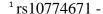
## Table of Polymorphisms - Susceptibility and Severity of Spike Protein Injury (SPI)

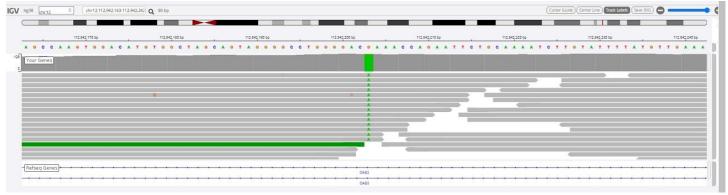
DNA Plasticity from Natural Vaccine effects on COVID-19.

Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
OAS1	G to A/A <sup>1</sup>	rs10774671	Blocks COVID replication	Yes. None on COVID; related to rs10752637 T-G/G Alzheimer's	Associated with severity ↑
OAS3; OAS1	G to A/A <sup>2</sup> T to G/G <sup>3</sup>	rs10735079; (LD) rs4766664 (LD) is Linkage	Interferon inducible genes - antiviral defense	Biorxiv - Genetic Variant protective and inherited from Neanderthals	Associated with critical illness, Blocks viral replication ↑

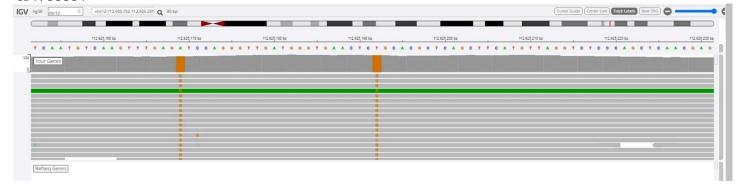




#### <sup>2</sup> rs10775079 -

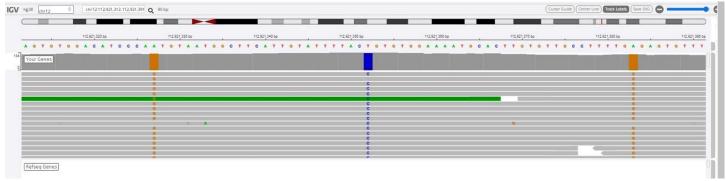


## <sup>3</sup> rs4766664 -



Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
		Disequalibrium			
SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and XCR1	T-C/C <sup>4</sup>	rs4767027	Reduced COVID-19 susceptibility	Biorxiv - Genetic Variant protective and inherited from Neanderthals	Associated with critical illness - decreased hospitalization risk \
OAS1	G-A/A <sup>5</sup>	rs1131454	Destroys COVID-19 RNA	Yes. Not related to COVID	Mediated decay of COVID-19 RNA; decreased viral loads ↑
DPP9	Normal <sup>6</sup>	rs2109069	Severe COVID lung attack	GWAS - Nature, 12/11/20;	Associated with severity of spike

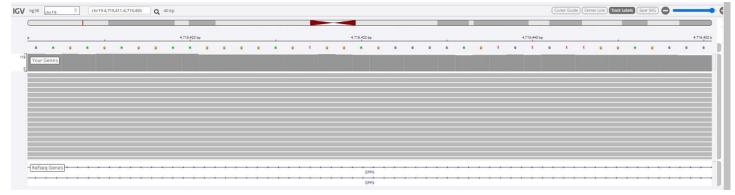
<sup>4</sup> rs4767027 -



<sup>5</sup> rs1131454 -



<sup>6</sup> rs2109069 -



Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				Genetic mechanisms of critical illness in SPI.	protein injury/illness ↓
DPP9	Normal <sup>7</sup>	rs12610495; (LD) rs2109069 <sup>8</sup>	Severe COVID	Map on SNPedia, GWAS too;	Ideopathic lung fibrosis, defeats antigen presentation ↓
SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and	Normal <sup>9</sup>	rs73064425	$\begin{array}{c} adjusted\_risk = o_{R^N\!/\!\mu} \\ \text{where N is the} \\ \text{number of effect} \\ \text{alleles.} \end{array}$	No	Associated with critical illness ↓

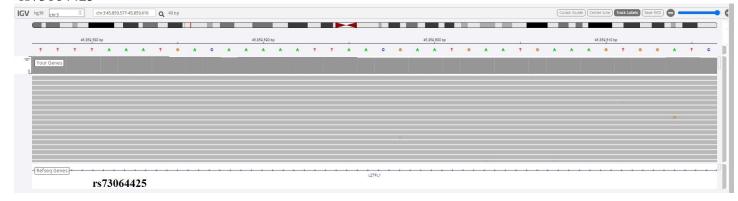
## <sup>7</sup> rs12610495



## 8 rs2109069 -

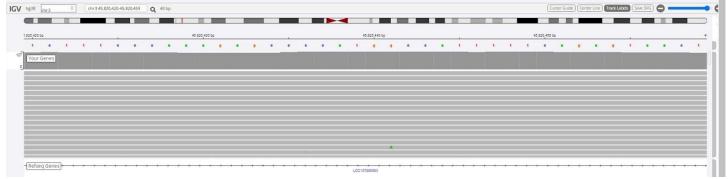


## <sup>9</sup> rs73064425 -

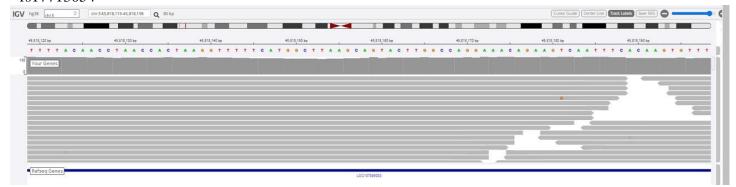


Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
XCR1					
SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and XCR1	Normal <sup>10</sup>	rs13078854	121 negative v 1,131 severe cases.	No	Associated with severity ↓
SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and XCR1	Normal <sup>11</sup>	rs17713054	250 of 2K hospitalized	Yes - doubles risk of severe COVID (spike protein injury)	Associated with hospitalization ↓
SLC6A20,	Normal <sup>12</sup>	rs2271616	1,131 of 15,434	No	Associated with

<sup>10</sup> rs13078854 -



<sup>11</sup> rs17713054 -

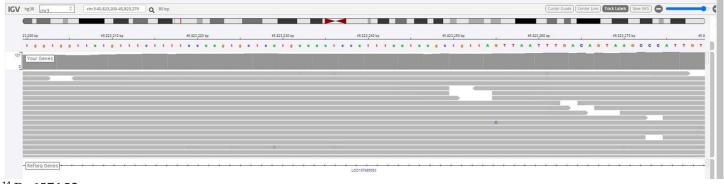


<sup>12</sup> rs2271616 -

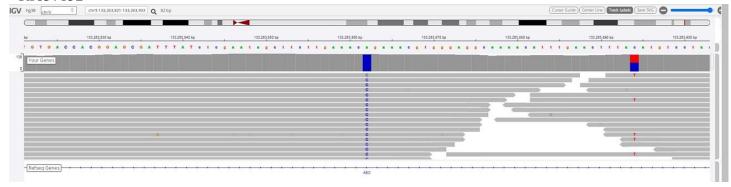


Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
LZTFL1, CCR9, FYCO1, CXCR6 and XCR1			hospitalized		susceptibility \
SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and XCR1	Normals <sup>13</sup>	rs10490770	24K hospitalized of 2M controls	Yes - higher susceptibility to respiratory failure	Associated with hospitalization ↓
ABO	a-CC <sup>14</sup>	rs657152	Cross replicating associations with rs11385942	Yes - blood type specific	Blood group A associated with respiratory failure \pm
ABO	a-CC <sup>15</sup>	rs657152	I am blood type O	PubMed N Engl	Blood group O

<sup>13</sup> rs10490770 -

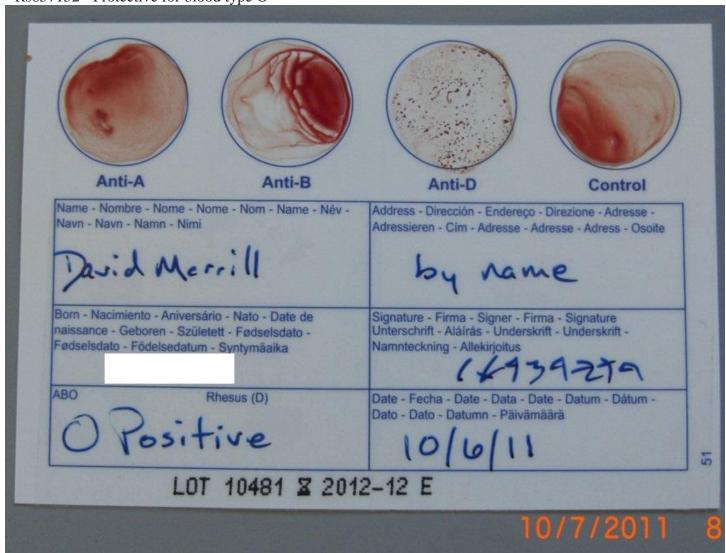


<sup>14</sup> Rs657152 -



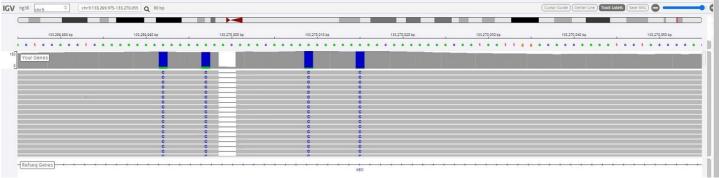
Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				J Med 2020 Jun 17	associated with a protective effect
LZTFL1	Normal	rs11385942	Bad allele	Yes - 3X respiratory failure susceptibility	Respiratory failure ↓

 $^{15}$  Rs657152 - Protective for blood type O

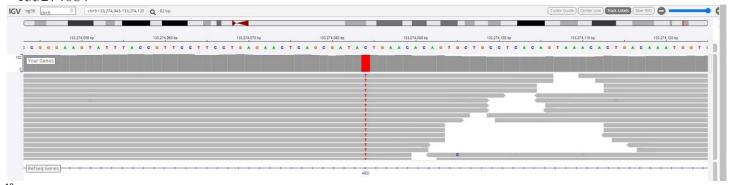


Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
ABO	a-CC <sup>16</sup>	rs9411378	Good mutation - for me, with blood type O	No - GWAS located Chr9: 133270015	Blood group A associated with COVID-19 positivity ↑
ABO	C-TT <sup>17</sup>	rs912805253	Bad for blood type A, protective for blood type O	European Journal of Medicine 7/20/22 Host Genomics	Blood group O associated with protection from SPI ↑
IFNAR2	A-AG <sup>18</sup>	rs2236757	Bad	Genome ucsc.edu 7 SNP associated with severe SPI	Associated with critical illness ↓
SLC6A20	normal <sup>19</sup>	rs2531743	Bad	Genome Wide	Associated with

<sup>16</sup> rs9411378 -



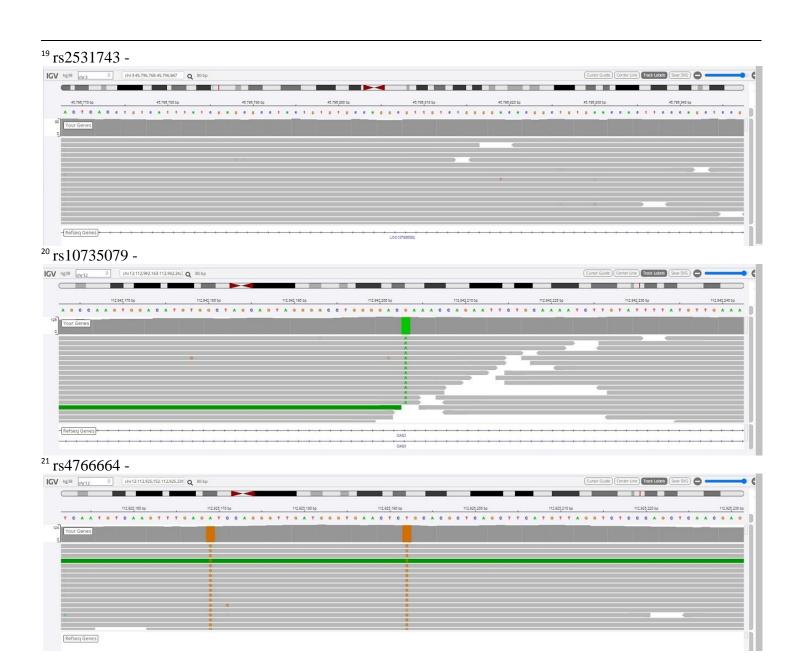
<sup>17</sup> 133274084 -



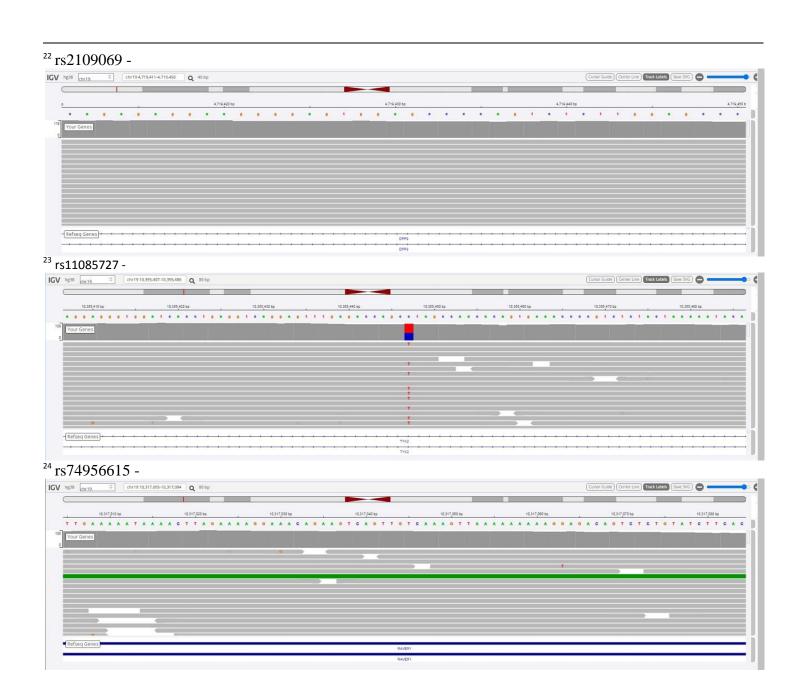
<sup>18</sup> rs2236757 -



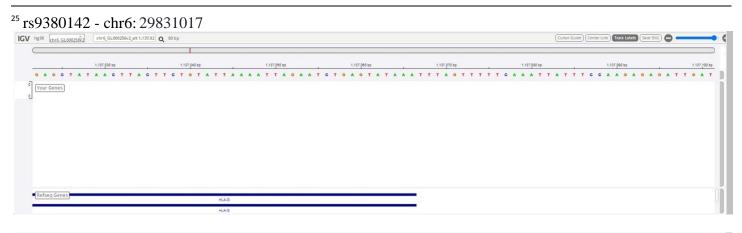
Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				Analysis medrxiv.org	Positive Tests ↓
IFNAR2	t-TC	rs13050728	Good strengthen the protective role of IFN pathway against severe COVID-19	GWAS -	Associated with severity, critical respiratory \( \psi
OAS3; OAS1	G-AA <sup>20</sup> T-GG <sup>21</sup>	rs10735079; rs4766664	Good	Biorxiv - Genetic Variant protective against SPI	Reduces risk of intensive care ↑
DPP9	Normal <sup>22</sup>	rs2109069	Bad	GWAS Catalog	Associated with



Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				Intron Variant	critical illness severity ↓
ICAM5/TYK2	c-TC <sup>23</sup> Normal	rs1108572(7); (LD) rs74956615	Good	eBioMedicine - Host genetic factors	Associated with critical illness ↓
TYK2	Normal <sup>24</sup>	rs74956615	Bad	Regeneron - Genome-wide analysis	Associated with severity↓
HLA-G	GAP Normal <sup>25</sup>	rs9380142 chr6: 29831017	Bad	Human Genomics -	Associated with critical illness ↓

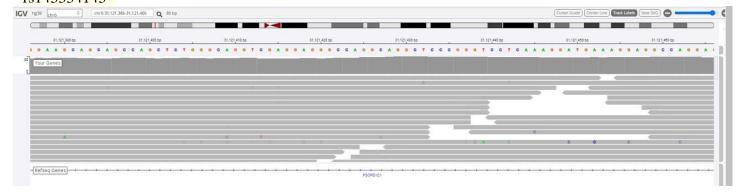


Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				Update on Human Genetic Susceptability to SPI	
CCHCR1	normal <sup>26</sup>	rs143334143	Bad mutation	Yes - 1.9x risk for becoming critically ill	Associated with critical illness; 1.9x risk. Genome.ucsc.edu
HLA-DPB1	Gap in genome <sup>27</sup>	rs2071351	Bad	Human Genomics -	Blocks Immune Response





<sup>26</sup> rs143334143 -



Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				Update on Human Genetic Susceptability to SPI	Pathway, susceptability↓
ACE2	normal <sup>28</sup>	rs190509934	Good	Medrxiv.org Genome-Wide Analysis	Associated with ACE 2 entry susceptability - Novel Risk Variant in ACE2
MUC5B <sup>□</sup>	Normal <sup>29</sup>	rs35705950	Bad	SNPedia pneumonia and pulmonary fibrosis	Associated with severity specifically lung issues ↓

## <sup>27</sup> rs2071351 -



#### <sup>28</sup> rs190509934 -



## <sup>29</sup> rs35705950 -

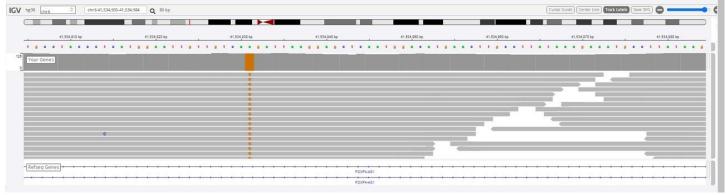


Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
TMPRSS2	normal <sup>30</sup>	rs3787946	Good	News - Medical Life Sciences Dec 23, 2020 - COVID Severitygenetic variance	Connected to thymus and adaptive immunity ↑
FOXP4	Normal <sup>31</sup>	rs1886814	Bad	NCBI - Insights into Genetic Factors	emphysema- associated variant rs2894439 ↓
LINC01276	Normal <sup>32</sup>	rs2894439	Bad	NCBI - Insights into Genetic Factors	emphysema- associated variant rs1886814 ↓
LZTFL1	Normal <sup>33</sup>	Rs71325088	Bad	SpringerLink -	Associated with

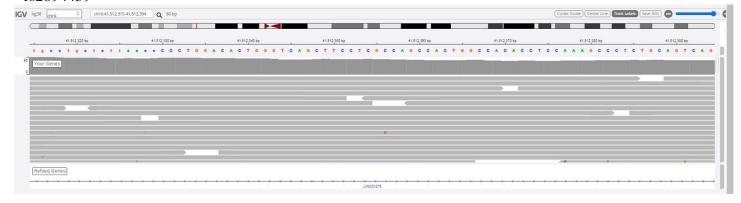
<sup>30</sup> rs3787946 -



<sup>31</sup> rs1886814 -



<sup>32</sup> rs2894439 -



Location	DNA Polymorphism	Variant	Allele Effects	SNPedia & other Articles	Outcomes
				Replication of LZTFL1 gene region susceptability	severity - lowest P-value ↓
NOTCH4	Normal <sup>34</sup>	rs3131294	Bad	Ncbi - Update Human Genetic Susceptability SPI	Affects severity
OAS1	c-TT <sup>35</sup>	rs6489867	Bad	Isaric.org - Genetic Mechanisms of Critical Illness in SPI	1.3 ratio affecting severity  SpringerLink - did not reach statistical significance↓↑

# <sup>33</sup> Rs71325088 -(Cursor Guide) (Center Line) Track Labels (Save SVG) IGV ng38 chr3 □ chr345,821,420-45,821,499 Q 80 bp <sup>34</sup> rs3131294 -(GV hg38 thr6 0 chr6.32,180,106.32,180,186 Q 80 bp Cursor Guide Center Line Track Labels (Save SVG) Refseq Genes <sup>35</sup> rs6489867 -Cunor Guide Center Line Track Labels (Save SVG) \_\_\_\_

Refseq Genes