

Supplementary Table 2. Difference in genera abundance between those who did and did not meet recommendations of 60 or more minutes of daily moderate-to-vigorous physical activity.

Genus	Unadjusted			Adjusted ^b		
	log ₂ FC ^a	SE	P _{FDR}	log ₂ FC ^a	SE	P _{FDR}
<i>Abiotrophia</i>	0.814	0.508	6.19E-01	0.737	0.556	5.56E-01
<i>Acetanaerobacterium</i>	0.187	0.294	9.53E-01	0.162	0.300	9.28E-01
<i>Acidaminococcus</i>	-2.582	2.938	9.53E-01	-5.415	2.998	4.21E-01
<i>Actinomyces</i>	-0.226	0.144	6.34E-01	-0.269	0.147	4.21E-01
<i>Adlercreutzia</i>	-0.475	0.208	3.69E-01	-0.529	0.216	1.86E-01
<i>Agathobacter</i>	-0.313	0.161	5.44E-01	-0.227	0.163	5.25E-01
<i>Akkermansia</i>	-0.345	0.576	9.55E-01	-0.321	0.592	9.28E-01
<i>Alistipes</i>	0.030	0.221	9.59E-01	-0.006	0.227	9.96E-01
<i>Allisonella</i>	1.085	1.233	9.53E-01	2.218	1.200	4.21E-01
<i>Alloprevotella</i>	-4.792	2.935	5.99E-01	-2.383	2.997	8.21E-01
<i>Alloscardovia</i>	-0.464	1.702	9.55E-01	-0.335	2.841	9.76E-01
<i>Anaerococcus</i>	0.009	0.489	9.91E-01	0.101	0.512	9.73E-01
<i>Anaerofilum</i>	0.264	0.356	9.53E-01	0.135	0.366	9.56E-01
<i>Anaerofustis</i>	-0.450	0.300	6.34E-01	-0.575	0.306	4.21E-01
<i>Anaerostipes</i>	0.039	0.110	9.55E-01	0.025	0.113	9.73E-01
<i>Anaerotruncus</i>	-0.136	0.273	9.55E-01	0.395	0.320	6.13E-01
<i>Anaerovorax</i>	0.391	2.535	9.59E-01	0.479	2.999	9.76E-01
<i>Angelakisella</i>	-0.075	0.328	9.55E-01	-0.299	0.342	7.97E-01
<i>Atopobium</i>	-0.440	0.335	7.04E-01	-0.499	0.344	5.10E-01
<i>Bacteroides</i>	0.134	0.186	9.53E-01	0.293	0.188	4.83E-01
<i>Barnesiella</i>	-0.173	0.859	9.55E-01	-0.121	0.929	9.76E-01
<i>Bifidobacterium</i>	-0.318	0.207	6.34E-01	-0.327	0.210	4.83E-01
<i>Bilophila</i>	0.089	0.255	9.55E-01	0.118	0.264	9.31E-01
<i>Blautia</i>	-0.084	0.079	8.48E-01	-0.116	0.082	5.24E-01
<i>Butyricicoccus</i>	-0.138	0.164	9.53E-01	-0.112	0.168	8.40E-01
<i>Butyricimonas</i>	0.127	0.599	9.55E-01	0.230	0.625	9.56E-01
<i>Butyrivibrio</i>	2.639	2.939	9.53E-01	9.768	2.997	4.04E-02
CAG-352	0.605	1.198	9.55E-01	1.543	1.138	5.37E-01
CAG-56	0.092	0.330	9.55E-01	0.013	0.346	9.96E-01
<i>Campylobacter</i>	0.731	0.581	7.20E-01	0.622	0.633	7.58E-01
<i>Candidatus_Soleaferrea</i>	-0.586	0.166	2.39E-02	-0.545	0.165	4.04E-02
<i>Candidatus_Stoquefichus</i>	-0.838	0.666	7.20E-01	-0.076	0.700	9.79E-01
<i>Caproiciproducens</i>	0.798	0.539	6.34E-01	-0.002	0.522	9.99E-01
<i>Catabacter</i>	-0.308	0.316	9.19E-01	-0.019	0.337	9.96E-01
<i>Catenibacterium</i>	0.955	1.679	9.55E-01	1.002	1.579	8.50E-01
<i>Christensenellaceae_R-7_group</i>	-0.176	0.230	9.53E-01	-0.071	0.242	9.73E-01
<i>Clostridium_sensu_stricto_1</i>	-0.169	0.237	9.53E-01	-0.235	0.250	7.72E-01
<i>Collinsella</i>	-0.404	0.247	5.99E-01	-0.399	0.254	4.83E-01
<i>Coprobacillus</i>	-0.366	0.502	9.53E-01	-0.159	0.528	9.72E-01
<i>Coprobacter</i>	0.844	1.312	9.53E-01	0.654	1.540	9.31E-01
<i>Coprococcus_1</i>	-0.077	0.280	9.55E-01	-0.238	0.290	8.02E-01
<i>Coprococcus_2</i>	0.106	0.511	9.55E-01	-0.372	0.531	8.40E-01
<i>Coprococcus_3</i>	0.057	0.215	9.55E-01	0.048	0.226	9.73E-01
<i>Corynebacterium</i>	-0.530	0.305	5.99E-01	-0.676	0.320	2.97E-01
<i>Corynebacterium_1</i>	-0.073	0.858	9.59E-01	-0.083	1.080	9.96E-01
<i>Cuneatibacter</i>	0.337	0.743	9.55E-01	-1.033	0.820	6.06E-01
<i>Defluviitaleaceae_UCG-011</i>	0.213	0.865	9.55E-01	-0.842	0.987	7.97E-01
<i>Desulfovibrio</i>	-0.037	0.603	9.73E-01	0.037	0.633	9.96E-01
<i>Dialister</i>	-0.268	0.394	9.53E-01	-0.279	0.407	8.40E-01
<i>Dielma</i>	-0.477	0.352	7.04E-01	-0.705	0.362	4.06E-01
DNF00809	-0.170	0.248	9.53E-01	-0.378	0.252	4.88E-01
<i>Dorea</i>	-0.087	0.137	9.53E-01	-0.123	0.143	7.97E-01
DTU089	-0.109	0.268	9.55E-01	-0.086	0.280	9.72E-01
<i>Eggerthella</i>	-0.538	0.246	4.33E-01	-0.527	0.248	2.97E-01
<i>Eisenbergiella</i>	-0.163	0.303	9.55E-01	0.495	0.349	5.24E-01
<i>Enterorhabdus</i>	2.311	2.110	8.48E-01	2.824	1.937	5.10E-01
<i>Erysipelatoclostridium</i>	0.036	0.204	9.55E-01	0.081	0.208	9.48E-01

Genus	Unadjusted			Adjusted ^b		
	log ₂ FC ^a	SE	p _{FDR}	log ₂ FC ^a	SE	p _{FDR}
<i>Erysipelotrichaceae_UCG-003</i>	-0.323	0.188	5.99E-01	-0.334	0.190	4.35E-01
<i>Eubacterium</i>	-1.404	0.587	3.69E-01	-1.754	0.636	8.97E-02
<i>Ezakiella</i>	0.624	0.382	5.99E-01	0.086	0.422	9.73E-01
<i>F0332</i>	-0.770	0.522	6.34E-01	-0.600	0.582	7.35E-01
<i>Faecalibacterium</i>	0.210	0.145	6.34E-01	0.229	0.150	4.88E-01
<i>Faecalitalea</i>	0.159	0.394	9.55E-01	0.374	0.407	7.72E-01
<i>Family_XIII_AD3011_group</i>	-0.415	0.202	5.44E-01	-0.455	0.201	2.40E-01
<i>Family_XIII_UCG-001</i>	0.311	0.290	8.48E-01	0.081	0.302	9.73E-01
<i>Fingoldia</i>	0.632	0.536	7.71E-01	-1.094	0.657	4.68E-01
<i>Flavonifractor</i>	-0.186	0.229	9.53E-01	0.256	0.220	6.38E-01
<i>Fournierella</i>	-0.412	0.416	9.10E-01	-0.622	0.406	4.88E-01
<i>Fusicatenibacter</i>	0.108	0.138	9.53E-01	0.120	0.140	7.97E-01
<i>Fusobacterium</i>	0.351	1.132	9.55E-01	0.965	1.351	8.40E-01
<i>Gallicola</i>	-0.035	0.759	9.80E-01	-0.375	0.891	9.31E-01
<i>GCA-900066225</i>	-0.325	0.246	7.04E-01	-0.313	0.251	6.09E-01
<i>GCA-900066575</i>	0.102	0.245	9.55E-01	-0.132	0.256	9.31E-01
<i>GCA-900066755</i>	-0.548	0.393	6.86E-01	-0.472	0.407	6.38E-01
<i>Gemella</i>	-0.311	0.226	6.92E-01	-0.377	0.231	4.68E-01
<i>Gordonibacter</i>	-1.019	0.222	3.82E-04	-0.799	0.222	1.89E-02
<i>Granulicatella</i>	0.146	0.222	9.53E-01	0.213	0.231	7.72E-01
<i>Haemophilus</i>	0.071	0.337	9.55E-01	-0.302	0.359	7.97E-01
<i>Harryflintia</i>	-0.413	0.490	9.53E-01	-0.426	0.510	7.97E-01
<i>Holdemanella</i>	0.261	0.896	9.55E-01	-0.217	0.939	9.73E-01
<i>Holdemania</i>	-0.186	0.194	9.26E-01	-0.098	0.196	9.31E-01
<i>Howardella</i>	0.413	2.161	9.55E-01	0.516	2.146	9.73E-01
<i>Hungatella</i>	-0.097	0.301	9.55E-01	0.362	0.324	6.71E-01
<i>Hydrogenoanaerobacterium</i>	-0.434	0.860	9.55E-01	-0.219	1.024	9.73E-01
<i>Intestinibacter</i>	-0.457	0.174	3.15E-01	-0.482	0.176	8.97E-02
<i>Intestinimonas</i>	0.129	0.281	9.55E-01	-0.191	0.280	8.40E-01
<i>Lachnoclostridium</i>	-0.232	0.142	5.99E-01	-0.202	0.144	5.25E-01
<i>Lachnospira</i>	-0.142	0.257	9.55E-01	-0.250	0.269	7.72E-01
<i>Lachnospiraceae_FCS020_group</i>	0.081	0.216	9.55E-01	0.017	0.226	9.96E-01
<i>Lachnospiraceae_ND3007_group</i>	0.157	0.259	9.55E-01	0.131	0.268	9.31E-01
<i>Lachnospiraceae_NK4A136_group</i>	0.050	0.254	9.55E-01	-0.118	0.261	9.31E-01
<i>Lachnospiraceae_NK4B4_group</i>	2.394	1.024	3.69E-01	3.047	1.100	8.97E-02
<i>Lachnospiraceae_UCG-001</i>	-0.149	0.336	9.55E-01	-0.260	0.348	8.40E-01
<i>Lachnospiraceae_UCG-003</i>	0.628	1.435	9.55E-01	4.678	1.643	8.87E-02
<i>Lachnospiraceae_UCG-004</i>	0.188	0.257	9.53E-01	0.222	0.266	7.97E-01
<i>Lachnospiraceae_UCG-010</i>	-0.050	0.268	9.55E-01	0.009	0.274	9.96E-01
<i>Lactobacillus</i>	0.938	0.409	3.69E-01	0.213	0.453	9.31E-01
<i>Lactococcus</i>	-0.728	0.298	3.69E-01	-0.442	0.324	5.37E-01
<i>Leuconostoc</i>	0.505	0.601	9.53E-01	1.037	0.664	4.83E-01
<i>Marvinbryantia</i>	0.057	0.264	9.55E-01	-0.124	0.273	9.31E-01
<i>Megamonas</i>	2.076	1.599	7.04E-01	7.749	1.629	3.56E-04
<i>Megasphaera</i>	-1.882	1.570	7.59E-01	-3.448	1.612	2.97E-01
<i>Merdibacter</i>	-0.114	0.546	9.55E-01	0.491	0.567	7.97E-01
<i>Methanobrevibacter</i>	-0.537	1.001	9.55E-01	-0.699	1.051	8.40E-01
<i>Mogibacterium</i>	2.042	0.365	4.07E-06	0.891	0.393	2.40E-01
<i>Moryella</i>	-0.332	1.821	9.55E-01	-0.431	2.999	9.76E-01
<i>Murdochiella</i>	0.202	0.516	9.55E-01	-0.256	0.552	9.31E-01
<i>Negativibacillus</i>	-1.227	0.412	1.33E-01	-0.858	0.436	4.04E-01
<i>Negativicoccus</i>	0.122	1.123	9.59E-01	0.215	1.618	9.76E-01
<i>Odoribacter</i>	0.205	0.363	9.55E-01	0.119	0.383	9.72E-01
<i>Olsenella</i>	2.729	2.100	7.04E-01	-0.405	2.557	9.76E-01
<i>Oribacterium</i>	0.006	0.807	9.95E-01	0.020	1.063	9.96E-01
<i>Oscillibacter</i>	-0.413	0.239	5.99E-01	-0.173	0.246	8.40E-01
<i>Oscillospira</i>	0.318	0.480	9.53E-01	0.158	0.508	9.72E-01
<i>Oxalobacter</i>	0.115	0.758	9.59E-01	-0.352	0.722	9.31E-01
<i>Paeniclostridium</i>	0.473	0.866	9.55E-01	-1.821	1.016	4.21E-01

Genus	Unadjusted			Adjusted ^b		
	log ₂ FC ^a	SE	P _{FDR}	log ₂ FC ^a	SE	P _{FDR}
<i>Parabacteroides</i>	0.442	0.230	5.44E-01	0.426	0.235	4.21E-01
<i>Paraprevotella</i>	1.384	1.035	7.04E-01	0.138	1.083	9.76E-01
<i>Parasutterella</i>	-0.599	0.366	5.99E-01	-0.435	0.372	6.38E-01
<i>Parvimonas</i>	-0.144	0.358	9.55E-01	-0.158	0.369	9.31E-01
<i>Pediococcus</i>	0.550	1.043	9.55E-01	-1.321	1.224	7.06E-01
<i>Peptococcus</i>	-1.129	0.733	6.34E-01	-1.406	0.851	4.68E-01
<i>Peptoniphilus</i>	0.112	0.380	9.55E-01	-0.329	0.431	8.39E-01
<i>Peptostreptococcus</i>	-1.169	1.159	9.00E-01	-0.336	1.552	9.73E-01
<i>Phascolarctobacterium</i>	-0.100	0.513	9.55E-01	-0.219	0.538	9.37E-01
<i>Phoceae</i>	-0.213	0.283	9.53E-01	-0.170	0.289	8.91E-01
<i>Porphyromonas</i>	0.289	0.425	9.53E-01	-0.211	0.452	9.31E-01
<i>Prevotella</i>	0.212	0.421	9.55E-01	0.196	0.444	9.31E-01
<i>Prevotella_2</i>	4.805	2.938	5.99E-01	9.577	2.998	4.23E-02
<i>Prevotella_6</i>	-0.207	0.693	9.55E-01	-1.377	0.772	4.21E-01
<i>Prevotella_7</i>	1.742	0.750	3.69E-01	0.907	0.763	6.38E-01
<i>Prevotella_9</i>	1.531	0.788	5.44E-01	0.220	0.844	9.73E-01
<i>Pyramidobacter</i>	-0.272	2.065	9.59E-01	-4.518	2.982	4.88E-01
<i>Raoultibacter</i>	-0.874	0.704	7.20E-01	-0.208	0.788	9.73E-01
<i>Rikenellaceae_RC9_gut_group</i>	1.073	2.935	9.55E-01	9.385	2.998	4.52E-02
<i>Romboutsia</i>	-0.360	0.201	5.99E-01	-0.144	0.213	8.40E-01
<i>Roseburia</i>	-0.060	0.213	9.55E-01	-0.137	0.216	8.50E-01
<i>Rothia</i>	-0.237	0.308	9.53E-01	-0.153	0.311	9.31E-01
<i>Ruminiclostridium_1</i>	0.102	1.029	9.59E-01	-2.783	1.158	1.96E-01
<i>Ruminiclostridium_5</i>	-0.114	0.158	9.53E-01	-0.263	0.163	4.73E-01
<i>Ruminiclostridium_6</i>	-0.701	0.353	5.44E-01	-0.470	0.370	6.06E-01
<i>Ruminiclostridium_9</i>	0.173	0.221	9.53E-01	-0.042	0.232	9.76E-01
<i>Ruminococcaceae_NK4A214_group</i>	-0.321	0.301	8.48E-01	-0.337	0.323	7.35E-01
<i>Ruminococcaceae_UCG-002</i>	-0.143	0.263	9.55E-01	-0.393	0.263	4.88E-01
<i>Ruminococcaceae_UCG-003</i>	-0.029	0.301	9.59E-01	-0.309	0.304	7.35E-01
<i>Ruminococcaceae_UCG-004</i>	-0.091	0.234	9.55E-01	-0.081	0.242	9.72E-01
<i>Ruminococcaceae_UCG-005</i>	0.036	0.282	9.59E-01	-0.192	0.283	8.40E-01
<i>Ruminococcaceae_UCG-007</i>	-0.488	0.448	8.48E-01	-0.456	0.465	7.58E-01
<i>Ruminococcaceae_UCG-008</i>	0.335	0.647	9.55E-01	0.146	0.737	9.73E-01
<i>Ruminococcaceae_UCG-009</i>	0.505	0.479	8.51E-01	0.589	0.484	6.22E-01
<i>Ruminococcaceae_UCG-010</i>	-0.102	0.413	9.55E-01	-0.422	0.412	7.35E-01
<i>Ruminococcaceae_UCG-011</i>	0.713	0.787	9.53E-01	-0.528	0.800	8.40E-01
<i>Ruminococcaceae_UCG-013</i>	0.014	0.166	9.59E-01	-0.293	0.177	4.68E-01
<i>Ruminococcaceae_UCG-014</i>	-0.366	0.489	9.53E-01	-0.839	0.495	4.65E-01
<i>Ruminococcus_1</i>	-0.023	0.244	9.59E-01	-0.030	0.254	9.76E-01
<i>Ruminococcus_2</i>	-0.641	0.440	6.34E-01	-0.751	0.459	4.68E-01
<i>S5-A14a</i>	0.017	0.558	9.86E-01	-0.489	0.644	8.39E-01
<i>Sarcina</i>	-0.475	1.276	9.55E-01	-5.593	1.308	1.72E-03
<i>Scardovia</i>	0.082	0.634	9.59E-01	0.001	0.737	9.99E-01
<i>Sellimonas</i>	-0.724	0.371	5.44E-01	-0.723	0.379	4.21E-01
<i>Senegalimassilia</i>	0.215	0.862	9.55E-01	0.280	0.895	9.72E-01
<i>Shuttleworthia</i>	0.089	0.744	9.59E-01	-0.550	0.809	8.40E-01
<i>Slackia</i>	-0.380	0.616	9.55E-01	0.123	0.615	9.73E-01
<i>Solobacterium</i>	-0.235	0.267	9.53E-01	-0.258	0.272	7.72E-01
<i>Staphylococcus</i>	-0.228	0.540	9.55E-01	-0.416	0.632	8.40E-01
<i>Streptococcus</i>	0.059	0.170	9.55E-01	-0.021	0.175	9.76E-01
<i>Subdoligranulum</i>	-0.137	0.178	9.53E-01	-0.140	0.186	8.39E-01
<i>Succiniclacticum</i>	0.461	1.499	9.55E-01	1.691	1.459	6.38E-01
<i>Sutterella</i>	0.846	0.571	6.34E-01	0.838	0.604	5.25E-01
<i>Terrisporobacter</i>	-0.394	0.271	6.34E-01	-0.661	0.278	1.98E-01
<i>Turicibacter</i>	-0.243	0.258	9.32E-01	-0.752	0.258	8.19E-02
<i>Tyzzereella</i>	-0.378	0.575	9.53E-01	-1.138	0.618	4.21E-01
<i>Tyzzereella_3</i>	0.522	0.993	9.55E-01	-0.500	1.064	9.31E-01
<i>Tyzzereella_4</i>	-0.124	0.572	9.55E-01	-0.026	0.619	9.96E-01
<i>UBA1819</i>	-0.331	0.189	5.99E-01	-0.009	0.220	9.96E-01

Genus	Unadjusted			Adjusted ^b		
	log ₂ FC ^a	SE	p _{FDR}	log ₂ FC ^a	SE	p _{FDR}
<i>UC5-1-2E3</i>	-0.915	0.525	5.99E-01	-0.954	0.555	4.54E-01
<i>Unknown</i>	-0.133	0.071	5.99E-01	-0.081	0.085	7.72E-01
<i>Varibaculum</i>	-0.367	0.955	9.55E-01	-0.327	1.045	9.72E-01
<i>Veillonella</i>	0.397	0.626	9.53E-01	0.128	0.689	9.76E-01
<i>Victivallis</i>	1.035	1.361	9.53E-01	5.172	1.898	8.97E-02
<i>Weissella</i>	1.339	1.076	7.20E-01	0.318	1.197	9.73E-01

^aInterpreted as the log₂ fold change between those who did and did not meet recommendations (positive: increased abundance in those who met recommendations; negative: decreased abundance in those who met recommendations).

^bAdjusted for maternal education, household income, location of residence, sex, child race, breastfeeding status at 1-month, BMI category at age 10, and dietary pattern at age 10. N=315 due to some missing covariates.