**Analyses for the CSHL poster**

By Tuuli Lappalainen April 25, 2012

Many of these analyses are already done, and doing the rest within a week is realistic. However, not all of this is needed for the poster – it’s fine if some of these don’t work out.

1. Introduction, study design
2. mRNA QC

* PCA of 5 replicates before and after normalization
* Numbers: variation between labs / between samples

1. eQTLs

* Numbers of eQTLs, eQTL sharing
* Indel enrichment in eQTLs?
* Trans-eQTL analysis of SVs (run some SNPs as a null)?
* Stats if we can get close to causal variants

1. sQTLs

* Numbers of sQTLs, sQTL sharing
* Example barplot
* Overlap with eQTLs??

1. Overlap of QTLs and functional elements of the genome

* Enrichment plot (horizontal boxplot)

1. ASE

* Basic stats
* ASE frequency versus effect size
* ASE distance MDS plot + genetic distance + expression distance
* Epistasis : loss of nsSNP with DER allele higher expressed

1. miRNAs

* Something to make the point that we have miRNA data. Some basic numbers: how many known (and novel?) miRNAs do we quantify?
* any evidence of correlation with target genes?

1. Loss of function

* Example plot of the diabetes gene
* Enrichment of ASE in nonsense sites