Building transcripts in major eye tissues

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.

De novo transcriptomes improve sample mapping rates

Next 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 denovo trancripts improved mapping rates, but especially in ocular tissues.q

Usage of novel transcripts in novel eye tissues

Novel loci in eye tissues