Table S1. The proportion of relative abundance in each treatment microbiota

<table>
<thead>
<tr>
<th>OTU</th>
<th>CTL</th>
<th>LFD</th>
<th>HFD</th>
<th>Family</th>
<th>Genus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Otu01</td>
<td>21.56±1.76</td>
<td>11.68±1.15</td>
<td>22.55±2.66</td>
<td>Lachnospiraceae</td>
<td>-</td>
</tr>
<tr>
<td>Otu02</td>
<td>31.5±1.91</td>
<td>34.86±2.61</td>
<td>28.44±1.40</td>
<td>Bacteroidaceae</td>
<td>Bacteroides</td>
</tr>
<tr>
<td>Otu03</td>
<td>19.5±2.65</td>
<td>11.81±1.26</td>
<td>7.38±2.29</td>
<td>S24-7</td>
<td>-</td>
</tr>
<tr>
<td>Otu05</td>
<td>0.08±0.02</td>
<td>6.98±0.68</td>
<td>3.32±0.94</td>
<td>Alcaligenaceae</td>
<td>Sutterella</td>
</tr>
<tr>
<td>Otu06</td>
<td>9.20±1.78</td>
<td>1.38±0.29</td>
<td>1.07±0.56</td>
<td>Lactobacillaceae</td>
<td>Lactobacillus</td>
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<tr>
<td>Otu07</td>
<td>1.52±0.26</td>
<td>0.66±0.14</td>
<td>0.61±0.41</td>
<td>Order Clostridiales_unclassified</td>
<td>-</td>
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<tr>
<td>Otu08</td>
<td>1.07±0.12</td>
<td>1.73±0.22</td>
<td>4.92±0.90</td>
<td>Ruminococcaceae</td>
<td>-</td>
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<tr>
<td>Otu09</td>
<td>1.46±0.25</td>
<td>1.20±0.27</td>
<td>0.62±0.30</td>
<td>Phylum Firmicutes_unclassified</td>
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<td>Otu10</td>
<td>0.15±0.03</td>
<td>5.43±0.54</td>
<td>1.94±0.28</td>
<td>Erysipelotrichaceae</td>
<td>Clostridium</td>
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<tr>
<td>Otu12</td>
<td>2.53±0.41</td>
<td>0.30±0.08</td>
<td>1.47±0.39</td>
<td>Lachnospiraceae</td>
<td>Clostridium</td>
</tr>
<tr>
<td>Otu13</td>
<td>0±0</td>
<td>0.01±0</td>
<td>4.79±0.58</td>
<td>Streptococcaceae</td>
<td>Lactococcus</td>
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<tr>
<td>Otu14</td>
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<td>2.03±0.26</td>
<td>3.86±1.16</td>
<td>Porphyromonadaceae</td>
<td>Parabacteroides</td>
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<td>Otu15</td>
<td>0.34±0.06</td>
<td>1.57±0.45</td>
<td>1.42±0.11</td>
<td>Lachnospiraceae</td>
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<tr>
<td>Otu16</td>
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<td>2.26±0.53</td>
<td>4.11±0.81</td>
<td>Peptococcaceae</td>
<td>rc4-4</td>
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<td>Otu17</td>
<td>0.13±0.03</td>
<td>1.15±0.32</td>
<td>1.01±0.20</td>
<td>[Mogibacteriaceae]</td>
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<tr>
<td>Otu18</td>
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<td>1.34±0.26</td>
<td>0.98±0.27</td>
<td>Lachnospiraceae</td>
<td>Coprococcus</td>
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<td>Otu21</td>
<td>0.56±0.42</td>
<td>1.56±1.18</td>
<td>1.39±0.71</td>
<td>Verrucomicrobiaceae</td>
<td>Akkermansia</td>
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<tr>
<td>Otu23</td>
<td>0.25±0.15</td>
<td>1.91±1.52</td>
<td>1.81±0.94</td>
<td>Deferribacteraceae</td>
<td>Mucispirillum</td>
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<tr>
<td>Otu27</td>
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<td>1.47±0.34</td>
<td>0.68±0.19</td>
<td>Erysipelotrichaceae</td>
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</tr>
<tr>
<td>Otu29</td>
<td>0.16±0.16</td>
<td>1.01±0.35</td>
<td>0.11±0.09</td>
<td>Order RF32_unclassified</td>
<td>-</td>
</tr>
</tbody>
</table>

Values show mean ± SD
Figure S1. Estimated function in each treatment based on 16S rRNA gene

*p < 0.01 in ANOVA