Title: Gut microbiota composition and diversity and its relation to metabolic health and obesity status in older adults

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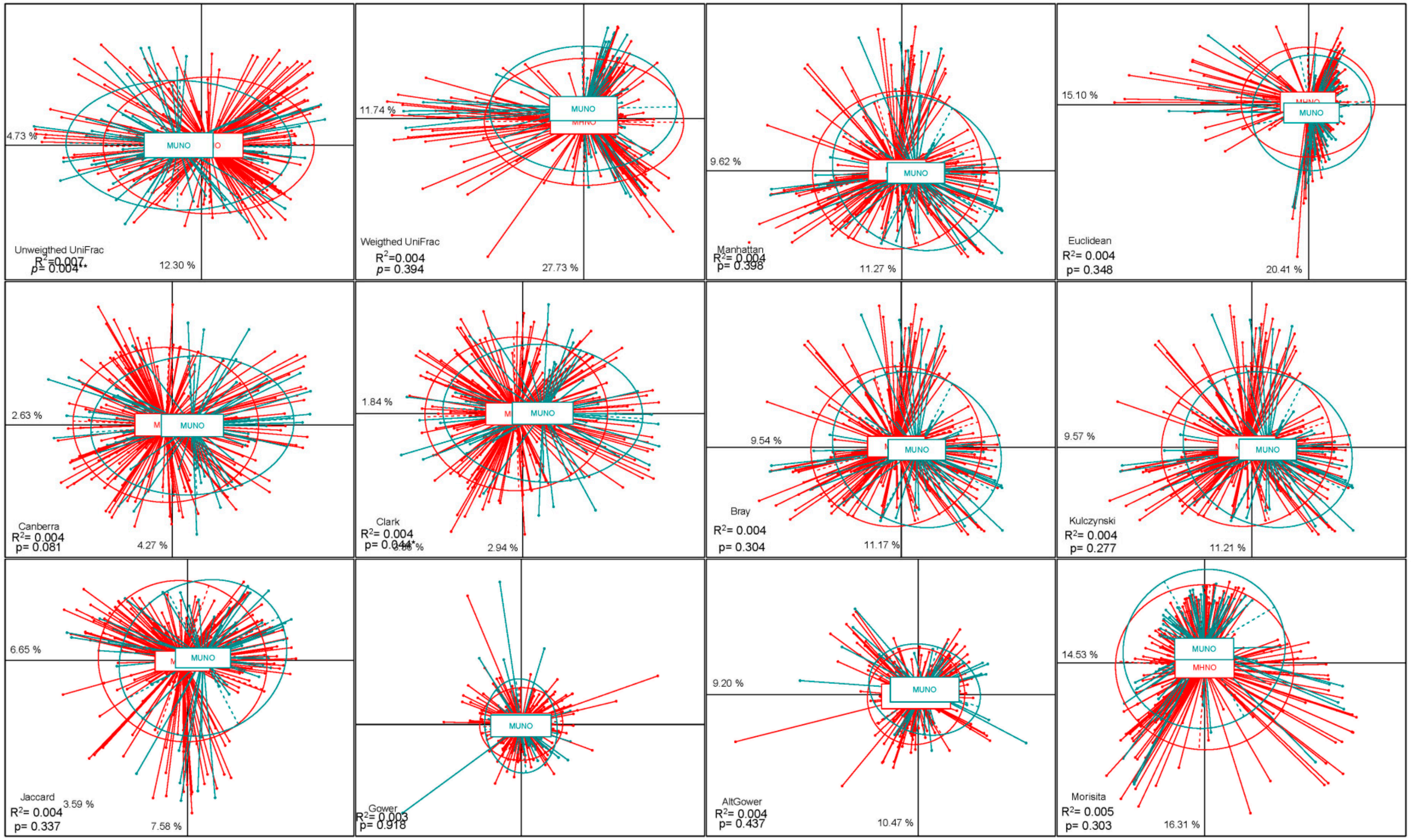

Fig. S1 Principal co-ordinate analysis between MUNO and MHNO groups based on different dissimilarity distance matrix. Subjects are colour coded according to Mets group; MHNO (red), MUNO (green). P-values were calculated from *adonis* test, *p < 0.05.

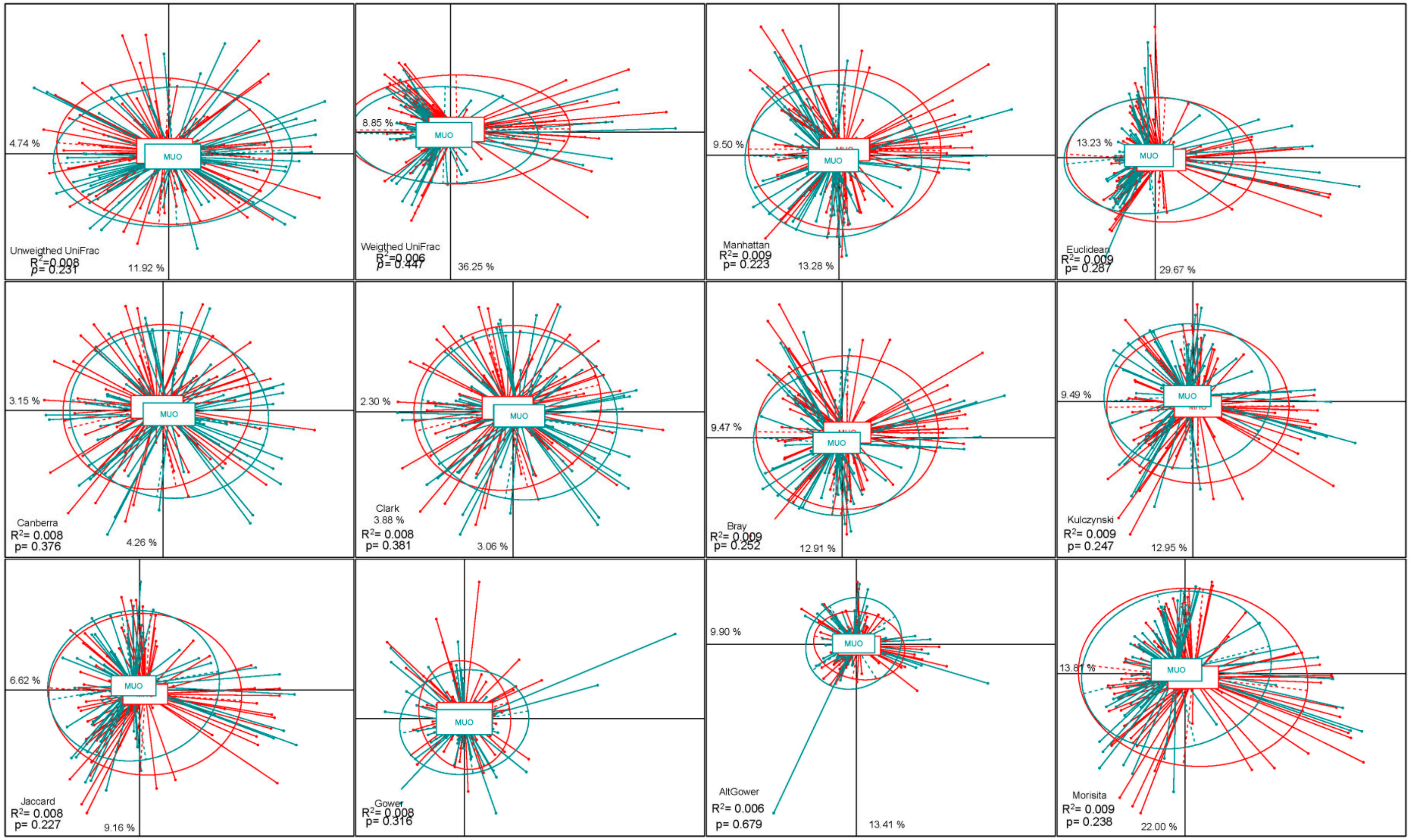

Fig. S2 Principal co-ordinate analysis between MUO and MHO groups based on different dissimilarity distance matrix. Subjects are colour coded according to Mets group; MHO (red), MUO (green). P-values were calculated from *adonis* test, *p < 0.05

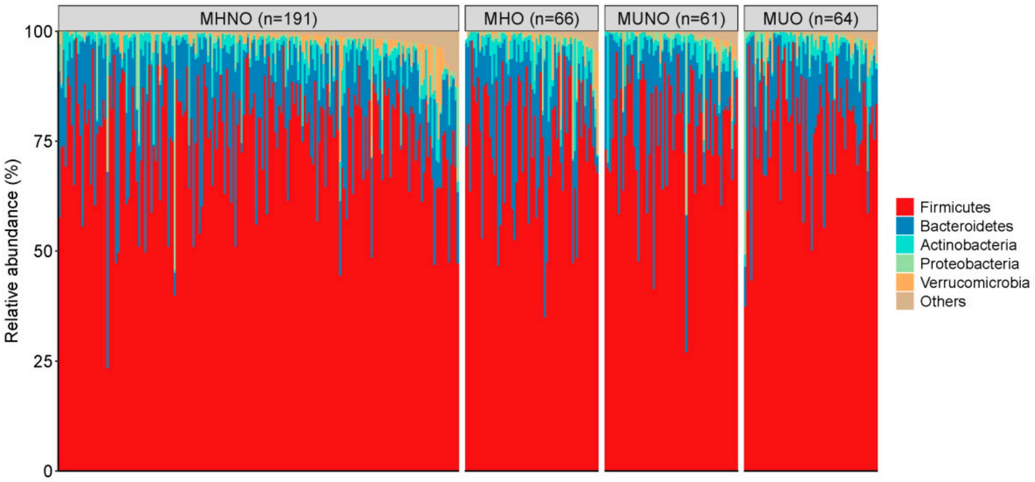

Fig. S3 Gut microbiota composition of MCR cohort at the phylum level.

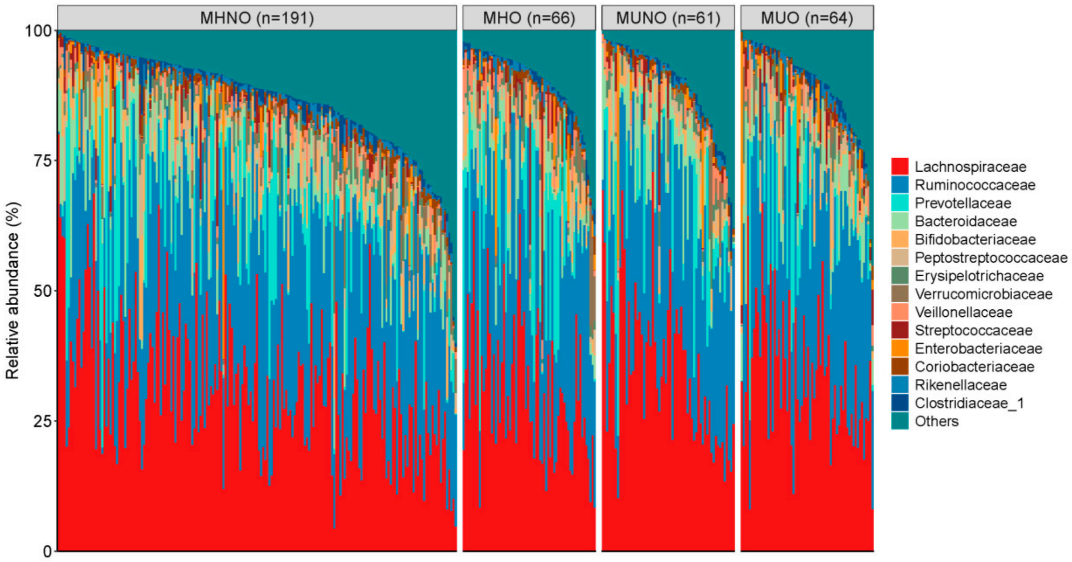

Fig. S4 Gut microbiota composition of MCR cohort at the family level.

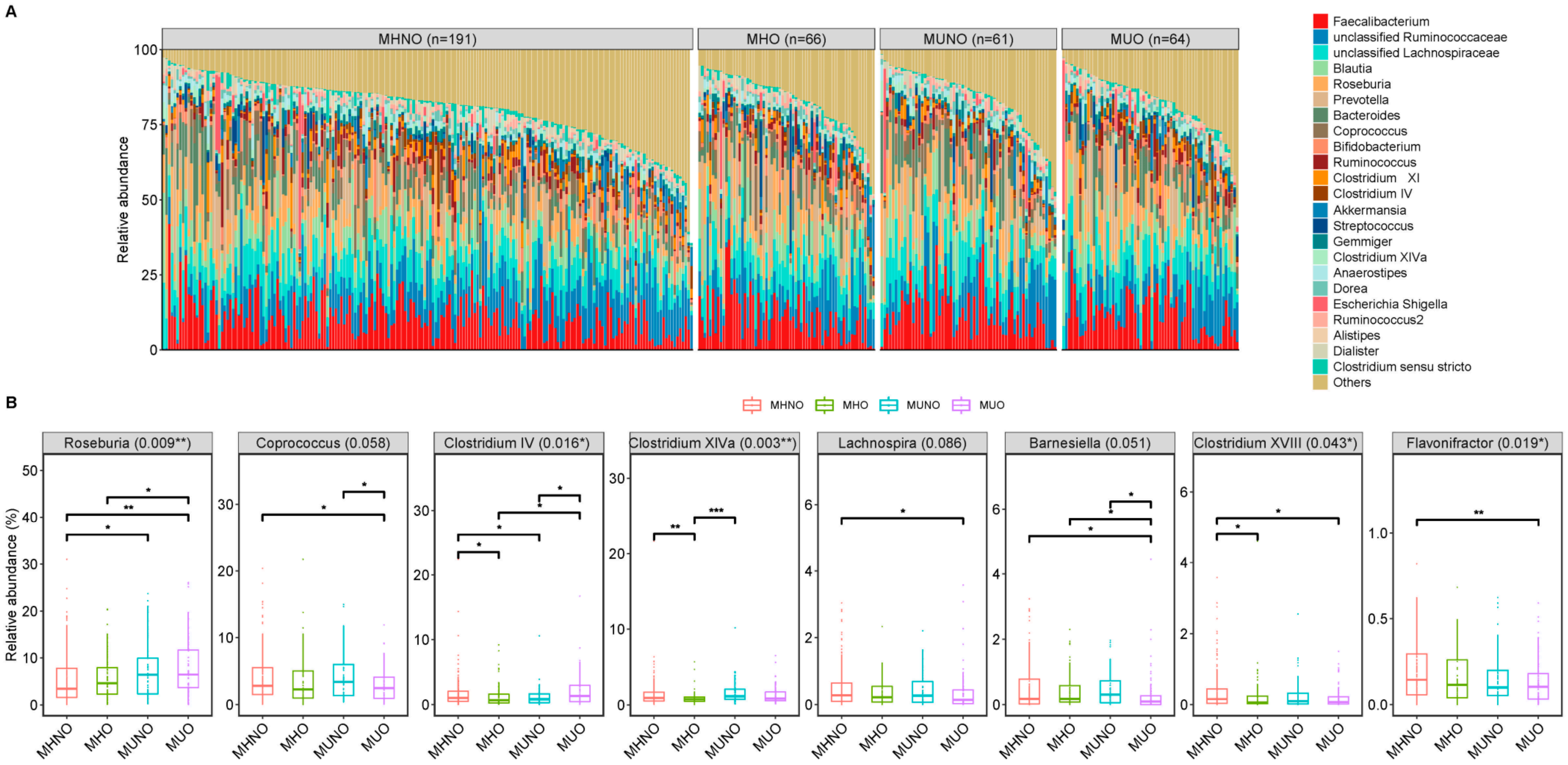

Fig. S5 Gut microbiota composition of MCR cohort at the genus level. (A) bar chart, (B) significantly different genus between MetS groups

Table S1 Linear regression between MetS risk factors and alpha diversity

Variables	Chao1				PD whole tree				Simpson				Shannon				Observed species			
	Coefficient	R^2	p value	FDR	Coefficient	R^2	p value	FDR	Coefficient	R^2	p value	FDR	Coefficient	R^2	p value	FDR	Coefficient	R^2	p value	FDR
BMI	-1.167	0.033	0.355	0.476	-0.105	0.045	0.210	0.359	-0.001	0.048	0.071	0.171	-0.012	0.053	0.095	0.228	-1.307	0.045	0.165	0.330
SBP	-0.437	0.033	0.239	0.410	-0.035	0.045	0.155	0.311	0.000	0.040	0.614	0.670	-0.002	0.047	0.452	0.602	-0.278	0.042	0.317	0.476
DBP	-0.580	0.032	0.357	0.476	-0.046	0.044	0.266	0.389	0.000	0.041	0.430	0.574	0.002	0.047	0.610	0.731	-0.309	0.041	0.510	0.557
WC	-0.608	0.034	0.196	0.393	-0.033	0.043	0.292	0.389	0.000	0.050	**0.041**	0.124	-0.005	0.054	0.072	0.216	-0.458	0.044	0.193	0.331
HbA1C	-0.549	0.032	0.554	0.665	-0.046	0.044	0.456	0.515	-0.001	0.045	0.125	0.251	-0.008	0.053	0.136	0.234	-0.522	0.043	0.451	0.557
Fasting glucose	-9.217	0.039	0.084	0.202	-0.654	0.050	0.065	0.157	-0.005	0.051	**0.026**	0.105	-0.064	0.057	**0.037**	0.147	-7.110	0.050	0.074	0.178
Total cholesterol	14.802	0.048	**0.011**	**0.034**	1.063	0.061	**0.006**	**0.037**	0.006	0.057	**0.013**	0.077	0.089	0.065	**0.008**	**0.045**	11.850	0.061	**0.007**	**0.040**
Triglyceride	-24.634	0.050	**0.006**	**0.022**	-1.346	0.054	**0.023**	0.069	-0.003	0.042	0.399	0.574	-0.069	0.051	0.176	0.265	-14.507	0.053	**0.029**	0.088
HDL-C	2.815	0.031	0.859	0.859	-0.193	0.041	0.854	0.854	0.003	0.041	0.587	0.670	0.038	0.047	0.673	0.734	1.948	0.041	0.869	0.869
Fat percent	-0.443	0.031	0.649	0.708	-0.046	0.042	0.472	0.515	0.000	0.040	0.840	0.840	-0.001	0.046	0.920	0.920	-0.477	0.042	0.511	0.557
LDL-C	22.537	0.061	**0.001**	**0.006**	1.571	0.074	**0.000**	**0.003**	0.007	0.057	**0.010**	0.077	0.110	0.068	**0.003**	**0.038**	16.454	0.069	**0.001**	**0.008**
VLDL-C	-56.416	0.052	**0.004**	**0.022**	-2.968	0.054	**0.023**	0.069	-0.008	0.042	0.306	0.524	-0.172	0.052	0.126	0.234	-32.851	0.053	**0.025**	0.088

P values < 0.05 are in bold.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption)

Table S2 Permutational multivariate analysis of variance using Bray-Curtis distance matrices

Variable	R^2	p value	FDR
Glucose	0.004	**0.016**	0.088
BMI	0.004	**0.022**	0.088
HbA1c	0.004	**0.022**	0.088
WC	0.004	**0.048**	0.144
Fat percent	0.004	0.067	0.161
LDL-C	0.003	0.138	0.249
Triglyceride	0.003	0.145	0.249
VLDL-C	0.003	0.226	0.339
HDL-C	0.003	0.439	0.533
SBP	0.003	0.444	0.533
Total Cholesterol	0.002	0.520	0.567
DBP	0.002	0.579	0.579

P value < 0.05 are in bold.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).

Table S3 Abundant taxa at phylum level within metabolic health groups.

Subjects Without Obesity					
Phylum	**MHNO (%)**	**MUNO (%)**	**Log2FC**	**P value**	**Adjusted p value**
Euryarchaeota	0.067 ± 0.12	0.051 ± 0.091	-1.364	**0.023**	0.09
Bacteroidetes	15.561 ± 11.806	15.377 ± 12.041	0.214	0.254	0.677
Actinobacteria	3.569 ± 4.275	2.933 ± 4.057	-0.205	0.445	0.889
Verrucomicrobia	1.831 ± 3.822	1.306 ± 3.641	-1.094	0.555	0.889
Lentisphaerae	0.012 ± 0.036	0.017 ± 0.079	-0.211	0.794	0.911
Firmicutes	75.944 ± 13.024	77.489 ± 13.516	0.022	0.86	0.911
Proteobacteria	1.922 ± 5.445	2.176 ± 6.093	0.095	0.911	0.911

Subjects With Obesity					
Phylum	**MHO (%)**	**MUO (%)**	**Log2FC**	**P value**	**Adjusted p value**
Firmicutes	75.041 ± 14.418	78.358 ± 12.944	0.295	**0.007**	0.054
Actinobacteria	4.007 ± 4.409	3.185 ± 3.756	-0.429	0.067	0.178
Bacteroidetes	16.69 ± 14.585	14.271 ± 12.41	-0.088	0.761	0.968
Verrucomicrobia	1.584 ± 3.964	1.234 ± 2.455	-0.557	0.824	0.968
Euryarchaeota	0.071 ± 0.168	0.072 ± 0.193	0.193	0.893	0.968
Lentisphaerae	0.015 ± 0.074	0.005 ± 0.023	-0.144	0.929	0.968
Proteobacteria	1.88 ± 4.268	2.303 ± 6.731	-0.017	0.968	0.968

P value < 0.05 are in bold.

Adjusted p values were calculated by DESeq2 test with Benjamini–Hochberg correction.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).

Table S4 Abundant taxa at family level within metabolic health groups.

Subjects Without Obesity

	MHNO (%)	MUNO (%)	Log2FC	P value	Adjusted p value
Lachnospiraceae	31.40 ± 13.63	35.20 ± 14.57	0.436	**0.003**	**0.04**
Bacteroidaceae	5.70 ± 6.789	6.74 ± 7.68	0.732	**0.013**	0.123
Methanobacteriaceae	0.06 ± 0.12	0.05 ± 0.09	-1.174	**0.041**	0.283
Pasteurellaceae	0.06 ± 0.29	0.06 ± 0.25	1.352	**0.049**	0.283
Ruminococcaceae	28.31 ± 9.95	28.95 ± 10.28	0.197	0.101	0.447
Micrococcaceae	0.005 ± 0.01	0.007 ± 0.02	0.919	0.108	0.447
Streptococcaceae	1.15 ± 2.75	1.24 ± 3.45	0.591	0.176	0.609
Actinomycetaceae	0.02 ± 0.03	0.02 ± 0.06	0.439	0.213	0.609
Oxalobacteraceae	0.004 ± 0.01	0.006 ± 0.01	0.67	0.228	0.609
Porphyromonadaceae	1.04 ± 1.05	0.97 ± 0.89	0.315	0.231	0.609
Coriobacteriaceae	1.12 ± 1.18	0.95 ± 0.78	-0.194	0.276	0.64
Erysipelotrichaceae	1.70 ± 1.97	1.51 ± 1.92	0.225	0.287	0.64
Peptostreptococcaceae	2.20 ± 2.82	1.65 ± 2.01	-0.307	0.366	0.755
Peptococcaceae_1	0.03 ± 0.07	0.03 ± 0.06	-0.586	0.39	0.755
Rikenellaceae	1.13 ± 1.61	0.82 ± 0.78	0.144	0.606	0.971
Sutterellaceae	0.13 ± 0.17	0.11 ± 0.20	-0.162	0.673	0.971
Acidaminococcaceae	0.63 ± 0.82	0.63 ± 0.94	-0.179	0.684	0.971
Verrucomicrobiaceae	1.79 ± 3.80	1.29 ± 3.62	-0.75	0.718	0.971
Bifidobacteriaceae	2.42 ± 3.71	1.95 ± 3.60	-0.117	0.737	0.971
Lactobacillaceae	0.50 ± 2.63	0.56 ± 2.17	0.884	0.751	0.971
Clostridiaceae_1	1.17 ± 2.02	0.81 ± 1.44	-0.288	0.771	0.971
Victivallaceae	0.01 ± 0.03	0.016 ± 0.07	-0.18	0.825	0.971
Eubacteriaceae	0.01 ± 0.02	0.004 ± 0.008	-0.12	0.854	0.971
Clostridiales_Incertae_Sedis_XIII	0.03 ± 0.04	0.032 ± 0.06	-0.089	0.876	0.971
Prevotellaceae	6.51 ± 11.41	5.904 ± 11.19	-0.197	0.945	0.971
Veillonellaceae	1.25 ± 1.91	1.471 ± 2.10	-0.084	0.95	0.971
Enterobacteriaceae	1.15 ± 5.15	1.375 ± 5.98	-0.137	0.965	0.971
Desulfovibrionaceae	0.19 ± 0.26	0.25 ± 0.34	0.012	0.971	0.971

Subjects With Obesity

	MHO (%)	MUO (%)	Log2FC	P value	Adjusted p value
Ruminococcaceae	27.98 ± 9.09	29.23 ± 9.24	0.26	0.051	0.781
Bifidobacteriaceae	2.65 ± 3.70	2.03 ± 3.41	-0.709	0.061	0.781
Lachnospiraceae	30.83 ± 13.40	33.37 ± 12.74	0.241	0.081	0.781
Desulfovibrionaceae	0.18 ± 0.26	0.19 ± 0.25	0.57	0.138	0.921
Coriobacteriaceae	1.33 ± 1.42	1.12 ± 1.29	-0.281	0.159	0.921
Peptostreptococcaceae	1.95 ± 2.26	1.98 ± 2.61	0.459	0.202	0.968
Bacteroidaceae	4.83 ± 5.45	5.56 ± 6.40	0.346	0.276	0.968
Rikenellaceae	1.23 ± 1.68	1.04 ± 1.34	-0.348	0.332	0.968
Erysipelotrichaceae	2.08 ± 2.30	1.84 ± 2.67	-0.222	0.425	0.968
Clostridiaceae_1	0.92 ± 1.29	0.95 ± 1.45	0.321	0.452	0.968
Clostridiales_Incertae_Sedis_XIII	0.05 ± 0.07	0.04 ± 0.07	-0.407	0.468	0.968

Peptococcaceae_1	0.03 ± 0.06	0.03 ± 0.09	-0.474	0.591	0.968
Micrococcaceae	0.004 ± 0.01	0.01 ± 0.03	0.364	0.592	0.968
Actinomycetaceae	0.02 ± 0.03	0.02 ± 0.03	0.197	0.629	0.968
Porphyromonadaceae	0.90 ± 0.77	0.72 ± 0.90	-0.152	0.652	0.968
Pasteurellaceae	0.02 ± 0.05	0.06 ± 0.25	0.596	0.684	0.968
Oxalobacteraceae	0.004 ± 0.009	0.004 ± 0.01	0.359	0.689	0.968
Methanobacteriaceae	0.07 ± 0.16	0.07 ± 0.19	-0.282	0.696	0.968
Eubacteriaceae	0.009 ± 0.04	0.007 ± 0.03	-0.331	0.709	0.968
Prevotellaceae	9.19 ± 14.74	6.49 ± 12.15	-0.846	0.794	0.968
Verrucomicrobiaceae	1.58 ± 3.96	1.23 ± 2.45	-0.578	0.797	0.968
Enterobacteriaceae	1.23 ± 4.18	1.78 ± 6.74	0.654	0.838	0.968
Streptococcaceae	2.19 ± 6.74	1.69 ± 2.99	0.252	0.876	0.968
Sutterellaceae	0.23 ± 0.43	0.12 ± 0.15	-0.134	0.884	0.968
Victivallaceae	0.02 ± 0.07	0.005 ± 0.02	-0.134	0.933	0.968
Veillonellaceae	2.08 ± 2.81	1.44 ± 2.68	0.113	0.951	0.968
Lactobacillaceae	0.26 ± 0.81	1.70 ± 6.10	0.199	0.951	0.968
Acidaminococcaceae	0.48 ± 0.66	0.48 ± 0.54	-0.018	0.968	0.968

P values < 0.05 are in bold.

Adjusted p values were calculated by DESeq2 test with Benjamini–Hochberg correction.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).

Table S5 Abundant taxa at genus level within metabolic health groups.

Subjects Without Obesity					
Genus	**MHNO (%)**	**MUNO (%)**	**Log2FC**	**P value**	**Adjusted p value**
Flavonifractor	0.16 ± 0.15	0.12 ± 0.16	-0.628	**0.037**	0.89
Roseburia	5.60 ± 5.50	7.45 ± 6.45	0.354	0.093	0.89
Clostridium_XI	2.19 ± 2.81	1.64 ± 2.00	-0.597	0.096	0.89
Rothia	0.005 ± 0.01	0.007 ± 0.01	0.912	0.102	0.89
Haemophilus	0.06 ± 0.28	0.06 ± 0.24	1.142	0.105	0.89
unclassified Lachnospiraceae	9.34 ± 4.26	10.62 ± 4.47	0.123	0.114	0.89
Butyricicoccus	0.21 ± 0.19	0.25 ± 0.20	0.322	0.14	0.89
Dorea	1.29 ± 0.94	1.48 ± 1.24	0.227	0.144	0.89
unclassified Oxalobacteraceae	0.004 ± 0.01	0.006 ± 0.01	0.841	0.153	0.89
unclassified Coriobacteriaceae	0.24 ± 0.31	0.19 ± 0.24	-0.419	0.17	0.89
unclassified Peptostreptococcaceae	0.007 ± 0.01	0.004 ± 0.01	-1.115	0.17	0.89
Slackia	0.041 ± 0.09	0.04 ± 0.07	0.75	0.173	0.89
unclassified Ruminococcaceae	12.37 ± 7.62	11.64 ± 8.62	-0.278	0.192	0.89
Holdemania	0.012 ± 0.02	0.012 ± 0.01	-0.506	0.195	0.89
Bifidobacterium	2.42 ± 3.70	1.95 ± 3.60	-0.486	0.198	0.89
Faecalibacterium	10.78 ± 7.32	12.45 ± 8.35	0.265	0.198	0.89
Barnesiella	0.48 ± 0.67	0.48 ± 0.52	0.495	0.228	0.945
Lachnospira	0.86 ± 0.93	0.69 ± 0.66	-0.318	0.236	0.945
Gemmiger	1.31 ± 1.19	1.46 ± 1.58	0.279	0.273	0.992
Ruminococcus	2.36 ± 2.83	1.96 ± 2.05	-0.291	0.303	0.992
Butyricimonas	0.05 ± 0.07	0.04 ± 0.05	-0.431	0.318	0.992
Allisonella	0.02 ± 0.11	0.03 ± 0.05	0.579	0.354	0.992
Methanobrevibacter	0.06 ± 0.11	0.05 ± 0.08	-1.047	0.363	0.992
Sporobacter	0.004 ± 0.0	0.003 ± 0.01	-0.46	0.371	0.992
Clostridium_IV	0.78 ± 1.01	0.78 ± 1.35	0.222	0.417	0.992
Ruminococcus2	0.90 ± 0.92	1.06 ± 1.28	-0.161	0.418	0.992
Sutterella	0.09 ± 0.15	0.07 ± 0.19	-0.41	0.438	0.992
Peptococcus	0.03 ± 0.07	0.03 ± 0.06	-0.51	0.473	0.992
Mogibacterium	0.03 ± 0.05	0.03 ± 0.06	-0.437	0.484	0.992
Collinsella	0.67 ± 0.83	0.61 ± 0.67	-0.209	0.502	0.992
Clostridium_XVIII	0.36 ± 0.56	0.26 ± 0.4	-0.226	0.51	0.992
Asaccharobacter	0.04 ± 0.06	0.03 ± 0.05	-0.242	0.534	0.992
unclassified Desulfovibrionaceae	0.03 ± 0.10	0.02 ± 0.07	-0.496	0.544	0.992
Parasutterella	0.04 ± 0.10	0.04 ± 0.07	0.369	0.548	0.992
Howardella	0.04 ± 0.07	0.04 ± 0.05	-0.28	0.555	0.992
Alistipes	1.13 ± 1.62	0.82 ± 0.78	-0.17	0.573	0.992
Anaerofilum	0.003 ± 0.01	0.005 ± 0.009	0.281	0.589	0.992
Turicibacter	0.16 ± 0.35	0.11 ± 0.22	-0.297	0.597	0.992
Anaerotruncus	0.008 ± 0.01	0.01 ± 0.023	0.201	0.604	0.992
Victivallis	0.01 ± 0.03	0.03 ± 0.07	0.433	0.629	0.992
Eggerthella	0.02 ± 0.05	0.01 ± 0.02	-0.244	0.637	0.992

Clostridium_XlVb	0.15 ± 0.27	0.11 ± 0.19	-0.171	0.641	0.992
Coprococcus	3.93 ± 3.54	3.92 ± 3.26	0.086	0.688	0.992
Clostridium_sensu_stricto	1.16 ± 2.01	0.78 ± 1.42	-0.402	0.702	0.992
Actinomyces	0.02 ± 0.026	0.02 ± 0.05	0.127	0.723	0.992
unclassified Erysipelotrichaceae	0.68 ± 1.16	0.49 ± 0.99	-0.151	0.727	0.992
Parabacteroides	0.16 ± 0.30	0.20 ± 0.29	0.148	0.728	0.992
Enterorhabdus	0.03 ± 0.04	0.02 ± 0.04	0.222	0.736	0.992
Akkermansia	1.79 ± 3.80	1.29 ± 3.62	-0.863	0.738	0.992
Oscillibacter	0.28 ± 0.29	0.25 ± 0.21	-0.082	0.738	0.992
Lactobacillus	0.5 ± 2.61	0.56 ± 2.17	0.831	0.755	0.992
Anaerostipes	1.39 ± 1.77	1.30 ± 1.40	-0.071	0.782	0.992
Odoribacter	0.06 ± 0.13	0.05 ± 0.05	0.083	0.783	0.992
Bilophila	0.06 ± 0.08	0.06 ± 0.07	-0.078	0.827	0.992
Gordonibacter	0.007 ± 0.02	0.009 ± 0.02	-0.116	0.83	0.992
unclassified Porphyromonadaceae	0.26 ± 0.727	0.19 ± 0.633	-0.314	0.852	0.992
Desulfovibrio	0.10 ± 0.21	0.17 ± 0.31	-0.149	0.859	0.992
Veillonella	0.05 ± 0.13	0.06 ± 0.15	0.172	0.864	0.992
Clostridium_XlVa	1.18 ± 1.77	1.43 ± 1.73	-0.035	0.87	0.992
unclassified Veillonellaceae	0.02 ± 0.04	0.03 ± 0.11	-0.176	0.893	0.992
Catenibacterium	0.47 ± 1.40	0.61 ± 1.52	0.467	0.894	0.992
Alloprevotella	0.22 ± 0.73	0.08 ± 0.23	-0.404	0.901	0.992
Blautia	6.65 ± 5.24	7.05 ± 5.77	0.015	0.913	0.992
Paraprevotella	0.15 ± 0.53	0.13 ± 0.31	-0.16	0.922	0.992
Prevotella	6.00 ± 11.16	5.6 ± 11.09	-0.362	0.926	0.992
unclassified Prevotellaceae	0.15 ± 0.80	0.08 ± 0.18	0.16	0.937	0.992
Olsenella	0.07 ± 0.38	0.03 ± 0.07	0.126	0.937	0.992
Dialister	1.02 ± 1.79	1.06 ± 1.74	0.149	0.959	0.992
Bacteroides	5.70 ± 6.78	6.73 ± 7.68	0.013	0.962	0.992
Escherichia/Shigella	1.00 ± 4.85	1.25 ± 5.97	-0.083	0.98	0.992
Phascolarctobacterium	0.55 ± 0.79	0.52 ± 0.92	0.027	0.985	0.992
Streptococcus	1.15 ± 2.75	1.23 ± 3.45	0.004	0.992	0.992

Subjects With Obesity

Genus	MHO (%)	MUO (%)	Log2FC	P value	Adjusted p value
unclassified Coriobacteriaceae	0.25 ± 0.30	0.23 ± 0.57	-0.773	**0.02**	0.61
Blautia	7.01 ± 4.48	7.11 ± 5.98	-0.397	**0.023**	0.61
Odoribacter	0.06 ± 0.07	0.04 ± 0.05	-0.811	**0.034**	0.61
Enterorhabdus	0.03 ± 0.05	0.02 ± 0.03	-1.644	**0.041**	0.61
Dorea	1.41 ± 1.05	1.34 ± 1.03	-0.395	0.05	0.61
Bifidobacterium	2.65 ± 3.70	2.02 ± 3.41	-0.744	0.058	0.61
Roseburia	5.82 ± 4.70	7.92 ± 6.32	0.426	0.061	0.61
Gemmiger	1.56 ± 1.92	1.55 ± 1.72	-0.516	0.083	0.61
Howardella	0.05 ± 0.06	0.04 ± 0.05	-0.94	0.085	0.61
Asaccharobacter	0.04 ± 0.05	0.03 ± 0.05	-0.741	0.089	0.61
Slackia	0.05 ± 0.08	0.03 ± 0.05	-0.885	0.099	0.61

Anaerofilum	0.006 ± 0.009	0.005 ± 0.009	-0.852	0.102	0.61
Alistipes	1.22 ± 1.68	1.03 ± 1.34	-0.56	0.112	0.621
Mogibacterium	0.05 ± 0.07	0.04 ± 0.07	-0.857	0.144	0.712
Allisonella	0.019 ± 0.04	0.01 ± 0.02	-1.239	0.148	0.712
Barnesiella	0.42 ± 0.50	0.34 ± 0.71	-1.577	0.16	0.72
Coprococcus	3.61 ± 3.78	2.87 ± 2.58	-0.363	0.181	0.743
Flavonifractor	0.13 ± 0.15	0.11 ± 0.12	-0.501	0.186	0.743
unclassified Lachnospiraceae	9.33 ± 4.05	10.11 ± 4.45	-0.137	0.201	0.76
Collinsella	0.84 ± 1.07	0.75 ± 0.98	-0.342	0.247	0.887
Gordonibacter	0.008 ± 0.01	0.006 ± 0.01	-0.642	0.267	0.915
unclassified Ruminococcaceae	11.53 ± 8.14	12.22 ± 7.70	-0.217	0.315	0.984
Anaerotruncus	0.01 ± 0.02	0.017 ± 0.03	0.453	0.316	0.984
Anaerostipes	0.96 ± 0.95	0.85 ± 0.96	-0.293	0.338	0.984
Peptococcus	0.03 ± 0.06	0.03 ± 0.09	-0.835	0.355	0.984
Clostridium_XlVa	0.84 ± 0.76	1.19 ± 1.21	0.177	0.355	0.984
unclassified Peptostreptococcaceae	0.008 ± 0.02	0.004 ± 0.01	-0.801	0.378	0.984
unclassified Erysipelotrichaceae	0.90 ± 1.31	0.7 ± 1.11	-0.419	0.383	0.984
Butyricimonas	0.05 ± 0.06	0.05 ± 0.08	-0.425	0.413	0.99
Bilophila	0.07 ± 0.1	0.06 ± 0.08	-0.323	0.444	0.99
Holdemania	0.01 ± 0.02	0.01 ± 0.02	0.293	0.488	0.99
Sporobacter	0.005 ± 0.01	0.004 ± 0.01	-0.388	0.5	0.99
Ruminococcus2	0.92 ± 0.83	1.02 ± 1.52	0.17	0.501	0.99
unclassified Veillonellaceae	0.008 ± 0.02	0.009 ± 0.03	-0.634	0.51	0.99
unclassified Desulfovibrionaceae	0.04 ± 0.122	0.028 ± 0.12	-0.676	0.514	0.99
Veillonella	0.03 ± 0.05	0.07 ± 0.17	0.433	0.516	0.99
Clostridium_XlVb	0.15 ± 0.27	0.14 ± 0.17	-0.231	0.558	0.99
unclassified Prevotellaceae	0.25 ± 0.73	0.14 ± 0.77	-1.119	0.568	0.99
Faecalibacterium	11.26 ± 7.91	11.21 ± 7.91	0.13	0.608	0.99
Ruminococcus	2.24 ± 2.45	2.48 ± 2.32	0.124	0.656	0.99
Desulfovibrio	0.08 ± 0.23	0.10 ± 0.20	0.465	0.657	0.99
Clostridium_XI	1.94 ± 2.24	1.98 ± 2.61	0.149	0.683	0.99
Turicibacter	0.14 ± 0.29	0.12 ± 0.19	-0.215	0.688	0.99
Butyricicoccus	0.22 ± 0.19	0.2 ± 0.15	-0.084	0.722	0.99
Haemophilus	0.02 ± 0.04	0.06 ± 0.24	0.474	0.744	0.99
unclassified Porphyromonadaceae	0.19 ± 0.51	0.09 ± 0.20	0.459	0.768	0.99
Akkermansia	1.58 ± 3.96	1.23 ± 2.45	-0.728	0.78	0.99
Bacteroides	4.83 ± 5.45	5.56 ± 6.40	0.084	0.787	0.99
Actinomyces	0.02 ± 0.02	0.02 ± 0.03	-0.103	0.81	0.99
Sutterella	0.16 ± 0.40	0.05 ± 0.08	-0.318	0.819	0.99
Olsenella	0.09 ± 0.32	0.03 ± 0.06	-0.391	0.824	0.99
Catenibacterium	0.75 ± 1.88	0.78 ± 2.09	-0.689	0.832	0.99
Dialister	1.47 ± 2.47	0.67 ± 1.26	-0.675	0.835	0.99
Rothia	0.004 ± 0.01	0.01 ± 0.02	0.126	0.847	0.99
Clostridium_sensu_stricto	0.92 ± 1.29	0.95 ± 1.45	-0.08	0.853	0.99

Prevotella	8.73 ± 14.64	6.16 ± 12.04	-0.58	0.858	0.99
Parabacteroides	0.17 ± 0.22	0.19 ± 0.24	-0.073	0.87	0.99
Paraprevotella	0.05 ± 0.14	0.08 ± 0.21	0.262	0.878	0.99
Alloprevotella	0.14 ± 0.47	0.10 ± 0.26	-0.491	0.88	0.99
Phascolarctobacterium	0.40 ± 0.61	0.45 ± 0.55	-0.196	0.882	0.99
Victivallis	0.015 ± 0.07	0.005 ± 0.02	-0.213	0.886	0.99
Escherichia/Shigella	1.18 ± 4.15	1.49 ± 6.65	0.398	0.902	0.99
Eggerthella	0.009 ± 0.02	0.015 ± 0.06	-0.124	0.903	0.99
Parasutterella	0.07 ± 0.21	0.07 ± 0.14	0.074	0.922	0.99
Clostridium_XVIII	0.26 ± 0.56	0.21 ± 0.33	-0.039	0.928	0.99
Streptococcus	2.19 ± 6.74	1.69 ± 2.99	0.079	0.961	0.99
Methanobrevibacter	0.07 ± 0.16	0.07 ± 0.19	0.056	0.967	0.99
Lactobacillus	0.26 ± 0.81	1.69 ± 6.06	0.131	0.968	0.99
unclassified Oxalobacteraceae	0.004 ± 0.009	0.004 ± 0.01	0.024	0.978	0.99
Lachnospira	0.69 ± 0.64	0.71 ± 0.93	0.009	0.979	0.99
Oscillibacter	0.22 ± 0.16	0.26 ± 0.33	-0.006	0.984	0.99
Clostridium_IV	0.77 ± 1.27	1.16 ± 2.28	-0.004	0.99	0.99

P values < 0.05 are in bold.

Adjusted p values were calculated by DESeq2 test with Benjamini–Hochberg correction.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).

Table S6 Significant results of linear regression between metabolic health markers and phylum relative abundance

Health markers	Genus	Coefficient	R^2	p value	FDR
Glucose	Verrucomicrobia	-0.612	0.021	**<0.001**	**0.009**

P values < 0.05 are in bold. Only significant results are shown.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).

Table S7 Significant results of linear regression between metabolic health markers and family relative abundance

Health markers	Genus	Coefficient	R^2	p value	FDR
Fat percent	Acidaminococcaceae	-0.024	0.032	**0.001**	**0.010**
BMI	Clostridiales_Incertae_Sedis_XIII	0.002	0.065	**0.008**	**0.047**
Lowest Rib Circumference	Acidaminococcaceae	0.001	0.068	**0.005**	**0.047**
Fat percent	Clostridiales_Incertae_Sedis_XIII	0.001	0.064	**0.012**	**0.047**
Fat percent	Pasteurellaceae	-0.007	0.023	**0.004**	**0.047**
Glucose	Verrucomicrobiaceae	-0.608	0.021	**0.001**	**0.009**

P values < 0.05 are in bold. Only significant results are shown.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).

Table S8 Significant results of linear regression between metabolic health markers and genus relative abundance

Health markers	**Genus**	**Coefficient**	**R^2**	**p value**	**FDR**
HDL-C	Blautia	2.84E+00	0.050	**<0.001**	**0.003**
Glucose	Akkermansia	-6.08E-01	0.021	**<0.001**	**0.009**
Waist circumference	Gemmiger	2.27E-02	0.030	**<0.001**	**0.007**
BMI	Anaerostipes	-5.45E-02	0.067	**0.002**	**0.019**
Waist circumference	Anaerostipes	-1.80E-02	0.061	**0.005**	**0.031**
Total cholesterol	Clostridium_IV	2.29E-01	0.052	**0.003**	**0.018**
LDL-C	Clostridium_IV	2.71E-01	0.055	**0.002**	**0.018**
Triglyceride	Collinsella	2.20E-01	0.054	**0.002**	**0.015**
VLDL-C	Collinsella	5.10E-01	0.056	**0.001**	**0.015**
Fat percent	Phascolarctobacterium	-2.18E-02	0.032	**0.001**	**0.017**
DBP	Parabacteroides	4.88E-03	0.031	**0.003**	**0.039**
HbA1C	Paraprevotella	1.06E-02	0.029	**0.003**	**0.034**
BMI	Mogibacterium	1.83E-03	0.065	**0.008**	**0.047**
Waist circumference	Mogibacterium	7.29E-04	0.068	**0.005**	**0.047**
Fat percent	Mogibacterium	1.35E-03	0.064	**0.012**	**0.047**
SBP	Allisonella	8.85E-04	0.031	**0.003**	**0.034**
BMI	Anaerofilum	2.39E-04	0.034	**0.010**	**0.023**
Waist circumference	Anaerofilum	1.05E-04	0.041	**0.002**	**0.009**
Triglyceride	Anaerofilum	2.01E-03	0.040	**0.002**	**0.009**
Fat percent	Anaerofilum	2.15E-04	0.039	**0.002**	**0.009**
VLDL-C	Anaerofilum	4.29E-03	0.038	**0.003**	**0.009**

P values < 0.05 are in bold. Only significant results are shown.

Permutational multivariate analysis adjusted for age, sex, disease status (CVD and T2DM), medication use (blood pressure, cholesterol lowering and diabetes medication), lifestyle factors (DASH score, smoking status and alcohol consumption).