

Joshua D. Hoffman, Nicole Narayan, Mera K. Tilley

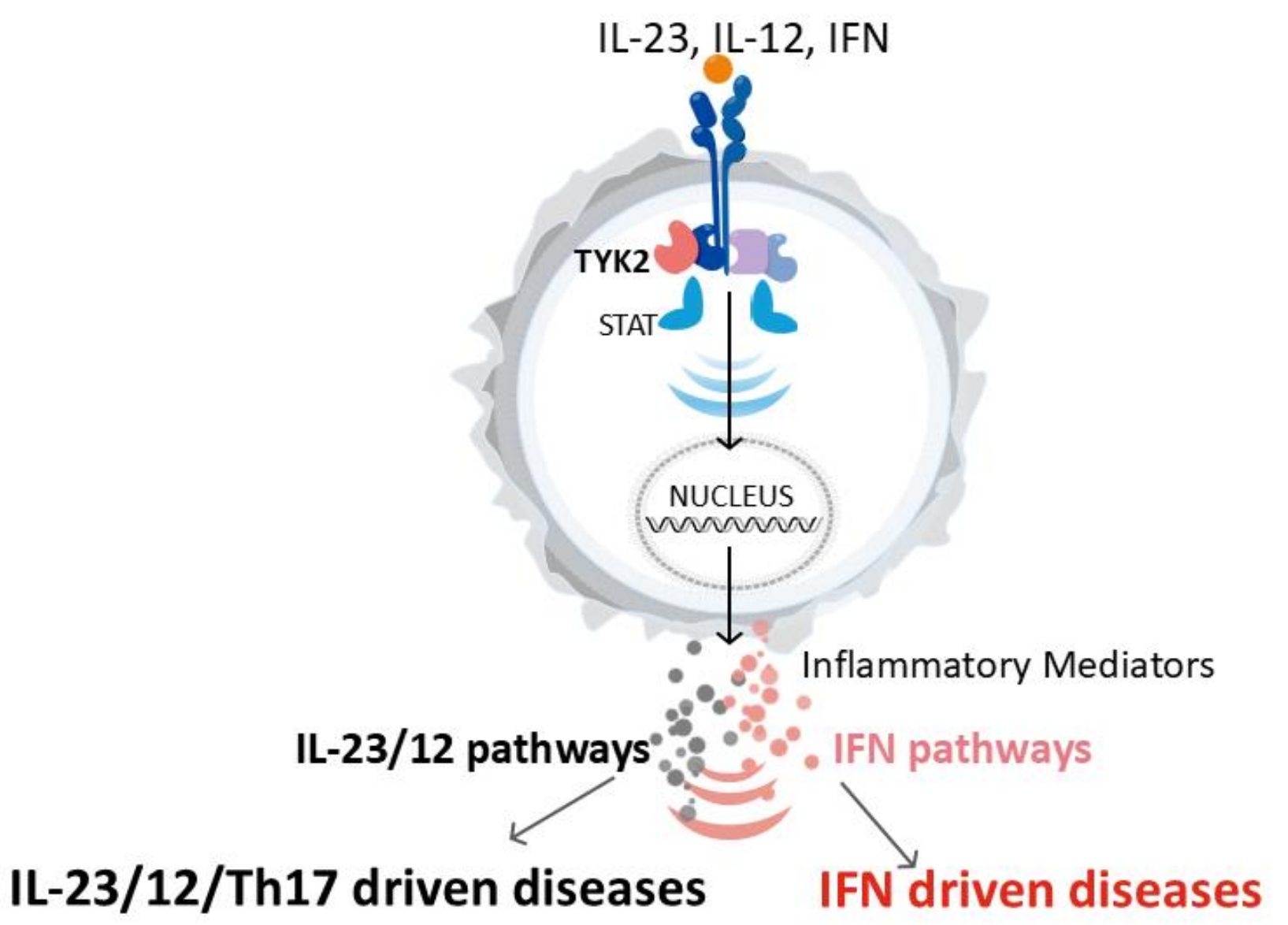
## Background

### New therapies are needed for SLE

- Systemic Lupus Erythematosus (SLE) is a chronic inflammatory multi-organ disease that affects >3.4 million people worldwide.<sup>1</sup>
- The biological heterogeneity in SLE leads to suboptimal results with conventional therapies, which causes the need for better understanding of pathological mechanisms and for development of new SLE targeted approaches.<sup>2</sup>

### TYK2 modulates key inflammatory pathways of SLE

- Genome Wide Association Studies (GWAS) identified SLE-related variants at the *Tyrosine Kinase 2 (TYK2)* locus.<sup>3</sup>
- Human **TYK2 loss-of-function variants protect** from a wide array of immune-mediated diseases, including SLE.<sup>4</sup>
- TYK2 mediates signaling from key proinflammatory cytokines, including **IL-23, IL-12, and type I IFN through STAT phosphorylation**.
- TYK2-mediated effects in other pathways are less studied.



## Objectives

This study aimed to reveal **new TYK2-mediated pathways in SLE** by integrating **SLE GWAS** summary statistics and **proteomics** data made available through UK Biobank.

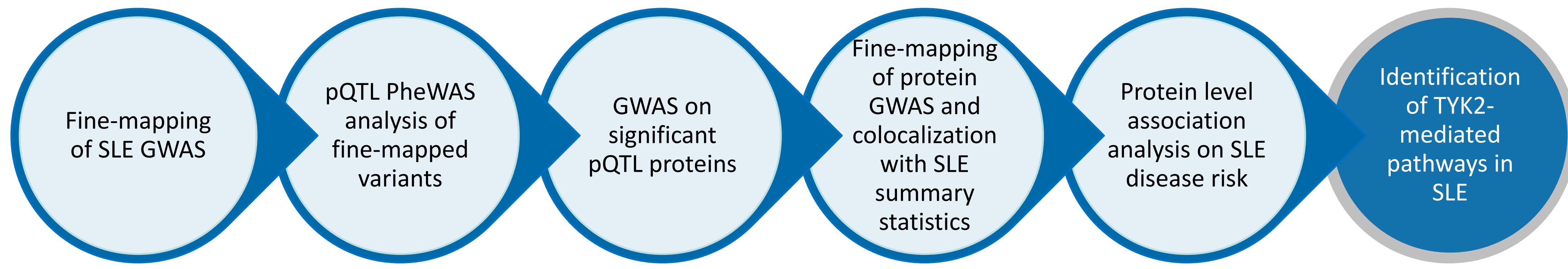
### Databases

- SLE GWAS** summary statistics from NHGRI-EBI GWAS Catalog.<sup>5</sup>
- Trans-protein-quantitative trait locus (**pQTL**) Phenome-wide association study (**PheWAS**) using Olink data from UK Biobank.<sup>6</sup>
- Protein level association analysis on SLE disease risk database from UK Biobank.<sup>6</sup>

### Statistical interaction methods

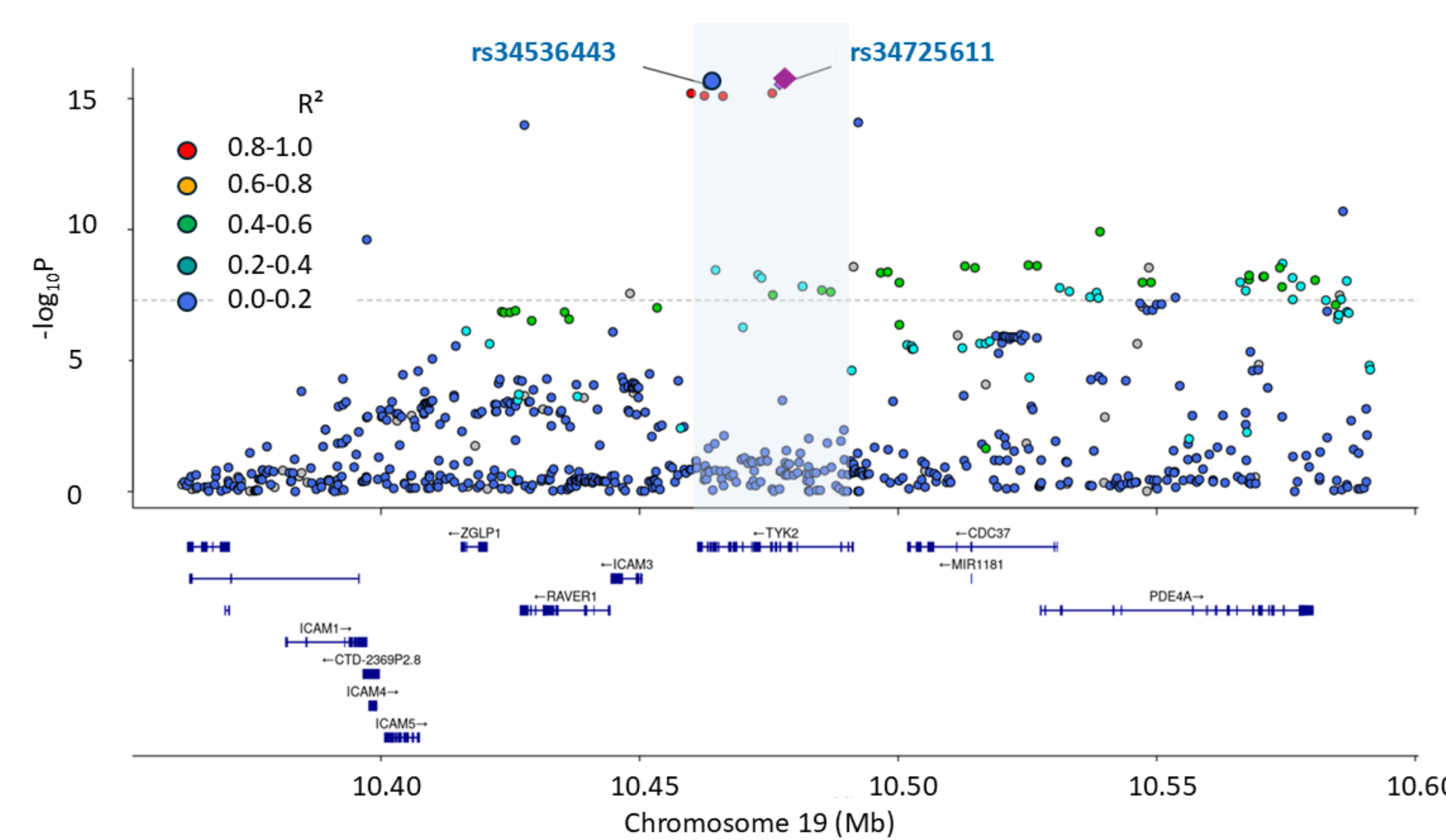
- Fine-mapping using susieR package.<sup>7</sup>
- Colocalization with Coloc R package.<sup>8</sup>

## Methods

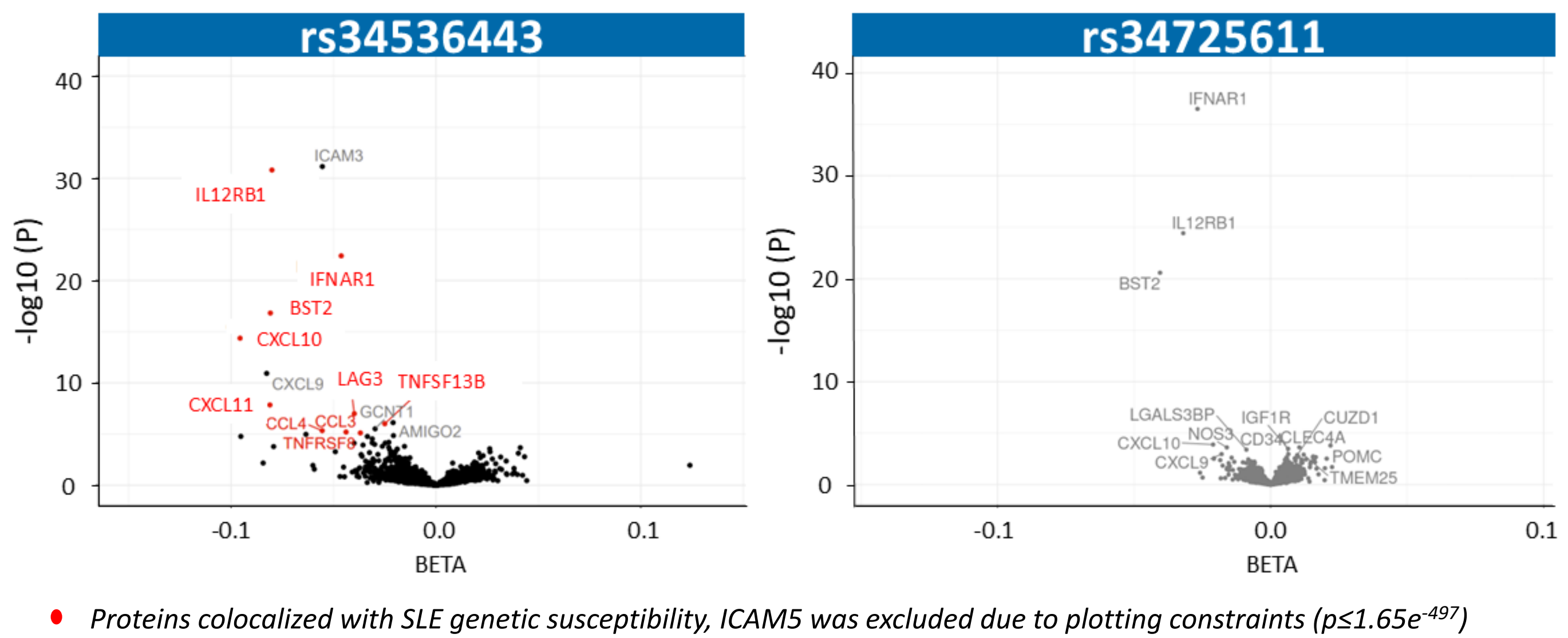


## Results

### SLE GWAS identified 2 independent variant sets at the TYK2 locus



### pQTL pheWAS analysis uncovered unique proteins associated with SLE-related TYK2 variants



• Proteins colocalized with SLE genetic susceptibility, ICAM5 was excluded due to plotting constraints ( $p \leq 1.65e^{-497}$ )

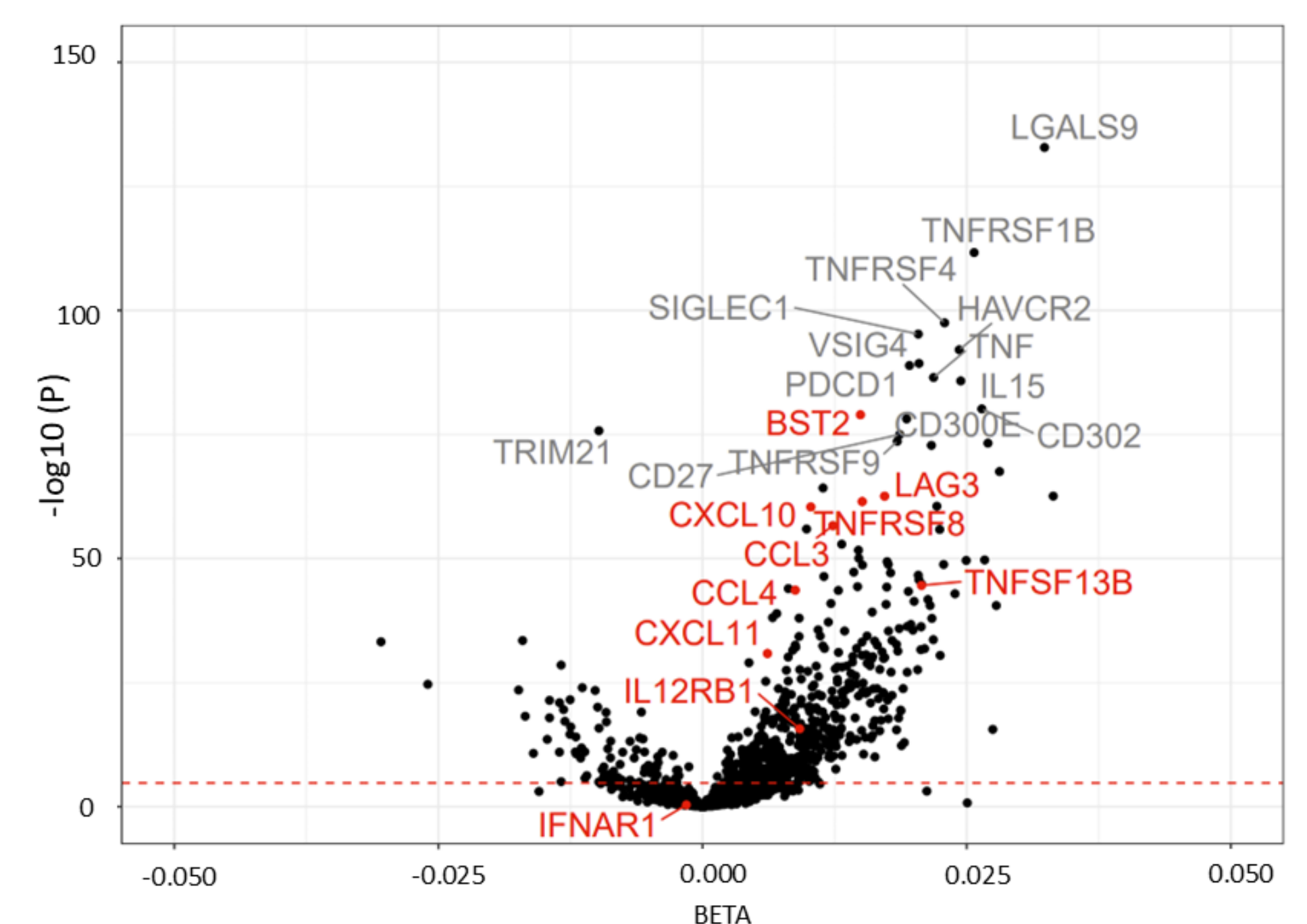
- Fine-mapping of GWAS discovered 2 independent single nucleotide polymorphisms (SNPs) at the *TYK2* locus related with SLE.
  - Rs34536443 (G>C)** is a well-characterized pharmacomimetic **TYK2 loss-of-kinase function allele (P1104A)**.
  - Rs34725611 (A>G)** is an intronic variant with unknown function.

- pQTL PheWAS screen identified >12 proteins that significantly associated with at least one SLE-related TYK2 variant based on a Benjamini-Hochberg correction.
- 10 TYK2-variant associated proteins colocalized with SLE disease susceptibility.

### Colocalized TYK2 variant-related proteins associated with T-cell and B-cell pathways along with IL-23/12 and type I IFN-signaling

Protein Name	Posterior Probability of Inclusion	Immunological Function
IL12RB1	1	IL-23/12-mediated signaling
IFNAR1	1	Type I IFN-mediated signaling
CXCL10	0.997	T-cell chemotaxis
BST2	0.996	B-cell activation
CXCL11	0.986	T-cell chemotaxis
TNFSF13B	0.986	B-cell and T-cell proliferation
LAG3	0.934	T-cell activation
CCL3	0.861	T-cell chemotaxis
TNFRSF8	0.781	NF-κB-mediated signaling
CCL4	0.45	T-cell chemotaxis

### Colocalized TYK2 variant-related proteins showed increased levels in SLE pathogenesis



- Most colocalized proteins associated with T-cell and B-cell regulation.
- Colocalization of IL12RB1 and IFNAR1 supported TYK2-mediated IL-23/12 and type I IFN-signaling.
- Almost all colocalized proteins were significantly increased in SLE cohorts compared to population controls.
  - IFNAR1 protein levels were not associated with SLE.

## Conclusions

Proteogenomic data of this study discovered new TYK2-mediated pathways in SLE pathogenesis in addition to its well-known IL-23/12 and type I IFN-regulation, hence **identified new potential mechanisms that might underlie the protective effects of TYK2 loss-of-function** variants in multiple autoimmune diseases.

- Association of IL12RB1 and IFNAR1 protein levels with TYK2 variants in SLE validated the known TYK2-mediated regulation of IL-23/IL12, and type I IFN pathways in SLE.
- Proteogenomic signatures demonstrated that the **TYK2 loss-of-function allele (P1104A)** also associated with several mediators of **T-cell and B-cell pathways in SLE pathogenesis**, which might contribute to the reported protective effects of TYK2 loss-of-function variants in SLE.

## References

<sup>1</sup>Tian J et al. Ann Rheum Dis, 2023  
<sup>2</sup>Karmakar A et al. Clin Exp Med, 2024  
<sup>3</sup>Contreras-Cubas C et al. Sci Rep, 2019  
<sup>4</sup>Dendrou CA et al. Sci Transl Med, 2016  
<sup>5</sup>Langefeld CD et al. Nat Comm, 2017  
<sup>6</sup>Bycroft C et al. Nature, 2018  
<sup>7</sup>Wang G et al. J of the Royal Stat Society, 2020  
<sup>8</sup>Wallace C. Gen Epi, 2023

## Disclosures

Commercial support was provided by Alumis Inc. All authors are employed by Alumis and have no other relationships or conflicts of interest to disclose.

## Contact Details

Email: [Jhoffman@alumis.com](mailto:Jhoffman@alumis.com)