

Supplementary Information for “*GIGYF1* loss of function is associated with clonal mosaicism and adverse metabolic health”

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Figure S1 | Relationship between bioinformatically predicted function and LOY association for *GIGYF1* and *CHEK2* moderate-impact variants. Y-axis shows the PAR-LOYq association of each variant assessed by absolute Z-score divided by minor allele count.

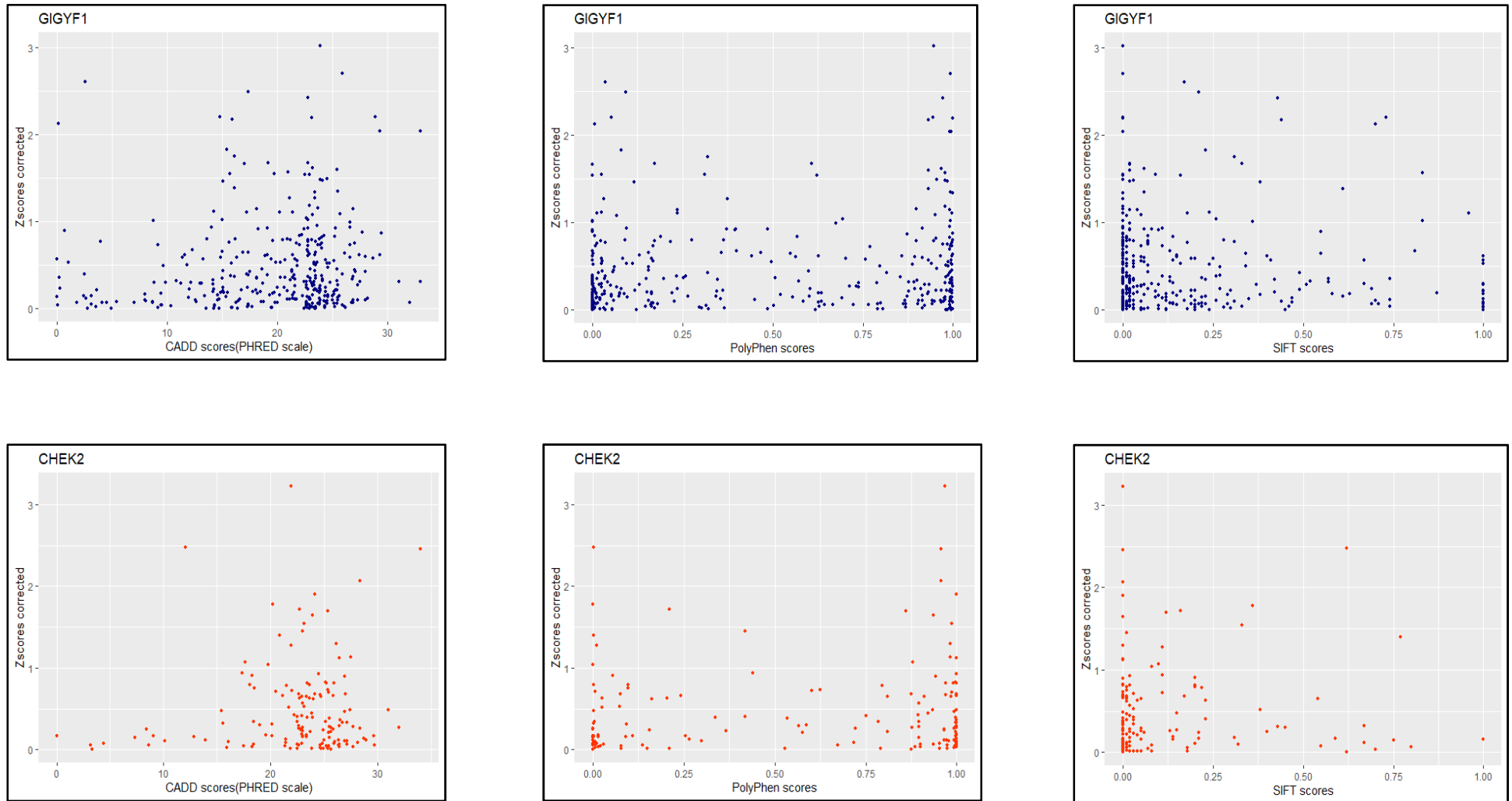


Figure S2 | Impact of GIGYF1 loss of function carriers on genetically-defined principal components. GIGYF1 carriers are highlighted in red, all other analysed samples in black. Analysis performed in maximum available sample-size (N=184,972).

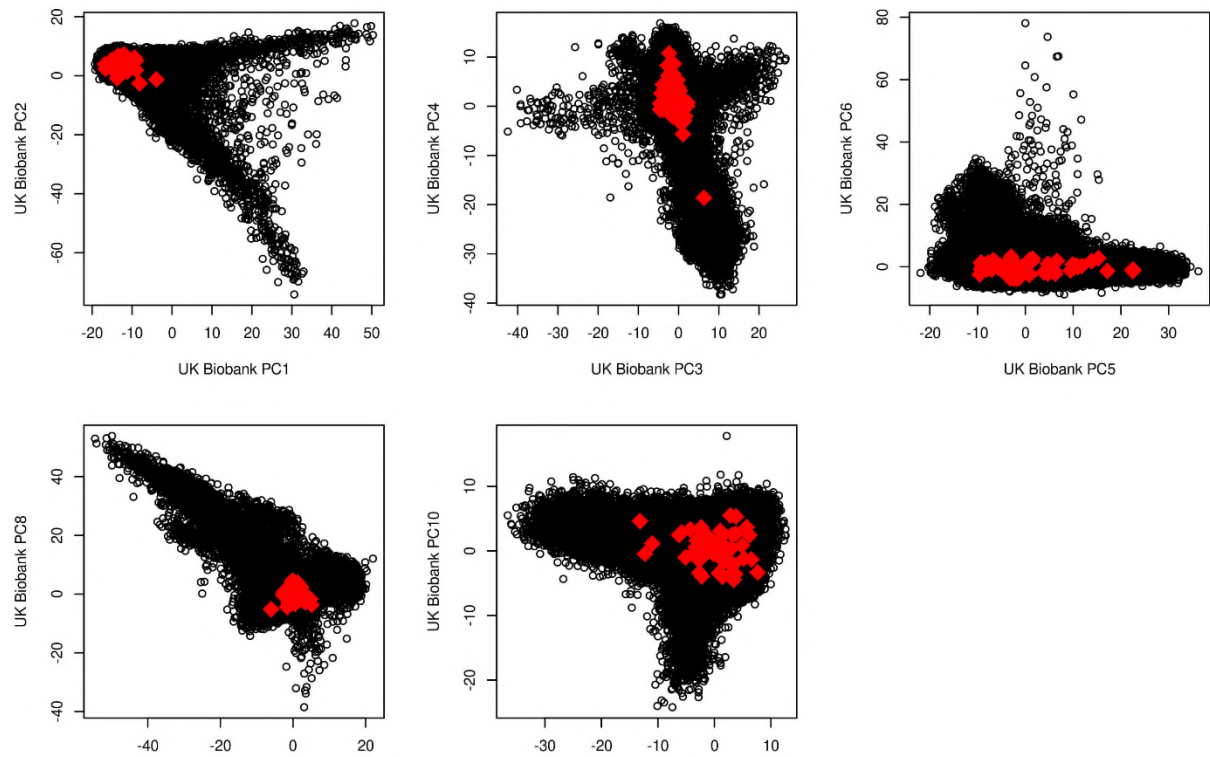


Figure S3 | Geographical distribution of GIGYF1 loss of function carriers by location of birth.
GIGYF1 carriers are highlighted in red, all other analysed samples in black. Analysis performed in maximum available sample-size (N=184,972).



Figure S4 | Regional association of common variants with Type 2 Diabetes, LOY and related traits in the region around GIGYF1 (+/- 500kb). Highlighted variants are the lead variant associated with T2D r2221781 (red) and lead eQTL for GIGYF1 rs221792 (purple).

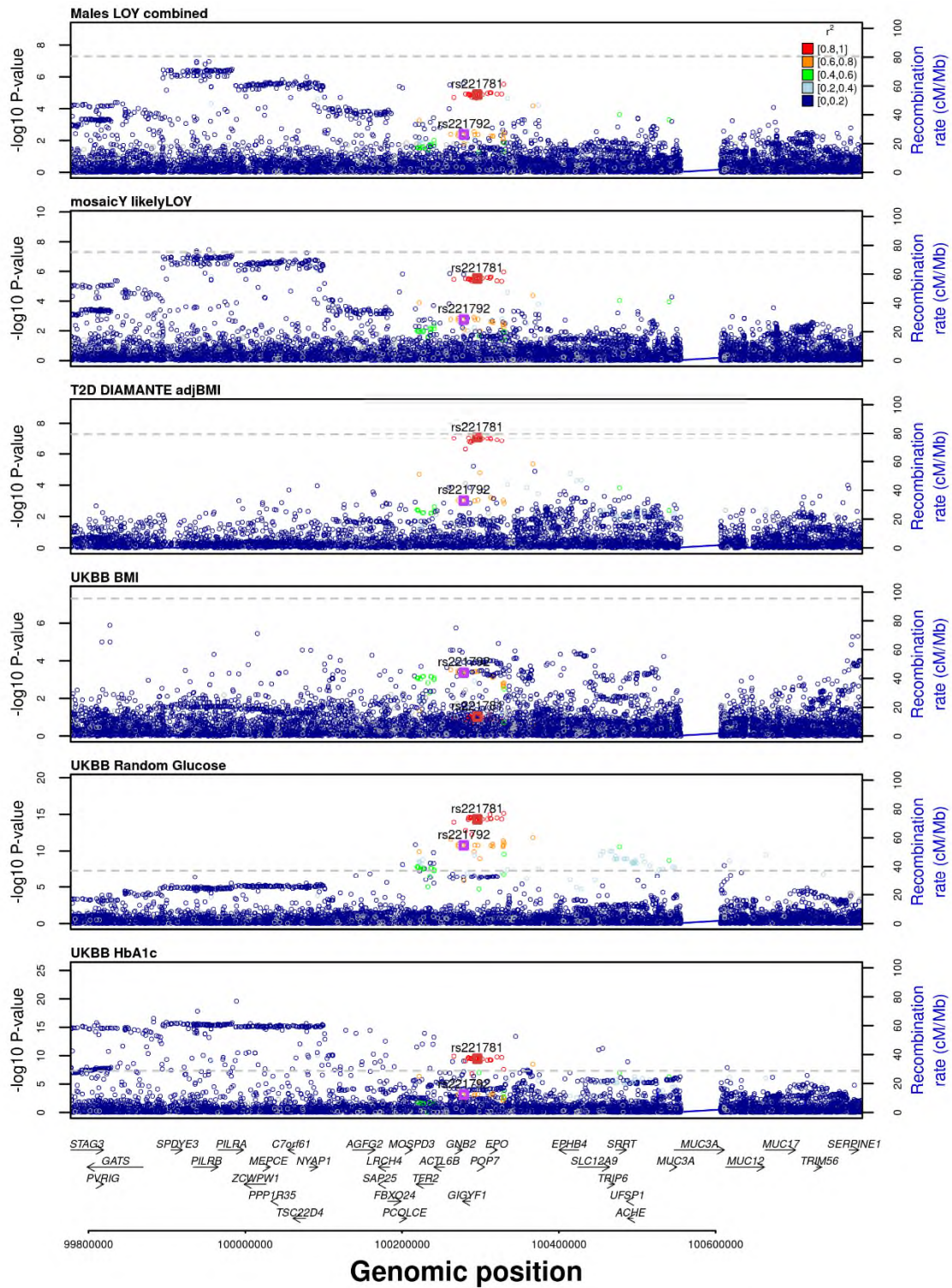


Figure S5 | Multi-tissue eQTL associations in GTEx for common variant rs221781. The solid pink line represents the null effect. Each square represents the beta estimate from a linear regression model of the variant against mRNA transcript abundance. Test statistic is a two-sided P-value and no correction for multiple testing has been made.

