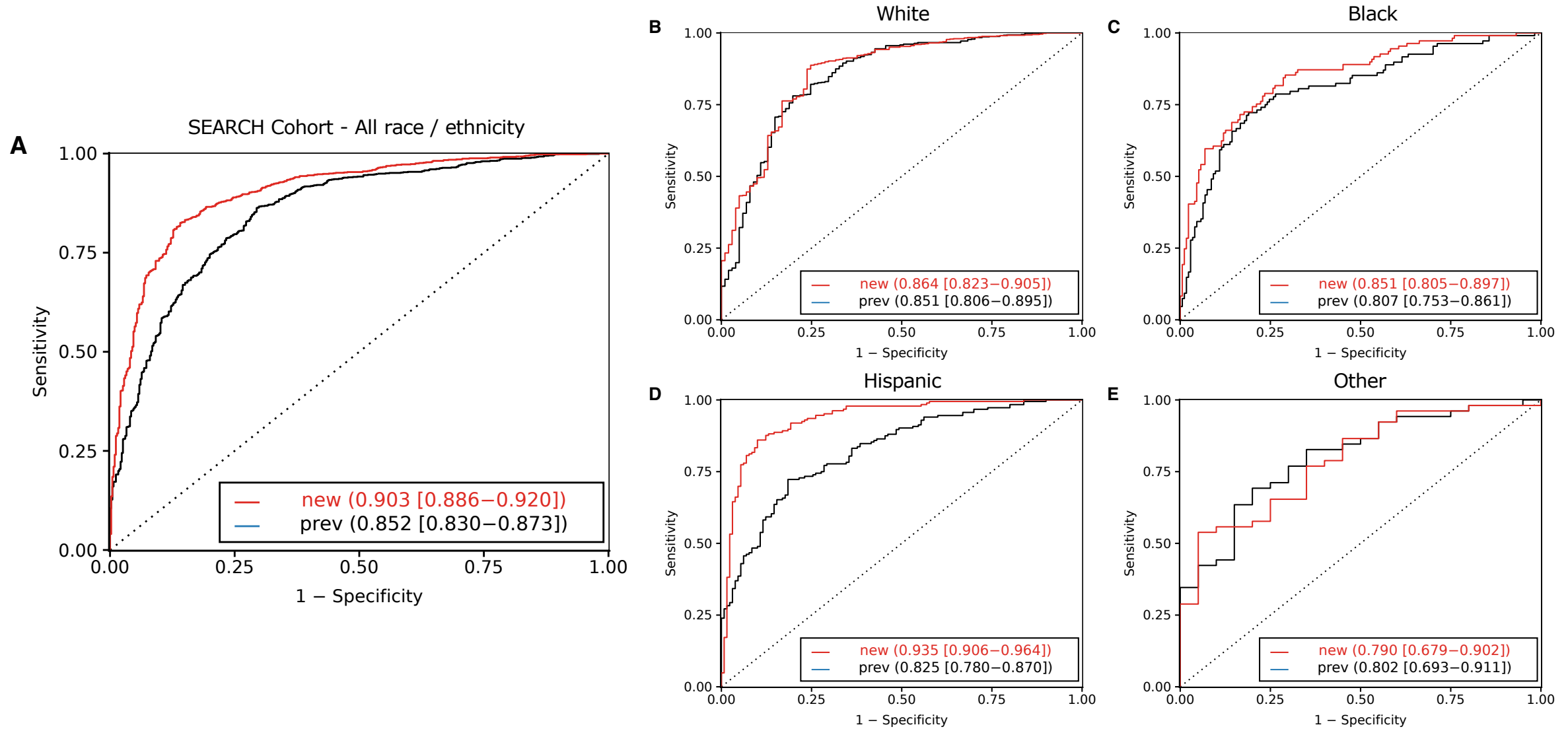


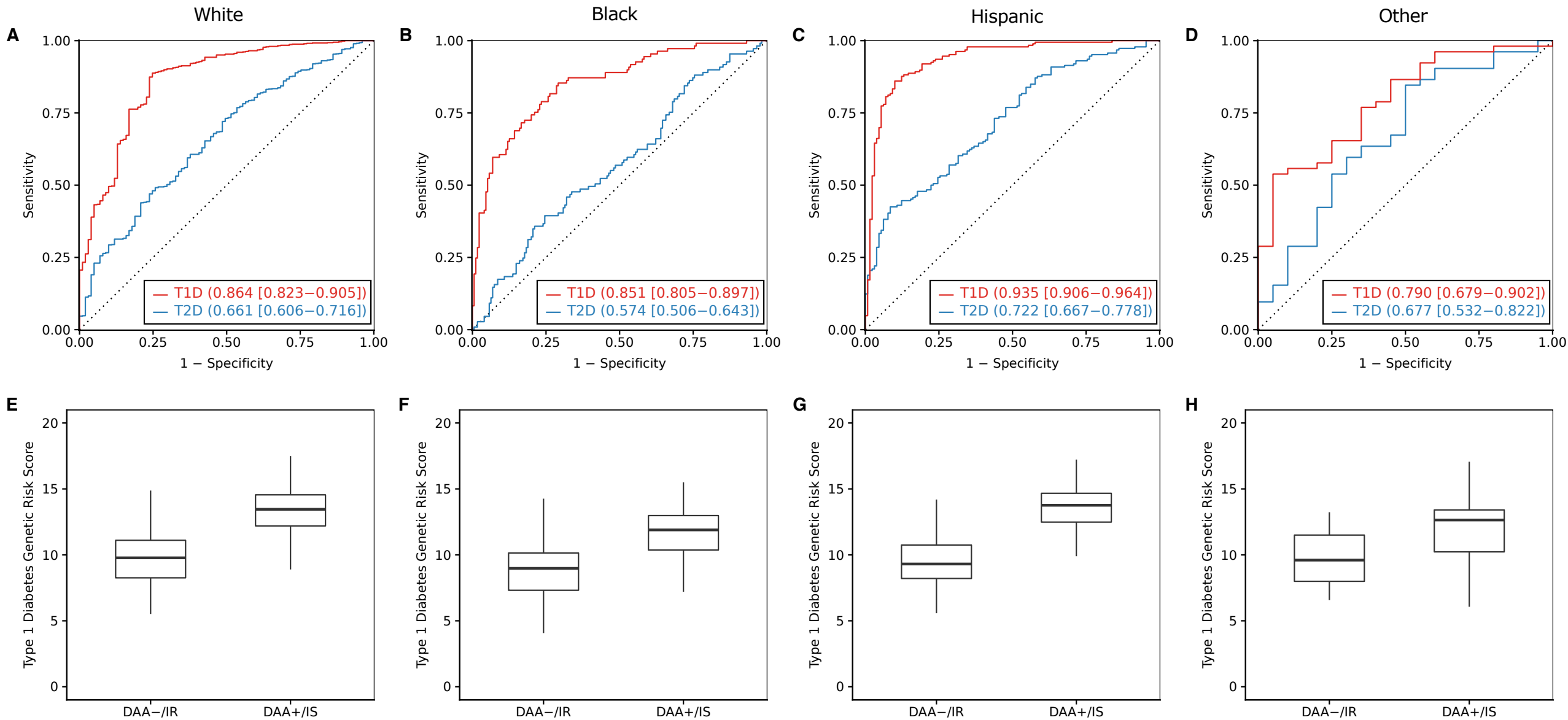


## Supplementary Figure 1 – ROC plots 30 SNP T1D GRS1 vs 67 SNP T1D GRS2



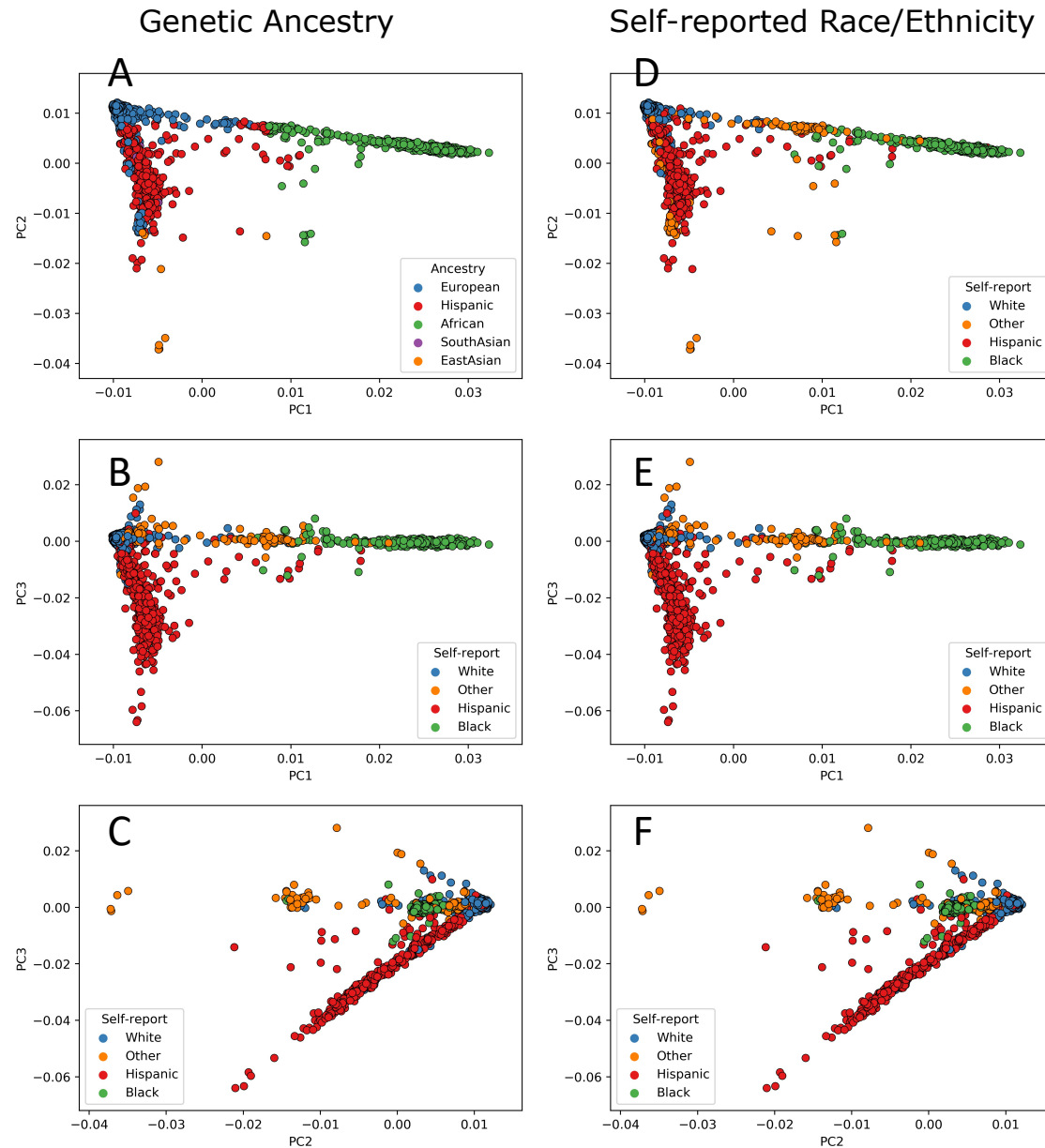
Supplementary Figure 1. ROC AUC comparison of original 30 SNP type 1 diabetes genetic risk score (T1D GRS1) (black lines) against improved 67 SNP T1D GRS2 (red lines) to discriminate diabetes autoantibody positive insulin sensitive (DAA+/IS) from diabetes autoantibody negative insulin resistant (DAA-/IR) stratified by self-reported race/ethnicity.

# Supplementary Figure 2 – ROC plots and box plots by race



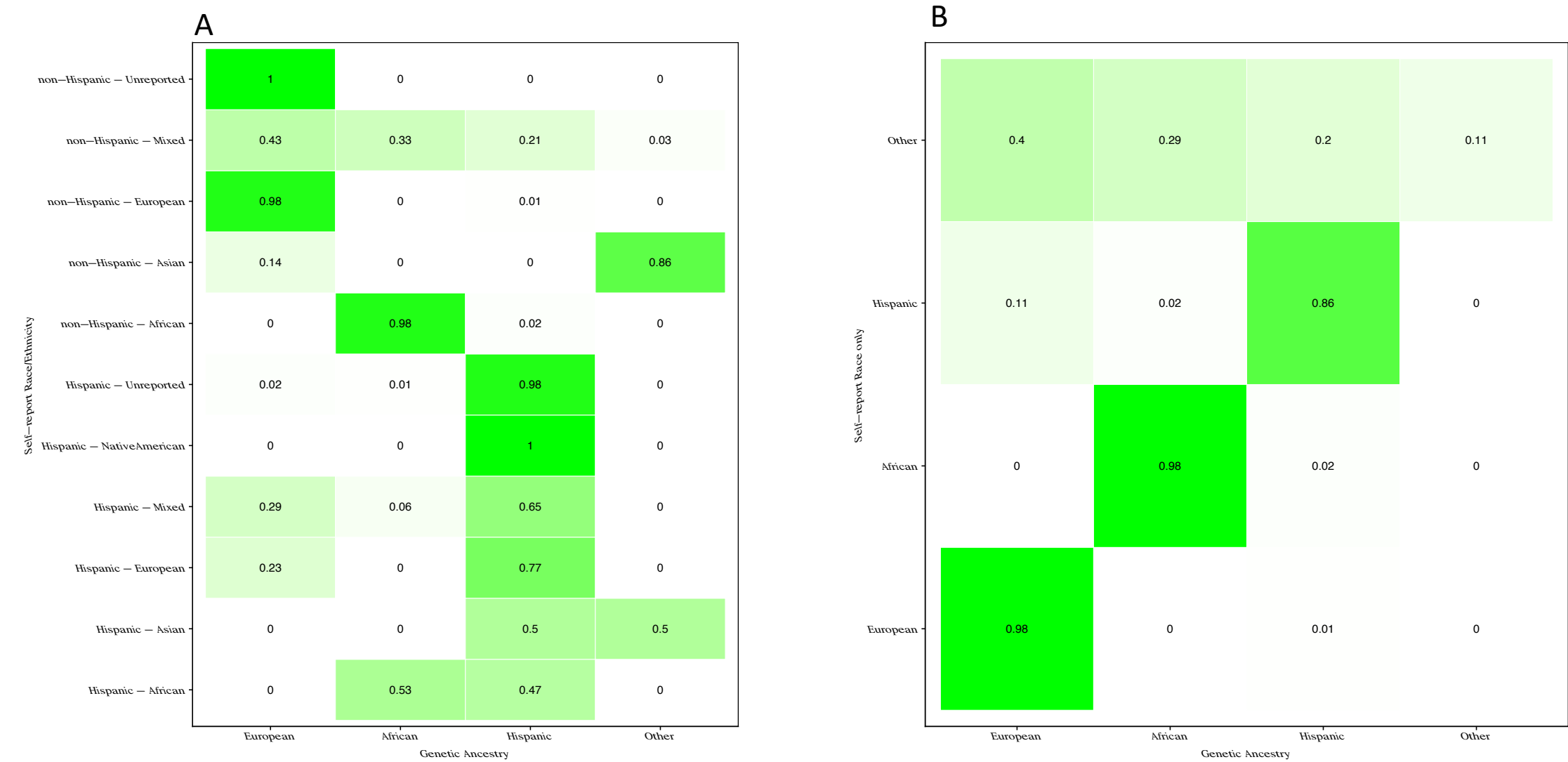
Supplementary Figure 2. ROC AUC comparison of 67 SNP type 1 diabetes genetic risk score (red lines) against T2D GRS (blue lines) to discriminate diabetes autoantibody positive insulin sensitive (DAA+/IS) from diabetes autoantibody negative insulin resistant (DAA-/IR) stratified by self-reported race/ethnicity (A-D). E-H display box plots of 67 SNP T1D GRS comparing DAA+/IS and DAA-/IR, stratified by self reported ethnic groups.

## Supplementary Figure 3 – Principal Components Analysis of ethnicity



Supplementary Figure 3. Result of principle components analysis for principle components 1-3, with genetically defined ethnicity (panels A-C) compared to self reported ethnicity (panels D-F)

# Supplementary Figure 4– Concordance of ethnicity



Supplementary Figure 4. We compared genetically defined ancestry to self-reported race/ethnicity. Genetically defined most likely ancestry is on the x axis, Each row of the y axis represents a self-defined ancestry and totalling 1, with groups collapsed into 3 major racial ethnic categories (B) showing very high concordance with genetically defined ancestry.

## Supplementary Figure 5 – Z-score to raw values T1D

Within cohort Z-score normalization (T1D GRS2)

$$\bar{x} = 12.230, \bar{s}_x = 2.559$$

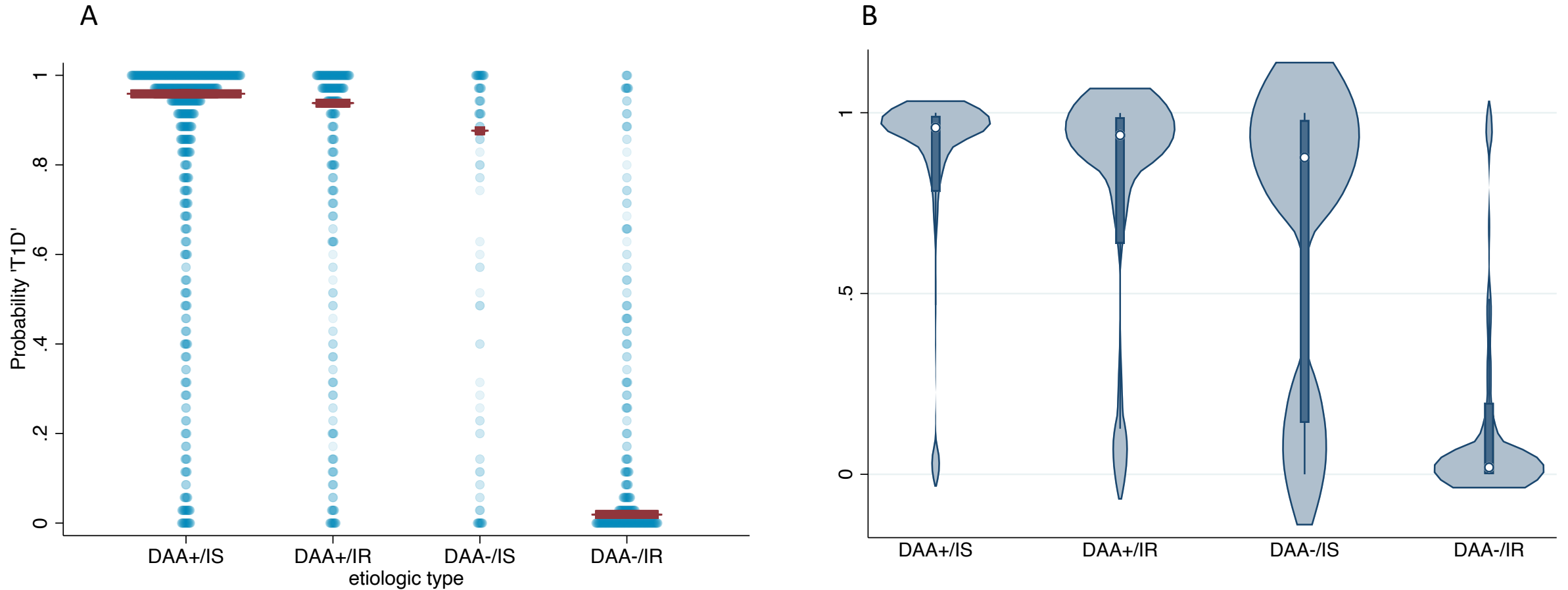
$$z = \frac{(x - \bar{x})}{\bar{s}_x}$$

Within cohort Z-score normalization (T2D GRS)

$$\bar{y} = 11.177, \bar{s}_y = 0.339$$

$$z = \frac{(y - \bar{y})}{\bar{s}_y}$$

## Supplementary Figure 6



Supplementary Figure 6. Probability of “T1D” based on gaussian mixture model assuming two distributions defined by DAA+/IS and DAA-/IR (see methods and Figure 3). 6A shows a dotplot with blue dots for each individual (red line = median), when stratified by etiologic type. 6B shows the same data represented by median (white circles), interquartile range (bars), range (whiskers), and density plot (violins)