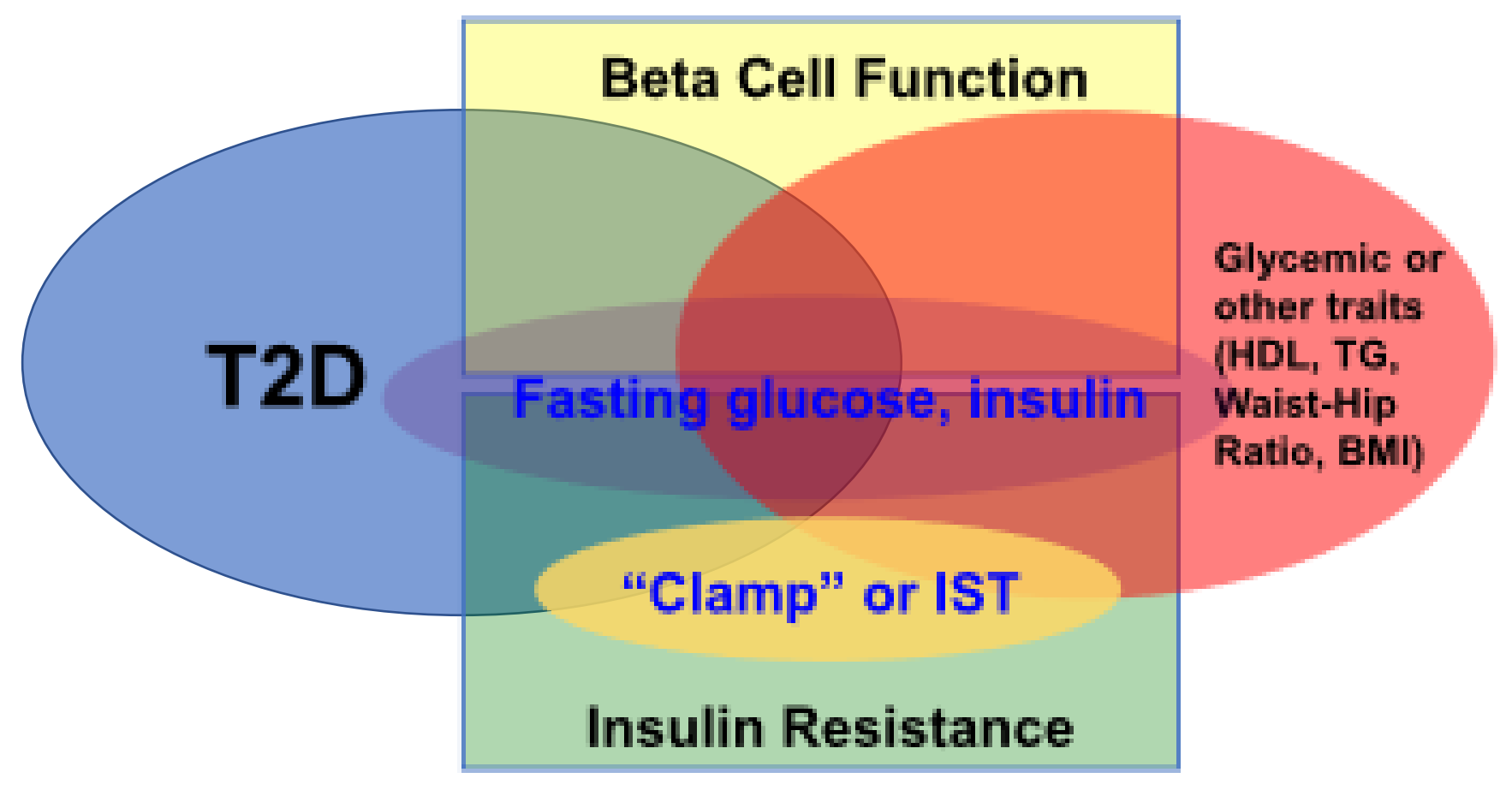


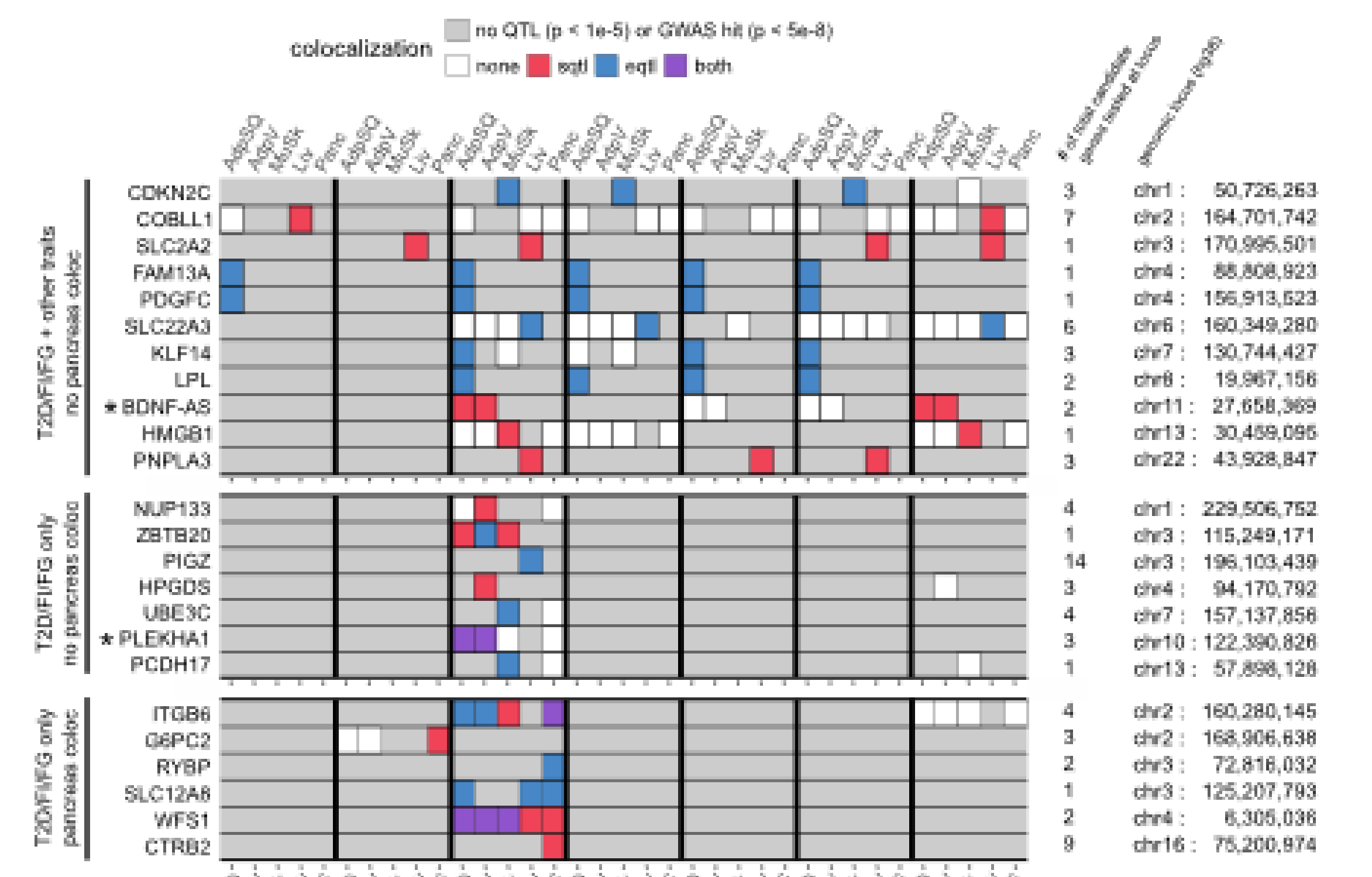
Michael J Gludemans^{1,2*}, Brunilda Balliu^{3*}, Daniel Nachun^{4,5}, Matthew G Durrant⁴, Erik Ingelsson⁶, Martin Wabitsch⁷, Thomas Quertermous^{6,8}, Stephen B Montgomery^{2,4}, Joshua W Knowles^{6,8,9}, Ivan Cárcamo-Orive^{6,8}

1. Department of Biomedical Data Science, Stanford University. 2. Department of Pathology, Stanford University. 3. Department of Computational Medicine, UCLA. 4. Department of Genetics, Stanford University. 5. Department of Immunology, Stanford University. 6. Department of Medicine, Division of Cardiovascular Medicine, Stanford University. 7. Department of Pediatrics and Adolescent Medicine, Division of Pediatric Endocrinology, Ulm University, Ulm, Germany. 8. Diabetes Research Center, Stanford University. 9. Prevention Research Center, Stanford University.

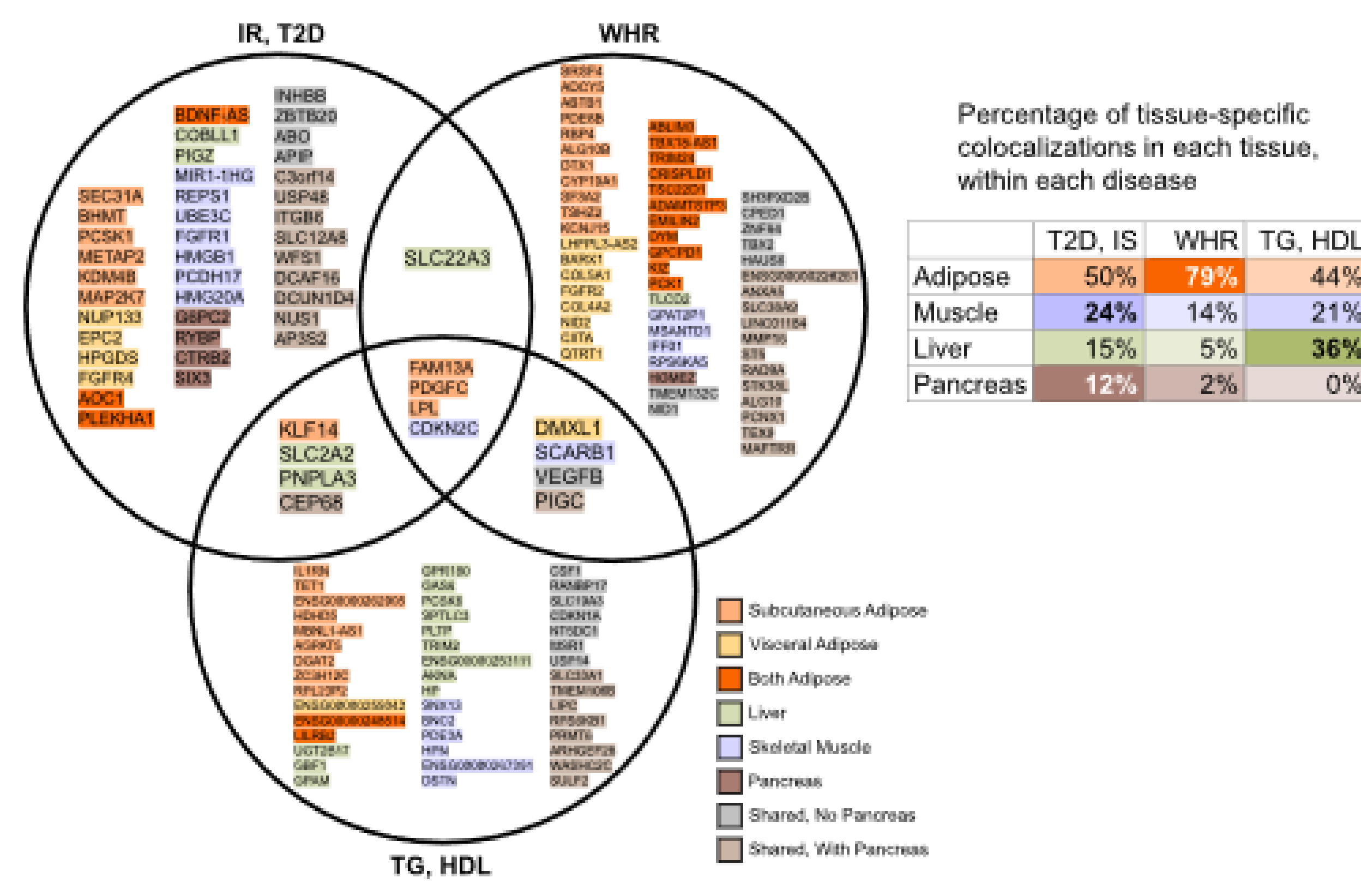
Insulin resistance (IR) leads to type 2 diabetes (T2D) and other diseases, but is hard to study directly



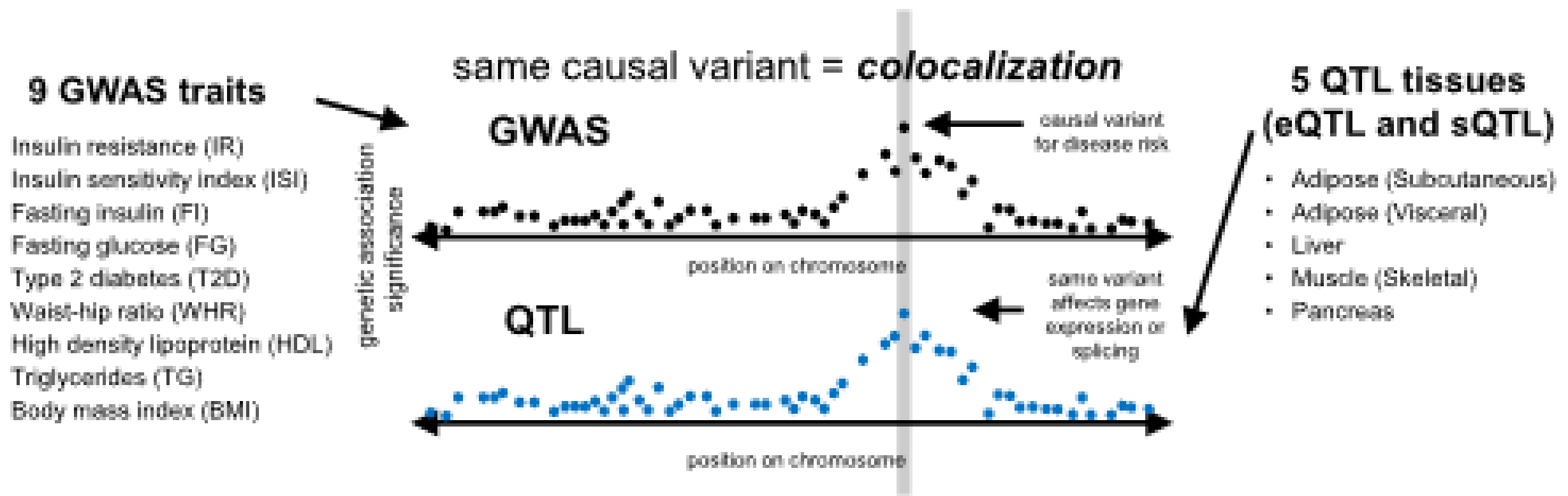
Uniquely colocalized IR and T2D loci show various patterns of tissue and trait sharing



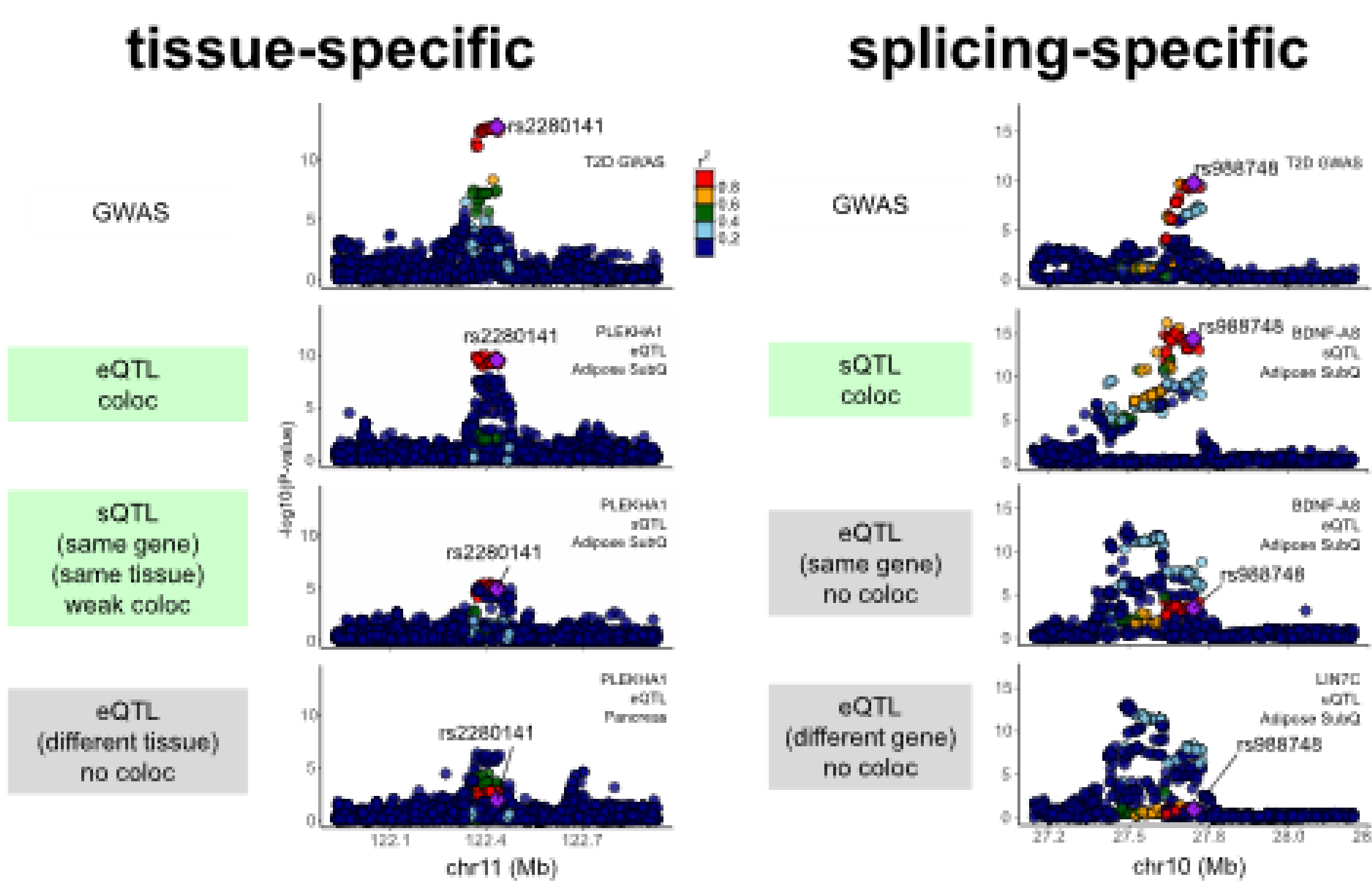
Loci with single colocalized genes show tissue-specificity patterns according to trait cluster



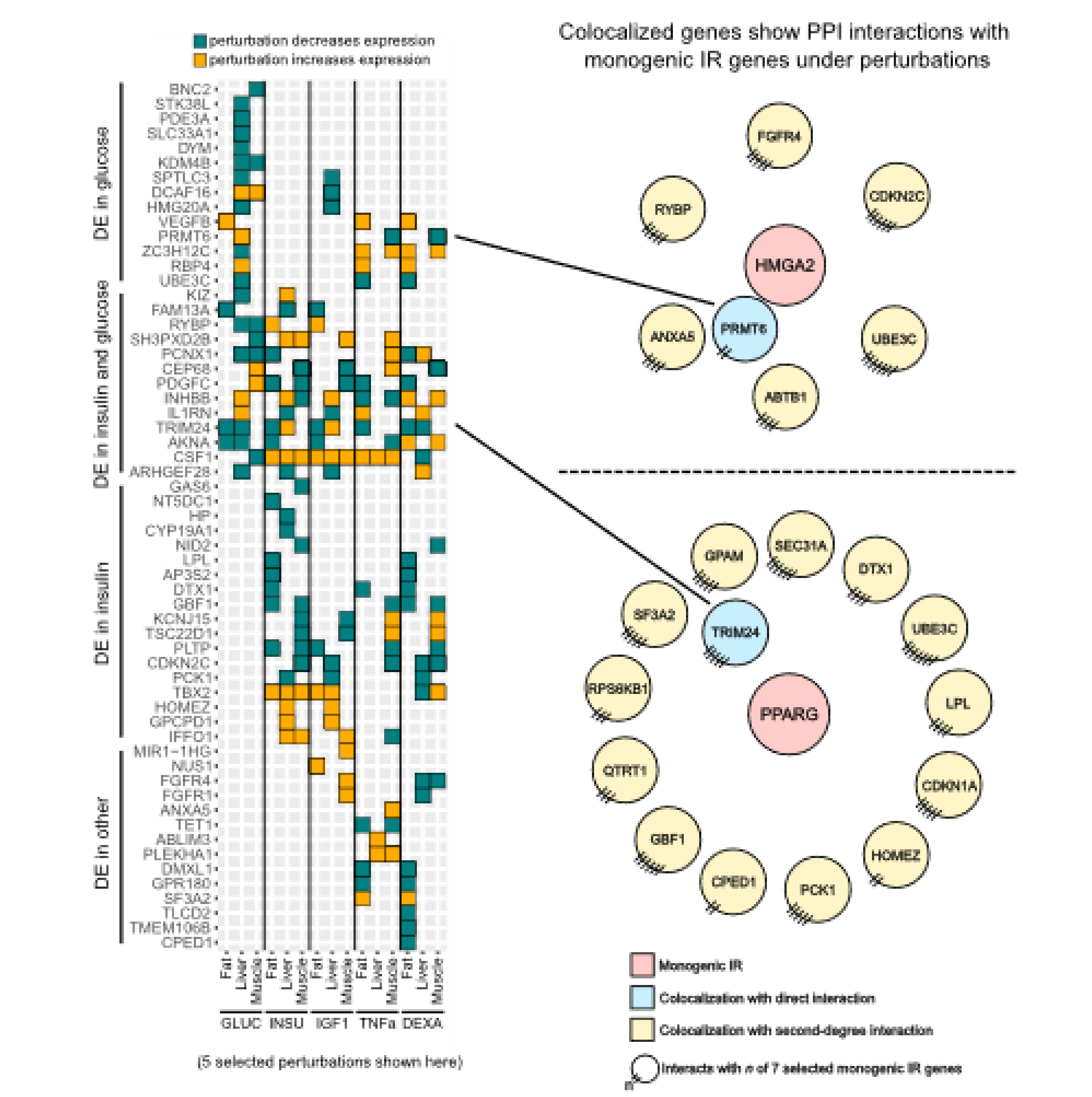
Genetic associations were integrated across 9 IR-related traits and 5 IR- or T2D- relevant human tissues



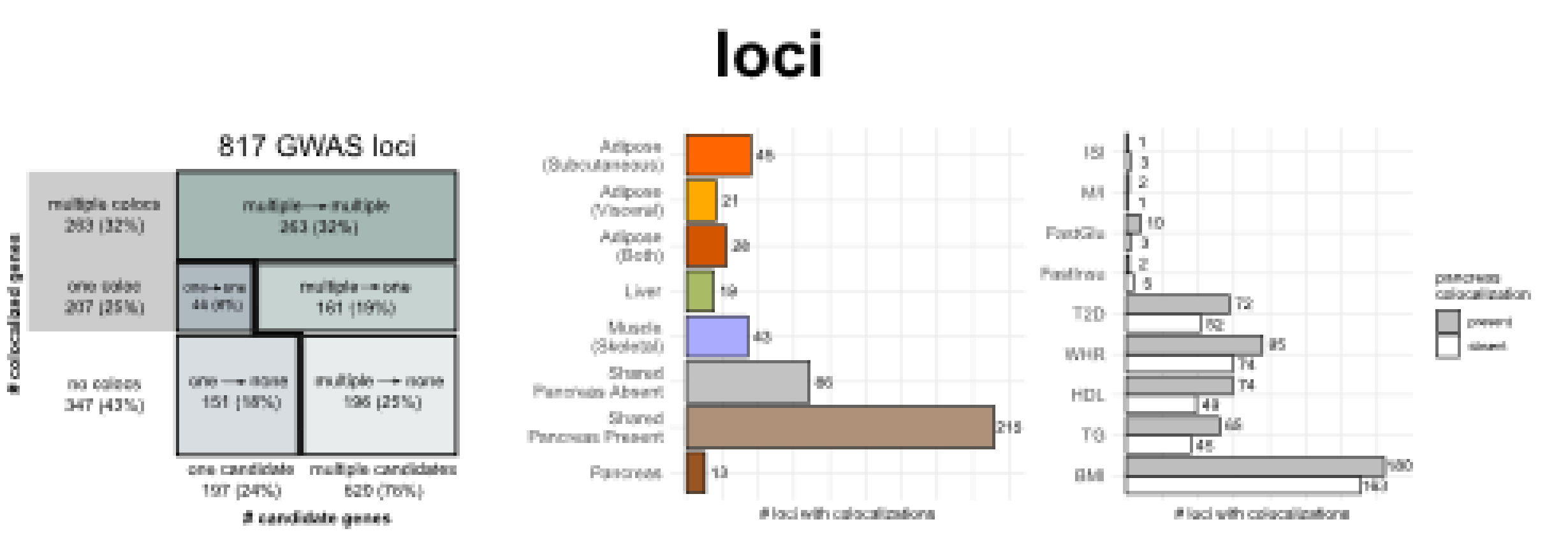
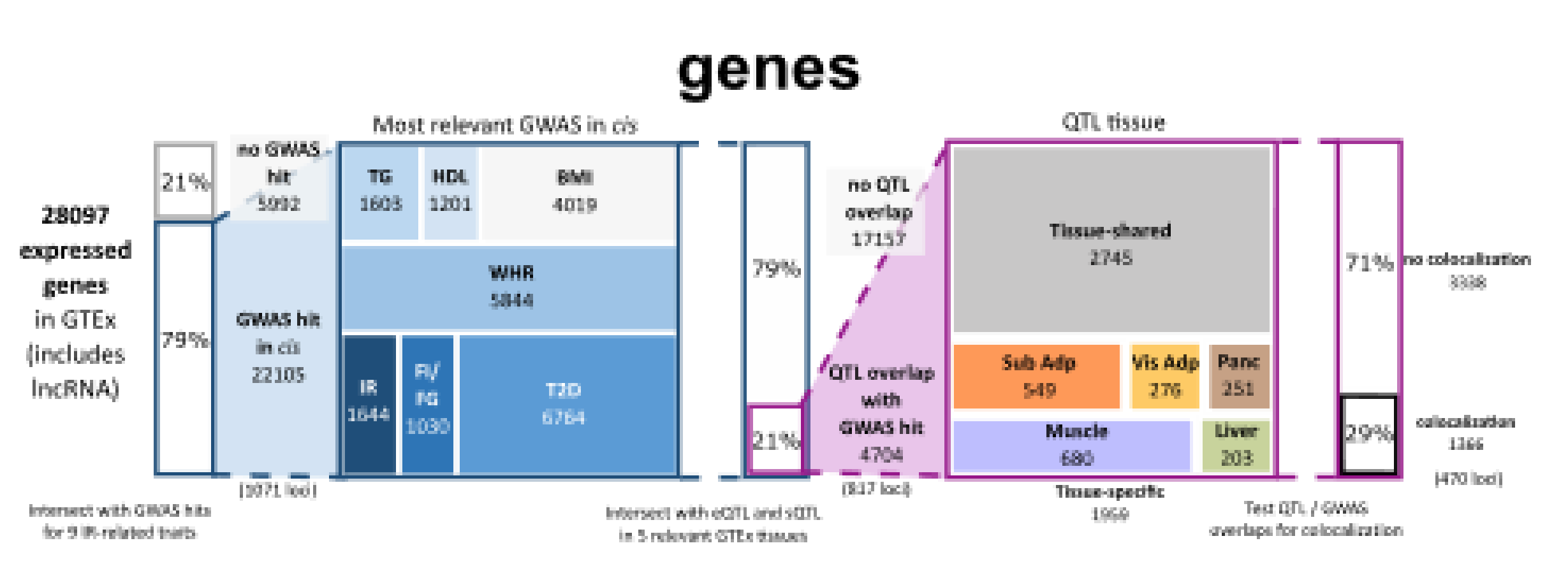
Tissue-specific genes and splicing-specific genes exist



Candidate causal genes show varied patterns of response to a panel of 21 perturbagens in fat, liver, and muscle cells



Colocalization analysis found 1366 genes associated with 470 IR-related GWAS loci



Funding, data, and code availability

M.J.G. was funded by a Stanford Graduate Fellowship and by NLM training grant T15 LM 007033.

A generalized version of the heatmap-producing code is available at <https://github.com/mikegludemans/post-coloc-toolkit>.

For further questions about this project or about applying the methodology to your own diseases of interest, contact me at mgloud@stanford.edu.