Figure 1 –Clustering on WT (todo qiong/sent table and no of clusters)

Figure 2 – Plot lines WT for Hnf6, Pdx1, Foxa1, Nkx2-2, Nkx6-1, Ptfi1(to do qiong)

Figure 3- De-novo motifs estimated from the sequence (100bps) around the top 500 Hnf6 peaks. Number represents the proportion of hits of the motif in the Hnf6 peaks.

Figure 4 – ChIP-Seq profiles of Hnf6 , Foxa2 , Pdx1 and Gata6 on PP cells around Pdx1, Hnf6, Nkx2-2 and Nkx6-1 genes.

Figure 5 – Genes in the vicinity of Hnf6 peaks. Out of the 5123 genes close to an Hnf6 peak (20kbs from the TSS); 780 are associated to clusters with ES and/or DE specific expression, while 1437 genes are associated to clusters with higher expression in pancreas progenitors and latter differentiation stages (III, VIII and IX).

Figure 6 – Co-binding statistics of Hnf6, Foxa2, Ptx1 and Gata6 peaks. (todo ivan)

Figure 7 – A statistical test accessing the number of observed (and expected) Hnf6 peaks around genes in each clusters indicates an significant enrichment of Hnf6 peaks closes to cluster VIII and IX (adjusted p-value > 0.005; z-test), which have high expression in both PE, PP and BC cell stages. On the other hand, genes with expression specific to ES and/or DE stages (cluster I, V) are significantly depleted of Hnf6 peaks (adjusted p-value < 0.005; z-test).

Figure 8 – PCA plot with 2-3 clones of wild type (WT) cells and cells with a homozygous (Hom) and heterozygous (Het) mutations in the Hnf6 gene. While all clones of ES and DE cells group together there is a clear tendency of mutants PE and PP cells towards ES cells.

Figure 9 - Genes up (715) or down (561) expressed in both Homozygous and Heterozygous clones during PE and PP stage. GO enrichment analysis indicates up regulated genes are associated to embryonic development, while down regulated genes are associated to pancreatic development (todo qiong).

Figure10 - A statistical test accessing the number of observed (and expected) Hnf6 peaks around genes in up/down regulated in Heterozygous and Homozygous clones (compared to WT). We observe an enrichment of Hnf6 peaks in genes down-regulated on Hnf6 Het. (PE, PC, BC) and genes down-regulated in Hnf6 Hom. (PE, PP; adjusted p-value < 0.0001; z-test). Inversely, there is a depletion of Hnf6 peaks in the vicinity of gene UP regulated on PE Het. and Hom. clones (adjusted p-value<0.05; z-test).

Figure 11 – ChIP-Seq profiles of Hnf6 , Foxa2 , Pdx1 and Gata6 on PP cells around selected genes and expression profiles of PE and PP clones (todo qiong/ivan).

Great Analysis – I performed the analysis for 500, 1000, 2500 and 5000 top Hnf6 peaks. It is very interesting that the top p-value term is “Transcription factors expressed in progenitors of exocrine pancreatic cells.” This includes the following factors (FOXA2, HNF1B, HNF4A, NR5A2, ONECUT1, PROX1, SOX9). We can make a plot out of this, once you select interesting condition to look at.