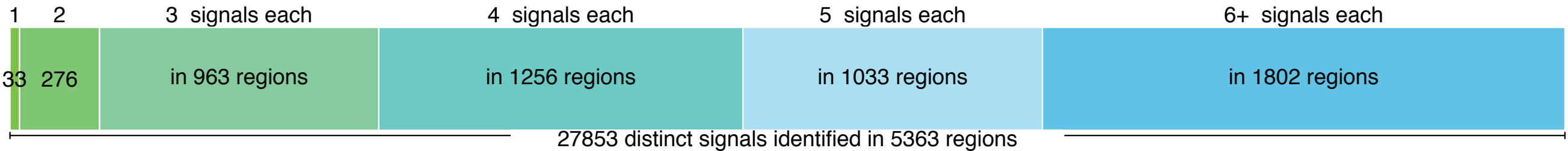
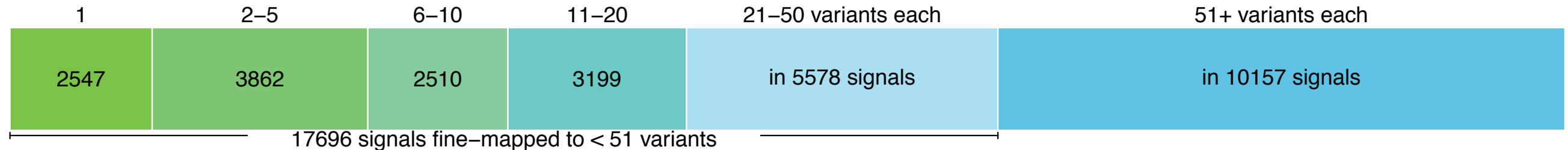


A. Summary of fine-mapping across all biomarkers

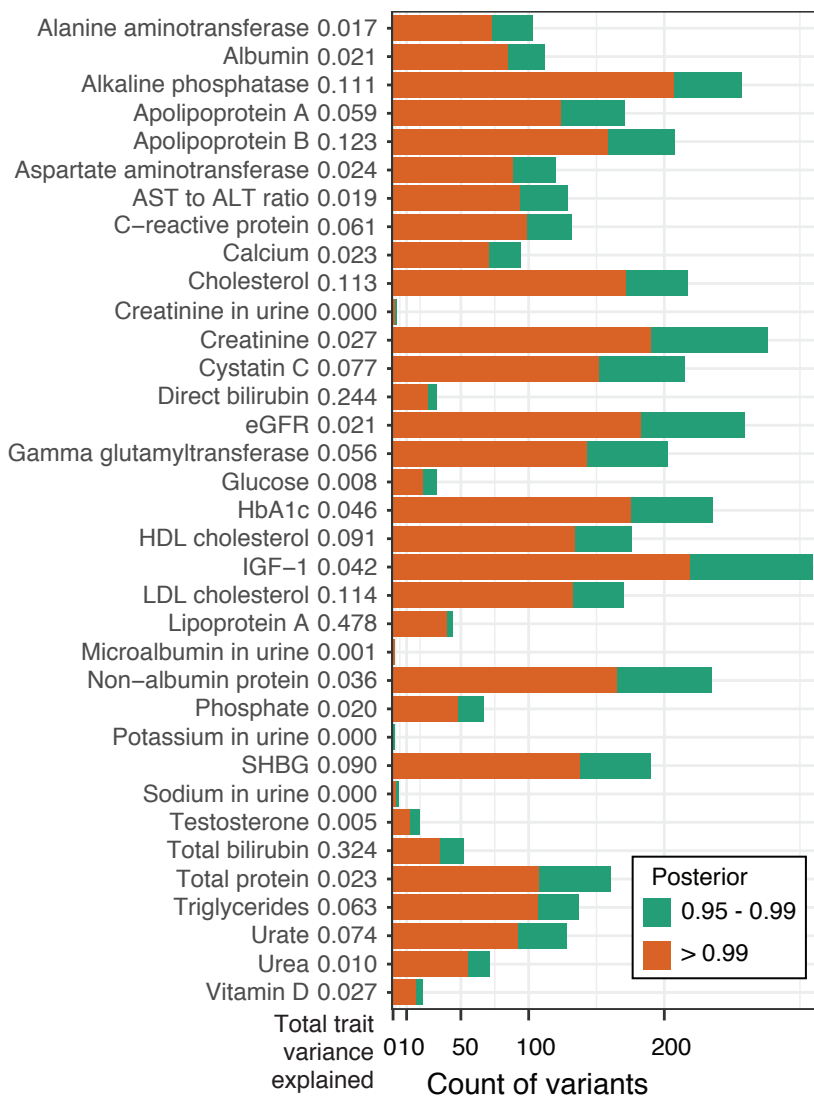
Number of distinct signals per region



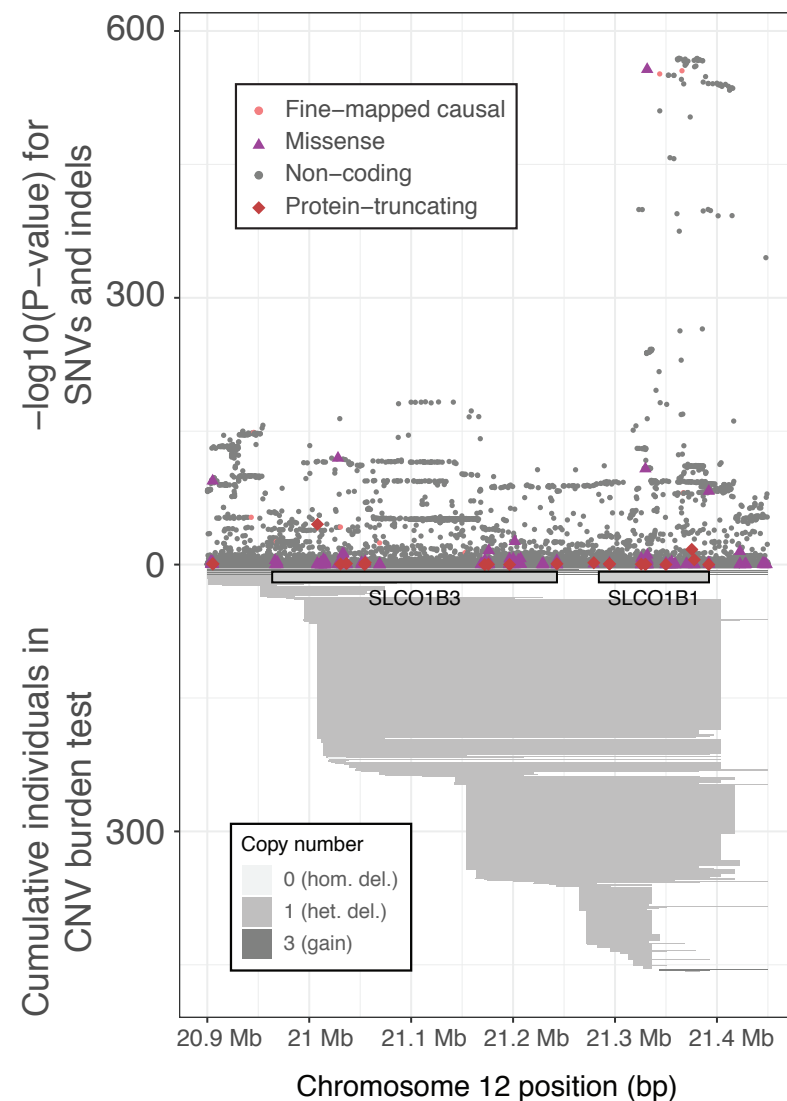
Number of variants in each signal



B. Number of fine-mapped variants per trait



C. Allelic series at SLCO1B1/SLCO1B3



D. Pleiotropy at HGFAC in common and rare variants

