

**Table S1. Taxonomic ranks of each bacterial identified in the HFD, HFD NE and HFD EE groups**

| <b>TAXA ABBREVIATION</b>      | <b>TAXA ID</b>                                                                                                             |
|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|
| <b>s_C21_c20</b>              | k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;<br>f_Desulfovibrionaceae;g_Desulfovibrio;s_C21_c20 |
| <b>s_muciniphila</b>          | k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;<br>f_Verrucomicrobiaceae;g_Akkermansia;s_muciniphila |
| <b>c_Sva0725</b>              | k_Bacteria;p_Acidobacteria;c_Sva0725                                                                                       |
| <b>o_Sva0725</b>              | k_Bacteria;p_Acidobacteria;c_Sva0725;o_Sva0725                                                                             |
| <b>g_Akkermansia</b>          | k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;<br>f_Verrucomicrobiaceae;g_Akkermansia               |
| <b>f_Verrucomicrobiaceae</b>  | k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;<br>f_Verrucomicrobiaceae                             |
| <b>o_Verrucomicrobiales</b>   | k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales                                                       |
| <b>p_Verrucomicrobia</b>      | k_Bacteria;p_Verrucomicrobia                                                                                               |
| <b>c_Verrucomicrobiae</b>     | k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae                                                                            |
| <b>f_Clostridiaceae</b>       | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae                                                      |
| <b>g_SMB53</b>                | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_Clostridiaceae;g_SMB53                                          |
| <b>g_Allobaculum</b>          | k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;<br>f_Erysipelotrichaceae;g_Allobaculum                     |
| <b>g_Odoribacter</b>          | k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;<br>f_[Odoribacteraceae];g_Odoribacter                            |
| <b>f_Odoribacteraceae</b>     | k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;<br>f_[Odoribacteraceae]                                          |
| <b>g_Fusibacter</b>           | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_[Acidaminobacteraceae];g_Fusibacter                             |
| <b>s_reuteri</b>              | k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;<br>g_Lactobacillus;s_reuteri                       |
| <b>g_Alkaliphilus</b>         | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_Clostridiaceae;g_Alkaliphilus                                   |
| <b>g_Tepidimicrobium</b>      | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_[Tissierellaceae];g_Tepidimicrobium                             |
| <b>g_Clostridiisalibacter</b> | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_Clostridiaceae;g_Clostridiisalibacter                           |
| <b>g_Rikenella</b>            | k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;<br>g_Rikenella                                   |
| <b>g_Syntrophococcus</b>      | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;<br>g_Syntrophococcus                               |
| <b>s_sucromutans</b>          | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;<br>g_Syntrophococcus;s_sucromutans                 |
| <b>f_Dehalobacteriaceae</b>   | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_Dehalobacteriaceae                                              |
| <b>g_Dehalobacterium</b>      | k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;<br>f_Dehalobacteriaceae;g_Dehalobacterium                            |

p\_: Phylum; c\_: Class; o\_: Order; f\_: Family; g\_: Genus; s\_: Specie

Experimental groups: mice fed with a high fat diet for 12 weeks in standard housing conditions (HFD); mice fed for 24 weeks with a high fat diet and maintained in standard housing (HFD NE) or in environmental enrichment (HFD EE) conditions.