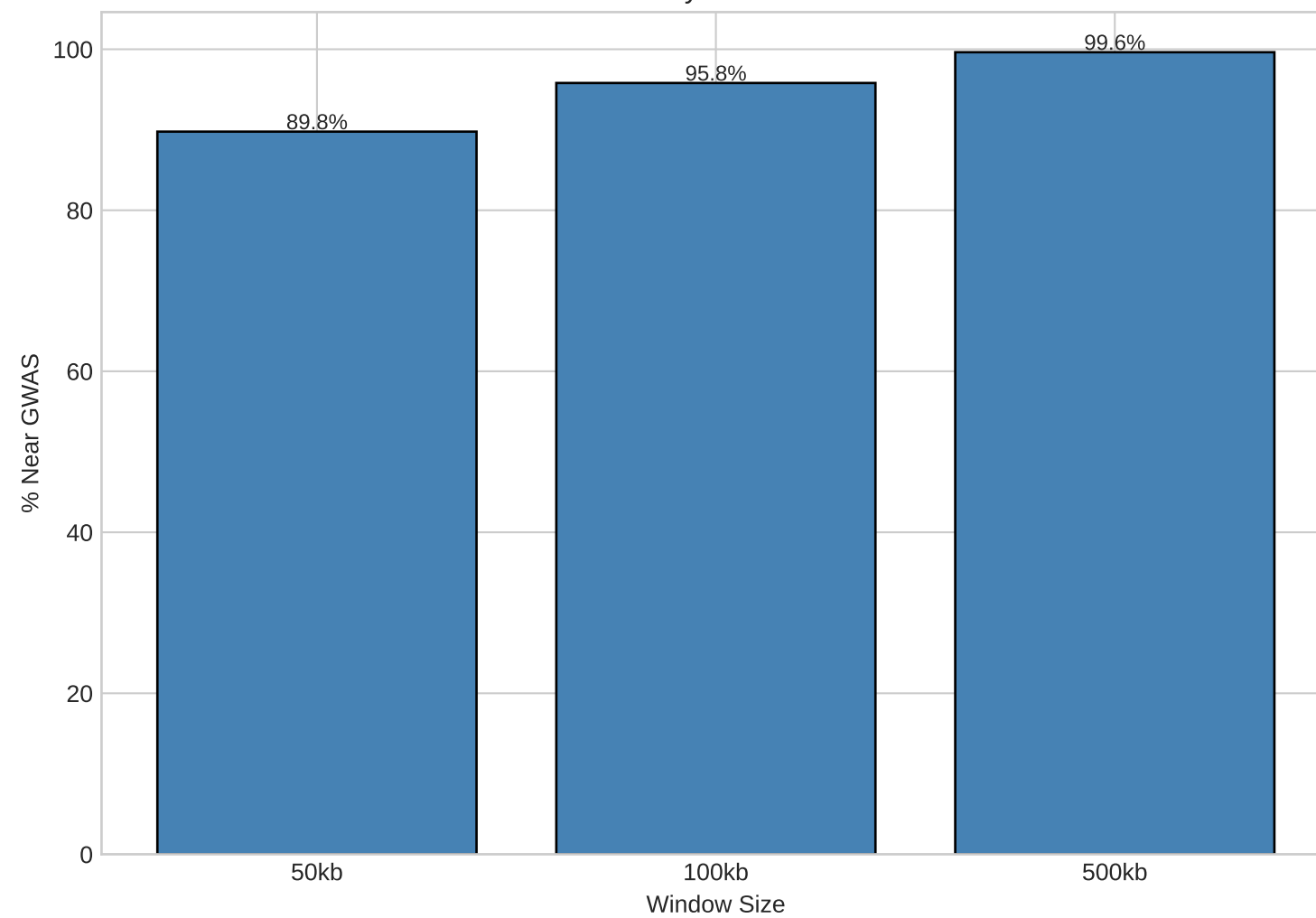
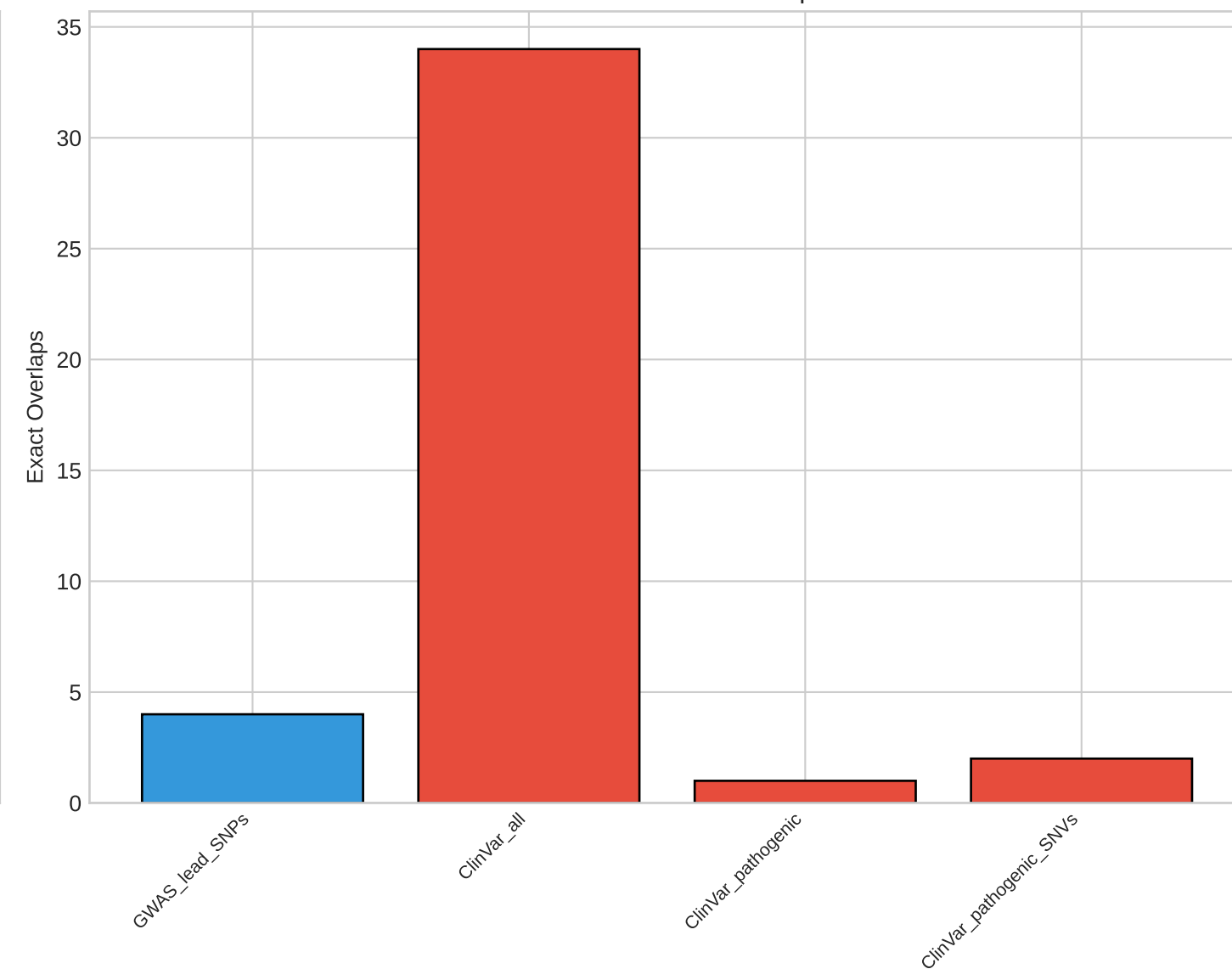


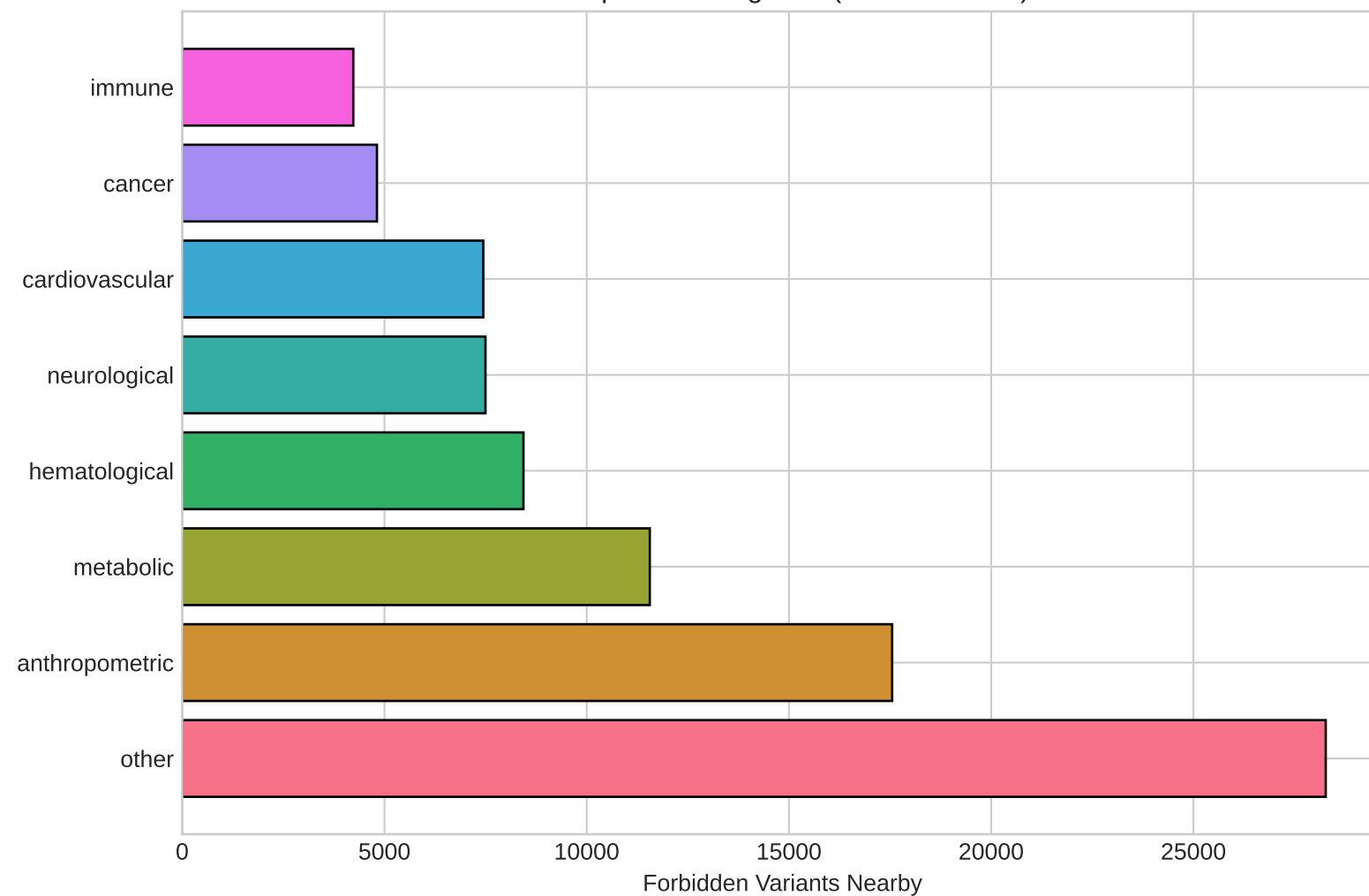
A. Proximity to GWAS Loci



B. Exact Position Overlaps



C. Top Trait Categories (100kb window)



D. Summary of Findings

KEY FINDINGS

Total Forbidden Variants: 29,957

PROXIMITY ANALYSIS:

- 95.8% within 100kb of GWAS loci

EXACT OVERLAPS:

- GWAS lead SNPs: 4
- ClinVar variants: 37

INTERPRETATION:

- Low exact overlap expected (forbidden variants don't exist in human populations)
- Proximity enrichment suggests forbidden sites cluster near disease-relevant regulatory regions