Uncovering novel genetic factors of pediatric sepsis through new tools for **precision genomic medicine.**

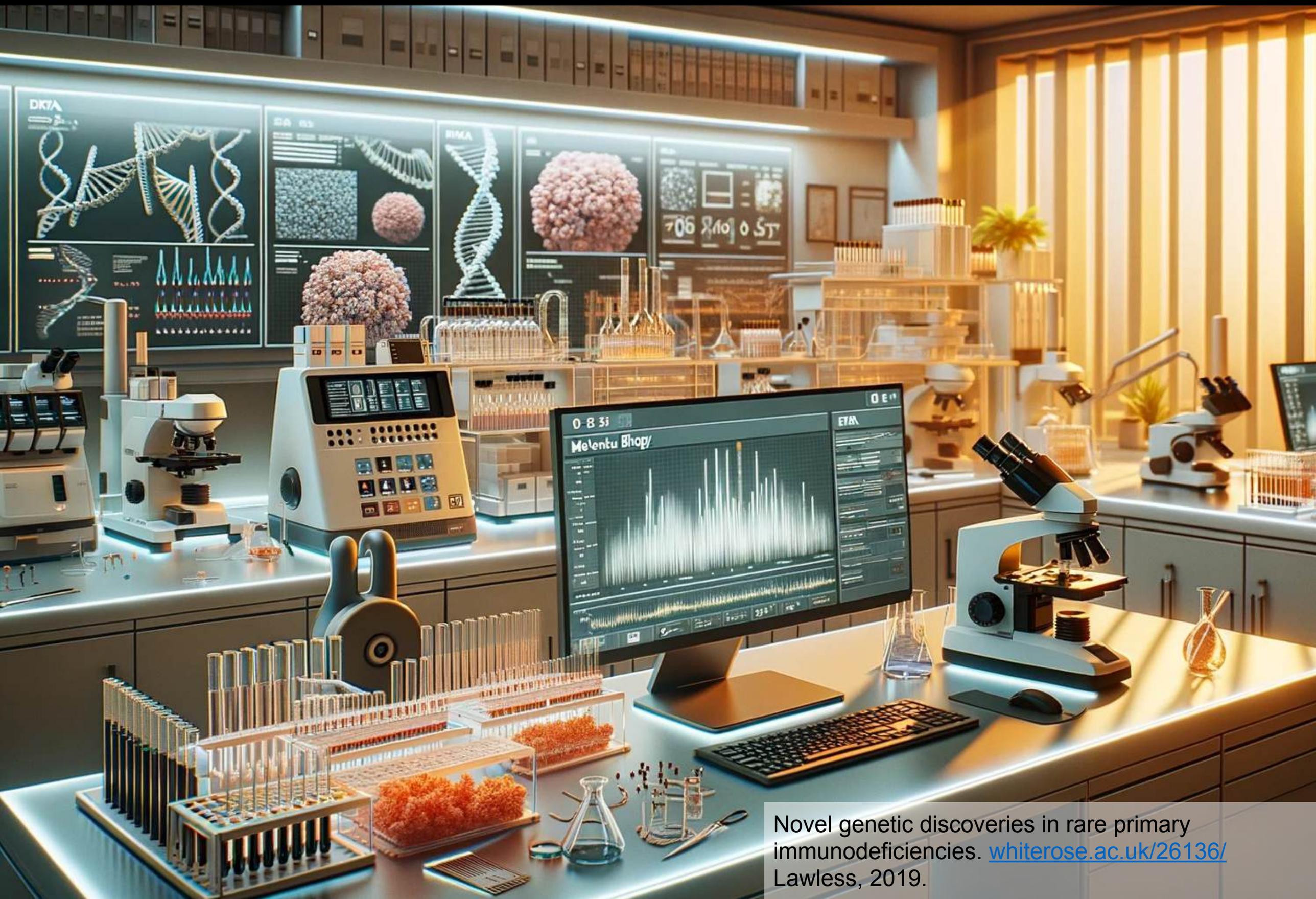
Dylan Lawless
Pauline Rogg
Manon Bouzereau
Robin Fallegger
Zaira Seferbekovatbd
Sina Ruger
Shweta Pipaliya
Valeriia Timonina
Konstantin Pipadin
Ali Saadat
Zhi Ming Xu
Christian Thorball
Flavia Hodell
Philipp Agyeman
Jacques Fellay
Luregn J. Schlapbach
for the Swiss Pediatric Sepsis Study

“Learn the facts, Steed-Asprey used to say, then try on the stories like clothes.”

Tinker, Tailor, Soldier, Spy.
John le Carré

A face behind the research

Decoding the puzzle



Novel genetic discoveries in rare primary immunodeficiencies. whiterose.ac.uk/26136/ Lawless, 2019.

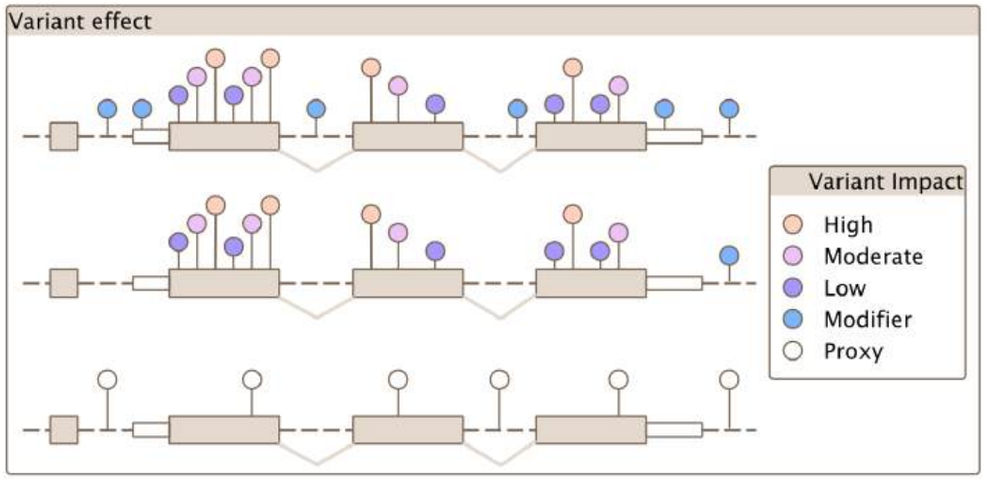
Journey’s verdict

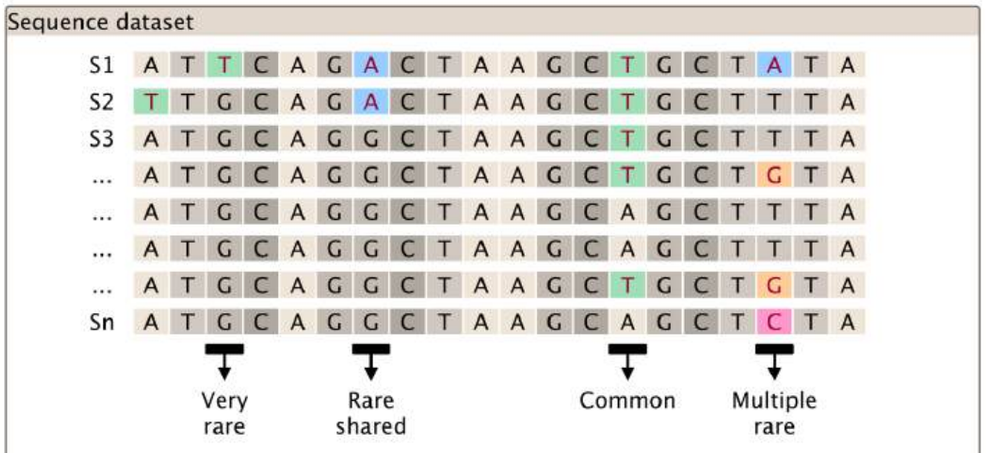
JACI. The Ever-Increasing Array of Novel Inborn Errors of Immunity: an Interim Update by the IUIS Committee 10.1007/s10875-021-00980-1 Tangye et al., 2021.

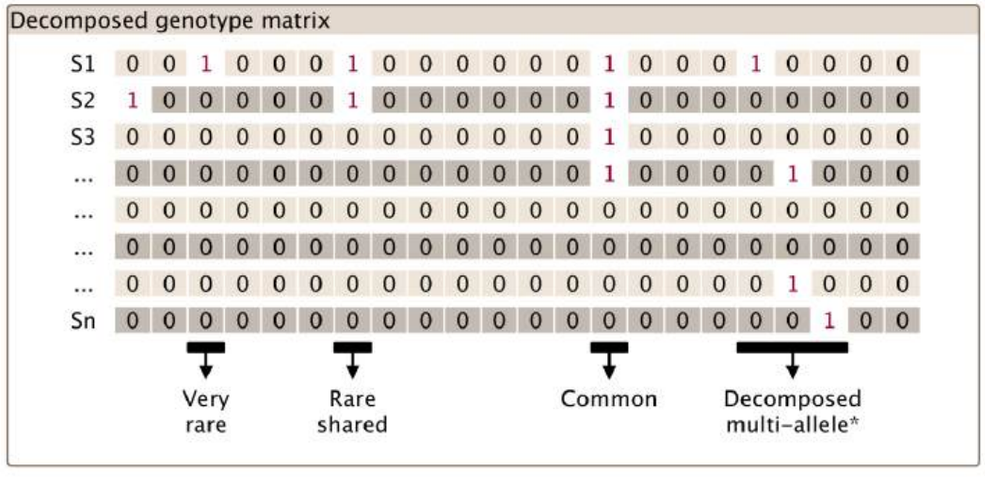
Blood. Germline TET2 Loss-Of-Function Causes Childhood Immunodeficiency and Lymphoma. 10.1182/blood.2020005844 Jarmila Stremenova Spegarova*, and Dylan Lawless*, et. al.

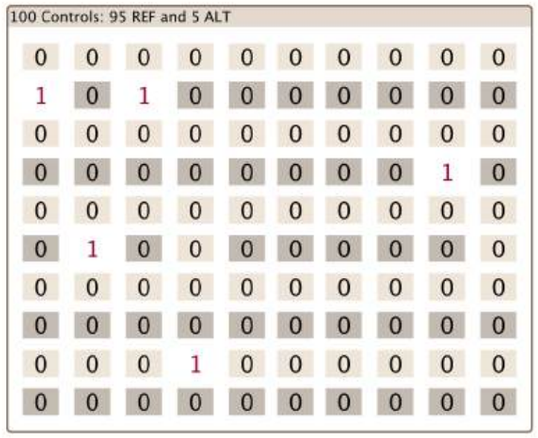
Scale

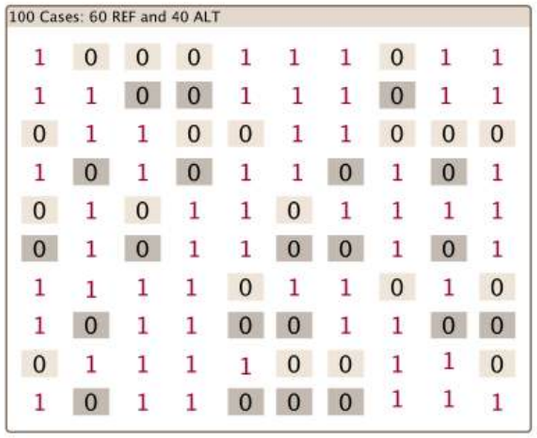
From wet to dry

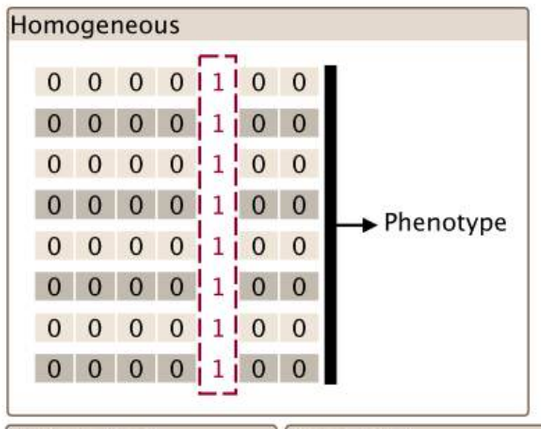


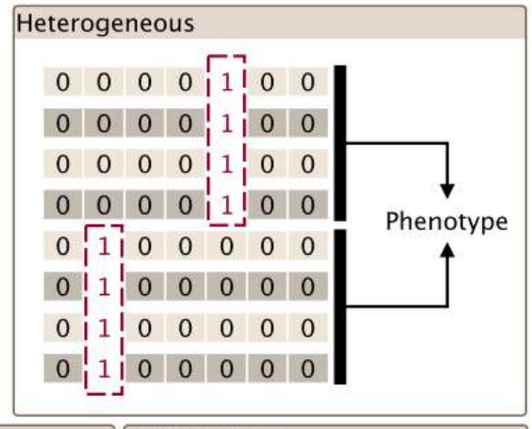


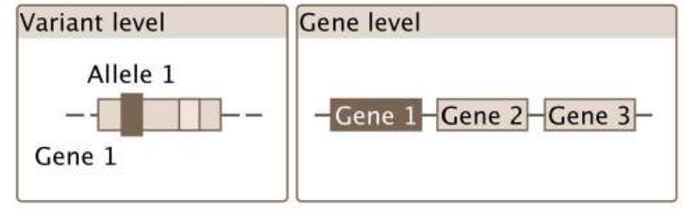


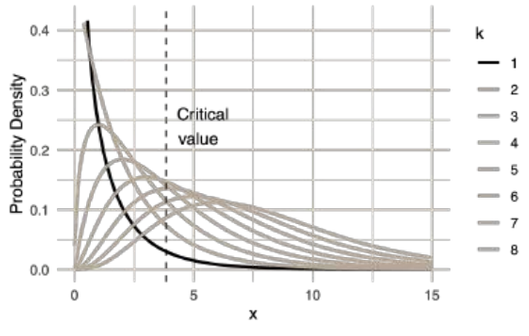


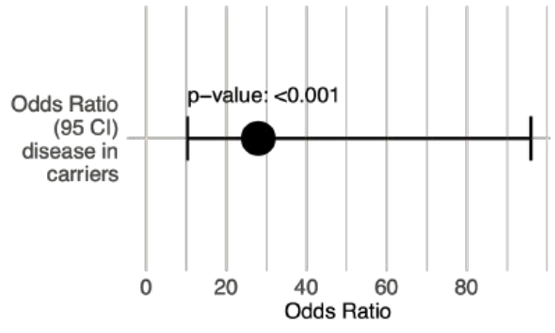












From wet to dry

From wet to dry

Variant annotation

Variant	Set	Sample	Genotype	Age	Sex	Cohort AF	CADD phred	REVEL	ClinVar	FATHMM	OMIM	PANTHER	Gene ontology	...	GnomAD AF
1	A	S1	0	18	0	.3	25.90	.902	PL	.7	179615	11539	0002331	...	3E-05
1	A	...	0	21	1	.3	25.90	.902	PL	.7	179615	11539	0002331	...	3E-05
1	A	Sn	1	45	0	.3	25.90	.902	PL	.7	179615	11539	0002331	...	3E-05
2	A	S1	1	18	0	.01	29.3	.783	P	.9	179615	11539	0002331	...	7E-06
2	A	...	0	21	1	.01	29.3	.783	P	.9	179615	11539	0002331	...	7E-06
2	A	Sn	0	45	0	.01	29.3	.783	P	.9	179615	11539	0002331	...	7E-06
3	B	S1	1	18	0	.5	25.9	.888	PL	NA	147660	10960	0002331	...	3E-05
3	B	...	0	21	1	.5	25.9	.888	PL	NA	147660	10960	0002331	...	3E-05
3	B	Sn	0	45	0	.5	25.9	.888	PL	NA	147660	10960	0002331	...	3E-05
4	B	S1	0	18	0	.02	12.1	NA	NA	NA	147660	10960	0002331	...	3E-05
4	B	...	0	21	1	.02	12.1	NA	NA	NA	147660	10960	0002331	...	3E-05
4	B	Sn	0	45	0	.02	12.1	NA	NA	NA	147660	10960	0002331	...	3E-05

Set level

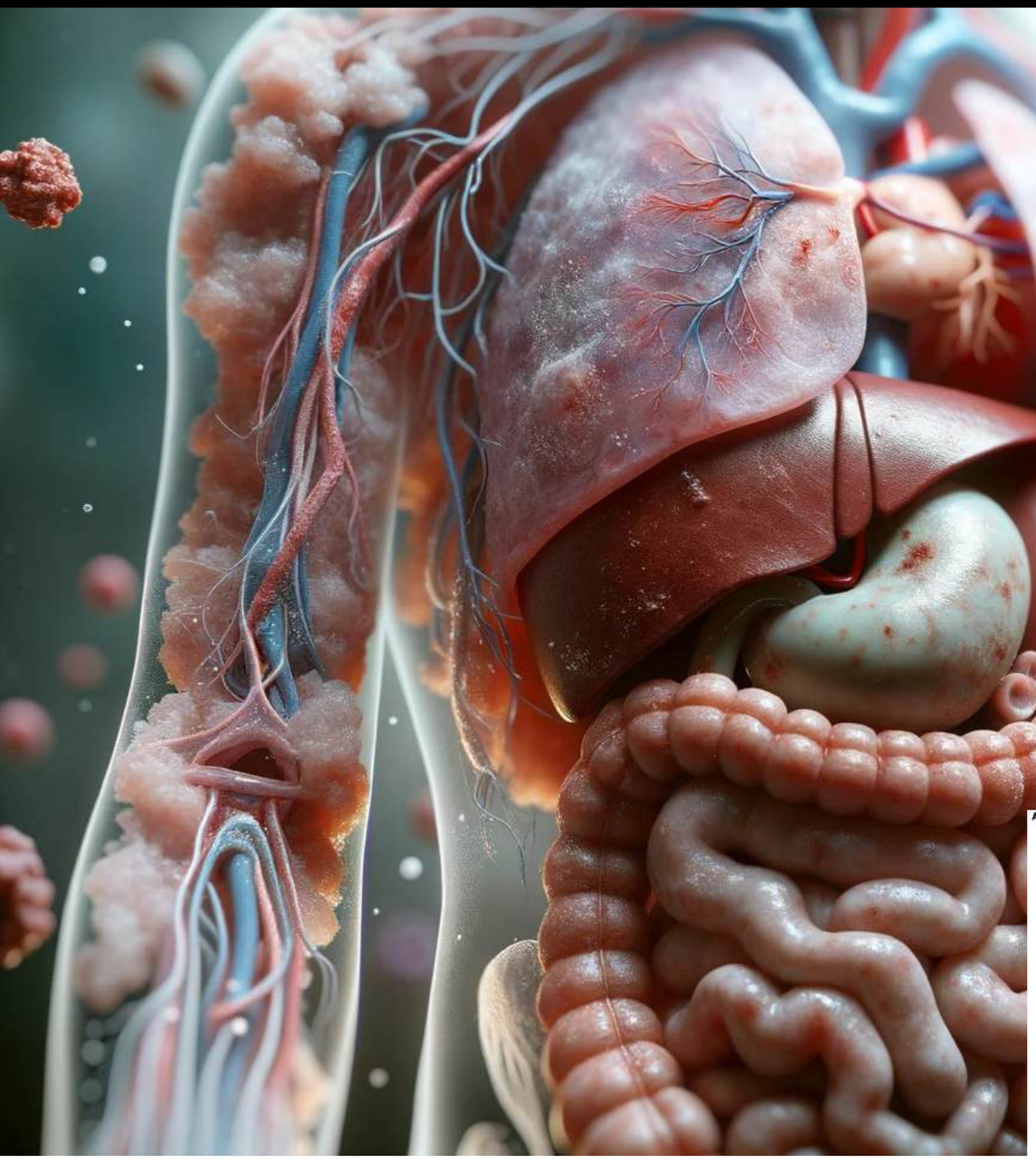
Sample level

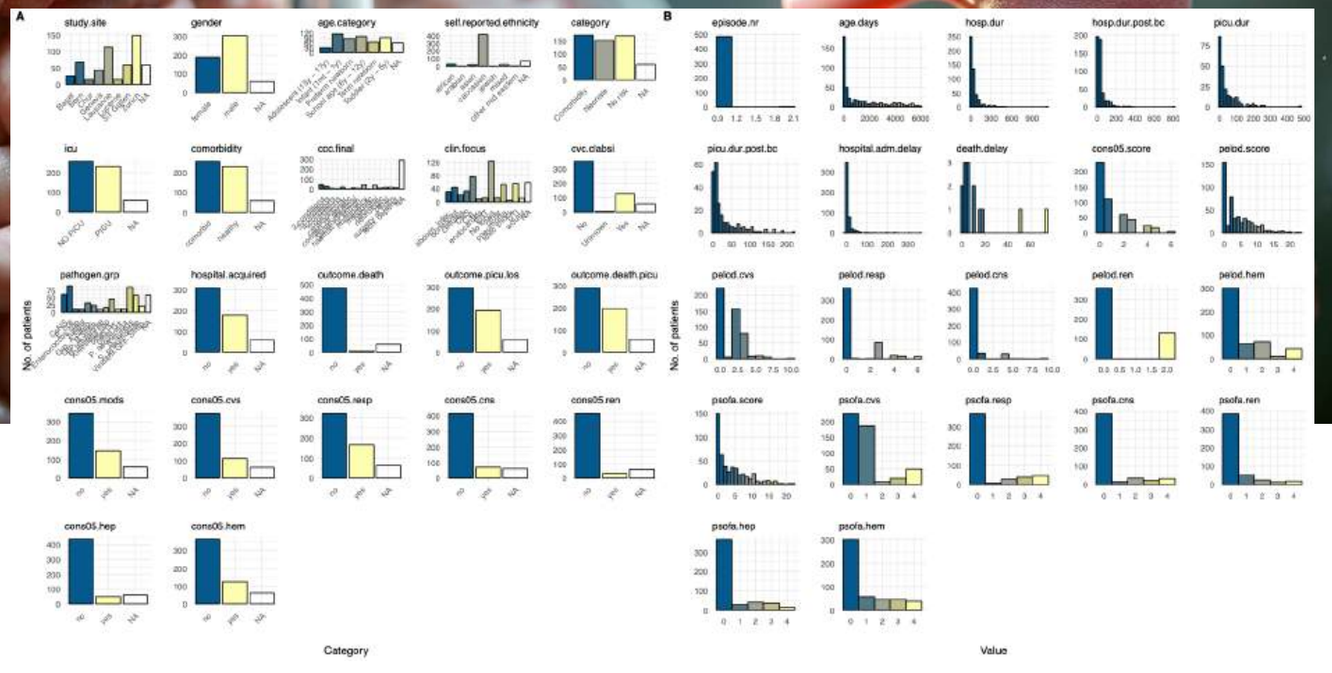
Variant level

Gene level

Ontology level

Sepsis



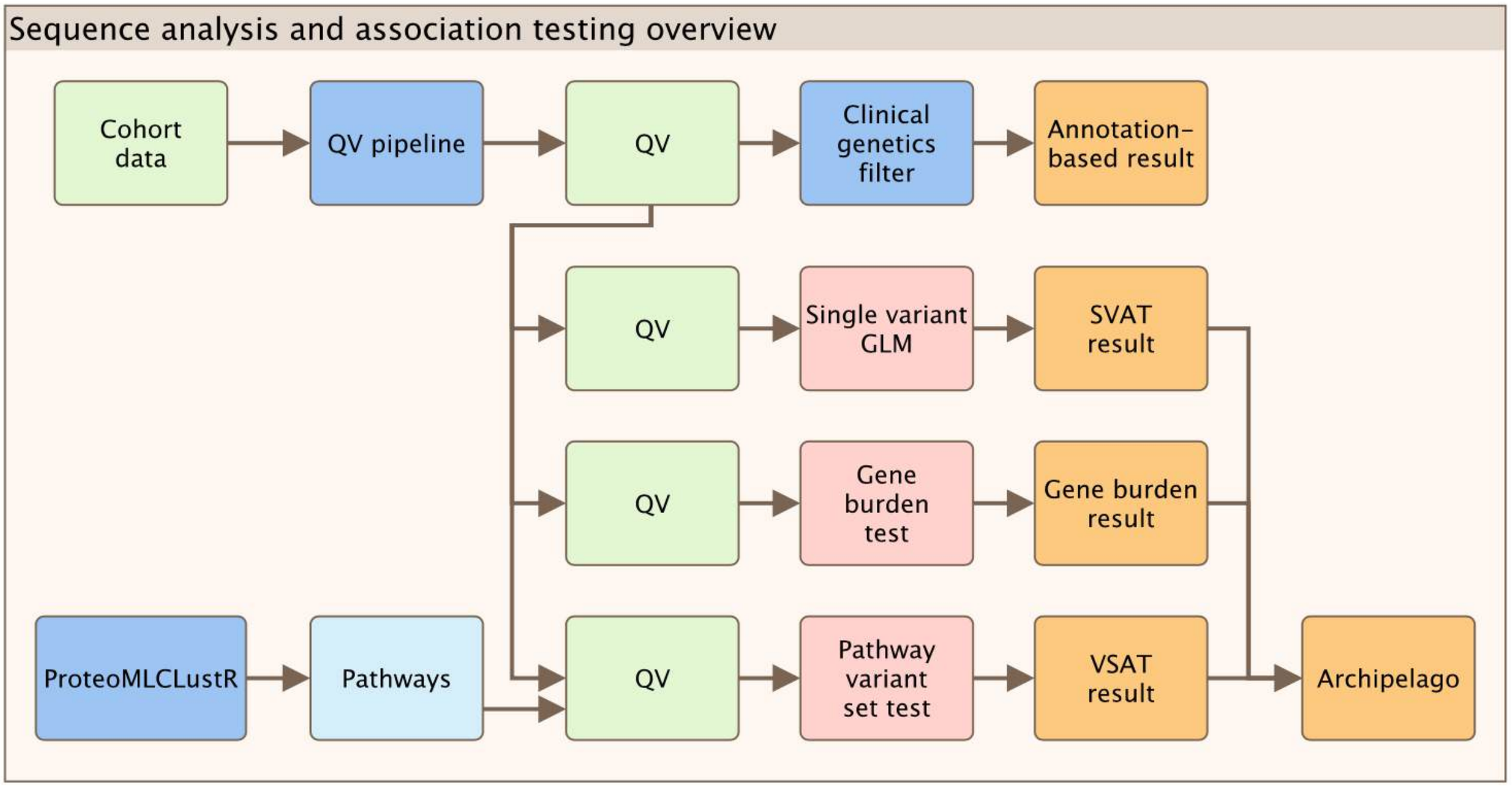


940 patients

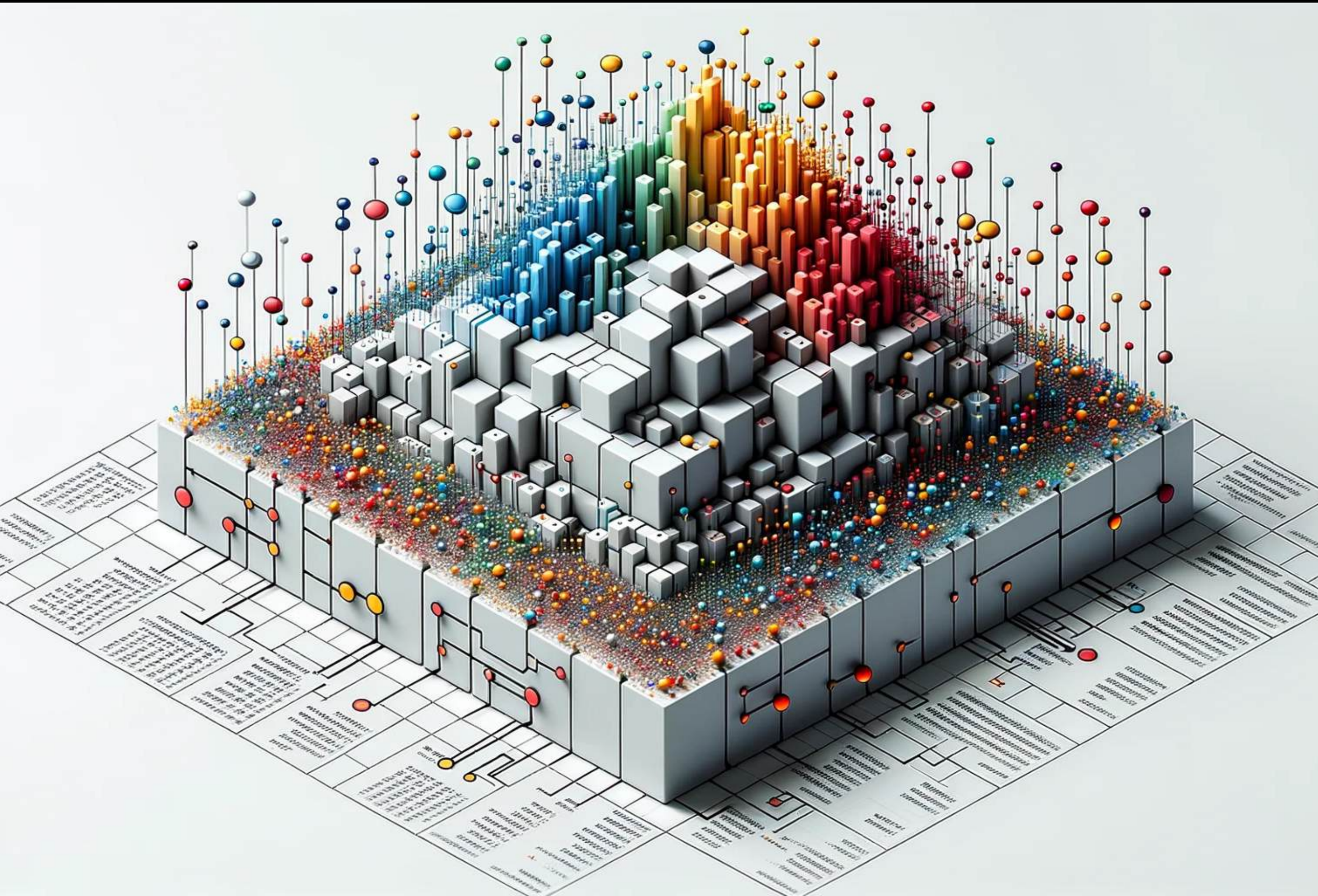
548 cases

392 controls

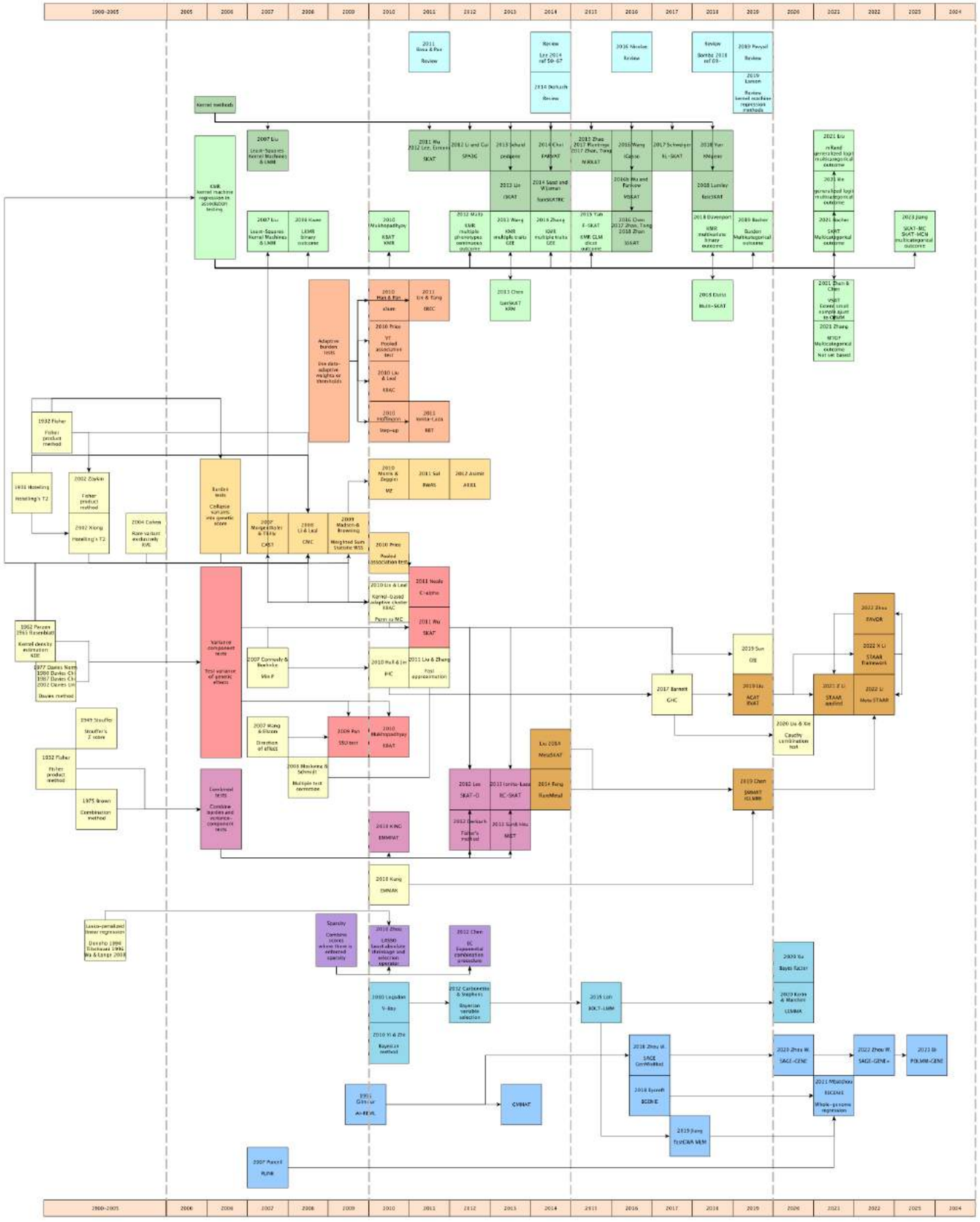
From dot to network



Collapse



Variant analysis history



	bib	Reference	method	Category_sim	Category	Description
\cite{	1931hotellingGe }	1931 Hotelling (1992	Hotelling's T2	Reference me	Statistical tes	Introduces the concept c
\cite{	1932fisherStatis }	1932 Fisher (1992 re	Fisher product	Reference me	NA	NA
\cite{	1949stoufferAm }	1949 Stouffer	Stouffer's Z sc	Reference me	NA	NA
\cite{	1956rosenblattF }	1956 Rosenblatt	Kernel density	Kernel	Kernel densit	Builds upon the previous
\cite{	1975brown400 }	1975 Brown	Combination r	Reference me	Meta-analysi	Introduces the Brown-Fo
\cite{	1977daviesHypc }	1977 Davies Norm	Davies metho	Reference me	Hypothesis te	discusses methods for hy
\cite{	1979neymanC }	1979 Neyman	C-alpha	Reference methods		
\cite{	1980daviesAlgo }	1980 Davies Chi	Davies metho	Reference me	Distribution t	derives the distribution
\cite{	1987daviesHypc }	1987 Davies Chi	Davies metho	Reference me	Hypothesis te	is a continuation of Davi
\cite{	1995gilmourAve }	1995 Gilmour	GMMAT	Reference me	Linear mixed	Introduces the average
\cite{	1999devlinGeno }	1999 Devlin	Genomic contr	Reference me	Genomic cont	Introduces the genomic
\cite{	1kg2012integra }	2012 1KG	1kG	Reference me	Human genor	Presents an integrated
\cite{	2002daviesHypc }	2002 Davies Lin	Davies metho	Reference me	Hypothesis te	is a further continuation
\cite{	2002xiongGener }	2002 Xiong	Hotelling's T2	Reference me	Genome asso	Introduces the generaliz
\cite{	2002zaykinTrun }	2002 Zaykin	Fisher product	Reference me	Meta-analysi	Introduces the truncate
\cite{	2004cohenMulti }	2004 Cohen	Rare variant e	Reference me	Rare alleles (s	A combination of metho
\cite{	2005whitlockCo }	2005 Whitlock	Weighted Z	Reference me	Meta-analysi	Introduces the weighte
\cite{	2006pricePincip }	2006 Price	PCA	Reference me	Population st	Describes the use of prir
\cite{	2007conneelyM }	2007 Conneely & Boe	Min P	Reference me	Multiple testi	presents a rapid metho
\cite{	2007liuSemipar }	2007 Liu	Least-Squares	Kernel	Kernel metho	presents a method for s
\cite{	2007morgenthal }	2007 Morgenthaler	CAST	Burden test	Genetic assoc	presents the cohort alle
\cite{	2007purcellPlink }	2007 Purcell	Plink	Software imp	Genome-wide	Presents PLINK, a popula
\cite{	2007wangImpro }	2007 Wang & Elston	Direction of ef	Adaptive bur	Linkage diseq	presents a weighted sco
\cite{	2008hofmannKe }	2008 Hofmann		Kernel (book	Kernel metho	provides an overview o
\cite{	2008kweePowe }	2008 Kwee	LKMR binary c	Kernel	Kernel metho	presents a powerful and
\cite{	2008liMethods }	2008 Li & Leal	CMC	Burden test	Rare variant	Introduces the combine
\cite{	2008liuEstimatic }	2008 Liu		Kernel	Kernel machir	The method proposed b
\cite{	2008moskvinaM }	2008 Moskvina & Sc	Multiple test	Reference me	Multiple testi	This paper by Moskvina
\cite{	2009madsenGro }	2009 Madsen & Brov	WSS Weighte	Adaptive Bur	Burden tests	Madsen and Browning p
\cite{	2009mukhopadh }	2009 Mukhopadhya	KBAT Associat	Kernel	Kernel machir	The KBAT method propo
\cite{	2009panAsympt }	2009 Pan	SSU test The s	Regression	Regression	The SSU method by Pan
\cite{	2010hallInnovat }	2010 Hall & Jin	iHC	Enforce sparsi	Tests that en	Hall and Jin introduce th
\cite{	2010hanDataAd }	2010 Han & Pan	aSum	Adaptive bur	Adaptive bur	The aSum method by Ha
\cite{	2010hoffmannCc }	2010 Hoffmann	StepUp	Combined tes	Combined tes	The StepUp method by
\cite{	2010kangVariar }	2010 Kang	EMMAX	Variance com	Variance com	Kang et al.'s EMMAX m
\cite{	2010kingEvoluti }	2010 King	EMMPAT Evol	Combined tes	Generalized r	King's EMMPAT metho
\cite{	2010liuNovel }	2010 Liu & Leal	KBAC Kernel-b	Kernel	Kernel machir	The method proposed b
\cite{	2010logsdonVar }	2010 Logsdon	V-Bay	Bayesian	Bayesian met	Logsdon et al. present a
\cite{	2010morrisEvalu }	2010 Morris & Zeggi	MZ	Review	Review paper	As mentioned previousl
\cite{	2010pricePoolec }	2010 Price	VT Pooled ass	Burden test	Burden tests	Price et al. present pool
\cite{	2010willerMeta }	2010 Willer	METAL	Meta analysi	Meta-analysi	Presents METAL, a tool
\cite{	2010zhouAssocia }	2010 Zhou	LASSO Least a	Enforce sparsi	Regression, T	Zhou's method uses LAS
\cite{	2011basuCompa }	2011 Basu & Pan (Review)		Review	Review paper	This paper by Basu and
\cite{	2011ionita-lazaN }	2011 Ionita-Laza	RBT Replicatio	Adaptive Bur	Adaptive bur	Ionita-Laza's RBT metho
\cite{	2011linGeneral }	2011 Lin & Tang	EREC		Generalized r	The EREC method by Lin
\cite{	2011nealeTestir }	2011 Neale	C-alpha	Variance com	Adaptive bur	Neale's C-alpha test is d
\cite{	2011sulOptimal }	2011 Sul	RWAS	Adaptive Bur	Burden tests	Sul's RWAS method is a
\cite{	2011wuRareVar }	2011 Wu	SKAT	Variance com	Kernel machir	As previously mentione
\cite{	2011yiBayesian }	2011 Yi & Zhi	Bayesian meth	Bayesian	Bayesian met	Yi and Zhi introduce a Ba
\cite{	2011zhangFast }	2011 Zhang & Liu	Fast approximation		Regression	The method proposed b

Variant analysis history

Score statistic

phenotype

$Gi = (G_{i1},..,G_{im})'$ allele counts (0, 1, 2)

S_j is positive or negative depending on variant j's direction of effect.

Estimated mean of y under the null hypothesis ($H_0 : \beta = 0$). Obtained by application of the null model $h(\mu_i) = \boldsymbol{\alpha_0} + \boldsymbol{\alpha}' \boldsymbol{X_i}$.

Score statistic of the marginal model for variant j.

$$S_j = \sum_{i=1}^{n} G_{ij} (y_i - \mu_i) \qquad (2)$$

Burden summary

Allele count for variant j in individual i

w_j is a threshold indicator or weight for variant j

Combined genetic score for individual i

Summary genetic score for burden tests.

$$C_i = \sum_{j=1}^{m} w_j G_{ij}, \qquad (3)$$

Burden statistic

Score statistic for variant j

Weight for variant j

Burden test statistic

$$Q_{\text{burden}} = \left(\sum_{j=1}^{m} w_j S_j \right)^2 \qquad (4)$$

Variance-component

Square of score statistic S_j^2

Weight w_j^2

SKAT test statistic

$$Q_{\text{SKAT}} = \sum_{j=1}^{m} w_j^2 S_j^2 \qquad (5)$$

Fisher combination

SKAT p-value term

Fisher statistic

Burden test p-value term

$$\text{Fisher} = -2\log(p_{\text{SKAT}}) - 2\log(p_{\text{burden}}), \qquad (6)$$

SKAT-O

SKAT test statistic term

Combining parameter ρ

Burden test statistic term

Parameter ρ constraint

$$Q_\rho = (1-\rho)\, Q_{\text{SKAT}} + \rho Q_{\text{burden}}, \quad 0 \le \rho \le 1, \qquad (7)$$

Kernel

I: The identity matrix of size $N \times N$.

σ_ϵ^2: The error variance component.

V: The marginal variance matrix of the response vector y.

σ_K^2: The variance component for the random effects associated with the

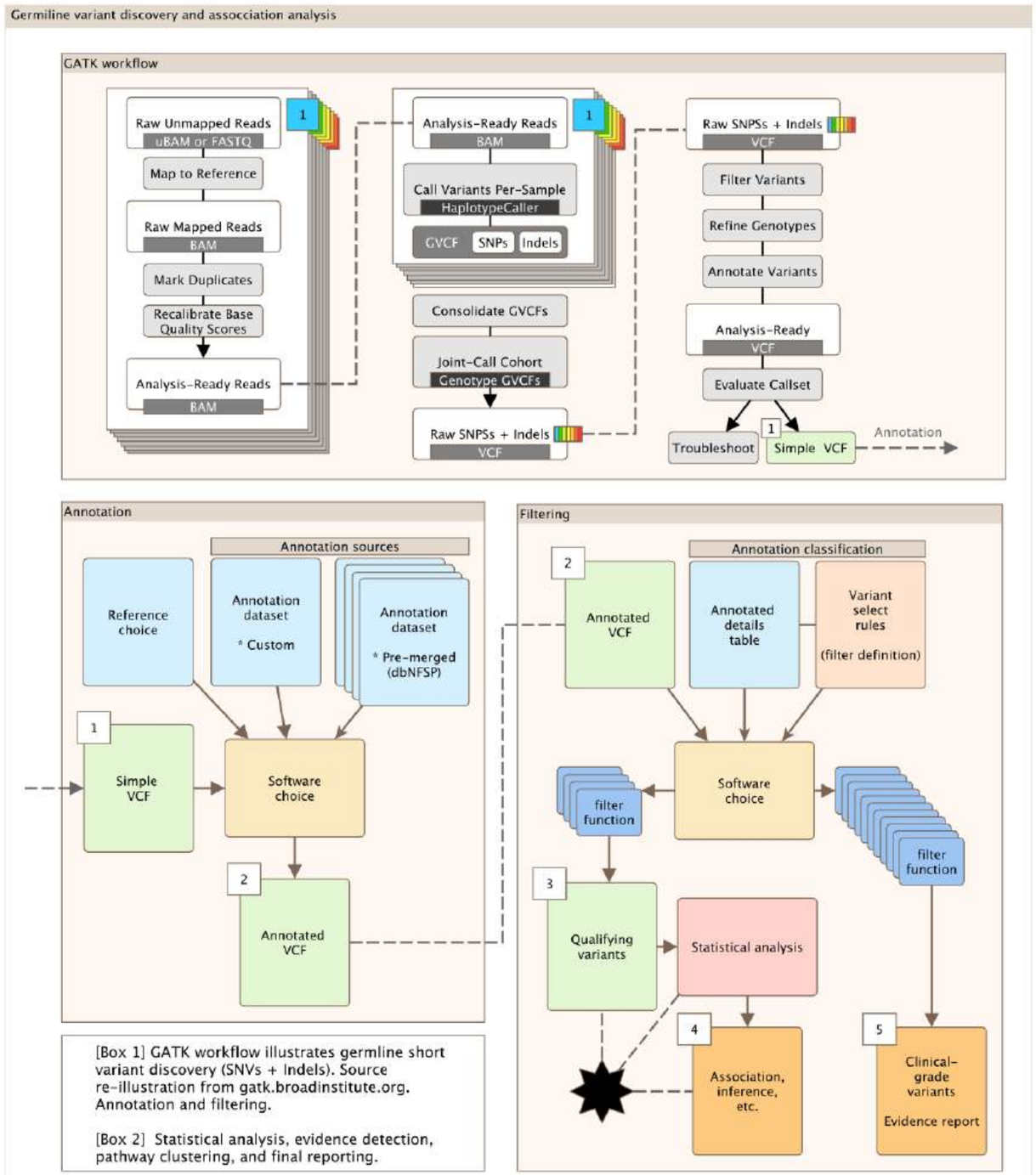
K: The kernel matrix of size $N \times N$, representing the covariance structure of the genetic random effects.

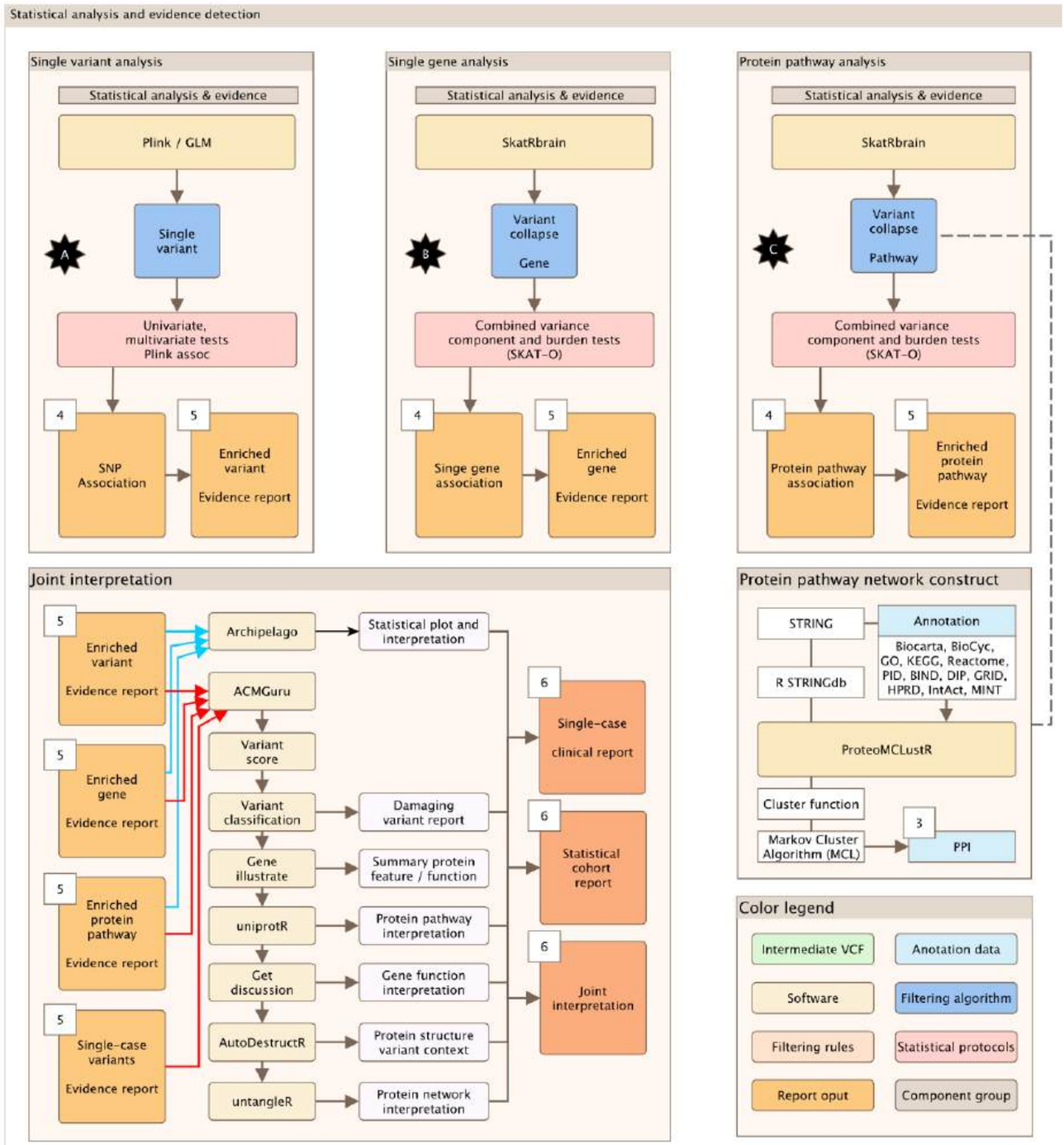
$$V = \sigma_\epsilon^2 I + \sigma_K^2 K \qquad (16)$$

$$f \sim \text{MVN}(0, \sigma_K^2 K) \qquad (15)$$

$$y_i = \alpha_0 + X_i'\alpha + f(G_i) + \epsilon_i \qquad (13)$$

Modular


Germiline variant discovery and assocciation analysis
GATK workflow
Raw Unmapped Reads
uBAM or FASTQ
Map to Reference
Raw Mapped Reads
BAM
Mark Duplicates
Recalibrate Base Quality Scores
Analysis-Ready Reads
BAM
Call Variants Per-Sample
HaplotypeCaller
GVCF
SNPs
Indels
Consolidate GVCFs
Joint-Call Cohort
Genotype GVCFs
Raw SNPSs + Indels
VCF
Raw SNPSs + Indels
VCF
Filter Variants
Refine Genotypes
Annotate Variants
Analysis-Ready
VCF
Evaluate Callset
Troubleshoot
Simple VCF
Annotation
Annotation
Annotation sources
Reference choice
Annotation dataset
* Custom
Annotation dataset
* Pre-merged (dbNFSP)
Simple VCF
Software choice
Annotated VCF
Filtering
Annotation classification
Annotated VCF
Annotated details table
Variant select rules
(filter definition)
filter function
Software choice
filter function
Qualifying variants
Statistical analysis
Association, inference, etc.
Clinical-grade variants
Evidence report
[Box 1] GATK workflow illustrates germline short variant discovery (SNVs + Indels). Source re-illustration from gatk.broadinstitute.org. Annotation and filtering.
[Box 2] Statistical analysis, evidence detection, pathway clustering, and final reporting.


Statistical analysis and evidence detection
Single variant analysis
Statistical analysis & evidence
Plink / GLM
Single variant
Univariate, multivariate tests Plink assoc
SNP Association
Enriched variant
Evidence report
Single gene analysis
Statistical analysis & evidence
SkatRbrain
Variant collapse
Gene
Combined variance component and burden tests (SKAT-O)
Singe gene association
Enriched gene
Evidence report
Protein pathway analysis
Statistical analysis & evidence
SkatRbrain
Variant collapse
Pathway
Combined variance component and burden tests (SKAT-O)
Protein pathway association
Enriched protein pathway
Evidence report
Joint interpretation
Enriched variant
Evidence report
Enriched gene
Evidence report
Enriched protein pathway
Evidence report
Single-case variants
Evidence report
Archipelago
ACMGuru
Variant score
Variant classification
Gene illustrate
uniprotR
Get discussion
AutoDestructR
untangleR
Statistical plot and interpretation
Damaging variant report
Summary protein feature / function
Protein pathway interpretation
Gene function interpretation
Protein structure variant context
Protein network interpretation
Single-case clinical report
Statistical cohort report
Joint interpretation
Protein pathway network construct
STRING
Annotation
Biocarta, BioCyc, GO, KEGG, Reactome, PID, BIND, DIP, GRID, HPRD, IntAct, MINT
R STRINGdb
ProteoMCLustR
Cluster function
Markov Cluster Algorithm (MCL)
PPI
Color legend
Intermediate VCF
Anotation data
Software
Filtering algorithm
Filtering rules
Statistical protocols
Report oput
Component group

Single case reports

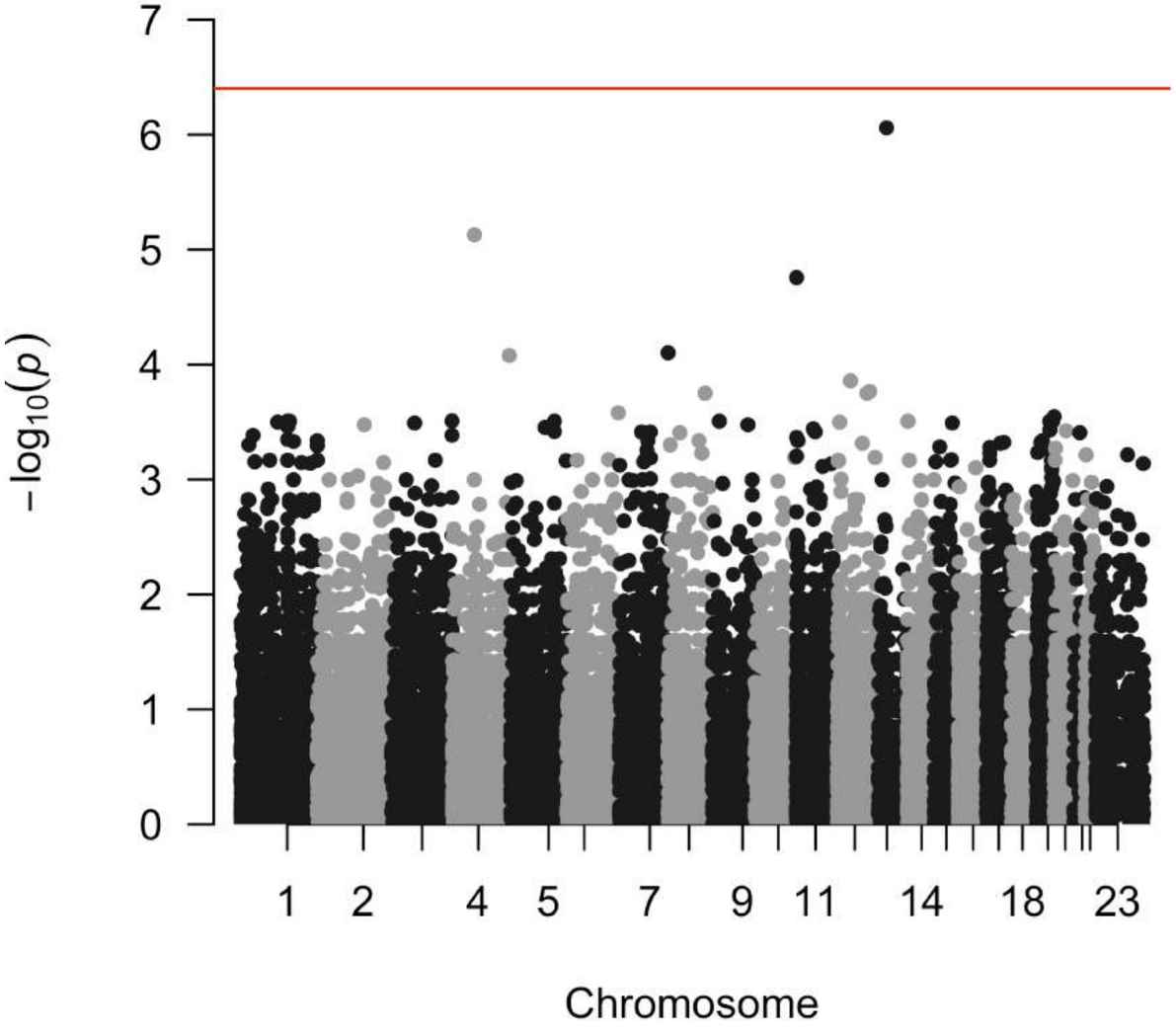
Single-case variants
ACMG/AMP score >6 likely pathogenic
or >10 pathogenic

ACMG score	Consequence	IMPACT	unique_variants
14	stop_gained	HIGH	2
14	splice_acceptor_variant	HIGH	3
14	frameshift_variant	HIGH	6
12	stop_gained	HIGH	1
10	splice_donor_variant	HIGH	1
9	stop_gained	HIGH	3
8	splice_acceptor_variant	HIGH	1
8	stop_gained	HIGH	2
8	stop_lost	HIGH	2
8	splice_donor_variant	HIGH	3
8	frameshift_variant	HIGH	7
7	stop_gained	HIGH	4
7	missense_variant	MODERATE	2
6	splice_acceptor_variant	HIGH	1
6	stop_gained&NMD_transcript_variant	HIGH	1
6	stop_gained	HIGH	2
6	frameshift_variant	HIGH	7
6	missense_variant&splice_region&NMD	MODERATE	1
6	missense_variant	MODERATE	2

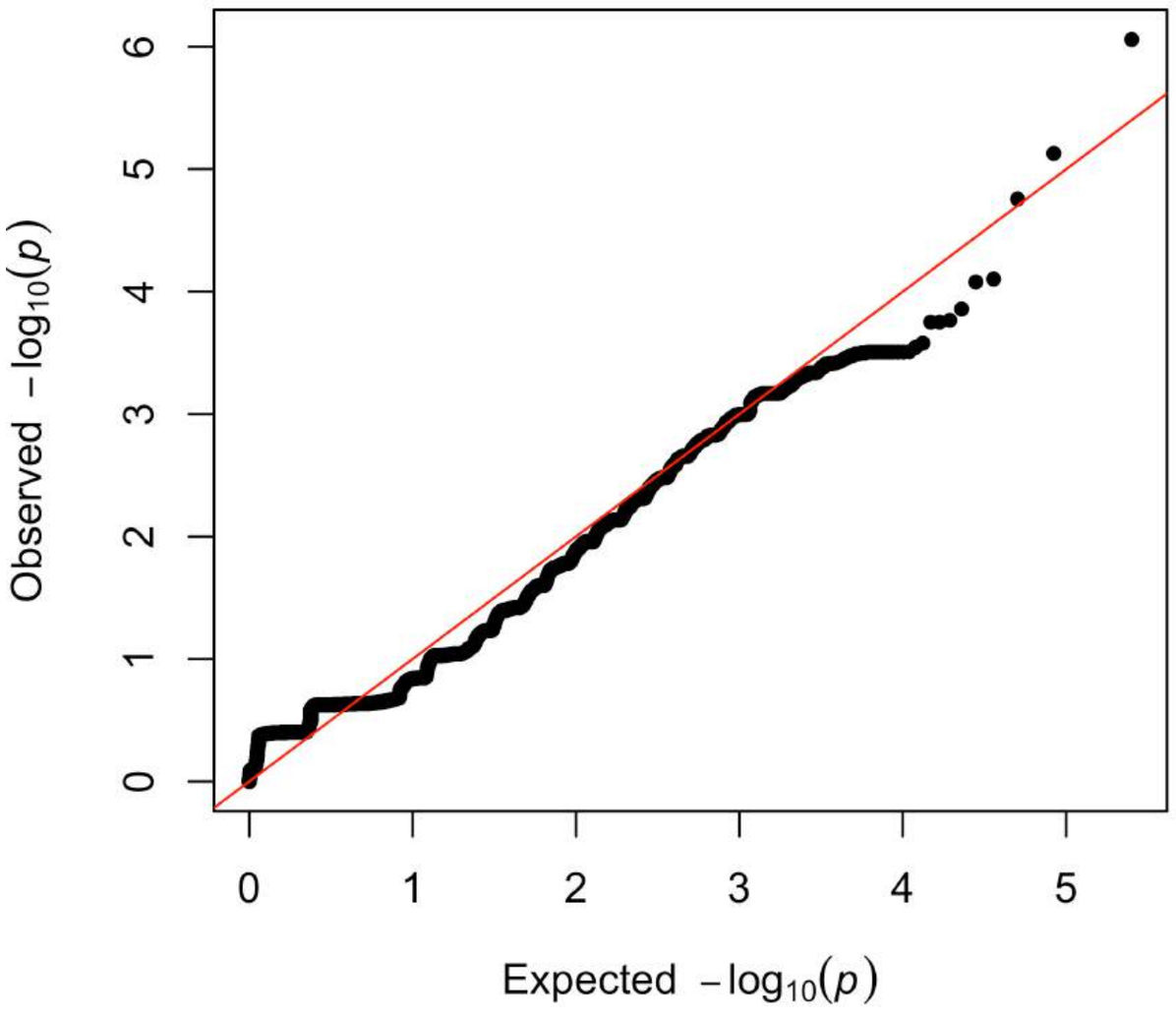
Single-case variant genes

Symbol	Consequence
ACD	frameshift_variant
CFHR1	frameshift_variant
CFHR1	frameshift_variant
CFHR1	frameshift_variant
CFHR1	frameshift_variant
CFHR1	splice_acceptor_variant
CFTR	missense_variant
CFTR	splice_donor_variant
IFIH1	frameshift_variant
IFIH1	splice_acceptor_variant
IL17F	frameshift_variant
IL17F	splice_donor_variant
IL17F	splice_donor_variant
NLRC4	stop_gained
NLRP1	frameshift_variant

Single variants



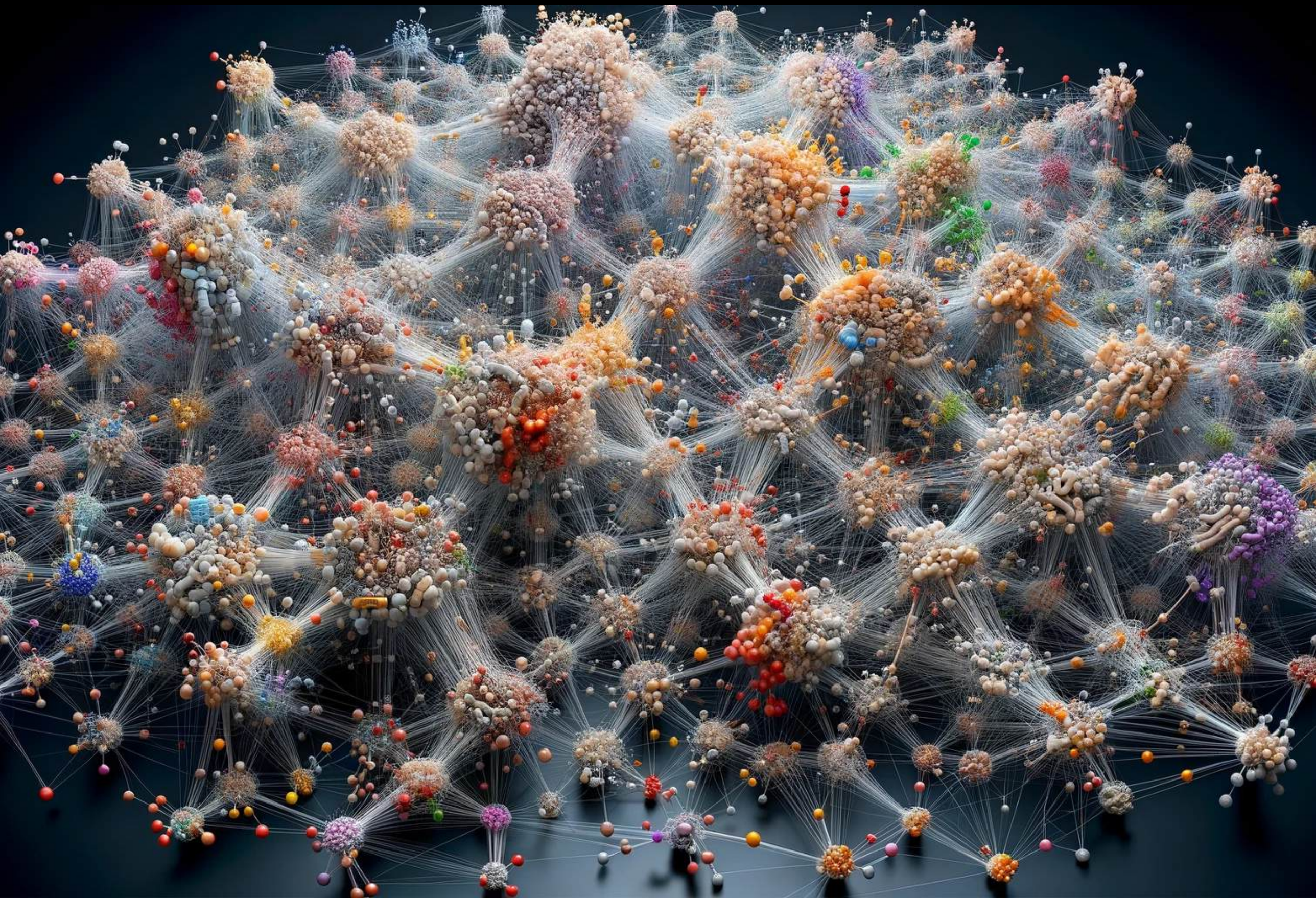
125’975 variant tests



$$\chi^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i}$$

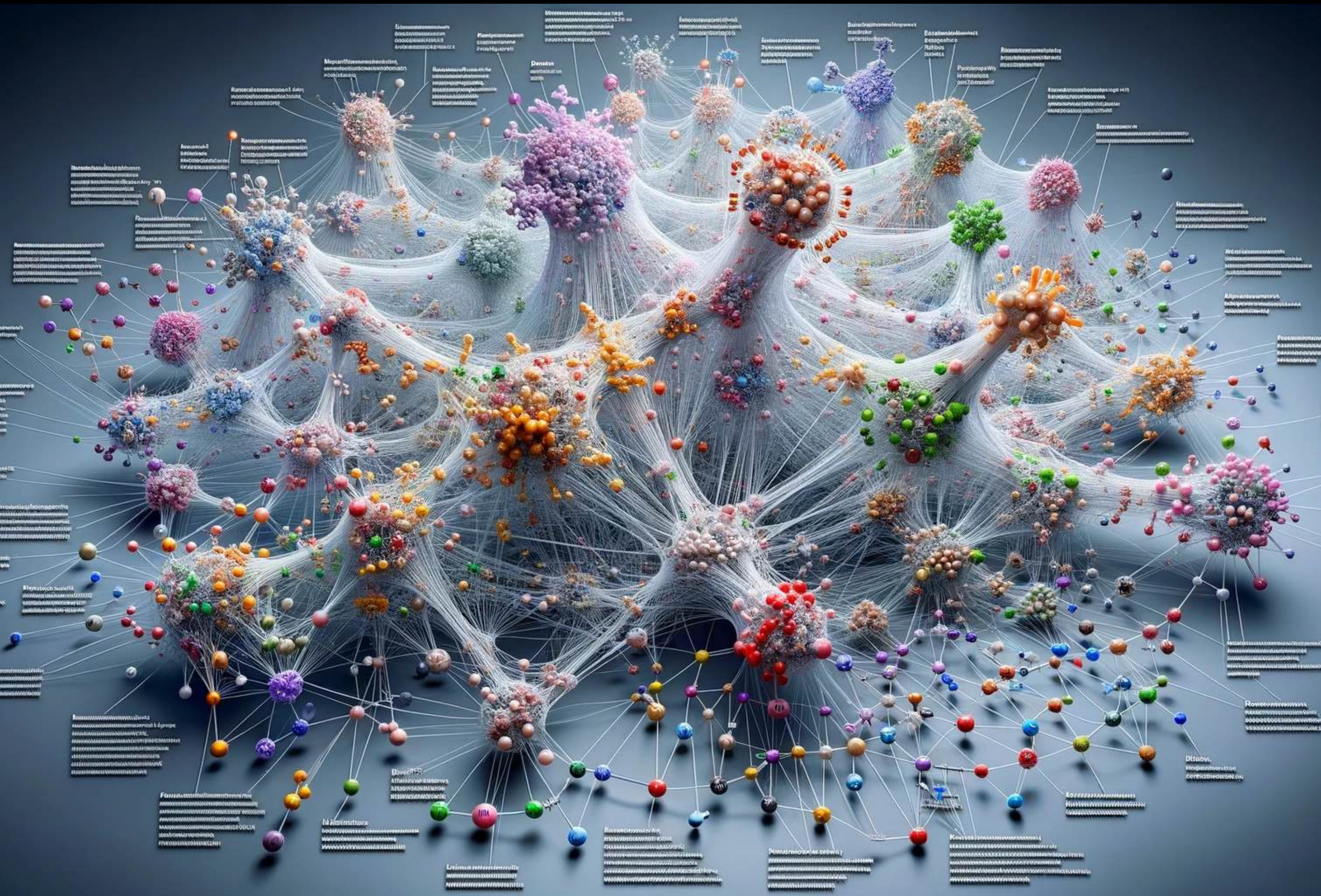
$$h_{(\mu_i)} = \alpha_0 \cdot \alpha'_{X_i} + \beta'_{G_i}$$

Pathways



Pathways

Pathways



ProteoMCLustR

Input:

$N_i,\ i = 1, \ldots, n$:

Nodes (genes) in the STRING database

$E_{ij},\ i, j = 1, \ldots, n$:

Edges (interactions) between nodes in STRING database

S : Score threshold for edges

I : Iteration limit

$L_{\text{min}}, L_{\text{max}}$: Size limits for clusters

e, r : Expansion & inflation parameters for MCL algorithm

Algorithm:

1. Preprocess $(N_i, E_{ij}, S) \rightarrow (N_i', E_{ij}')$
2. ChooseInflation $(N_i', E_{ij}', L_{\text{min}}, L_{\text{max}}) \rightarrow$ inflation
3. RunMCL $(N_i', E_{ij}', I, L_{\text{min}}, L_{\text{max}}, \text{inflation}, e, r)$

3.1. Initialize $M_{ij}^{(0)} = \dfrac{E_{ij}'}{\sum_{k=1}^{n} E_{ik}'}$

3.2. Iterate until convergence:

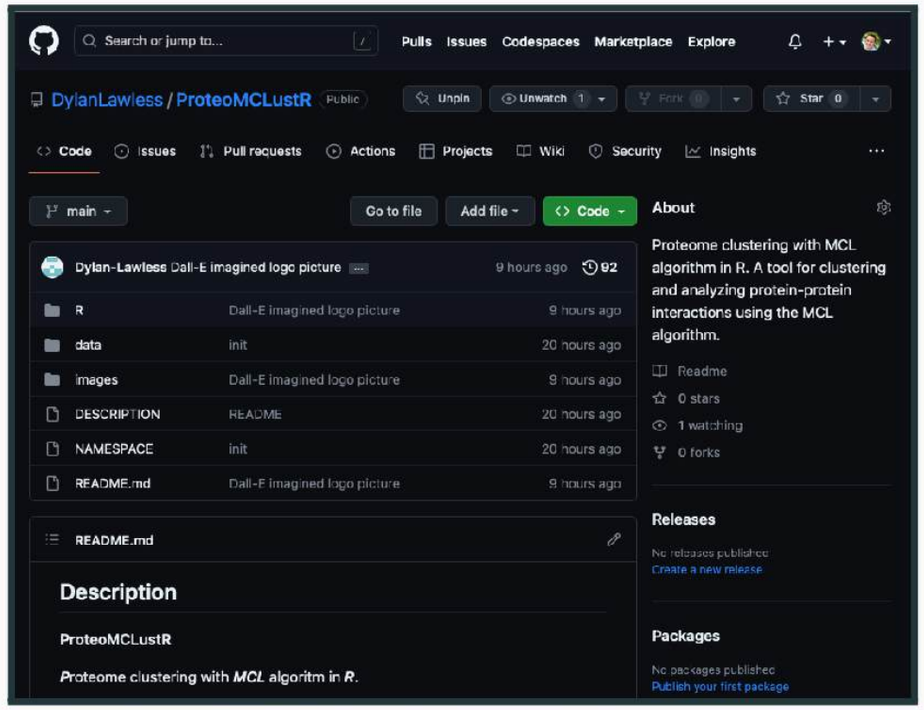
3.2.1. Expansion $M^{(k)} = (M^{(k-1)})^e$

3.2.2. Inflation $M_{ij}^{(k)} = \dfrac{(M_{ij}^{(k-1)})^r}{\sum_{k=1}^{n} (M_{ik}^{(k-1)})^r}$

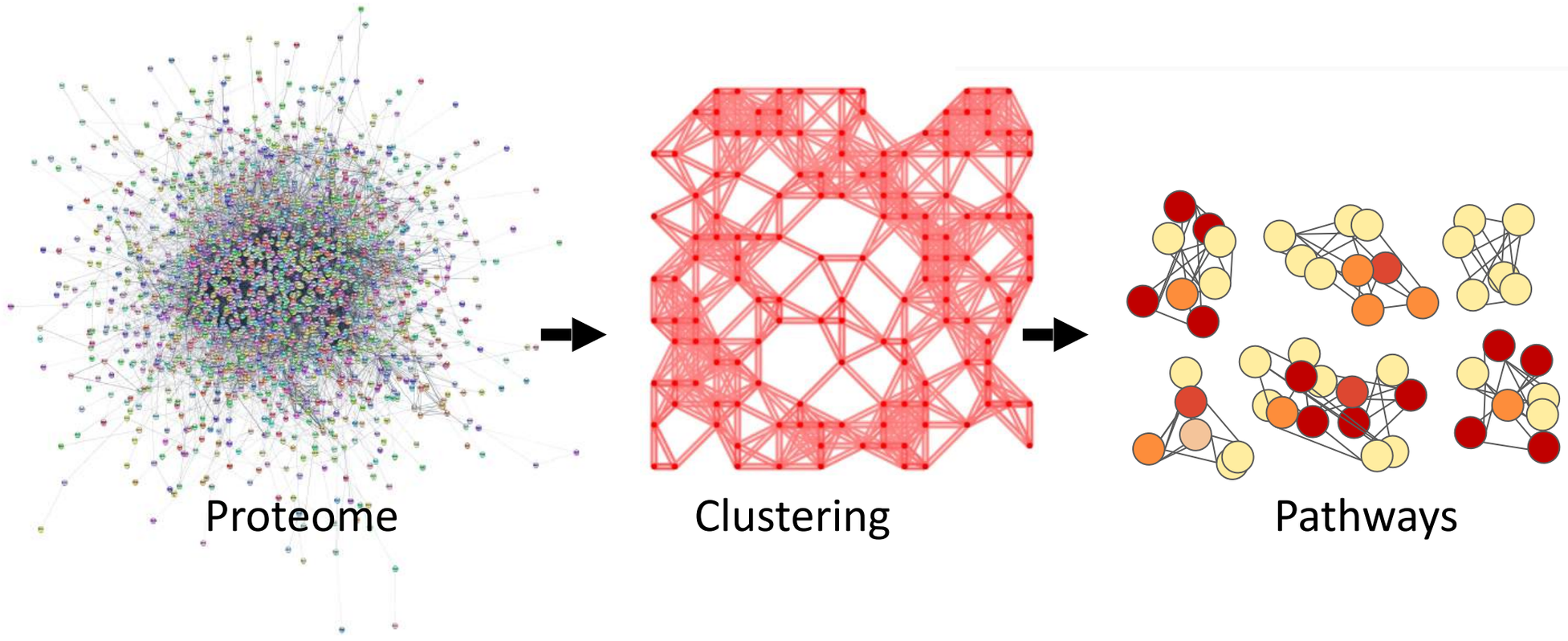
3.3. Extract clusters from converged matrix $M^{(\text{final})}$

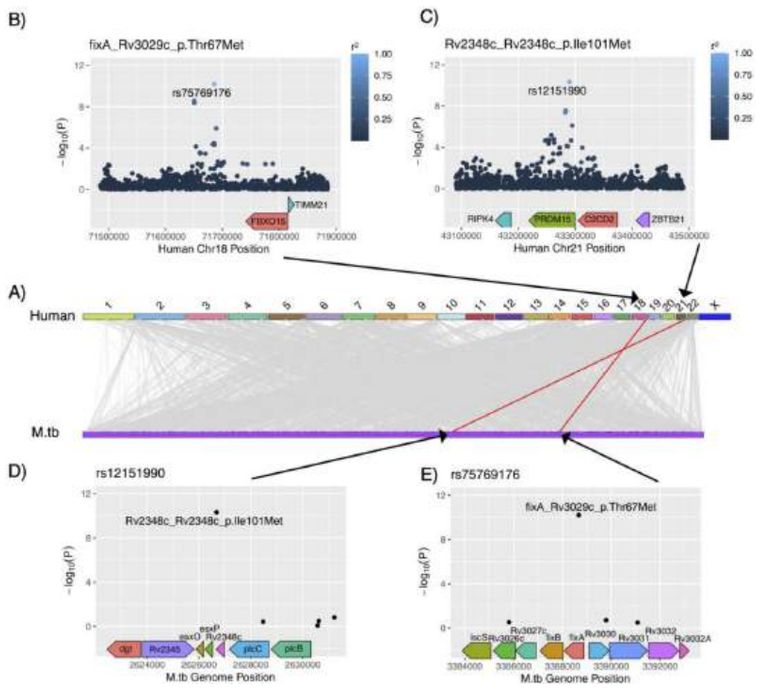
Output:

Clusters: Set of optimized node (gene) clusters



ProteoMCLustR



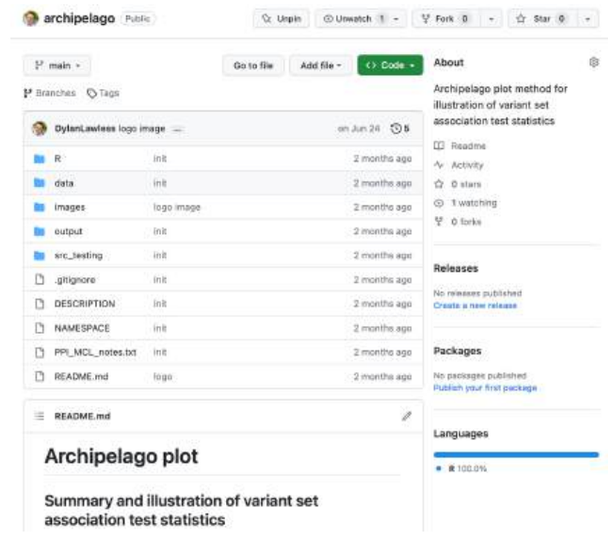


Genome-to-genome analysis reveals associations between human and mycobacterial genetic variation in tuberculosis patients from Tanzania

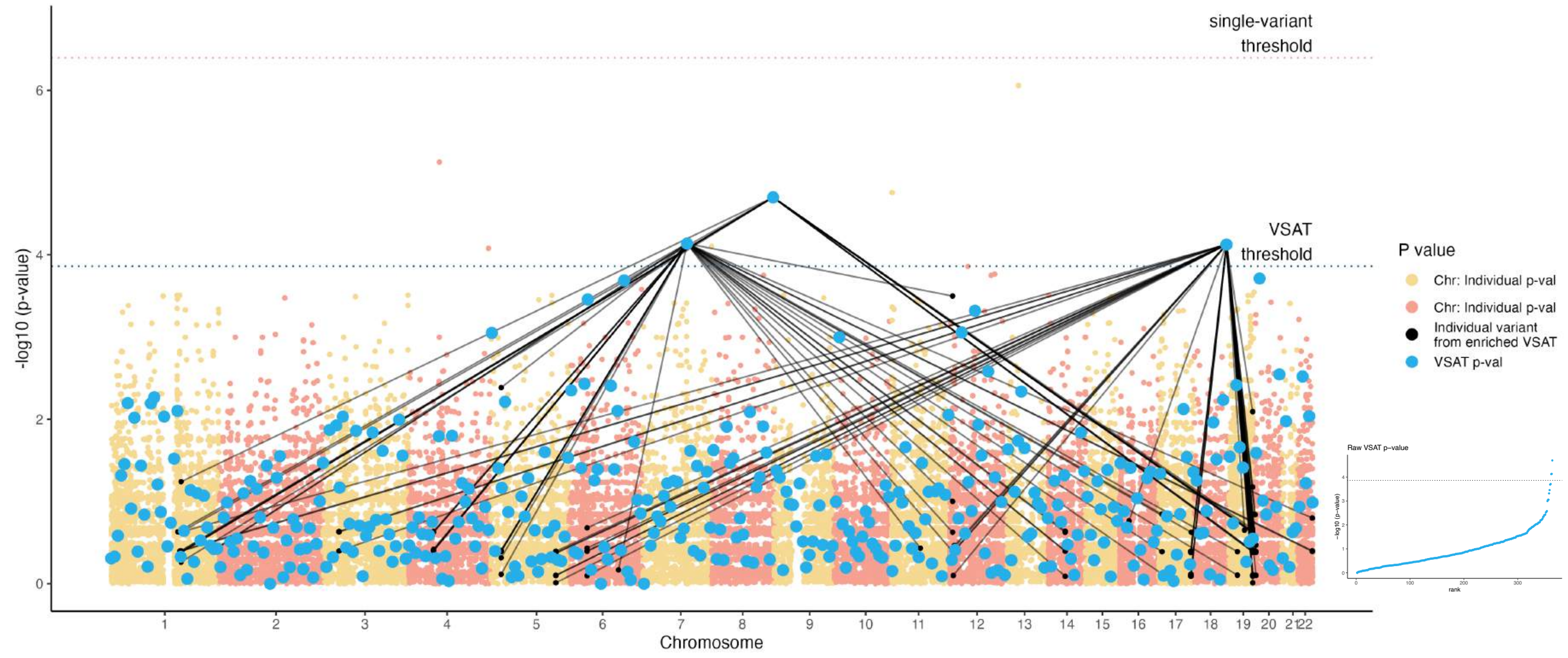
Zhi Ming Xu, Michaela Zwyer, Daniela Brites, Hellen Hiza, Mohamed Sasamalo, Miriam Reinhard, Anna Doetsch, Sonia Borrell, Olivier Naret, Sina Rüeger, Dylan Lawless, Faima Isihaka, Hosiana Temba, Thomas Maroa, Rastard Naftari, Christian Beisel, Jerry Hella, Klaus Reither, Damien Portevin, Sebastien Gagneux, Jacques Fellay

doi: https://doi.org/10.1101/2023.05.11.23289848

Archipelago



Archipelago

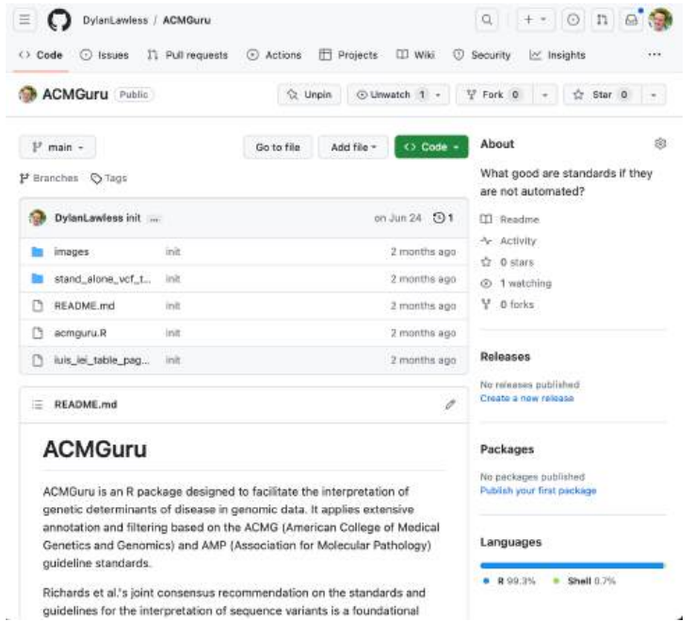


Pre-print. Archipelago plot method for illustration of variant set association test statistics. 2023 Lawless and Fellay.

Evidence

ACMGuru

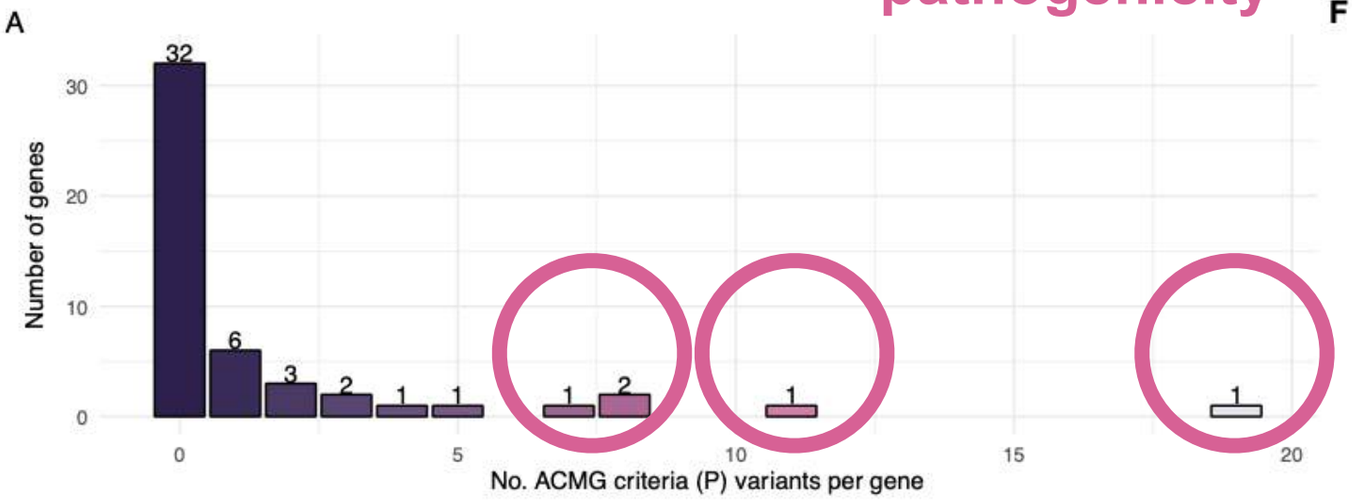
- Joint consensus recommendation on the standards and guidelines for the interpretation of sequence variants (Richards 2015).
- Standards and guidelines for the interpretation and reporting of sequence variants in cancer (Li 2017).
- Technical standards for the interpretation and reporting of constitutional copy-number variants (Riggs 2020).
- Effective variant filtering and expected candidate variant yield in studies of rare human disease (Pedersen 2021).
- ...

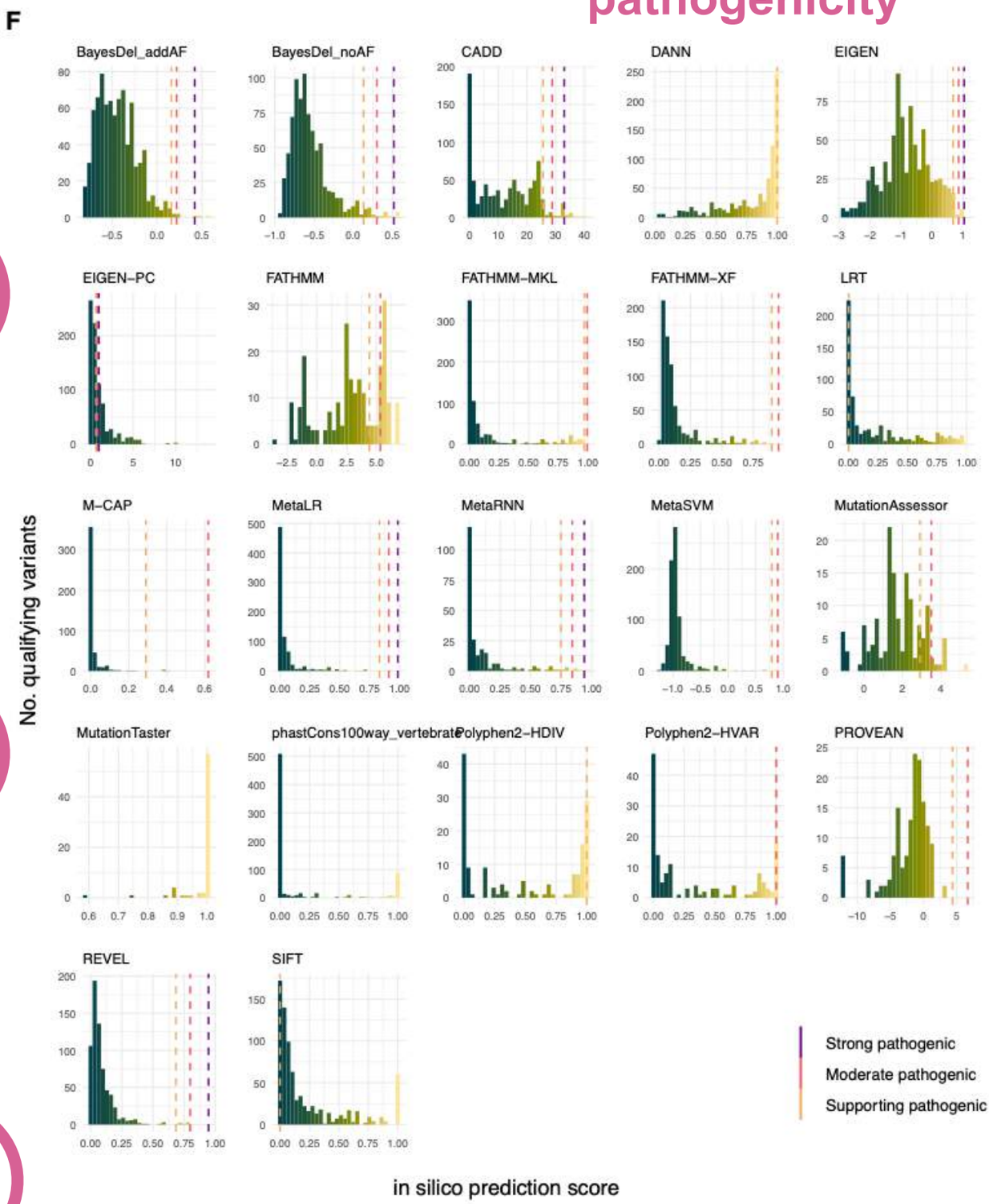


Evidence: scoring

Evident pathogenicity

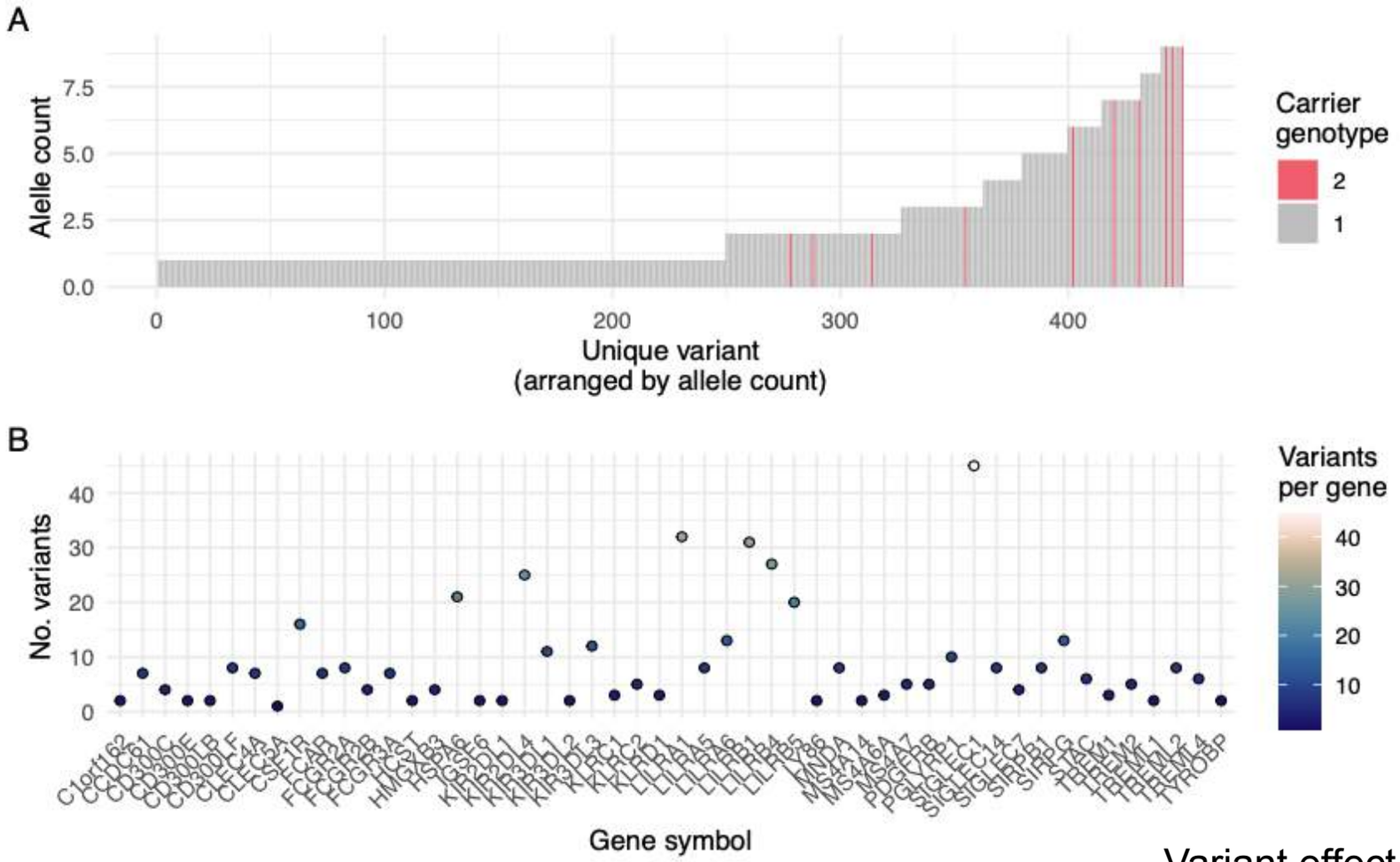
Predicted pathogenicity





Evidence: technical

Distribution within enriched pathway



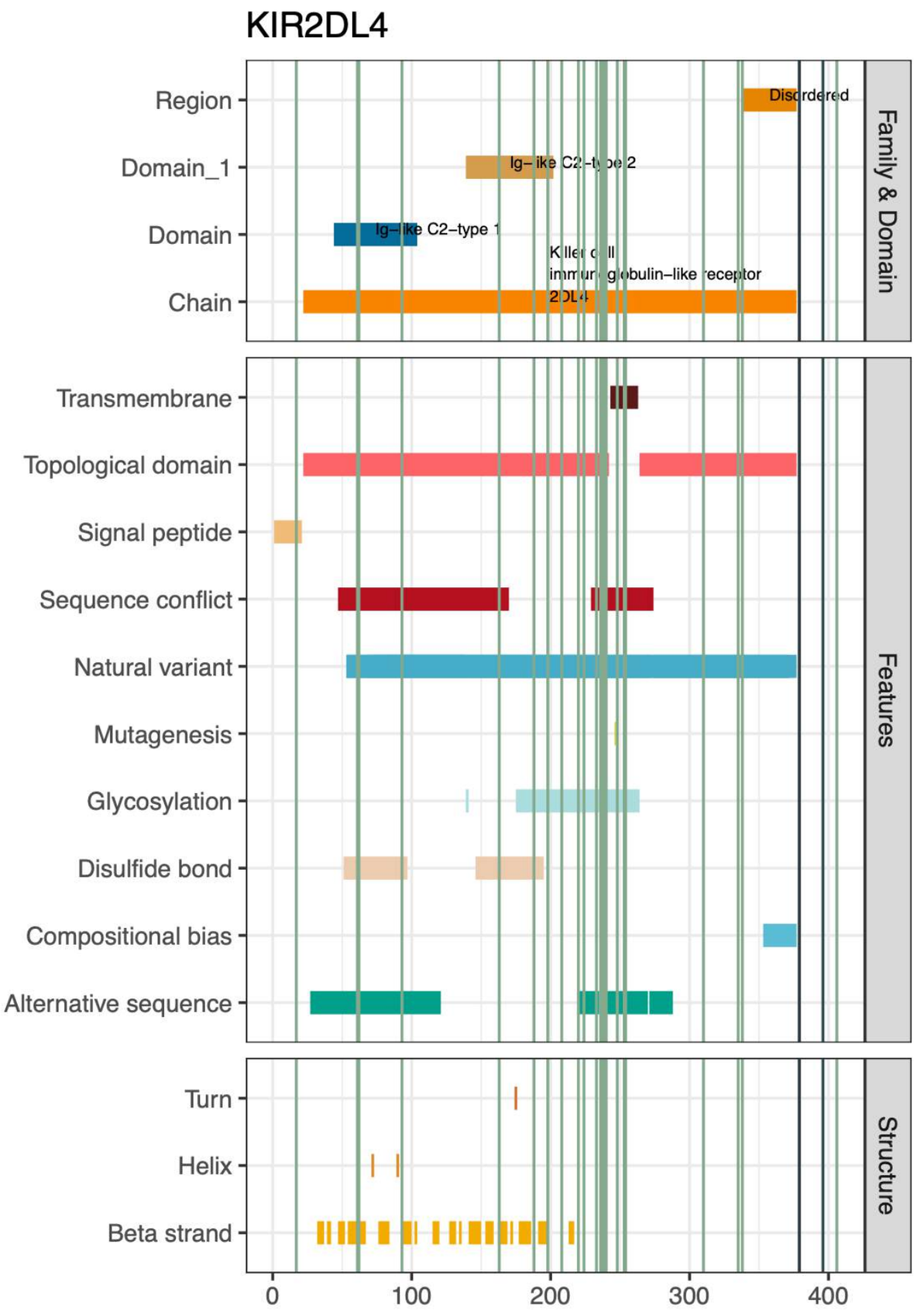
Enriched pathway variants,
ACMG/AMP score >6, likely pathogenic

SYMBOL	HGVSp	Consequence	sample.id	genotype
KIR2DL4	ENSP00000379580.3:p.Ala379Val	missense_variant	GE076	1
KIR2DL4	ENSP00000379580.3:p.Asp310LysfsTer5	frameshift_variant	GE076	1
LILRA1	ENSP00000251372.3:p.Glu416Asp	missense_variant	P501	1
LILRA1	ENSP00000251372.3:p.Glu416Gly	missense_variant	P501	1
LILRA1	ENSP00000251372.3:p.Leu277Pro	missense_variant	ZH114	1
LILRA1	ENSP00000251372.3:p.Ser414Pro	missense_variant	P501	1
LILRA1	NA	splice_acceptor_variant	P501	1
LILRA1	NA	splice_acceptor_variant	ZH114	1
SIRPG	ENSP00000305529.3:p.Arg342Cys	missense_variant	LAU176	1
SIRPG	ENSP00000305529.3:p.Pro136GlnfsTer29	frameshift_variant	LAU176	1

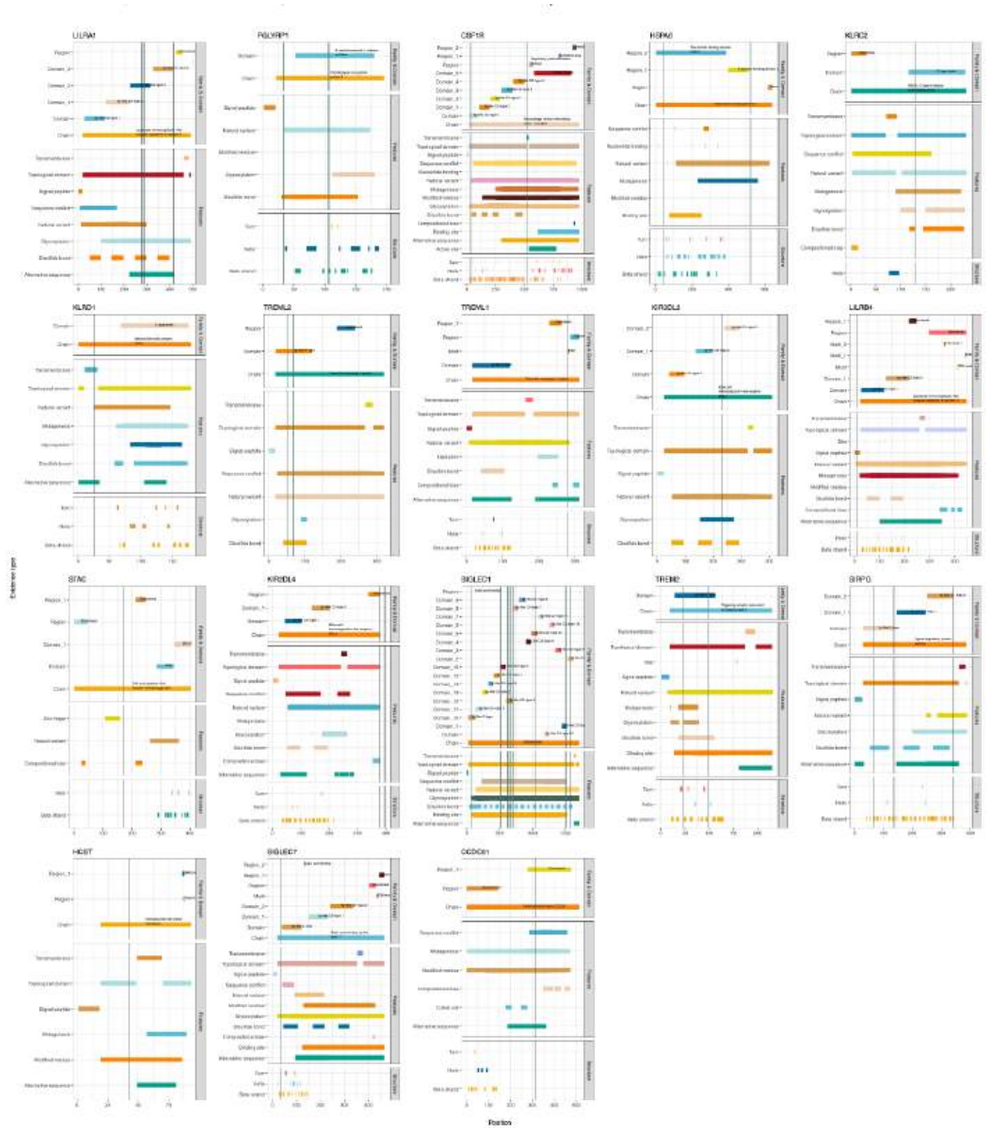
Variant effect summaries

Consequence	IMPACT	genotype	unique_variants
frameshift_variant&splice_region_variant	HIGH	1	1
start_lost	HIGH	1	1
stop_gained&splice_region_variant	HIGH	1	1
stop_lost	HIGH	1	1
splice_donor_variant	HIGH	1	3
splice_acceptor_variant	HIGH	1	4
frameshift_variant	HIGH	1	8
stop_gained	HIGH	1	17
inframe_deletion&splice_region_variant	MODERATE	1	1
inframe_deletion	MODERATE	1	2
missense_variant&splice_region_variant	MODERATE	1	9
missense_variant	MODERATE	2	9
missense_variant	MODERATE	1	305

Evidence: protein function

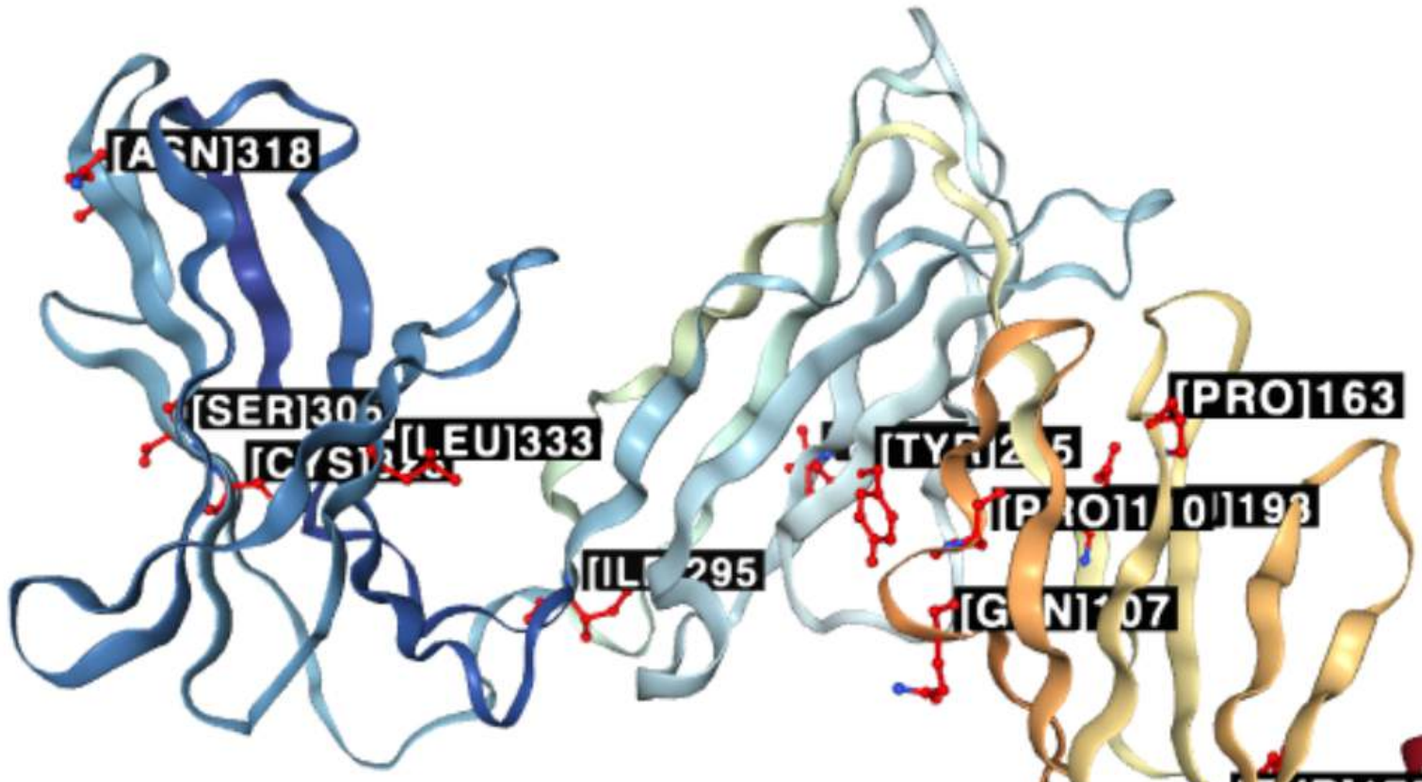


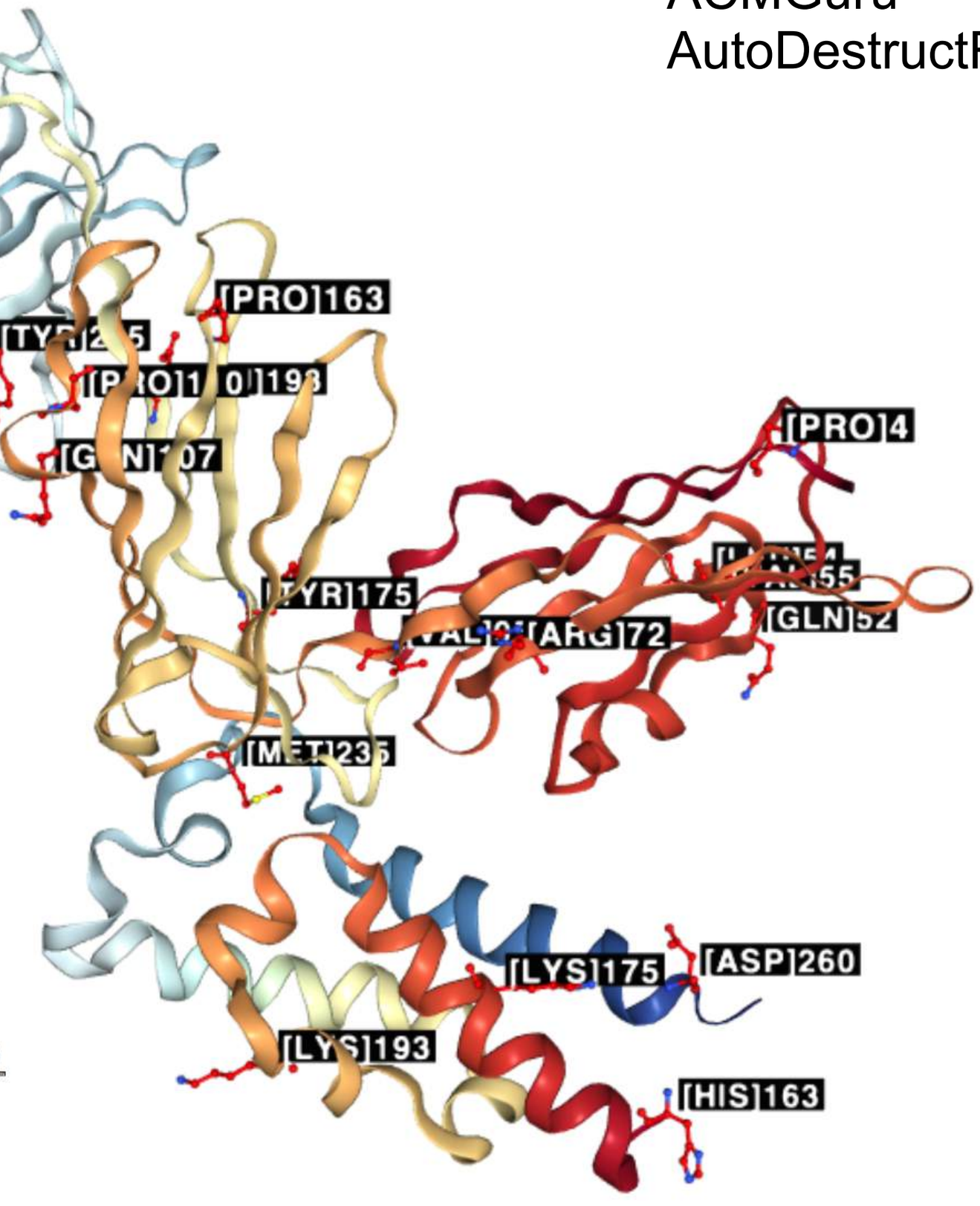
ACMGuru
gene-illustrate

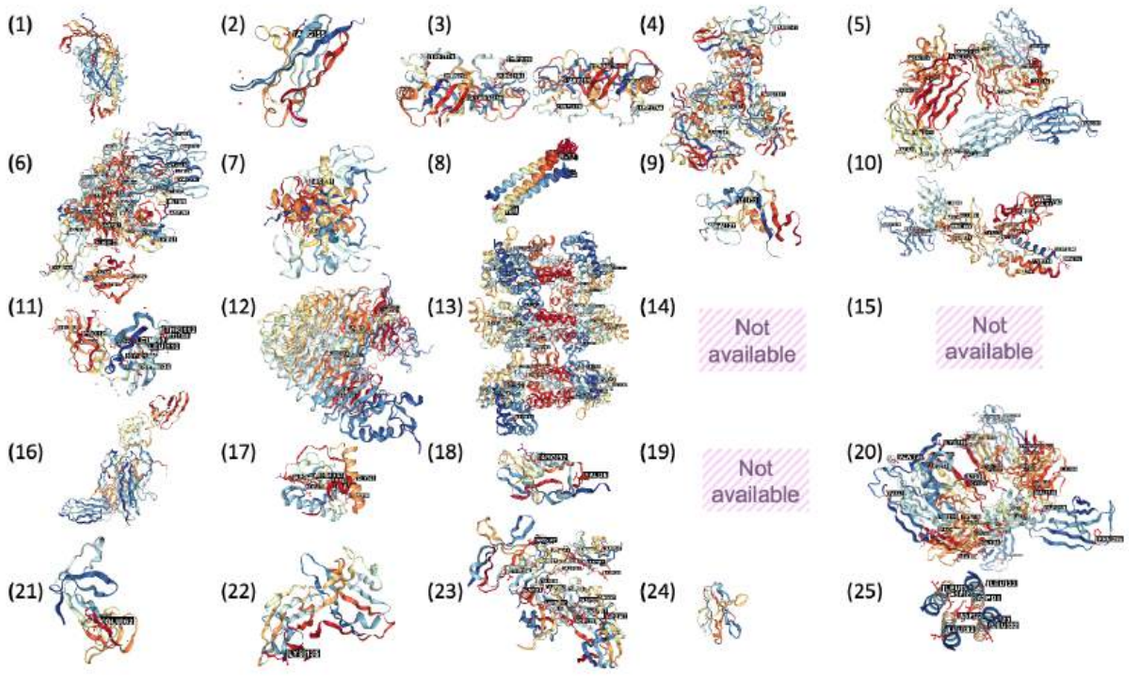


Evidence: protein structural

ACMGuru
AutoDestructR



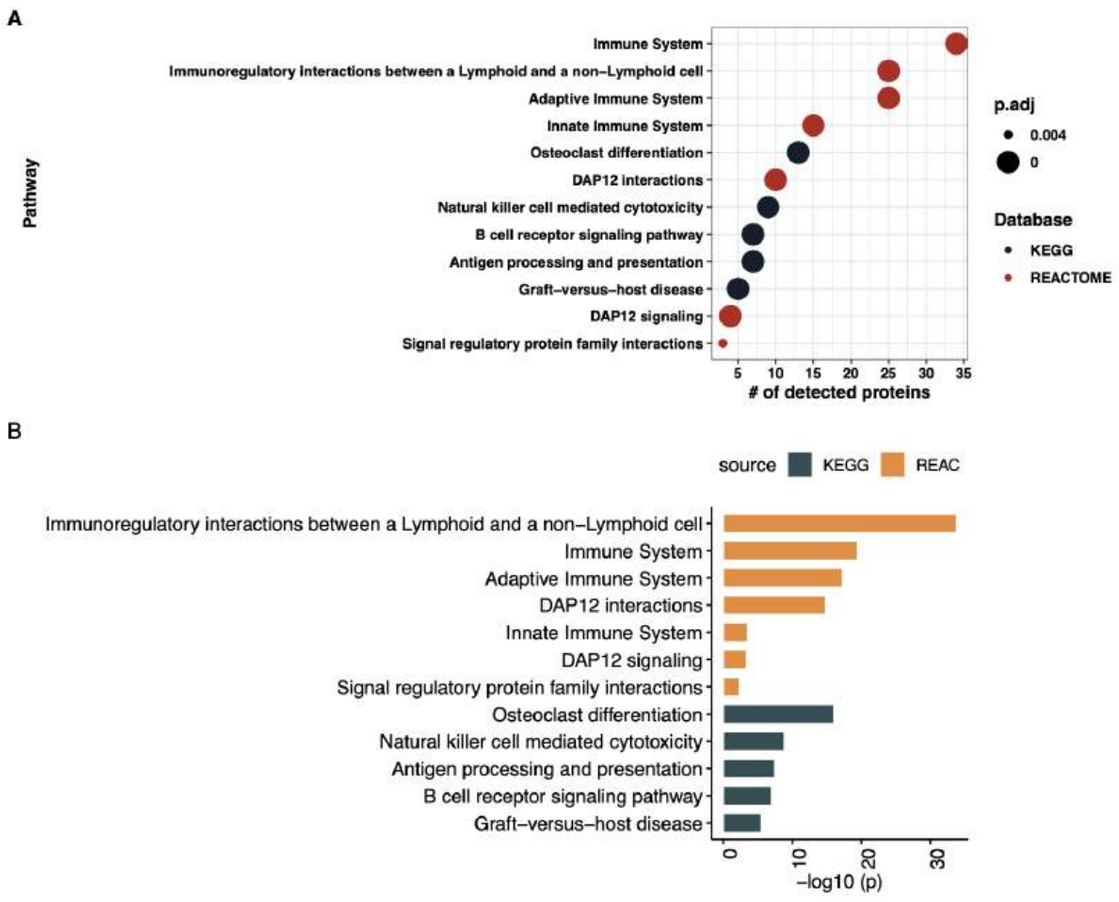




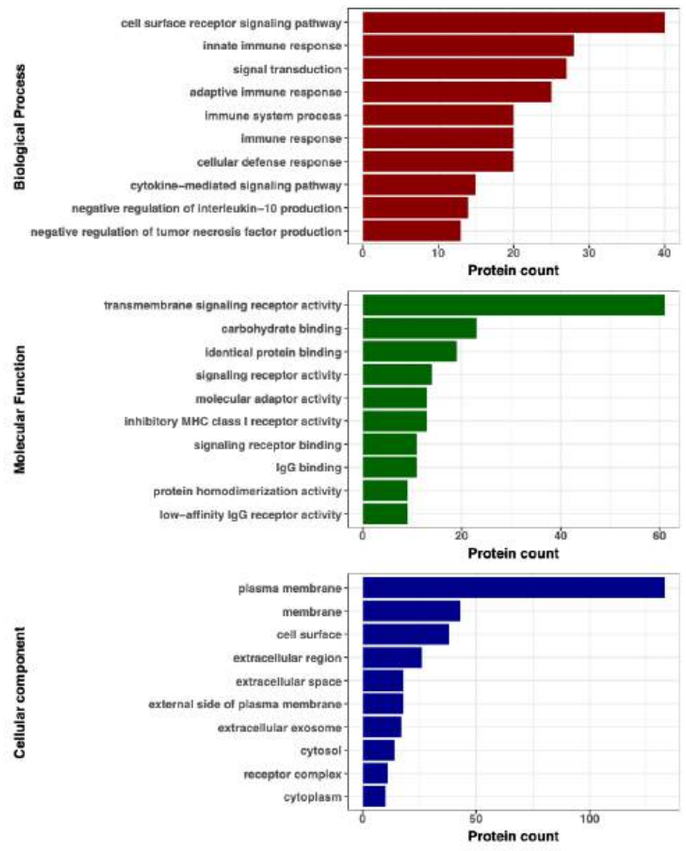
Evidence: pathway function

ACMGuru
uniprotR

Kegg and Reactome pathway interpretation

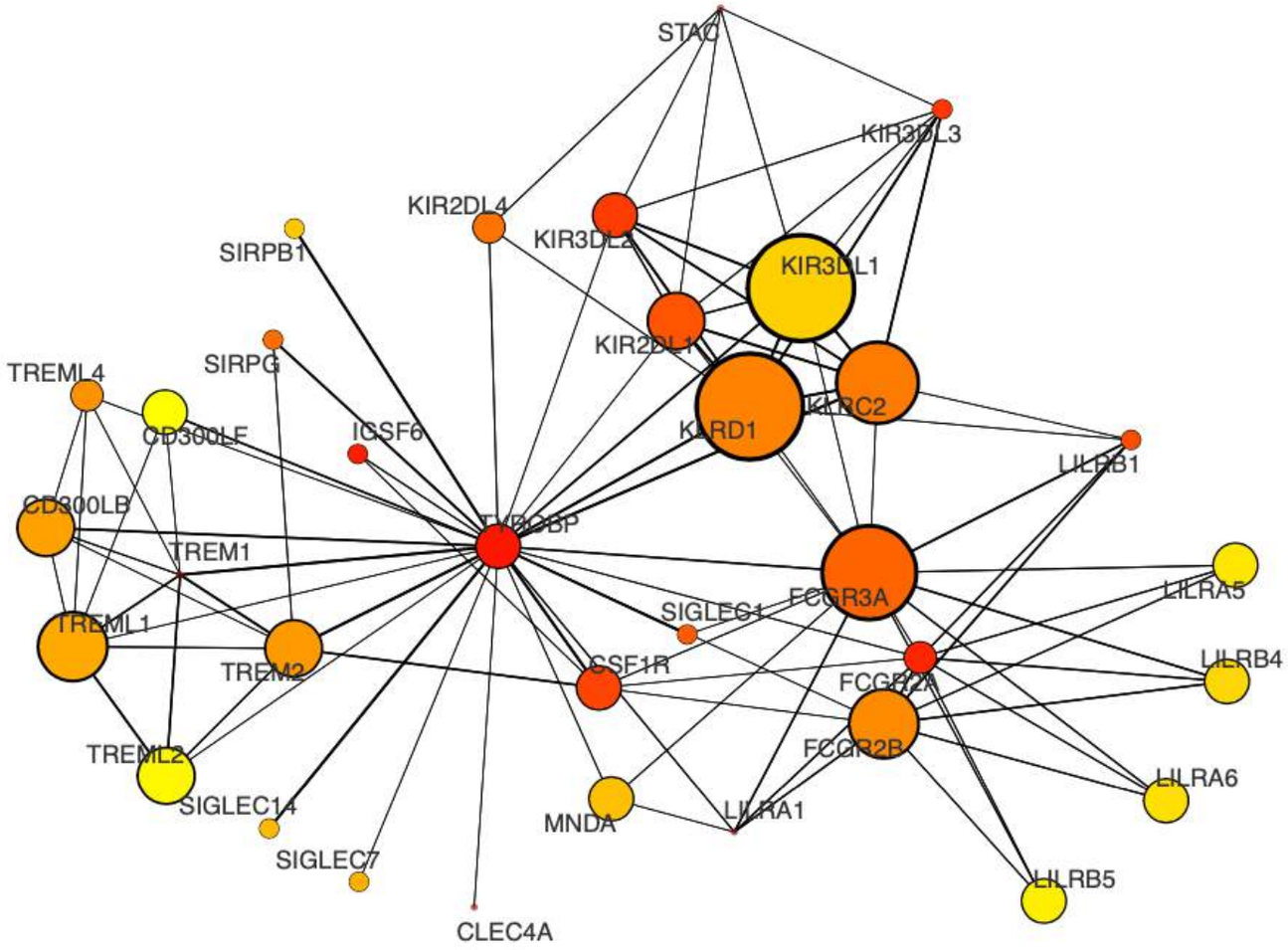


Gene Ontology (GO) pathway interpretation



Goterm	Count	%
cell surface receptor signaling pathway	40	22.22%
innate immune response	28	15.56%
signal transduction	27	15.00%
adaptive immune response	25	13.89%
cellular defense response	20	11.11%
immune response	20	11.11%
immune system process	20	11.11%
cytokine−mediated signaling pathway	15	8.33%
negative regulation of interleukin−10 production	14	7.78%
negative regulation of tumor necrosis factor production	13	7.22%
Goterm	**Count**	**%**
transmembrane signaling receptor activity	61	33.89%
carbohydrate binding	23	12.78%
identical protein binding	19	10.56%
signaling receptor activity	14	7.78%
inhibitory MHC class I receptor activity	13	7.22%
molecular adaptor activity	13	7.22%
IgG binding	11	6.11%
signaling receptor binding	11	6.11%
low−affinity IgG receptor activity	9	5.00%
protein homodimerization activity	9	5.00%
Goterm	**Count**	**%**
plasma membrane	133	73.89%
membrane	43	23.89%
cell surface	38	21.11%
extracellular region	26	14.44%
external side of plasma membrane	18	10.00%
extracellular space	18	10.00%
extracellular exosome	17	9.44%
cytosol	14	7.78%
receptor complex	11	6.11%
cytoplasm	10	5.56%

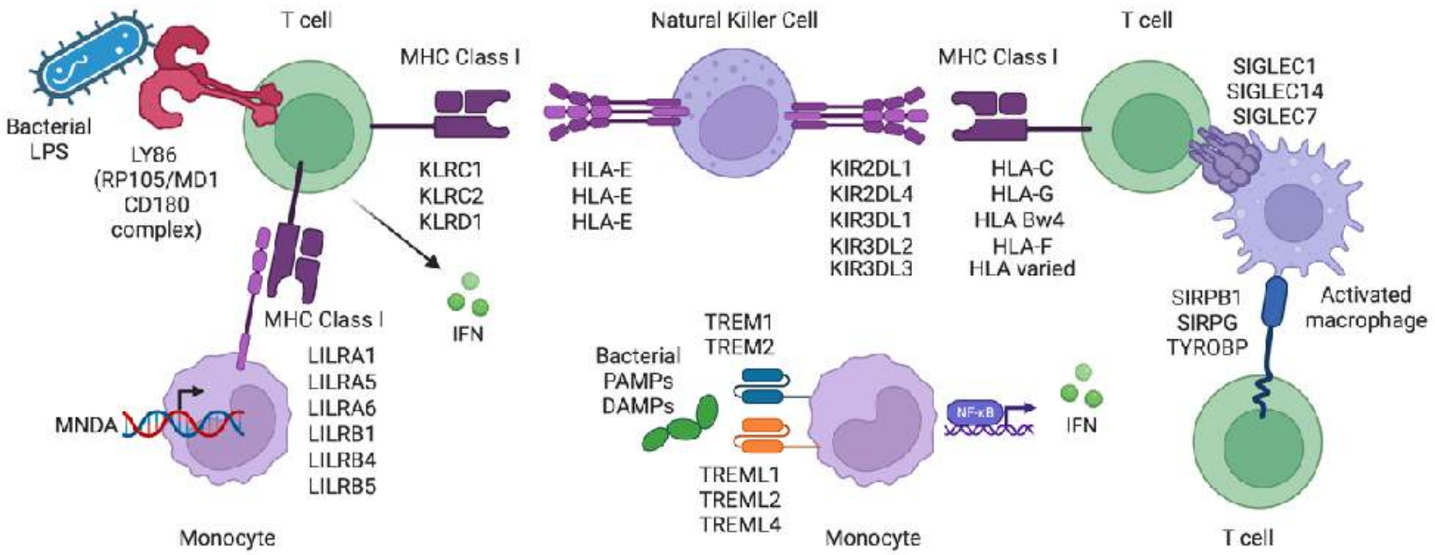
Evidence: Pathway interpretation



ACMGuru
untangleR
getDiscussion

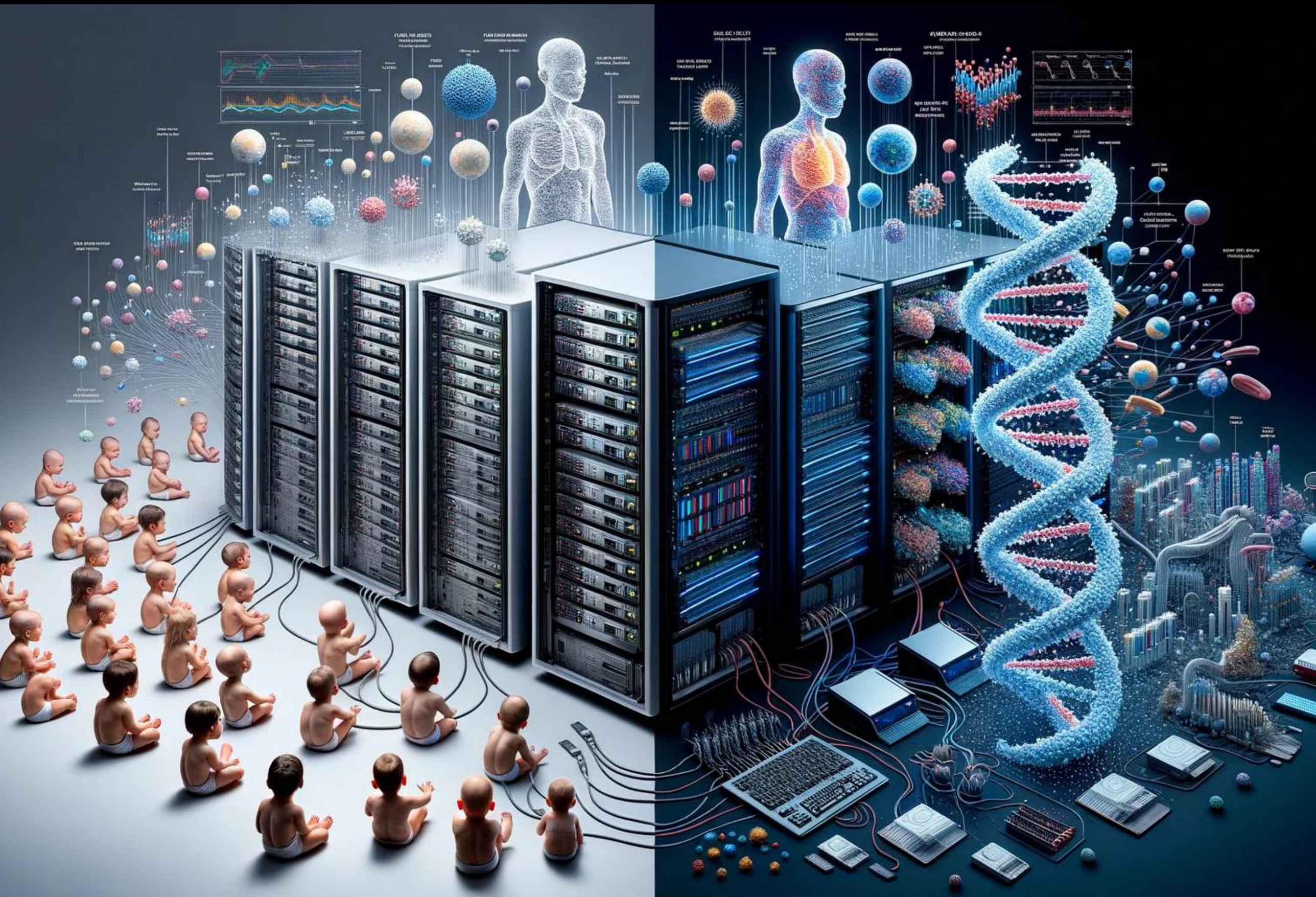
- **KIR2DL4, KIR3DL3, KLRD1**: Regulate NK cell activity, central to innate immune response.
- **LILRA1, LILRB1, LILRB4**: MCH class I
- **TREML1,2,4:** Pathogen recognition
- **SIGLEC1**: Pathogen recognition, macrophage activation
- **SIRPG**: immunomodulation; can lead to sepsis' hallmark overactive response.

- **Key Processes**
- Antigen presentation
- Signaling receptors
- Interactions between lymphoid & non-lymphoid cells
- Adaptive & innate immune responses



Now

Scale and test



Scale and test

Scale and test

Cluster Specs

- 419 compute nodes
- 2 Intel(R) per node (36 cores each)
- 3 TB SSD disk
- 512 GB RAM/node min

Max Requirements

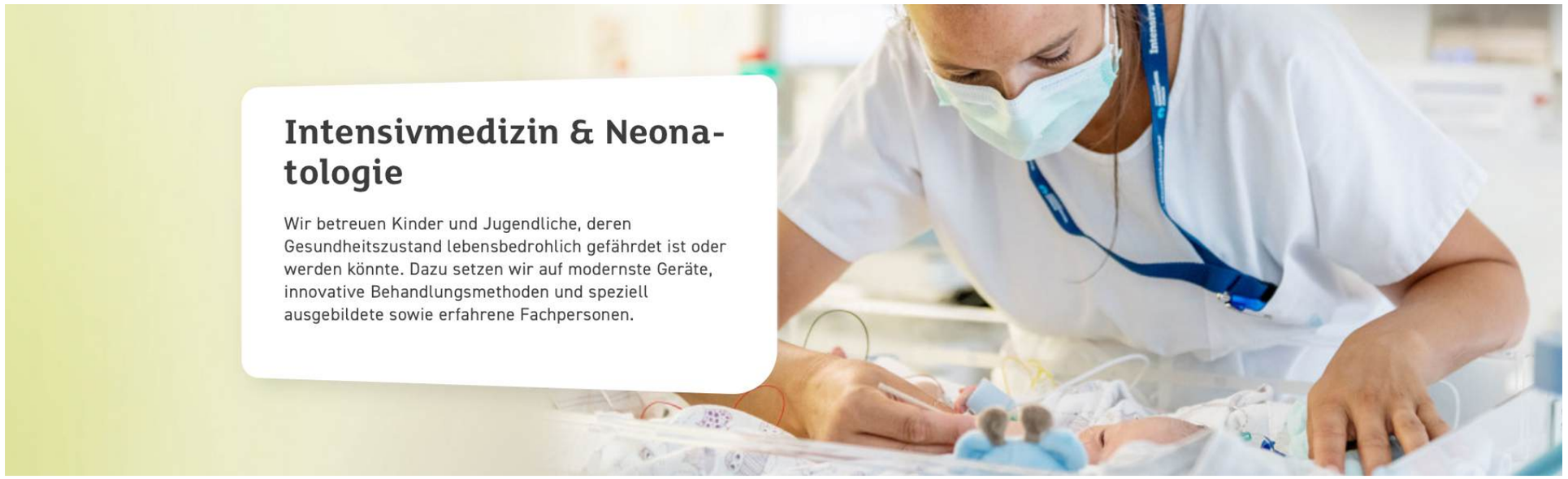
- Time: 24 hours
- 24 CPUs/node; 80GB per CPU
- 1000 job array
- Occasionally 500GB RAM

Runtimes for 1000 sample

- GATK pipeline: < 8 hours
- Clustering: < 10 hours (parallel to GATK)
- Statistical analysis: < 2 hours

A face behind the research

Thanks



UNIVERSITÄTS-
KINDERSPITAL
ZÜRICH

Forschungszentrum für das Kind FZK

Prof Luregn Schlapbach

Prof Matthias Baumgartner

Prof Jacques Felley

Organizing committee

Reto Huber (Chair)
Matthias Baumgartner
Micaela Belendez
Barbara Brotschi
Maya Horst
Karin Kucian
Nicole Meili
Michelle Seiler
Ana Stücklin
Martin Theiler
Huub van Hedel
Flavia Wehrle
Stephan Wüest

Poster jury

Patrick Meyer (Chair)
Martin Baumgartner
Sophie Böttcher
Barbara Brotschi
Suzanne Dhaini
Sean Froese
Raphael Morscher
Jana Pachlopnik
Paolo Paioni

Oral jury

Matthias Baumgartner
Martin Baumgartner
Barbara Brotschi
Sean Froese
Johannes Häberle
Reto Huber
Maya Horst
Uchenna Kennedy
Karin Kucian
Nicole Meili
Ola Sabet

EPFL

University of Zurich[UZH]

CHUV

SIB Swiss Institute of Bioinformatics

health2030 genome center

SwissPedHealth Lighthouse project