



FARGEN

Ílegur hava týdning!

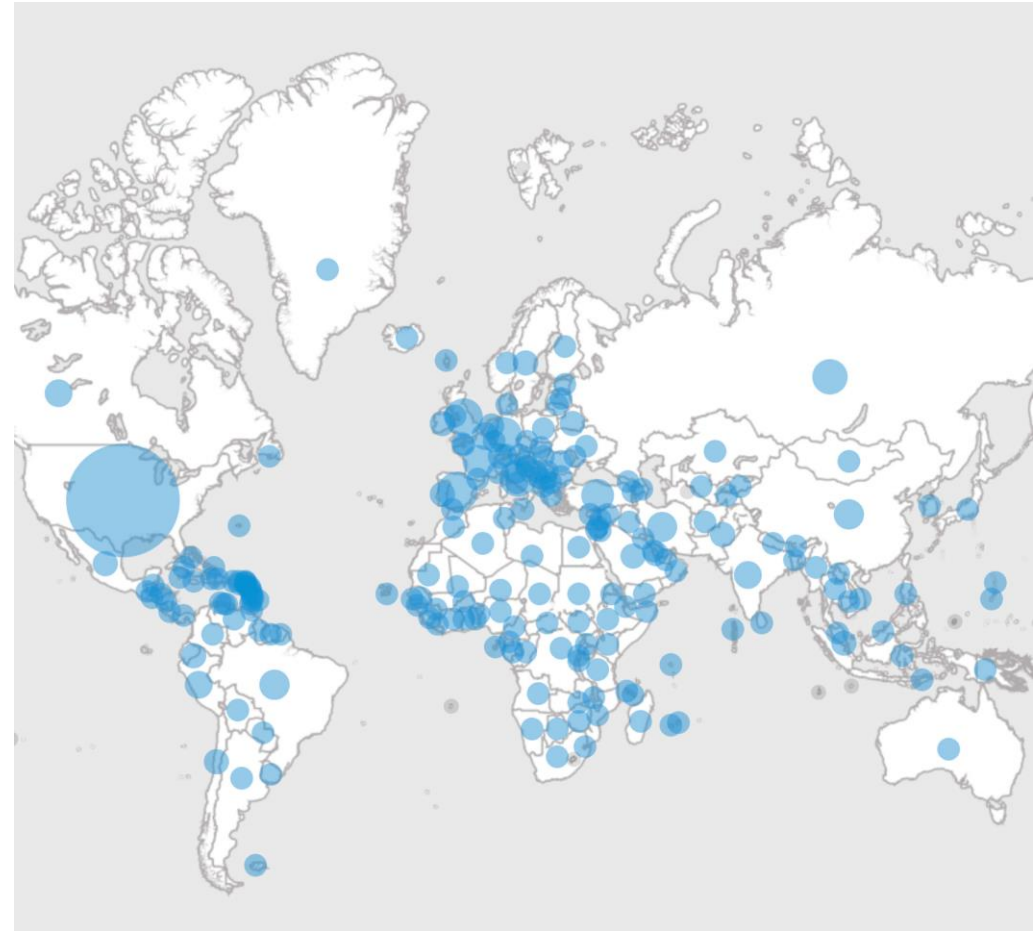
Ávirkan hjá ílegum á sjúkugongdina fyri COVID-19

Leivur Nattestad Lydersen, Cand. Polyt.

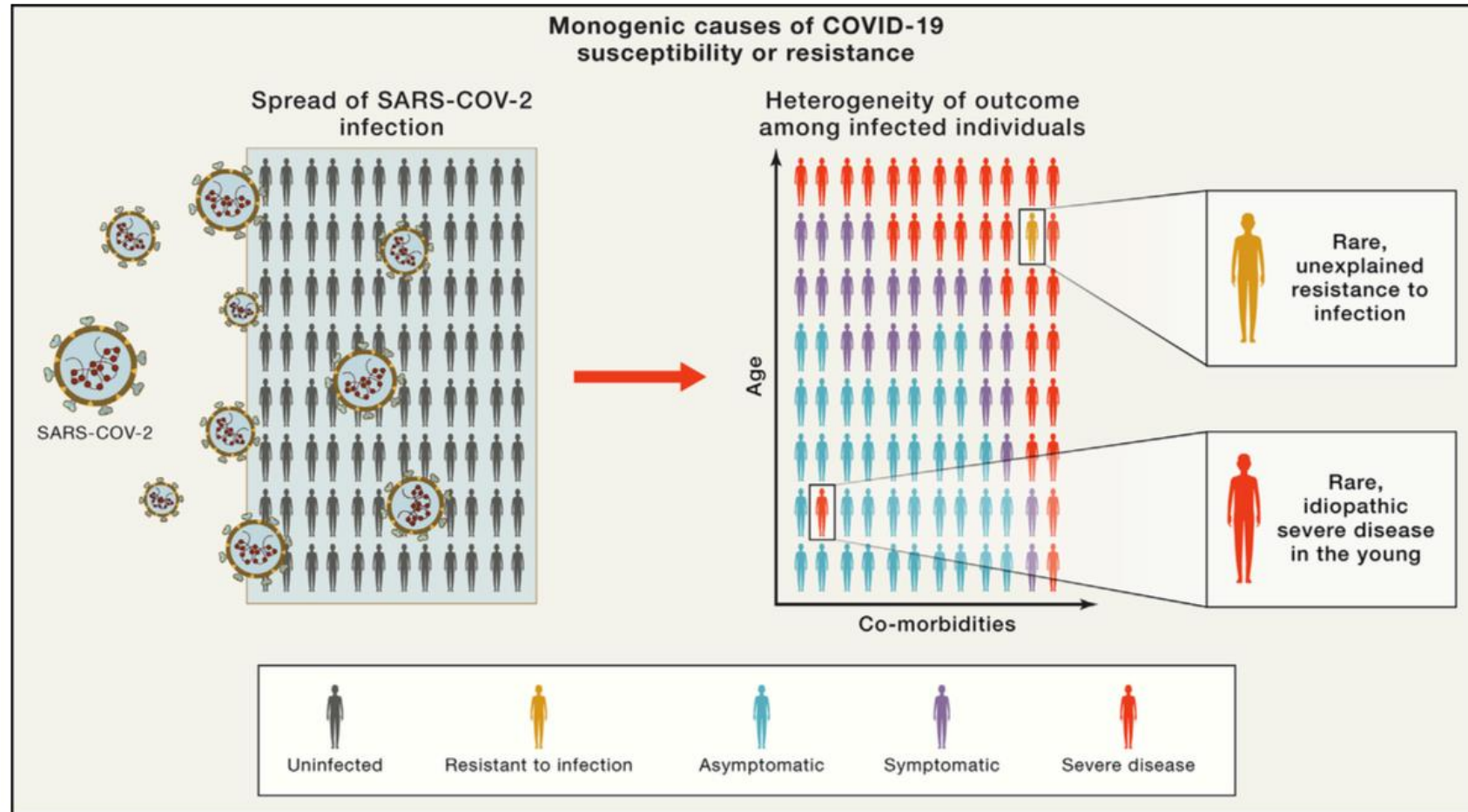
Vísindavøka á ferð - 2022

COVID-19 tann 14. september 2022

- 228 tjóðir ávirkaðar...higartil
 - 614 milliónir smittað
 - 6,5 millónir deyð
- Ymiskt, hvussu korona ávirkar
 - Alt frá ongi sjúkueyðkenni til lívshættislig sjúkueyðkenni
- Kann ílegusamansetingin hava týdning?



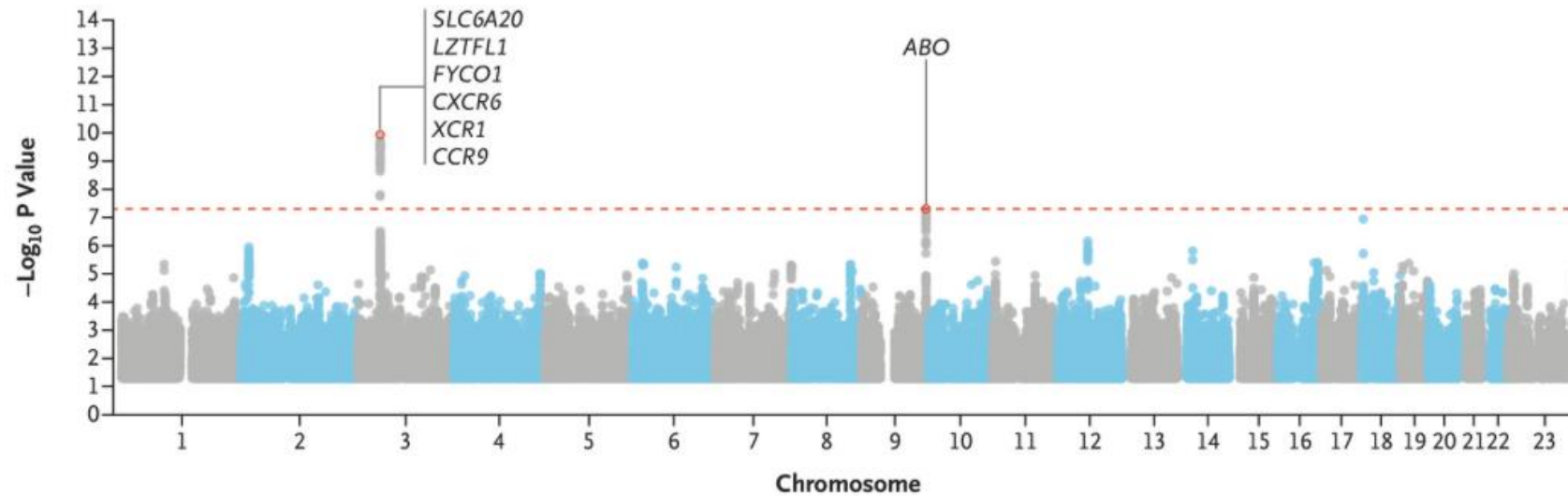
Hví tosa um ílegusamanseting?





ORIGINAL ARTICLE

Genomewide Association Study of Severe Covid-19 with Respiratory Failure

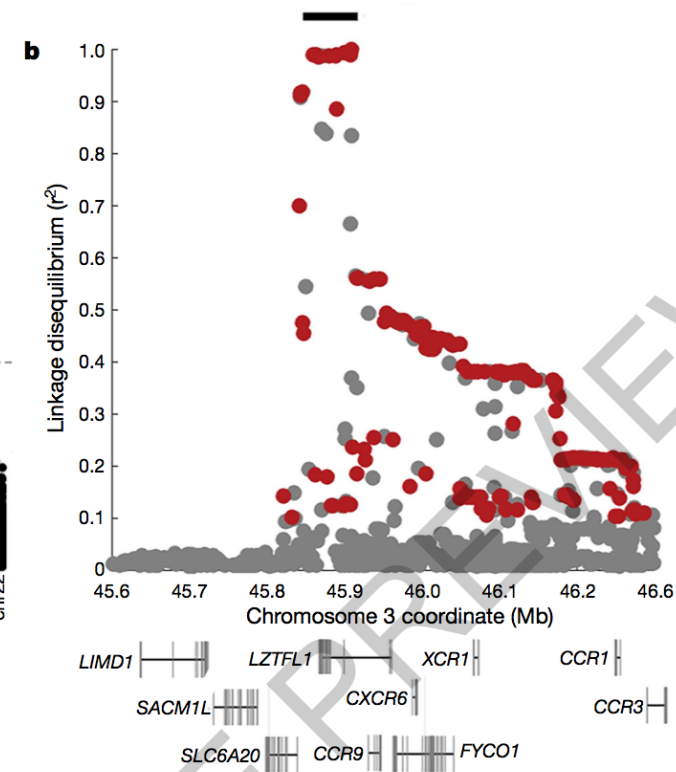
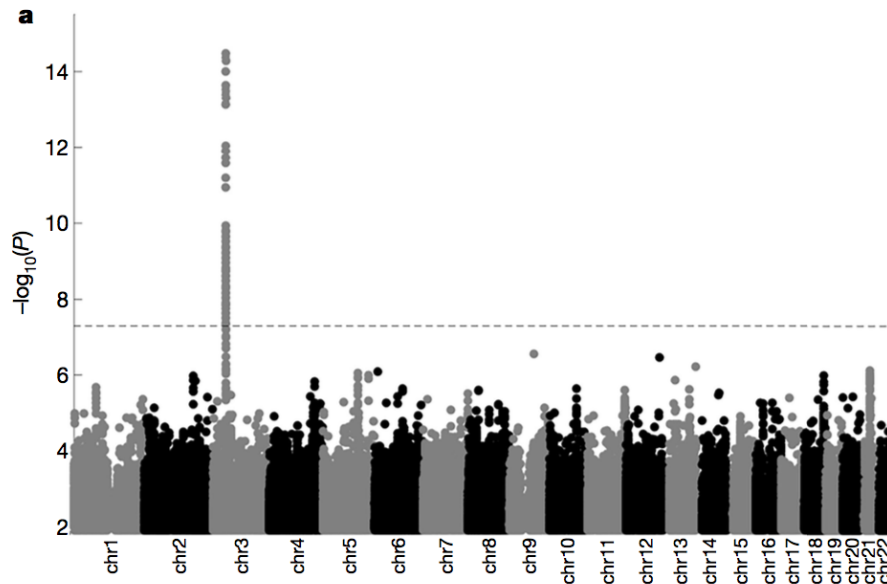
The Severe Covid-19 GWAS Group*



The major genetic risk factor for severe COVID-19 is inherited from Neanderthals

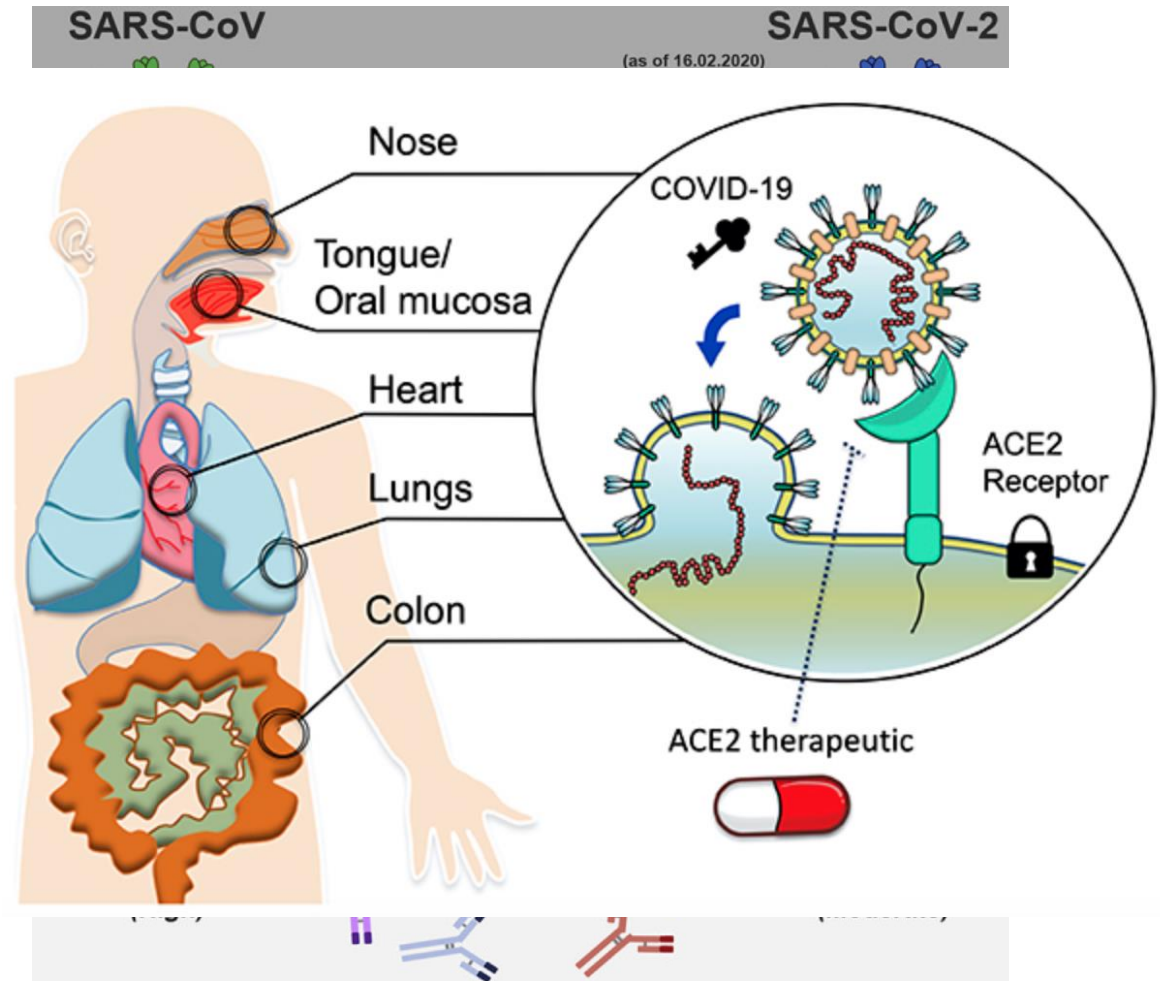
Hugo Zeberg  & Svante Pääbo 

Nature (2020) | [Cite this article](#)



Hvat vistu vit um koronuvirusið beinanvegin?

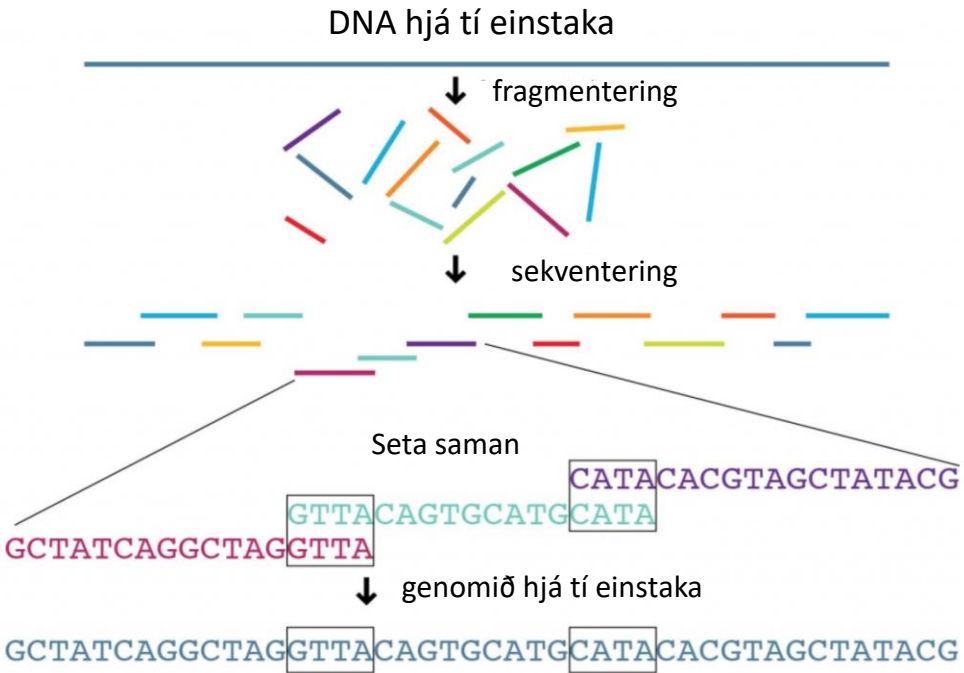
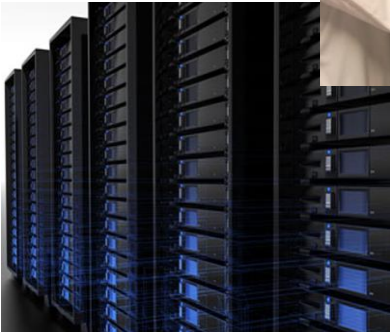
- Líkskapur millum SARS-CoV og COVID-19 (Lu et al. 2020)
- ACE2 er hurðin inn í kyknuna
- Reseptorur í yvirflatanum á ymsum kyknum
- Tal av reseptorum kann hava ávirkan á sjúkugongdina
- ACE2 er eitt móguligt target fyri eina vaccinu



Í Føroyum kanna vit, um ávísar ílegur hava samband við ymisk sjúkueyðkenni

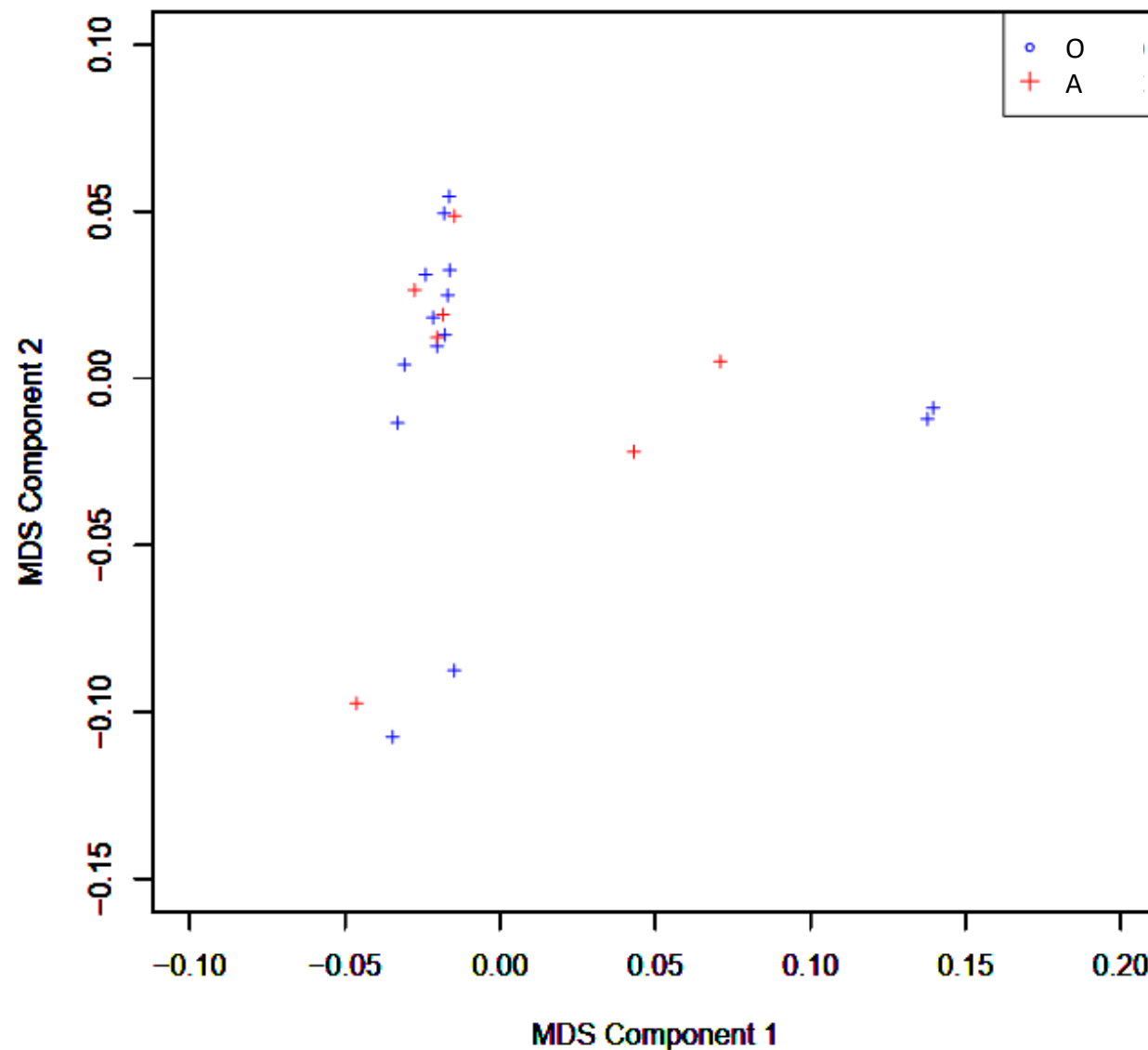
	Øll	Kvinnur	Menn	
	Kanning 1	Kanning 2	Kanning 3	Kanning 4
Case'ir (F/M)	41 (22/19)	62 (30/32)	66 (31/35)	58 (33/25)
Miðal aldur (SD)	40.27 (±18.83)	39.55 (±23.07)	38.13 (±23.02)	41.78 (±20.01)
Kontrollar (F/M)	87 (45/42)	66 (37/29)	62 (36/26)	70 (34/36)
Miðal aldur (SD)	40.53 (±20.77)	41.29 (±16.97)	42.92 (±16.25)	39.35 (±20.24)

Blóðroynd til ílegulesing

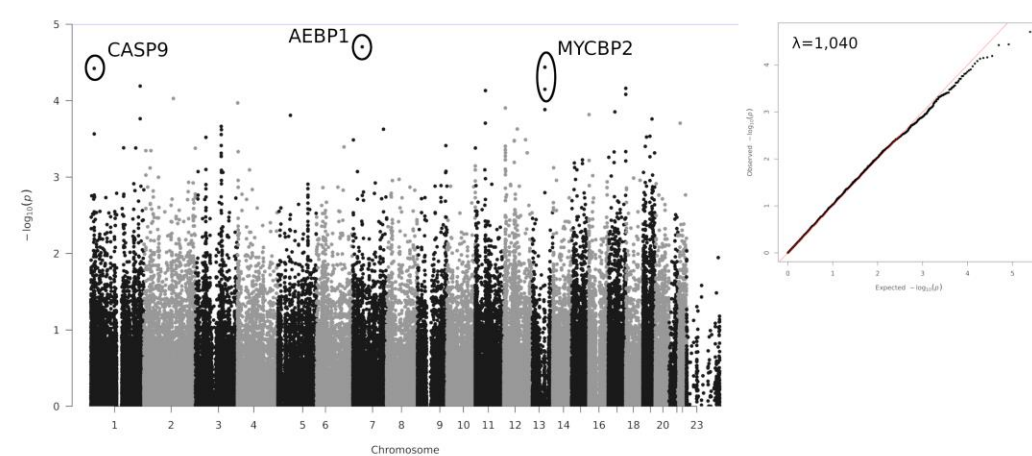
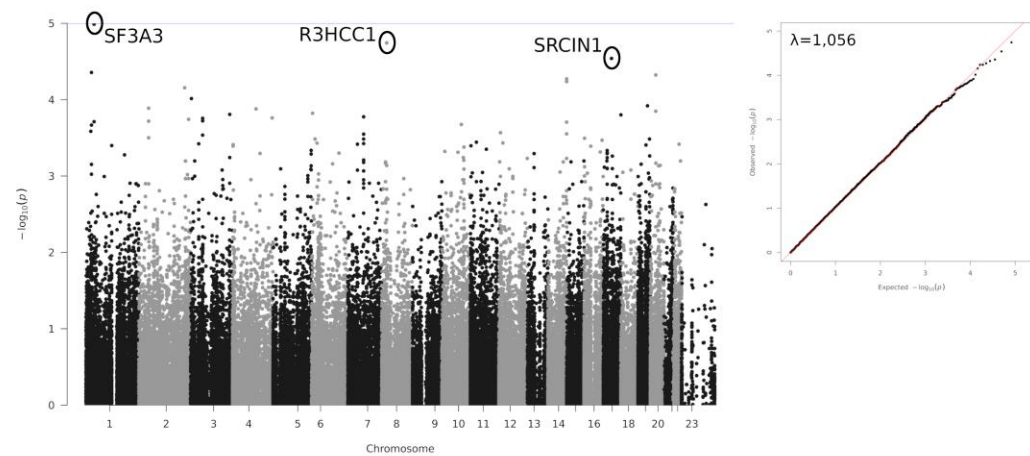
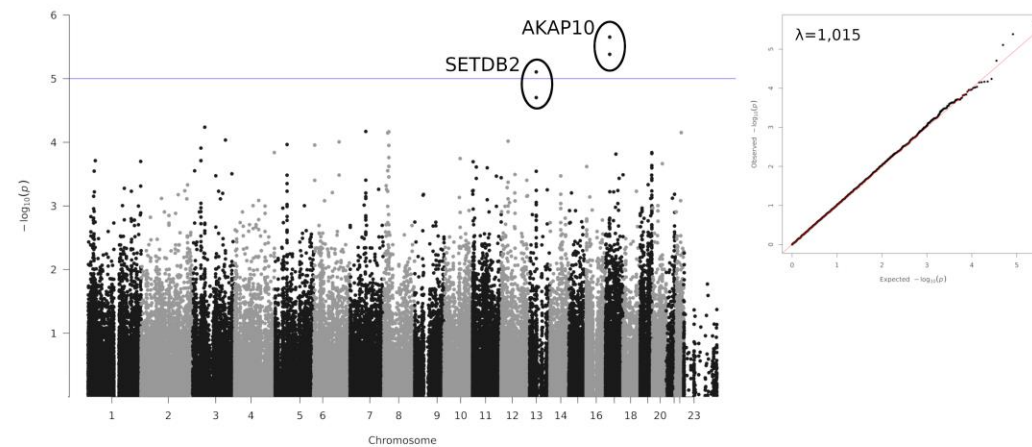
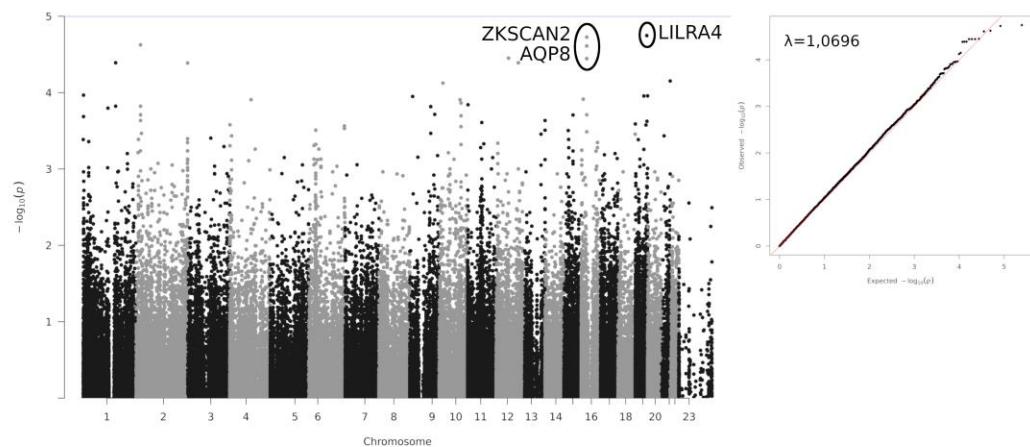


Føroyar í mun til Europa

- Føroyingar bólka seg fyri seg sjálvar
- Kann hava týdning fyri sjúkugongd og viðgerð
- COVID-19-sjúklingarnir bólka seg væl saman

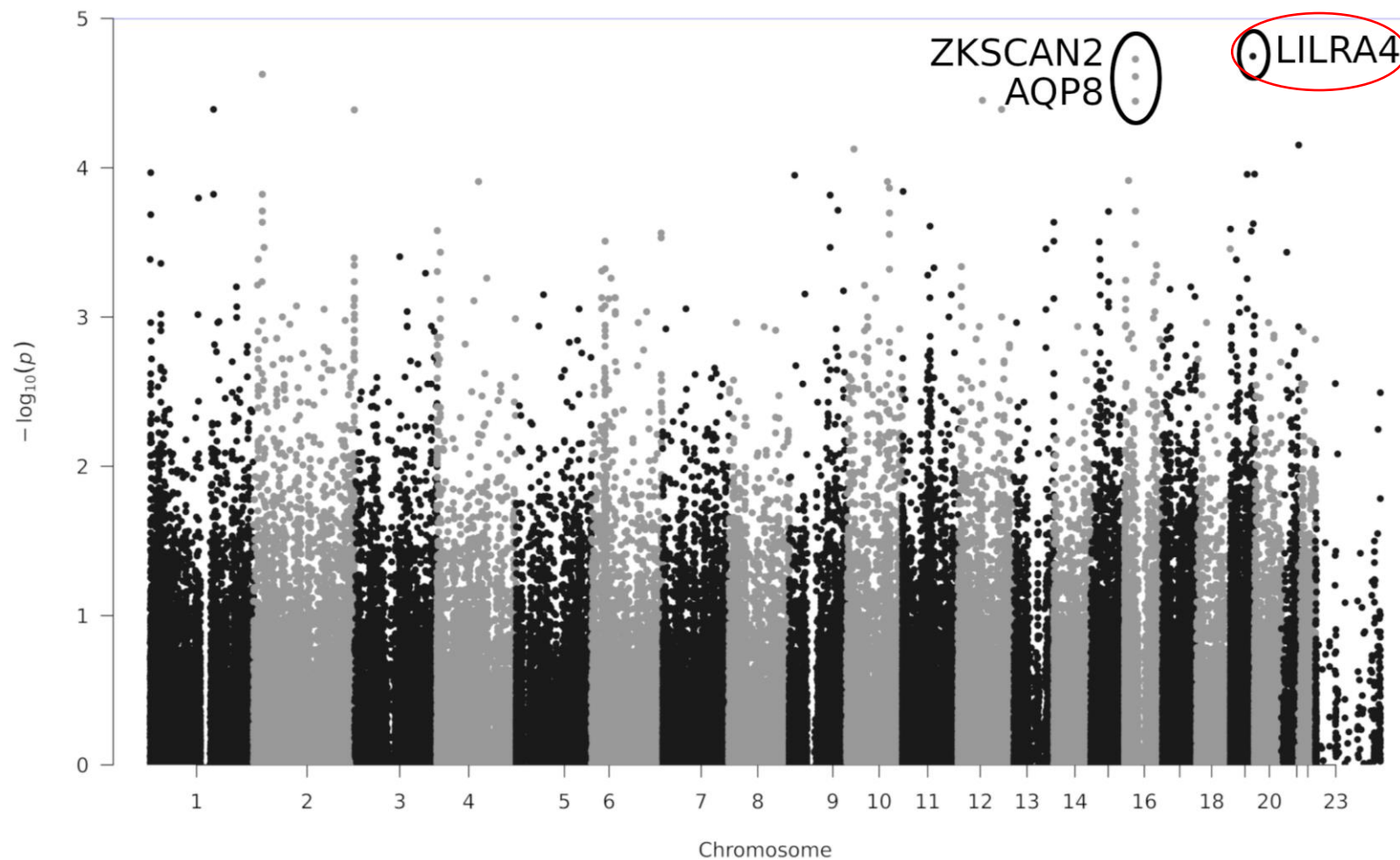


GWAS – Genome Wide Association Study



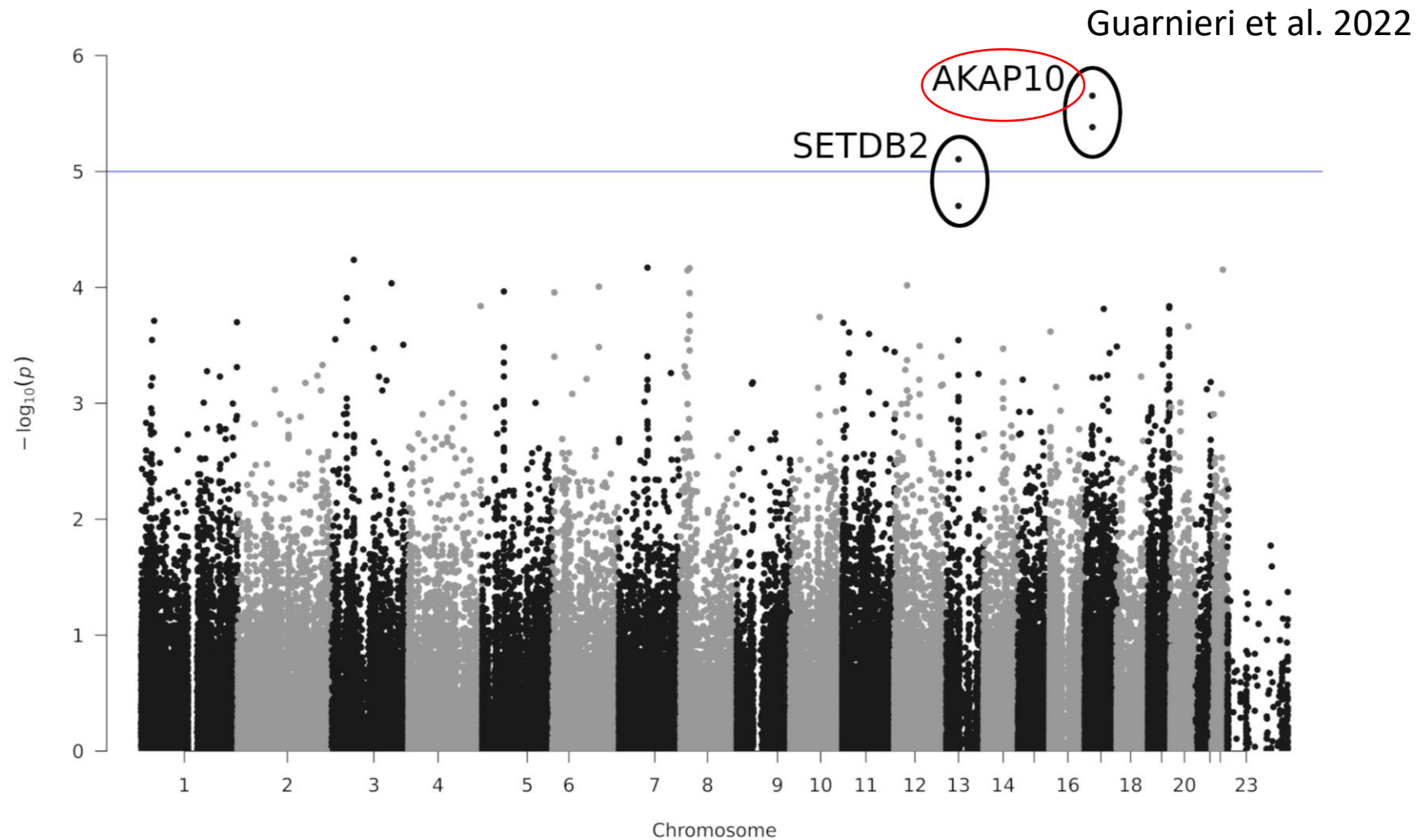
GWAS – Genome Wide Association Study

Zhang et al. 2021



Lydersen et al. 2022 í gerð

GWAS – Genome Wide Association Study



Lydersen et al. 2022 í gerð

Úrslit

Table 2. The table shows missense variants nominal significant associated with severity of COVID-19 from the four association analyses. The cases comprise individuals with more severe COVID-19 symptoms, larger number of symptoms, higher grade of self-reported severity of COVID-19, and individuals with COVID-19 symptoms 2 years post-infection. The table includes the gene name, genomic position (hg38), RSID from dbSNP, minor allele frequency (MAF) in cases and controls, p-value, odds ratio (OR (95% CI)), protein change, and references to COVID-19 or viral related research for the genes comprising the associated single variants (reference).

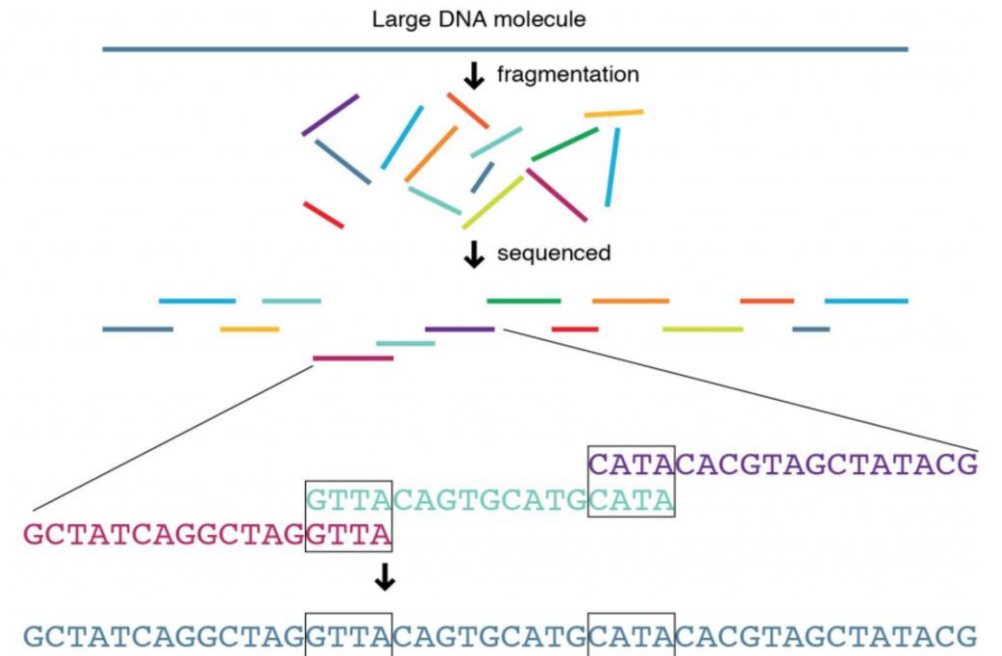
Gene	Genomic pos.	RSID:A1/A2	MAF		P	OR (95% CI)	Protein	Covid-19 or viral related research
			Cases	Controls				
<i>Analysis 1: mild to severe covid-19 symptoms:</i>								
<i>AQP8</i>	chr16:25228484	rs2287798:C/G	0.56	0.29	2.45x10 ⁻⁵	3.17 (1.84-5.47)	p.Ala260Pro	Mariajoseph-Antony et al. 2020 (14)
<i>ZKSCAN2</i>	chr16:25251957	rs2112811:A/G	0.33	0.11	3.58x10 ⁻⁵	3.78 (1.96-7.28)	p.Leu253Phe	na
<i>HS1BP3</i>	chr2:20619123	rs35579164:C/G	0.16	0.03	1.51x10 ⁻⁴	6.37 (2.19-18.54)	p.Pro348Arg	na
<i>GABBR2</i>	chr9:98293840	rs10985765:C/T	0.32	0.12	1.53x10 ⁻⁴	3.38 (1.76-6.49)	p.Thr869Ala	Shcherbak et al. 2022 (15)
<i>TBC1D2</i>	chr9:98229148	rs1573025:A/C	0.32	0.12	1.53x10 ⁻⁴	3.38 (1.76-6.49)	p.Gly261Val	Taylor et al. 2020 (16)
<i>Analysis 2: number of covid-19 symptoms:</i>								
<i>AKAP10</i>	chr17:19909228	rs203462:T/C	0.57	0.28	2.22x10 ⁻⁶	3.44 (2.04-5.79)	p.Ile646Val	Guarnieri et al. 2022 (17)
<i>AKAP10</i>	chr17:19958145	rs2108978:C/T	0.57	0.29	4.14x10 ⁻⁶	3.31 (1.97-5.56)	p.Arg249His	Guarnieri et al. 2022 (17)
<i>KIR2DS4</i>	chr19:54837865	rs1130494:G/C	0.25	0.08	1.45x10 ⁻⁴	4.07 (1.90-8.71)	p.Met120Ile	Hajeer et al. 2022 (18)
<i>KIR2DS4</i>	chr19:54835110	rs1130478:T/G	0.17	0.03	1.50x10 ⁻⁴	6.65 (2.21-20.00)	p.Gln22His	Hajeer et al. 2022 (18)
<i>LOXL2</i>	chr8:23309840	rs1063582:T/G	0.35	0.15	1.74x10 ⁻⁴	3.08 (1.69-5.62)	p.Met570Leu	Peng et al. 2021 (19)
<i>DUSP13</i>	chr10:75107995	rs41280430:C/G	0.12	0.01	1.80x10 ⁻⁴	18.03 (2.34-138.7)	p.Gly122Arg	Reay et al. 2021 (20)
<i>Analysis 3: graded severity of covid-19:</i>								
<i>EGF</i>	chr4:109993271	rs4698803:A/T	0.46	0.23	1.32x10 ⁻⁴	2.81 (1.64-4.82)	p.Glu920Val	na
<i>WBSCR28</i>	chr7:73861235	rs11770052:T/A	0.12	0.31	1.68x10 ⁻⁴	0.30 (0.16-0.57)	p.Ile14Asn	na
<i>Analysis 4: having symptoms after 2 years (follow-up):</i>								
<i>OMG</i>	chr17:31296270	rs11080149:T/C	0.26	0.08	1.40x10 ⁻⁴	4.05 (1.90-8.62)	p.Gly21Asp	Assavapongpaiboon et al. 2022 (21)
<i>SPRTN</i>	chr1:231352778	rs2437150:C/T	0.19	0.42	1.72x10 ⁻⁴	0.33 (0.18-0.59)	p.Pro296Leu	na

RSID:A1/A2: Single nucleotide polymorphism: minor allele and major allele
na: not available

Niðurstøða

Vit hava

- Ílegulisið øll tey smittaðu, sum vildu luttaka frá fyrstu bylgju
- Kanna ílegur saman við øðrum faktorum
 - Tal av sjúkueyðkennum, andaneyð, sjúkugongd
- Ikki stórir munur millum case'ir og kontrollar
- Flestu ílegur, vit funnu, høvdu samband við immunverjuna
- Íleguupplýsingar hjálpa til við viðgerð
- Íleguupplýsingar hjálpa til við váðameting



Takk til

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