

SQANTI3 report

Unique Genes: 12925

Unique Isoforms: 76071

Gene classification

| Category | # Genes |
|-----------------|---------|
| Annotated Genes | 12018 |
| Novel Genes | 907 |

Splice Junction Classification

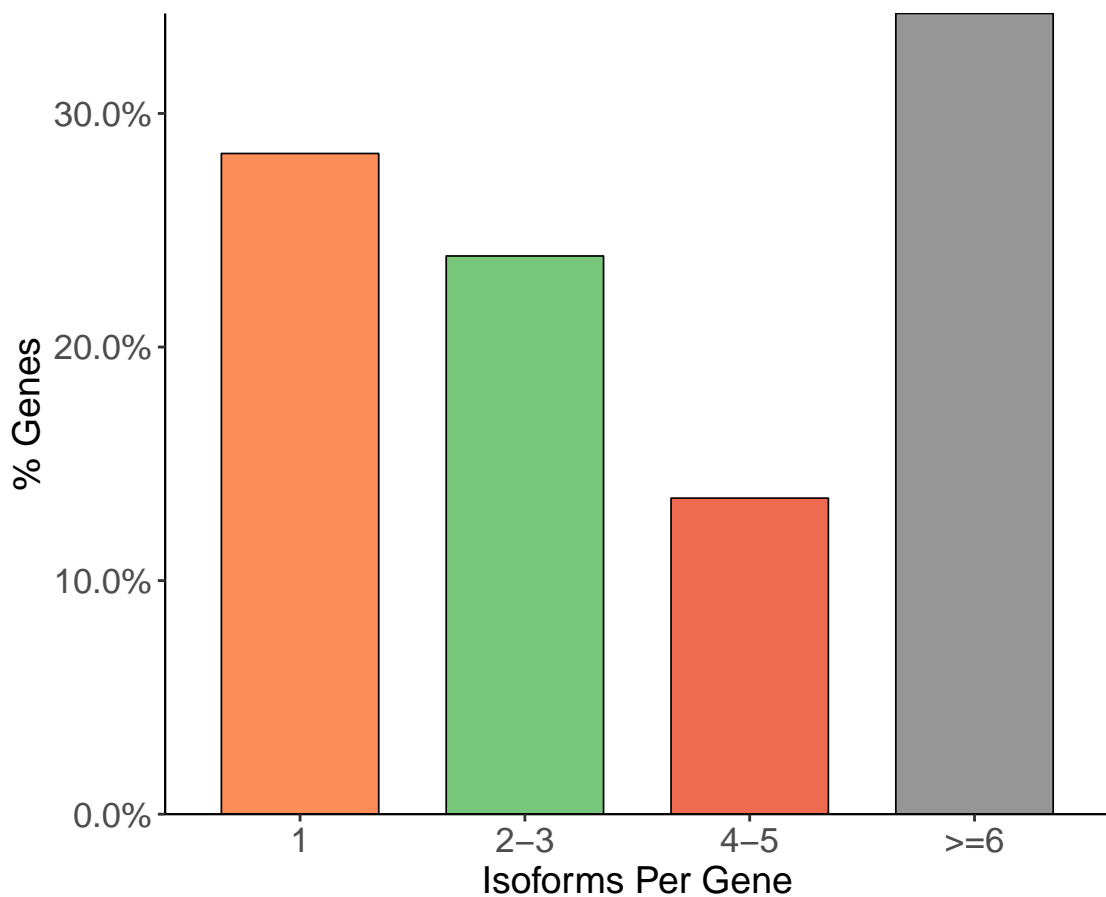
| Category | # SJs | Percent |
|---------------------|--------|---------|
| Known canonical | 117293 | 81.41 |
| Known Non–canonical | 61 | 0.04 |
| Novel canonical | 26714 | 18.54 |
| Novel Non–canonical | 9 | 0.01 |

*Characterization of transcripts
based on splice junctions*

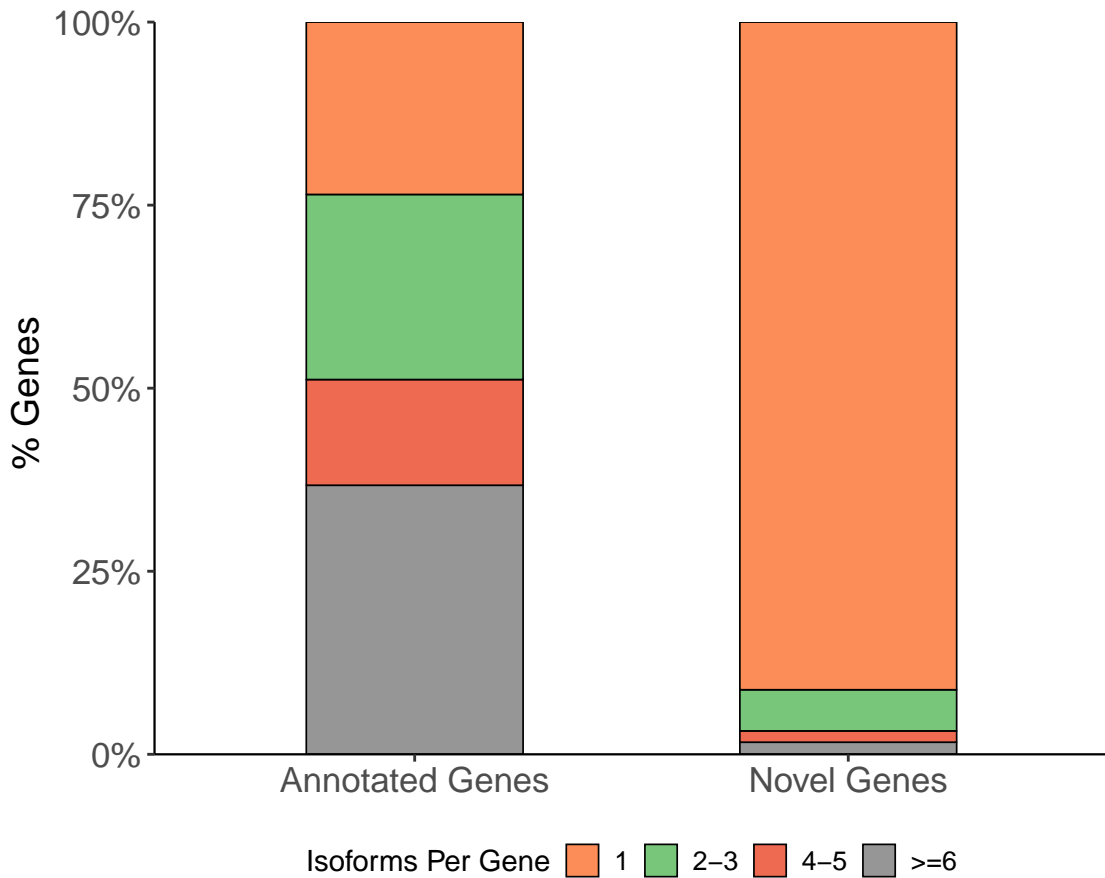
| Category | # Isoforms |
|------------------|------------|
| FSM | 21131 |
| ISM | 8777 |
| NIC | 20769 |
| NNC | 23161 |
| Genic Genomic | 87 |
| Antisense | 489 |
| Fusion | 1021 |
| Intergenic | 636 |
| Genic Intron | 0 |

Gene Characterization

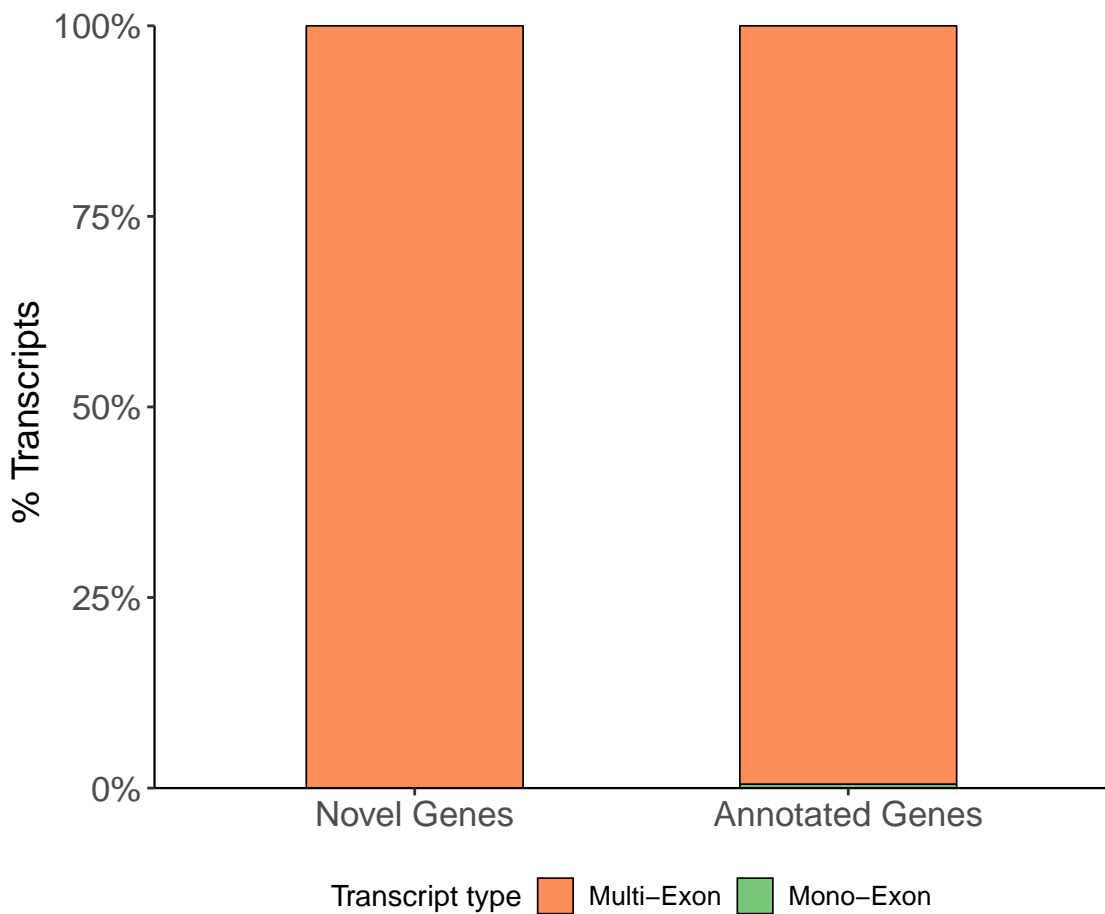
Number of Isoforms per Gene



Number of Isoforms per Gene, Known vs Novel Genes



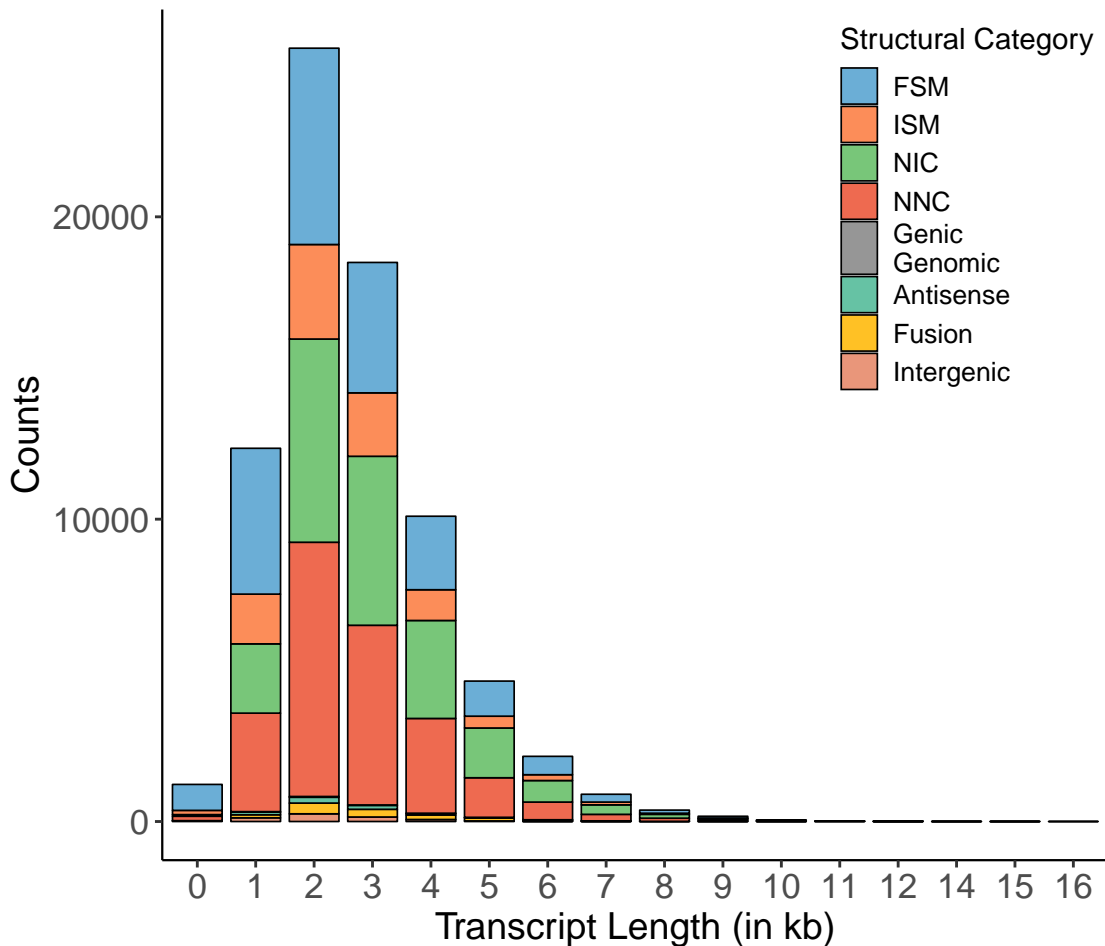
Distribution of Mono- vs Multi-Exon Transcripts



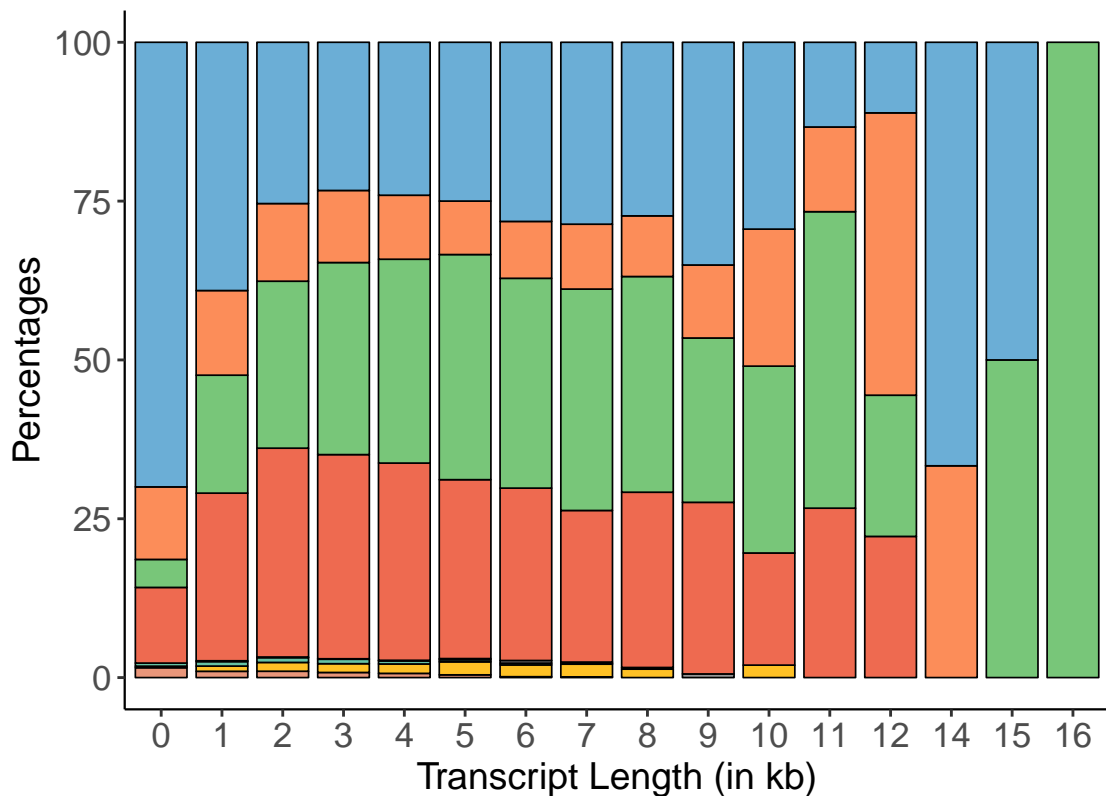
Structural Category

- FSM
- ISM
- NIC
- NNC
- Genic
- Genomic
- Antisense
- Fusion
- Intergenic

Transcript Length (in kb)



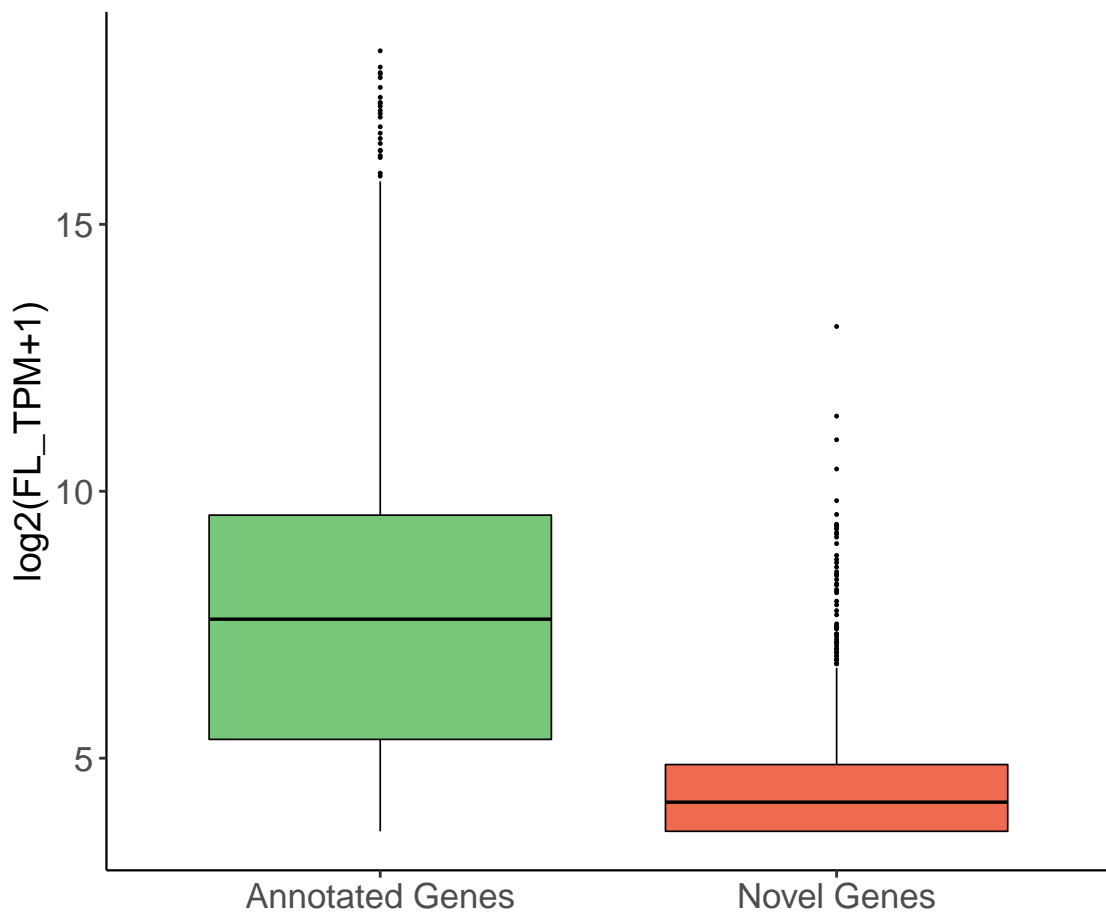
Classifications by Transcript Length, normalized



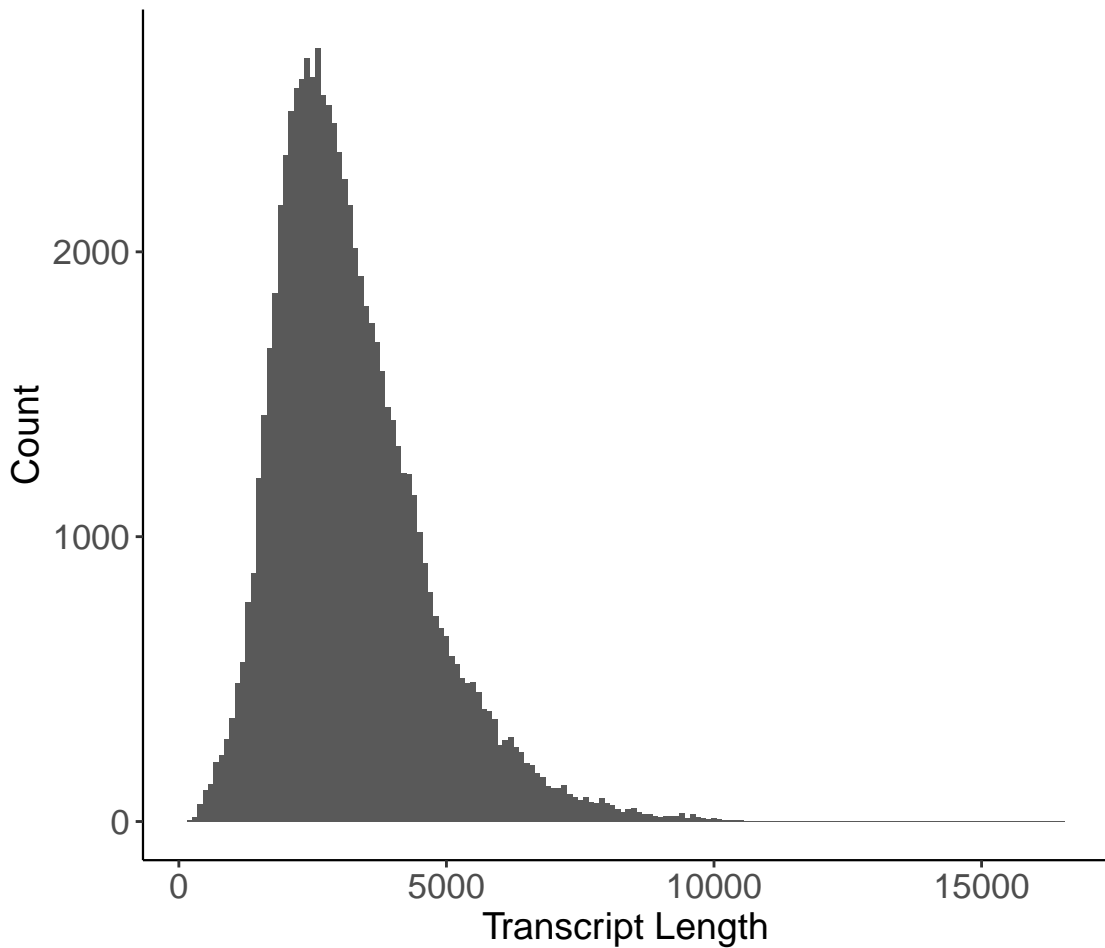
Structural Category

| | | | |
|-----|-----|-----------|------------|
| FSM | NIC | Genic | Fusion |
| ISM | NNC | Genomic | Intergenic |
| | | Antisense | |

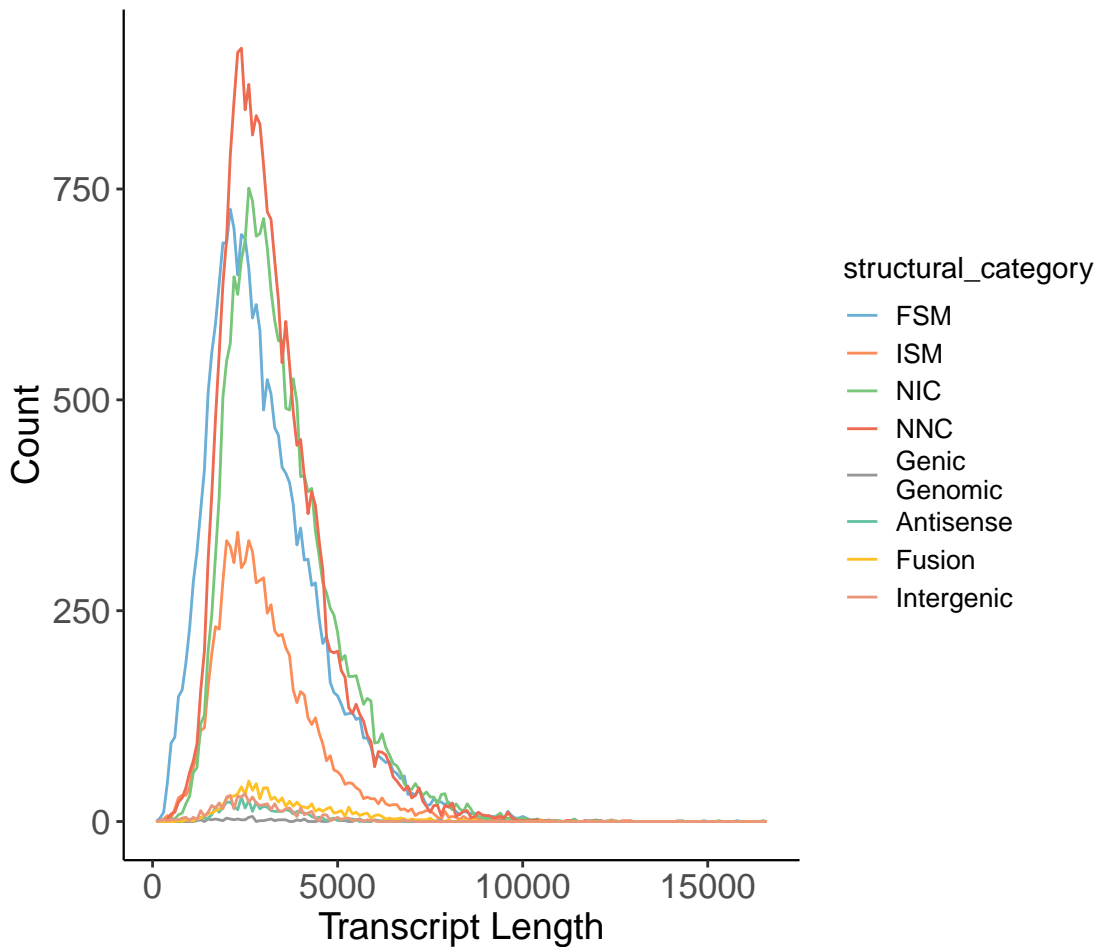
Number of FL reads per Gene by type of gene annotation



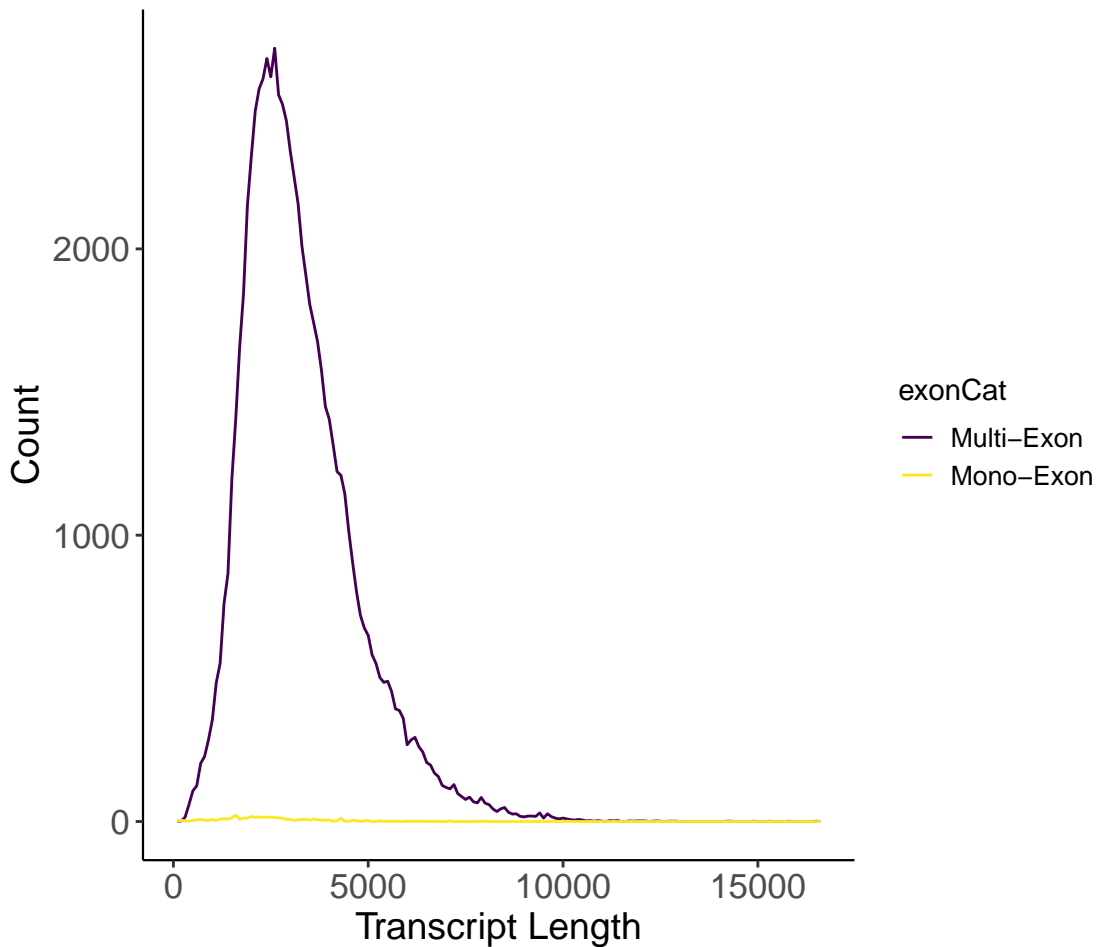
Transcript Lengths, all transcripts



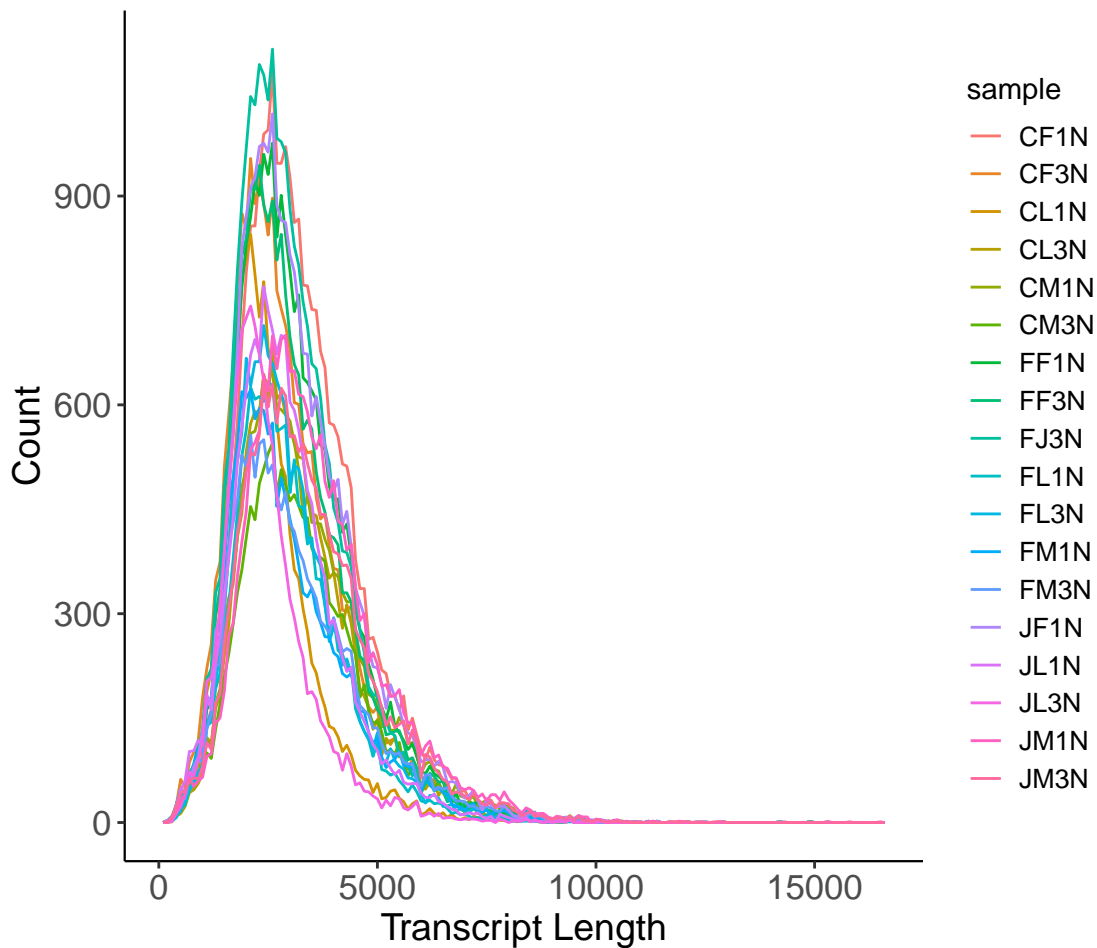
Transcript Lengths, by structural category



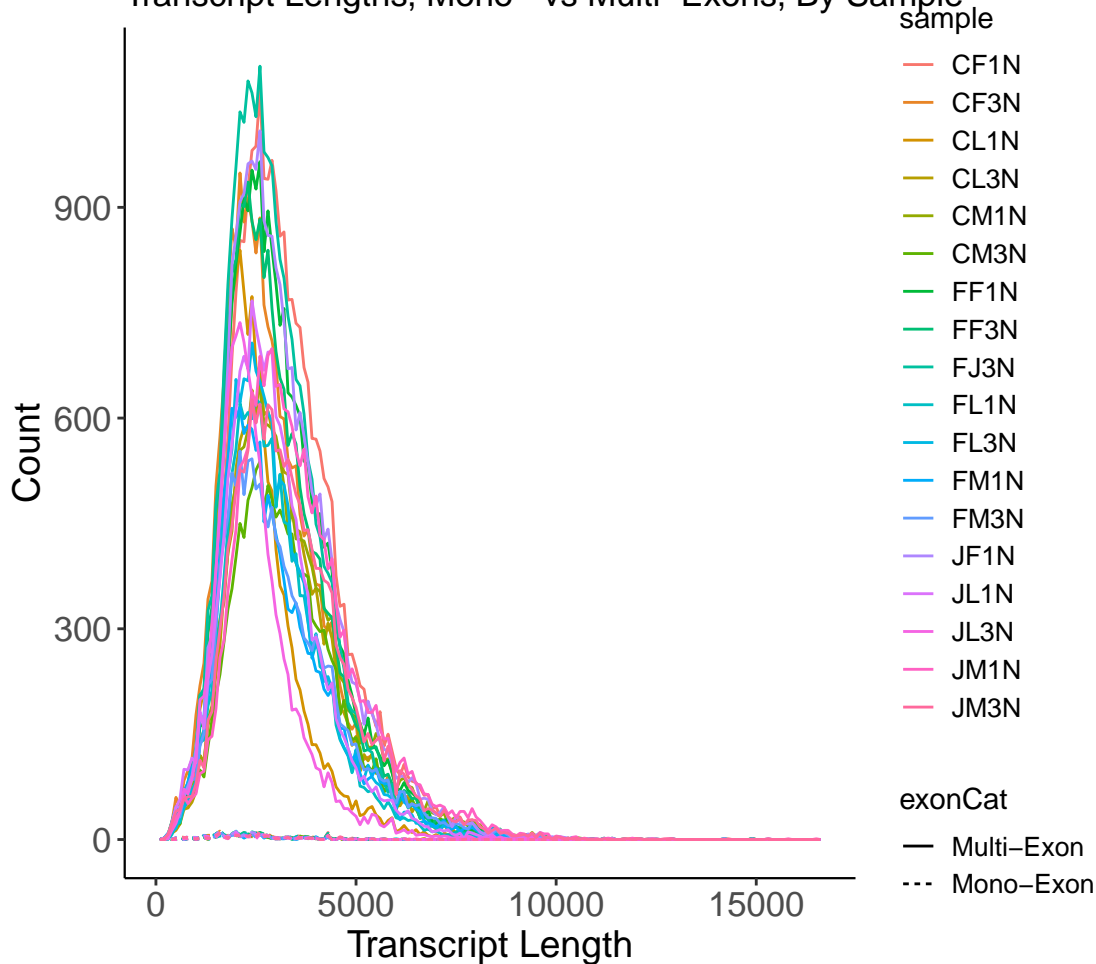
Transcript Lengths, Mono- vs Multi-Exons



Transcript Lengths, By Sample

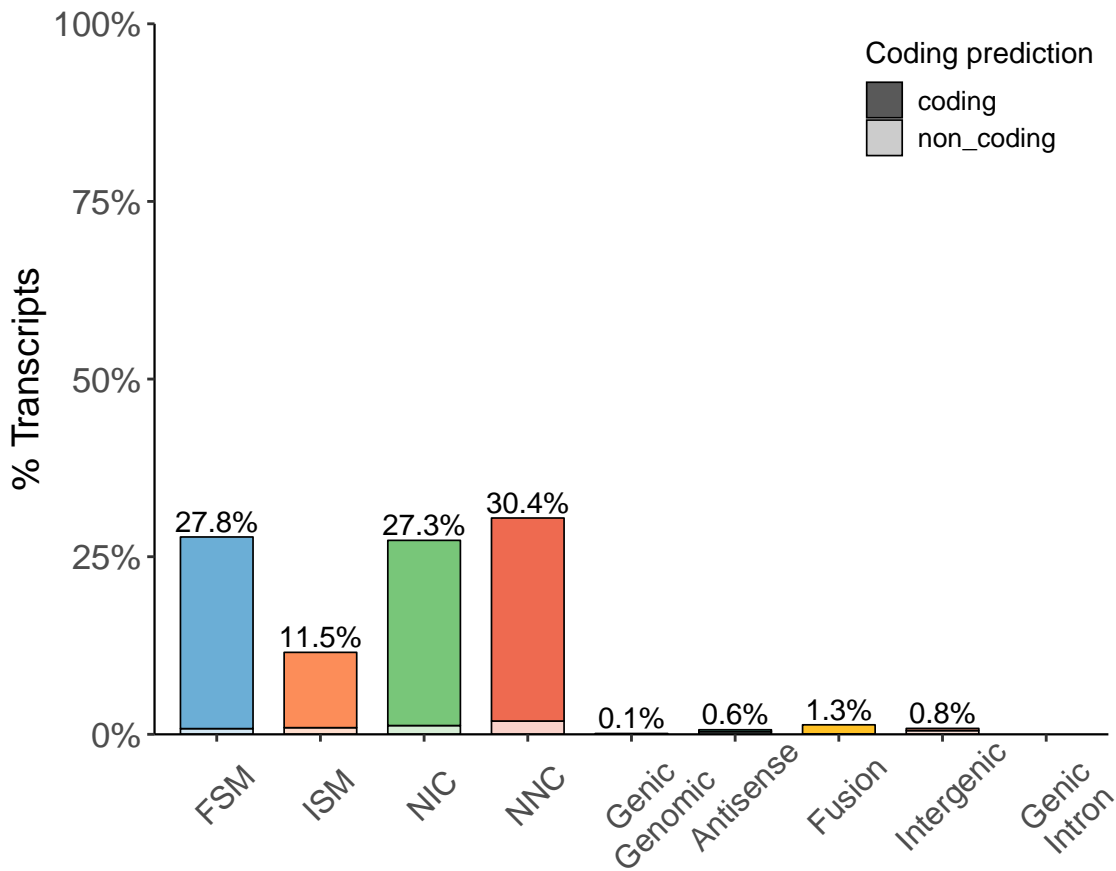


Transcript Lengths, Mono- vs Multi-Exons, By Sample

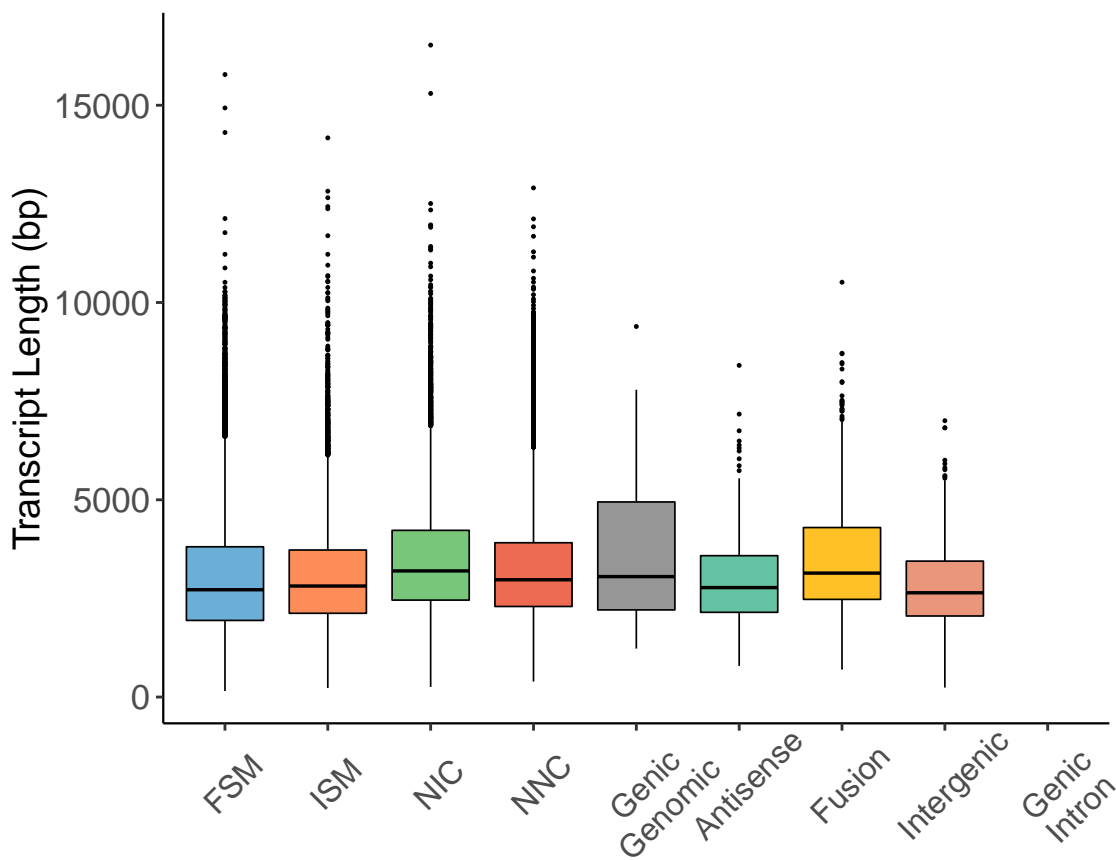


*Structural Isoform Characterization
by Splice Junctions*

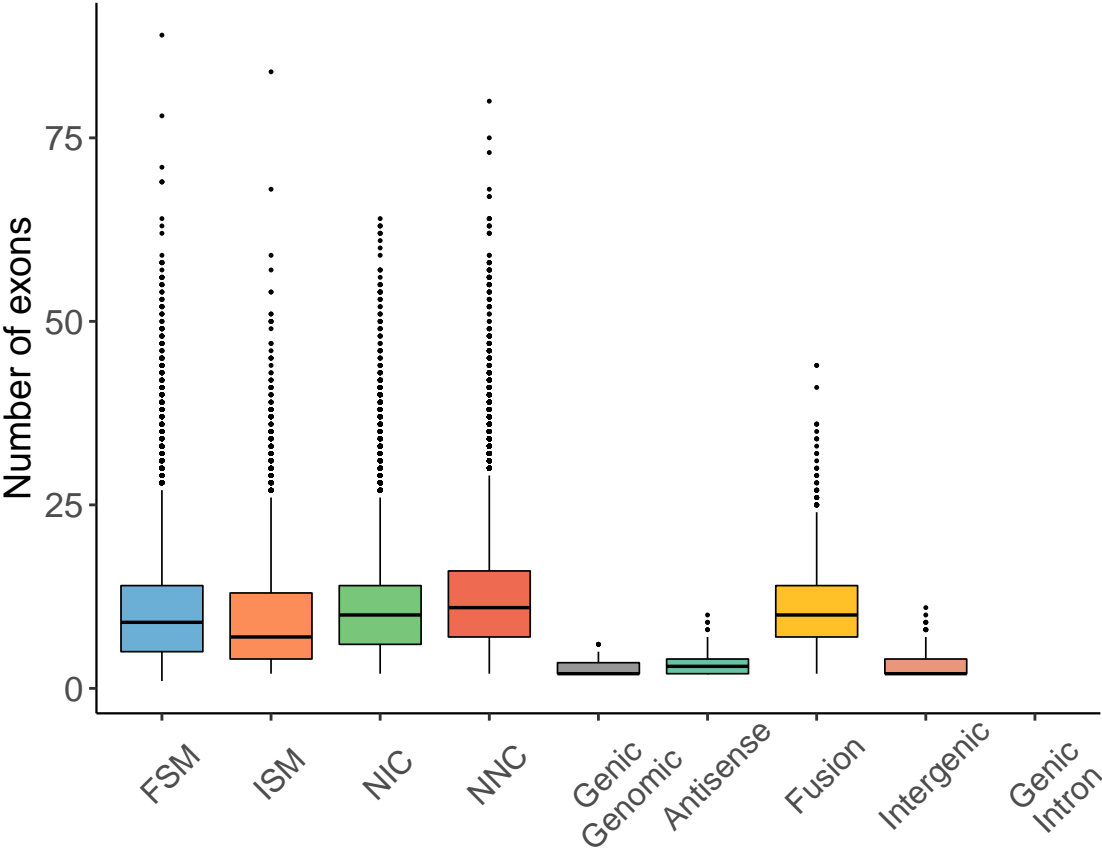
Isoform distribution across structural categories



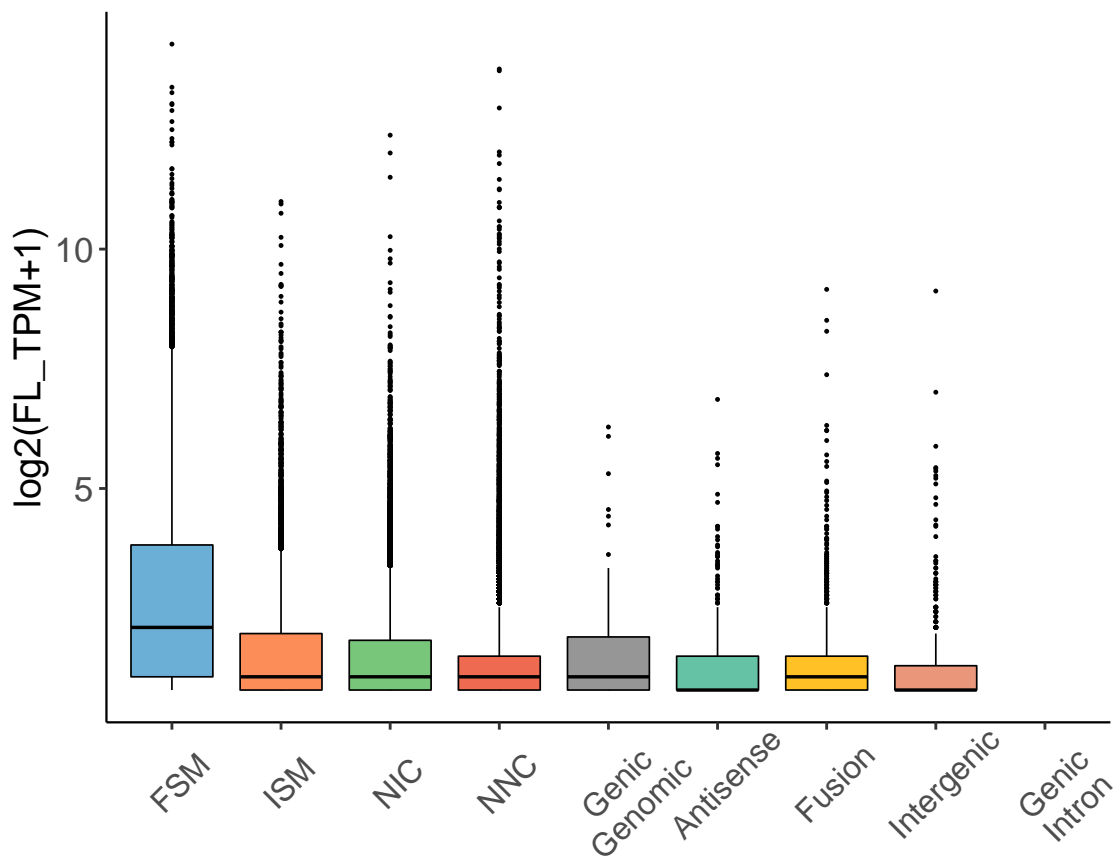
Transcript Lengths by Structural Classification



Exon Counts by Structural Classification

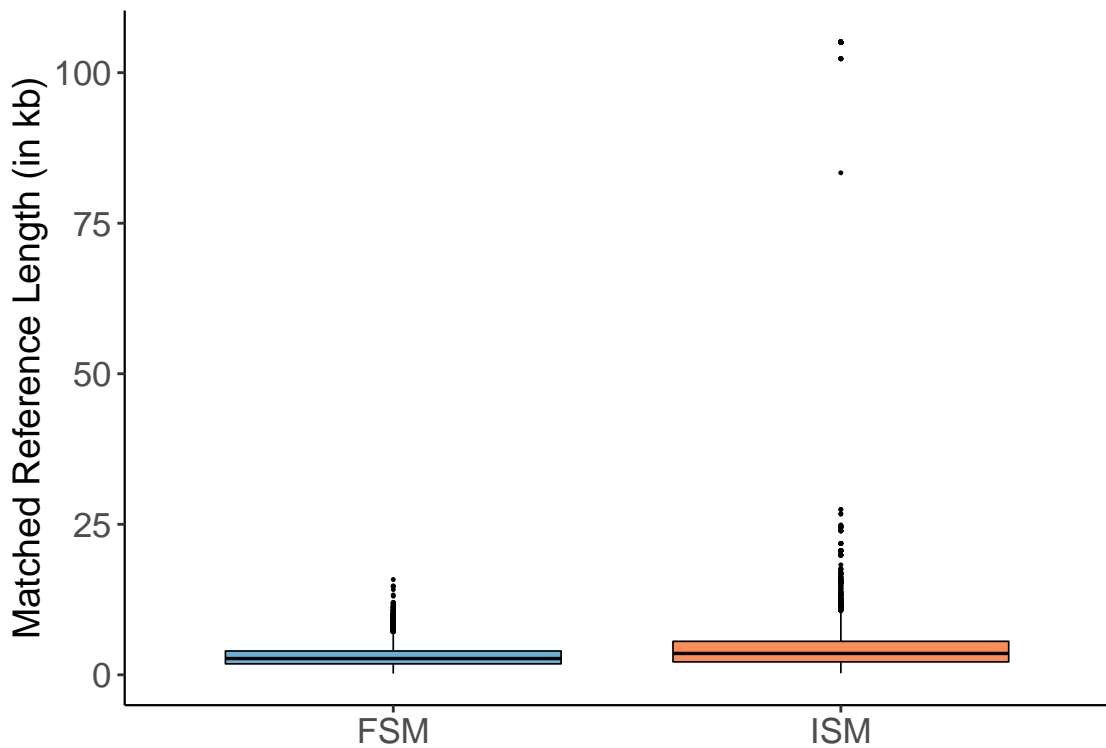


FL Count (normalized) by Structural Category



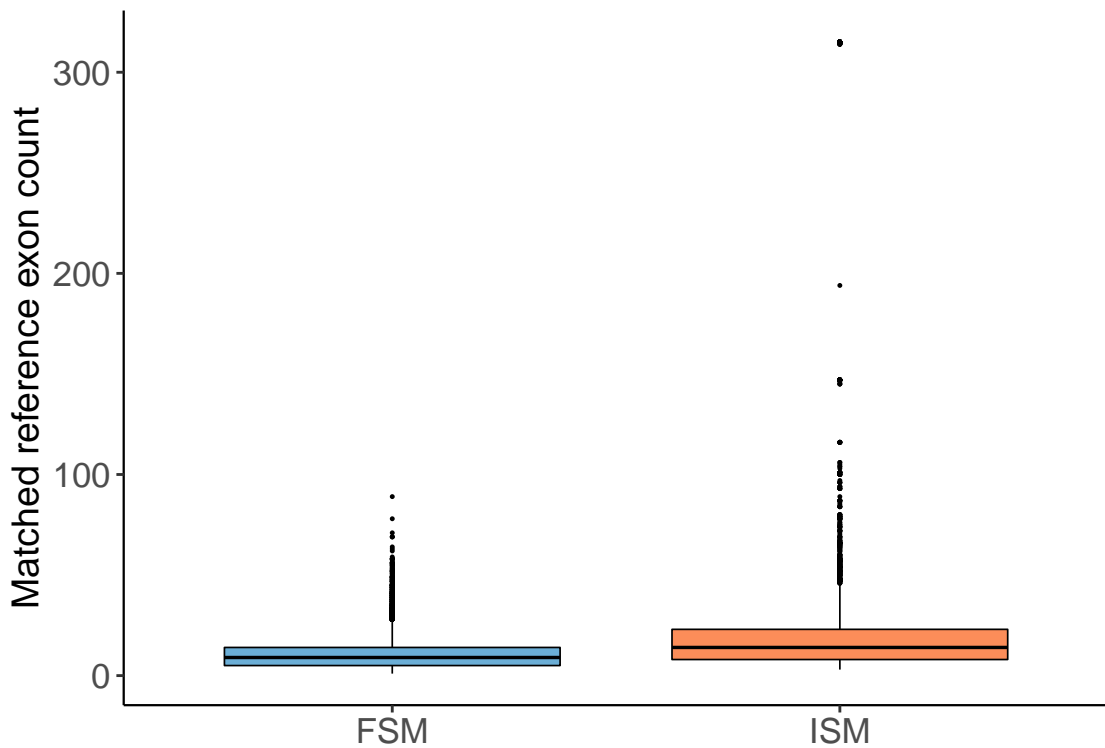
Length Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories



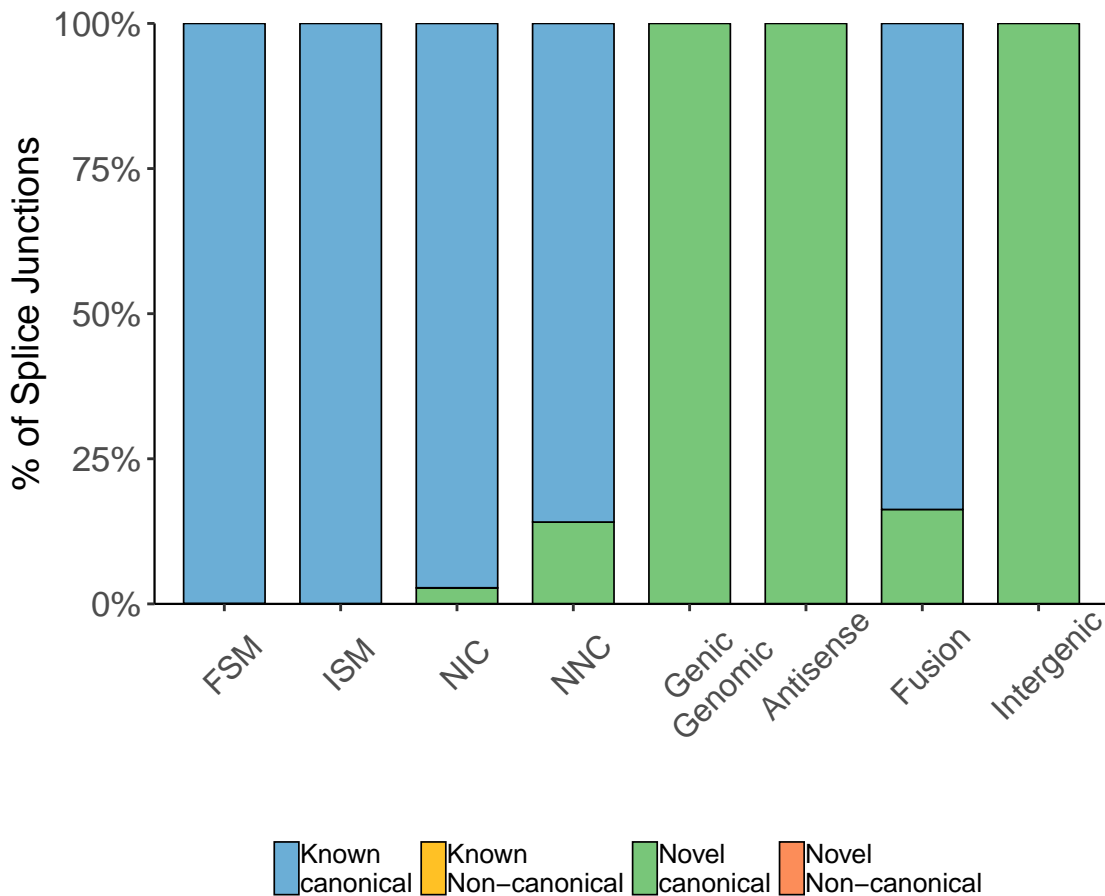
Exon Count Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories

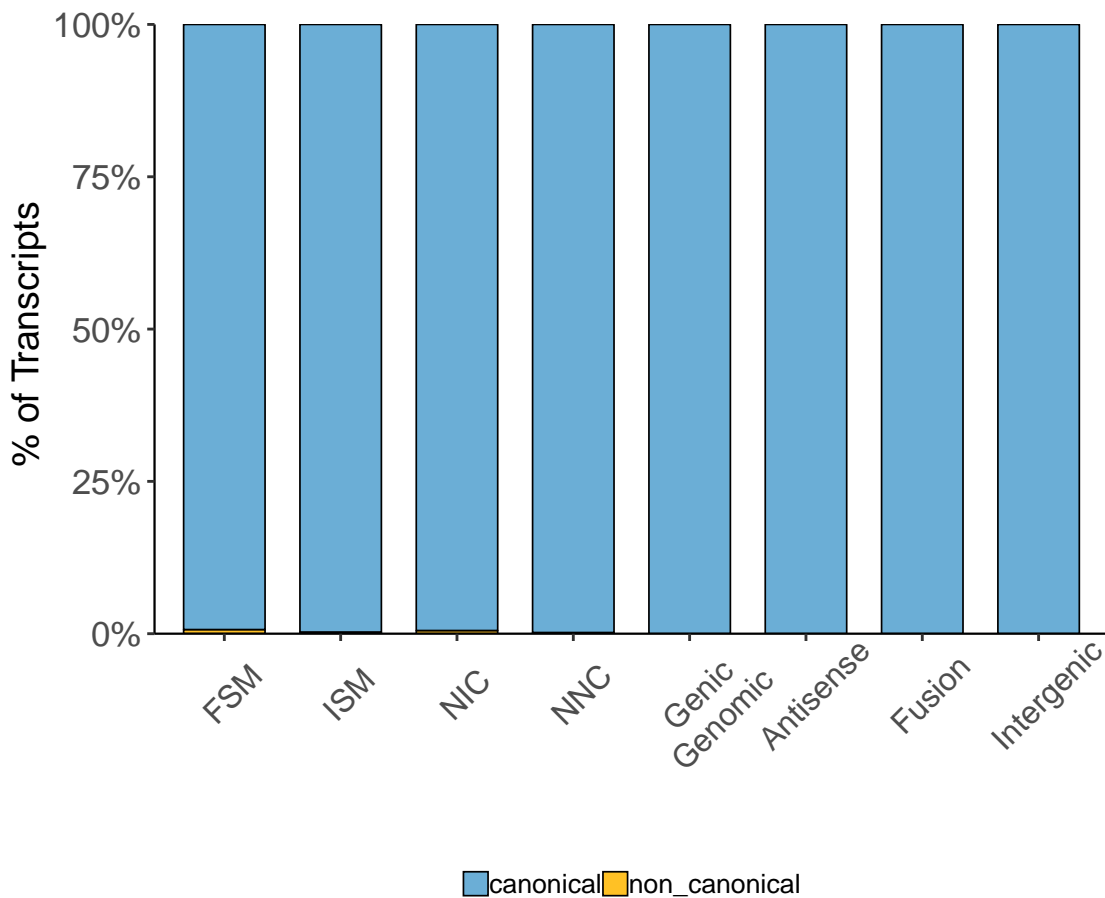


Splice Junction Characterization

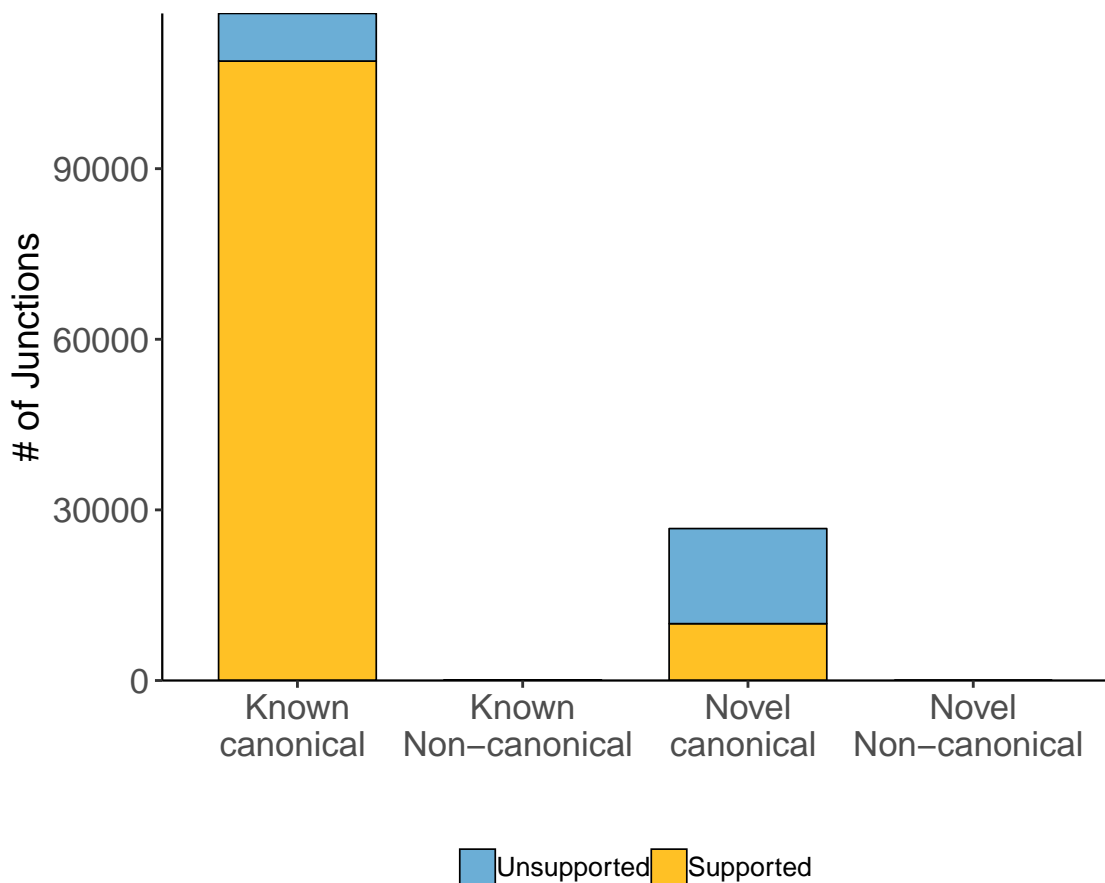
Distribution of Splice Junctions by Structural Classification



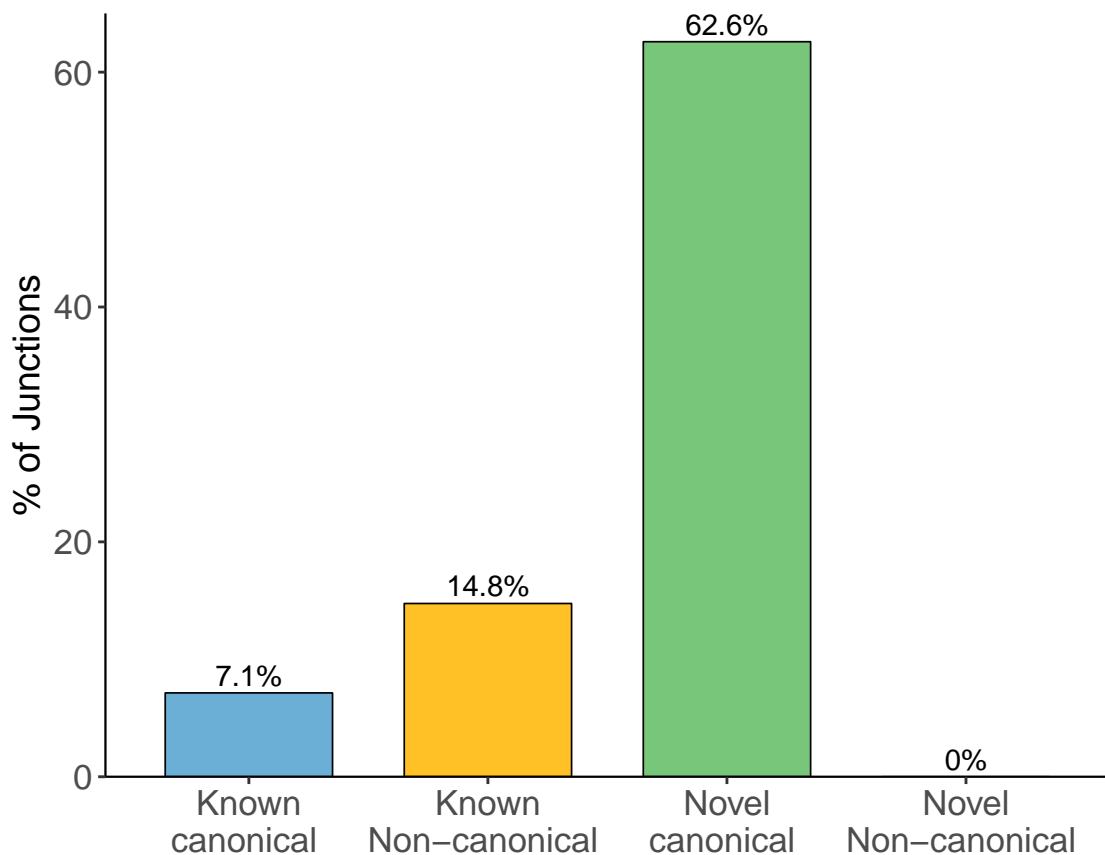
Distribution of Transcripts by Splice Junctions



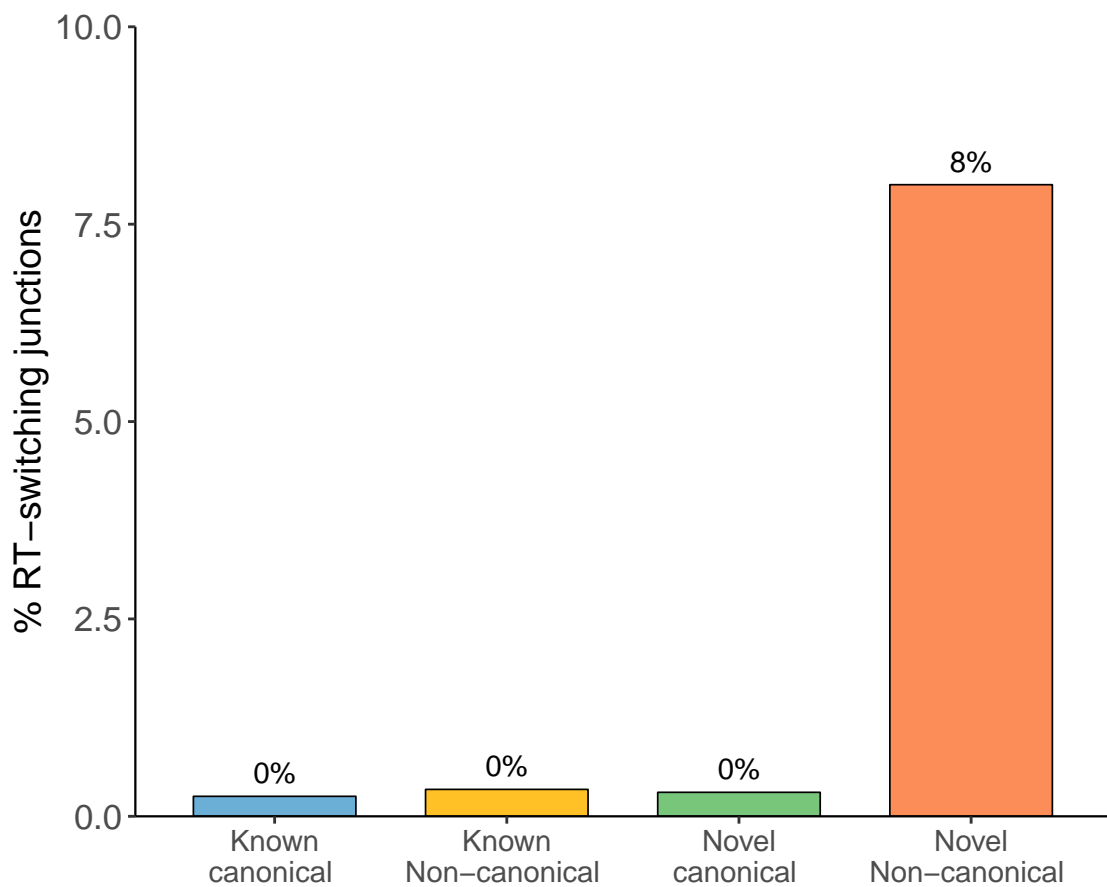
Unique junctions w/ or w/out short read coverage



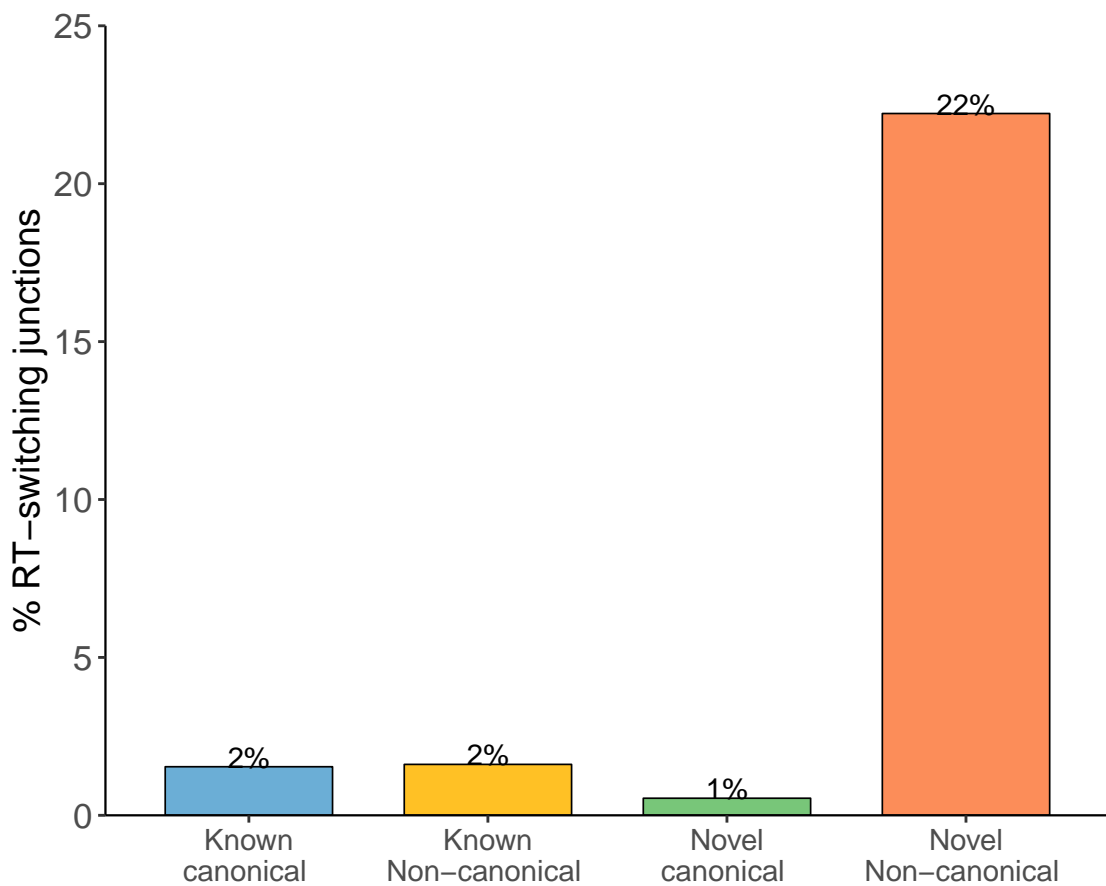
Unique junctions w/out short read coverage (percentage)



RT-switching, all junctions



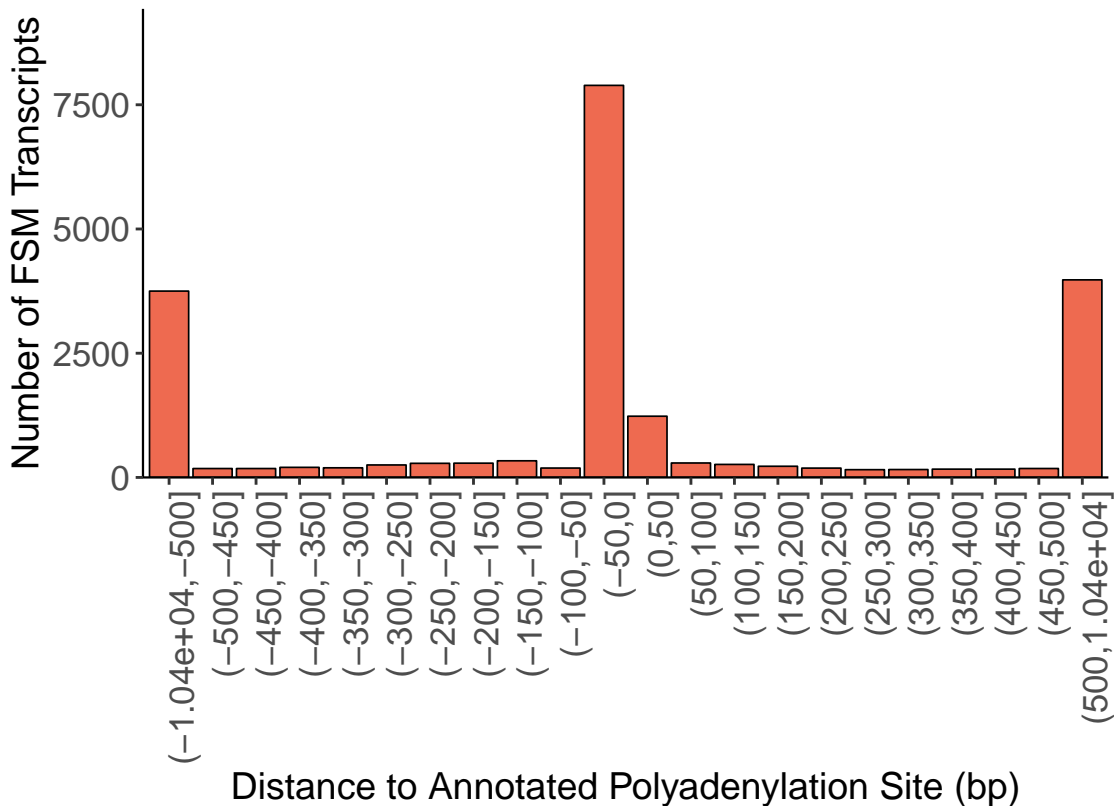
RT-switching, unique junctions



Comparison with Annotated TSS and PolyA Sites

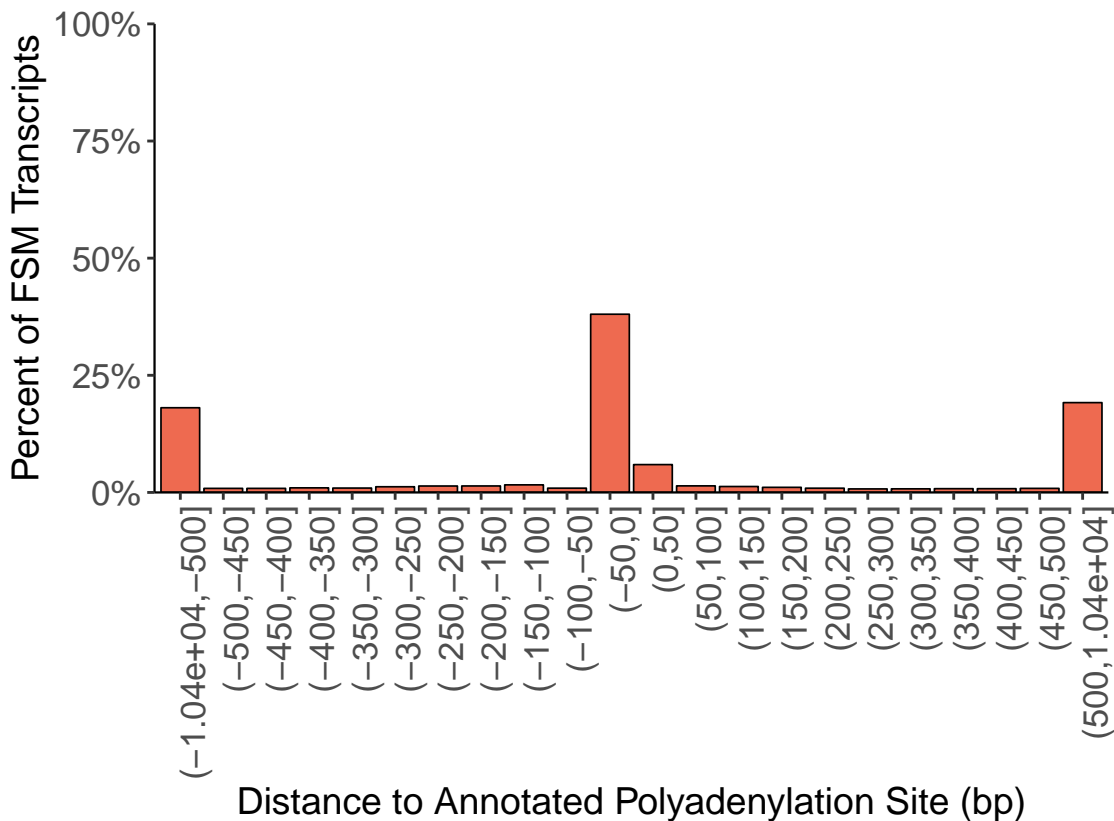
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



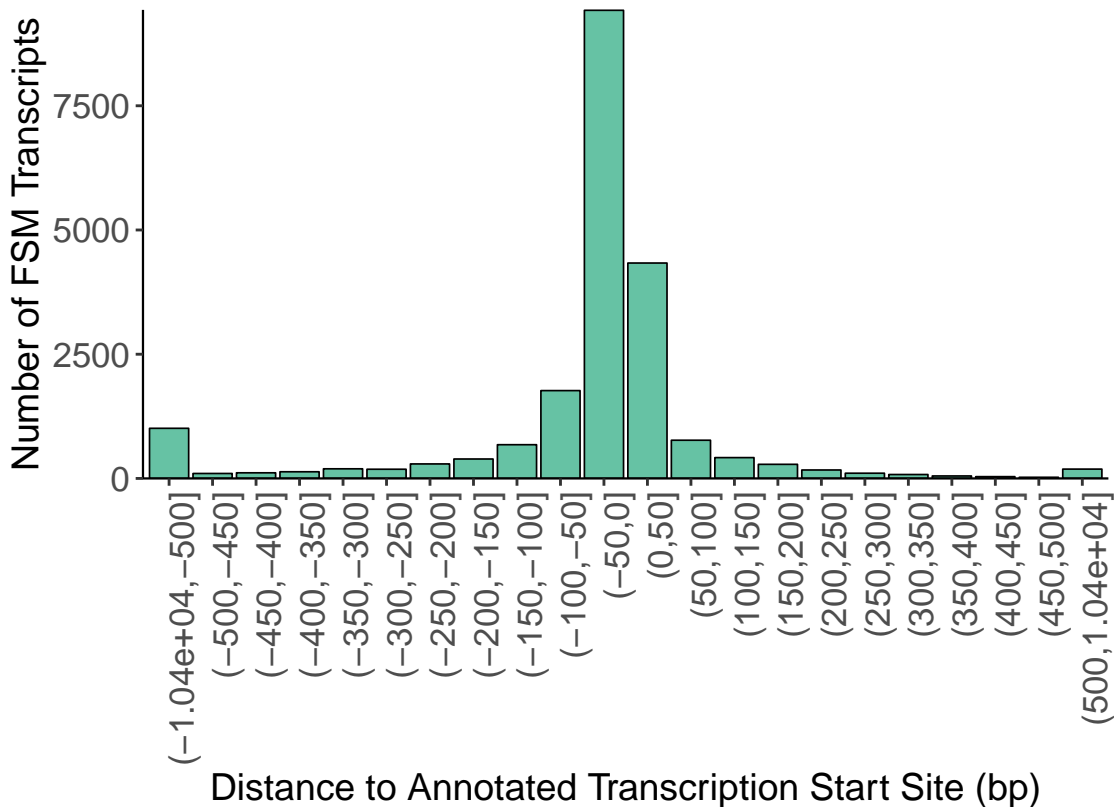
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



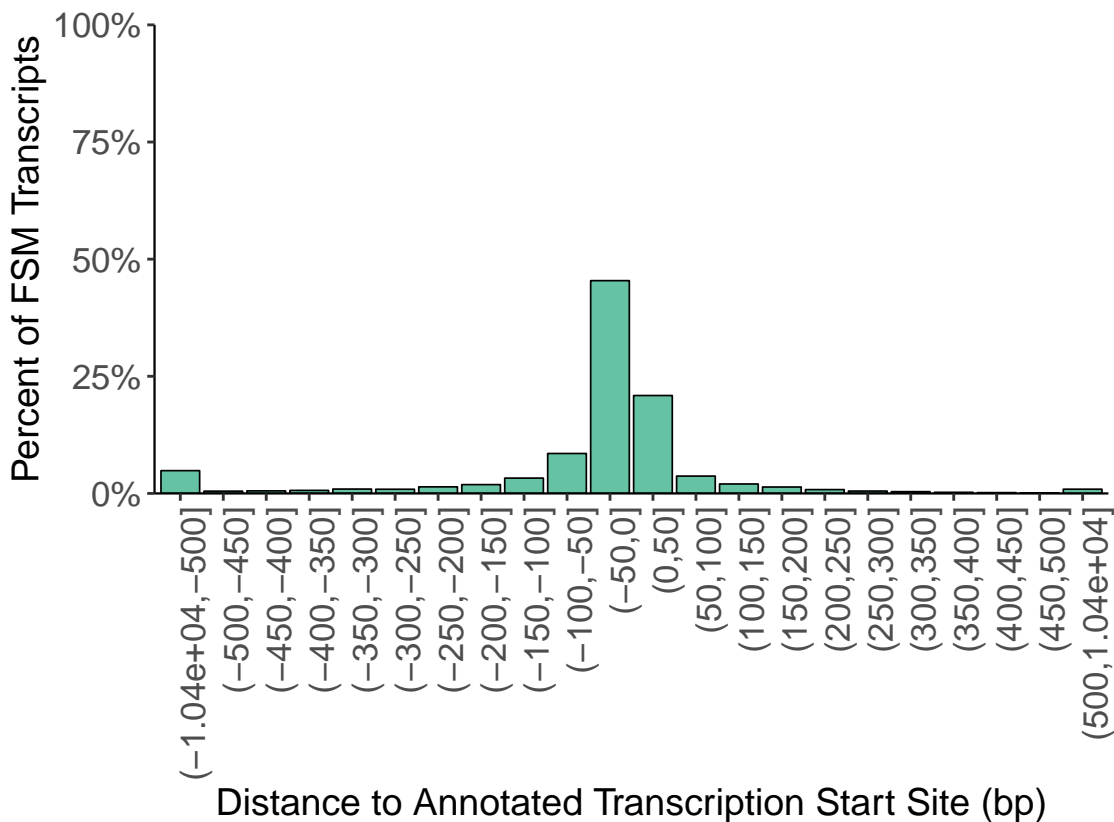
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



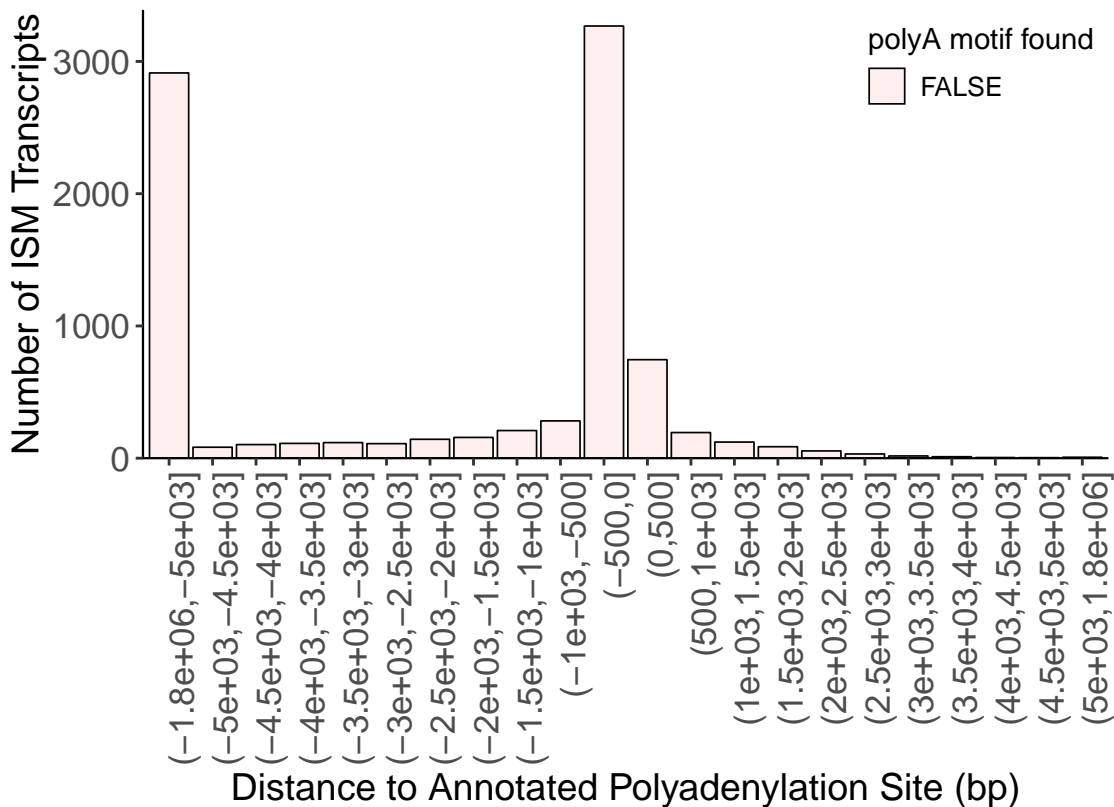
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



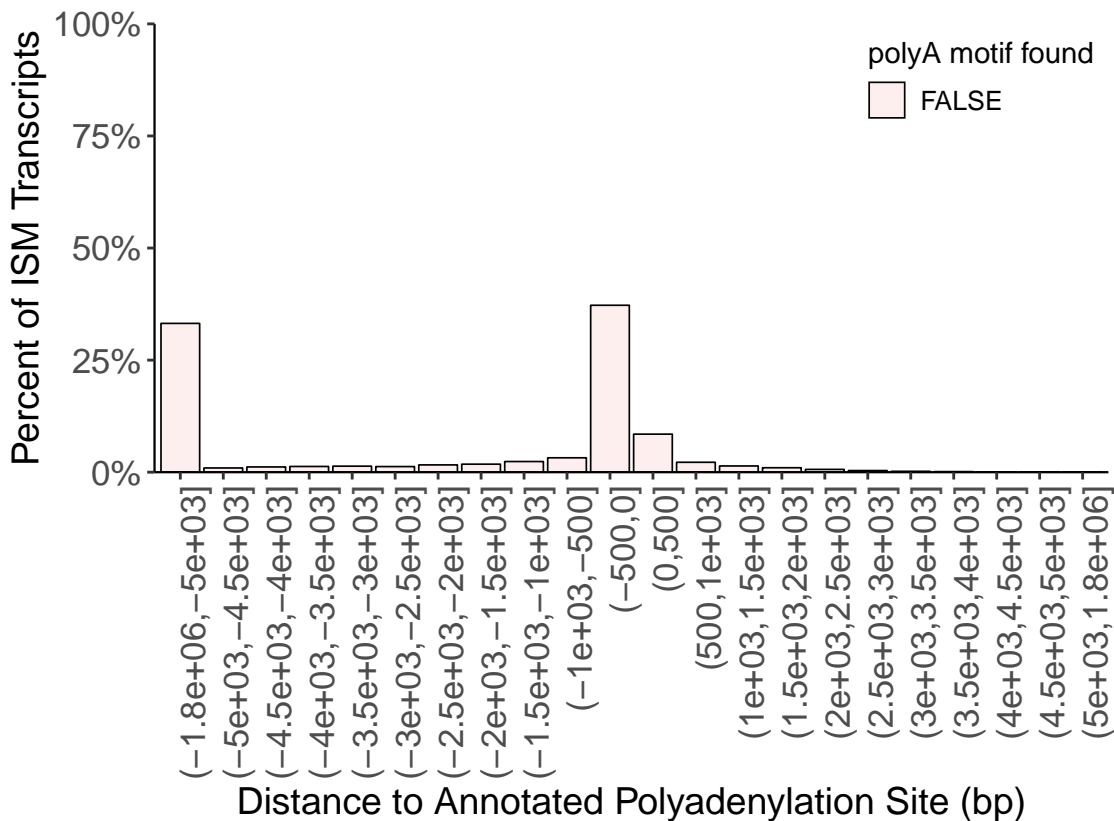
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



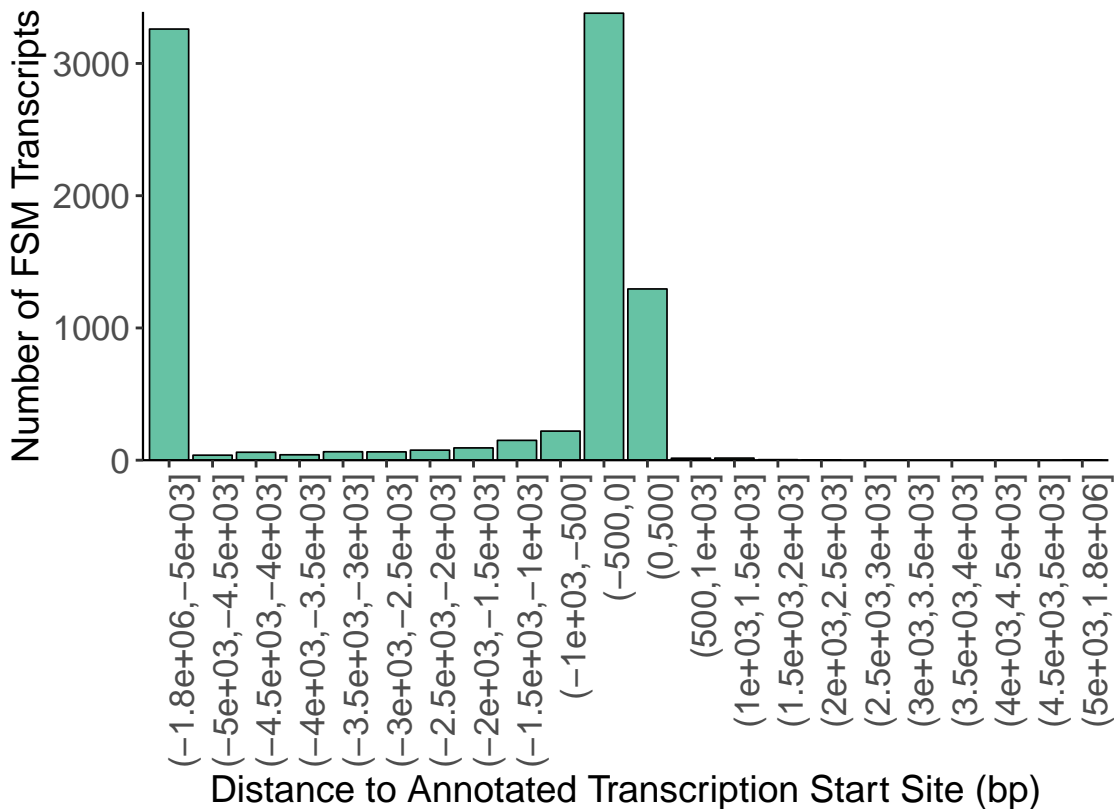
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



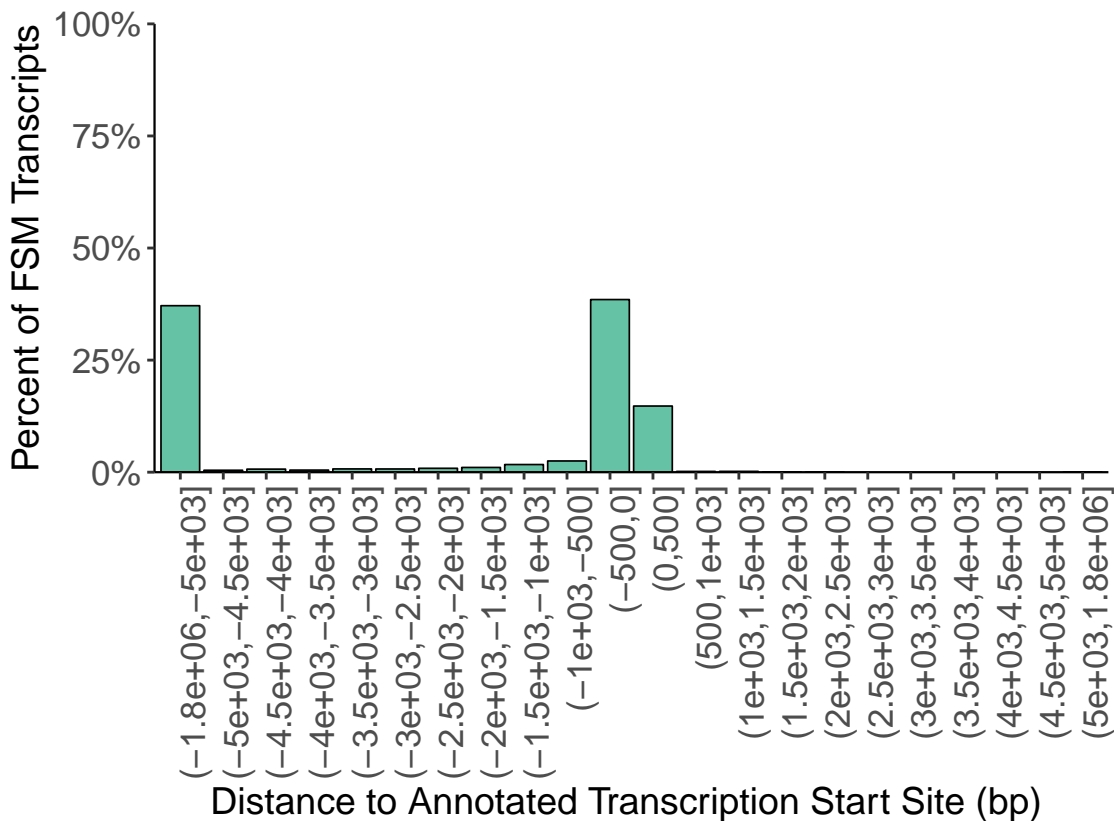
Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site, ISM only

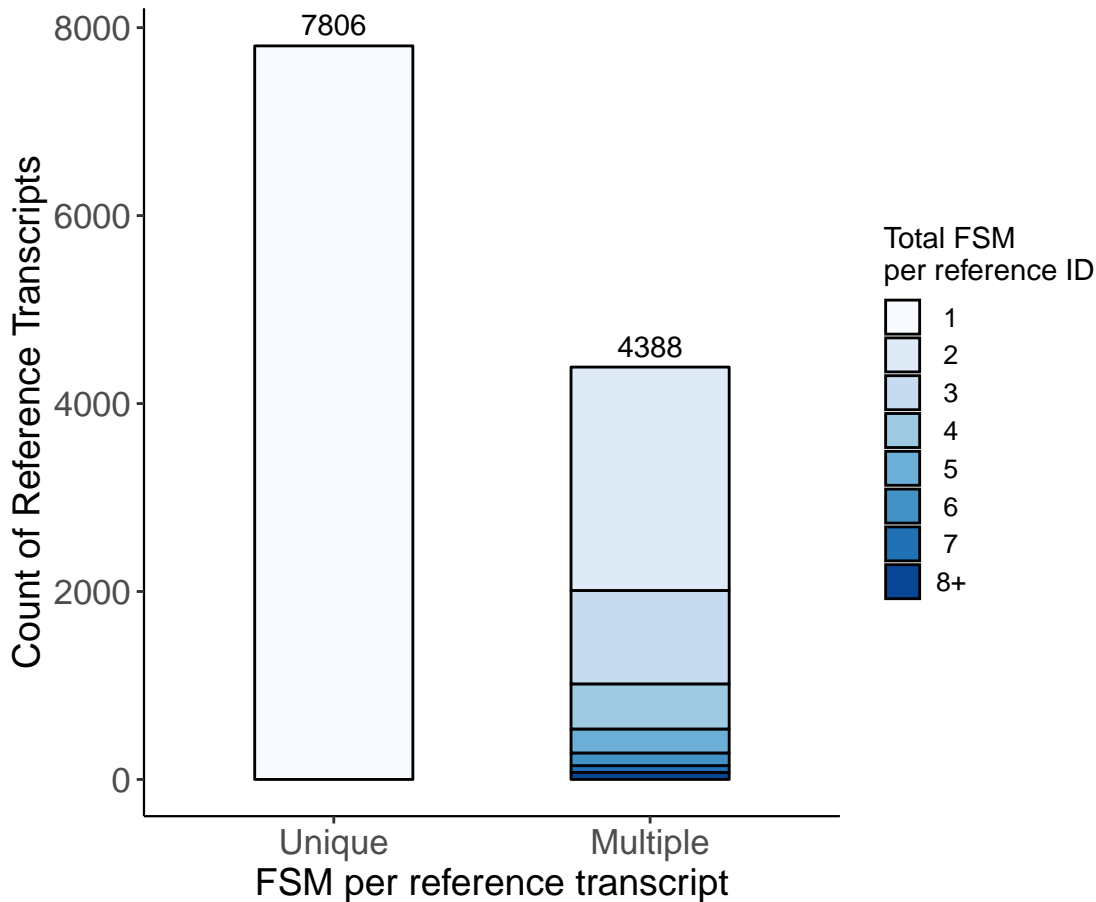
Negative values indicate downstream of annotated TSS



*Accumulation of FSM and ISM
to the same reference transcript*

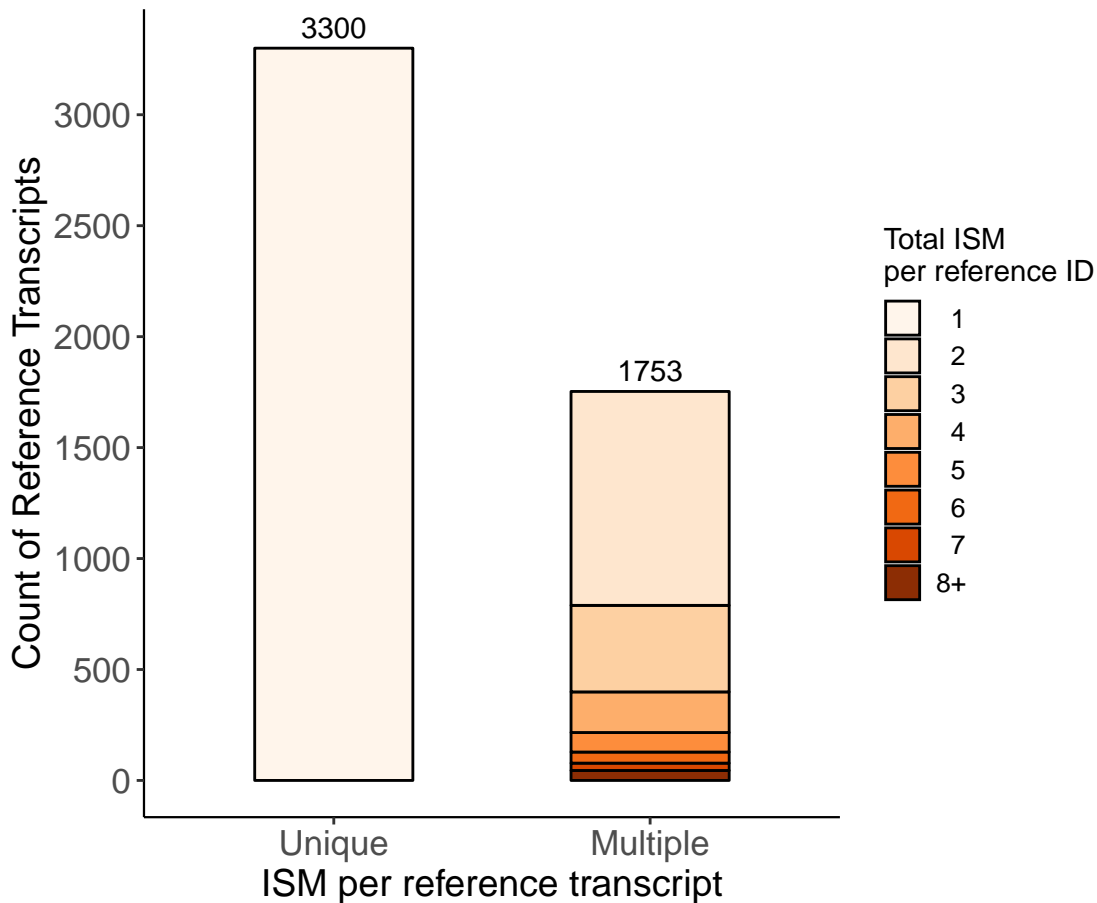
Reference transcript redundance

Only FSM



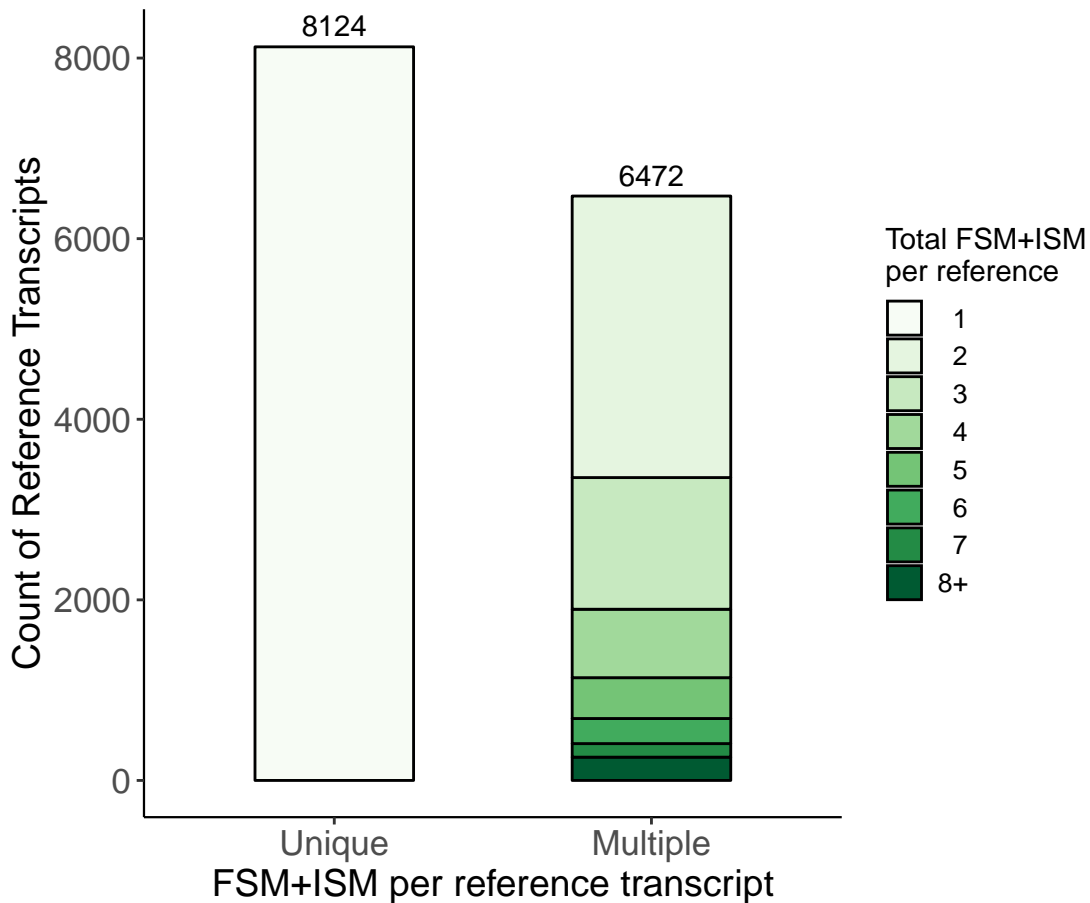
Reference transcript redundance

Only ISM



Reference transcript redundance

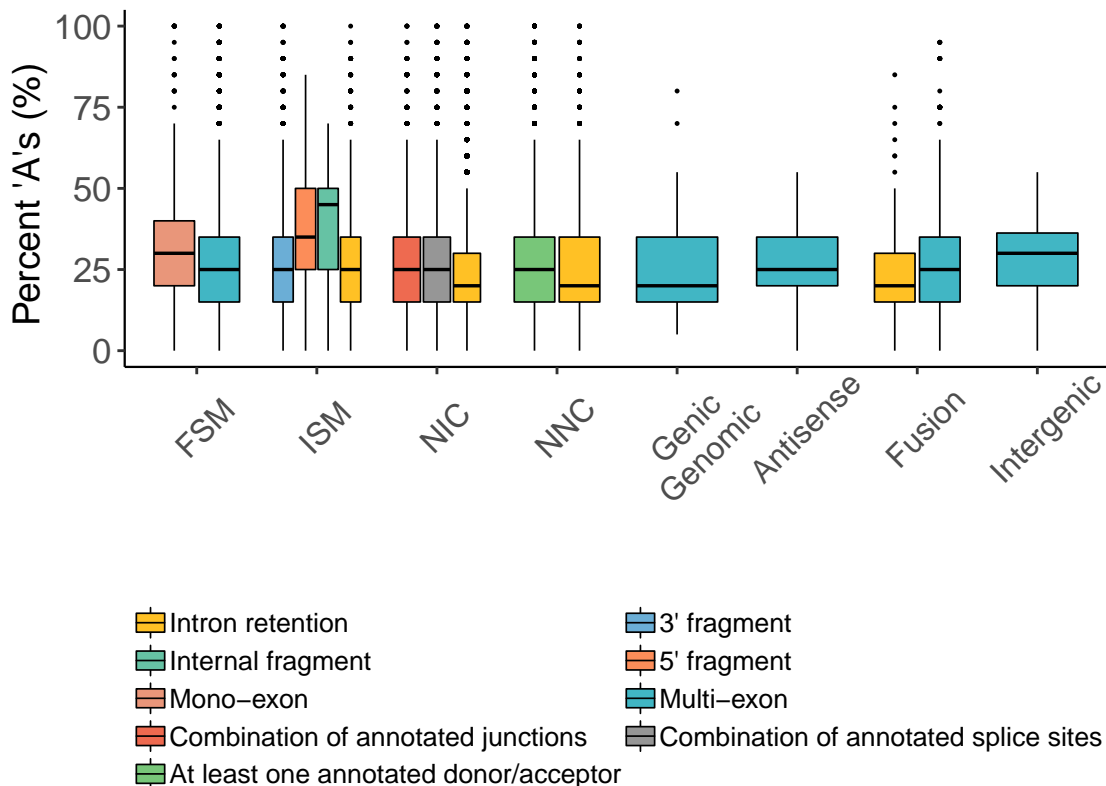
FSM+ISM



Intra-Priming Quality Check

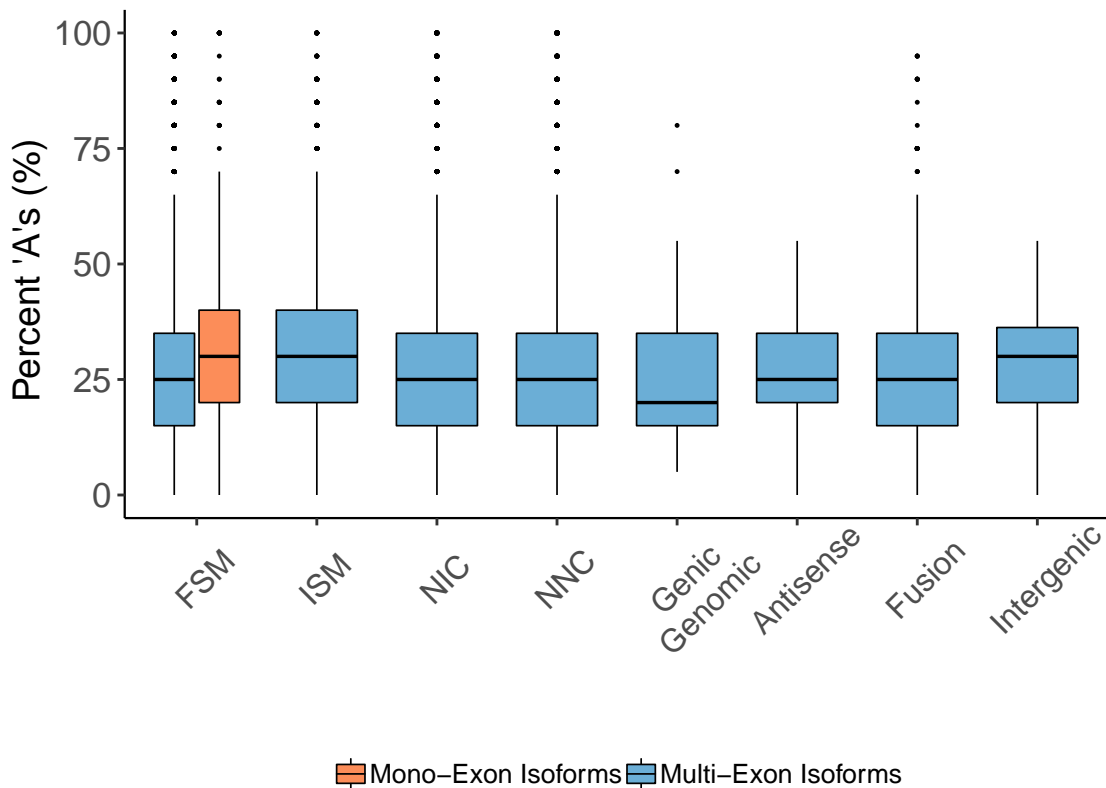
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



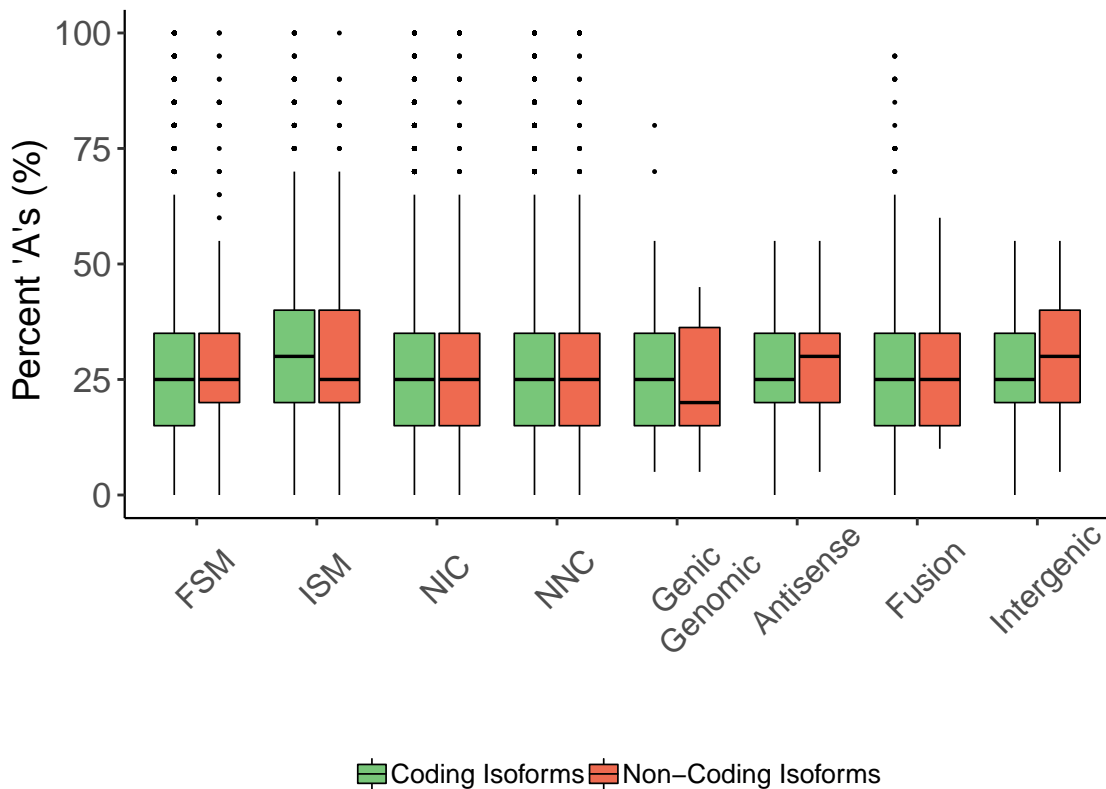
Possible Intra-Priming, Mono- vs Multi-Exon

Percent of genomic 'A's in downstream 20 bp



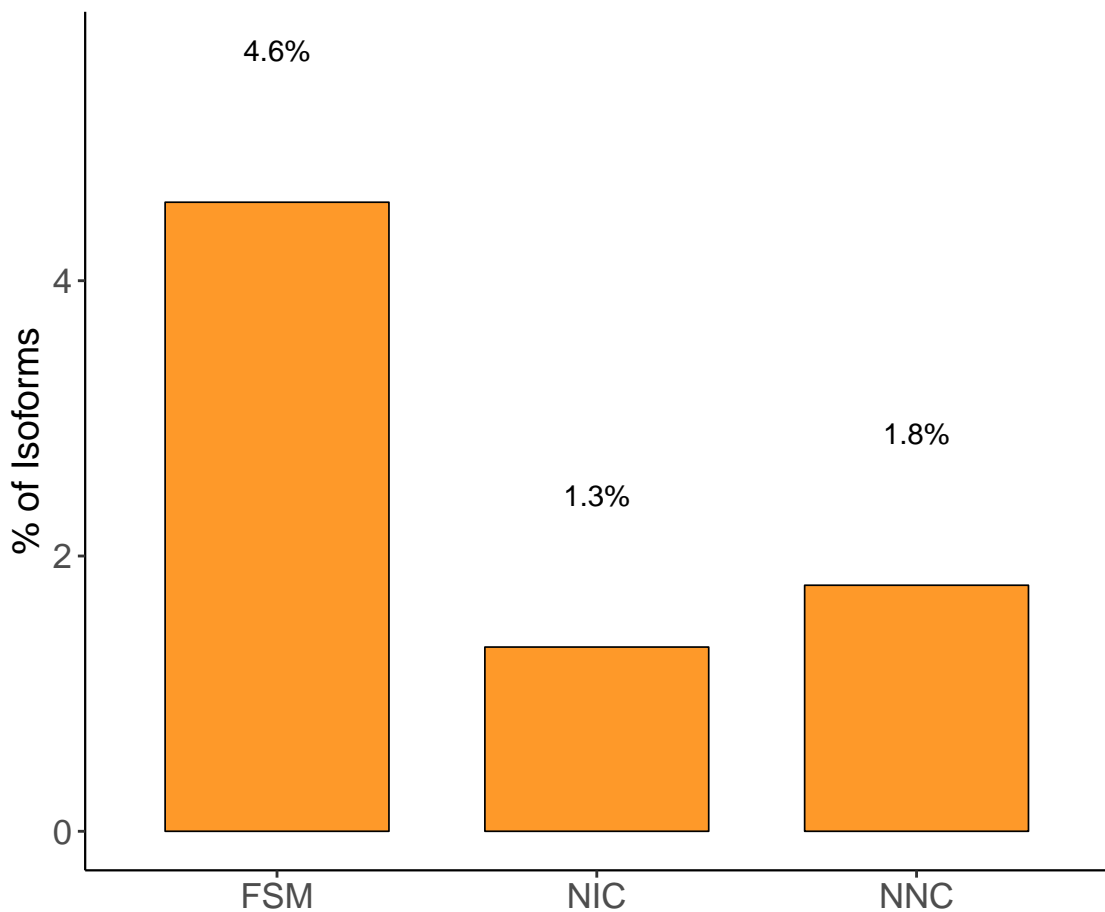
Possible Intra-Priming, Coding vs Non-Coding

Percent of genomic 'A's in downstream 20 bp

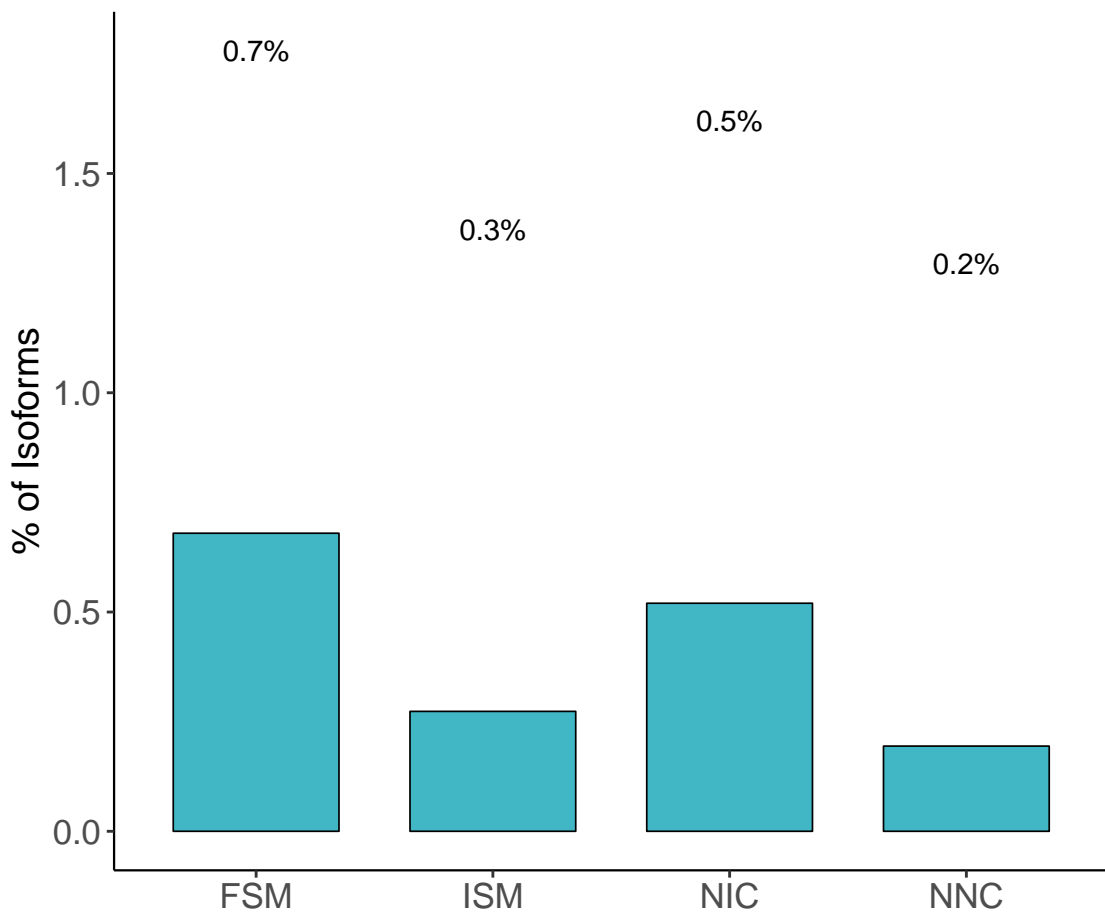


Quality Controls

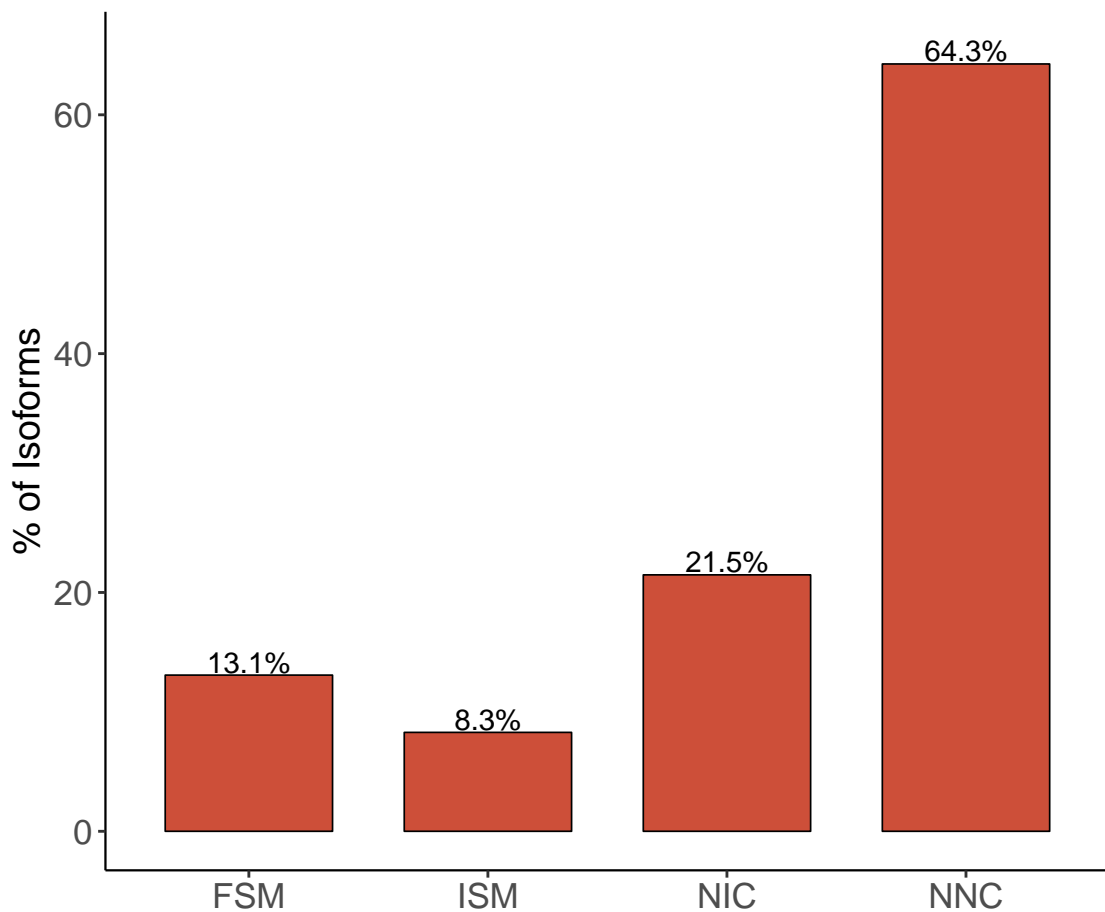
Incidence of RT-switching



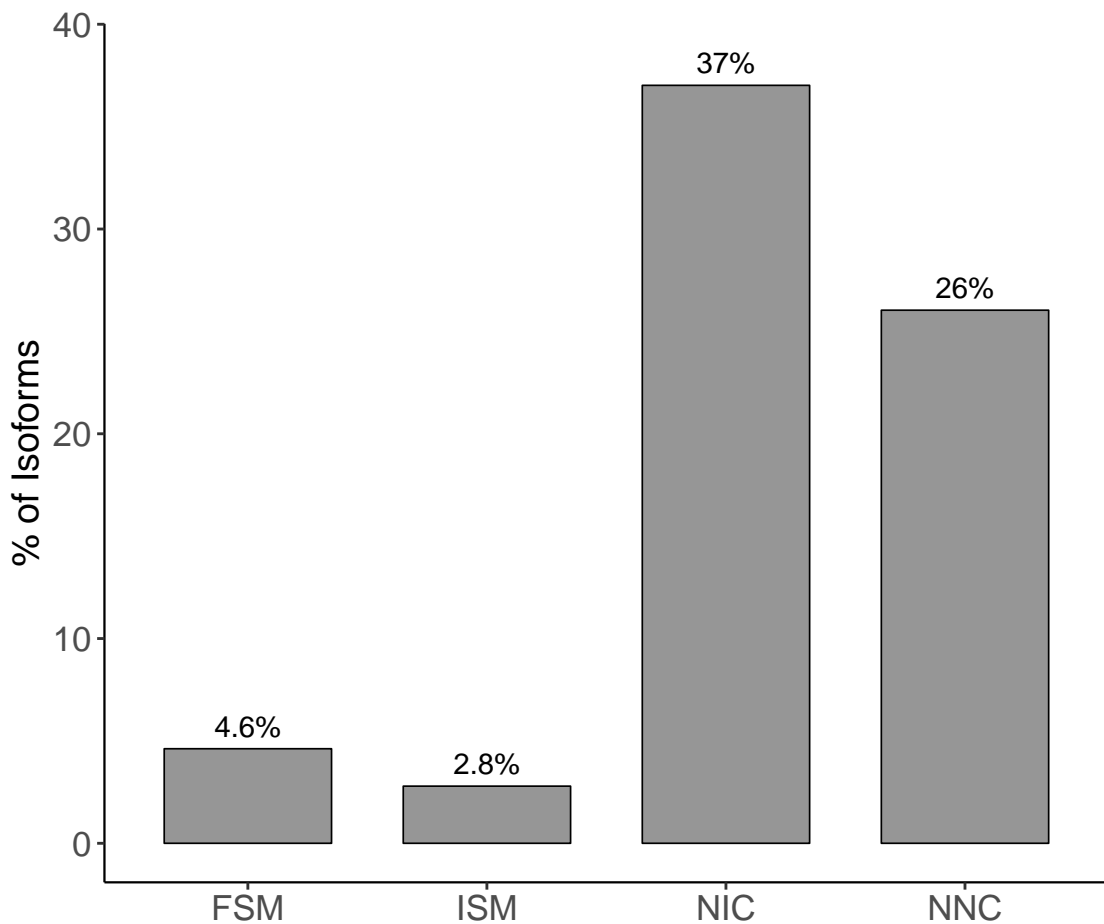
Incidence of Non-Canonical Junctions



Incidence of SJ without SR coverage Junctions



Incidence of NMD by structural category



Quality control attributes across structural categories

