

Supplementary Material

Table of Contents

Abbreviations used	2
Online Table I. Spearman correlation between traits and OTU richness and diversity	3
Online Table II: OTUs associated with BMI at FDR < 0.05 level.....	4
Online Table III. OTUs associated with TG at FDR < 0.05 level.....	5
Online Table IV. OTUs associated with HDL at FDR < 0.05 level	6
Online Table V. Associated Taxonomies at FDR < 0.05 level.....	7
Online Table VI. The association between microbes and the SNPs associated with lipids and BMI at P value 1×10^{-5}	12
Online Table VII. The associations between microbes and the combined BMI and lipid genetic risk scores at P < 0.05 level	13
Online Figure I. The workflow of the two-part model.....	14
Online Figure II. The number of OTUs associated with TG, HDL and BMI at FDR < 0.05 and their overlaps with each other	15
Online Figure III. The amount of variance in BMI and lipids explained by the gut microbiome.....	16
Online Figure IV. The variation of lipids explained by age, gender, BMI, genetic and microbial risk.	17

Abbreviations used

BMI: body mass index

FDR: false discovery rate, ≤ 0.05

HDL: high-density lipoprotein cholesterol

LDL: low-density lipoprotein cholesterol

OTU: operational taxonomic unit

P: P value

R: Spearman correlation coefficient

TC: total cholesterol

TG: triglycerides

Online Table I. Spearman correlation between traits and OTU richness and diversity

	Age		Gender*		Adjusted for age and gender									
	R	P	R	P	BMI		TG		HDL		LDL		TC	
					R	P	R	P	R	P	R	P	R	P
Richness [#]	0.23	5.87x10⁻¹²	-0.09	0.0055	-0.12	3.8x10⁻⁴	-0.13	1.37x10⁻⁴	0.112	8.3x10⁻⁴	-0.0028	0.93	0.0021	0.95
Diversity [§]	0.21	1.08x10⁻¹⁰	-0.1	0.0023	-0.08	0.013	-0.12	0.00032	0.12	0.00054	-0.054	0.11	-0.04	0.2

*Gender: negative value indicates the OTU diversity is less in men than in women

[#]Richness: the number of OTUs per sample

[§]Diversity: Shannon's diversity index

R: Spearman correlation coefficient; P: P value. Numbers in bold indicate the significant correlations at P < 0.05.

BMI: body mass index; TG: triglyceride, HDL: high-density lipoprotein cholesterol; LDL: low-density lipoprotein cholesterol, TC: total cholesterol

Online Table II: OTUs associated with BMI at FDR < 0.05 level

OTU	Summary of OTUs reads				Binary Model				Quantitative model				Meta Analysis		Final P value
	No. Absent	No. Present	ln(Counts+1)/Present	Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value	Meta P value		
251395.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	357	536	8.0391791	-1.459	0.273	-5.354	1.10E-07	-0.065	0.10897	-0.593	0.5532	-4.17385	2.99E-05	1.10E-07	
4299281.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	478	415	29.3903614	-1.38	0.266	-5.181	2.74E-07	0.0589	0.08229	0.716	0.4745	-3.1293	0.00175	2.74E-07	
182031.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	94	799	210.914894	-1.415	0.437	-3.237	0.001	-0.188	0.04836	-3.893	0.0001	-5.02084	5.14E-07	5.14E-07	
316911.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	141	752	16.5345745	-1.157	0.368	-3.142	0.002	-0.369	0.09303	-3.972	7.83E-05	-5.00767	5.51E-07	5.51E-07	
4368791.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	521	372	18.8763441	-1.082	0.274	-3.95	8.44E-05	-0.325	0.10276	-3.159	0.0017	-4.9975	5.81E-07	5.81E-07	
3069358.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	249	644	20.628882	-1.145	0.299	-3.833	1E-04	-0.267	0.08203	-3.255	0.0012	-4.98997	6.04E-07	6.04E-07	
193129.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	177	716	29.2192737	-1.146	0.338	-3.394	7E-04	-0.251	0.07019	-3.583	0.0004	-4.91257	8.99E-07	8.99E-07	
1703711.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	189	704	30.6221591	-1.187	0.333	-3.593	3E-04	-0.26	0.0783	-3.323	0.0009	-4.87056	1.11E-06	1.11E-06	
345717.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	611	282	5.36879433	-1.148	0.288	-3.983	7.36E-05	-0.463	0.15855	-2.919	0.0038	-4.85021	1.23E-06	1.23E-06	
295743.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	507	386	37.8626943	-1.302	0.271	-4.808	1.79E-06	-0.15	0.08019	-1.876	0.0614	-4.6998	2.60E-06	1.79E-06	
312766.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	477	416	4.82451923	-1.012	0.272	-3.728	2E-04	-0.417	0.14126	-2.953	0.0033	-4.70153	2.58E-06	2.58E-06	
584417.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	466	427	29.3747073	-1.215	0.268	-4.54	6.39E-06	-0.16	0.0801	-1.995	0.0466	-4.59813	4.26E-06	4.26E-06	
192201.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	66	827	103.347037	0.528	0.515	1.0259	0.305	0.3327	0.07278	4.571	5.60E-06	3.93593	8.29E-05	5.60E-06	
179664.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	282	611	119.807725	-1.111	0.288	-3.861	1E-04	-0.152	0.06108	-2.481	0.0134	-4.46737	7.92E-06	7.92E-06	
192144.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	519	374	2.36898396	1.032	0.271	3.8107	1E-04	0.5482	0.22986	2.385	0.0176	4.361738	1.29E-05	1.29E-05	
4307785.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	536	357	5.72630252	-0.76	0.274	-2.771	0.006	-0.535	0.16527	-3.239	0.0013	-4.22667	2.37E-05	2.37E-05	
183187.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	442	451	8.9002217	-0.663	0.269	-2.468	0.014	-0.445	0.12881	-3.457	0.0006	-4.16803	3.07E-05	3.07E-05	
189878.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales_f_Lachnospiraceae	493	400	45.675	-1.12	0.268	-4.173	3.30E-05	0.1346	0.08124	1.657	0.0984	-1.76714	0.0721	3.30E-05	
3997272.k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_B24-7(Barnesiellaceae)	169	724	32.1643646	-1.388	0.34	-4.083	4.84E-05	0.0261	0.0739	0.353	0.7241	-2.62344	0.0087	4.84E-05	
811768.k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Rhodocyclales	574	319	4.46081505	-1.134	0.279	-4.061	5.33E-05	-0.266	0.15556	-1.708	0.0885	-4.06153	4.88E-05	4.88E-05	
165137.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	187	706	9.28328612	0.073	0.33	0.2199	0.826	0.3841	0.0961	3.997	7.11E-05	2.964569	0.0003	7.11E-05	
119310.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	675	218	5.2018349	-1.231	0.311	-3.959	8.13E-05	-0.171	0.15264	-1.123	0.2627	-5.75786	0.00035	8.13E-05	
218924.k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae	277	616	10.25	-1.141	0.288	-3.957	8.20E-05	-0.042	0.09572	-0.44	0.6599	-3.09614	0.00196	8.20E-05	
313600.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	695	198	8.88888889	-1.276	0.323	-3.955	8.25E-05	0.2321	0.16568	1.401	0.1629	-1.79703	0.07233	8.25E-05	
174353.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	442	451	8.1286031	-1.025	0.269	-3.809	1E-04	-0.187	0.10549	-1.77	0.0774	-3.93068	8.47E-05	8.47E-05	
329767.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	542	351	20.8347578	-1.067	0.275	-3.874	1E-04	-0.006	0.09295	-0.066	0.9477	-2.77363	0.00554	0.00011	
42458.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	693	200	3.59	-0.49	0.323	-1.515	0.13	-0.309	0.2352	-3.86	0.0002	-3.74711	0.00018	0.00015	
162844.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales_f_Lachnospiraceae	187	706	5.51133144	0.881	0.329	2.6772	0.008	0.3055	0.14116	2.676	0.0078	3.775683	0.00016	0.00016	
178389.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	335	558	136.121864	-1.033	0.276	-3.748	2E-04	0.0147	0.05648	0.261	0.7946	-2.75514	0.01408	0.00019	
326539.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	784	109	7.02752394	-1.433	0.413	-3.467	6E-04	-0.415	0.23032	-1.804	0.0741	-3.70933	0.00021	0.00021	
182864.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_f_Blaustia	480	413	2.24213075	0.994	0.268	3.713	2E-04	-0.027	0.23519	-0.114	0.909	2.53766	0.01128	0.00022	
4455005.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Mogibacteriaceae	611	282	9.5567759	-0.506	0.294	-1.721	0.086	-0.502	0.14162	-3.547	0.0005	-3.69396	0.00022	0.00022	
174571.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	545	348	2.94258784	0.315	0.277	1.1385	0.255	0.7033	0.19011	3.7	0.0003	3.393005	0.00069	0.00025	
370063.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	439	454	10.4515419	-0.741	0.269	-2.753	0.006	-0.268	0.11093	-2.418	0.016	-3.64883	0.00027	0.00027	
165334.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae	622	271	27.1586716	-0.966	0.296	-3.266	0.001	-0.209	0.11001	-1.904	0.058	-3.64259	0.00027	0.00027	
4474703.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	153	740	13.4810811	-0.856	0.36	-2.378	0.018	-0.271	0.09811	-2.762	0.0059	-3.62579	0.00029	0.00029	
34789.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae	669	224	3.61160714	-0.709	0.315	-2.253	0.025	-0.628	0.21808	-2.879	0.0044	-3.60455	0.00031	0.00031	
447859.k_Bacteria_p_Tenericutes_c_RF3o_M16151-28	813	80	4.85	-1.698	0.47	-3.612	3E-04	0.0055	0.25501	0.022	0.9828	-5.25905	0.01144	0.00032	
191874.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales_f_Ruminococcus	586	307	2.51140065	-0.072	0.284	-0.254	0.8	-0.805	0.22455	-3.585	0.0004	-3.68623	0.00073	0.00039	
556564.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	516	377	9.47214854	-0.974	0.275	-3.539	4E-04	-0.083	0.11135	-0.744	0.4572	-3.01902	0.00254	0.00042	
531038.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	735	158	14.8987342	-1.247	0.352	-3.539	4E-04	0.1229	0.13891	0.885	0.3777	-1.8692	0.06159	0.00042	
192741.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	475	418	6.99043062	-0.951	0.269	-3.535	4E-04	-0.099	0.12736	-0.775	0.4388	-3.03738	0.00239	0.00043	
175962.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	814	79	6.65822785	-1.665	0.473	-3.521	5E-04	0.5688	0.26691	2.131	0.0364	-1.00058	0.31703	0.00045	
184665.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	14	879	83.252597	0	0	0	1	0.2822	0.08058	3.502	0.0005	2.467139	0.01362	0.00048	
180503.k_Bacteria_p_Verrucomicrobia_c_Verrucomicrobia_o_Verrucomicrobiales_f_Abitarmatium_mauritii	245	648	282.804012	-0.579	0.304	-1.903	0.057	-0.147	0.04887	-3.01	0.0027	-3.46369	0.00053	0.00053	
289562.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcales	833	60	11.25	-1.845	0.537	-3.439	6E-04	-0.227	0.2555	-0.887	0.379	-3.04473	0.00233	0.00061	
201772.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	373	520	2.55	0.92	0.271	3.3987	7E-04	-0.065	0.19264	-0.34	0.7342	2.1547	0.03119	0.00071	
317749.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	543	350	5.90857148	-0.931	0.275	-3.391	7E-04	-0.059	0.14057	-0.422	0.6736	-2.68712	0.00071	0.00073	
15305_Archaea_f_Thaumarchaeota_c_Methanobrevibacterium_f_Methanobrevibacterium	393	500	337.278	-0.54	0.274	-1.968	0.049	-0.153	0.05439	-2.821	0.0005	-3.37555	0.00074	0.00074	
447980.k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Bacteroidaceae_f_Rikenellaceae	64	829	51.3281062	-0.411	0.521	-0.788	0.431	-0.223	0.06623	-3.369	0.0008	-2.93054	0.00338	0.00079	
437939.k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Bacteroidaceae_f_Bacteroides	436	457	26.249453	-0.838	0.268	-3.13	0.002	-0.131	0.08486	-1.541	0.1241	-3.29409	0.00099	0.00099	
293858.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	196	697	78.1764706	-1.067	0.323	-3.302	1E-03	-0.068	0.05614	-1.219	0.2231	-3.18846	0.00143	0.001	
173921.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae	528	365	4.03013699	-0.89	0.272	-3.274	0.001	-0.197	0.15345	-1.285	0.1998	-3.21401	0.00131	0.0011	
366748.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	41	852	98.1760563	-0.469	0.643	-0.73	0.466	-0.226	0.06907	-3.267	0.0011	-2.81825	0.00483	0.00113	
2824376.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	461	432	40.4791667	0.874	0.268	3.2654	0.001	0.0706	0.07766	0.909	0.3638	2.9436	0.00324	0.00113	
177757.k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Odoribacteraceae_f_Odoribacter	316	577	5.7712305	-0.763	0.281	-2.717	0.007	-0.213	0.11305	-1.887	0.0596	-3.24838	0.00116	0.00116	
4480944.k_Bacteria_p_Firmicutes_c_Clostridia	53	840	294.242857	-1.23	0.568	-2.166	0.031	-0.113	0.04644	-2.434	0.0151	-3.24734	0.00116	0.00116	
178137.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae	50	843	17.9632266	1.026	0.587	1.7483	0.081	0.2493	0.08786	2.837	0.0047	3.235756	0.00121	0.00121	
196275.k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales	52	841	240.737218	-1.844	0.571	-3.229	0.001	0.0033	0.05013	0.066					

Online Table III. OTUs associated with TG at FDR < 0.05 level

OTU	Summary of OTU reads				Binary Model				Quantitative model				Meta Analysis		
	No. Abund	No. Present	Estimate	Log2(Count+0.5)	Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value	Meta P value	Final P value
03123X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	277	710	29.2937374	-0.27614159	0.00504952	-4.8891281	8.09E-06	-0.06653288	0.01251631	-7.88246059	0.00015858	5.818680484	5.92E-09	5.88E-09	5.88E-09
179645X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	182	411	119.8772504	-0.1793582	0.01180868	-2.4404224	0.00667672	-0.04379151	0.01402743	-4.0494202	5.88E-05	-5.26977899	1.52E-07	1.52E-07	1.52E-07
101751X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	403	483	67.02098485	-0.254004	0.04887913	-5.288861507	1.91E-07	-0.03984641	0.01231395	-9.0007777	0.00376505	-4.55955242	1.52E-05	1.91E-07	
4065051X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	144	749	30.1775200	-0.23112745	0.06569792	-3.548054969	0.00047727	0.0466674	0.01322072	-3.70875104	0.00027251	-5.16647833	6.28E-07	3.28E-07	
182031X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	94	789	201.9148934	-0.15291926	0.07933836	-1.92741277	0.05424663	-0.04532231	0.00686706	-5.12625107	7.71E-07	-4.9534404	7.22E-07	3.71E-07	
215195X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	357	538	308.1791504	-0.25173727	0.04915249	-5.1740385	1.80E-07	-0.01244002	0.01929884	-6.64985258	0.01598213	-6.05058363	5.11E-05	3.80E-07	
175922X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	814	79	6.65229704	-0.42072094	0.08425915	-5.07685429	4.61E-07	0.02237846	0.03045273	1.90136204	0.06058898	-2.8020232	0.02570264	6.61E-07	
17453X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	462	651	8.28868394	-0.2224973	0.08292792	-4.61647818	4.48E-06	0.07726275	0.01884336	-3.937725	0.01665664	-5.07292383	4.97E-07	4.97E-07	
171789X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	543	350	5.50879129	-0.24137138	0.04911821	-4.7924183	2.18E-06	-0.07869111	0.01402025	-2.35120211	0.01927517	-5.02089907	5.62E-07	5.62E-07	
262476X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	461	428	40.4792887	-0.19935643	0.08870789	-2.80421214	7.18E-05	0.04491422	0.01491666	-1.0897997	0.02032762	-4.96464236	6.18E-07	6.18E-07	
4176702X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	153	740	13.46188199	-0.23138307	0.05745249	-3.61230911	0.00062366	-0.05947652	0.01739903	-3.46932459	0.00087756	-4.94160382	7.75E-07	7.75E-07	
808564X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	240	644	20.62888199	-0.21648027	0.03828477	-4.02131525	6.21E-05	-0.04533424	0.01504465	-2.96029278	0.0038947	-4.95269293	8.82E-07	8.82E-07	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	466	427	29.5740704	-0.20182462	0.04829202	-4.17898793	1.22E-05	-0.03786049	0.01479603	-2.5430903	0.0109960	-4.97937298	2.16E-06	2.16E-06	
1187911X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	189	704	30.6215900	-0.22819834	0.05955504	-3.78977139	0.00051531	0.03887041	0.01308741	-2.76429212	0.0058487	-4.92455884	1.77E-06	3.70E-06	
4368791X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	521	322	18.8734409	-0.20579677	0.09375151	-3.96694293	7.47E-05	-0.08224551	0.01124459	-5.48179752	0.01134459	-5.48179752	4.55E-06	4.55E-06	
117078X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Chloroflexales	403	483	7.12629396	-0.18280103	0.04284166	-3.78576228	0.00043916	-0.05812601	0.02052101	-2.71889158	0.00789415	-4.97309297	4.67E-06	4.67E-06	
10071X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Chloroflexales	684	209	37.22059496	-0.00807948	0.05737055	-0.17107219	0.86424071	0.15921419	0.02251704	4.78E-06	0.13146071	0.00489461	4.78E-06	4.78E-06	
139973X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Chloroflexales	767	126	8.39625190	-0.25416882	0.06112658	-3.67458716	0.00021613	0.11619701	0.01448283	-2.71261194	0.0076406	-4.77667875	7.65E-06	7.65E-06	
17838X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	353	558	1.38612848	-0.36687774	0.09597978	-4.16570882	3.40E-05	0.03217963	0.00989695	-2.12626249	0.03727266	-4.4203747	9.33E-06	9.33E-06	
4407781X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	536	357	5.73910232	-0.31797607	0.04904874	-4.43847854	1.02E-05	-0.04972469	0.01902389	-1.58063019	0.11407458	-4.2777302	7.26E-05	1.02E-05	
174749X_Bacteroidetes_Firmicutes_Bacteroidetes_Syntrophomonadaceae	580	783	22.88017899	-0.21146688	0.04888111	-4.00711807	1.10E-06	0.02182441	0.01191842	-6.05026104	0.00479731	-5.22252399	0.00029787	1.99E-05	
101730X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	507	386	37.3033681	-0.21355878	0.06687076	-4.20068174	1.10E-06	-0.01630023	0.01008878	-1.98023768	0.7983214	-1.8912671	0.03101044	4.24E-05	
4488481X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	53	880	246.3428751	-0.14523426	0.10178752	-1.40866756	0.11480446	-0.03547683	0.00812759	-1.45137894	1.58E-05	-4.06143565	1.87E-05	1.58E-05	
108979X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	7	880	246.3428751	0	0	0	0	0	0	0	0	0	0	0	
841891X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Chloroflexales	181	712	24.58132325	-0.25651089	0.05971151	-4.20374051	1.96E-05	-0.07486562	0.01374641	-3.424214	0.17862285	-3.98814868	7.24E-05	1.96E-05	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	511	382	16.5507487	-0.13085857	0.08081117	-2.67868811	0.00761078	0.06642677	0.01988524	-1.35287561	0.00899505	-4.9393671	2.24E-05	2.24E-05	
370053X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	403	464	10.45154185	-0.19894241	0.08262325	-3.12627015	4.10E-05	-0.08075554	0.02066237	-1.89716033	0.01680265	-4.18831617	1.25E-05	1.25E-05	
1620251X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	66	827	103.3470375	-0.10888147	0.02049554	-1.17464181	0.24045593	0.05462602	0.01286818	4.18914693	0.00678415	0.18300231	2.97E-05	2.97E-05	
4181952X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	756	137	5.39410084	-0.27892217	0.06671015	-3.11973042	3.21E-05	-0.02915197	0.01426759	-4.97813917	0.016917295	-2.9702384	0.00069433	3.21E-05	
4412959X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	240	653	56.1182944	-0.16977942	0.05442628	-3.1912449	0.00087031	-0.06279322	0.01554568	-2.52811902	0.00074054	-4.1928497	6.88E-05	3.48E-05	
201658X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	196	697	78.1764709	-0.05489679	0.08662628	-0.9058029	0.34862789	-0.02467001	0.0202738	-4.1388469	0.010105	-3.6558497	0.00036304	6.92E-05	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	455	458	46.87878029	-0.18817792	0.04705151	-4.05117795	4.41E-06	-0.03199411	0.01721292	-1.77092802	0.0800207	-4.12049475	1.09E-05	4.09E-05	
420001X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	678	417	29.20268169	-0.19766127	0.06218411	-4.09791887	1.43E-05	0.00768029	0.01189173	0.44051129	0.4706986	-2.3384817	0.00041044	6.24E-05	
967968X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	41	853	98.17050534	-0.25345043	0.11571327	-2.19123202	0.02662636	-0.0473871	0.01238275	-3.56288691	0.00081761	-4.96016724	7.90E-06	4.69E-05	
302741X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	475	418	6.99043022	-0.17090089	0.04803483	-4.09988023	4.93E-05	-0.07249248	0.02188003	-2.78857575	0.43082838	-4.27314612	0.00047041	4.93E-05	
178385X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	311	382	3.2127272	-0.20616456	0.05005811	-4.07736032	4.97E-05	-0.09685157	0.01600097	-3.70911414	0.17183634	-1.9055701	0.00174970	4.97E-05	
187155X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	70	623	9.58661625	-0.13761764	0.08009597	-1.52768848	0.13084621	0.07989042	0.01932965	4.03047076	0.0047066	-3.91429693	9.07E-05	6.00E-05	
448891X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	538	355	16.45702651	-0.19751312	0.04901246	-4.02520461	1.18E-05	-0.04548688	0.01474247	-1.46277901	0.14497377	-3.86100567	0.00011161	6.88E-05	
4448734X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	807	86	20.0212531	-0.32782724	0.01884884	-3.99911849	6.89E-05	-0.03188119	0.01741505	-1.98575325	0.32713708	-1.98575325	0.00046029	6.88E-05	
214824X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Bacteroidetes	277	616	10.35	-0.23074888	0.02505409	-3.99546742	6.98E-05	-0.05666806	0.01717755	-0.97027204	0.32291641	-4.99737768	0.00069335	6.98E-05	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales_Ruminococales	226	667	3.15742189	-0.08472789	0.05614037	-1.76982137	0.07710004	0.10081371	0.02779469	3.84460213	0.00031451	3.95787863	7.69E-05	7.69E-05	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	680	214	7.74860759	-0.22827493	0.07574602	-3.96645904	7.89E-05	-0.03718482	0.01878266	-1.3118472	0.18917669	-3.7892975	0.00019077	7.98E-05	
188565X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	227	656	77.85283275	-0.21742973	0.05489693	-3.96499904	7.94E-05	0.00028130	0.01137719	0.302008	0.17194648	-2.1457722	0.01125918	7.94E-05	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	426	417	14.84889472	-0.18810889	0.04889419	-4.09176817	1.43E-05	0.00768029	0.01189173	1.86477967	0.01044761	-2.9944814	0.00037727	1.43E-05	
840804X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	363	526	11.41581881	-0.07893732	0.04613203	-1.95886859	0.11706818	0.07154168	0.04825756	3.9165247	0.00000553	3.81617103	0.00000031	0.0001	
279370X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	226	657	24.26179694	-0.21118924	0.05412851	-3.87766693	0.00011310	-0.01174178	0.01051033	-1.11661178	0.26475751	-1.51737004	0.00041930	0.0001	
174645X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	18	875	13.1022871	-0.2635472	0.01911887	-4.0142198	0	0	0	0	0	0	0	0	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	826	67	10.28865472	-0.35141987	0.05144654	-3.84288183	0.00013027	0.05241671	0.01739884	1.46032059	0.00043066	-1.72521392	0.00497494	0.0001	
4172061X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	9	884	58.5070721	0	0	0	0	0	0	0	0	0	0	0	
317814X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	196	607	6.62072704	-0.17710526	0.05849698	-3.62491799	0.00255841	-0.04861931	0.02077709	-2.38359705	0.01741805	-1.81428129	0.00013628	0.0001	
101731X_Bacteroidetes_Firmicutes_Clostridia_Clostridiales	44	849	41.70789164	-0.17159214	0.03188641	-3.18866041	0.00087629	-0.02348117	-0.0573179	0.9300					

Online Table IV. OTUs associated with HDL at FDR < 0.05 level

OTU	Summary of OTUs reads			Binary Model				Quantitative model				Meta Analysis		Final P value
	No. Absent	No. Present	meanCountsInPresents	Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value	Meta P value	
193129;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	177	716	29.21927374	0.018331026	0.032	0.564057	0.57286	0.03984	0.007	5.8651	6.88E-09	4.4956	6.94E-06	6.88E-09
295743;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	507	386	37.8626943	0.122685905	0.026	4.733554	2.57E-06	0.02005	0.009	2.35404	0.019076	4.9828	6.27E-07	6.27E-07
175962;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	814	79	6.658227848	0.223957556	0.045	4.985222	7.44E-07	-0.0303	0.03	-1.00598	0.317662	2.7932	0.0052188	7.44E-07
113051;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mgibacteriaceae(Clostridiales)	508	385	4.314285714	-0.12083975	0.026	-4.65974	3.65E-06	0.01236	0.015	0.83048	0.406791	-2.688	0.0071978	3.65E-06
4368791;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	521	372	18.87634409	0.118317674	0.026	4.524347	6.88E-06	0.02053	0.011	1.83527	0.067273	4.474	7.68E-06	6.88E-06
337551;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae	410	483	9.472049689	0.116365873	0.026	4.498691	7.75E-06	-0.0005	0.012	-0.03848	0.96932	3.1351	0.0017182	7.75E-06
584417;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	466	427	29.37470726	0.097383288	0.026	3.78927	0.00016	0.02068	0.009	2.41863	0.016	4.3713	1.24E-05	1.24E-05
4437359;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	240	653	16.13782542	0.096066021	0.029	3.325076	0.00092	0.02543	0.009	2.87733	0.004143	4.3706	1.24E-05	1.24E-05
317749;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	543	350	5.908571429	0.11175989	0.026	4.269655	2.17E-05	0.0271	0.015	1.83592	0.067228	4.297	1.73E-05	1.73E-05
42458;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	693	200	3.59	0.070718932	0.031	2.286521	0.02346	0.08481	0.023	3.6213	0.000374	4.1299	3.63E-05	3.63E-05
173927;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	535	358	4.695530726	0.106889805	0.026	4.088196	4.74E-05	-0.009	0.016	-0.55498	0.579258	2.4844	0.0129752	4.74E-05
2251911;k_Bacteria;p_Actinobacteria;c_Coribacteriales;o_Coribacteriales;f_Coribacteriaceae;f_Eggerthella	435	458	16.80786026	-0.079963225	0.026	-3.10686	0.00195	-0.0218	0.008	-2.57326	0.010392	-4.002	6.27E-05	6.27E-05
183187;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	442	451	8.490022173	0.082655619	0.026	3.220094	0.00132	0.03198	0.013	2.40295	0.01667	3.9639	7.37E-05	7.37E-05
4299281;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	478	415	29.39036145	0.101014626	0.026	3.93547	8.95E-05	0.00372	0.009	0.39325	0.694338	3.0479	0.0023047	8.95E-05
4329572;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	659	234	2.525641026	0.113346572	0.029	3.898278	0.0001	0.03632	0.026	1.37324	0.171015	3.712	0.0002056	0.0001042
334023;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	858	35	35.82857143	0.153900681	0.066	2.318709	0.02064	0.1176	0.034	3.41094	0.001818	3.8418	0.0001222	0.0001222
289562;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	833	60	11.25	0.196011066	0.051	3.823676	0.00014	0.02262	0.031	0.72944	0.468772	3.2042	0.0013542	0.0001407
1144764;k_Bacteria;p_Tenericutes;c_Mollicutes;o_RF39	819	74	30.16216216	0.164267233	0.047	3.529651	0.00044	0.03784	0.021	1.8125	0.074197	3.7489	0.0001776	0.0001776
179664;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	282	611	119.8772504	0.066338916	0.028	2.395923	0.01678	0.0174	0.006	2.89692	0.003904	3.7315	0.0001903	0.0001903
278483;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mgibacteriaceae(Clostridiales;f_Lachnospiraceae)	341	552	6.128623188	0.090648156	0.026	3.43529	0.00062	0.0214	0.012	1.77002	0.077281	3.6697	0.0002429	0.0002429
192741;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	475	418	6.990430622	0.075201731	0.026	2.914949	0.00365	0.02744	0.013	2.19181	0.028949	3.6001	0.000318	0.000318
183845;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales;f_Lachnospiraceae	651	242	4.842975207	0.103503442	0.029	3.578355	0.00036	0.01852	0.021	0.87148	0.384373	3.1356	0.001715	0.0003645
581201;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	706	187	2.550802139	0.112899977	0.032	3.571211	0.00037	-0.0318	0.029	-1.09585	0.274583	1.743	0.0813406	0.0003744
182031;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	94	799	210.9148936	0.079620105	0.042	1.888973	0.05922	0.01438	0.005	3.08755	0.002088	3.51	0.000448	0.000448
44502124;k_Bacteria;p_Firmicutes;c_Bacillo_Lactobacillales;f_Streptococcales;f_Streptococcus	600	293	4.436860968	-0.073469638	0.027	-2.68752	0.00733	-0.0353	0.015	-2.28411	0.023093	-3.502	0.000461	0.000461
178759;k_Bacteria;p_Tenericutes;c_RF3_o_ML6151-28	813	80	4.85	0.140080873	0.045	3.109324	0.00193	0.0629	0.034	1.86792	0.065628	3.4938	0.0004762	0.0004762
307180;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	813	80	3.3375	0.143205532	0.045	3.188739	0.00148	0.06731	0.038	1.77308	0.080222	3.4847	0.0004926	0.0004926
34413;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae	198	695	6.509352518	0.106717445	0.031	3.466451	0.00055	-0.0021	0.013	-0.16834	0.866366	2.3232	0.0201661	0.0005527
13997;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blaustia	767	126	8.396825397	-0.115002791	0.037	-3.12404	0.00184	-0.0324	0.018	-1.781	0.077402	-3.451	0.0005583	0.0005583
2631109;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcales	410	483	24.79917184	0.088650446	0.026	3.43626	0.00062	0.00853	0.01	0.87183	0.383736	3.037	0.0023893	0.0006172
334864;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	832	61	8.901639344	0.174417751	0.051	3.430814	0.00063	0.02239	0.031	0.7263	0.47063	2.9274	0.0034177	0.0006295
590980;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales	692	201	3.417910448	0.105153609	0.031	3.428499	0.00063	0.02507	0.025	1.01158	0.312978	3.1291	0.0017532	0.0006348
295100;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae	675	218	9.247706422	0.102173935	0.03	3.412629	0.00067	0.01186	0.016	0.73475	0.463298	2.9232	0.0034649	0.0006725
1177803;k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Phytothecococcales;f_Mgibacteriaceae(Clostridiales)	655	238	4.714285714	0.072363682	0.029	2.475191	0.0135	0.04241	0.018	2.33196	0.020552	3.3845	0.0007132	0.0007132

Online Table V. Associated Taxonomies at FDR < 0.05 level.

A. Association with BMI

No	Taxonomy	Summary of OTUs reads			Binary Model				Quantitative model				Meta Analysis		Asso. Z value	Asso. P value	Replication in Goodrich et al Cell 2014			
		No. Absent	No. Present	mean/Counting	Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value	Meta P value			BMI p-value	BMI q-value	higher in	Replicated (same direction)?
1	k__Archaea	388	505	358.73267	0.55549	0.275	-2.01832	0.0488576	0.142	0.05132	-2.667059	0.0079	3.303	0.000955	-3.30445	0.000955	0.01111	0.0090523	Lean	yes
2	k__Bacteria__Actinobacteria__Coriobacteriia__Coriobacteriales__Coriobacterium__Coriobacterium	623	70	22.8	0.65224	0.5	1.30461	0.1923625	0.144	0.22461	0.509454	0.6121	1.2803	0.200431	1.303623	0.192363	na	na	na	na
3	k__Bacteria__Actinobacteria__Coriobacteriia__Coriobacteriales__Coriobacterium__Aggrius	435	458	16.80786	0.36538	0.27	1.35266	0.1765096	0.1817	0.0934	1.945107	0.0524	2.3275	0.0199386	2.527502	0.019939	0.03094	0.0489024	Obese	na
4	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales	2	891	1100.3726	0	0	0	1	-0.211	0.07675	-2.743257	0.0062	-1.935	0.0529738	-2.73669	0.006206	0.96374	0.9659907	Lean	na
5	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidia__Bacteroides	5	888	407.75563	0	0	0	1	-0.09	0.06543	-1.374341	0.1697	0.971	0.3315418	-1.37322	0.169684	0.25619	0.452895	Obese	na
6	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidia__Bifidobacteriales	34	859	110.97206	1.22304	0.702	-1.74289	0.0816977	0.184	0.06634	-2.771448	0.0057	3.186	0.0014337	-3.18577	0.001444	na	na	na	na
8	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidia__Oribacteriales	219	674	10.047478	0.70765	0.312	-2.26976	0.0234606	0.281	0.09376	-2.993717	0.0029	3.711	0.0002062	-3.71126	0.000206	0.09847	0.2501123	Lean	na
9	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__Oribacteriales__Bacteroides	410	483	7.132594	0.70155	0.269	-2.60651	0.0093	0.203	0.11963	-1.788543	0.0743	-3.101	0.0019288	-3.10099	0.001929	0.01111	0.0487732	Lean	yes
10	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__Oribacteriales__Oribacterium	316	577	5.7712305	-0.7628	0.281	-2.71656	0.0067245	-0.213	0.11305	-1.887461	0.0596	3.248	0.0016006	-3.24838	0.001601	0.4991	0.6787126	Lean	no
11	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__Bifidobacteriales	125	768	39.302083	-1.96141	0.382	-5.13159	3.53E-07	-0.123	0.06672	-1.8435	0.0656	4.903	9.45E-07	-5.09276	3.53E-07	0.00042	0.0048162	Lean	no
12	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__S24.7	658	235	104	-0.13883	0.311	-0.44679	0.6551338	0.0053	0.0895	0.058857	0.9531	0.274	0.7838023	0.46664	0.655134	na	na	na	na
6	k__Bacteria__Bacteroidetes__Bacteroidia__Bacteroidales__S24.7__Bifidobacteriales	169	724	32.164365	1.38817	0.34	-0.08314	4.84E-05	0.0261	0.0739	0.353089	0.7241	2.623	0.0087048	-4.06305	4.84E-05	na	na	na	na
13	k__Bacteria__Cyanobacteria	429	464	12.336207	0.83649	0.269	-3.11308	0.0019107	0.02	0.09551	-0.201665	0.8403	2.337	0.0194278	-3.10378	0.001911	0.08209	0.1999995	Lean	na
14	k__Bacteria__Firmicutes__Bacilli__Gemmatimonadetes__Bacillales	524	369	2.9691599	0.86606	0.272	-3.18725	0.0014865	0.1332	0.20317	0.655495	0.5126	2.7097	0.0067335	-3.177304	0.001487	na	na	na	na
18	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Christensenellales	232	661	38.255673	-1.15395	0.308	-3.74953	0.0001886	-0.221	0.06884	-3.203697	0.0014	4.896	9.79E-07	-4.89591	9.79E-07	1.4E-05	0.001262	Lean	yes
19	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Clostridiales	84	809	11.820766	1.97282	0.459	-4.29898	1.91E-05	0.144	0.09265	-1.551265	0.1212	4.119	3.80E-05	-4.27669	1.91E-05	0.03398	0.109537	Lean	yes
20	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Clostridiales__O2006	399	494	6.194332	0.63374	0.273	-2.32201	0.0204576	0.096	0.11774	0.815897	0.4127	1.06	0.289279	-2.31785	0.020458	0.02320	0.0870564	Lean	na
16	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Clostridiales__Lachnospiraceae	841	52	26.480769	0.82703	0.577	1.43435	0.1518249	0.158	0.29305	-0.539179	0.5923	0.6347	0.5256501	1.433115	0.151825	na	na	na	na
21	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Dehalobacteriaceae__Dehalobacterium	612	281	2.8398577	0.92868	0.288	-3.21917	0.0013322	0.2352	0.1993	1.180252	0.2389	1.436	0.1509167	-3.20895	0.001332	1.2E-05	0.0013899	Lean	yes
22	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae	1	892	162.47534	0	0	0	1	0.5962	0.16716	3.566374	0.0004	2.5121	0.0120001	-3.552703	0.000381	0.00384	0.0224942	Obese	yes
23	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae__Blautia	51	842	8.965057	0.83747	0.579	1.44625	0.1484588	0.2827	0.10553	2.679315	0.0075	2.9117	0.0039944	-2.911726	0.003994	0.01068	0.0478067	Obese	yes
14	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae__Coprococcus	414	479	6.565762	0.28385	0.274	-1.03594	0.3005114	-0.108	0.1313	-0.8237	0.4105	1.314	0.1888383	-1.31402	0.188838	0.06599	0.1728847	Obese	na
25	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae__Lachnospira	181	712	24.563202	-0.74132	0.334	-2.21794	0.026811	0.0748	0.07709	0.970723	0.332	0.88	0.3789766	-2.21426	0.026811	1.8E-05	0.000463	Lean	na
15	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Moryella__Moryella__Lachnospiraceae	341	552	6.1286232	-0.75558	0.276	-2.73381	0.006385	-0.176	0.12198	-1.442962	0.1496	2.947	0.0032045	-2.94741	0.003205	na	na	na	na
17	k__Bacteria__Firmicutes__Clostridia__Clostridiales__Moryella__Moryella__Lachnospiraceae	655	238	4.7142857	-0.97996	0.305	-3.21463	0.0013532	-0.064	0.16365	-0.391057	0.6961	2.542	0.01102	-3.20445	0.001353	na	na	na	na
26	k__Bacteria__Firmicutes__Euryarchaeota__Euryarchaeota__Euryarchaeota__Euryarchaeota__Euryarchaeota	303	590	13.142373	0.81877	0.283	-2.89079	0.0039363	-0.106	0.0928	-1.141882	0.2541	2.845	0.0044377	-2.88322	0.003936	0.03923	0.1202065	Lean	yes
27	k__Bacteria__Firmicutes__Euryarchaeota__Euryarchaeota__Euryarchaeota__Euryarchaeota__Euryarchaeota	312	581	3.0791738	0.61668	0.282	-2.18677	0.0289532	-0.095	0.14963	-0.631966	0.5277	1.0978	0.2728668	-2.184123	0.028953	0.72728	0.8903074	Obese	na
28	k__Bacteria__Proteobacteria__Betaproteobacteria__Burkholderiales__Hofmanniellales	574	319	4.462815	-1.13397	0.279	-4.06053	3.33E-05	0.266	0.15556	-1.708398	0.0885	4.062	4.88E-05	-4.06513	4.88E-05	na	na	na	na
30	k__Bacteria__Proteobacteria__Betaproteobacteria__Oribacteriales__Oribacteriales__Oribacterium	194	699	25.858369	0.96695	0.325	-2.97563	0.0030003	-0.002	0.07532	-0.021299	0.983	2.113	0.0345712	-2.96743	0.003003	0.73611	0.8667375	Obese	na
29	k__Bacteria__Proteobacteria__Betaproteobacteria__Oribacteriales__Oribacteriales__Oribacterium	309	584	11.383562	-0.90382	0.283	-3.18835	0.0014809	-0.01	0.09419	-0.111219	0.9116	2.326	0.0200178	-3.1784	0.001481	0.12497	0.2597026	Obese	na
31	k__Bacteria__Proteobacteria__Gammaproteobacteria	467	426	36.5	-0.32004	0.269	-1.1878	0.2352283	0.0747	0.08862	0.841296	0.3995	0.244	0.8075108	-1.187	0.235228	0.87708	0.9457519	Obese	na
32	k__Bacteria__Proteobacteria__Gammaproteobacteria__Pasteurellales__Pasteurellales	538	355	15.467606	0.44765	0.274	-1.6314	0.101161	0.1084	0.11432	0.948472	0.3435	0.483	0.6293654	-1.62972	0.101161	0.04855	0.1138688	Lean	na
13	k__Bacteria__Tenericutes	323	570	90.261404	-1.04539	0.281	-3.73863	0.0002129	-0.083	0.06531	-1.272254	0.2038	3.517	0.0004362	-3.70325	0.000213	6.6E-07	1.532E-05	Lean	yes
34	k__Bacteria__Tenericutes__Tenericutes__Tenericutes__Tenericutes__Tenericutes	245	648	282.80401	-0.57871	0.304	-1.90288	0.0573794	-0.147	0.04887	-3.009647	0.0027	3.464	0.0005328	-3.46369	0.000533	0.03277	0.101414	Lean	yes

B. Association with TG

No	Taxonomy	Summary of OTUs reads			Association with TG											
					Binary Model				Quantitative model			Meta Analysis		Asso. Z value	Asso. P value	
		No. Absent	No Present	meanCounts/Presents	Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value			Meta P value
1	k_Archaea	388	505	358.7326733	-0.031873486	0.04970027	-0.641314	0.521484	-0.031034	0.01005	-3.087107	0.0021333	-2.62483	0.00866918	-3.071013	0.002133
2	k_Bacteriophyta	823	70	22.8	0.239065921	0.089767865	2.663157	0.007881	0.087195	0.03879	2.247853	0.0279322	3.433252	0.00059639	3.433252	0.000596
3	k_Bacteriophyta	435	458	16.80786026	0.198117942	0.04825651	4.1055174	4.41E-05	0.029459	0.01712	1.720466	0.0860306	4.102494	4.09E-05	4.102494	4.09E-05
4	k_Bacteriophyta	2	891	1100.372615	0	0	0	1	-0.063453	0.01366	-4.64663	3.89E-06	-3.26499	0.00109469	-4.617389	3.89E-06
5	k_Bacteriophyta	34	859	110.9720605	-0.233515756	0.128155448	-1.822129	0.068772	-0.031233	0.01206	-2.590027	0.0097602	-3.11419	0.00184451	-3.11419	0.001845
6	k_Bacteriophyta	169	724	32.16436464	-0.222027892	0.061491765	-3.610693	0.000322	-0.002757	0.0132	-0.208848	0.8346261	-2.69076	0.007129	-3.596534	0.000322
7	k_Bacteriophyta	5	888	407.7556306	0	0	0	1	-0.035561	0.01172	-3.033716	0.0024863	-2.139	0.03243586	-3.024999	0.002486
8	k_Bacteriophyta	219	674	10.04747774	-0.173269955	0.056016681	-3.093185	0.002042	-0.053708	0.01703	-3.153657	0.0016845	-4.40166	1.07E-05	-4.401663	1.07E-05
9	k_Bacteriophyta	410	483	7.126293996	-0.182801929	0.048294166	-3.785176	0.000164	-0.055813	0.02053	-2.718839	0.0067894	-4.57921	4.67E-06	-4.57921	4.67E-06
10	k_Bacteriophyta	316	577	5.771230503	-0.153492833	0.050525733	-3.037914	0.002452	-0.030771	0.02027	-1.518288	0.1294942	-3.21402	0.0013089	-3.214021	0.001309
11	k_Bacteriophyta	125	768	39.30208333	-0.23249752	0.069412471	-3.349506	0.000844	-0.014161	0.01222	-1.158849	0.2468802	-3.17917	0.00147699	-3.33806	0.000844
12	k_Bacteriophyta	658	235	104	-0.145474903	0.055750961	-2.60937	0.009224	-0.032007	0.01656	-1.823798	0.0694747	-3.12469	0.00177994	-3.124688	0.001779
13	k_Bacteriophyta	429	464	12.3362069	-0.138333805	0.048455185	-2.854881	0.004406	0.007312	0.01838	0.397871	0.6909099	-1.73237	0.08320769	-2.847562	0.004406
14	k_Bacteriophyta	524	369	2.989159892	0.068459431	0.049179484	1.3920323	0.164261	0.127423	0.03506	3.634305	0.0003187	3.528802	0.00041745	3.599597	0.000319
15	k_Bacteriophyta	341	552	6.128623188	-0.142927333	0.049771082	-2.871694	0.004418	-0.020779	0.02174	-0.955723	0.3396342	-2.70054	0.00692266	-2.864255	0.004418
16	k_Bacteriophyta	841	52	26.48076923	0.019646294	0.103952459	0.1889931	0.850141	-0.050124	0.041	-1.222448	0.2275071	-0.71974	0.47168448	-1.206805	0.227507
17	k_Bacteriophyta	655	238	4.714285714	-0.018680005	0.055220341	-0.33839	0.735149	-0.04216	0.03271	-1.288963	0.1986339	-1.14805	0.25094614	-1.28531	0.198684
18	k_Bacteriophyta	232	661	38.25567322	-0.207634965	0.055510036	-3.740494	0.000195	-0.028444	0.01238	-2.2973	0.0219152	-4.25443	2.10E-05	-4.254429	2.10E-05
19	k_Bacteriophyta	84	809	11.82076638	-0.089573123	0.083857894	-1.068154	0.285741	-0.029917	0.01699	-1.760686	0.0786712	-1.99825	0.04568906	-1.998255	0.045689
20	k_Bacteriophyta	399	494	6.194331984	-0.138746841	0.04909921	-2.825847	0.004821	-0.028931	0.02182	-1.325821	0.1855168	-2.92932	0.003397	-2.929324	0.003397
21	k_Bacteriophyta	612	281	2.839857651	-0.049643503	0.052238925	-0.950316	0.342211	0.047951	0.04026	1.191024	0.2346639	0.168732	0.8660757	1.18843	0.234664
22	k_Bacteriophyta	1	892	162.4753363	0	0	0	1	0.076232	0.03025	2.519944	0.0119119	1.778192	0.07537238	2.514743	0.011912
23	k_Bacteriophyta	51	842	8.956057007	0.174056271	0.104240734	1.6697529	0.095321	0.067328	0.01896	3.551936	0.0004038	3.6809	0.00023241	3.6809	0.000232
24	k_Bacteriophyta	414	479	6.565762004	-0.200419653	0.048957273	-4.093767	4.63E-05	-0.016482	0.02314	-0.712148	0.4762735	-3.38357	0.00071551	-4.073501	4.63E-05
25	k_Bacteriophyta	181	712	24.56320225	-0.256516089	0.059751151	-4.293074	1.96E-05	-0.017697	0.01317	-1.343248	0.1796229	-3.96811	7.24E-05	-4.269845	1.96E-05
26	k_Bacteriophyta	303	590	13.14237288	-0.018201919	0.051303452	-0.354789	0.722832	-0.003904	0.0171	-0.228289	0.8195013	-0.41215	0.68023193	-0.412147	0.680232
27	k_Bacteriophyta	312	581	3.079173838	0.139203541	0.050703606	2.7454367	0.006165	0.04176	0.02843	1.469119	0.1423466	2.974074	0.00239875	2.974074	0.002399
28	k_Bacteriophyta	574	319	4.460815047	-0.157246343	0.05049469	-3.114116	0.001904	-0.055273	0.03041	-1.817483	0.0700931	-3.47621	0.00050856	-3.476207	0.000509
29	k_Bacteriophyta	194	699	25.8583691	-0.090380776	0.058741052	-1.538631	0.124251	-0.015322	0.01392	-1.101052	0.271256	-1.86489	0.06219723	-1.864887	0.062197
30	k_Bacteriophyta	309	584	11.38356164	-0.0111639	0.051346578	-0.256373	0.797722	-0.009998	0.01786	-0.559699	0.5759013	-0.57677	0.56409377	-0.576772	0.564094
31	k_Bacteriophyta	467	426	36.5	-0.153559956	0.048315151	-3.178298	0.001533	-0.029222	0.014	-2.087271	0.0374645	-3.71167	0.0002059	-3.711667	0.000206
32	k_Bacteriophyta	538	355	15.46760563	-0.197553312	0.049081246	-4.025026	6.18E-05	-0.024457	0.01674	-1.460777	0.1449738	-3.86309	0.00011196	-4.005721	6.18E-05
33	k_Bacteriophyta	323	570	90.26140351	-0.260678392	0.05028562	-5.183955	2.69E-07	-0.014884	0.01153	-1.291312	0.1971237	-4.54932	5.38E-06	-5.14392	2.69E-07
34	k_Bacteriophyta	245	648	282.8040123	-0.020267247	0.054891488	-0.369224	0.712049	-0.02419	0.00916	-2.641565	0.008453	-2.1231	0.0337451	-2.633417	0.008453

C. Association with HDL

No	Taxonomy	Summary of OTUs reads			Association with HDL											
		No. Absent	No. Present	Count/Prevalence	Binary Model			Quantitative model			Meta Analysis		Asso. Z value	Asso. P value		
					Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value			Meta Z value	Meta P value
1	k__Archaea	388	505	358.73267	0.029222	0.0264	1.10731	0.2684619	0.0085207	0.0056	1.5168	0.129939	1.8533	0.06384	1.8532947	0.0638401
2	k__Bacteria_p__Actinobacteria_c__Coriobacteriia_o__Coriobacteriales_f__Co	823	70	22.8	-0.05037	0.0478	-1.0527	0.2927651	0.0061629	0.0215	0.2871	0.774972	-0.542	0.587968	-1.052075	0.2927651
3	k__Bacteria_p__Actinobacteria_c__Coriobacteriia_o__Coriobacteriales_f__Co	435	458	16.80786	-0.07996	0.0257	-3.1069	0.001951	-0.021842	0.0085	-2.5733	0.010392	-4.002	6.27E-05	4.002297	6.27E-05
4	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales	2	891	1100.3726	0	0	0	1	0.0176423	0.0074	2.3951	0.016821	1.6904	0.090949	2.3906027	0.0168207
5	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroi	34	859	110.97206	0.039644	0.0682	0.58134	0.5611593	0.0032455	0.0065	0.4983	0.618384	0.7632	0.445372	0.763154	0.4453716
6	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__S24-7/Ba	169	724	32.164365	0.058767	0.0328	1.78919	0.0739247	-0.012005	0.0074	-1.6142	0.106926	0.1237	0.901566	1.7870791	0.0739247
7	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroi	5	888	407.75563	0	0	0	1	0.0135655	0.0063	2.1579	0.031202	1.5235	0.127646	2.154487	0.031202
8	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Odoriba	219	674	10.047478	0.037017	0.0299	1.23837	0.215907	0.0198754	0.0094	2.121	0.03429	2.3717	0.017705	2.3717319	0.0177049
9	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Odoriba	410	483	7.126294	0.063726	0.0258	2.47262	0.013599	0.0112126	0.0119	0.9446	0.345319	2.4122	0.015856	2.4676839	0.013599
10	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Odoriba	316	577	5.7712305	0.036532	0.027	1.35546	0.1756157	0.0154917	0.0113	1.3682	0.171787	1.9239	0.054362	1.9239399	0.0543621
11	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenella	125	768	39.302083	0.056229	0.037	1.77181	0.0767687	0.0056321	0.0067	0.8399	0.401215	1.845	0.06504	1.8449854	0.0650397
12	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__S24-7	658	235	104	0.03023	0.0297	1.01741	0.3092335	-0.005317	0.01	-0.5306	0.596175	0.3443	0.730616	1.0168317	0.3092335
13	k__Bacteria_p__Cyanobacteria	429	464	12.336207	0.055553	0.0258	2.15394	0.0315133	0.0063305	0.0098	0.6473	0.517766	1.978	0.047928	2.1505299	0.0315133
14	k__Bacteria_p__Firmicutes_c__Bacilli_o__Gemellales/Bacillales	524	369	2.9891599	-0.00395	0.0262	-0.1509	0.8801077	-0.03484	0.0174	-2.0041	0.045795	-1.519	0.128776	-1.9972813	0.0457946
15	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Mogibacteriace	341	552	6.1286232	0.090648	0.0264	3.43529	0.0006194	0.0213975	0.0121	1.77	0.077281	3.6697	0.000243	3.6696563	0.0002429
16	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae/f	841	52	26.480769	-0.07073	0.0552	-1.282	0.200164	0.0236992	0.0225	1.054	0.297177	-0.169	0.866032	-1.2810846	0.200164
17	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Peptostreptoco	655	238	4.7142857	0.072364	0.0292	2.47519	0.0135022	0.0424122	0.0182	2.332	0.020552	3.3845	0.000713	3.3844619	0.0007132
18	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Christensenella	232	661	38.255673	0.030382	0.0297	1.0229	0.3066352	0.0203002	0.0068	2.9839	0.002951	2.8249	0.004729	2.9727634	0.0029513
19	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae	84	809	11.820766	0.073237	0.0445	1.64547	0.1002273	-0.004459	0.0092	-0.4842	0.628346	0.82	0.412199	1.6437525	0.1002273
20	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae	399	494	6.194332	0.068515	0.0261	2.62522	0.0088082	-0.020476	0.0125	-1.64	0.101643	0.6947	0.487235	2.6194105	0.0088082
21	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Dehalobacteria	612	281	2.8398577	0.020734	0.0278	0.74701	0.4552546	0.0183758	0.0234	0.7837	0.433891	1.0813	0.27955	1.0813314	0.2795497
22	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae	1	892	162.47534	0	0	0	1	-0.006431	0.0161	-0.3987	0.690234	-0.282	0.77809	-0.3985382	0.6902335
23	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae	51	842	8.956057	-0.03594	0.0554	-0.6482	0.5170312	-0.017523	0.01	-1.7576	0.079318	-1.699	0.089233	-1.755465	0.0791798
24	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae	414	479	6.565762	0.069521	0.0261	2.65877	0.0079837	-0.008081	0.0131	-0.6161	0.538117	1.4404	0.149742	2.6527596	0.0079837
25	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae	181	712	24.563202	0.037279	0.032	1.16334	0.2450059	0.0061753	0.0074	0.8333	0.404937	1.411	0.158256	1.4109616	0.1582559
26	k__Bacteria_p__Firmicutes_c__Erysipelotrichi_o__Erysipelotrichales_f__Erysi	303	590	13.142373	-0.01526	0.0273	-0.5599	0.5756993	0.0029155	0.009	0.3233	0.746591	-0.167	0.867166	-0.5596777	0.5756993
27	k__Bacteria_p__Firmicutes_c__Erysipelotrichi_o__Erysipelotrichales_f__Erysi	312	581	3.0791738	-0.08626	0.0269	-3.2073	0.0013878	-0.002619	0.0136	-0.1925	0.847429	-2.397	0.016539	-3.1971864	0.0013878
28	k__Bacteria_p__Proteobacteria_c__Betaproteobacteria_o__Burkholderiales/f	574	319	4.460815	0.064251	0.0269	2.38995	0.0170583	0.031191	0.0168	1.8617	0.065581	2.9985	0.002713	2.9985243	0.0027129
29	k__Bacteria_p__Proteobacteria_c__Deltaproteobacteria_o__Desulfuovibrionia	194	699	25.858369	0.050299	0.0312	1.6121	0.1072946	-0.003298	0.0075	-0.4374	0.661945	0.8296	0.40676	1.6104733	0.1072946
30	k__Bacteria_p__Proteobacteria_c__Deltaproteobacteria_o__Desulfuovibrionia	309	584	11.383562	0.062805	0.0272	2.30934	0.0211535	-0.018021	0.0096	-1.8867	0.059699	0.2986	0.765279	2.3052341	0.0211535
31	k__Bacteria_p__Proteobacteria_c__Gammaproteobacteria	467	426	36.5	0.066791	0.0257	2.59742	0.0095482	0.0002591	0.008	0.0325	0.974087	1.8556	0.063506	2.5917742	0.0095482
32	k__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Pasteurellales	538	355	15.467606	0.078975	0.0262	3.01706	0.0026252	0.000774	0.0101	0.077	0.93868	2.1817	0.029128	3.0085291	0.0026252
33	k__Bacteria_p__Tenericutes	323	570	90.261404	0.064681	0.027	2.3932	0.0169091	0.0158099	0.0065	2.449	0.014628	3.4154	0.000637	3.4154259	0.0006368
34	k__Bacteria_p__Verrucomicrobia_c__Verrucomicrobiae_o__Verrucomicrobia	245	648	282.80401	-0.03369	0.0291	-1.1561	0.2479695	0.010003	0.0049	2.0354	0.042215	0.6195	0.535592	2.0313902	0.0422154

D. Association with LDL

No	Taxonomy	Summary of OTUs reads			Association with LDL											
		No. Absent	No. Present	meanCountInPresent	Binary Model				Quantitative model				Meta Analysis		Asso. Z value	Asso. P value
					Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value	Meta P value		
1	k__Archaea	388	505	358.7926733	0.08532	0.05862	1.455503	0.145883	0.014	0.01198	1.12868	0.25957429	1.825484	0.067928	1.825484	0.067928
2	k__Bacteria__Actinobacteria__Coriobacteriia__Coriobacteriales__Coriobacteraceae__Coffeinivibrio	823	70	22.8	0.18903	0.10621	1.779696	0.075468	0.051	0.04592	1.104029	0.27358837	2.031126	0.042242	2.031126	0.042242
3	k__Bacteria__Actinobacteria__Coriobacteriia__Coriobacteriales__Coriobacteraceae__Eggerthella	435	458	16.80786026	0.11134	0.05739	1.940087	0.052685	0.006	0.01989	0.320942	0.74840228	1.596815	0.110307	1.9374909	0.052685
4	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales	2	891	1100.372615	0	0	0	1	-0.032	0.01638	-1.928613	0.05409814	-1.361923	0.173222	-1.92605	0.054098
5	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	34	859	110.9720605	0.22043	0.1514	1.455932	0.145765	-0.034	0.01443	-2.344312	0.01929028	-0.625944	0.531352	-2.339873	0.01929
6	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	169	724	32.16436464	-0.00311	0.07313	-0.042513	0.966099	-0.017	0.01654	-1.05436	0.29207175	-0.775052	0.438309	-1.053358	0.292072
7	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	5	888	407.7556306	0	0	0	1	-0.014	0.01398	-1.034811	0.3010403	-0.731293	0.4646	-1.034205	0.30104
8	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	219	674	10.04747774	-0.07771	0.06644	-1.169692	0.242439	-0.045	0.02047	-2.190746	0.02881446	-2.372292	0.017678	-2.372292	0.017678
9	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	410	483	7.126293996	-0.10736	0.05736	-1.871629	0.061586	-0.062	0.02538	-2.426796	0.0156015	-3.031627	0.002432	-3.031627	0.002432
10	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	316	577	5.771230503	-0.09969	0.05987	-1.665163	0.096233	-0.019	0.0245	-0.768143	0.44271924	-1.718981	0.085618	-1.718981	0.085618
11	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	125	768	39.30208333	-0.03399	0.08246	-0.412226	0.680273	0.018	0.01489	1.185475	0.23619877	0.546206	0.584925	1.1845415	0.236199
12	k__Bacteriap__Bacteroidetes__Bacteroidia__Bacteroidales__Bacteroidales__Bacteroidaceae	658	235	104	-0.06647	0.06603	-1.006612	0.314395	-0.028	0.0198	-1.404966	0.1613747	-1.701656	0.08882	-1.701656	0.08882
13	k__Bacteriap__Cyanobacteria	429	464	12.3362069	-0.09468	0.05738	-1.650018	0.099293	0.012	0.02264	0.551303	0.58169438	-0.775965	0.43777	-1.648291	0.099293
14	k__Bacteriap__Firmicutes__Bacilli__Gemmatimonadetes__Gemmatimonadetes	524	369	2.989159892	0.02533	0.05812	0.435749	0.663125	0.003	0.04084	0.074684	0.94905076	0.360791	0.178256	0.4356032	0.663125
15	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Mollicutes__Mollicutes	341	552	6.128623188	-0.06359	0.05899	-1.077971	0.28134	-0.029	0.02657	-1.094487	0.274223	-1.534919	0.124804	-1.534919	0.124804
16	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Clostridiales__Lachnospiraceae	841	52	26.48076923	0.38113	0.12206	3.122418	0.001852	0.18	0.07179	2.51094	0.01546218	3.913406	9.10E-05	3.9134057	9.10E-05
17	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Mollicutes__Mollicutes	655	238	4.714285714	0.00602	0.0652	0.092368	0.926427	-0.103	0.04039	-2.545515	0.0115547	-1.720474	0.085346	-2.52546	0.011555
18	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Christensenellaceae	232	661	38.25567322	-0.00814	0.06605	-0.123174	0.901998	0.003	0.01539	0.197543	0.84346402	0.052557	0.958085	0.1974646	0.843464
19	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Clostridiales	84	809	11.82076638	0.14736	0.09894	1.489347	0.136751	0.027	0.02051	1.320646	0.18699491	1.985217	0.04712	1.985217	0.04712
20	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Clostridiales__Lachnospiraceae	399	494	6.194331984	0.04373	0.05821	0.751291	0.452677	0.053	0.02773	1.920841	0.05533171	1.886011	0.059293	1.9162624	0.055332
21	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Clostridiales__Lachnospiraceae	612	281	2.839857651	0.07698	0.06165	1.248603	0.21214	0.023	0.04718	0.48349	0.62912974	1.223759	0.221043	1.2477039	0.21214
22	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae	1	892	162.4753363	0	0	0	1	-0.078	0.03576	-2.176524	0.02977923	-1.536553	0.124403	-2.173014	0.029779
23	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae__Blautia	51	842	8.956057007	-0.05312	0.12325	-0.430973	0.666593	-0.007	0.02227	-0.326275	0.74429768	-0.535277	0.592458	-0.535277	0.592458
24	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae__Coprococcus	414	479	6.565762004	-0.05132	0.05832	-0.879999	0.379098	-0.071	0.02941	-2.412324	0.01622998	-2.321617	0.020254	-2.403702	0.01623
25	k__Bacteriap__Firmicutes__Clostridia__Clostridiales__Lachnospiraceae__Lachnospira	181	712	24.56320225	-0.13729	0.07112	-1.930349	0.053882	-0.007	0.01674	-0.391297	0.69569562	-1.639726	0.101062	-1.927786	0.053882
26	k__Bacteriap__Firmicutes__Frypanobacteriia__Frypanobacteriales__Frypanobacteriaceae__Frypanobacter	303	590	13.14237288	0.08155	0.06051	1.347604	0.17813	0.035	0.02075	1.698302	0.08998164	2.151041	0.031473	2.1510409	0.031473
27	k__Bacteriap__Firmicutes__Frypanobacteriia__Frypanobacteriales__Frypanobacteriaceae__Frypanobacter	312	581	3.079173838	-3.21E-06	0.06012	-5.35E-05	0.999957	0.007	0.03204	0.218836	0.82685506	0.154632	0.877111	0.2187368	0.826855
28	k__Bacteriap__Proteobacteria__Betaproteobacteria__Burkholderiales__Rhodocyclaceae	574	319	4.460815047	-0.03585	0.05993	-0.598158	0.549887	0.041	0.03541	1.164805	0.24497944	0.399304	0.689669	1.1626305	0.244979
29	k__Bacteriap__Proteobacteria__Betaproteobacteria__Burkholderiales__Rhodocyclaceae	194	699	25.8583691	-0.04258	0.06943	-0.613296	0.539837	0.007	0.01628	0.405226	0.68543999	-0.14708	0.883069	-0.613059	0.539837
30	k__Bacteriap__Proteobacteria__Betaproteobacteria__Burkholderiales__Rhodocyclaceae	309	584	11.38356164	0.0043	0.06062	0.070891	0.9435	0.019	0.0206	0.903702	0.36652946	0.688626	0.491059	0.9029933	0.366529
31	k__Bacteriap__Proteobacteria__Gammaproteobacteria	467	426	36.5	-0.07801	0.05731	-1.361354	0.173747	-0.038	0.01761	-2.168206	0.03070248	-2.489842	0.01278	-2.489842	0.01278
32	k__Bacteriap__Proteobacteria__Gammaproteobacteria__Pasteurellales__Pasteurellaceae	538	355	15.46760563	-0.05814	0.05844	-0.994794	0.320107	-0.047	0.02243	-2.089419	0.03739165	-2.174848	0.029642	-2.174848	0.029642
33	k__Bacteriap__Tenericutes	323	570	90.26140351	-0.13584	0.06009	-2.260652	0.024022	4E-04	0.01409	0.030623	0.97558098	-1.574136	0.115456	-2.256774	0.024022
34	k__Bacteriap__Tenericutes__Mollicutes__Mollicutes	245	648	282.8040123	-0.03897	0.0648	-0.601344	0.547764	0.01	0.01094	0.877709	0.38042939	0.195156	0.845271	0.8771054	0.380429

E. Association with TC.

No	Taxonomy	Summary of OTUs reads			Association with TC											
		No. Absent	No. Present	meanCounts/Presents	Binary Model				Quantitative model				Meta Analysis		Std. Z value	Asso. P value
					Estimate	s.e.	T value	P value	Estimate	s.e.	T value	P value	Meta Z value	Meta P value		
1	k__Archaea	388	505	358.7326733	0.094513	0.0633	1.49312303	0.13576	0.0083	0.0128	0.648611	0.516887	1.5131505	0.130242	1.51315	0.13024
2	k__Bacteria_p__Actinobacteria_c__Coriobacteriales_o__Coriobacteraceae_g__Collaredactinonema	823	70	22.8	0.201735	0.1147	1.75876895	0.078961	0.09485	0.04793	1.97908	0.051981	2.6163184	0.008888	2.61632	0.00889
3	k__Bacteria_p__Actinobacteria_c__Coriobacteriales_o__Coriobacteriaceae_g__Eggerthella	435	458	16.80786026	0.106938	0.062	1.72480238	0.084911	0.00761	0.02128	0.357786	0.72067	1.4710926	0.141266	1.72288	0.08491
4	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales	2	891	1100.372615	0	0	0	1	-0.03449	0.01762	-1.95764	0.050586	-1.382378	0.168856	-1.955	0.05059
5	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__Rikenellaceae	34	859	110.9720605	0.159131	0.1636	0.97265355	0.33099	-0.04027	0.01555	-2.58905	0.009788	-1.139232	0.254606	-2.5832	0.00979
6	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__S24-7/Barnesiellaceae	169	724	32.16436464	-0.04329	0.07896	-0.5483379	0.583598	-0.02576	0.01767	-1.45726	0.145479	-1.416917	0.156507	-1.4557	0.14548
7	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__Bacteroides	5	888	407.7556306	0	0	0	1	-0.01332	0.01503	-0.88606	0.375826	-0.626223	0.531168	-0.8856	0.37583
8	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Odoribacteraceae	219	674	10.04747774	-0.11395	0.0717	-1.5892516	0.11236	-0.04275	0.02195	-1.94813	0.051818	-2.497729	0.012499	-2.4977	0.0125
9	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Odoribacteraceae_g__Butyrivibrio	410	483	7.126293996	-0.11871	0.06194	-1.9165791	0.055612	-0.06566	0.02742	-2.39443	0.01703	-3.04064	0.002361	-3.0406	0.00236
10	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Odoribacteraceae_g__Odoribacter	316	577	5.771230503	-0.13137	0.0646	-2.0335694	0.042292	-0.00677	0.02604	-0.2601	0.79488	-1.619709	0.105295	-2.0306	0.04229
11	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae	125	768	39.30208333	-0.07814	0.08901	-0.8778199	0.380279	0.01901	0.01599	1.188777	0.234887	0.2195251	0.826241	1.18784	0.2348
12	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__S24-7	658	235	104	-0.09796	0.07127	-1.3744736	0.169641	-0.0396	0.02185	-1.81216	0.071259	-2.246604	0.024665	-2.2466	0.02467
13	k__Bacteria_p__Cyanobacteria	429	464	12.3362069	-0.09597	0.06198	-1.5485533	0.121845	0.02139	0.02426	0.881773	0.378361	-0.471042	0.637611	-1.5471	0.12185
14	k__Bacteria_p__Firmicutes_c__Bacilli_o__Gemellales/Bacillales	524	369	2.989159892	0.056479	0.06274	0.9002184	0.368248	0.03218	0.04296	0.749212	0.454212	1.1654328	0.243844	1.16543	0.24384
15	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Magbacteriaceae(Clostridiales/Lachnospiraceae	341	552	6.128623188	-0.05317	0.06372	-0.8344071	0.404276	-0.01002	0.02851	-0.35133	0.725477	-0.838032	0.402012	-0.838	0.40201
16	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae/Lachnospiraceae	841	52	26.48076923	0.304537	0.13214	2.30468119	0.021414	0.16968	0.07395	2.294583	0.026173	3.1991158	0.001378	3.19912	0.00138
17	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Pyrospiraceae(Magbacteriaceae/Clostridiales	655	238	4.714285714	0.066863	0.07037	0.95016061	0.342289	-0.06855	0.04294	-1.59638	0.111753	-0.453051	0.650512	-1.5904	0.11175
18	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Christensenellaceae	232	661	38.25567322	-0.05606	0.0713	-0.7861758	0.431974	0.00999	0.01625	0.614629	0.539013	-0.121227	0.903472	-0.7858	0.43197
19	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae	84	809	11.82076638	0.159967	0.10685	1.49718434	0.134701	0.00762	0.02226	0.34251	0.732057	1.2998111	0.193666	1.49582	0.1347
20	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae_g__O2406	309	404	6.194331984	0.048177	0.06286	0.76645533	0.443609	0.02047	0.02972	0.688909	0.491206	1.0284898	0.30372	1.02849	0.30372
21	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Dehalobacteriaceae_g__Dehalobacterium	612	281	2.839857651	0.066697	0.0666	1.00150503	0.316856	0.05977	0.04934	1.211529	0.226725	1.5625493	0.118159	1.56255	0.11816
22	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae	1	892	162.4753363	0	0	0	1	-0.05033	0.03868	-1.30107	0.193573	-0.919297	0.35794	-1.3001	0.19357
23	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Blautia	51	842	8.956057007	-0.04754	0.1331	-0.3571525	0.721063	0.00811	0.02409	0.336823	0.726334	-0.014374	0.988532	-0.357	0.72106
24	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Coproccoccus	414	479	6.565762004	-0.0645	0.06297	-1.0244093	0.305921	-0.0875	0.03109	-2.81442	0.00509	-2.704759	0.006835	-2.8013	0.00509
25	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Lachnospira	181	712	24.56320225	-0.22652	0.07659	-2.9576853	0.003182	0.00061	0.01801	0.038884	0.97298	-2.061738	0.039233	-2.9496	0.00318
26	k__Bacteria_p__Firmicutes_c__Erysipelotrichia_o__Erysipelotrichales_f__Erysipelotrichaceae_g__cc_115	303	590	13.14237288	0.065539	0.06538	1.00250652	0.316372	0.0437	0.02225	1.964265	0.049972	2.0945511	0.036211	2.09456	0.03621
27	k__Bacteria_p__Firmicutes_c__Erysipelotrichia_o__Erysipelotrichales_f__Erysipelotrichaceae_g__Holdemania	312	581	3.079173838	-0.03313	0.06491	-0.5104387	0.609871	0.01965	0.03515	0.559132	0.576289	0.0343342	0.972611	0.55881	0.57629
28	k__Bacteria_p__Proteobacteria_c__Betaproteobacteria_o__Burkholderiales/Rhodocyclales	574	319	4.460815047	-0.02753	0.06472	-0.4253414	0.670691	0.04364	0.03945	1.10614	0.26951	0.4801195	0.631142	1.10419	0.26951
29	k__Bacteria_p__Proteobacteria_c__Deltaproteobacteria_o__Desulfosulfolobales_f__Desulfosulfolobaceae	194	699	25.8583691	-0.03672	0.07498	-0.489738	0.62444	-0.00408	0.01761	-0.23169	0.816844	-0.509947	0.610089	-0.5099	0.61009
30	k__Bacteria_p__Proteobacteria_c__Deltaproteobacteria_o__Desulfosulfolobales_f__Desulfosulfolobaceae_g__Bilophia	309	584	11.38356164	-0.059928	0.06543	0.91585269	0.359993	-0.00343	0.02243	-0.15292	0.878512	0.5931853	0.589759	0.91518	0.35999
31	k__Bacteria_p__Proteobacteria_c__Gammaproteobacteria	467	426	36.5	-0.06323	0.06191	-1.0212402	0.307419	-0.04804	0.01871	-2.56781	0.010579	-2.529303	0.011429	-2.5263	0.01058
32	k__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Pasteurellales_f__Pasteurellaceae	538	355	15.46760563	-0.05664	0.06311	-0.8974532	0.36972	-0.05617	0.02397	-2.34313	0.019682	-2.283497	0.022401	-2.3124	0.01968
33	k__Bacteria_p__Tenericutes	323	570	90.26140351	-0.1802	0.06479	-2.7812277	0.00553	0.01477	0.01503	0.982871	0.326091	-1.267419	0.205005	-2.7744	0.00553
34	k__Bacteria_p__Verrucomicrobia_c__Verrucomicrobiales_f__Verrucomicrobiales_g__Akermansia	245	648	282.8040123	-0.06493	0.06995	-0.9282257	0.353543	0.00059	0.01186	0.497201	0.619217	-0.304607	0.760666	-0.9277	0.35354

Online Table VI. The association between microbes and the SNPs associated with lipids and BMI at P value 1×10^{-5}

None of the associations were significant at FDR 0.05 level after correcting for multiple tests.

A. Association with lipid-associated SNPs

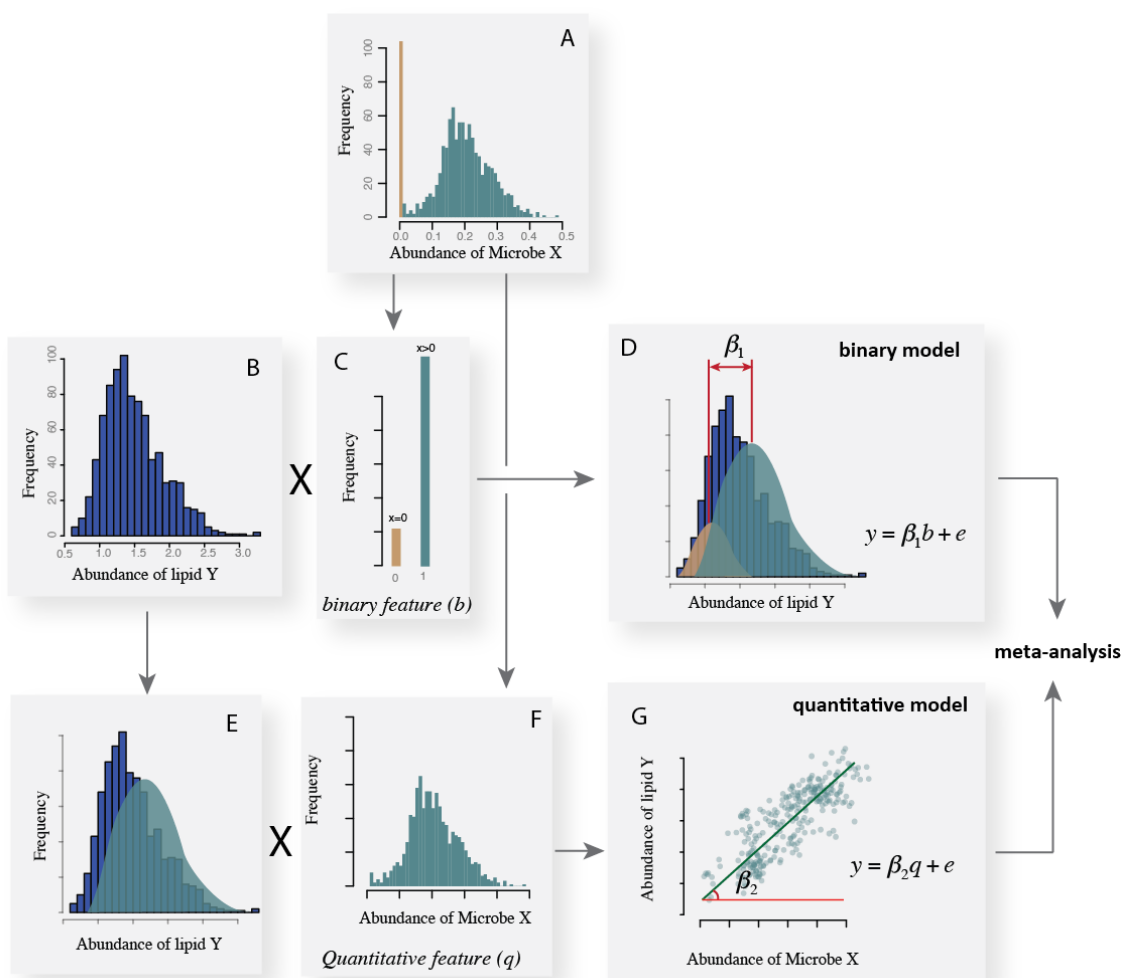
PValue	SNPName	SNPChr	SNPChrPos	Microbe	SNPType	AlleleAssessed	OverallZScore	DatasetsWhere	DatasetsZScore	DatasetsNrSam	FDR
1.03E-05	rs4660293	1	40028180	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_GG_3998460	A/G	G	4.4106452	LLD	4.4106452	893	1
1.36E-05	rs12328675	2	165540800	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_GG_2612154	T/C	C	4.3499897	LLD	4.3499897	893	1
1.79E-05	rs3136441	11	46743247	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_1945574	T/C	C	4.2893612	LLD	4.2893612	893	1
2.35E-05	rs2814982	6	34546560	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_263839	C/T	T	4.2287593	LLD	4.2287593	893	1
2.35E-05	rs2290159	3	12628920	k__Bacteria_p__Actinobacteria_c__Coriobacteriales_f__Coriobacteraceae_GG_412475	G/C	C	4.2287593	LLD	4.2287593	893	1
3.99E-05	rs4942486	13	32953388	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_4409643	T/C	T	-4.1076336	LLD	-4.1076336	893	1
5.18E-05	rs9376090	6	135411228	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_197302	T/C	C	-4.047109	LLD	-4.047109	893	1
5.18E-05	rs10128711	11	18632984	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_539352	T/C	T	-4.047109	LLD	-4.047109	893	1
5.19E-05	rs12748152	1	27138393	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_288810	C/T	T	4.047109	LLD	4.047109	893	1
5.90E-05	rs838880	12	125261593	k__Bacteria_p__Firmicutes_c__Bacilli_o__Lactobacillales_f__Lactobacillaceae_GG_259975	T/C	C	4.0168561	LLD	4.0168561	893	1
6.70E-05	rs2814982	6	34546560	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_GG_379905	C/T	T	3.9866094	LLD	3.9866094	893	1
6.70E-05	rs7134375	12	20473758	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_208879	C/A	A	3.9866094	LLD	3.9866094	893	1
6.70E-05	rs7134375	12	20473758	k__Bacteria_p__Firmicutes_c__Gemmatimonadetes_c__Gemmatimonadetes_f__Gemmatimonadaceae_GG_151512	C/A	A	3.9866094	LLD	3.9866094	893	1
6.70E-05	rs7134375	12	20473758	k__Bacteria_p__Firmicutes_c__Gemmatimonadetes_c__Gemmatimonadetes_f__Gemmatimonadaceae_GG_151512	C/A	A	3.9866094	LLD	3.9866094	893	1
6.70E-05	rs2290159	3	12628920	k__Bacteria_p__Lentisphaerae_c__Lentisphaeria_o__Victivallales	G/C	C	3.9866094	LLD	3.9866094	893	1
6.70E-05	rs2290159	3	12628920	k__Bacteria_p__Lentisphaerae_c__Lentisphaeria_o__Victivallales_f__Victivallaceae	G/C	C	3.9866094	LLD	3.9866094	893	1
7.62E-05	rs7134375	12	20473758	k__Bacteria_p__Firmicutes_c__Bacilli_o__Lactobacillales_f__Lactobacillaceae_GG_4168094	C/A	A	3.9563688	LLD	3.9563688	893	1
7.62E-05	rs7134375	12	20473758	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Porphyromonadaceae_GG_554296	C/A	A	3.9563688	LLD	3.9563688	893	1
7.62E-05	rs2290159	3	12628920	k__Bacteria_p__Lentisphaerae	G/C	C	3.9563688	LLD	3.9563688	893	1
7.62E-05	rs2290159	3	12628920	k__Bacteria_p__Lentisphaerae_c__Lentisphaeria	G/C	C	3.9563688	LLD	3.9563688	893	1
7.62E-05	rs10128711	11	18632984	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_208810	T/C	T	3.9563688	LLD	3.9563688	893	1
8.63E-05	rs11246602	11	51512090	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_193850	T/C	C	-3.9261344	LLD	-3.9261344	893	1
8.63E-05	rs645040	3	135926622	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_198051	T/G	G	-3.9261344	LLD	-3.9261344	893	1
9.78E-05	rs10128711	11	18632984	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_f__Faecalibacterium	T/C	T	-3.895906	LLD	-3.895906	893	1
9.78E-05	rs10128711	11	18632984	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_f__Faecalibacterium	T/C	T	-3.895906	LLD	-3.895906	893	1
9.78E-05	rs10128711	11	18632984	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_f__Faecalibacterium	T/C	T	-3.895906	LLD	-3.895906	893	1

B. Association with BMI-associated SNPs

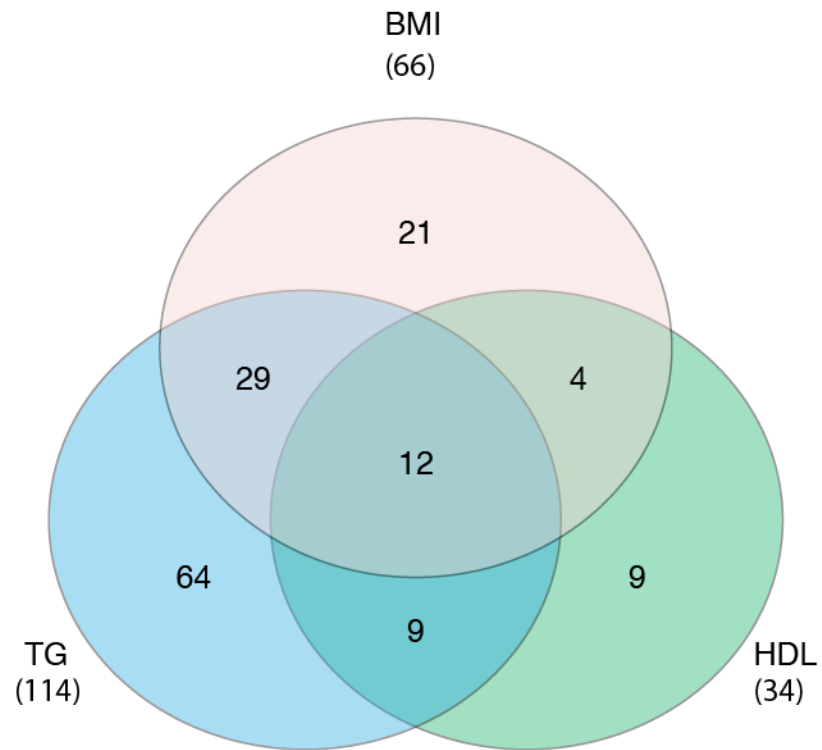
SNPName	SNPChr	SNPChrPos	Microbe	SNPType	AlleleAssessed	OverallZScore	DatasetsWhere	DatasetsZScore	DatasetsNrSam	FDR
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_1703711	A/G	A	4.4713281	LLD	4.4713281	893	0.85
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_370063	A/G	A	4.3499897	LLD	4.3499897	893	1
rs13201877	6	137675541	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_34139	A/G	G	4.1984681	LLD	4.1984681	893	1
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_322719	A/G	A	4.1984681	LLD	4.1984681	893	1
rs7164727	15	73093991	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_192201	C/T	C	4.1681835	LLD	4.1681835	893	1
rs1460676	2	164567689	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Dehalobacteriaceae_f__Dehalobacterium	T/C	C	-4.1379053	LLD	-4.1379053	893	1
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_4439795	A/G	A	4.1379053	LLD	4.1379053	893	1
rs1516725	3	185824004	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_207252	C/T	T	4.0773681	LLD	4.0773681	893	1
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_288588	A/G	A	4.0168561	LLD	4.0168561	893	1
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_GG_312766	A/G	A	4.0168561	LLD	4.0168561	893	1
rs1460676	2	164567689	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Dehalobacteriaceae	T/C	C	-3.9563688	LLD	-3.9563688	893	1
rs4787491	16	30015337	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_GG_584417	A/G	A	3.9563688	LLD	3.9563688	893	1
rs4787491	16	30015337	k__Bacteria_p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Dodonbacteriaceae_f__Bifidobacterium	A/G	A	3.895906	LLD	3.895906	893	1

Online Figure I. The workflow of the two-part model

A. The distribution of microbe X. The brown bar indicates the number of subjects with zero value of microbe X, i.e. none of this particular microbe (also called “spike”) and the green bars indicate the destruction of non-zero. The spike shows the departure of the distribution from a normal distribution. **B.** The distribution of lipid Y. After transformation, the lipid distribution is close to a normal distribution. **C.** The binary feature of microbe X. The subjects are divided into two groups (zero vs non-zero). **D.** The binary model to test whether the lipid level is significantly different between the two groups (zero vs non-zero). **E.** The distribution of lipid Y for the subjects with non-zero. **F.** Quantitative feature of microbe X: the distribution of non-zero values. **G.** The quantitative model to test whether the abundance of lipid X is associated with the abundance of microbe X. The signals from the binary model and quantitative model are combined using meta-analysis.

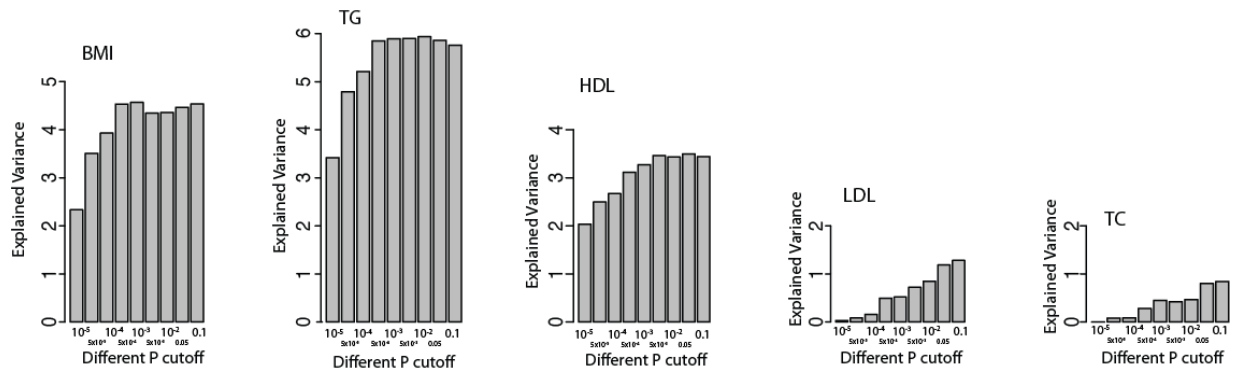


Online Figure II. The number of OTUs associated with TG, HDL and BMI at FDR < 0.05 and their overlaps with each other



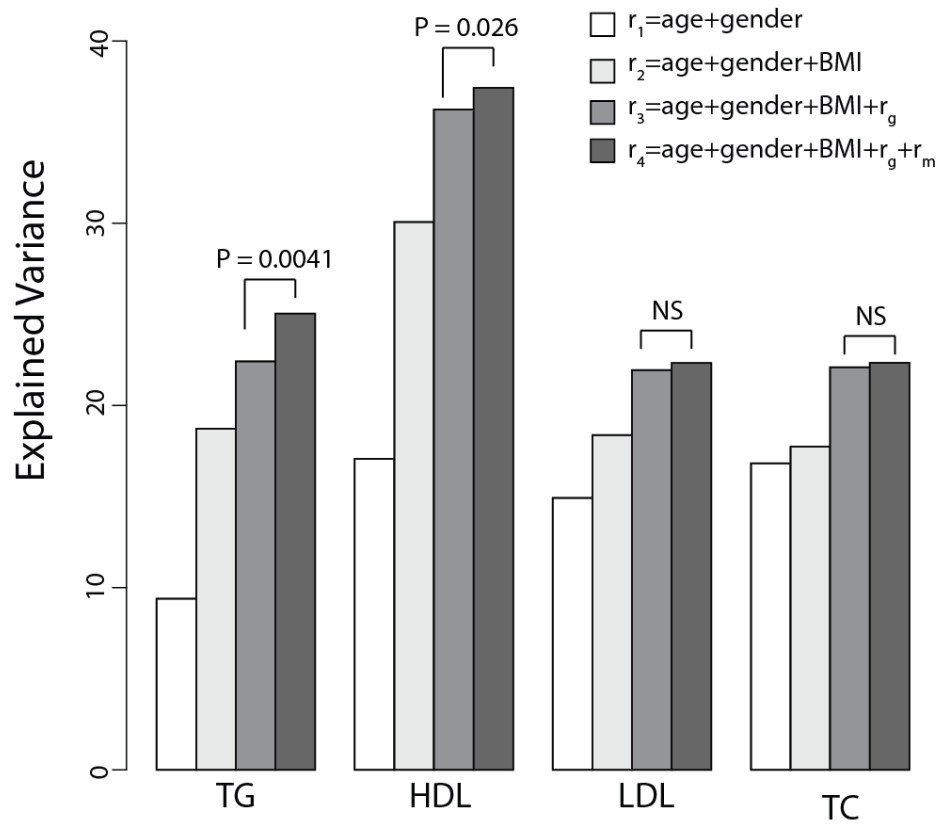
Online Figure III. The amount of variance in BMI and lipids explained by the gut microbiome

The x-axis refers to the different significance levels at which OTUs were identified. The Y-axis refers to the variance explained by the OTUs.



Online Figure IV. The variation of lipids explained by age, gender, BMI, genetic and microbial risk.

The significance of microbial contribution is indicated as the P value of the ANOVA test that compared the performance of the risk models r_3 and r_4 .



NS=not significant