	Methylprednisolone (N=83)	Control (N=90)	p-value*
Any adverse event	29 (34.9)	30 (33.3)	0.87
Shock requiring vasopressors	0 (0.0)	1 (1.1)	1.00
Acure renal failure	2 (2.4)	4 (4.4)	0.68
Disseminated intravascular coagulation	2 (2.4)	1 (1.1)	0.61
Acute myocardial infarction	1 (1.2)	1 (1.1)	1.00
Stroke	0 (0.0)	1 (1.1)	1.00
Pulmonary embolism	1 (1.2)	1 (1.1)	1.00
Bacterial superinfection	1 (1.2)	1 (1.1)	1.00
Agitation	9 (10.8)	2 (2.2)	0.03
Hyperglycemia	8 (9.6)	0 (0.0)	0.002
Hypokalemia	6 (7.2)	13 (14.4)	0.15
Pneumothorax	1 (1.2)	0 (0.0)	0.48
Transaminases elevation	2 (2.4)	2 (2.2)	1.00
Bradycardia/QT elongation	7 (8.4)	2 (2.2)	0.09
Diarrhea	1 (1.2)	6 (6.7)	0.12

Data are n (%). *P-value of Fisher's exact test

Table S1: **Distribution of study patients according to study group and in-hospital adverse events.**

	Methylprednisolone (n=83)	Control (n=90)	p-value*
Antibiotics	74 (89.2)	81 (90.0)	1.00
Azithromycin	31 (37.4)	44 (48.9)	0.17
Antivirals	36 (43.4)	75 (83.3)	<0.001
Hydroxychloroquine	67 (80.7)	81 (90.0)	0.09
Vitamins	21 (25.3)	28 (31.1)	0.40
Anticoagulants	60 (72.3)	61 (67.8)	0.62
Noninvasive ventilation	72 (86.7)	66 (73.3)	0.04
High-flow nasal cannula	10 (12.0)	18 (20.0)	0.21

*P-value of Fisher's exact test

Table S2: **Concomitant in-hospital treatments.**

Methylprednisolone (N=83)	Control (N=90)	OR (95% CI)	p-value
19	40	0.37 (0.19-0.72)	0.003
22	40	0.45 (0.24-0.86)	0.01
24	40	0.51 (0.27-0.96)	0.04
19	37	0.43 (0.22-0.83)	0.01
19	35	0.47 (0.65-0.97)	0.02
22	37	0.52 (0.27-0.98)	0.04
24	35	0.64 (0.34-1.21)	0.17

Table S3. **Sensitivity Analyses**

Legend: MP denoted methylprednisolone. Since the primary composite outcome includes two variable that may be influenced by medical decision making (transfer to ICU and decision to intubate), we performed sensitivity analysis by examining scenarios to bias against our hypotheses. If 3 or 5 more patients in the MP group had met the composite outcome, or if 3 or 5 fewer in the control group had met the composite outcome, then the findings were still statistically significant. Only in the scenarios when 10 patients (5 in each group) hypothetically experienced a different primary composite outcome were non-significant findings.

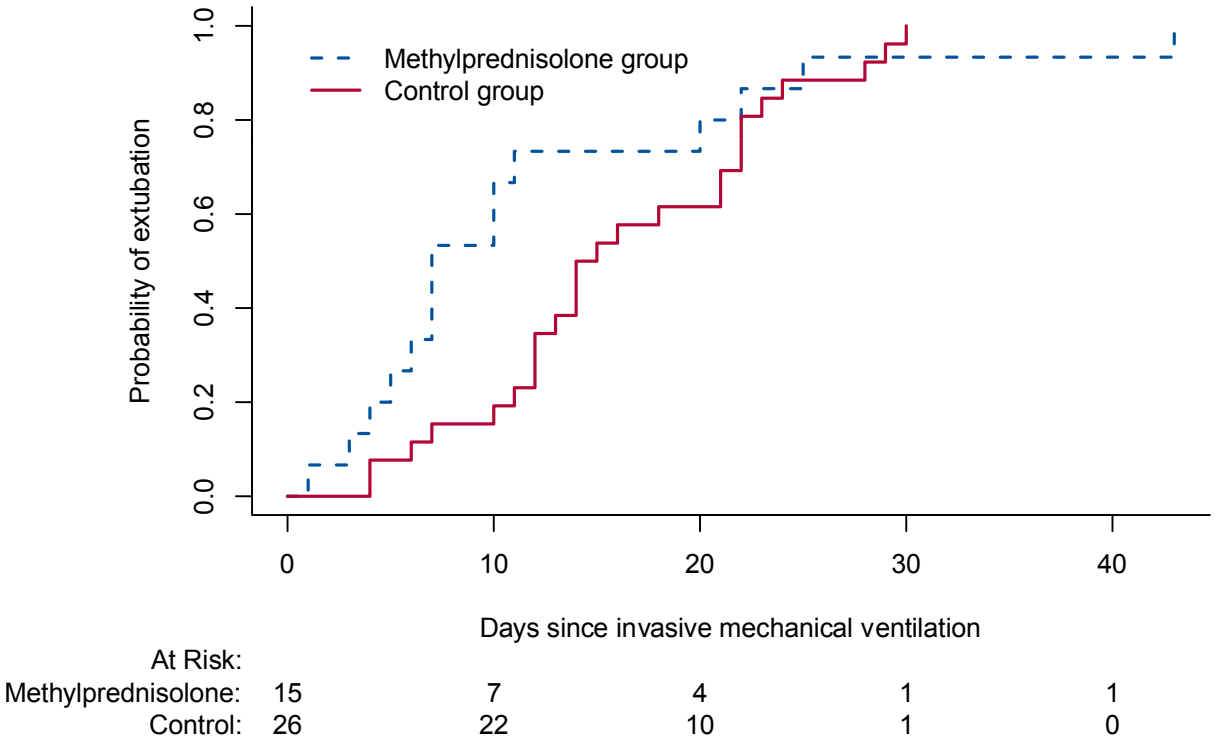

Figure S1. **Kaplan-Meier curve showing time to removal of mechanical ventilation in MP vs. control.**

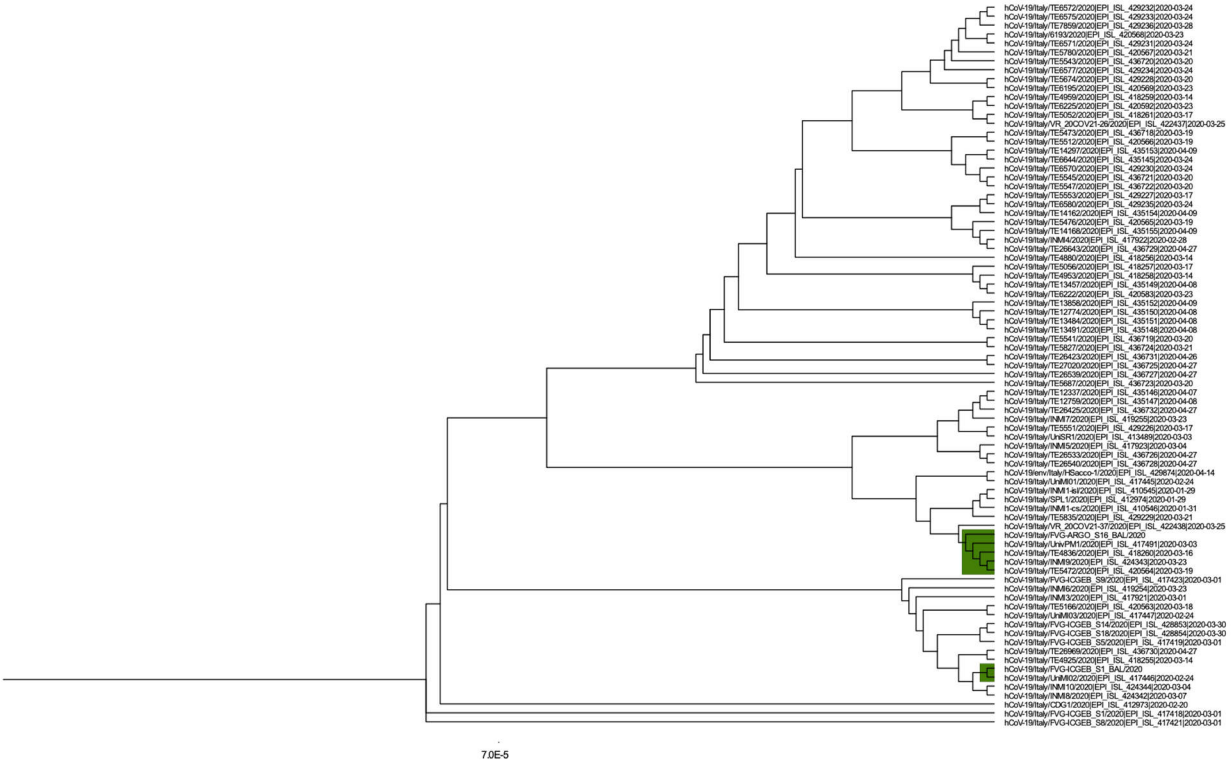

Figure S2. **Phylogenetic Italian subtree showing almost no differences between previously Italian sequenced virus and sequences obtained from of our samples.**

The quantity and quality of the RNA solution was assessed using Qubit 2.0 fluorometer (Thermo Fisher Scientific) and Agilent 2100 Bioanalyzer (Agilent Technologies). For each nasopharyngeal swab 10ng of total RNA was processed using Trio RNA-Seq Library Preparation Kit (NuGEN Technologies). All the obtained libraries have been quality-checked and quantified before been equimolarly pooled and sequenced for metatranscriptome analysis using Illumina MiSEQ 2x250bp paired-end mode following standard procedures. Sequenced reads that passed the quality check (Phred score ≥30), were trimmed using filterAndTrim function of Bioconductor DADA2 package. the filtered reads were assembled *de novo* using Megahit (v.1.2.9) with default parameter settings. Megahit generated multiple contigs but in all cases the longest contigs ware identified as

"Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2 complete genome" with 99% of identity and 0 gaps with a mean coverage raging form 400x to1200x.

Phylogenetic trees were inferred using the maximum likelihood method implemented in the MEGAX program using the 79 Europe/Italy GISAID sequences available by 05/10/2020.