Supplementary Methods:

We used DESeq2 for differential abundance analysis[1]; We followed their standard procedure to generate an adjusted p-value. DESeq2 has an internal step for scaling and normalization before calculating p-values. The input is the absolute abundance table without any normalization. We did not change any default value of their parameters. The output is a tab-delimited table, including the p-value, adjusted p-value, and Log2 foldchange of each OTU.

We used MaAsLin2[2] for determining the multivariable association between covariates and microbial features; we used their recommended procedure to perform the test. The input is the absolute abundance table without any normalization. Here are the parameters that we used, min_abundance(0.00001), min_prevalence(0.001), max_significance(0.25), standardize(TRUE), analysis method (CPLM which stands for Compound Poisson Linear Models). The output is tab-delimited table includes the p-value, q-value, coefficient, and standard error of each covariate compared to our fixed effect variables.

BiomMiner[3] is a workflow which utilizes highly popular/cited statistical methods to analyze and visualizes metagenomics dataset. For each method, BiomMiner follows the recommended standard procedure without prior modification. It visualizes each report using carefully studied methods to be easy to understand and sophisticated enough to present the research. The aggregated report is an HTML platform.

Supplementary References:

1 Love, M. I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology* **15**, 550, doi:10.1186/s13059-014-0550-8 (2014).
2 *https://huttenhower.sph.harvard.edu/maaslin/*.
3 Shamsaddini, A., Dadkhah, K. & Gillevet, P. M. BiomMiner: An advanced exploratory microbiome analysis and visualization pipeline. *PLoS One* **15**, e0234860, doi:10.1371/journal.pone.0234860 (2020).

Supplementary Tables

Table S1: Characteristics of Subject Groups Based on HE

	Controls (n=40)	**All Cirrhosis (n=163)**			**P value between all groups***	**P value comparing Cirr-L and Cirr-LR[#]**
		No-HE (n=63)	**HE (n=100)**			
			Cirr-L (n=43)	**Cirr-LR (n=57)**		
Age	58.6±10.3	60.1±7.4	57.9±9.8	61.1±7.6	0.09	0.08
Gender (male)	24 (60%)	46 (73%)	34 (79%)	46 (80%)	0.09	0.90
Proton pump inhibitor	NA	25 (40%)	25 (59%)	41 (71%)	0.002	0.15
Type 2 Diabetes	NA	27 (42%)	12 (23%)	22 (28%)	0.28	0.26
MELD score	NA	9.3±3.8	13.3±4.7	12.8±4.8	<0.0001	0.60
Alcohol-related etiology	NA	10 (16%)	22 (51%)	24 (42%)	<0.0001	0.37
Daily caloric intake	2229±239	2138±421	2098±398	2104±581	0.36	0.95
Shannon diversity	2.78±0.27	2.56±0.0.35	2.35±0.63	1.70±0.74	<0.0001	<0.0001
Hospitalizations in 90 days	NA	3 (5%)	24 (56%)	17 (30%)	<0.0001	0.008
Death in 1 year	NA	0 (0%)	7 (16%)	7 (12%)	<0.0001	0.56

Data presented as raw number (%) or mean±SD. *: ANOVA, Chi-square tests as appropriate, #Chi-square and unpaired t-tests as appropriate, Cirr-L: patients with cirrhosis on lactulose only, Cirr-LR: patients with cirrhosis on lactulose and rifaximin, NA: not applicable

Table S2: Kruskal-Wallis Comparison of Controls versus Cirrhosis Bacterial Species

Lineage	LOG2FC	Direction	pvalue
Lactobacillus_timonensis	11.66	Cirrhosis	0.015264
Lactobacillus_reuteri	10.79	Cirrhosis	0.005677
Lactobacillus_sp_UMNPBX3	10.53	Cirrhosis	0.022538
Lactobacillus_antri	10.51	Cirrhosis	0.001222
Citrobacter_sp_CFNIH10	10.46	Cirrhosis	0.0225
Citrobacter_farmeri	10.39	Cirrhosis	0.012415
Morganella_morganii	10.29	Cirrhosis	0.027143
Klebsiella_sp_2N3	10.24	Cirrhosis	0.002351
Klebsiella_sp_MS_92_3	10.23	Cirrhosis	5.93E-04
Lactobacillus_plantarum	10.1	Cirrhosis	0.00104
Klebsiella_michiganensis	9.88	Cirrhosis	7.64E-06
Klebsiella_sp_HMSC16A12	9.62	Cirrhosis	0.008356
Lactobacillus_sp_HMSC066G01	9.47	Cirrhosis	0.004498
Citrobacter_braakii	9.41	Cirrhosis	0.027096
Lactobacillus_gastricus	9.4	Cirrhosis	0.029906
Lactobacillus_sp_HMSC077C11	9.3	Cirrhosis	0.022528
Pluralibacter_gergoviae	9.25	Cirrhosis	0.048071
Enterobacter_cloacae_complex_Hoffmann_cluster_IV	9.24	Cirrhosis	0.012521
Lactobacillus_delbrueckii	9.23	Cirrhosis	0.005729
Klebsiella_pneumoniae	9.19	Cirrhosis	3.50E-04
Lactobacillus_gasseri	9.17	Cirrhosis	1.51E-05
Lactobacillus_brevis	9.11	Cirrhosis	0.039855
Lactobacillus_sp_HMSC24D01	9.05	Cirrhosis	0.003639
Microvirgula_aerodenitrificans	9	Cirrhosis	0.002938
Lactobacillus_pentosus	9	Cirrhosis	0.032999
Citrobacter_amalonaticus	8.99	Cirrhosis	0.027216
Lactobacillus_johnsonii	8.87	Cirrhosis	0.00894
Enterobacter_cloacae_complex_Hoffmann_cluster_III	8.87	Cirrhosis	0.027143
Klebsiella_variicola	8.85	Cirrhosis	7.65E-04
Enterococcus_avium	8.83	Cirrhosis	0.015276
Enterobacter_asburiae	8.77	Cirrhosis	3.64E-04
Citrobacter_werkmanii	8.62	Cirrhosis	0.003636
Megasphaera_micronuciformis	8.57	Cirrhosis	4.00E-06
Streptococcus_sp_HMSC071H03	8.57	Cirrhosis	0.027236
Klebsiella_sp_4_1_44FAA	8.51	Cirrhosis	0.027182
Lactobacillus_rhamnosus	8.47	Cirrhosis	0.007423
Lactobacillus_sp_HMSC072E07	8.41	Cirrhosis	0.018524

Lactobacillus_sp_HMSC068B07	8.4	Cirrhosis	0.027263
Lactobacillus_sp_HMSC056D05	8.37	Cirrhosis	0.048095
Klebsiella_sp_HMSC25G12	8.35	Cirrhosis	0.033026
Bifidobacterium_dentium	8.34	Cirrhosis	0.00397
Veillonella_sp_3_1_44	8.31	Cirrhosis	2.82E-05
Lactobacillus_taiwanensis	8.3	Cirrhosis	0.009959
Lactobacillus_frumenti	8.3	Cirrhosis	0.027295
Weissella_confusa	8.29	Cirrhosis	0.004171
Veillonella_parvula	8.28	Cirrhosis	1.49E-05
Lactobacillus_casei	8.27	Cirrhosis	3.19E-04
Lactobacillus_sakei	8.25	Cirrhosis	0.018473
Campylobacter_curvus	8.23	Cirrhosis	0.01526
Klebsiella_oxytoca	8.22	Cirrhosis	0.037517
Bifidobacterium_breve	8.19	Cirrhosis	0.018511
Veillonella_sp_6_1_27	8.18	Cirrhosis	4.22E-05
Selenomonas_artemidis	8.18	Cirrhosis	0.005542
Lactobacillus_parabuchneri	8.15	Cirrhosis	0.018514
Klebsiella_quasivariicola	8.13	Cirrhosis	0.004494
Lactobacillus_jensenii	8.13	Cirrhosis	0.0404
Lactobacillus_salivarius	8.11	Cirrhosis	0.005428
Chryseobacterium_bovis	8.11	Cirrhosis	0.005552
Lactobacillus_fermentum	8.09	Cirrhosis	3.09E-06
Lactobacillus_paracasei	8.06	Cirrhosis	0.007183
Campylobacter_concisus	7.95	Cirrhosis	0.001426
Lactobacillus_sp_HMSC075D02	7.93	Cirrhosis	0.00233
Fusobacterium_nucleatum	7.9	Cirrhosis	0.017204
Acinetobacter_sp_WCHA34	7.79	Cirrhosis	0.022489
Lactobacillus_coleohominis	7.77	Cirrhosis	0.012465
Campylobacter_sp_10_1_50	7.74	Cirrhosis	0.001847
Lactococcus_raffinolactis	7.73	Cirrhosis	0.009143
Klebsiella_sp_A_Nf5	7.69	Cirrhosis	0.010239
Ruminococcaceae_bacterium_CPB6	7.58	Cirrhosis	0.027773
Veillonella_rodentium	7.46	Cirrhosis	9.63E-04
Enterobacter_cloacae_complex_sp_ECNIH7	7.46	Cirrhosis	0.027184
Salmonella_enterica	7.43	Cirrhosis	0.003779
Enterobacter_hormaechei	7.38	Cirrhosis	0.015208
Veillonella_atypica	7.35	Cirrhosis	4.22E-05
Veillonella_sp_HPA0037	7.22	Cirrhosis	2.57E-04
Arcobacter_butzleri	7.2	Cirrhosis	0.033017

Enterococcus_italicus	7.19	Cirrhosis	0.003612
Enterococcus_sp_HMSC064A12	7.19	Cirrhosis	0.047826
Streptococcus_sp_HMSC066E07	7.18	Cirrhosis	0.0102
Klebsiella_sp_HMSC16C06	7.11	Cirrhosis	0.033026
Acidaminococcus_fermentans	7.09	Cirrhosis	0.02494
Selenomonas_noxia	7.08	Cirrhosis	0.048213
Moraxella_osloensis	7.07	Cirrhosis	0.008387
Campylobacter_gracilis	7.03	Cirrhosis	0.002533
Inediibacterium_massiliense	6.99	Cirrhosis	0.027285
Klebsiella_sp_X1_16S_Nf21	6.94	Cirrhosis	0.048084
Enterococcus_sp_HMSC035B04	6.61	Cirrhosis	0.03958
Haemophilus_sp_oral_taxon_036	6.58	Cirrhosis	0.010214
Citrobacter_sp_FDAARGOS_156	6.55	Cirrhosis	0.033189
Veillonella_tobetsuensis	6.51	Cirrhosis	0.001023
Klebsiella_quasipneumoniae	6.32	Cirrhosis	0.001179
Veillonella_dispar	6.24	Cirrhosis	5.45E-04
Selenomonas_sp_Marseille_P3560	6.17	Cirrhosis	0.048019
Escherichia_marmotae	6.03	Cirrhosis	0.041039
Selenomonas_flueggei	6.02	Cirrhosis	0.027242
Anaeroglobus_geminatus	5.99	Cirrhosis	0.0111
Bifidobacterium_sp_TRE_H	5.67	Cirrhosis	0.046728
Shigella_dysenteriae	5.59	Cirrhosis	0.049692
Streptococcus_dysgalactiae	5.55	Cirrhosis	0.032973
Streptococcus_vestibularis	5.5	Cirrhosis	0.010483
Escherichia_albertii	5.12	Cirrhosis	0.020809
Streptobacillus_moniliformis	5.1	Cirrhosis	0.036412
Streptococcus_sp_DD10	4.99	Cirrhosis	0.02943
Rothia_sp_HMSC065C03	4.87	Cirrhosis	0.041329
Lactobacillus_ruminis	4.86	Cirrhosis	1.83E-04
Escherichia_sp_KTE31	4.75	Cirrhosis	0.013486
Anaerotruncus_sp_AT3	4.72	Cirrhosis	0.026469
Lelliottia_amnigena	4.64	Cirrhosis	0.013606
Rothia_sp_HMSC069D01	4.59	Cirrhosis	0.002333
Streptococcus_sp_NPS_308	4.48	Cirrhosis	0.015037
Atopobium_parvulum	4.47	Cirrhosis	6.87E-04
Rothia_sp_HMSC062H08	4.39	Cirrhosis	0.010541
Citrobacter_freundii	4.38	Cirrhosis	0.001093
Rothia_sp_HMSC065C12	4.38	Cirrhosis	0.045088
Escherichia_sp_1_1_43	4.37	Cirrhosis	0.038322

Streptococcus_sp_oral_taxon_071	4.33	Cirrhosis	0.041857
Rothia_sp_HMSC064F07	4.29	Cirrhosis	0.009002
Rothia_sp_HMSC071C12	4.24	Cirrhosis	0.006978
Rothia_sp_HMSC069C04	4.2	Cirrhosis	0.011984
Streptococcus_sp_F0441	4.13	Cirrhosis	0.019316
Kytococcus_sedentarius	4.13	Cirrhosis	0.044445
Streptococcus_macedonicus	4.1	Cirrhosis	0.029185
Rothia_sp_HMSC076D04	4.09	Cirrhosis	0.028262
Rothia_sp_HMSC08A08	4.08	Cirrhosis	0.016054
Rothia_sp_HMSC061D12	4.06	Cirrhosis	0.029631
Rothia_sp_HMSC066G02	4.03	Cirrhosis	0.025311
Clostridium_hylemonae	4.01	Cirrhosis	0.013938
Rothia_sp_HMSC071F11	3.96	Cirrhosis	0.013962
Rothia_sp_HMSC066G07	3.94	Cirrhosis	0.012003
Rothia_sp_HMSC071B01	3.92	Cirrhosis	0.00111
Rothia_mucilaginosa	3.91	Cirrhosis	0.003078
Rothia_sp_HMSC075F09	3.86	Cirrhosis	0.020462
Streptococcus_sp_HMSC076C09	3.84	Cirrhosis	0.042837
Rothia_sp_HMSC068F09	3.78	Cirrhosis	0.00183
Lachnospiraceae_bacterium_M18_1	3.76	Cirrhosis	0.007962
Rothia_sp_HMSC065G12	3.75	Cirrhosis	0.010676
Rothia_sp_HMSC072B03	3.69	Cirrhosis	0.009969
Rothia_sp_HMSC069C01	3.61	Cirrhosis	0.028529
Clostridium_butyricum	3.6	Cirrhosis	0.01555
Rothia_sp_HMSC036D11	3.49	Cirrhosis	0.003687
Rothia_sp_HMSC065D02	3.4	Cirrhosis	0.022872
Rothia_sp_HMSC072E10	3.38	Cirrhosis	0.020296
Rothia_sp_HMSC065B04	3.28	Cirrhosis	0.047892
Clostridium_disporicum	3.21	Cirrhosis	0.017891
Bacteroides_eggerthii	3.18	Cirrhosis	0.033532
Rothia_sp_HMSC062F03	3.14	Cirrhosis	0.023502
Rothia_sp_HMSC078H08	3.08	Cirrhosis	0.001796
Lachnoclostridium_phocaeense	3.02	Cirrhosis	0.0024
Stomatobaculum_longum	2.97	Cirrhosis	0.004073
Holdemania_massiliensis	2.96	Cirrhosis	0.027128
Bacteroides_sp_Marseille_P3166	2.83	Cirrhosis	0.003028
Bacteroides_clarus	2.82	Cirrhosis	0.028529
Dielma_fastidiosa	2.78	Cirrhosis	0.006394
Coprobacillus_sp_29_1	2.69	Cirrhosis	0.015189

Alistipes_sp_CHKCI003	2.68	Cirrhosis	0.005776
Clostridium_sp_AT4	2.65	Cirrhosis	0.039406
Neglecta_timonensis	2.64	Cirrhosis	0.040983
Clostridiales_bacterium_KA00274	2.62	Cirrhosis	2.97E-04
Lachnospiraceae_bacterium_3_1_57FAA_CT1	2.57	Cirrhosis	0.021633
Blautia_sp_Marseille_P2398	2.56	Cirrhosis	0.041312
Porphyromonas_gulae	2.55	Cirrhosis	0.016052
Holdemania_sp_Marseille_P2844	2.54	Cirrhosis	0.026485
Clostridium_sp_ASF502	2.54	Cirrhosis	0.035232
Raoultibacter_timonensis	2.47	Cirrhosis	0.022131
Catonella_morbi	2.31	Cirrhosis	0.001883
Parabacteroides_sp_HGS0025	2.31	Cirrhosis	0.046793
Intestinibacillus_massiliensis	2.29	Cirrhosis	0.01936
Campylobacter_sp_P0106	2.26	Cirrhosis	4.65E-04
Blautia_schinkii	2.23	Cirrhosis	0.049875
Candidatus_Saccharibacteria_oral_taxon_TM7x	2.21	Cirrhosis	0.001148
Clostridium_sp_KLE_1755	2.14	Cirrhosis	0.011819
Gemmiger_formicilis	2.14	Cirrhosis	0.047571
Alistipes_sp_Marseille_P5061	2.1	Cirrhosis	0.014137
Pseudoflavonifractor_capillosus	2.05	Cirrhosis	0.007214
Clostridium_sp_D5	2.04	Cirrhosis	0.028336
Gabonibacter_massiliensis	2.04	Cirrhosis	0.029357
Clostridium_leptum	2.03	Cirrhosis	0.024634
Eisenbergiella_massiliensis	2	Cirrhosis	0.002022
Lachnospiraceae_bacterium_28_4	1.93	Cirrhosis	7.07E-04
Enterorhabdus_mucosicola	1.93	Cirrhosis	0.031004
Coprobacter_fastidiosus	1.92	Cirrhosis	0.010977
Coprococcus_eutactus	1.9	Cirrhosis	1.92E-04
Alistipes_putredinis	1.9	Cirrhosis	0.013632
Anaerotignum_lactatifermentans	1.89	Cirrhosis	0.00312
Raoultibacter_massiliensis	1.89	Cirrhosis	0.044636
Asaccharospora_irregularis	1.87	Cirrhosis	8.89E-05
Eubacterium_limosum	1.87	Cirrhosis	0.022337
Bacteroides_oleiciplenus	1.86	Cirrhosis	0.02345
Roseburia_inulinivorans	1.85	Cirrhosis	0.024854
Lachnospiraceae_bacterium_2_1_58FAA	1.85	Cirrhosis	0.035558
Anaeromassilibacillus_sp_Marseille_P3371	1.83	Cirrhosis	2.85E-04
Lachnospiraceae_bacterium_3_1	1.83	Cirrhosis	0.001213
Eubacterium_rectale	1.83	Cirrhosis	0.006041

Streptococcus_agalactiae	1.83	Cirrhosis	0.032699
Ruminococcus_gauvreauii	1.77	Cirrhosis	0.022625
Eggerthella_sp_YY7918	1.75	Cirrhosis	0.001625
Gordonibacter_pamelaeae	1.72	Cirrhosis	0.017637
Faecalicatena_contorta	1.72	Cirrhosis	0.039341
Ileibacterium_massiliense	1.71	Cirrhosis	0.00419
Ruminococcaceae_bacterium_cv2	1.71	Cirrhosis	0.040961
Absiella_dolichum	1.69	Cirrhosis	3.32E-04
Bacteroides_sp_4_3_47FAA	1.69	Cirrhosis	0.01438
Oribacterium_sp_oral_taxon_078	1.69	Cirrhosis	0.039976
Coprobacillus_sp_8_1_38FAA	1.67	Cirrhosis	2.98E-06
Bacteroides_stercoris	1.67	Cirrhosis	0.006347
Butyricimonas_synergistica	1.67	Cirrhosis	0.010905
Erysipelotrichaceae_bacterium_6_1_45	1.66	Cirrhosis	0.016479
Actinomyces_georgiae	1.65	Cirrhosis	0.046072
Enterorhabdus_caecimuris	1.64	Cirrhosis	0.003032
Ruthenibacterium_lactatiformans	1.63	Cirrhosis	0.005406
Anaerotignum_neopropionicum	1.62	Cirrhosis	0.007533
Burkholderiales_bacterium_1_1_47	1.62	Cirrhosis	0.009967
Eubacterium_sp_YI	1.62	Cirrhosis	0.039692
Bacteroides_sp_HMSC068A09	1.6	Cirrhosis	0.004988
Blautia_sp_Marseille_P3201T	1.6	Cirrhosis	0.005624
Clostridioides_difficile	1.6	Cirrhosis	0.006857
Odoribacter_laneus	1.6	Cirrhosis	0.039495
Marvinbryantia_formatexigens	1.59	Cirrhosis	0.001069
Ruminococcus_faecis	1.58	Cirrhosis	0.006605
Coprobacter_secundus	1.57	Cirrhosis	7.69E-05
Fusobacterium_naviforme	1.57	Cirrhosis	4.34E-04
Streptococcus_pasteurianus	1.57	Cirrhosis	5.50E-04
Lachnospiraceae_bacterium_7_1_58FAA	1.56	Cirrhosis	0.010805
Anaerotruncus_sp_G32012	1.56	Cirrhosis	0.027541
Lachnospiraceae_bacterium_A2	1.55	Cirrhosis	0.017683
Fusicatenibacter_saccharivorans	1.54	Cirrhosis	0.002023
Erysipelotrichaceae_bacterium_21_3	1.54	Cirrhosis	0.018764
Johnsonella_ignava	1.53	Cirrhosis	0.006062
Oscillibacter_sp_1_3	1.53	Cirrhosis	0.007029
Roseburia_hominis	1.52	Cirrhosis	0.00641
Firmicutes_bacterium_ASF500	1.52	Cirrhosis	0.023108
Adlercreutzia_equolifaciens	1.5	Cirrhosis	0.004188

Peptoniphilus_asaccharolyticus	1.5	Cirrhosis	0.01587
Provencibacterium_massiliense	1.49	Cirrhosis	0.002226
Eubacterium_hallii	1.48	Cirrhosis	0.024022
Dorea_sp_5_2	1.46	Cirrhosis	2.18E-04
Ruminococcaceae_bacterium_Marseille_P2935	1.46	Cirrhosis	0.006034
Murdochiella_vaginalis	1.46	Cirrhosis	0.033735
Parabacteroides_sp_Marseille_P3668	1.45	Cirrhosis	0.044412
Sharpea_azabuensis	1.44	Cirrhosis	8.92E-04
Clostridium_sp_SY8519	1.43	Cirrhosis	9.53E-04
Clostridium_sp_M62_1	1.41	Cirrhosis	0.003325
Blautia_sp_KLE_1732	1.39	Cirrhosis	0.014532
Catenibacterium_mitsuokai	1.37	Cirrhosis	0.004312
Alistipes_ihumii	1.37	Cirrhosis	0.007964
Bacteroides_gallinarum	1.37	Cirrhosis	0.010211
Bacteroides_fluxus	1.34	Cirrhosis	0.039964
Clostridium_sp_SN20	1.33	Cirrhosis	0.012776
Alistipes_sp_Marseille_P2431	1.32	Cirrhosis	0.005285
Enterococcus_gilvus	1.32	Cirrhosis	0.012857
Coprococcus_comes	1.31	Cirrhosis	1.44E-04
Eubacterium_sp_SB2	1.3	Cirrhosis	0.0012
Clostridium_methylpentosum	1.3	Cirrhosis	0.001506
Lachnospiraceae_bacterium_A4	1.3	Cirrhosis	0.004676
Alistipes_shahii	1.3	Cirrhosis	0.012776
Subdoligranulum_sp_4_3_54A2FAA	1.29	Cirrhosis	0.002804
Erysipelotrichaceae_bacterium_2_2_44A	1.29	Cirrhosis	0.003494
Faecalibaculum_rodentium	1.26	Cirrhosis	1.07E-04
Roseburia_intestinalis	1.26	Cirrhosis	3.16E-04
Bacteroides_sp_Marseille_P3208T	1.25	Cirrhosis	0.00989
Bittarella_massiliensis	1.24	Cirrhosis	0.001261
Streptococcus_orisratti	1.24	Cirrhosis	0.007857
Clostridium_saccharolyticum	1.23	Cirrhosis	2.49E-05
Parasutterella_excrementihominis	1.23	Cirrhosis	0.003624
Slackia_piriformis	1.23	Cirrhosis	0.033564
Catabacter_hongkongensis	1.22	Cirrhosis	0.014704
Treponema_porcinum	1.21	Cirrhosis	2.98E-05
Ruminococcus_sp_YE71	1.21	Cirrhosis	0.00235
Clostridium_sp_SS2_1	1.21	Cirrhosis	0.017985
Eubacterium_sp_14_2	1.2	Cirrhosis	3.88E-04
Clostridium_phoceensis	1.2	Cirrhosis	8.49E-04

Murdochiella_massiliensis	1.2	Cirrhosis	0.002364
Ruminococcus_torques	1.18	Cirrhosis	0.002896
Fournierella_massiliensis	1.17	Cirrhosis	5.38E-05
Alistipes_finegoldii	1.17	Cirrhosis	0.027967
Eubacterium_eligens	1.16	Cirrhosis	0.002657
Bacteroides_salanitronis	1.15	Cirrhosis	5.67E-04
Peptoniphilus_phoceensis	1.15	Cirrhosis	0.003342
Bariatricus_massiliensis	1.14	Cirrhosis	0.005362
Faecalibacterium_prausnitzii	1.13	Cirrhosis	6.86E-04
Bulleidia_extructa	1.13	Cirrhosis	0.005676
Alistipes_onderdonkii	1.13	Cirrhosis	0.016186
Lachnoanaerobaculum_saburreum	1.12	Cirrhosis	7.40E-04
Lactobacillus_rogosae	1.11	Cirrhosis	7.34E-04
Fusicatenibacter_sp_2789STDY5834925	1.11	Cirrhosis	7.96E-04
Phascolarctobacterium_succinatutens	1.11	Cirrhosis	0.032608
Blautia_sp_SF_50	1.11	Cirrhosis	0.042644
Sutterella_sp_KLE1602	1.1	Cirrhosis	0.013667
Ruminococcus_sp_AT10	1.09	Cirrhosis	4.23E-04
Lachnospiraceae_bacterium_1_1_57FAA	1.08	Cirrhosis	0.002734
Holdemania_filiformis	1.08	Cirrhosis	0.004687
Anaerotruncus_colihominis	1.07	Cirrhosis	5.26E-04
Acetivibrio_ethanolgignens	1.06	Cirrhosis	0.001115
Anaerofustis_stercorihominis	1.05	Cirrhosis	0.011573
Parabacteroides_sp_CT06	1.04	Cirrhosis	0.013025
Coprococcus_sp_HPP0048	1.03	Cirrhosis	0.026669
Pseudoflavonifractor_sp_Marseille_P3106	1.02	Cirrhosis	5.79E-04
Bacteroides_nordii	-1	Control	0.023214
Monoglobus_pectinilyticus	-1.37	Control	1.92E-05
Alistipes_inops	-1.4	Control	0.017719
Bacteroides_coprocola	-1.87	Control	0.029882
Faecalitalea_cylindroides	-1.95	Control	5.00E-04
Lachnobacterium_bovis	-2.58	Control	4.79E-04
Butyrivibrio_crossotus	-2.77	Control	5.30E-04
Ruminococcus_champanellensis	-2.78	Control	2.66E-06

Table S3: DESeq2 Comparison of Resistomes Control vs Cirrhosis

Resistomes Lineage	LOG2FC	Direction	pvalue
Klebsiella_sp	8.79	Cirrhosis	8.01E-04
Exiguobacterium_sp	7.94	Cirrhosis	0.002848
Serratia_marcescens	5.46	Cirrhosis	1.01E-06
Haemophilus_influenzae	5.08	Cirrhosis	0.001338
Streptococcus_oralis	4.92	Cirrhosis	0.00466
Vibrio_parahaemolyticus	4.62	Cirrhosis	1.41E-05
Riemerella_anatipestifer	4.3	Cirrhosis	0.019943
Streptococcus_australis	4.29	Cirrhosis	4.12E-05
Acinetobacter_nosocomialis	3.95	Cirrhosis	6.46E-04
Streptococcus_pneumoniae	3.83	Cirrhosis	0.037213
Salmonella_enterica	3.61	Cirrhosis	0.003114
Enterococcus_faecium	3.61	Cirrhosis	0.0114
Achromobacter_insuavis	3.57	Cirrhosis	0.03141
Staphylococcus_aureus	3.56	Cirrhosis	1.82E-04
Escherichia_coli	3.09	Cirrhosis	0.001287
Citrobacter_amalonaticus	3.08	Cirrhosis	0.023368
Mycobacterium_tuberculosis	3.06	Cirrhosis	0.016948
Citrobacter_freundii	2.86	Cirrhosis	9.73E-04
Klebsiella_pneumoniae	2.82	Cirrhosis	0.009835
Acinetobacter_baumannii	2.78	Cirrhosis	0.015969
Acidaminococcus_fermentans	2.15	Cirrhosis	0.023939
uncultured_bacterium	1.17	Cirrhosis	0.002329
Campylobacter_fetus	1.12	Cirrhosis	0.045666
mixed_culture	1.05	Cirrhosis	0.023757

Table S4: DESeq2 Comparison of ARO terms Control vs Cirrhosis

Lineage DESeq2	LOG2FC	Direction	pvalue
aadA16	7.98	Cirrhosis	2.38E-05
CTX_M_76	7.79	Cirrhosis	0.01756
efmA	7.58	Cirrhosis	0.001967
CTX_M_117	7.48	Cirrhosis	3.16E-06
SHV_160	6.89	Cirrhosis	7.60E-05
QnrB8	6.88	Cirrhosis	3.12E-06
ANT_3_IIa	6.4	Cirrhosis	2.98E-05
CTX_M_50	6.34	Cirrhosis	1.00E-06
Klebsiella_pneumoniae_KpnG	6.16	Cirrhosis	1.00E-06
tet_45	5.98	Cirrhosis	9.52E-05
FosA5	5.93	Cirrhosis	0.001071
RlmA_II	5.87	Cirrhosis	0.00239
aadA	5.6	Cirrhosis	0.011444
FosA6	5.58	Cirrhosis	0.00256
vanD	5.55	Cirrhosis	0.021856
TEM_205	5.46	Cirrhosis	5.41E-05
oqxA	5.4	Cirrhosis	1.80E-06
Klebsiella_pneumoniae_acrA	5.35	Cirrhosis	3.36E-05
AAC_6_Ib10	5.22	Cirrhosis	0.001958
sul1	5.2	Cirrhosis	1.30E-04
mphB	5.18	Cirrhosis	3.87E-06
vanSA	5.06	Cirrhosis	0.018476
catI	4.98	Cirrhosis	1.21E-06
FosA2	4.97	Cirrhosis	0.031619
pmrA	4.93	Cirrhosis	0.013391
tet_C	4.88	Cirrhosis	4.05E-06
ramA	4.87	Cirrhosis	3.29E-04
aadA8b	4.85	Cirrhosis	0.032478
aadA24	4.79	Cirrhosis	0.04115
Klebsiella_pneumoniae_OmpK37	4.6	Cirrhosis	1.04E-06
TEM_40	4.56	Cirrhosis	0.004099
mphA	4.55	Cirrhosis	0.006717
TEM_102	4.55	Cirrhosis	0.02493
SRT_2	4.38	Cirrhosis	0.040797
AAC_3_IV	4.31	Cirrhosis	0.005449
SHV_11	4.21	Cirrhosis	0.022617
tet_D	4.16	Cirrhosis	5.46E-04
patA	4.14	Cirrhosis	0.019495
Klebsiella_pneumoniae_KpnH	4.12	Cirrhosis	1.24E-06
Enterobacter_cloacae_acrA	4.04	Cirrhosis	0.006217
EreD	4.03	Cirrhosis	0.014354
tetA_46	3.86	Cirrhosis	0.001434
tet_A	3.73	Cirrhosis	0.003181

tetB_46	3.72	Cirrhosis	0.00363
H_NS	3.64	Cirrhosis	1.30E-04
Klebsiella_pneumoniae_KpnF	3.64	Cirrhosis	4.50E-04
AAC_6_Ib7	3.64	Cirrhosis	0.043031
oqxB	3.61	Cirrhosis	5.23E-04
APH_6_Id	3.55	Cirrhosis	3.97E-04
cpxA	3.47	Cirrhosis	2.46E-04
mdtM	3.47	Cirrhosis	0.001144
Klebsiella_pneumoniae_KpnE	3.43	Cirrhosis	3.96E-06
SAT_1	3.43	Cirrhosis	0.013674
sul2	3.42	Cirrhosis	3.07E-04
APH_3_Ib	3.41	Cirrhosis	4.24E-05
emrA	3.41	Cirrhosis	0.001773
Escherichia_coli_ampH	3.38	Cirrhosis	0.001227
mdtC	3.36	Cirrhosis	4.17E-05
mdtH	3.36	Cirrhosis	0.001207
marA	3.36	Cirrhosis	0.002196
pmrF	3.35	Cirrhosis	0.001038
bacA	3.31	Cirrhosis	4.60E-04
mdtB	3.3	Cirrhosis	3.19E-04
gadX	3.28	Cirrhosis	6.09E-04
Escherichia_coli_mdfA	3.28	Cirrhosis	0.00198
arnA	3.28	Cirrhosis	0.002518
aadA22	3.28	Cirrhosis	0.049927
CRP	3.24	Cirrhosis	0.001963
Tet_X4	3.22	Cirrhosis	0.008158
mdtK	3.21	Cirrhosis	0.002943
tolC	3.16	Cirrhosis	0.005914
mdtN	3.13	Cirrhosis	0.009376
Escherichia_coli_emrE	3.13	Cirrhosis	0.014692
Escherichia_coli_ampC1_beta_lactamase	3.12	Cirrhosis	0.01132
Tet_X3	3.11	Cirrhosis	0.016357
yojI	3.09	Cirrhosis	0.001309
aadS	3.09	Cirrhosis	0.032282
acrB	3.06	Cirrhosis	0.006765
acrE	3.05	Cirrhosis	0.014596
mdtG	3.02	Cirrhosis	0.018732
mdtP	3.01	Cirrhosis	0.018393
acrS	3.01	Cirrhosis	0.024064
mdtA	3	Cirrhosis	0.009166
acrF	3	Cirrhosis	0.019808
emrR	2.99	Cirrhosis	0.004823
eptA	2.97	Cirrhosis	0.027021
baeS	2.95	Cirrhosis	0.024986
emrB	2.92	Cirrhosis	0.028064
evgS	2.88	Cirrhosis	0.023217

acrD	2.87	Cirrhosis	0.02227
arlS	2.76	Cirrhosis	0.043254
mphE	2.66	Cirrhosis	0.039672
mdtO	2.64	Cirrhosis	0.040901
kdpE	2.63	Cirrhosis	0.030919
tlrC	1.26	Cirrhosis	0.024299
MexB	1.26	Cirrhosis	0.039048
CblA_1	1.11	Cirrhosis	0.035662
vanSG	-1.13	Control	7.18E-06
vanXYG	-1.29	Control	1.00E-06

Table S5: DESeq2 Comparison of AMR genes Control vs Cirrhosis

Lineage (DESeq2)	LOG2FC	Direction	pvalue
quinolone_resistance_protein_qnr	6.75	Cirrhosis	1.02E-06
KPC_beta_lactamase	6.38	Cirrhosis	0.025915
CTX_M_beta_lactamase	5.73	Cirrhosis	1.00E-06
fosfomycin_thiol_transferase	5.56	Cirrhosis	5.61E-06
non_erm_23S_ribosomal_RNA_methyltransferase_G748	5.03	Cirrhosis	0.012382
ANT_3	4.63	Cirrhosis	1.00E-06
General_Bacterial_Porin_with_reduced_permeability_to_beta_lactams	4.35	Cirrhosis	1.49E-06
CMY_beta_lactamase	4.18	Cirrhosis	0.035015
blaZ_beta_lactamase	4.16	Cirrhosis	0.024347
sulfonamide_resistant_sul	4.06	Cirrhosis	3.13E-04
SHV_beta_lactamase	3.14	Cirrhosis	7.77E-04
macrolide_phosphotransferase_MPH	3.13	Cirrhosis	0.011087
streptothricin_acetyltransferase_SAT	3.12	Cirrhosis	0.003593
antibiotic_resistant_isoleucyl_tRNA_synthetase_ileS	3.08	Cirrhosis	0.018339
APH_3	3.05	Cirrhosis	0.002415
undecaprenyl_pyrophosphate_related_proteins	2.79	Cirrhosis	0.019842
ATP_binding_cassette_ABC_antibiotic_efflux_pump	2.72	Cirrhosis	3.39E-04
resistance_nodulation_cell_division_RND_antibiotic_efflux_pump	2.5	Cirrhosis	0.012729
ACI_beta_lactamase	2	Cirrhosis	0.001094
tetracycline_resistant_ribosomal_protection_protein	1.3	Cirrhosis	0.003761
glycopeptide_resistance_gene_cluster	1.24	Cirrhosis	0.001917

Table S6: Kruskal-Wallis Comparison of No HE versus Prior HE Bacterial Species

Lineage	LOG2FC	Direction	pvalue
Clostridium_sphenoides	-12.71	Prior HE	0.027112
Hafnia_sp_HMSC23F03	-11.05	Prior HE	0.041813
Lactobacillus_sp_HMSC08B12	-9.43	Prior HE	0.02713
Neisseria_bacilliformis	-8.57	Prior HE	0.017542
Enterococcus_casseliflavus	-7.48	Prior HE	0.027138
Lactobacillus_sp_HMSC061B07	-7.44	Prior HE	0.007254
Lactobacillus_acidophilus	-7.35	Prior HE	0.006721
Pediococcus_claussenii	-7.16	Prior HE	0.017491
Lactobacillus_sp_HMSC078F07	-7.15	Prior HE	0.02714
Enterococcus_sp_HMSC063H10	-7.07	Prior HE	0.041849
Inediibacterium_massiliense	-6.99	Prior HE	2.75E-04
Lactobacillus_sp_HMSC068B07	-6.8	Prior HE	0.007601
Enterococcus_sp_255_ESPC	-6.7	Prior HE	0.041853
Enterococcus_sp_HMSC035B04	-6.58	Prior HE	0.001833
Lactobacillus_sp_HMSC056D05	-6.36	Prior HE	0.029378
Lactobacillus_sp_HMSC077C11	-6.28	Prior HE	0.005373
Lactobacillus_paracasei	-6.15	Prior HE	0.015794
Escherichia_sp_KTE96	-6.07	Prior HE	0.041845
Lactobacillus_delbrueckii	-5.87	Prior HE	2.65E-04
Neisseria_lactamica	-5.67	Prior HE	0.041809
Bifidobacterium_sp_TRE_D	-5.64	Prior HE	0.004635
Bifidobacterium_mongoliense	-5.52	Prior HE	0.041849
Paeniglutamicibacter_antarcticus	-5.49	Prior HE	0.0113
Bifidobacterium_callitrichos	-5.29	Prior HE	0.017516
Bifidobacterium_sp_TRE_1	-5.29	Prior HE	0.027135
Bifidobacterium_aesculapii	-5.22	Prior HE	0.03331
Lactobacillus_rossiae	-5.04	Prior HE	0.007252
Bifidobacterium_subtile	-5	Prior HE	0.027135
Streptococcus_sp_M334	-4.89	Prior HE	0.001045
Weissella_sp_DD23	-4.81	Prior HE	0.017541
Bifidobacterium_reuteri	-4.78	Prior HE	0.001452
Leuconostoc_mesenteroides	-4.68	Prior HE	0.019226
Bifidobacterium_lemurum	-4.64	Prior HE	0.027128
Bifidobacterium_sp_TRE_H	-4.62	Prior HE	0.00739
Kingella_oralis	-4.61	Prior HE	0.046563
Streptococcus_sp_HMSC076C08	-4.58	Prior HE	0.027089
Leptospira_sp_JW3_C_A1	-4.46	Prior HE	0.011288

Megasphaera_micronuciformis	-4.44	Prior HE	0.030664
Campylobacter_showae	-4.32	Prior HE	0.041845
Blautia_producta	-4.28	Prior HE	6.51E-05
Bifidobacterium_saguini	-4.25	Prior HE	0.00205
Aerococcus_sp_HMSC23C02	-4.25	Prior HE	0.027133
Colwellia_echini	-4.17	Prior HE	0.027133
Bifidobacterium_breve	-3.94	Prior HE	0.00964
Streptococcus_sp_HMSC077D04	-3.59	Prior HE	0.002638
Veillonella_sp_6_1_27	-3.58	Prior HE	0.022356
Veillonella_parvula	-3.56	Prior HE	0.023193
Streptococcus_sp_oral_taxon_058	-3.54	Prior HE	0.00158
Veillonella_sp_3_1_44	-3.51	Prior HE	0.024751
Streptococcus_sp_CCUG_49591	-3.5	Prior HE	0.02017
Parvimonas_micra	-3.48	Prior HE	0.043364
Bifidobacterium_longum	-3.44	Prior HE	0.016517
Lautropia_mirabilis	-3.42	Prior HE	0.01015
Bifidobacterium_sp_12_1_47BFAA	-3.38	Prior HE	0.03324
Streptococcus_sp_HMSC073F11	-3.37	Prior HE	0.011038
Streptococcus_sp_F0441	-3.35	Prior HE	0.038454
Streptococcus_mitis	-3.27	Prior HE	0.004997
Streptococcus_sp_HMSC070B10	-3.26	Prior HE	0.03203
Veillonella_rodentium	-3.24	Prior HE	0.03528
Campylobacter_curvus	-3.23	Prior HE	0.039533
Streptococcus_sp_NLAE_zl_C503	-2.99	Prior HE	0.021089
Oxalobacter_formigenes	-2.95	Prior HE	0.018667
Streptococcus_sp_UMB0029	-2.94	Prior HE	0.035476
Coprobacillus_sp_8_1_38FAA	-2.93	Prior HE	0.024559
Streptococcus_sp_HMSC063B03	-2.92	Prior HE	0.029331
Streptococcus_pseudopneumoniae	-2.83	Prior HE	0.021052
Gabonia_massiliensis	-2.59	Prior HE	0.008626
Asaccharospora_irregularis	-2.43	Prior HE	0.034456
Clostridium_butyricum	-2.41	Prior HE	0.019365
Streptococcus_pneumoniae	-2.33	Prior HE	0.026626
Veillonella_atypica	-2.11	Prior HE	0.003229
Campylobacter_sp_10_1_50	-2.05	Prior HE	0.001687
Olsenella_provencensis	-2.05	Prior HE	0.035881
Veillonella_tobetsuensis	-2.04	Prior HE	0.004597
Campylobacter_concisus	-1.99	Prior HE	0.002245
Veillonella_sp_HPA0037	-1.99	Prior HE	0.006568

Lactobacillus_fermentum	-1.96	Prior HE	0.003434
Veillonella_dispar	-1.95	Prior HE	0.040455
Sutterella_wadsworthensis	-1.89	Prior HE	0.00992
Clostridium_sp_L2_50	-1.82	Prior HE	0.008786
Clostridium_bolteae	-1.77	Prior HE	0.014293
Prevotella_amnii	-1.54	Prior HE	0.03658
Tannerella_sp_oral_taxon_HOT_286	-1.51	Prior HE	0.024385
Bacteroides_paurosaccharolyticus	-1.5	Prior HE	0.010049
Mogibacterium_diversum	-1.44	Prior HE	0.032918
Intestinibacillus_massiliensis	-1.42	Prior HE	0.002908
Alistipes_sp_CHKCI003	-1.42	Prior HE	0.046751
Lachnospiraceae_bacterium_2_1_46FAA	-1.34	Prior HE	0.00197
Olsenella_umbonata	-1.33	Prior HE	0.046302
Clostridium_disporicum	-1.26	Prior HE	0.001283
Absiella_dolichum	-1.25	Prior HE	0.022078
Holdemania_massiliensis	-1.12	Prior HE	0.008361
Ruminococcaceae_bacterium_D16	-1.04	Prior HE	0.028704
Bifidobacterium_scardovii	-1.01	Prior HE	0.003206
Bacteroides_sp_AR20	1	No HE	0.001628
bacterium_LF_3	1.03	No HE	0.00997
Tyzzerella_nexilis	1.1	No HE	7.75E-05
Coprococcus_sp_HPP0048	1.11	No HE	3.11E-05
Clostridium_sp_HMSC19A11	1.11	No HE	2.22E-04
Peptoniphilus_sp_HMSC062D09	1.11	No HE	0.004956
Lachnospiraceae_bacterium_1_4_56FAA	1.16	No HE	7.24E-05
Emergencia_timonensis	1.17	No HE	0.025267
Clostridium_leptum	1.18	No HE	3.05E-04
Eisenbergiella_massiliensis	1.22	No HE	0.002074
Bacteroides_thetaiotaomicron	1.27	No HE	0.019027
Christensenella_timonensis	1.29	No HE	0.038347
Lachnospiraceae_bacterium_9_1_43BFAA	1.36	No HE	1.19E-04
Ileibacterium_massiliense	1.36	No HE	1.48E-04
Clostridium_sp_AT4	1.39	No HE	6.98E-04
Prevotella_falsenii	1.4	No HE	0.004245
Gabonibacter_massiliensis	1.42	No HE	0.015268
Enorma_phocaeensis	1.47	No HE	0.01169
Enterococcus_cecorum	1.49	No HE	0.034486
Bariatricus_massiliensis	1.5	No HE	0.010063
Coprococcus_sp_HPP0074	1.6	No HE	2.40E-04

Clostridium_sp_KLE_1755	1.6	No HE	9.16E-04
Lachnospiraceae_bacterium_A4	1.65	No HE	7.71E-06
Holdemania_sp_Marseille_P2844	1.77	No HE	0.002152
Ruminococcus_gauvreauii	1.78	No HE	8.37E-08
Adlercreutzia_equolifaciens	1.82	No HE	0.002855
Alistipes_inops	1.83	No HE	0.001675
Enterococcus_gilvus	2.07	No HE	0.016756
Clostridiales_bacterium_CHKCI001	2.09	No HE	0.01463
Lachnospiraceae_bacterium_M18_1	2.14	No HE	0.004674
Dielma_fastidiosa	2.15	No HE	0.004401
Cloacibacillus_porcorum	2.38	No HE	0.008659
Enorma_massiliensis	2.39	No HE	5.56E-04
Ruminococcaceae_bacterium_D5	2.5	No HE	0.009786
Negativibacillus_massiliensis	2.59	No HE	9.39E-05
Eubacterium_callanderi	2.73	No HE	3.39E-04
Senegalimassilia_anaerobia	2.94	No HE	8.97E-04
Clostridium_scindens	2.96	No HE	3.60E-04
Lachnoclostridium_phocaeense	3	No HE	0.000674
Lachnospira_multipara	3	No HE	0.030754
Collinsella_ihuae	3.27	No HE	0.006426
Streptococcus_pyogenes	3.77	No HE	0.032948
Fusobacterium_perfoetens	4.17	No HE	0.030754
Clostridiales_bacterium_Marseille_P2846	4.32	No HE	0.015309
Citrobacter_portucalensis	4.75	No HE	0.012085
Megasphaera_elsdenii	5.11	No HE	0.036244
Kluyvera_cryocrescens	8.2	No HE	5.94E-04
Prevotella_sp_oral_taxon_299	8.4	No HE	0.030754
Enterobacter_sp_BIDMC_29	10.08	No HE	0.015211
Megasphaera_sp_ASD88	10.45	No HE	0.012075
Kluyvera_ascorbata	10.57	No HE	0.012279

Table S7: DESeq2 Comparison of ARO terms No HE vs Prior HE

Lineage	LOG2FC	Direction	pvalue
tetU	-6.62	Prior HE	1.64E-05
ErmX	-4.21	Prior HE	0.017726
tetS	-4.02	Prior HE	0.028251
vanZA	-3.77	Prior HE	0.001993
efmA	-3.7	Prior HE	0.001209
vanRA	-3.11	Prior HE	0.022796
vanD	-3.05	Prior HE	0.026556
CTX_M_76	-2.93	Prior HE	6.49E-04
vanHD	-2.87	Prior HE	0.012827
vanSA	-2.7	Prior HE	1.77E-04
tet44	-2.38	Prior HE	0.010112
MexA	-2.21	Prior HE	0.018543
ErmC	-2.03	Prior HE	4.29E-04
ANT_6_Ia	-1.92	Prior HE	9.72E-05
PDC_3	-1.87	Prior HE	0.004275
aadS	-1.84	Prior HE	0.008296
arlS	-1.77	Prior HE	0.001127
SHV_126	-1.65	Prior HE	0.014703
Bifidobacteria_intrinsic_ileS_conferring_resistance_to_mupirocin	-1.63	Prior HE	0.017417
mexJ	-1.61	Prior HE	0.034514
TriC	-1.56	Prior HE	0.01828
Tet_X3	-1.55	Prior HE	0.023154
Tet_X4	-1.53	Prior HE	0.024412
MuxC	-1.49	Prior HE	0.003973
Klebsiella_pneumoniae_KpnE	-1.35	Prior HE	0.004959
macB	-1.31	Prior HE	0.01627
cdeA	-1.29	Prior HE	0.014446
tlrC	-1.28	Prior HE	0.038061
Campylobacter_coli_chloramphenicol_acetyltransferase	1	No HE	0.030701
Pseudomonas_aeruginosa_CpxR	1.07	No HE	0.001614
aadA22	1.09	No HE	0.00101
APH_6_Ic	1.19	No HE	0.003567
AAC_3_IV	1.22	No HE	4.36E-04
QnrB8	1.24	No HE	0.013442
dfrA14	1.33	No HE	0.005042
aadA8	2.37	No HE	0.018973

Table S8: DESeq2 Comparison of AMR genes No HE vs Prior HE

Lineage	LOG2FC	Direction	pvalue
vanZ	-3.3	Prior HE	0.005011
RbpA_bacterial_RNA_polymerase_binding_protein	-2.71	Prior HE	0.019651
KPC_beta_lactamase	-2.44	Prior HE	0.023482
PDC_beta_lactamase	-2.31	Prior HE	8.45E-05
antibiotic_resistant_isoleucyl_tRNA_synthetase_ileS	-1.54	Prior HE	0.031918
multidrug_and_toxic_compound_extrusion_MATE_transporter	-1.08	Prior HE	0.01371
quinolone_resistance_protein_qnr	1.66	No HE	1.18E-06

Table S9: DESeq2 Comparison of Resistomes No HE vs Prior HE

Lineage	LOG2FC	Direction	pvalue
Listeria_monocytogenes	-4.52	Prior HE	0.013184
Staphylococcus_aureus	-2.15	Prior HE	1.76E-04
Transposon_Tn4551	-1.54	Prior HE	0.033926
Bifidobacterium_bifidum	-1.53	Prior HE	0.036106
Streptomyces_rishiriensis	-1.25	Prior HE	0.039764
Streptococcus_oralis	-1.23	Prior HE	3.67E-05
Pseudomonas_fluorescens	-1.23	Prior HE	0.026737

Table S10: DESeq2 Comparison of bacterial species between patients with/without hospitalizations

Lineage	LOG2FC	Direction	P-value
Lactobacillus_johnsonii	-4.82	Yes	0.025568
Lactobacillus_taiwanensis	-3.05	Yes	0.022549
Lactobacillus_reuteri	-2.24	Yes	0.008086
Veillonella_rodentium	-2.1	Yes	0.026939
Veillonella_sp_6_1_27	-1.95	Yes	0.030128
Dialister_pneumosintes	-1.41	Yes	0.004617
Megasphaera_elsdenii	5.64	No	0.004679
Bifidobacterium_angulatum	4.92	No	0.019657
Intestinibacillus_massiliensis	4.88	No	0.002948
bacterium_LF_3	4.84	No	0.006838
Clostridium_disporicum	4.8	No	0.030494
Holdemania_sp_Marseille_P2844	4.5	No	0.006876
Bifidobacterium_adolescentis	4.4	No	0.003838
Negativibacillus_massiliensis	4.01	No	0.036816
Gordonibacter_pamelaeae	3.88	No	0.001004
Stomatobaculum_longum	3.81	No	0.006674
Gemmiger_formicilis	3.3	No	0.00467
Eggerthella_sp_YY7918	3.12	No	0.019952
Clostridium_leptum	3	No	0.020136
Ileibacterium_massiliense	2.95	No	0.005354
Ruminococcus_bromii	2.95	No	0.032055
Fusobacterium_nucleatum	2.86	No	0.006738
Sharpea_azabuensis	2.79	No	0.016735
Clostridium_sp_Marseille_P3244	2.67	No	0.008697
Erysipelotrichaceae_bacterium_21_3	2.61	No	0.016633
Coprobacillus_sp_8_1_38FAA	2.59	No	9.74E-04
Eubacterium_sp_YI	2.54	No	0.003218
Massilioclostridium_coli	2.54	No	0.003429
Lachnospiraceae_bacterium_1_1_57FAA	2.54	No	0.020971
Dorea_longicatena	2.35	No	0.005021
Barnesiella_intestinihominis	2.31	No	0.021871
Bittarella_massiliensis	2.19	No	0.004025
Lachnospira_pectinoschiza	2.18	No	0.014039
Angelakisella_massiliensis	2.17	No	0.029552
Gordonibacter_massiliensis	2.04	No	0.025837
Enterococcus_faecium	1.77	No	0.030714
Lactobacillus_antri	1.73	No	0.040165
Streptococcus_sp_NLAE_zl_C503	1.72	No	0.004432
Bilophila_wadsworthia	1.7	No	0.035182
Streptococcus_sp_oral_taxon_058	1.54	No	9.46E-05
Streptococcus_oralis	1.43	No	0.04173
Streptococcus_sp_HMSC076C09	1.12	No	0.048357
Streptococcus_sp_HMSC077D04	1.04	No	0.034966

Table S11: MAAsLin2 Comparison of bacterial species between those patients who were hospitalized within 90 days compared to those who were not

Bacterial species	Coefficient	Std Error	p-value	q-value
Clostridium_aerotolerans	7.592922	0.69483	3.81E-21	4.49E-18
Clostridium_sphenoides	7.874307	0.847236	1.01E-16	5.96E-14
Ruminococcaceae_bacterium_CPB6	7.228162	0.840646	6.79E-15	2.67E-12
Campylobacter_helveticus	7.687291	0.908964	1.57E-14	4.63E-12
Desulfotomaculum_guttoideum	7.416556	0.90159	6.16E-14	1.45E-11
Pseudomonas_lundensis	6.755691	0.871955	9.90E-13	1.94E-10
Corynebacterium_argentoratense	5.402029	0.771889	6.61E-11	1.11E-08
Clostridium_sp._Marseille_P2415	5.287963	0.765265	1.07E-10	1.58E-08
Enterobacter_sp._BIDMC_29	6.503206	0.974658	3.85E-10	5.04E-08
MELD score	0.408795	0.063203	1.14E-09	1.34E-07
Ethanoligenens_harbinense	5.716702	0.909251	2.91E-09	3.12E-07
Lactobacillus_timonensis	4.293639	0.691846	4.43E-09	4.34E-07
Megasphaera_massiliensis	-4.14289	0.676906	6.86E-09	6.21E-07
Lactobacillus_animalis	5.604159	0.941611	1.61E-08	1.35E-06
bacterium_LF_3	-3.22386	0.545662	2.00E-08	1.57E-06
Pectobacterium_polaris	6.154924	1.081076	5.76E-08	4.24E-06
Desulfovibrio_sp._6_1_46AFAA	5.710722	1.00972	6.92E-08	4.79E-06
Bacteroides_eggerthii	2.348308	0.442954	3.74E-07	2.32E-05
Desulfovibrio_fairfieldensis	5.732978	1.079928	3.61E-07	2.32E-05
Bacteroides_paurosaccharolyticus	3.779167	0.728369	6.30E-07	3.71E-05
Atopobium_minutum	6.261503	1.214486	7.33E-07	4.11E-05
Lactobacillus_johnsonii	4.090141	0.807571	1.11E-06	5.94E-05
Actinomyces_radicidentis	4.491694	0.92451	2.79E-06	0.000143
Cloacibacillus_porcorum	-6.06685	1.261112	3.43E-06	0.000169
Enterobacter_sp._IF2SW_B1	4.573978	0.962688	4.45E-06	0.00021
Bifidobacterium_thermophilum	-2.99791	0.64201	6.33E-06	0.000287
Proteus_columbae	5.108279	1.098859	6.92E-06	0.000302
Dysgonomonas_gadei	5.12005	1.14555	1.47E-05	0.000619
Bifidobacterium_adolescentis	-2.19538	0.511809	3.08E-05	0.001251
Scardovia_wiggsiae	1.997282	0.473705	4.13E-05	0.001622
Raoultibacter_timonensis	-5.46954	1.33649	6.73E-05	0.002559
Candidatus_Stoquefichus_sp._SB1	-3.71245	0.909349	7.00E-05	0.002577
Christensenella_timonensis	-3.72828	0.916579	7.42E-05	0.002648
Duodenibacillus_massiliensis	-4.87447	1.230323	0.000111	0.003861
Yersinia_nurmii	2.769388	0.703742	0.000123	0.004153
Massilioclostridium_coli	-1.23365	0.317172	0.000147	0.004799
Parabacteroides_johnsonii	1.800856	0.464988	0.000156	0.00497
Lactobacillus_sp._HMSC068F07	3.290518	0.853568	0.000167	0.005175
Campylobacter_gracilis	1.435931	0.373565	0.000174	0.005257

Lactobacillus_harbinensis	-8.01303	2.093762	0.000185	0.005455
Blautia_producta	2.888703	0.756252	0.00019	0.00547
Hepatic Encephalopathy	0.535402	0.140563	0.000198	0.005557
Selenomonas_bovis	-7.67085	2.043571	0.000243	0.006657
Collinsella_stercoris	2.444294	0.657371	0.000277	0.007403
Bifidobacterium_animalis	-4.96262	1.343721	0.000303	0.007894
Streptococcus_sobrinus	2.376968	0.644452	0.000308	0.007894
Clostridium_disporicum	3.625167	0.995139	0.000363	0.009103
Erysipelotrichaceae_bacterium_5_2_54FAA	2.271604	0.625182	0.000376	0.009218
Porphyromonas_sp._KLE_1280	-8.77541	2.451715	0.000456	0.010953
Lactulose use	0.559616	0.1567	0.000469	0.011043
Ruminococcus_champanellensis	-1.54246	0.435404	0.000519	0.011979
Citrobacter_sp._KTE30	3.054304	0.868945	0.000571	0.012943
Lactobacillus_sp._HMSC17G08	-4.9796	1.420702	0.000591	0.013147
Proteus_sp._HMSC10D02	3.729865	1.066438	0.000607	0.013246
Clostridium_saccharogumia	-1.89447	0.542932	0.000625	0.013381
Provencibacterium_massiliense	-1.26232	0.363108	0.000653	0.013743
Angelakisella_massiliensis	-0.79168	0.229573	0.00072	0.014615
Collinsella_bouchesdurhonensis	-2.62445	0.760592	0.000715	0.014615
Lactobacillus_futsaii	2.877955	0.844736	0.00083	0.016569
Mycoplasma_salivarium	-15.5189	4.567722	0.000857	0.016824
Klebsiella_michiganensis	2.735671	0.809119	0.000906	0.017407
Oxalobacter_formigenes	-3.93273	1.164266	0.000916	0.017407
Clostridium_bolteae	1.650174	0.489302	0.000933	0.017445
Clostridium_sporosphaeroides	2.277428	0.681949	0.001043	0.018896
Neisseria_bacilliformis	2.709928	0.811015	0.001036	0.018896
Ileibacterium_massiliense	-1.11513	0.335045	0.001083	0.019329
Lactobacillus_taiwanensis	2.723624	0.821353	0.001128	0.019841
Actinomyces_bouchesdurhonensis	-2.70429	0.819411	0.001189	0.020604
Cloacibacillus_evryensis	-4.31111	1.312972	0.001258	0.021168
Ruminococcus_bicirculans	-1.56326	0.475868	0.001251	0.021168
Holdemania_sp._Marseille_P2844	-2.63234	0.808462	0.001378	0.022859
Anaerotruncus_rubiinfantis	-1.31537	0.404821	0.001409	0.023047
Prevotella_saccharolytica	-4.80998	1.497158	0.001588	0.025627
Ruminococcus_flavefaciens	-2.24962	0.706631	0.001746	0.027801
Bifidobacterium_angulatum	-2.66402	0.845295	0.001937	0.030422
Clostridium_butyricum	1.792873	0.571922	0.002044	0.031685
Synergistes_sp._3_1_syn1	-4.12855	1.323008	0.00214	0.032734
Lactobacillus_agilis	2.674522	0.865816	0.002366	0.035282
Lelliottia_nimipressuralis	3.049747	0.98722	0.002365	0.035282
Anaerosporobacter_mobilis	-2.15087	0.697961	0.002422	0.035666
Alistipes_indistinctus	-2.25561	0.735589	0.002542	0.036966
Eubacterium_sp._YI	-1.06046	0.346712	0.002605	0.037421
Veillonella_seminalis	-6.39904	2.095705	0.002648	0.037584
Prevotella_sp._oral_taxon_299	-4.74509	1.572264	0.002959	0.041495
Bacteroides_helcogenes	1.029002	0.344354	0.003246	0.044319

Enterococcus_sp._6D12_DIV0197	3.062361	1.025735	0.003273	0.044319
Neisseria_sp._GT4A_CT1	-7.97085	2.666363	0.003234	0.044319
Lachnospiraceae_bacterium_1_1_57FAA	-1.26778	0.425598	0.003342	0.044735
Gordonibacter_pamelaeae	-1.79977	0.609281	0.003608	0.047757
Gardnerella_sp._30_4	3.11223	1.057321	0.003725	0.04876

Table S12: Hospitalizations according to ARG patterns using MaAsLin2

AMR Gene family	**Coefficient**	**Std Error**	**p-value**	**q-value**
MELD score	0.416846	0.065426	2.01E-09	2.11E-07
ANT (2)	3.944935	0.969324	7.46E-05	0.004
Hepatic Encephalopathy	0.553297	0.146857	0.0002	0.008
On lactulose	0.578707	0.164193	0.0006	0.015
Llm_23S_ribosomal_RNA_methyltransferase	-1.37914	0.446251	0.0024	0.048
Aminocoumarin resistant parY	-0.65035	0.232716	0.006	0.049
Rifamycin resistant beta-subunit of RNA polymerase (rpoB)	-0.56267	0.23582	0.01	0.050
ARO term	**Coefficient**	**Std Error**	**p-value**	**q-value**
MELD score	0.416846	0.065426	2.01E-09	2.39E-06
dfrA12	5.20263	1.178382	1.88E-05	0.011
ANT(2)_Ia	3.944935	0.969324	7.46E-05	0.017
lnuA	3.741122	0.89308	4.67E-05	0.017
MexE	5.585521	1.359197	6.39E-05	0.017
Hepatic Encephalopathy	0.553297	0.146857	0.000233	0.046
OXY_1_6	5.006226	1.363162	0.00033	0.049
vanVB	3.681022	0.994075	0.000295	0.049
OXY_1_4	4.689606	1.292108	0.000385	0.050
Resistomes	**Coefficient**	**Std Error**	**p-value**	**q-value**
MELD score	0.416846	0.065426	2.01E-09	3.49E-07
Hepatic Encephalopathy	0.553297	0.146857	0.000233	0.020
On lactulose	0.578707	0.164193	0.000557	0.032
Gram negative bacterium	4.221368	1.360246	0.002272	0.046
Nocardia farcinica	-0.6116	0.206644	0.00356	0.049
Streptomyces niveus	-1.50058	0.518148	0.004322	0.049
Citrobacter freundii	1.032339	0.359189	0.004618	0.050
Streptomyces rishiriensis	-0.65035	0.232716	0.005849	0.046

Table S13: DESeq2 Comparison of bacterial species between patients with/without death

Lineage	LOG2FC	Direction	pvalue
Pseudomonas_lundensis	-6.44	Death_1Year_Yes	0.002397
Clostridium_sphenoides	-5.93	Death_1Year_Yes	0.002397
Campylobacter_helveticus	-4.32	Death_1Year_Yes	0.002397
Desulfotomaculum_guttoideum	-2.58	Death_1Year_Yes	0.002397
Lactobacillus_frumenti	-2.32	Death_1Year_Yes	1.19E-07
Asaccharospora_irregularis	-2.32	Death_1Year_Yes	1.57E-05
Aerococcus_sp_HMSC23C02	-2.32	Death_1Year_Yes	0.002397
Neisseria_bacilliformis	-1.58	Death_1Year_Yes	1.57E-05
Colwellia_echini	-1.58	Death_1Year_Yes	0.002397
Lactobacillus_gallinarum	-1.58	Death_1Year_Yes	0.002397
Lactobacillus_parabuchneri	-1.58	Death_1Year_Yes	0.002397
Aerococcus_christensenii	-1	Death_1Year_Yes	0.002397
Bacillus_paralicheniformis	-1	Death_1Year_Yes	0.002397
Butyricimonas_synergistica	-1	Death_1Year_Yes	0.002397
Chryseobacterium_bovis	-1	Death_1Year_Yes	0.002397
Lachnospira_multipara	-1	Death_1Year_Yes	0.002397
Lactobacillus_coleohominis	-1	Death_1Year_Yes	0.002397
Lactobacillus_sp_HMSC078F07	-1	Death_1Year_Yes	0.002397
Neisseria_gonorrhoeae	-1	Death_1Year_Yes	0.002397
Propionibacterium_sp_HMSC067A02	-1	Death_1Year_Yes	0.002397
Lactobacillus_sp_HMSC066G01	1	Death_1Year_No	9.14E-04
Enterococcus_avium	1	Death_1Year_No	0.049566
Oscillibacter_sp_KLE_1745	1.22	Death_1Year_No	0.008788
Bacteroides_helcogenes	1.46	Death_1Year_No	0.043766
Bacteroides_sp_2_1_16	1.49	Death_1Year_No	0.004573
Lactobacillus_fermentum	1.59	Death_1Year_No	0.019971
Veillonella_sp_HPA0037	1.66	Death_1Year_No	0.029392
Bacteroides_caecimuris	1.67	Death_1Year_No	0.013637
Ileibacterium_massiliense	1.68	Death_1Year_No	0.022419
Acetivibrio_ethanolgignens	1.68	Death_1Year_No	0.035462
Streptococcus_sp_HMSC057G03	1.73	Death_1Year_No	0.007257
Lactobacillus_gastricus	1.77	Death_1Year_No	0.007156
Actinomyces_oris	1.77	Death_1Year_No	0.034493
Lactobacillus_plantarum	1.81	Death_1Year_No	8.58E-04
Bacteroides_sp_1_1_30	1.91	Death_1Year_No	0.023112
Parabacteroides_sp_2_1_7	1.92	Death_1Year_No	0.037014
Lactobacillus_antri	1.94	Death_1Year_No	0.004144

Veillonella_atypica	2	Death_1Year_No	0.038635
Streptococcus_anginosus	2.04	Death_1Year_No	0.025737
Streptococcus_sp_HMSC061E03	2.07	Death_1Year_No	0.043553
Lactobacillus_sp_UMNPBX3	2.12	Death_1Year_No	0.023456
Parabacteroides_distasonis	2.18	Death_1Year_No	0.019821
Streptococcus_vestibularis	2.21	Death_1Year_No	0.026362
Enterococcus_faecium	2.27	Death_1Year_No	8.74E-04
Bacteroides_uniformis	2.27	Death_1Year_No	0.04533
Lachnospiraceae_bacterium_5_1_57FAA	2.3	Death_1Year_No	0.038733
Streptococcus_sp_HMSC078H03	2.45	Death_1Year_No	0.045263
Lachnospiraceae_bacterium_3_1_57FAA_CT1	2.46	Death_1Year_No	0.022816
Sellimonas_intestinalis	2.5	Death_1Year_No	0.001221
Lactobacillus_vaginalis	2.53	Death_1Year_No	0.042067
Lactobacillus_johnsonii	3.61	Death_1Year_No	0.027163
Anaerostipes_hadrus	5.41	Death_1Year_No	0.043505
Bifidobacterium_adolescentis	5.58	Death_1Year_No	0.010899
Lachnospira_pectinoschiza	5.82	Death_1Year_No	0.018895
Bacteroides_bouchesdurhonensis	5.83	Death_1Year_No	0.037008
Absiella_dolichum	5.97	Death_1Year_No	0.027067
Neglecta_timonensis	6.88	Death_1Year_No	0.043507

Table S14: MaAsLin2 Comparison of bacterial species between those patients who died within 1 year compared to those who were not

Bacterial species	Coefficient	Std Error	p-value	q-value
Clostridium_sphenoides	8.290692	0.604374	7.31E-29	8.61E-26
Campylobacter_helveticus	8.156014	0.600078	1.63E-28	9.61E-26
Pseudomonas_lundensis	7.664528	0.694685	1.96E-21	7.68E-19
Pseudomonas_stutzeri	6.547608	0.802033	8.88E-14	2.61E-11
Pectobacterium_polaris	7.317731	1.011614	1.81E-11	4.25E-09
Bacillus_paralicheniformis	4.926454	0.724337	1.93E-10	3.38E-08
Desulfotomaculum_guttoideum	7.115187	1.047297	2.01E-10	3.38E-08
Lactobacillus_rossiae	4.758192	0.742356	1.54E-09	2.27E-07
Neisseria_gonorrhoeae	4.508563	0.713589	2.48E-09	3.25E-07
Colwellia_echini	4.665834	0.749125	3.95E-09	4.65E-07
Alcanivorax_hongdengensis	4.836703	0.78729	6.09E-09	6.53E-07
Leptospira_sp._JW3_C_A1	4.77791	0.789937	9.87E-09	9.69E-07
Aerococcus_sp._HMSC23C02	4.898015	0.8239	1.66E-08	1.50E-06
Paeniglutamicibacter_antarcticus	4.723313	0.800015	2.04E-08	1.50E-06
Prevotella_copri	-5.84785	0.98715	1.85E-08	1.50E-06
Propionibacterium_sp._HMSC067A02	4.880055	0.826335	2.02E-08	1.50E-06
Pseudomonas_sp._Ep_R1	5.450812	0.951841	4.90E-08	3.39E-06
MELD score	0.481243	0.10545	9.92E-06	0.000649
Alistipes_indistinctus	-5.70684	1.255507	1.07E-05	0.000664
Gabonia_massiliensis	2.973682	0.674186	1.88E-05	0.001106
Clostridium_butyricum	2.589304	0.605233	3.22E-05	0.001725
Klebsiella_michiganensis	3.741447	0.872796	3.11E-05	0.001725
Barnesiella_intestinihominis	-4.22453	1.009611	4.69E-05	0.002402
Alistipes_ihumii	-3.49826	0.843706	5.45E-05	0.002676
Bacteroides_eggerthii	3.135202	0.778519	8.68E-05	0.004089
Proteus_sp._HMSC10D02	4.950639	1.266186	0.000136	0.006153
Tidjanibacter_massiliensis	-2.72215	0.699378	0.000145	0.006333
Gordonibacter_urolithinfaciens	-2.90821	0.77325	0.000237	0.00995
Clostridium_disporicum	4.510528	1.20907	0.000264	0.01074
Neisseria_bacilliformis	3.48207	0.937241	0.00028	0.010979
Dielma_fastidiosa	-4.63552	1.251799	0.000292	0.011105
Serratia_sp._Leaf51	4.748093	1.292285	0.000324	0.011945
Massilioclostridium_coli	-1.80045	0.501644	0.00044	0.015708
Neglecta_timonensis	-2.58713	0.726337	0.000485	0.016787
Asaccharospora_irregularis	2.733496	0.775377	0.000551	0.018541
Alistipes_putredinis	-2.08029	0.597276	0.000639	0.020899
bacterium_LF_3	-3.15239	0.909875	0.000681	0.021667
Hepatic Encephalopathy	0.640503	0.186403	0.000751	0.023276
Lachnospiraceae_bacterium_5_1_63FAA	-1.66308	0.486888	0.000805	0.024321
Eubacterium_hallii	1.759866	0.517625	0.00085	0.024423
Lactobacillus_ghanensis	3.033717	0.892015	0.000847	0.024423
Paraprevotella_clara	-2.08575	0.619777	0.000956	0.026811

Acidaminococcus_intestini	-2.36197	0.735324	0.001591	0.043591
Eubacterium_sulci	-4.67244	1.45954	0.001649	0.044135
Fusicatenibacter_saccharivorans	-1.33235	0.422874	0.001942	0.049924
Veillonella_sp._3_1_44	2.487249	0.78971	0.001949	0.049924

Table S15: Death according to ARG patterns using MaAsLin2

AMR Gene family	**Coefficient**	**Std Error**	**p-value**	**q-value**
ANT(2)	4.933638	0.800366	5.80E-09	6.09E-07
MELD score	0.488417	0.107213	1.05E-05	0.00055
Hepatic Encephalopathy	0.672385	0.190429	0.000545	0.019066
ARO term	**Coefficient**	**Std Error**	**p-value**	**q-value**
TriB	17.01624	1.941014	2.96E-15	3.52E-12
MexE	6.344279	1.015945	3.85E-09	2.29E-06
ANT(2__)_Ia	4.933638	0.800366	5.80E-09	2.30E-06
dfrA12	6.441504	1.057267	8.34E-09	2.48E-06
tetS	2.921262	0.539251	2.25E-07	5.36E-05
MELD score	0.488417	0.107213	1.05E-05	0.002078
AAC(6)_Ia	4.934291	1.107515	1.59E-05	0.002705
tet(B)	2.372869	0.540336	2.07E-05	0.003077
LnuP	3.637684	0.871269	4.94E-05	0.006526
CfxA6	-3.15404	0.851239	0.000293	0.034839
TEM_48	4.566194	1.254481	0.00037	0.040072
mexM	3.594843	1.00494	0.000463	0.045909
Hepatic Encephalopathy	0.672385	0.190429	0.000545	0.048503
TEM_219	1.777728	0.505381	0.000571	0.048503
Resistomes	**Coefficient**	**Std Error**	**p-value**	**q-value**
MELD score	0.488417	0.107213	1.05E-05	0.001823
Legionella pneumophila	2.136465	0.583204	0.000341	0.019754
uncultured_organism	-3.15404	0.851239	0.000293	0.019754
Hepatic Encephalopathy	0.672385	0.190429	0.000545	0.023696
Gram negative bacterium	3.911547	1.152632	0.000875	0.030437
Desulfitobacterium hafniense	-3.222	0.996429	0.001492	0.043275
On Lactulose	0.630089	0.216487	0.004137	0.088609
Acidaminococcus fermentans	-4.77778	1.66093	0.004583	0.088609
Enterobacter hormaechei	2.013171	0.680997	0.003598	0.088609

TABLE S16: Differences between Type 2 Diabetes and Cirrhosis ARO terms

Lineage	LOG2FC	Direction	pvalue
tetO	14.62	Cirrhosis	1.00E-06
Bifidobacteria_intrinsic_ileS_conferring_resistance_to_mupirocin	14.44	Cirrhosis	1.00E-06
Mef_En2	13.88	Cirrhosis	1.00E-06
adeF	13.65	Cirrhosis	1.00E-06
TEM_83	13.65	Cirrhosis	1.00E-06
ErmF	13.59	Cirrhosis	1.00E-06
sul1	13.01	Cirrhosis	1.00E-06
msbA	12.68	Cirrhosis	1.00E-06
ErmB	12.62	Cirrhosis	1.00E-06
acrB	12.36	Cirrhosis	1.00E-06
CfxA6	12.2	Cirrhosis	1.00E-06
mdtM	12.18	Cirrhosis	1.00E-06
yojI	12	Cirrhosis	1.00E-06
cpxA	11.93	Cirrhosis	1.00E-06
tetM	11.72	Cirrhosis	1.00E-06
Bifidobacterium_adolescentis_rpoB_conferring_resistance_to_rifampicin	11.62	Cirrhosis	1.00E-06
aad_6	11.6	Cirrhosis	1.00E-06
mdtN	11.5	Cirrhosis	1.00E-06
emrB	11.3	Cirrhosis	1.00E-06
dfrF	10.91	Cirrhosis	1.00E-06
Escherichia_coli_mdfA	10.89	Cirrhosis	1.00E-06
CblA_1	10.87	Cirrhosis	1.00E-06
CTX_M_83	10.87	Cirrhosis	1.00E-06
cepA_beta_lactamase	10.67	Cirrhosis	1.00E-06
acrE	10.61	Cirrhosis	1.00E-06
CfxA	10.46	Cirrhosis	1.00E-06
CTX_M_86	10.46	Cirrhosis	1.00E-06
bacA	10.43	Cirrhosis	1.00E-06
mdtH	10.35	Cirrhosis	1.00E-06
CTX_M_16	10.32	Cirrhosis	1.00E-06
CTX_M_50	10.32	Cirrhosis	1.00E-06
aadA12	10.15	Cirrhosis	1.00E-06
cdeA	10.15	Cirrhosis	1.00E-06
QnrB8	10.15	Cirrhosis	1.00E-06
CfxA4	9.97	Cirrhosis	1.00E-06
CTX_M_9	9.97	Cirrhosis	1.00E-06
dfrA15	9.97	Cirrhosis	1.00E-06

mdtO	9.97	Cirrhosis	1.00E-06
CfxA2	9.7	Cirrhosis	1.00E-06
CTX_M_87	9.7	Cirrhosis	1.00E-06
cmx	9.69	Cirrhosis	1.00E-06
mdtC	9.69	Cirrhosis	1.00E-06
acrS	9.36	Cirrhosis	1.00E-06
TEM_80	9.36	Cirrhosis	1.00E-06
gadW	9.17	Cirrhosis	1.00E-06
pmrF	9	Cirrhosis	1.00E-06
oleB	8.94	Cirrhosis	1.00E-06
Klebsiella_pneumoniae_acrA	8.92	Cirrhosis	1.00E-06
SHV_155	8.81	Cirrhosis	1.00E-06
lsaC	8.66	Cirrhosis	1.79E-06
MexC	8.65	Cirrhosis	1.00E-06
ANT_6_Ia	8.56	Cirrhosis	1.00E-06
tet32	8.49	Cirrhosis	1.00E-06
tetU	8.41	Cirrhosis	1.00E-06
vanSD	8.27	Cirrhosis	1.00E-06
vanRG	8.23	Cirrhosis	1.00E-06
vanRD	8.22	Cirrhosis	1.00E-06
OprN	8.2	Cirrhosis	1.00E-06
APH_3_IIb	8.2	Cirrhosis	1.00E-06
TEM_157	8.19	Cirrhosis	1.00E-06
CfxA5	8.02	Cirrhosis	1.00E-06
CTX_M_90	8.02	Cirrhosis	1.00E-06
emrA	8.01	Cirrhosis	1.00E-06
aadA16	7.98	Cirrhosis	1.00E-06
PDC_3	7.81	Cirrhosis	1.00E-06
NmcA_beta_lactamase	7.8	Cirrhosis	1.00E-06
SHV_126	7.77	Cirrhosis	1.00E-06
AAC_3_Ib	7.7	Cirrhosis	1.00E-06
efmA	7.65	Cirrhosis	2.46E-06
vanD	7.51	Cirrhosis	0.022647
CMY_71	7.36	Cirrhosis	1.00E-06
CTX_M_117	7.36	Cirrhosis	1.00E-06
aadS	7.3	Cirrhosis	1.00E-06
TEM_40	7.28	Cirrhosis	1.09E-06
DES_1	7.26	Cirrhosis	1.00E-06
Enterobacter_cloacae_acrA	7.26	Cirrhosis	1.00E-06

mdtK	7.23	Cirrhosis	1.00E-06
ramA	7.04	Cirrhosis	1.00E-06
emeA	7.01	Cirrhosis	0.004884
aadA5	7	Cirrhosis	1.76E-05
TEM_6	7	Cirrhosis	1.76E-05
ErmC	6.97	Cirrhosis	1.00E-06
arlS	6.89	Cirrhosis	1.00E-06
TEM_95	6.89	Cirrhosis	1.00E-06
adeS	6.85	Cirrhosis	3.54E-05
efrA	6.85	Cirrhosis	3.54E-05
tolC	6.79	Cirrhosis	1.00E-06
Klebsiella_pneumoniae_KpnE	6.74	Cirrhosis	1.00E-06
catA8	6.67	Cirrhosis	1.00E-06
gadX	6.67	Cirrhosis	1.00E-06
Escherichia_coli_ampC	6.63	Cirrhosis	1.00E-06
Pseudomonas_aeruginosa_CpxR	6.57	Cirrhosis	6.10E-05
adeB	6.51	Cirrhosis	1.00E-06
TEM_81	6.51	Cirrhosis	1.00E-06
TEM_1	6.32	Cirrhosis	6.70E-04
MexA	6.29	Cirrhosis	1.07E-06
TEM_219	6.21	Cirrhosis	0.001353
APH_2_Ig	6.04	Cirrhosis	0.003131
cmlA6	5.95	Cirrhosis	1.00E-06
mdtA	5.95	Cirrhosis	1.00E-06
tetB_46	5.86	Cirrhosis	1.00E-06
ugd	5.84	Cirrhosis	1.00E-06
oqxB	5.82	Cirrhosis	1.00E-06
pmrA	5.78	Cirrhosis	3.70E-06
AAC_6_Ib3	5.76	Cirrhosis	1.79E-06
AAC_6_Im	5.76	Cirrhosis	1.79E-06
TEM_206	5.7	Cirrhosis	0.012626
catI	5.68	Cirrhosis	1.00E-06
TaeA	5.67	Cirrhosis	1.00E-06
TEM_217	5.67	Cirrhosis	1.00E-06
Escherichia_coli_acrA	5.61	Cirrhosis	1.00E-06
mexN	5.57	Cirrhosis	1.00E-06
vanRF	5.32	Cirrhosis	0.048336
TEM_178	5.3	Cirrhosis	7.45E-04
TEM_57	5.3	Cirrhosis	7.45E-04

APH_2_IIIa	5.17	Cirrhosis	6.29E-04
APH_3_Ia	5.17	Cirrhosis	6.29E-04
APH_6_Ic	5.16	Cirrhosis	4.87E-05
Tet_X3	5.15	Cirrhosis	1.00E-06
CfxA3	5.11	Cirrhosis	1.00E-06
patB	4.98	Cirrhosis	1.00E-06
RlmA_II	4.77	Cirrhosis	1.61E-05
TriC	4.73	Cirrhosis	1.01E-06
Klebsiella_pneumoniae_KpnH	4.57	Cirrhosis	1.00E-06
aadA	4.54	Cirrhosis	3.77E-05
TEM_33	4.54	Cirrhosis	3.77E-05
patA	4.53	Cirrhosis	1.00E-06
mexJ	4.52	Cirrhosis	1.06E-06
vanXYG	4.47	Cirrhosis	2.70E-06
PC1_beta_lactamase_blaZ	4.47	Cirrhosis	2.86E-05
mexK	4.45	Cirrhosis	1.00E-06
vanSA	4.19	Cirrhosis	1.00E-04
evgA	4.14	Cirrhosis	1.00E-06
mexW	3.99	Cirrhosis	1.01E-06
Klebsiella_pneumoniae_OmpK37	3.94	Cirrhosis	1.00E-06
MuxC	3.93	Cirrhosis	1.00E-06
srmB	3.66	Cirrhosis	1.00E-06
msrC	3.65	Cirrhosis	1.00E-06
Tet_X4	3.63	Cirrhosis	1.00E-06
smeR	3.62	Cirrhosis	5.15E-05
mexH	3.55	Cirrhosis	1.00E-06
Pseudomonas_aeruginosa_soxR	3.55	Cirrhosis	0.043554
Erm_35	3.54	Cirrhosis	1.87E-04
emrK	3.51	Cirrhosis	1.00E-06
efpA	3.48	Cirrhosis	1.00E-06
vanRA	3.42	Cirrhosis	4.46E-05
mphA	3.4	Cirrhosis	2.90E-06
AxyY	3.33	Cirrhosis	1.03E-06
EreA2	3.27	Cirrhosis	0.03659
aadA24	3.22	Cirrhosis	9.07E-04
TEM_53	3.22	Cirrhosis	9.07E-04
Streptomyces_rishiriensis_parY_mutant_ conferring_resistance_to_aminocoumarin	3.16	Cirrhosis	1.00E-06
macB	3.11	Cirrhosis	1.00E-06
mel	3.05	Cirrhosis	1.00E-06

otr_A	2.96	Cirrhosis	0.005336
vanXD	2.93	Cirrhosis	0.001084
msrE	2.92	Cirrhosis	4.08E-06
lmrD	2.92	Cirrhosis	0.040443
APH_3_IIIa	2.86	Cirrhosis	1.02E-06
tetX	2.83	Cirrhosis	1.00E-06
Nocardia_rifampin_resistant_beta_subunit_of_RNA_polymerase_rpoB2	2.8	Cirrhosis	1.00E-06
SAT_4	2.75	Cirrhosis	1.51E-06
mexI	2.69	Cirrhosis	1.00E-06
CTX_M_76	2.67	Cirrhosis	8.37E-06
MuxB	2.62	Cirrhosis	1.88E-06
catS	2.57	Cirrhosis	1.47E-06
vanI	2.48	Cirrhosis	3.07E-06
TEM_102	2.38	Cirrhosis	0.006295
tlrC	2.31	Cirrhosis	1.40E-06
LlmA_23S_ribosomal_RNA_methyltransferase	2.29	Cirrhosis	0.001588
MexB	2.25	Cirrhosis	5.01E-06
MexD	2.06	Cirrhosis	3.75E-04
adeK	2.04	Cirrhosis	0.037499
AAC_3_IIb	2.02	Cirrhosis	1.02E-06
smeF	1.95	Cirrhosis	0.04268
tetA_46	1.93	Cirrhosis	0.010021
mtrD	1.87	Cirrhosis	0.001932
vanTG	1.87	Cirrhosis	0.017352
smeE	1.86	Cirrhosis	4.11E-05
evgS	1.84	Cirrhosis	6.55E-06
kdpE	1.82	Cirrhosis	1.55E-06
SHV_11	1.69	Cirrhosis	0.043402
OXA_184	1.66	Cirrhosis	0.032493
tet_C	1.65	Cirrhosis	0.034882
SAT_1	1.56	Cirrhosis	0.013294
arnA	1.51	Cirrhosis	0.00664
qepA	1.38	Cirrhosis	0.033017
tetW	1.16	Cirrhosis	0.042933
tet_W_N_W	1.12	Cirrhosis	0.023633
ACI_1	1.11	Cirrhosis	1.00E-06
APH_6_Id	-1.1	T2D	1.00E-06
mphE	-1.22	T2D	1.00E-06
sul2	-1.23	T2D	1.00E-06

AAC_6_Ib7	-1.25	T2D	7.30E-05
lsaE	-1.26	T2D	0.007313
Enterococcus_faecalis_chloramphenicol_acetyltransferase	-1.27	T2D	1.25E-04
AAC_3_IIe	-1.31	T2D	4.14E-06
mexQ	-1.74	T2D	1.00E-06
TEM_47	-1.77	T2D	0.004306
sdiA	-1.87	T2D	1.00E-06
FosA5	-1.93	T2D	1.00E-06
Erm_49	-1.96	T2D	0.004757
catP	-1.98	T2D	2.19E-06
AAC_3_IIc	-2	T2D	3.86E-06
smeB	-2.23	T2D	1.00E-06
AAC_3_IId	-2.29	T2D	1.00E-06
OXA_209	-2.31	T2D	1.00E-06
lmrC	-2.33	T2D	1.08E-06
floR	-2.4	T2D	1.87E-06
LnuP	-2.46	T2D	0.023913
Escherichia_coli_ampC1_beta_lactamase	-2.62	T2D	1.00E-06
ErmT	-2.67	T2D	1.00E-06
MuxA	-2.71	T2D	1.00E-06
cmlA1	-2.81	T2D	0.001553
mdsA	-2.81	T2D	0.001553
TEM_110	-2.87	T2D	1.00E-06
ErmQ	-3.13	T2D	0.011063
vanHD	-3.42	T2D	1.00E-06
vanRC	-3.44	T2D	1.00E-06
novA	-3.45	T2D	1.00E-06
OXA_347	-3.49	T2D	1.00E-06
aadA3	-3.54	T2D	5.98E-05
vanRE	-3.58	T2D	0.007747
vanRM	-3.67	T2D	1.02E-06
FosA6	-3.92	T2D	1.00E-06
CMY_9	-4.03	T2D	1.00E-06
arr_3	-4.3	T2D	1.00E-06
opmE	-4.5	T2D	1.00E-06
APH_2_If	-4.6	T2D	1.00E-06
CTX_M_141	-4.62	T2D	1.00E-06
dfrA32	-4.73	T2D	9.21E-05
Escherichia_coli_emrE	-4.8	T2D	1.00E-06

CTX_M_66	-4.92	T2D	1.00E-06
aadA13	-5.83	T2D	1.00E-06
rmtF	-6.41	T2D	1.00E-06
tetB_60	-6.49	T2D	1.00E-06
mtrA	-6.67	T2D	1.00E-06
vmlR	-6.9	T2D	1.00E-06
mtrC	-7.05	T2D	1.00E-06
lnuF	-7.58	T2D	1.00E-06
CcrA_beta_lactamase	-7.6	T2D	3.82E-04
salA	-8.27	T2D	1.00E-06
LEN_34	-8.45	T2D	1.00E-06
rphA	-8.8	T2D	1.00E-06
catII_from_Escherichia_coli_K_12	-8.83	T2D	1.00E-06
FosA4	-8.83	T2D	1.00E-06
CTX_M_77	-9.02	T2D	1.00E-06
DHA_17	-9.09	T2D	1.00E-06
vanXB	-9.24	T2D	1.00E-06
DHA_15	-9.43	T2D	1.00E-06
dfrA19	-9.46	T2D	1.00E-06
smeA	-9.77	T2D	1.00E-06
dfrA7	-10.07	T2D	1.00E-06
DHA_12	-10.21	T2D	1.00E-06
CMY_117	-11.88	T2D	1.00E-06

Table S17: AMR Gene Family differences Type 2 Diabetes vs Cirrhosis

Lineage	LOG2FC	Direction	pvalue
Erm_23S_ribosomal_RNA_methyltransferase	14.34	Cirrhosis	1.00E-06
CfxA_beta_lactamase	14.25	Cirrhosis	1.00E-06
ABC_F_ATP_binding_cassette_ribosomal_protection_protein	13.4	Cirrhosis	1.00E-06
pmr_phosphoethanolamine_transferase	13.06	Cirrhosis	1.00E-06
APH_2	12.81	Cirrhosis	1.00E-06
sulfonamide_resistant_sul	12.57	Cirrhosis	1.00E-06
aminocoumarin_resistant_parY	12.27	Cirrhosis	1.00E-06
trimethoprim_resistant_dihydrofolate_reductase_dfr	11.86	Cirrhosis	1.00E-06
lincosamide_nucleotidyltransferase_LNU	11.7	Cirrhosis	1.00E-06
chloramphenicol_acetyltransferase_CAT	10.89	Cirrhosis	1.00E-06
ANT_3	10.88	Cirrhosis	1.00E-06
ciprofloxacin_phosphotransferase	9.8	Cirrhosis	1.00E-06
macrolide_phosphotransferase_MPH	9.8	Cirrhosis	1.00E-06
kdpDE	9.66	Cirrhosis	1.00E-06
OXA_beta_lactamase	9.31	Cirrhosis	1.00E-06
vanY	9.1	Cirrhosis	0.024397
fosfomycin_thiol_transferase	8.31	Cirrhosis	1.00E-06
VIM_beta_lactamase	8.31	Cirrhosis	1.00E-06
PDC_beta_lactamase	8.07	Cirrhosis	1.00E-06
NmcA_beta_lactamase	7.99	Cirrhosis	1.00E-06
SHV_beta_lactamase	5.79	Cirrhosis	1.00E-06
antibiotic_resistant_isoleucyl_tRNA_synthetase_ileS	5.63	Cirrhosis	1.00E-06
CARB_beta_lactamase	5.33	Cirrhosis	4.26E-05
CMY_beta_lactamase	5.33	Cirrhosis	4.26E-05
vanX	5.23	Cirrhosis	0.001235
rifamycin_resistant_beta_subunit_of_RNA_polymerase_rpoB	5.15	Cirrhosis	1.00E-06
tetracycline_resistant_ribosomal_protection_protein	4.95	Cirrhosis	1.00E-06
non_erm_23S_ribosomal_RNA_methyltransferase_G748	4.89	Cirrhosis	2.14E-06
resistance_nodulation_cell_division_RND_antibiotic_efflux_pump	4.68	Cirrhosis	1.00E-06
APH_6	4.53	Cirrhosis	1.00E-06
vanS	4.34	Cirrhosis	1.00E-06
multidrug_and_toxic_compound_extrusion_MATE_transporter	3.63	Cirrhosis	1.00E-06
ACI_beta_lactamase	3.36	Cirrhosis	1.05E-06
ATP_binding_cassette_ABC_antibiotic_efflux_pump	3.21	Cirrhosis	1.00E-06
RbpA_bacterial_RNA_polymerase_binding_protein	2.86	Cirrhosis	0.016622
Llm_23S_ribosomal_RNA_methyltransferase	2.85	Cirrhosis	5.68E-05
tetracycline_inactivation_enzyme	2.74	Cirrhosis	1.02E-06
glycopeptide_resistance_gene_cluster	2.41	Cirrhosis	1.87E-05
cepA_beta_lactamase	2.3	Cirrhosis	0.008537
ANT_6	1.65	Cirrhosis	5.48E-05
AAC_3	1.1	Cirrhosis	0.028115
macrolide_esterase	-1.64	T2D	1.00E-06
vanZ	-2.01	T2D	1.00E-06

CcrA_beta_lactamase	-2.83	T2D	8.27E-04
APH_4	-3.94	T2D	1.00E-06
vanW	-4.29	T2D	1.00E-06
SRT_beta_lactamase	-4.92	T2D	1.00E-06
undecaprenyl_pyrophosphate_related_proteins	-5.46	T2D	1.00E-06
CepS_beta_lactamase	-6.76	T2D	1.00E-06
rifampin_phosphotransferase	-6.81	T2D	1.00E-06
rifampin_ADP_ribosyltransferase_Arr	-7.94	T2D	1.00E-06
ACC_beta_lactamase	-9.81	T2D	1.00E-06

Table S18: Resistomes Type 2 Diabetes vs Cirrhosis

Lineage	LOG2FC	Direction	pvalue
Bifidobacterium_adolescentis	15.31	Cirrhosis	1.00E-06
Campylobacter_jejuni	14.77	Cirrhosis	1.00E-06
Enterococcus_faecium	14.29	Cirrhosis	1.00E-06
Klebsiella_pneumoniae	14.26	Cirrhosis	1.00E-06
Enterobacter_hormaechei	13.17	Cirrhosis	1.00E-06
Campylobacter_coli	13.14	Cirrhosis	1.00E-06
uncultured_bacterium	12.99	Cirrhosis	1.00E-06
Transposon_Tn4551	12.89	Cirrhosis	1.00E-06
Enterobacter_asburiae	12.2	Cirrhosis	1.00E-06
Streptococcus_australis	12.19	Cirrhosis	1.00E-06
Brucella_melitensis	11.95	Cirrhosis	1.00E-06
Butyrivibrio_fibrisolvens	11.95	Cirrhosis	1.00E-06
Streptococcus_agalactiae	11.95	Cirrhosis	1.00E-06
Prevotella_intermedia	11.72	Cirrhosis	1.00E-06
Shigella_sp	10.38	Cirrhosis	1.00E-06
Streptococcus_pyogenes	10.38	Cirrhosis	1.00E-06
Macrococcus_caseolyticus	9.97	Cirrhosis	1.00E-06
Neisseria_gonorrhoeae	9.97	Cirrhosis	1.00E-06
Pseudomonas_sp	9.58	Cirrhosis	1.00E-06
Shigella_sonnei	9.58	Cirrhosis	1.00E-06
Campylobacter_fetus	9.44	Cirrhosis	1.00E-06
Streptomyces_ambofaciens	8.5	Cirrhosis	1.00E-06
Plasmid_pNG2	8.29	Cirrhosis	1.17E-05
Proteus_mirabilis	8.27	Cirrhosis	0.022835
Parabacteroides_distasonis	7.9	Cirrhosis	1.00E-06
Bacteroides_coprosuis	7.55	Cirrhosis	1.00E-06
Desulfitobacterium_hafniense	7.39	Cirrhosis	1.01E-06
Bifidobacterium_bifidum	7.18	Cirrhosis	1.00E-06
Klebsiella_aerogenes	6.49	Cirrhosis	1.25E-06
Mycobacterium_tuberculosis	6.45	Cirrhosis	1.00E-06
Klebsiella_sp	6.19	Cirrhosis	2.73E-06
Haemophilus_parainfluenzae	6.02	Cirrhosis	0.020293
Staphylococcus_pseudintermedius	5.39	Cirrhosis	0.035511
Vibrio_parahaemolyticus	5.18	Cirrhosis	1.00E-06
Klebsiella_oxytoca	4.78	Cirrhosis	1.00E-06
Paenibacillus_sp	4.5	Cirrhosis	1.00E-06
Salmonella_enterica	4.47	Cirrhosis	1.00E-06
Streptococcus_oralis	4.19	Cirrhosis	3.51E-06
Pseudomonas_fluorescens	3.93	Cirrhosis	1.00E-06
Achromobacter_insuavis	3.64	Cirrhosis	1.42E-06
Streptomyces_niveus	2.96	Cirrhosis	2.23E-05
Streptomyces_rimosus	2.64	Cirrhosis	0.008216
Nocardia_farcinica	2.57	Cirrhosis	1.00E-06

Acinetobacter_nosocomialis	2.55	Cirrhosis	1.00E-06
Streptomyces_antibioticus	2.52	Cirrhosis	1.00E-06
Citrobacter_youngae	2.22	Cirrhosis	0.007497
Streptomyces_fradiae	2.14	Cirrhosis	3.54E-06
Serratia_marcescens	2.1	Cirrhosis	3.13E-05
Stenotrophomonas_maltophilia	1.59	Cirrhosis	7.41E-06
Clostridioides_difficile	1.54	Cirrhosis	2.94E-04
Haemophilus_influenzae	1.49	Cirrhosis	0.017403
mixed_culture	1.28	Cirrhosis	0.02752
Enterococcus_faecalis	1.05	Cirrhosis	0.045903
Shigella_dysenteriae	-1.28	T2D	1.02E-06
Citrobacter_amalonaticus	-1.33	T2D	1.00E-06
Enterococcus_casseliflavus	-1.62	T2D	2.28E-04
Citrobacter_freundii	-1.63	T2D	1.00E-06
Vibrio_cholerae	-2.57	T2D	1.00E-06
Proteobacteria	-3.2	T2D	0.001385
Plasmid_pGT633	-3.64	T2D	1.00E-06
Lactococcus_lactis	-3.67	T2D	1.00E-06
Mycolicibacterium_smegmatis	-3.75	T2D	0.045636
Vibrio_anguillarum	-4.19	T2D	1.70E-06
Francisella_tularensis	-4.57	T2D	1.00E-06
Pantoea_agglomerans	-4.78	T2D	9.43E-05
Enterococcus_gallinarum	-4.85	T2D	1.00E-06
Rhodococcus_hoagii	-5.21	T2D	1.00E-06
Staphylococcus_sciuri	-5.87	T2D	1.00E-06
Citrobacter_braakii	-6.3	T2D	1.00E-06
Aeromonas_salmonicida	-6.95	T2D	1.00E-06
Legionella_pneumophila	-7.83	T2D	1.00E-06
Geobacillus_stearothermophilus	-7.89	T2D	1.00E-06
Proteus_vulgaris	-8.2	T2D	1.00E-06
Brachyspira_pilosicoli	-11.9	T2D	1.00E-06

Table S19: Differences between CKD and Cirrhosis ARO terms

Lineage	LOG2FC	Direction	pvalue
Bifidobacterium_adolescentis_rpoB_ conferring_resistance_to_rifampicin	15.52	Cirrhosis	1.00E-06
adeF	14.65	Cirrhosis	1.00E-06
Mef_En2	13.87	Cirrhosis	1.00E-06
ErmF	13.6	Cirrhosis	1.00E-06
acrD	12.23	Cirrhosis	1.00E-06
aad_6	11.67	Cirrhosis	1.00E-06
CfxA5	11.6	Cirrhosis	1.00E-06
Escherichia_coli_ampC1_beta_lactamase	11.49	Cirrhosis	1.00E-06
Tet_X3	11.16	Cirrhosis	1.00E-06
cdeA	11.09	Cirrhosis	1.00E-06
Tet_X4	11.07	Cirrhosis	1.00E-06
cepA_beta_lactamase	10.7	Cirrhosis	1.00E-06
APH_3_Ib	10.59	Cirrhosis	1.00E-06
baeS	10.56	Cirrhosis	1.00E-06
mexH	10.46	Cirrhosis	1.00E-06
bacA	10.43	Cirrhosis	1.00E-06
acrS	10.38	Cirrhosis	1.00E-06
QnrB8	10.11	Cirrhosis	1.00E-06
SAT_4	10.03	Cirrhosis	1.00E-06
aadA8b	9.84	Cirrhosis	1.00E-06
catI	9.56	Cirrhosis	1.00E-06
Escherichia_coli_emrE	9.38	Cirrhosis	1.00E-06
arnA	8.73	Cirrhosis	1.00E-06
MexC	8.73	Cirrhosis	1.00E-06
TEM_205	8.69	Cirrhosis	1.00E-06
ANT_6_Ia	8.6	Cirrhosis	1.00E-06
mexN	8.19	Cirrhosis	1.00E-06
APH_3_IIb	8.14	Cirrhosis	1.00E-06
OprN	8.07	Cirrhosis	1.00E-06
NmcA_beta_lactamase	7.89	Cirrhosis	1.00E-06
PDC_3	7.86	Cirrhosis	1.00E-06
AAC_3_Ib	7.79	Cirrhosis	1.00E-06
SHV_126	7.76	Cirrhosis	1.02E-06
SHV_160	7.67	Cirrhosis	1.49E-06
TriC	7.49	Cirrhosis	1.10E-06
aadA24	7.48	Cirrhosis	2.79E-04

MexA	7.47	Cirrhosis	1.33E-06
mexJ	7.44	Cirrhosis	1.31E-06
catS	7.42	Cirrhosis	1.00E-06
opmE	7.41	Cirrhosis	3.65E-06
lsaA	7.31	Cirrhosis	0.014443
SHV_155	7.26	Cirrhosis	1.00E-06
LlmA_23S_ribosomal_RNA_methyltransferase	7.1	Cirrhosis	8.14E-06
CTX_M_76	6.64	Cirrhosis	0.00859
arlS	6.56	Cirrhosis	1.00E-06
APH_6_Ic	6.55	Cirrhosis	0.001035
tetA_46	6.53	Cirrhosis	1.00E-06
Pseudomonas_aeruginosa_CpxR	6.48	Cirrhosis	8.63E-04
adeB	6.45	Cirrhosis	1.03E-06
lsaC	6.42	Cirrhosis	1.51E-04
catB3	6.39	Cirrhosis	0.00182
tetS	6.39	Cirrhosis	0.003276
AxyY	6.37	Cirrhosis	1.00E-06
adeK	6.36	Cirrhosis	0.002129
TEM_1	6.3	Cirrhosis	0.002913
TEM_76	6.21	Cirrhosis	0.004798
SRT_2	6.17	Cirrhosis	0.004426
RlmA_II	6.12	Cirrhosis	6.96E-06
MexF	5.98	Cirrhosis	0.009169
tetB_46	5.91	Cirrhosis	1.00E-06
smeF	5.86	Cirrhosis	0.016748
QnrS1	5.83	Cirrhosis	0.021289
efmA	5.82	Cirrhosis	5.21E-04
TEM_219	5.81	Cirrhosis	0.022222
ACI_1	5.79	Cirrhosis	1.00E-06
ErmC	5.76	Cirrhosis	1.00E-06
tlrC	5.75	Cirrhosis	1.00E-06
mexK	5.74	Cirrhosis	1.00E-06
lmrC	5.7	Cirrhosis	0.030325
vanRC	5.69	Cirrhosis	2.96E-04
patB	5.67	Cirrhosis	1.02E-06
OprJ	5.67	Cirrhosis	0.030499
efrB	5.53	Cirrhosis	0.001353
TaeA	5.51	Cirrhosis	1.02E-06
MuxC	5.43	Cirrhosis	1.00E-06

patA	5.43	Cirrhosis	1.00E-06
aadS	5.42	Cirrhosis	1.00E-06
smeR	5.27	Cirrhosis	1.84E-04
pmrA	5.1	Cirrhosis	9.86E-05
mexQ	5.06	Cirrhosis	1.00E-06
MexB	5.03	Cirrhosis	1.00E-06
MexD	5.03	Cirrhosis	1.10E-06
Enterobacter_cloacae_acrA	4.96	Cirrhosis	1.22E-06
srmB	4.87	Cirrhosis	1.00E-06
mexI	4.87	Cirrhosis	1.00E-06
dfrA17	4.83	Cirrhosis	1.00E-06
mtrD	4.83	Cirrhosis	1.28E-06
KPC_12	4.81	Cirrhosis	0.029381
OXY_4_1	4.81	Cirrhosis	0.029381
PC1_beta_lactamase_blaZ	4.77	Cirrhosis	3.30E-04
smeS	4.68	Cirrhosis	0.004563
lmrD	4.67	Cirrhosis	0.039248
efrA	4.65	Cirrhosis	0.004939
tetU	4.44	Cirrhosis	1.00E-06
carA	4.44	Cirrhosis	0.002335
RbpA	4.44	Cirrhosis	0.023937
Nocardia_rifampin_resistant_beta_ subunit_of_RNA_polymerase_rpoB2	4.42	Cirrhosis	1.00E-06
otr_A	4.36	Cirrhosis	0.003221
mexY	4.32	Cirrhosis	0.027566
vanRD	4.29	Cirrhosis	1.05E-06
smeE	4.26	Cirrhosis	1.00E-06
MuxB	4.18	Cirrhosis	1.02E-06
tetX	4.14	Cirrhosis	1.00E-06
smeB	4.1	Cirrhosis	1.00E-06
oleB	4.02	Cirrhosis	1.00E-06
AAC_3_IIb	3.99	Cirrhosis	1.00E-06
novA	3.97	Cirrhosis	6.17E-04
AAC_6_Im	3.96	Cirrhosis	4.61E-04
macB	3.94	Cirrhosis	1.00E-06
CTX_M_50	3.92	Cirrhosis	1.00E-06
vanSA	3.9	Cirrhosis	0.007172
Streptomyces_rishiriensis_parY_mutant_ conferring_resistance_to_aminocoumarin	3.89	Cirrhosis	1.00E-06
efpA	3.87	Cirrhosis	1.00E-06

msrC	3.83	Cirrhosis	1.00E-06
mexW	3.82	Cirrhosis	1.77E-06
vanSD	3.82	Cirrhosis	1.77E-05
ramA	3.66	Cirrhosis	9.52E-06
msrE	3.65	Cirrhosis	5.88E-05
MuxA	3.57	Cirrhosis	1.27E-06
vanXD	3.55	Cirrhosis	0.038097
Bifidobacteria_intrinsic_ileS_ conferring_resistance_to_mupirocin	3.53	Cirrhosis	1.00E-06
EreA2	3.53	Cirrhosis	0.016658
CblA_1	3.51	Cirrhosis	1.00E-06
mphE	3.44	Cirrhosis	1.00E-06
vanHD	3.44	Cirrhosis	0.041956
OXA_184	3.43	Cirrhosis	4.62E-04
tet_C	3.42	Cirrhosis	2.86E-06
vanRA	3.4	Cirrhosis	0.001503
vanD	3.4	Cirrhosis	0.048939
FosA5	3.33	Cirrhosis	0.006181
msbA	3.31	Cirrhosis	1.00E-06
Klebsiella_pneumoniae_KpnE	3.3	Cirrhosis	1.00E-06
CTX_M_69	3.3	Cirrhosis	0.024235
mel	3.29	Cirrhosis	1.00E-06
qepA	3.26	Cirrhosis	6.75E-06
FosA6	3.25	Cirrhosis	8.44E-04
vanXYG	3.21	Cirrhosis	0.002331
tetW	3.2	Cirrhosis	1.00E-06
Klebsiella_pneumoniae_KpnH	3.18	Cirrhosis	1.00E-06
oqxA	3.18	Cirrhosis	2.94E-06
CRP	3.13	Cirrhosis	1.00E-06
vanI	3.12	Cirrhosis	1.64E-05
baeR	3.1	Cirrhosis	1.00E-06
ugd	3.09	Cirrhosis	1.00E-06
Klebsiella_pneumoniae_KpnG	3.06	Cirrhosis	1.16E-06
mdtB	3.05	Cirrhosis	1.00E-06
SHV_11	3.04	Cirrhosis	0.011778
CfxA6	3.03	Cirrhosis	3.30E-06
acrB	3.01	Cirrhosis	1.00E-06
Escherichia_coli_ampC	3	Cirrhosis	1.00E-06
CTX_M_117	2.97	Cirrhosis	9.14E-05
Klebsiella_pneumoniae_acrA	2.96	Cirrhosis	4.13E-05

dfrA14	2.96	Cirrhosis	0.033072
SAT_1	2.95	Cirrhosis	2.74E-04
mdtO	2.86	Cirrhosis	1.00E-06
APH_3_IIIa	2.86	Cirrhosis	1.00E-06
mdtA	2.86	Cirrhosis	1.01E-06
mdtK	2.81	Cirrhosis	1.08E-06
sdiA	2.79	Cirrhosis	0.005375
emrB	2.77	Cirrhosis	1.44E-06
Escherichia_coli_ampH	2.76	Cirrhosis	1.21E-06
tolC	2.75	Cirrhosis	1.20E-06
H_NS	2.73	Cirrhosis	1.24E-06
Klebsiella_pneumoniae_OmpK37	2.73	Cirrhosis	2.33E-06
Escherichia_coli_mdfA	2.71	Cirrhosis	1.27E-06
mdtP	2.7	Cirrhosis	2.65E-06
cpxA	2.69	Cirrhosis	1.38E-06
emrR	2.67	Cirrhosis	1.05E-06
mdtG	2.67	Cirrhosis	2.64E-06
aadA16	2.61	Cirrhosis	0.00221
mdtE	2.58	Cirrhosis	2.80E-05
CfxA	2.57	Cirrhosis	2.35E-06
TEM_157	2.57	Cirrhosis	3.45E-04
AAC_6_Ib10	2.55	Cirrhosis	0.02211
Escherichia_coli_acrA	2.54	Cirrhosis	8.86E-06
Erm_35	2.54	Cirrhosis	0.013394
tet_W_N_W	2.51	Cirrhosis	1.00E-06
CfxA2	2.51	Cirrhosis	6.53E-06
CfxA4	2.51	Cirrhosis	6.70E-06
pmrF	2.51	Cirrhosis	9.06E-06
Klebsiella_pneumoniae_KpnF	2.5	Cirrhosis	6.93E-05
mdtF	2.49	Cirrhosis	4.88E-05
tetM	2.43	Cirrhosis	4.37E-06
acrE	2.39	Cirrhosis	8.45E-05
marA	2.39	Cirrhosis	1.67E-04
tetQ	2.37	Cirrhosis	2.21E-06
APH_3_Ia	2.36	Cirrhosis	0.016164
tetO	2.34	Cirrhosis	2.67E-06
lnuC	2.33	Cirrhosis	4.23E-04
mdtH	2.31	Cirrhosis	9.90E-05
emrA	2.31	Cirrhosis	2.84E-04

eptA	2.28	Cirrhosis	3.33E-04
kdpE	2.21	Cirrhosis	1.63E-06
CfxA3	2.21	Cirrhosis	2.90E-04
mdtC	2.18	Cirrhosis	1.80E-04
acrF	2.12	Cirrhosis	0.00141
mdtM	2.09	Cirrhosis	0.003141
ANT_3_IIa	2.09	Cirrhosis	0.016791
TEM_40	2.05	Cirrhosis	0.037867
mdtN	2.04	Cirrhosis	0.004039
ErmG	2.02	Cirrhosis	0.011967
TEM_116	1.98	Cirrhosis	0.025737
tet_D	1.98	Cirrhosis	0.026618
gadX	1.81	Cirrhosis	0.010844
evgS	1.7	Cirrhosis	0.035113
lsaE	-1	CKD	0.028029
AAC_3_IIc	-1.09	CKD	0.032367
OXA_347	-1.2	CKD	1.01E-06
yojI	-1.35	CKD	1.00E-06
TEM_102	-1.64	CKD	1.00E-06
CTX_M_141	-2.09	CKD	0.005648
sul1	-2.5	CKD	1.00E-06
SHV_99	-2.91	CKD	0.009639
CMY_9	-3.14	CKD	2.58E-04
LnuP	-3.17	CKD	3.44E-05
ErmQ	-3.94	CKD	9.49E-05
SHV_46	-4.29	CKD	6.32E-04
OKP_B_5	-4.39	CKD	4.45E-04
MCR_1_4	-4.9	CKD	1.05E-06
ACT_32	-5.19	CKD	1.00E-06
npmA	-5.63	CKD	1.98E-05
APH_2_If	-6.81	CKD	1.00E-06
Sed1_beta_lactamase	-6.88	CKD	1.00E-06
ACT_38	-7.73	CKD	1.00E-06
CTX_M_21	-7.92	CKD	1.00E-06
CTX_M_42	-10.3	CKD	1.00E-06
SHV_67	-13.8	CKD	1.00E-06

Table S20: Differences between CKD and Cirrhosis AMR Gene Families

Lineage	LOG2FC	Direction	pvalue
resistance_nodulation_cell_division_RND_antibiotic_efflux_pump	16.42	Cirrhosis	1.00E-06
Erm_23S_ribosomal_RNA_methyltransferase	13.36	Cirrhosis	1.00E-06
CfxA_beta_lactamase	13.25	Cirrhosis	1.00E-06
pmr_phosphoethanolamine_transferase	13.08	Cirrhosis	1.00E-06
APH_3	11.47	Cirrhosis	1.00E-06
glycopeptide_resistance_gene_cluster	11.46	Cirrhosis	1.00E-06
kdpDE	11.26	Cirrhosis	1.00E-06
cepA_beta_lactamase	11.13	Cirrhosis	1.00E-06
CTX_M_beta_lactamase	11.08	Cirrhosis	1.00E-06
macrolide_phosphotransferase_MPH	10.77	Cirrhosis	1.00E-06
fosfomycin_thiol_transferase	9.35	Cirrhosis	1.00E-06
NmcA_beta_lactamase	7.9	Cirrhosis	1.00E-06
PDC_beta_lactamase	6.89	Cirrhosis	1.02E-06
CMY_beta_lactamase	6.78	Cirrhosis	6.52E-04
ACI_beta_lactamase	6.23	Cirrhosis	1.00E-06
non_erm_23S_ribosomal_RNA_methyltransferase_G748	5.21	Cirrhosis	1.05E-04
ACT_beta_lactamase	5.2	Cirrhosis	4.87E-04
vanX	4.89	Cirrhosis	0.007295
multidrug_and_toxic_compound_extrusion_MATE_transporter	4.86	Cirrhosis	1.00E-06
Llm_23S_ribosomal_RNA_methyltransferase	4.68	Cirrhosis	5.81E-05
blaZ_beta_lactamase	4.61	Cirrhosis	0.002519
tetracycline_inactivation_enzyme	4.3	Cirrhosis	1.00E-06
vanS	4.14	Cirrhosis	1.02E-06
KPC_beta_lactamase	4.11	Cirrhosis	0.041692
rifamycin_resistant_beta_subunit_of_RNA_polymerase_rpoB	4.03	Cirrhosis	1.00E-06
SHV_beta_lactamase	3.86	Cirrhosis	1.00E-06
antibiotic_resistant_isoleucyl_tRNA_synthetase_ileS	3.84	Cirrhosis	1.00E-06
aminocoumarin_resistant_parY	3.68	Cirrhosis	1.00E-06
ABC_F_ATP_binding_cassette_ribosomal_protection_protein	3.56	Cirrhosis	1.00E-06
AAC_3	3.43	Cirrhosis	1.00E-06
AAC_6	3.3	Cirrhosis	4.53E-06
OXA_beta_lactamase	3.09	Cirrhosis	9.88E-04
ampC_type_beta_lactamase	2.82	Cirrhosis	1.00E-06
undecaprenyl_pyrophosphate_related_proteins	2.75	Cirrhosis	1.04E-06
streptothricin_acetyltransferase_SAT	2.72	Cirrhosis	1.99E-06
General_Bacterial_Porin_with_reduced_permeability_to_beta_lactams	2.68	Cirrhosis	9.08E-06
major_facilitator_superfamily_MFS_antibiotic_efflux_pump	2.65	Cirrhosis	1.00E-06

tetracycline_resistant_ribosomal_protection_protein	2.53	Cirrhosis	1.00E-06
quinolone_resistance_protein_qnr	2.53	Cirrhosis	3.14E-04
trimethoprim_resistant_dihydrofolate_reductase_dfr	2.49	Cirrhosis	1.03E-06
lincosamide_nucleotidyltransferase_LNU	2.11	Cirrhosis	0.002805
TEM_beta_lactamase	2.09	Cirrhosis	0.001479
small_multidrug_resistance_SMR_antibiotic_efflux_pump	1.92	Cirrhosis	0.012084
CblA_beta_lactamase	-1.09	CKD	1.00E-06
RbpA_bacterial_RNA_polymerase_binding_protein	-2.38	CKD	1.00E-06
OXY_beta_lactamase	-2.4	CKD	1.00E-06
SRT_beta_lactamase	-2.76	CKD	1.00E-06
sulfonamide_resistant_sul	-2.97	CKD	1.00E-06
APH_2	-3.93	CKD	1.00E-06
ANT_3	-3.97	CKD	1.00E-06
BUT_beta_lactamase	-4.39	CKD	5.44E-05
Bleomycin_resistant_protein	-6.17	CKD	1.00E-06
MIR_beta_lactamase	-6.53	CKD	1.00E-06
16S_rRNA_methyltransferase_A1408	-6.85	CKD	1.04E-06
defensin_resistant_mprF	-8.5	CKD	1.00E-06
CKO_beta_lactamase	-10.55	CKD	1.00E-06

Table S21: Differences between CKD and Cirrhosis Resistomes

Lineage	LOG2FC	Direction	pvalue
Escherichia_coli	16.79	Cirrhosis	1.00E-06
Bifidobacterium_bifidum	14.14	Cirrhosis	1.00E-06
Enterobacter_hormaechei	13.14	Cirrhosis	1.00E-06
Streptococcus_pyogenes	12.95	Cirrhosis	1.00E-06
Staphylococcus_aureus	12.41	Cirrhosis	1.00E-06
Citrobacter_freundii	12.29	Cirrhosis	1.00E-06
Streptococcus_agalactiae	11.96	Cirrhosis	1.00E-06
Campylobacter_jejuni	11.42	Cirrhosis	1.00E-06
Shigella_sonnei	11.14	Cirrhosis	1.00E-06
Salmonella_enterica	10.29	Cirrhosis	1.00E-06
Streptococcus_suis	10.29	Cirrhosis	1.00E-06
Acinetobacter_nosocomialis	10.24	Cirrhosis	1.00E-06
Aeromonas_media	10.24	Cirrhosis	1.00E-06
Stenotrophomonas_maltophilia	10.15	Cirrhosis	1.00E-06
Butyrivibrio_fibrisolvens	9.24	Cirrhosis	1.00E-06
Plasmid_pNG2	8.2	Cirrhosis	8.68E-04
Shigella_flexneri	8.1	Cirrhosis	1.00E-06
Streptomyces_lividans	8.1	Cirrhosis	1.00E-06
Clostridium_perfringens	8.02	Cirrhosis	2.12E-06
Parabacteroides_distasonis	7.83	Cirrhosis	1.00E-06
Citrobacter_koseri	7.83	Cirrhosis	1.04E-06
Desulfovibrio_desulfuricans	7.83	Cirrhosis	1.04E-06
Achromobacter_insuavis	7.72	Cirrhosis	1.00E-06
Acidaminococcus_fermentans	7.06	Cirrhosis	1.00E-06
Klebsiella_oxytoca	6.69	Cirrhosis	1.00E-06
Streptococcus_australis	6.66	Cirrhosis	1.00E-06
Streptomyces_fradiae	6.19	Cirrhosis	1.00E-06
Bacillus_subtilis	5.95	Cirrhosis	0.028627
Streptomyces_lincolnensis	5.86	Cirrhosis	0.035853
Haemophilus_influenzae	5.61	Cirrhosis	1.36E-06
Transposon_Tn4551	5.6	Cirrhosis	1.00E-06
Clostridioides_difficile	5.51	Cirrhosis	1.00E-06
Prevotella_intermedia	5.47	Cirrhosis	1.00E-06
Citrobacter_youngae	5.45	Cirrhosis	5.16E-04
Streptomyces_antibioticus	5.19	Cirrhosis	1.00E-06
Streptomyces_rimosus	5.17	Cirrhosis	0.010737
Streptococcus_pneumoniae	5.12	Cirrhosis	1.00E-06
Enterococcus_gallinarum	4.92	Cirrhosis	0.007394
Burkholderia_cepacia	4.75	Cirrhosis	1.90E-04

Streptomyces_ambofaciens	4.66	Cirrhosis	1.00E-06
Streptomyces_niveus	4.6	Cirrhosis	4.02E-04
Desulfitobacterium_hafniense	4.59	Cirrhosis	3.73E-06
Nocardia_farcinica	4.43	Cirrhosis	1.00E-06
Streptomyces_thermotolerans	4.38	Cirrhosis	0.002098
Enterobacter_cloacae	4.33	Cirrhosis	1.00E-06
Vibrio_parahaemolyticus	4.22	Cirrhosis	1.00E-06
Serratia_marcescens	4.07	Cirrhosis	0.00139
Paenibacillus_sp	3.91	Cirrhosis	1.00E-06
Streptomyces_rishiriensis	3.88	Cirrhosis	1.00E-06
Bifidobacterium_adolescentis	3.75	Cirrhosis	1.00E-06
mixed_culture	3.58	Cirrhosis	1.00E-06
Mycobacterium_tuberculosis	3.53	Cirrhosis	1.06E-06
Campylobacter_coli	3.24	Cirrhosis	1.00E-06
Bacteroides_vulgatus	2.76	Cirrhosis	1.17E-06
Bacteroides_fragilis	2.73	Cirrhosis	1.00E-06
Citrobacter_amalonaticus	2.56	Cirrhosis	1.29E-04
uncultured_bacterium	2.55	Cirrhosis	1.00E-06
Enterococcus_faecalis	2.43	Cirrhosis	0.0021
uncultured_organism	2.2	Cirrhosis	1.61E-06
Shigella_dysenteriae	2	Cirrhosis	0.034339
Capnocytophaga_ochracea	1.98	Cirrhosis	0.004919
Neisseria_gonorrhoeae	1.66	Cirrhosis	0.028076
Bacteroides_thetaiotaomicron	1.14	Cirrhosis	0.028355
Klebsiella_pneumoniae	-1.49	CKD	1.00E-06
Acinetobacter_baumannii	-3.04	CKD	1.00E-06
Enterobacter_asburiae	-3.18	CKD	1.00E-06
Bacteroides_coprosuis	-3.2	CKD	1.00E-06
Legionella_pneumophila	-3.24	CKD	1.00E-06
Morganella_morganii	-3.53	CKD	1.00E-06
Vibrio_cholerae	-4	CKD	1.00E-06
Aeromonas_salmonicida	-5.7	CKD	3.18E-05
Providencia_stuartii	-6.93	CKD	1.00E-06
Ralstonia_pickettii	-7.21	CKD	1.00E-06
Buttiauxella_agrestis	-9.33	CKD	1.00E-06
Proteobacteria	-10.75	CKD	1.00E-06
Citrobacter_sedlakii	-11.91	CKD	1.00E-06
Citrobacter_sp	-12.75	CKD	1.00E-06

Table S22: Average Model Accuracy for Naïve Predictions in Cirrhosis Vs CKD &Diabetes

AMR	**Classification Accuracy**	**Sensitivity**	**Specificity**	**Area Under the Curve**
Classification Tree	0.95164	0.92308	0.986	0.9846
CN2 rules	0.96376	0.99144	0.96262	0.9976
kNN	0.8346	0.8346	0.8346	0.8346
Logistic regression	0.91616	0.85268	0.96378	0.9869
Naive Bayes	0.88354	0.8419	0.96144	0.98716
Neural Network	0.92292	0.86968	0.96494	0.99076
Random Forest	0.98338	0.97866	0.99184	0.99992
SVM	0.79372	0.8419	0.82012	0.96534
ARG	**Classification Accuracy**	**Sensitivity**	**Specificity**	**Area Under the Curve**
Classification Tree	0.97616	0.97616	0.97616	0.97616
CN2 rules	0.9854	1	0.98204	0.99992
kNN	0.92002	0.82762	0.97846	0.98712
Logistic regression	0.98464	0.95904	0.9988	0.99944
Naive Bayes	0.91	0.85996	0.994	0.91
Neural Network	0.98464	0.96554	0.9964	0.99964
Random Forest	1	1	1	1
SVM	0.68694	0.9806	0.53702	0.68694
Resistome	**Classification Accuracy**	**Sensitivity**	**Specificity**	**Area Under the Curve**
Classification Tree	0.95684	0.96576	0.97224	0.98276
CN2 rules	0.92606	0.97218	0.91304	0.9936
kNN	0.84586	0.72014	0.97464	0.9579
Logistic regression	0.93298	0.91024	0.97464	0.9939
Naive Bayes	0.9121	0.88032	0.9831	0.99454
Neural Network	0.94454	0.92522	0.97708	0.99596
Random Forest	0.99618	0.99144	0.9988	1
SVM	0.82734	0.88886	0.83094	0.96416