

- 1 **Table S1** The results of Spearman abundance correlation analysis of naive TB group at the genus level. Only significant correlations with $p \leq$
2 0.10 after false discovery rate correction and $|r| \geq 0.6$ are displayed.

genus_a	genus_b	r	p value	p(FDR)
k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Sordariales;f_Chaetomiaceae;g_Chaetomium	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Sporormiaceae;g_Preussia	0.84171 4438	1.99 E-08	6.63E- 05
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Sporormiaceae;g_Preussia	0.69113 5301	4.66 E-05	0.01384 1455
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Tannerellaceae;g_Parabacteroides	k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Hypocreales_fam_Incertae_sedis;g_Acremonium	0.62104 4363	4.21 E-04	0.05311 5464
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Ophiocordycipitaceae;g_Purpureocillium	0.61229 0503	5.34 E-04	0.05991 1637
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Sordariales;f_Chaetomiaceae;g_Chaetomium	0.67091 7616	9.33 E-05	0.01965 6126
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Candidatus_Soleaferrea	k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Sordariales;f_Chaetomiaceae;g_Chaetomium	0.61664 6135	4.75 E-04	0.05761 2038
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	k_Fungi;p_Basidiomycota;c_Tremellomycetes;o_Filobasidiales;f_Filobasidiaceae;g_Naganishia	0.63715 7663	2.66 E-04	0.03952 5623
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	k_Fungi;p_Basidiomycota;c_Tremellomycetes;o_Filobasidiales;f_Filobasidiaceae;g_Naganishia	0.66654 3575	1.08 E-04	0.02053 1352
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae;g_Peptococcus	k_Fungi;p_Basidiomycota;c_Tremellomycetes;o_Filobasidiales;f_Filobasidiaceae;g_Naganishia	0.67940 8031	7.01 E-05	0.01785 7232
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Fungi;p_Basidiomycota;c_Tremellomycetes;o_Filobasidiales;f_Filobasidiaceae;g_Naganishia	0.82871 5682	5.14 E-08	9.17E- 05
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	0.67805 3565	7.34 E-05	0.01808 7092

k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelatoclostridiaceae;g_Erysipelatoclostridium	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	- 0.67288 5288	8.74 E-05	0.01946 2767
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Dorea	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	0.61176 5529	5.42 E-04	0.05991 1637
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggertellaceae;g_Senegalimassilia	0.88187 0578	5.63 E-10	5.02E- 06
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	- 0.62083 7673	4.23 E-04	0.05311 5464
k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.74857 0772	4.62 E-06	0.00257 4383
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.64327 9274	2.22 E-04	0.03412 3129
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.69315 2306	4.34 E-05	0.01357 0443
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NC2004	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.83004 9647	4.68 E-08	9.17E- 05
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.74923 2369	4.49 E-06	0.00257 4383
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.66470 4912	1.14 E-04	0.02077 0399
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.65221 4656	1.69 E-04	0.02841 5762
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.60825 9974	5.95 E-04	0.06167 4054

k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.84021 4102	2.23 E-08	6.63E- 05
k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.60173 5329	7.06 E-04	0.06835 4388
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_ventriosum	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.61558 6422	4.89 E-04	0.05806 15
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.67040 2081	9.49 E-05	0.01965 6126
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.63325 7896	2.98 E-04	0.04149 7623
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.60804 3024	5.98 E-04	0.06167 4054
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae	0.66354 2153	1.19 E-04	0.02113 1411
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelatoclostridiaceae;g_Erysipelatoclostridium	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Paraprevotella	- 0.61833 2908	4.53 E-04	0.05611 5434
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Paraprevotella	0.61126 3074	5.49 E-04	0.05991 1637
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_ventriosum	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.62927 8194	3.34 E-04	0.04509 8296
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_ND3007	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.63348 9194	2.96 E-04	0.04149 7623
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_010	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.63108 9338	3.17 E-04	0.04348 5792

k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.60752 7022	6.06 E-04	0.06167 4054
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.61636 6025	4.78 E-04	0.05761 2038
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.70483 7492	2.82 E-05	0.00966 5989
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Dorea	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelatoclostridiaceae;g_Erysipelatoclostridium	- 0.60288 1778	6.85 E-04	0.06736 3391
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelatoclostridiaceae;g_Erysipelatoclostridium	- 0.65329 9279	1.64 E-04	0.02806 5138
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Faecalitalea	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	0.64245 0152	2.28 E-04	0.03438 4553
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	0.61111 1111	5.51 E-04	0.05991 1637
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.67459 0748	8.25 E-05	0.01905 2335
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NC2004	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.67161 8875	9.11 E-05	0.01965 6126
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.75170 4569	4.00 E-06	0.00254 8907
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.82158 1175	8.38 E-08	1.24E- 04
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gauvreauii	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.66801 813	1.03 E-04	0.02053 1352

k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.60085 0164	7.22 E-04	0.06918 6955
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.75219 4057	3.92 E-06	0.00254 8907
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.69609 7918	3.90 E-05	0.01286 2362
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoraceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	0.73052 4104	1.02 E-05	0.00452 8124
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostridia_UCG_014;g_Clostridia_UCG_014	0.71124 9962	2.21 E-05	0.00819 8748
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_FCS020	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.72488 9217	1.28 E-05	0.00544 653
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.72334 8345	1.37 E-05	0.00553 6282
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.68057 6071	6.74 E-05	0.01785 7232
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.67739 4971	7.51 E-05	0.01808 7092
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.63656 3857	2.71 E-04	0.03955 7672
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.61254 3267	5.31 E-04	0.05991 1637
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_hallii	0.68621 8034	5.54 E-05	0.01593 6016
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	0.63385 1025	2.93 E-04	0.04149 7623

k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoraceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	0.64493 7142	2.11 E-04	0.03345 0035
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	0.61358 308	5.16 E-04	0.05991 1637
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	0.62299 5352	3.99 E-04	0.05147 9976
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_ventriosum	0.60546 5334	6.40 E-04	0.06410 6662
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Peptostreptococcaceae;g_Intestinibacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_ventriosum	0.60271 8495	6.88 E-04	0.06736 3391
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_FCS020	0.67940 8031	7.01 E-05	0.01785 7232
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoraceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NC2004	0.66536 5612	1.12 E-04	0.02075 5384
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Veillonellaceae;g_Megasphaera	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NC2004	0.68118 0431	6.60 E-05	0.01785 7232
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136	0.67428 3683	8.34 E-05	0.01905 2335
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136	0.75773 4131	3.02 E-06	0.00224 2982
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136	0.72039 1329	1.54 E-05	0.00596 7725
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoraceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136	0.66737 8999	1.05 E-04	0.02053 1352
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_001	0.70727 1896	2.57 E-05	0.00916 7815

k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae; g_Eubacterium_siraeum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Lachnospiraceae_UCG_001	0.73900 5235	7.07 E-06	0.00369 7584
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f _Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Lachnospiraceae_UCG_001	0.65418 6503	1.59 E-04	0.02783 9096
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f _Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Lachnospiraceae_UCG_001	0.60932 352	5.78 E-04	0.06134 0644
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_O xalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Lachnospiraceae_UCG_001	0.64452 5913	2.14 E-04	0.03345 0035
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae; g_Faecalibacterium	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Lachnospiraceae_UCG_004	0.60985 3589	5.70 E-04	0.06121 0159
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_E nterobacteriaceae;g_Escherichia_Shigella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Roseburia	- 0.61271 6131	5.28 E-04	0.05991 1637
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae; g_Eubacterium_siraeum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Ruminococcus_gauvreauii	0.75951 2427	2.78 E-06	0.00224 2982
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f _Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g _Ruminococcus_gauvreauii	0.60736 3576	6.09 E-04	0.06167 4054
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g _NK4A214	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_copr ostanoligenes;g_Eubacterium_coprostanoligenes	0.76480 5329	2.15 E-06	0.00191 357
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae; g_Ruminococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_copr ostanoligenes;g_Eubacterium_coprostanoligenes	0.69263 5903	4.42 E-05	0.01357 0443
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f _Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_copr ostanoligenes;g_Eubacterium_coprostanoligenes	0.73632 1143	7.94 E-06	0.00372 6189
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae; g_Negativibacillus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g _NK4A214	0.73775 2684	7.47 E-06	0.00369 7584

k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	0.62423 7033	3.85 E-04	0.05121 16
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	0.65021 8649	1.80 E-04	0.02917 3582
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	0.65167 4069	1.72 E-04	0.02841 5762
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	0.80695 1431	2.14 E-07	2.38E- 04
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Negativibacillus	0.81152 1928	1.61 E-07	2.05E- 04
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae;g_Peptococcus	0.76548 8112	2.08 E-06	0.00191 357
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_AD3011	0.62360 7673	3.92 E-04	0.05135 3204
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_UCG_001	0.66635 0336	1.08 E-04	0.02053 1352

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4 **Table S2** The results of Spearman abundance correlation analysis of TB2MT group at the genus level. Only significant correlations with $p \leq 0.10$
5 after false discovery rate correction and $|r| \geq 0.6$ are displayed.

genus_a	genus_b	r	p value	p(FDR)
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter	k_Fungi;p_Basidiomycota;c_Tremellomycetes;o_Tremellales;f_Tremellaceae;g_Cryptococcus	0.71962291 7	1.08E-05	0.012073
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellace	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroida	-	1.04E-05	0.012073

ac;g_Prevotella	ceae;g_Bacteroides	0.72052372		
		9		
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellac eae;g_Copro bacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiell aceae;g_Barnesiella	0.71962291	1.08E-05	0.012073
		7		
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Peptostreptococcaceae;g_Terrisporobacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiell aceae;g_Barnesiella	0.71962291	1.08E-05	0.012073
		7		
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Peptostreptococcaceae;g_Terrisporobacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiell aceae;g_Copro bacter	1	0	0
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Butyricimonas	0.68545808	4.07E-05	0.036303
		2		
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospirace ae;g_Lachnospiraceae_ND3007	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Odoribacter	0.69127671	3.29E-05	0.032601
		2		
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospirace ae;g_Lachnospiraceae_ND3007	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.66735534	7.67E-05	0.049174
		1		
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcac eae;g_Subdoligranulum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Agathobacter	0.66715001	7.73E-05	0.049174
		2		
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospirace	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira	0.74232499	4.03E-06	0.011958

ac;g_Eubacterium_hallii	ceae;g_Dorea			
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_FCS020	0.71962291 7	1.08E-05	0.012073
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobacea e;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_UCG_001	0.66101519 1	9.48E-05	0.056327
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirac eae;g_NK4A214	0.66822128	7.45E-05	0.049174
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_ Pasteurellaceae;g_Haemophilus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirac eae;g_NK4A214	0.80143043 9	1.75E-07	7.80E-04
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierel ales;f_Anaerovoracaceae;g_Family_XIII_UCG_001	0.66822128	7.45E-05	0.049174

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7 **Table S3** The results of Spearman abundance correlation analysis of TB6MT group at the genus level. Only significant correlations with $p \leq 0.10$

8 after false discovery rate correction and $|r| \geq 0.6$ are displayed.

genus_a	genus_b	r	p value	p(FDR)
k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Chaetothyriales;f_Herpotri chiellaceae;g_Phialophora	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Cladosp oriaceae;g_Cladosporium	0.763456622	1.43E-04	0.06691 5869

k_Fungi;p_Basidiomycota;c_Microbotryomycetes;o_Sporidiobolales;f_Sporidiobolaceae;g_Rhodotorula	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Cladosporiaceae;g_Cladosporium	0.764478479	1.38E-04	0.06691 5869
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Sporormiaceae;g_Preussia	0.764060308	1.40E-04	0.06691 5869
k_Fungi;p_Basidiomycota;c_Wallemyomycetes;o_Wallemyales;f_Wallemyaceae;g_Wallemya	k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	0.747108382	2.37E-04	0.08352 8931
k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Sordariales;f_Chaetomiaceae;g_Chaetomium	k_Fungi;p_Ascomycota;c_Saccharomycetes;o_Saccharomycetales;f_Dobryomycetaceae;g_Meyerozyma	0.80468873	3.26E-05	0.02107 149
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_ND3007	k_Fungi;p_Ascomycota;c_Saccharomycetes;o_Saccharomycetales;f_Saccharomycetaceae;g_Saccharomyces	-0.728914386	4.00E-04	0.09198 3371
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	-0.76045555	1.57E-04	0.06767 8414
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium_sensu_stricto_1	k_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Agaricales;f_Pleurotaceae;g_Pleurotus	0.756534362	1.78E-04	7.25E- 02
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Veillonellaceae;g_Dialister	k_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Agaricales;f_Pleurotaceae;g_Pleurotus	0.730548891	3.82E-04	0.09198 3371
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Erysipelotrichum	k_Fungi;p_Basidiomycota;c_Tremellomycetes;o_Filobasidiales;f_Filobasidium	1	6.08E-	9.4224E

aceae;g_Holdemanella	basidiaceae;g_Naganishia		132	-129
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Fungi;p_Mucoromycota;c_Mucoromycetes;o_Mucorales;f_Mucoraceae;g_Mucor	0.726483157	4.27E-04	0.09198 3371
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Copro bacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella	0.726483157	4.27E-04	0.09198 3371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.834073745	9.0765E-06	0.00639 4806
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gauvreauii	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.839254327	7.06E-06	5.80E-03
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.839254327	7.06E-06	5.80E-03
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculaceae	0.76260079	1.47E-04	6.69E-02
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	k_Bacteria;p_Desulfobacterota;c_Desulfovibrionia;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila	0.763882021	1.41E-04	6.69E-02
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Candidatus_Soleaferrea	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus	0.726483157	4.27E-04	0.09198 3371

k_Bacteria;p_Firmicutes;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarectobacterium	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	-0.740299011	2.90E-04	9.20E-02
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_FCS020	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.726483157	4.27E-04	0.091983371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_NK4A136	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.726483157	0.000427278	0.091983371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gauvreauii	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.99382716	1.12E-17	1.23996E-14
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.742795681	0.00026938	0.090769438
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellaes;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.99382716	1.11996E-17	1.23996E-14
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellaes;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_eligens	0.726483157	0.000427278	0.091983371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	0.73297674	0.000356982	0.091983371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae	1	6.079E-04	9.4224E-02

ae;g_Lachnospiraceae_NK4A136	ceae;g_Lachnospiraceae_FCS020		132	-129
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_FCS020	1	6.08E- 132	9.4224E -129
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospirace ae;g_Roseburia	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_ND3007	0.838076781	7.48207E -06	0.00579 8605
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_NK4A136	1	6.079E- 132	9.4224E -129
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospirace ae;g_Ruminococcus_gauvreauii	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_UCG_001	0.726483157	0.000427 278	0.09198 3371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Lachnospiraceae_UCG_001	0.726483157	0.000427 278	0.09198 3371
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobacea e;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Ruminococcus_gauvreauii	0.747409319	0.000234 991	0.08352 8931
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Ruminococcus_gauvreauii	1	0	0
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobacea ae;g_Monoglobus	0.747409319	0.000234 991	0.08352 8931

k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Veillonellaceae;g_Veillonella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Butyricicocaceae;g_Butyricicoccus	-0.739040883	3.00E-04	0.09198 3371
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10 **Table S4** The results of Spearman abundance correlation analysis of HS group at the genus level. Only significant correlations with $p \leq 0.10$ after
11 false discovery rate correction and $|r| \geq 0.6$ are displayed.

genus_a	genus_b	r	p value	p(FDR)
k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Chaetothyriales;f_Trichomeriaceae;g_Knufia	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Dothideales;f_Aureobasidiaceae;g_Aureobasidium	0.648783657	0.00108 9453	0.091586 029
k_Fungi;p_Ascomycota;c_Saccharomycetes;o_Saccharomycetales;f_Phaeffomycetaceae;g_Wickerhamomyces	k_Fungi;p_Ascomycota;c_Dothideomycetes;o_Dothideales;f_Aureobasidiaceae;g_Aureobasidium	0.691396509	3.66E-04	0.053431 21
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Paraprevotella	k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Chaetothyriales;f_Herpotrichiellaceae;g_Exophiala	-0.717948398	1.68E-04	0.036593 78
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Chaetothyriales;f_Herpotrichiellaceae;g_Exophiala	-0.699003856	2.95E-04	0.047845 589
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Chaetothyriales;f_Herpotrichiellaceae;g_Phialophora	-0.65589389	9.19E-04	0.081860 02
k_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Hypocreaceae	k_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae	0.659257012	8.46E-	0.081077

eae;g_Trichoderma	ceae;g_Talaromyces		04	183
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium	k_Fungi;p_Ascomycota;c_Saccharomycetes;o_Saccharomycetales;f_Trichomonascaceae;g_Trichomonascus	0.767456359	3.07E-05	0.016991 198
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	k_Fungi;p_Ascomycota;c_Saccharomycetes;o_Saccharomycetales;f_Trichomonascaceae;g_Trichomonascus	0.667705736	6.85E-04	0.071736 373
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Senegalimassilia	k_Fungi;p_Mucoromycota;c_Mucoromycetes;o_Mucorales;f_Mucoraceae;g_Mucor	0.642860512	0.00125 1718	0.097710 696
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Selenomonadaceae;g_Megamonas	k_Bacteria;p_Actinobacteriota;c_Actinobacteriia;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium	-0.743660647	7.29E-05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gnavus	k_Bacteria;p_Actinobacteriota;c_Actinobacteriia;o_Micrococcales;f_Micrococccaceae;g_Rothia	0.66672294	7.03E-04	0.071736 373
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Eggerthella	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	-0.64234346	0.00126 681	0.097710 696
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_oxidoreducens	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	0.771359859	2.63E-05	0.016769 859
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Flavonifractor	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Eggerthella	0.782455037	1.68E-05	0.013720 782

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostridia_UCG_014;g_Clostridia_UCG_014	k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Senegalimassilia	0.64216818	0.00127 1961	0.097710 696
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Sutterellaceae;g_Parasutterella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	0.694173294	3.39E- 04	0.051798 987
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella	0.645193551	0.00118 551	0.096037 059
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella	0.704680164	2.51E- 04	0.043799 119
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.728342411	1.21E- 04	0.029499 5
k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.766004534	3.24E- 05	0.016991 198
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.745072019	6.94E- 05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_010	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.682091675	4.71E- 04	0.059983 267
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.717068133	1.73E-	0.036703

e;g_Monoglobus	ceae;g_Butyricimonas		04	047
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Butyricimonas	0.745151515	6.92E-05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellaes;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Butyricimonas	0.886715433	3.91E-08	3.48E-04
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostridia_UCG_014;g_Clostridia_UCG_014	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Odoribacter	0.651944221	0.001010455	0.087921 125
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Odoribacter	0.741586008	7.82E-05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Colidextribacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Odoribacter	0.668569011	6.70E-04	0.071439 879
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Odoribacter	0.646082296	0.001161084	0.095800 19
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Sutterellaceae;g_Sutterella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifila ceae;g_Odoribacter	0.706597807	2.37E-04	0.043095 292
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotella ceae;g_Prevotella	0.641186308	0.001301145	0.099098 302

k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Colidextribacter	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellaaceae;g_Prevotella	0.671812157	6.17E-04	0.071439879
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Sutterellaceae;g_Sutterella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotellaaceae;g_Prevotella	0.687429281	4.08E-04	0.056819329
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	-0.669883321	6.48E-04	0.071439879
k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.841914359	9.01E-07	0.001605142
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostridia_UCG_014;g_Clostridia_UCG_014	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.646211197	0.001157577	0.09580019
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.862640617	2.42E-07	7.18E-04
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_ventriosum	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.70128004	2.77E-04	0.046960008
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	-0.650008499	0.001058236	0.089808982
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	-0.65344938	9.75E-04	0.085985

ac;g_Ruminococcus_gnavus	eae;g_Alistipes		04	349
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobacea e;g_Monoglobus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.680366079	4.93E- 04	0.061922 061
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_c oprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.642576314	0.00125 9994	0.097710 696
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirace ae;g_Flavonifractor	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	-0.751875284	5.46E- 05	0.024341 767
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirace ae;g_NK4A214	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.743638778	7.29E- 05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae ;g_Peptococcus	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.651705022	0.00101 6258	0.087921 125
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.743554632	7.31E- 05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.687414886	4.08E- 04	0.056819 329
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Sutterellaceae;g_Sutterella	k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellac eae;g_Alistipes	0.728636476	1.20E- 04	0.029499 5

k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotricostriaceae;g_Erysipelatoclostridium	-0.711035366	2.08E-04	0.040239608
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_010	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotricostriaceae;g_Erysipelotrichaceae_UCG_003	0.682390896	4.67E-04	0.059983267
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Veillonellaceae;g_Dialister	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotricostriaceae;g_Erysipelotrichaceae_UCG_003	0.643380303	0.001236702	0.097710696
k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenellaceae_R_7	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	-0.693106912	3.49E-04	0.051798987
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_ND3007	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	-0.656643594	9.02E-04	0.081651541
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gnavus	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	0.669599817	6.53E-04	0.071439879
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaeae;g_Ruminococcus	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	-0.670357881	6.41E-04	0.071439879
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaeae;g_Subdoligranulum	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium_innocuum	-0.728055055	1.22E-04	0.0294995
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostrid	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotric	0.67464905	5.73E-	0.069045

ia_UCG_014;g_Clostridia_UCG_014	haceae;g_Holdemanella		04	501
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae; ;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotric haceae;g_Holdemanella	0.796862097	9.06E- 06	0.010087 094
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Haemophilus	k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotric haceae;g_Turicibacter	0.693552273	3.44E- 04	0.051798 987
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae; g_Ruminococcus_gnavus	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae; g_Streptococcus	0.66839233	6.73E- 04	0.071439 879
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostridia_UCG_014;g_Clostridia_UCG_014	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae; g_Christensenellaceae_R_7	0.684940867	4.36E- 04	0.058927 072
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae; g_Coprococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae; g_Christensenellaceae_R_7	0.753217698	5.21E- 05	0.024341 767
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae; g_Lachnoclostridium	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae; g_Christensenellaceae_R_7	-0.665696667	7.21E- 04	0.072182 838
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae; g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae; g_Christensenellaceae_R_7	0.687815032	4.04E- 04	0.056819 329
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae; g_NK4A214	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christensenellaceae; g_Christensenellaceae_R_7	0.672801322	6.02E- 04	0.071439 879

k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae; ;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christens enellaceae;g_Christensenellaceae_R_7	0.736713721	9.22E- 05	0.026512 123
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christens enellaceae;g_Christensenellaceae_R_7	0.760370618	4.01E- 05	0.019843 43
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christens enellaceae;g_Christensenellaceae_R_7	0.658354806	8.65E- 04	0.081632 595
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Sutterellaceae;g_Sutterella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Christensenellales;f_Christens enellaceae;g_Christensenellaceae_R_7	0.711934448	2.02E- 04	0.040038 795
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostri dia_vadinBB60;g_Clostridia_vadinBB60	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostri dia_UCG_014;g_Clostridia_UCG_014	0.868858754	1.56E- 07	6.96E-04
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospirace ae;g_Coprococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostri dia_UCG_014;g_Clostridia_UCG_014	0.664170153	7.49E- 04	0.073078 264
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcac eae;g_Eubacterium_siraeum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostri dia_UCG_014;g_Clostridia_UCG_014	0.821635012	2.75E- 06	0.003505 798
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae ;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostri dia_UCG_014;g_Clostridia_UCG_014	0.735755574	9.52E- 05	0.026516 695
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostri	0.836498761	1.23E-	0.001829

les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	dia_UCG_014;g_Clostridia_UCG_014		06	36
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_UCG_014;f_Clostridia_UCG_014;g_Clostridia_UCG_014	0.85171424	4.96E-07	0.001104 342
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.705558112	2.44E-04	0.043542 509
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Flavonifractor	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	-0.739975028	8.27E-05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Eubacterium_siraeum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.676103534	5.52E-04	0.067386 434
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae;g_Peptococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.6666118	7.04E-04	0.071736 373
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.722832072	1.45E-04	0.033357
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Oxalobacteraceae;g_Oxalobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridia_vadinBB60;f_Clostridia_vadinBB60;g_Clostridia_vadinBB60	0.697200257	3.11E-04	0.049464 931
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter	0.668876081	6.65E-04	0.071439 879

k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales; f_Enterobacteriaceae;g_Escherichia_Shigella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Anaerostipes	-0.663883239	7.54E- 04	0.073078 264
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Moraxellaceae;g_Acinetobacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Blautia	-0.656999891	8.94E- 04	0.081651 541
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae; g_Flavonifractor	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Coprococcus	-0.731777713	1.09E- 04	0.029315 343
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella les;f_Anaerovoracaceae;g_Family_XIII_AD3011	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Coprococcus	0.699114424	2.94E- 04	0.047845 589
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_Sutterellaceae;g_Sutterella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Coprococcus	0.719677356	1.60E- 04	0.035555 507
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae; g_Candidatus_Soleaferrea	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Dorea	0.669261652	6.59E- 04	0.071439 879
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae; g_Lachnospiraceae_FCS020	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Eubacterium_ventriosum	0.656466741	9.06E- 04	0.081651 541
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae; g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira ceae;g_Eubacterium_ventriosum	0.66878803	6.67E- 04	0.071439 879
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospira	0.700948429	2.79E-	0.046960

ae;g_Lachnospiraceae_ND3007	ceae;g_Fusicatenibacter		04	008
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter	0.645419536	0.00117 9258	0.096037 059
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaeae;g_Ruminococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter	0.739729546	8.33E- 05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_FCS020	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium	-0.664503022	7.43E- 04	0.073078 264
k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_ND3007	0.777646047	2.05E- 05	0.015132 952
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaeae;g_Ruminococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_ND3007	0.744951166	6.97E- 05	0.024755 225
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_004	0.658111421	8.70E- 04	0.081632 595
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Colidextribacter	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_010	0.775819311	2.21E- 05	0.015132 952
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaeae;g_Subdoligranulum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospiraceae_UCG_010	0.64341966	0.00123 5571	0.097710 696

k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_torques	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Roseburia	0.766345357	3.20E-05	0.016991198
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Subdoligranulum	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gnavus	-0.650820288	0.001037969	0.088935977
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Veillonellaceae;g_Dialister	k_Bacteria;p_Firmicutes;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_gnavus	-0.683645952	4.52E-04	0.059983267
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	0.696083697	3.21E-04	0.050156263
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus	k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	0.714993749	1.84E-04	0.038196885
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierellales;f_Peptostreptococcaceae;g_Romboutsia	k_Bacteria;p_Firmicutes;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	0.71227169	2.00E-04	0.040038795
k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_NK4A214	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	0.728790999	1.20E-04	0.0294995
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Sutterellaceae;g_Sutterella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Eubacterium_coprostanoligenes;g_Eubacterium_coprostanoligenes	0.739875047	8.29E-05	0.024755225
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonadales;f_Veillonellaceae;g_Dialister	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Roseburia	0.783583413	1.61E-05	0.013720198

ales;f_Veillonellaceae;g_Dialister	eae;g_Colidextribacter		05	782
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirac	-0.708141479	2.26E-	0.042928
les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	eae;g_Flavonifractor		04	084
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirac	-0.722532116	1.46E-	0.033357
f_Sutterellaceae;g_Sutterella	eae;g_Flavonifractor		04	
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirac	0.656412181	9.07E-	0.081651
les;f_Anaerovoracaceae;g_Family_XIII_AD3011	eae;g_NK4A214		04	541
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Oscillospirac	0.686183875	4.22E-	0.057851
f_Sutterellaceae;g_Sutterella	eae;g_NK4A214		04	922
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococc	0.666391412	7.08E-	0.071736
;g_Peptococcus	aceae;g_Eubacterium_siraeum		04	373
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococc	0.782321422	1.69E-	0.013720
f_Oxalobacteraceae;g_Oxalobacter	aceae;g_Eubacterium_siraeum		05	782
k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcaceae	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococc	0.707377827	2.32E-	0.042993
;g_Peptococcus	aceae;g_Negativibacillus		04	409
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Veillonellales_Selenomonad	k_Bacteria;p_Firmicutes;c_Clostridia;o_Oscillospirales;f_Ruminococc	0.683085253	4.59E-	0.059983
ales;f_Veillonellaceae;g_Dialister	aceae;g_Subdoligranulum		04	267

k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptostreptococcales_Tissierella	k_Bacteria;p_Firmicutes;c_Clostridia;o_Peptococcales;f_Peptococcace	0.676300578	5.49E-	0.067386
les;f_Anaerovoracaceae;g_Family_XIII_UCG_001	ae;g_Peptococcus		04	434

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