

## Supplementary Information

### Deep sequencing-derived Metagenome Assembled Genomes from the gut microbiome of liver transplant patients

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**Table S1:** Patient-level demographic and clinical data at the time of stool sample collection.

<b>Patient (sample) ID</b>	<b>Gender</b>	<b>Age</b>	<b>Years from LT</b>	<b>MASLD</b>	<b>NAS</b>
N1153	M	65	1	0	0
N1154	F	57	1	1	1
N1155	F	58	6	1	5
N1156	M	49	1	0	1
N1157	M	56	1	1	2
N1158	F	69	3	1	5
N1161	F	67	2	1	3
N1162	M	64	1	1	3
N1163	F	67	2	1	4
N1164	M	70	5	1	1
N1165	F	66	4	1	5
N1166	F	51	3	1	3
N1167	M	56	2	1	6
N1168	M	48	1	1	1
N1169	M	66	4	1	2
N1170	F	71	3	1	4
N1171	M	65	7	0	0
N1173	M	65	1	0	0
N1174	M	73	8	1	3
N1175	F	71	3	0	0
N1191	F	59	6	0	1

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**Table S2:** The alpha diversity of LT samples estimated by two common diversity indices.

<b>Sample ID</b>	<b>Berger Parker's</b>	<b>Simpson's</b>
N1153	0.17923	0.9315
N1154	0.17923	0.9315
N1155	0.38627	0.821
N1156	0.50674	0.68476
N1157	0.22601	0.88095
N1158	0.26606	0.89682
N1161	0.64889	0.57263
N1162	0.34406	0.7665
N1163	0.16557	0.92355
N1164	0.60842	0.62081
N1165	0.26837	0.88239
N1166	0.39028	0.82495
N1167	0.38029	0.7623
N1168	0.09781	0.95689
N1169	0.19855	0.94229
N1170	0.37164	0.84607
N1171	0.22865	0.90037
N1173	0.44123	0.68477
N1174	0.72495	0.43669
N1175	0.68508	0.51626
N1191	0.78571	0.3798

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**Table S3:** The completeness and contamination of total 219 high quality MAGs.

<b>Metagenome assembled genome (MAGs) with sample ID</b>	<b>Completeness (%)</b>	<b>Contamination (%)</b>
Oscillospiraceae_N1154.9	100	0.14
<i>Proteus_mirabilis</i> _N1162.4	100	0
<i>Methanobrevibacter_smithii</i> _N1173.2	100	0
<i>Megasphaera</i> _N1156.1	100	0.6
<i>Megasphaera</i> _N1153.15	100	0.4
<i>Laribacter_hongkongensis</i> _N1166.2	100	0.54
<i>Fusobacterium_ulcerans</i> _N1166.6	100	2.25
<i>Bilophila_wadsworthia</i> _N1167.5	100	0.59
<i>Bifidobacterium_longum</i> _N1168.11	100	0
<i>Bifidobacterium_longum</i> _N1161.4	100	0
<i>Acidaminococcus_intestini</i> _N1155.5	100	0
<i>Phascolarctobacterium_faecium</i> _N1165.7	99.98	1.5
<i>Megasphaera</i> _N1165.12	99.88	0.6
<i>Pseudomonas_aeruginosa</i> _N1163.10	99.68	0.11
<i>Escherichia_coli</i> _N1167.8	99.67	0.48
<i>Escherichia_coli</i> _N1165.14	99.67	3.81
<i>Escherichia_coli</i> _N1164.9	99.67	3.5
<i>Escherichia_coli</i> _N1156.2	99.67	0.39
<i>Collinsella</i> _N1155.20	99.63	1.61
<i>Escherichia_coli</i> _N1174.2	99.62	0.15
<i>Escherichia_coli</i> _N1161.2	99.62	0.26
<i>Escherichia_coli</i> _N1175.5	99.62	0.65
Rikenellaceae_N1169.12	99.52	0.64
<i>Eubacterium_rectale</i> _N1173.20	99.52	0.24
<i>Eubacterium_rectale</i> _N1153.19	99.52	0
<i>Bacteroides_ovatus</i> _N1155.13	99.51	0.04
<i>Bacteroides_xylanisolvans</i> _N1156.6	99.46	0
<i>Dysgonomonas</i> _N1175.7	99.45	3.28
<i>Phocaeicola_dorei</i> _N1165.11	99.44	1.5
<i>Parabacteroides_distasonis</i> _N1170.16	99.42	0
<i>Ruminococcus_torques</i> _N1169.17	99.42	0
<i>Ruminococcus_torques</i> _N1154.4	99.42	0
<i>Bilophila_wadsworthia</i> _N1156.5	99.41	0.11
<i>Megasphaera</i> _N1191.6	99.4	0
<i>Acidaminococcus_intestini</i> _N1162.2	99.4	0
<i>Phascolarctobacterium_faecium</i> _N1153.9	99.38	1.5
<i>Escherichia_coli</i> _N1162.8	99.37	0.15
<i>Parasutterella_excrementihominis</i> _N1169.9	99.37	0.11
<i>Blautia_obeum</i> _N1166.13	99.37	0.21

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<b>Metagenome assembled genome (MAGs) with sample ID</b>	<b>Completeness (%)</b>	<b>Contamination (%)</b>
<i>Blautia_obeum</i> _N1161.8	99.37	0
<i>Blautia_obeum</i> _N1155.8	99.37	0
<i>Clostridium_leptum</i> _N1154.8	99.33	0
Oscillospiraceae_N1175.8	99.32	0.68
Acidaminococcaceae_N1164.8	99.28	2.1
<i>Alistipes_finegoldii</i> _N1153.12	99.28	0.48
<i>Bacteroides_stercoris</i> _N1156.3	99.26	0
<i>Bacteroides_fragilis</i> _N1167.13	99.26	0
<i>Parabacteroides_merdae</i> _N1162.1	99.25	1.53
<i>Phocaeicola_vulgatus</i> _N1158.23	99.25	0
<i>Hafnia_paralvei</i> _N1164.7	99.24	0.7
<i>Parabacteroides_merdae</i> _N1154.6	99.23	0.51
<i>Bacteroides_dorei</i> _N1154.10	99.23	0.85
Bacillota_N1167.4	99.22	1.48
<i>Eggerthella_lenta</i> _N1168.12	99.19	0
<i>Collinsella_aerofaciens</i> _N1173.11	99.19	1.61
<i>Bacteroides</i> _N1166.4	99.19	0.33
<i>Limosilactobacillus_fermentum</i> _N1170.28	99.18	0
<i>Bacteroides_dorei</i> _N1169.20	99.06	1.5
Lachnospiraceae_N1167.6	99.05	0
Lachnospiraceae_N1169.13	99.03	1.71
Lachnospiraceae_N1171.17	99.02	0
<i>Bifidobacterium_longum</i> _N1173.10	99.01	0.55
<i>Streptococcus_salivarius</i> _N1170.6	98.92	1.49
<i>Limosilactobacillus_fermentum</i> _N1168.2	98.91	1.2
<i>Bacteroides_fragilis</i> _N1157.4	98.88	0.93
<i>Oligella_urethralis</i> _N1163.6	98.88	0
Fusobacteriaceae_N1165.6	98.88	2.25
<i>Phocaeicola_vulgatus</i> _N1153.13	98.87	0.4
<i>Ruminococcus_torques</i> _N1166.11	98.83	0.29
<i>Ruminococcus_torques</i> _N1158.3	98.83	0.74
<i>Bifidobacterium_longum</i> _N1170.9	98.82	2.59
<i>Bacteroides_ovatus</i> _N1154.5	98.81	0.16
<i>Alistipes_finegoldii</i> _N1164.6	98.8	0.48
Lachnospiraceae_N1164.3	98.78	0
<i>Blautia_obeum</i> _N1154.19	98.73	0
<i>Ruminococcus_bromii</i> _N1169.23	98.66	1.01
Bacillota_N1157.17	98.66	0
Oscillospiraceae_N1158.12	98.64	0.68
<i>Faecalibacterium_prausnitzii</i> _N1158.17	98.64	0
<i>Prevotella_buccae</i> _N1167.1	98.64	0.34

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<b>Metagenome assembled genome (MAGs) with sample ID</b>	<b>Completeness (%)</b>	<b>Contamination (%)</b>
<i>Anaerostipes_hadrus</i> _N1170.23	98.52	2.35
<i>Ruthenibacterium_lactatiformans</i> _N1158.15	98.52	0
<i>Blautia_obeum</i> _N1153.3	98.33	0.63
<i>Fusicatenibacter_saccharivorans</i> _N1153.7	98.31	0.65
<i>Ruminococcus_bromii</i> _N1173.14	98.28	9.48
<i>Collinsella</i> _N1154.15	98.19	1.09
<i>Bacteroides_vulgatus</i> _N1163.8	98.16	0
<i>Bacteroides_uniformis</i> _N1164.4	98.14	0.19
<i>Dialister_invisus</i> _N1170.8	98.1	0.63
<i>Dialister_invisus</i> _N1167.7	98.1	1.92
<i>Dialister_invisus</i> _N1156.8	98.1	0.63
<i>Blautia_obeum</i> _N1173.21	98.1	1.11
<i>Bacteroides_fragilis</i> _N1162.6	98.1	0
<i>Ruminococcus_bromii</i> _N1170.3	97.99	0.67
Oscillospiraceae_N1170.17	97.99	1.68
Oscillospiraceae_N1158.9	97.99	0.34
Oscillospiraceae_N1157.1	97.99	0
Bacillota_N1164.14	97.99	1.34
Bacillota_N1161.10	97.99	0
<i>Clostridium_leptum</i> _N1155.7	97.99	1.34
<i>Blautia</i> _N1171.6	97.99	2.01
<i>Faecalibacterium_prausnitzii</i> _N1155.22	97.96	0
<i>Bacteroides_caccae</i> _N1161.1	97.96	0
<i>Akkermansia_muciniphila</i> _N1173.3	97.96	0.68
<i>Akkermansia_muciniphila</i> _N1170.24	97.96	0
<i>Akkermansia_muciniphila</i> _N1167.9	97.96	0
<i>Akkermansia_muciniphila</i> _N1164.13	97.96	0.68
<i>Akkermansia_muciniphila</i> _N1157.9	97.96	0
<i>Akkermansia</i> _N1175.9	97.96	0
<i>Akkermansia</i> _N1174.3	97.96	0.68
<i>Ruminococcus_gnavus</i> _N1154.12	97.95	0.58
Bacillota_N1170.38	97.95	2.64
<i>Parabacteroides_distasonis</i> _N1155.19	97.93	1.73
<i>Enterocloster_bolteae</i> _N1154.17	97.79	0.68
<i>Bacteroides_uniformis</i> _N1157.12	97.79	0.99
Oscillospiraceae_N1175.6	97.77	1.42
<i>Monoglobus_pectinilyticus</i> _N1170.19	97.76	0.34
<i>Bacteroides_uniformis</i> _N1171.14	97.74	0.12
<i>Citrobacter_freundii</i> _N1163.9	97.72	1.24
<i>Parabacteroides_distasonis</i> _N1157.2	97.7	0.77
<i>Blautia_obeum</i> _N1156.9	97.67	0.02

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<b>Metagenome assembled genome (MAGs) with sample ID</b>	<b>Completeness (%)</b>	<b>Contamination (%)</b>
<i>Bacteroides intestinalis</i> _N1163.1	97.67	0.75
<i>Ruminococcus bromii</i> _N1158.13	97.65	1.01
Bacillota_N1170.15	97.65	0.67
<i>Eubacterium siraeum</i> _N1169.1	97.65	0.34
<i>Clostridium bolteae</i> _N1158.18	97.63	0.11
<i>Acidaminococcus intestini</i> _N1191.4	97.6	0
<i>Collinsella intestinalis</i> _N1153.5	97.58	0.81
<i>Parabacteroides distasonis</i> _N1171.13	97.55	0.77
<i>Bacteroides uniformis</i> _N1153.20	97.51	0
<i>Parabacteroides distasonis</i> _N1169.6	97.5	1.06
<i>Phascolarctobacterium succinatutens</i> _N1169.7	97.45	1.8
Bacteroidaceae_N1166.5	97.4	1.05
<i>Ruminococcus bromii</i> _N1168.8	97.32	1.34
Oscillospiraceae_N1169.2	97.32	0.67
Oscillospiraceae_N1157.15	97.32	0.67
<i>Flavonifractor plautii</i> _N1154.2	97.32	2.48
Bacillota_N1173.4	97.32	1.34
Bacillota_N1170.14	97.32	0
Bacillota_N1155.18	97.32	1.34
<i>Prevotella copri</i> _N1169.11	97.3	0.84
<i>Ruthenibacterium lactatiformans</i> _N1170.7	97.28	0.34
<i>Gemmiger formicilis</i> _N1153.8	97.28	0.82
<i>Faecalibacterium prausnitzii</i> _N1167.10	97.28	0
<i>Faecalibacterium prausnitzii</i> _N1157.5	97.25	0
<i>Roseburia faecis</i> _N1169.18	97.18	1.45
Bacillota_N1158.14	97.15	3.15
<i>Blautia obeum</i> _N1168.5	96.92	0
Oscillospiraceae_N1170.4	96.91	1.36
Lachnospiraceae_N1170.2	96.84	1.41
<i>Citrobacter koseri</i> _N1155.12	96.83	3.56
<i>Parabacteroides merdae</i> _N1155.11	96.82	1.15
<i>Ruminococcus torques</i> _N1163.11	96.78	0.7
Lachnospiraceae_N1154.11	96.72	0
<i>Ruminococcus bromii</i> _N1171.1	96.64	0.67
Bacillota_N1158.5	96.64	1.01
<i>Barnesiella intestinhominis</i> _N1169.5	96.6	0
<i>Gemmiger formicilis</i> _N1163.2	96.6	0.02
Bacillota_N1169.16	96.55	0.19
<i>Roseburia hominis</i> _N1158.16	96.38	0.48
<i>Roseburia intestinalis</i> _N1157.13	96.38	1.33

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<b>Metagenome assembled genome (MAGs) with sample ID</b>	<b>Completeness (%)</b>	<b>Contamination (%)</b>
<i>Parabacteroides_distasonis</i> _N1158.8	96.35	1.86
Bacillota_N1166.7	96.31	2.51
Blautia_N1153.11	96.27	0.32
<i>Ruminococcus_bicirculans</i> _N1170.34	96.24	0.23
<i>Holdemanella</i> _N1154.3	96.23	0.71
Pseudomonadota_N1163.16	96.09	2
<i>Bacteroides_caccae</i> _N1191.7	96.08	3.18
<i>Bacteroides_caccae</i> _N1161.11	96.05	1.04
<i>Parabacteroides_distasonis</i> _N1163.7	95.99	1.67
Pseudomonadota_N1164.5	95.7	0
<i>Ruminococcus_torques</i> _N1164.15	95.62	3.19
<i>Flavonifractor_plautii</i> _N1157.3	95.61	1.48
<i>Ruminococcus_torques</i> _N1171.5	95.32	0
<i>Anaerotignum_lactatifermentans</i> _N1155.9	95.3	0.08
<i>Anaerotignum</i> _N1164.1	95.3	0
<i>Phocaeicola_vulgatus</i> _N1191.2	95.11	0.56
Blautia_N1161.12	94.96	0.02
<i>Bilophila_wadsworthia</i> _N1163.4	94.84	1.28
<i>Clostridium</i> _N1158.21	94.63	1.63
Oscillospiraceae_N1169.15	94.63	0.9
Pseudomonadota_N1170.29	94.62	1.24
<i>Escherichia_coli</i> _N1173.17	94.61	0.1
Bacteroidetes_N1169.19	94.49	0.56
Bacillota_N1170.26	94.41	1.01
Bacillota_N1157.18	94.38	0.53
Bacteroidetes_N1169.14	94.18	0.75
<i>Ruthenibacterium_lactatiformans</i> _N1164.2	94.01	0
<i>Ruminococcus_torques</i> _N1161.5	93.82	0
<i>Ruminococcus_torques</i> _N1168.1	93.29	0.63
<i>Blautia_obeum</i> _N1165.9	93.12	0.02
Oscillospiraceae_N1170.21	93.11	1.34
Oscillospiraceae_N1173.1	92.95	3.08
<i>Ruminococcus</i> _N1154.16	92.87	1.2
Lachnospiraceae_N1171.8	92.87	0.88
<i>Parabacteroides_distasonis</i> _N1154.14	92.74	0.77
Oscillospiraceae_N1170.18	92.62	0
Oscillospiraceae_N1158.22	92.62	1.01
<i>Ruthenibacterium_lactatiformans</i> _N1157.19	92.17	0.5
<i>Roseburia</i> _N1157.16	92.15	2.52
<i>Phascolarctobacterium_succinatutens</i> _N1191.10	92.14	1.95
<i>Clostridium_leptum</i> _N1170.10	92.09	2.85



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<b>Metagenome assembled genome (MAGs) with sample ID</b>	<b>Completeness (%)</b>	<b>Contamination (%)</b>
<i>Clostridium</i> _N1161.6	91.64	2.32
<i>Escherichia_coli</i> _N1166.10	91.55	0.45
Bacillota_N1170.22	91.49	0.71
<i>Roseburia_inulinivorans</i> _N1156.7	91.46	1.04
Bacillota_N1171.4	91.42	1.01
<i>Bifidobacterium_longum</i> _N1153.4	91.27	1.83
<i>Gemmiger_formicilis</i> _N1165.4	91.15	0.85
Lachnospiraceae_N1171.2	90.9	0.21
<i>Parabacteroides_merdae</i> _N1162.11	90.89	0.64
<i>Bacteroides_ovatus</i> _N1158.6	90.87	2.07
Bacillota_N1174.1	90.83	1.07
<i>Anaerostipes_hadrus</i> _N1168.10	90.66	4.61
<i>Escherichia_coli</i> _N1155.6	90.44	3.37
<i>Bacteroides_finegoldii</i> _N1170.30	90.43	0.63
<i>Coprococcus</i> _N1153.14	90.07	0.63
<i>Collinsella_aerofaciens</i> _N1165.2	89.15	0.95
<i>Akkermansia_muciniphila</i> _N1191.18	94.69	0

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**Table S4:** The relative abundance of MAGs in each data set.

Sample ID	Organism	Relative Abundance (%)	
N1153	<i>Blautia obeum</i> N1153.3	32.9	
	<i>Bifidobacterium longum</i> N1153.4	0.6	
	<i>Collinsella intestinalis</i> N1153.5	0.7	
	<i>Fusicatenibacter saccharivorans</i> N1153.7	4.58	
	<i>Gemmiger formicilis</i> N1153.8	3.07	
	<i>Phascolarctobacterium faecium</i> N1153.9	3.91	
	<i>Blautia</i> N1153.11	7.8	
	<i>Alistipes finegoldii</i> N1153.12	2.01	
	<i>Bacteroides vulgatus</i> N1153.13	14.19	
	<i>Coprococcus</i> N1153.14	2.67	
	<i>Megasphaera</i> N1153.15	1.23	
	<i>Eubacterium rectale</i> N1153.19	3.75	
	<i>Bacteroides uniformis</i> N1153.20	3.97	
	N1154	<i>Flavonifractor plautii</i> N1154.2	1.88
		<i>Holdemanella</i> N1154.3	2.39
		<i>Ruminococcus torques</i> N1154.4	4.11
		<i>Bacteroides ovatus</i> N1154.5	15.67
		<i>Parabacteroides merdae</i> N1154.6	4.71
		<i>Clostridium leptum</i> N1154.8	2.45
Ruminococcaceae N1154.9		1.51	
<i>Bacteroides dorei</i> N1154.10		9.1	
Lachnospiraceae N1154.11		2.92	
<i>Ruminococcus gnavus</i> N1154.12		3.88	
<i>Parabacteroides distasonis</i> N1154.14		2.81	
<i>Collinsella</i> N1154.15		0.61	
Ruminococcus N1154.16		2.29	
<i>Clostridium bolteae</i> N1154.17		3.66	
<i>Blautia obeum</i> N1154.19		41.46	
N1155		<i>Acidaminococcus intestini</i> N1155.5	10.42
		<i>Escherichia coli</i> N1155.6	5.81
		<i>Clostridium leptum</i> N1155.7	2.43
		<i>Blautia obeum</i> N1155.8	11.41
	<i>Anaerotignum lactatifermentans</i> N1155.9	1.26	
	<i>Parabacteroides merdae</i> N1155.11	3.13	
	<i>Citrobacter koseri</i> N1155.12	5.4	
	<i>Bacteroides ovatus</i> N1155.13	36.58	
	Bacillota N1155.18	2.23	
	<i>Parabacteroides distasonis</i> N1155.19	2.32	
	<i>Collinsella</i> N1155.20	1.61	
	<i>Faecalibacterium prausnitzii</i> N1155.22	1.6	

## Supplementary Information

Sample ID	Organism	Relative Abundance (%)	
N1156	<i>Megasphaera</i> N1156.1	2.77	
	<i>Escherichia coli</i> N1156.2	41.51	
	<i>Bacteroides stercoris</i> N1156.3	20.85	
	<i>Bilophila wadsworthia</i> N1156.5	2.34	
	<i>Bacteroides xylanisolvens</i> N1156.6	11.09	
	<i>Roseburia inulinivorans</i> N1156.7	1.89	
	<i>Dialister invisus</i> N1156.8	8	
	<i>Blautia obeum</i> N1156.9	3.89	
	N1157	Ruminococcaceae N1157.1	6.26
<i>Parabacteroides distasonis</i> N1157.2		7.23	
<i>Flavonifractor plautii</i> N1157.3		3.66	
<i>Bacteroides fragilis</i> N1157.4		16.61	
<i>Faecalibacterium prausnitzii</i> N1157.5		2.82	
<i>Akkermansia muciniphila</i> N1157.9		11.64	
<i>Bacteroides uniformis</i> N1157.12		15.16	
<i>Roseburia intestinalis</i> N1157.13		7.99	
Ruminococcaceae N1157.15		9.71	
<i>Roseburia</i> N1157.16		1.9	
Bacillota N1157.17		3.36	
Bacillota N1157.18		2.22	
<i>Ruthenibacterium lactatiformans</i> N1157.19		2.11	
N1158		<i>Ruminococcus torques</i> N1158.3	4.8
		Bacillota N1158.5	2.06
		<i>Bacteroides ovatus</i> N1158.6	4.5
		<i>Parabacteroides distasonis</i> N1158.8	2.3
		Oscillospiraceae N1158.9	14.56
		Oscillospiraceae N1158.12	9.42
	<i>Ruminococcus bromii</i> N1158.13	1.73	
	Bacillota N1158.14	1.83	
	<i>Ruthenibacterium lactatiformans</i> N1158.15	3.89	
	<i>Roseburia hominis</i> N1158.16	3.13	
	<i>Faecalibacterium prausnitzii</i> N1158.17	6.97	
	<i>Clostridium bolteae</i> N1158.18	4.13	
	<i>Clostridium</i> N1158.21	4.19	
	Oscillospiraceae N1158.22	3.5	
	<i>Phocaeicola vulgatus</i> N1158.23	15.11	
	N1161	<i>Bacteroides caccae</i> N1161.1	4.93
		<i>Escherichia coli</i> N1161.2	55.97
<i>Bifidobacterium longum</i> N1161.4		1.56	

## Supplementary Information

Sample ID	Organism	Relative Abundance (%)
	<i>Ruminococcus torques</i> N1161.5	2.03
	<i>Clostridium</i> N1161.6	2.83
	<i>Blautia obeum</i> N1161.8	6.72
	Bacillota N1161.10	1.98
	<i>Bacteroides caccae</i> N1161.11	3.5
	<i>Blautia</i> N1161.12	1.84
N1162	<i>Parabacteroides merdae</i> N1162.1	20.94
	<i>Acidaminococcus intestini</i> N1162.2	1.51
	<i>Proteus mirabilis</i> N1162.4	25.55
	<i>Bacteroides fragilis</i> N1162.6	9.61
	<i>Escherichia coli</i> N1162.8	31.47
	<i>Parabacteroides merdae</i> N1162.11	2.11
N1163	<i>Bacteroides intestinalis</i> N1163.1	9.87
	<i>Gemmiger formicilis</i> N1163.2	2.55
	<i>Bilophila wadsworthia</i> N1163.4	1.88
	<i>Oligella urethralis</i> N1163.6	4.32
	<i>Parabacteroides distasonis</i> N1163.7	2.62
	<i>Bacteroides vulgatus</i> N1163.8	11.82
	<i>Citrobacter freundii</i> N1163.9	19.97
	<i>Pseudomonas aeruginosa</i> N1163.10	11.71
	<i>Ruminococcus torques</i> N1163.11	2.07
	Pseudomonadota N1163.16	1.17
N1164	<i>Anaerotignum</i> N1164.1	1.41
	<i>Ruthenibacterium lactatiformans</i> N1164.2	2.96
	Lachnospiraceae N1164.3	4.97
	<i>Bacteroides uniformis</i> N1164.4	4.44
	Pseudomonadota N1164.5	1.02
	<i>Alistipes finegoldii</i> N1164.6	3.14
	<i>Hafnia paralvei</i> N1164.7	9.53
	Acidaminococcaceae N1164.8	2.91
	<i>Escherichia coli</i> N1164.9	50.66
	<i>Akkermansia muciniphila</i> N1164.13	4.46
	Bacillota N1164.14	2.21
	<i>Ruminococcus torques</i> N1164.15	2.46
N1165	<i>Collinsella aerofaciens</i> N1165.2	0.79
	<i>Gemmiger formicilis</i> N1165.4	1.11
	Fusobacteriaceae N1165.6	29.43
	<i>Phascolarctobacterium faecium</i> N1165.7	3.4
	<i>Blautia obeum</i> N1165.9	9.12

## Supplementary Information

Sample ID	Organism	Relative Abundance (%)
	<i>Bacteroides dorei</i> N1165.11	10.8
	<i>Megasphaera</i> N1165.12	20.27
	<i>Escherichia coli</i> N1165.14	8.3
N1166	<i>Laribacter hongkongensis</i> N1166.2	3.54
	<i>Bacteroides</i> N1166.4	20.33
	Bacteroidaceae N1166.5	4.19
	<i>Fusobacterium ulcerans</i> N1166.6	8.01
	Bacillota N1166.7	1.14
	<i>Escherichia coli</i> N1166.10	35.21
	<i>Ruminococcus torques</i> N1166.11	2.14
	<i>Blautia obeum</i> N1166.13	4
N1167	<i>Prevotella buccae</i> N1167.1	2.09
	Bacillota N1167.4	1.57
	<i>Bilophila wadsworthia</i> N1167.5	5.94
	Lachnospiraceae N1167.6	12.14
	<i>Dialister invisus</i> N1167.7	2.27
	<i>Escherichia coli</i> N1167.8	21.45
	<i>Akkermansia muciniphila</i> N1167.9	10.3
	<i>Faecalibacterium prausnitzii</i> N1167.10	2.53
	<i>Bacteroides fragilis</i> N1167.13	14.82
N1168	<i>Ruminococcus torques</i> N1168.1	8.79
	<i>Lactobacillus fermentum</i> N1168.2	1
	<i>Blautia obeum</i> N1168.5	34.36
	<i>Ruminococcus bromii</i> N1168.8	1.74
	<i>Anaerostipes hadrus</i> N1168.10	2.99
	<i>Bifidobacterium longum</i> N1168.11	2.77
	<i>Eggerthella lenta</i> N1168.12	1.8
N1169	<i>Eubacterium siraeum</i> N1169.1	1.87
	Oscillospiraceae N1169.2	4.72
	<i>Barnesiella intestinihominis</i> N1169.5	3.99
	<i>Parabacteroides distasonis</i> N1169.6	2.91
	<i>Phascolarctobacterium succinatutens</i> N1169.7	1.26
	<i>Parasutterella excrementihominis</i> N1169.9	1.78
	<i>Prevotella copri</i> N1169.11	4.16
	Rikenellaceae N1169.12	5.95
	Lachnospiraceae N1169.13	7.81
	Bacteroidetes N1169.14	1.3
	Oscillospiraceae N1169.15	2.15
	Bacillota N1169.16	2.65

## Supplementary Information

Sample ID	Organism	Relative Abundance (%)
	<i>Ruminococcus torques</i> N1169.17	6.61
	<i>Roseburia faecis</i> N1169.18	4.29
	Bacteroidetes N1169.19	2.49
	<i>Bacteroides dorei</i> N1169.20	11.04
	<i>Ruminococcus bromii</i> N1169.23	2.34
N1170	Lachnospiraceae N1170.2	4.11
	<i>Ruminococcus bromii</i> N1170.3	2.08
	Oscillospiraceae N1170.4	1.97
	<i>Streptococcus salivarius</i> N1170.6	2.54
	<i>Ruthenibacterium lactatiformans</i> N1170.7	2.46
	<i>Dialister invisus</i> N1170.8	2.77
	<i>Bifidobacterium longum</i> N1170.9	0.88
	<i>Clostridium leptum</i> N1170.10	1.27
	Bacillota N1170.14	1.7
	Bacillota N1170.15	1.24
	<i>Parabacteroides distasonis</i> N1170.16	4.79
	Oscillospiraceae N1170.17	8.06
	Oscillospiraceae N1170.18	2.02
	<i>Monoglobus pectinilyticus</i> N1170.19	2.43
	Oscillospiraceae N1170.21	1.58
	Bacillota N1170.22	0.88
	<i>Anaerostipes hadrus</i> N1170.23	1.88
	<i>Akkermansia muciniphila</i> N1170.24	19.21
	Bacillota N1170.26	0.95
	<i>Lactobacillus fermentum</i> N1170.28	1.05
	Pseudomonadota N1170.29	0.74
	<i>Bacteroides fingoldii</i> N1170.30	3.23
	<i>Ruminococcus bicirculans</i> N1170.34	1.1
	Bacillota N1170.38	2.27
N1171	<i>Ruminococcus bromii</i> N1171.1	1.99
	Lachnospiraceae N1171.2	5.44
	Bacillota N1171.4	1.17
	<i>Ruminococcus torques</i> N1171.5	6.44
	<i>Blautia</i> N1171.6	12.41
	Lachnospiraceae N1171.8	2.37
	<i>Parabacteroides distasonis</i> N1171.13	2.6
	<i>Bacteroides uniformis</i> N1171.14	9.44
	Lachnospiraceae N1171.17	3.69
N1173	Oscillospiraceae N1173.1	1.43
	<i>Methanobrevibacter smithii</i> N1173.2	1.29

## Supplementary Information

<b>Sample ID</b>	<b>Organism</b>	<b>Relative Abundance (%)</b>
	<i>Akkermansia muciniphila</i> N1173.3	25.31
	Bacillota N1173.4	4.99
	Lachnospiraceae N1173.8	1.68
	<i>Bifidobacterium longum</i> N1173.10	1.27
	<i>Collinsella aerofaciens</i> N1173.11	1.43
	<i>Ruminococcus bromii</i> N1173.14	1.4
	<i>Escherichia coli</i> N1173.17	27.25
	<i>Eubacterium rectale</i> N1173.20	3.37
	<i>Blautia obeum</i> N1173.21	9.1
N1174	Bacillota N1174.1	1.31
	<i>Escherichia coli</i> N1174.2	17.55
	<i>Akkermansia</i> N1174.3	72.49
N1175	<i>Escherichia coli</i> N1175.5	9.88
	Oscillospiraceae N1175.6	3.1
	<i>Dysgonomonas</i> N1175.7	2.12
	Oscillospiraceae N1175.8	16.76
	<i>Akkermansia</i> N1175.9	54.38
N1191	<i>Phocaeicola vulgatus</i> N1191.2	3.96
	<i>Acidaminococcus intestini</i> N1191.4	1.36
	<i>Megasphaera</i> N1191.6	3.18
	<i>Bacteroides caccae</i> N1191.7	3.49
	<i>Phascolarctobacterium succinatutens</i> N1191.10	0.91
	<i>Akkermansia muciniphila</i> N1191.18	35

## Supplementary Information

Phylum	NAS (0-2)											NAS (3-4)					NAS (>=5)			
	N1153	N1154	N1156	N1157	N1164	N1168	N1169	N1171	N1173	N1175	N1191	N1161	N1162	N1163	N1166	N1174	N1155	N1158	N1165	N1167
Fusobacteria	0	0.021	0.0001	0	6.4E-05	0.0004	0	0.00029	0	0	0	0.00017	1.5E-05	0	0.07924	0	0.000523	0	0.1117	0.00017
Euryarchaeota	0	1E-04	0	0	0	0.0002	0.000766	0	0.014	0	4.39E-05	0	0	0	0	0	0.000242	0	0	0
Verrucomicrobia	0	0	0	0.1557	0.05263	0	0.005131	0	0.347	0.687	0.7855	0.00026	0	0.00011	3.12E-05	0.7267	7.29E-05	0	0	0.1747

Figure S1. Differential abundance of three key phyla among different NAS groups.