



SUPPLEMENTARY FIGURE 6. A) Predicted *PAX6* Transcription factor binding motif likely affected by allelic imbalance of the variant rs10842991 (highlighted in purple). B) The *ADCY5* rs11708067 risk A allele was associated with increased methylation levels (y-axis, while genotypes are shown on the x-axis). C) Chromatin Capture (Capture C) in the human beta-cell line EndoB1H1 showed interactions between the *ADCY5* promoter (peak) and the flanking regions of the promoter. The x-axis shows the position on the chromosome in Mb while the y-axis indicates mapped reads per fragment. D) Chromatin Capture (Capture C) in the human beta-cell line EndoB1H1 focussed at the genomic region (~47kb) near the variant rs11708067 (highlighted) and variants in high LD ($r^2 > 0.8$) with it (variants are depicted as black dots). Fragments containing rs11708067 (red) or other high LD variants (dark grey) are highlighted. The x-axis shows the position on the chromosome in bp while the y-axis indicates normalised mapped reads per fragment. The two fragments with P-values have a significant (FDR < 0.05) number of normalised read counts over background: The fragment with the P-value on the left (in red) contains rs11708067 while the fragment with the P-value on the right harbours rs2877716, rs6798189, rs56371916.