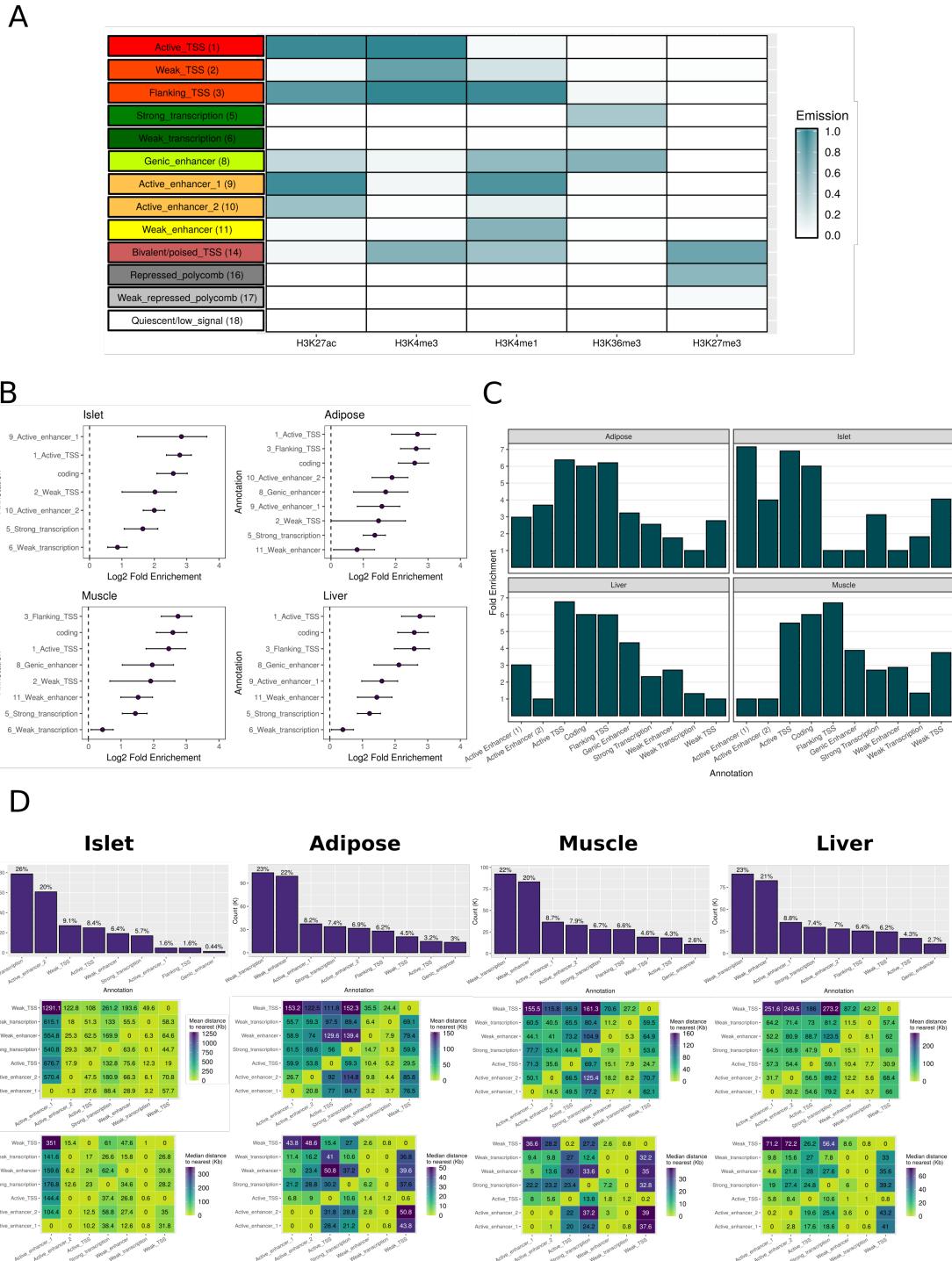
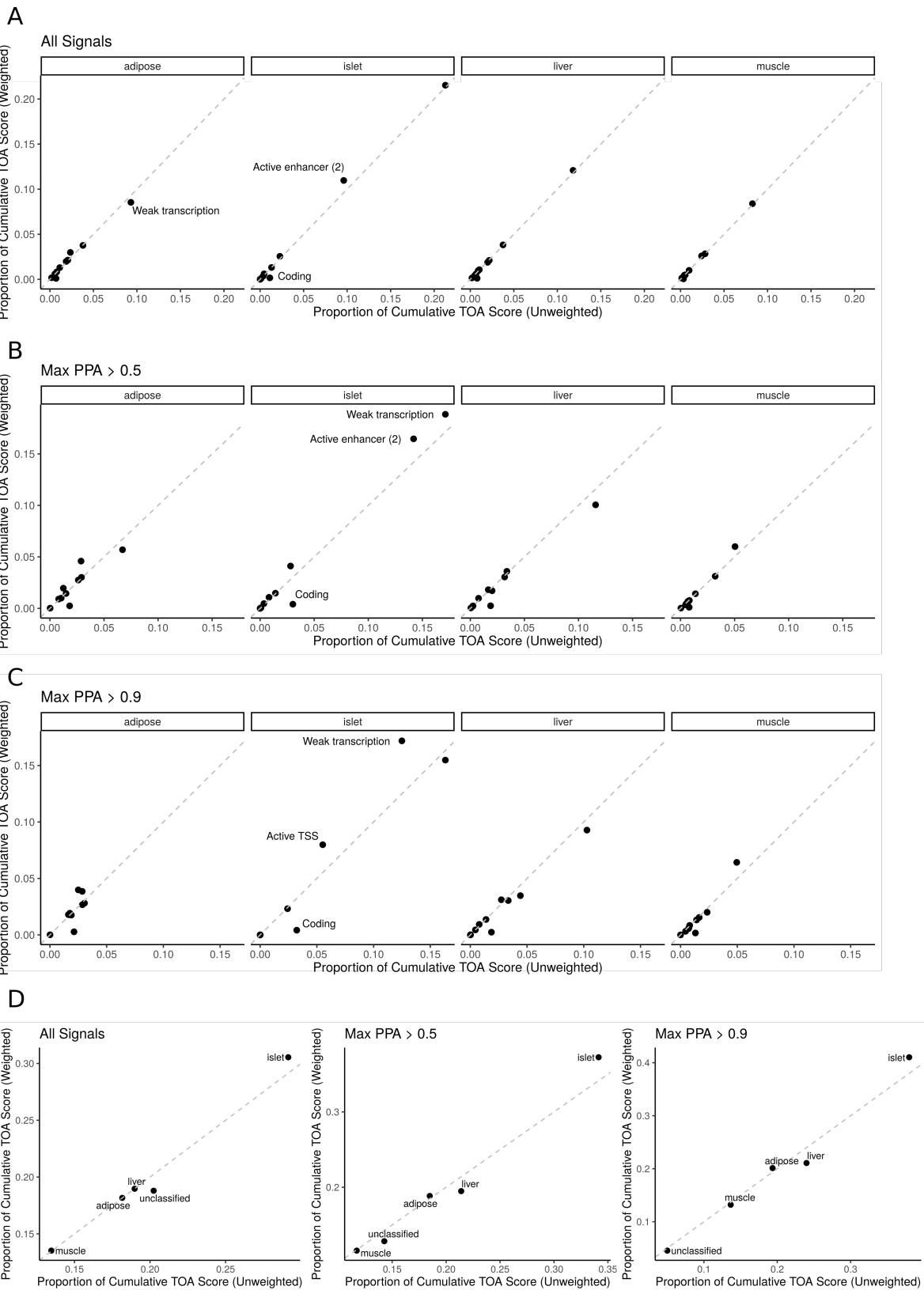


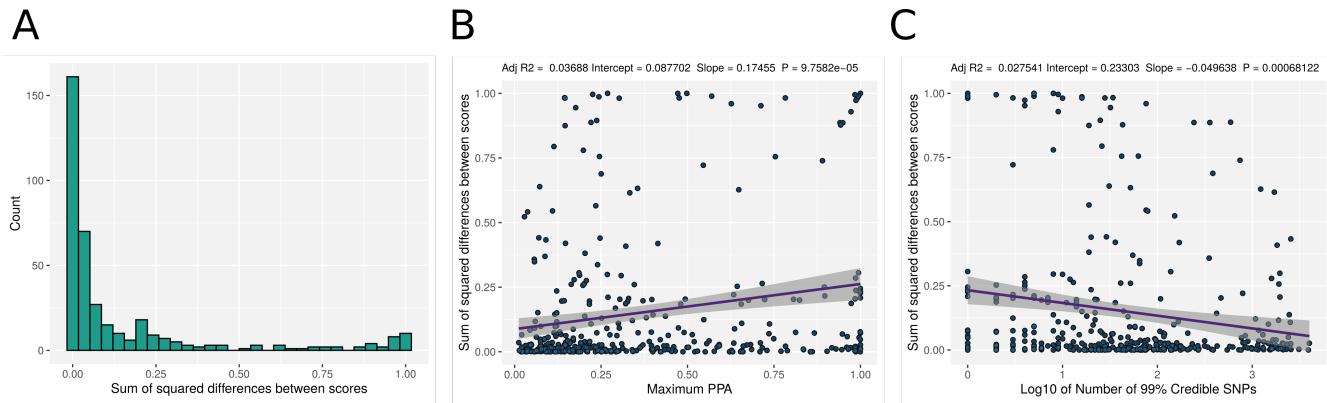
## **Suplementary Figures**



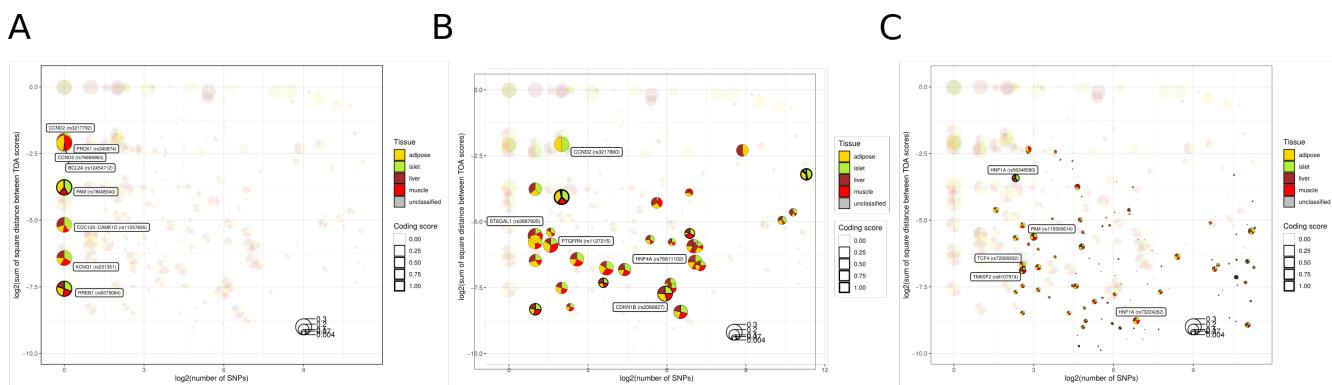
**Supplementary Figure 1.** Epigenomic annotations are enriched for variants associated with type 2 diabetes.



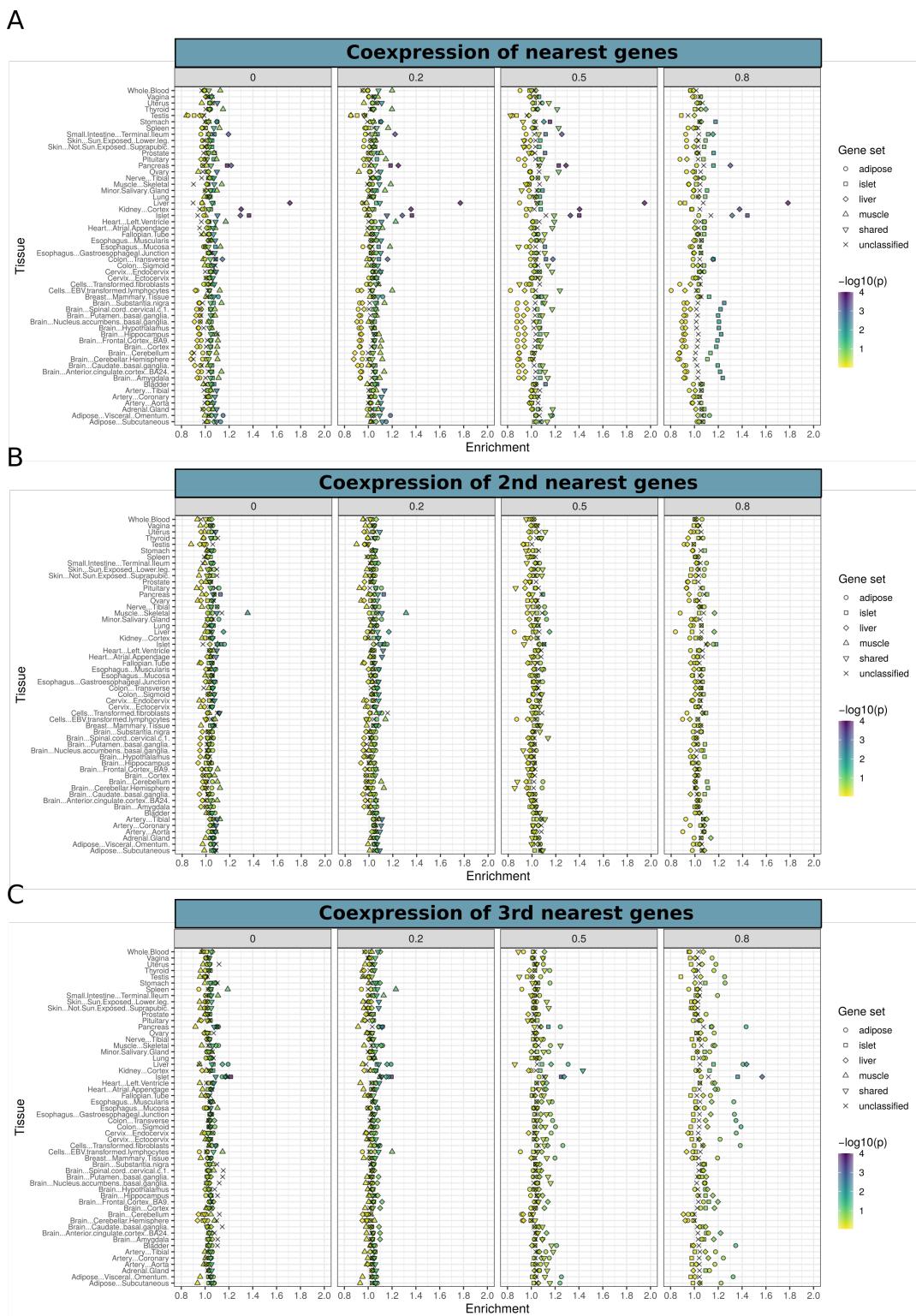
**Supplementary Figure 2. Comparison of GWAS effect size weighted and unweighted TOA scores.**



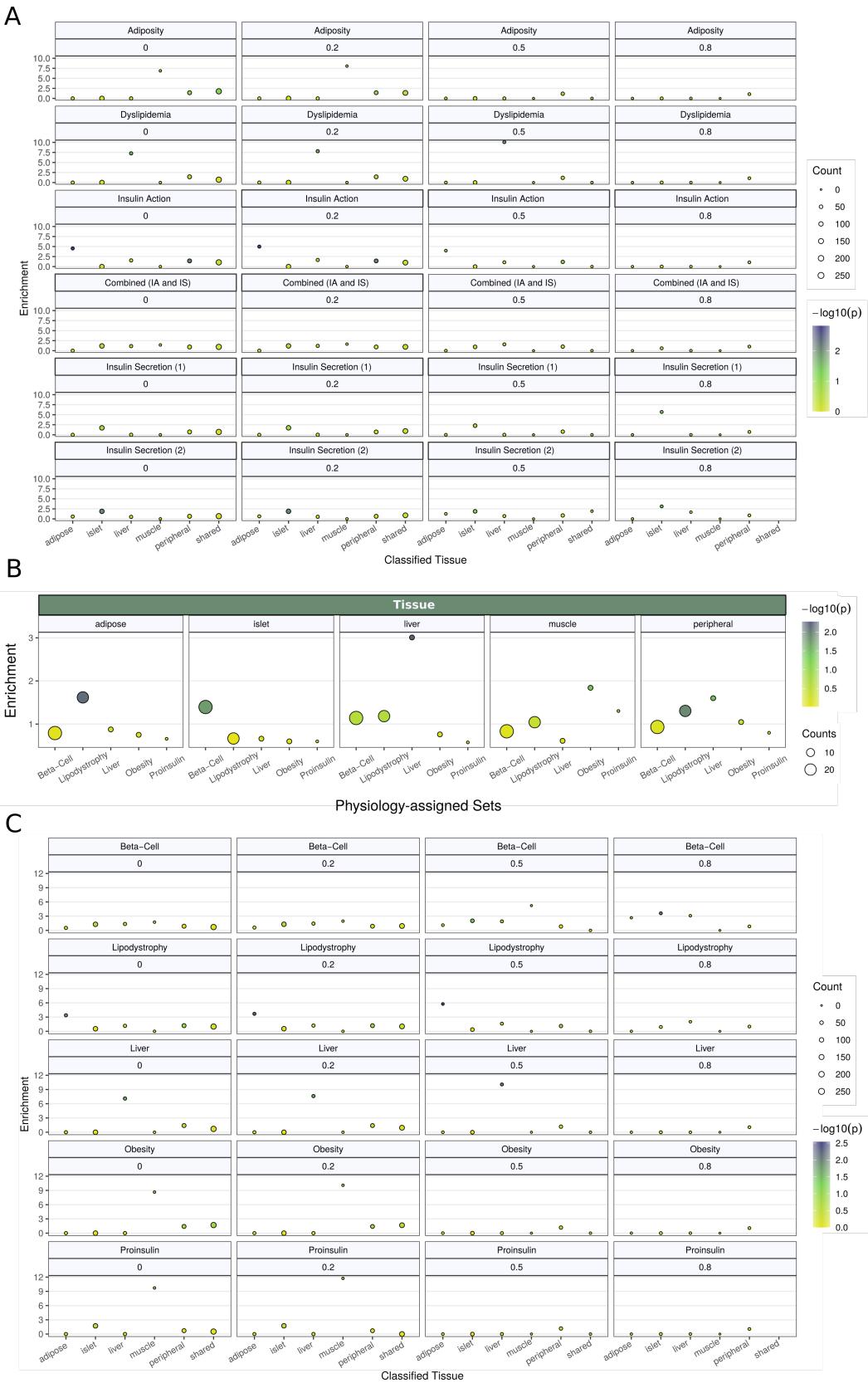
**Supplementary Figure 3.** The relationship between credible set resolution and tissue specificity.



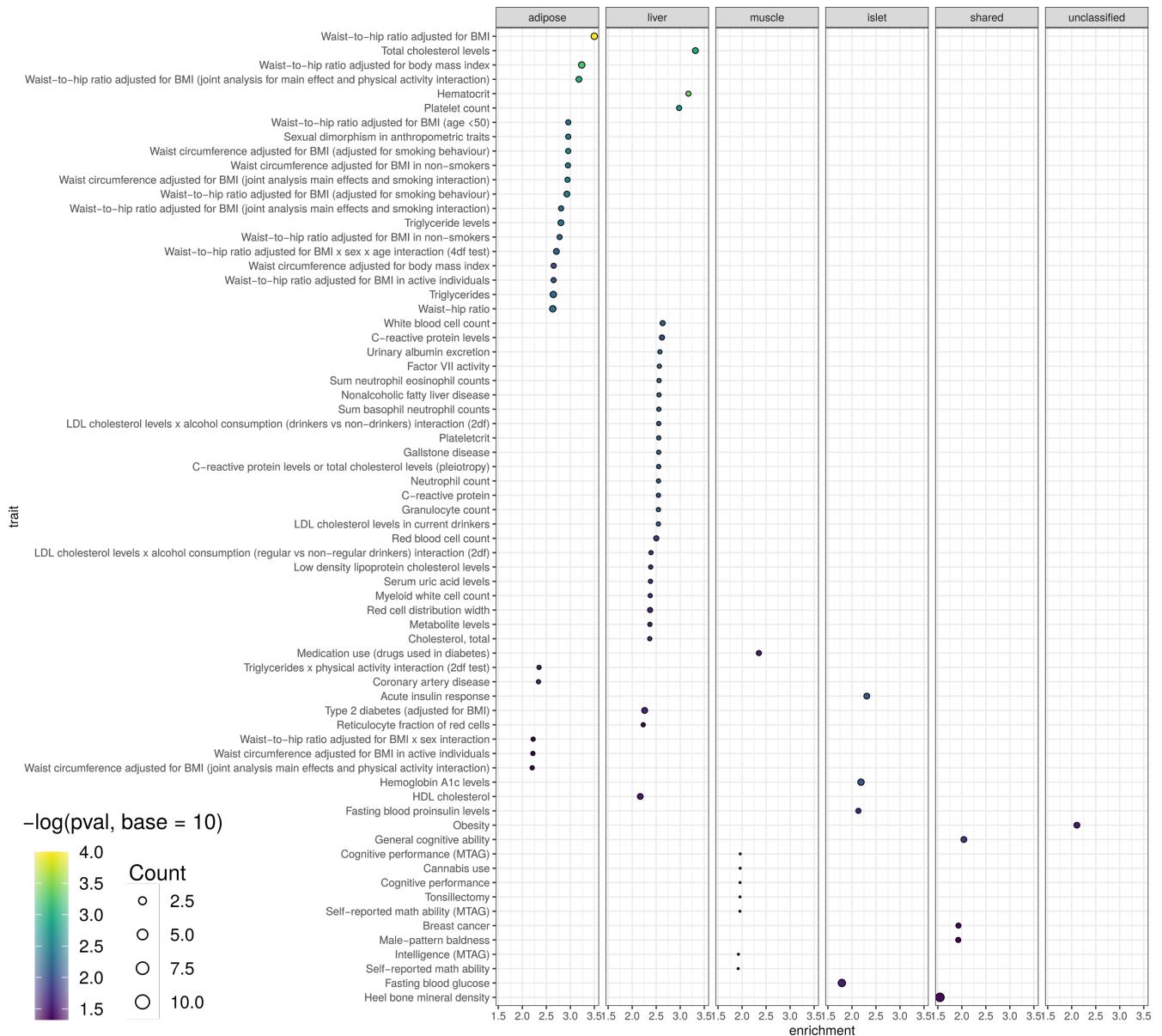
**Supplementary Figure 4.** Fine-mapping resolution and TOA score diversity at shared signals.

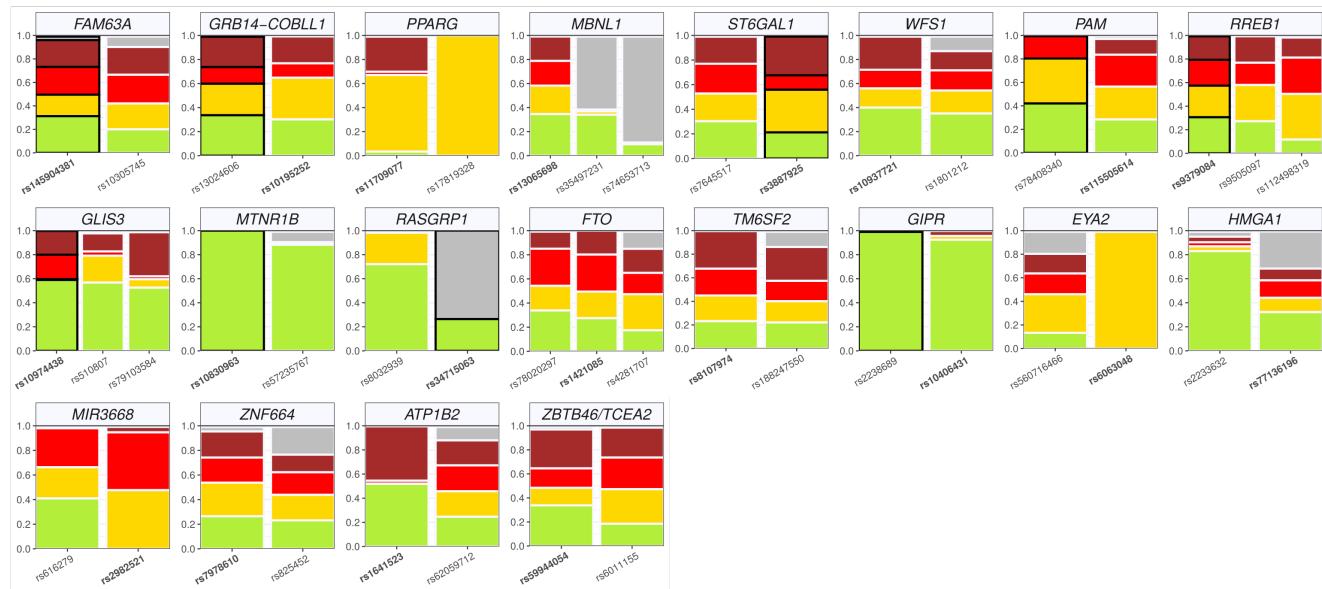
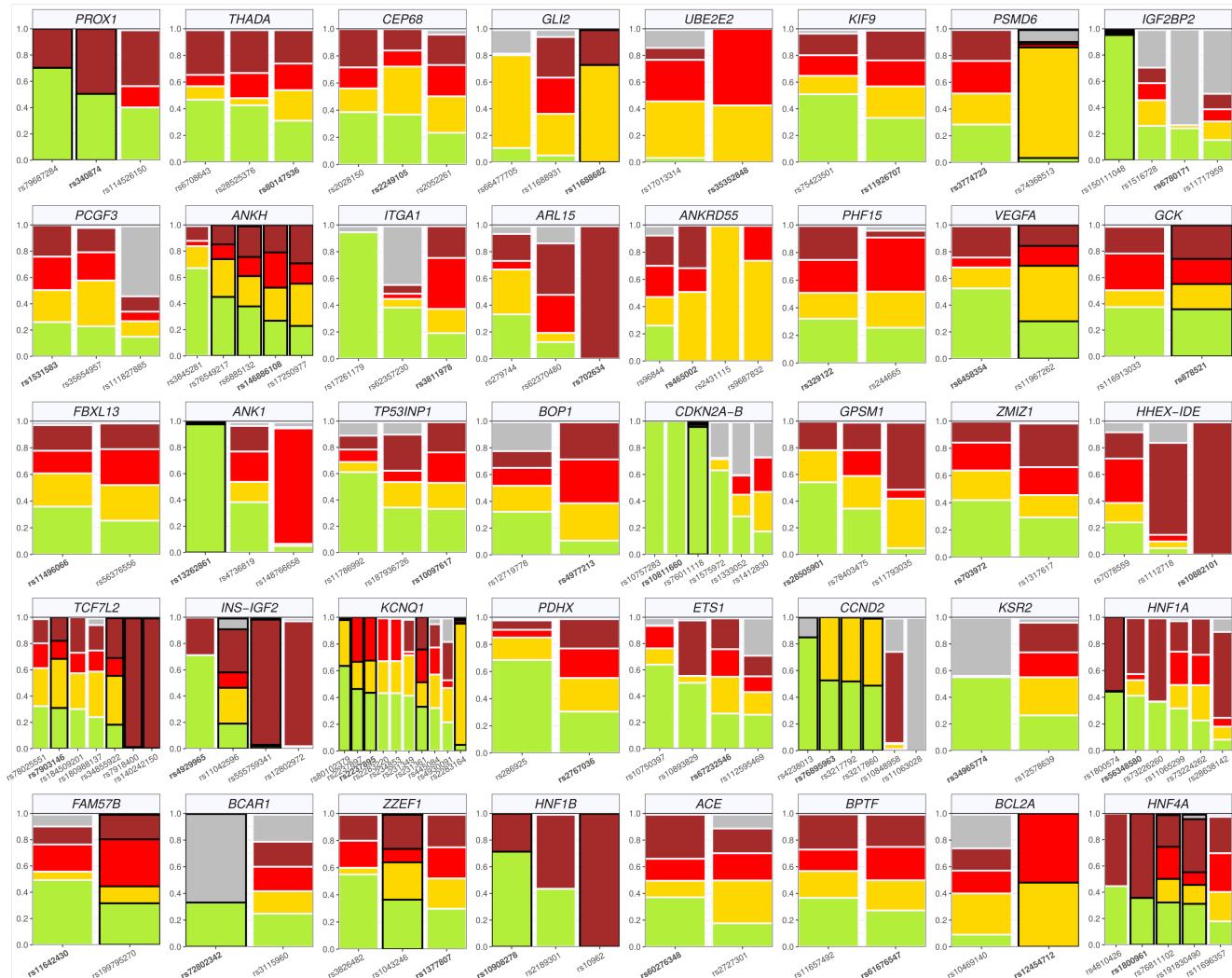


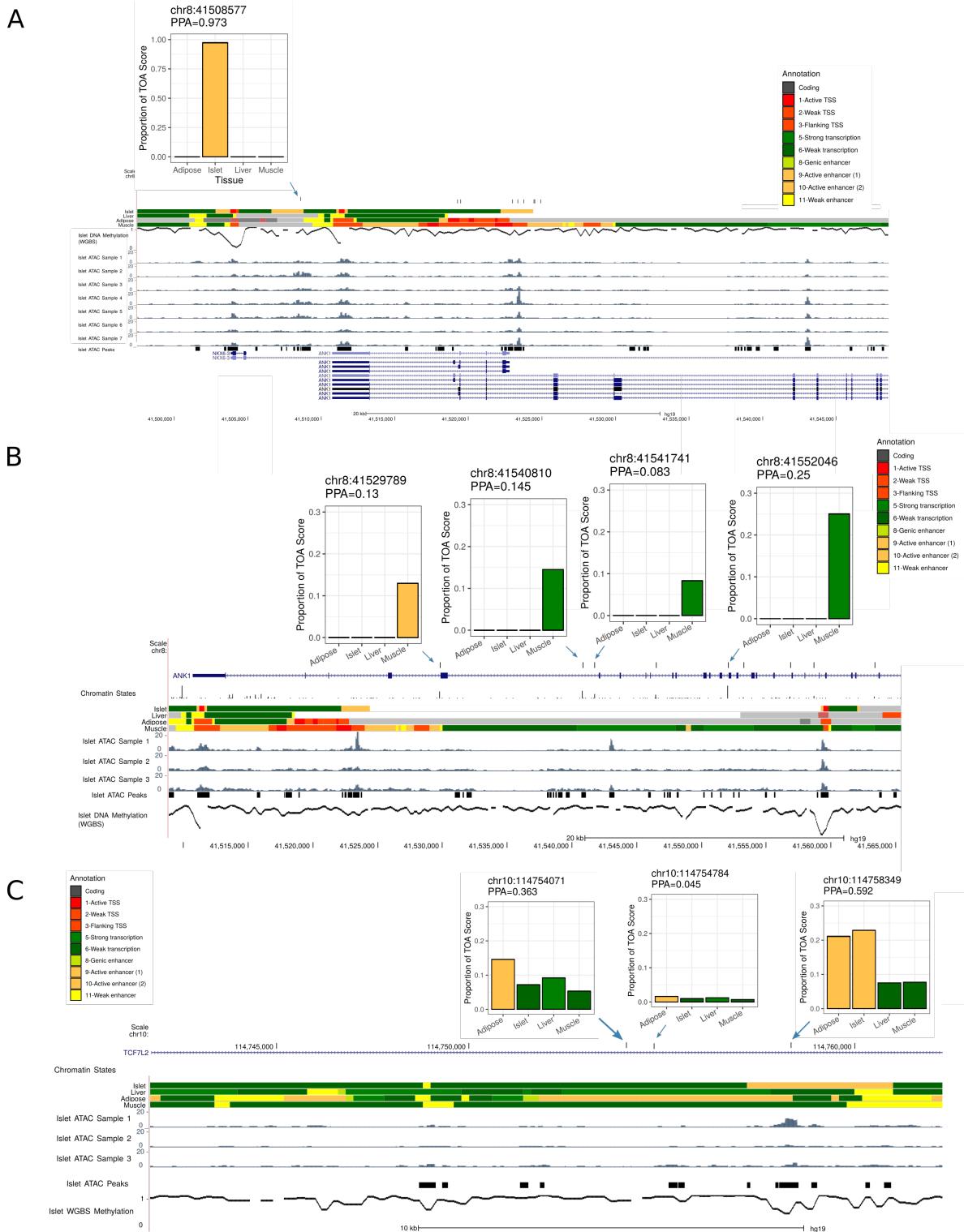
**Supplementary Figure 5.** Coexpression of proximal genes to tissue-assigned signals.



**Supplementary Figure 6. Comparison of sets of epigenomic- and physiology-assigned signals.**



**A****B****Supplementary Figure 8. Multiple tissues implicated by epigenomic scores at heterogenous loci.**



**Supplementary Figure 9.** Epigenomic profiles of fine-mapped signals at T2D-associated loci.