

1 **A catalog of associations between rare coding variants and COVID-19 outcomes**

2 J. A. Kosmicki^{1†}, J. E. Horowitz^{1†}, N. Banerjee¹, R. Lanche¹, A. Marcketta¹, E. Maxwell¹, X. Bai¹,
3 D. Sun¹, J. D. Backman¹, D. Sharma¹, H. M. Kang¹, C. O’Dushlaine¹, A. Yadav¹, A. J. Mansfield¹,
4 A. H. Li¹, K. Watanabe¹, L. Gurski¹, S. E. McCarthy¹, A. E. Locke¹, S. Khalid¹, S. O’Keeffe¹, J.
5 Mbatchou¹, O. Chazara², Y. Huang³, E. Kvikstad⁵, A. O’Neill², P. Nioi⁴, M. M. Parker⁴, S.
6 Petrovski², H. Runz³, J. D. Szustakowski⁵, Q. Wang², E. Wong⁶, A. Cordova-Palomera⁶, E. N.
7 Smith⁶, S. Szalma⁶, X. Zheng⁷, S. Esmaceli⁷, J. W. Davis⁷, Y-P. Lai⁸, X. Chen⁸, A. E. Justice⁹, J.
8 B. Leader⁹, T. Mirshahi⁹, D. J. Carey⁹, A. Verma¹⁰, G. Sirugo¹⁰, M. D. Ritchie¹⁰, D. J. Rader¹⁰, G.
9 Povysil¹¹, D. B. Goldstein^{11,12}, K. Kiryluk^{11,13}, E. Pairo-Castineira^{14,15}, K. Rawlik¹⁴, D. Pasko¹⁶, S.
10 Walker¹⁶, A. Meynert¹⁵, A. Kousathanas¹⁶, L. Moutsianas¹⁶, A. Tenesa^{14,15,17}, M. Caulfield^{16,18}, R.
11 Scott^{16,19}, J. F. Wilson^{15,17}, J. K. Baillie^{14,15,20}, G. Butler-Laporte^{21,22}, T. Nakanishi^{21,23-25}, M.
12 Lathrop^{23,26}, J.B. Richards^{21-23,27}, Regeneron Genetics Center*, UKB Exome Sequencing
13 Consortium*, M. Jones¹, S. Balasubramanian¹, W. Salerno¹, A. R. Shuldiner¹, J. Marchini¹, J. D.
14 Overton¹, L. Habegger¹, M. N. Cantor¹, J. G. Reid¹, A. Baras^{1‡}, G. R. Abecasis^{1‡}, M. A. Ferreira^{1‡}

15

16 From:

17 ¹Regeneron Genetics Center, 777 Old Saw Mill River Rd., Tarrytown, NY 10591, USA

18 ²Centre for Genomics Research, Discovery Sciences, BioPharmaceuticals R&D, AstraZeneca,
19 Cambridge CB2 0AA, UK

20 ³Biogen, 300 Binney St, Cambridge, MA 02142, USA

21 ⁴Alnylam Pharmaceuticals, 675 West Kendall St, Cambridge, MA 02142, USA

22 ⁵Bristol Myers Squibb, Route 206 and Province Line Road, Princeton, NJ 08543, USA

23 ⁶Takeda California Inc., 9625 Towne Centre Dr, San Diego, CA 92121, USA

- 24 ⁷AbbVie, Inc., 1 N. Waukegan Rd, North Chicago, IL 60064, USA
- 25 ⁸Pfizer, Inc., 1 Portland Street, Cambridge MA 02139, USA
- 26 ⁹Geisinger, Danville, PA, 17822, USA
- 27 ¹⁰Department of Genetics, Perelman School of Medicine, University of Pennsylvania,
28 Philadelphia, PA, 19104, USA
- 29 ¹¹Institute for Genomic Medicine, Columbia University Irving Medical Center, New York, NY
30 10032, USA
- 31 ¹²Department of Genetics & Development, Columbia University, New York, NY 10032, USA
- 32 ¹³Division of Nephrology, Department of Medicine, Vagelos College of Physicians & Surgeons,
33 Columbia University, New York, NY 10032, USA
- 34 ¹⁴Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh, EH25 9RG, UK
- 35 ¹⁵MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of
36 Edinburgh, Western General Hospital, Crewe Road, Edinburgh, EH4 2XU, UK
- 37 ¹⁶Genomics England, London EC1M 6BQ, UK
- 38 ¹⁷Centre for Global Health Research, Usher Institute of Population Health Sciences and
39 Informatics, Teviot Place, Edinburgh EH8 9AG, UK
- 40 ¹⁸William Harvey Research Institute, Barts and the London School of Medicine and Dentistry,
41 Queen Mary University of London, London EC1M 6BQ, UK
- 42 ¹⁹Great Ormond Street Hospital for Children NHS Foundation Trust, London WC1N 3JH, UK
- 43 ²⁰Intensive Care Unit, Royal Infirmary of Edinburgh, 54 Little France Drive, Edinburgh, EH16
44 5SA, UK
- 45 ²¹Lady Davis Institute, Jewish General Hospital, Montréal, Québec H3T 1E2, Canada
- 46 ²²Department of Epidemiology, Biostatistics and Occupational Health, McGill University,
47 Montréal, Québec H3A 0G4, Canada

48 ²³Department of Human Genetics, McGill University, Montréal, Québec H3A 0G4, Canada

49 ²⁴Kyoto-McGill International Collaborative School in Genomic Medicine, Graduate School of
50 Medicine, Kyoto University, Kyoto 606-8501, Japan

51 ²⁵Research Fellow, Japan Society for the Promotion of Science

52 ²⁶Canadian Centre for Computational Genomics, McGill University, Montréal, Québec H3A
53 0G4, Canada

54 ²⁷Department of Twins Research, King's College London, London WC2R 2LS, UK

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56 *A complete list of investigators is provided in the Supplementary Appendix.

57 †J. A. Kosmicki and J. E. Horowitz contributed equally to this manuscript.

58 ‡A. Baras, G. R. Abecasis and M. A. Ferreira jointly supervised this work.

59 Correspondence to: manuel.ferreira@regeneron.com and goncalo.abecasis@regeneron.com

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61 **ABSTRACT**

62 Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) causes coronavirus disease-19
63 (COVID-19), a respiratory illness that can result in hospitalization or death. We investigated
64 associations between rare genetic variants and seven COVID-19 outcomes in 543,213 individuals,
65 including 8,248 with COVID-19. After accounting for multiple testing, we did not identify any
66 clear associations with rare variants either exome-wide or when specifically focusing on (i) 14
67 interferon pathway genes in which rare deleterious variants have been reported in severe COVID-
68 19 patients; (ii) 167 genes located in COVID-19 GWAS risk loci; or (iii) 32 additional genes of
69 immunologic relevance and/or therapeutic potential. Our analyses indicate there are no significant
70 associations with rare protein-coding variants with detectable effect sizes at our current sample
71 sizes. Analyses will be updated as additional data become available, with results publicly
72 browsable at <https://rgc-covid19.regeneron.com>.

73

74 **MAIN TEXT**

75 The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1] causes coronavirus
76 disease 2019 (COVID-19) [2]. COVID-19 ranges in clinical presentation from asymptomatic
77 infection to flu-like illness with respiratory failure, hyperactive immune responses and death [3-
78 5]. It is currently estimated that SARS-CoV-2 has infected >100 million individuals and has been
79 attributed to >2 million recorded deaths worldwide. Known risk factors for severe disease include
80 male sex, older age, ancestry, obesity and underlying cardiovascular, renal, and respiratory
81 diseases [6-9], among others.

82
83 Since the start of the SARS-CoV-2 pandemic, host genetic analysis of common genetic variation
84 among SARS-CoV-2 patients have identified at least nine genome-wide significant loci that
85 modulate COVID-19 susceptibility and severity, including variants in/near *LZTFL1*, *IFNAR2*,
86 *DPP9* and the *HLA* region [10-13]. However, to date, there has been no assessment of the
87 contribution of rare genetic variation to COVID-19 disease susceptibility or severity through large
88 population-based exome-wide association analyses.

89
90 To identify rare variants (RVs, minor allele frequency [MAF]<1%) associated with COVID-19
91 susceptibility and severity, we generated exome-wide sequencing data for 543,213 individuals
92 from three studies (Geisinger Health System [GHS], Penn Medicine BioBank [PMBB] and UK
93 Biobank [UKB]) and three ancestries (African, European and South Asian) (**Supplementary**
94 **Table 1**). Of these, 8,248 had COVID-19, and among those 2,085 (25.28%) were hospitalized and
95 590 (7.15%) had severe disease (i.e. requiring ventilation or resulting in death; **Supplementary**
96 **Table 2**). Using these data, we tested the association between RVs and seven COVID-19

97 outcomes: five related to disease susceptibility and two related to disease severity among COVID-
98 19 cases (**Supplementary Table 3**). In a separate paper [13], we used these same phenotypes to
99 validate the association with common risk variants reported in previous COVID-19 GWAS[10-
100 12], thus demonstrating that our phenotypes are calibrated with those used in other studies.

101
102 For each phenotype, exome-wide association analyses were performed separately in each study
103 and ancestry using REGENIE[14], testing single RVs (~7 million) and a burden of RVs in 18,886
104 protein-coding genes. The genomic inflation factor (λ_{GC}) for RVs was often <1 in individual
105 studies, caused by a large proportion of variants having a minor allele count (MAC) of 0 in cases
106 (**Supplementary Table 4**). In meta-analyses across studies and ancestries, we found no RV
107 associations at a conservative $P < 9.6 \times 10^{-10}$, which corresponds to a Bonferroni correction for the
108 number of variants and traits tested. The most significant associations with RVs are listed in **Table**
109 **1**, all observed with our COVID-19 hospitalization phenotype (2,085 hospitalized cases vs.
110 534,965 COVID-19 negative or unknown controls). Of these, we highlight an association with an
111 RV in the promoter of *EEF2* (rs532051930:A, MAF=0.003%, OR=93.9, 95% CI 20.3-434.5,
112 $P=6.2 \times 10^{-9}$; **Supplementary Figure 1A**), a translation elongation factor which plays a key role in
113 viral replication[15, 16].

114
115 Despite not reaching our threshold for genome-wide significance, we highlight the association
116 with *EEF2* because: (i) it was supported by two independent studies (**Supplementary Figure 1B**);
117 (ii) five additional RVs in the 89 bp promoter of *EEF2* (out of 50 tested) had an independent and
118 directionally-consistent predisposing association with the same hospitalization phenotype
119 ($P < 0.05$; **Supplementary Table 5**); (iii) rs532051930 is predicted by DeepSEA [17] to be a

120 regulatory variant and to disrupt binding of several transcription factors, including GABP, which
121 has been linked to RV-induced aberrant gene expression [18]; (iv) rs532051930 is located at the
122 peak of the transcription initiation region for *EEF2* (**Supplementary Figure 1C**) [19], suggesting
123 that it might affect RNA polymerase II binding; and (v) among a subset of 1,988 individuals with
124 available RNA-seq data from liver tissue, the only individual who was a carrier for rs532051930:A
125 had the second highest expression of *EEF2* (**Supplementary Figure 1D**). These results raise the
126 possibility that rs532051930 and potentially other promoter RVs increase *EEF2* transcription and,
127 consequently, increase risk of hospitalization due to SARS-CoV-2 infection.

128
129 Given these supporting observations and the established role of *EEF2* in viral replication, we
130 studied the genetic association with rs532051930 in greater detail, to understand if it was likely to
131 be a true-positive association. First, we reviewed sequencing reads for all 26 carriers of this variant,
132 to visually validate the heterozygote genotype call produced by the calling algorithm. Sequencing
133 reads were consistent with a heterozygote call for all 26 individuals. Second, we determined if the
134 association with this rare variant was robust to the association test used (**Supplementary Table**
135 **6**). A Firth test applied to a joint analysis of data across the two studies, adjusting for study specific
136 covariates as an offset, resulted in $P=5.5 \times 10^{-8}$. Similar results were obtained by: (i) an
137 approximation to this approach, which combines log-likelihood curves calculated at a grid of
138 values with the Firth penalty, applied using approximate derivatives; (ii) a *P*-value-based meta-
139 analysis, for which there is evidence of better type-I error control [20]; and (iii) the BinomiRare
140 test [21], which uses a test statistic based on allele counts in cases only, adjusts for covariates and
141 combines data across studies. We also applied tests without covariates and these uniformly led to
142 less significant associations, but this is expected since the covariates explain variation in the

143 phenotype. Third, we attempted to replicate this association by querying whether this variant was
144 present in an additional 4,341 COVID-19 cases with exome- or whole-genome sequence data
145 generated as part of the GenOMICC (n=2,969) [11], Columbia University COVID-19 Biobank
146 (n=1,152) and Biobanque Quebec (n=220) [22] studies. We found no carriers for this variant in
147 these additional COVID-19 cases (**Supplementary Table 7**). Given these findings, we conclude
148 that it is not certain that there is a true association between rs532051930 and COVID-19 risk,
149 illustrating the importance of replication.

150
151 Next, we addressed the possibility that associations with protein-coding RVs might help pinpoint
152 target genes of common risk variants identified in GWAS of COVID-19. To this end, we focused
153 on 167 genes located within 500 kb of the nine common variants associated with COVID-19
154 hospitalization in a separate analysis [13]. Of the 334 gene burden tests performed (167 genes x 2
155 burden tests), which considered both pLoF variants alone (M1 burden test) or pLoF plus
156 deleterious missense variants (M3 burden test), 17 had a nominally significant association with the
157 same COVID-19 hospitalization phenotype (**Supplementary Table 6**). Of these, burden tests for
158 one gene – *CHAF1A* (OR=25 for the M1 burden test, 95% CI 4.9-128.5, $P=1.0 \times 10^{-4}$) – remained
159 borderline significant after correcting for the 334 tests performed ($P < 0.05/334 = 1.5 \times 10^{-4}$).
160 *CHAF1A* is located 317 kb from the lead common variant at locus 19p13.3 [13], is highly
161 expressed in EBV-transformed B-cells [23] and encodes a component of the chromatin assembling
162 factor complex that affects cell differentiation, including the differentiation of pre-B cells into B-
163 cells and macrophages [24].

164

165 We then examined the association with 14 genes in the interferon pathway, given recent reports
166 that deleterious RVs in these genes may be implicated in severe clinical outcomes [25, 26]. Given
167 the larger sample size in our studies, we examined whether there was any evidence for association
168 between the COVID-19 hospitalization phenotype (2,085 cases vs. 534,965 controls) and the
169 burden of rare (MAF<0.1%) pLoF variants (M1 burden test) or pLoF plus deleterious missense
170 variants (M3 burden test) in these 14 genes, three of which are located within 500 kb of a COVID-
171 19 GWAS risk variant (*IFNAR1*, *IFNAR2* and *TICAM1*). Of the 14 genes, only two genes had a
172 nominal significant association: *STAT2* and *TLR7* (**Table 2**). However, neither remained
173 significant after correcting for the 28 tests performed (both with $P>0.05/28=0.0018$). Further, these
174 results were unchanged when testing COVID-19 severe cases (N=590), or when restricting the
175 burden tests to include variants with a MAF<1% or singleton variants (**Supplementary Table 7**).
176 Therefore, as recently reported by others [22], we found no evidence for an association between
177 RVs in these 14 interferon signaling genes and risk of COVID-19.

178
179 Lastly, we performed the same analysis for an additional 32 genes that are involved in the etiology
180 of SARS-CoV-2 infection (*ACE2*, *TMPRSS2*), encode therapeutic targets for COVID-19 obtained
181 through ClinicalTrials.gov (e.g. *IL6R*, *JAK1*) or have been implicated in other immune or
182 infectious diseases through GWAS (e.g. *IL33*). After correcting for multiple testing, there were
183 also no significant associations with a burden of deleterious RVs for this group of COVID-19
184 therapeutic target genes (**Supplementary Table 8**).

185
186 In summary, we provide a catalog of RV associations with COVID-19 outcomes based on exome-
187 sequence data, capturing genetic variation not assayed by array genotyping or imputation. We did

188 not find any convincing associations with current sample sizes, but will continue to expand our
189 analyses and update results periodically at <https://rgc-covid19.regeneron.com>.

190 **METHODS**

191

192 **Participating Studies**

193 *Geisinger Health System (GHS)*. The GHS MyCode Community Health Initiative study has been
194 described previously [27]. Briefly, the GHS study is a health system-based cohort from central and
195 eastern Pennsylvania (USA) with ongoing recruitment since 2006. A subset of 144,182 MyCode
196 participants sequenced as part of the GHS-Regeneron Genetics Center DiscovEHR partnership
197 were included in this study. Information on COVID-19 outcomes were obtained through GHS's
198 COVID-19 registry. Patients were identified as eligible for the registry based on relevant lab results
199 and ICD-10 diagnosis codes; patient charts were then reviewed to confirm COVID-19 diagnoses.
200 The registry contains data on outcomes, comorbidities, medications, supplemental oxygen use and
201 ICU admissions.

202

203 *Penn Medicine BioBank (PMBB) study*. PMBB study participants are recruited through the
204 University of Pennsylvania Health System, which enrolls participants during hospital or clinic
205 visits. Participants donate blood or tissue and allow access to EHR information[28]. The PMBB
206 COVID-19 registry consists of patients who have positive qPCR testing for SARS-COV-2. We
207 then used electronic health records to classify COVID-19 patients into hospitalized and severe
208 (ventilation or death) categories.

209

210 *UK Biobank (UKB) study*. We studied the host genetics of SARS-CoV-2 infection in participants
211 of the UK Biobank study, which took place between 2006 and 2010 and includes approximately
212 500,000 adults aged 40-69 at recruitment. In collaboration with UK health authorities, the UK

213 Biobank has made available regular updates on COVID-19 status for all participants, including
214 results from four main data types: qPCR test for SARS-CoV-2, anonymized electronic health
215 records, primary care and death registry data. We report results based on the 12 September 2020
216 data refresh and excluded from the analysis 28,547 individuals with a death registry event prior to
217 2020.

218

219 **COVID-19 phenotypes used for genetic association analyses**

220 We grouped participants from each study into three broad COVID-19 disease categories
221 (**Supplementary Table 2**): (i) positive – those with a positive qPCR or serology test for SARS-
222 CoV-2, or a COVID-19-related ICD10 code (U07), hospitalization or death; (ii) negative – those
223 with only negative qPCR or serology test results for SARS-CoV-2 and no COVID-19-related
224 ICD10 code (U07), hospitalization or death; and (iii) unknown – those with no qPCR or serology
225 test results and no COVID-19-related ICD10 code (U07), hospitalization or death. We then used
226 these broad COVID-19 disease categories, in addition to hospitalization and disease severity
227 information, to create seven COVID-19-related phenotypes for genetic association analyses, as
228 detailed in **Supplementary Table 3**.

229

230 **Array genotyping**

231 Genotyping was performed on one of four SNP array types: Illumina OmniExpress Exome array
232 (OMNI; 59345 samples from GHS), Illumina Global Screening Array (GSA; PMBB and 82,527
233 samples from GHS), Applied Biosystems UK BiLEVE Axiom Array (49,950 samples from UKB),
234 or Applied Biosystems UK Biobank Axiom Array (438,427 samples from UKB). We retained
235 variants with a minor allele frequency (MAF) >1%, <10% missingness, Hardy-Weinberg

236 equilibrium test P -value $> 10^{-15}$. Array data were then used: (i) to define ancestry subsets; and (ii)
237 to generate a polygenic risk score (PRS) predictor, as part of the exome-wide association analyses
238 carried out in REGENIE (see below).

239

240 **Exome sequencing**

241 *Sample Preparation and Sequencing.* Genomic DNA samples normalized to approximately 16
242 ng/ul were transferred to the Regeneron Genetics Center from the UK Biobank in 0.5ml 2D matrix
243 tubes (Thermo Fisher Scientific) and stored in an automated sample biobank (LiCONiC
244 Instruments) at -80°C prior to sample preparation. Exome capture was completed using a high-
245 throughput, fully-automated approach developed at the Regeneron Genetics Center. Briefly, DNA
246 libraries were created by enzymatically shearing 100ng of genomic DNA to a mean fragment size
247 of 200 base pairs using a custom NEBNext Ultra II FS DNA library prep kit (New England
248 Biolabs) and a common Y-shaped adapter (Integrated DNA Technologies [IDT]) was ligated to
249 all DNA libraries. Unique, asymmetric 10 base pair barcodes were added to the DNA fragment
250 during library amplification with KAPA HiFi polymerase (KAPA Biosystems) to facilitate
251 multiplexed exome capture and sequencing. Equal amounts of sample were pooled prior to
252 overnight exome capture, approximately 16 hours, with either (i) a slightly modified version of
253 IDT's xGen probe library (for UKB, PMBB and 81,620 samples of GHS); or (ii) NimbleGen
254 VCRome (58,856 samples of GHS). Captured fragments were bound to streptavidin-coupled
255 Dynabeads (Thermo Fisher Scientific) and non-specific DNA fragments removed through a series
256 of stringent washes using the xGen Hybridization and Wash kit according to the manufacturer's
257 recommended protocol (Integrated DNA Technologies). The captured DNA was PCR amplified
258 with KAPA HiFi and quantified by qPCR with a KAPA Library Quantification Kit (KAPA

259 Biosystems). The multiplexed samples were pooled and then sequenced using: (i) for UKB
260 samples – 75 bp paired-end reads with two 10 base pair index reads on the Illumina NovaSeq 6000
261 platform using S2 or S4 flow cells; (ii) for GHS samples captured with VCRome – 75 bp paired-
262 end reads with two 8 bp index reads on the Illumina HiSeq 2500; (iii) for GHS captured with IDT
263 – two 8 bp index reads on the Illumina HiSeq 2500 or two 10 bp index reads on the Illumina
264 NovaSeq 6000 on S4 flow cells; (iv) for UPENN-PMBB – two 10 bp index reads on the Illumina
265 NovaSeq 6000 on S4 flow cells.

266

267 *Variant calling and quality control.* Sample read mapping and variant calling, aggregation and
268 quality control were performed via the SPB protocol described in Van Hout et al. [29]. Briefly, for
269 each sample, NovaSeq WES reads are mapped with BWA MEM to the hg38 reference genome.
270 Small variants are identified with WeCall and reported as per-sample gVCFs. These gVCFs are
271 aggregated with GLnexus into a joint-genotyped, multi-sample VCF (pVCF). SNV genotypes with
272 read depth (DP) less than seven and indel genotypes with read depth less than ten are changed to
273 no-call genotypes. After the application of the DP genotype filter, a variant-level allele balance
274 filter is applied, retaining only variants that meet either of the following criteria: (i) at least one
275 homozygous variant carrier or (ii) at least one heterozygous variant carrier with an allele balance
276 (AB) greater than the cutoff ($AB \geq 0.15$ for SNVs and $AB \geq 0.20$ for indels).

277

278 *Identification of low-quality variants from exome-sequencing using machine learning.* Briefly, in
279 each study, we defined a set of positive control and negative control variants based on: (i)
280 concordance in genotype calls between array and exome sequencing data; (ii) Mendelian
281 inconsistencies in the exome sequencing data; (iii) differences in allele frequencies between exome

282 sequencing batches (UKB and GHS); (iv) variant loadings on 20 principal components derived
283 from the analysis of variants with a MAF<1%; (v) transmitted singletons. The model was then
284 trained on up to 30 available WeCall/GLnexus site quality metrics, including, for example, allele
285 balance and depth of coverage. We split the data into training (80%) and test (20%) sets. We
286 performed a grid search with 5-fold cross-validation on the training set to identify the
287 hyperparameters that return the highest accuracy during cross-validation, which are then applied
288 to the test set to confirm accuracy. This approach identified as low-quality a total of 7 million
289 variants in the UKB study (86% in the buffer region), 7.2 million across the two GHS datasets
290 (IDT and VCRome; 84% in the buffer region) and 1.1 million in the PMBB study (88% in the
291 buffer region). These variants were removed from analysis in the respective studies.

292
293 *Gene burden masks.* Briefly, for each gene region as defined by Ensembl [30], genotype
294 information from multiple rare coding variants was collapsed into a single burden genotype, such
295 that individuals who were: (i) homozygous reference (Ref) for all variants in that gene were
296 considered homozygous (RefRef); (ii) heterozygous for at least one variant in that gene were
297 considered heterozygous (RefAlt); (iii) and only individuals that carried two copies of the
298 alternative allele (Alt) of the same variant were considered homozygous for the alternative allele
299 (AltAlt). We did not phase rare variants; compound heterozygotes, if present, were considered
300 heterozygous (RefAlt). We did this separately for four classes of variants: (i) predicted loss of
301 function (pLoF), which we refer to as an “M1” burden mask; (ii) pLoF or missense (“M2”); (iii)
302 pLoF or missense variants predicted to be deleterious by 5/5 prediction algorithms (“M3”); (iv)
303 pLoF or missense variants predicted to be deleterious by 1/5 prediction algorithms (“M4”).
304 Variants were annotated using SnpEff 4.3[31] and the most severe consequence for each variant

305 was chosen, considering complete protein-coding transcripts for each gene. The following variants
306 were considered to be pLoF variants: frameshift-causing indels, variants affecting splice acceptor
307 and donor sites, variants leading to stop gain, stop loss and start loss. The five missense deleterious
308 algorithms used were SIFT [32], PolyPhen2 (HDIV), PolyPhen2 (HVAR) [33], LRT [34], and
309 MutationTaster [35]. For each gene, and for each of these four groups, we considered five separate
310 burden masks, based on the frequency of the alternative allele of the variants that were screened
311 in that group: <1%, <0.1%, <0.01%, <0.001% and singletons only. Each burden mask was then
312 tested for association with the same approach used for individual variants (see below).

313

314 **Genetic association analyses**

315 Association analyses in each study were performed using the genome-wide Firth logistic
316 regression test implemented in REGENIE [14]. In this implementation, Firth's approach is applied
317 when the p-value from standard logistic regression score test is below 0.05. As the Firth penalty
318 (*i.e.* Jeffrey's invariant prior) corresponds to a data augmentation procedure where each
319 observation is split into a case and a control with different weights, it can handle variants with no
320 minor alleles among cases. With no covariates, this corresponds to adding 0.5 in every cell of a
321 2x2 table of allele counts versus case-control status.

322 We included in step 1 of REGENIE (*i.e.* prediction of individual trait values based on the
323 genetic data) array variants with a minor allele frequency (MAF) >1%, <10% missingness, Hardy-
324 Weinberg equilibrium test P -value > 10^{-15} and linkage-disequilibrium (LD) pruning (1000 variant
325 windows, 100 variant sliding windows and $r^2 < 0.9$). The exception was the GHS study, for which
326 we used exome (not array) variants in step 1; we did this because two different exome capture
327 technologies (IDT and VCRome) were used to sequence the GHS samples, and so it was important

328 to capture in step 1 of REGENIE any differences in exome sequencing performance between IDT
329 and VCRome. We excluded from step 1 any SNPs with high inter-chromosomal LD, in the major
330 histo-compatibility (MHC) region, or in regions of low complexity.

331 The association model used in step 2 of REGENIE included as covariates (i) age, age², sex,
332 age-by-sex and age²-by-sex; (ii) 10 ancestry-informative principle components (PCs) derived from
333 the analysis of a set of LD-pruned (50 variant windows, 5 variant sliding windows and $r^2 < 0.5$)
334 common variants from the array (imputed for the GHS study) data; (iii) an indicator for exome
335 sequencing batch (GHS: two IDT batches, one VCRome batch; UKB: six IDT batches); and (iv)
336 20 PCs derived from the analysis of exome variants with a MAF between 2.6×10^{-5} (roughly
337 corresponding to a minor allele count [MAC] of 20) and 1%. We corrected for PCs built from rare
338 variants because previous studies demonstrated PCs derived from common variants do not
339 adequately correct for fine-scale population structure [36, 37].

340 Within each study, association analyses were performed separately for five different
341 continental ancestries defined based on the array data: African (AFR), Admixed American (AMR),
342 European (EUR) and South Asian (SAS). We determined continental ancestries by projecting each
343 sample onto reference principle components calculated from the HapMap3 reference panel.
344 Briefly, we merged our samples with HapMap3 samples and kept only SNPs in common between
345 the two datasets. We further excluded SNPs with MAF < 10%, genotype missingness > 5% or
346 Hardy-Weinberg Equilibrium test p-value < 10^{-5} . We calculated PCs for the HapMap3 samples
347 and projected each of our samples onto those PCs. To assign a continental ancestry group to each
348 non-HapMap3 sample, we trained a kernel density estimator (KDE) using the HapMap3 PCs and
349 used the KDEs to calculate the likelihood of a given sample belonging to each of the five
350 continental ancestry groups. When the likelihood for a given ancestry group was > 0.3, the sample

351 was assigned to that ancestry group. When two ancestry groups had a likelihood >0.3 , we
352 arbitrarily assigned AFR over EUR, AMR over EUR, AMR over EAS, SAS over EUR, and AMR
353 over AFR. Samples were excluded from analysis if no ancestry likelihoods were >0.3 , or if more
354 than three ancestry likelihoods were > 0.3 .

355 Results were subsequently meta-analyzed across studies and ancestries using an inverse
356 variance-weighted fixed-effects meta-analysis.

357

358 **Gene expression analysis in participants of the GHS study**

359 For a subset of individuals from the GHS study ($n=1,988$, ascertained through the Geisinger
360 Bariatric Surgery Clinic), RNA was extracted from liver biopsies conducted during bariatric
361 surgery to evaluate liver disease. Individuals had class 3 obesity ($BMI>40\text{kg/m}^2$) or class 2 obesity
362 ($BMI\ 35\text{-}39\ \text{kg/m}^2$) with an obesity-related co-morbidity (e.g. type-2 diabetes, hypertension, sleep
363 apnea, non-alcoholic fatty liver disease). RNA libraries were prepared using polyA-extraction and
364 then sequenced with 75bp paired-end reads with two 10 bp index reads on the Illumina NovaSeq
365 6000 on S4 flow cells. RNA-seq data were then analyzed using the GTEx v8 workflow[38], using
366 STAR [39] and RNASeqQC [40], except that GENCODE v32 was used in lieu of v26. Briefly: (i)
367 raw expression counts were normalized with TMM (Trimmed Mean of M-values) as implemented
368 in edgeR [40]; (ii) a rank-based inverse normal transformation was applied to the normalized
369 expression values; (iii) principal components (PCs) analysis was performed on data from 25,078
370 genes with TPM >0.1 in $>20\%$ samples, to identify latent factors accounting for variation in gene
371 expression; (iv) gene expression levels were adjusted for the top 100 PCs to improve power to
372 identify cis-regulatory effects.

373

374 **Frequency of *EEF2* rare promoter variant in COVID-19 cases from independent studies**

375 To help understand if the association between COVID-19 risk and rs532051930 in *EEF2* was
376 likely to be a true-positive association, we determine its frequency in 4,341 cases from three
377 additional studies.

378 *GenOMICC* ($n=2,969$). Individuals with severe COVID-19 were ascertained as described
379 previously[11]. DNA samples were then whole-genome sequenced on the Illumina NovaSeq 6000
380 platform, aligned to the human reference genome hg38 and variant called to GVCF stage on the
381 DRAGEN pipeline (software v01.011.269.3.2.22, hardware v01.011.269) at Genomics England.
382 rs532051930 +/-50bp was genotyped with the GATK GenotypeGVCFs tool v4.1.8.1 and filtered
383 to minimum depth 8X. Ancestry for individuals with array genotyping was inferred using
384 ADMIXTURE[41] populations defined in 1000 Genomes[42]. When one individual had a
385 probability > 80% of pertaining to one ancestry, then the individual was assigned to this ancestry,
386 otherwise the individual was considered to be of admixed ancestry, as performed in the Million
387 veteran program [43]. Somalier v0.2.12[44] was used to estimate ancestry for samples with whole-
388 genome sequencing data. Predictions from Somalier were compared against predictions from
389 ADMIXTURE for 1833 samples with both array genotyping and whole-genome sequencing data.
390 Of these, the ancestry assignment matched between the two approaches for 1832 samples.
391 Somalier predictions were used for the remaining 927 samples, of which 813 could be confidently
392 ($\geq 95\%$ probability) assigned to a population; the remaining 114 were assigned to admixed
393 ancestry.

394 *Columbia University COVID-19 biobank* ($n=1,152$). This cohort has previously been
395 described in detail[22]. Briefly, 1,152 COVID-19 patients that were treated for COVID-19 at the
396 Columbia University Irving Medical Center were recruited to the Columbia University COVID-

397 19 Biobank between March and May 2020. All patients had PCR-confirmed SARS-CoV-2
398 infection and the vast majority had severe COVID-19 requiring hospitalization. For all cases,
399 exomes were captured with the IDT xGen Exome Research Panel V1.0 and sequenced on
400 Illumina's NovaSeq 6000 platform with 150 bp paired-end reads according to standard protocols.
401 All cases were processed with the same bioinformatic pipeline for variant calling. In brief, reads
402 were aligned to human reference GRCh37 using DRAGEN and duplicates were marked with
403 Picard. Variants were called according to the Genome Analysis Toolkit (GATK) Best Practices
404 recommendations v3.66[45]. Finally, variants were annotated with ClinEff[31] and the IGM's in-
405 house tool ATAV[46]. A centralized database was used to store variant and per site coverage data
406 for all samples enabling well controlled analyses without the need of generating jointly called VCF
407 files (see Ren et al. 2020 for details[46]). For each patient, we performed ancestry classification
408 into one of the six major ancestry groups (European, African, Latinx, East Asian, South Asian and
409 Middle Eastern) using a neural network trained on a set of samples with known ancestry labels.
410 We used a 50% probability cut-off to assign an ancestry label to each sample and labeled samples
411 that did not reach 50% for any of the ancestral groups as "Admixed".

412 We only included samples that had at least 90% of the consensus coding sequence (CCDS
413 release 20[47]) covered at $\geq 10x$ and $\leq 3\%$ contamination levels according to VerifyBamID[48].
414 Additionally, we removed samples with a discordance between self-declared and sequence-derived
415 gender and samples with an inferred relationship of second-degree or closer according to
416 KING[49]. All cases had at least 10x coverage at the position of rs532051930.

417 *Biobanque Québec Covid-19 (n=220)*. The Biobanque Québec COVID-19
418 (www.BQC19.ca) is a provincial biobank prospectively enrolling patients with suspected COVID-
419 19, or COVID-19 confirmed through SARS-CoV-2 PCR testing and was previously described[22].

420 For this study, we used results from patients with available WGS data and who were recruited at
421 the Jewish General Hospital (JGH) in Montreal. The JGH is a university affiliated hospital serving
422 a large multi-ethnic adult population and the Québec government designated the JGH as the primary
423 COVID-19 reference center early in the pandemic. In total, Biobanque Quebec contained 533
424 participants with WGS, including 62 cases of COVID-19 who required invasive ventilatory support
425 (BiPAP, high flow oxygen, or endotracheal intubation) or died, 128 COVID-19 patients who were
426 hospitalized but did not require invasive ventilatory support, 30 individuals with COVID-19 did not
427 require hospitalization, and 313 SARS-CoV-2 PCR-negative participants. Using genetic PCAs
428 derived from genome-wide genotyping, 76% of participants were of European ancestry, 9% were
429 of African ancestry, 7% were of east Asian ancestry, and 5% were of south Asian ancestry.

430 We performed WGS at a mean depth of 30x on all individuals using Illumina's Novaseq
431 6000 platform (Illumina, San Diego, CA, USA). Sequencing results were analyzed using the
432 McGill Genome Center bioinformatics pipelines[50], in accordance with Genome Analysis
433 Toolkit (GATK) best practices recommendations[45]. Reads were aligned to the GRCh38
434 reference genome. Variant quality control was performed using the variantRecalibrator and
435 applyVQSR functions from GATK.

436

437 **Results availability**

438 All genotype-phenotype association results reported in this study are available for browsing using
439 the RGC's COVID-19 Results Browser (<https://rgc-covid19.regeneron.com>). Data access and use
440 is limited to research purposes in accordance with the Terms of Use (<https://rgc-covid19.regeneron.com/terms-of-use>). The COVID-19 Results Browser provides a user-friendly
441 interface to explore genetic association results, enabling users to query summary statistics across
442

443 multiple cohorts and association studies using genes, variants or phenotypes of interest. Results
444 are displayed in an interactive tabular view ordered by p-value – enabling filtering, sorting,
445 grouping and viewing additional statistics – with link outs to individual GWAS reports, including
446 interactive Manhattan and QQ plots. LocusZoom views of LD information surrounding variants
447 of interest are also available, with LD calculated using the respective source genetic datasets.

448 The data resource supporting the COVID-19 Results Browser was built using a processed
449 version of the raw association analysis outputs. Using the RGC’s data engineering toolkit based in
450 Apache Spark and Project Glow (<https://projectglow.io/>), association results were annotated,
451 enriched and partitioned into a distributed, columnar data store using Apache Parquet. Processed
452 Parquet files were registered with AWS Athena, which enables efficient, scalable queries on
453 unfiltered association result datasets. Additionally, “filtered” views of associations significant at a
454 threshold of p-value < 0.001 were stored in AWS RDS Aurora databases for low latency queries
455 to service primary views of top associations. APIs into RDS and Athena are managed behind the
456 scenes such that results with a p-value>0.001 are pulled from Athena as needed.

457

458 **Competing interests**

459 J.E.H., J.A.K., A.D., D.S., N.B, A.Y., A.M., R.L., E.M., X.B., D.S., F.S.P.K., J.D.B., C.O’D.,
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468 implementation or interpretation of this study. S.S., E.W., A.C.P., and E.N.S. are employed by
469 Takeda. S.S. holds shares in Takeda and Janssen. The other authors declare no competing interests.

470

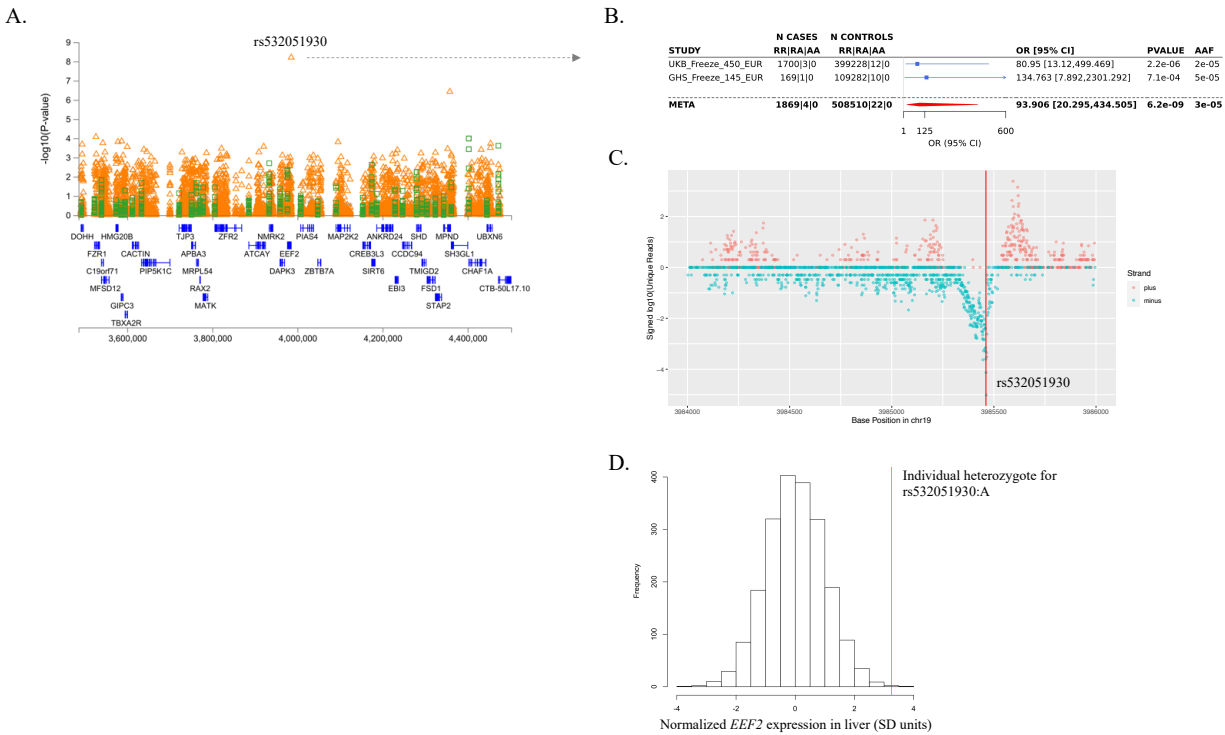
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515 **Supplementary Figures**



516

517

518 **Supplementary Figure 1. Association between a rare promoter variant in *EEF2***

519 **(rs532051930:A) and the COVID-19 hospitalization phenotype. (A) Regional association plot**

520 **centered on rs532051930. Orange triangles: individual rare variants (MAF<0.5%). Green squares:**

521 **burden tests. Grey circles: individual common variants (MAF>0.5%). (B) Forest plot showing**

522 **association in the two individual datasets included in the meta-analysis of this variant. (C) Results**

523 **from a population-scale PROcap (Precision Run-On 5' cap sequencing) study [19], which profiles**

524 **transcription start sites of nascent RNAs attached to RNA polymerase. The variant rs532051930**

525 **(vertical red line) is located 2 bp away from the peak of transcription initiation. (D) Distribution**

526 **of *EEF2* expression among 1,918 individuals from the GHS study with available RNA-seq data**

527 **from liver tissue. Vertical red line indicates expression levels for the only individual who was**

528 **heterozygote for the rare promoter variant rs532051930.**

529 **TABLES**

530

531 **Table 1. Top rare variant associations identified in this study ($P < 10^{-8}$), all observed with the**
532 **phenotype COVID-19 positive and hospitalized (cases) vs. COVID-19 negative or unknown**
533 **(controls).**

Variant	Effect allele	Odds Ratio [95% CI]	P-value	N cases with 0 1 2 copies of effect allele	N controls with 0 1 2 copies of effect allele	Effect allele frequency	Gene	Variant effect
rs374698271	T	81.60 [18.71,355.81]	4.65E-09	1698 5 0	399222 18 0	0.00003	<i>RFX2</i>	Intronic
rs532051930	A	93.90 [20.29,434.50]	6.17E-09	1869 4 0	508510 22 0	0.00003	<i>EEF2</i>	5 prime UTR
rs751932982	A	22.68 [7.89,65.23]	6.92E-09	1869 2 2	508247 44 8	0.00006	<i>FAM9B</i>	Intronic

534

535 **Table 2.** Association between the phenotype COVID-19 positive and hospitalized (cases) vs
 536 COVID-19 negative or unknown (controls) and 14 genes related to interferon signaling that were
 537 recently reported to contain rare (MAF<0.1%), deleterious variants in patients with severe
 538 COVID-19 [14, 23].

Variants included in burden test	Gene	Odds Ratio (95% CI)	P-value	N cases with RR RA AA genotype*	N controls with RR RA AA genotype*	AAF
pLoF, MAF<0.1%	<i>IFNAR1</i>	0.805[0.146;4.438]	8.00E-01	2019 1 0	525406 359 0	0.00034
	<i>IFNAR2</i>	2.077[0.620;6.961]	2.40E-01	2082 3 0	534277 688 0	0.00064
	<i>IKBKG</i>	0.491[0.005;50.219]	7.60E-01	1873 0 0	508491 31 10	0.00005
	<i>IRF3</i>	0.956[0.251;3.643]	9.50E-01	2083 2 0	534559 406 0	0.00038
	<i>IRF7</i>	1.165[0.426;3.185]	7.70E-01	2082 3 0	534124 841 0	0.00079
	<i>IRF9</i>	0.371[0.003;53.766]	7.00E-01	1873 0 0	508479 53 0	0.00005
	<i>STAT1</i>	0.365[0.001;126.712]	7.40E-01	1873 0 0	508490 42 0	0.00004
	<i>STAT2</i>	0.355[0.028;4.438]	4.20E-01	1873 0 0	508405 127 0	0.00012
	<i>TBK1</i>	0.365[0.011;11.964]	5.70E-01	1873 0 0	508445 87 0	0.00009
	<i>TICAM1</i>	3.730[0.189;73.610]	3.90E-01	1872 1 0	508368 164 0	0.00016
	<i>TLR3</i>	1.128[0.144;8.834]	9.10E-01	2084 1 0	534674 291 0	0.00027
	<i>TLR7</i>	7.627[1.872;31.075]	4.60E-03	1872 0 1	508503 25 4	0.00003
	<i>TRAF3</i>	0.368[0.000;733.638]	8.00E-01	1873 0 0	508504 28 0	0.00003
	<i>UNC93B1</i>	1.302[0.272;6.238]	7.40E-01	1938 2 0	516861 409 0	0.0004
pLoF or missense predicted deleterious, MAF<0.1%	<i>IFNAR1</i>	0.756[0.234;2.444]	6.40E-01	2083 2 0	534219 746 0	0.0007
	<i>IFNAR2</i>	1.968[0.598;6.469]	2.70E-01	2082 3 0	534253 712 0	0.00067
	<i>IKBKG</i>	0.446[0.010;19.737]	6.80E-01	1873 0 0	508452 70 10	0.00009
	<i>IRF3</i>	0.786[0.238;2.592]	6.90E-01	2083 2 0	534413 552 0	0.00052
	<i>IRF7</i>	1.137[0.519;2.492]	7.50E-01	2080 5 0	533486 1479 0	0.00138
	<i>IRF9</i>	0.371[0.003;53.766]	7.00E-01	1873 0 0	508479 53 0	0.00005
	<i>STAT1</i>	0.365[0.038;3.488]	3.80E-01	2018 0 0	526009 218 0	0.00021
	<i>STAT2</i>	2.600[1.272;5.314]	8.80E-03	2073 12 0	533405 1559 1	0.00146
	<i>TBK1</i>	1.114[0.445;2.790]	8.20E-01	2081 4 0	533861 1103 1	0.00103
	<i>TICAM1</i>	3.657[0.188;71.218]	3.90E-01	1872 1 0	508365 167 0	0.00016
	<i>TLR3</i>	0.805[0.435;1.493]	4.90E-01	2077 8 0	532355 2609 1	0.00244
	<i>TLR7</i>	1.580[0.627;3.979]	3.30E-01	2001 3 1	525830 477 163	0.00076
	<i>TRAF3</i>	3.013[0.527;17.217]	2.10E-01	2019 1 0	525523 242 0	0.00023
	<i>UNC93B1</i>	1.665[0.774;3.582]	1.90E-01	2075 10 0	533331 1634 0	0.00153

* RR: individuals who have genotype Reference/Reference for all variants included in burden test. RA: individuals who have genotype Reference/Alternate for at least one variant. AA: individuals who have genotype Alternate/Alternate for at least one variant.

539

540 **SUPPLEMENTARY TABLES**

541

542 **Supplementary Tables 1 to 10 are provided in a separate document.**

543

544 **Supplementary Table 1.** Demographics and clinical characteristics of study participants.

545

546 **Supplementary Table 2.** Breakdown of COVID-19 status across the four studies included in the
547 analysis.

548

549 **Supplementary Table 3.** Definitions used for the seven COVID-19 phenotypes analyzed.

550

551 **Supplementary Table 4.** Genomic inflation factor (λ_{GC}) observed in the analysis of exome
552 sequence variants for each of the eight phenotypes tested.

553

554 **Supplementary Table 5.** Association between the COVID-19 hospitalization phenotype and 50
555 rare variants in the promoter of *EEF2*.

556

557 **Supplementary Table 6.** Evidence for association between the COVID-19 hospitalization
558 phenotype and rs532051930 across different association tests.

559

560 **Supplementary Table 7.** No carriers of the rare variant rs532051930 in the promoter of *EEF2*
561 were observed in an additional 4,122 individuals with COVID-19.

562

563 **Supplementary Table 8.** Results from burden association tests for 167 genes located in eight loci
564 described in Horowitz et al. [13].

565

566 **Supplementary Table 9.** Results from burden association tests for 14 genes related to interferon
567 signaling and recently reported to contain rare (MAF<0.1%), deleterious variants in patients with
568 severe COVID-19.

569

570 **Supplementary Table 10.** Results from burden association tests for an additional 32 genes that
571 are involved in the etiology of SARS-CoV-2, encode therapeutic targets or have been implicated
572 in other immune or infectious diseases through GWAS.

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686

687 **SUPPLEMENTARY TEXT**

688

689 **Regeneron Genetics Center (RGC) Research Team and Contribution Statements**

690 All authors/contributors are listed in alphabetical order.

691

692 **RGC Management and Leadership Team**

693 Goncalo Abecasis, Ph.D., Aris Baras, M.D., Michael Cantor, M.D., Giovanni Coppola, M.D.,

694 Aris Economides, Ph.D., Luca A. Lotta, M.D., Ph.D., John D. Overton, Ph.D., Jeffrey G. Reid,

695 Ph.D., Alan Shuldiner, M.D.

696 Contribution: All authors contributed to securing funding, study design and oversight. All

697 authors reviewed the final version of the manuscript.

698

699 **Sequencing and Lab Operations**

700 Christina Beechert, Caitlin Forsythe, M.S., Erin D. Fuller, Zhenhua Gu, M.S., Michael Lattari,

701 Alexander Lopez, M.S., John D. Overton, Ph.D., Thomas D. Schleicher, M.S., Maria

702 Sotiropoulos Padilla, M.S., Louis Widom, Sarah E. Wolf, M.S., Manasi Pradhan, M.S., Kia

703 Manoochehri, Ricardo H. Ulloa.

704 Contribution: C.B., C.F., A.L., and J.D.O. performed and are responsible for sample genotyping.

705 C.B, C.F., E.D.F., M.L., M.S.P., L.W., S.E.W., A.L., and J.D.O. performed and are responsible

706 for exome sequencing. T.D.S., Z.G., A.L., and J.D.O. conceived and are responsible for

707 laboratory automation. M.P., K.M., R.U., and J.D.O are responsible for sample tracking and the

708 library information management system.

709

710 **Clinical Informatics**

711 Nilanjana Banerjee, Ph.D., Michael Cantor, M.D. M.A., Dadong Li, Ph.D., Deepika Sharma,

712 MHI

713 Contribution: All authors contributed to the development and validation of clinical phenotypes

714 used to identify study subjects and (when applicable) controls.

715

716 **Genome Informatics**

717 Xiaodong Bai, Ph.D., Suganthi Balasubramanian, Ph.D., Andrew Blumenfeld, Gisu Eom, Lukas

718 Habegger, Ph.D., Alicia Hawes, B.S., Shareef Khalid, Jeffrey G. Reid, Ph.D., Evan K. Maxwell,

719 Ph.D., William Salerno, Ph.D., Jeffrey C. Staples, Ph.D.

720 Contribution: X.B., A.H., W.S. and J.G.R. performed and are responsible for analysis needed to

721 produce exome and genotype data. G.E. and J.G.R. provided compute infrastructure

722 development and operational support. S.B., and J.G.R. provide variant and gene annotations and

723 their functional interpretation of variants. E.M., J.S., A.B., L.H., J.G.R. conceived and are

724 responsible for creating, developing, and deploying analysis platforms and computational

725 methods for analyzing genomic data.

726

727 **Analytical Genetics**

728 Gonçalo R. Abecasis, Ph.D., Joshua Backman, Ph.D., Manuel A. Ferreira, Ph.D., Lauren Gurski,

729 Jack A. Kosmicki, Ph.D., Alexander H. Li, Ph.D., Adam E. Locke, Ph.D., Anthony Marcketta,

730 Jonathan Marchini, Ph.D., Joelle Mbatchou, Ph.D., Shane McCarthy, Ph.D., Colm O'Dushlaine,

731 Ph.D., Dylan Sun, Kyoko Watanabe, Ph.D.

732 Contribution: J.A.K. and M.A.F. performed association analyses and led manuscript writing
733 group. J.B. identified low-quality variants in exome sequence data using machine learning. L.G.
734 and K.W. helped with visualization of association results. A.H.L., A.E.L., A.M. and D.S.
735 prepared the analytical pipelines to perform association analyses. J.M. and J.M. developed and
736 helped deploy REGENIE. S.M. and C.O'D. helped defined COVID-19 phenotypes. G.R.A.
737 supervised all analyses. All authors contributed to and reviewed the final version of the
738 manuscript.

739

740 **Immune, Respiratory, and Infectious Disease Therapeutic Area Genetics**

741 Julie E. Horowitz, PhD.

742 Contribution: J.E.H. helped defined COVID-19 phenotypes, interpret association results and led
743 the manuscript writing group.

744

745 **Research Program Management**

746 Marcus B. Jones, Ph.D., Michelle LeBlanc, Ph.D., Jason Mighty, Ph.D., Lyndon J. Mitnaul,
747 Ph.D.

748 Contribution: All authors contributed to the management and coordination of all research
749 activities, planning and execution. All authors contributed to the review process for the final
750 version of the manuscript.

751

752 **UK Biobank Exome Sequencing Consortium Research Team**

753

754 **¹Bristol Myers Squibb**

755 Oleg Moiseyenko, Carlos Rios, Saurabh Saha

756

757 **²Regeneron Pharmaceuticals Inc.**

758 Listed in pages 38 to 40.

759

760 **³Biogen Inc.**

761 Sally John, Chia-Yen Chen, David Sexton, Paola G. Bronson, Christopher D. Whelan, Varant

762 Kupelian, Eric Marshall, Timothy Swan, Susan Eaton, Jimmy Z. Liu, Stephanie Loomis, Megan

763 Jensen, Saranya Duraisamy, Ellen A. Tsai, Heiko Runz

764

765 **⁴Alnylam Pharmaceuticals**

766 Aimee M. Deaton, Margaret M. Parker, Lucas D. Ward, Alexander O. Flynn-Carroll, Greg

767 Hinkle, Paul Nioi

768

769 **⁵AstraZeneca**

770 Olympe Chazara, Sri VV. Deevi, Xiao Jiang, Amanda O'Neill, Slavé Petrovski, Katherine

771 Smith, Quanli Wang

772

773 **⁶Takeda California Inc**

774 Jason Tetrault, Dorothee Diogo, Aldo Cordova Palomera, Emily Wong, Rajesh Mikkilineni,

775 David Merberg, Sunita Badola, Erin N. Smith, Sandor Szalma

776

777 ⁷**Pfizer, Inc**

778 Yi-Pin Lai, Xing Chen, Xinli Hu, Melissa R. Miller

779

780 ⁸**Abbvie**

781 Xiuwen Zheng, Bridget Riley-Gillis, Jason Grundstad, Sahar Esmaeeli, Jeff Waring, J. Wade

782 Davis

783

784 ¹Bristol Myers Squibb, Route 206 and Province Line Road, Princeton, NJ 08543, USA

785 ²Regeneron Pharmaceuticals Inc., 777 Old Saw Mill River Road, Tarrytown, New York 10591,

786 USA

787 ³Biogen Inc., 225 Binney Street, Cambridge, MA 02139, USA

788 ⁴Alnylam Pharmaceuticals, 675 West Kendall St, Cambridge, MA 02142, USA

789 ⁵AstraZeneca Centre for Genomics Research, Discovery Sciences, BioPharmaceuticals R&D,

790 Cambridge, UK

791 ⁶Takeda California Inc., 9625 Towne Centre Dr, San Diego, CA 92121, USA

792 ⁷ Pfizer, Inc., 1 Portland Street, Cambridge MA 02139, USA

793 ⁸ AbbVie, Inc., 1 N. Waukegan Rd, North Chicago, IL 60064, USA

794

795

796 **GenOMICC Consortium**

797 Sara Clohisey¹, Fiona Griffiths¹, James Furniss¹, James Furniss¹, Trevor Paterson¹, Tony
798 Wackett¹, Ruth Armstrong¹, Wilna Oosthuizen¹, Nick Parkinson¹, Max Head Fourman¹, Andrew
799 Law¹, Veronique Vitart², Lucija Klaric², Anne Richmond², Chris P. Ponting², Andrew D.
800 Bretherick², Charles Hinds³, Timothy Walsh⁴, Sean Keating⁴, Clark D Russell^{1,5}, Malcolm G.
801 Semple^{6,7}, Kathy Rowan⁸, Elvina Gountouna⁹, Nicola Wrobel¹⁰, Lee Murphy¹⁰, Angie Fawkes¹⁰,
802 Richard Clark¹⁰, Audrey Coutts¹⁰, Lorna Donnelly¹⁰, Tammy Gilchrist¹⁰, Katarzyna Hafezi¹⁰,
803 Louise Macgillivray¹⁰, Alan Maclean¹⁰, Sarah McCafferty¹⁰, Kirstie Morrice¹⁰, , Angie Fawkes¹⁰,
804 Julian Knight¹¹, Charlotte Summers¹², Manu Shankar-Hari^{13,14}, Peter Horby¹⁵, Alistair
805 Nichol^{16,17,18}, David Maslove¹⁹, Lowell Ling²⁰, Danny McAuley^{21,22}, Hugh Montgomery²³, Peter
806 J.M. Openshaw^{24,25}.

807 ¹Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh, EH25 9RG, UK

808 ²MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of
809 Edinburgh, Western General Hospital, Crewe Road, Edinburgh, EH4 2XU, UK

810 ³William Harvey Research Institute, Barts and the London School of Medicine and Dentistry,
811 Queen Mary University of London, London EC1M 6BQ, UK

812 ⁴Intensive Care Unit, Royal Infirmary of Edinburgh, 54 Little France Drive, Edinburgh, EH16
813 5SA, UK

814 ⁵Centre for Inflammation Research, The Queen's Medical Research Institute, University of
815 Edinburgh, 47 Little France Crescent, Edinburgh, UK

816 ⁶NIHR Health Protection Research Unit for Emerging and Zoonotic Infections, Institute of
817 Infection, Veterinary and Ecological Sciences University of Liverpool, Liverpool, L69 7BE, UK

818 ⁷Respiratory Medicine, Alder Hey Children's Hospital, Institute in The Park, University of
819 Liverpool, Alder Hey Children's Hospital, Liverpool, UK

820 ⁸Intensive Care National Audit & Research Centre, London, UK

821 ⁹Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine,
822 University of Edinburgh, Western General Hospital, Crewe Road, Edinburgh, EH4 2XU, UK

823 ¹⁰Edinburgh Clinical Research Facility, Western General Hospital, University of Edinburgh,

824 EH4 2XU, UK

825 ¹¹Wellcome Centre for Human Genetics, University of Oxford, Oxford, UK

826 ¹²Department of Medicine, University of Cambridge, Cambridge, UK

827 ¹³Department of Intensive Care Medicine, Guy's and St. Thomas NHS Foundation Trust,

828 London, UK

829 ¹⁴School of Immunology and Microbial Sciences, King's College London, UK

830 ¹⁵Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University

831 of Oxford, Old Road Campus, Roosevelt Drive, Oxford, OX3 7FZ, UK

832 ¹⁶Clinical Research Centre at St Vincent's University Hospital, University College Dublin,

833 Dublin, Ireland

834 ¹⁷Australian and New Zealand Intensive Care Research Centre, Monash University, Melbourne,

835 Australia

836 ¹⁸Intensive Care Unit, Alfred Hospital, Melbourne, Australia

837 ¹⁹Department of Critical Care Medicine, Queen's University and Kingston Health Sciences

838 Centre, Kingston, ON, Canada

839 ²⁰Department of Anaesthesia and Intensive Care, The Chinese University of Hong Kong, Prince

840 of Wales Hospital, Hong Kong, China

841 ²¹Wellcome-Wolfson Institute for Experimental Medicine, Queen's University Belfast, Belfast,

842 Northern Ireland, UK

843 ²²Department of Intensive Care Medicine, Royal Victoria Hospital, Belfast, Northern Ireland,

844 UK

845 ²³UCL Centre for Human Health and Performance, London, W1T 7HA, UK

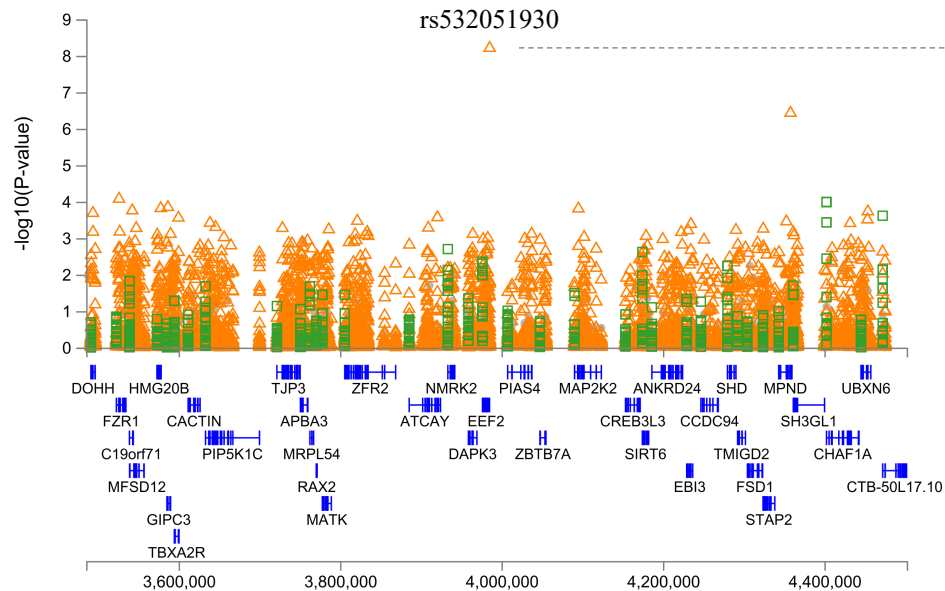
846 ²⁴National Heart and Lung Institute, Imperial College London, London, UK

847 ²⁵Imperial College Healthcare NHS Trust: London, London, UK

848

SUPPLEMENTARY FIGURES

A.

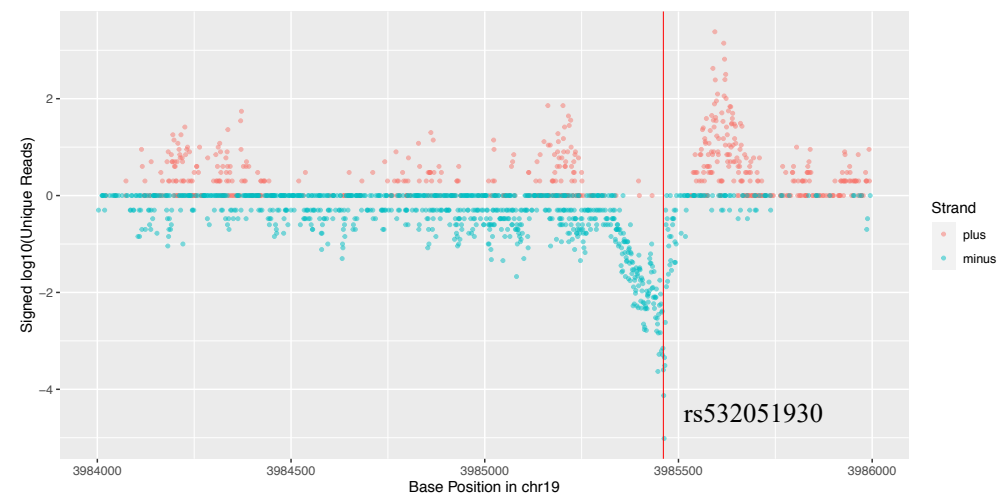


B.

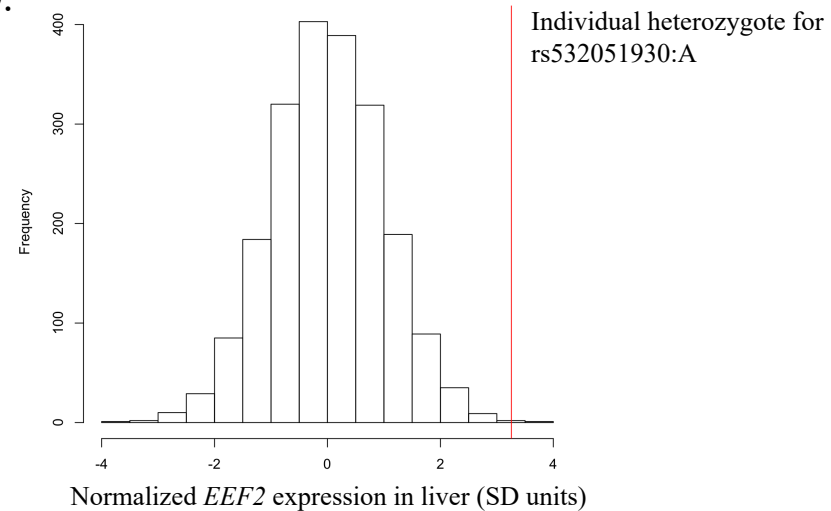
STUDY	N CASES	N CONTROLS	OR [95% CI]	PVALUE	AAF
	RR RA AA	RR RA AA			
UKB_Freeze_450_EUR	1700 3 0	399228 12 0	80.95 [13.12,499.469]	2.2e-06	2e-05
GHS_Freeze_145_EUR	169 1 0	109282 10 0	134.763 [7.892,2301.292]	7.1e-04	5e-05
META	1869 4 0	508510 22 0	93.906 [20.295,434.505]	6.2e-09	3e-05

OR (95% CI) scale: 1, 125, 600

C.



D.



Supplementary Figure 1. Association between a rare promoter variant in *EEF2* (rs532051930:A) and the COVID-19 hospitalization phenotype. (A) Regional association plot centered on rs532051930. Orange triangles: individual rare variants (MAF<0.5%). Green squares: burden tests. Grey circles: individual common variants (MAF>0.5%). (B) Forest plot showing association in the two individual datasets included in the meta-analysis of this variant. (C) Results from a population-scale PROcap (Precision Run-On 5' cap sequencing) study [19], which profiles transcription start sites of nascent RNAs attached to RNA polymerase. The variant rs532051930 (vertical red line) is located 2 bp away from the peak of transcription initiation. (D) Distribution of *EEF2* expression among 1,918 individuals from the GHS study with available RNA-seq data from liver tissue. Vertical red line indicates expression levels for the only individual who was heterozygote for the rare promoter variant rs532051930.

SUPPLEMENTARY TABLES

Supplementary Table 1. Demographics and clinical characteristics of study participants.

Demographics	COVID-19 Positive		Covid-19 Negative or Unknown
	Hospitalized	Not Hospitalized	
UK Biobank			
Total N	1848	5400	416935
AFR ancestry, n (%)	80 (3.8)	134 (2.2)	8495 (1.8)
EUR ancestry, n (%)	1703 (81.9)	5030 (83.2)	399240 (85.7)
SAS ancestry, n (%)	65 (3.1)	236 (3.9)	9200 (1.9)
Average Age, y (% >60y)	59.7 (57)	52.6 (22)	56.2 (36)
Female, n (%)	737 (39.8)	2896 (53.6)	229572 (55.1)
Hypertension, n (%)	884 (47.8)	1214 (22.5)	96851 (23.2)
Cardiovascular Disease, n (%)	265 (14.3)	330 (6.1)	24859 (5.8)
Type 2 Diabetes, n (%)	342 (18.5)	378 (7)	25335 (6.1)
Chronic kidney disease, n (%)	134 (7.3)	112 (2.1)	8096 (1.9)
Asthma, n (%)	343 (18.5)	886 (16.4)	59229 (14.2)
COPD, n (%)	208 (11.2)	164 (3)	10117 (2.4)
GHS			
Total N	170	664	109292
EUR ancestry, n (%)	170 (100)	664 (100)	109292 (100)
Average Age, y (% >60y)	67.81 (76.47)	54.74 (39.0)	55.75 (44.14)
Female, n (%)	90 (52.94)	435 (65.51)	68226 (62.42)
Hypertension, n (%)	138 (81.17)	343 (51.65)	53658 (49.09)
Cardiovascular Disease, n (%)	77 (45.29)	108 (16.26)	17269 (15.80)
Type 2 Diabetes, n (%)	73 (42.94)	158 (23.79)	23290 (21.30)
Chronic kidney disease, n (%)	64 (37.64)	94 (14.15)	14246 (13.03)
Asthma, n (%)	15 (8.82)	47 (7.07)	6975 (6.38)
COPD, n (%)	47(27.64)	67 (10.09)	10822 (9.90)
PMBB			
Total N	67	99	959
AFR ancestry, n (%)	67 (100)	99 (100)	959 (100)
Average Age, y (% >60y)	62.58 (61.19)	47.64 (19.19)	56.24 (43.27)
Female, n (%)	38 (56.7)	72 (72.7)	641 (66.8)
Hypertension, n (%)	59 (88.1)	52 (52.5)	704 (73.4)
Cardiovascular Disease, n (%)	40 (59.7)	17 (17.2)	359 (37.4)
Type 2 Diabetes, n (%)	50 (74.6)	31 (31.3)	440 (45.9)
Chronic kidney disease, n (%)	42 (62.7)	13 (13.1)	300 (31.3)
Asthma, n (%)	18 (26.9)	23 (23.2)	294 (30.7)
COPD, n (%)	20 (29.9)	8 (8.1)	145 (15.1)

Supplementary Table 2. Breakdown of COVID-19 status across the four studies included in the analysis.

COVID-19 status	Positive qPCR or serology for SARS-CoV-2	ICD10 U07 diagnosis or hospitalization	Severe COVID-19 (ventilation or death)	Negative qPCR or serology test for SARS-CoV-2				
					UK Biobank	GHS	PMBB	Total
Positive	Yes	Yes	Yes	Yes or No or NA	382	49	27	458
	Yes	Yes	No or NA	Yes or No or NA	1119	121	40	1,280
	Yes	No or NA	Yes	Yes or No or NA	0	0	0	0
	Yes	No or NA	No or NA	Yes or No or NA	5400	664	99	6,163
	No or NA	Yes	Yes	No or NA	122	0	0	122
	No or NA	Yes	No or NA	No or NA	77	0	0	77
	No or NA	No or NA	Yes	No or NA	0	0	0	0
	No or NA	Yes	Yes	Yes	37	0	0	37
	No or NA	Yes	No or NA	Yes	111	0	0	111
	No or NA	No or NA	Yes	Yes	0	0	0	0
				Total = 7248	Total = 834	Total = 166	Total = 8248	
Negative	No or NA	No or NA	No or NA	Yes	32,867	15,574	959	49,400
Unknown	NA	No or NA	No or NA	NA	384,068	93,718	7,779	485,565
Total					424,183	110,126	8,904	543,213

Supplementary Table 3. Definitions used for the seven COVID-19 phenotypes analyzed.

Broad phenotype category	Phenotype	Case/control group	Definition			Sample size with genetic data			
			COVID-19 status	Hospitalized	Severe disease	UK Biobank	GHS	PMBB	Total
Risk of infection	COVID-19 positive vs. COVID-19 negative or unknown	Cases	Positive	Yes, No or NA	Yes, No or NA	7,248	834	166	8,248
		Controls	Negative or unknown	No or NA	No or NA	416,935	109,292	8,738	534,965
	COVID-19 positive vs. COVID-19 negative	Cases	Positive	Yes, No or NA	Yes, No or NA	7,248	834	166	8,248
		Controls	Negative	No or NA	No or NA	32,867	15,574	959	49,400
	COVID-19 positive and not hospitalized vs. COVID-19 negative or unknown	Cases	Positive	No	No	5,400	664	99	6,163
		Controls	Negative or unknown	No or NA	No or NA	416,935	109,292	8,738	534,965
	COVID-19 positive and hospitalized vs. COVID-19 negative or unknown	Cases	Positive	Yes (or death)	Yes, No or NA	1,848	170	67	2,085
		Controls	Negative or unknown	No or NA	No or NA	416,935	109,292	8,738	534,965
COVID-19 positive and severe vs. COVID-19 negative or unknown	Cases	Positive	Yes, No or NA	Yes	541	49	NA	590	
	Controls	Negative or unknown	No or NA	No or NA	416,935	109,292	NA	526,227	
Risk of adverse outcomes amongst infected individuals	COVID-19 positive and hospitalized vs. COVID-19 positive and not hospitalized	Cases	Positive	Yes (or death)	Yes, No or NA	1,703	170	67	1,940
		Controls	Positive	No	No	5,030	664	99	5,793
	COVID-19 positive and severe vs. COVID-19 positive and not hospitalized	Cases	Positive	Yes, No or NA	Yes	523	49	NA	572
		Controls	Positive	No	No	5,164	664	NA	5,828

Supplementary Table 4. Genomic inflation factor (lambda GC) observed in the analysis of exome sequence variants for each of the seven phenotypes tested.

Phenotype	Study	Ancestry	N cases	N controls	Exome-sequencing variants with MAF<0.5% & MAC>=5			Exome-sequencing variants with MAF<0.5% & MAC>25			Exome-sequencing variants with MAF>0.5%		
					N variants	Proportion of variants with MAC=0 in cases	Lambda GC	N variants	Proportion of variants with MAC=0 in cases	Lambda GC	N variants	Proportion of variants with MAC=0 in cases	Lambda GC
COVID19_positive_hospitalized_vs_COVID19_negative_or_unknown_combined	UKB Freeze 450	SAS	65	9200	798145	0.873	0.202	222553	0.719	0.774	227664	0.193	1.254
	UPENN-PMBB Freeze One	AFR	67	8738	890983	0.857	0.215	279379	0.708	0.748	486699	0.132	1.099
	UKB Freeze 450	AFR	80	8495	812651	0.830	0.268	248412	0.653	0.803	380222	0.120	0.947
	GHS Freeze 145 Exome	EUR	170	109292	2899753	0.933	0.042	889226	0.815	0.23	172227	0.046	0.997
	UKB Freeze 450	EUR	1703	399240	6411484	0.849	0.126	2074846	0.622	0.555	166323	0.000	1.004
	Meta-analysis	ALL	2085	534965	8053662	0.832	0.126	2833904	0.599	0.554	352116	0.043	1.02
COVID19_positive_hospitalized_vs_COVID19_positive_not_hospitalized_combined	UPENN-PMBB Freeze One	AFR	67	99	NA	NA	NA	NA	NA	NA	330315	0.012	0.183
	GHS Freeze 145 Exome	EUR	170	664	209299	0.549	0.866	NA	NA	NA	173449	0.035	1.079
	UKB Freeze 450	EUR	1703	5030	424564	0.072	1.099	112045	0.000	1.043	166403	0.000	1.037
	Meta-analysis	ALL	1940	5793	462977	0.126	1.017	128932	0.000	1.021	398264	0.009	0.388
COVID19_positive_not_hospitalized_vs_COVID19_negative_or_unknown_combined	UPENN-PMBB Freeze One	AFR	99	8738	893407	0.796	0.338	280294	0.596	0.992	487296	0.076	0.961
	UKB Freeze 450	AFR	134	8495	816964	0.736	0.48	250786	0.492	1.218	379423	0.050	0.998
	UKB Freeze 450	SAS	236	9200	808557	0.652	0.622	226850	0.325	1.326	227147	0.016	1.016
	GHS Freeze 145 Exome	EUR	664	109292	2907752	0.824	0.167	892254	0.559	0.731	172221	0.001	1.016
	UKB Freeze 450	EUR	5030	399240	6440585	0.722	0.345	2086994	0.387	1.074	166350	0.000	1.019
	Meta-analysis	ALL	6163	534965	8091286	0.710	0.345	2849393	0.385	1.059	351738	0.020	0.982
COVID19_positive_severe_vs_COVID19_negative_or_unknown_combined	UKB Freeze 450	SAS	18	9200	796240	0.961	0.04	222161	0.910	0.163	226990	0.496	0.749
	UKB Freeze 450	AFR	33	8495	811241	0.919	0.132	248076	0.831	0.346	379346	0.302	0.821
	GHS Freeze 145 Exome	EUR	49	109292	2895469	0.976	0.013	888545	0.932	0.08	172229	0.246	0.785
	UKB Freeze 450	EUR	490	399240	6400400	0.931	0.034	2070233	0.812	0.176	166321	0.001	1.02
	Meta-analysis	ALL	590	526227	7876462	0.917	0.037	2721522	0.783	0.214	225588	0.090	0.889
	UKB Freeze 450	AFR	33	134	NA	NA	NA	NA	NA	NA	235941	0.109	0.234
COVID19_positive_severe_vs_COVID19_positive_not_hospitalized_combined	GHS Freeze 145 Exome	EUR	49	664	194798	0.818	0.273	NA	NA	NA	170209	0.228	1.141
	UKB Freeze 450	EUR	490	5030	373269	0.327	1.078	87177	0.043	1.013	166184	0.001	0.998
	Meta-analysis	ALL	572	5828	410271	0.365	0.912	101899	0.035	0.968	301689	0.056	0.593
	UPENN-PMBB Freeze One	AFR	166	959	195274	0.331	1.345	NA	NA	NA	484596	0.023	0.974
COVID19_positive_vs_COVID19_negative_combined	UKB Freeze 450	AFR	214	766	141313	0.206	1.071	NA	NA	NA	387132	0.013	0.938
	UKB Freeze 450	SAS	301	844	149617	0.129	1.111	NA	NA	NA	228543	0.004	1.07
	GHS Freeze 145 Exome	EUR	834	15574	896282	0.505	0.889	239671	0.091	1.024	172248	0.000	1.019
	UKB Freeze 450	EUR	6733	31257	1361423	0.143	1.15	417941	0.001	1.015	166646	0.000	1
	Meta-analysis	ALL	8248	49400	1745716	0.203	1.023	575968	0.005	1.025	471978	0.006	0.984
	UPENN-PMBB Freeze One	AFR	166	8738	897805	0.700	0.519	282679	0.434	1.219	486918	0.029	0.972
COVID19_positive_vs_COVID19_negative_or_unknown_combined	UKB Freeze 450	AFR	214	8495	821371	0.636	0.666	253263	0.335	1.356	379070	0.015	1.02
	UKB Freeze 450	SAS	301	9200	812263	0.595	0.735	228572	0.246	1.267	226861	0.007	1.012
	GHS Freeze 145 Exome	EUR	834	109292	2910461	0.799	0.205	893247	0.509	0.844	172192	0.001	1.026
	UKB Freeze 450	EUR	6733	399240	6455895	0.675	0.446	2093385	0.315	1.175	166339	0.000	1.017
	Meta-analysis	ALL	8248	534965	8111082	0.663	0.443	2857926	0.315	1.161	351576	0.009	0.996

Supplementary Table 5. Association between the COVID-19 hospitalization phenotype and 50 rare variants in the promoter of EEF2.

rs ID	hg38	Effect allele	Odds ratio	95% LCI	95% UCI	SE	P-value	Effect allele frequency	N cases with 0112 copies of effect allele	N controls with 0112 copies of effect allele	Studies analyzed
rs532051930	19:3985461:G:A	A	93.9065	20.2954	434.505	0.7816	6.18E-09	2.55E-05	1869/410	508510/2220	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs374797871	19:3985414:A:G	G	24.2157	1.84809	317.299	1.3127	0.0152	0.000547	146/110	172151/180	UKB Freeze 450 AFR UPENN-PMBB Freeze One AFR Meta
rs754033543	19:3985383:T:C	C	18.9215	1.73245	206.658	1.2198	0.0159	0.00027	1702/110	399219/210	UKB Freeze 450 EUR Meta
rs542049090	19:3985437:A:G	G	18.6529	1.72231	202.014	1.2155	0.0161	0.00026	1769/110	407947/200	UKB Freeze 450 EUR UPENN-PMBB Freeze One AFR Meta
rs897131413	19:3985457:G:C	C	17.7894	1.63807	193.191	1.2169	0.0180	0.00047	1872/110	508477/470	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs370100022	19:3985421:G:A	A	5.21063	1.10233	24.6302	0.7925	0.0373	0.000140	1936/200	517585/1440	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR UKB Freeze 450 SAS Meta
rs546488032	19:3985433:G:A	A	6.19102	0.776398	49.3674	1.0593	0.0852	0.000057	1937/110	517671/561	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR UKB Freeze 450 SAS Meta
rs201347619	19:3985401:T:A	A	0.364401	0.0678296	1.95767	0.8578	0.2393	0.004028	147/000	170941/381	UKB Freeze 450 AFR UPENN-PMBB Freeze One AFR Meta
rs369523513	19:3985436:G:A	A	0.36233	0.0593301	2.21276	0.9232	0.2715	0.000116	2020/000	525596/1201	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 AFR UKB Freeze 450 EUR UPENN-PMBB Freeze One AFR Meta
rs373888946	19:3985451:G:T	T	0.363709	0.0429819	3.07768	1.0896	0.3533	0.000204	1873/000	508319/2080	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs907273439	19:3985443:G:C	C	2.35632	0.354027	15.6831	0.9671	0.3755	0.000234	1871/210	508270/2370	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs190787427	19:3985426:G:C	C	0.361534	0.0260517	5.0172	1.342	0.4484	0.000117	1938/000	517565/1220	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR UKB Freeze 450 SAS Meta
rs377104055	19:3985429:T:C	C	0.361136	0.0234969	5.55049	1.3941	0.4650	0.000087	1850/000	416400/730	UKB Freeze 450 AFR UKB Freeze 450 EUR UPENN-PMBB Freeze One AFR Meta
rs200921166	19:3985402:C:T	T	0.360523	0.00840259	15.4668	1.9179	0.5948	0.000064	1703/000	399187/510	UKB Freeze 450 EUR Meta
rs774095261	19:3985425:C:A	A	0.352361	0.00521284	23.8177	2.1498	0.6275	0.000020	1850/000	416437/170	UKB Freeze 450 AFR UKB Freeze 450 EUR UPENN-PMBB Freeze One AFR Meta
rs529755390	19:3985441:T:C	C	0.361172	0.00447913	29.123	2.2398	0.6493	0.000049	1873/000	508368/500	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs77439048	19:3985423:A:C	C	0.377494	0.00480048	29.6849	2.227	0.6618	0.000062	1873/000	508457/630	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs1196793724	19:3985434:C:G	G	0.364183	0.00328972	40.3162	2.4015	0.6740	0.000044	1703/000	399202/350	UKB Freeze 450 EUR Meta
rs529755390	19:3985441:T:A	A	0.364438	0.0027381	48.5061	2.4955	0.6859	0.000047	1703/000	399119/380	UKB Freeze 450 EUR Meta
NA	rs5441:T:TCGCCGGCCAGC	CGCCGAC	0.364656	0.00182461	72.878	2.7029	0.7090	0.000044	1873/000	508368/450	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs190787427	19:3985426:G:A	A	0.365569	0.00170724	78.2788	2.7381	0.7132	0.000042	1703/000	399120/340	UKB Freeze 450 EUR Meta
rs1280637004	19:3985463:G:A	A	0.364255	0.000412394	321.736	3.4611	0.7704	0.000024	1703/000	399215/190	UKB Freeze 450 EUR Meta
rs363082396	19:3985435:C:A	A	0.364183	0.000353722	374.953	3.5393	0.7753	0.000034	1873/000	508468/350	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
NA	19:3985425:C:G	G	0.364111	0.000282174	469.838	3.6545	0.7822	0.000021	1703/000	399217/170	UKB Freeze 450 EUR Meta
rs374912847	19:3985392:G:A	A	0.362584	0.000204629	642.464	3.8163	0.7904	0.000014	1703/000	399229/110	UKB Freeze 450 EUR Meta
NA	19:3985455:G:A	A	0.363455	0.000175147	754.222	3.8969	0.7951	0.000016	1703/000	399227/130	UKB Freeze 450 EUR Meta
rs750678552	19:3985430:C:G	G	0.35912	0.000113616	1135.11	4.1116	0.8033	0.000432	65/000	919280	UKB Freeze 450 SAS Meta
rs776567094	19:3985428:G:A	A	0.365423	6.02E-05	2218.87	4.4447	0.8208	0.000019	1703/000	399218/150	UKB Freeze 450 EUR Meta
rs369523513	19:3985436:G:C	C	0.366851	5.09E-05	2645.82	4.5325	0.8249	0.000018	1873/000	508462/180	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
NA	19:3985417:G:C	C	0.363855	2.93E-05	4571.18	4.8096	0.8335	0.000014	1703/000	399224/110	UKB Freeze 450 EUR Meta
rs1027642860	19:3985460:A:C	C	0.36092	1.49E-05	8736.83	5.1503	0.8431	0.000009	1703/000	399229/70	UKB Freeze 450 EUR Meta
rs779559837	19:3985438:G:A	A	0.391097	3.10E-05	4928.25	4.8172	0.8455	0.000110	170/000	109251/240	GHS Freeze 145 MegaFreeze EUR Meta
NA	19:3985444:C:T	T	0.382166	1.81E-05	8071.45	5.0807	0.8498	0.000022	1873/000	508485/220	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs776029459	19:3985405:C:G	G	0.374486	1.16E-05	12130.2	5.2989	0.8530	0.000017	1873/000	508513/170	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
NA	19:3985411:A:G	G	0.364948	5.36E-06	24871	5.6784	0.8591	0.000006	1703/000	399231/50	UKB Freeze 450 EUR Meta
rs995814367	19:3985458:G:A	A	0.365204	3.21E-06	41519	5.9395	0.8653	0.000012	1703/000	399229/100	UKB Freeze 450 EUR Meta
rs764194249	19:3985408:G:A	A	0.365204	2.04E-06	65358.2	6.171	0.8703	0.000006	1703/000	399234/50	UKB Freeze 450 EUR Meta
NA	19:3985442:G:A	A	0.366228	1.12E-06	119957	6.4794	0.8768	0.000009	1703/000	399223/70	UKB Freeze 450 EUR Meta
rs77439048	19:3985423:A:G	G	0.366667	6.02E-07	223245	6.7957	0.8826	0.000015	1703/000	399223/120	UKB Freeze 450 EUR Meta
rs886610889	19:3985452:A:ACGG	ACCG	0.383391	9.78E-07	150305	6.5711	0.8840	0.000046	170/000	109273/100	GHS Freeze 145 MegaFreeze EUR Meta
rs748898673	19:3985399:A:C	C	0.366228	4.01E-07	334091	7.002	0.8859	0.000009	1703/000	399233/70	UKB Freeze 450 EUR Meta
rs560636284	19:3985439:G:A	A	0.92441	0.310456	2.75251	0.5567	0.8877	0.000897	1870/310	507593/9130	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta
rs776567094	19:3985428:G:C	C	0.365825	2.96E-07	451572	7.1563	0.8882	0.000009	1703/000	399218/70	UKB Freeze 450 EUR Meta
rs1019385884	19:3985467:G:A	A	0.366008	2.35E-07	569136	7.2741	0.8901	0.000007	1703/000	399229/60	UKB Freeze 450 EUR Meta
rs1037024876	19:3985452:A:G	G	0.34294	5.19E-08	2.24E+06	8.0119	0.8937	0.000023	1700/000	109273/50	GHS Freeze 145 MegaFreeze EUR Meta
rs754780163	19:3985431:G:A	A	0.366888	1.38E-07	973791	7.5469	0.8943	0.000012	1703/000	399227/100	UKB Freeze 450 EUR Meta
NA	19:3985432:C:G	G	0.367034	7.63E-10	1.77E+08	10.2002	0.9217	0.000006	1703/000	399235/50	UKB Freeze 450 EUR Meta
NA	19:3985449:A:G	G	0.375987	7.77E-10	1.82E+08	10.2028	0.9236	0.000027	1700/000	109282/60	GHS Freeze 145 MegaFreeze EUR Meta
NA	19:3985446:G:A	A	0.367402	2.56E-13	5.28E+11	14.2826	0.9441	0.000006	1703/000	399232/50	UKB Freeze 450 EUR Meta
rs373344045	19:3985424:G:A	A	1.06354	0.140046	8.07673	1.0344	0.9525	0.000243	1872/110	508283/2470	GHS Freeze 145 MegaFreeze EUR UKB Freeze 450 EUR Meta

Supplementary Table 6. Evidence for association between the COVID-19 hospitalization phenotype and rs532051930 across different association tests.

Approach	Association test in individual studies	Approach used to combine results across studies	Association in UKB Europeans			Association in GHS Europeans			Association in UKB+GHS Europeans		
			OR (95% CI)	SE*	P-value	OR (95% CI)	SE*	P-value	OR (95% CI)	SE*	P-value
1 (default)	REGENIE Firth exact test, with covariates and LOCO	Inverse-variance fixed-effects meta-analysis	80.9 (13.1 - 499.5)	0.93	2.20E-06	134.8 (7.9 - 2301.3)	1.45	7.07E-04	93.9 (20.3 - 434.5) 0.78 6.17E-09		
2		Sample size weighted meta-analysis							NA 3.14E-08		
3		Meta-analysis of log-likelihood curves							85.6 (17.2 - 425.8) 0.82 5.51E-08		
4		Firth exact test, no covariates	65.7 (16.9 - 195.3)	0.90	3.49E-06	92.1 (9.9 - 395.0)	1.4	0.00127	72.5 (16.4 - 321.0)	0.76	1.64E-08
5		Fisher's exact test (no covariates)	58.7 (10.6 - 218.5)	0.98	3.35E-05	64.6 (1.48 - 456.8)	1.75	0.017	60.1 (11.2 - 321.6)	0.86	1.70E-06
6		Logistic regression, with covariates	71.6 (15.6 - 241.7)	0.99	1.55E-05	106.5 (5.61 - 648.2)	1.74	0.00733	78.9 (14.6 - 425.0)	0.86	3.73E-07
7		Logistic regression, no covariates	58.7 (13.4 - 185.0)	0.96	2.37E-05	64.7 (3.51 - 340.4)	1.67	0.0123	60.2 (11.7 - 308.4)	0.83	9.00E-07
8		BinomiRare test, with covariates	Meta-analysis NA			NA			NA 2.96E-07		
9		Firth exact test, with covariates	Mega-analysis (UKB+GHS combined)			NA			85.8 (17.2 - 427.2) 0.82 5.48E-08		
10		Firth exact test, no covariates							54.4 (11.8 - 250.5) 0.78 2.91E-07		
11		Fisher's exact test (no covariates)							49.4 (9.7 - 251.0) 0.83 2.53E-06		
12		Logistic regression, with covariates							78.7 (14.6 - 424.9) 0.86 3.88E-07		
13		Logistic regression, no covariates							49.5 (9.9 - 246.2) 0.82 1.89E-06		

*Re-calculated from the OR and p-value

Supplementary Table 7. No carriers of the rare variant rs532051930 in the promoter of EEF2 were observed in an additional 4,341 individuals with COVID-19.

Study	Reference	N COVID-19 cases							Heterozygote for rs532051930:A	
		Total	Hospitalized	Severe	Of European	African	Asian	Hispanic/other ancestry		
GenOMICC	PMID 33307546	2969	2969	2969	2110	145	375	NA	339	0
Columbia University COVID-19 Biobank	https://www.medrxiv.org/content/10.1101/2020.12.18.20248226v2	1152	1082	479	67	463	33	506	83	0
Biobanque Québec Covid-19	https://www.medrxiv.org/content/10.1101/2020.12.18.20248226v2	220	128	62	154	30	29	7	0	0

Supplementary Table 8. Results from burden association tests for 167 genes located in eight loci described by Horowitz et al. (2021).

Trait	Gene	Burden test	MAF	Odds Ratio [95% CI]	P-value	N cases with RRR/AA genotype ^a	N controls with RRR/AA genotype ^a	AAF	GWAS SNP	Distance to GWAS SNP, bp	Distance to GWAS SNP, rank
COVID19 positive hospitalized vs COVID19 negative or unknown	CHAF1A	M1	<1%	25.2164.947.128.539	1.00E-04	1935/30	517687/450	0.00005	19:4719431:G:A	316669	16
COVID19 positive hospitalized vs COVID19 negative or unknown	CHAF1A	M3	<1%	25.2164.947.128.539	1.00E-04	1935/30	517687/450	0.00005	19:4719431:G:A	316669	16
COVID19 positive hospitalized vs COVID19 negative or unknown	SLC22A31	M1	<1%	5.5831.807.17.256	2.80E-03	1844/60	4160714020	0.00049	16:89117727	78271	3
COVID19 positive hospitalized vs COVID19 negative or unknown	SLC22A31	M3	<1%	5.5831.807.17.256	2.80E-03	1844/60	4160714020	0.00049	16:89117727	78271	3
COVID19 positive hospitalized vs COVID19 negative or unknown	SARDH	M1	<1%	2.3671.315.4.259	4.00E-03	20721/21	53347174871	0.0014	9:133270015:A:C	393873	25
COVID19 positive hospitalized vs COVID19 negative or unknown	SHD	M1	<1%	5.2831.619.17.242	5.80E-03	1869/40	5082902420	0.00024	19:4719431:G:A	439368	22
COVID19 positive hospitalized vs COVID19 negative or unknown	CTB-SOL17.10	M1	<1%	5.7261.598.20.518	7.40E-03	2017/30	5256251400	0.00014	19:4719431:G:A	247081	13
COVID19 positive hospitalized vs COVID19 negative or unknown	CTB-SOL17.10	M3	<1%	5.7261.598.20.518	7.40E-03	2017/30	5256251400	0.00014	19:4719431:G:A	247081	13
COVID19 positive hospitalized vs COVID19 negative or unknown	DBH	M1	<1%	0.3200.128.0.796	1.40E-02	2083/20	53276122040	0.00205	9:133270015:A:C	366356	22
COVID19 positive hospitalized vs COVID19 negative or unknown	SIGLEC14	M1	<1%	6.5441.434.29.868	1.50E-02	1936/20	5176259512	0.00012	19:51739497	96143	6
COVID19 positive hospitalized vs COVID19 negative or unknown	OLIG2	M1	<1%	12.0461.255.115.574	3.10E-02	1872/10	508456760	0.00008	21:33252612:A:G	225750	7
COVID19 positive hospitalized vs COVID19 negative or unknown	OLIG2	M3	<1%	12.0461.255.115.574	3.10E-02	1872/10	508456760	0.00008	21:33252612:A:G	225750	7
COVID19 positive hospitalized vs COVID19 negative or unknown	PSORS1C2	M1	<1%	5.1761.151.23.275	3.20E-02	1871/20	5083501820	0.00018	6:31153649:G:A	15699	4
COVID19 positive hospitalized vs COVID19 negative or unknown	PPP2R1A	M3	<1%	5.4291.129.26.105	3.50E-02	1871/20	508371950	0.00019	19:51739497	450599	33
COVID19 positive hospitalized vs COVID19 negative or unknown	SH3GL1	M1	<1%	10.8041.173.99.499	3.60E-02	1872/10	508459730	0.00007	19:4719431:G:A	357832	17
COVID19 positive hospitalized vs COVID19 negative or unknown	MCB	M1	<1%	2.1061.007.4.401	4.80E-02	2077/80	53392110431	0.00098	6:31153649:G:A	344544	18
COVID19 positive hospitalized vs COVID19 negative or unknown	MCB	M3	<1%	2.1061.007.4.401	4.80E-02	2077/80	53392110431	0.00098	6:31153649:G:A	344544	18
COVID19 positive hospitalized vs COVID19 negative or unknown	ATP6V1G2	M3	<1%	8.5960.965.76.602	5.40E-02	1872/10	508475570	0.00006	6:31153649:G:A	391758	21
COVID19 positive hospitalized vs COVID19 negative or unknown	ATP6V1G2	M1	<1%	8.5960.965.76.602	5.40E-02	1872/10	508475570	0.00006	6:31153649:G:A	391758	21
COVID19 positive hospitalized vs COVID19 negative or unknown	SRFBF6	M1	<1%	5.0250.971.25.993	5.40E-02	2016/20	5259752520	0.00024	9:133270015:A:C	61853	2
COVID19 positive hospitalized vs COVID19 negative or unknown	MYDGF	M3	<1%	0.3430.115.1.024	5.50E-02	2085/00	5344694960	0.00046	19:4719431:G:A	61427	2
COVID19 positive hospitalized vs COVID19 negative or unknown	XCR1	M1	<1%	3.0680.967.9.733	5.70E-02	2017/30	5254323330	0.00032	3:45859597:C:T	161348	6
COVID19 positive hospitalized vs COVID19 negative or unknown	C6orf15	M3	<1%	3.0030.965.9.351	5.80E-02	2016/40	5254652991	0.00029	6:31153649:G:A	42269	7
COVID19 positive hospitalized vs COVID19 negative or unknown	LARS2	M3	<1%	1.3550.987.1.861	6.00E-02	2036/481	52945998238	0.00041	3:45859597:C:T	465144	11
COVID19 positive hospitalized vs COVID19 negative or unknown	PRRC2A	M3	<1%	0.7160.505.1.016	6.10E-02	2063/220	529433100257	0.00037	6:31153649:G:A	469140	34
COVID19 positive hospitalized vs COVID19 negative or unknown	LMD1	M3	<1%	2.2020.962.5.038	6.20E-02	2079/60	5340539120	0.00085	3:45859597:C:T	264718	8
COVID19 positive hospitalized vs COVID19 negative or unknown	FTFR1	M1	<1%	9.5210.887.102.209	6.30E-02	2019/10	525731340	0.00003	19:51739497	6444	1
COVID19 positive hospitalized vs COVID19 negative or unknown	SIGLEC14	M3	<1%	3.5350.936.13.249	6.30E-02	2003/20	52627319818	0.00021	19:51739497	96143	6
COVID19 positive hospitalized vs COVID19 negative or unknown	CTBA	M3	<1%	2.8430.930.8.693	6.70E-02	2080/50	5344055600	0.00053	16:89117727	474375	20
COVID19 positive hospitalized vs COVID19 negative or unknown	OLIG1	M1	<1%	7.3540.856.63.204	6.90E-02	1872/10	508454780	0.00008	21:33252612:A:G	182366	5
COVID19 positive hospitalized vs COVID19 negative or unknown	OLIG1	M3	<1%	7.3540.856.63.204	6.90E-02	1872/10	508454780	0.00008	21:33252612:A:G	182366	5
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF615	M1	<1%	0.3680.121.1.117	7.80E-02	2085/00	5341548101	0.00076	19:51739497	253382	17
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF615	M3	<1%	0.3680.121.1.117	7.80E-02	2085/00	5341548101	0.00076	19:51739497	253382	17
COVID19 positive hospitalized vs COVID19 negative or unknown	KDM4B	M3	<1%	2.1460.916.5.028	7.90E-02	2077/80	5318617781	0.00166	19:4719431:G:A	313459	15
COVID19 positive hospitalized vs COVID19 negative or unknown	CPNE7	M1	<1%	2.5090.871.7.222	8.80E-02	2079/60	5342237420	0.00007	16:89117727	458170	18
COVID19 positive hospitalized vs COVID19 negative or unknown	DBH	M3	<1%	0.8240.657.1.033	9.30E-02	2021/640	5140432088735	0.01957	9:133270015:A:C	366356	22
COVID19 positive hospitalized vs COVID19 negative or unknown	SURF1	M1	<1%	1.7340.905.3.321	9.70E-02	2075/100	53551145440	0.00136	9:133270015:A:C	81897	6
COVID19 positive hospitalized vs COVID19 negative or unknown	CTSL	M3	<1%	2.0460.869.4.823	1.00E-01	2076/90	53271612472	0.00017	16:89117727	41119	4
COVID19 positive hospitalized vs COVID19 negative or unknown	FEM1A	M1	<1%	3.7780.670.21.285	1.30E-01	2015/30	5259143130	0.0003	19:4719431:G:A	72423	4
COVID19 positive hospitalized vs COVID19 negative or unknown	FEM1A	M3	<1%	3.7780.670.21.285	1.30E-01	2015/30	5259143130	0.0003	19:4719431:G:A	72423	4
COVID19 positive hospitalized vs COVID19 negative or unknown	LZTFL1	M3	<1%	2.5780.756.8.800	1.30E-01	2082/30	5345044601	0.00043	3:45859597:C:T	33284	1
COVID19 positive hospitalized vs COVID19 negative or unknown	SURF2	M3	<1%	0.4710.176.1.262	1.30E-01	2084/10	5340389270	0.00086	9:133270015:A:C	86577	7
COVID19 positive hospitalized vs COVID19 negative or unknown	ARRDC5	M3	<1%	2.5130.744.8.487	1.40E-01	2080/50	5342637020	0.00066	19:4719431:G:A	171614	7
COVID19 positive hospitalized vs COVID19 negative or unknown	FLOT1	M3	<1%	1.9690.802.4.836	1.40E-01	2077/80	53372212421	0.00117	6:31153649:G:A	425534	26
COVID19 positive hospitalized vs COVID19 negative or unknown	RLON3	M1	<1%	19.0790.389.936.241	1.40E-01	1872/10	508458870	0.00009	19:51739497	427650	32
COVID19 positive hospitalized vs COVID19 negative or unknown	SLC6A20	M1	<1%	0.4620.161.1.328	1.50E-01	2085/00	5344619040	0.00084	3:45859597:C:T	101161	5
COVID19 positive hospitalized vs COVID19 negative or unknown	MAF7B	M3	<1%	0.4730.168.1.330	1.60E-01	2084/10	5340788870	0.00083	5:163300447	202947	4
COVID19 positive hospitalized vs COVID19 negative or unknown	SARDH	M3	<1%	1.2930.905.1.848	1.60E-01	2053/41	52807169913	0.00045	9:133270015:A:C	393873	25
COVID19 positive hospitalized vs COVID19 negative or unknown	TSC1	M3	<1%	0.7410.490.1.121	1.60E-01	2069/160	52819067687	0.00633	9:133270015:A:C	373781	23
COVID19 positive hospitalized vs COVID19 negative or unknown	MUC2J	M1	<1%	0.3670.086.1.555	1.70E-01	2020/00	5252635011	0.00048	6:31153649:G:A	169691	10
COVID19 positive hospitalized vs COVID19 negative or unknown	MUC2J	M3	<1%	0.3670.086.1.555	1.70E-01	2020/00	5252635011	0.00048	6:31153649:G:A	169691	10
COVID19 positive hospitalized vs COVID19 negative or unknown	PLIN5	M1	<1%	0.4860.172.1.374	1.70E-01	2084/10	5340329312	0.00087	19:4719431:G:A	195904	11
COVID19 positive hospitalized vs COVID19 negative or unknown	PLIN5	M3	<1%	0.4860.172.1.374	1.70E-01	2084/10	5340329312	0.00087	19:4719431:G:A	195904	11
COVID19 positive hospitalized vs COVID19 negative or unknown	LMD1	M1	<1%	11.5390.303.439.203	1.90E-01	1872/10	5084311010	0.0001	3:45859597:C:T	264718	8
COVID19 positive hospitalized vs COVID19 negative or unknown	MVD	M1	<1%	0.3620.078.1.673	1.90E-01	1938/00	5173333990	0.00038	16:89117727	462503	19
COVID19 positive hospitalized vs COVID19 negative or unknown	NCR3	M3	<1%	0.3730.086.1.608	1.90E-01	2020/00	5253514140	0.00039	6:31153649:G:A	435417	30
COVID19 positive hospitalized vs COVID19 negative or unknown	RNF166	M3	<1%	2.0520.696.6.046	1.90E-01	2016/10	5251575980	0.00057	16:89117727	420160	15
COVID19 positive hospitalized vs COVID19 negative or unknown	SACML	M1	<1%	3.2930.554.19.385	1.90E-01	1937/10	5175841480	0.00014	3:45859597:C:T	170132	7
COVID19 positive hospitalized vs COVID19 negative or unknown	CCDC94	M1	<1%	3.7630.497.28.456	2.00E-01	2019/10	5256061590	0.00015	19:4719431:G:A	472285	23
COVID19 positive hospitalized vs COVID19 negative or unknown	SACML	M3	<1%	1.9820.690.5.692	2.00E-01	2080/50	534178861	0.00074	3:45859597:C:T	170132	7
COVID19 positive hospitalized vs COVID19 negative or unknown	TRAPP2L	M1	<1%	0.7590.498.1.158	2.00E-01	2069/160	528171678311	0.00635	16:89117727	260577	8
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF616	M1	<1%	0.4930.166.1.465	2.00E-01	2004/10	5255309400	0.00089	19:51739497	375320	28
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF616	M3	<1%	0.4930.166.1.465	2.00E-01	2004/10	5255309400	0.00089	19:51739497	375320	28
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF836	M1	<1%	0.3630.076.1.725	2.00E-01	2085/00	5346153500	0.00033	19:51739497	415374	31
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF836	M3	<1%	0.3630.076.1.725	2.00E-01	2085/00	5346153500	0.00033	19:51739497	415374	31
COVID19 positive hospitalized vs COVID19 negative or unknown	CEACAM18	M1	<1%	0.3650.075.1.733	2.10E-01	2005/00	5260424280	0.0004	19:51739497	260855	18
COVID19 positive hospitalized vs COVID19 negative or unknown	CEACAM18	M3	<1%	0.3650.075.1.733	2.10E-01	2005/00	5260424280	0.0004	19:51739497	260855	18
COVID19 positive hospitalized vs COVID19 negative or unknown	DNAK28	M1	<1%	0.5610.228.1.381	2.10E-01	2083/20	53383711280	0.00015	21:33252612:A:G	235614	8
COVID19 positive hospitalized vs COVID19 negative or unknown	APRT	M3	<1%	0.5020.168.1.501	2.20E-01	2084/10	5341318340	0.00078	16:89117727	300830	10
COVID19 positive hospitalized vs COVID19 negative or unknown	BAG6	M3	<1%	0.7130.416.1.224	2.20E-01	2076/90	5316253373	0.00312	6:31153649:G:A	485481	36
COVID19 positive hospitalized vs COVID19 negative or unknown	HMMR	M3	<1%	0.6880.377.1.254	2.20E-01	2078/70	53222927306	0.00256	5:163300447	160245	3
COVID19 positive hospitalized vs COVID19 negative or unknown	SLC6A20	M3	<1%	0.7210.428.1.216	2.20E-01	2076/90	53123637272	0.00348	3:45859597:C:T	101161	5
COVID19 positive hospitalized vs COVID19 negative or unknown	SPAC49	M1	<1%	0.3680.075.1.806	2.20E-01	2085/00	5345234402	0.00041	9:133270015:A:C	386068	24
COVID19 positive hospitalized vs COVID19 negative or unknown	VARS2	M1	<1%	0.7680.503.1.174	2.20E-01	2069/160	529226572910	0.00537	6:31153649:G:A	239238	14
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF841	M1	<1%	0.5620.225.1.399	2.20E-01	2083/20	53369412710	0.00119	19:51739497	325609	22
COVID19 positive hospitalized vs COVID19 negative or unknown	ZNF841	M3	<1%	0.5620.225.1.399	2.20E-01	2083/20	53369412710	0.00119	19:51739497	325609	22
COVID19 positive hospitalized vs COVID19 negative or unknown	DNR1	M1	<1%	0.3650.071.1.871	2.30E-01	1938/00	5175144180	0.0004	6:31153649:G:A	268430	17
COVID19 positive hospitalized vs COVID19 negative or unknown	FYXO1	M3	<1%	1.2700.862.1.871	2.30E-01	2055/00	52745749416	0.00703	3:45859597:C:T	62167	3
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNGR2	M1	<1%	8.3960.261.270.048	2.30E-01	1872/10	508441910	0.00009	21:33252612:A:G	150931	3
COVID19 positive hospitalized vs COVID19 negative or unknown	TCF7L1	M3	<1%	0.5060.							

COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SURF6</i>	M3	<-1%	1.442(0.785,2.651)	2.40E-01	2071140	53257323884	0.00224	9-133270015:A:C	61853	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AC074141.1</i>	M1	<-1%	0.515(0.167,1.587)	2.50E-01	2084110	53424971511	0.00067	19-51739497	133034	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AC074141.1</i>	M3	<-1%	0.515(0.167,1.587)	2.50E-01	2084110	53424971511	0.00067	19-51739497	133034	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MED22</i>	M1	<-1%	2.725(0.493,5.068)	2.50E-01	1872110	5083491930	0.00019	9-133270015:A:C	71489	4
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CXNG1</i>	M3	<-1%	2.100(0.575,7.670)	2.60E-01	2081410	5343705950	0.00056	5-16330447	13809	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MBXG1</i>	M3	<-1%	0.315(0.042,3.346)	2.60E-01	2081410	5344773146	0.00018	19-4719431:G:A	61427	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>YCR3</i>	M1	<-1%	0.363(0.063,2.083)	2.60E-01	1873100	5082313010	0.00029	6-31153649:G:A	435417	30
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SON</i>	M3	<-1%	1.154(0.897,1.483)	2.60E-01	20147010	5183731657022	0.01553	21-33252612:A:G	290480	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	<-1%	1.968(0.598,6.469)	2.70E-01	2082310	5342537120	0.00067	21-33252612:A:G	10690	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SPG7</i>	M1	<-1%	1.418(0.762,2.638)	2.70E-01	2075100	53298619781	0.00185	16-8911727	390690	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GALNS</i>	M1	<-1%	0.370(0.061,2.257)	2.80E-01	1953100	5167243030	0.00029	16-8911727	303289	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>POU5F1</i>	M3	<-1%	0.363(0.057,2.295)	2.80E-01	1873100	5082352970	0.00029	6-31153649:G:A	10951	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SIGLEC8</i>	M1	<-1%	2.359(0.503,11.052)	2.80E-01	2017130	5253673980	0.00038	19-51739497	287119	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF432</i>	M1	<-1%	1.745(0.629,4.839)	2.80E-01	2078710	53534414210	0.00133	19-51739497	294222	21
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF432</i>	M3	<-1%	1.745(0.629,4.839)	2.80E-01	2078710	53534414210	0.00133	19-51739497	294222	21
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DNX30A</i>	M3	<-1%	1.265(0.809,1.979)	3.00E-01	2061240	53010348557	0.00456	21-33252612:A:G	325694	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SURF2</i>	M1	<-1%	0.532(0.161,1.757)	3.00E-01	2084110	5343116540	0.00061	9-133270015:A:C	86577	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SURF4</i>	M1	<-1%	5.574(0.219,142.075)	3.00E-01	1937110	517635961	0.0001	9-133270015:A:C	93448	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IGLON5</i>	M3	<-1%	1.781(0.591,5.367)	3.10E-01	2080510	5341278380	0.00078	19-51739497	427650	32
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SIGLEC8</i>	M3	<-1%	2.209(0.485,10.070)	3.10E-01	2082310	5345534120	0.00039	19-51739497	287119	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ADAMTSL2</i>	M3	<-1%	0.674(0.308,1.477)	3.20E-01	2081410	53353814200	0.00134	9-133270015:A:C	264725	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ARRDC5</i>	M1	<-1%	4.900(0.209,114.787)	3.20E-01	1872110	5084061260	0.00012	19-4719431:G:A	171614	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GFI1B</i>	M3	<-1%	0.761(0.444,1.304)	3.20E-01	2075100	5112532382	0.00303	9-133270015:A:C	283337	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LIM2</i>	M3	<-1%	1.580(0.643,3.881)	3.20E-01	2078710	53377511900	0.00111	19-51739497	359297	25
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>OBP2B</i>	M1	<-1%	1.214(0.828,1.778)	3.20E-01	2053320	52819467710	0.00633	9-133270015:A:C	64687	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>OBP2B</i>	M3	<-1%	1.214(0.828,1.778)	3.20E-01	2053320	52819467710	0.00633	9-133270015:A:C	64687	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PBRCA2</i>	M1	<-1%	0.635(0.262,1.553)	3.20E-01	1870310	50556129710	0.00291	6-31153649:G:A	469140	34
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CDT1</i>	M1	<-1%	2.121(0.474,9.487)	3.30E-01	2015130	5257924350	0.00041	16-8911727	313896	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RPL7A</i>	M3	<-1%	0.364(0.048,2.778)	3.30E-01	1953100	5168042230	0.00021	9-133270015:A:C	78228	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TCF19</i>	M1	<-1%	0.369(0.050,2.706)	3.30E-01	1938100	5174372941	0.00028	6-31153649:G:A	5820	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>XCR1</i>	M3	<-1%	1.753(0.566,5.428)	3.30E-01	2081410	5342906750	0.00063	3-45859597:C:T	161348	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CDSN</i>	M3	<-1%	0.680(0.310,1.494)	3.40E-01	2074110	53140135631	0.00333	6-31153649:G:A	37625	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CEL</i>	M1	<-1%	0.802(0.513,1.256)	3.40E-01	2070150	530001494420	0.00465	9-133270015:A:C	208022	16
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCR9</i>	M1	<-1%	0.354(0.041,3.080)	3.50E-01	1938100	5175451870	0.00018	3-45859597:C:T	35336	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CTU2</i>	M3	<-1%	1.180(0.834,1.670)	3.50E-01	2047380	52641585446	0.008	16-8911727	411197	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SPIC19</i>	M3	<-1%	0.689(0.317,1.498)	3.50E-01	2081410	53329516682	0.00156	9-133270015:A:C	386068	24
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CEL</i>	M3	<-1%	0.832(0.564,1.229)	3.60E-01	2064210	528589635521	0.00598	9-133270015:A:C	208022	16
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CRYZL1</i>	M1	<-1%	0.363(0.042,3.132)	3.60E-01	1938100	5175202120	0.0002	21-33252612:A:G	337178	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FAM163B</i>	M3	<-1%	1.436(0.647,3.191)	3.70E-01	2066190	53039645690	0.00427	9-133270015:A:C	309006	21
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MPND</i>	M1	<-1%	0.376(0.044,3.228)	3.70E-01	2020010	5255402241	0.00021	19-4719431:G:A	375838	18
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>C21orf62</i>	M1	<-1%	0.362(0.038,3.417)	3.80E-01	1938100	5175671650	0.00016	21-33252612:A:G	458851	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>C21orf62</i>	M3	<-1%	0.362(0.038,3.417)	3.80E-01	1938100	5175671650	0.00016	21-33252612:A:G	458851	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PIEZO1</i>	M1	<-1%	0.722(0.350,1.488)	3.80E-01	2080510	53324317220	0.00161	16-8911727	402123	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ACSF3</i>	M3	<-1%	0.874(0.642,1.189)	3.90E-01	2048370	5242131073517	0.01006	16-8911727	17046	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HMMR</i>	M1	<-1%	0.722(0.342,1.522)	3.90E-01	2080510	53323917215	0.00162	5-16330447	160245	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SHD</i>	M3	<-1%	1.511(0.585,3.902)	3.90E-01	2082310	53391810452	0.00098	19-4719431:G:A	439368	22
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M1	<-1%	3.730(0.189,73.610)	3.90E-01	1872110	5083881640	0.00016	19-4719431:G:A	96807	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M3	<-1%	3.657(0.188,71.218)	3.90E-01	1872110	5083651670	0.00016	19-4719431:G:A	96807	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SURF1</i>	M3	<-1%	1.308(0.702,2.439)	4.00E-01	2072130	53262723380	0.00219	9-133270015:A:C	81897	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CXCR6</i>	M1	<-1%	0.364(0.034,3.941)	4.10E-01	1940010	5170721980	0.00019	3-45859597:C:T	86884	4
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DDX39B</i>	M3	<-1%	0.367(0.034,3.973)	4.10E-01	1873100	5082652670	0.00026	6-31153649:G:A	376784	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IL17C</i>	M3	<-1%	1.666(0.496,5.595)	4.10E-01	2081410	5342617040	0.00066	16-8911727	479086	21
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UBXN6</i>	M1	<-1%	0.368(0.034,3.984)	4.10E-01	2020010	5255831820	0.00017	19-4719431:G:A	273934	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PPF1R18</i>	M1	<-1%	0.365(0.031,4.278)	4.20E-01	1873100	5083561760	0.00017	6-31153649:G:A	476381	35
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF614</i>	M1	<-1%	2.130(0.339,13.393)	4.20E-01	2082310	5347092560	0.00024	19-51739497	273639	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF614</i>	M3	<-1%	2.130(0.339,13.393)	4.20E-01	2082310	5347092560	0.00024	19-51739497	273639	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ETFB</i>	M3	<-1%	1.329(0.655,2.696)	4.30E-01	2077810	53321317511	0.00164	19-51739497	394287	29
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ACSF3</i>	M1	<-1%	0.683(0.258,1.808)	4.40E-01	2082310	5340938720	0.00081	16-8911727	17046	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ANKRD11</i>	M3	<-1%	1.168(0.788,1.733)	4.40E-01	2056290	5283966233	0.00062	16-8911727	150750	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DNAJC28</i>	M3	<-1%	0.762(0.384,1.512)	4.40E-01	2079610	53303119340	0.00181	21-33252612:A:G	235614	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FYCO1</i>	M1	<-1%	1.425(0.575,3.534)	4.40E-01	2080510	53386510982	0.00103	3-45859597:C:T	62167	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GALNS</i>	M3	<-1%	0.747(0.357,1.563)	4.40E-01	2080510	53314118231	0.00017	16-8911727	303289	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>BNGR2</i>	M3	<-1%	3.072(0.176,53.618)	4.40E-01	1872110	5084061260	0.00012	21-33252612:A:G	150931	4
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PLIN3</i>	M3	<-1%	0.591(0.154,2.274)	4.40E-01	2084110	5345134511	0.00042	19-4719431:G:A	119760	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PLIN3</i>	M3	<-1%	1.203(0.756,1.912)	4.40E-01	2064210	530811413321	0.00391	19-4719431:G:A	214973	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAFIP2L1</i>	M3	<-1%	0.856(0.575,1.273)	4.40E-01	2064210	527447780414	0.00703	16-8911727	260577	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ADAMTSL2</i>	M1	<-1%	0.727(0.317,1.669)	4.50E-01	2081410	53374412147	0.00115	9-133270015:A:C	264725	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GART</i>	M1	<-1%	1.393(0.591,3.285)	4.50E-01	2078710	53341715480	0.00145	21-33252612:A:G	251511	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IL10RB</i>	M1	<-1%	2.965(0.174,50.555)	4.50E-01	1937110	5175841480	0.00014	21-33252612:A:G	13853	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SLC2A6</i>	M1	<-1%	0.377(0.030,4.670)	4.50E-01	2085010	5348011631	0.00015	9-133270015:A:C	202005	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF649</i>	M1	<-1%	0.367(0.027,4.993)	4.50E-01	1873100	5083631690	0.00017	19-51739497	151120	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF649</i>	M3	<-1%	0.367(0.027,4.993)	4.50E-01	1873100	5083631690	0.00017	19-51739497	151120	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AIF1</i>	M1	<-1%	0.364(0.025,5.368)	4.60E-01	1938100	5175871450	0.00014	6-31153649:G:A	461680	32
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SEMA6B</i>	M1	<-1%	0.359(0.023,5.521)	4.60E-01	1873100	5084071250	0.00012	19-4719431:G:A	176518	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SEMA6B</i>	M3	<-1%	0.359(0.023,5.521)	4.60E-01	1873100	5084071250	0.00012	19-4719431:G:A	176518	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>EBI3</i>	M1	<-1%	0.366(0.031,5.744)	4.70E-01	1873100	5083811690	0.00014	19-4719431:G:A	489881	24
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FLDT1</i>	M1	<-1%	0.365(0.023,5.722)	4.70E-01	1873100	5083971350	0.00013	6-31153649:G:A	425534	26
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MED22</i>	M3	<-1%	0.600(0.150,4.401)	4.70E-01	2084110	5344844810	0.00045	9-133270015:A:C	71489	4
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NKG7</i>	M3	<-1%	1.921(0.3							

COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LTB</i>	M3	<1%	0.359 0.018;7.128	5.00E-01	1873 00	50844587 0	0.00009	6:31153649:G:A	427059	27
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NUDCD2</i>	M3	<1%	0.607 0.142;2.598	5.00E-01	2084 10	534582383 0	0.00036	5:163300447	153519	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SURF4</i>	M3	<1%	0.612 0.149;2.513	5.00E-01	2084 10	534492472 1	0.00044	9:133270015:A:C	93448	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>C6orf13</i>	M1	<1%	0.370 0.019;7.362	5.10E-01	1873 00	508407124 1	0.00012	6:31153649:G:A	42269	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CDT1</i>	M3	<1%	0.840 0.506;1.412	5.10E-01	2073 20	5320382920 7	0.00274	16:8911727	313896	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FPF3</i>	M3	<1%	0.363 0.017;7.326	5.10E-01	1873 00	516947800 0	0.00008	19:51739497	29161	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FPF2</i>	M3	<1%	0.365 0.019;7.103	5.10E-01	1953 00	516947800 0	0.00008	19:51739497	29161	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MPND</i>	M3	<1%	1.146 0.765;1.717	5.10E-01	2059 251	5287726178 15	0.0058	19:4719431:G:A	375838	18
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GTFC3</i>	M3	<1%	1.236 0.644;2.372	5.20E-01	2074 110	53249624690 0	0.00231	9:133270015:A:C	239004	17
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MVD</i>	M3	<1%	0.778 0.361;1.676	5.20E-01	2080 50	5332716871 1	0.00158	16:8911727	465203	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CBFA2T3</i>	M1	<1%	2.336 0.164;3.240	5.30E-01	1872 10	5083481831 1	0.00018	16:8911727	240752	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCNG1</i>	M1	<1%	0.370 0.017;7.948	5.30E-01	2020 00	525664101 0	0.00001	5:163300447	138809	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IL17C</i>	M1	<1%	0.364 0.016;8.237	5.30E-01	1873 00	508415117 0	0.00011	16:8911727	479086	21
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AC018753.18</i>	M3	<1%	1.134 0.757;1.697	5.40E-01	2058 270	5288706077 18	0.00572	19:51739497	127267	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HIST1</i>	M3	<1%	1.169 0.709;1.925	5.40E-01	2067 180	5308044459 2	0.00389	19:51739497	26071	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PLIN3</i>	M1	<1%	0.640 0.151;2.712	5.40E-01	2084 10	534575389 1	0.00036	19:4719431:G:A	119760	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>APRT</i>	M1	<1%	0.637 0.147;2.755	5.50E-01	1939 10	5168004700 0	0.00045	16:8911727	308030	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FPF3</i>	M3	<1%	0.379 0.016;9.247	5.50E-01	1940 00	51720169 0	0.00007	19:51739497	84251	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF577</i>	M1	<1%	0.710 0.232;2.175	5.50E-01	2083 20	5342357291 1	0.00068	19:51739497	133034	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF577</i>	M3	<1%	0.710 0.232;2.175	5.50E-01	2083 20	5342357291 1	0.00068	19:51739497	133034	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCR3</i>	M3	<1%	0.839 0.467;1.509	5.60E-01	2076 90	5327052252 8	0.00212	3:45859597:C:T	404806	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>REXO4</i>	M1	<1%	1.410 0.440;4.521	5.60E-01	2081 40	534520442 3	0.00042	9:133270015:A:C	136937	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ABO</i>	M1	<1%	1.163 0.694;1.949	5.70E-01	2068 170	5312053752 8	0.00352	9:133270015:A:C	14414	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ABO</i>	M3	<1%	1.163 0.694;1.949	5.70E-01	2068 170	5312053752 8	0.00352	9:133270015:A:C	14414	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CR2L1</i>	M3	<1%	0.755 0.288;1.982	5.70E-01	2082 30	5339231044 11	0.00097	21:33252612:A:G	337178	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DPP9</i>	M1	<1%	0.364 0.011;2.326	5.70E-01	1938 00	5176291030 0	0.00001	19:4719431:G:A	42868	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GTE2H4</i>	M1	<1%	0.648 0.147;2.863	5.70E-01	1872 10	508061471 0	0.00046	6:31153649:G:A	244613	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GTE2H4</i>	M3	<1%	0.648 0.147;2.863	5.70E-01	1872 10	508061471 0	0.00046	6:31153649:G:A	244613	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NFKB1L1</i>	M1	<1%	0.362 0.010;2.546	5.70E-01	1938 00	5176261060 0	0.00001	6:31153649:G:A	394045	22
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAP2</i>	M1	<1%	0.647 0.146;2.879	5.70E-01	2084 10	5345564081 1	0.00038	19:4719431:G:A	395299	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAP2</i>	M3	<1%	0.647 0.146;2.879	5.70E-01	2084 10	5345564081 1	0.00038	19:4719431:G:A	395299	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AC018753.18</i>	M1	<1%	1.121 0.745;1.688	5.80E-01	2059 260	5290958581 8	0.00551	19:51739497	127267	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DDI1</i>	M3	<1%	0.897 0.612;1.314	5.80E-01	2061 240	5281776786 2	0.00634	6:31153649:G:A	268430	17
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GTFC3</i>	M1	<1%	1.613 0.302;8.614	5.80E-01	2018 20	525364401 0	0.00038	9:133270015:A:C	239004	17
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IER3</i>	M3	<1%	0.366 0.011;2.404	5.80E-01	1873 00	51778929 0	0.00009	6:31153649:G:A	409714	23
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RPL13</i>	M1	<1%	0.386 0.014;11.051	5.80E-01	2020 00	52571055 0	0.00005	16:8911727	443332	17
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RPL13</i>	M3	<1%	0.386 0.014;11.051	5.80E-01	2020 00	52571055 0	0.00005	16:8911727	443332	17
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CXCR6</i>	M3	<1%	1.374 0.439;4.303	5.90E-01	2082 30	53396110040 0	0.00094	3:45859597:C:T	86884	4
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DDX39B</i>	M1	<1%	0.369 0.010;3.799	5.90E-01	1873 00	5083881440 0	0.00014	6:31153649:G:A	376784	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>EBI3</i>	M3	<1%	0.659 0.147;2.957	5.90E-01	2084 10	534573871 1	0.00036	19:4719431:G:A	489881	24
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HLA-C</i>	M1	<1%	0.819 0.399;1.682	5.90E-01	1932 60	51586918594 0	0.00018	6:31153649:G:A	115519	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HLA-C</i>	M3	<1%	0.819 0.399;1.682	5.90E-01	1932 60	51586918594 0	0.00018	6:31153649:G:A	115519	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SNAI3</i>	M1	<1%	2.035 0.154;26.820	5.90E-01	1937 10	5176251043 0	0.00011	16:8911727	439280	16
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CYBA</i>	M1	<1%	0.365 0.009;15.232	6.00E-01	1873 00	50843995 0	0.00009	16:8911727	474375	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LTA</i>	M3	<1%	0.370 0.009;15.194	6.00E-01	1873 00	50845082 0	0.00008	6:31153649:G:A	419093	24
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC10</i>	M1	<1%	1.257 0.533;2.964	6.00E-01	2080 50	53269122740 0	0.00212	19:51739497	328399	23
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ETFB</i>	M1	<1%	0.382 0.010;15.023	6.10E-01	2018 00	526137900 0	0.00009	19:51739497	394287	29
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IER3</i>	M1	<1%	0.365 0.008;17.529	6.10E-01	1873 00	508462700 0	0.00007	6:31153649:G:A	409714	23
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MAT2B</i>	M1	<1%	0.365 0.008;17.788	6.10E-01	1873 00	508463690 0	0.00007	5:163300447	202947	4
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RPL7A</i>	M1	<1%	0.364 0.007;18.601	6.10E-01	1873 00	508464680 0	0.00007	9:133270015:A:C	78228	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TMEM50B</i>	M3	<1%	1.489 0.318;6.964	6.10E-01	2004 10	5261173530 0	0.00033	21:33252612:A:G	198205	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCR9</i>	M3	<1%	0.845 0.435;1.640	6.20E-01	2075 100	53174932160 0	0.003	3:45859597:C:T	35336	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PIEZO1</i>	M3	<1%	0.954 0.793;1.149	6.20E-01	1973 1111	5046093025181 0	0.02844	16:8911727	402123	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC11</i>	M1	<1%	1.211 0.569;2.576	6.20E-01	2010 80	5244917726 0	0.00017	19:51739497	475425	34
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TMEM8C</i>	M1	<1%	0.366 0.007;19.640	6.20E-01	1873 00	508459730 0	0.00007	9:133270015:A:C	244620	18
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AVKRD1</i>	M1	<1%	0.370 0.006;21.174	6.30E-01	1873 00	5084261060 0	0.00001	16:8911727	150750	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HLA-B</i>	M1	<1%	0.370 0.006;21.195	6.30E-01	1873 00	508450820 0	0.00008	6:31153649:G:A	200833	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HLA-B</i>	M3	<1%	0.370 0.006;21.195	6.30E-01	1873 00	508450820 0	0.00008	6:31153649:G:A	200833	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LTB</i>	M1	<1%	0.364 0.006;22.319	6.30E-01	1873 00	508475570 0	0.00006	6:31153649:G:A	427059	27
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC11</i>	M3	<1%	1.204 0.567;2.557	6.30E-01	2077 80	53318017916 0	0.00167	19:51739497	475425	34
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	<1%	0.756 0.234;2.444	6.40E-01	2083 20	5342197460 0	0.0007	21:33252612:A:G	72443	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NRM</i>	M1	<1%	1.796 0.152;21.204	6.40E-01	1952 10	5168252020 0	0.0002	6:31153649:G:A	464989	33
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GFIIB</i>	M1	<1%	0.367 0.004;30.523	6.60E-01	1873 00	508466660 0	0.00006	9:133270015:A:C	283337	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PLIN4</i>	M1	<1%	1.140 0.639;2.037	6.60E-01	2072 130	53200729499 0	0.00277	19:4719431:G:A	214973	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SDN</i>	M1	<1%	0.364 0.004;34.635	6.60E-01	1940 00	517207630 0	0.00006	21:33252612:A:G	290480	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>HIST1</i>	M1	<1%	1.189 0.532;2.654	6.70E-01	2078 70	5332191745 1	0.00163	19:51739497	26071	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LRG1</i>	M3	<1%	1.270 0.427;3.778	6.70E-01	2083 20	5346053600 0	0.00034	19:4719431:G:A	181492	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC6</i>	M1	<1%	0.708 0.143;3.510	6.70E-01	1872 10	5076878450 0	0.00083	19:51739497	219416	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC6</i>	M3	<1%	0.708 0.143;3.510	6.70E-01	1872 10	5076878450 0	0.00083	19:51739497	219416	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TNF</i>	M3	<1%	1.319 0.364;4.770	6.70E-01	1950 30	5163886390 0	0.00062	6:31153649:G:A	422092	25
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LST1</i>	M1	<1%	0.366 0.003;43.447	6.80E-01	1873 00	508483490 0	0.00005	6:31153649:G:A	433650	29
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LST1</i>	M3	<1%	0.366 0.003;43.447	6.80E-01	1873 00	508483490 0	0.00005	6:31153649:G:A	433650	29
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MC1D1</i>	M1	<1%	1.676 0.149;18.821	6.80E-01	1872 10	5083641680 0	0.00017	6:31153649:G:A	375365	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MC1D1</i>	M3	<1%	1.676 0.149;18.821	6.80E-01	1872 10	5083641680 0	0.00017	6:31153649:G:A	375365	19
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TNFAIP3L1</i>	M1	<1%	0.367 0.003;43.093	6.80E-01	1873 00	508485470 0	0.00005	19:4719431:G:A	67562	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCR1</i>	M1	<1%	0.364 0.003;36.469	6.90E-01	1940 00	508483490 0	0.00003	3:45859597:C:T	34368	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LMZ</i>	M1	<1%	0.370 0.003;49.414	6.90E-01	1940 00	517211590 0	0.00006	19:51739497	359297	25
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF613</i>	M3	<1%	1.380 0.280;6.797	6.90E-01	2083 20	5345424230 0	0.0004			

COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FSD1</i>	M1	<1%	0.3690 0.001 117.744	7.30E-01	1873 00	50849438 0	0.00004	19:4719431:G:A	414685	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GBGT1</i>	M3	<1%	1.0490 0.804 1.368	7.30E-01	202757 1	521986 12948 31	0.01217	9:133270015:A:C	116439	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC12</i>	M1	<1%	1.182 0.460 3.036	7.30E-01	2080 50	53398 1982 2	0.00092	19:51739497	247857	16
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC12</i>	M3	<1%	1.1790 0.459 3.029	7.30E-01	2080 50	53398 0983 2	0.00092	19:51739497	247857	16
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CDH15</i>	M1	<1%	1.3040 0.277 6.149	7.40E-01	2083 20	53454 431 0	0.00004	16:8911727	54104	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>POL3F1</i>	M1	<1%	0.3570 0.01166 756	7.40E-01	1873 00	508577 540	0.00002	6:31153649:G:A	10051	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FAM163B</i>	M1	<1%	0.3690 0.001 163.914	7.50E-01	1873 00	508499 330	0.00003	9:133270015:A:C	309006	21
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STKLD1</i>	M1	<1%	1.1660 0.455 2.987	7.50E-01	2080 50	533984 980 1	0.00092	9:133270015:A:C	106458	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TMEM50B</i>	M1	<1%	0.3680 0.001 185.287	7.50E-01	1873 00	508494 380 0	0.00004	21:33252612:A:G	198205	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF350</i>	M1	<1%	0.7610 0.144 4.027	7.50E-01	2084 10	534690 274 1	0.00026	19:51739497	225356	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF350</i>	M3	<1%	0.7610 0.144 4.027	7.50E-01	2084 10	534690 274 1	0.00026	19:51739497	225356	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCDC94</i>	M3	<1%	1.2030 0.364 3.973	7.60E-01	2083 20	534347 617 1	0.00058	19:4719431:G:A	472285	23
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DPCR1</i>	M1	<1%	0.8230 0.237 2.860	7.60E-01	2083 20	534233 731 1	0.00068	6:31153649:G:A	219027	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DPCR1</i>	M3	<1%	0.8230 0.237 2.860	7.60E-01	2083 20	534233 731 1	0.00068	6:31153649:G:A	219027	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>DP99</i>	M3	<1%	1.0640 0.709 1.598	7.60E-01	2060 250	5285226 30 13	0.00603	19:4719431:G:A	42868	1
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PPR3</i>	M1	<1%	0.3690 0.001 218.142	7.60E-01	1873 00	508510 22 0	0.00002	19:51739497	84251	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PSORS1C1</i>	M1	<1%	0.8980 0.453 1.780	7.60E-01	2079 60	533000 1964 1	0.00184	6:31153649:G:A	24017	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PSORS1C1</i>	M3	<1%	0.8980 0.453 1.780	7.60E-01	2079 60	533000 1964 1	0.00184	6:31153649:G:A	24017	5
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RNF166</i>	M1	<1%	1.2730 0.270 6.009	7.60E-01	2018 20	525472 8880	0.00027	16:8911727	420160	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCR3</i>	M1	<1%	0.8560 0.309 2.372	7.70E-01	2017 30	525195 5682	0.00054	3:45859597:C:T	404806	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF175</i>	M1	<1%	0.8880 0.400 1.975	7.70E-01	2081 40	533617 1345 3	0.00126	19:51739497	166168	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ZNF175</i>	M3	<1%	0.8880 0.400 1.975	7.70E-01	2081 40	533617 1345 3	0.00126	19:51739497	166168	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PABPN1L</i>	M1	<1%	0.8340 0.238 2.922	7.80E-01	2083 20	534695 951	0.00056	16:8911727	253991	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RALGDS</i>	M1	<1%	1.2520 0.274 5.532	7.90E-01	2083 20	534643 331 0	0.00031	9:133270015:A:C	171429	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TMEM8C</i>	M3	<1%	0.8440 0.235 3.029	7.90E-01	2083 20	534301 6640	0.00062	9:133270015:A:C	244620	18
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CBX16</i>	M3	<1%	0.9240 0.509 1.677	7.90E-01	2076 81	532445 571 3	0.00236	19:4719431:G:A	27393	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFAR1</i>	M1	<1%	0.8050 0.146 4.438	8.00E-01	2019 10	5254063 599	0.00034	21:33252612:A:G	72443	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NRM</i>	M3	<1%	0.8500 0.238 3.033	8.00E-01	2083 20	534283 682 0	0.00064	6:31153649:G:A	464989	33
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>REXO4</i>	M3	<1%	1.0970 0.527 2.285	8.00E-01	2077 80	533569 13924	0.00131	9:133270015:A:C	136937	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CACFD1</i>	M3	<1%	0.9190 0.453 1.861	8.10E-01	2080 50	533381 1583 1	0.00148	9:133270015:A:C	190051	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LARS2</i>	M1	<1%	0.8080 0.140 4.671	8.10E-01	2004 10	526142 3280	0.00031	3:45859597:C:T	465144	11
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PPP1R18</i>	M3	<1%	0.9090 0.427 1.937	8.10E-01	2079 60	534061 8968	0.00085	6:31153649:G:A	476381	33
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PPP2R1A</i>	M1	<1%	0.3660 0.000 1508.610	8.10E-01	1873 00	508508 24 0	0.00002	19:51739497	450599	35
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UHRF1</i>	M1	<1%	0.3680 0.000 1325.460	8.10E-01	1873 00	508517 15 0	0.00001	19:4719431:G:A	190042	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UHRF1</i>	M3	<1%	0.3680 0.000 1325.460	8.10E-01	1873 00	508517 15 0	0.00001	19:4719431:G:A	190042	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CDH15</i>	M3	<1%	1.0690 0.605 1.891	8.20E-01	2071 30	5327262 3316	0.0021	16:8911727	54104	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MUC22</i>	M1	<1%	0.8710 0.247 3.070	8.30E-01	1913 20	4252524 129	0.00051	6:31153649:G:A	142943	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MUC22</i>	M3	<1%	0.8710 0.247 3.070	8.30E-01	1913 20	4252524 129	0.00051	6:31153649:G:A	142943	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC10</i>	M1	<1%	1.1190 0.395 3.165	8.30E-01	1934 40	515732 20000	0.00193	19:51739497	328399	23
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CPNE7</i>	M3	<1%	1.0480 0.644 1.708	8.50E-01	2067 180	530935 40300	0.00377	16:8911727	458170	18
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>LTA</i>	M1	<1%	0.3670 0.000 12959.200	8.50E-01	1873 00	508522 10 0	0.00001	6:31153649:G:A	419093	24
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>RALGDS</i>	M3	<1%	0.9540 0.589 1.545	8.50E-01	2069 160	530761 41986	0.00393	9:133270015:A:C	171429	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>AF1</i>	M3	<1%	0.8520 0.143 5.082	8.60E-01	2084 10	534686 2790	0.00026	6:31153649:G:A	461680	32
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>PABPN1L</i>	M3	<1%	0.9160 0.358 2.345	8.60E-01	2081 40	535859 11051	0.00103	16:8911727	253991	7
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC5</i>	M3	<1%	1.0360 0.692 1.549	8.60E-01	2060 250	5284846 10116	0.00573	19:51739497	127267	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TNF</i>	M1	<1%	0.3680 0.000 2777.100	8.60E-01	1873 00	508514 180	0.00002	6:31153649:G:A	423092	25
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CACFD1</i>	M1	<1%	1.1910 0.145 9.818	8.70E-01	2019 10	5255941 710	0.00016	9:133270015:A:C	190051	14
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CLDN22</i>	M3	<1%	0.8940 0.241 3.316	8.70E-01	2083 20	534613 3502	0.00033	19:51739497	372356	27
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SH3GL1</i>	M3	<1%	0.8950 0.240 3.344	8.70E-01	2083 20	534346 6190	0.00058	19:4719431:G:A	357832	17
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TNFAIP8L1</i>	M3	<1%	1.1900 0.143 9.890	8.70E-01	2019 10	525556 2090	0.0002	19:4719431:G:A	67562	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TSC1</i>	M1	<1%	0.9120 0.307 2.703	8.70E-01	2082 30	5342227 430	0.00069	9:133270015:A:C	373781	23
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SFT42</i>	M1	<1%	0.3730 0.000 129089.000	8.80E-01	1700 0	109274 180	0.00008	6:31153649:G:A	222162	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SFT42</i>	M3	<1%	0.3730 0.000 129089.000	8.80E-01	1700 0	109274 180	0.00008	6:31153649:G:A	222162	13
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MDC1</i>	M3	<1%	0.9140 0.244 3.430	8.90E-01	2083 20	534403 5620	0.00053	6:31153649:G:A	453185	31
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>USG10L</i>	M1	<1%	0.9590 0.522 1.761	8.90E-01	2078 70	5327272 262	0.00209	19:51739497	406887	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCHCR1</i>	M3	<1%	0.9710 0.605 1.557	9.00E-01	2068 170	530623 4332 0	0.00407	6:31153649:G:A	11058	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>GBGT1</i>	M1	<1%	0.9680 0.588 1.596	9.00E-01	2071 30	531599 3355 11	0.00316	9:133270015:A:C	116439	10
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TUBB</i>	M1	<1%	0.3810 0.000 1930640.000	9.00E-01	1873 00	508521 11 0	0.00001	6:31153649:G:A	433143	28
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TUBB</i>	M3	<1%	0.3810 0.000 1930640.000	9.00E-01	1873 00	508521 11 0	0.00001	6:31153649:G:A	433143	28
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MDC1</i>	M1	<1%	0.9270 0.245 3.513	9.10E-01	2083 20	534414 5150	0.00051	6:31153649:G:A	453185	31
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NFKB1L1</i>	M3	<1%	1.1320 0.140 9.129	9.10E-01	2084 10	534693 2720	0.00025	6:31153649:G:A	394045	22
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ADAMTS13</i>	M1	<1%	1.0760 0.256 4.523	9.20E-01	2083 20	534440 5250	0.00049	9:133270015:A:C	152428	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>ADAMTS13</i>	M3	<1%	1.0760 0.256 4.523	9.20E-01	2083 20	534440 5250	0.00049	9:133270015:A:C	152428	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CBF4T3</i>	M3	<1%	1.0280 0.613 1.725	9.20E-01	2070 50	530741 42231	0.00395	16:8911727	240752	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>FSD1</i>	M3	<1%	0.9450 0.314 2.841	9.20E-01	2083 20	534118 8340	0.00078	19:4719431:G:A	414685	20
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SGLEC5</i>	M1	<1%	1.0230 0.680 1.537	9.20E-01	2061 240	529067 5821 6	0.00553	19:51739497	127267	8
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CLDN22</i>	M1	<1%	1.1050 0.137 8.938	9.30E-01	1937 10	517581 8331	0.00018	19:51739497	372356	27
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IL1ORB</i>	M3	<1%	0.9230 0.141 6.047	9.30E-01	2017 10	525901 3260	0.00031	21:33252612:A:G	13853	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>BAG6</i>	M3	<1%	1.0570 0.137 8.174	9.60E-01	2004 10	5261932 743	0.00027	6:31153649:G:A	485481	36
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STKLD1</i>	M3	<1%	1.0160 0.526 1.960	9.60E-01	2076 90	533250 17132	0.00161	9:133270015:A:C	106458	9
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CCHCR1</i>	M1	<1%	0.9910 0.597 1.647	9.70E-01	2070 50	531208 37489	0.00352	6:31153649:G:A	11058	3
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>NUDC2</i>	M1	<1%	1.0390 0.135 8.008	9.70E-01	2084 10	5347492 160	0.00002	5:163300447	153519	12
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SPG7</i>	M3	<1%	1.0040 0.786 1.283	9.70E-01	2025 600	5196851 5227 53	0.01433	16:8911727	390690	2
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>CD5N</i>	M1	<1%	0.9860 0.255 4.140	9.80E-01	2076 90	5326832 2820	0.00213	6:31153649:G:A	37625	6
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>KDM4B</i>	M1	<1%	0.9720 0.142 6.666	9.80E-01	1939 10	5166456 5250	0.00006	19:4719431:G:A	313459	15
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>MG7</i>	M1	<1%	0.9770 0.140 6.842	9.80E-01	1937 10	508762 560	0.00025	19:51739497	36731	26
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>SNAB</i>	M3	<								

Supplementary Table 9. Results from burden association tests for 14 genes related to interferon signaling.

Trait	Gene	Burden test	MAF	Odds Ratio [95% CI]	P-value	N cases with		N controls with		AAF
						RR RA AA genotype*	RR RA AA genotype*			
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M1	<0.1%	0.8 (0.15, 4.44)	0.8033	2019 1 0	525406 359 0	3.41E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M1	<0.1%	2.08 (0.62, 6.96)	0.2361	2082 3 0	534277 688 0	6.43E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IKBKG</i>	M1	<0.1%	0.49 (0.0, 50.22)	0.7634	1873 0 0	508491 31 10	5.00E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF3</i>	M1	<0.1%	0.96 (0.25, 3.64)	0.9476	2083 2 0	534559 406 0	3.80E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF7</i>	M1	<0.1%	1.16 (0.43, 3.18)	0.766	2082 3 0	534124 84 10	7.86E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF9</i>	M1	<0.1%	0.37 (0.0, 53.77)	0.696	1873 0 0	508479 53 0	5.19E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT1</i>	M1	<0.1%	0.37 (0.0, 126.71)	0.7357	1873 0 0	508490 42 0	4.11E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT2</i>	M1	<0.1%	0.35 (0.03, 4.44)	0.4215	1873 0 0	508405 127 0	1.24E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TBK1</i>	M1	<0.1%	0.37 (0.01, 11.96)	0.5714	1873 0 0	508445 87 0	8.52E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M1	<0.1%	3.73 (0.19, 73.61)	0.387	1872 1 0	508368 164 0	1.62E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR3</i>	M1	<0.1%	1.13 (0.14, 8.83)	0.909	2084 1 0	534674 29 10	2.72E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR7</i>	M1	<0.1%	7.63 (1.87, 31.08)	0.004584	1872 0 1	508503 25 4	3.43E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAF3</i>	M1	<0.1%	0.37 (0.0, 733.64)	0.7966	1873 0 0	508504 28 0	2.74E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UNC93B1</i>	M1	<0.1%	1.3 (0.27, 6.24)	0.741	1938 2 0	516861 409 0	3.96E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M1	<1%	0.8 (0.15, 4.44)	0.8033	2019 1 0	525406 359 0	3.41E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M1	<1%	2.08 (0.62, 6.96)	0.2361	2082 3 0	534277 688 0	6.43E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IKBKG</i>	M1	<1%	0.49 (0.0, 50.22)	0.7634	1873 0 0	508491 31 10	5.00E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF3</i>	M1	<1%	1.82 (0.54, 6.13)	0.3334	2082 2 1	534509 455 1	4.29E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF7</i>	M1	<1%	1.16 (0.43, 3.18)	0.766	2082 3 0	534124 84 10	7.86E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF9</i>	M1	<1%	0.37 (0.0, 53.77)	0.696	1873 0 0	508479 53 0	5.19E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT1</i>	M1	<1%	0.37 (0.0, 126.71)	0.7357	1873 0 0	508490 42 0	4.11E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT2</i>	M1	<1%	0.35 (0.03, 4.44)	0.4215	1873 0 0	508405 127 0	1.24E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TBK1</i>	M1	<1%	0.37 (0.01, 11.96)	0.5714	1873 0 0	508445 87 0	8.52E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M1	<1%	3.73 (0.19, 73.61)	0.387	1872 1 0	508368 164 0	1.62E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR3</i>	M1	<1%	1.13 (0.14, 8.83)	0.909	2084 1 0	534674 29 10	2.72E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR7</i>	M1	<1%	7.63 (1.87, 31.08)	0.004584	1872 0 1	508503 25 4	3.43E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAF3</i>	M1	<1%	0.37 (0.0, 733.64)	0.7966	1873 0 0	508504 28 0	2.74E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UNC93B1</i>	M1	<1%	1.3 (0.27, 6.24)	0.741	1938 2 0	516861 409 0	3.96E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M1	singleton	0.37 (0.0, 44.0)	0.6857	1873 0 0	508477 55 0	5.39E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M1	singleton	0.36 (0.0, 179.42)	0.7463	1873 0 0	508500 32 0	3.13E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IKBKG</i>	M1	singleton	0.55 (0.0, 2706.13)	0.8906	1873 0 0	508523 7 2	1.08E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF3</i>	M1	singleton	0.37 (0.0, 113.18)	0.7313	1873 0 0	508495 37 0	3.62E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF7</i>	M1	singleton	0.37 (0.0, 64.55)	0.7071	1873 0 0	508481 51 0	5.00E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF9</i>	M1	singleton	0.37 (0.0, 249.69)	0.7666	1873 0 0	508505 27 0	2.64E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT1</i>	M1	singleton	0.37 (0.0, 301.54)	0.7688	1873 0 0	508502 30 0	2.94E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT2</i>	M1	singleton	0.37 (0.0, 37.61)	0.6705	1873 0 0	508487 45 0	4.41E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TBK1</i>	M1	singleton	0.36 (0.0, 86.69)	0.7179	1873 0 0	508501 31 0	3.04E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M1	singleton	18.3 (1.71, 196.34)	0.01636	1872 1 0	508489 43 0	4.31E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR3</i>	M1	singleton	15.34 (1.46, 161.33)	0.02294	1939 1 0	517242 28 0	2.79E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR7</i>	M1	singleton	12.49 (2.71, 57.56)	0.001198	1872 0 1	508520 10 2	1.57E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAF3</i>	M1	singleton	0.37 (0.0, 8930.06)	0.8463	1873 0 0	508514 18 0	1.76E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UNC93B1</i>	M1	singleton	0.37 (0.0, 186.54)	0.7539	1873 0 0	508489 43 0	4.21E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	<0.1%	0.76 (0.23, 2.44)	0.64	2083 2 0	534219 746 0	6.96E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	<0.1%	1.97 (0.6, 6.47)	0.2651	2082 3 0	534253 712 0	6.66E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IKBKG</i>	M3	<0.1%	0.45 (0.01, 19.74)	0.6761	1873 0 0	508452 70 10	8.82E-05		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF3</i>	M3	<0.1%	0.79 (0.24, 2.59)	0.692	2083 2 0	534413 552 0	5.16E-04		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF7</i>	M3	<0.1%	1.14 (0.52, 2.49)	0.7481	2080 5 0	533486 1479 0	1.38E-03		
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF9</i>	M3	<0.1%	0.37 (0.0, 53.77)	0.696	1873 0 0	508479 53 0	5.19E-05		

COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT1</i>	M3	<0.1%	0.37 (0.04, 3.49)	0.3816	2018 0 0	526009 218 0	2.06E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT2</i>	M3	<0.1%	2.6 (1.27, 5.31)	0.008795	2073 12 0	533405 1559 1	1.46E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TBK1</i>	M3	<0.1%	1.11 (0.45, 2.79)	0.8171	2081 4 0	533861 1103 1	1.03E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M3	<0.1%	3.66 (0.19, 71.22)	0.392	1872 1 0	508365 167 0	1.65E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR3</i>	M3	<0.1%	0.81 (0.43, 1.49)	0.4921	2077 8 0	532355 2609 1	2.44E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR7</i>	M3	<0.1%	1.58 (0.63, 3.98)	0.3321	2001 3 1	525830 477 163	7.64E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAF3</i>	M3	<0.1%	3.01 (0.53, 17.22)	0.2148	2019 1 0	525523 242 0	2.30E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UNC93B1</i>	M3	<0.1%	1.66 (0.77, 3.58)	0.1922	2075 10 0	533331 1634 0	1.53E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	<1%	0.76 (0.23, 2.44)	0.64	2083 2 0	534219 746 0	6.96E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	<1%	1.97 (0.6, 6.47)	0.2651	2082 3 0	534253 712 0	6.66E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IKBK G</i>	M3	<1%	1.04 (0.54, 2.01)	0.9101	1935 0 3	516444 949 339	1.57E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF3</i>	M3	<1%	1.38 (0.46, 4.15)	0.5704	2082 2 1	534363 601 1	5.65E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF7</i>	M3	<1%	1.14 (0.52, 2.49)	0.7481	2080 5 0	533486 1479 0	1.38E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF9</i>	M3	<1%	0.37 (0.0, 53.77)	0.696	1873 0 0	508479 53 0	5.19E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT1</i>	M3	<1%	0.37 (0.04, 3.49)	0.3816	2018 0 0	526009 218 0	2.06E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT2</i>	M3	<1%	2.6 (1.27, 5.31)	0.008795	2073 12 0	533405 1559 1	1.46E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TBK1</i>	M3	<1%	1.11 (0.45, 2.79)	0.8171	2081 4 0	533861 1103 1	1.03E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M3	<1%	3.66 (0.19, 71.22)	0.392	1872 1 0	508365 167 0	1.65E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR3</i>	M3	<1%	0.83 (0.42, 1.32)	0.4285	2070 15 0	530068 4895 2	4.57E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR7</i>	M3	<1%	1.58 (0.63, 3.98)	0.3321	2001 3 1	525830 477 163	7.64E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAF3</i>	M3	<1%	0.89 (0.48, 1.65)	0.711	2076 9 0	532255 2706 4	2.54E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UNC93B1</i>	M3	<1%	1.66 (0.77, 3.58)	0.1922	2075 10 0	533331 1634 0	1.53E-03
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	singleton	0.37 (0.01, 20.63)	0.6273	1873 0 0	508465 67 0	6.56E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	singleton	0.36 (0.0, 138.92)	0.7352	1873 0 0	508498 34 0	3.33E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IKBK G</i>	M3	singleton	0.55 (0.0, 2553.85)	0.889	1873 0 0	508522 8 2	1.18E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF3</i>	M3	singleton	0.37 (0.0, 46.47)	0.687	1940 0 0	517212 58 0	5.59E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF7</i>	M3	singleton	2.94 (0.17, 51.0)	0.4591	2004 1 0	526371 99 0	9.46E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>IRF9</i>	M3	singleton	0.37 (0.0, 249.69)	0.7666	1873 0 0	508505 27 0	2.64E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT1</i>	M3	singleton	0.37 (0.01, 19.67)	0.6207	1873 0 0	508458 74 0	7.25E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>STAT2</i>	M3	singleton	35.11 (4.02, 306.33)	0.001283	2018 2 0	525651 114 0	1.10E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TBK1</i>	M3	singleton	0.37 (0.02, 8.91)	0.5401	2005 0 0	526361 109 0	1.03E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TICAM1</i>	M3	singleton	17.91 (1.68, 190.85)	0.01686	1872 1 0	508486 46 0	4.60E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR3</i>	M3	singleton	0.93 (0.14, 6.19)	0.943	2084 1 0	534786 178 1	1.69E-04
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TLR7</i>	M3	singleton	4.02 (1.16, 13.91)	0.02818	1939 0 1	517197 55 18	8.96E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>TRAF3</i>	M3	singleton	0.37 (0.01, 21.93)	0.6308	1873 0 0	508461 71 0	6.96E-05
COVID19 positive hospitalized vs COVID19 negative or unknown	<i>UNC93B1</i>	M3	singleton	0.38 (0.01, 12.45)	0.5832	1953 0 0	516939 88 0	8.48E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR1</i>	M1	<0.1%	2.62 (0.18, 38.8)	0.4837	571 1 0	516685 342 0	3.31E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR2</i>	M1	<0.1%	1.97 (0.17, 22.68)	0.5855	589 1 0	525553 674 0	6.41E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IKBK G</i>	M1	<0.1%	14.74 (1.12, 193.22)	0.04042	539 0 0	508491 31 10	5.01E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF3</i>	M1	<0.1%	3.02 (0.6, 15.18)	0.1793	589 1 0	525854 373 0	3.55E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF7</i>	M1	<0.1%	2.68 (0.39, 18.58)	0.3189	588 2 0	525395 832 0	7.92E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF9</i>	M1	<0.1%	0.42 (0.0, 5297.95)	0.8575	539 0 0	508479 53 0	5.21E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT1</i>	M1	<0.1%	0.38 (0.0, 3004.31)	0.8315	539 0 0	508490 42 0	4.13E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT2</i>	M1	<0.1%	0.37 (0.0, 38.82)	0.6778	539 0 0	508405 127 0	1.25E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TBK1</i>	M1	<0.1%	0.38 (0.0, 211.44)	0.7619	539 0 0	508445 87 0	8.54E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TICAM1</i>	M1	<0.1%	0.89 (0.05, 15.25)	0.9349	539 0 0	508368 164 0	1.61E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR3</i>	M1	<0.1%	0.41 (0.01, 21.61)	0.6594	590 0 0	525950 277 0	2.63E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR7</i>	M1	<0.1%	42.12 (0.51, 3486.63)	0.0969	539 0 0	508503 25 4	3.24E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TRAF3</i>	M1	<0.1%	0.43 (0.0, 281622.0)	0.9011	539 0 0	508504 28 0	2.75E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>UNC93B1</i>	M1	<0.1%	3.35 (0.18, 61.63)	0.4157	538 1 0	508128 404 0	3.98E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR1</i>	M1	<1%	2.62 (0.18, 38.8)	0.4837	571 1 0	516685 342 0	3.31E-04

COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR2</i>	M1	<1%	1.97 (0.17, 22.68)	0.5855	589 1 0	525553 674 0	6.41E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IKBKKG</i>	M1	<1%	14.74 (1.12, 193.22)	0.04042	539 0 0	508491 31 10	5.01E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF3</i>	M1	<1%	3.02 (0.6, 15.18)	0.1793	589 1 0	525854 373 0	3.55E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF7</i>	M1	<1%	2.68 (0.39, 18.58)	0.3189	588 2 0	525395 832 0	7.92E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF9</i>	M1	<1%	0.42 (0.0, 5297.95)	0.8575	539 0 0	508479 53 0	5.21E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT1</i>	M1	<1%	0.38 (0.0, 3004.31)	0.8315	539 0 0	508490 42 0	4.13E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT2</i>	M1	<1%	0.37 (0.0, 38.82)	0.6778	539 0 0	508405 127 0	1.25E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TBK1</i>	M1	<1%	0.38 (0.0, 211.44)	0.7619	539 0 0	508445 87 0	8.54E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TICAM1</i>	M1	<1%	0.89 (0.05, 15.25)	0.9349	539 0 0	508368 164 0	1.61E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR3</i>	M1	<1%	0.41 (0.01, 21.61)	0.6594	590 0 0	525950 277 0	2.63E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR7</i>	M1	<1%	42.12 (0.51, 3486.63)	0.0969	539 0 0	508503 25 4	3.24E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TRAF3</i>	M1	<1%	0.43 (0.0, 281622.0)	0.9011	539 0 0	508504 28 0	2.75E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>UNC93B1</i>	M1	<1%	3.35 (0.18, 61.63)	0.4157	538 1 0	508128 404 0	3.98E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR1</i>	M1	singleton	0.37 (0.0, 165.53)	0.7518	539 0 0	508477 55 0	5.40E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR2</i>	M1	singleton	0.48 (0.0, 901579.0)	0.9216	539 0 0	508500 32 0	3.14E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IKBKKG</i>	M1	singleton	0.58 (0.0, 711727.0)	0.939	490 0 0	399233 6 1	1.00E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF3</i>	M1	singleton	24.01 (0.35, 1669.95)	0.1419	539 0 0	508495 37 0	3.63E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF7</i>	M1	singleton	0.45 (0.0, 19828.4)	0.8843	539 0 0	508481 51 0	5.01E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF9</i>	M1	singleton	0.45 (0.0, 564343.0)	0.9115	539 0 0	508505 27 0	2.65E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT1</i>	M1	singleton	0.38 (0.0, 9818.87)	0.8505	539 0 0	508502 30 0	2.95E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT2</i>	M1	singleton	0.39 (0.0, 13826.4)	0.861	539 0 0	508487 45 0	4.42E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TBK1</i>	M1	singleton	0.38 (0.0, 28255.6)	0.8649	539 0 0	508501 31 0	3.04E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TICAM1</i>	M1	singleton	15.49 (0.28, 860.18)	0.1812	539 0 0	508489 43 0	4.22E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR3</i>	M1	singleton	0.38 (0.0, 18335.2)	0.8602	539 0 0	508509 23 0	2.26E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR7</i>	M1	singleton	0.4 (0.0, 3891300000.0)	0.9371	490 0 0	399229 9 2	1.63E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TRAF3</i>	M1	singleton	0.42 (0.0, 1871470.0)	0.9114	539 0 0	508514 18 0	1.77E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>UNC93B1</i>	M1	singleton	0.42 (0.0, 20393.0)	0.8758	539 0 0	508489 43 0	4.22E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	<0.1%	1.07 (0.15, 7.68)	0.9458	589 1 0	525500 727 0	6.91E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	<0.1%	1.88 (0.17, 20.82)	0.6068	589 1 0	525529 698 0	6.63E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IKBKKG</i>	M3	<0.1%	12.55 (0.99, 159.28)	0.051	539 0 0	508452 70 10	8.84E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF3</i>	M3	<0.1%	2.53 (0.54, 11.8)	0.2388	589 1 0	525713 514 0	4.89E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF7</i>	M3	<0.1%	3.07 (0.81, 11.64)	0.09817	587 3 0	524764 1463 0	1.39E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF9</i>	M3	<0.1%	0.42 (0.0, 5297.95)	0.8575	539 0 0	508479 53 0	5.21E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT1</i>	M3	<0.1%	0.38 (0.01, 14.6)	0.6027	590 0 0	526009 218 0	2.07E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT2</i>	M3	<0.1%	1.64 (0.36, 7.55)	0.5246	587 3 0	524718 1508 1	1.44E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>TBK1</i>	M3	<0.1%	1.96 (0.33, 11.47)	0.456	588 2 0	525137 1089 1	1.04E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>TICAM1</i>	M3	<0.1%	0.89 (0.05, 15.22)	0.9349	539 0 0	508365 167 0	1.64E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR3</i>	M3	<0.1%	0.74 (0.24, 2.26)	0.5951	588 2 0	523680 2546 1	2.42E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR7</i>	M3	<0.1%	1.22 (0.29, 5.15)	0.7855	557 0 0	517105 467 160	7.59E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TRAF3</i>	M3	<0.1%	14.61 (1.54, 138.27)	0.01935	571 1 0	516792 235 0	2.28E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>UNC93B1</i>	M3	<0.1%	3.13 (1.26, 7.77)	0.01414	584 6 0	524612 1615 0	1.54E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	<1%	1.07 (0.15, 7.68)	0.9458	589 1 0	525500 727 0	6.91E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	<1%	1.88 (0.17, 20.82)	0.6068	589 1 0	525529 698 0	6.63E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IKBKKG</i>	M3	<1%	1.41 (0.48, 4.17)	0.5303	556 0 1	516444 949 339	1.57E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF3</i>	M3	<1%	2.53 (0.54, 11.8)	0.2388	589 1 0	525713 514 0	4.89E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF7</i>	M3	<1%	3.07 (0.81, 11.64)	0.09817	587 3 0	524764 1463 0	1.39E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF9</i>	M3	<1%	0.42 (0.0, 5297.95)	0.8575	539 0 0	508479 53 0	5.21E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT1</i>	M3	<1%	0.38 (0.01, 14.6)	0.6027	590 0 0	526009 218 0	2.07E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT2</i>	M3	<1%	1.64 (0.36, 7.55)	0.5246	587 3 0	524718 1508 1	1.44E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>TBK1</i>	M3	<1%	1.96 (0.33, 11.47)	0.456	588 2 0	525137 1089 1	1.04E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>TICAM1</i>	M3	<1%	0.89 (0.05, 15.22)	0.9349	539 0 0	508365 167 0	1.64E-04

COVID19 positive severe vs COVID19 negative or unknown	<i>TLR3</i>	M3	<1%	0.97 (0.41, 2.26)	0.9396	585 5 0	521403 4822 2	4.59E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR7</i>	M3	<1%	1.22 (0.29, 5.15)	0.7855	557 0 0	517105 467 160	7.59E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TRAF3</i>	M3	<1%	1.27 (0.49, 3.25)	0.6217	587 3 0	523530 2693 4	2.57E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>UNC93B1</i>	M3	<1%	3.13 (1.26, 7.77)	0.01414	584 6 0	524612 1615 0	1.54E-03
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR1</i>	M3	singleton	0.37 (0.0, 119.72)	0.738	539 0 0	508465 67 0	6.58E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IFNAR2</i>	M3	singleton	0.47 (0.0, 448932.0)	0.9144	539 0 0	508498 34 0	3.34E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IKBK1</i>	M3	singleton	0.57 (0.0, 614503.0)	0.9374	490 0 0	399232 7 1	1.13E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF3</i>	M3	singleton	20.95 (0.32, 1352.58)	0.1525	539 0 0	508480 52 0	5.11E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF7</i>	M3	singleton	0.42 (0.0, 600.62)	0.8166	557 0 0	517640 92 0	8.88E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>IRF9</i>	M3	singleton	0.45 (0.0, 564343.0)	0.9115	539 0 0	508505 27 0	2.65E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT1</i>	M3	singleton	0.38 (0.0, 269.14)	0.7735	539 0 0	508458 74 0	7.27E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>STAT2</i>	M3	singleton	0.4 (0.0, 128.93)	0.7543	572 0 0	516919 108 0	1.04E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TBK1</i>	M3	singleton	0.38 (0.0, 184.6)	0.7614	557 0 0	517628 104 0	1.00E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TICAM1</i>	M3	singleton	15.0 (0.27, 819.65)	0.1846	539 0 0	508486 46 0	4.52E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR3</i>	M3	singleton	0.41 (0.01, 15.67)	0.6287	590 0 0	526065 161 1	1.55E-04
COVID19 positive severe vs COVID19 negative or unknown	<i>TLR7</i>	M3	singleton	11.63 (0.84, 161.65)	0.06761	539 0 0	508468 49 15	7.76E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>TRAF3</i>	M3	singleton	0.4 (0.0, 689.93)	0.8098	539 0 0	508461 71 0	6.97E-05
COVID19 positive severe vs COVID19 negative or unknown	<i>UNC93B1</i>	M3	singleton	0.42 (0.0, 250.75)	0.7916	572 0 0	516939 88 0	8.50E-05

* RR: individuals who have genotype Reference/Reference for all variants included in burden test. RA: individuals who have genotype Reference/Alternate for at least one variant. AA: individuals who have genotype Alternate/Alternate for at least one variant.

Supplementary Table 10. Results from burden association tests for 32 additional genes of biological or therapeutic interest.

Trait	Gene	Burden test	MAF	Odds Ratio [95% CI]	P-value	N cases with RR RA AA genotype*	N controls with RR RA AA genotype*	AAF
COVID19 positive hospitalized vs COVID19 negative or unknown	IL23R	M1	<1%	3.849[0.853;17.373]	8.00E-02	1871 2 0	508324 208 0	0.00021
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1A	M3	<1%	2.350[0.835;6.611]	1.10E-01	2016 4 0	525349 415 1	0.0004
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNL3	M1	<1%	14.959[0.345;647.891]	1.60E-01	1872 1 0	508438 940	0.00009
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1A	M1	<1%	4.218[0.574;31.008]	1.60E-01	2019 1 0	525641 124 0	0.00012
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNL1	M3	<1%	0.369[0.086;1.585]	1.80E-01	2085 0 0	534569 395 1	0.00037
COVID19 positive hospitalized vs COVID19 negative or unknown	TMPRSS2	M1	<1%	2.526[0.646;9.876]	1.80E-01	1936 4 0	516764 506 0	0.00049
COVID19 positive hospitalized vs COVID19 negative or unknown	C5	M1	<1%	2.077[0.702;6.144]	1.90E-01	2081 4 0	534324 640 1	0.0006
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNL1	M1	<1%	0.369[0.081;1.687]	2.00E-01	2085 0 0	534607 357 1	0.00033
COVID19 positive hospitalized vs COVID19 negative or unknown	IL17RC	M3	<1%	1.643[0.749;3.604]	2.20E-01	2080 5 0	533824 1140 1	0.00107
COVID19 positive hospitalized vs COVID19 negative or unknown	VEGFA	M3	<1%	0.558[0.219;1.418]	2.20E-01	2083 2 0	533873 1091 1	0.00102
COVID19 positive hospitalized vs COVID19 negative or unknown	IL7R	M1	<1%	1.668[0.692;4.019]	2.50E-01	2079 6 0	533848 1117 0	0.00105
COVID19 positive hospitalized vs COVID19 negative or unknown	IL12B	M3	<1%	2.200[0.438;11.048]	3.40E-01	2017 1 0	526033 194 0	0.00018
COVID19 positive hospitalized vs COVID19 negative or unknown	IL23A	M3	<1%	0.366[0.046;2.919]	3.40E-01	1938 0 0	517449 282 1	0.00027
COVID19 positive hospitalized vs COVID19 negative or unknown	IL17RA	M1	<1%	0.359[0.040;3.220]	3.60E-01	2020 0 0	525537 228 0	0.00022
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNLR1	M3	<1%	0.366[0.040;3.321]	3.70E-01	1938 0 0	517531 201 0	0.00019
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1B	M3	<1%	0.369[0.039;3.491]	3.80E-01	2005 0 0	526208 262 0	0.00025
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNL3	M3	<1%	3.464[0.185;64.982]	4.10E-01	1939 1 0	517141 129 0	0.00013
COVID19 positive hospitalized vs COVID19 negative or unknown	JAK1	M1	<1%	1.942[0.398;9.474]	4.10E-01	1937 1 0	517541 189 2	0.00019
COVID19 positive hospitalized vs COVID19 negative or unknown	JAK1	M3	<1%	1.942[0.398;9.474]	4.10E-01	1937 1 0	517541 189 2	0.00019
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNLR1	M1	<1%	0.365[0.030;4.527]	4.30E-01	1938 0 0	517571 161 0	0.00015
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1B	M1	<1%	0.368[0.030;4.481]	4.30E-01	1873 0 0	508320 212 0	0.00021
COVID19 positive hospitalized vs COVID19 negative or unknown	JAK2	M1	<1%	0.366[0.029;4.555]	4.30E-01	1938 0 0	517530 202 0	0.00019
COVID19 positive hospitalized vs COVID19 negative or unknown	IL23R	M3	<1%	0.847[0.054;1.296]	4.40E-01	2067 18 0	529085 586 119	0.00551
COVID19 positive hospitalized vs COVID19 negative or unknown	VEGFA	M1	<1%	0.661[0.218;2.002]	4.60E-01	2083 2 0	534217 747 1	0.0007
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1R1	M1	<1%	0.666[0.222;1.995]	4.70E-01	1936 2 0	517281 444 7	0.00044
COVID19 positive hospitalized vs COVID19 negative or unknown	IL7R	M3	<1%	1.269[0.666;2.419]	4.70E-01	2075 10 0	532768 2197 0	0.00205
COVID19 positive hospitalized vs COVID19 negative or unknown	TMPRSS2	M3	<1%	1.341[0.606;2.967]	4.70E-01	2077 8 0	533498 1467 0	0.00137
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNG	M3	<1%	0.366[0.020;6.537]	4.90E-01	1873 0 0	508402 130 0	0.00013
COVID19 positive hospitalized vs COVID19 negative or unknown	BTK	M3	<1%	0.497[0.061;4.077]	5.10E-01	2020 0 0	525622 114 29	0.00016
COVID19 positive hospitalized vs COVID19 negative or unknown	IL6	M3	<1%	0.369[0.019;7.067]	5.10E-01	1953 0 0	516905 122 0	0.00012
COVID19 positive hospitalized vs COVID19 negative or unknown	IL6R	M1	<1%	0.377[0.020;7.210]	5.20E-01	1940 0 0	517152 118 0	0.00011
COVID19 positive hospitalized vs COVID19 negative or unknown	IL12B	M1	<1%	0.365[0.016;8.562]	5.30E-01	1873 0 0	508442 90 0	0.00009
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1R1	M3	<1%	0.739[0.283;1.931]	5.40E-01	2082 3 0	534274 684 7	0.00065
COVID19 positive hospitalized vs COVID19 negative or unknown	IL6	M1	<1%	0.367[0.014;9.615]	5.50E-01	1873 0 0	508423 109 0	0.00011
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNGR1	M3	<1%	0.651[0.149;2.841]	5.70E-01	2084 1 0	534532 433 0	0.0004
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNL2	M3	<1%	1.481[0.380;5.766]	5.70E-01	2082 3 0	534408 557 0	0.00052
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNB1	M3	<1%	0.828[0.423;1.623]	5.80E-01	2011 7 0	524038 2186 3	0.00208
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNG	M1	<1%	0.364[0.011;12.464]	5.80E-01	1873 0 0	508453 79 0	0.00008
COVID19 positive hospitalized vs COVID19 negative or unknown	JAK2	M3	<1%	0.850[0.481;1.503]	5.80E-01	2075 10 0	532245 2171 46	0.00255
COVID19 positive hospitalized vs COVID19 negative or unknown	IL4R	M1	<1%	1.931[0.154;24.219]	6.10E-01	1937 1 0	517553 179 0	0.00017
COVID19 positive hospitalized vs COVID19 negative or unknown	PDCD1	M3	<1%	0.367[0.005;29.373]	6.50E-01	1873 0 0	508473 59 0	0.00006
COVID19 positive hospitalized vs COVID19 negative or unknown	IL17A	M1	<1%	0.364[0.004;35.613]	6.70E-01	1873 0 0	508492 40 0	0.00004
COVID19 positive hospitalized vs COVID19 negative or unknown	IL23A	M1	<1%	0.365[0.002;57.511]	7.00E-01	1873 0 0	508494 38 0	0.00004
COVID19 positive hospitalized vs COVID19 negative or unknown	ACE2	M1	<1%	0.392[0.002;61.868]	7.20E-01	1873 0 0	508485 44 3	0.00005
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1RAP	M3	<1%	1.272[0.349;4.641]	7.20E-01	2083 2 0	534386 579 0	0.00054
COVID19 positive hospitalized vs COVID19 negative or unknown	IL4R	M3	<1%	1.534[0.147;16.057]	7.20E-01	2017 1 0	526039 188 0	0.00018
COVID19 positive hospitalized vs COVID19 negative or unknown	PDCD1	M1	<1%	0.367[0.002;83.673]	7.20E-01	1873 0 0	508492 40 0	0.00004
COVID19 positive hospitalized vs COVID19 negative or unknown	CSF2	M3	<1%	0.368[0.001;136.635]	7.40E-01	1873 0 0	508491 41 0	0.00004
COVID19 positive hospitalized vs COVID19 negative or unknown	BTK	M1	<1%	0.363[0.001;230.098]	7.60E-01	1873 0 0	508505 27 0	0.00003
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNGR1	M1	<1%	0.807[0.145;4.481]	8.10E-01	2084 1 0	534629 336 0	0.00031

COVID19 positive hospitalized vs COVID19 negative or unknown	ACE2	M3	<1%	0.944[0.582;1.533]	8.20E-01	2079 2 4	532861 1626 478	0.00241
COVID19 positive hospitalized vs COVID19 negative or unknown	CCR5	M1	<1%	0.939[0.521;1.690]	8.30E-01	2077 8 0	532508 2453 4	0.0023
COVID19 positive hospitalized vs COVID19 negative or unknown	CCR5	M3	<1%	0.939[0.521;1.690]	8.30E-01	2077 8 0	532508 2453 4	0.0023
COVID19 positive hospitalized vs COVID19 negative or unknown	IL1RAP	M1	<1%	1.281[0.142;11.540]	8.30E-01	1872 1 0	508333 199 0	0.0002
COVID19 positive hospitalized vs COVID19 negative or unknown	CSF2	M1	<1%	0.370[0.000;6631.170]	8.40E-01	1873 0 0	508515 17 0	0.00002
COVID19 positive hospitalized vs COVID19 negative or unknown	IL17RC	M1	<1%	1.113[0.317;3.899]	8.70E-01	2083 2 0	534378 587 0	0.00055
COVID19 positive hospitalized vs COVID19 negative or unknown	IL17A	M3	<1%	0.885[0.140;5.608]	9.00E-01	1872 1 0	508249 283 0	0.00028
COVID19 positive hospitalized vs COVID19 negative or unknown	C5	M3	<1%	0.984[0.670;1.445]	9.30E-01	2059 26 0	529016 5928 21	0.00558
COVID19 positive hospitalized vs COVID19 negative or unknown	IL6R	M3	<1%	1.089[0.143;8.291]	9.30E-01	2084 1 0	534746 219 0	0.0002
COVID19 positive hospitalized vs COVID19 negative or unknown	IL17RA	M3	<1%	1.009[0.713;1.429]	9.60E-01	2052 33 0	527528 7417 20	0.00697
COVID19 positive hospitalized vs COVID19 negative or unknown	IL33	M3	<1%	0.988[0.649;1.505]	9.60E-01	2063 22 0	529239 5720 6	0.00536
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNB1	M1	<1%	0.987[0.470;2.070]	9.70E-01	1946 7 0	515284 174 2	0.00169
COVID19 positive hospitalized vs COVID19 negative or unknown	IL33	M1	<1%	0.993[0.652;1.513]	9.70E-01	2063 22 0	529265 5694 6	0.00533
COVID19 positive hospitalized vs COVID19 negative or unknown	IFNL2	M1	<1%	0.992[0.240;4.100]	9.90E-01	2083 2 0	534469 496 0	0.00046

* RR: individuals who have genotype Reference/Reference for all variants included in burden test. RA: individuals who have genotype Reference/Alternate for at least one variant. AA: individuals who have genotype Alternate/Alternate for at least one variant.