



Figure S4. Chromatin accessibility changes associated with progression to clinical T1D. Normalized read coverage plots of ATAC-seq and RNA-seq libraries around the *CAPG* (A) and *SLAMF7* (B) loci in progressors (red) and non-progressors (turquoise). DARs are indicated by grey rectangles at the right-hand side. Boxplot showing normalized (logCPM) chromatin accessibility data (non-adjusted for age) in differentially accessible regions linked to *CAPG* (C) and *SLAMF7*. pHiC shows promoter-enhancer interactions in primary CD4⁺ T cells predicted by promoter-capture Hi-C (pHiC) (34) overlapping the DAR. ChromHMM shows ChromHMM tracks from Roadmap for primary human CD4⁺ T cells. Abbreviations are: TssA, active Transcription Start Site; TssAFlnk, flanking active Transcription Start Site; TssBiv, bivalent/poised TSS; Tx, strong transcription; TxFlnk, transcription at gene 5' and 3'; TxWk, weak transcription; BivFlnk, flanking bivalent Transcription Start Site/enhancer; Enh, enhancers; EnhBiv, bivalent enhancer; EnhG, genic enhancers; Het, heterochromatin; Quies, quiescent/low; ReprPC, repressed polycomb; ReprPCWk, weak repressed polycomb; ZNF/Rpts, ZNF genes and repeats. (D). Shown are the median (central horizontal line), interquartile range (boxes), values of the upper and lower quartiles (whiskers), outliers beyond 1.5 IQR (circles).