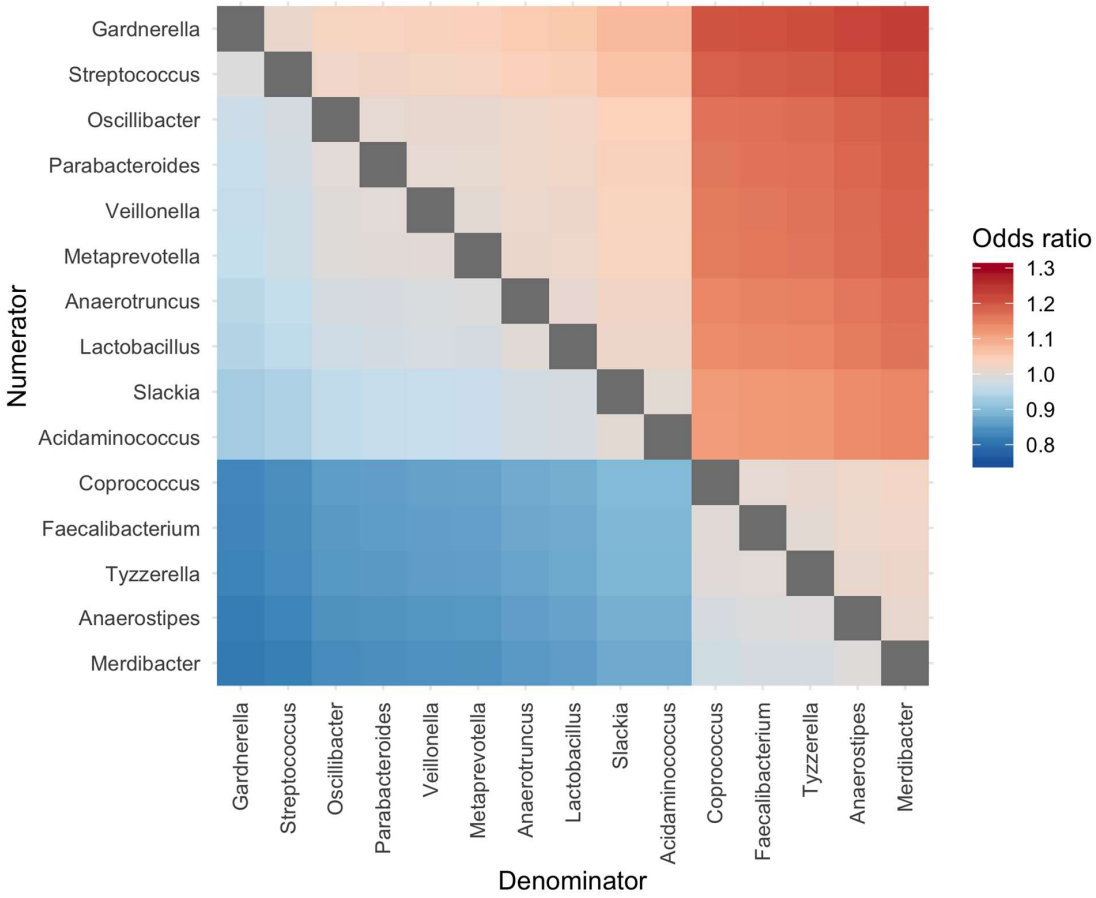
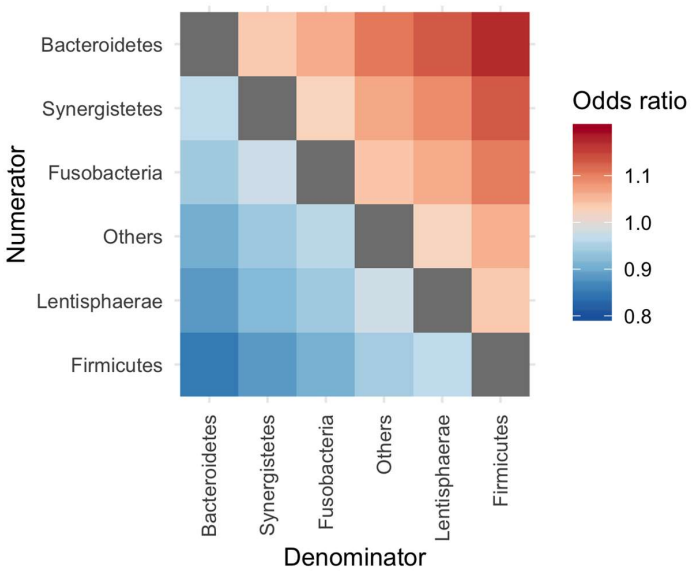
SUPPLEMENTARY MATERIALS

Figure A1: Genus-level pairwise odds ratios of for IBS vs. control



Agnello M, *et al. BMJ Open Gastro* 2020; 7:e000345. doi: 10.1136/bmjgast-2019-000345

Figure A2: Phylum-level pairwise odds ratios of for IBS vs. control



Agnello M, *et al. BMJ Open Gastro* 2020; 7:e000345. doi: 10.1136/bmjgast-2019-000345

Table A1: Wilcoxon rank-sum tests of all species for control vs. IBS

Species	W	Adjusted p-value (q-value)
Flavonifractor plautii	689555	<0.01
Faecalibacterium prausnitzii	1167612	<0.01
Faecalimonas umbilicata	737862	<0.01
Eggerthella lenta	746138	<0.01
Erysipelatoclostridium ramosum	754745	<0.01
Hungatella hathewayi	757205	<0.01
Ruthenibacterium lactatiformans	757359	<0.01
Blautia hydrogenotrophica	758420	<0.01
Coprococcus catus	1140868	<0.01
Lactobacillus salivarius	764651	<0.01
Anaerostipes caccae	764956	<0.01
Neglecta timonensis	765163	<0.01
Lactobacillus fermentum	768811	<0.01
Streptococcus mutans	769761	<0.01
Agathobaculum desmolans	769840	<0.01
Lachnoclostridium phocaeense	771022	<0.01
Anaerotignum lactatifermentans	771722	<0.01
Campylobacter ureolyticus	772758	<0.01
Clostridium perfringens	774222	<0.01
Collinsella tanakaei	775017	<0.01
Eubacterium limosum	775614	<0.01
Lactobacillus reuteri	776210	<0.01
Megasphaera massiliensis	776633	<0.01
Peptoniphilus coxii	776888	<0.01
Anaerotruncus colihominis	778600	<0.01
Streptococcus pneumoniae	778671	<0.01
Corynebacterium pyruviciproducens	780024	<0.01
Anaerococcus senegalensis	780339	<0.01
Streptococcus anginosus	780707	<0.01
Corynebacterium pseudogenitalium	781035	<0.01
Emergencia timonensis	781650	<0.01
Absiella dolichum	782046	<0.01
Gardnerella vaginalis	782491	<0.01
Intestinimonas butyriciproducens	783027	<0.01
Actinomyces neuii	784006	<0.01
Lactobacillus rhamnosus	784739	<0.01
Butyricicoccus pullicaecorum	784744	<0.01
Gordonibacter urolithinfaciens	786220	<0.01
Facklamia hominis	786298	<0.01
Lagierella massiliensis	786818	<0.01
Lactobacillus jensenii	787688	<0.01
Anaerococcus octavius	787708	<0.01
Lactobacillus iners	787925	<0.01
Holdemania filiformis	787955	<0.01
Streptococcus agalactiae	788242	<0.01
Corynebacterium riegelii	788593	<0.01
Slackia piriformis	788695	<0.01
Paraprevotella xylaniphila	789025	<0.01
Prevotella bergensis	789451	<0.01
Atopobium vaginae	790527	<0.01
Blautia obeum	1111638	<0.01
Eisenbergiella tayi	791367	<0.01
Cloacibacillus evryensis	794011	<0.01
Fusobacterium nucleatum	794076	<0.01

Dielma fastidiosa	794330	<0.01
Faecalicatena contorta	794487	<0.01
Peptococcus niger	794863	<0.01
Porphyromonas somerae	795539	<0.01
Sneathia amnii	795557	<0.01
Anaerococcus provencensis	797210	<0.01
Negativicoccus massiliensis	797265	<0.01
Megasphaera elsdenii	797884	<0.01
Prevotellamassilia timonensis	798167	<0.01
Murdochiella massiliensis	798672	<0.01
Acidaminococcus intestini	799358	<0.01
Coprobacillus cateniformis	800413	<0.01
Parabacteroides faecis	800966	<0.01
Prevotella bivia	801257	<0.01
Faecalitalea cylindroides	801472	<0.01
Dorea longicatena	1100287	<0.01
Staphylococcus aureus	803486	<0.01
Gabonia massiliensis	803853	<0.01
Porphyromonas uenonis	804116	<0.01
Porphyromonas asaccharolytica	805347	<0.01
Alistipes indistinctus	806071	<0.01
Victivallis vadensis	806235	<0.01
Lactobacillus ruminis	806292	<0.01
Peptoniphilus lacrimalis	806893	<0.01
Odoribacter laneus	807315	<0.01
Dialister succinatiphilus	807967	<0.01
Tyzzerella nexilis	808241	<0.01
Allisonella histaminiformans	809395	<0.01
Dakarella massiliensis	810101	<0.01
Bacteroides coprophilus	810548	<0.01
Collinsella bouchesdurhonensis	810711	<0.01
Ileibacterium massiliense	810763	<0.01
Bacteroides xylanisolvens	810765	<0.01
Bacteroides ovatus	811506	<0.01
Bifidobacterium bifidum	811750	<0.01
Peptoniphilus duerdenii	812220	<0.01
Blautia schinkii	1090133	<0.01
Mobiluncus curtisii	812422	<0.01
Prevotella timonensis	813321	<0.01
Gemmiger formicilis	1087059	<0.01
Mitsuokella jalaludinii	816135	<0.01
Dialister propionicifaciens	817243	<0.01
Bacteroides clarus	817446	<0.01
Mitsuokella multacida	817493	<0.01
Coprococcus comes	1084334	<0.01
Oxalobacter formigenes	818498	<0.01
Peptostreptococcus anaerobius	818609	<0.01
Bacteroides eggerthii	819412	<0.01
Parabacteroides johnsonii	820089	<0.01
Methanosphaera stadtmanae	820898	<0.01
Bacteroides nordii	821663	<0.01
Duodenibacillus massiliensis	821736	<0.01
Anaerostipes hadrus	1080201	<0.01
Dialister invisus	822939	<0.01
Lactococcus lactis	823118	<0.01
Alistipes ihumii	823493	<0.01
Parabacteroides goldsteinii	825222	<0.01
Blautia massiliensis	1075875	<0.01
Bacteroides coprocola	827440	<0.01
Bacteroides intestinalis	828825	<0.01

Campylobacter hominis	829583	<0.01
Corynebacterium jeikeium	830068	<0.01
Barnesiella intestinihominis	830391	<0.01
Prevotella disiens	831028	<0.01
Turicibacter sanguinis	832247	<0.01
Casaltella massiliensis	834540	<0.01
Peptoniphilus urinimassiliensis	835250	<0.01
Holdemanella biformis	840439	<0.01
Prevotella buccalis	841886	<0.01
Bacteroides salyersiae	847065	<0.01
Slackia isoflavoniconvertens	847858	<0.01
Akkermansia muciniphila	1054285	<0.01
Prevotella copri	1053364	<0.01
Catenibacterium mitsuokai	851442	<0.01
Bacteroides massiliensis	1048729	<0.01
Collinsella aerofaciens	1048456	<0.01
Butyricimonas virosa	855382	<0.01
Butyrivibrio crossotus	856192	<0.01
Phascolarctobacterium succinatutens	857057	<0.01
Negativibacillus massiliensis	858049	<0.01
Anaerococcus vaginalis	858098	<0.01
Alistipes timonensis	859728	<0.01
Prevotella corporis	863307	<0.01
Coprobacter fastidiosus	863677	<0.01
Alistipes shahii	1033851	<0.01
Bacteroides finegoldii	868794	<0.01
Sutterella wadsworthensis	1028995	<0.01
Ruminococcus callidus	876595	<0.01
Desulfovibrio piger	877791	<0.01
Alistipes finegoldii	879087	<0.01
Ruminococcus bromii	1023135	<0.01
Dorea formicigenerans	1018650	<0.01
Odoribacter splanchnicus	1016082	<0.01
Corynebacterium singulare	890365	<0.01
Parasutterella excrementihominis	1005275	0.01
Others	897286	0.01
Roseburia hominis	898403	0.01
Bilophila wadsworthia	900481	0.02
Intestinibacter bartlettii	900722	0.02
Ruminococcus lactaris	999935	0.02
Bacteroides fragilis	906821	0.04
Bacteroides caccae	989559	0.08
Parabacteroides merdae	915586	0.1
Methanobrevibacter smithii	916965	0.12
Roseburia inulinivorans	982354	0.15
Coprococcus eutactus	980108	0.19
Bacteroides plebeius	980007	0.19
Parabacteroides distasonis	925598	0.24
Phascolarctobacterium faecium	926380	0.26
Senegalimassilia anaerobia	926938	0.26
Bifidobacterium adolescentis	974988	0.27
Roseburia intestinalis	974494	0.28
Bacteroides vulgatus	928398	0.29
Finegoldia magna	932446	0.39
Eubacterium ramulus	969166	0.4
Alistipes obesi	967614	0.44
Bacteroides uniformis	960274	0.68
Roseburia faecis	945495	0.79
Blautia stercoris	955009	0.86

Table A2: Logistic regression for control vs. IBS at species level (Full model)

	Variable	OR	95% CI	p-value
Species	*Dorea formicigenerans*	1.09	1.03-1.15	<0.01
	Flavonifractor plautii	1.10	1.04-1.17	<0.01
	Tyzzerella nexilis	0.90	0.84-0.96	<0.01
	Anaerococcus provencensis	1.14	1.03-1.27	0.01
	Blautia hydrogenotrophica	1.10	1.03-1.17	0.01
	Faecalimonas umbilicata	1.09	1.02-1.17	0.01
	Gardnerella vaginalis	1.16	1.04-1.28	0.01
	Lactobacillus jensenii	1.18	1.04-1.34	0.01
	Prevotella copri	1.06	1.01-1.10	0.01
	Staphylococcus aureus	0.89	0.80-0.98	0.01
	Corynebacterium pyruviciproducens	1.12	1.02-1.22	0.02
	Lactobacillus salivarius	1.24	1.04-1.48	0.02
	Streptococcus agalactiae	1.15	1.02-1.30	0.02
	Anaerostipes hadrus	0.92	0.85-0.99	0.03
	Bacteroides finegoldii	1.06	1.01-1.11	0.03
	Bilophila wadsworthia	1.05	1.01-1.11	0.03
	Acidaminococcus intestini	1.06	1.00-1.13	0.04
	Clostridium perfringens	1.16	1.00-1.35	0.05
	Slackia piriformis	1.07	1.00-1.14	0.05
	Blautia massiliensis	0.94	0.87-1.00	0.06
	Lactobacillus fermentum	1.22	0.99-1.49	0.06
	Murdochiella massiliensis	1.11	1.00-1.24	0.06
	Coprococcus catus	0.95	0.91-1.00	0.07
	Negativicoccus massiliensis	0.89	0.79-1.01	0.07
	Slackia isoflavoniconvertens	1.06	0.99-1.13	0.07
	Bacteroides coprocola	1.06	0.99-1.13	0.09
	Bacteroides massiliensis	1.04	0.99-1.08	0.09
	Megasphaera massiliensis	1.06	0.99-1.14	0.09
	Streptococcus pneumoniae	1.07	0.99-1.16	0.09
	Alistipes indistinctus	1.05	0.99-1.12	0.10
	Anaerococcus vaginalis	0.94	0.87-1.01	0.10
	Bacteroides fragilis	1.04	0.99-1.09	0.10
	Alistipes finegoldii	1.04	0.99-1.09	0.12
	Bacteroides eggerthii	1.05	0.99-1.11	0.12
	Coprobacillus cateniformis	0.93	0.84-1.02	0.12
	Lachnoclostridium phocaeense	1.10	0.98-1.24	0.12
	Prevotella timonensis	0.93	0.84-1.02	0.12
	Streptococcus mutans	1.11	0.97-1.28	0.13
	Neglecta timonensis	1.06	0.98-1.13	0.14
	Dialister invisus	1.03	0.99-1.08	0.15
	Coprococcus comes	1.04	0.98-1.09	0.17
	Corynebacterium jeikeium	0.93	0.85-1.03	0.17
	Peptoniphilus urinimassiliensis	1.07	0.97-1.17	0.17
	Sutterella wadsworthensis	0.96	0.92-1.02	0.17

	Faecalibacterium prausnitzii	0.96	0.91-1.02	0.18
	Paraprevotella xylaniphila	1.08	0.97-1.21	0.18
	Coprobacter fastidiosus	0.96	0.91-1.02	0.19
	Parasutterella excrementihominis	0.97	0.93-1.02	0.19
	Bacteroides nordii	1.04	0.98-1.09	0.20
	Desulfovibrio piger	0.96	0.91-1.02	0.20
	Blautia obeum	1.04	0.98-1.11	0.21
	Collinsella aerofaciens	1.03	0.98-1.08	0.21
	Anaerococcus octavius	1.06	0.96-1.18	0.22
	Atopobium vaginae	0.92	0.80-1.05	0.22
	Eubacterium limosum	0.95	0.87-1.03	0.22
	Gemmiger formicilis	1.03	0.98-1.09	0.22
	Alistipes shahii	0.97	0.92-1.02	0.23
	Methanosphaera stadtmanae	0.94	0.85-1.04	0.23
	Allisonella histaminiformans	0.96	0.89-1.03	0.25
	Collinsella tanakaei	1.05	0.97-1.14	0.25
	Streptococcus anginosus	1.05	0.97-1.14	0.25
	Lactococcus lactis	0.96	0.90-1.03	0.26
	Peptoniphilus coxii	1.06	0.96-1.18	0.26
	Corynebacterium singulare	0.96	0.89-1.03	0.27
	Absiella dolichum	1.06	0.96-1.17	0.28
	Eisenbergiella tayi	0.95	0.88-1.04	0.28
	Peptococcus niger	1.06	0.95-1.19	0.29
	Phascolarctobacterium succinatutens	1.03	0.97-1.10	0.29
	Mobiluncus curtisii	0.94	0.84-1.05	0.30
	Bacteroides ovatus	1.03	0.97-1.08	0.32
	Catenibacterium mitsuokai	0.97	0.90-1.03	0.32
	Parabacteroides goldsteinii	1.03	0.97-1.09	0.32
	Ruminococcus callidus	1.03	0.98-1.08	0.32
	Bacteroides coprophilus	0.95	0.86-1.05	0.33
	Porphyromonas uenonis	0.95	0.85-1.06	0.33
	Holdemanella biformis	1.03	0.97-1.11	0.34
	Roseburia hominis	0.98	0.94-1.02	0.34
	Bacteroides intestinalis	1.03	0.97-1.09	0.36
	Faecalicatena contorta	1.05	0.95-1.15	0.36
	Turicibacter sanguinis	0.97	0.91-1.03	0.36
	Campylobacter ureolyticus	1.05	0.95-1.16	0.37
	Erysipelatoclostridium ramosum	1.03	0.97-1.09	0.37
	Lactobacillus iners	1.04	0.96-1.12	0.37
	Ruthenibacterium lactatiformans	1.04	0.96-1.12	0.37
	Bacteroides salyersiae	1.02	0.97-1.08	0.39
	Duodenibacillus massiliensis	0.96	0.88-1.05	0.39
	Mitsuokella multacida	0.95	0.85-1.07	0.41
	Anaerococcus senegalensis	1.04	0.94-1.15	0.43
	Alistipes timonensis	0.98	0.92-1.04	0.44
	Porphyromonas somerae	1.04	0.94-1.16	0.45
	Eggerthella lenta	1.02	0.97-1.08	0.46
	Odoribacter splanchnicus	1.02	0.96-1.08	0.50
	Prevotella disiens	0.97	0.90-1.05	0.50

	Cloacibacillus evryensis	1.03	0.94-1.13	0.51
	Intestinibacter bartlettii	1.02	0.97-1.07	0.51
	Alistipes ihumii	1.02	0.96-1.08	0.54
	Dorea longicatena	0.98	0.92-1.05	0.55
	Lactobacillus rhamnosus	1.04	0.91-1.20	0.55
	Corynebacterium riegelii	1.03	0.91-1.17	0.59
	Hungatella hathewayi	1.02	0.94-1.11	0.59
	Peptostreptococcus anaerobius	0.98	0.89-1.07	0.59
	Blautia schinkii	0.99	0.93-1.04	0.61
	Dakarella massiliensis	1.02	0.95-1.09	0.61
	Lactobacillus reuteri	0.96	0.82-1.13	0.61
	Prevotellamassilia timonensis	0.97	0.88-1.08	0.61
	Others	1.01	0.96-1.07	0.61
	Dialister succinatiphilus	0.98	0.88-1.08	0.63
	Bacteroides clarus	0.98	0.91-1.06	0.64
	Emergencia timonensis	0.98	0.90-1.07	0.64
	Ruminococcus bromii	0.99	0.95-1.03	0.64
	Mitsuokella jalaludinii	1.03	0.91-1.17	0.65
	Campylobacter hominis	0.98	0.89-1.07	0.67
	Ileibacterium massiliense	1.03	0.91-1.16	0.67
	Porphyromonas asaccharolytica	1.02	0.93-1.12	0.67
	Intestinimonas butyriciproducens	1.02	0.94-1.10	0.68
	Odoribacter laneus	1.02	0.94-1.10	0.69
	Butyricimonas virosa	1.01	0.96-1.07	0.70
	Fusobacterium nucleatum	0.98	0.87-1.10	0.71
	Dielma fastidiosa	0.98	0.89-1.09	0.73
	Oxalobacter formigenes	1.01	0.94-1.09	0.73
	Akkermansia muciniphila	0.99	0.95-1.03	0.74
	Lactobacillus ruminis	1.02	0.93-1.12	0.74
	Parabacteroides faecis	0.98	0.89-1.09	0.74
	Bifidobacterium bifidum	1.01	0.95-1.07	0.75
	Collinsella bouchesdurhonensis	1.02	0.93-1.11	0.75
	Bacteroides xylanisolvens	1.01	0.92-1.11	0.77
	Prevotella bergensis	1.02	0.90-1.16	0.77
	Parabacteroides johnsonii	1.01	0.95-1.07	0.78
	Peptoniphilus duerdenii	0.99	0.89-1.09	0.78
	Gabonia massiliensis	1.01	0.93-1.10	0.79
	Victivallis vadensis	1.01	0.92-1.12	0.80
	Anaerotignum lactatifermentans	1.01	0.96-1.06	0.82
	Lagierella massiliensis	1.01	0.90-1.14	0.83
	Peptoniphilus lacrimalis	1.01	0.91-1.13	0.83
	Barnesiella intestinihominis	1.01	0.95-1.07	0.85
	Butyricicoccus pullicaecorum	1.01	0.92-1.11	0.85
	Facklamia hominis	1.01	0.89-1.15	0.86
	Gordonibacter urolithinfaciens	1.01	0.91-1.13	0.86
	Sneathia amnii	1.01	0.89-1.15	0.86
	Butyrivibrio crossotus	1.01	0.94-1.08	0.89
	Holdemania filiformis	0.99	0.93-1.07	0.89
	Corynebacterium pseudogenitalium	1.01	0.92-1.09	0.90

	Faecalitalea cylindroides	0.99	0.91-1.08	0.90
	Negativibacillus massiliensis	1.00	0.95-1.05	0.90
	Prevotella corporis	1.00	0.94-1.08	0.90
	Ruminococcus lactaris	1.00	0.95-1.04	0.91
	Actinomyces neuii	1.01	0.90-1.13	0.92
	Anaerostipes caccae	1.00	0.91-1.10	0.92
	Anaerotruncus colihominis	1.00	0.91-1.09	0.92
	Agathobaculum desmolans	1.00	0.93-1.07	0.93
	Dialister propionicifaciens	1.00	0.90-1.12	0.96
	Megasphaera elsdenii	1.00	0.91-1.11	0.96
	Prevotella buccalis	1.00	0.92-1.08	0.97
	Prevotella bivia	1.00	0.92-1.08	0.98
	Casaltella massiliensis	1.00	0.89-1.12	1.00
Sex	Male	1.00	0.68-1.48	1.00
	Female	Referent	-	-
Age (years)	>34 to 42	0.99	0.73-1.34	0.95
	>42 to 52	0.97	0.71-1.32	0.84
	>52 to 81	1.17	0.85-1.61	0.34
	18 to 34	Referent	-	-
Age-sex interaction	Male:Age(>34 to 42)	0.78	0.46-1.32	0.36
	Male:Age(>42 to 52)	0.64	0.36-1.11	0.11
	Male:Age(>52 to 81)	0.70	0.39-1.24	0.22
Race	African American	1.10	0.47-2.60	0.82
	Asian/Oceania/Pacific Islander/Hawaii	0.54	0.32-0.91	0.02
	Latin American/Hispanic	0.52	0.29-0.91	0.02
	Mixed	0.41	0.23-0.73	<0.01
	Unknown	0.85	0.69-1.03	0.10
	Caucasian/European/American	Referent	-	-
Antibiotic use in preceding year	Penicillins	1.32	1.03-1.68	0.03
	Tetracyclines	1.82	1.21-2.74	<0.01
	Cephalosporins	1.85	1.07-3.19	0.03
	Quinolones	1.94	1.27-2.96	<0.01
	Lincomycins	2.01	0.86-4.70	0.11
	Macrolides	1.42	1.00-2.03	0.05
	Sulfonamides	2.06	0.99-4.28	0.05
	Glycopeptides	4.54	0.47-43.82	0.19
	Aminoglycosides	1.33	0.19-9.02	0.77
Family history of gut disorders	Irritable bowel syndrome	5.46	3.97-7.50	<0.01
	Ulcerative colitis	1.01	0.56-1.83	0.97
	Crohn's disease	0.95	0.54-1.70	0.87
	Diverticulitis	1.38	0.99-1.92	0.06

Table A3: Wilcoxon rank-sum tests of all genera for control vs. IBS (Full model)

Genera	W	Adjusted p-value (q-value)
Coprococcus	1179627	<0.01
Faecalibacterium	1163613	<0.01
Eggerthella	770212	<0.01
Erysipelatoclostridium	791029	<0.01
Anaerotruncus	801546	<0.01
Anaerotignum	803232	<0.01
Ruminococcus	1097436	<0.01
Lactobacillus	807118	<0.01
Dorea	1091291	<0.01
Streptococcus	814404	<0.01
Acidaminococcus	818999	<0.01
Veillonella	819511	<0.01
Megasphaera	825183	<0.01
Parabacteroides	833676	<0.01
Holdemania	834106	<0.01
Intestinimonas	834662	<0.01
Absiella	835493	<0.01
Oscillibacter	835722	<0.01
Ezakiella	837373	<0.01
Negativicoccus	838035	<0.01
Gardnerella	839454	<0.01
Lactonifactor	839648	<0.01
Enterococcus	840819	<0.01
Fusobacterium	840974	<0.01
Pediococcus	842982	<0.01
Anaerostipes	1060480	<0.01
Delftia	843055	<0.01
Dysgonomonas	843234	<0.01
Fournierella	843775	<0.01
Escherichia	844066	<0.01
Weissella	844235	<0.01
Bacillus	844983	<0.01
Enterobacter	845500	<0.01
Facklamia	845530	<0.01
Faecalicatena	846124	<0.01
Metaprevotella	846635	<0.01
Actinomyces	847186	<0.01
Methanomassiliicoccus	847248	<0.01
Tyzzerella	847502	<0.01
Roseburia	1055655	<0.01
Gemella	848338	<0.01
Solobacterium	849380	<0.01
Lachnobacterium	850470	<0.01
Peptococcus	851064	<0.01
Faecalicoccus	851333	<0.01
Gordonibacter	851473	<0.01

Congobacterium	851663	<0.01
Atopobium	852412	<0.01
Others	852829	<0.01
Sneathia	853370	<0.01
Brachyspira	854096	<0.01
Alistipes	1049295	<0.01
Faecalitalea	854853	<0.01
Staphylococcus	856466	<0.01
Leuconostoc	857384	<0.01
Allisonella	858648	<0.01
Bacteroides	858719	<0.01
Olsenella	859298	<0.01
Megamonas	859931	<0.01
Subdoligranulum	860231	<0.01
Varibaculum	860304	<0.01
Libanicoccus	860577	<0.01
Brevibacterium	861083	<0.01
Dakarella	861932	<0.01
Gabonibacter	862713	<0.01
Campylobacter	866059	<0.01
Mobiluncus	871161	<0.01
Peptostreptococcus	871745	<0.01
Dialister	871946	<0.01
Oxalobacter	873138	<0.01
Merdibacter	875844	<0.01
Mitsuokella	876718	<0.01
Lactococcus	878407	<0.01
Methanosphaera	879070	<0.01
Porphyromonas	879190	<0.01
Slackia	881984	<0.01
Barnesiella	883193	<0.01
Prevotella	1020284	<0.01
Howardella	884120	<0.01
Peptoniphilus	885929	<0.01
Casaltella	888989	<0.01
Holdemanella	890229	<0.01
Odoribacter	1012078	0.01
Blautia	894512	0.01
Catenibacterium	896945	0.01
Sutterella	1006440	0.01
Anaerococcus	898817	0.01
Massiliprevotella	899259	0.02
Collinsella	999236	0.03
Haemophilus	909314	0.05
Butyrivibrio	910588	0.06
Butyricimonas	910757	0.06
Bilophila	911466	0.06
Bifidobacterium	991807	0.06
Parasutterella	990540	0.07
Clostridium	913916	0.08
Eubacterium	989367	0.08
Desulfovibrio	915748	0.09
Akkermansia	985090	0.12
Finegoldia	933834	0.42

Ruminiclostridium	936081	0.48
Phascolarctobacterium	966393	0.5
Corynebacterium	961897	0.64
Methanobrevibacter	961447	0.65
Turicibacter	942853	0.67

Table A4: Logistic regression for control vs. IBS at genus level (Full model)

	Variable	OR	95% CI	p-value
Genus	*Faecalibacterium*	0.94	0.90-0.98	0.01
	Gardnerella	1.13	1.03-1.23	0.01
	Lactobacillus	1.07	1.02-1.13	0.01
	Veillonella	1.09	1.02-1.16	0.01
	Anaerotruncus	1.08	1.01-1.15	0.02
	Tyzzerella	0.94	0.88-0.99	0.02
	Coprococcus	0.94	0.89-0.99	0.03
	Merdibacter	0.92	0.85-0.99	0.03
	Metaprevotella	1.09	1.01-1.17	0.03
	Slackia	1.05	1.01-1.10	0.03
	Acidaminococcus	1.05	1.00-1.11	0.04
	Anaerostipes	0.93	0.86-1.00	0.04
	Eggerthella	1.05	1.00-1.09	0.05
	Lactococcus	0.95	0.89-1.00	0.07
	Ezakiella	1.09	0.98-1.22	0.1
	Blautia	1.1	0.98-1.25	0.11
	Lactonifactor	1.1	0.98-1.24	0.12
	Negativicoccus	1.07	0.98-1.17	0.12
	Staphylococcus	0.94	0.87-1.02	0.13
	Anaerotignum	1.03	0.99-1.08	0.14
	Megasphaera	1.04	0.98-1.10	0.16
	Dakarella	1.04	0.98-1.10	0.18
	Ruminococcus	0.97	0.92-1.02	0.19
	Dialister	1.03	0.99-1.07	0.21
	Campylobacter	0.96	0.89-1.03	0.22
	Faecalicatena	1.05	0.97-1.14	0.22
	Congobacterium	1.05	0.97-1.15	0.23
	Methanomassiliicoccus	1.05	0.96-1.15	0.25
	Fournierella	1.05	0.96-1.15	0.26
	Methanosphaera	0.95	0.87-1.04	0.26
	Mitsuokella	0.95	0.88-1.04	0.27
	Mobiluncus	0.95	0.86-1.04	0.28
	Peptostreptococcus	0.96	0.90-1.03	0.28
	Atopobium	0.95	0.86-1.05	0.29
	Massiliprevotella	1.03	0.98-1.08	0.29
	Alistipes	0.97	0.91-1.03	0.33
	Peptococcus	1.05	0.95-1.16	0.33
	Erysipelatoclostridium	1.03	0.97-1.08	0.34
	Roseburia	0.98	0.93-1.03	0.36
	Absiella	1.03	0.96-1.11	0.4
	Enterococcus	1.03	0.96-1.12	0.4
	Fusobacterium	1.03	0.96-1.12	0.4
	Facklamia	1.04	0.95-1.13	0.44
	Bacteroides	0.96	0.87-1.06	0.45

	Holdemanella	1.02	0.96-1.08	0.46
	Gordonibacter	1.02	0.97-1.07	0.5
	Megamonas	1.02	0.96-1.09	0.5
	Sneathia	0.97	0.87-1.07	0.51
	Others	0.98	0.93-1.04	0.53
	Allisonella	0.98	0.92-1.04	0.55
	Odoribacter	1.01	0.97-1.06	0.55
	Dorea	1.02	0.96-1.09	0.56
	Casaltella	0.98	0.90-1.06	0.57
	Haemophilus	0.98	0.93-1.04	0.58
	Faecalitalea	1.02	0.94-1.10	0.64
	Holdemania	0.99	0.93-1.05	0.68
	Libanicoccus	0.98	0.88-1.09	0.72
	Actinomyces	0.99	0.92-1.06	0.73
	Catenibacterium	0.99	0.94-1.05	0.76
	Varibaculum	1.01	0.94-1.09	0.76
	Howardella	0.99	0.93-1.06	0.79
	Prevotella	1.00	0.97-1.04	0.8
	Barnesiella	1.00	0.94-1.05	0.86
	Porphyromonas	0.99	0.92-1.08	0.89
	Anaerococcus	1.00	0.93-1.08	0.96
	Intestinimonas	1.00	0.94-1.07	0.96
	Peptoniphilus	1.00	0.92-1.09	0.97
	Oxalobacter	1.00	0.94-1.07	0.99
	Oscillibacter	1.10	1.03-1.16	<0.01
	Parabacteroides	1.09	1.03-1.16	<0.01
	Streptococcus	1.12	1.06-1.18	<0.01
Sex	Male	1.09	0.76-1.58	0.64
	Female	Referent	-	-
Age (years)	>34 to 42	1.06	0.79-1.41	0.72
	>42 to 52	1.02	0.76-1.38	0.88
	>52 to 81	1.35	0.99-1.83	0.05
	18 to 34	Referent	-	-
Age-sex interaction	Male:Age(>34 to 42)	0.7	0.42-1.17	0.17
	Male:Age(>42 to 52)	0.61	0.35-1.04	0.07
	Male:Age(>52 to 81)	0.54	0.31-0.93	0.03
Race	African American	1.33	0.57-3.08	0.51
	Asian/Oceania/Pacific Islander/Hawaii	0.52	0.32-0.85	0.01
	Latin American/Hispanic	0.54	0.31-0.93	0.03
	Mixed	0.45	0.26-0.78	<0.01
	Unknown	0.87	0.72-1.05	0.16
	Caucasian/European/American	Referent	-	-
Antibiotic use in preceding year	Penicillins	1.24	0.98-1.58	0.07
	Tetracyclines	1.73	1.17-2.56	0.01
	Cephalosporins	1.88	1.11-3.17	0.02
	Quinolones	2.06	1.37-3.10	<0.01
	Lincomycins	2.24	0.98-5.14	0.06
	Macrolides	1.46	1.04-2.05	0.03
	Sulfonamides	1.62	0.79-3.32	0.19

	Glycopeptides	4.81	0.58-39.96	0.15
	Aminoglycosides	1.09	0.17-6.87	0.92
Family history of gut disorders	Irritable bowel syndrome	5.15	3.80-6.98	<0.01
	Ulcerative colitis	0.96	0.54-1.68	0.88
	Crohn's disease	1.25	0.91-1.71	0.18
	Diverticulitis	0.96	0.56-1.67	0.89

Table A5: Wilcoxon rank-sum tests of all phyla for control vs. IBS (Full model)

Phyla	W	Adjusted p-value (q-value)
Verrucomicrobia	967675	0.46
Lentisphaerae	872461	<0.01
Firmicutes	912685	0.11
Bacteroidetes	832432	<0.01
Actinobacteria	928450	0.34
Proteobacteria	967385	0.46
Euryarchaeota	976484	0.34
Fusobacteria	840477	<0.01
Synergistetes	844810	<0.01
Others	862726	<0.01

Table A6: Logistic regression for control vs. IBS at phylum level (Full model)

	Variable	OR	CI	p.value
Phyla	*Lentisphaerae*	1.02	0.95-1.10	0.50
	Firmicutes	0.99	0.86-1.14	0.87
	Bacteroidetes	1.15	1.03-1.28	0.01
	Fusobacteria	1.09	1.03-1.15	<0.01
	Synergistetes	1.11	1.05-1.18	<0.01
	Others	1.05	0.95-1.15	0.35
Sex	Male	0.84	0.60-1.18	0.32
	Female	Referent	-	-
Age	>34 to 42	1.12	0.85-1.47	0.44
	>42 to 52	1.13	0.86-1.49	0.38
	>52 to 81	1.53	1.16-2.02	<0.01
	18 to 34	Referent	-	-
Age-sex interaction	Male:Age(>34 to 42)	0.81	0.50-1.31	0.39
	Male:Age(>42 to 52)	0.65	0.39-1.08	0.1
	Male:Age(>52 to 81)	0.65	0.39-1.08	0.1
Race	African American	1.41	0.64-3.10	0.39
	Asian/Oceania/Pacific Islander/Hawaii	0.49	0.31-0.79	<0.01
	Latin American/Hispanic	0.6	0.36-1.00	0.05
	Mixed	0.5	0.29-0.87	0.01
	Unknown	0.87	0.72-1.03	0.11
	Caucasian/European/American	Referent	-	-
Antibiotic use in preceding year	Penicillins	1.43	1.15-1.79	<0.01
	Tetracyclines	1.92	1.32-2.78	<0.01
	Cephalosporins	1.97	1.20-3.25	0.01
	Quinolones	2.46	1.68-3.62	<0.01
	Lincomycins	2.53	1.15-5.58	0.02
	Macrolides	1.62	1.17-2.24	<0.01
	Sulfonamides	1.95	0.98-3.89	0.06
	Glycopeptides	6.32	0.77-51.88	0.09
	Aminoglycosides	1.1	0.18-6.56	0.92
Family history of gut disorders	Irritable bowel syndrome	5.47	4.09-7.32	<0.01
	Ulcerative colitis	0.96	0.57-1.64	0.89
	Crohn's disease	1.02	0.61-1.71	0.93
	Diverticulitis	1.3	0.96-1.75	0.09

Table A7: Participant characteristics and distribution in control and IBS groups in the subgroup on antibiotics (n=1010)

	Control (n = 270)		IBS (n = 740)		p-value
Age [n, median (25th-75th percentile)]	270	41(34-50)	740	42(34-53)	0.14
Gender [n, (%)]					
Female	183	(67.78)	561	(75.81)	0.01
Male	87	(32.22)	179	(24.19)	0.01
Region of the U.S. [n, (%)]					
Midwest	49	(18.22)	131	(17.70)	0.91
Northeast	49	(18.22)	143	(19.32)	0.68
South	77	(28.62)	226	(30.54)	0.51
West	94	(34.94)	240	(32.43)	0.44
Race [n, (%)]					
Caucasian/European/American	144	(53.33)	452	(61.08)	0.01
African American	1	(0.37)	9	(1.22)	0.32
Asian/Oceanian/Pacific Islander/Hawaiian	11	(4.10)	13	(1.80)	<0.01
Latin American/Hispanic	8	(2.96)	18	(2.43)	0.71
Mixed	11	(4.10)	14	(1.89)	0.02
Unknown	95	(35.19)	234	(31.62)	0.23
Antibiotics in the preceding year [n, (%)]	**349**		**1,283**		
Penicillins	160	(45.85)	416	(32.42)	<0.01
Tetracyclines	45	(12.89)	184	(14.34)	0.54
Cephalosporins	23	(6.59)	110	(8.57)	0.27
Quinolones	37	(10.60)	211	(16.45)	<0.01
Lincomycins	8	(2.29)	59	(4.60)	0.07
Macrolides	62	(17.77)	211	(16.45)	0.61
Sulfonamides	11	(3.15)	67	(5.22)	0.14
Glycopeptides	1	(0.29)	19	(1.48)	<0.01
Aminoglycosides	2	(0.57)	6	(0.47)	0.28
Family history of gut disorders [n, (%)]	**49**	**(17.17)**	**377**	**(44.92)**	**<0.01**
IBS	21	(10.88)	203	(26.72)	0.16
Ulcerative colitis	7	(3.63)	27	(3.55)	0.09
Crohn's disease	4	(2.07)	33	(4.34)	0.99
Diverticulitis	17	(8.81)	114	(15.00)	0.60

Figure A3: Species-level pairwise odds ratios for IBS vs. control in the subgroup on antibiotics

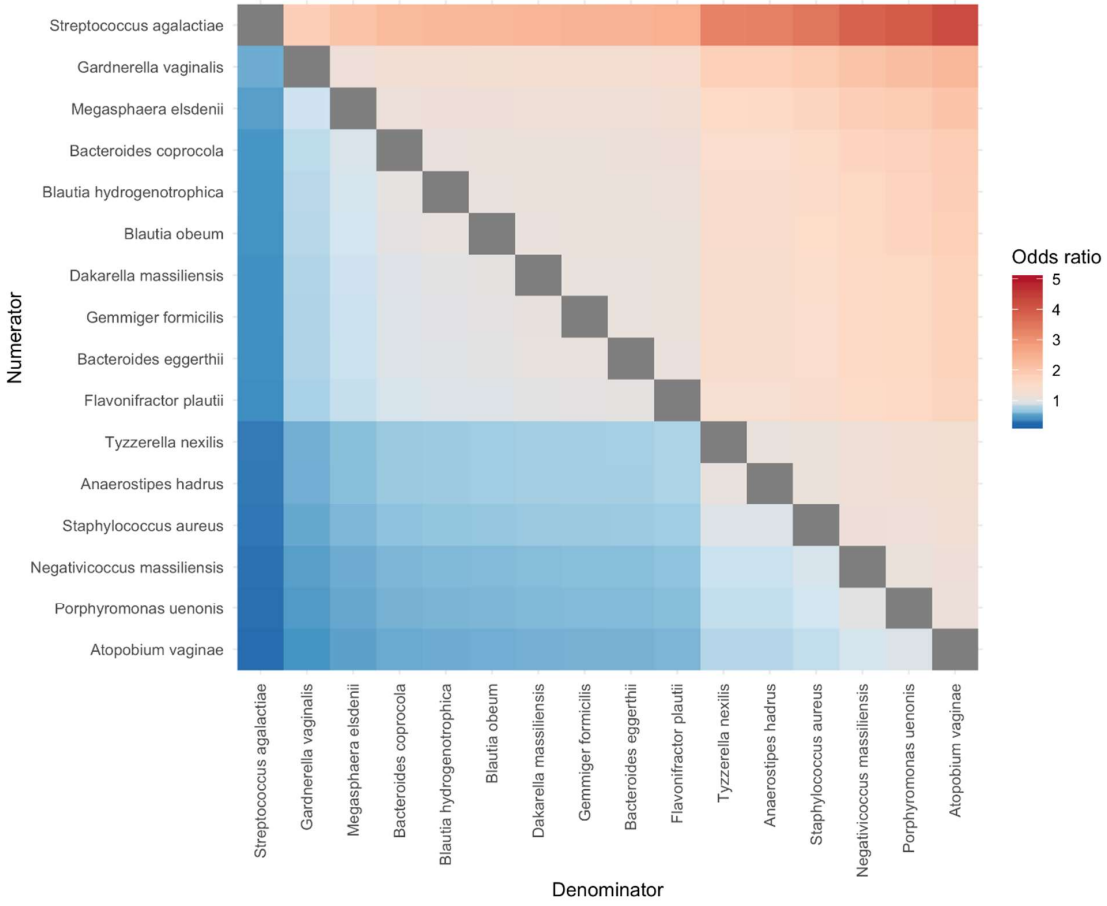


Figure A4: Genus-level pairwise odds ratios for IBS vs. control in the subgroup on antibiotics