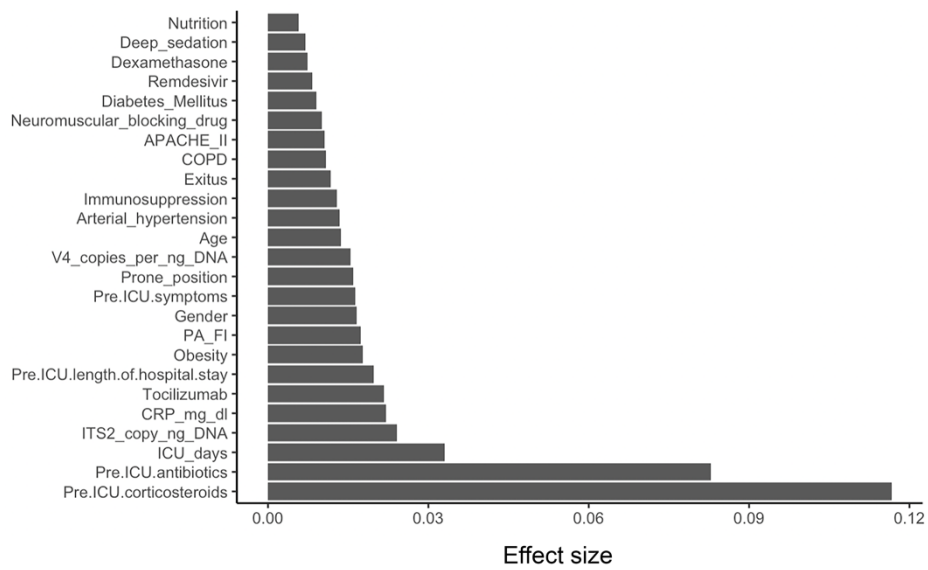


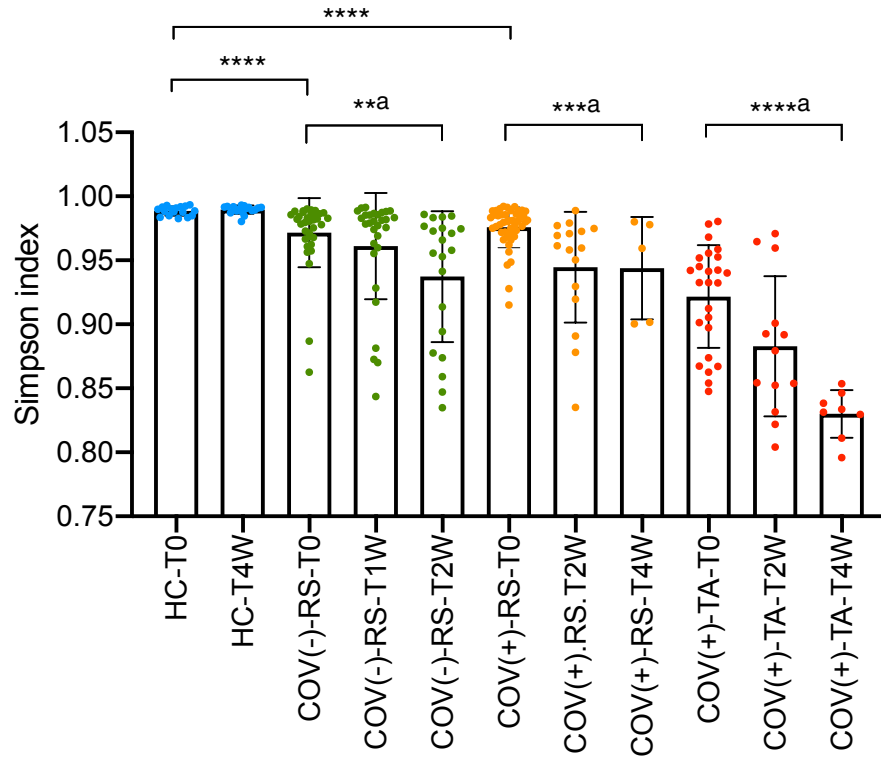
Supplementary Figure S1. a, Bacterial load in critically ill patients as assessed by qPCR of the V4 region of the 16S rRNA gene on ICU admission **b**, Bacterial richness as assessed by the Chao1 index analysis of the 16S rRNA sequences on ICU admission day. *** $p < 0.0001$, Mann–Whitney test.

Contribution of clinical factors to data's effect size



	Df	SumOfSqs	R2	F	Pr(>F)	FDR
Pre.ICU.corticosteroids	8	2.088	0.117	1.204	0.106	0.372
Pre.ICU.antibiotics	7	1.483	0.083	0.978	0.536	0.807
ICU_days	1	0.592	0.033	2.730	0.003	0.075
ITS2_copy_ng_DNA	1	0.433	0.024	1.996	0.025	0.258
CRP_mg_dl	1	0.395	0.022	1.824	0.050	0.295
Tocilizumab	1	0.387	0.022	1.788	0.031	0.258
Pre.ICU.length.of.hospital.stay	1	0.354	0.020	1.634	0.059	0.295
Obesity	1	0.316	0.018	1.460	0.113	0.372
PA_FI	1	0.311	0.017	1.433	0.119	0.372
Gender	1	0.297	0.017	1.370	0.142	0.394
Pre.ICU.symptoms	1	0.293	0.016	1.350	0.176	0.440
Prone_position	2	0.285	0.016	0.657	0.925	0.963
V4_copies_per_ng_DNA	1	0.276	0.015	1.272	0.211	0.480
Age	1	0.245	0.014	1.131	0.289	0.577
Arterial_hypertension	1	0.241	0.013	1.110	0.300	0.577
Immunosuppression	1	0.230	0.013	1.060	0.364	0.650
Exitus	1	0.210	0.012	0.968	0.450	0.750
COPD	1	0.193	0.011	0.893	0.561	0.807
APACHE_II	1	0.190	0.011	0.876	0.581	0.807
Neuromuscular_blocking_drug	1	0.181	0.010	0.835	0.620	0.816
Diabetes_Mellitus	1	0.161	0.009	0.744	0.745	0.931
Remdesivir	1	0.148	0.008	0.684	0.803	0.956
Dexamethasone	1	0.132	0.007	0.611	0.902	0.963
Deep_sedation	1	0.125	0.007	0.579	0.914	0.963
Nutrition	1	0.103	0.006	0.474	0.963	0.963
Residual	38	8.234	0.460	NA	NA	NA
Total	77	17.902	1.000	NA	NA	NA

Supplementary Figure S2. Analysis of covariates with potential effect on microbiome variation in samples collected at baseline from ICU-COV(-) and ICU-COV(+) patients using the adonis test.



Supplementary Figure S3. Bacterial evenness as assessed by the Simpson index analysis of the 16S rRNA sequences. ** $P < 0.001$; *** $P < 0.0001$; **** $P < 0.00001$, Mann-Whitney test unless 3 groups were tested then Kruskal-Wallis test was applied (a).

microbiome of ICU-COV(+) patients. Only taxa found significantly different between groups were plotted ($FDR < 0.05$). MaAsLin2 tool was used for comparison analysis.