Supplementary table 1: Univariate analysis results for 90- day hospitalizations.

RNA				DNA			
Variable	**Est**	**p-value**	**OR (95% CI)**	**Variable**	**Est**	**p-value**	**OR (95% CI)**
Age	-0.0637	0.0411	0.94 (0.88, 1.00)	**Age**	-0.0650	0.0371	0.94 (0.88, 1.00)
Male	-1.0380	0.0270	0.35 (0.14, 0.89)	**Male**	-0.9808	0.0353	0.38 (0.15, 0.93)
Alcoholic etiology	0.1603	0.6640	1.17 (0.57, 2.42)	**Alcoholic etiology**	0.1943	0.5944	1.21 (0.59, 2.48)
Diabetes	-0.4054	0.4158	0.67 (0.25, 1.77)	**Diabetes**	-0.4430	0.3724	0.64 (0.24, 1.70)
HE	0.7855	0.0773	2.19 (0.92, 5.24)	**HE**	0.8049	0.0700	2.24 (0.94, 5.34)
Infection	1.1908	0.0092	3.29 (1.34, 8.06)	**Infection**	1.2095	0.0081	3.35 (1.37, 8.20)
Beta_blocker	-0.4417	0.3435	0.64 (0.26, 1.60)	**Beta_blocker**	-0.4699	0.3127	0.63 (0.25, 1.56)
PPI	0.6286	0.1620	1.88 (0.78, 4.53)	**PPI**	0.5978	0.1825	1.82 (0.76, 4.38)
MELD	0.1042	0.0014	1.11 (1.04, 1.18)	**MELD**	0.1054	0.0012	1.11 (1.04, 1.19)
Bacteroides	-1.4404	0.0179	0.24 (0.07, 0.78)	***Bacteroides***	-1.0761	0.0252	0.34 (0.13, 0.88)
Escherichia	-0.2162	0.6650	0.81 (0.30, 2.14)	***Bifidobacterium***	0.5237	0.2530	1.69 (0.69, 4.14)
Klebsiella	1.2083	0.0737	3.35 (0.89, 12.59)	***Colinsella***	-0.0940	0.8683	0.91 (0.30, 2.76)
Raoultella	0.9946	0.0765	2.70 (0.90, 8.13)	***Citrobacter***	1.1914	0.1096	3.29 (0.77, 14.16)
Enterococcus	1.9870	0.0012	7.29 (2.19, 24.29)	***Escherichia***	-0.2420	0.6660	0.79 (0.26, 2.36)
Clostridiales_XIVa	-0.4070	0.3582	0.67 (0.28, 1.59)	***Klebsiella***	0.8629	0.2792	2.37 (0.50, 11.31)
Lachno_incertae sedis	-1.4949	0.0035	0.22 (0.08, 0.61)	***Pluralibacter***	-0.7438	0.5001	0.48 (0.06, 4.13)
Roseburia	-0.9544	0.0624	0.39 (0.14, 1.05)	***Enterococcus***	1.2404	0.0185	3.46 (1.23, 9.71)
Lachno_Ruminococcus	-0.7032	0.2950	0.50 (0.13, 1.85)	***Catenibacter***	-12.6009	0.9639	<0.01 (<0.01, >999)
Parabacteroides	-1.1701	0.0097	0.31 (0.13, 0.75)	***Anerostipes***	-0.6266	0.2543	0.53 (0.18, 1.57)

Prevotella	-1.1781	0.0736	0.31 (0.09, 1.12)	***Blautia***	-1.0426	0.0204	0.35 (0.15, 0.85)
Alistipes	-1.5466	0.0081	0.21 (0.07, 0.67)	***Clostridiales_XIV***	-0.1217	0.7888	0.89 (0.36, 2.16)
Fecalibacterium	-0.6712	0.1566	0.51 (0.20, 1.29)	***Dorea***	-0.7638	0.2534	0.47 (0.13, 1.73)
Oscillibacter	-1.7992	0.0889	0.17 (0.02, 1.32)	***Fusicanibacter***	-0.7091	0.2342	0.49 (0.15, 1.58)
Veillonella	0.9089	0.0620	2.48 (0.96, 6.45)	***Lachno_incertaesedis***	-1.7060	0.0003	0.18 (0.07, 0.46)
				Roseburia	-2.0988	0.0063	0.12 (0.03, 0.55)
				Lachno_Ruminococcus	-1.5141	0.0020	0.22 (0.08, 0.58)
				Lactobacillus	0.3711	0.4243	1.45 (0.58, 3.60)
				Parabacteroides	-0.8809	0.0717	0.41 (0.16, 1.08)
				Fecalibacterium	-0.9036	0.0459	0.41 (0.17, 0.98)
				Subdoligranulum	-2.3957	0.0221	0.09 (0.01, 0.71)
				Streptococcus	-0.5635	0.2119	0.57 (0.24, 1.38)
				Veillonella	0.7673	0.1370	2.15 (0.78, 5.92)

All variables with $p<0.20$ were included in the multi-variable analysis, bacterial taxa are at the genus level. HE: hepatic encephalopathy, PPI: proton pump inhibitor, MELD: model for end-stage liver disease.