* Stuff about building the transcriptome
  + Bar graphs of novel isoforms and novel loci
  + Novel exons by type
  + Number of reference transcripts in txomes?
  + Salmon variance?
  + Number of samples transcripts are constructed in?
* Stuff about the transcriptomes in the eye
  + PIU
  + Upset of things being shared
  + CDS/NC/UTR
* Novel loci in the fetal eye
  + Heatmap
  + Expression over time
  + Conservation?
* Stuff about webapp/pipeline(todo)

Overall numbers of Transcriptome build

We built transcripts in several major ocular subtissues from adult and Fetal Cornea, Retinal Pigmented Epithelium(RPE), and Retina, as well as other major body tissues. Initially, XXX distinct transcripts were constructed, which contained XXX reference transcripts and XXX novel transcript. We found that many of these transcripts were detected in one or two samples, and so to refine our set of transcriptomes, we designed a rigorous filtering and processing pipeline(methods). We were left with a total of XXX reference and XXX novel transcripts. Novel transcripts can be broken into two categories, novel isoforms, which are novel variations of known genes, and novel loci, which are previously unreported, entirely novel regions of transcribed sequence. (Figure 1)

Novel isoforms can be broken down into three main catagories – modifcations of known exons, getting longer or shorter, whole novel exons, ie a completely unreported novel exon, or a novel arrangement of exons due to exon omission. We can also attributed these catagories as originating from 3 distinct biological phenomena – alternative splicing, alternative first exons(alternative promoter usage), or alternative last exons( alternative polyadenylation). For each novel exon, we identified the potential biological process leading to the inclusion/exclusion of this exon(fig).

De novo transcriptomes improve sample mapping rates

As an initial benchmark of the accuracy of our transcriptome builds, we quantified transcript expression of our samples using the alignment free quantification tool salmon using both our set of transcriptomes and the gencode VXX reference. We found that globally, salmon mapping rates increased when using the denovo transcriptomes to build salmon indexes

Usage of novel transcripts in novel eye tissues

Novel transcripts are generally specific to a single subtissue.(upset) The majority of novel transcripts have their novel region in the UTR of

Novel loci in eye tissues