.014 ± 0.020 | 0.076 ± 0.082 | 0.174 ± 0.173 | 0.307 ± 0.174 | 0.323 ± 0.102 | **0.0311** | **< 0.0001** | **0.0041** | -0.6775 | **0.0055** |
| Blautia hydrogenotrophica (T); S5a36 | 0.496 | 0.552 ± 0.170 | 0.090 ± 0.092 | 0.116 ± 0.166 | 0.005 ± 0.010 | 0.269 ± 0.231 | 0.042 ± 0.045 | **0.0006** | > 0.01 | > 0.01 | 0.4554 | 0.0880 |
| Faecalibacterium prausnitzii (T); ATCC 27768\* | 0.879 | 0.070 ± 0.078 | 0.067 ± 0.082 | 0.080 ± 0.064 | 0.362 ± 0.137 | 0.163 ± 0.028 | 0.148 ± 0.086 | **0.0015** | > 0.01 | > 0.01 | -0.5749 | 0.0250 |
| Verrucomicrobium spinosum (T); DSM 4136T | 0.442 | 0.060 ± 0.056 | 0.087 ± 0.057 | 0.119 ± 0.058 | 0.210 ± 0.147 | 0.160 ± 0.131 | 0.231 ± 0.240 | **0.0024** | > 0.01 | > 0.01 | -0.4001 | 0.1395 |
| Desulfovibrio desulfuricans subsp. desulfuricans (T); Essex 6 | 0.598 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.163 ± 0.185 | 0.224 ± 0.219 | 0.321 ± 0.481 | 0.196 ± 0.107 | **0.0062** | **0.0015** | > 0.01 | -0.5678 | 0.0272 |
| Alistipes shahii (T); WAL 8301\* | 0.714 | 0.147 ± 0.213 | 0.702 ± 0.557 | 0.030 ± 0.029 | 0.011 ± 0.016 | 0.123 ± 0.129 | 0.010 ± 0.014 | **0.0016** | **0.0096** | > 0.01 | 0.7849 | **0.0005** |
| Bacillus funiculus (T); NAF001 | 0.374 | 0.499 ± 0.552 | 0.331 ± 0.219 | 0.061 ± 0.054 | 0.033 ± 0.033 | 0.125 ± 0.263 | 0.010 ± 0.022 | **0.0067** | **0.0020** | > 0.01 | 0.1783 | **0.0026** |
| Prevotella salivae (T); JCM 12084 | 0.629 | 0.045 ± 0.044 | 0.064 ± 0.049 | 0.160 ± 0.148 | 0.258 ± 0.211 | 0.136 ± 0.091 | 0.083 ± 0.034 | **0.0042** | > 0.01 | > 0.01 | -0.3489 | 0.2024 |
| Allobaculum stercoricanis (T); type strain: DSM 13633\* | 0.486 | 0.047 ± 0.051 | 0.032 ± 0.021 | 0.089 ± 0.052 | 0.139 ± 0.091 | 0.103 ± 0.061 | 0.309 ± 0.133 | > 0.01 | **0.0002** | **0.0342** | -0.6706 | **0.0062** |
| Blautia hydrogenotrophica (T); S5a36; X95624\* | 0.705 | 0.553 ± 0.315 | 0.047 ± 0.057 | 0.061 ± 0.098 | 0.013 ± 0.030 | 0.121 ± 0.127 | 0.028 ± 0.033 | **0.0008** | **0.0210** | > 0.01 | 0.2509 | 0.3671 |
| Eubacterium ruminantium (T); GA195 | 0.597 | 0.000 ± 0.000 | 0.036 ± 0.049 | 0.411 ± 0.572 | 0.188 ± 0.218 | 0.066 ± 0.101 | 0.000 ± 0.000 | **0.0061** | > 0.01 | **0.0095** | -0.1940 | 0.4884 |
| Eubacterium rectale (T); L34627 | 0.821 | 0.035 ± 0.036 | 0.026 ± 0.026 | 0.082 ± 0.083 | 0.129 ± 0.139 | 0.110 ± 0.127 | 0.262 ± 0.161 | > 0.01 | **0.0100** | > 0.01 | -0.5151 | 0.0494 |
| Acetanaerobacterium elongatum (T); Z7\* | 0.517 | 0.602 ± 0.518 | 0.136 ± 0.194 | 0.016 ± 0.035 | 0.027 ± 0.021 | 0.013 ± 0.018 | 0.086 ± 0.096 | **0.0067** | **0.0129** | > 0.01 | 0.3312 | 0.2278 |
| Allobaculum stercoricanis (T); type strain: DSM 13633 | 0.488 | 0.054 ± 0.107 | 0.052 ± 0.045 | 0.081 ± 0.077 | 0.122 ± 0.086 | 0.180 ± 0.095 | 0.172 ± 0.048 | > 0.01 | **0.0057** | > 0.01 | -0.6647 | **0.0069** |
| Bacteroides stercoris (T); ATCC 43183 (T). | 0.657 | 0.321 ± 0.412 | 0.258 ± 0.096 | 0.026 ± 0.032 | 0.005 ± 0.010 | 0.026 ± 0.041 | 0.007 ± 0.015 | **< 0.0001** | **< 0.0001** | > 0.01 | 0.9111 | **< 0.0001** |
| Clostridium xylanolyticum (T); ATCC 4963 | 0.758 | 0.494 ± 0.451 | 0.146 ± 0.157 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.000 ± 0.000 | **< 0.0001** | **< 0.0001** | > 0.01 | 0.7265 | **0.0022** |

\*These bacterial groups showed statistically significant interactions between iron treatment and genotype.

1Obtained with the SeqMatch tool of RDP.

SM Table 3. Bacterial taxa affected by host genotype.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Bacterial taxa | Percent abundance of bacterial group [mean ± SD] for the different treatments | | | | | | *P-value* for factorial ANOVA | Correlations of  bacterial taxa with histology scores | |
| WT Fe ade,  sham-inj. | TNFΔARE  Fe ade,  sham-inj. | WT Fe def, sham-inj. | TNFΔARE  Fe def,  sham-inj. | WT Fe def, iron-inj. | TNFΔARE  Fe def,  iron-inj. | R | *P-value* |
| Phylum level |  |  |  |  |  |  |  |  |  |
| Proteobacteria | 10.26 ± 3.69 | 5.14 ± 2.15 | 6.34 ± 3.02 | 5.08 ± 2.23 | 6.24 ± 1.32 | 4.87 ± 2.28 | **0.0024** | 0.0228 | 0.9356 |
| Family level |  |  |  |  |  |  |  |  |  |
| Helicobacteraceae | 4.60 ± 4.69 | 0.56 ± 0.61 | 2.93 ± 2.58 | 0.69 ± 0.50 | 2.06 ± 1.44 | 0.78 ± 0.96 | **0.0019** | -0.1184 | 0.6743 |
| Peptosreptococcaceae | 0.20 ± 0.24 | 1.35 ± 1.08 | 0.43 ± 0.17 | 0.82 ± 0.32 | 0.75 ± 0.22 | 1.00 ± 0.71 | **0.0023** | 0.2095 | 0.4536 |
| Genus level |  |  |  |  |  |  |  |  |  |
| *Helicobacter* | 4.27 ± 4.39 | 0.50 ± 0.58 | 2.70 ± 2.37 | 0.60 ± 0.44 | 1.87 ± 1.30 | 0.71 ± 0.87 | **0.0016** | -0.1190 | 0.6727 |
| *Peptosreptococcaceae Insertae Sedis* | 0.18 ± 0.20 | 1.28 ± 1.03 | 0.40 ± 0.16 | 0.75 ± 0.29 | 0.71 ± 0.19 | 0.94 ± 0.66 | **0.0025** | 0.2181 | 0.4349 |

SM Table 4. OTUs affected by genotype.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Highest match in RDP database (type strain) | Sequence similarity score  to closest type strain1 | Percent abundance of bacterial group [mean ± SD] for the different treatments | | | | | |  | Correlations of  bacterial taxa with histology scores | |
| WT Fe ade,  sham-inj. | TNFΔARE  Fe ade,  sham-inj. | WT Fe def, sham-inj. | TNFΔARE  Fe def,  sham-inj. | WT Fe def, iron-inj. | TNFΔARE  Fe def,  iron-inj. | *P-value* for factorial ANOVA | *R* | *P-value* |
| Helicobacter ganmani (T); CMRI H02 | 0.916 | 2.984 ± 3.193 | 0.313 ± 0.388 | 1.802 ± 1.699 | 0.333 ± 0.263 | 1.160 ± 0.903 | 0.499 ± 0.690 | **0.0018** | -0.1269 | 0.6522 |
| Clostridium oroticum (T); M59109\* | 0.805 | 5.447 ± 3.306 | 0.050 ± 0.069 | 0.375 ± 0.316 | 0.347 ± 0.428 | 0.012 ± 0.017 | 0.136 ± 0.234 | **0.0027** | -0.3498 | 0.2013 |
| Clostridium orbiscindens (T); DSM 6740\* | 0.662 | 1.059 ± 0.366 | 0.421 ± 0.275 | 0.207 ± 0.197 | 0.769 ± 0.142 | 0.420 ± 0.199 | 0.308 ± 0.188 | **0.0028** | 0.6086 | 0.0161 |
| Bacteroides eggerthii (T); L16485\* | 0.712 | 0.448 ± 0.701 | 0.430 ± 0.402 | 0.030 ± 0.034 | 0.009 ± 0.012 | 0.848 ± 0.369 | 0.020 ± 0.032 | **0.0093** | 0.7715 | **0.0008** |
| Allobaculum stercoricanis (T); type strain: DSM 13633\* | 0.515 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.024 ± 0.023 | 0.030 ± 0.042 | 0.000 ± 0.000 | 1.452 ± 1.632 | **0.0072** | -0.3288 | 0.2314 |
| Bacteroides capillosus (T); ATCC 29799 | 0.614 | 0.041 ± 0.065 | 0.160 ± 0.066 | 0.117 ± 0.154 | 0.303 ± 0.157 | 0.399 ± 0.497 | 0.495 ± 0.213 | **0.0088** | -5932 | 0.0198 |
| Clostridium oroticum (T); M59109\* | 0.760 | 1.572 ± 0.881 | 0.027 ± 0.060 | 0.116 ± 0.085 | 0.076 ± 0.037 | 0.019 ± 0.031 | 0.072 ± 0.103 | **0.0013** | -0.4056 | 0.1336 |
| Clostridium oroticum (T); M59109\* | 0.746 | 1.231 ± 0.748 | 0.014 ± 0.019 | 0.124 ± 0.129 | 0.064 ± 0.058 | 0.005 ± 0.012 | 0.046 ± 0.067 | **0.0014** | -0.3527 | 0.1973 |
| Helicobacter ganmani (T); CMRI H02 | 0.932 | 0.390 ± 0.380 | 0.041 ± 0.057 | 0.372 ± 0.361 | 0.065 ± 0.065 | 0.242 ± 0.167 | 0.080 ± 0.123 | **0.0027** | -0.2054 | 0.4627 |
| Blautia hydrogenotrophica (T); S5a36 | 0.496 | 0.552 ± 0.170 | 0.090 ± 0.092 | 0.116 ± 0.166 | 0.005 ± 0.010 | 0.269 ± 0.231 | 0.042 ± 0.045 | **< 0.0001** | 0.4554 | 0.0880 |
| Faecalibacterium prausnitzii (T); ATCC 27768\* | 0.879 | 0.070 ± 0.078 | 0.067 ± 0.082 | 0.080 ± 0.064 | 0.362 ± 0.137 | 0.163 ± 0.028 | 0.148 ± 0.086 | **0.0092** | -0.5749 | 0.0250 |
| Helicobacter ganmani (T); CMRI H02 | 0.958 | 0.362 ± 0.366 | 0.035 ± 0.060 | 0.240 ± 0.310 | 0.042 ± 0.046 | 0.168 ± 0.116 | 0.054 ± 0.050 | **0.0046** | -0.0973 | 0.7302 |
| Allobaculum stercoricanis (T); type strain: DSM 13633\* | 0.486 | 0.047 ± 0.051 | 0.032 ± 0.021 | 0.089 ± 0.052 | 0.139 ± 0.091 | 0.103 ± 0.061 | 0.309 ± 0.133 | **0.0086** | -0.6706 | **0.0062** |
| Blautia hydrogenotrophica (T); S5a36; X95624\* | 0.705 | 0.553 ± 0.315 | 0.047 ± 0.057 | 0.061 ± 0.098 | 0.013 ± 0.030 | 0.121 ± 0.127 | 0.028 ± 0.033 | **0.0004** | 0.2509 | 0.3671 |
| Helicobacter ganmani (T); CMRI H02 | 0.791 | 0.240 ± 0.256 | 0.042 ± 0.075 | 0.237 ± 0.202 | 0.028 ± 0.052 | 0.146 ± 0.139 | 0.073 ± 0.093 | **0.0091** | -0.06707 | 0.8123 |
| Clostridium symbiosum (T); M59112 | 0.715 | 0.299 ± 0.608 | 0.000 ± 0.000 | 0.276 ± 0.378 | 0.012 ± 0.027 | 0.055 ± 0.105 | 0.000 ± 0.000 | **0.0091** | -0.2051 | 0.4633 |
| Parabacteroides distasonis (T); M86695\* | 0.724 | 0.597 ± 0.613 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.078 ± 0.134 | 0.015 ± 0.022 | **0.0057** | -0.3185 | 0.2472 |

\*These bacterial groups showed statistically significant interactions between iron treatment and genotype.

1Obtained with the SeqMatch tool of RDP.

SM Table 5. Bacterial taxa affected by the interaction of iron treatment and genotype

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Bacterial taxa | Percent abundance of bacterial group [mean ± SD] for the different treatments | | | | | | Interaction treatment genotype | Correlations of  bacterial taxa with histology scores | |
| WT Fe ade,  sham-inj. | TNFΔARE  Fe ade, sham-inj. | WT Fe def, sham-inj. | TNFΔARE  Fe def, sham-inj. | WT Fe def, iron-inj. | TNFΔARE  Fe def,  iron-inj. | *P-value* | R | *P-value* |
|  |  |  |
| Genus level | |  |  |  |  |  |  |  |  |
| *Dorea* | 2.59 ± 1.39 | 0.14 ± 0.13 | 0.32 ± 0.26 | 0.42 ± 0.33 | 0.17 ± 0.17 | 0.22 ± 0.24 | **0.0003a** | -0.3674 | 0.178 |

a The significant difference was within the Fe ade, sham-inj.

SM Table 6. Bacterial taxa affected by the interaction of iron treatment and genotype.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Closest related type strain | Sequence similarity score  to closest type strain1 | Percent abundance of bacterial group [mean ± SD] for the different treatments | | | | | |  | Correlation parameters of  bacterial taxa with histology scores | |
| WT Fe ade,  sham-inj. | TNFΔARE  Fe ade,  sham-inj. | WT Fe def, sham-inj. | TNFΔARE  Fe def,  sham-inj. | WT Fe def, iron-inj. | TNFΔARE  Fe def,  iron-inj. | *P-value* | *R* | *P-value* |
| Clostridium oroticum (T); M59109 | 0.805 | 5.447 ± 3.306 | 0.050 ± 0.069 | 0.375 ± 0.316 | 0.347 ± 0.428 | 0.012 ± 0.017 | 0.136 ± 0.234 | **< 0.0001**a | -0.3498 | 0.2013 |
| Bacteroides eggerthii (T); L16485 | 0.712 | 0.448 ± 0.701 | 0.430 ± 0.402 | 0.030 ± 0.034 | 0.009 ± 0.012 | 0.848 ± 0.369 | 0.020 ± 0.032 | **0.0020**c | 0.7715 | **0.0008** |
| Allobaculum stercoricanis (T); type strain: DSM 13633 | 0.515 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.024 ± 0.023 | 0.030 ± 0.042 | 0.000 ± 0.000 | 1.452 ± 1.632 | **0.0013**c | -0.3288 | 0.2314 |
| Clostridium oroticum (T); M59109 | 0.760 | 1.572 ± 0.881 | 0.027 ± 0.060 | 0.116 ± 0.085 | 0.076 ± 0.037 | 0.019 ± 0.031 | 0.072 ± 0.103 | **< 0.0001**a | -0.4056 | 0.1336 |
| Clostridium oroticum (T); M59109 | 0.748 | 0.037 ± 0.035 | 0.476 ± 0.360 | 0.356 ± 0.319 | 0.060 ± 0.088 | 0.381 ± 0.340 | 0.298 ± 0.236 | **0.0078**a | 0.4233 | 0.1140 |
| Allobaculum stercoricanis (T); DSM 13633 (T). | 0.494 | 0.146 ± 0.192 | 0.050 ± 0.064 | 0.181 ± 0.158 | 0.237 ± 0.118 | 0.222 ± 0.100 | 0.566 ± 0.163 | **0.0057**c | -0.7037 | **0.0034** |
| Clostridium lituseburense (T); M59107 | 0.885 | 0.107 ± 0.083 | 0.085 ± 0.061 | 0.156 ± 0.090 | 0.481 ± 0.154 | 0.249 ± 0.163 | 0.215 ± 0.112 | **0.0098**b | -0.6560 | **0.0079** |
| Clostridium oroticum (T); M59109 | 0.746 | 1.231 ± 0.748 | 0.014 ± 0.019 | 0.124 ± 0.129 | 0.064 ± 0.058 | 0.005 ± 0.012 | 0.046 ± 0.067 | **0.0002**a | -0.3527 | 0.1973 |
| Allobaculum stercoricanis (T); type strain: DSM 13633 | 0.504 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.010 ± 0.014 | 0.031 ± 0.041 | 0.000 ± 0.000 | 1.036 ± 1.210 | **0.0097**b | -0.3217 | 0.2423 |
| Faecalibacterium prausnitzii (T); ATCC 27768 | 0.879 | 0.070 ± 0.078 | 0.067 ± 0.082 | 0.080 ± 0.064 | 0.362 ± 0.137 | 0.163 ± 0.028 | 0.148 ± 0.086 | **0.0008**b | -0.5749 | 0.0250 |
| Alistipes shahii (T); WAL 8301 | 0.714 | 0.147 ± 0.213 | 0.702 ± 0.557 | 0.030 ± 0.029 | 0.011 ± 0.016 | 0.123 ± 0.129 | 0.010 ± 0.014 | **0.0057**a | 0.7849 | **0.0005** |
| Parabacteroides distasonis (T); M86695 | 0.763 | 0.024 ± 0.055 | 0.215 ± 0.208 | 0.082 ± 0.085 | 0.068 ± 0.096 | 0.223 ± 0.179 | 0.016 ± 0.036 | **0.0010**ac | 0.5017 | 0.0567 |
| Parabacteroides distasonis (T); M86695 | 0.724 | 0.597 ± 0.613 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.000 ± 0.000 | 0.078 ± 0.134 | 0.015 ± 0.022 | **0.0065**a | -0.3185 | 0.2472 |

a The significant difference was within the Fe def, iron-inj.

b The significant difference was within the Fe ade, sham-inj.

c The significant difference was within the Fe ade, iron-inj.

1Obtained with the SeqMatch tool of RDP.