Table 2: Shotgun species differentially abundant between the IBS and Control groups

Species	IBS (IQR)	Control (IQR)	Wilcoxon Statistic	p-value	q-value
Ruminococcus_gnavus	0.0136 (0 - 0.187)	0 (0 - 0)	1209	< 0.001	< 0.001
Clostridium_bolteae	0.016 (0 - 0.0873)	0 (0 - 0.00248)	1189	< 0.001	< 0.001
Clostridiales_bacterium_1_7_47FAA	0 (0 - 0.0122)	0 (0 - 0)	1401	< 0.001	< 0.001
Anaerotruncus_colihominis	0 (0 - 0.0266)	0 (0 - 0)	1457	< 0.001	0.00029
Lachnospiraceae_bacterium_1_4_56FAA	0.000465 (0 - 0.0453)	0 (0 - 0)	1433	< 0.001	0.00029
Flavonifractor_plautii	0.000835 (0 - 0.0266)	0 (0 - 0)	1480.5	< 0.001	0.000871
Clostridium_clostridioforme	0 (0 - 0.0209)	0 (0 - 0)	1612	0.0001	0.000871
Clostridium_hathewayi	0.00177 (0 - 0.0316)	0 (0 - 0)	1468	0.000106	0.000871
Clostridium_symbiosum	0.00164 (0 - 0.0882)	0 (0 - 0)	1515	0.000201	0.00147
Ruminococcus_torques	0.557 (0.266 - 1.33)	0.249 (0.107 - 0.568)	1428	0.000245	0.00161
Alistipes_senegalensis	0 (0 - 0.016)	0.0155 (0 - 0.0885)	3027	0.000365	0.00218
Prevotella_copri	0 (0 - 0)	0 (0 - 0.596)	2835	0.000607	0.00309
Eggerthella_lenta	0 (0 - 0.00447)	0 (0 - 0)	1645.5	0.000612	0.00309
Lachnospiraceae_bacterium_5_1_57FAA	0 (0 - 0)	0 (0 - 0)	1885	0.00116	0.00546
Lachnospiraceae_bacterium_3_1_46FAA	0.0729 (0.0207 - 0.2)	0.0212 (0.00171 - 0.0787)	1534.5	0.00135	0.0059
Clostridium_asparagiforme	0 (0 - 0.0113)	0 (0 - 0)	1651	0.00177	0.00705
Barnesiella_intestinihominis	0.558 (0 - 1.75)	1.41 (0.587 - 2.35)	2968.5	0.00182	0.00705
Clostridium_citroniae	0.00289 (0 - 0.0237)	0 (0 - 0.00399)	1630	0.00194	0.00709
Eubacterium_eligens	0.669 (0.0405 - 1.27)	1.18 (0.395 - 2.12)	2947	0.00258	0.00874
Lachnospiraceae_bacterium_7_1_58FAA	0.0273 (0.0102 - 0.0683)	0.0121 (0.00511 - 0.0273)	1579.5	0.00266	0.00874
Coprococcus_sp_ART55_1	0 (0 - 0)	0 (0 - 4.25)	2817.5	0.00376	0.0118
Lachnospiraceae_bacterium_3_1_57FAA_CT1	0.000675 (0 - 0.0517)	0 (0 - 0.000522)	1675	0.004	0.0119
Clostridium_ramosum	0 (0 - 0)	0 (0 - 0)	1927.5	0.00532	0.0152
Coprococcus_catus	0.238 (0.0985 - 0.426)	0.338 (0.239 - 0.512)	2877	0.0068	0.0186
Eubacterium_biforme	0 (0 - 0.37)	0.222 (0 - 0.86)	2815	0.00721	0.0189
Ruminococcus_lactaris	0 (0 - 0.488)	0.41 (0 - 0.99)	2814.5	0.00986	0.0249
Bacteroides_massiliensis	0 (0 - 0)	0 (0 - 1.19)	2729	0.0108	0.0253
Lachnospiraceae_bacterium_2_1_58FAA	0.00245 (0 - 0.0446)	0 (0 - 0.0101)	1735	0.0111	0.0253
Haemophilus_parainfluenzae	0 (0 - 0.0112)	0.00638 (0 - 0.0493)	2788.5	0.0115	0.0253
Clostridium_nexile	0 (0 - 0.00897)	0 (0 - 0)	1846.5	0.0119	0.0253
Clostridium_innocuum	0 (0 - 0.00333)	0 (0 - 0)	1869.5	0.012	0.0253

Bacteroides_xylanisolvens	0.00587 (0 - 0.103)	0.0561 (0.00379 - 0.163)	2807	0.0144	0.0296
Oxalobacter_formigenes	0 (0 - 0)	0 (0 - 0)	2575	0.0167	0.0332
Alistipes_putredinis	1.29 (0 - 3.26)	3.05 (0.483 - 4.23)	2796.5	0.0177	0.0342
Paraprevotella_clara	0 (0 - 0.014)	0 (0 - 0.179)	2714	0.0192	0.036
Odoribacter_splanchnicus	0.357 (0 - 0.687)	0.573 (0.0488 - 0.883)	2772	0.0217	0.0395
Eubacterium_sp_3_1_31	0 (0 - 0)	0 (0 - 0)	1951	0.0266	0.0472
Streptococcus_sanguinis	0 (0 - 0)	0 (0 - 0)	1960.5	0.0388	0.0672
Coprobacter_fastidiosus	0 (0 - 0.0321)	0.0187 (0 - 0.0646)	2695	0.0413	0.0695
Streptococcus_anginosus	0 (0 - 0)	0 (0 - 0)	1959	0.0452	0.0731
Erysipelotrichaceae_bacterium_2_2_44A	0 (0 - 0.00105)	0 (0 - 0)	1940.5	0.0456	0.0731
Blautia_hydrogenotrophica	0 (0 - 0)	0 (0 - 0)	1984	0.0522	0.0816
Dorea_formicigenerans	0.478 (0.235 - 0.619)	0.322 (0.196 - 0.494)	1826	0.0553	0.0845
Roseburia_hominis	0.172 (0.0312 - 0.446)	0.313 (0.0873 - 0.842)	2680	0.0661	0.0987
Streptococcus_parasanguinis	0.0395 (0.00359 - 0.167)	0.021 (0 - 0.0848)	1857	0.0728	0.102
Roseburia_inulinivorans	0.646 (0.127 - 1.88)	0.386 (0.0729 - 0.811)	1854	0.0729	0.102
Clostridiaceae_bacterium_JC118	0 (0 - 0.00671)	0 (0 - 0)	1952	0.0733	0.102
Pseudoflavonifractor_capillosus	0 (0 - 0.00126)	0 (0 - 0)	1972.5	0.0797	0.109
Bacteroides_plebeius	0 (0 - 0)	0 (0 - 0)	2523	0.0845	0.112
Methanobrevibacter_smithii	0 (0 - 0.31)	0 (0 - 0.51)	2608	0.0854	0.112
Streptococcus_mitis_oralis_pneumoniae	0 (0 - 0)	0 (0 - 0)	2057.5	0.0887	0.114
Bacteroides_eggerthii	0 (0 - 0)	0 (0 - 0.415)	2562.5	0.101	0.128
Bacteroides_clarus	0 (0 - 0)	0 (0 - 0.00842)	2523	0.105	0.13
Lachnospiraceae_bacterium_8_1_57FAA	0 (0 - 0.0333)	0 (0 - 0.0626)	2573	0.112	0.136
Lachnospiraceae_bacterium_1_1_57FAA	0 (0 - 0.141)	0 (0 - 0.0226)	1943	0.115	0.137
Gordonibacter_pamelaeae	0 (0 - 0.0207)	0 (0 - 0.0036)	1965.5	0.127	0.149
Bifidobacterium_longum	0.689 (0.12 - 1.74)	0.399 (0.185 - 0.983)	1919	0.131	0.152
Bacteroides_uniformis	4.36 (1.9 - 8.98)	2.79 (0.91 - 6.16)	1922	0.135	0.153
Lactococcus_lactis	0 (0 - 0)	0 (0 - 0)	2039.5	0.142	0.156
Alistipes_shahii	0.305 (0 - 0.798)	0.527 (0.0792 - 1.05)	2591.5	0.145	0.156
Alistipes_sp_AP11	0 (0 - 0)	0 (0 - 0)	2066.5	0.145	0.156
Clostridium_leptum	0.022 (0 - 0.0836)	0.00645 (0 - 0.0575)	1938	0.148	0.156
Rothia_mucilaginosa	0 (0 - 0.000285)	0 (0 - 0)	2041	0.176	0.183
Faecalibacterium_prausnitzii	7.3 (2.85 - 11.7)	8.63 (4.98 - 11.8)	2564	0.185	0.186

Bacteroidales_bacterium_ph8	0.237 (0 - 0.861)	0.426 (0.12 - 0.731)	2560	0.187	0.186
Streptococcus_vestibularis	0 (0 - 0)	0 (0 - 0)	2085.5	0.189	0.186
Ruminococcus_obeum	0.541 (0.314 - 0.897)	0.671 (0.398 - 1.01)	2560	0.191	0.186
Streptococcus_salivarius	0.108 (0.0388 - 0.495)	0.0772 (0.0214 - 0.334)	1966.5	0.194	0.186
Alistipes_finegoldii	0.0235 (0 - 0.15)	0.0635 (0.00754 - 0.216)	2552.5	0.195	0.186
Escherichia_coli	0.084 (0 - 0.662)	0.0307 (0 - 0.192)	1977.5	0.204	0.191
Eubacterium_siraeum	0.0725 (0.00105 - 0.881)	0.229 (0.00867 - 1.43)	2538	0.222	0.206
Bifidobacterium_animalis	0 (0 - 0)	0 (0 - 0)	2076	0.227	0.207
Clostridium_sp_L2_50	0 (0 - 0)	0 (0 - 0)	2406	0.231	0.208
Bacteroides_finegoldii	0 (0 - 0)	0 (0 - 0)	2448	0.234	0.208
Coprococcus_comes	0.442 (0.25 - 0.914)	0.644 (0.348 - 0.939)	2523.5	0.251	0.219
Bacteroides_stercoris	0 (0 - 0.15)	0 (0 - 0.417)	2488	0.254	0.219
Erysipelotrichaceae_bacterium_21_3	0 (0 - 0)	0 (0 - 0)	2107	0.259	0.221
Paraprevotella_xylaniphila	0 (0 - 0)	0 (0 - 0.00141)	2448	0.272	0.229
Clostridium_bartlettii	0.0333 (0.00441 - 0.122)	0.057 (0.00256 - 0.259)	2499	0.295	0.245
Collinsella_aerofaciens	0.504 (0.0122 - 1.14)	0.34 (0.184 - 0.687)	2026	0.298	0.245
Bacteroides_fragilis	0 (0 - 0.305)	0 (0 - 0.0349)	2063	0.312	0.248
Ruminococcus_callidus	0 (0 - 0.0831)	0.0007 (0 - 0.227)	2472	0.312	0.248
Parasutterella_excrementihominis	0 (0 - 0.0163)	0 (0 - 0.0429)	2468	0.313	0.248
Ruminococcus_sp_5_1_39BFAA	0 (0 - 2.4)	0 (0 - 1.14)	2066	0.333	0.26
Bacteroides_dorei	0.45 (0 - 3)	0.179 (0 - 1.48)	2048	0.342	0.264
Sutterella_wadsworthensis	0 (0 - 0.31)	0.058 (0 - 0.395)	2463	0.35	0.267
Streptococcus_infantis	0 (0 - 0)	0 (0 - 0)	2143.5	0.353	0.267
Bacteroides_faecis	0 (0 - 0.0018)	0 (0 - 0.0715)	2428	0.377	0.281
Phascolarctobacterium_succinatutens	0 (0 - 0)	0 (0 - 0)	2133	0.387	0.281
Desulfovibrio_piger	0 (0 - 0)	0 (0 - 0.013)	2407	0.387	0.281
Bifidobacterium_pseudocatenulatum	0 (0 - 0)	0 (0 - 0)	2394	0.392	0.281
Alistipes_indistinctus	0 (0 - 0.0732)	0.0191 (0 - 0.0722)	2445	0.397	0.281
Streptococcus_gordonii	0 (0 - 0)	0 (0 - 0)	2157	0.398	0.281
Eubacterium_ramulus	0.154 (0.0184 - 0.379)	0.115 (0.0223 - 0.263)	2072	0.403	0.282
Lachnospiraceae_bacterium_5_1_63FAA	0.0563 (0.0179 - 0.15)	0.0427 (0.0167 - 0.0952)	2079.5	0.423	0.293
Desulfovibrio_desulfuricans	0 (0 - 0)	0 (0 - 0)	2150.5	0.428	0.293
Streptococcus_australis	0 (0 - 0)	0 (0 - 0.00326)	2386	0.46	0.31

Parahactoroidos distaconis	0.158 (0 - 0.609)	0.099 (0 - 0.394)	2099	0.469	0.31
Parabacteroides_distasonis	•	•			
Eubacterium_rectale	5.13 (2.08 - 11.2)	5.71 (1.3 - 14.5)	2427	0.469	0.31
Ruminococcus_bromii	2.83 (0 - 6.62)	1.05 (0 - 4.27)	2101	0.472	0.31
Streptococcus_thermophilus	0.0132 (0 - 0.237)	0.00267 (0 - 0.164)	2108	0.481	0.313
Turicibacter_sanguinis	0 (0 - 0)	0 (0 - 0)	2348	0.501	0.323
Catenibacterium_mitsuokai	0 (0 - 0)	0 (0 - 0)	2362	0.51	0.324
Veillonella_dispar	0 (0 - 0)	0 (0 - 0)	2166	0.512	0.324
Bacteroides_caccae	0.609 (0 - 1.84)	0.764 (0.0777 - 1.32)	2398.5	0.543	0.34
Bacteroides_ovatus	0.536 (0.0777 - 1.77)	0.409 (0.102 - 1.4)	2130	0.563	0.349
Bacteroides_coprocola	0 (0 - 0)	0 (0 - 0)	2338	0.59	0.359
Ruminococcaceae_bacterium_D16	0 (0 - 0)	0 (0 - 0)	2345.5	0.595	0.359
Dialister_invisus	0.448 (0 - 4.74)	0 (0 - 5.34)	2147	0.596	0.359
Bifidobacterium_catenulatum	0 (0 - 0)	0 (0 - 0)	2336	0.607	0.363
Eubacterium_ventriosum	0.141 (0 - 0.392)	0.0795 (0.0131 - 0.265)	2155	0.635	0.376
Bacteroides_vulgatus	2.07 (0.287 - 4.6)	2.12 (0.828 - 3.16)	2168	0.68	0.399
Erysipelotrichaceae_bacterium_6_1_45	0 (0 - 0.00156)	0 (0 - 0.000795)	2189.5	0.689	0.4
Adlercreutzia_equolifaciens	0.0424 (0 - 0.113)	0.0267 (0.0016 - 0.0942)	2178	0.711	0.41
Bacteroides_salyersiae	0 (0 - 0)	0 (0 - 0)	2316.5	0.737	0.42
Bilophila_wadsworthia	0.0124 (0 - 0.0455)	0.0125 (0 - 0.0354)	2189	0.746	0.42
Bifidobacterium_adolescentis	0.354 (0 - 1.91)	0.455 (0 - 1.23)	2190	0.748	0.42
Coprococcus_eutactus	0 (0 - 0)	0 (0 - 0)	2300	0.779	0.429
Eubacterium_hallii	1.2 (0.507 - 1.91)	1.19 (0.624 - 1.92)	2325	0.783	0.429
Burkholderiales_bacterium_1_1_47	0 (0 - 0.0184)	0 (0 - 0.00985)	2316.5	0.783	0.429
Bacteroides_intestinalis	0 (0 - 0)	0 (0 - 0)	2298.5	0.812	0.439
Parabacteroides_goldsteinii	0 (0 - 0)	0 (0 - 0)	2296	0.815	0.439
Parabacteroides_merdae	0.437 (0 - 1.24)	0.43 (0 - 0.9)	2215	0.834	0.441
Holdemania_filiformis	0.005 (0 - 0.0346)	0.0059 (0 - 0.0231)	2307	0.838	0.441
Bacteroides_nordii	0 (0 - 0)	0 (0 - 0)	2235	0.839	0.441
Dorea_longicatena	0.812 (0.256 - 1.53)	0.881 (0.358 - 1.39)	2298	0.876	0.448
Bacteroides_thetaiotaomicron	0.159 (0 - 0.624)	0.159 (0 - 0.377)	2227	0.877	0.448
Parabacteroides_johnsonii	0 (0 - 0)	0 (0 - 0)	2286	0.882	0.448
Anaerostipes_hadrus	0.0305 (0.0104 - 0.0955)	` '	2296	0.883	0.448
Bifidobacterium_bifidum	0 (0 - 0.191)	0 (0 - 0.0933)	2236	0.887	0.448
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Roseburia_intestinalis	0.39 (0.0263 - 2.06)	0.425 (0.0663 - 2.06)	2286.5	0.916	0.459
Bacteroides_cellulosilyticus	0 (0 - 0.728)	0 (0 - 0.667)	2244.5	0.935	0.464
Akkermansia_muciniphila	0.0551 (0 - 1.51)	0.0478 (0 - 1.66)	2279	0.94	0.464
Veillonella_parvula	0 (0 - 0.023)	0 (0 - 0.0184)	2269	0.975	0.478
Veillonella_atypica	0 (0 - 0)	0 (0 - 0)	2259.5	0.99	0.48
Alistipes_onderdonkii	0.348 (0 - 1.2)	0.313 (0.0781 - 0.761)	2259.5	0.993	0.48

Shotgun compositional analysis performed on 139 samples (IBS: n= 78 and Control: n=58)

Median abundance % represented as inter-quartile range (IQR)