

Supplementary Methods

Detailed Microbial and Bioinformatics Methods

Microbial DNA were isolated from stool samples as previously described[1]. **16S rRNA Bacterial community analysis:** The V1 and V2 hyper-variable regions of the bacterial 16S ribosomal RNA (rRNA) gene were sequenced on a PGM Ion Torrent Next-generation sequencer using Multitag fusion primers targeting the V1–V2 region (27F: 5'-AGAGTTTGATCCTGGCTCAG-3', 355R: 5'-GCTGCCTCCCGTAGGAGT-3'). Amplicons for 96 samples were then sequenced together to generate >20,000 x 400 base reads per sample. Quality Control: A negative control (water) and a known positive control were used in each batch of microbial DNA sequencing to assess laboratory variability and contamination[2].

Fungal community analysis: Similarly, the ITS1 regions of the fungal 18S ribosomal RNA (rRNA) gene were sequenced on a PGM Ion Torrent Next-generation sequencer using Multitag fusion primers (ITS1F: 5'-CTTGGTCATTTAGAGGAAGTAA-3' ; ITS2: 5'-GCTGCGTTCTTCATCGATGC-3'). Amplicons for 96 samples were sequenced together to generate >10,000 x 400 base reads per sample. The mycobiome is generally less diverse than the microbiome and thus required fewer reads to interrogate this community[3].

We used >1000 reads for bacteria and >100 reads for fungi given the relatively lower abundance of fungal taxa as the lowest number chosen to be acceptable. Fungal primers produced strong PCR product for about 73% of the samples while the rest either did not produce any product or the products were very weak. All the samples were repeated with bacterial primers and essentially all samples produced strong PCR products which indicated that the DNA was good quality and was not degraded. Due to the dramatic difference in product intensity it was harder to normalize the barcoded products for pooling which resulted in a wide range for read numbers for the fungal samples. We used a cutoff of 100 reads per sample as that was clearly above the negative control and is the break point in supplementary figure 1.

This was a conservative approach as we did not want to subjectively bias the results. It should be noted that if noise was introduced into the analysis by the samples with low reads, it would have made the LEFSE analysis less sensitive and would have exclude more taxa in from the results. Also the results that were found are biologically plausible and change with the underlying cirrhosis and antibiotic use severity. This low-read phenomenon is the result of two issues, first that the mycobiome is rarer than bacteria and, second, that the genome size of fungi is an order of magnitude larger than bacterial genomes.

Overall Bio-informatics analysis:

We used the Microbiome Analysis Center's Portal to organize raw data, track clinical metadata, and track analysis between the groups at baseline and/if they develop infections and are re-sampled. The portal consists of a Drupal based interface wrapped around a MYSQL database that uses PHP to manage the relational database

(http://mbac.gmu.edu/mbac/display_detail.php?tb=research&id=4). The system has built in safeguards to curate the data, keep is secure, and to assure quality control. Raw 16S rRNA and fungal ITS1 gene sequence data were utilized for bioinformatics analysis after chimeric sequences were removed using UChime[4]. The remaining clean 16S sequences were clustered into operational taxonomic units (OTUs) using the USEARCH algorithm[5]. A sequence identity of 97% were used to generate OTUs representing bacterial species. The taxonomic identity of reference sequences were determined using the RDP11 Classifier[6] and QIIME Pipeline. **Bio-statistical Analysis:** Bacterial and fungal community composition were characterized using OTU counts generated as described above. OTU counts were converted to measures of relative abundance to account for variation in sequencing coverage between samples and compared to between groups in the cross-sectional and prospective studies as well as within groups in the prospective study. Statistical analysis was carried out using the statistical software package R (www.r-project.org). Alpha (α) diversity (richness and evenness of taxa within a population) were

reported using the Shannon Index[7]. Changes in abundance of individual bacterial and fungal taxa were also analyzed using traditional univariate statistical methods. We used LEfSe to determine the features most likely to explain differences between the subject groups[8]

Supplementary Table1: Comparison between the three inpatient groups

	No infection (n=19)	Culture negative infection (n=22)	Culture positive infection (n=25)
Age (years)	54.9±9.6	55.3±8.9	56.4±8.9
Gender (men/women)	11/8	14/8	20/5
Etiology (HCV, alcohol, HCV+alcohol, NAFLD, others)	3/4/2/6/4	6/5/7/2/0	7/7/5/3/2/1
MELD score	20.5±6.6	17.8±5.9	20.8±6.4
Prior Hepatic encephalopathy	9	13	18*
Lactulose only /Any Rifaximin	5/4	5/8	6/12
SBP prophylaxis	1	0	3
Proton Pump Inhibitors	8	15	15
Non-selective beta-blockers	4	6	6
Diabetes	6	6	6

Supplementary table 2: Comparison between outpatients on and not on SBP prophylaxis

Outpatients	Not on SBP prophylaxis (n=65)	On SBP Prophylaxis (n=12)
Age (years)	58.3±5.3	55.7±7.7
Gender (men/women)	48/17	10/2
Etiology (HCV, alcohol, HCV+alcohol, NAFLD, others)	30/8/10/14/8	3/3/1/4/1
MELD score	12.4±6.4	17.6±6.6*
Prior Hepatic encephalopathy	14	7*
Lactulose/Lactulose+Rifaximin	1/13	1/6*
Proton Pump Inhibitors	33	5
Non-selective beta-blockers	23	4
Diabetes	29	4

Supplementary table 3: Comparison between outpatients on and not on rifaximin

Outpatients	Not on rifaximin (n=63)	Rifaximin use (n=14)
Age (years)	58.6±4.3	55.1±9.2
Gender (men/women)	45/17	12/2
Etiology (HCV, alcohol, HCV+alcohol, NAFLD, others)	27/10/11/16/13	6/2/1/2/3
MELD score	11.9±6.3	18.8±5.2*
Prior Hepatic encephalopathy	8	14
Lactulose use	8	8
SBP prophylaxis	6	6*
Proton Pump Inhibitors	24	6
Non-selective beta-blockers	21	6
Diabetes	29	4

Supplementary table 4: LEFSe Comparison between inpatients

<i>Phylum_Order_Family_Genus</i>	Group with higher LDA	P value
Admitted without infection vs. Admitted with Culture negative infection		
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae</i>	Uninfected	0.03
<i>Basidiomycota_Ustilaginomycetes_Ustilaginales_Ustilaginales_Incertaesedis</i>	Uninfected	0.04
<i>Ascomycota_Eurotiomycetes_Onygenales_Arthrodermataceae</i>	Culture negative	0.04
<i>Ascomycota_Pezizomycetes_Pezizales_Tuberaceae</i>	Culture negative	0.012
<i>Ascomycota_Dothideomycetes_Pleosporales_Venturiaceae</i>	Culture negative	0.04
<i>Ascomycota_Sordariomycetes_Hypocreales_Clavicipitaceae</i>	Culture negative	0.012
<i>Firmicutes_Bacilli_Lactobacillales_Leuconostocaceae</i>	Culture negative	0.012
Admitted without infection vs. Admitted with Culture positive infection		
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXI</i>	Uninfected	0.015
<i>Firmicutes_Clostridia_Clostridiales_Ruminococcaceae</i>	Uninfected	0.005
<i>Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae</i>	Uninfected	0.04
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Uninfected	0.005
Admitted with culture-negative infection vs. Admitted with Culture positive infection		
<i>Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae</i>	Culture negative	0.002
<i>Ascomycota_Sordariomycetes_Hypocreomycetidae_Incertaesedis_Plectosphaerellaceae</i>	Culture negative	0.02
<i>Ascomycota_Sordariomycetes_Hypocreales_Clavicipitaceae</i>	Culture negative	0.013
<i>Firmicutes_Clostridia_Clostridiales_Ruminococcaceae</i>	Culture negative	0.006
<i>Basidiomycota_Agaricomycetes_Polyporales_Sistotremataceae</i>	Culture negative	0.02
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Culture negative	0.005
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Culture negative	0.018

Supplementary table 5: LEFSe Comparison between cirrhotic outpatients

Phylum_Order_Family_Genus	Group with higher LDA	P value
Outpatient not on anything vs outpatient on lactulose only		
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrimonadaceae</i>	Not on anything	0.014
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Not on anything	0.03
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae</i>	Not on anything	0.029
<i>Ascomycota_Eurotiomycetes_Eurotiales_Trichocomaceae</i>	On lactulose	0.012
<i>Ascomycota_Sordariomycetes_Hypocreales_Hypocreaceae</i>	On lactulose	0.01
<i>Firmicutes_Bacilli_Bacillales_Bacillales_IncertaeSedisXI</i>	On lactulose	0.01
<i>Ascomycota_Eurotiomycetes_Pyrenulales_Massariaceae</i>	On lactulose	0.01
<i>Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae</i>	On lactulose	0.032
<i>Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae</i>	On lactulose	0.01
<i>Basidiomycota_Agaricomycetes_Agaricales_Hebelomataceae</i>	On lactulose	0.014
<i>Ascomycota_Lecanoromycetes_Lecanorales_Parmeliaceae</i>	On lactulose	0.0002
<i>Basidiomycota_Agaricomycetes_Agaricomycetidae_Incertaesedis_Agaricomycetidae_Incertaesedis_Incertaesedis</i>	On lactulose	0.0002
<i>Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae</i>	On lactulose	0.001
<i>Bacteroidetes_Flavobacteriia_Flavobacteriales_Flavobacteriaceae</i>	On lactulose	0.0103
Outpatient not on anything vs outpatient on rifaximin (no SBPP)		
<i>Ascomycota_Sordariomycetes_Microascales_Halosphaeriaceae</i>	On rifaximin	9.01E-05
<i>Basidiomycota_Agaricomycetes_Polyporales_Meruliaceae</i>	On rifaximin	0.010
<i>Zygomycota_Mucoromycotina_Incertaesedis_Mucorales_Phycomycetaceae</i>	On rifaximin	9.01E-05
<i>Basidiomycota_Agaricomycetes_Agaricomycetidae_Incertaesedis_Agaricomycetidae_Incertaesedis_Incertaesedis</i>	On rifaximin	9.01E-05
<i>Chytridiomycota_Chytridiomycetes_Rhizophydiales_Rhizophydiaceae</i>	On rifaximin	9.01E-05
Outpatient not on anything vs outpatient on SBP prophylaxis		
<i>Basidiomycota_Agaricostilbomycetes_Agaricostilbales_Agaricostilbaceae</i>	On SBPP	0.03
<i>Proteobacteria_Gammaproteobacteria_Aeromonadales_Succinivibrionaceae</i>	On SBPP	1.62E-06
<i>Proteobacteria_Epsilonproteobacteria_Campylobacteriales_Campylobacteraceae</i>	On SBPP	0.0008
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Marinilabiliaceae</i>	On SBPP	0.001
<i>Basidiomycota_Agaricomycetes_Sebacinales_SebacinalesGroupA</i>	On SBPP	1.62E-06
Outpatient not on anything vs outpatient on lactulose, rifaximin and SBP prophylaxis		
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrimonadaceae</i>	Not on anything	0.049
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Not on anything	0.027
<i>Proteobacteria_Betaproteobacteria_Burkholderiales_Sutterellaceae</i>	Not on anything	0.02
<i>Ascomycota_Eurotiomycetes_Onygenales_Arthrodermataceae</i>	On L, R, SBPP	0.099
<i>Ascomycota_Eurotiomycetes_Eurotiales_Trichocomaceae</i>	On L, R, SBPP	0.03
<i>Ascomycota_Saccharomycetes_Saccharomycetales_Saccharomycetaceae</i>	On L, R, SBPP	0.02
<i>Proteobacteria_Epsilonproteobacteria_Campylobacteriales_Campylobacteraceae</i>	On L, R, SBPP	0.04
<i>Firmicutes_Bacilli_Lactobacillales_Enterococcaceae</i>	On L, R, SBPP	4.59E-05
<i>Proteobacteria_Betaproteobacteria_Burkholderiales_Burkholderiales_i</i>	On L, R, SBPP	0.046

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<i>Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae</i>	On L, R, SBPP	0.002
<i>Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae</i>	On L, R, SBPP	0.04
<i>Actinobacteria_Actinobacteria_Actinomycetales_Promicromonosporaceae</i>	On L, R, SBPP	0.002
<i>Proteobacteria_Betaproteobacteria_Burkholderiales_Comamonadaceae</i>	On L, R, SBPP	0.001
<i>Actinobacteria_Actinobacteria_Actinomycetales_Corynebacteriaceae</i>	On L, R, SBPP	0.002
<i>Actinobacteria_Actinobacteria_Actinomycetales_Propionibacteriaceae</i>	On L, R, SBPP	0.002
<i>Proteobacteria_Betaproteobacteria_Hydrogenophilales_Hydrogenophilaceae</i>	On L, R, SBPP	0.002
<i>Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae</i>	On L, R, SBPP	0.03

Supplementary Table 6: LEFSe Comparison between healthy controls and outpatient cirrhosis

<i>Phylum_Order_Family_Genus</i>	Group with higher LDA	P value
Healthy controls vs. outpatients not on anything		
<i>Basidiomycota_Agaricomycetes_Agaricales_Marasmiaceae</i>	Controls	0.03
<i>Basidiomycota_Agaricomycetes_Thelephorales_Thelephoraceae</i>	Controls	0.009
<i>Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae</i>	Controls	0.04
<i>Ascomycota_Pezizomycetes_Pezizales_Tuberaceae</i>	Controls	0.02
<i>Ascomycota_Dothideomycetes_Pleosporales_Lophiostomataceae</i>	Controls	0.007
<i>Ascomycota_Dothideomycetes_Dothideomycetes_Incertaedis_Incertaedis_Gloniaceae</i>	Controls	1.29E-06
<i>Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae</i>	Controls	0.04
<i>Ascomycota_Dothideomycetes_Pleosporales_Montagnulaceae</i>	Controls	0.03
<i>Synergistetes_Synergistia_Synergistales_Synergistaceae</i>	Controls	0.002
<i>Basidiomycota_Agaricomycetes_Russulales_Russulaceae</i>	Controls	0.03
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Controls	0.009
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisXII</i>	Controls	0.002
<i>Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae</i>	Controls	0.002
<i>Basidiomycota_Agaricomycetes_Boletales_Sclerodermataceae</i>	Controls	1.23E-05
<i>Firmicutes_Clostridia_Clostridiales_Peptococcaceae1</i>	Controls	0.01
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisIV</i>	Controls	0.0002
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisXI</i>	Controls	0.01
<i>Basidiomycota_Agaricomycetes_Sebacinales_SebacinalesGroupA</i>	Controls	0.001
<i>Basidiomycota_Agaricomycetes_Agaricales_Hebelomataceae</i>	Controls	2.63E-05
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisXIII</i>	Controls	0.006
<i>Ascomycota_Pezizomycetes_Pezizales_Pyronemataceae</i>	Controls	0.01
<i>Actinobacteria_Actinobacteria_Actinomycetales_Propionibacteriaceae</i>	Controls	0.0004
<i>Ascomycota_Dothideomycetes_Dothideomycetes_Incertaedis_Incertaedis_Myxotrichaceae</i>	Controls	0.03
<i>Glomeromycota_Glomeromycetes_Glomerales_Glomeraceae</i>	Controls	0.03
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Controls	0.006
<i>Firmicutes_Bacilli_Lactobacillales_Enterococcaceae</i>	Not on anything	0.04
<i>Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae</i>	Not on anything	0.01
<i>Ascomycota_Sordariomycetes_Hypocreales_Clavicipitaceae</i>	Not on anything	0.02
Healthy controls vs. outpatients on lactulose only		
<i>Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae</i>	Controls	0.04
<i>Ascomycota_Sordariomycetes_Hypocreales_Nectriaceae</i>	Controls	0.04
<i>Ascomycota_Dothideomycetes_Dothideomycetes_Incertaedis_Incertaedis_Gloniaceae</i>	Controls	0.04
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrimonadaceae</i>	Controls	0.01
<i>Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae</i>	Controls	0.009
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Controls	0.004
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisXIII</i>	Controls	0.02
<i>Ascomycota_Eurotiomycetes_Eurotiales_Trichocomaceae</i>	Controls	0.02
<i>Fusobacteria_Fusobacteriia_Fusobacteriales_Fusobacteriaceae</i>	On Lactulose	0.002
<i>Basidiomycota_Agaricomycetes_Agaricomycetidae_Incertaedis_Ag</i>	On Lactulose	0.01

<i>aricomycetidae_Incertaesedis_Incertaesedis</i>		
<i>Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae</i>	On Lactulose	0.01
Healthy controls vs. outpatients on rifaximin (no SBPP)		
<i>Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae</i>	Controls	0.03
<i>Ascomycota_Pezizomycetes_Pezizales_Tuberaceae</i>	Controls	0.04
<i>Ascomycota_Dothideomycetes_Dothideomycetes_Incertaesedis_Incertaesedis_Gloniaceae</i>	Controls	0.01
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrromonadaceae</i>	Controls	0.0003
<i>Basidiomycota_Agaricomycetes_Agaricales_Inocybaceae</i>	Controls	0.01
<i>Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae</i>	Controls	0.01
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Controls	0.0007
<i>Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae</i>	Controls	0.03
<i>Basidiomycota_Agaricomycetes_Boletales_Sclerodermataceae</i>	Controls	0.01
<i>Firmicutes_Clostridia_Clostridiales_Clostridiaceae1</i>	Controls	0.009
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisIV</i>	Controls	0.04
<i>Basidiomycota_Agaricomycetes_Agaricales_Hebelomataceae</i>	Controls	0.04
<i>Firmicutes_Clostridia_Clostridiales_Ruminococcaceae</i>	Controls	0.009
<i>Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae</i>	Controls	0.007
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXIII</i>	Controls	0.008
<i>Proteobacteria_Betaproteobacteria_Burkholderiales_Sutterellaceae</i>	Controls	0.02
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Controls	0.0001
<i>Actinobacteria_Actinobacteria_Actinomycetales_Micrococcaceae</i>	On Rifaximin	0.04
<i>Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae</i>	On Rifaximin	0.002
<i>Proteobacteria_Gammaproteobacteria_Pseudomonadales_Pseudomonadaceae</i>	On Rifaximin	0.04
Healthy controls vs. outpatient on lactulose, rifaximin and SBP prophylaxis		
<i>Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae</i>	Controls	0.02
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrromonadaceae</i>	Controls	0.02
<i>Basidiomycota_Agaricomycetes_Agaricales_Inocybaceae</i>	Controls	0.04
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Controls	0.002
<i>Ascomycota_Eurotiomycetes_Onygenales_Arthrodermataceae</i>	Controls	0.02
<i>Ascomycota_Saccharomycetes_Saccharomycetales_Saccharomycetaceae</i>	Controls	0.04
<i>Actinobacteria_Actinobacteria_Coriobacteriales_Coriobacteriaceae</i>	Controls	0.04
<i>Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae</i>	Controls	0.02
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXIII</i>	Controls	0.01
<i>Proteobacteria_Betaproteobacteria_Burkholderiales_Sutterellaceae</i>	Controls	0.01
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Controls	0.03
<i>Proteobacteria_Epsilonproteobacteria_Campylobacteriales_Campylobacteraceae</i>	On L, R, SBPP	0.04
<i>Firmicutes_Bacilli_Lactobacillales_Enterococcaceae</i>	On L, R, SBPP	0.021397569
<i>Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xanthomonadaceae</i>	On L, R, SBPP	0.04
<i>Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae</i>	On L, R, SBPP	0.01
<i>Actinobacteria_Actinobacteria_Actinomycetales_Promicromonosporaceae</i>	On L, R, SBPP	0.04
<i>Proteobacteria_Betaproteobacteria_Burkholderiales_Comamonadaceae</i>	On L, R, SBPP	0.04

<i>Actinobacteria_Actinobacteria_Actinomycetales_Actinomycetaceae</i>	On L, R, SBPP	0.04
<i>Actinobacteria_Actinobacteria_Actinomycetales_Corynebacteriaceae</i>	On L, R, SBPP	0.04
<i>Proteobacteria_Betaproteobacteria_Hydrogenophilales_Hydrogenophilaceae</i>	On L, R, SBPP	0.04

Supplementary Table 7: LEFSe Comparison between healthy controls and inpatient cirrhosis

<i>Phylum_Order_Family_Genus</i>	Group with higher LDA	P value
Healthy controls vs. Admitted with no infection		
<i>Actinobacteria_Actinobacteria_Actinomycetales_Micrococcaceae</i>	Uninfected	0.03
<i>Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae</i>	Uninfected	0.01
<i>Fusobacteria_Fusobacteriia_Fusobacteriales_Fusobacteriaceae</i>	Uninfected	0.01
<i>Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae</i>	Uninfected	0.001
<i>Actinobacteria_Actinobacteria_Actinomycetales_Actinomycetaceae</i>	Uninfected	0.012
<i>Basidiomycota_Agaricomycetes_Thelephorales_Thelephoraceae</i>	Controls	0.04
<i>Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae</i>	Controls	0.02
<i>Ascomycota_Pezizomycetes_Pezizales_Tuberaceae</i>	Controls	0.004
<i>Ascomycota_Sordariomycetes_Hypocreales_Nectriaceae</i>	Controls	0.01
<i>Ascomycota_Dothideomycetes_Dothideomycetes_Incertaedis_Incertaedis_Gloniaceae</i>	Controls	0.004
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Porphyromonadaceae</i>	Controls	0.002
<i>Basidiomycota_Agaricomycetes_Agaricales_Inocybaceae</i>	Controls	0.02
<i>Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae</i>	Controls	0.001
<i>Synergistetes_Synergistia_Synergistales_Synergistaceae</i>	Controls	0.008
<i>Basidiomycota_Tremellomycetes_Tremellales_Tremellales_Incertaedis</i>	Controls	0.04
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae</i>	Controls	0.0006
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisXII</i>	Controls	0.04
<i>Basidiomycota_Agaricomycetes_Boletales_Sclerodermataceae</i>	Controls	0.004
<i>Ascomycota_Eurotiomycetes_Onygenales_Arthrodermataceae</i>	Controls	0.02
<i>Firmicutes_Clostridia_Clostridiales_Clostridiaceae1</i>	Controls	0.007
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisIV</i>	Controls	0.01
<i>Basidiomycota_Agaricomycetes_Agaricales_Hebelomataceae</i>	Controls	0.01
<i>Firmicutes_Clostridia_Clostridiales_Ruminococcaceae</i>	Controls	0.0001
<i>Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae</i>	Controls	0.0008
<i>Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaedisXIII</i>	Controls	0.0001
<i>Ascomycota_Eurotiomycetes_Eurotiales_Trichocomaceae</i>	Controls	0.002
<i>Actinobacteria_Actinobacteria_Actinomycetales_Propionibacteriaceae</i>	Controls	0.04
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Controls	7.67E-05
Healthy controls vs. Admitted with culture-negative infection		
<i>Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae</i>	Culture negative	0.03
<i>Proteobacteria_Gammaproteobacteria_Pseudomonadales_Moraxellaceae</i>	Culture negative	0.03
<i>Actinobacteria_Actinobacteria_Actinomycetales_Micrococcaceae</i>	Culture negative	0.03
<i>Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae</i>	Culture negative	0.0003
<i>Firmicutes_Bacilli_Bacillales_Staphylococcaceae</i>	Culture negative	0.03
<i>Fusobacteria_Fusobacteriia_Fusobacteriales_Fusobacteriaceae</i>	Culture negative	0.007
<i>Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae</i>	Culture negative	0.0002
<i>Ascomycota_Sordariomycetes_Hypocreales_Clavicipitaceae</i>	Culture negative	0.003
<i>Firmicutes_Bacilli_Lactobacillales_Leuconostocaceae</i>	Culture negative	0.01
<i>Basidiomycota_Agaricomycetes_Thelephorales_Thelephoraceae</i>	Controls	0.027

Ascomycota_Dothideomycetes_Dothideomycetes_Incertaesedis_Incertaesedis_Gloniaceae	Controls	0.0031
Basidiomycota_Agaricomycetes_Agaricales_Agaricaceae	Controls	0.04
Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrimonadaceae	Controls	0.03
Synergistetes_Synergistia_Synergistales_Synergistaceae	Controls	0.009
Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae	Controls	0.002
Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXII	Controls	0.02
Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae	Controls	0.02
Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae	Controls	0.02
Basidiomycota_Ustilaginomycotina_Incertaesedis_Malasseziales_Malasseziales_Incertaesedis	Controls	0.04
Actinobacteria_Actinobacteria_Coriobacteriales_Coriobacteriaceae	Controls	0.01
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae	Controls	8.30E-05
Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae	Controls	0.008
Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXIII	Controls	0.003
Ascomycota_Eurotiomycetes_Eurotiales_Trichocomaceae	Controls	0.012
Ascomycota_Pezizomycetes_Pezizales_Pyronemataceae	Controls	0.04
Healthy controls vs. Admitted with culture-positive infection		
Proteobacteria_Gammaproteobacteria_Aeromonadales_Succinivibrionaceae	Culture positive	0.002
Basidiomycota_Agaricomycetes_Sebacinales_SebacinalesGroupA	Culture positive	0.03
Bacteroidetes_Bacteroidia_Bacteroidales_Porphyrimonadaceae	Culture positive	0.0001
Firmicutes_Bacilli_Lactobacillales_Enterococcaceae	Culture positive	0.005
Actinobacteria_Actinobacteria_Actinomycetales_Micrococcaceae	Culture positive	0.02
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae	Culture positive	0.0005
Firmicutes_Clostridia_Clostridiales_Clostridiaceae1	Culture positive	0.02
Fusobacteria_Fusobacteriia_Fusobacteriales_Fusobacteriaceae	Culture positive	0.02
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae	Culture positive	0.01
Basidiomycota_Agaricomycetes_Thelephorales_Thelephoraceae	Controls	0.01
Proteobacteria_Deltaproteobacteria_Desulfovibrionales_Desulfovibrionaceae	Controls	0.0001
Ascomycota_Dothideomycetes_Dothideomycetes_Incertaesedis_Incertaesedis_Gloniaceae	Controls	0.02
Basidiomycota_Agaricomycetes_Agaricales_Agaricaceae	Controls	0.03
Basidiomycota_Agaricomycetes_Agaricales_Inocybaceae	Controls	0.007
Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae	Controls	0.0004
Synergistetes_Synergistia_Synergistales_Synergistaceae	Controls	0.01
Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae	Controls	2.76E-07
Basidiomycota_Agaricomycetes_Boletales_Sclerodermataceae	Controls	0.004
Firmicutes_Clostridia_Clostridiales_Peptococcaceae1	Controls	0.03
Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisIV	Controls	0.01
Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXI	Controls	0.03
Ascomycota_Saccharomycetes_Saccharomycetales_Dipodascaceae	Controls	0.03
Actinobacteria_Actinobacteria_Coriobacteriales_Coriobacteriaceae	Controls	0.0007
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae	Controls	1.11E-06
Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae	Controls	8.25E-05
Firmicutes_Clostridia_Clostridiales_Clostridiales_IncertaeSedisXIII	Controls	7.56E-05
Ascomycota_Eurotiomycetes_Eurotiales_Trichocomaceae	Controls	0.02
Ascomycota_Pezizomycetes_Pezizales_Pyronemataceae	Controls	0.03

<i>Actinobacteria_Actinobacteria_Actinomycetales_Propionibacteriaceae</i>	Controls	0.01
<i>Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidales_incertae_sedi</i> <i>s</i>	Controls	0.01
<i>Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae</i>	Controls	0.005
<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Controls	1.27E-07

Supplementary Table 8: LEFSe findings pre/post PPI therapy

Comparison	<i>Phylum_Order_Family_Genus</i>	Group with higher LDA	P value
Cirrhosis pre vs post	<i>Firmicutes_Bacilli_Lactobacillales_Streptococcaceae</i>	Cirrhosis Post	0.0001
	<i>Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae</i>	Cirrhosis Post	0.018
	<i>Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae</i>	Cirrhosis Pre	0.03
Control pre vs post	<i>Firmicutes_Bacilli_Lactobacillales_Streptococcaceae</i>	Control Post	0.0008
	<i>Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae</i>	Control Pre	0.04
	<i>Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae</i>	Control Pre	0.03
Cirrhosis post vs Control post	<i>Firmicutes_Clostridia_Clostridiales_Syntrophomonadaceae</i>	Cirrhosis Post	0.02
	<i>Firmicutes_Clostridia_Clostridiales_Lachnospiraceae</i>	Control Post	0.01
	<i>Firmicutes_Clostridia_Clostridiales_Eubacteriaceae</i>	Control Post	0.04
	<i>Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae</i>	Control Post	0.02
	<i>Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae</i>	Control Post	0.01
	<i>Verrucomicrobia_Verrucomicrobiae_Verrucomicrobiales_Verrucomicrobiaceae</i>	Control Post	0.04
	<i>Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae</i>	Control Post	0.03

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Suppl Fig 1 NUMBER OF READS

