

# ANNEXA report

2025-10-16

ANNEXA version: 3.2.6

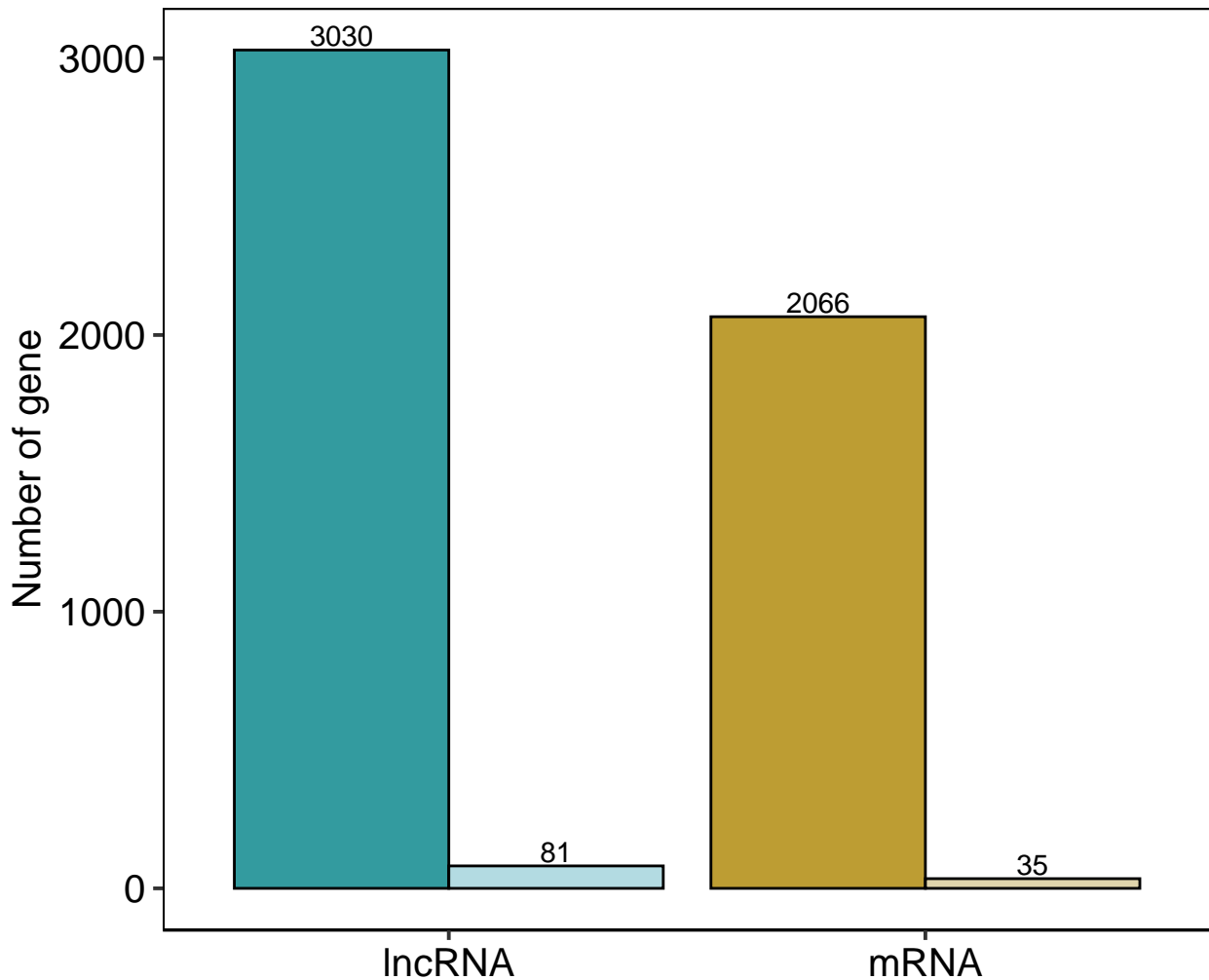
## ANNEXA command line:

```
nextflow run /Users/nhoffmann/github/ANNEXA  
-profile docker  
--input ../sample.txt  
--gtf ../chr1.gtf  
--fa ../chr1.fa  
--maxCpu 2  
--maxMemory 8  
-resume
```

## *Gene Characterization*

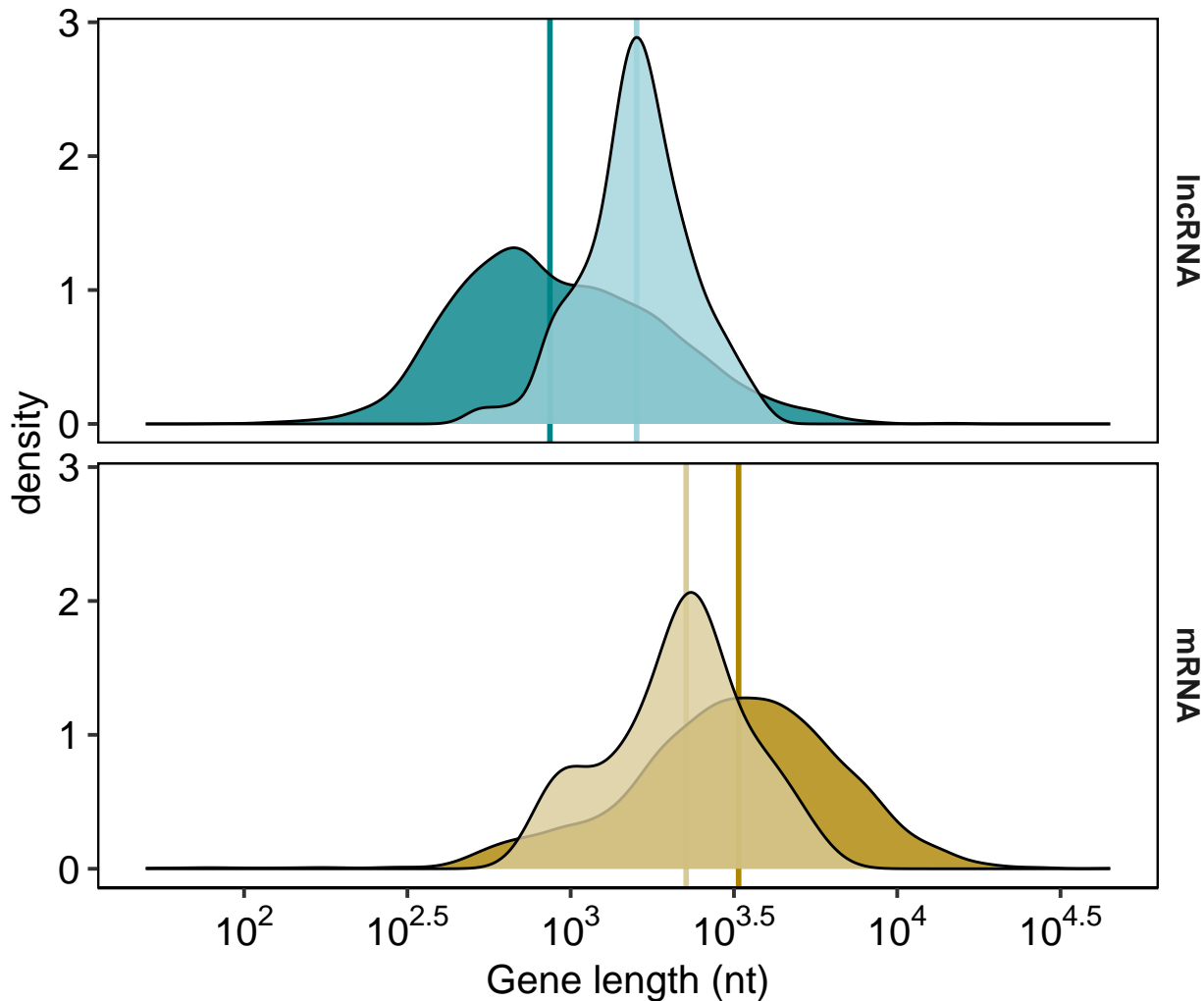
# Number of genes

Source    IncRNA known    IncRNA novel    mRNA known    mRNA novel

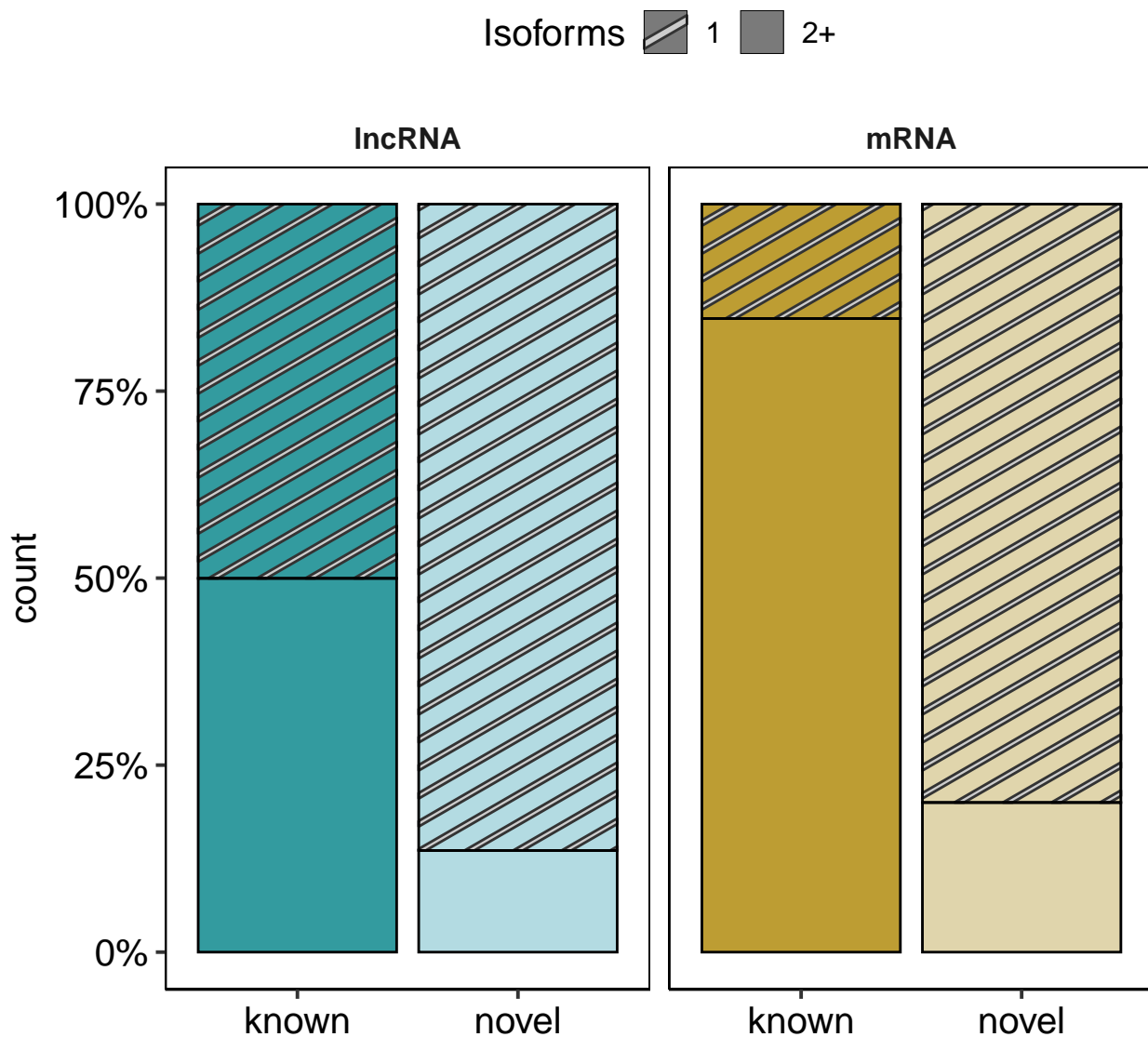


# Gene length distribution

Source    IncRNA known    IncRNA novel    mRNA known    mRNA novel

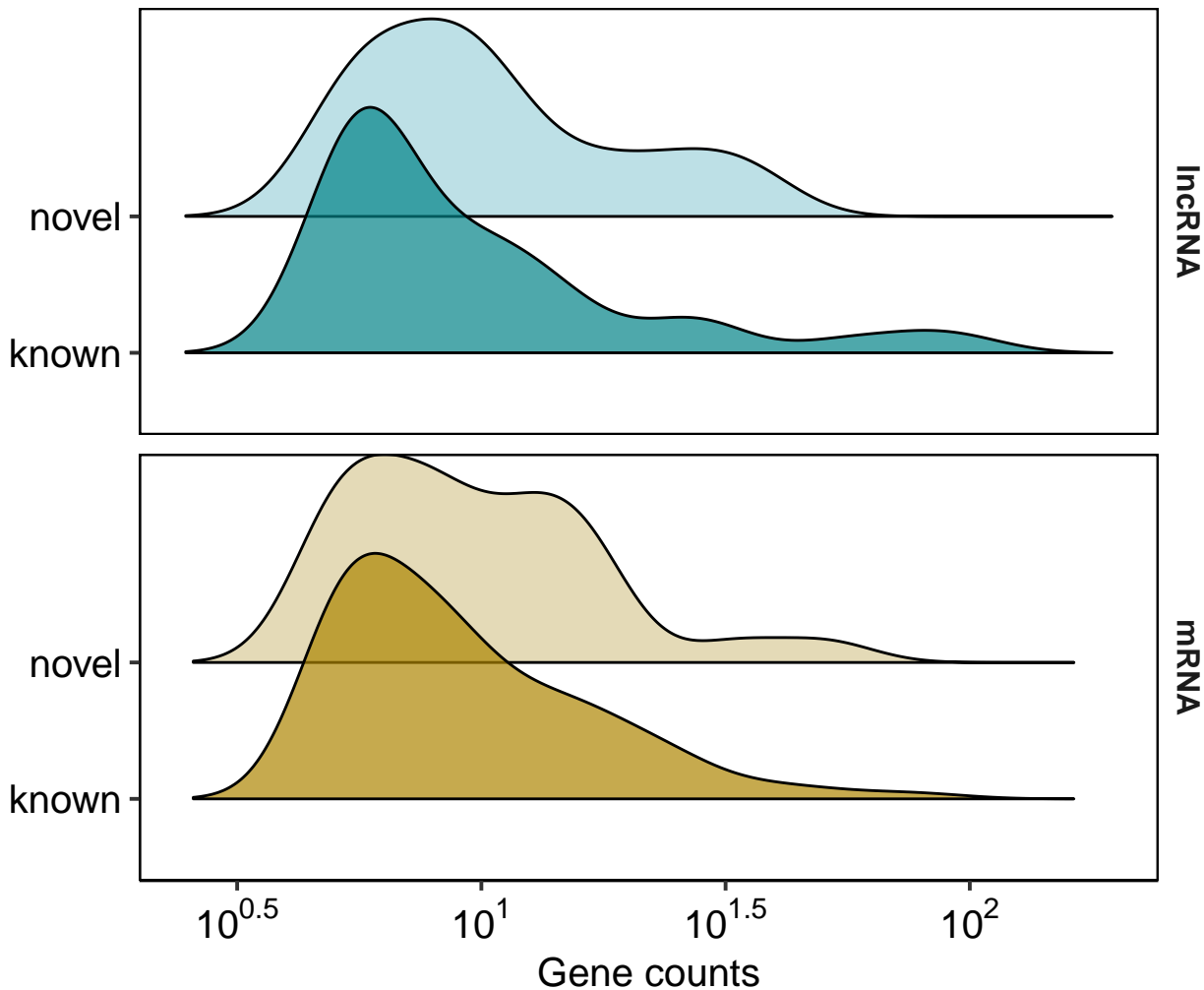


# Proportion of mono versus multi-isoform genes



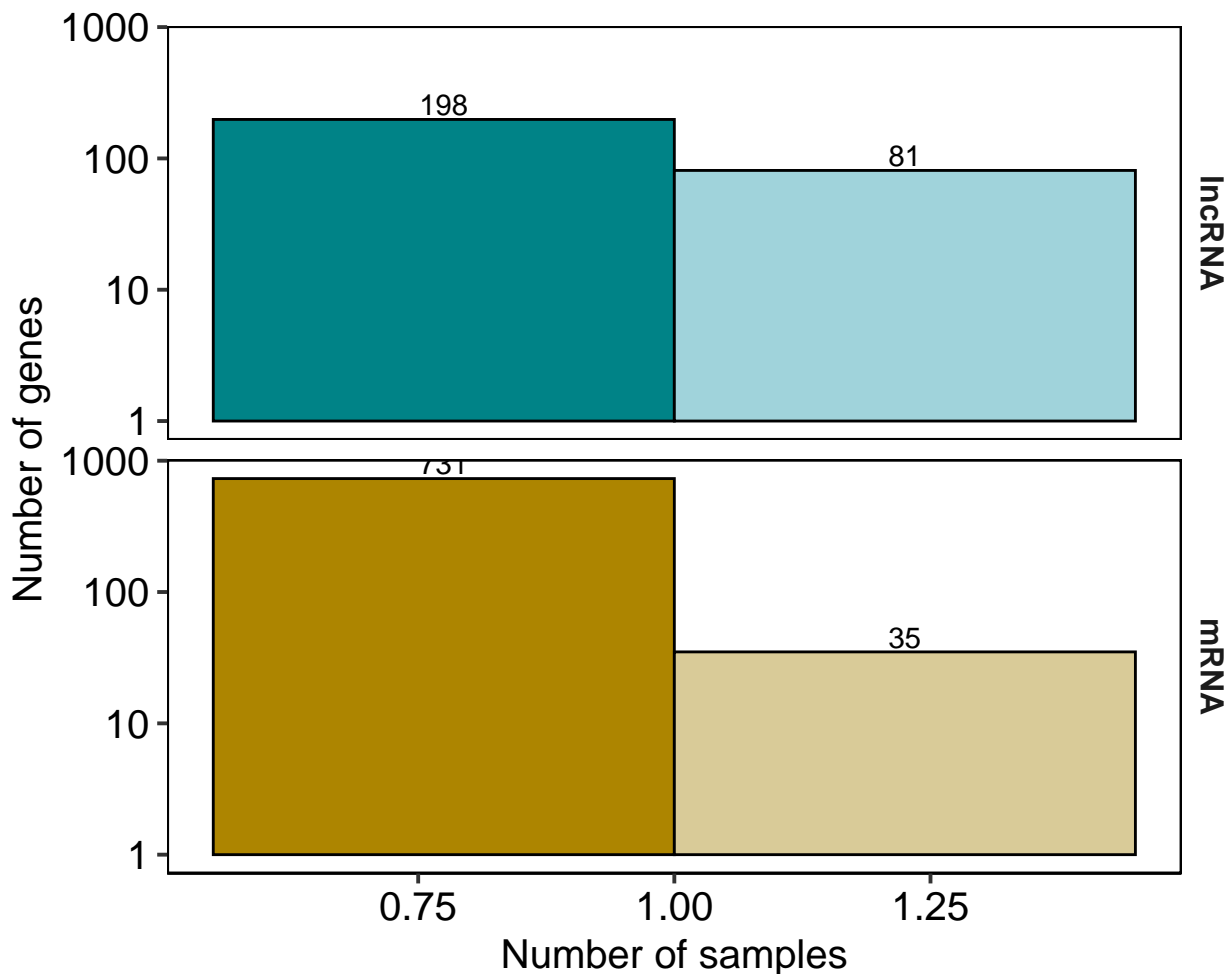
# Distribution of gene counts

Source    IncRNA known    IncRNA novel    mRNA known    mRNA novel



# Number of genes according to his breadth of expression (gene count >1)

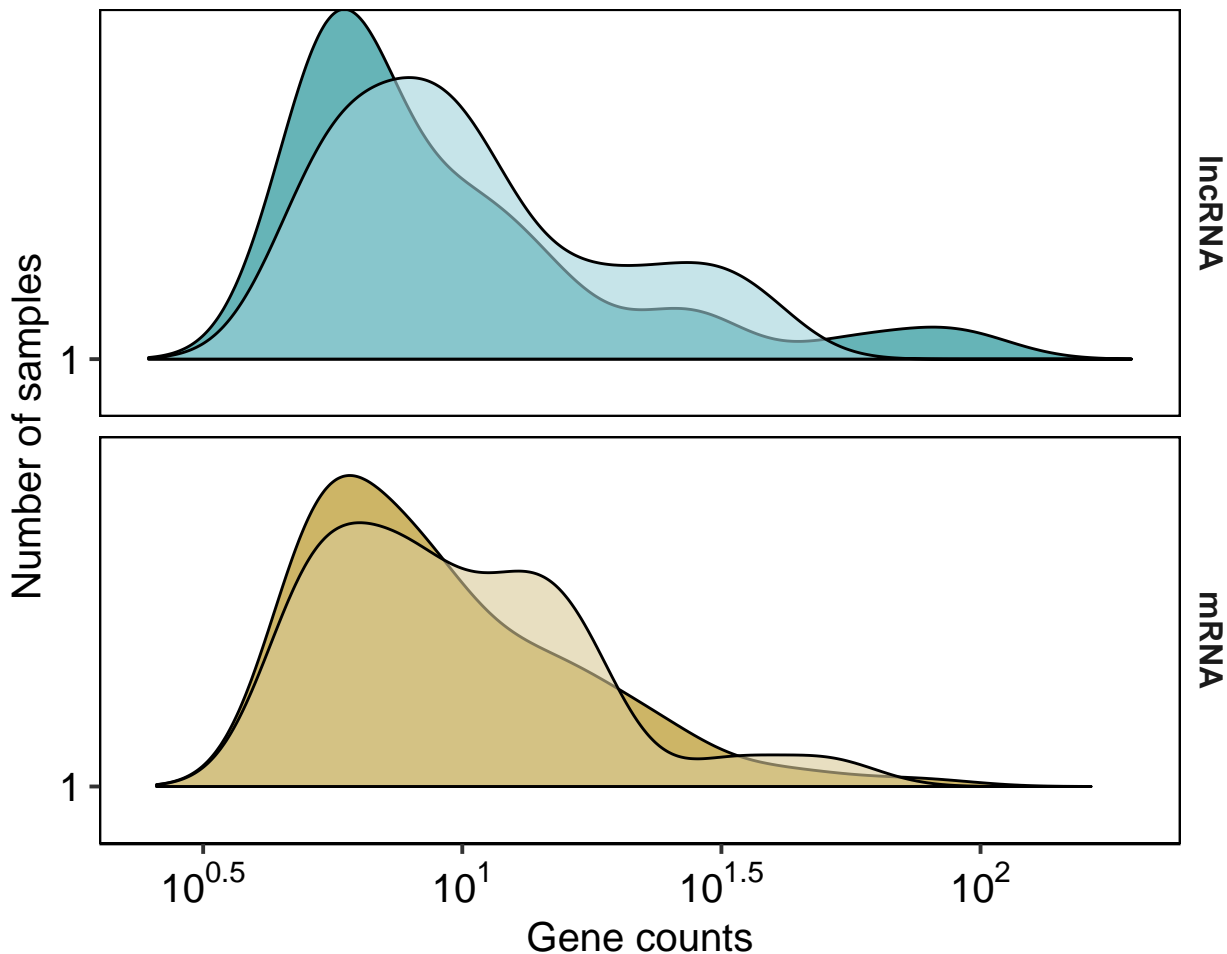
Source IncRNA known IncRNA novel mRNA known mRNA novel





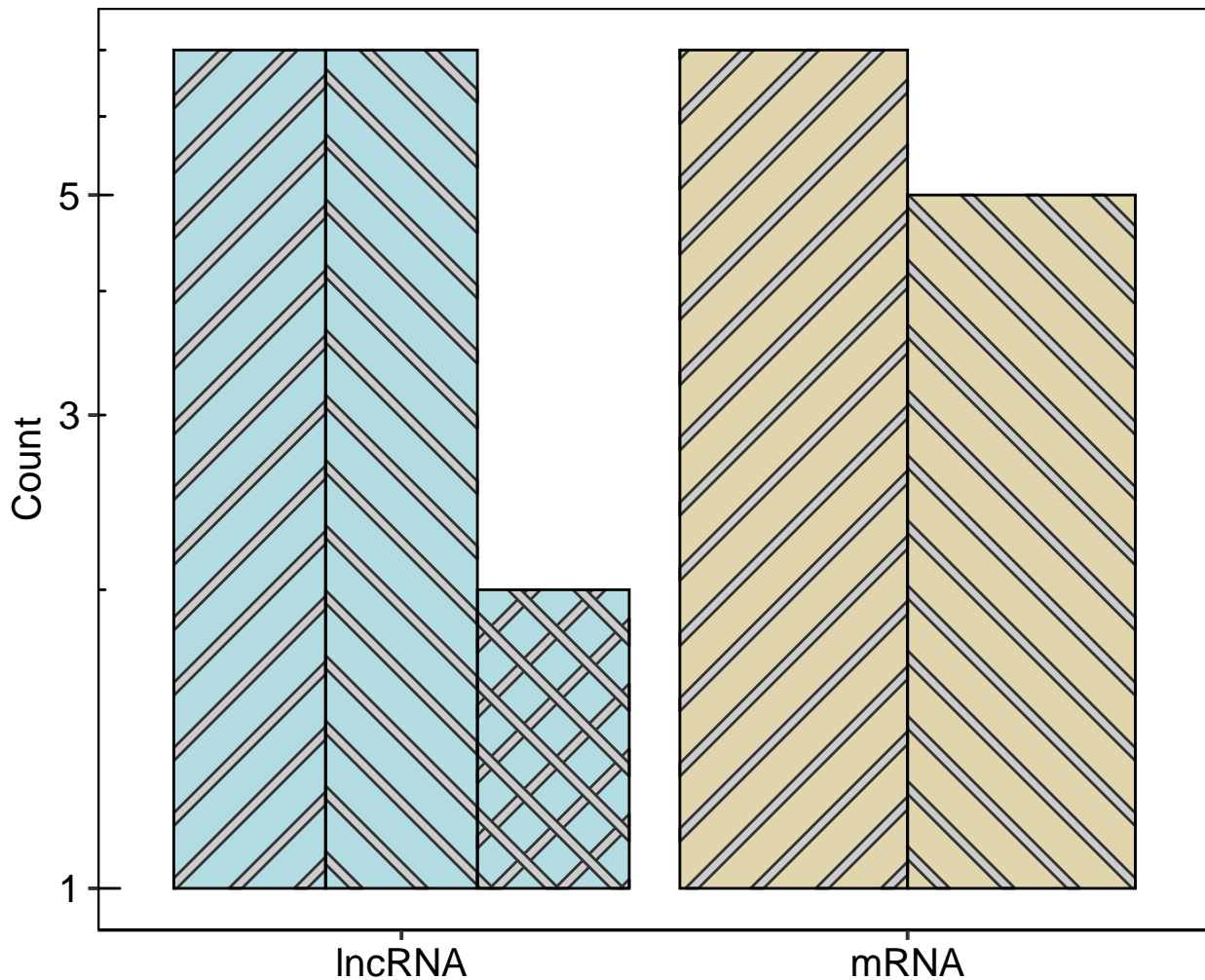
# Gene counts separated by number of samples with at least 1 count

Source   IncRNA known   IncRNA novel   mRNA known   mRNA novel



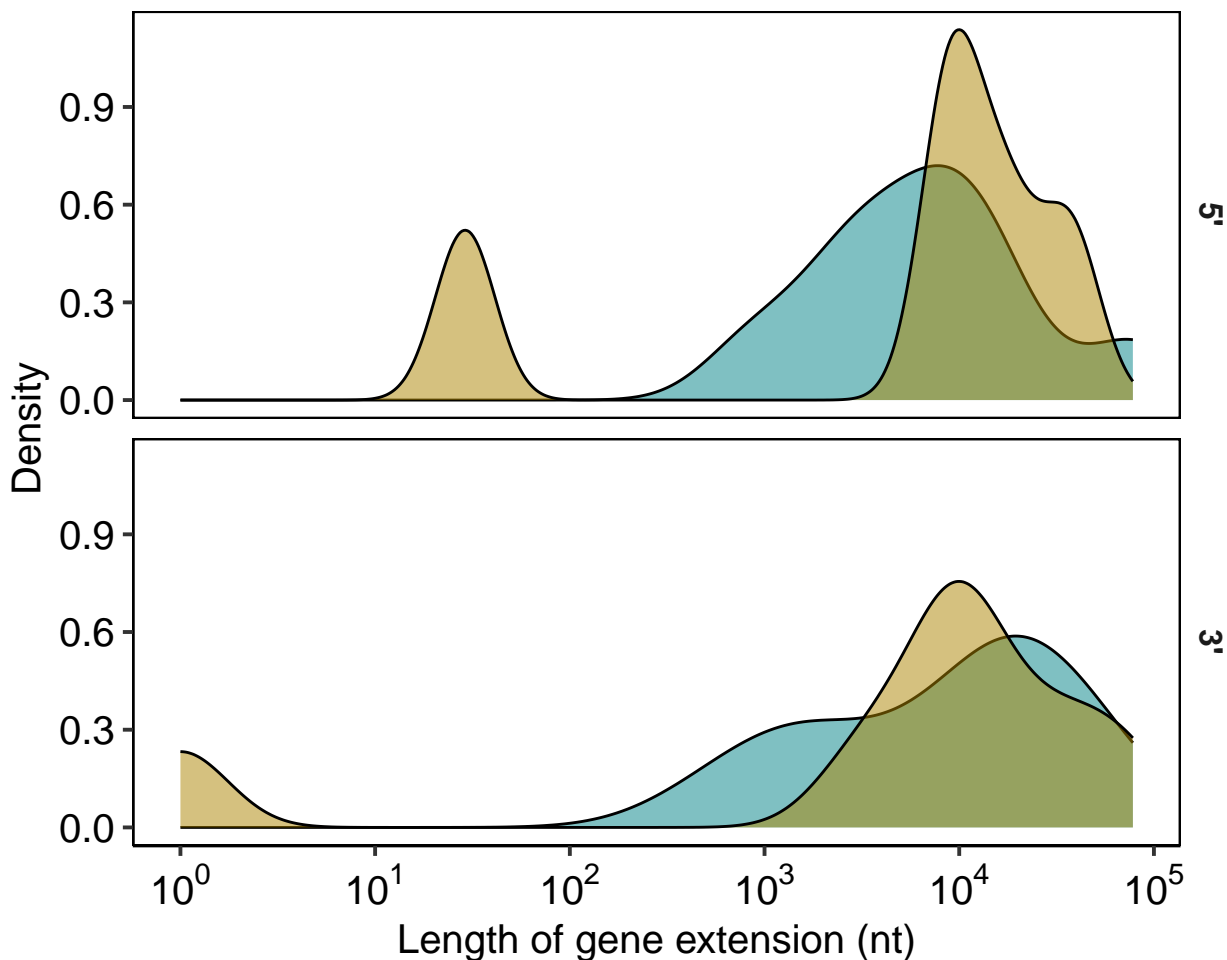
# Number of 5' and 3' gene extensions

Gene extension  3'  5'  5'-3'



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

Source ■ lncRNA known ■ mRNA known

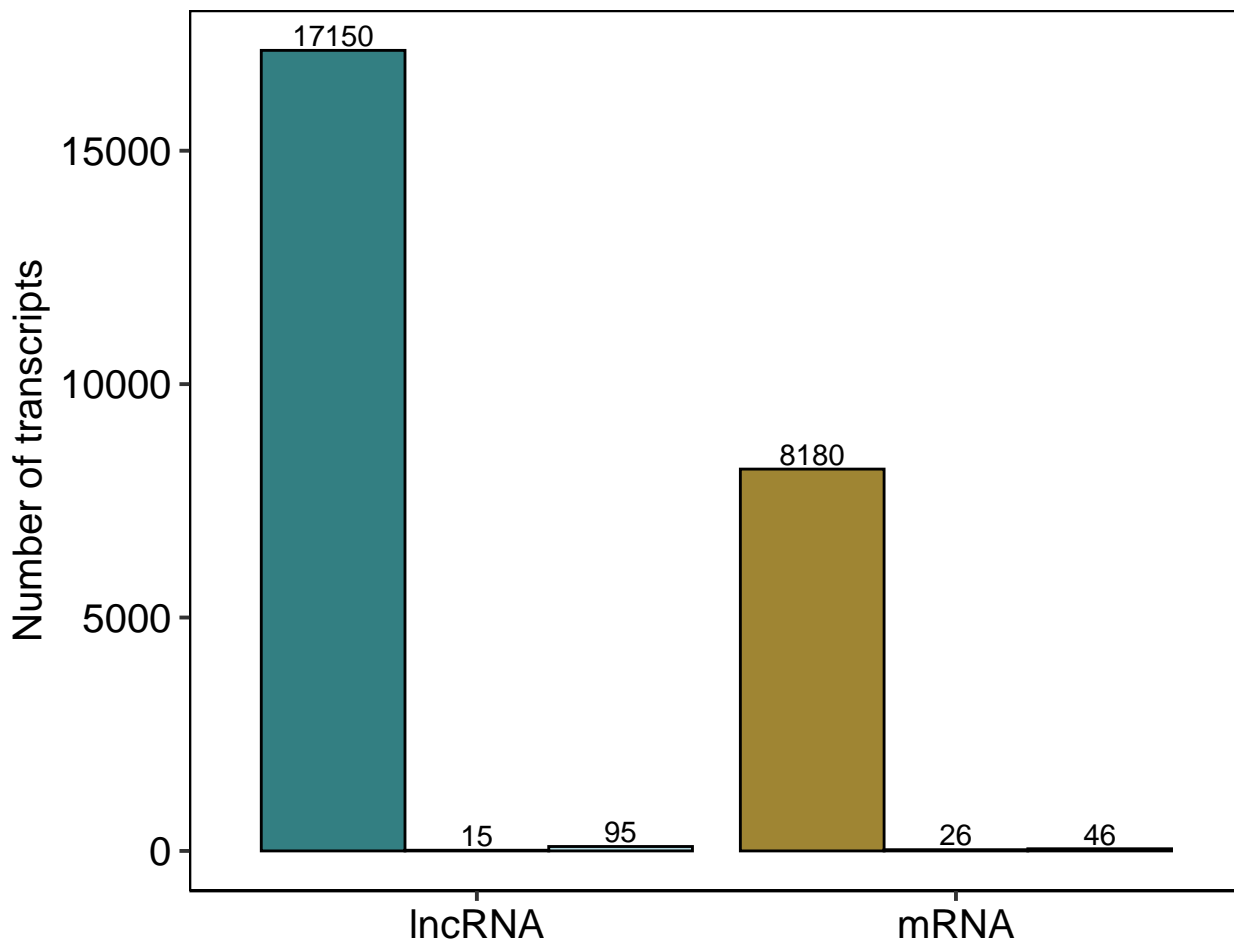


## *Transcript Characterization*

# Number of transcripts

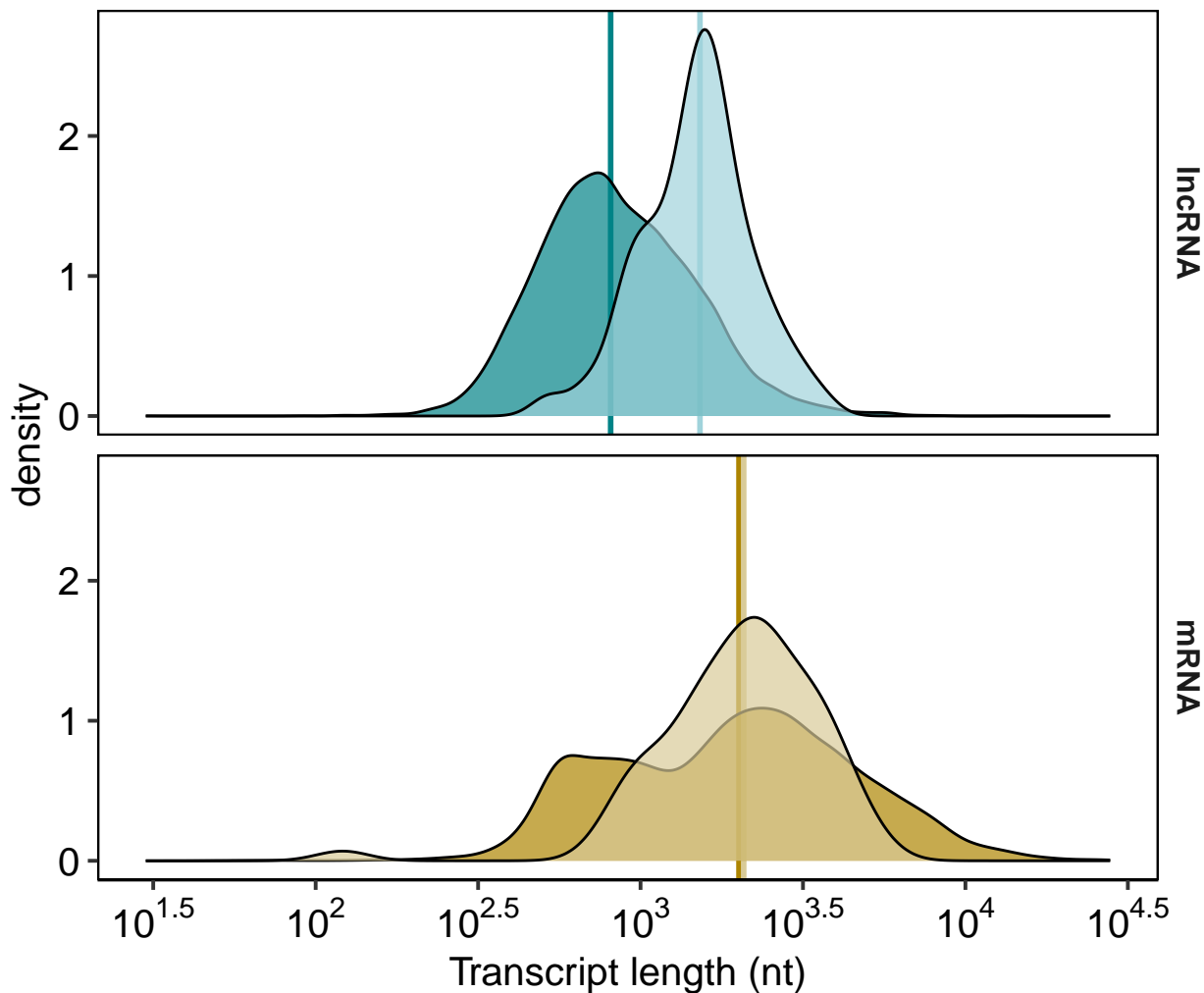
K=known, N=novel

K in K gene	N in N gene	N in K gene
N in K gene	K in K gene	N in N gene



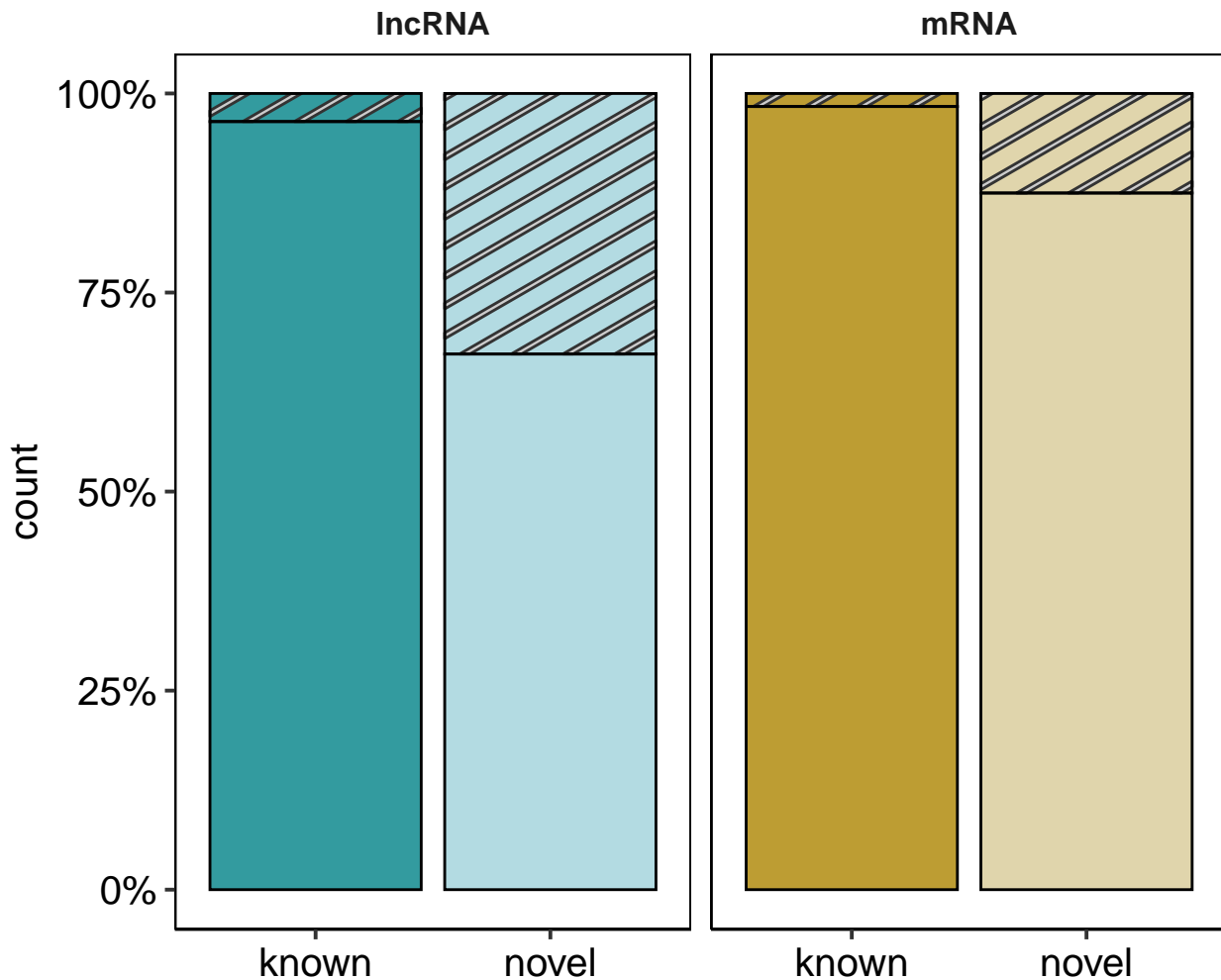
# Transcript length distribution

Source    IncRNA known    IncRNA novel    mRNA known    mRNA novel



# Proportion of mono versus multi exonic transcripts





Exons 1 2+

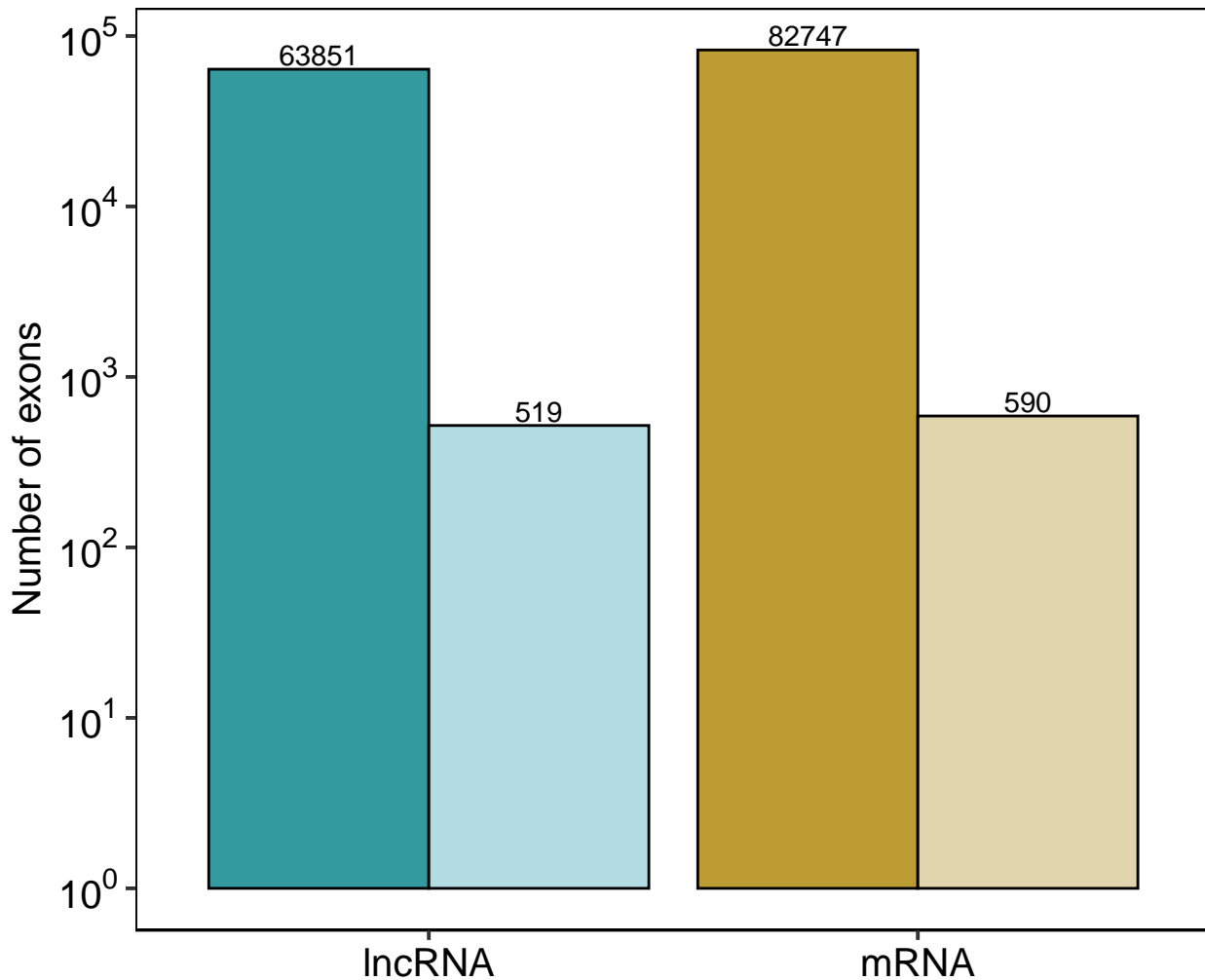


## *Exon Characterization*



# Number of exons

Source    lncRNA known    lncRNA novel    mRNA known    mRNA novel



# Exon length distribution

Source  lncRNA known  lncRNA novel  mRNA known  mRNA novel

