



**SUPPLEMENTARY FIGURE 4. Enrichment of refined islet regulatory states in FG GWAS data** A) FGWAS Log2 Fold Enrichment including 95% CI ( $\log_2FE$ , x-axis) of all chromatin states (y-axis) in FG GWAS regions. In addition, CDS is shown to also include the effect of protein-coding regions. Significantly enriched annotations are shown in black. B) FG FGWAS maximum likelihood model determined through cross-validation.  $\log_2FE$  and 95% CI (x-axis) of annotations included in the maximum likelihood model (y-axis) are shown. C) Single feature  $\log_2FE$  (x-axis) for different enhancer states (grey panels) defined from different combinations of epigenetic marks (y-axis) including ChIP+ATAC+Meth, ChIP+ATAC, ChIP+Meth and ChIP-only. Enhancers are defined as follows: Strong enhancers are marked by both H3K4me1 and H3K27ac, weak Enhancers are defined by H3K4me1 only, gene enhancers are marked by H3K4me1 and H3K36me3, other enhancers are marked by H3K4me1, H3K4me3 and H3K27ac and are often referred to as TSS upstream regions (only included in the FGWAS T2D model for ChIP-only and ChIP+Meth chromatin states). D) Single feature  $\log_2FE$  including 95% CI (x-axis) results of various annotations derived from ChIP-seq (ChIP-only), ATAC-seq, WGBS methylation status and CDS are shown. E) Maximum likelihood FGWAS nested model combining ChIP-only, ATAC-peaks and LMR states (y-axis) showing  $\log_2FE$  enrichment (x-axis) which was used for the LRT in Supplementary Figure S3F. F) Chi-square distribution (black curved line) with the indicated results of a maximum likelihood ratio test based on the maximum likelihood difference between a model including LMRs or ATAC-seq peaks compared to the ChIP-only model. The dashed line indicates significance (P-value<0.05). For all FGWAS enrichment plots the axis has been truncated at -6 to facilitate visualisation and accurate values are provided in the supplementary tables.