

Supplemental Tables and Figures

Table S2. The relative abundance of bacteria in TB and HC groups at phylum levels

phylum name	TB-mean(%)	HC-mean(%)	P_value
<i>p__Firmicutes</i>	58.11	66.24	0.155
<i>p__Proteobacteria</i>	9.398	19.11	0.1044
<i>p__Bacteroidota</i>	24.02	2.263	1.46E-06
<i>p__Actinobacteriota</i>	5.963	12	0.004326
<i>p__Fusobacteriota</i>	1.277	0.009737	0.06611
<i>p__Synergistota</i>	0.5824	0.002554	0.7768
<i>p__Verrucomicrobiota</i>	0.3275	0.1074	1
<i>p__Desulfobacterota</i>	0.2287	0.05699	0.1272
<i>p__Patescibacteria</i>	0.02128	0.136	3.84E-07

Comparisons of the relative abundances of intestinal bacteria between the TB and HC groups were conducted at the phylum levels (Wilcoxon Rank Sum test), TB: tuberculosis; HC: healthy control.

Table S3. The relative abundance of bacteria in genus level

genus name	TB-mean(%)	HC-mean(%)	P_value
<i>g__Bacteroides</i>	13.63	1.795	1.68E-05
<i>g__Prevotella</i>	8.035	0.01277	0.002179
<i>g__Escherichia-Shigella</i>	7.285	13.53	0.0895
<i>g__Faecalibacterium</i>	6.927	6.027	0.9487
<i>g__Blautia</i>	6.601	13.36	0.0001037
<i>g__Megamonas</i>	5.411	0.04837	0.9206
<i>g__Bifidobacterium</i>	4.742	7.959	0.01173
<i>g__Veillonella</i>	4.289	0.1772	0.1655
<i>g__Subdoligranulum</i>	3.796	6.597	0.01489
<i>g__Phascolarctobacterium</i>	2.437	0.0573	0.09631
<i>g__Roseburia</i>	2.333	0.8862	0.617
<i>g__Lactobacillus</i>	1.913	0.8072	0.432
<i>g__Clostridium_innocuum_group</i>	1.689	0.05794	4.00E-05
<i>g__Dialister</i>	1.543	0.1227	0.5056
<i>g__Enterococcus</i>	1.461	0.2123	0.6806
<i>g__Lachnoclostridium</i>	1.442	0.1518	0.00818
<i>g__unclassified_f__Lachnospiraceae</i>	1.302	0.728	0.4517
<i>g__Fusobacterium</i>	1.277	0.009418	0.0658
<i>g__Agathobacter</i>	1.144	2.397	0.002732
<i>g__Erysipelatoclostridium</i>	1.116	0.0083	0.0001058
<i>g__Klebsiella</i>	0.9926	3.815	0.001527
<i>g__Eubacterium_hallii_group</i>	0.9166	4.313	1.46E-05
<i>g__Ruminococcus_gnavus_group</i>	0.8855	1.047	0.7867
<i>g__Ruminococcus_torques_group</i>	0.8817	1.598	0.001862

<i>g__Anaerostipes</i>	0.8808	1.555	0.0006838
<i>g__Collinsella</i>	0.8325	2.999	0.001058
<i>g__Alistipes</i>	0.6959	0.2602	0.3482
<i>g__Streptococcus</i>	0.6755	1.247	0.006078
<i>g__Butyricicoccus</i>	0.6575	0.5232	0.1055
<i>g__Ruminococcus</i>	0.6328	2.692	0.00306
<i>g__Megasphaera</i>	0.5929	0.9507	0.9148
<i>g__Dorea</i>	0.5844	3.987	9.54E-06
<i>g__Lachnospiraceae_NK4A136_group</i>	0.5838	0.3236	0.3179
<i>g__Pyramidobacter</i>	0.5809	0.0006385	0.8546
<i>g__Fusicatenibacter</i>	0.5606	3.142	4.61E-05
<i>g__Parabacteroides</i>	0.5377	0.08252	0.0007242
<i>g__norank_f__Eubacterium_coprostanoligenes_group</i>	0.5005	0.4956	0.1674
<i>g__Parasutterella</i>	0.4935	0.08492	0.008549
<i>g__Haemophilus</i>	0.482	0.04326	0.8057
<i>g__Romboutsia</i>	0.4805	3.435	5.00E-05
<i>g__Coprococcus</i>	0.3861	0.7058	0.009789
<i>g__Akkermansia</i>	0.3269	0.1074	0.791
<i>g__Paraprevotella</i>	0.302	0.01277	0.6974
<i>g__Catenibacterium</i>	0.2922	0	0.1765
<i>g__Prevotellaceae_UCG-003</i>	0.2484	0	0.2785
<i>g__Intestinibacter</i>	0.248	0.8592	0.03976
<i>g__UCG-002</i>	0.2317	0.1137	0.992
<i>g__Staphylococcus</i>	0.2316	0	0.07331
<i>g__Barnesiella</i>	0.2313	0.05507	0.6596
<i>g__Eubacterium_ventriosum_group</i>	0.2225	0.1253	0.961
<i>g__norank_f__Ruminococcaceae</i>	0.2211	0.06481	0.774
<i>g__Eubacterium_eligens_group</i>	0.2188	0.019	0.4837
<i>g__Erysipelotrichaceae_UCG-003</i>	0.2008	1.421	2.47E-06
<i>g__Flavonifractor</i>	0.199	0.01101	0.0004114
<i>g__Clostridium_sensu_stricto_1</i>	0.1949	2.154	0.000218
<i>g__Bilophila</i>	0.1794	0.007502	0.01339
<i>g__Eubacterium_siraeum_group</i>	0.1565	0.01038	0.2639
<i>g__Clostridioides</i>	0.1499	0	0.04719
<i>g__Adlercreutzia</i>	0.1469	0.5995	0.01332
<i>g__NK4A214_group</i>	0.1396	0.1318	0.1499
<i>g__Christensenellaceae_R-7_group</i>	0.135	0.01341	0.0875
<i>g__Holdemanella</i>	0.1348	0	0.04721
<i>g__Monoglobus</i>	0.1293	0.6722	0.003405
<i>g__Terrisporobacter</i>	0.119	0.1705	0.07577
<i>g__UCG-005</i>	0.1163	0.006545	0.2069
<i>g__Ruminococcus_gauvreauii_group</i>	0.1141	0.4013	0.0001447
<i>g__CAG-56</i>	0.1108	0.3692	0.02554
<i>g__Sellimonas</i>	0.108	0.005587	0.05243

<i>g__Oscillibacter</i>	0.1021	0.004469	0.02156
<i>g__Turicibacter</i>	0.09761	0.3269	0.01344
<i>g__unclassified_f__Enterobacteriaceae</i>	0.07778	1.001	0.01201
<i>g__norank_f__Coriobacteriales_Incertae_Sedis</i>	0.03009	0.1338	0.181
<i>g__Eisenbergiella</i>	0.02128	0.1612	0.9413
<i>g__CAG-352</i>	0.01877	0.363	0.3026
<i>g__Enterobacter</i>	0.003773	0.6233	1.57E-05
<i>g__Weissella</i>	0.002225	0.1528	8.81E-08
<i>g__Pediococcus</i>	0	0.103	0.07089

Comparisons of the relative abundances of intestinal bacteria between the TB and HC groups were conducted at genus levels (Wilcoxon Rank Sum test), TB: tuberculosis; HC: healthy control.

Table S4. The relative abundance of fungi at the phylum level

phylum name	TB-mean(%)	HC-mean(%)	P_value
<i>p__Ascomycota</i>	84.89	68.46	0.000781
<i>p__unclassified_k__Fungi</i>	11.18	17.88	0.008158
<i>p__Basidiomycota</i>	3.71	12.33	0.000206
<i>p__Mucoromycota</i>	0.2235	1.187	0.0103
<i>p__Chytridiomycota</i>	0.0001815	0.1358	0.01564

Comparisons of the relative abundances of intestinal fungus between the TB and HC groups were conducted at the phylum levels (Wilcoxon Rank Sum test), TB: tuberculosis; HC: healthy control.

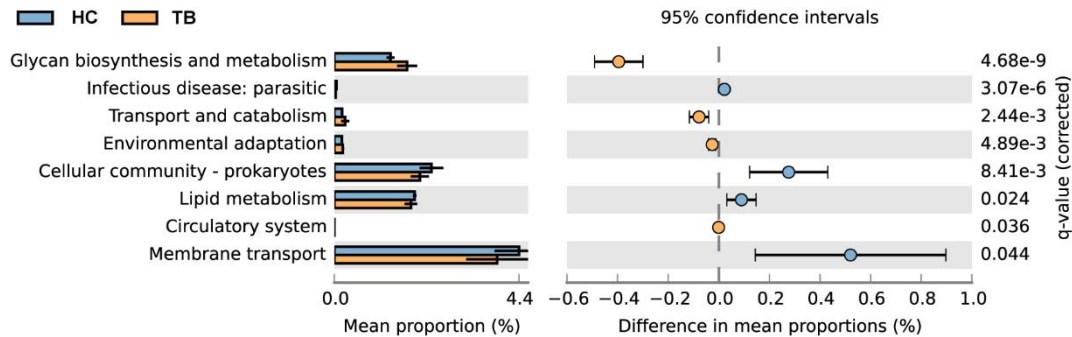
Table S5. The relative abundance of fungi at the genus level

genus name	TB-mean(%)	HC-mean(%)	P_value
<i>g__Saccharomyces</i>	53.67	14.28	0.002249
<i>g__Candida</i>	21.61	22.26	0.432
<i>g__unclassified_k__Fungi</i>	11.18	17.88	0.008158
<i>g__Pichia</i>	3.249	0.7105	0.4941
<i>g__Aspergillus</i>	1.884	7.49	0.01224
<i>g__Cutaneotrichosporon</i>	1.64	4.64	0.01951
<i>g__unclassified_p__Ascomycota</i>	1.316	9.142	0.004802
<i>g__Apiotrichum</i>	0.9514	5.095	0.002257
<i>g__Talaromyces</i>	0.5429	0.02751	0.5779
<i>g__Fusicolla</i>	0.482	0.001495	0.768
<i>g__Rhodotorula</i>	0.2562	0.2612	0.008303
<i>g__Starmerella</i>	0.2446	0.0001495	0.768
<i>g__unclassified_f__Trichosporonaceae</i>	0.2339	0.0001495	0.5534
<i>g__Penicillium</i>	0.2057	1.604	0.000562

<i>g__Eremothecium</i>	0.1755	0	0.4633
<i>g__Trichosporon</i>	0.1648	0.08178	0.05354
<i>g__Cladosporium</i>	0.1594	0.5631	0.008389
<i>g__Trichoderma</i>	0.1509	2.055	0.1176
<i>g__unclassified_o__Saccharomycetales</i>	0.1465	0.205	0.4502
<i>g__Alternaria</i>	0.1285	1.783	0.03333
<i>g__Vanrija</i>	0.1159	0.02033	0.3791
<i>g__Diutina</i>	0.1005	0.01435	0.8923
<i>g__Malassezia</i>	0.04557	0.4294	0.001765
<i>g__Dipodascus</i>	0.04303	4.058	0.254
<i>g__unclassified_o__Malasseziales</i>	0.0413	0.1567	0.7184
<i>g__Mucor</i>	0.0335	0.1247	0.04872
<i>g__Rhizopus</i>	0.02805	0.6758	0.009821
<i>g__Coprinellus</i>	0.02079	0.2779	0.03947
<i>g__unclassified_f__Didymellaceae</i>	0.01707	0.3195	0.001223
<i>g__Xeromyces</i>	0.01371	0.3736	0.006748
<i>g__Wallemia</i>	0.01307	0.1529	0.352
<i>g__unclassified_o__Chaetothyriales</i>	0.01262	0.3259	0.4167
<i>g__unclassified_f__Dipodascaceae</i>	0.009985	0.5444	0.1001
<i>g__unclassified_f__Aureobasidiaceae</i>	0.00826	0.05083	0.6186
<i>g__unclassified_f__Aspergillaceae</i>	0.007444	0.302	0.03478
<i>g__Exophiala</i>	0.005174	0.1867	0.1122
<i>g__Auricularia</i>	0.002632	0.1944	0.274
<i>g__unclassified_p__Chytridiomycota</i>	0.0001815	0.1355	0.04374
<i>g__Periconia</i>	0	0.3487	0.2159
<i>g__Gilbertella</i>	0	0.3084	0.2159
<i>g__Curvularia</i>	0	0.2157	0.2159
<i>g__Flammulina</i>	0	0.1843	0.2159
<i>g__Filobasidium</i>	0	0.1745	0.008496
<i>g__Xerochrysium</i>	0	0.1601	0.000939
<i>g__Lodderomyces</i>	0	0.1334	0.008496

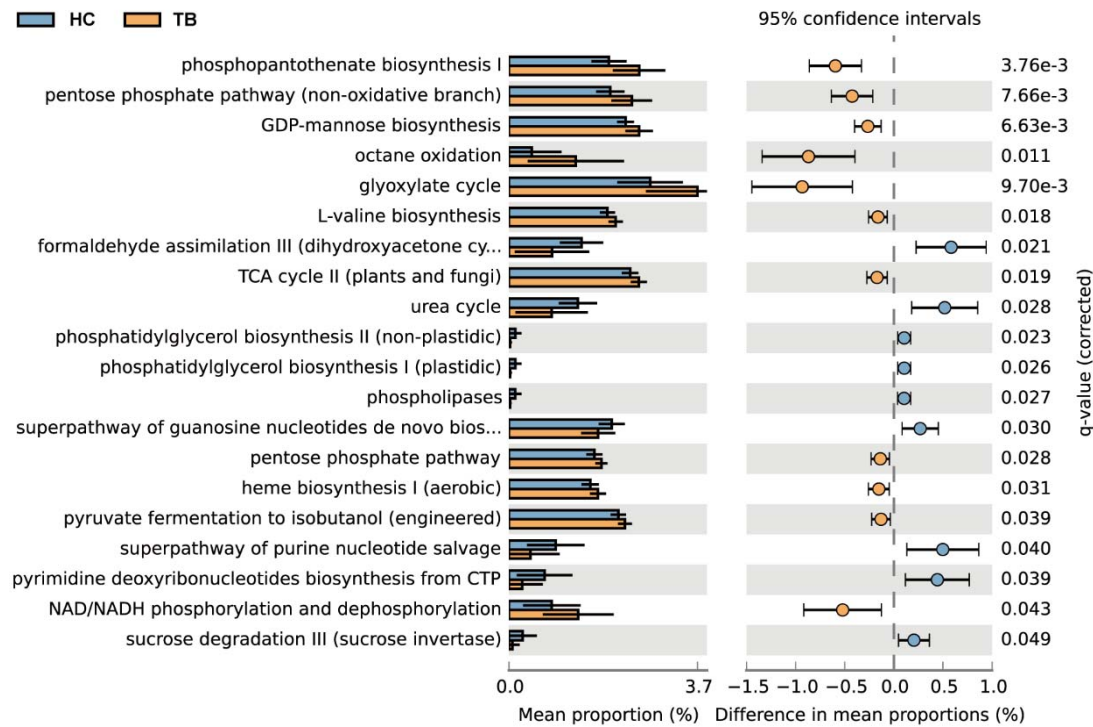
Comparisons of the relative abundances of intestinal fungus between the TB and HC groups were conducted at the genus levels (Wilcoxon Rank Sum test), TB: tuberculosis; HC: healthy control.

Figure S1. The different bacterial functions were evaluated between the two groups (Welch's t-test, $p < 0.05$).



The potential enriched pathways of the microbiota were predicted using PICRUST2 based on the 16S rRNA gene. The different bacterial functions were evaluated between the two groups with Welch's t-test. TB: tuberculosis; HC: healthy control.

Figure S2. The different fungal functions were evaluated between the two groups (Welch's t-test, $p < 0.05$).



The potential enriched pathways of the mycobiota were predicted using PICRUST2 based on the ITS2 gene. The different bacterial functions were evaluated between the two groups with Welch's t-test. TB: tuberculosis; HC: healthy control.