Figures S1 – S7. Manhattan plots showing COGS gene prioritisation scores for the seven COVID-19 host GWAS.

Dots represent genes, and selected genes exceeding a lenient COGS prioritisation score cutoff of 0.3 are labelled, based on Promoter Capture Hi-C data from 17 human primary blood cell types (including endothelial precursors). Some labels were removed to avoid overprinting, and most genes without conventional names were not labelled. Please refer to Table S1 for full information.
A1: very severe respiratory confirmed covid vs. not hospitalized covid (Figure S1)
A2: very severe respiratory confirmed covid vs. population (Figure S2)
B2: hospitalized covid vs. population (Figure S4)
C2: covid vs. population (Figure S6)

COGS score

Chromosome

MEF2D

OAS3

UBXN6

DPP9

HDGFL2

SAFB2

SAFB

VRK3

ZNF473

IFNAR2

IFNAR1

TRIB3

SOX12
D1: predicted covid from self-reported symptoms vs. predicted or self-reported non-covid (Figure S7)
Figures S8 – S11. Example profiles of SNP-level posterior probabilities, promoter interactions and H3K27ac signals in potentially causal cell types for three prioritised genes

Top: –log10-p-values from the summary statistics of GWAS meta-analysis produced by COVID-19hg consortium (Figure S8: B2 [hospitalized covid vs. population]; Figure S9: A2 [very severe respiratory confirmed covid vs. population]; Figure S10: B1 [hospitalized covid vs. not hospitalized covid]; Figure S11: A1 [very severe respiratory confirmed covid vs. not hospitalized covid], respectively).

Second from top: SNP-level posterior probabilities of variant being causal for the respective GWAS generated by Wakefield’s Bayesian prioritisation procedure.

Third from top: Arcs showing promoter interactions detected for the prioritised gene (Figure S8: OAS3; Figure S9: IFNAR1; Figure S10: ETS1; Figure S11: CCR1, respectively) in one of the 17 human primary blood cell types from Javierre et al. (2016) used in the COGS prioritisation procedure.

Fourth from top: Pileups of H3K27ac ChIP-seq signal for the same cell type as above in the analysed locus (OAS3 and CCR1: macrophages from Pacheco et al., BMC Genomics 2015, accession GSE68798; IFNAR1: B cells from Andersson, Nature 2017, accession GSE40668; ETS1: CD4+ T cells, ENCODE project, accession ENCSR561KOM).

Bottom panel: The locations of the annotated genes in the analysed locus.

The genomic coordinates are on the GRCh37 assembly.
OAS3 in B2: hospitalized covid vs. population (Figure S8)

GWAS SNP $-\log_{10}(p)$

Posterior probability of variant being causal

H3K27ac ChIP-seq signal in MACROPHAGES

OAS3 promoter interactions in MACROPHAGES
IFNAR1 in A2: very severe respiratory confirmed covid vs. population (Figure S9)

GWAS SNP $-\log_{10}(p)$

Posterior probability of variant being causal

H3K27ac ChIP–seq signal in total B cells

IFNAR1 promoter interactions in total B cells

promoter–promoter–interaction
promoter–PIR–interaction

IL10RB–AS1
IL10RB
USP11P1
IFNAR2
AP000295.9
AP000295.10
IFNAR1
IFNGR2
ETS1 in B1: hospitalized covid vs. not hospitalized covid (Figure S10)
CCR1 in A1: very severe respiratory confirmed covid vs. not hospitalized covid (Figure S11)
Table S2. The numbers of genes showing elevated COGS prioritisation scores per GWAS

<table>
<thead>
<tr>
<th>GWAS</th>
<th>COGS&gt;=0.75</th>
<th>0.3&lt;COGS&lt;0.75</th>
<th>Examples of prioritised coding genes</th>
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<tbody>
<tr>
<td>A1</td>
<td>0</td>
<td>8</td>
<td>PDE3B, CCR1</td>
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<tr>
<td>A2</td>
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<td>42</td>
<td>DPP9, IFNAR2, TYK2, ICAM4</td>
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<tr>
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<td>19</td>
<td>MFHAS1, CCR1, CCR2, ETS1, KCNJ5, NFKBIA</td>
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<tr>
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<td>DPP9, IFNAR2, FOXP4, OAS3</td>
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<td>SLC6A20</td>
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<td>IFNAR2, IFNAR1, DPP9</td>
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<tr>
<td>D1</td>
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<td>IGFBP3, IGFBP1</td>
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