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## Supplementary Material



### Novel Microbial Signatures in the Faecal Microbiome Associated with Severe Alcoholic Hepatitis: *Bacteroides Finegoldii* and *Veillonella Dispar*

Rizwana Hasan<sup>1,2,#</sup>, Ashish Kumar<sup>3,#</sup>, Sudeep Bose<sup>2</sup>, Rahul Roy<sup>1</sup>, Anil Arora<sup>3</sup>, Praveen Sharma<sup>3</sup>, Sai Pawan Nagumantri<sup>1</sup>, Debarati Paul<sup>2</sup> and Sangeeta Choudhury<sup>1,\*</sup>

<sup>1</sup>Department of Research, Sir Ganga Ram Hospital, New Delhi 110060, India

<sup>2</sup>Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh 201313, India

<sup>3</sup>Institute of Liver Gastroenterology & Pancreaticobiliary Sciences, Sir Ganga Ram Hospital, New Delhi 110060, India

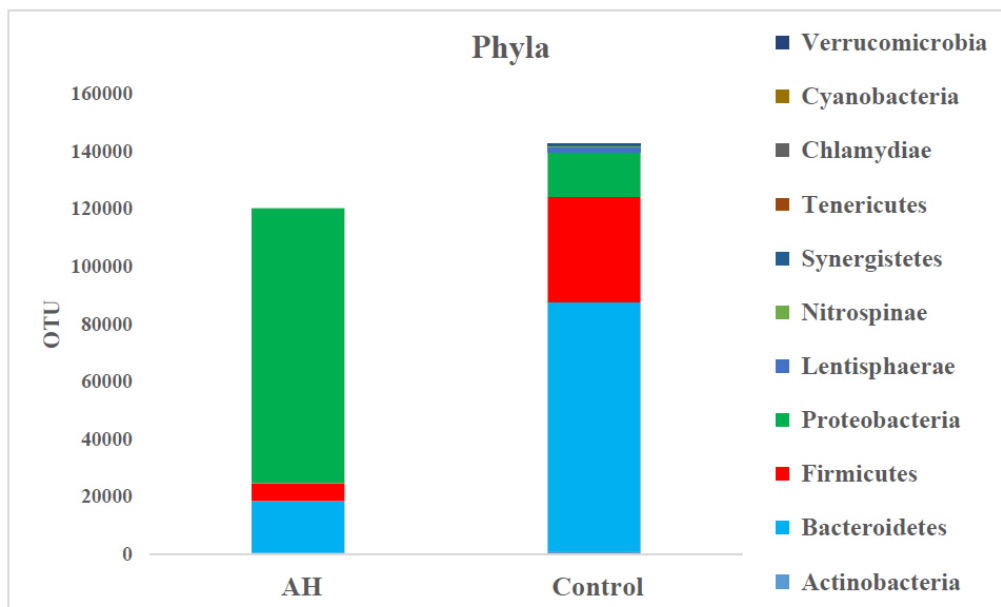


Fig. (1). OTU of bacterial phyla in the microbiota of AH and control.

Table S1. Normalized data by DESeq2 algorithm at Genus-species level ( $p < 0.005$ ).

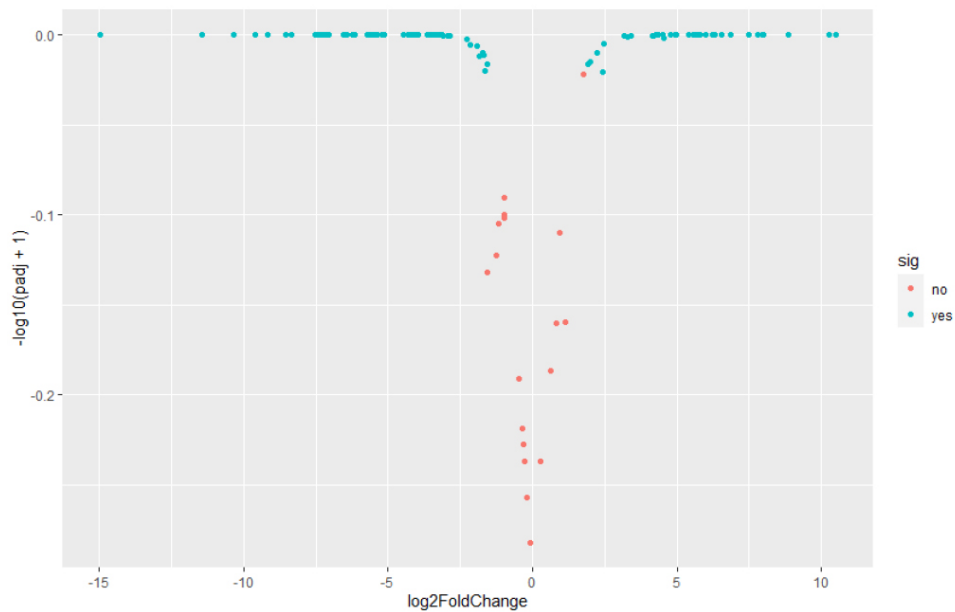
S. No.	OTU	Base Mean	log2 Fold Change	lfcSE	stat	P value	P adj
1	<i>Prevotella copri</i>	22218.573	-14.990	0.6057	-24.747	3.37E-135	4.48E-133
2	<i>Prevotella stercorea</i>	981.450	-10.338	0.9699	-10.658	1.60E-26	1.06E-24
3	<i>Eubacterium eligens</i>	110.496	-7.385	0.7004	-10.544	5.42E-26	2.40E-24
4	<i>Roseburia faecis</i>	123.887	-7.540	0.7245	-10.408	2.29E-25	7.62E-24
5	<i>Succinivibrio dextrinosolvens</i>	2532.643	-11.453	1.2100	-9.465	2.92E-21	7.78E-20
6	<i>Dialister succinatiphilus</i>	618.128	-9.599	1.1010	-8.718	2.83E-18	6.27E-17
7	<i>Sutterella sp.</i>	439.847	-9.154	1.0612	-8.627	6.32E-18	1.20E-16
8	<i>Dorea longicatena</i>	57.327	-6.424	0.7508	-8.556	1.17E-17	1.94E-16
9	<i>Gemmiger formicilis</i>	114.392	-7.371	0.8629	-8.542	1.32E-17	1.95E-16
10	<i>Victivallis vadensis</i>	282.067	-8.564	1.0150	-8.437	3.26E-17	4.33E-16
11	<i>Desulfovibrio piger</i>	244.253	-8.367	1.0064	-8.314	9.28E-17	1.12E-15

S. No.	OTU	Base Mean	log2 Fold Change	lfcSE	stat	P value	P adj
12	<i>Coprococcus eutactus</i>	35.160	-5.719	0.7246	-7.893	2.95E-15	3.27E-14
13	<i>Odoribacter splanchnicus</i>	32.104	-5.585	0.7215	-7.741	9.86E-15	1.01E-13
14	<i>Catenibacterium mitsuokai</i>	30.036	-5.489	0.7139	-7.689	1.48E-14	1.40E-13
15	<i>Escherichia coli</i>	224.624	7.946	1.0430	7.619	2.56E-14	2.27E-13
16	<i>Ruminococcus flavefaciens</i>	129.597	-7.487	0.9867	-7.588	3.26E-14	2.71E-13
17	<i>Ruminococcus bromii</i>	49.814	-6.193	0.8355	-7.412	1.24E-13	9.72E-13
18	<i>Mitsuokella multacida</i>	109.021	-7.244	0.9859	-7.348	2.02E-13	1.49E-12
19	<i>Collinsella aerofaciens</i>	49.015	-6.165	0.8448	-7.298	2.93E-13	2.05E-12
20	<i>Butyrivibrio crossotus</i>	104.037	-7.176	0.9896	-7.251	4.13E-13	2.74E-12
21	<i>Veillonella dispar</i>	1776.612	10.251	1.4312	7.163	7.90E-13	5.00E-12
22	<i>Lactobacillus rogosae</i>	36.118	-5.733	0.8091	-7.086	1.38E-12	8.34E-12
23	<i>Bacteroides finegoldii</i>	2421.088	10.507	1.5105	6.956	3.50E-12	2.02E-11
24	<i>Oscillibacter sp.</i>	23.991	-5.144	0.7424	-6.929	4.23E-12	2.34E-11
25	<i>Haemophilus parainfluenzae</i>	66.729	-6.557	0.9663	-6.785	1.16E-11	6.18E-11
26	<i>Clostridium cocleatum</i>	102.033	6.870	1.0269	6.690	2.23E-11	1.14E-10
27	<i>Olsenella umbonata</i>	67.144	-6.558	0.9824	-6.676	2.46E-11	1.21E-10
28	<i>Megasphaera hominis</i>	65.643	-6.522	0.9911	-6.581	4.67E-11	2.22E-10
29	<i>Clostridium aldenense</i>	576.283	8.866	1.3680	6.481	9.13E-11	4.19E-10
30	<i>Bacteroides plebeius</i>	99.110	-7.055	1.0933	-6.452	1.10E-10	4.88E-10
31	<i>Alistipes putredinis</i>	101.388	-7.080	1.1039	-6.414	1.42E-10	6.08E-10
32	<i>Bacteroides caccae</i>	53.032	-6.227	0.9741	-6.393	1.63E-10	6.76E-10
33	<i>Bacteroides fragilis</i>	182.097	7.490	1.2159	6.160	7.29E-10	2.94E-09
34	<i>Sutterella wadsworthensis</i>	145.823	-5.675	0.9252	-6.134	8.55E-10	3.34E-09
35	<i>Klebsiella pneumoniae</i>	11042.257	8.010	1.3125	6.103	1.04E-09	3.96E-09
36	<i>Alistipes sp.</i>	24.032	-5.121	0.8510	-6.018	1.77E-09	6.53E-09
37	<i>Mitsuokella jalaludini</i>	35.949	-5.674	0.9510	-5.967	2.42E-09	8.69E-09
38	<i>Serratia rubidaea</i>	86.639	6.559	1.1216	5.848	4.97E-09	1.74E-08
39	<i>Pseudobutyrvibrio ruminis</i>	51.735	-6.156	1.0548	-5.836	5.33E-09	1.82E-08
40	<i>Klebsiella variicola</i>	7185.937	7.783	1.3487	5.771	7.90E-09	2.57E-08
41	<i>Bacteroides vulgatus</i>	85.078	-5.590	0.9688	-5.770	7.93E-09	2.57E-08
42	<i>Clostridium ramosum</i>	56.423	5.985	1.1012	5.435	5.48E-08	1.74E-07
43	<i>Paraprevotella clara</i>	33.950	-5.565	1.0290	-5.408	6.38E-08	1.97E-07
44	<i>Streptococcus sinensis</i>	76.388	6.320	1.2018	5.258	1.45E-07	4.39E-07
45	<i>Ruminococcus gnavreuii</i>	14.008	-4.317	0.8279	-5.214	1.85E-07	5.48E-07
46	<i>Enterobacter sacchari</i>	47.080	5.731	1.1051	5.186	2.15E-07	6.21E-07
47	<i>Bacteroides coprocola</i>	26.247	-5.201	1.0056	-5.172	2.31E-07	6.54E-07
48	<i>Dorea formicigenerans</i>	11.977	-4.082	0.8038	-5.079	3.80E-07	1.05E-06
49	<i>Veillonella tobetsuensis</i>	45.927	5.684	1.1214	5.069	4.00E-07	1.07E-06
50	<i>Eubacterium xylanophilum</i>	29.618	-5.355	1.0567	-5.067	4.04E-07	1.07E-06
51	<i>Escherichia/Shigella coli</i>	41.522	5.551	1.1141	4.982	6.30E-07	1.64E-06
52	<i>Clostridium innocuum</i>	37.326	5.421	1.0925	4.962	6.99E-07	1.79E-06
53	<i>Streptococcus australis</i>	51.390	5.792	1.1832	4.895	9.82E-07	2.46E-06
54	<i>Streptococcus peroris</i>	51.388	5.791	1.1845	4.889	1.01E-06	2.49E-06
55	<i>[Eubacterium] bifforme</i>	15.589	-4.458	0.9129	-4.884	1.04E-06	2.52E-06
56	<i>Oxalobacter formigenes</i>	14.094	-4.301	0.8860	-4.854	1.21E-06	2.87E-06
57	<i>Enterococcus faecium</i>	47.447	5.687	1.1760	4.836	1.32E-06	3.09E-06
58	<i>Veillonella rogosae</i>	15.856	4.346	0.9388	4.629	3.68E-06	8.43E-06
59	<i>Streptococcus salivarius</i>	9.209	-3.661	0.7919	-4.623	3.78E-06	8.52E-06
60	<i>Eubacterium hallii</i>	11.262	-3.975	0.8672	-4.584	4.57E-06	1.01E-05
61	<i>Clostridium bartlettii</i>	29.375	4.762	1.0452	4.556	5.20E-06	1.13E-05
62	<i>Eubacterium siraeum</i>	13.193	-4.197	0.9380	-4.474	7.66E-06	1.64E-05
63	<i>Bilophila wadsworthia</i>	69.317	-4.191	0.9382	-4.467	7.92E-06	1.67E-05
64	<i>Bifidobacterium longum</i>	207.261	4.931	1.1096	4.444	8.82E-06	1.83E-05
65	<i>Streptococcus sanguinis</i>	27.954	4.996	1.1247	4.442	8.93E-06	1.83E-05

S. No.	OTU	Base Mean	log2 Fold Change	lfcSE	stat	P value	P adj
66	<i>Bacteroides stercoris</i>	11.914	-4.046	0.9229	-4.384	1.16E-05	2.35E-05
67	<i>Parabacteroides distasonis</i>	5708.398	6.220	1.4421	4.313	1.61E-05	3.20E-05
68	<i>Blautia producta</i>	7.834	-3.382	0.7939	-4.260	2.05E-05	4.00E-05
69	<i>Escherichia vulneris</i>	15.564	4.258	1.0097	4.217	2.47E-05	4.76E-05
70	<i>[Ruminococcus] gnavus</i>	72.281	-4.082	0.9731	-4.195	2.73E-05	5.18E-05
71	<i>Klebsiella sp.</i>	19.165	4.500	1.0769	4.179	2.93E-05	5.49E-05
72	<i>Roseburia sp.</i>	7.990	-3.429	0.8280	-4.141	3.45E-05	6.38E-05
73	<i>Parabacteroides merdae</i>	9.198	-3.649	0.8900	-4.100	4.13E-05	7.52E-05
74	<i>Escherichia/Shigella coli/dysenteriae</i>	19.678	4.521	1.1046	4.093	4.26E-05	7.66E-05
75	<i>Bacteroides dorei</i>	8.902	-3.600	0.8846	-4.069	4.72E-05	8.37E-05
76	<i>Bacteroides pectinophilus</i>	8.612	-3.521	0.8808	-3.998	6.40E-05	0.000111
77	<i>Barnesiella intestinihominis</i>	8.598	-3.517	0.8805	-3.994	6.49E-05	0.000112
78	<i>Veillonella parvula</i>	16.710	4.297	1.0902	3.942	8.08E-05	0.000137
79	<i>Clostridium sp.</i>	7.504	-3.330	0.8612	-3.866	0.0001105	0.000185
80	<i>Megamonas rupellensis</i>	7.960	-3.408	0.8821	-3.863	0.0001118	0.0001859
81	<i>Lactobacillus ruminis</i>	7.570	-3.338	0.8649	-3.859	0.000113	0.0001867
82	<i>Alistipes shahii</i>	7.784	-3.366	0.8874	-3.793	0.000148	0.000238
83	<i>Cronobacter turicensis</i>	16.787	4.283	1.1288	3.794	0.0001480	0.000238
84	<i>Weissella confusa</i>	7.310	-3.242	0.8728	-3.714	0.0002038	0.0003226
85	<i>Roseburia intestinalis</i>	6.687	-3.132	0.8493	-3.688	0.0002263	0.0003542
86	<i>Clostridium butyricum</i>	146.160	4.201	1.1503	3.652	0.0002603	0.0004026
87	<i>Alistipes senegalensis</i>	6.054	-2.945	0.8190	-3.596	0.0003228	0.0004935
88	<i>Bifidobacterium ruminantium</i>	5.754	-2.867	0.8344	-3.436	0.000589	0.0008814
89	<i>Veillonella alcalescens</i>	8.601	3.424	0.9957	3.439	0.0005845	0.0008814
90	<i>Comamonas kerstersii</i>	5.976	-2.902	0.8461	-3.429	0.0006053	0.0008945
91	<i>Streptococcus thermophilus</i>	19.630	4.153	1.2179	3.410	0.0006501	0.0009501
92	<i>Lactococcus lactis</i>	12.650	-3.113	0.9343	-3.332	0.0008622	0.0012464
93	<i>Salmonella enterica</i>	7.035	3.159	0.9586	3.295	0.0009827	0.0014054
94	<i>Bacteroides faecichinchillae</i>	8.165	3.304	1.0585	3.121	0.0018008	0.0025479
95	<i>Bacteroides thetaiotaomicron</i>	1586.554	4.527	1.5037	3.011	0.0026051	0.0036471
96	<i>Alistipes indistinctus</i>	4.086	-2.261	0.7740	-2.921	0.003484	0.004828
97	<i>Morganella morgani</i>	4.463	2.482	0.9407	2.638	0.0083400	0.0114352
98	<i>Serratia symbiotica</i>	4.337	2.454	0.9347	2.626	0.0086449	0.0117323
99	<i>Ruminococcus faecis</i>	4.071	-2.167	0.8344	-2.597	0.0094031	0.0126324
100	<i>Eubacterium ramulus</i>	3.407	-1.906	0.7441	-2.561	0.0104324	0.0138751
101	<i>Eubacterium hadrum</i>	3.148	-1.742	0.7312	-2.382	0.0172124	0.0226658
102	<i>Bacteroides nordii</i>	7.443	2.252	0.9529	2.363	0.0181331	0.0236441
103	<i>Bifidobacterium catenulatum</i>	3.013	-1.682	0.7247	-2.321	0.020270208	0.026174152
104	<i>Bacteroides intestinalis</i>	3.507	-1.860	0.8128	-2.288	0.0221361	0.0283087
105	<i>Trabulsiella odontotermitis</i>	3.097	1.992	0.9018	2.209	0.027174059	0.034420475
106	<i>Blautia wexlerae</i>	2.888	-1.557	0.7180	-2.169	0.030092459	0.037757519
107	<i>Shigella boydii</i>	2.956	1.923	0.8920	2.156	0.031096357	0.038652481
108	<i>Butyrivimonas virosa</i>	3.212	-1.659	0.8012	-2.070	0.038411337	0.04730285
109	<i>Subdoligranulum sp.</i>	90.029	2.448	1.1905	2.056	0.039734731	0.048483663
110	<i>Lactococcus piscium</i>	2.679	1.767	0.8718	2.027	0.042634205	0.051548629
111	<i>Roseburia inulinivorans</i>	2.491	-0.966	0.7425	-1.301	0.193149875	0.231431832
112	<i>Bacteroides cellulosilyticus</i>	2.489	-0.987	0.8010	-1.232	0.217763231	0.258593837
113	<i>Bulleidia p-1630-c5</i>	2.470	-0.972	0.7996	-1.215	0.224246054	0.263935621
114	<i>Streptococcus pseudopneumoniae</i>	12.149	-1.178	0.9899	-1.190	0.233890951	0.272872777
115	<i>Clostridium nexile</i>	1.499	0.948	0.8408	1.128	0.259352353	0.287475976
116	<i>Veillonella atypica</i>	1.498	0.948	0.8407	1.128	0.259376821	0.287475976
117	<i>Ruminococcus gnavus</i>	1.499	0.948	0.8408	1.128	0.259352353	0.287475976
118	<i>Mangrovibacter plantisponsor</i>	1.503	0.949	0.8410	1.128	0.259247253	0.287475976
119	<i>Bifidobacterium breve</i>	1.499	0.948	0.8408	1.128	0.259352353	0.287475976

S. No.	OTU	Base Mean	log2 Fold Change	lfcSE	stat	P value	P adj
120	<i>Leuconostoc lactis</i>	1.499	0.948	0.8408	1.128	0.259352353	0.287475976
121	<i>Bacteroides uniformis</i>	62.018	-1.248	1.1941	-1.045	0.295994784	0.325349639
122	<i>Faecalibacterium prausnitzii</i>	2494.768	-1.550	1.5756	-0.984	0.325136001	0.354451542
123	<i>Bacteroides xylanisolvens</i>	203.884	1.126	1.3685	0.823	0.410735537	0.44412867
124	<i>Streptococcus lactarius</i>	13.577	0.824	1.0148	0.812	0.41673373	0.446980533
125	<i>Bacteroides sp.</i>	13.243	0.636	0.9559	0.666	0.505498047	0.537849922
126	<i>Ruminiclostridium siraenum</i>	1.870	-0.451	0.7092	-0.637	0.524434042	0.553569267
127	<i>Roseburia hominis</i>	1.830	-0.346	0.7075	-0.489	0.624563359	0.654070289
128	<i>Bacteroides massiliensis</i>	1.817	-0.308	0.7071	-0.435	0.663543323	0.689462984
129	<i>Bacteroides salyersiae</i>	1.804	-0.267	0.7069	-0.378	0.705798082	0.725400232
130	<i>Clostridium leptum</i>	1.685	0.264	0.7221	0.366	0.714491958	0.725400232
131	<i>Coprococcus catus</i>	1.685	0.264	0.7221	0.366	0.714491958	0.725400232
132	<i>Blautia faecis</i>	1.778	-0.178	0.7070	-0.251	0.801465977	0.807537689
133	<i>Eubacterium rectale</i>	1.751	-0.076	0.7083	-0.107	0.914401455	0.914401455
134	<i>Yersinia enterocolitica</i>	3.600	-1.916	0.8579	-2.233	NA	NA
135	<i>Butyrivimonas sp.</i>	18.591	-4.697	0.9891	-4.749	NA	NA
136	<i>Blautia obeum</i>	2.101	-0.886	0.7249	-1.223	NA	NA
137	<i>Lachnoclostridium clostridioforme</i>	2.589	-1.435	0.7578	-1.893	NA	NA
138	<i>Parasutterella excrementihominis</i>	3.866	-2.106	0.7924	-2.658	NA	NA
139	<i>Clostridium chartatabidum</i>	6.155	-2.964	0.8780	-3.376	NA	NA
140	<i>Blautia luti</i>	2.272	-1.113	0.7370	-1.510	NA	NA
141	<i>Alistipes Alistipes</i>	8.208	-3.446	0.9100	-3.786	NA	NA
142	<i>Clostridium vincentii</i>	5.919	-2.905	0.8525	-3.407	NA	NA
143	<i>Raoultella planticola</i>	3.168	-1.600	0.8389	-1.908	NA	NA

Note: – lfcSE – log fold change standard error; P adj – adjusted p-values



**Fig. (2).** Mapping AH and healthy control gene expression pattern at species levels using the Volcano plot scattered diagram. X-axis shows differential gene expression pattern (log2FoldChange) at the species level. Y-axis shows the magnitude of change (p-adj value; statistical significance of difference). Significant values are represented as green dots and non-significant as red dots.

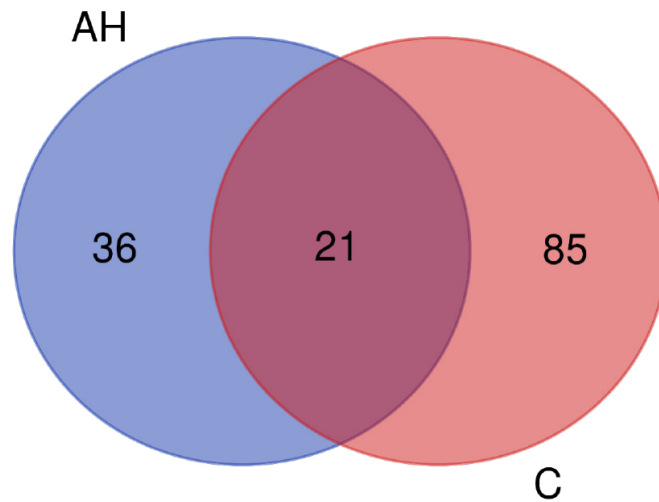


Fig. (3). Venn diagram for OTUs at the species level, different colours represent different groups of the microbiome.

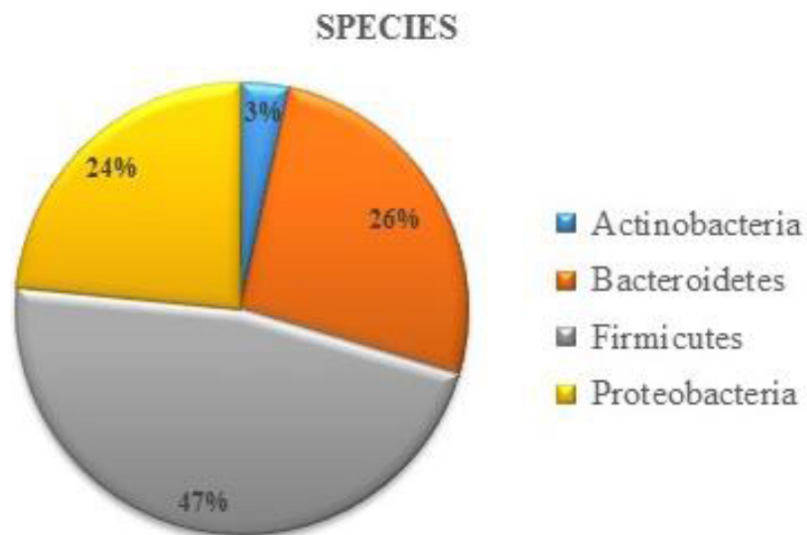


Fig. (4). Total species percentage according to phyla, maximum coverage is from firmicutes phylum.

Table S2. Abundance and sensitivity by receiver operating characteristic (ROC) curve.

Test Result Variable(s)	Area Under the Curve (AUC)				
	Area	Std. Error <sup>a</sup>	Asymptotic Sig. <sup>b</sup>	Asymptotic 95% Confidence Interval	
				Lower Bound	Upper Bound
<i>Klebsiella pneumoniae</i>	0.906	0.095	0.027	0.72	1
<i>Klebsiella variicola</i>	0.938	0.075	0.017	0.79	1
<i>Parabacteroides distasonis</i>	0.844	0.117	0.062	0.614	1
<i>Bacteroides finegoldii</i>	0.672	0.161	0.35	0.356	0.988
<i>Bacteroides thetaiotaomicron</i>	0.781	0.141	0.126	0.505	1
<i>Veillonella dispar</i>	0.422	0.17	0.671	0.088	0.756
<i>Clostridium aldenense</i>	0.625	0.175	0.497	0.281	0.969

Note – a - Under the nonparametric assumption, b- Null hypothesis: true area=0.5

Table S3. Co-occurrence network of AH microbiota at genera level.

Source	Target	Correlation	P value
<i>Dorea</i>	<i>Lachnospira</i>	1	3.00E-04
<i>Dorea</i>	<i>Roseburia</i>	1	3.00E-04
<i>Lachnospira</i>	<i>Roseburia</i>	1	3.00E-04
<i>Coprococcus</i>	<i>Dorea</i>	0.9971	3.00E-04
<i>Coprococcus</i>	<i>Lachnospira</i>	0.9971	3.00E-04
<i>Coprococcus</i>	<i>Roseburia</i>	0.9971	3.00E-04
<i>Dorea</i>	<i>Eubacterium</i>	0.9912	3.00E-04
<i>Eubacterium</i>	<i>Lachnospira</i>	0.9912	3.00E-04
<i>Eubacterium</i>	<i>Roseburia</i>	0.9912	3.00E-04
<i>Porphyromonadaceae</i>	<i>Tannerellaceae</i>	0.9895	3.00E-04
<i>Catenibacterium</i>	<i>Dorea</i>	0.9883	3.00E-04
<i>Catenibacterium</i>	<i>Lachnospira</i>	0.9883	3.00E-04
<i>Catenibacterium</i>	<i>Roseburia</i>	0.9883	3.00E-04
<i>Coprococcus</i>	<i>Eubacterium</i>	0.9883	3.00E-04
<i>Eubacterium</i>	<i>Odoribacteraceae</i>	0.9883	3.00E-04
<i>Mediterraneibacter</i>	<i>Sutterella</i>	0.986	3.00E-04
<i>Catenibacterium</i>	<i>Eubacterium</i>	0.9854	3.00E-04
<i>Mediterraneibacter</i>	<i>Ruminococcus</i>	0.9806	3.00E-04
<i>Catenibacterium</i>	<i>Coprococcus</i>	0.9795	3.00E-04
<i>Coprococcus</i>	<i>Odoribacteraceae</i>	0.9766	3.00E-04
<i>Dialister</i>	<i>Oscillibacter</i>	0.9736	3.00E-04
<i>Dorea</i>	<i>Odoribacteraceae</i>	0.9707	3.00E-04
<i>Lachnospira</i>	<i>Odoribacteraceae</i>	0.9707	3.00E-04
<i>Odoribacteraceae</i>	<i>Roseburia</i>	0.9707	3.00E-04
<i>Ruminococcus</i>	<i>Sutterella</i>	0.9653	3.00E-04
<i>Catenibacterium</i>	<i>Odoribacteraceae</i>	0.9649	3.00E-04
<i>Odoribacteraceae</i>	<i>Prevotellaceae</i>	0.9561	1.00E-03
<i>Catenibacterium</i>	<i>Dialister</i>	0.9502	1.00E-03
<i>Eubacterium</i>	<i>Prevotellaceae</i>	0.9444	1.00E-03
<i>Dorea</i>	<i>Sutterella</i>	0.9437	1.00E-03
<i>Lachnospira</i>	<i>Sutterella</i>	0.9437	1.00E-03
<i>Roseburia</i>	<i>Sutterella</i>	0.9437	1.00E-03
<i>Coprococcus</i>	<i>Sutterella</i>	0.9409	1.00E-03
<i>Catenibacterium</i>	<i>Oscillibacter</i>	0.9356	1.00E-03
<i>Dialister</i>	<i>Prevotellaceae</i>	0.9356	1.00E-03
<i>Coprococcus</i>	<i>Oscillibacter</i>	0.9327	1.00E-03
<i>Coprococcus</i>	<i>Prevotellaceae</i>	0.9327	1.00E-03
<i>Eubacterium</i>	<i>Sutterella</i>	0.9298	1.00E-03
<i>Oscillibacter</i>	<i>Ruminococcus</i>	0.9298	1.00E-03
<i>Dorea</i>	<i>Oscillibacter</i>	0.9297	1.00E-03
<i>Lachnospira</i>	<i>Oscillibacter</i>	0.9297	1.00E-03
<i>Oscillibacter</i>	<i>Roseburia</i>	0.9297	1.00E-03
<i>Catenibacterium</i>	<i>Ruminococcus</i>	0.927	1.00E-03
<i>Dialister</i>	<i>Dorea</i>	0.9268	1.00E-03
<i>Dialister</i>	<i>Lachnospira</i>	0.9268	1.00E-03
<i>Dialister</i>	<i>Roseburia</i>	0.9268	1.00E-03
<i>Dorea</i>	<i>Prevotellaceae</i>	0.9268	1.00E-03
<i>Lachnospira</i>	<i>Prevotellaceae</i>	0.9268	1.00E-03
<i>Odoribacteraceae</i>	<i>Oscillibacter</i>	0.9268	1.00E-03
<i>Prevotellaceae</i>	<i>Roseburia</i>	0.9268	1.00E-03
<i>Catenibacterium</i>	<i>Sutterella</i>	0.9214	1.00E-03
<i>Catenibacterium</i>	<i>Prevotellaceae</i>	0.9209	1.00E-03

Source	Target	Correlation	P value
<i>Coprococcus</i>	<i>Dialister</i>	0.9209	1.00E-03
<i>Bacteroidaceae</i>	<i>Tannerellaceae</i>	0.9188	1.00E-03
<i>Oscillibacter</i>	<i>Prevotellaceae</i>	0.918	1.00E-03
<i>Dorea</i>	<i>Mediterraneibacter</i>	0.9178	1.00E-03
<i>Lachnospira</i>	<i>Mediterraneibacter</i>	0.9178	1.00E-03
<i>Mediterraneibacter</i>	<i>Roseburia</i>	0.9178	1.00E-03
<i>Eubacterium</i>	<i>Mediterraneibacter</i>	0.9164	1.00E-03
<i>Dorea</i>	<i>Ruminococcus</i>	0.9158	1.00E-03
<i>Lachnospira</i>	<i>Ruminococcus</i>	0.9158	1.00E-03
<i>Roseburia</i>	<i>Ruminococcus</i>	0.9158	1.00E-03
<i>Bacteroidaceae</i>	<i>Porphyromonadaceae</i>	0.9156	1.00E-03
<i>Dialister</i>	<i>Eubacterium</i>	0.9151	1.00E-03
<i>Eubacterium</i>	<i>Oscillibacter</i>	0.9151	1.00E-03
<i>Eubacterium</i>	<i>Ruminococcus</i>	0.913	1.00E-03
<i>Dialister</i>	<i>Ruminococcus</i>	0.9102	1.00E-03
<i>Odoribacteraceae</i>	<i>Sutterella</i>	0.9102	1.00E-03
<i>Catenibacterium</i>	<i>Mediterraneibacter</i>	0.9094	1.00E-03
<i>Dialister</i>	<i>Odoribacteraceae</i>	0.9092	1.00E-03
<i>Faecalibacterium</i>	<i>Ruminococcus</i>	0.9085	1.00E-03
<i>Coprococcus</i>	<i>Mediterraneibacter</i>	0.908	1.00E-03
<i>Coprococcus</i>	<i>Ruminococcus</i>	0.9074	1.00E-03
<i>Odoribacteraceae</i>	<i>Ruminococcus</i>	0.9074	1.00E-03
<i>Faecalibacterium</i>	<i>Mediterraneibacter</i>	0.9065	1.00E-03
<i>Oscillibacter</i>	<i>Sutterella</i>	0.899	1.00E-03
<i>Mediterraneibacter</i>	<i>Odoribacteraceae</i>	0.8968	1.00E-03
<i>Prevotellaceae</i>	<i>Sutterella</i>	0.885	1.00E-03
<i>Faecalibacterium</i>	<i>Sutterella</i>	0.8827	1.00E-03
<i>Dialister</i>	<i>Sutterella</i>	0.8822	1.00E-03
<i>Bacteroidaceae</i>	<i>Subdoligranulum</i>	0.8812	1.00E-03
<i>Mediterraneibacter</i>	<i>Oscillibacter</i>	0.873	1.00E-03
<i>Bilophila</i>	<i>Dialister</i>	0.8704	1.00E-03
<i>Prevotellaceae</i>	<i>Ruminococcus</i>	0.8654	1.00E-04
<i>Not_Assigned</i>	<i>Ruminococcus</i>	0.8627	1.00E-04
<i>Dialister</i>	<i>Mediterraneibacter</i>	0.8548	1.00E-04
<i>Mediterraneibacter</i>	<i>Prevotellaceae</i>	0.852	1.00E-04
<i>Bilophila</i>	<i>Oscillibacter</i>	0.8515	1.00E-04
<i>Not_Assigned</i>	<i>Sutterella</i>	0.8416	1.00E-04
<i>Bilophila</i>	<i>Prevotellaceae</i>	0.8407	1.00E-04
<i>Mediterraneibacter</i>	<i>Not_Assigned</i>	0.834	1.00E-04
<i>Erysipelatoclostridium</i>	<i>Veillonella</i>	0.8333	1.00E-04
<i>Klebsiella</i>	<i>Serratia</i>	0.8316	1.00E-04
<i>Not_Assigned</i>	<i>Oscillibacter</i>	0.8297	1.00E-04
<i>Dialister</i>	<i>Not_Assigned</i>	0.8223	1.00E-04
<i>Catenibacterium</i>	<i>Not_Assigned</i>	0.8125	1.00E-04
<i>Bifidobacterium</i>	<i>Streptococcus</i>	0.806	1.00E-04
<i>Dorea</i>	<i>Not_Assigned</i>	0.8027	1.00E-04
<i>Lachnospira</i>	<i>Not_Assigned</i>	0.8027	1.00E-04
<i>Not_Assigned</i>	<i>Roseburia</i>	0.8027	1.00E-04
<i>Coprococcus</i>	<i>Not_Assigned</i>	0.8002	1.00E-04
<i>Enterococcus</i>	<i>Escherichia</i>	0.7887	1.00E-04
<i>Bilophila</i>	<i>Catenibacterium</i>	0.7867	1.00E-04
<i>Eubacterium</i>	<i>Not_Assigned</i>	0.7855	1.00E-04
<i>Bilophila</i>	<i>Coprococcus</i>	0.784	1.00E-04
<i>Bilophila</i>	<i>Dorea</i>	0.7813	1.00E-04

Source	Target	Correlation	P value
<i>Bilophila</i>	<i>Lachnospira</i>	0.7813	1.00E-04
<i>Bilophila</i>	<i>Roseburia</i>	0.7813	1.00E-04
<i>Not Assigned</i>	<i>Odoribacteraceae</i>	0.7806	1.00E-04
<i>Bilophila</i>	<i>Odoribacteraceae</i>	0.7732	2.00E-04
<i>Bilophila</i>	<i>Eubacterium</i>	0.7678	2.00E-04
<i>Faecalibacterium</i>	<i>Not Assigned</i>	0.767	2.00E-04
<i>Enterocloster</i>	<i>Erysipelatoclostridium</i>	0.7613	2.00E-04
<i>Faecalibacterium</i>	<i>Oscillibacter</i>	0.7597	3.00E-04
<i>Not Assigned</i>	<i>Prevotellaceae</i>	0.7584	3.00E-04
<i>Catenibacterium</i>	<i>Faecalibacterium</i>	0.7463	4.00E-04
<i>Bilophila</i>	<i>Ruminococcus</i>	0.7461	4.00E-04
<i>Bilophila</i>	<i>Sutterella</i>	0.7435	4.00E-04
<i>Dorea</i>	<i>Faecalibacterium</i>	0.7409	4.00E-04
<i>Faecalibacterium</i>	<i>Lachnospira</i>	0.7409	4.00E-04
<i>Faecalibacterium</i>	<i>Roseburia</i>	0.7409	4.00E-04
<i>Coprococcus</i>	<i>Faecalibacterium</i>	0.7355	5.00E-04
<i>Dialister</i>	<i>Faecalibacterium</i>	0.7355	5.00E-04
<i>Porphyromonadaceae</i>	<i>Subdoligranulum</i>	0.7342	5.00E-04
<i>Subdoligranulum</i>	<i>Tannerellaceae</i>	0.7342	5.00E-04
<i>Eubacterium</i>	<i>Faecalibacterium</i>	0.7301	6.00E-04
<i>Faecalibacterium</i>	<i>Odoribacteraceae</i>	0.7247	7.00E-04
<i>Enterocloster</i>	<i>Veillonella</i>	0.7149	9.00E-04
<i>Bifidobacterium</i>	<i>Subdoligranulum</i>	0.7142	9.00E-04
<i>Bacteroidaceae</i>	<i>Bifidobacterium</i>	0.7054	0.0011
<i>Klebsiella</i>	<i>Subdoligranulum</i>	-0.7187	8.00E-04
<i>Klebsiella</i>	<i>Tannerellaceae</i>	-0.7388	5.00E-04
<i>Catenibacterium</i>	<i>Enterococcus</i>	-0.7522	3.00E-04
<i>Coprococcus</i>	<i>Enterococcus</i>	-0.7522	3.00E-04
<i>Dialister</i>	<i>Enterococcus</i>	-0.7522	3.00E-04
<i>Dorea</i>	<i>Enterococcus</i>	-0.7522	3.00E-04
<i>Enterococcus</i>	<i>Eubacterium</i>	-0.7522	3.00E-04
<i>Enterococcus</i>	<i>Lachnospira</i>	-0.7522	3.00E-04
<i>Enterococcus</i>	<i>Odoribacteraceae</i>	-0.7522	3.00E-04
<i>Enterococcus</i>	<i>Oscillibacter</i>	-0.7522	3.00E-04
<i>Enterococcus</i>	<i>Prevotellaceae</i>	-0.7522	3.00E-04
<i>Enterococcus</i>	<i>Roseburia</i>	-0.7522	3.00E-04
<i>Klebsiella</i>	<i>Porphyromonadaceae</i>	-0.7555	3.00E-04
<i>Bilophila</i>	<i>Erysipelatoclostridium</i>	-0.7558	3.00E-04
<i>Bacteroidaceae</i>	<i>Serratia</i>	-0.7604	2.00E-04
<i>Enterocloster</i>	<i>Oscillibacter</i>	-0.7609	2.00E-04
<i>Ruminococcus</i>	<i>Veillonella</i>	-0.7738	2.00E-04
<i>Sutterella</i>	<i>Veillonella</i>	-0.7738	2.00E-04
<i>Mediterraneibacter</i>	<i>Veillonella</i>	-0.7743	2.00E-04
<i>Dialister</i>	<i>Enterocloster</i>	-0.7756	2.00E-04
<i>Enterocloster</i>	<i>Faecalibacterium</i>	-0.7851	1.00E-04
<i>Escherichia</i>	<i>Not Assigned</i>	-0.7851	1.00E-04
<i>Catenibacterium</i>	<i>Enterocloster</i>	-0.7879	1.00E-04
<i>Coprococcus</i>	<i>Enterocloster</i>	-0.7904	1.00E-04
<i>Dorea</i>	<i>Enterocloster</i>	-0.7928	1.00E-04
<i>Enterocloster</i>	<i>Lachnospira</i>	-0.7928	1.00E-04
<i>Enterocloster</i>	<i>Roseburia</i>	-0.7928	1.00E-04
<i>Bilophila</i>	<i>Enterocloster</i>	-0.7965	1.00E-04
<i>Enterocloster</i>	<i>Odoribacteraceae</i>	-0.8076	1.00E-04
<i>Enterocloster</i>	<i>Eubacterium</i>	-0.8101	1.00E-04



Source	Target	Correlation	P value
<i>Enterocloster</i>	<i>Ruminococcus</i>	-0.8205	1.00E-04
<i>Enterocloster</i>	<i>Prevotellaceae</i>	-0.8297	1.00E-04
<i>Enterocloster</i>	<i>Mediterraneibacter</i>	-0.8351	1.00E-04
<i>Enterocloster</i>	<i>Sutterella</i>	-0.8369	1.00E-04
<i>Faecalibacterium</i>	<i>Veillonella</i>	-0.8536	1.00E-04
<i>Bacteroidaceae</i>	<i>Klebsiella</i>	-0.8679	1.00E-04

Table S4. Co-occurrence network of HC microbiota at genera level.

Source	Target	Correlation	P value
<i>Bacteroidaceae</i>	<i>Porphyromonadaceae</i>	0.9156	<0.001
<i>Bacteroidaceae</i>	<i>Tannerellaceae</i>	0.9188	<0.001
<i>Catenibacterium</i>	<i>Coprococcus</i>	0.9795	<0.001
<i>Catenibacterium</i>	<i>Dialister</i>	0.9502	<0.001
<i>Catenibacterium</i>	<i>Dorea</i>	0.9883	<0.001
<i>Catenibacterium</i>	<i>Eubacterium</i>	0.9854	<0.001
<i>Catenibacterium</i>	<i>Lachnospira</i>	0.9883	<0.001
<i>Catenibacterium</i>	<i>Mediterraneibacter</i>	0.9094	<0.001
<i>Catenibacterium</i>	<i>Odoribacteraceae</i>	0.9649	<0.001
<i>Catenibacterium</i>	<i>Oscillibacter</i>	0.9356	<0.001
<i>Catenibacterium</i>	<i>Prevotellaceae</i>	0.9209	<0.001
<i>Catenibacterium</i>	<i>Roseburia</i>	0.9883	<0.001
<i>Catenibacterium</i>	<i>Ruminococcus</i>	0.927	<0.001
<i>Catenibacterium</i>	<i>Sutterella</i>	0.9214	<0.001
<i>Coprococcus</i>	<i>Dialister</i>	0.9209	<0.001
<i>Coprococcus</i>	<i>Dorea</i>	0.9971	<0.001
<i>Coprococcus</i>	<i>Eubacterium</i>	0.9883	<0.001
<i>Coprococcus</i>	<i>Lachnospira</i>	0.9971	<0.001
<i>Coprococcus</i>	<i>Mediterraneibacter</i>	0.908	<0.001
<i>Coprococcus</i>	<i>Odoribacteraceae</i>	0.9766	<0.001
<i>Coprococcus</i>	<i>Oscillibacter</i>	0.9327	<0.001
<i>Coprococcus</i>	<i>Prevotellaceae</i>	0.9327	<0.001
<i>Coprococcus</i>	<i>Roseburia</i>	0.9971	<0.001
<i>Coprococcus</i>	<i>Ruminococcus</i>	0.9074	<0.001
<i>Coprococcus</i>	<i>Sutterella</i>	0.9409	<0.001
<i>Dialister</i>	<i>Dorea</i>	0.9268	<0.001
<i>Dialister</i>	<i>Eubacterium</i>	0.9151	<0.001
<i>Dialister</i>	<i>Lachnospira</i>	0.9268	<0.001
<i>Dialister</i>	<i>Odoribacteraceae</i>	0.9092	<0.001
<i>Dialister</i>	<i>Oscillibacter</i>	0.9736	<0.001
<i>Dialister</i>	<i>Prevotellaceae</i>	0.9356	<0.001
<i>Dialister</i>	<i>Roseburia</i>	0.9268	<0.001
<i>Dialister</i>	<i>Ruminococcus</i>	0.9102	<0.001
<i>Dorea</i>	<i>Eubacterium</i>	0.9912	<0.001
<i>Dorea</i>	<i>Lachnospira</i>	1.00	<0.001
<i>Dorea</i>	<i>Mediterraneibacter</i>	0.9178	<0.001
<i>Dorea</i>	<i>Odoribacteraceae</i>	0.9707	<0.001
<i>Dorea</i>	<i>Oscillibacter</i>	0.9297	<0.001
<i>Dorea</i>	<i>Prevotellaceae</i>	0.9268	<0.001
<i>Dorea</i>	<i>Roseburia</i>	1.00	<0.001
<i>Dorea</i>	<i>Ruminococcus</i>	0.9158	<0.001
<i>Dorea</i>	<i>Sutterella</i>	0.9437	<0.001
<i>Eubacterium</i>	<i>Lachnospira</i>	0.9912	<0.001

Source	Target	Correlation	P value
<i>Eubacterium</i>	<i>Mediterraneibacter</i>	0.9164	<0.001
<i>Eubacterium</i>	<i>Odoribacteraceae</i>	0.9883	<0.001
<i>Eubacterium</i>	<i>Oscillibacter</i>	0.9151	<0.001
<i>Eubacterium</i>	<i>Prevotellaceae</i>	0.9444	<0.001
<i>Eubacterium</i>	<i>Roseburia</i>	0.9912	<0.001
<i>Eubacterium</i>	<i>Ruminococcus</i>	0.913	<0.001
<i>Eubacterium</i>	<i>Sutterella</i>	0.9298	<0.001
<i>Faecalibacterium</i>	<i>Mediterraneibacter</i>	0.9065	<0.001
<i>Faecalibacterium</i>	<i>Ruminococcus</i>	0.9085	<0.001
<i>Lachnospira</i>	<i>Mediterraneibacter</i>	0.9178	<0.001
<i>Lachnospira</i>	<i>Odoribacteraceae</i>	0.9707	<0.001
<i>Lachnospira</i>	<i>Oscillibacter</i>	0.9297	<0.001
<i>Lachnospira</i>	<i>Prevotellaceae</i>	0.9268	<0.001
<i>Lachnospira</i>	<i>Roseburia</i>	1.00	<0.001
<i>Lachnospira</i>	<i>Ruminococcus</i>	0.9158	<0.001
<i>Lachnospira</i>	<i>Sutterella</i>	0.9437	<0.001
<i>Mediterraneibacter</i>	<i>Roseburia</i>	0.9178	<0.001
<i>Mediterraneibacter</i>	<i>Ruminococcus</i>	0.9806	<0.001
<i>Mediterraneibacter</i>	<i>Sutterella</i>	0.986	<0.001
<i>Odoribacteraceae</i>	<i>Oscillibacter</i>	0.9268	<0.001
<i>Odoribacteraceae</i>	<i>Prevotellaceae</i>	0.9561	<0.001
<i>Odoribacteraceae</i>	<i>Roseburia</i>	0.9707	<0.001
<i>Odoribacteraceae</i>	<i>Ruminococcus</i>	0.9074	<0.001
<i>Odoribacteraceae</i>	<i>Sutterella</i>	0.9102	<0.001
<i>Oscillibacter</i>	<i>Prevotellaceae</i>	0.918	<0.001
<i>Oscillibacter</i>	<i>Roseburia</i>	0.9297	<0.001
<i>Oscillibacter</i>	<i>Ruminococcus</i>	0.9298	<0.001
<i>Porphyromonadaceae</i>	<i>Tannerellaceae</i>	0.9895	<0.001
<i>Prevotellaceae</i>	<i>Roseburia</i>	0.9268	<0.001
<i>Roseburia</i>	<i>Ruminococcus</i>	0.9158	<0.001
<i>Roseburia</i>	<i>Sutterella</i>	0.9437	<0.001
<i>Ruminococcus</i>	<i>Sutterella</i>	0.9653	<0.001

**Table S5. Linear Discriminant Analysis (LDA) Effect Size (LEfSe) of taxa.**

Taxa Phylum. Class. Order. Family. Genus. Species	changes	fold change	fdr adjusted
<b>Carbohydrate</b>			
Bacteria.Terrabacteriagroup.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcuspseudopneumoniae	high	4.9714	0.0832
Bacteria.Terrabacteriagroup.Firmicutes.Clostridia.Eubacteriales.Lachnospiraceae.Enterocloster	low	5.1255	0.0851
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroidesvulgatus	high	4.4400	0.0403*
Bacteria.Proteobacteria.Alphaproteobacteria	high	4.4416	0.0517
Bacteria.Terrabacteriagroup.Firmicutes.Erysipelotrichia.Erysipelotrichales	high	3.8304	0.0380*
Bacteria.Terrabacteriagroup.Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae	high	4.1290	0.0576
Bacteria.Terrabacteriagroup.Firmicutes.Clostridia.Eubacteriales.Lachnospiraceae.Enterocloster.Enteroclosteraldensis	low	5.1255	0.0851
Bacteria.Terrabacteriagroup.Firmicutes.Clostridia.Eubacteriales.Oscillospiraceae.Ruminococcus	high	4.1398	0.0788
Bacteria.Terrabacteriagroup.Firmicutes.Erysipelotrichia	high	3.8304	0.0380*
<b>Protien</b>			
Bacteria.Terrabacteriagroup.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus	high	2.5480	0.0277*
Bacteria.Terrabacteriagroup.Actinobacteria.Actinomycetia.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium	high	2.3659	0.0424*
Bacteria.Terrabacteriagroup.Actinobacteria	high	3.0746	0.0019*
Bacteria.Terrabacteriagroup.Actinobacteria.Actinomycetia	normal	2.6189	0.0186*
Bacteria.Terrabacteriagroup.Actinobacteria.Actinomycetia.Bifidobacteriales	high	2.6113	0.0424*
Bacteria.Terrabacteriagroup.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae	high	2.5445	0.0244*
Bacteria.Terrabacteriagroup.Actinobacteria.Actinomycetia.Bifidobacteriales.Bifidobacteriaceae	high	2.3316	0.0424*
<b>Fat</b>			

Taxa Phylum. Class. Order. Family. Genus. Species	changes	fold change	fdR adjusted
Bacteria.FCBgroup	normal	5.3978	0.0007**
Bacteria.Terrabacteriagroup.Firmicutes.Clostridia.Eubacteriales.Lachnospiraceae.Enterocloster	low	5.4262	0.0007**
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella	normal	5.0195	0.0001**
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae	normal	5.0828	0.0001**
Bacteria.Terrabacteriagroup.Firmicutes.Clostridia.Eubacteriales.Lachnospiraceae.Enterocloster.Enteroclosteraldensis	low	5.4262	0.0007**
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup.Bacteroidetes.Bacteroidia.Bacteroidales	normal	5.3975	0.0007**
Bacteria.Terrabacteriagroup.Firmicutes.Clostridia	low	5.3247	0.0007**
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup	normal	5.3978	0.0007**
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup.Bacteroidetes	normal	5.3978	0.0007**
Bacteria.FCBgroup.Bacteroidetes_Chlorobigroup.Bacteroidetes.Bacteroidia	normal	5.3975	0.0007**
Bacteria.Terrabacteriagroup.Firmicutes	low	5.3414	0.0007**
Bacteria.Terrabacteriagroup	low	5.3392	0.0007**

Note: (\*P < .05, \*\*P ≤ .001)

Table 6(A). Diet intake of enrolled subjects [caloric values of cooked preparations].

Preparation	Quantity for one serving	Calories (Kcal)
<b>1. Cereal</b>		
Rice	1 cup	170
Roti	1 no.	80
Paratha	1 no.	150
Puri	1 no.	80
Bread	2 slices	170
Kichidi	1 bowl	200
<b>2. Pulse</b>		
Plain dhal	½ bowl	100
Sambar	1 bowl	110
<b>3. Vegetable</b>		
Vegetables with high Calorie Value		100
Vegetables with low Calorie Value		20
With gravy	1 bowl	170
Dry	1 bowl	150
<b>4. Non-Vegetarian food</b>		
Boiled egg	1 no.	90
Omelette	1 no.	160
Fried egg	1 no.	160
Mutton curry	¼ bowl	260
Chicken curry	¼ bowl	240
Fish fried	2 big pieces	190
<b>5. Sweets and Desserts</b>		
Barfi	2 small pieces	400
Fruit cake	1 piece	270
Ice-cream	½ cup	200
<b>6. Beverages</b>		
Tea	1 cup	75
Coffee	1 cup	110
Milk	1 cup	180
<b>7. Fruits</b>		
Apple	1 medium	107
Banana	1 medium	120

**Table 6(B). Statistical assessment of diet intake in AH and HC.**

Nutrient content	Normal Range	Mean $\pm$ SD		P-value
		AH (n=12)	HC (n=6)	
Total Calories	1,600-2,400 Kcal/day	1512.2 $\pm$ 348.9	2392.5 $\pm$ 119.9	0.004
		low (n=7), within normal range (n=5)	within normal range (n=6)	
Carbohydrates	282 gm/day	284.7 $\pm$ 92.5	204.4 $\pm$ 31.1	0.039
		low (n=8), High (n=4)	low (n=4), High (n=2)	
Protein	60-80 gm/day	56.9 $\pm$ 14.4	81.3 $\pm$ 18.7	0.015
		low (n=5), within normal range (n=7)	High (n=1), within normal range (n=5)	
Fat	44-77 gm/day	28.6 $\pm$ 8.5	47.9 $\pm$ 6.7	0.001
		low (n=12)	low (n=2), within normal range (n=4)	
Fibre	30-38 gm/day	33.2 $\pm$ 5.2	34 $\pm$ 4	0.779
		low (n=3), within normal range (n=9)	within normal range (n=6)	

**Note:** kcal: kilocalorie; gm: gram; HC; healthy control; AH: alcoholic hepatitis; SD - Standard Deviation

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