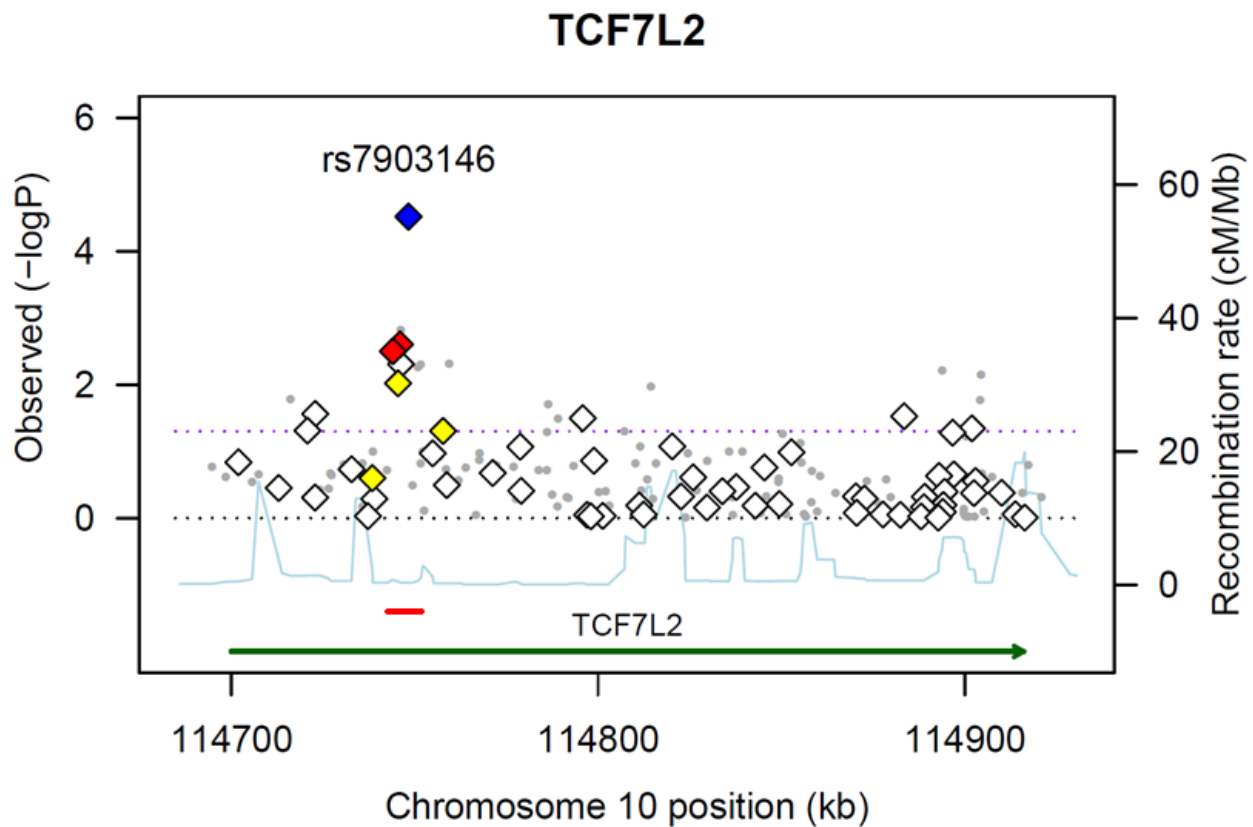


Supplementary Figure 1. Regional association plot for *TCF7L2* +/- 10kb (C10:114,689,999-114,926,060). SNPs analyzed are plotted with their $-\log_{10}$ P-values of association with T2D versus the genomic position (NCBI Build 36.1). The *TCF7L2* gene position was taken from the UCSC genome browser (green) and the core region of association (C10:114,744,078-114,748,339) analyzed by direct sequence analysis is depicted in red. SNPs genotyped on the Affymetrix 6.0 array are denoted with diamonds. The most significantly associated SNP (rs7903146) is depicted as a blue diamond with its correlated proxies (red= $r^2 \geq 0.80$; orange= $0.80 > r^2 \geq 0.50$; yellow= $0.50 > r^2 \geq 0.20$). SNPs imputed from a HapMap phase II hybrid panel (1:1, YRI:CEU) are depicted as gray circles. Estimated recombination rates from HapMap are plotted in the background to depict the LD structure in the region.



Supplementary Figure 2. Regional association plot for *TCF7L2* +/- 10kb (C10:114,689,999-114,926,060). SNPs analyzed are plotted with their $-\log_{10}$ P-values of association with T2D versus the genomic position (NCBI Build 36.1). The *TCF7L2* gene position was taken from the UCSC genome browser (green) and the core region of association (C10:114,744,078-114,748,339) analyzed by direct sequence analysis is depicted in red. SNPs genotyped on the Affymetrix 6.0 array are denoted with diamonds. The most significantly associated SNP (rs7903146) is depicted as a blue diamond with its correlated proxies (red= $r^2 \geq 0.80$; orange= $0.80 > r^2 \geq 0.50$; yellow= $0.50 > r^2 \geq 0.20$). SNPs imputed from the 1000 Genomes Project YRI dataset are depicted as gray circles. Estimated recombination rates from HapMap are plotted in the background to depict the LD structure in the region.

