

Genomski čimbenici u patogenezi COVID-19



Lucija Klarić
UKRI Innovation Fellow

MRC Human Genetics Unit, Institute of Genetics and Cancer
University of Edinburgh

27/04/2021

Genomski čimbenici u patogenezi COVID-19

Article | Published: 11 December 2020

Genetic mechanisms of critical illness in COVID-19

Erola Pairo-Castineira, Sara Clohisey, Lucija Klaric, Andrew D. Bretherick, Konrad Rawlik, Dorota Pasko, Susan Walker, Nick Parkinson, Max Head Fourman, Clark D. Russell, James Furniss, Anne Richmond, Elvina Gountouna, Nicola Wrobel, David Harrison, Bo Wang, Yang Wu, Alison Meynert, Fiona Griffiths, Wilna Oosthuyzen, Athanasios Kousathanas, Loukas Moutsianas, Zhiyan Yang, Ranran Zhai, Chenqing Zheng, Graeme Grimes, Rupert Beale, Jonathan Millar, Barbara Shih, Sean Keating, Marie Zechner, Chris Haley, David J. Porteous, Caroline Hayward, Jian Yang, Julian Knight, Charlotte Summers, Manu Shankar-Hari, Paul Klenerman, Lance Turtle, Antonia Ho, Shona C. Moore, Charles Hinds, Peter Horby, Alistair Nichol, David Maslove, Lowell Ling, Danny McAuley, Hugh Montgomery, Timothy Walsh, Alexandre C. Pereira, Alessandra Renieri, The GenOMICC Investigators, The ISARIC4C Investigators, The COVID-19 Human Genetics Initiative, 23andMe Investigators, BRACOVID Investigators, Gen-COVID Investigators, Xia Shen, Chris P. Ponting, Angie Fawkes, Albert Tenesa, Mark Caulfield, Richard Scott, Kathy Rowan, Lee Murphy, Peter J. M. Openshaw, Malcolm G. Semple, Andrew Law, Veronique Vitart, James F. Wilson & J. Kenneth Baillie✉ -Show fewer authors

Nature 591, 92–98(2021) | Cite this article

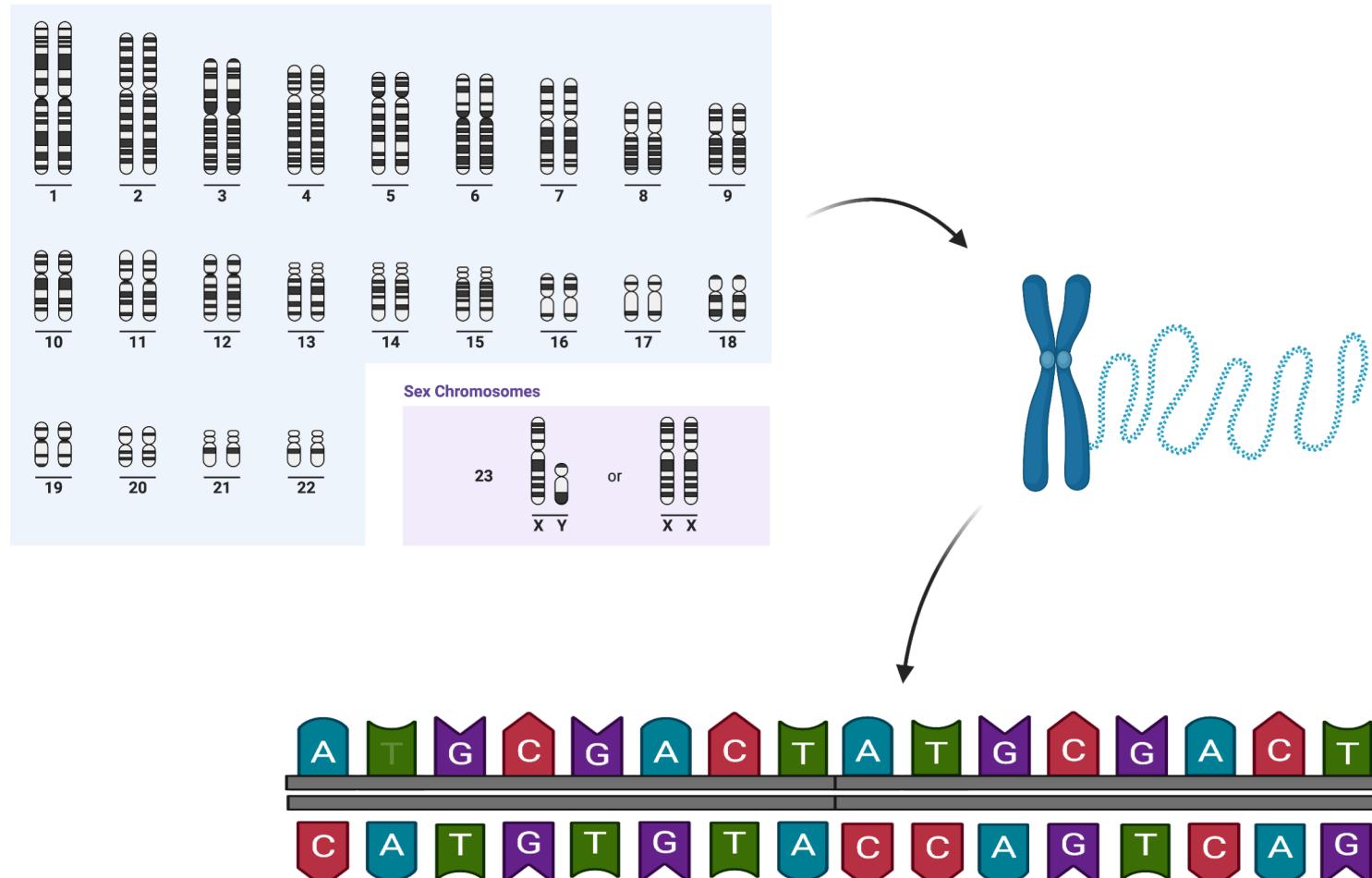
238k Accesses | 52 Citations | 2724 Altmetric | Metrics



THE UNIVERSITY
of EDINBURGH

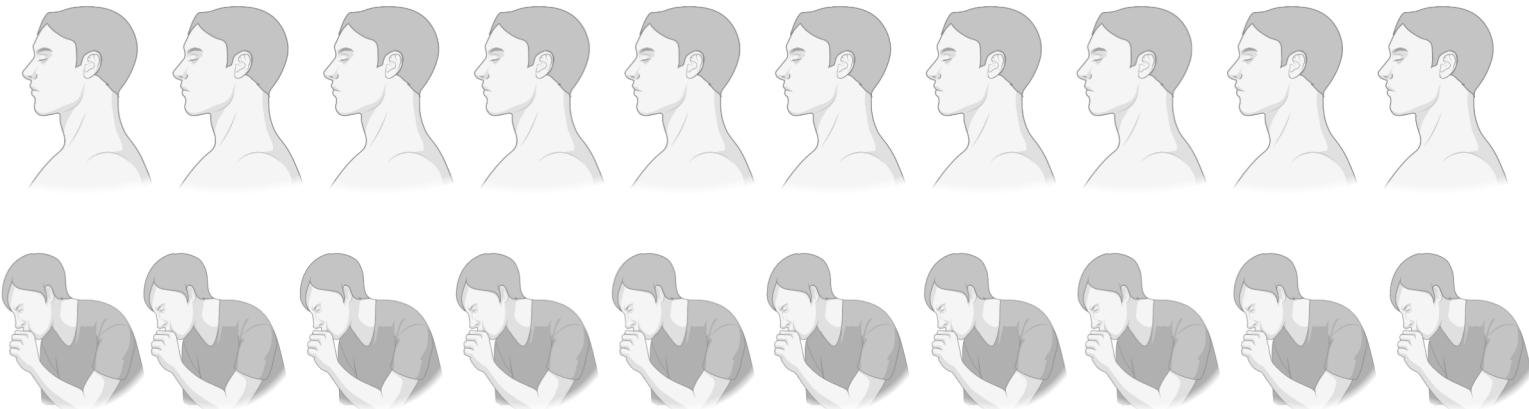
Cjelogenomske studije asocijacija (*engl* GWAS)

- *engl* Genome-wide Association Study – GWAS

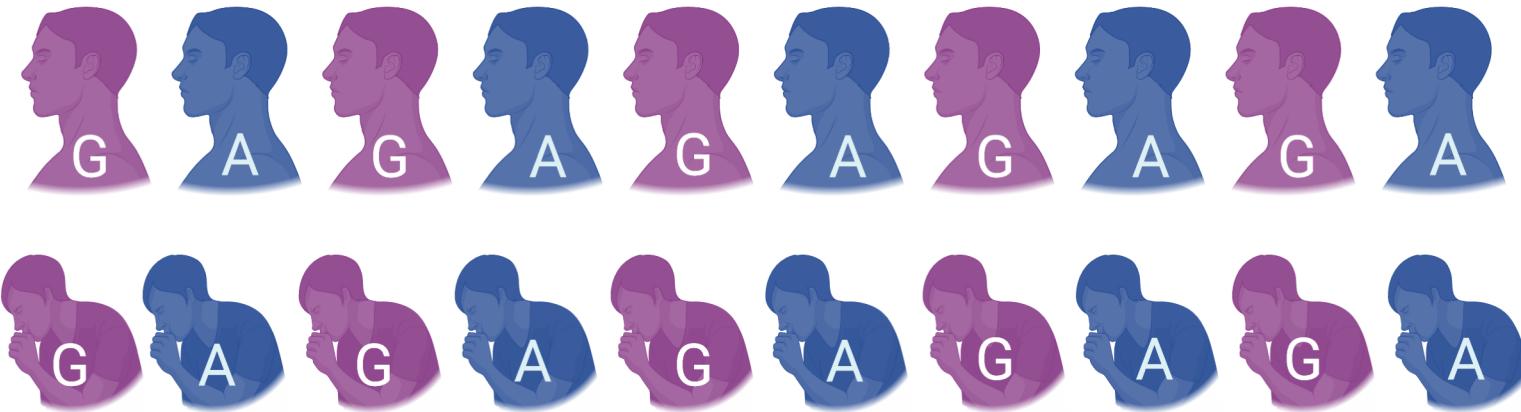
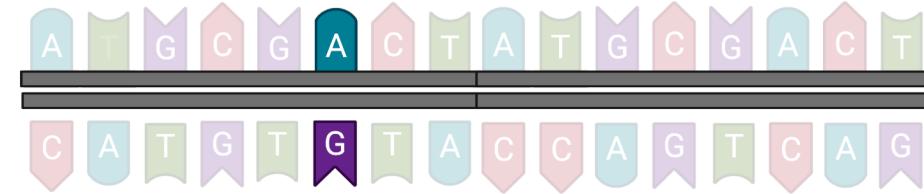


THE UNIVERSITY
of EDINBURGH

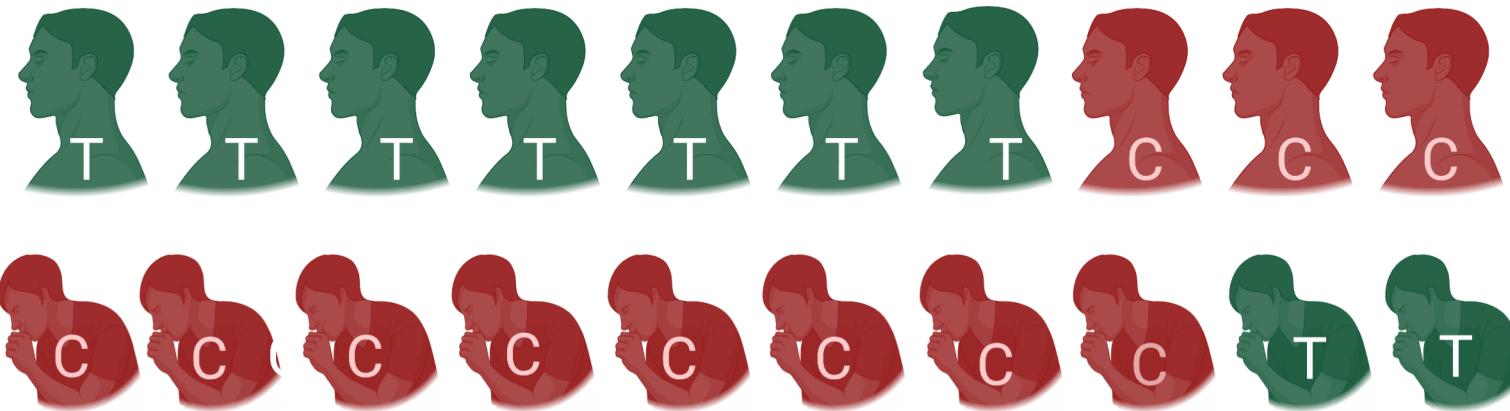
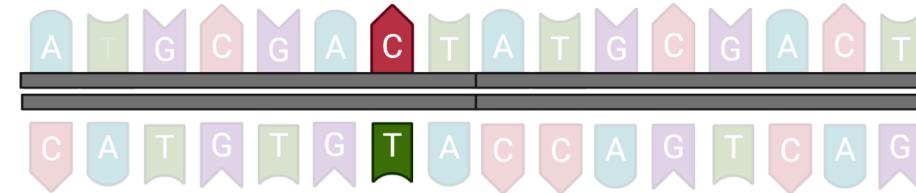
Cjelogenomske studije asocijacija (engl GWAS)



Cjelogenomske studije asocijacija (*engl GWAS*)



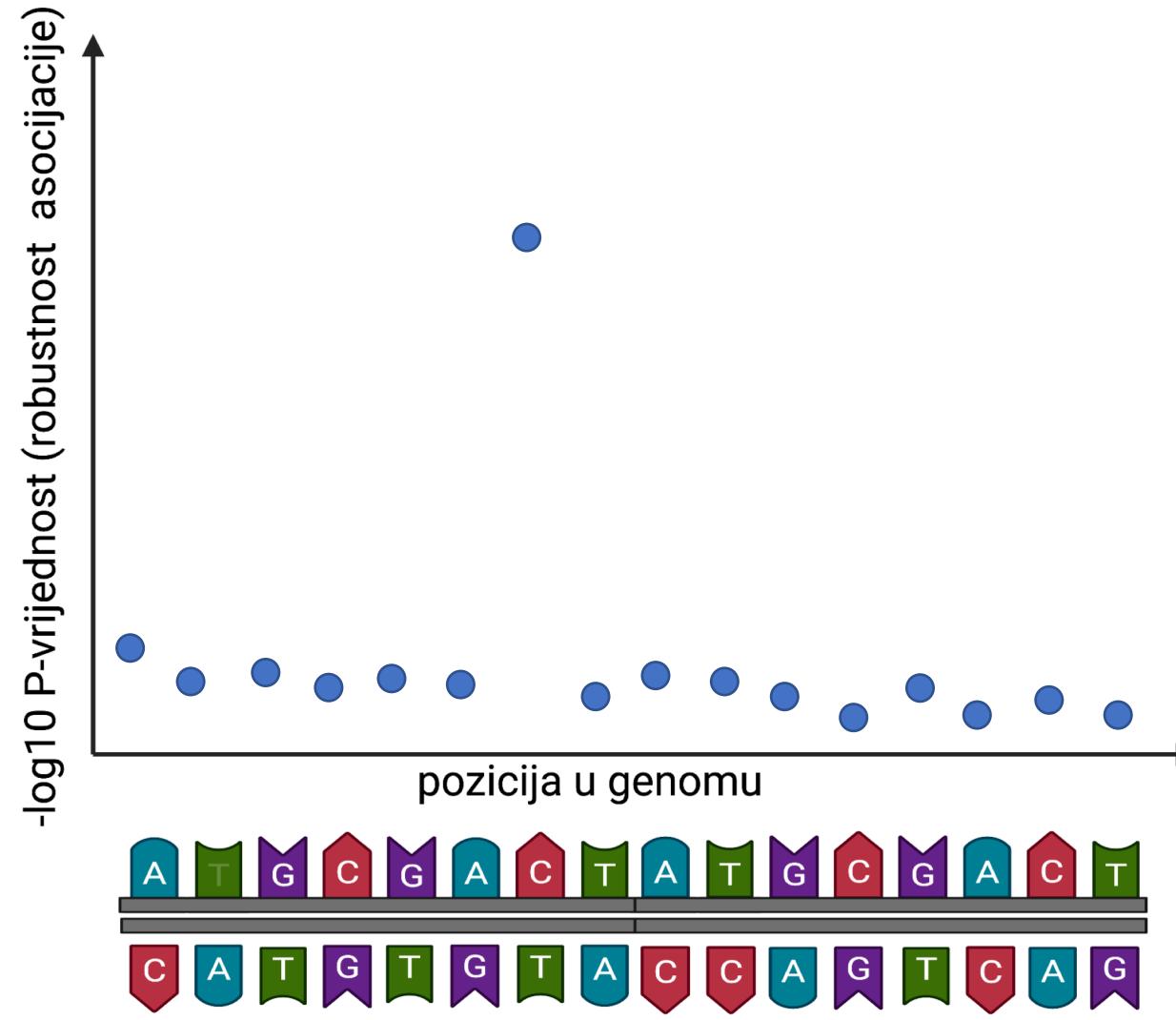
Cjelogenomske studije asocijacija (*engl GWAS*)



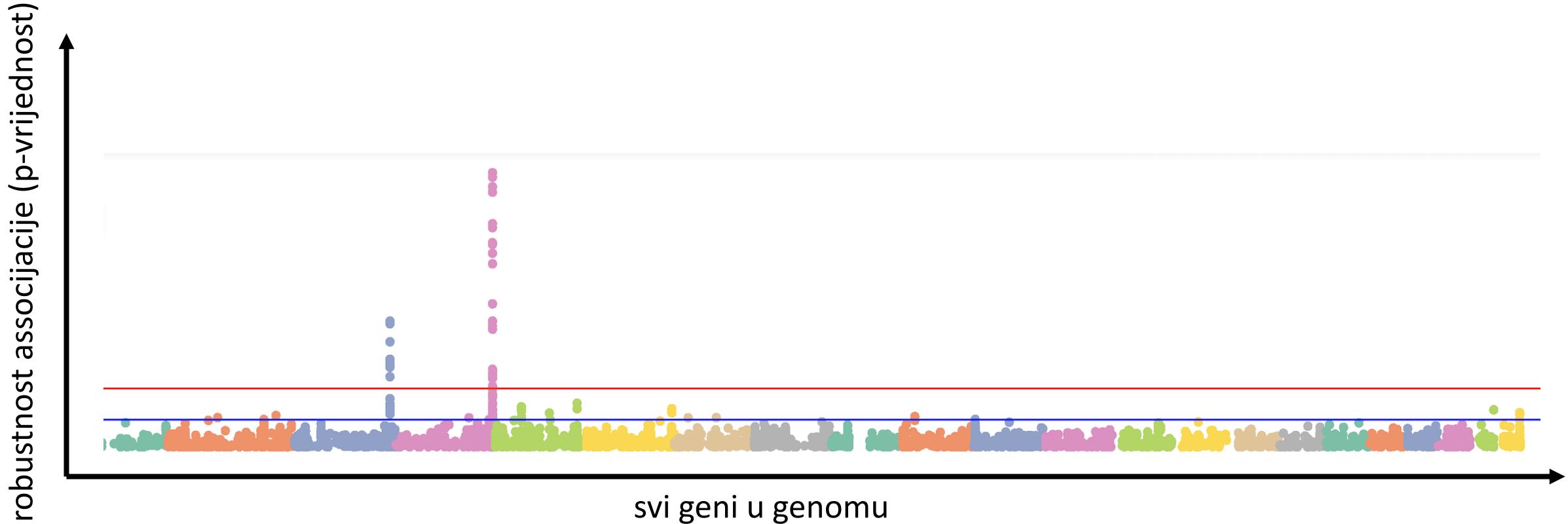
Cjelogenomske studije asocijacija (*engl GWAS*)



Cjelogenomske studije asocijacija (*engl GWAS*)

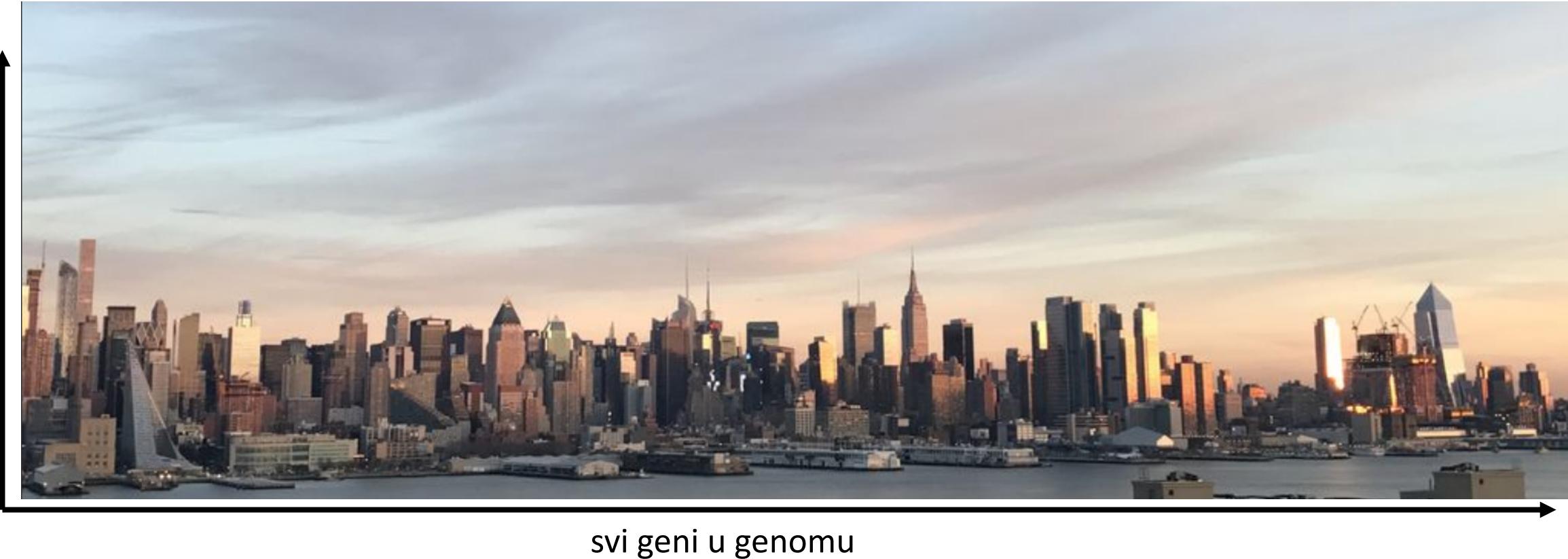


Cjelogenomske studije asocijacija (*engl GWAS*)



Cjelogenomske studije asocijacija (*engl GWAS*)

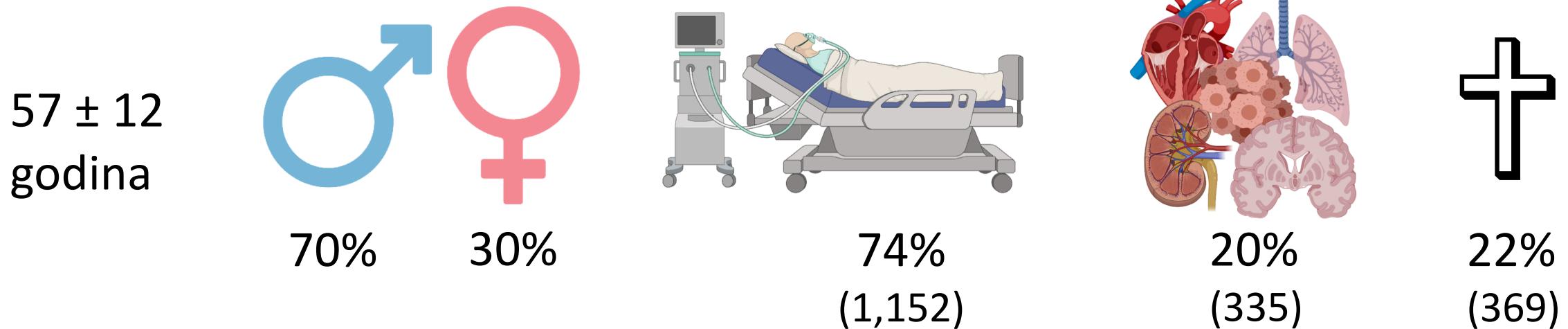
robustnost asocijacija (p-vrijednost)



Genetska predispozicija za teški oblik COVID-19



- pacijenti sa intenzivnih jedinica diljem Ujedinjenog Kraljevstva (206)
- 1,676 pacijenata Europskog podrijetla



THE UNIVERSITY
of EDINBURGH



Genetska predispozicija za teški oblik COVID-19

- UK biobanka
 - biomedicinska baza (500,000 sudionika)
 - genetika, klinički fenotipovi, elektronički medicinski zapisi, razni upitnici
- 8,380 “zdravih” sudionika
 - odgovarajuće karakteristike: spol, tjelesni indeks mase (*engl. BMI*), socio-ekonomski status

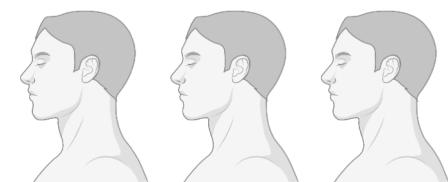


biobank^{uk}

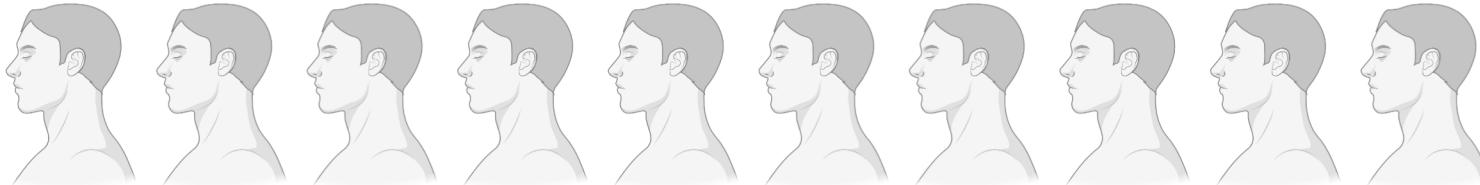


THE UNIVERSITY
of EDINBURGH

MRC
Human
Genetics
Unit



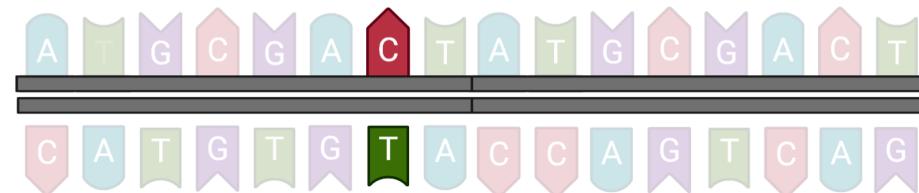
Cjelogenomske studije asocijacija (engl GWAS)



biobank^{uk}



GenOM|CC

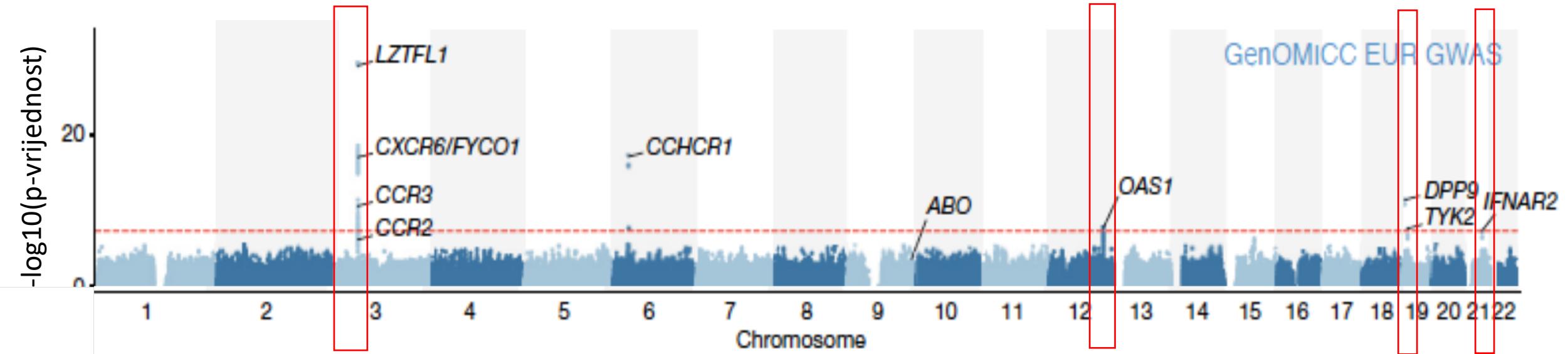


× 4,500,000



THE UNIVERSITY
of EDINBURGH

Genetska predispozicija za teški oblik COVID-19



Genetska predispozicija za teški oblik COVID-19

LZTFL1



Dob: ~2 -15x

OAS1



BMI: ~1.5-2.5x

DPP9

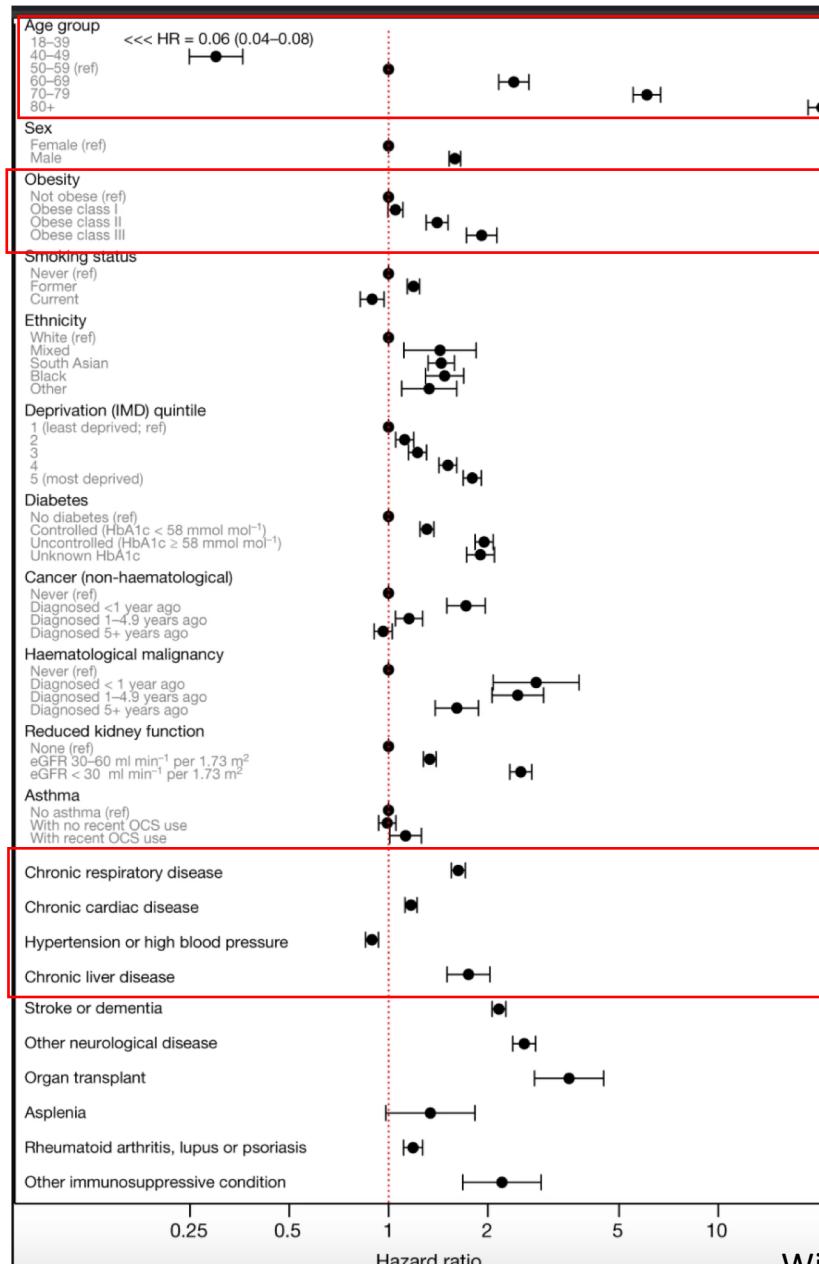


TYK2



Kronične
bolesti pluća,
srca i jetre:
~1.3-1.8x

IFNAR2



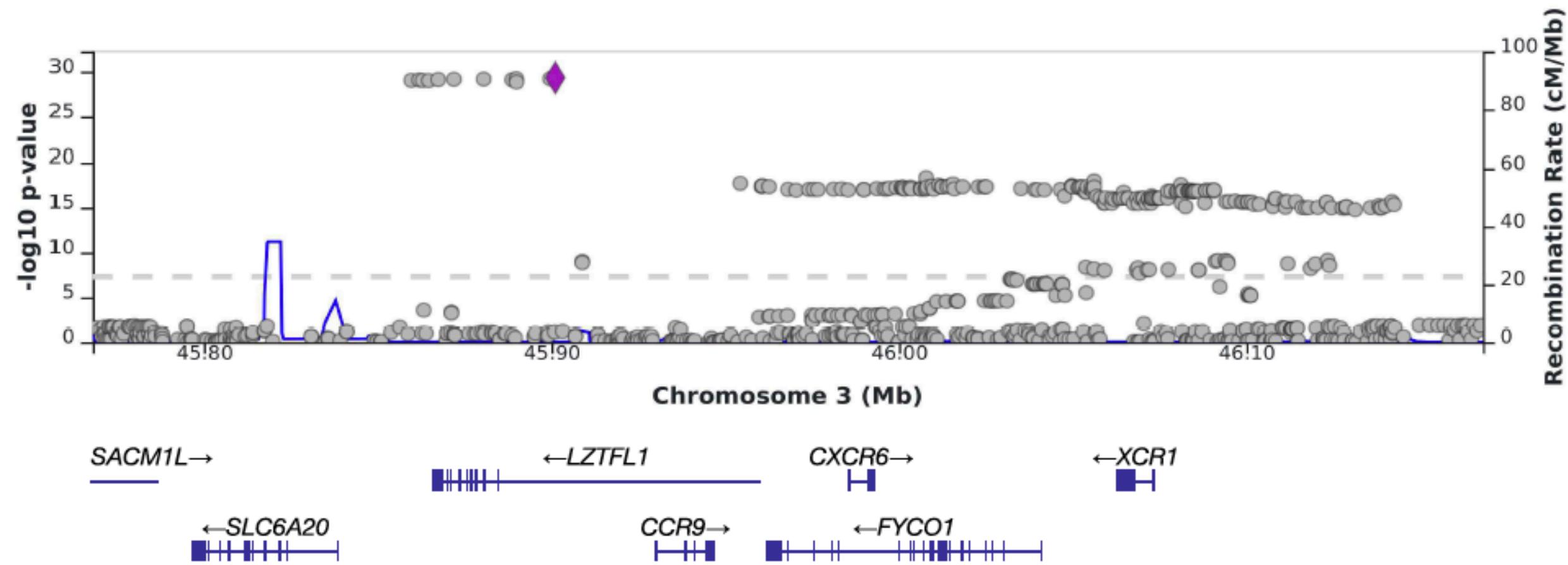
0.5 0.7 1 1.5 2 2.5

0.25 0.5 1 2 5 10

Hazard ratio

Genetska predispozicija za teški oblik COVID-19

- *LZTFL1* – interakcija sa Bardet-Biedl Syndrome proteinima
- *FYCO1* – potencijalno povezan sa beta-koronavirusima
- *CXCR6, CCR9, CCR2, CCR3* – kemokinski receptori vezani uz regulaciju upalnih procesa



Genetska predispozicija za teški oblik COVID-19

- **Rani odgovor:**
 - *OAS1* – RNAza L; degradacije virusne RNA i inhibicija replikacije virusa
 - *IFNAR2* – intereferon receptor – aktivacija protuvirusnog odgovora
- **Kasni odgovor (eksesivni upalni odgovor):**
 - *DPP9* – serinska proteaza (citokini, uključujući CXCL10); aktivacija "inflamasoma" (upalni odgovor na infekcije)
 - idiopatska fibroza pluća
 - *TYK2* – tirozin kinaza (JAK); sudjeluje u interferonskom signalnom putu

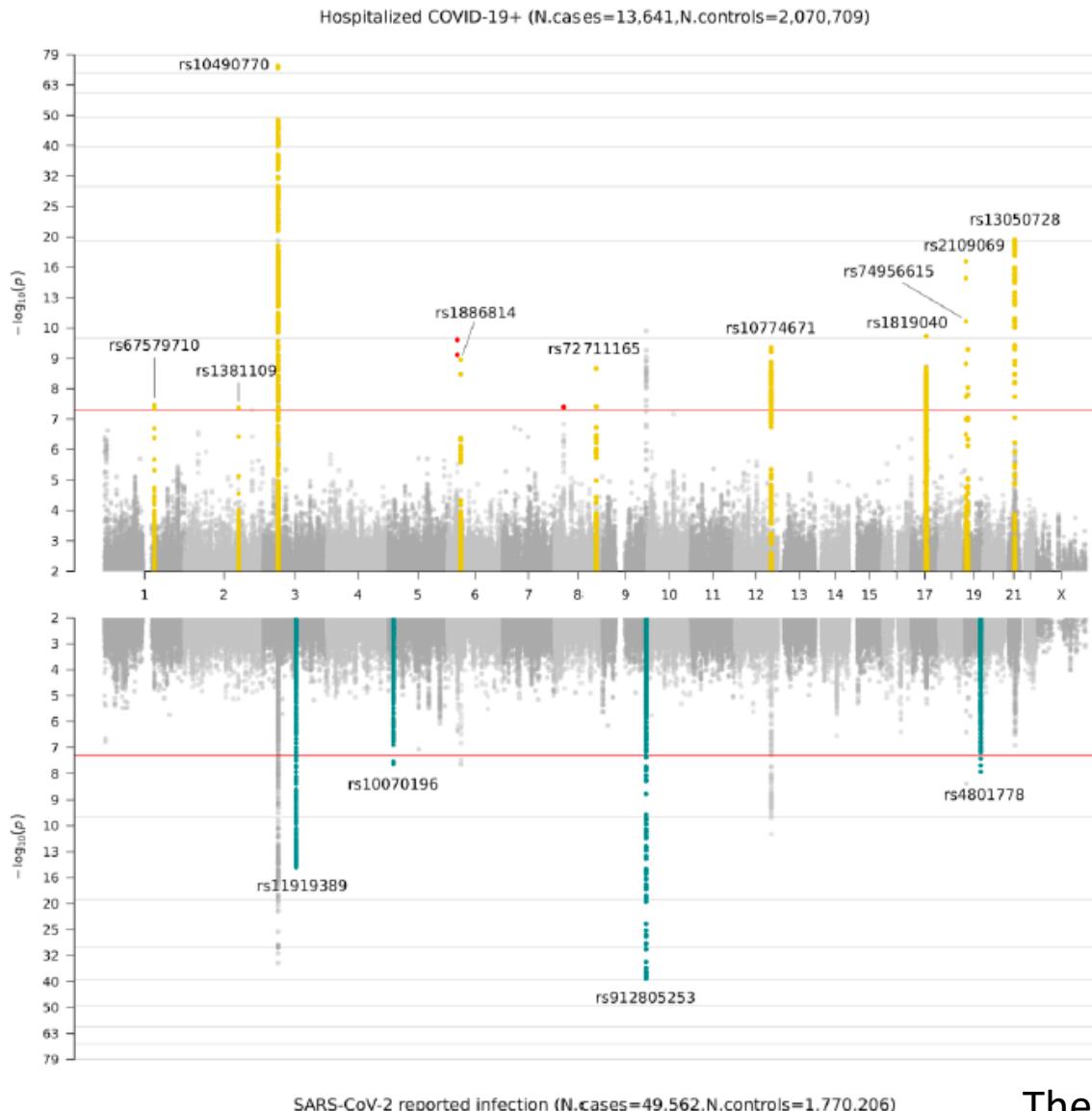
Genetska predispozicija za teški oblik COVID-19

- Host Genetics Initiative
 - 46 studija iz 19 zemalja diljem svijeta



Genetska predispozicija za teški oblik COVID-19

- Host Genetic Initiative



The COVID-19 Host Genetics Initiative, medRxiv, 2021



Zaključci

- 5 genetskih regija
 - rani odgovor: *IFNAR2*, *OAS1*
 - oštećenje pluća: *DPP9*, *TYK2*, *LZTLF1-CCR2-CCR3-CCR9-CXCR6*
- razumijevanje bioloških procesa -> bolja terapija
- Potencijal za nove terapije:
 - *OAS1* – inhibitori fosfodiesteraze 12
 - *TYK2* – inhibitor JAK kinaze (baricitinib)
 - *IFNAR2* – tretman interferonima – neuspješan

Article | Published: 11 December 2020

Genetic mechanisms of critical illness in COVID-19

Erola Pairo-Castineira, Sara Clohisey, Lucija Klaric, Andrew D. Bretherick, Konrad Rawlik, Dorota Pasko,
Susan Walker, Nick Parkinson, Max Head Fourman, Clark D. Russell, James Furniss, Anne Richmond,
Elvina Gountouna, Nicola Wrobel, David Harrison, Bo Wang, Yang Wu, Alison Meynert, Fiona Griffiths,
Wilna Oosthuyzen, Athanasios Kousathanas, Loukas Moutsianas, Zhiyan Yang, Ranran Zhai, Chenqing
Zheng, Graeme Grimes, Rupert Beale, Jonathan Millar, Barbara Shih, Sean Keating, Marie Zechner,
Chris Haley, David J. Porteous, Caroline Hayward, Jian Yang, Julian Knight, Charlotte Summers, Manu
Shankar-Hari, Paul Klenerman, Lance Turtle, Antonia Ho, Shona C. Moore, Charles Hinds, Peter Horby,
Alistair Nichol, David Maslove, Lowell Ling, Danny McAuley, Hugh Montgomery, Timothy Walsh,
Alexandre C. Pereira, Alessandra Renieri, The GenOMICC Investigators, The ISARIC4C Investigators,
The COVID-19 Human Genetics Initiative, 23andMe Investigators, BRACOVID Investigators, Gen-COVID
Investigators, Xia Shen, Chris P. Ponting, Angie Fawkes, Albert Tenesa, Mark Caulfield, Richard Scott,
~~Kathy Rowan, Lee Murphy, Peter J. M. Openshaw, Malcolm G. Semple, Andrew Law, Veronique Vitart,~~
James F. Wilson & J. Kenneth Baillie  -Show fewer authors

University of Edinburgh

MRC Human Genetics Unit, Institute of Genetics and Cancer
Roslin Institute



T
of