

Table S5a. Associated taxonomies with Body mass index (BMI) at FDR < 0.05 level ^a

Taxonomie	Summary of OTUs reads			Binary model				Quantitative model				Meta analysis		Final association	
	No. Absent	No. Present	mean counts in presents	Estimate	s.e.	t value	P value	Estimate	s.e.	t value	P value	Meta z value	Meta P value	z	P value
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Cardiobacteriales_f_Cardiobacteriaceae_g_Cardiobacterium	71	4	1.75	-4.24195	2.37290	-1.78766	0.07804	-5.52718	0.11621	-47.56072	0.01338	-2.99501	0.00274	-2.99501	0.00274
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae_g_Alistipes	16	59	53.17	-3.67338	1.25130	-2.93565	0.00447	-0.10021	0.26910	-0.37238	0.71102	-2.27248	0.02306	-2.84328	0.00447
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_[Paraprevotellaceae]_g_Paraprevotella	21	54	130.56	3.25642	1.12945	2.88319	0.00519	0.03801	0.34127	0.11138	0.91175	2.05485	0.03989	2.79517	0.00519
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Clostridium	5	70	129.89	2.61207	2.15636	1.21133	0.22973	0.72489	0.27335	2.65187	0.00998	2.67109	0.00756	2.67109	0.00756
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Prevotellaceae_g__	71	4	2.25	-0.27906	2.41506	-0.11555	0.90833	-2.24329	0.02838	-79.03470	0.00805	-1.95510	0.05057	-2.64978	0.00805
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Prevotellaceae_g_Prevotella	1	74	1607.95	0.00000	0.00000	0.00000	1.00000	0.33719	0.12479	2.70211	0.00861	1.85762	0.06322	2.62708	0.00861
k_Archaea_p_Euryarchaeota_c_Methanobacteria_o_Methanobacteriales_f_Methanobacteriaceae_g_Methanobrevibacter	49	26	31.38	-0.44387	1.13651	-0.39056	0.69728	-1.12528	0.39786	-2.82833	0.00953	-2.10823	0.03501	-2.59250	0.00953
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Citrobacter	66	9	9.33	4.18009	1.57318	2.65710	0.00970	0.09168	1.37712	0.06657	0.94909	1.87393	0.06094	2.58628	0.00970
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g__	6	69	38.58	-0.13521	1.98847	-0.06800	0.94598	0.70845	0.26806	2.64287	0.01026	1.76725	0.07719	2.56703	0.01026
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Acidaminococcus	38	37	331.81	2.70483	1.06660	2.53594	0.01338	0.23528	1.06049	0.29640	0.24872	0.01287	2.48728	0.01287	
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_[Odoribacteraceae]_g_Odoribacter	3	72	46.57	0.82753	2.78051	0.29762	0.76685	-0.75739	0.29845	-2.53775	0.01342	-1.53863	0.12390	-2.47244	0.01342
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Enterobacter	66	9	2.67	-2.75462	1.63425	1.68555	0.09621	2.65084	1.19708	2.21443	0.06872	2.46338	0.01376	2.46338	0.01376
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_[Eubacterium]	27	48	66.77	-0.07356	1.11868	-0.06575	0.94776	0.47227	0.18553	2.54549	0.01441	1.68389	0.09220	2.46691	0.01441
k_Bacteria_p_Cyanobacteria_c_Chloroplast_o_Streptophyta_f_g__	51	24	10.63	2.78753	1.11435	2.50149	0.01464	0.48019	0.63407	0.75731	0.45728	2.25176	0.02434	2.44113	0.01464
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Megamonas	61	14	178.79	0.30809	1.37636	0.22384	0.82352	0.85183	0.29729	2.86532	0.01537	1.87141	0.06129	2.42355	0.01537
k_Bacteria_p_Cyanobacteria_c_4C0d-2_o_Y52_f_g__	49	26	26.58	-1.16649	1.11858	-1.04283	0.30051	-0.97098	0.40491	-2.38000	0.02499	-2.31708	0.02050	-2.31708	0.02050
k_Bacteria_p_Firmicutes_c_Bacilli_o_Turicibacteriales_f_Turicibacteraceae_g_Turicibacter	59	16	13.88	1.10087	1.30605	0.84290	0.40208	1.12218	0.43689	2.56858	0.02336	2.19590	0.02810	2.26755	0.02336
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae_g_Christensenella	64	11	4.45	-3.23294	1.46582	-2.20556	0.03061	-1.04834	1.23857	-0.84640	0.42192	-2.09673	0.03602	-2.16213	0.03061
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Veillonella	15	61	66.15	-0.20052	1.39277	-0.14398	0.88592	0.53177	0.24093	2.20713	0.03128	1.42134	0.15522	2.15355	0.03128
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g__	70	5	29.00	-1.21748	2.14394	-0.56787	0.57189	-0.77258	0.14000	-5.51839	0.03130	-1.92224	0.05458	-2.15319	0.03130
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus	29	46	161.57	2.24965	1.07070	2.10110	0.03913	0.02393	0.27279	0.08772	0.93051	1.52027	0.12844	2.06278	0.03913
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g__	6	69	305.32	0.24939	2.08736	0.11947	0.90523	0.36601	0.17720	2.06558	0.04280	1.51655	0.12938	2.02567	0.04280
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Pantoea	32	43	269.12	1.37740	1.07161	1.28535	0.20279	0.37846	0.24448	1.54802	0.12949	1.97265	0.04854	1.97265	0.04854

^a Statistics associated to the two part model for association analysis between the trait and microbes adjusting for age and gender. The binomial analysis that tests for association of detecting a microbe with the trait, where s.e. represents the standard error of the estimate, t-value of a t test for the estimate and its associated probability (P value). The quantitative analysis tests for association between the trait and the abundance of the microbe for the subjects where that microbe is present, where s.e. represents the standard error of the estimate, t-value of a t test for the estimate and its associated probability (P value). The Meta analysis combine the effect of both binary and quantitative analysis, a meta P value was derived using an unweighted Z method. The final association P value per microbe-trait pair was assigned from the minimum of P values from the binary analysis, quantitative analysis, and meta-analysis.

Table S5b. Associated taxonomies with Triglycerides at FDR < 0.05 level ^a

Taxonomie	Summary of OTUs reads			Binary model				Quantitative model				Meta analysis		Final association	
	No. Absent	No. Present	mean counts in presents	Estimate	s.e.	t value	P value	Estimate	s.e.	t value	P value	Meta z value	Meta P value	z	P value
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Dialister	17	58	268.71	-75.53458	22.52918	-3.35274	0.00128	-0.42802	2.06444	-0.20733	0.83652	-2.42339	0.01538	-3.22084	0.00128
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_g__	67	8	5.63	101.77620	30.59668	3.32638	0.00139	-82.60462	58.64759	-1.40849	0.21803	1.38978	0.16459	3.19725	0.00139
k_Bacteria_p_Fusobacteria_c_Fusobacteriia_o_Fusobacteriales_f_Leptotrichiaceae_g_Leptotrichia	69	6	2.67	33.97669	37.24747	0.91219	0.36471	-58.45030	9.29023	-6.29159	0.00811	-1.23109	0.21829	-2.64744	0.00811
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Oribacterium	59	16	2.88	62.41962	23.64636	2.63971	0.01017	16.93305	52.48570	0.32262	0.75211	2.04069	0.04128	2.57012	0.01017
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Lachnospira	9	75	288.77	0.00000	0.00000	0.00000	1.00000	-9.43567	3.79208	-2.48826	0.01515	-1.71737	0.08591	-2.42873	0.01515
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_[Mogibacteriaceae]_g_Mogibacterium	67	8	2.13	29.00754	32.78823	0.88469	0.37927	-66.69096	20.12746	-3.31343	0.02116	-1.00824	0.31334	-2.30511	0.02116
k_Bacteria_p_TM7_c_TM7-3_o_CW040_f_g__	25	50	155.90	-40.58598	21.04268	-1.92875	0.05770	-3.95866	3.02501	-1.30864	0.19702	-2.25427	0.02418	-2.25427	0.02418
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Phascalocartobacterium	12	63	301.17	13.04554	27.79236	0.46939	0.64021	8.48866	3.75927	2.25806	0.02759	1.88829	0.05899	2.20304	0.02759
k_Bacteria_p_Firmicutes_c_Bacilli_o_Gemellales_f_Gemellaceae_g__	36	39	7.87	40.40409	19.77700	2.04298	0.04472	12.83030	11.63355	1.10287	0.27740	2.18743	0.02871	2.18743	0.02871
k_Bacteria_p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_Attopobium	52	23	5.39	47.54758	21.39399	2.22247	0.02939	-18.08059	20.05529	-0.90154	0.37803	0.91687	0.35921	2.17818	0.02939
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Coprobaillus	6	15	4.93	54.46843	24.72433	2.20303	0.03079	-18.83968	31.35802	-0.60079	0.55915	1.1414	0.26522	2.15973	0.03079
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_[Tissierellaceae]_g_WAL_1855D	65	10	4.00	63.21708	28.94208	2.18426	0.03220	-49.29793	61.30630	-0.80413	0.44777	0.97777	0.32819	2.14191	0.03220
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus	29	46	161.57	-39.88948	20.35123	-1.96005	0.05386	-3.66895	3.38111	-1.08513	0.28391	-2.12099	0.03392	-2.12099	0.03392
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Leuconostocaceae_g_Weissella	61	14	7.00	15.93906	26.21858	0.60793	0.54515	12.11592	5.09175	2.37952	0.03653	1.90636	0.05660	2.09096	0.03653
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Ruminococcus	0	75	308.87	0.00000	0.00000	0.00000	1.00000	-12.14391	5.72785	-2.12015	0.03744	-1.47144	0.14117	-2.08093	0.03744
k_Bacteria_p_Proteobacteria_c_Epsilonproteobacteria_o_Campylobacteriales_f_Campylobacteraceae_g_Campylobacter	62	13	3.92	53.26154	26.04491	2.04499	0.04451	-103.67951	45.88597	-2.25950	0.04741	0.01881	0.98499	2.00924	0.04451
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Catenibacterium	48	27	61.48	-41.98303	20.62267	-2.03577	0.04545	-0.50362	4.92345	-0.10229	0.91938	-1.48609	0.13725	-2.00043	0.04545
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Erwinia	49	26	13.69	-6.62846	21.29569	-0.31126	0.75650	11.25878	5.36355	2.09913	0.04698	1.18539	0.23586	1.98647	0.04698

^a Statistics associated to the two part model for association analysis between the trait and microbes adjusting for age and gender. The binomial analysis that tests for association of detecting a microbe with the trait, where s.e. represents the standard error of the estimate, t-value of a t test for the estimate and its associated probability (P value). The quantitative analysis tests for association between the trait and the abundance of the microbe for the subjects where that microbe is present, where s.e. represents the standard error of the estimate, t-value of a t test for the estimate and its associated probability (P value). The Meta analysis combine the effect of both binary and quantitative analysis, a meta P value was derived using an unweighted Z method. The final association P value per microbe-trait pair was assigned from the minimum of P values from the binary analysis, quantitative analysis, and meta-analysis.

Table S5c. Associated taxonomies with High-density lipoprotein (HDL) at FDR < 0.05 level ^a

Taxonomie	Summary of OTUs reads			Binary model				Quantitative model				Meta analysis		Final association	
	No. Absent	No. Present	mean counts in presents	Estimate	s.e.	t value	P value	Estimate	s.e.	t value	P value	Meta z value	Meta P value	z	P value
k_Bacteria_p_Tenericutes_c_Mollicutes_o_Anaeroplasmatales_f_Anaeroplasmataceae_g_	71	4	687.50	7.70278	6.47966	1.18876	0.23844	-10.39396	0.01165	-892.05595	0.00071	-1.55944	0.11889	-3.38428	0.00071
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Oribacterium	59	16	2.88	1.71378	3.53338	0.48503	0.62913	-19.03891	5.11684	-3.72084	0.00257	-1.79074	0.07334	-3.01544	0.00257
k_Bacteria_p_Firmicutes_c_Bacilli_o_Bacillales_f_Staphylococcaceae_g_Staphylococcus	71	4	2.75	18.30074	6.17725	2.96260	0.00413	-8.84490	15.41236	-0.57388	0.66832	1.72499	0.08453	2.86795	0.00413
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Oxalobacteraceae_g_Oxalobacter	42	33	9.12	6.31233	2.82518	2.23431	0.02857	4.51120	2.97952	1.51407	0.14047	2.59043	0.00959	2.59043	0.00959
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Catenibacterium	48	27	61.48	7.56556	2.89679	2.61170	0.01096	1.05257	1.54711	0.68035	0.50279	2.27275	0.02304	2.54405	0.01096
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_	17	58	36.62	-8.19344	3.32906	-2.46119	0.01625	-0.03991	0.52314	-0.07630	0.93946	-1.75313	0.07958	-2.40335	0.01625
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae_g_Alistipes	16	59	53.17	-0.59856	3.58254	-0.16708	0.86778	-1.87315	0.80143	-2.33727	0.02303	-1.72498	0.08453	-2.27301	0.02303
k_Bacteria_p_Firmicutes_c_Bacilli_o_Gemellales_f_Gemellaceae_g_	36	39	7.87	-5.03986	2.84586	-1.77094	0.08080	-1.58707	1.07656	-1.47421	0.14912	-2.25475	0.02415	-2.25475	0.02415
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Cardiobacteriales_f_Cardiobacteriaceae_g_Cardiobacterium	71	4	1.75	9.78147	6.46054	1.51403	0.13440	21.38645	3.19541	6.69286	0.09442	2.24119	0.02501	2.24119	0.02501
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Bacteroidaceae_g_Bacteroides	0	75	4087.83	0.00000	0.00000	0.00000	1.00000	-2.47105	1.10913	-2.22791	0.02901	-1.54385	0.12262	-2.18334	0.02901
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Bifidobacteriales_f_Bifidobacteriaceae_g_	68	7	5.00	10.66025	4.83020	2.20700	0.03050	-12.34710	4.71863	-2.61667	0.05901	0.19470	0.84563	2.16350	0.03050
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pseudomonadales_f_Moraxellaceae_g_Acinetobacter	64	11	2.45	8.08179	3.98966	2.02568	0.04650	10.40523	9.35575	1.11217	0.29836	2.14305	0.03211	2.14305	0.03211
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Bifidobacteriales_f_Bifidobacteriaceae_g_Alloscardovia	67	8	15.25	-4.62636	4.67216	-0.99020	0.32539	-2.71062	1.13746	-2.38304	0.06293	-2.01040	0.04439	-2.01040	0.04439
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Escherichia	54	21	8.67	-0.97245	3.29060	-0.29552	0.76844	2.38835	1.12297	2.12681	0.04752	1.19304	0.23285	1.98162	0.04752
k_Bacteria_p_Firmicutes_c_Bacilli_o_Bacillales_f_Planococcaceae_g_	62	13	2.46	-1.60995	3.24600	-0.42095	0.67505	8.09224	3.58647	2.25632	0.04767	1.10387	0.26965	1.98034	0.04767
k_Bacteria_p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_Atopobium	52	23	5.39	-6.18905	3.07532	-2.01249	0.04791	-0.12069	1.53345	-0.07870	0.93805	-1.45373	0.14602	-1.97817	0.04791
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Dehalobacteriaceae_g_Dehalobacterium	48	27	6.04	3.98383	2.98866	1.33298	0.18674	3.92576	2.59107	1.51511	0.14280	1.96979	0.04886	1.96979	0.04886

^a Statistics associated to the two part model for association analysis between the trait and microbes adjusting for age and gender. The binomial analysis that tests for association of detecting a microbe with the trait, where s.e. represents the standard error of the estimate, *t*-value of a *t* test for the estimate and its associated probability (*P* value). The quantitative analysis tests for association between the trait and the abundance of the microbe for the subjects where that microbe is present, where s.e. represents the standard error of the estimate, *t*-value of a *t* test for the estimate and its associated probability (*P* value). The Meta analysis combine the effect of both binary and quantitative analysis, a meta *P* value was derived using an unweighted Z method. The final association *P* value per microbe-trait pair was assigned from the minimum of *P* values from the binary analysis, quantitative analysis, and meta-analysis.

Table S5d. Associated taxonomies with Low-density lipoprotein (HDL) at FDR < 0.05 level ^a

Taxonomie	Summary of OTUs reads			Binary model				Quantitative model				Meta analysis		Final association	
	No. Absent	No. Present	mean counts in presents	Estimate	s.e.	t value	P value	Estimate	s.e.	t value	P value	Meta z value	Meta P value	z	P value
k_Bacteria_p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_	23	52	14.87	0.79347	5.15124	0.15403	0.87801	5.00216	1.69927	2.94371	0.00495	2.09589	0.03609	2.81054	0.00495
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_	6	69	305.32	-22.70412	8.82754	-2.57196	0.01218	-1.08496	0.75551	-1.43606	0.15571	-2.77657	0.00549	-2.77657	0.00549
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Prevotellaceae_g_	71	4	2.25	27.77277	10.15788	2.73411	0.00787	-12.63501	20.75306	-0.60883	0.65184	1.56023	0.11870	2.65771	0.00787
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Escherichia	54	21	8.67	-12.87293	5.15750	-2.49596	0.01485	0.11916	2.16502	0.05504	0.95671	-1.68410	0.09216	-2.43595	0.01485
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_g_	67	8	5.63	17.84628	7.37449	2.42000	0.01805	5.25760	7.90853	0.66480	0.53561	2.11011	0.03485	2.36468	0.01805
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Clostridium	71	4	1.25	-20.64467	10.40515	-1.98408	0.05106	-29.27143	12.88989	-2.27088	0.26407	-2.16926	0.03006	-2.16926	0.03006
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Clostridium	68	7	31.43	-0.87960	8.20209	-0.10724	0.91490	-5.75344	1.76883	-3.25267	0.03130	-1.59816	0.11001	-2.15328	0.03130
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_SMB53	53	22	3.14	-0.05586	5.21953	-0.01070	0.99149	10.33790	4.45099	2.32261	0.03146	1.51361	0.13013	2.15123	0.03146
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Leuconostocaceae_g_Weissella	61	14	7.00	8.17949	6.05740	1.35033	0.18114	8.24201	4.40721	1.87012	0.08830	2.15081	0.03149	2.15081	0.03149
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pseudomonadales_f_Pseudomonadaceae_g_Pseudomonas	61	14	27.07	-5.70772	6.05318	-0.94293	0.34887	-4.01931	1.71127	-2.34873	0.03857	-2.12520	0.03357	-2.12520	0.03357
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Dialister	17	58	268.71	-0.24483	5.65247	-0.04331	0.96557	-1.57944	0.74002	-2.13433	0.03729	-1.50313	0.13280	-2.08259	0.03729
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_g_	54	21	223.33	1.72619	5.27233	0.32741	0.74431	2.43587	1.09260	2.2942	0.03876	1.69200	0.09065	2.06670	0.03876
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Tissierellaceae_g_Peptoniphilus	68	7	7.14	-0.32745	8.21295	-0.03987	0.96831	-9.50340	3.25620	-2.91856	0.04331	-1.45698	0.14512	-2.02075	0.04331
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pasteurellales_f_Pasteurellaceae_g_Actinobacillus	65	10	3.10	2.55452	7.11844	0.35886	0.72075	-13.90841	5.87645	-2.36680	0.04984	-1.13411	0.25675	-1.96134	0.04984

^a Statistics associated to the two part model for association analysis between the trait and microbes adjusting for age and gender. The binomial analysis that tests for association of detecting a microbe with the trait, where s.e. represents the standard error of the estimate, *t*-value of a *t* test for the estimate and its associated probability (*P* value). The quantitative analysis tests for association between the trait and the abundance of the microbe for the subjects where that microbe is present, where s.e. represents the standard error of the estimate, *t*-value of a *t* test for the estimate and its associated probability (*P* value). The Meta analysis combine the effect of both binary and quantitative analysis, a meta *P* value was derived using an unweighted Z method. The final association *P* value per microbe-trait pair was assigned from the minimum of *P* values from the binary analysis, quantitative analysis, and meta-analysis.

Table S5e. Associated taxonomies with Total cholesterol (TC) at FDR < 0.05 level ^a

Taxonomie	Summary of OTUs reads			Binary model				Quantitative model				Meta analysis		Final association	
	No. Absent	No. Present	mean counts in presents	Estimate	s.e.	t value	P value	Estimate	s.e.	t value	P value	Meta z value	Meta P value	z	P value
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Anaerotruncus	35	40	5.48	-9.27950	5.74866	-1.61420	0.11086	-6.72385	2.77878	-2.41972	0.02056	-2.76497	0.00569	-2.76497	0.00569
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pasteurellales_f_Pasteurellaceae_g_	63	12	4.42	-18.95427	7.59835	-2.49453	0.01491	1.12192	6.19121	0.18121	0.86022	-1.59700	0.11026	-2.43460	0.01491
k_Bacteria_p_Firmicutes_c_Bacilli_o_Gemellales_f_Gemellaceae_g_	36	39	7.87	4.76046	5.75766	0.82681	0.41108	-5.97766	2.53353	-2.35942	0.02385	-1.01652	0.30938	-2.25958	0.02385
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae_g_Christensenella	64	11	4.45	-17.72210	7.88383	-2.24790	0.02765	9.16884	8.21083	1.11668	0.29655	-0.81912	0.41272	-2.20228	0.02765
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_g_	54	21	223.33	-3.93402	6.41354	-0.61339	0.54155	2.98066	1.24762	2.38909	0.02805	1.12158	0.26204	2.19662	0.02805
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_SMB53	53	22	3.14	-3.42593	6.34833	-0.53966	0.59110	10.51976	4.45741	2.36006	0.02912	1.16292	0.24486	-2.18186	0.02912
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_	6	69	305.32	-23.61437	10.89174	-2.16810	0.03346	0.39100	0.95821	0.40805	0.68456	-1.21644	0.22382	-2.12655	0.03346
k_Bacteria_p_Proteobacteria_c_Deltaproteobacteria_o_Desulfovibrionales_f_Desulfovibrionaceae_g_Desulfovibrio	28	47	205.96	6.29885	5.95658	1.05746	0.29384	2.52163	1.25830	2.00401	0.05125	2.12070	0.03395	2.12070	0.03395
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_[Paraprevotellaceae]_g_Paraprevotella	21	54	130.56	10.14829	6.31136	1.60794	0.11223	2.44311	1.70817	1.43025	0.15874	2.11961	0.03404	2.11961	0.03404
k_Bacteria_p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_Eggerthella	60	15	5.53	-15.04464	7.00762	-2.14690	0.03517	-0.64027	4.78001	-0.13395	0.89567	-1.58217	0.11361	-2.10639	0.03517
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Leuconostocaceae_g_Weissella	61	14	7.00	-0.06516	7.47518	-0.00872	0.99307	10.41354	4.43221	2.34952	0.03852	1.45706	0.14510	2.06928	0.03852
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Bifidobacteriales_f_Bifidobacteriaceae_g_Bifidobacterium	7	68	91.18	-2.49938	9.90983	-0.25221	0.80160	-2.91829	1.39534	-2.09145	0.04040	-1.62700	0.10374	-2.04964	0.04040
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Ruminococcus	0	75	308.87	0.00000	0.00000	0.00000	1.00000	-3.38723	1.63083	-2.07700	0.04137	-1.44236	0.14920	-2.03980	0.04137
k_Bacteria_p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_Adlercreutzia	60	15	3.47	-14.53509	7.00583	-2.07471	0.04159	5.99994	5.26070	1.14052	0.27632	-0.67104	0.50219	-2.03762	0.04159
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Peptococcaceae_g_	40	35	13.69	-3.96541	5.83952	-0.67906	0.49927	-5.88691	2.77386	-2.12228	0.04165	-1.91813	0.05509	-2.03701	0.04165
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Clostridium	71	4	1.25	-20.34598	12.80038	-1.58948	0.11633	-36.28571	11.20860	-3.23731	0.19073	-2.03560	0.04179	-2.03560	0.04179
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Sarcina	68	7	30.14	6.51830	9.90905	0.65781	0.51276	-10.72036	3.80527	-2.81724	0.04796	-0.93561	0.34948	-1.97770	0.04796
k_Bacteria_p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_	23	52	14.87	0.42868	6.27876	0.06827	0.94576	4.22936	2.10125	2.01278	0.04965	1.43614	0.15096	1.96297	0.04965

^a Statistics associated to the two part model for association analysis between the trait and microbes adjusting for age and gender. The binomial analysis that tests for association of detecting a microbe with the trait, where s.e. represents the standard error of the estimate, *t*-value of a *t* test for the estimate and its associated probability (*P* value). The quantitative analysis tests for association between the trait and the abundance of the microbe for the subjects where that microbe is present, where s.e. represents the standard error of the estimate, *t*-value of a *t* test for the estimate and its associated probability (*P* value). The Meta analysis combine the effect of both binary and quantitative analysis, a meta *P* value was derived using an unweighted Z method. The final association *P* value per microbe-trait pair was assigned from the minimum of *P* values from the binary analysis, quantitative analysis, and meta-analysis.