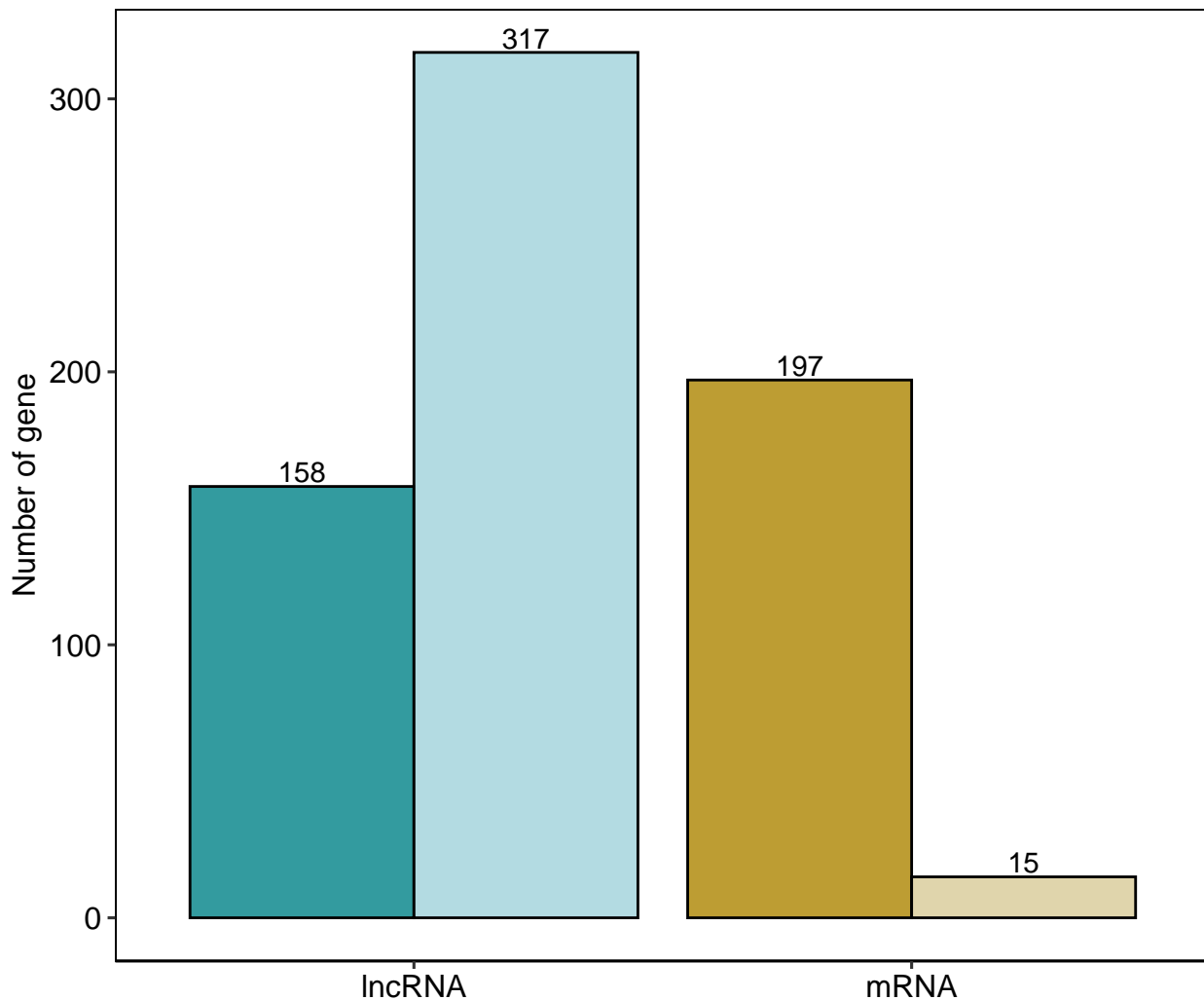


ANNEXA report

Gene Characterization

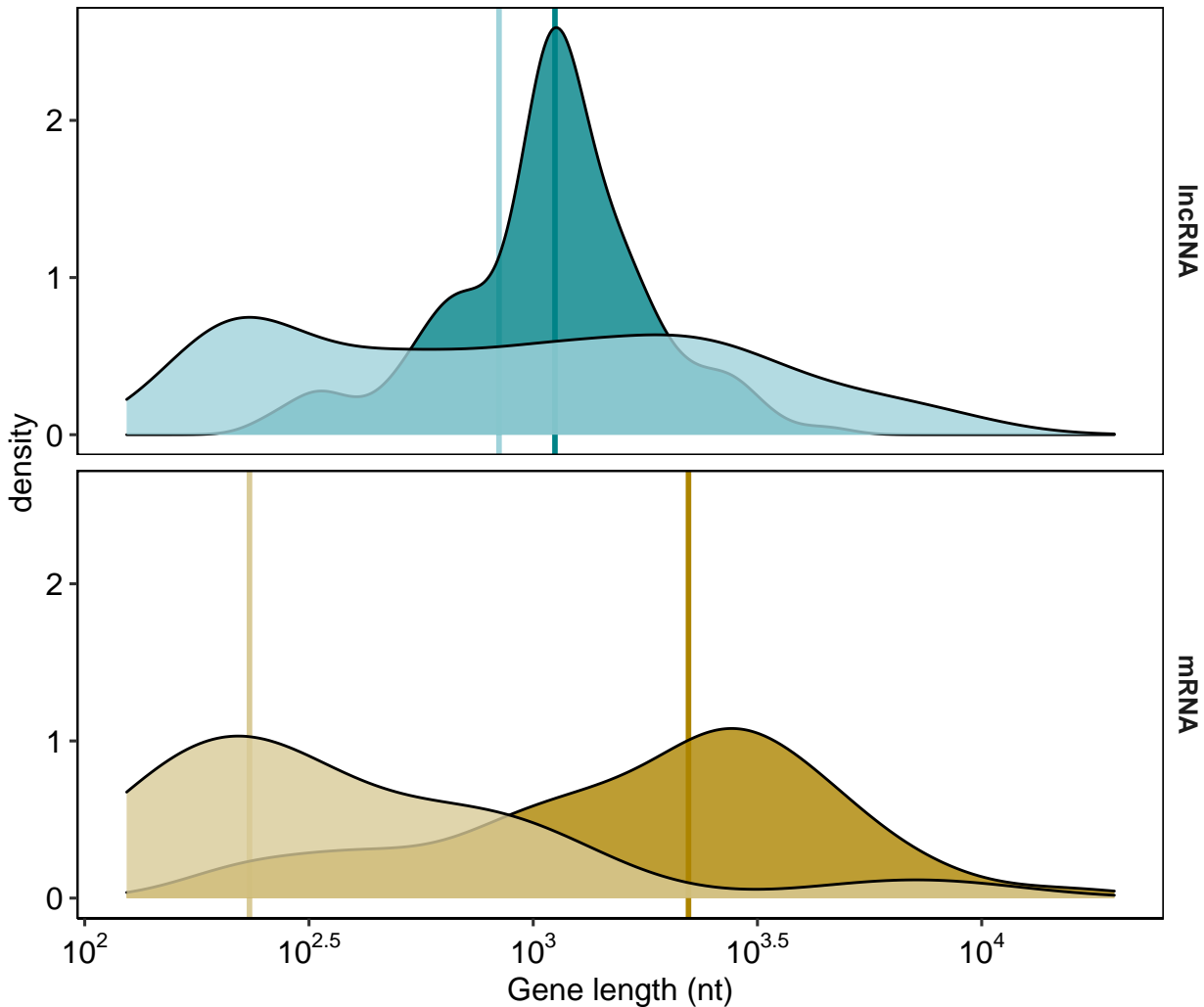
Number of genes

Source IncRNA known IncRNA novel mRNA known mRNA novel



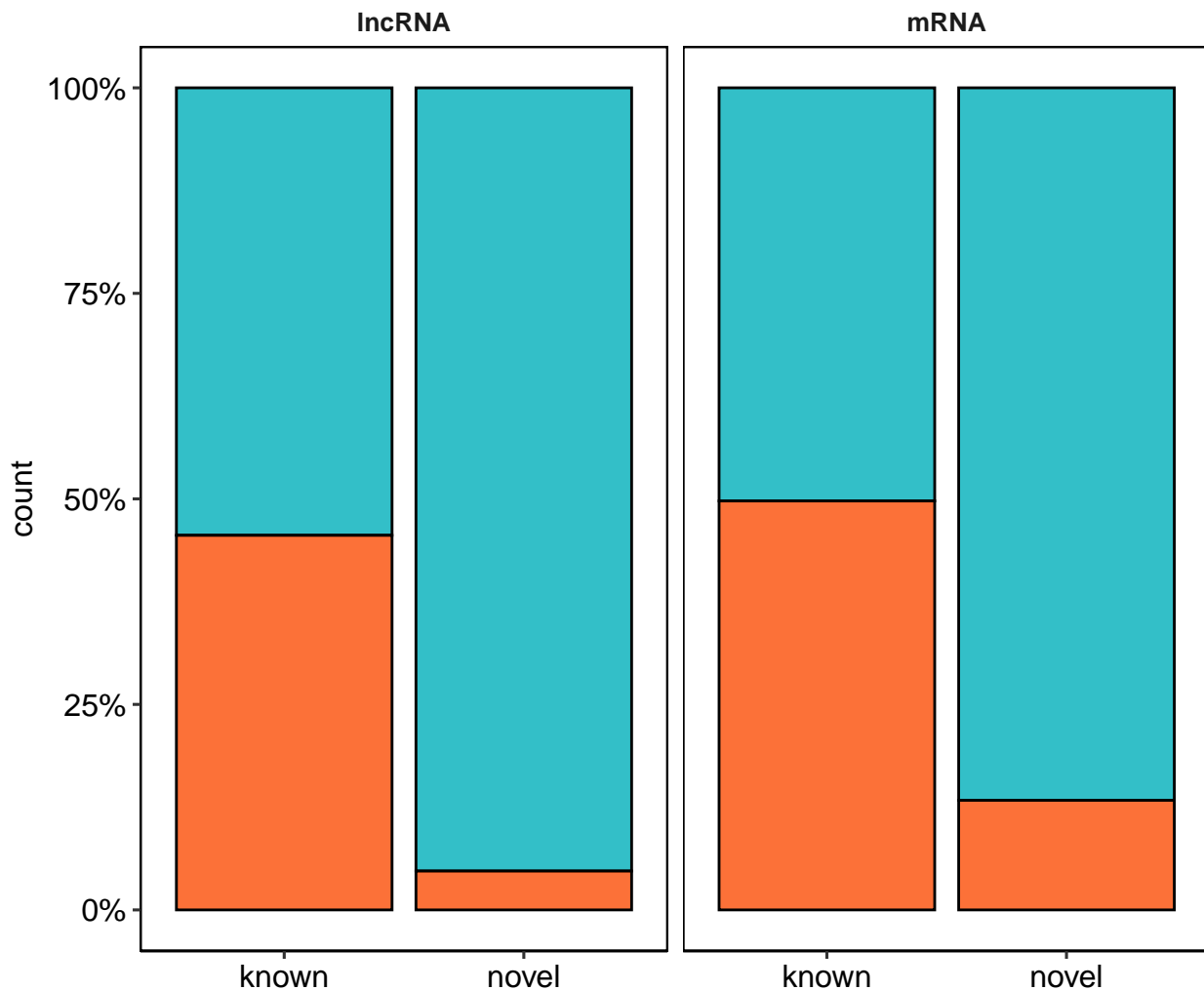
Gene length distribution

Source IncRNA known IncRNA novel mRNA known mRNA novel



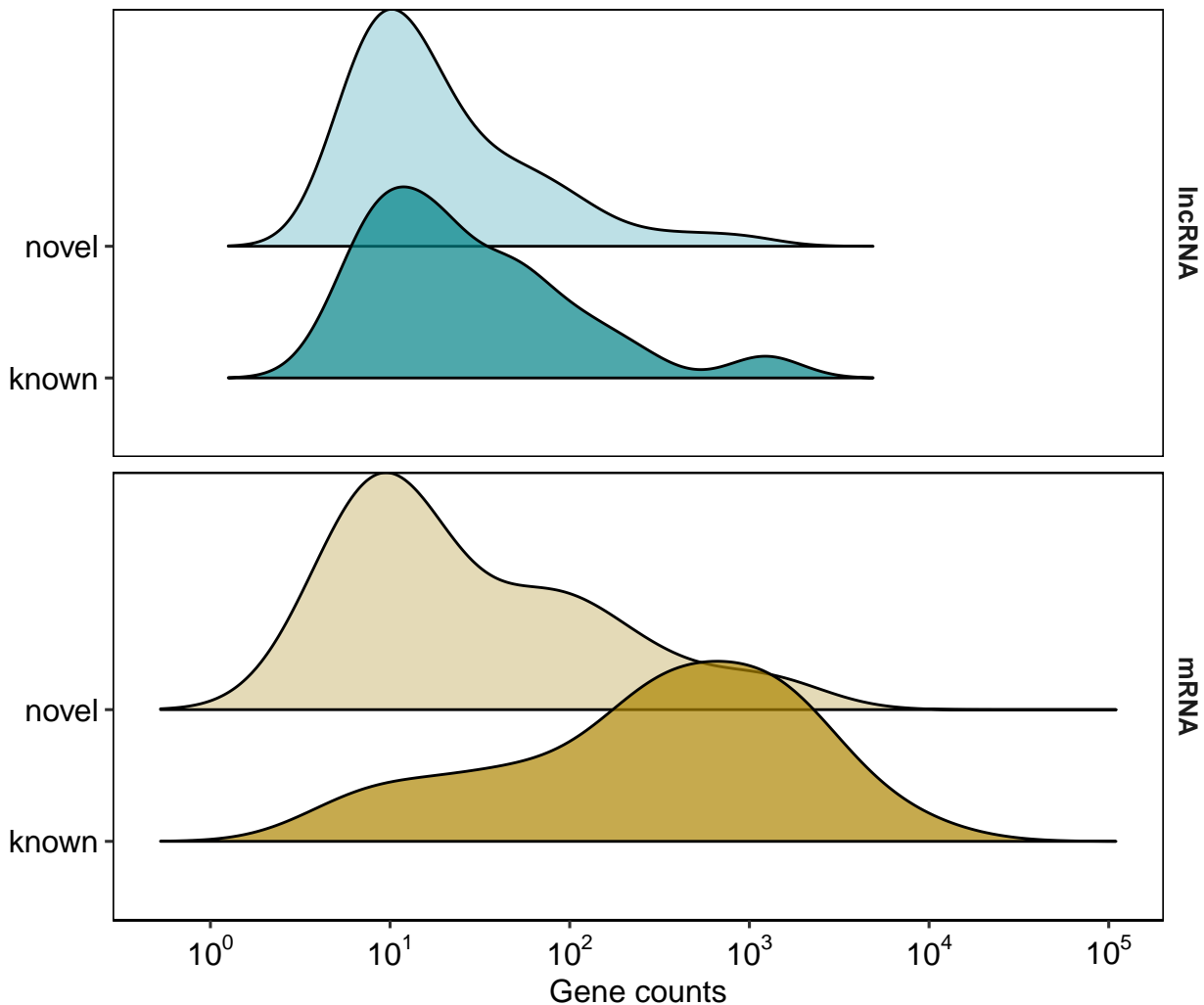
Proportion of mono versus multi-isoform genes

isoformes 1 2+



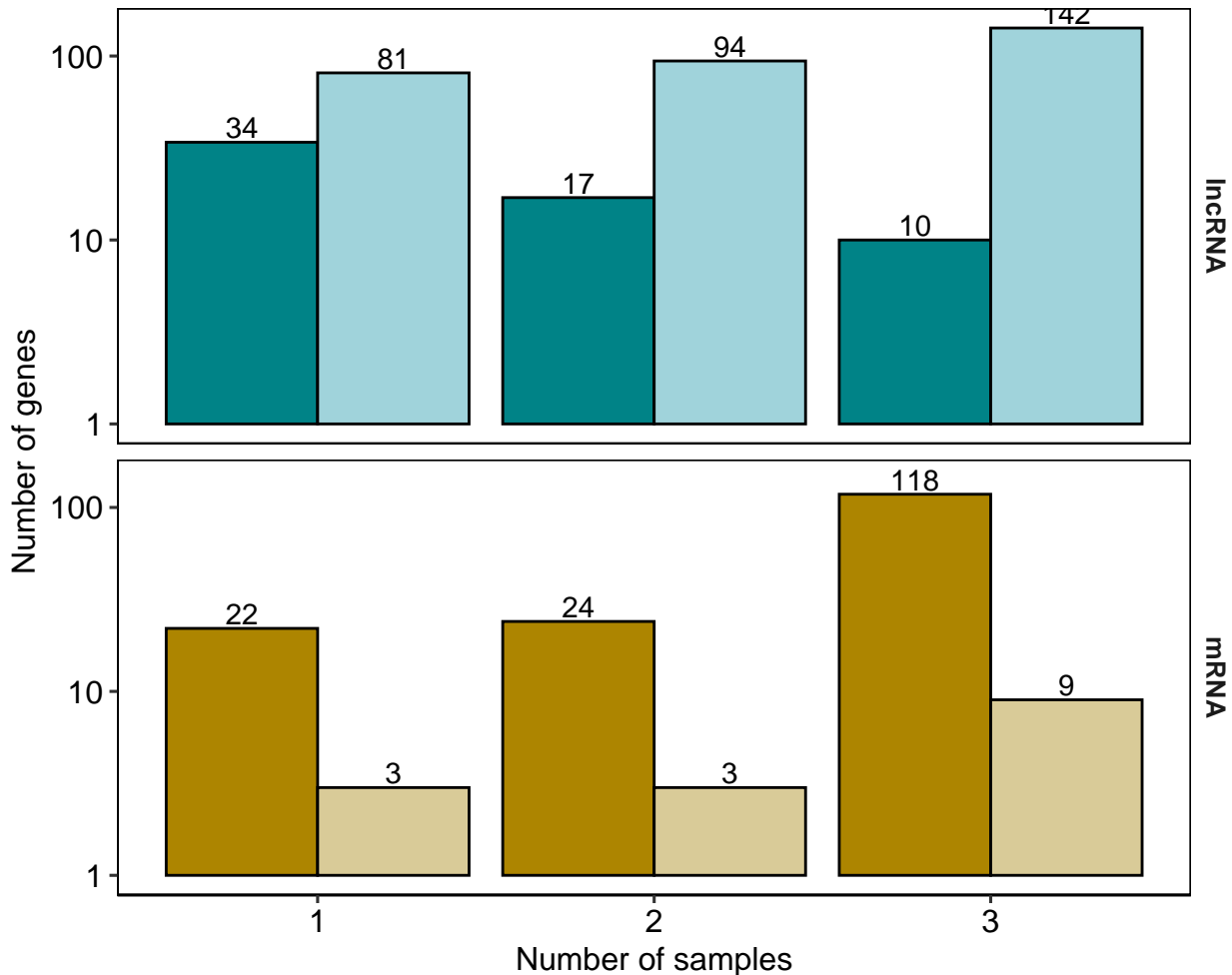
Distribution of gene counts

Source lncRNA known lncRNA novel mRNA known mRNA novel



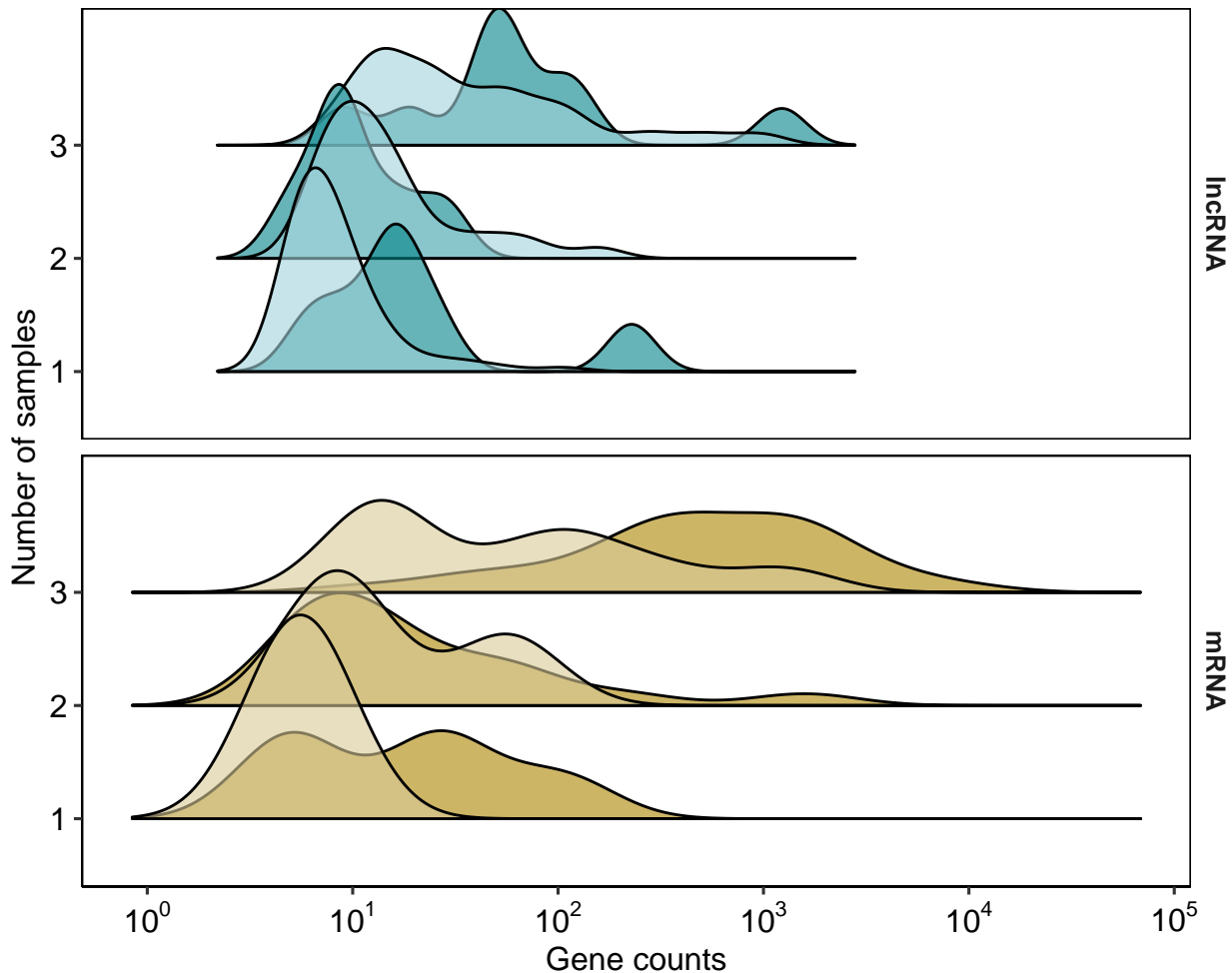
Number of genes according to his number of samples with more than 1 count

Source IncRNA known IncRNA novel mRNA known mRNA novel

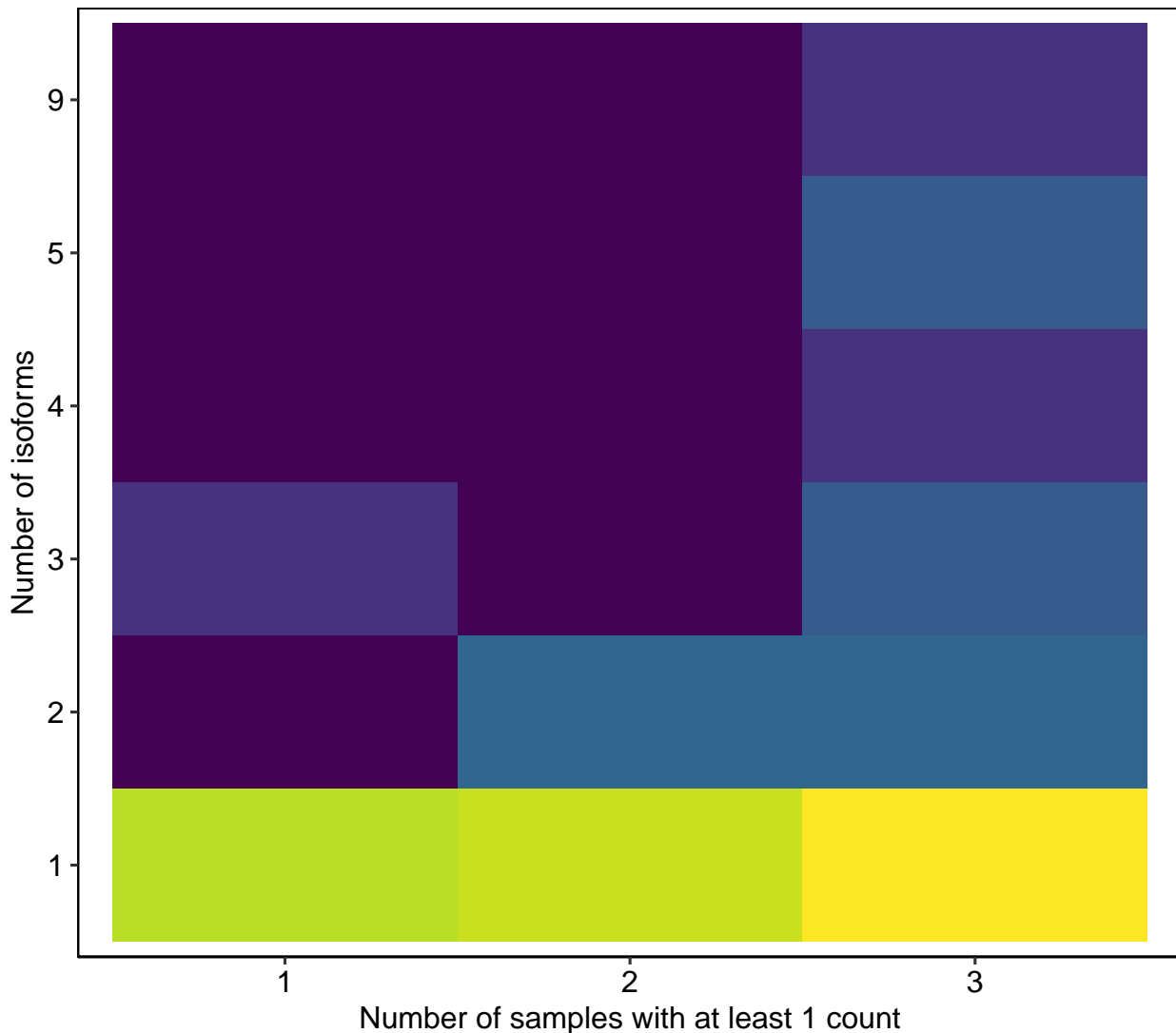


Gene counts separated by number of samples with at least 1 count

Source IncRNA known IncRNA novel mRNA known mRNA novel

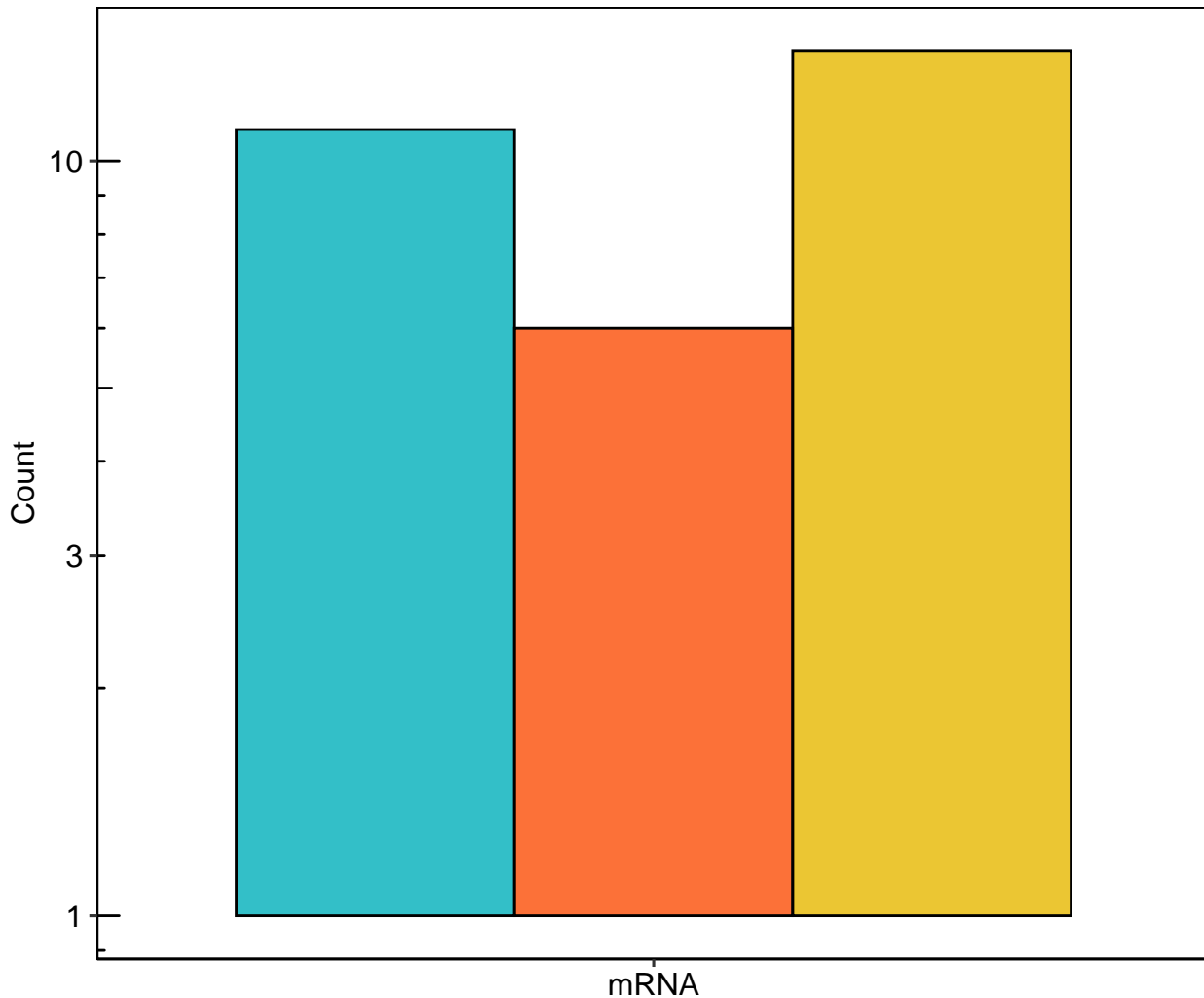


Number of novel genes (log) based on isoform number and number of samples with at least 1 count



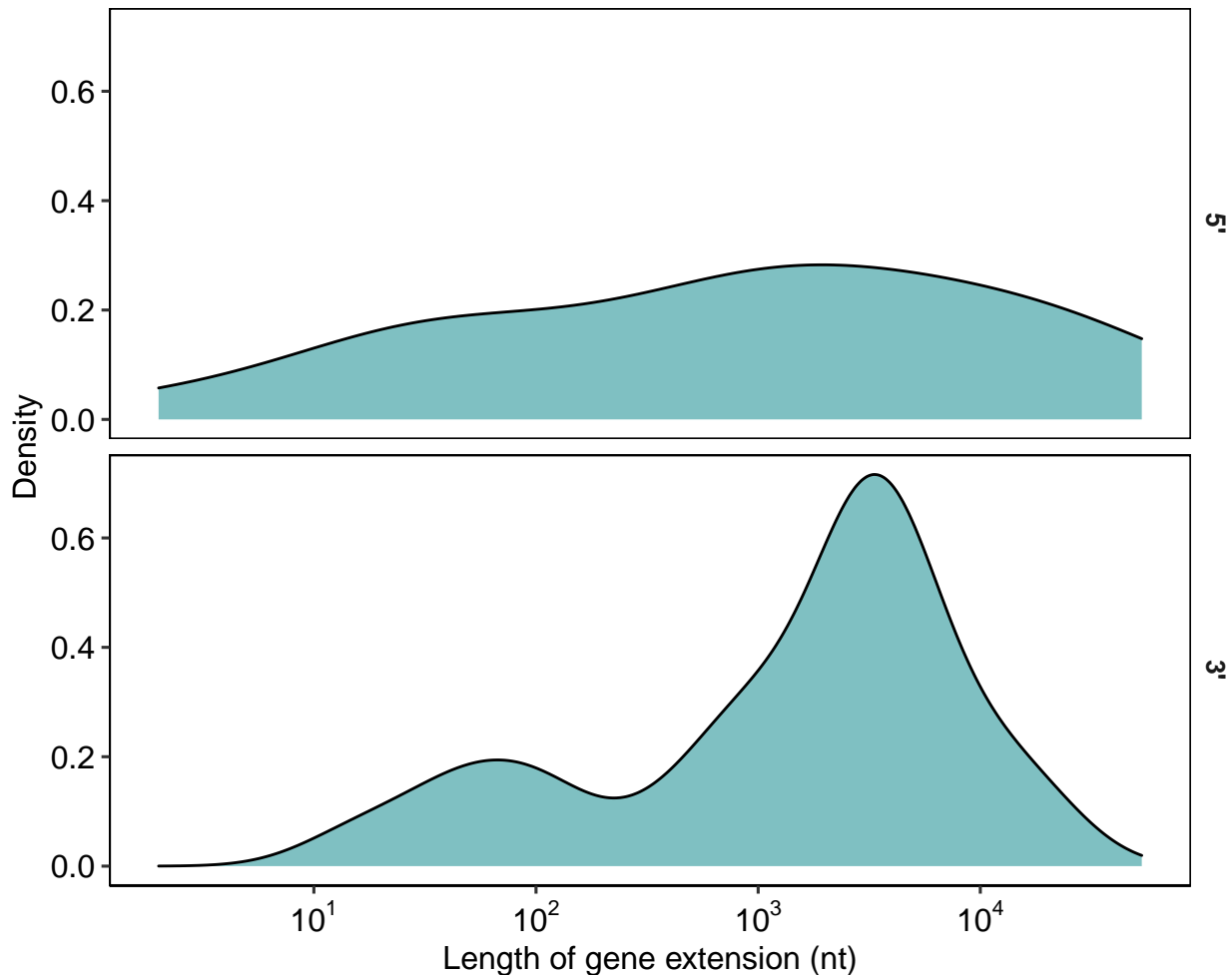
Number of 5' and 3' gene extensions

Gene extension 3' 5' 5'-3'



Distribution of 5' and 3' gene extensions (at genomic level)

Source  mRNA known

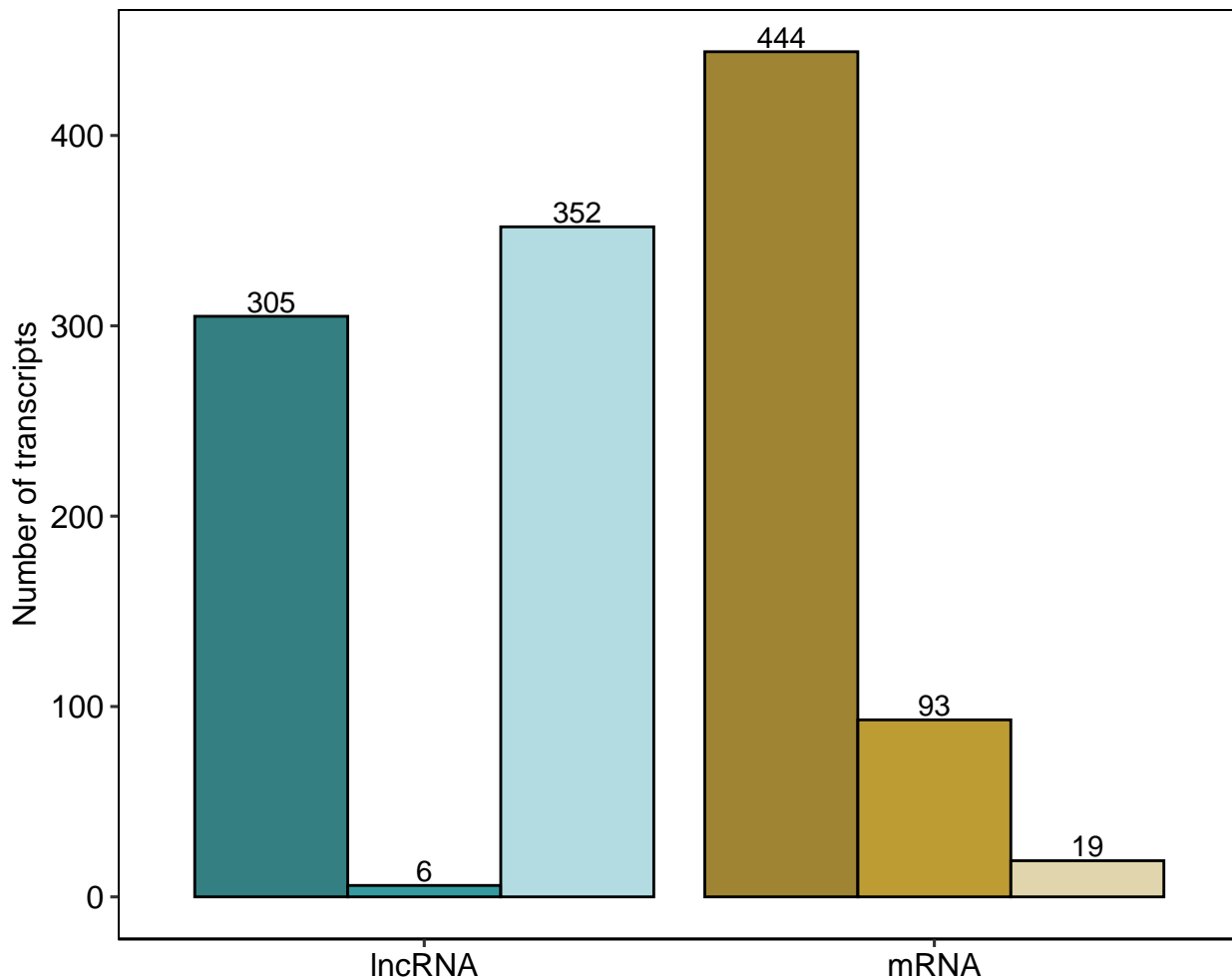


Transcript Characterization

Number of transcripts

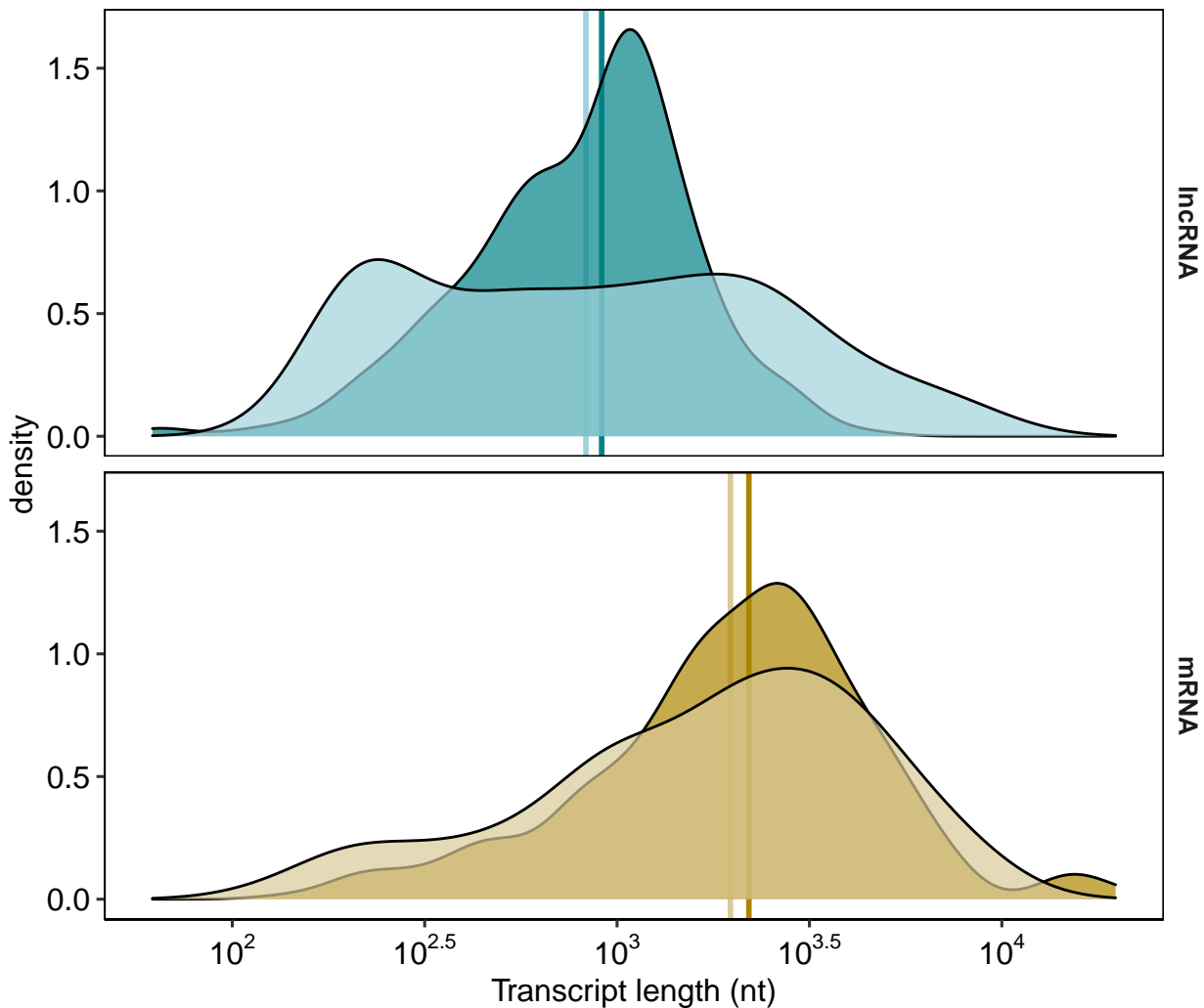
K=known, N=novel

| | | |
|-------------|-------------|-------------|
| K in K gene | N in N gene | N in K gene |
| N in K gene | K in K gene | N in N gene |



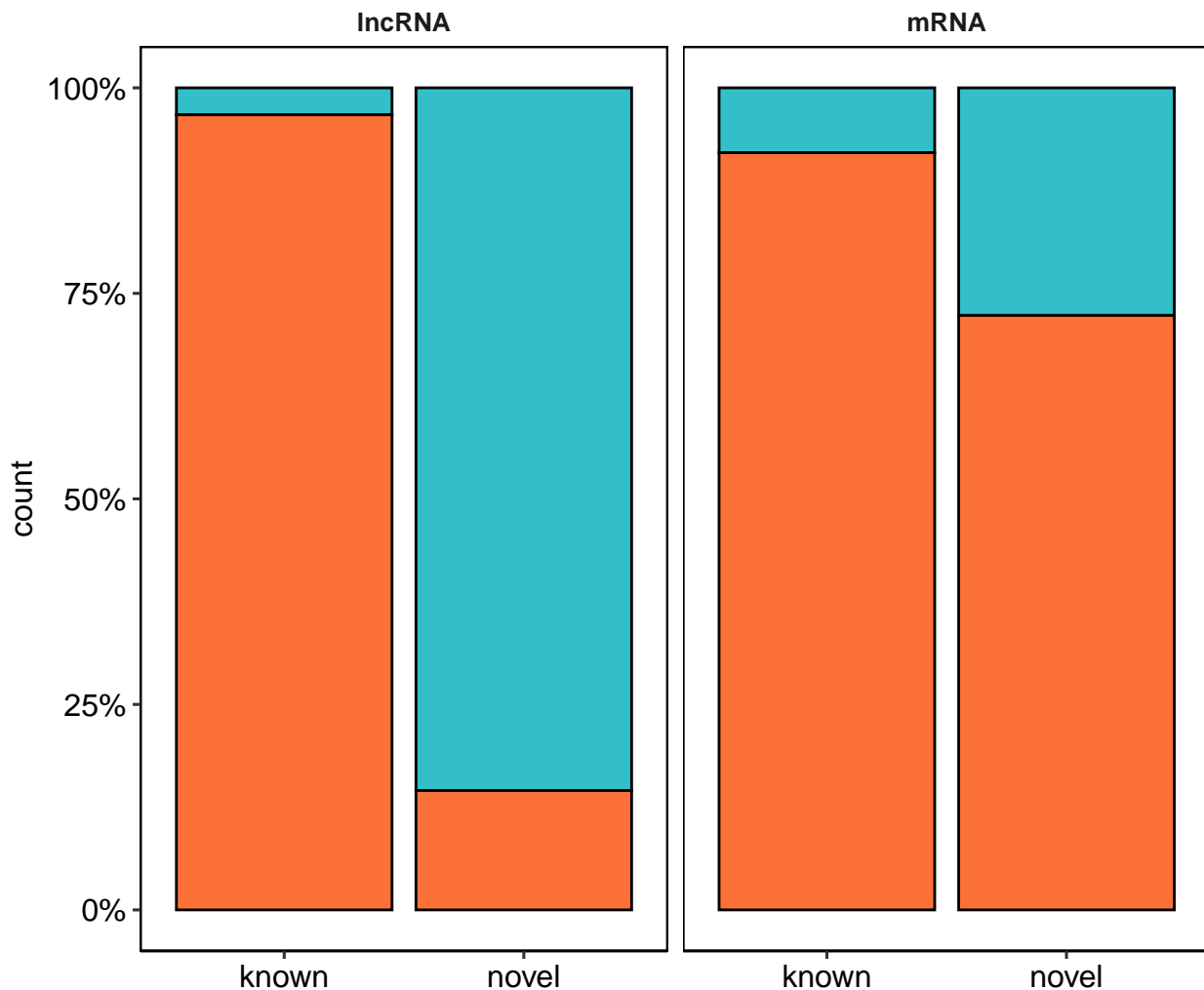
Transcript length distribution

Source lncRNA known lncRNA novel mRNA known mRNA novel



Proportion of mono versus multi exonic transcripts

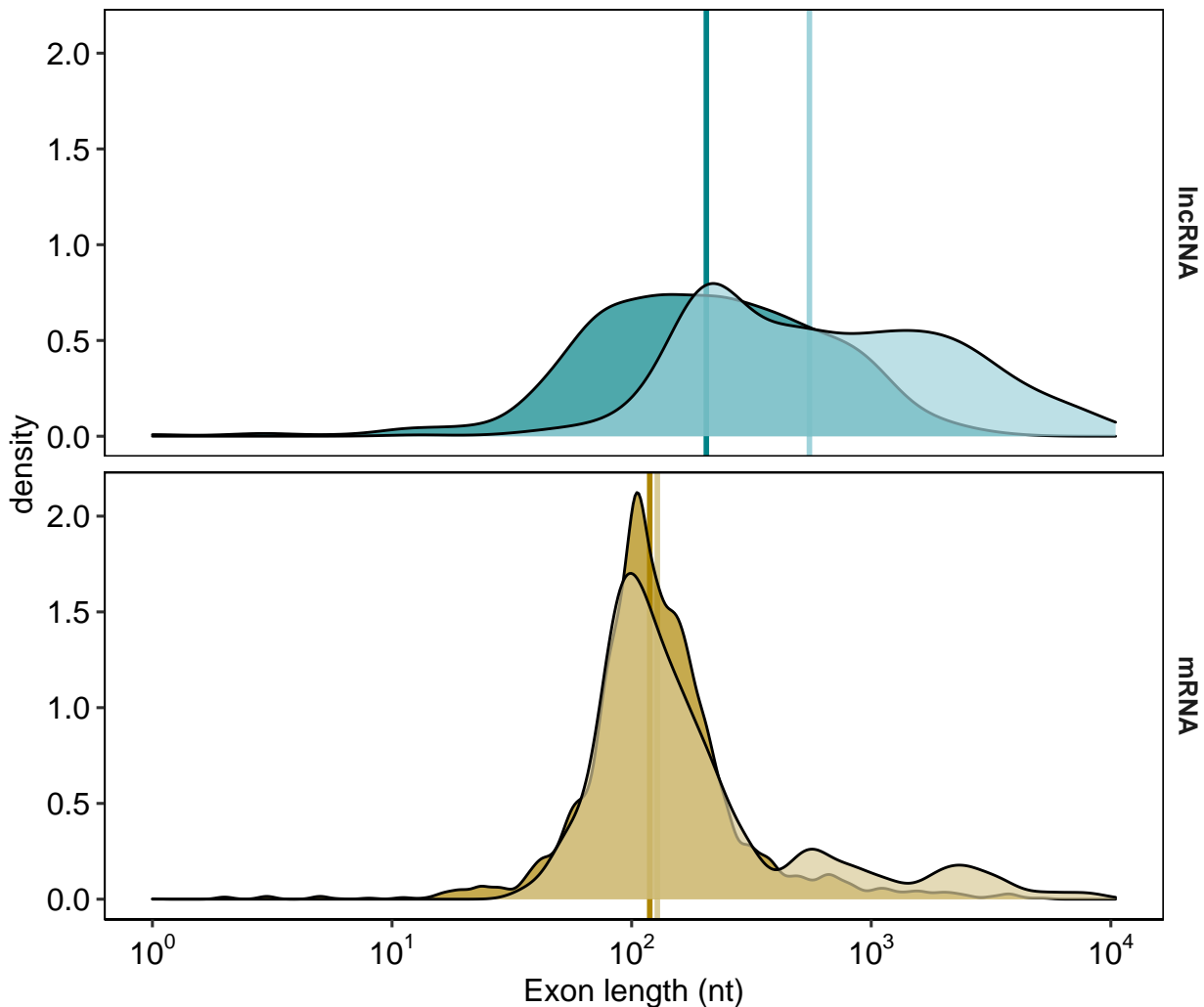
exons 1 2+



Exon Characterization

Exon length distribution

Source lncRNA known lncRNA novel mRNA known mRNA novel



Number of exons

Source IncRNA known IncRNA novel mRNA known mRNA novel

