

Table S2. Taxonomic ranks of each bacterial identified in the HFD NE and HFD EE groups

TAXA ABBREVIATION	TAXA ID
o_SM1D11	k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_SM1D11
f_Clostridiaceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae
f_Acidaminobacteraceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_[Acidaminobacteraceae]
f_Veillonellaceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Veillonellaceae
f_Peptostreptococcaceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Peptostreptococcaceae
g_SMB53	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Clostridiaceae;g_SMB53
g_Allobaculum	k_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales; f_Erysipelotrichaceae;g_Allobaculum
g_Fusibacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_[Acidaminobacteraceae];g_Fusibacter
g_Akaliphilus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Clostridiaceae;g_Akaliphilus
g_Tepidimicrobium	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_[Tissierellaceae];g_Tepidimicrobium
g_Clostridiisalibacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Clostridiaceae;g_Clostridiisalibacter
s_C21_c20	k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales; f_Desulfovibrionaceae;g_Desulfovibrio;s_C21_c20
s_reuteri	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae; g_Lactobacillus;s_reuteri
c_Sva0725	k_Bacteria;p_Acidobacteria;c_Sva0725
o_Sva0725	k_Bacteria;p_Acidobacteria;c_Sva0725;o_Sva0725
f_Bacteroidaceae	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales; f_Bacteroidaceae
f_Prevotellaceae	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales; f_Prevotellaceae
f_Dehalobacteriaceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Dehalobacteriaceae
g_Bacteroides	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales; f_Bacteroidaceae;g_Bacteroides
g_Syntrophococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae; g_Syntrophococcus
g_Prevotella	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales; f_Prevotellaceae;g_Prevotella
g_Dehalobacterium	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales; f_Dehalobacteriaceae;g_Dehalobacterium
g_Butyricimonas	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales; f_[Odoribacteraceae];g_Butyricimonas
s_sucromutans	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae; g_Syntrophococcus;s_sucromutans

c_ : Class; o_ : Order; f_ : Family; g_ : Genus; s_ : Specie.

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