



ESM Fig. 3 Promoters in islets have distinct chromatin state lineages. **(a)** Heatmap of the total read counts for H3K4me1, H3K4me3, H3K9me3, and H3K27me3 in ESCs, liver and islets, in +/-2 kb regions centered on the TSS of promoter regions associated with poised enhancers. The data are segregated into the identified promoter clusters (p1-p11) and the chromatin state for each cluster is indicated. **(b)** Heatmap of the fraction of poised enhancers in each enhancer cluster that is associated with the promoters in each promoter cluster. Darker blue is more deprived, and darker red is more enriched. **(c)** We next compared the frequency with which enhancers in each enhancer cluster (e1-e9) were associated with promoters in each promoter cluster (p1-p11) in ESCs and islets. **(d)** Box-whisker plot of gene expression levels in ESCs (light blue), Liver (dark blue), and in Islets (red) for genes associated with the indicated promoter clusters. **(e)** Box-whisker plot of specificity to islets as compared to 203 other mouse SAGE libraries for genes associated with the indicated promoter clusters. **(f)** Fold enrichment of significantly enriched GO and KEGG terms associated with genes with promoters in the indicated promoter clusters. Statistically significant differences were detected using a Kruskal-Wallis non-parametric test with a Dunn's multiple comparison correction, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$