

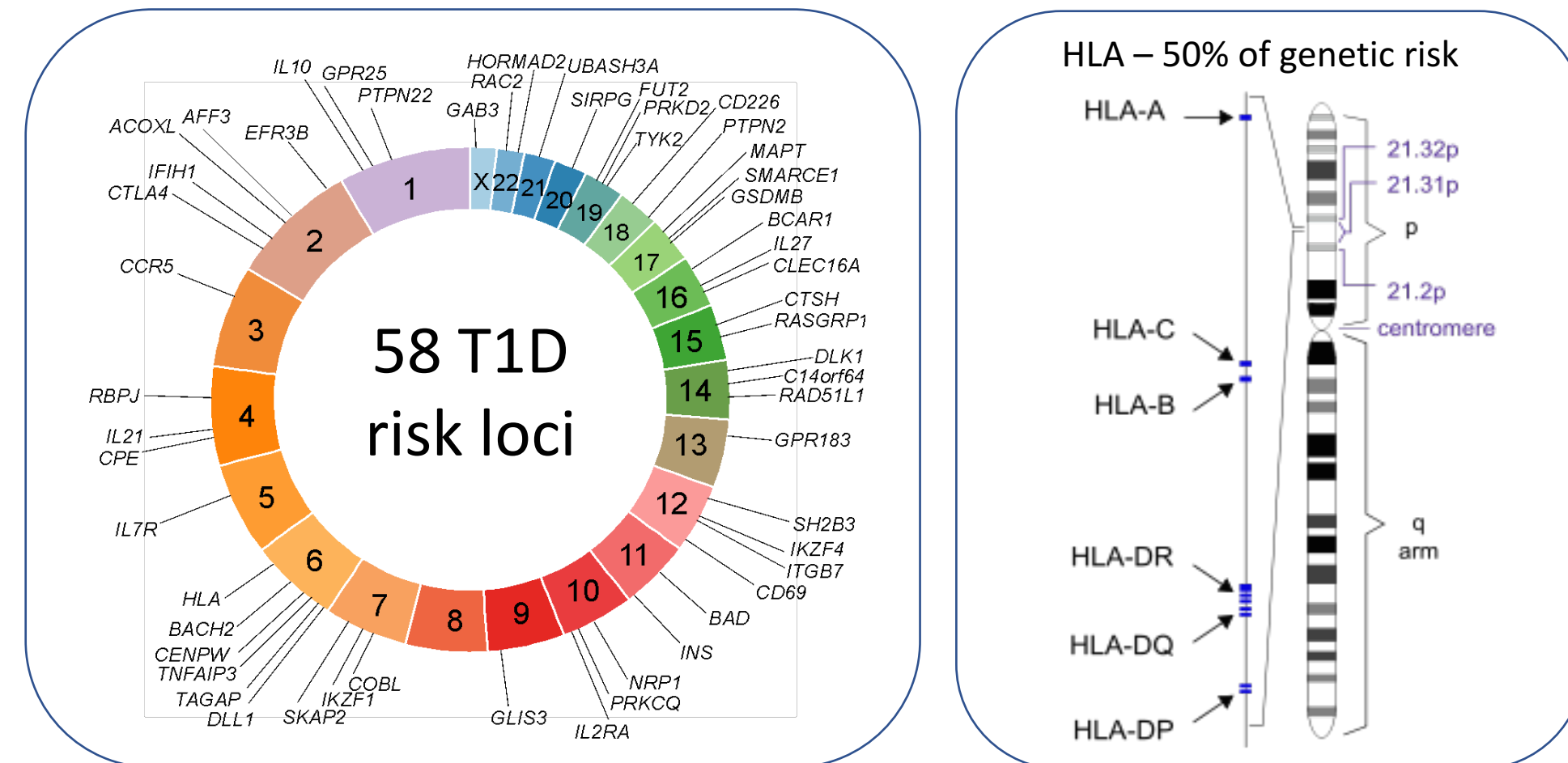
Type 1 Diabetes Risk Is Influenced by Both Immune Cell and Pancreatic Islet Regulatory Variation

Anthony Aylward, Nikita Kadakia, Mei-Lin Okino, Hudson Cooper, Ulupi Jhala, Kyle Gaulton

Department of Pediatrics, University of California San Diego, La Jolla, CA, USA

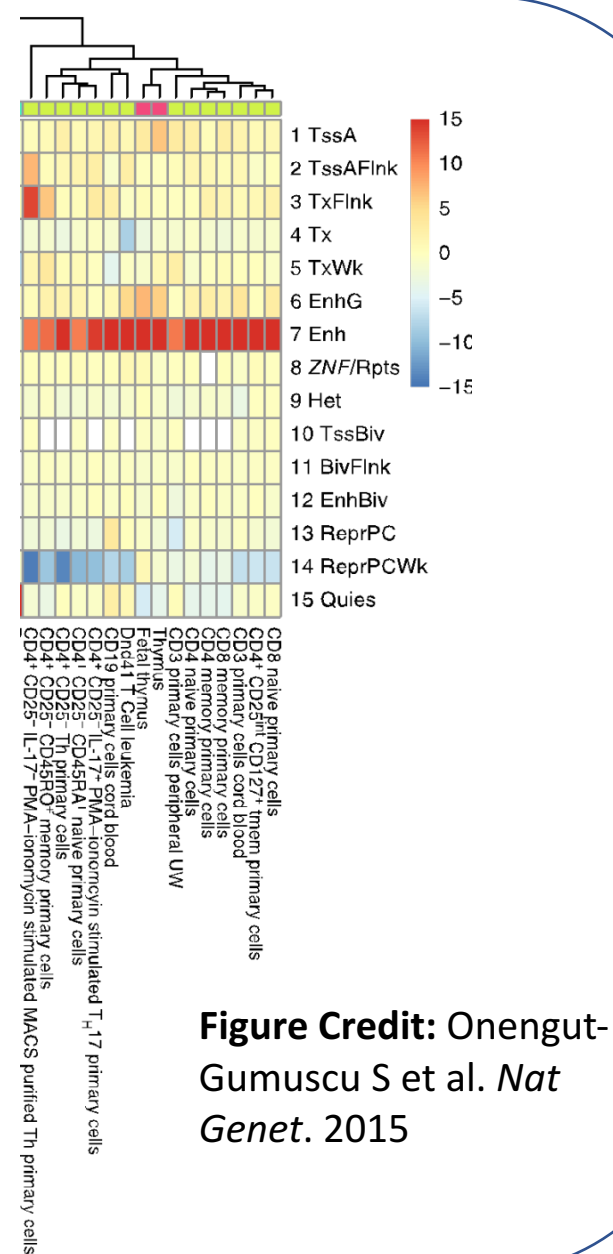
1. Background

Many genomic loci influence T1D risk, but causal mechanisms at most loci are unknown

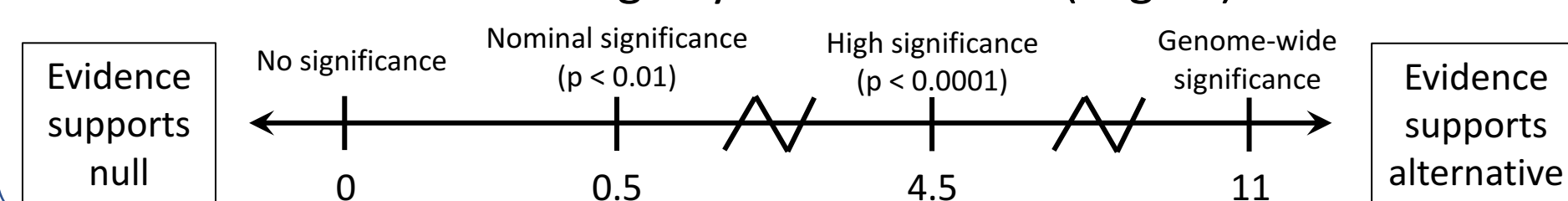


Previous studies identified enrichment of T1D variants in immune enhancers

- Most T1D risk variants lie in non-coding genomic regions, and probably have regulatory effects.
- Epigenomic maps from human cells can provide information about mechanisms of disease loci.
- A previous genetic fine-mapping study found that T1D variants are enriched predominantly in immune-related enhancers.

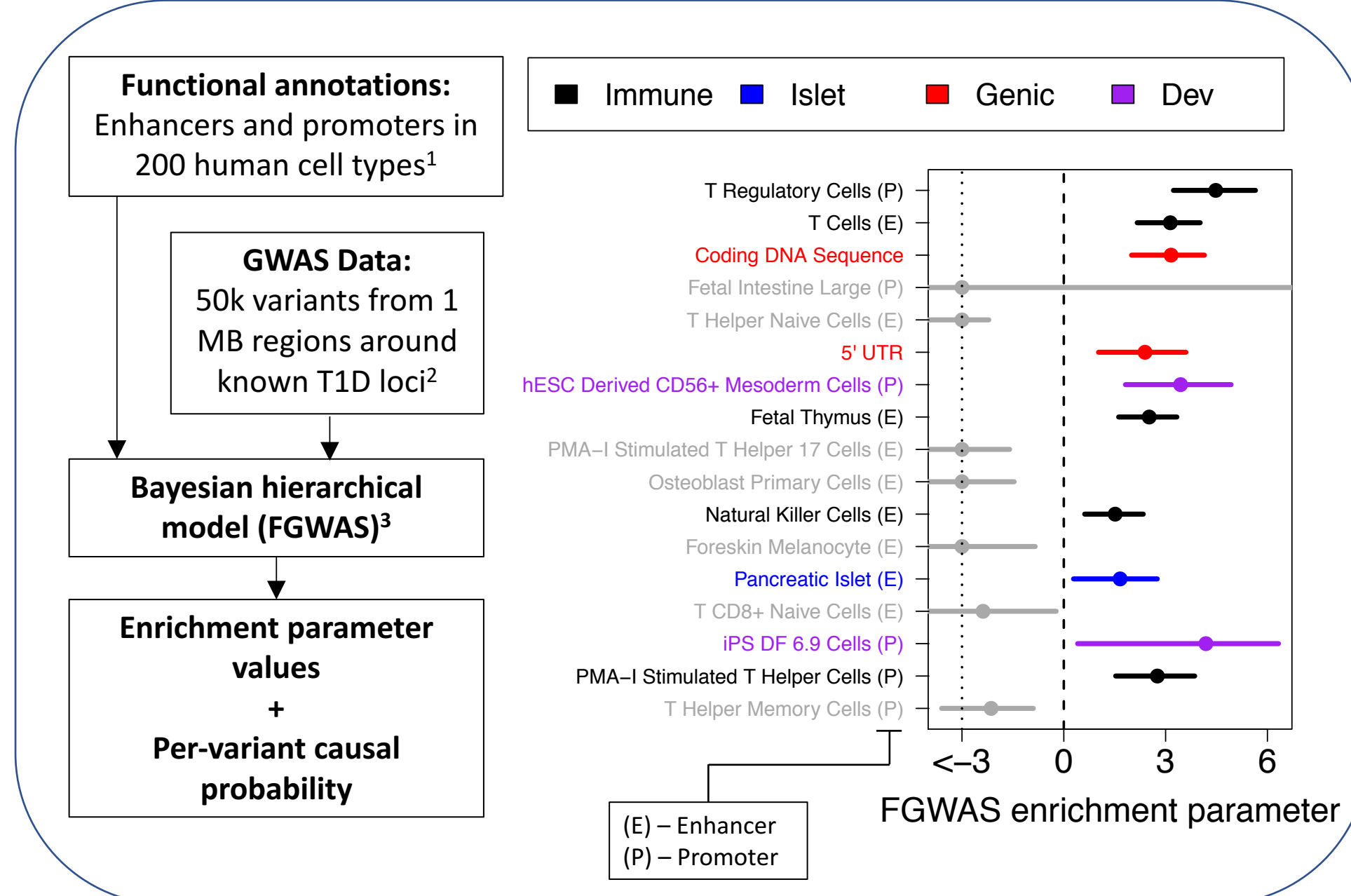


Statistics: Log Bayes Factor Scale (Log BF)

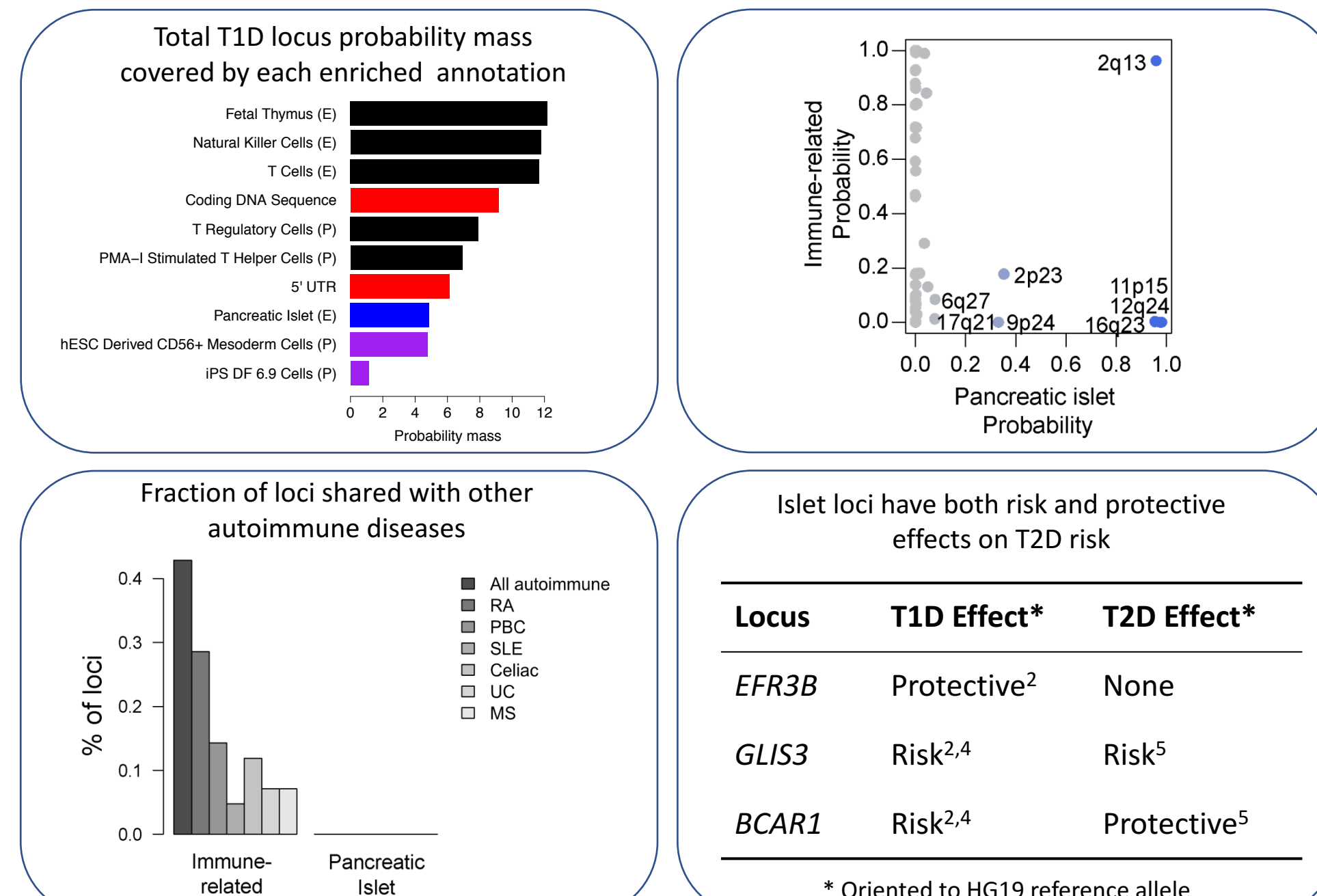


2. Modeling T1D risk using epigenome data

Statistical modeling reveals that regulatory sites in immune cells and pancreatic islets are enriched for T1D risk variants

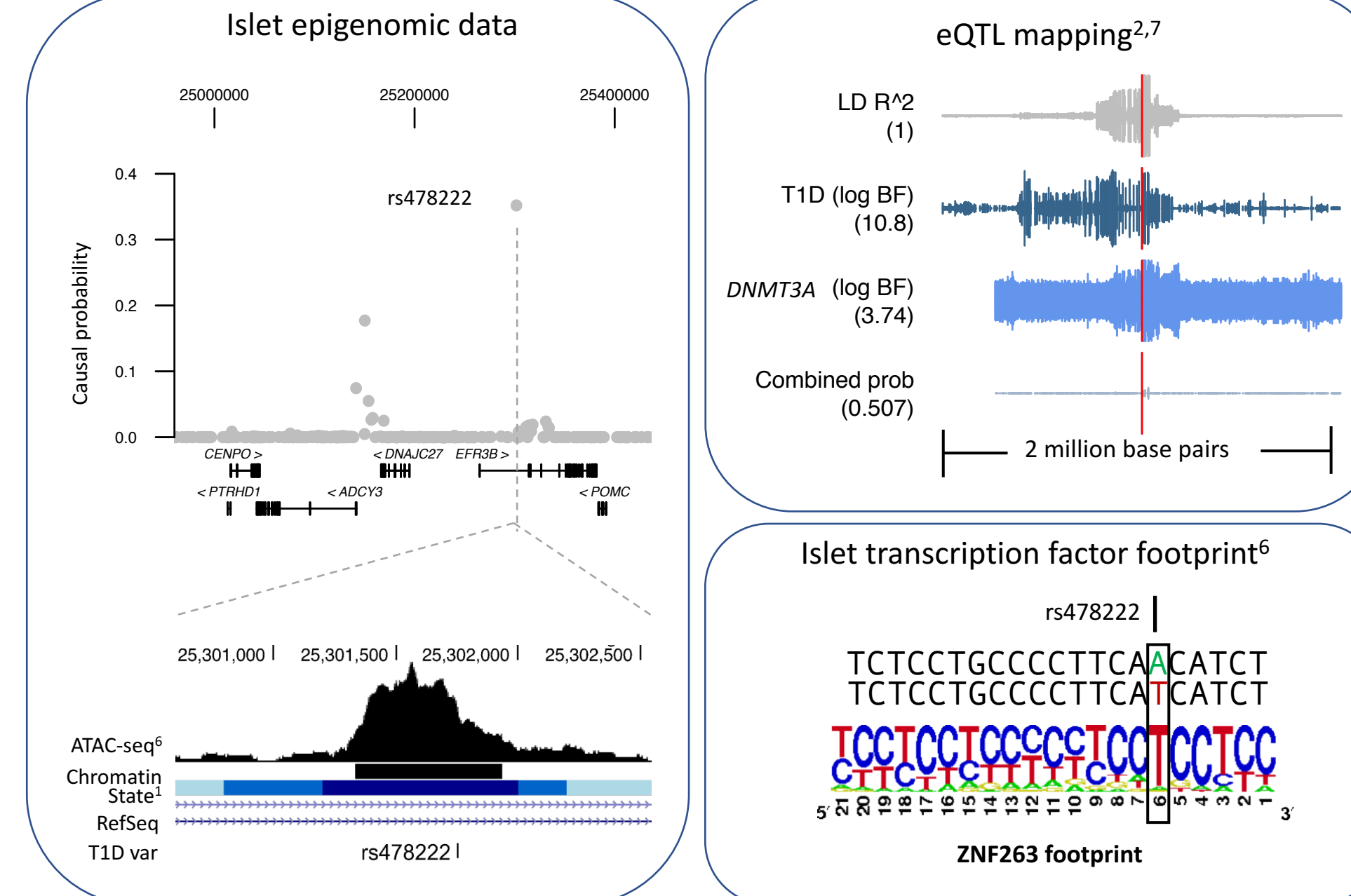


Variants in pancreatic islet enhancer regions represent a distinct subset of T1D loci

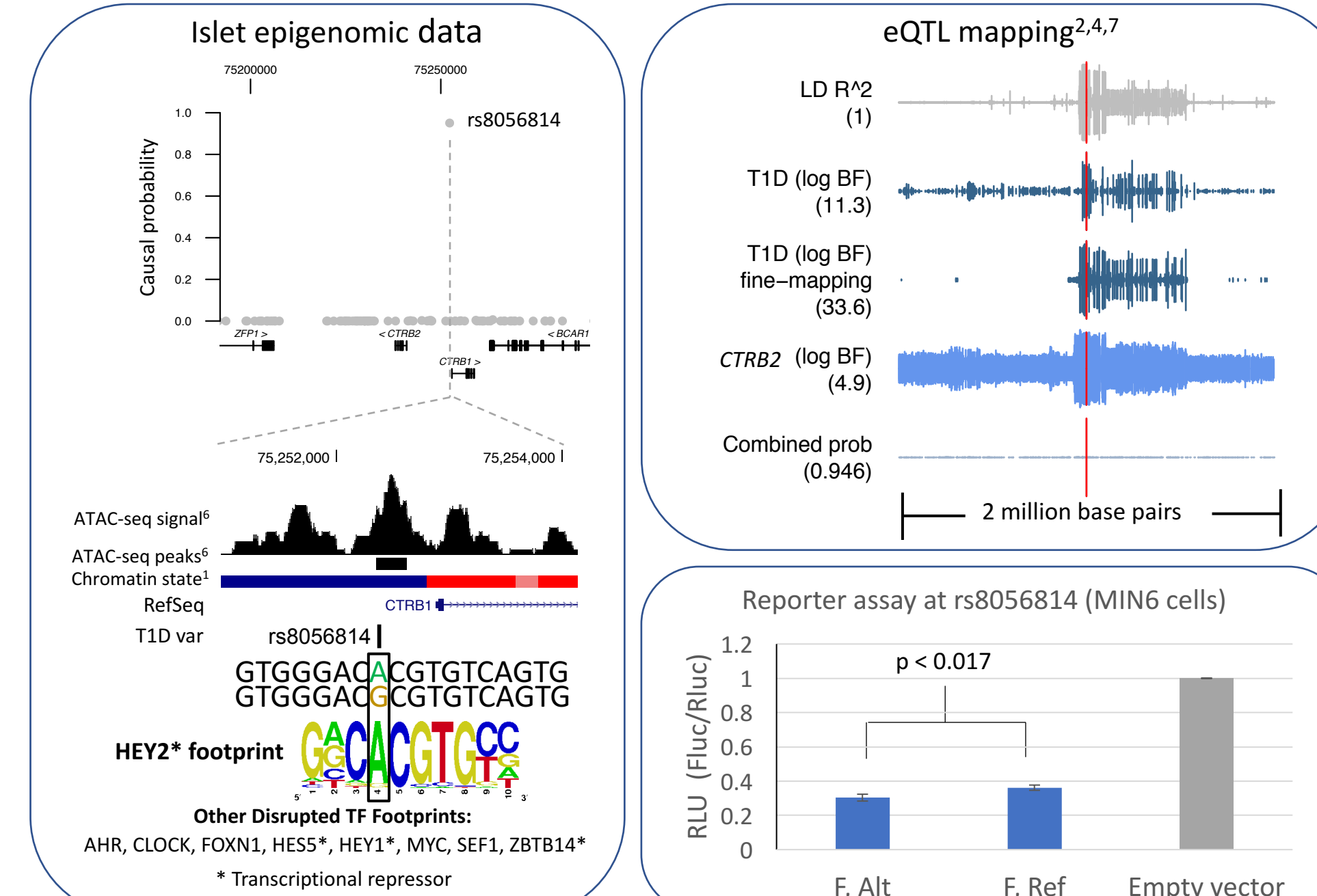


3. Candidate T1D variants affect islet regulation

EFR3B Locus: Candidate variant overlaps islet accessible chromatin and affects islet *DNMT3A* expression

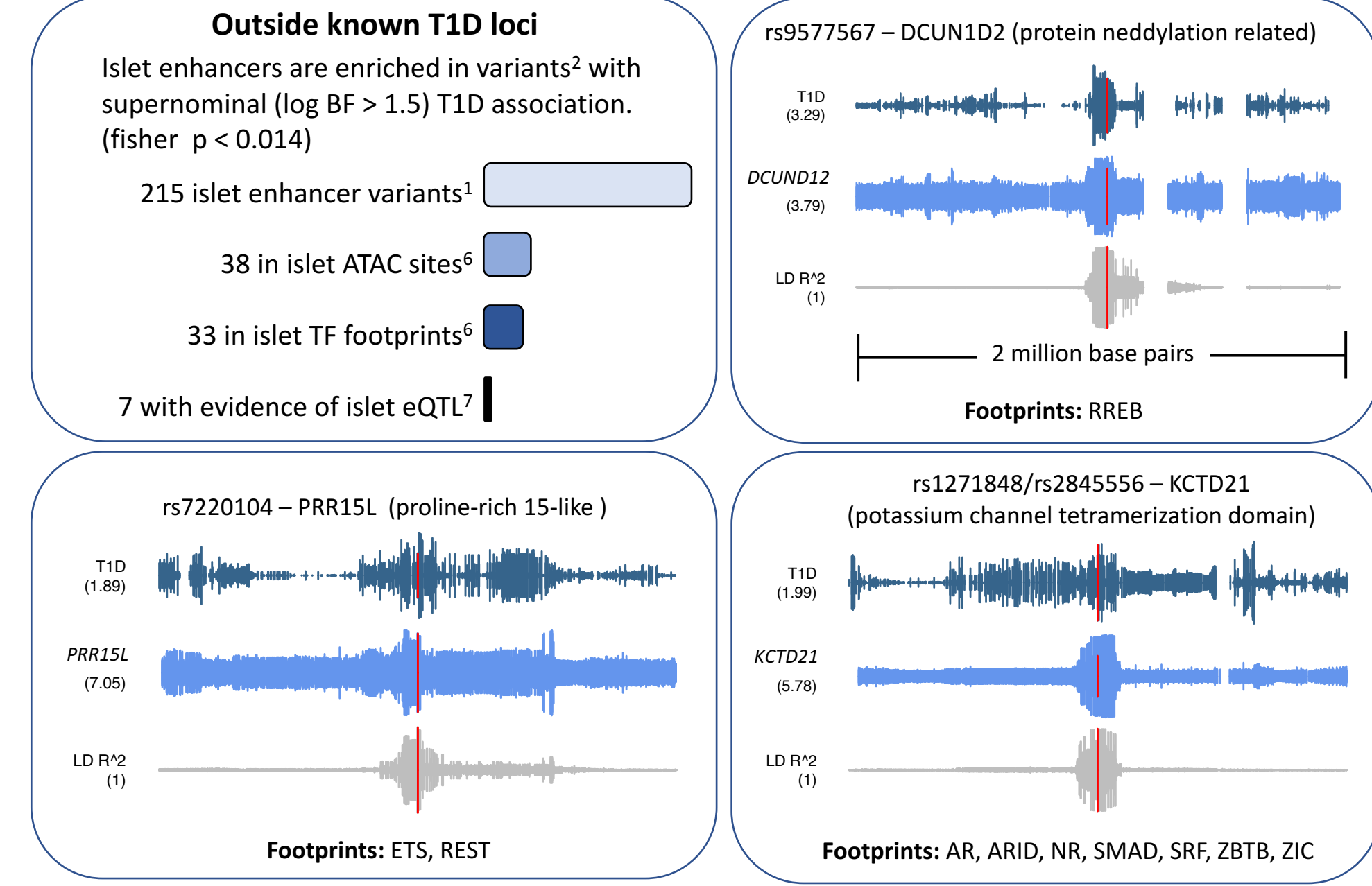


BCAR1 Locus: Candidate variant overlaps islet accessible chromatin and alters islet regulatory activity and *CTRB2* expression



4. Islet regulatory variants broadly influence T1D

Variants with nominal T1D association are enriched in pancreatic islet enhancers



Summary

- Statistical models demonstrate variants in both immune cell and pancreatic islet regulatory elements are enriched for T1D risk
- T1D loci can be partitioned into immune- and islet-related groups with distinct properties based on epigenomic annotations
- Evidence that pancreatic islet regulatory mechanisms underlie T1D risk at known loci, including *EFR3B* and *BCAR1*, in addition to several novel loci.

References

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