Evaluating the contribution of gut microbiome to the variance of porcine serum glucose and lipid concentration

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Running title: Gut microbiota associated with serum lipids

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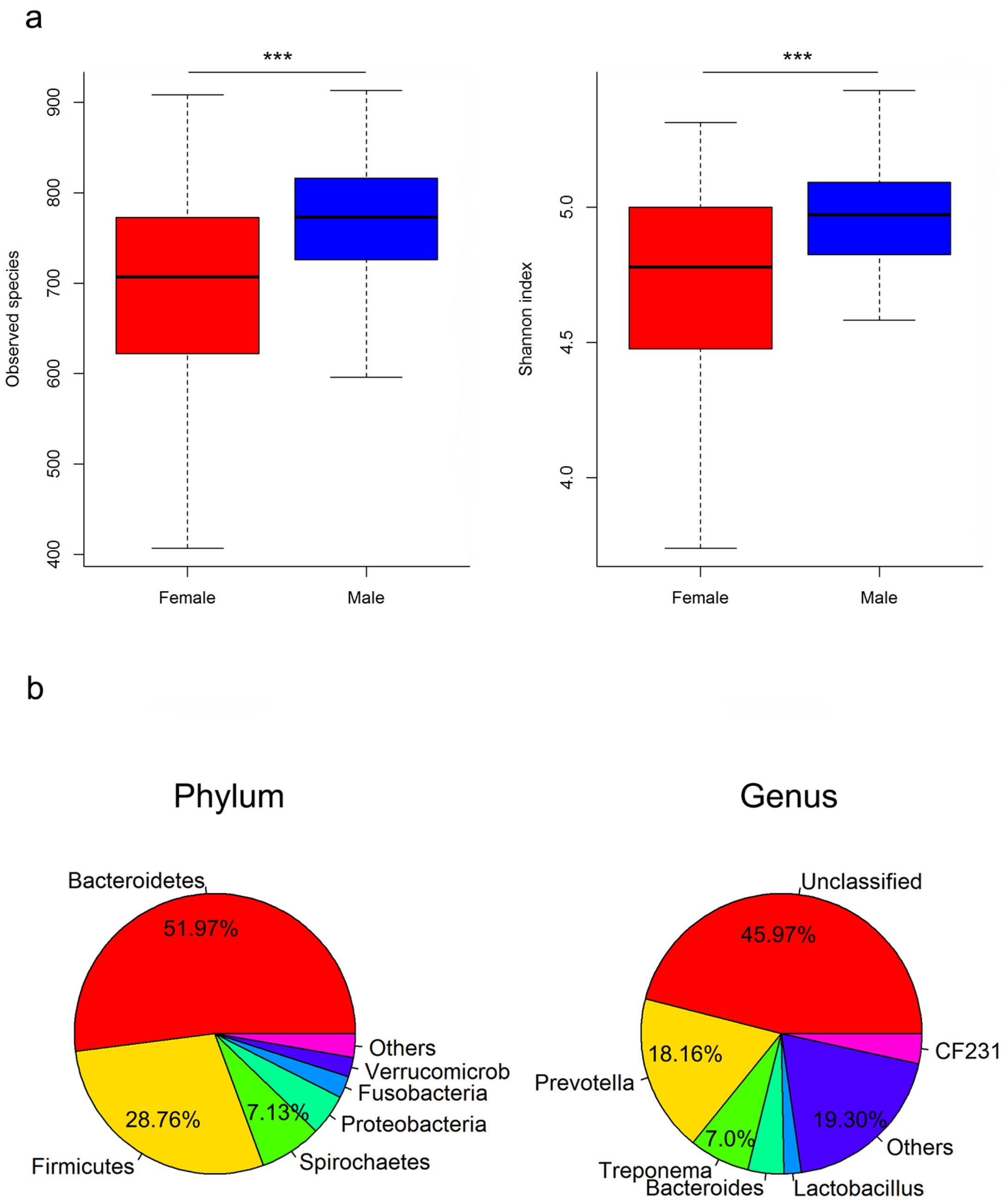
Supplementary Figure 1: α-diversity and microbial composition of porcine cecum luminal samples. **(a).** Boxplots of observed species and Shannon index between males and females; **(b).** Microbial composition of cecum luminal samples at phylum level and genus level.



Note:

Estimate_q: The estimated regression coefficient in the quantitative model

Estimate_b: The estimated regression coefficient in the binary model

T_value_q: The test statistics T value in the quantitative model

T_value_b: The test statistics T value in the binary model

meta_z_score: the compitative unweighted Z score in the meta-analysis

P_meta: the compitative P value in the meta-analysis

final_p_value: the minimum of P values from the binary analysis, quantitative analysis and meta-analysis

Supplementary Table 1: OTUs significantly associated with blood glucose (GLU)

ID	Estimate_q*	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	GLU_final_p_value
Otu363_Corynebacterium	-0.27	-0.74	-0.59	5.53E-01	-3.34	9.71E-04	-2.75	5.93E-03	9.71E-04
Otu197_Bacteroidales	-0.93	-1.52	-3.82	1.72E-04	-2.12	3.50E-02	-4.15	3.35E-05	3.35E-05
Otu2316_Bacteroidales	-0.63	-0.76	-2.02	4.57E-02	-3.37	8.74E-04	-3.77	1.66E-04	1.66E-04
Otu1540_Bacteroidales	1.29	0.37	2.88	4.53E-03	1.54	1.24E-01	3.09	1.98E-03	1.98E-03
Otu1100_Bacteroidales	-0.40	-0.66	-1.29	1.98E-01	-2.93	3.66E-03	-2.97	3.02E-03	3.02E-03
Otu891_Bacteroides	-0.17	-1.32	-0.55	5.82E-01	-4.69	4.61E-06	-3.63	2.85E-04	4.61E-06
Otu160_Bacteroides	-0.46	-1.20	-1.42	1.63E-01	-4.57	7.94E-06	-4.15	3.40E-05	7.94E-06
Otu152_Bacteroides	-0.38	-0.92	-1.57	1.20E-01	-4.10	5.71E-05	-3.94	7.99E-05	5.71E-05
Otu119_Bacteroides	0.07	-1.20	0.38	7.08E-01	-3.95	1.04E-04	2.48	1.32E-02	1.04E-04
Otu2183_Bacteroides	-0.11	-2.12	-0.59	5.54E-01	-3.86	1.43E-04	-3.11	1.89E-03	1.43E-04
Otu107_Bacteroides	-0.44	-0.72	-2.19	3.04E-02	-3.23	1.39E-03	-3.79	1.50E-04	1.50E-04
Otu2736_Bacteroides	-0.40	-1.34	-0.98	3.39E-01	-3.72	2.49E-04	-3.27	1.09E-03	2.49E-04
Otu2265_Bacteroides	-0.38	-0.84	-1.50	1.37E-01	-3.52	5.11E-04	-3.51	4.51E-04	4.51E-04
Otu251_Bacteroides	-0.13	-1.24	-0.24	8.15E-01	-3.43	7.01E-04	-2.56	1.04E-02	7.01E-04
Otu2237_Bacteroides	-0.64	-0.97	-2.54	1.18E-02	-1.88	6.10E-02	-3.11	1.90E-03	1.90E-03

Otu32_Bacteroides_coprophilus	-0.48	-1.18	-2.81	5.69E-03	-5.53	8.28E-08	-5.75	9.15E-09	9.15E-09
Otu188_Bacteroides_fragilis	-0.88	-0.71	-2.20	3.16E-02	-2.84	4.83E-03	-3.51	4.44E-04	4.44E-04
Otu108_Bacteroides_plebeius	-0.63	-0.64	-3.10	2.38E-03	-2.89	4.17E-03	-4.17	3.00E-05	3.00E-05
Otu27_BS11	-0.44	0.22	-3.10	2.25E-03	0.81	4.18E-01	1.59	1.12E-01	2.25E-03
Otu334_Paraprevotellaceae	-0.57	-1.01	-2.39	1.78E-02	-3.19	1.59E-03	-3.91	9.31E-05	9.31E-05
Otu380_Paraprevotellaceae	0.50	0.68	2.24	2.66E-02	3.02	2.79E-03	3.68	2.32E-04	2.32E-04
Otu71_Paraprevotellaceae	-0.32	-0.61	-1.88	6.15E-02	-2.57	1.06E-02	-3.13	1.76E-03	1.76E-03
Otu73_CF231	-0.72	-0.88	-3.56	4.43E-04	-1.00	3.20E-01	-3.19	1.44E-03	4.43E-04
Otu1530_Prevotella	0.03	-1.33	0.22	8.28E-01	-4.07	6.50E-05	2.67	7.58E-03	6.50E-05
Otu929_Prevotella	-0.69	-0.51	-3.22	1.51E-03	-1.56	1.20E-01	-3.34	8.31E-04	8.31E-04
Otu47_Prevotella	-0.37	-0.72	-1.57	1.21E-01	-2.91	3.99E-03	-3.13	1.73E-03	1.73E-03
Otu194_Prevotella	-0.19	-0.75	-0.80	4.22E-01	-3.17	1.73E-03	-2.78	5.40E-03	1.73E-03
Otu51_YRC22	-0.54	-0.20	-3.23	1.55E-03	-0.89	3.75E-01	-2.86	4.17E-03	1.55E-03
Otu2674_Parabacteroides	-1.42	0.11	-4.20	3.79E-05	NA	NA	-3.96	NA	3.79E-05
Otu2269_Parabacteroides	-1.09	-1.96	-3.25	1.31E-03	-2.24	2.59E-02	-3.85	1.19E-04	1.19E-04
Otu255_Parabacteroides	-1.11	-2.27	-3.52	5.16E-04	-1.30	1.96E-01	-3.37	7.51E-04	5.16E-04
Otu960_Parabacteroides	-0.95	-0.67	-2.67	8.10E-03	-2.12	3.49E-02	-3.36	7.68E-04	7.68E-04
Otu688_Parabacteroides	-0.78	-0.69	-2.52	1.24E-02	-2.13	3.44E-02	-3.26	1.10E-03	1.10E-03
Otu2415_Parabacteroides	-0.93	-1.09	-2.76	6.29E-03	-1.63	1.05E-01	-3.08	2.09E-03	2.09E-03
Otu331_S24-7	-0.51	-0.73	-1.95	5.22E-02	-2.33	2.05E-02	-3.01	2.60E-03	2.60E-03
Otu457_YS2	0.02	0.76	0.05	9.58E-01	3.38	8.45E-04	2.40	1.65E-02	8.45E-04
Otu2242_YS2	0.94	-0.01	3.15	2.01E-03	-0.04	9.70E-01	-2.16	3.10E-02	2.01E-03
Otu23_Turicibacter	0.81	1.27	3.75	2.20E-04	1.02	3.09E-01	3.33	8.63E-04	2.20E-04
Otu1839_Clostridiales	2.38	1.03	3.60	5.52E-04	4.48	1.15E-05	5.55	2.94E-08	2.94E-08
Otu596_Clostridiales	1.61	0.52	3.97	1.22E-04	2.33	2.04E-02	4.36	1.32E-05	1.32E-05
Otu1638_Clostridiales	1.23	0.69	2.76	6.64E-03	3.10	2.18E-03	4.09	4.38E-05	4.38E-05

Otu2107_Clostridiales	0.81	0.80	2.46	1.49E-02	3.38	8.49E-04	4.08	4.50E-05	4.50E-05
Otu2352_Clostridiales	1.46	0.25	3.70	3.21E-04	1.08	2.80E-01	3.31	9.37E-04	3.21E-04
Otu697_Clostridiales	-0.39	0.81	-0.66	5.09E-01	3.52	5.13E-04	-1.99	4.67E-02	5.13E-04
Otu455_Clostridiales	1.75	-0.22	3.47	7.90E-04	-0.97	3.34E-01	-1.69	9.11E-02	7.90E-04
Otu501_Clostridiales	1.00	0.44	2.87	4.69E-03	1.82	6.97E-02	3.28	1.03E-03	1.03E-03
Otu1925_Clostridiales	1.44	-0.06	3.10	2.43E-03	-0.27	7.89E-01	-1.96	5.05E-02	2.43E-03
Otu646_Christensenellaceae	-1.81	-0.65	-3.20	1.86E-03	-2.87	4.54E-03	-4.21	2.59E-05	2.59E-05
Otu803_Christensenellaceae	-0.74	-0.61	-2.04	4.29E-02	-2.14	3.31E-02	-2.94	3.30E-03	3.30E-03
Otu231_Clostridiaceae	0.75	1.90	3.13	2.00E-03	1.54	1.26E-01	3.27	1.08E-03	1.08E-03
Otu33_Clostridium_butyricum	0.64	1.28	2.65	8.64E-03	1.78	7.61E-02	3.11	1.86E-03	1.86E-03
Otu132_Lachnospiraceae	1.48	1.12	7.17	1.14E-11	2.71	7.25E-03	6.70	2.11E-11	1.14E-11
Otu1914_Lachnospiraceae	0.01	1.58	0.04	9.72E-01	5.94	1.01E-08	4.08	4.57E-05	1.01E-08
Otu509_Lachnospiraceae	1.11	1.17	3.90	1.34E-04	4.36	1.92E-05	5.72	1.05E-08	1.05E-08
Otu75_Lachnospiraceae	0.94	0.75	5.77	2.81E-08	2.14	3.36E-02	5.43	5.66E-08	2.81E-08
Otu2502_Lachnospiraceae	0.94	1.20	3.36	9.63E-04	4.65	5.57E-06	5.55	2.92E-08	2.92E-08
Otu849_Lachnospiraceae	1.11	1.27	4.04	7.45E-05	3.57	4.27E-04	5.29	1.21E-07	1.21E-07
Otu1335_Lachnospiraceae	1.38	0.92	3.41	8.86E-04	4.19	3.86E-05	5.26	1.43E-07	1.43E-07
Otu196_Lachnospiraceae	1.33	1.23	5.40	1.67E-07	1.40	1.62E-01	4.69	2.75E-06	1.67E-07
Otu1363_Lachnospiraceae	2.56	0.60	4.68	7.92E-06	2.70	7.50E-03	5.05	4.43E-07	4.43E-07
Otu1639_Lachnospiraceae	0.37	1.33	0.98	3.26E-01	5.06	8.58E-07	4.17	2.99E-05	8.58E-07
Otu1537_Lachnospiraceae	0.76	1.14	3.68	2.95E-04	3.27	1.25E-03	4.84	1.28E-06	1.28E-06
Otu1168_Lachnospiraceae	0.93	1.04	3.65	3.28E-04	3.27	1.22E-03	4.83	1.39E-06	1.39E-06
Otu1903_Lachnospiraceae	0.81	0.93	3.38	8.82E-04	3.40	7.96E-04	4.72	2.32E-06	2.32E-06
Otu144_Lachnospiraceae	0.99	0.80	4.82	2.69E-06	1.77	7.86E-02	4.56	5.06E-06	2.69E-06
Otu225_Lachnospiraceae	1.15	0.92	2.91	4.88E-03	3.80	1.83E-04	4.64	3.55E-06	3.55E-06
Otu1407_Lachnospiraceae	1.40	0.83	2.83	5.63E-03	3.73	2.35E-04	4.56	5.16E-06	5.16E-06

Otu242_Lachnospiraceae	1.08	0.44	4.61	7.55E-06	1.63	1.04E-01	4.32	1.59E-05	7.55E-06
Otu1731_Lachnospiraceae	1.43	0.86	2.47	1.53E-02	3.90	1.24E-04	4.43	9.46E-06	9.46E-06
Otu418_Lachnospiraceae	0.05	1.30	0.08	9.35E-01	4.51	1.02E-05	3.18	1.48E-03	1.02E-05
Otu344_Lachnospiraceae	0.77	1.00	2.76	6.27E-03	3.37	8.70E-04	4.29	1.81E-05	1.81E-05
Otu1870_Lachnospiraceae	1.05	0.81	3.34	9.97E-04	2.77	6.10E-03	4.27	1.99E-05	1.99E-05
Otu980_Lachnospiraceae	0.72	0.97	2.69	7.80E-03	3.42	7.43E-04	4.27	1.99E-05	1.99E-05
Otu617_Lachnospiraceae	1.08	0.65	4.30	2.49E-05	0.97	3.35E-01	3.66	2.50E-04	2.49E-05
Otu442_Lachnospiraceae	0.60	0.90	1.66	9.90E-02	4.12	5.24E-05	4.03	5.66E-05	5.24E-05
Otu96_Lachnospiraceae	0.92	0.85	4.06	6.68E-05	0.84	4.03E-01	3.41	6.47E-04	6.68E-05
Otu2735_Lachnospiraceae	1.58	0.51	3.46	7.07E-04	2.20	2.85E-02	3.94	8.04E-05	8.04E-05
Otu770_Lachnospiraceae	1.30	0.30	4.02	8.84E-05	1.18	2.39E-01	3.60	3.13E-04	8.84E-05
Otu2393_Lachnospiraceae	0.45	1.46	1.72	8.63E-02	3.84	1.60E-04	3.88	1.03E-04	1.03E-04
Otu87_Lachnospiraceae	1.04	0.29	3.94	1.10E-04	0.59	5.57E-01	3.15	1.64E-03	1.10E-04
Otu559_Lachnospiraceae	1.15	0.63	2.64	9.52E-03	2.81	5.30E-03	3.81	1.42E-04	1.42E-04
Otu1149_Lachnospiraceae	0.97	-0.25	3.86	1.46E-04	-0.31	7.54E-01	-2.46	1.37E-02	1.46E-04
Otu1625_Lachnospiraceae	0.96	1.10	3.64	3.37E-04	1.65	9.95E-02	3.70	2.16E-04	2.16E-04
Otu2651_Lachnospiraceae	1.06	0.57	2.72	7.60E-03	2.57	1.09E-02	3.69	2.27E-04	2.27E-04
Otu237_Lachnospiraceae	0.81	0.34	3.61	3.76E-04	0.43	6.64E-01	2.82	4.78E-03	3.76E-04
Otu1756_Lachnospiraceae	1.28	0.58	2.58	1.07E-02	2.46	1.47E-02	3.53	4.13E-04	4.13E-04
Otu2521_Lachnospiraceae	1.06	0.55	3.57	4.40E-04	1.41	1.59E-01	3.48	5.01E-04	4.40E-04
Otu901_Lachnospiraceae	0.59	0.79	1.10	2.75E-01	3.53	5.03E-04	3.23	1.23E-03	5.03E-04
Otu244_Lachnospiraceae	0.86	0.43	3.50	5.53E-04	0.96	3.40E-01	3.12	1.83E-03	5.53E-04
Otu1315_Lachnospiraceae	0.82	0.68	2.25	2.55E-02	2.66	8.24E-03	3.45	5.65E-04	5.65E-04
Otu2206_Lachnospiraceae	0.22	0.77	0.69	4.90E-01	3.48	5.89E-04	2.92	3.53E-03	5.89E-04
Otu1014_Lachnospiraceae	0.82	0.61	2.11	3.69E-02	2.74	6.59E-03	3.40	6.81E-04	6.81E-04
Otu2170_Lachnospiraceae	0.91	0.62	2.05	4.27E-02	2.78	5.92E-03	3.38	7.26E-04	7.26E-04

Otu677_Lachnospiraceae	1.23	0.81	1.58	1.19E-01	3.16	1.80E-03	3.31	9.31E-04	9.31E-04
Otu65_Lachnospiraceae	0.67	1.32	3.33	1.01E-03	0.75	4.54E-01	2.85	4.30E-03	1.01E-03
Otu1498_Lachnospiraceae	0.92	1.72	3.20	1.58E-03	1.39	1.66E-01	3.21	1.31E-03	1.31E-03
Otu292_Lachnospiraceae	-0.25	0.86	-0.36	7.23E-01	3.19	1.63E-03	-1.98	4.80E-02	1.63E-03
Otu1778_Lachnospiraceae	1.54	0.45	2.52	1.36E-02	1.97	5.02E-02	3.13	1.74E-03	1.74E-03
Otu129_Lachnospiraceae	0.52	0.53	2.36	1.94E-02	2.04	4.24E-02	3.09	2.01E-03	2.01E-03
Otu1652_Lachnospiraceae	-0.26	0.69	-0.39	6.96E-01	3.12	2.03E-03	-1.91	5.67E-02	2.03E-03
Otu136_Lachnospiraceae	0.89	0.11	3.12	2.03E-03	NA	NA	2.87	NA	2.03E-03
Otu2673_Lachnospiraceae	0.75	0.71	1.73	8.87E-02	2.68	7.89E-03	3.08	2.05E-03	2.05E-03
Otu1398_Lachnospiraceae	0.86	0.35	2.99	3.25E-03	1.41	1.60E-01	3.07	2.11E-03	2.11E-03
Otu200_Lachnospiraceae	0.83	1.29	2.86	4.67E-03	1.47	1.43E-01	3.04	2.40E-03	2.40E-03
Otu921_Lachnospiraceae	1.27	0.42	2.48	1.43E-02	1.85	6.57E-02	3.03	2.42E-03	2.42E-03
Otu1340_Lachnospiraceae	0.85	0.57	2.20	2.89E-02	2.05	4.16E-02	2.99	2.82E-03	2.82E-03
Otu2618_Lachnospiraceae	0.85	0.07	3.00	3.05E-03	0.28	7.79E-01	2.29	2.18E-02	3.05E-03
Otu241_Lachnospiraceae	0.85	0.83	1.36	1.82E-01	2.88	4.37E-03	2.96	3.09E-03	3.09E-03
Otu713_Lachnospiraceae	-0.01	0.69	-0.02	9.81E-01	2.98	3.23E-03	-2.07	3.89E-02	3.23E-03
Otu449_Lachnospiraceae	0.96	0.39	2.44	1.59E-02	1.72	8.62E-02	2.92	3.51E-03	3.51E-03
Otu385_Anaerostipes	1.14	0.75	1.89	6.31E-02	3.04	2.67E-03	3.44	5.87E-04	5.87E-04
Otu652_Blautia	1.75	0.27	4.52	1.29E-05	1.17	2.45E-01	3.91	9.35E-05	1.29E-05
Otu1994_Blautia	1.06	0.61	2.49	1.40E-02	2.66	8.42E-03	3.60	3.16E-04	3.16E-04
Otu180_Coprococcus	1.08	1.03	4.82	2.72E-06	3.09	2.27E-03	5.48	4.36E-08	4.36E-08
Otu291_Coprococcus	1.30	0.63	5.14	7.36E-07	2.49	1.35E-02	5.25	1.53E-07	1.53E-07
Otu908_Coprococcus	1.05	0.97	3.05	2.65E-03	4.23	3.38E-05	5.06	4.25E-07	4.25E-07
Otu285_Coprococcus	0.92	0.88	3.80	1.93E-04	3.17	1.70E-03	4.86	1.20E-06	1.20E-06
Otu428_Coprococcus	1.02	0.91	2.44	1.67E-02	4.11	5.50E-05	4.54	5.51E-06	5.51E-06
Otu612_Coprococcus	0.60	0.99	1.42	1.57E-01	4.39	1.67E-05	4.04	5.25E-05	1.67E-05

Otu2686_Coprococcus	0.57	0.93	1.92	5.69E-02	3.98	9.29E-05	4.11	3.96E-05	3.96E-05
Otu469_Coprococcus	1.47	0.53	2.77	7.06E-03	2.22	2.73E-02	3.47	5.28E-04	5.28E-04
Otu541_Coprococcus	0.37	0.76	1.30	1.94E-01	2.89	4.17E-03	2.94	3.24E-03	3.24E-03
Otu217_Lachnospira	0.94	0.92	3.70	2.97E-04	3.84	1.58E-04	5.23	1.70E-07	1.70E-07
Otu470_Lachnospira	1.22	0.27	4.07	7.26E-05	1.09	2.75E-01	3.58	3.47E-04	7.26E-05
Otu352_Pseudobutyrivibrio	0.96	0.35	3.31	1.12E-03	1.38	1.68E-01	3.28	1.05E-03	1.05E-03
Otu111_Roseburia	1.48	0.11	5.85	1.65E-08	NA	NA	5.52	NA	1.65E-08
Otu2600_Roseburia	1.52	0.11	5.17	4.85E-07	NA	NA	4.90	NA	4.85E-07
Otu247_Roseburia	-0.62	0.99	-0.91	3.66E-01	3.33	1.01E-03	-1.69	9.19E-02	1.01E-03
Otu684_Mogibacteriaceae	-1.12	-0.46	-2.54	1.22E-02	-2.06	4.05E-02	-3.22	1.28E-03	1.28E-03
Otu872_Peptococcaceae	-1.54	-0.12	-3.22	1.61E-03	-0.52	6.02E-01	-2.60	9.35E-03	1.61E-03
Otu302_Peptococcus	0.79	0.72	1.86	6.77E-02	2.87	4.49E-03	3.30	9.64E-04	9.64E-04
Otu138_Ruminococcaceae	-0.74	-0.77	-3.90	1.40E-04	-3.17	1.73E-03	-4.91	9.21E-07	9.21E-07
Otu2072_Ruminococcaceae	1.30	0.72	3.20	1.67E-03	3.21	1.53E-03	4.46	8.07E-06	8.07E-06
Otu315_Ruminococcaceae	-1.23	-0.34	-4.30	3.29E-05	-1.48	1.39E-01	-3.98	6.86E-05	3.29E-05
Otu318_Ruminococcaceae	-0.89	-0.68	-2.76	6.67E-03	-3.07	2.42E-03	-4.06	4.85E-05	4.85E-05
Otu254_Ruminococcaceae	-1.20	-0.56	-3.16	2.00E-03	-2.50	1.32E-02	-3.94	8.21E-05	8.21E-05
Otu1116_Ruminococcaceae	-1.17	-0.41	-3.65	3.72E-04	-1.82	6.94E-02	-3.80	1.44E-04	1.44E-04
Otu811_Ruminococcaceae	1.51	0.62	2.29	2.36E-02	2.77	6.03E-03	3.54	3.97E-04	3.97E-04
Otu89_Ruminococcaceae	-0.67	-0.12	-3.38	8.51E-04	-0.28	7.82E-01	-2.55	1.06E-02	8.51E-04
Otu952_Ruminococcaceae	1.13	0.55	2.20	2.90E-02	2.40	1.73E-02	3.23	1.25E-03	1.25E-03
Otu92_Ruminococcaceae	-0.57	-0.38	-2.98	3.26E-03	-1.51	1.32E-01	-3.14	1.67E-03	1.67E-03
Otu491_Ruminococcaceae	-0.64	-0.53	-2.14	3.41E-02	-2.09	3.79E-02	-2.97	3.02E-03	3.02E-03
Otu2095_Faecalibacterium	1.51	0.69	2.57	1.45E-02	2.21	2.77E-02	3.29	1.02E-03	1.02E-03
Otu266_Faecalibacterium	1.17	0.34	4.36	2.05E-05	1.13	2.59E-01	3.81	1.39E-04	2.05E-05
Otu240_Faecalibacterium	0.97	0.35	2.84	5.37E-03	1.56	1.21E-01	3.07	2.17E-03	2.17E-03

Otu1484_Oscillospira	-1.01	-0.26	-3.80	1.85E-04	-0.50	6.15E-01	-3.00	2.71E-03	1.85E-04
Otu833_Oscillospira	1.04	0.49	3.12	2.08E-03	1.52	1.31E-01	3.25	1.17E-03	1.17E-03
Otu487_Oscillospira	-0.91	-0.51	-1.95	5.41E-02	-2.23	2.65E-02	-2.93	3.38E-03	3.38E-03
Otu427_Ruminococcus	1.07	0.65	3.23	1.53E-03	2.77	6.01E-03	4.18	2.88E-05	2.88E-05
Otu1952_Ruminococcus	1.38	0.68	2.81	5.97E-03	3.01	2.87E-03	4.05	5.07E-05	5.07E-05
Otu521_Ruminococcus	0.79	0.84	3.27	1.25E-03	2.12	3.52E-02	3.77	1.62E-04	1.62E-04
Otu391_Ruminococcus	0.53	1.27	2.03	4.35E-02	3.31	1.08E-03	3.74	1.84E-04	1.84E-04
Otu328_Ruminococcus	0.56	0.65	2.25	2.57E-02	2.61	9.76E-03	3.41	6.62E-04	6.62E-04
Otu337_Ruminococcus	0.71	0.70	1.69	9.33E-02	3.14	1.92E-03	3.38	7.24E-04	7.24E-04
Otu1616_Ruminococcus	0.76	0.45	3.04	2.69E-03	1.19	2.37E-01	2.96	3.09E-03	2.69E-03
Otu379_Ruminococcus	0.65	0.49	2.44	1.56E-02	1.76	7.96E-02	2.95	3.18E-03	3.18E-03
Otu97_Anaerovibrio	0.65	0.65	2.09	3.92E-02	2.84	4.84E-03	3.45	5.60E-04	5.60E-04
Otu181_Megasphaera	0.49	-0.98	1.33	1.94E-01	-3.12	2.06E-03	1.26	2.07E-01	2.06E-03
Otu759_p-75-a5	1.61	0.25	3.36	1.04E-03	1.11	2.70E-01	3.10	1.94E-03	1.04E-03
Otu862_Fusobacteriaceae	-0.66	-1.01	-3.51	6.53E-04	-4.62	6.31E-06	-5.60	2.10E-08	2.10E-08
Otu3_Fusobacteriaceae	-0.59	-0.45	-5.06	9.41E-07	-1.44	1.50E-01	-4.49	7.29E-06	9.41E-07
Otu840_Fusobacteriaceae	-0.58	-0.68	-2.91	4.51E-03	-3.01	2.93E-03	-4.11	3.93E-05	3.93E-05
Otu2231_Fusobacteriaceae	-0.68	-1.17	-1.03	3.14E-01	-3.35	9.34E-04	-3.05	2.27E-03	9.34E-04
Otu43_Fusobacterium	-0.38	-0.82	-1.47	1.46E-01	-3.12	2.04E-03	-3.21	1.34E-03	1.34E-03
Otu28_Fusobacterium	-0.34	-0.54	-2.47	1.44E-02	-1.96	5.17E-02	-3.11	1.90E-03	1.90E-03
Otu319_Proteobacteria	-0.27	-0.96	-1.06	2.90E-01	-4.21	3.66E-05	-3.67	2.45E-04	3.66E-05
Otu321_Betaproteobacteria	-0.19	-0.83	-0.83	4.08E-01	-3.18	1.66E-03	-2.81	4.98E-03	1.66E-03
Otu112_Desulfovibrionaceae	-0.67	-0.81	-3.20	1.62E-03	-3.31	1.09E-03	-4.54	5.69E-06	5.69E-06
Otu591_Desulfovibrionaceae	-1.12	-0.19	-4.33	2.42E-05	-0.61	5.42E-01	-3.42	6.33E-04	2.42E-05
Otu199_Enterobacteriaceae	-0.10	-0.69	-0.36	7.20E-01	-2.98	3.22E-03	-2.34	1.94E-02	3.22E-03
Otu2813_Treponema	0.82	0.51	2.30	2.34E-02	2.30	2.23E-02	3.22	1.28E-03	1.28E-03

Otu1005_Treponema	0.70	0.44	2.72	7.22E-03	1.71	8.95E-02	3.10	1.93E-03	1.93E-03
Otu437_Anaeroplasma	0.46	0.91	0.70	4.84E-01	3.65	3.23E-04	3.04	2.38E-03	3.23E-04
Otu527_RF39	1.24	0.77	2.63	9.77E-03	3.50	5.54E-04	4.27	1.97E-05	1.97E-05
Otu484_RF39	1.79	0.50	3.07	3.00E-03	2.07	3.93E-02	3.56	3.77E-04	3.77E-04
Otu1146_RF39	1.63	0.60	2.34	2.13E-02	2.71	7.27E-03	3.53	4.22E-04	4.22E-04
Otu249_RF39	0.68	0.51	2.50	1.40E-02	2.29	2.26E-02	3.35	8.11E-04	8.11E-04
Otu278_RFP12	-0.52	-0.80	-2.61	9.57E-03	-2.03	4.38E-02	-3.26	1.12E-03	1.12E-03
Otu311_RFP12	-0.62	-0.34	-2.99	3.21E-03	-1.30	1.94E-01	-3.00	2.68E-03	2.68E-03

Supplementary table 2: OTUs significantly associated with total cholesterol (TC)

ID	**Estimate_q**	**Estimate_b**	**T_value_q**	**P_value_q**	**T_value_b**	**P_value_b**	**meta_z_score**	**P_meta**	**final_p_value**
Otu307_Treponema	0.02	-0.27	0.41	6.81E-01	-5.4	1.51E-07	3.42	6.20E-04	1.51E-07
Otu1069_Treponema	-0.03	-0.18	-0.53	5.95E-01	-4.0	8.02E-05	-3.16	1.55E-03	8.02E-05
Otu169_Prevotella	-0.02	-0.19	-0.45	6.55E-01	-4.0	8.72E-05	-3.09	2.00E-03	8.72E-05
Otu2043_Ruminococcaceae	-0.09	-0.18	-0.77	4.43E-01	-4.0	9.17E-05	-3.31	9.40E-04	9.17E-05
Otu68_Prevotella_stercorea	0.02	0.19	0.76	4.48E-01	3.9	1.46E-04	3.22	1.27E-03	1.46E-04
Otu1047_Treponema	0.02	-0.24	0.64	5.23E-01	-3.7	2.51E-04	2.14	3.26E-02	2.51E-04
Otu2306_Ruminococcaceae	-0.23	-0.13	-4.77	4.04E-06	-2.8	5.37E-03	-5.23	1.71E-07	1.71E-07
Otu13_Lactobacillus	-0.09	-0.22	-3.44	6.83E-04	-2.5	1.33E-02	-4.15	3.29E-05	3.29E-05
Otu521_Ruminococcus	-0.12	-0.25	-2.58	1.06E-02	-3.3	1.32E-03	-4.08	4.55E-05	4.55E-05
Otu2206_Lachnospiraceae	0.12	0.15	2.21	2.90E-02	3.6	3.91E-04	4.05	5.09E-05	5.09E-05
Otu1457_Ruminococcus	-0.20	-0.14	-2.43	1.66E-02	-3.3	9.57E-04	-4.03	5.58E-05	5.58E-05
Otu456_Ruminococcaceae	0.17	0.14	2.63	9.42E-03	3.0	3.30E-03	3.91	9.08E-05	9.08E-05
Otu350_Ruminococcus	-0.14	-0.13	-2.90	4.18E-03	-2.5	1.22E-02	-3.80	1.46E-04	1.46E-04
Otu117_Ruminococcaceae	-0.18	0.03	-4.20	3.77E-05	0.2	8.78E-01	2.81	5.03E-03	3.77E-05
Otu127_GMD14H09	0.14	0.04	3.70	2.85E-04	0.8	4.21E-01	3.13	1.72E-03	2.85E-04

Supplementary table 3: OTUs significantly associated with ratio of low density lipoprotein to high density lipoprotein (LDL/HDL)

ID	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	final_p_value
Otu30_Bacteroidetes	-0.11	-1.14	-2.57	1.08E-02	-5.26	3.17E-07	-5.42	6.05E-08	6.05E-08
Otu862_Fusobacteriaceae	0.25	0.34	3.09	2.52E-03	4.60	6.97E-06	5.31	1.07E-07	1.07E-07
Otu199_Enterobacteriaceae	0.36	0.22	4.01	1.31E-04	2.85	4.74E-03	4.70	2.58E-06	2.58E-06
Otu3_Fusobacteriaceae	0.19	0.16	4.75	3.94E-06	1.47	1.44E-01	4.30	1.73E-05	3.94E-06
Otu328_Ruminococcus	-0.02	-0.39	-0.24	8.14E-01	-4.63	6.14E-06	-3.36	7.69E-04	6.14E-06
Otu33_Clostridium_butyricum	-0.36	-0.29	-4.51	1.05E-05	-1.16	2.46E-01	-3.94	8.27E-05	1.05E-05
Otu43_Fusobacterium	0.28	0.35	2.36	2.22E-02	3.95	1.05E-04	4.36	1.30E-05	1.30E-05
Otu231_Clostridiaceae	-0.36	-0.22	-4.42	1.53E-05	-0.51	6.11E-01	-3.42	6.32E-04	1.53E-05
Otu394_Epulopiscium	-0.07	-0.41	-0.82	4.11E-01	-4.38	1.78E-05	-3.62	2.99E-04	1.78E-05
Otu2813_Treponema	-0.25	-0.28	-2.36	1.99E-02	-3.75	2.25E-04	-4.26	2.09E-05	2.09E-05
Otu2402_Treponema	-0.38	-0.17	-3.89	1.53E-04	-2.21	2.79E-02	-4.23	2.32E-05	2.32E-05
Otu259_Oscillospira	0.29	0.27	3.09	2.31E-03	2.80	5.51E-03	4.12	3.83E-05	3.83E-05
Otu15_Clostridium	-0.36	0.04	-4.13	4.94E-05	NA	NA	-3.89	NA	4.94E-05
Otu1922_Treponema	-0.26	-0.27	-2.22	2.83E-02	-3.59	4.08E-04	-4.05	5.12E-05	5.12E-05
Otu151_Prevotella	-0.05	-0.39	-0.73	4.69E-01	-4.06	6.73E-05	-3.33	8.67E-04	6.73E-05
Otu1384_Ruminococcaceae	0.51	0.14	3.93	1.28E-04	1.78	7.66E-02	3.96	7.48E-05	7.48E-05
Otu47_Prevotella	-0.05	0.33	-0.45	6.51E-01	3.99	8.75E-05	-2.45	1.41E-02	8.75E-05
Otu1014_Lachnospiraceae	0.11	-0.30	1.15	2.51E-01	-3.99	8.85E-05	1.96	5.00E-02	8.85E-05
Otu45_Treponema	-0.20	-0.14	-3.99	8.88E-05	-1.04	3.00E-01	-3.50	4.58E-04	8.88E-05
Otu101_Epulopiscium	0.31	0.26	2.33	2.27E-02	3.30	1.13E-03	3.91	9.10E-05	9.10E-05
Otu1410_Treponema	-0.34	-0.15	-3.84	1.73E-04	-1.76	7.90E-02	-3.90	9.73E-05	9.73E-05
Otu193_Mogibacteriaceae	0.32	0.64	3.88	1.34E-04	1.52	1.30E-01	3.77	1.63E-04	1.34E-04
Otu5_Escherichia	0.16	0.27	3.87	1.42E-04	1.33	1.86E-01	3.63	2.88E-04	1.42E-04
Otu1975_Treponema	-0.25	-0.22	-2.63	9.45E-03	-2.79	5.73E-03	-3.79	1.51E-04	1.51E-04

Otu366_Anaeroplasma	-0.32	-0.19	-2.99	3.44E-03	-2.43	1.56E-02	-3.78	1.58E-04	1.58E-04
Otu17_Phascolarctobacterium	0.36	0.04	3.80	1.87E-04	NA	NA	3.56	NA	1.87E-04
Otu13_Lactobacillus	-0.18	-0.10	-3.78	2.02E-04	-0.62	5.33E-01	-3.07	2.15E-03	2.02E-04
Otu16_Treponema	-0.13	-0.42	-2.79	5.77E-03	-2.47	1.41E-02	-3.69	2.26E-04	2.26E-04
Otu1047_Treponema	-0.11	-0.38	-1.92	5.62E-02	-3.34	9.84E-04	-3.68	2.33E-04	2.33E-04
Otu2022_Ruminococcus	0.16	-0.29	1.20	2.34E-01	-3.73	2.40E-04	1.76	7.91E-02	2.40E-04
Otu188_Bacteroides_fragilis	0.10	0.31	0.65	5.21E-01	3.68	2.85E-04	3.02	2.53E-03	2.85E-04
Otu649_Mogibacteriaceae	0.15	0.28	0.78	4.35E-01	3.68	2.86E-04	3.12	1.83E-03	2.86E-04
Otu1151_Prevotella	-0.17	-0.46	-2.17	3.10E-02	-3.00	2.99E-03	-3.62	2.89E-04	2.89E-04
Otu485_Epulopiscium	-0.04	-0.30	-0.37	7.13E-01	-3.65	3.20E-04	-2.80	5.03E-03	3.20E-04
Otu1616_Ruminococcus	-0.29	-0.12	-3.66	3.20E-04	-0.94	3.46E-01	-3.21	1.32E-03	3.20E-04
Otu42_Actinobacillus	0.19	0.19	2.66	8.89E-03	2.48	1.38E-02	3.59	3.29E-04	3.29E-04
Otu186_Prevotella	-0.16	-0.38	-2.38	1.84E-02	-2.74	6.59E-03	-3.59	3.32E-04	3.32E-04
Otu2674_Parabacteroides	0.42	0.04	3.63	3.48E-04	NA	NA	3.39	NA	3.48E-04
Otu2502_Lachnospiraceae	-0.16	-0.30	-1.71	8.89E-02	-3.40	8.04E-04	-3.57	3.53E-04	3.53E-04
Otu442_Lachnospiraceae	-0.01	-0.27	-0.14	8.91E-01	-3.60	3.82E-04	-2.61	9.09E-03	3.82E-04
Otu1800_Parabacteroides	0.39	0.20	3.60	3.87E-04	0.88	3.81E-01	3.13	1.76E-03	3.87E-04
Otu135_CF231	0.28	0.24	2.42	1.86E-02	2.68	7.94E-03	3.54	3.98E-04	3.98E-04
Otu111_Roseburia	-0.32	0.04	-3.59	3.99E-04	NA	NA	-3.35	NA	3.99E-04
Otu291_Coprococcus	0.00	-0.30	0.01	9.91E-01	-3.58	4.15E-04	2.49	1.28E-02	4.15E-04
Otu31_Treponema	-0.24	-0.30	-3.57	4.28E-04	-1.00	3.19E-01	-3.19	1.40E-03	4.28E-04
Otu104_Lactobacillus_reuteri	-0.11	-0.52	-2.03	4.39E-02	-2.98	3.14E-03	-3.51	4.42E-04	4.42E-04
Otu2449_Lachnospiraceae	-0.05	-0.39	-0.54	5.88E-01	-3.56	4.47E-04	-2.87	4.16E-03	4.47E-04
Otu2562_Mogibacteriaceae	0.32	0.22	3.36	9.08E-04	1.65	1.00E-01	3.51	4.52E-04	4.52E-04
Otu350_Ruminococcus	-0.23	-0.22	-2.47	1.45E-02	-2.52	1.25E-02	-3.49	4.76E-04	4.76E-04
Otu2306_Ruminococcaceae	-0.09	-0.29	-1.03	3.04E-01	-3.53	4.98E-04	-3.19	1.43E-03	4.98E-04

Otu468_Ruminococcus	-0.04	-0.26	-0.43	6.65E-01	-3.50	5.57E-04	-2.75	6.01E-03	5.57E-04
Otu2768_Clostridiaceae	-0.12	-0.27	-1.03	3.04E-01	-3.50	5.61E-04	-3.17	1.54E-03	5.61E-04
Otu816_Peptococcaceae	0.03	0.26	0.16	8.69E-01	3.47	6.11E-04	2.54	1.11E-02	6.11E-04
Otu32_Bacteroides_coprophilus	0.11	0.26	1.47	1.45E-01	3.43	7.16E-04	3.42	6.17E-04	6.17E-04
Otu141_S24-7	0.20	-0.23	3.44	6.96E-04	-0.66	5.08E-01	-1.93	5.36E-02	6.96E-04
Otu2231_Fusobacteriaceae	0.50	0.38	1.66	1.10E-01	3.21	1.49E-03	3.38	7.36E-04	7.36E-04
Otu44_Prevotella	-0.14	-0.38	-2.56	1.11E-02	-2.25	2.55E-02	-3.37	7.39E-04	7.39E-04
Otu1423_Treponema	-0.42	-0.13	-3.33	1.07E-03	-1.50	1.35E-01	-3.37	7.51E-04	7.51E-04
Otu195_Pasteurellaceae	0.28	0.21	2.22	2.95E-02	2.60	9.82E-03	3.37	7.65E-04	7.65E-04
Otu575_Ruminococcaceae	0.00	-0.26	-0.01	9.93E-01	-3.41	7.69E-04	-2.38	1.71E-02	7.69E-04
Otu872_Peptococcaceae	0.27	0.24	1.60	1.11E-01	3.19	1.59E-03	3.36	7.80E-04	7.80E-04
Otu106_Ruminococcus	-0.15	-0.25	-2.44	1.54E-02	-2.34	2.02E-02	-3.36	7.91E-04	7.91E-04
Otu161_rc4-4	0.29	0.32	3.38	8.36E-04	1.39	1.66E-01	3.34	8.30E-04	8.30E-04
Otu89_Ruminococcaceae	0.23	0.10	3.38	8.64E-04	0.68	4.96E-01	2.84	4.55E-03	8.64E-04
Otu413_Lachnospiraceae	0.06	-0.25	0.47	6.43E-01	-3.35	9.36E-04	2.01	4.42E-02	9.36E-04
Otu756_Dethiosulfovibrionaceae	0.28	0.23	2.03	4.40E-02	2.69	7.69E-03	3.31	9.38E-04	9.38E-04
Otu243_Lachnospiraceae	-0.29	0.01	-3.36	9.72E-04	0.16	8.71E-01	2.22	2.66E-02	9.72E-04
Otu2633_Phascolarctobacterium	0.29	0.01	3.31	1.09E-03	0.11	9.10E-01	2.39	1.69E-02	1.09E-03
Otu276_Ruminococcaceae	0.28	0.22	1.81	7.35E-02	2.84	4.89E-03	3.26	1.13E-03	1.13E-03
Otu683_Ruminococcaceae	-0.36	-0.18	-2.31	2.29E-02	-2.34	2.00E-02	-3.25	1.14E-03	1.14E-03
Otu432_Ruminococcus	-0.32	0.33	-1.33	1.92E-01	3.29	1.14E-03	-1.38	1.69E-01	1.14E-03
Otu1069_Treponema	-0.27	-0.19	-2.34	2.04E-02	-2.28	2.34E-02	-3.24	1.18E-03	1.18E-03
Otu596_Clostridiales	-0.02	-0.25	-0.20	8.45E-01	-3.25	1.33E-03	-2.41	1.61E-02	1.33E-03

Supplementary table 4: OTUs significantly associated with atherosclerosis index (AI)

ID	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	final_p_value
Otu862_Fusobacteriaceae	0.31	0.40	3.09	2.53E-03	4.22	3.5E-05	5.06	4.11E-07	4.11E-07
Otu13_Lactobacillus	-0.30	-0.32	-5.08	7.96E-07	-1.58	1.1E-01	-4.61	4.12E-06	7.96E-07
Otu30_Bacteroidetes	-0.17	-1.08	-3.00	3.00E-03	-3.78	2.0E-04	-4.73	2.22E-06	2.22E-06
Otu104_Lactobacillus_reuteri	-0.24	-0.71	-3.42	7.32E-04	-3.20	1.6E-03	-4.62	3.79E-06	3.79E-06
Otu350_Ruminococcus	-0.34	-0.39	-3.03	2.79E-03	-3.43	7.0E-04	-4.51	6.46E-06	6.46E-06
Otu328_Ruminococcus	0.01	-0.49	0.14	8.86E-01	-4.61	6.7E-06	3.08	2.05E-03	6.69E-06
Otu15_Clostridium	-0.51	0.05	-4.58	7.55E-06	NA	NA	-4.33	NA	7.55E-06
Otu2633_Phascolarctobacterium	0.50	0.05	4.59	7.74E-06	0.30	7.7E-01	3.37	7.44E-04	7.74E-06
Otu394_Epulopiscium	-0.15	-0.55	-1.33	1.85E-01	-4.52	9.7E-06	-4.07	4.76E-05	9.66E-06
Otu231_Clostridiaceae	-0.46	-0.11	-4.48	1.16E-05	-0.20	8.4E-01	-3.24	1.19E-03	1.16E-05
Otu17_Phascolarctobacterium	0.54	0.05	4.48	1.18E-05	NA	NA	4.23	NA	1.18E-05
Otu106_Ruminococcus	-0.26	-0.39	-3.22	1.51E-03	-2.84	4.9E-03	-4.23	2.29E-05	2.29E-05
Otu3_Fusobacteriaceae	0.22	0.19	4.32	2.40E-05	1.42	1.6E-01	3.99	6.66E-05	2.40E-05
Otu199_Enterobacteriaceae	0.39	0.26	3.49	7.54E-04	2.61	9.8E-03	4.21	2.56E-05	2.56E-05
Otu135_CF231	0.40	0.32	3.21	2.19E-03	2.88	4.4E-03	4.18	2.90E-05	2.90E-05
Otu816_Peptococcaceae	0.00	0.40	0.01	9.91E-01	4.22	3.4E-05	2.94	3.31E-03	3.44E-05
Otu2306_Ruminococcaceae	-0.23	-0.41	-2.05	4.17E-02	-3.84	1.6E-04	-4.11	3.96E-05	3.96E-05
Otu756_Dethiosulfovibrionaceae	0.41	0.38	2.38	1.84E-02	3.49	5.8E-04	4.10	4.15E-05	4.15E-05
Otu1616_Ruminococcus	-0.44	-0.08	-4.13	5.13E-05	-0.50	6.2E-01	-3.22	1.29E-03	5.13E-05
Otu43_Fusobacterium	0.31	0.39	2.39	2.06E-02	3.41	7.7E-04	4.02	5.94E-05	5.94E-05
Otu141_S24-7	0.31	-0.12	4.06	6.82E-05	-0.27	7.9E-01	-2.63	8.59E-03	6.82E-05
Otu16_Treponema	-0.16	-0.61	-2.71	7.21E-03	-2.85	4.7E-03	-3.90	9.67E-05	9.67E-05
Otu33_Clostridium_butyricum	-0.41	-0.34	-3.96	1.01E-04	-1.08	2.8E-01	-3.51	4.50E-04	1.01E-04
Otu2022_Ruminococcus	-0.06	-0.39	-0.29	7.69E-01	-3.94	1.1E-04	-2.94	3.23E-03	1.08E-04

Otu123_	0.32	-0.03	3.92	1.18E-04	-0.11	9.1E-01	-2.64	8.21E-03	1.18E-04
Otu366_Anaeroplasma	-0.44	-0.24	-3.04	2.96E-03	-2.49	1.4E-02	-3.85	1.20E-04	1.20E-04
Otu47_Prevotella	-0.13	0.42	-1.01	3.15E-01	3.90	1.3E-04	-2.00	4.55E-02	1.26E-04
Otu376_Ruminococcus	-0.32	-0.42	-2.52	1.24E-02	-2.93	3.7E-03	-3.82	1.35E-04	1.35E-04
Otu872_Peptococcaceae	0.17	0.37	0.79	4.31E-01	3.81	1.8E-04	3.21	1.33E-03	1.77E-04
Otu1749_Phascolarctobacterium	0.29	0.16	3.80	1.86E-04	1.00	3.2E-01	3.35	8.18E-04	1.86E-04
Otu1432_Lactobacillus_reuteri	-0.30	-0.28	-3.59	4.09E-04	-1.74	8.3E-02	-3.73	1.94E-04	1.94E-04
Otu1047_Treponema	-0.07	-0.54	-0.96	3.37E-01	-3.77	2.1E-04	-3.30	9.64E-04	2.09E-04
Otu1014_Lachnospiraceae	0.10	-0.36	0.76	4.49E-01	-3.72	2.5E-04	2.05	4.01E-02	2.53E-04
Otu151_Prevotella	-0.06	-0.46	-0.68	4.96E-01	-3.71	2.6E-04	-3.07	2.18E-03	2.59E-04
Otu161_rc4-4	0.39	0.49	3.51	5.31E-04	1.66	9.8E-02	3.62	2.94E-04	2.94E-04
Otu101_Epulopiscium	0.44	0.25	2.76	7.19E-03	2.43	1.6E-02	3.60	3.14E-04	3.14E-04
Otu139_Desulfovibrio	0.23	0.41	2.48	1.41E-02	2.64	8.9E-03	3.59	3.36E-04	3.36E-04
Otu42_Actinobacillus	0.23	0.24	2.61	1.01E-02	2.42	1.6E-02	3.52	4.31E-04	4.31E-04
Otu5_Escherichia	0.19	0.32	3.56	4.57E-04	1.23	2.2E-01	3.35	8.11E-04	4.57E-04
Otu195_Pasteurellaceae	0.38	0.26	2.55	1.27E-02	2.47	1.4E-02	3.49	4.75E-04	4.75E-04
Otu591_Desulfovibrionaceae	0.24	0.40	1.93	5.49E-02	3.05	2.5E-03	3.49	4.79E-04	4.79E-04
Otu2402_Treponema	-0.32	-0.24	-2.60	1.04E-02	-2.39	1.8E-02	-3.49	4.82E-04	4.82E-04
Otu145_S24-7	0.28	0.20	3.52	5.15E-04	0.96	3.4E-01	3.13	1.74E-03	5.15E-04
Otu38_Lactobacillus	-0.25	0.03	-3.52	5.25E-04	0.12	9.1E-01	2.37	1.79E-02	5.25E-04
Otu645_Clostridiales	-0.08	-0.36	-0.36	7.21E-01	-3.51	5.3E-04	-2.70	6.90E-03	5.34E-04
Otu1423_Treponema	-0.59	-0.13	-3.52	5.49E-04	-1.22	2.2E-01	-3.31	9.48E-04	5.49E-04
Otu410_YS2	0.52	0.22	2.93	4.51E-03	2.03	4.3E-02	3.44	5.91E-04	5.91E-04
Otu575_Ruminococcaceae	-0.17	-0.35	-0.96	3.41E-01	-3.48	5.9E-04	-3.10	1.92E-03	5.94E-04
Otu1384_Ruminococcaceae	0.57	0.08	3.50	5.99E-04	0.79	4.3E-01	2.99	2.81E-03	5.99E-04
Otu208_CF231	0.32	0.34	3.20	1.57E-03	1.69	9.2E-02	3.43	6.10E-04	6.10E-04

Otu257_Prevotella	0.31	0.23	2.60	1.04E-02	2.29	2.3E-02	3.42	6.28E-04	6.28E-04
Otu171_Prevotella	-0.26	-0.23	-3.05	2.62E-03	-1.77	7.7E-02	-3.38	7.32E-04	7.32E-04
Otu649_Mogibacteriaceae	0.17	0.33	0.73	4.69E-01	3.41	7.6E-04	2.89	3.81E-03	7.56E-04
Otu1975_Treponema	-0.31	-0.25	-2.35	2.00E-02	-2.45	1.5E-02	-3.36	7.69E-04	7.69E-04
Otu2813_Treponema	-0.14	-0.33	-1.04	3.00E-01	-3.40	7.9E-04	-3.10	1.91E-03	7.94E-04
Otu2768_Clostridiaceae	-0.15	-0.34	-1.02	3.07E-01	-3.38	8.3E-04	-3.08	2.04E-03	8.35E-04
Otu2709_Prevotella	0.22	0.30	2.62	9.35E-03	2.13	3.4E-02	3.33	8.54E-04	8.54E-04
Otu468_Ruminococcus	-0.06	-0.33	-0.54	5.90E-01	-3.36	9.0E-04	-2.73	6.35E-03	8.96E-04
Otu118_Bacteroidales	0.29	0.21	2.74	6.82E-03	1.99	4.8E-02	3.31	9.27E-04	9.27E-04
Otu454_Mogibacteriaceae	0.38	0.28	2.50	1.32E-02	2.20	2.8E-02	3.30	9.58E-04	9.58E-04
Otu57_CF231	0.33	-0.03	3.35	1.07E-03	-0.34	7.3E-01	-2.07	3.84E-02	1.07E-03
Otu31_Treponema	-0.28	-0.39	-3.31	1.07E-03	-1.00	3.2E-01	-3.02	2.53E-03	1.07E-03

Supplementary table 5: taxonomies significantly associated with blood glucose

Taxonomy	**Estimate_q**	**Estimate_b**	**T_value_q**	**P_value_q**	**T_value_b**	**P_value_b**	**meta_z_score**	**GLU_P_meta**	**final_p_value**
g_Coprococcus	1.69	0.11	6.11	4.11E-09	NA	NA	5.88	NA	4.11E-09
g_Roseburia	1.68	0.11	5.99	7.75E-09	NA	NA	5.77	NA	7.75E-09
f_Lachnospiraceae/Lachnospira	2.23	0.11	5.77	2.42E-08	NA	NA	5.58	NA	2.42E-08
g_Faecalibacterium	1.05	0.18	3.81	1.79E-04	0.49	0.62	3.75	2.74E-03	1.79E-04
o_Turicibacterales/Turicibacteraceae/Turicibacter	0.82	1.39	3.62	3.56E-04	1.59	0.11	3.64	2.70E-04	2.70E-04
g_Peptococcus	1.24	0.85	1.98	5.38E-02	3.14	0.00	3.56	3.75E-04	3.75E-04
f_Enterococcaceae	1.69	-1.39	1.43	1.72E-01	-3.31	0.00	3.27	1.78E-01	1.07E-03
g_Clostridium	0.06	0.78	0.06	9.55E-01	3.19	0.00	3.15	2.31E-02	1.61E-03
g_Pseudobutyrivibrio	0.63	0.67	1.38	1.70E-01	3.03	0.00	3.09	2.00E-03	2.00E-03
g_Mogibacterium	-1.30	-0.54	-2.08	4.12E-02	-2.29	0.02	-3.05	2.27E-03	2.27E-03
o_Actinomycetales	-0.93	-0.52	-2.18	3.14E-02	-2.32	0.02	-3.15	1.63E-03	1.63E-03

Taxonomy	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	GLU_P_meta	final_p_value
o_Bacillales	-1.03	-0.80	-0.99	3.27E-01	-3.20	0.00	-3.17	3.38E-03	1.55E-03
c_Actinobacteria	-0.97	-0.50	-2.32	2.18E-02	-2.23	0.03	-3.19	1.42E-03	1.42E-03
c_Deltaproteobacteria	-0.80	-1.06	-3.66	3.10E-04	-1.20	0.23	-3.61	6.77E-04	3.10E-04
f_Christensenellaceae	-1.05	-0.63	-3.45	6.83E-04	-1.71	0.09	-3.61	3.07E-04	3.07E-04
g_Fusobacterium	-0.40	-0.55	-3.07	2.47E-03	-2.14	0.03	-3.64	2.68E-04	2.68E-04
f_S24.7	-1.50	0.11	-3.93	1.09E-04	NA	NA	-3.87	NA	1.09E-04
f_Bacteroidaceae/Bacteroides	-1.16	0.11	-4.04	7.22E-05	NA	NA	-3.97	NA	7.22E-05
p_Fusobacteria/Fusobacteriia/Fusobacteriales/Fusobacteriaceae	-0.56	-0.53	-4.72	4.37E-06	-1.61	0.11	-4.59	1.17E-05	4.37E-06
o_Desulfovibrionales/Desulfovibrionaceae	-1.20	-1.02	-4.75	3.51E-06	-1.62	0.11	-4.64	9.72E-06	3.51E-06
f_Porphyromonadaceae	-1.71	0.11	-4.77	3.20E-06	NA	NA	-4.66	NA	3.20E-06
g_Parabacteroides	-1.88	0.11	-4.93	1.56E-06	NA	NA	-4.80	NA	1.56E-06

Supplementary table 6: Taxonomies significantly associated with total cholesterol (TC)

taxonomy	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	final_p_value
o_Lactobacillales/f_Lactobacillaceae/Lactobacillus	-0.08	-0.66	-2.80	5.50E-03	-3.97	9.57E-05	-4.72	2.34E-06	2.34E-06
f_BS11	-0.06	-0.13	-2.08	3.95E-02	-2.88	4.32E-03	-3.47	5.14E-04	5.14E-04
c_Bacilli	-0.14	0.02	-3.49	5.84E-04	NA	NA	-3.44	NA	5.84E-04
p_Fusobacteria/Fusobacteriia/Fusobacteriales/Fusobacteriaceae	0.08	0.09	3.40	8.23E-04	1.43	1.55E-01	3.37	7.47E-04	7.47E-04
g_Fusobacterium	0.08	0.12	2.70	7.71E-03	2.40	1.71E-02	3.57	3.57E-04	3.57E-04
g_Prevotella	0.19	0.02	3.72	2.45E-04	NA	NA	3.67	NA	2.45E-04
o_GMD14H09	0.14	0.05	3.75	2.36E-04	0.86	3.93E-01	3.68	1.35E-03	2.36E-04
c_Deltaproteobacteria	0.19	0.05	4.49	1.11E-05	0.30	7.63E-01	4.39	8.98E-04	1.11E-05

Supplementary table 7: Taxonomies significantly associated with high density lipoprotein (HDL)

taxonomy	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	final_p_value
f_Veillonellaceae	-0.32	0.02	-4.51	1.01E-05	NA	NA	-4.42	NA	1.01E-05
g_Phascolarctobacterium	-0.28	0.02	-4.41	1.54E-05	NA	NA	-4.32	NA	1.54E-05
p_Synergistetes/Synergistia/Synergistales	-0.10	-0.19	-0.95	3.44E-01	-3.85	1.53E-04	-3.79	8.17E-04	1.53E-04
f_Dethiosulfovibrionaceae	-0.11	-0.19	-1.03	3.06E-01	-3.83	1.65E-04	-3.77	7.05E-04	1.65E-04
g_CF231	-0.24	0.02	-3.59	4.02E-04	NA	NA	-3.54	NA	4.02E-04
g_Desulfovibrio	-0.03	-0.21	-0.60	5.46E-01	-3.29	1.16E-03	-3.25	6.47E-03	1.16E-03
c_Bacilli	0.15	0.02	3.25	1.33E-03	NA	NA	3.21	NA	1.33E-03
g_Anaeroplasma	0.22	0.01	3.42	7.82E-04	0.25	8.03E-01	3.36	1.07E-02	7.82E-04
g_Mitsuokella	0.31	0.39	0.78	4.52E-01	3.55	4.72E-04	3.50	2.66E-03	4.72E-04
o_Lactobacillales/f_Lactobacillaceae/Lactobacillus	0.12	0.10	3.66	3.07E-04	0.50	6.14E-01	3.61	3.63E-03	3.07E-04

Supplementary table 8: Taxonomies significantly associated with low density lipoprotein (LDL)

taxonomy	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	final_p_value
c_Deltaproteobacteria	0.17	-0.08	4.60	6.91E-06	-0.54	5.88E-01	-4.50	5.16E-03	6.91E-06
f_Enterococcaceae	-0.18	0.31	-0.41	6.86E-01	4.50	1.06E-05	-4.40	4.68E-03	1.06E-05
g_Vagococcus	-0.35	0.35	-0.33	7.45E-01	4.14	4.74E-05	-4.07	8.14E-03	4.74E-05
o_Desulfovibrionales/Desulfovibrionaceae	0.17	-0.01	4.03	7.63E-05	-0.11	9.12E-01	-3.96	6.55E-03	7.63E-05
c_Gammaproteobacteria	0.08	-0.02	3.66	3.07E-04	-0.08	9.40E-01	-3.61	1.25E-02	3.07E-04
p_Spirochaetes/Spirochaetes/Spirochaetales/Spirochaetaceae/Treponema	-0.09	0.02	-3.25	1.31E-03	NA	NA	-3.21	NA	1.31E-03
o_GMD14H09	0.11	-0.01	3.20	1.61E-03	-0.14	8.87E-01	-3.15	3.33E-02	1.61E-03
g_Mitsuokella	0.40	0.30	0.65	5.30E-01	3.55	4.60E-04	3.50	3.48E-03	4.60E-04
f_Enterobacteriaceae/Enterobacteriales/Escherichia	0.08	0.11	3.77	2.07E-04	1.52	1.29E-01	3.71	2.18E-04	2.07E-04
p_Proteobacteria	0.16	0.02	3.92	1.18E-04	NA	NA	3.85	NA	1.18E-04
g_Fusobacterium	0.09	0.13	3.29	1.20E-03	2.98	3.14E-03	4.38	1.19E-05	1.19E-05

f_Aeromonadaceae	0.05	0.29	0.28	7.81E-01	4.84	2.33E-06	4.72	4.06E-04	2.33E-06
p_Fusobacteria/Fusobacteriia/Fusobacteriales/Fusobacteriaceae	0.10	0.09	5.13	6.82E-07	1.64	1.02E-01	4.97	3.02E-06	6.82E-07

Supplementary table 9: Taxonomies significantly associated with ratio of low density lipoprotein to high density lipoprotein (LDL/HDL)

taxonomy	Estimate_q	Estimate_b	T_value_q	P_value_q	T_value_b	P_value_b	meta_z_score	P_meta	final_p_value
f_Aeromonadaceae	-0.06	0.54	-0.17	8.64E-01	4.41	1.56E-05	-4.32	3.35E-03	1.56E-05
g_Roseburia	-0.43	0.04	-4.35	2.01E-05	NA	NA	-4.26	NA	2.01E-05
g_Anaeroplasma	-0.36	-0.06	-3.72	2.71E-04	-0.72	4.71E-01	-3.64	2.04E-03	2.71E-04
c_Bacilli	-0.25	0.04	-3.49	5.78E-04	NA	NA	-3.44	NA	5.78E-04
o_Turicibacterales/Turicibacteraceae/Turicibacter	-0.26	-0.24	-3.39	8.31E-04	-0.80	4.25E-01	-3.34	3.42E-03	8.31E-04
o_Anaeroplasmatales/Anaeroplasmataceae	-0.33	-0.09	-3.37	9.23E-04	-1.09	2.78E-01	-3.31	1.88E-03	9.23E-04
f_Lactobacillaceae/Lactobacillus	-0.17	-0.31	-3.27	1.25E-03	-1.04	2.98E-01	-3.23	2.54E-03	1.25E-03
o_Spirochaetales/Spirochaetaceae/Treponema	-0.17	0.04	-3.16	1.76E-03	NA	NA	-3.13	NA	1.76E-03
g_Coprococcus	-0.31	0.04	-3.08	2.29E-03	NA	NA	-3.05	NA	2.29E-03
f_Paraprevotellaceae	0.41	0.04	3.08	2.33E-03	NA	NA	3.04	NA	2.33E-03
f_Porphyromonadaceae	0.39	0.04	3.13	1.95E-03	NA	NA	3.10	NA	1.95E-03
g_Desulfovibrio	0.21	0.20	2.54	1.20E-02	1.90	5.82E-02	3.12	1.83E-03	1.83E-03
p_Proteobacteria	0.27	0.04	3.18	1.69E-03	NA	NA	3.14	NA	1.69E-03
g_Actinobacillus	0.17	0.21	2.08	4.00E-02	2.78	5.84E-03	3.40	6.71E-04	6.71E-04
c_Gammaproteobacteria	0.16	0.43	3.53	5.01E-04	1.00	3.17E-01	3.48	1.53E-03	5.01E-04
g_rc4.4	0.32	0.30	3.19	1.65E-03	1.89	6.06E-02	3.55	3.81E-04	3.81E-04
f_Mogibacteriaceae	0.37	0.04	3.64	3.39E-04	NA	NA	3.58	NA	3.39E-04
o_Pasteurellales/Pasteurellaceae	0.19	0.20	2.60	1.05E-02	2.56	1.11E-02	3.61	3.10E-04	3.10E-04
g_Epulopiscium	0.06	-0.45	0.73	4.65E-01	-3.72	2.50E-04	3.66	3.82E-02	2.50E-04
p_Synergistetes/Synergistia/Synergistales	0.29	0.29	1.49	1.37E-01	3.81	1.77E-04	3.75	2.13E-04	1.77E-04
f_Peptococcaceae	0.33	0.44	3.48	6.10E-04	1.92	5.62E-02	3.77	1.61E-04	1.61E-04

c_Deltaproteobacteria/Dethiosulfovibrionaceae	0.29	0.01	3.95	1.02E-04	0.04	9.71E-01	3.89	5.55E-03	1.02E-04
f_Dethiosulfovibrionaceae									
o_Desulfovibrionales/Desulfovibrionaceae	0.35	0.09	4.03	7.60E-05	0.41	6.83E-01	3.96	2.02E-03	7.60E-05
f_Enterobacteriaceae/Enterobacteriales	0.16	0.34	3.45	6.70E-04	2.35	1.96E-02	4.06	5.00E-05	5.00E-05
g_CF231	0.42	0.04	4.14	4.78E-05	NA	NA	4.07	NA	4.78E-05
f_Veillonellaceae	0.47	0.04	4.14	4.74E-05	NA	NA	4.07	NA	4.74E-05
p_Fusobacteria/Fusobacteriia/Fusobacteriales/Fusobacteriaceae	0.15	0.28	3.59	4.19E-04	2.51	1.26E-02	4.26	2.06E-05	2.06E-05
g_Phascolarctobacterium	0.44	0.04	4.39	1.70E-05	NA	NA	4.30	NA	1.70E-05

Supplementary table 10: Taxonomies significantly associated with atherosclerosis index (AI)

taxonomy	**Estimate_q**	**Estimate_b**	**T_value_q**	**p_value_q**	**T_value_b**	**p_value_b**	**meta_z_score**	**p_meta**	**final_p_value**
c_Bacilli	-0.41	0.05	-4.66	5.17E-06	NA	NA	-4.56	NA	5.17E-06
o_Lactobacillales/f_Lactobacillaceae/Lactobacillus	-0.31	-0.57	-4.65	5.51E-06	-1.469	1.43E-01	-4.54	2.15E-05	5.51E-06
g_Roseburia	-0.52	0.05	-4.10	5.62E-05	NA	NA	-4.03	NA	5.62E-05
f_Aeromonadaceae	-0.09	0.60	-0.26	8.00E-01	3.802	1.82E-04	-3.74	1.36E-02	1.82E-04
g_Epulopiscium	-0.01	-0.54	-0.06	9.50E-01	-3.489	5.77E-04	-3.44	1.32E-02	5.77E-04
f_Clostridiaceae	-0.47	0.05	-3.49	5.77E-04	NA	NA	-3.44	NA	5.77E-04
g_Anaeroplasma	-0.46	-0.07	-3.49	6.22E-04	-0.615	5.39E-01	-3.42	4.32E-03	6.22E-04
o_Turicibacterales/Turicibacteraceae/Turicibacter	-0.33	-0.33	-3.30	1.11E-03	-0.853	3.95E-01	-3.26	3.63E-03	1.11E-03
o_Spirochaetales/Spirochaetaceae/Treponema	-0.22	0.05	-3.16	1.76E-03	NA	NA	-3.13	NA	1.76E-03
o_Anaeroplasmatales/Anaeroplasmataceae	-0.40	-0.09	-3.11	2.18E-03	-0.826	4.10E-01	-3.06	5.95E-03	2.18E-03
f_Mogibacteriaceae	0.37	0.05	2.82	5.21E-03	NA	NA	2.79	NA	5.21E-03
p_Proteobacteria	0.31	0.05	2.88	4.29E-03	NA	NA	2.86	NA	4.29E-03
f_Porphyromonadaceae	0.49	0.05	3.01	2.85E-03	NA	NA	2.98	NA	2.85E-03
o_Desulfovibrionales/Desulfovibrionaceae	0.38	0.26	3.33	9.95E-04	0.944	3.46E-01	3.29	2.75E-03	9.95E-04
c_Gammaproteobacteria	0.19	0.83	3.17	1.72E-03	1.537	1.26E-01	3.30	9.69E-04	9.69E-04

g_Actinobacillus	0.18	0.28	1.85	6.63E-02	2.910	3.96E-03	3.34	8.51E-04	8.51E-04
g_Desulfovibrio	0.24	0.36	2.15	3.25E-02	2.772	6.01E-03	3.45	5.51E-04	5.51E-04
g_rc4.4	0.40	0.40	3.07	2.43E-03	1.960	5.12E-02	3.52	4.27E-04	4.27E-04
o_Pasteurellales/Pasteurellaceae	0.23	0.26	2.44	1.62E-02	2.626	9.21E-03	3.54	3.98E-04	3.98E-04
f_Paraprevotellaceae	0.62	0.05	3.63	3.45E-04	NA	NA	3.58	NA	3.45E-04
c_Deltaproteobacteria	0.35	0.26	3.72	2.50E-04	0.678	4.99E-01	3.66	2.15E-03	2.50E-04
o_Enterobacteriales/Enterobacteriaceae/Escherichia	0.19	0.38	3.26	1.31E-03	2.043	4.22E-02	3.71	2.08E-04	2.08E-04
p_Fusobacteria/Fusobacteriia/Fusobacteriales/Fusobacteriaceae	0.16	0.34	2.99	3.17E-03	2.395	1.74E-02	3.77	1.64E-04	1.64E-04
f_Peptococcaceae	0.46	0.57	3.78	1.97E-04	1.965	5.06E-02	4.01	5.95E-05	5.95E-05
g_CF231	0.57	0.05	4.43	1.46E-05	NA	NA	4.33	NA	1.46E-05
f_Dethiosulfovibrionaceae	0.39	0.44	1.67	9.78E-02	4.507	1.03E-05	4.41	1.79E-05	1.03E-05
p_Synergistetes/Synergistia/Synergistales	0.36	0.44	1.53	1.27E-01	4.522	9.65E-06	4.42	2.59E-05	9.65E-06
f_Veillonellaceae	0.68	0.05	4.81	2.65E-06	NA	NA	4.70	NA	2.65E-06
g_Phascolarctobacterium	0.63	0.05	4.99	1.14E-06	NA	NA	4.87	NA	1.14E-06

Supplementary table 11. KEGG functional pathway significantly associated with blood glucose.

LEVEL1	LEVEL2	LEVEL3	Estimate	T_value	z_score	p_value
Metabolism	Energy Metabolism	Carbon fixation pathways in prokaryotes	-20.09	-5.75	-5.56	2.71E-08
Metabolism	Energy Metabolism	Nitrogen metabolism	-31.39	-5.74	-5.55	2.89E-08
Metabolism	Biosynthesis of Other Secondary Metabolites	Tropane, piperidine and pyridine alkaloid biosynthesis	-21.48	-5.44	-5.27	1.34E-07
Metabolism	Amino Acid Metabolism	Cysteine and methionine metabolism	-70.29	-5.36	-5.20	2.00E-07
Environmental Information Processing	Signal Transduction	MAPK signaling pathway - yeast	-11.57	-5.31	-5.16	2.53E-07
Metabolism	Metabolism of Other Amino Acids	D-Glutamine and D-glutamate metabolism	-29.77	-5.29	-5.14	2.71E-07
Metabolism	Xenobiotics Biodegradation and Metabolism	Ethylbenzene degradation	-11.45	-5.03	-4.90	9.53E-07
Metabolism	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	-10.37	-4.92	-4.79	1.65E-06
Metabolism	Nucleotide Metabolism	Purine metabolism	-39.82	-4.69	-4.58	4.54E-06

Metabolism	Biosynthesis of Other Secondary Metabolites	Isoquinoline alkaloid biosynthesis	-7.48	-4.64	-4.54	5.72E-06
Metabolism	Biosynthesis of Other Secondary Metabolites	Novobiocin biosynthesis	-22.49	-4.61	-4.50	6.69E-06
Metabolism	Metabolism of Cofactors and Vitamins	Folate biosynthesis	-11.34	-4.53	-4.44	9.15E-06
Metabolism	Xenobiotics Biodegradation and Metabolism	Naphthalene degradation	-9.80	-4.49	-4.40	1.09E-05
Environmental Information Processing	Signaling Molecules and Interaction	Cellular antigens	-3.28	-4.33	-4.25	2.16E-05
Metabolism	Xenobiotics Biodegradation and Metabolism	Toluene degradation	-4.54	-4.22	-4.14	3.51E-05
Metabolism	Amino Acid Metabolism	Tyrosine metabolism	-17.09	-4.19	-4.11	3.96E-05
Metabolism	Glycan Biosynthesis and Metabolism	Lipopolysaccharide biosynthesis proteins	-4.03	-4.09	-4.02	5.88E-05
Organismal Systems	Digestive System	Protein digestion and absorption	-2.40	-4.01	-3.94	8.13E-05
Metabolism	Glycan Biosynthesis and Metabolism	Lipopolysaccharide biosynthesis	-3.17	-4.00	-3.93	8.39E-05
Metabolism	Metabolism of Terpenoids and Polyketides	Prenyltransferases	-13.28	-3.98	-3.91	9.11E-05
Metabolism	Metabolism of Other Amino Acids	Taurine and hypotaurine metabolism	-14.02	-3.96	-3.90	9.74E-05
Metabolism	Amino Acid Metabolism	Glycine, serine and threonine metabolism	-33.63	-3.95	-3.88	1.03E-04
Metabolism	Metabolism of Cofactors and Vitamins	Nicotinate and nicotinamide metabolism	-18.05	-3.94	-3.87	1.09E-04
Metabolism	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - ganglio series	-3.13	-3.92	-3.86	1.14E-04
Metabolism	Metabolism of Cofactors and Vitamins	Riboflavin metabolism	-10.47	-3.89	-3.83	1.29E-04
Metabolism	Carbohydrate Metabolism	Butanoate metabolism	-17.05	-3.79	-3.73	1.94E-04
Environmental Information Processing	Membrane Transport	Bacterial secretion system	-16.45	-3.70	-3.65	2.63E-04
Metabolism	Enzyme Families	Peptidases	-34.45	-3.69	-3.63	2.80E-04
Metabolism	Glycan Biosynthesis and Metabolism	N-Glycan biosynthesis	-4.06	-3.67	-3.62	2.97E-04
Metabolism	Metabolism of Cofactors and Vitamins	Ubiquinone and other terpenoid-quinone biosynthesis	-3.79	-3.65	-3.60	3.19E-04
Cellular Processes	Transport and Catabolism	Peroxisome	-8.84	-3.65	-3.59	3.26E-04
Metabolism	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	-21.73	-3.61	-3.56	3.77E-04
Metabolism	Glycan Biosynthesis and Metabolism	Glycosaminoglycan degradation	-3.61	-3.59	-3.54	3.99E-04
Metabolism	Lipid Metabolism	Arachidonic acid metabolism	-3.05	-3.57	-3.52	4.24E-04
Metabolism	Metabolism of Terpenoids and Polyketides	Polyketide sugar unit biosynthesis	-12.97	-3.55	-3.50	4.58E-04

Metabolism	Glycan Biosynthesis and Metabolism	Glycosyltransferases	-10.87	-3.49	-3.44	5.74E-04
Metabolism	Metabolism of Cofactors and Vitamins	Biotin metabolism	-8.77	-3.44	-3.39	6.89E-04
Metabolism	Metabolism of Cofactors and Vitamins	Retinol metabolism	-3.95	-3.32	-3.27	1.06E-03
Metabolism	Nucleotide Metabolism	Pyrimidine metabolism	-27.69	-3.23	-3.19	1.44E-03
Metabolism	Metabolism of Other Amino Acids	Glutathione metabolism	-6.75	-3.21	-3.17	1.53E-03
Organismal Systems	Endocrine System	Adipocytokine signaling pathway	-4.15	-3.16	-3.13	1.76E-03
Metabolism	Metabolism of Cofactors and Vitamins	One carbon pool by folate	-14.57	-3.11	-3.08	2.07E-03
Metabolism	Amino Acid Metabolism	Phenylalanine metabolism	-12.20	-3.07	-3.04	2.40E-03
Metabolism	Biosynthesis of Other Secondary Metabolites	Streptomycin biosynthesis	-13.32	-3.02	-2.99	2.82E-03
Metabolism	Metabolism of Terpenoids and Polyketides	Biosynthesis of siderophore group nonribosomal peptides	-2.95	-2.99	-2.96	3.12E-03
Metabolism	Biosynthesis of Other Secondary Metabolites	Penicillin and cephalosporin biosynthesis	-3.53	-2.89	-2.86	4.19E-03
Metabolism	Biosynthesis of Other Secondary Metabolites	Stilbenoid, diarylheptanoid and gingerol biosynthesis	-0.43	-1.65	-2.83	4.64E-03
Environmental Information Processing	Signal Transduction	Phosphatidylinositol signaling system	-8.28	-2.84	-2.82	4.85E-03
Metabolism	Glycan Biosynthesis and Metabolism	Peptidoglycan biosynthesis	-21.48	-2.83	-2.80	5.05E-03
Metabolism	Metabolism of Other Amino Acids	beta-Alanine metabolism	-7.37	-2.78	-2.75	5.90E-03
Metabolism	Metabolism of Cofactors and Vitamins	Vitamin B6 metabolism	-10.32	-2.77	-2.74	6.14E-03
Metabolism	Xenobiotics Biodegradation and Metabolism	Drug metabolism - other enzymes	-15.31	-2.76	-2.73	6.26E-03
Metabolism	Metabolism of Terpenoids and Polyketides	Terpenoid backbone biosynthesis	-18.14	-2.70	-2.68	7.40E-03
Metabolism	Amino Acid Metabolism	Valine, leucine and isoleucine degradation	-4.66	-2.69	-2.66	7.73E-03
Metabolism	Metabolism of Terpenoids and Polyketides	Geraniol degradation	-2.09	-2.68	-2.66	7.85E-03
Metabolism	Energy Metabolism	Oxidative phosphorylation	-10.49	-2.67	-2.65	8.04E-03
Metabolism	Lipid Metabolism	Fatty acid metabolism	-5.54	-2.66	-2.64	8.37E-03
Metabolism	Xenobiotics Biodegradation and Metabolism	Aminobenzoate degradation	-6.85	-2.64	-2.61	8.94E-03
Metabolism	Metabolism of Other Amino Acids	Selenocompound metabolism	-20.28	-2.59	-2.57	1.01E-02
Metabolism	Metabolism of Cofactors and Vitamins	Lipoic acid metabolism	-2.90	-2.59	-2.57	1.02E-02
Metabolism	Lipid Metabolism	Steroid hormone biosynthesis	-1.21	-2.55	-2.53	1.14E-02

Metabolism	Metabolism of Terpenoids and Polyketides	Biosynthesis of vancomycin group antibiotics	-8.42	-2.50	-2.48	1.30E-02
Metabolism	Biosynthesis of Other Secondary Metabolites	Isoflavonoid biosynthesis	-0.81	-2.12	-2.47	1.37E-02
Organismal Systems	Excretory System	Proximal tubule bicarbonate reclamation	-2.84	-2.47	-2.45	1.42E-02
Metabolism	Carbohydrate Metabolism	Inositol phosphate metabolism	-5.45	-2.47	-2.45	1.43E-02
Cellular Processes	Transport and Catabolism	Lysosome	-2.78	-2.28	-2.27	2.32E-02
Metabolism	Carbohydrate Metabolism	Propanoate metabolism	-11.07	-2.27	-2.26	2.40E-02
Metabolism	Lipid Metabolism	Steroid biosynthesis	-0.71	-2.31	1.38	2.20E-02
Metabolism	Carbohydrate Metabolism	C5-Branched dibasic acid metabolism	16.42	2.49	2.47	1.36E-02
Environmental Information Processing	Signal Transduction	Two-component system	11.38	2.55	2.53	1.14E-02
Metabolism	Biosynthesis of Other Secondary Metabolites	Butirosin and neomycin biosynthesis	6.88	2.63	2.60	9.20E-03
Metabolism	Xenobiotics Biodegradation and Metabolism	Bisphenol degradation	12.37	2.64	2.61	8.96E-03
Metabolism	Enzyme Families	Protein kinases	9.13	2.67	2.65	8.12E-03
Metabolism	Carbohydrate Metabolism	Galactose metabolism	11.17	2.69	2.67	7.58E-03
Metabolism	Lipid Metabolism	Glycerolipid metabolism	10.02	2.82	2.79	5.24E-03
Metabolism	Amino Acid Metabolism	Valine, leucine and isoleucine biosynthesis	18.32	2.85	2.82	4.79E-03
Metabolism	Energy Metabolism	Photosynthesis	11.00	3.03	3.00	2.73E-03
Metabolism	Energy Metabolism	Photosynthesis proteins	11.43	3.12	3.09	2.01E-03
Metabolism	Carbohydrate Metabolism	Starch and sucrose metabolism	14.81	3.53	3.48	5.05E-04
Cellular Processes	Cell Motility	Cytoskeleton proteins	11.21	3.56	3.51	4.48E-04
Metabolism	Carbohydrate Metabolism	Fructose and mannose metabolism	20.46	3.72	3.66	2.48E-04
Organismal Systems	Endocrine System	Insulin signaling pathway	10.16	3.76	3.70	2.15E-04
Metabolism	Carbohydrate Metabolism	Pentose and glucuronate interconversions	15.93	3.77	3.71	2.06E-04
Metabolism	Lipid Metabolism	Primary bile acid biosynthesis	6.09	3.88	3.82	1.36E-04
Environmental Information Processing	Membrane Transport	ABC transporters	10.94	3.97	3.90	9.49E-05
Metabolism	Lipid Metabolism	Secondary bile acid biosynthesis	6.23	4.15	4.07	4.66E-05
Cellular Processes	Cell Motility	Bacterial chemotaxis	5.67	4.44	4.34	1.39E-05

Metabolism	Metabolism of Terpenoids and Polyketides	Biosynthesis of ansamycins	11.07	4.45	4.36	1.30E-05
Metabolism	Metabolism of Other Amino Acids	D-Arginine and D-ornithine metabolism	2.77	4.52	4.42	9.65E-06
Environmental Information Processing	Membrane Transport	Transporters	10.98	4.60	4.50	6.73E-06
Cellular Processes	Cell Motility	Bacterial motility proteins	7.09	4.64	4.53	5.76E-06
Cellular Processes	Cell Motility	Flagellar assembly	6.14	4.80	4.69	2.77E-06
Metabolism	Carbohydrate Metabolism	Pentose phosphate pathway	25.41	5.07	4.94	7.88E-07
Organismal Systems	Environmental Adaptation	Plant-pathogen interaction	21.32	5.15	5.01	5.47E-07