**Analyses for the CSHL poster**

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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