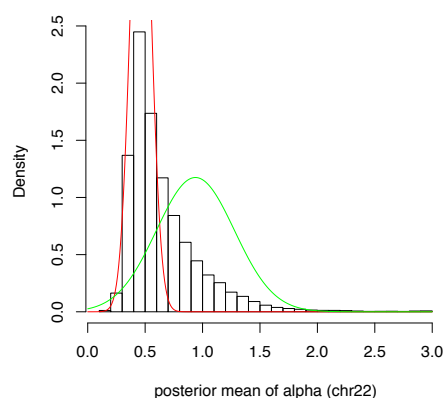
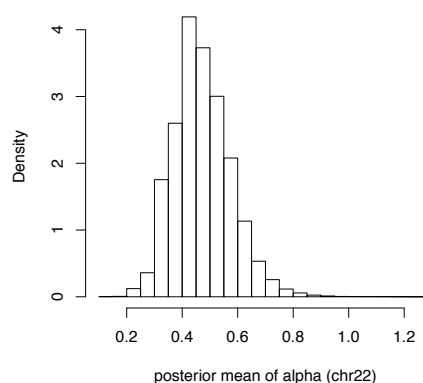


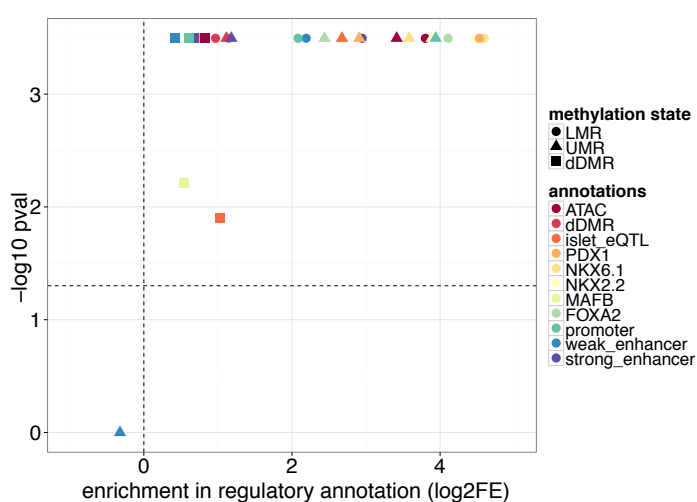
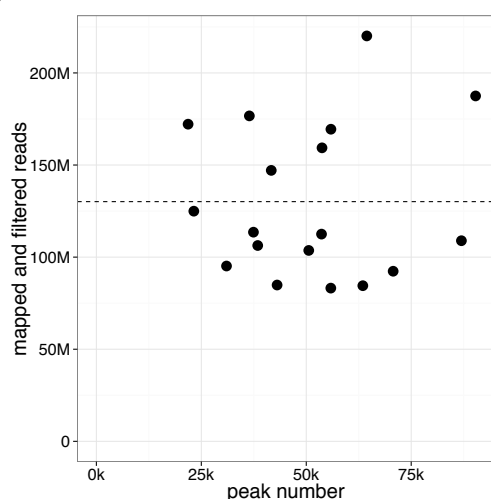
A



B



C



SUPPLEMENTARY FIGURE 2. Identification and removal of Partially Methylated Domains (PMDs) A-B) Density distribution of the alpha value (A) before and (B) after removing PMDs (green curve in (A)) on chromosome 22. Alpha values represent a summary statistic derived from DNA methylation of windows of 100 CpGs and represents an indication of the polarisation status of methylation values in the genome which is expected to contain either highly methylated or unmethylated regions. Distributions with $\alpha < 1$ indicate methylation levels that are bimodal with either 0 or 1 methylation. $\alpha = 1$ corresponds to a uniform distribution of methylation; and distributions with $\alpha > 1$ tend to have primarily intermediate methylation levels. The red and green curve in (A) represent the non-PMD (red) and PMD regions (green) in the genome. C) Number of peaks (x-axis) and mapped and filtered reads (y-axis) per ATAC-seq islet preparation. The dashed line indicates the mean read number. D) \log_2 Fold Enrichment (\log_2FE , x-axis) and associated $-\log_{10}$ Bonferroni adjusted P-values (y-axis) of LMRs (circle), UMRs (triangle) in various islet annotations (colours) is shown. These annotations include islet chromatin states, islet relevant TFBS (FOXA2, MAFB, NKX2.2, NKX.61, PDX1), islet eQTLs, WGBS derived T2D-associated islet disease DMRs (dDMRs) and ATAC-seq open chromatin peaks. dDMRs (square) were also tested for enrichment in the aforementioned islet regulatory annotations. The results cluster near $-\log_{10}$ P-value of 3.5 since most Bonferroni adjusted P-values were more extreme than 0.00032.