Figure 1 - Manhattan plots of GWAS before and after adjustment for GRS: Top row, genome-wide GWAS: Panel A, unadjusted; Panel B, after adjusting for GRS1; Panel C after adjustment for GRS2. Bottom row, high resolution plot of association scores for the full HLA region on Chr 6q: Panel D, unadjusted; Panel E, after adjustment for GRS1; Panel F, after adjustment for GRS2.
Figure 2- ROC curves comparing the ability of GRS1 and GRS2, and their components, to discriminate T1D. For each pair of curves in a panel, the figures show ROC AUCs and the p-value for their comparison by the DeLong algorithm. A HLA DR-DQ haplotypes and interaction terms, for GRS1 vs GRS2 in the T1DGC. B Both non-DR-DQ HLA and non-HLA loci, for GRS1 vs GRS2 in the T1DGC. C Full GRS1 versus full GRS2 in the T1DGC discovery dataset. D HLA DR-DQ haplotypes and interaction terms, for GRS1 vs GRS2 in the UK Biobank. E Both non-DR-DQ HLA and non-HLA loci, for GRS1 vs GRS2 in UK Biobank. F Full GRS1 versus full GRS2 in UK Biobank.
Figure 3- Comparison of the ability of GRS1 (left) and GRS2 (right) to discriminate type 1 diabetes (red) from controls (blue) in 3A and 3B respectively. Comparison of the ability of GRS1 (left) and GRS2 (right) to discriminate type 1 diabetes (red) from type 2 diabetes (yellow) in 3C and 3D respectively. Note the similar distribution of T1D GRS2 scores in the background population and in T2D cases.