

SQANTI3 report

Unique Genes: 7486
Unique Isoforms: 16160

Gene classification

| Category | # Genes |
|-----------------|----------------|
| Annotated Genes | 6487 |
| Novel Genes | 999 |

*Characterization of transcripts
based on splice junctions*

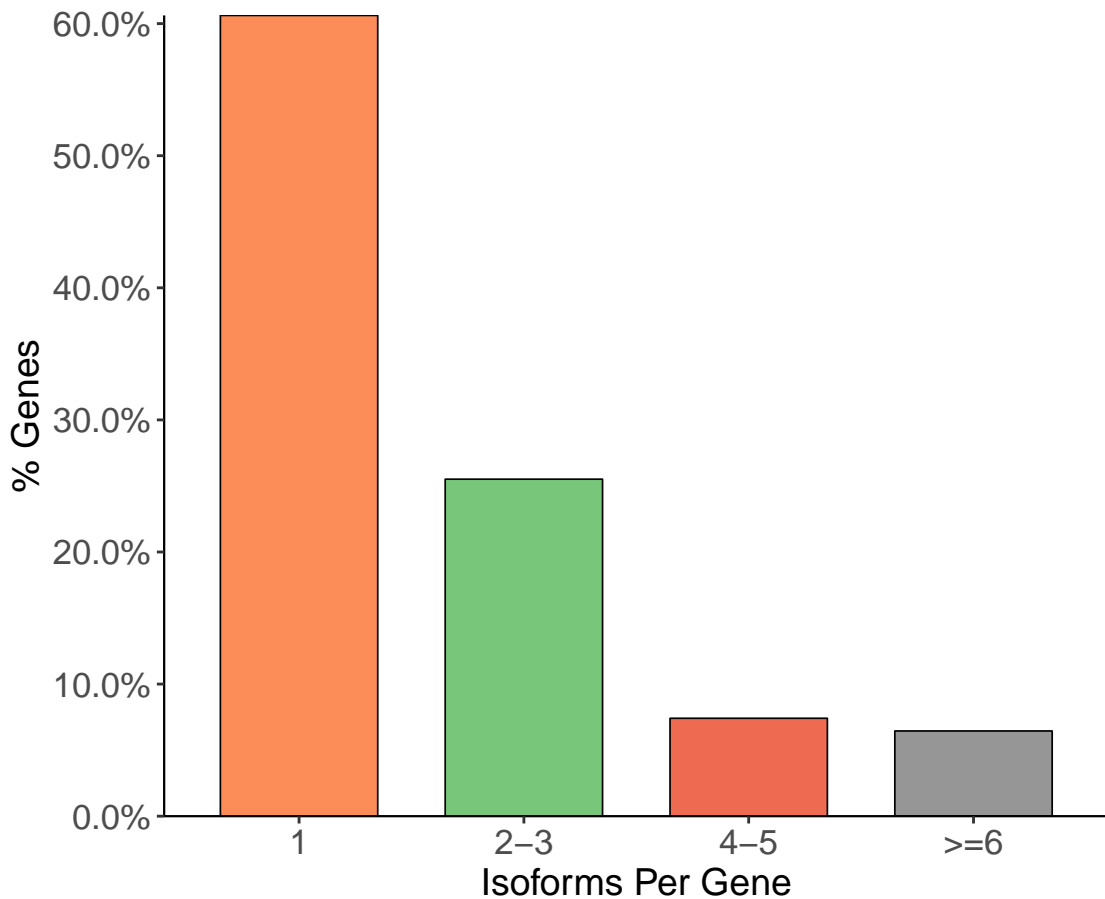
| Category | # Isoforms |
|------------------|-------------------|
| FSM | 12252 |
| ISM | 2299 |
| NIC | 244 |
| NNC | 228 |
| Genic Genomic | 116 |
| Antisense | 196 |
| Fusion | 0 |
| Intergenic | 825 |
| Genic Intron | 0 |

Splice Junction Classification

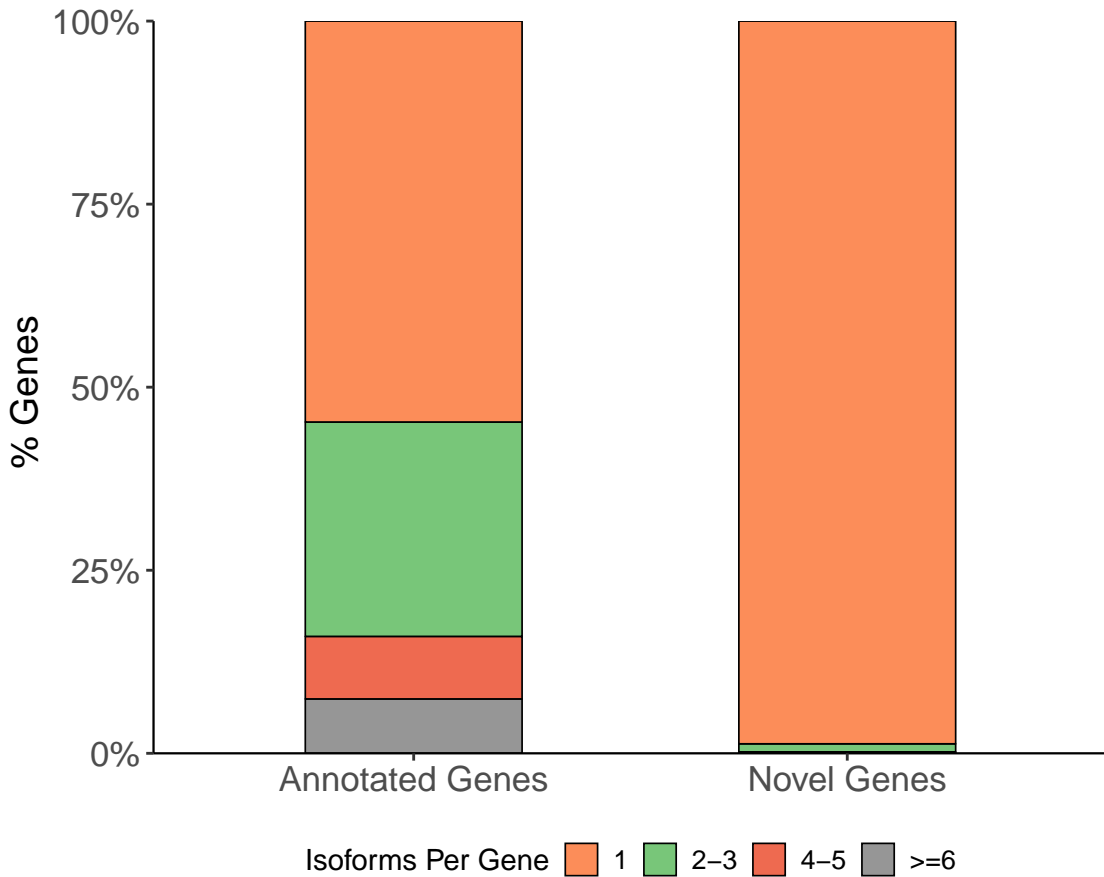
| Category | # SJs | Percent |
|---------------------|--------------|----------------|
| Known canonical | 47582 | 95.66 |
| Known Non-canonical | 1489 | 2.99 |
| Novel canonical | 426 | 0.86 |
| Novel Non-canonical | 243 | 0.49 |

Gene Characterization

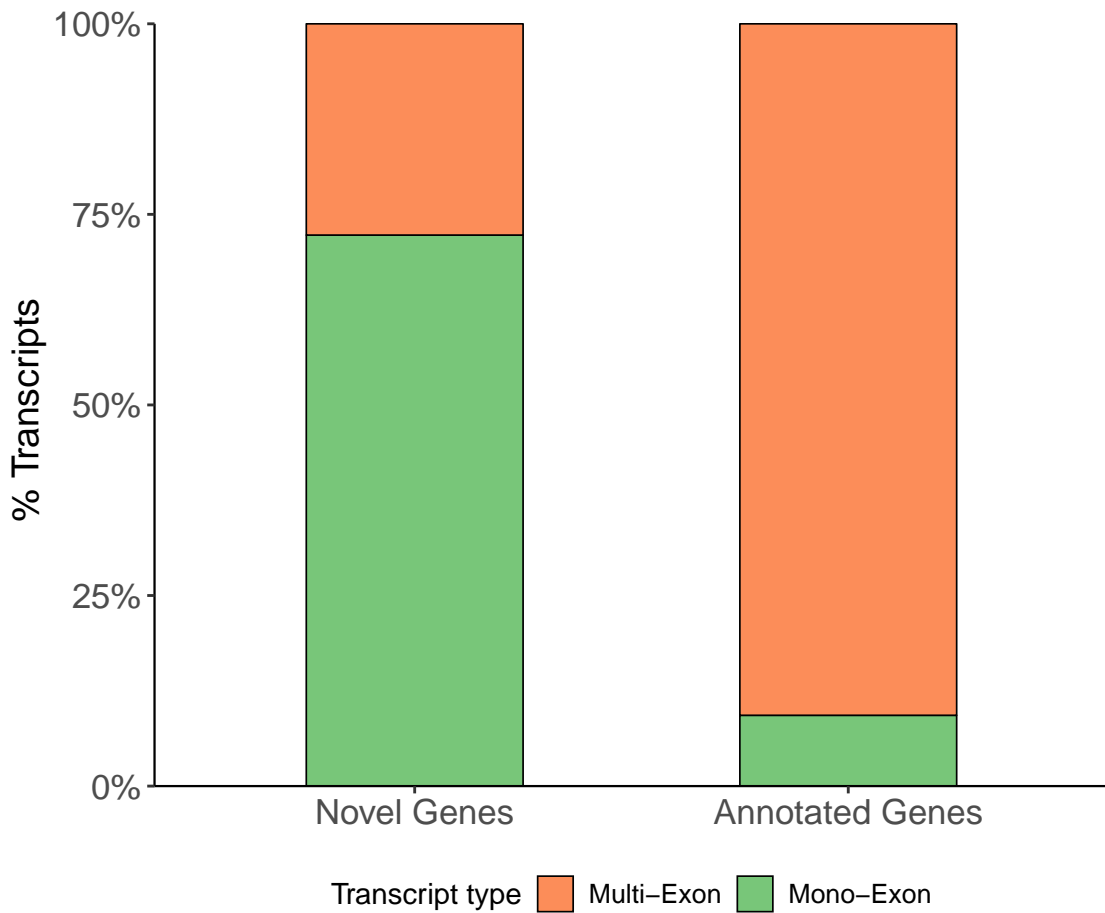
Number of Isoforms per Gene



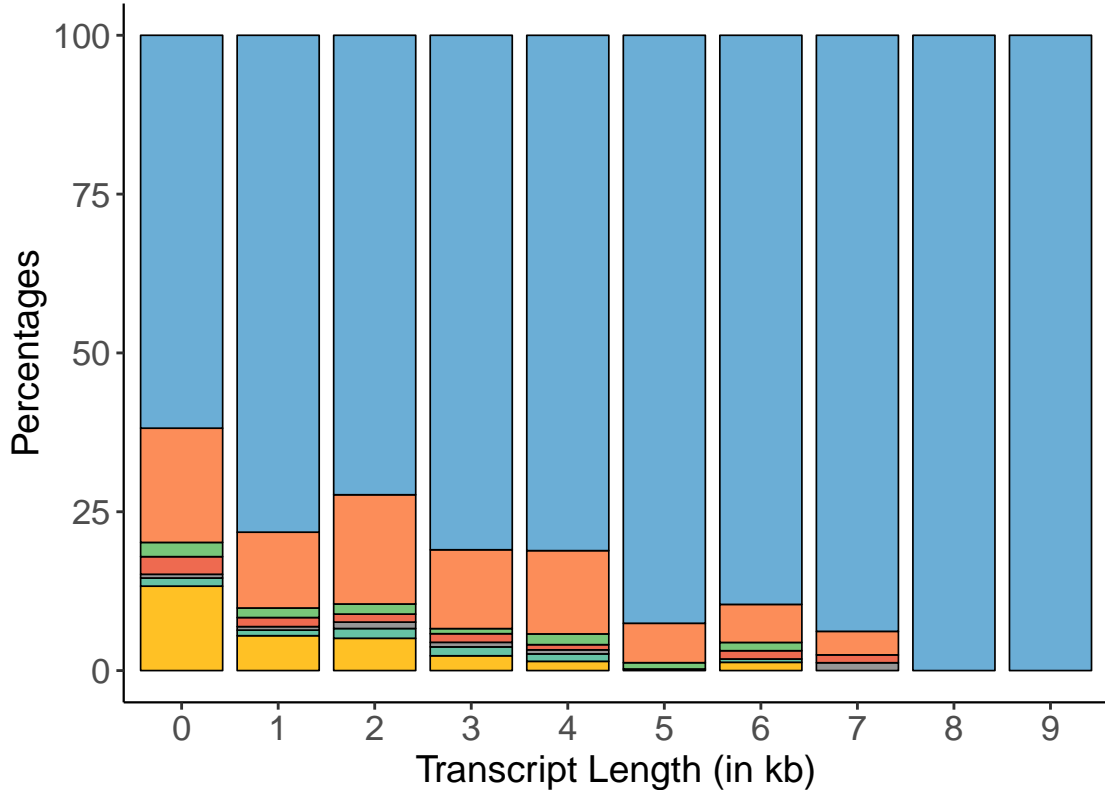
Number of Isoforms per Gene, Known vs Novel Genes



Distribution of Mono- vs Multi-Exon Transcripts



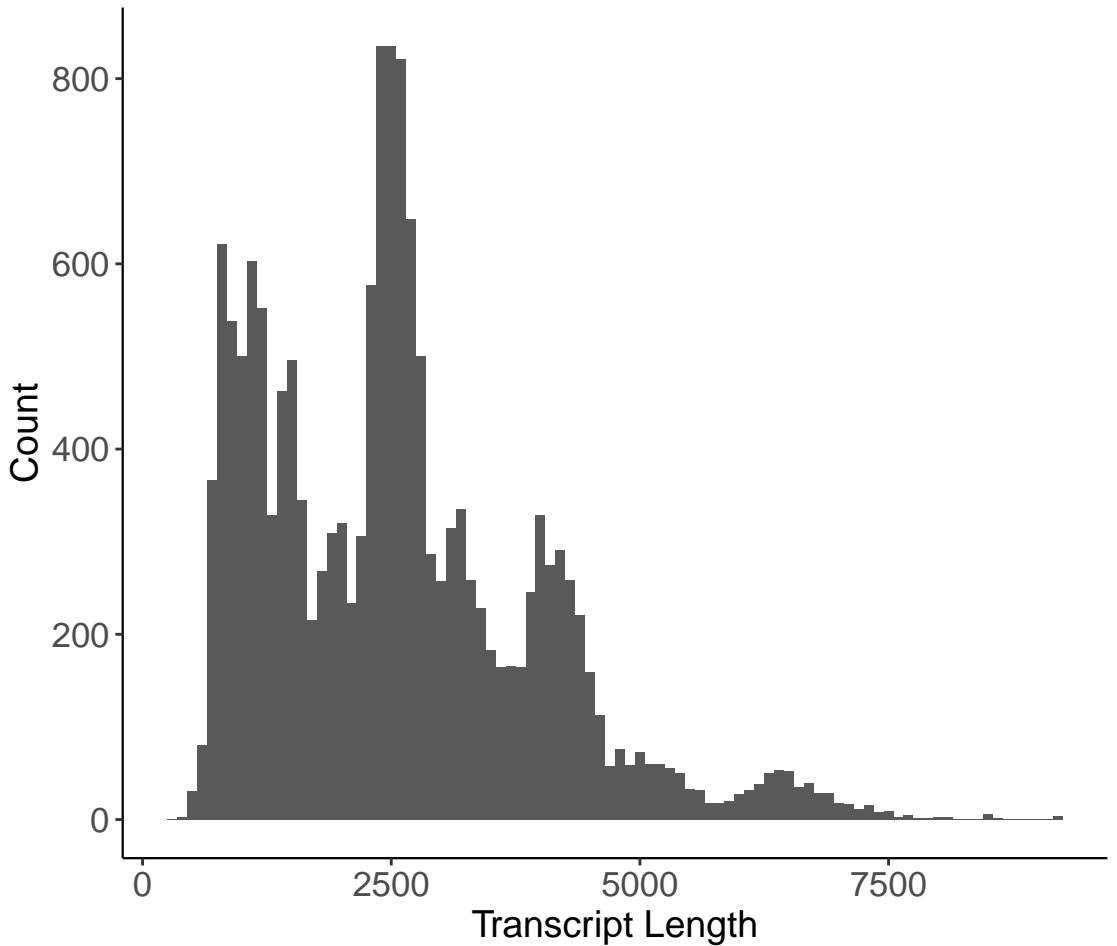
Classifications by Transcript Length, normalized



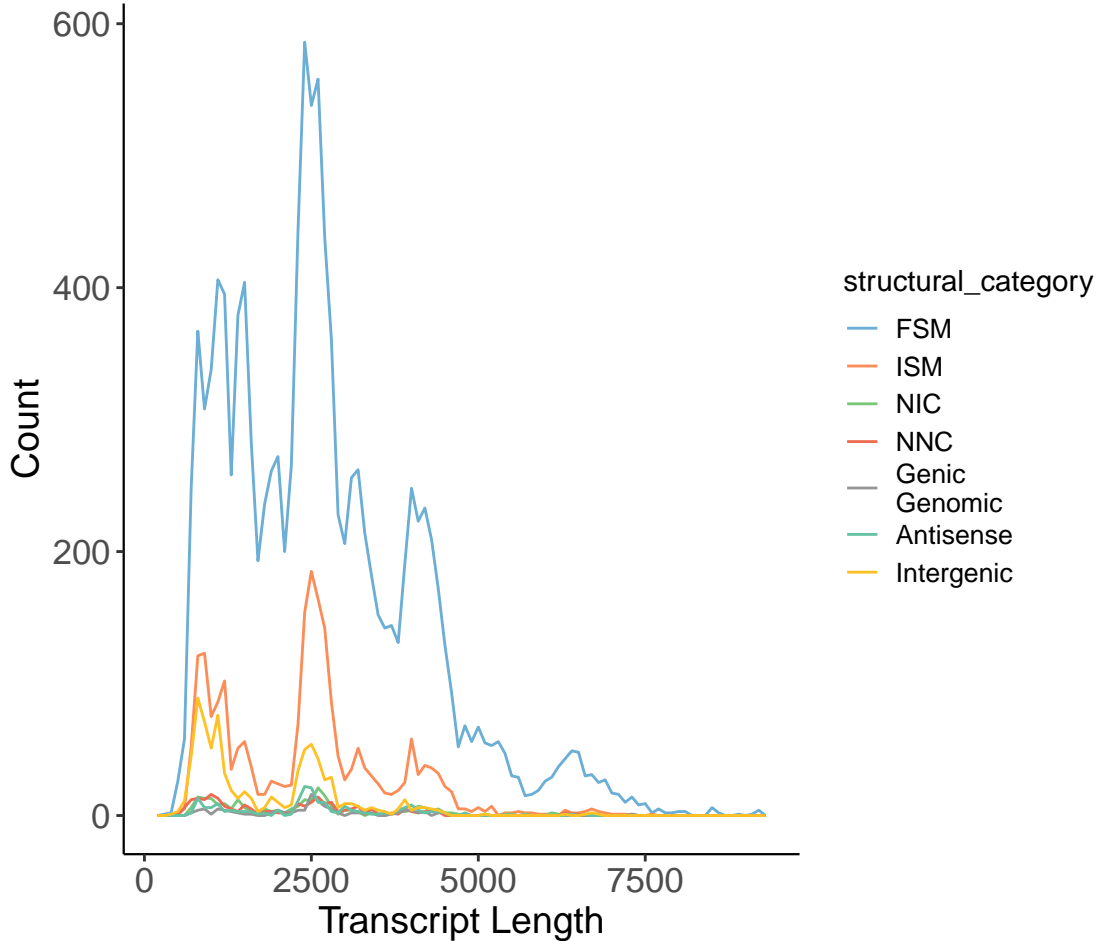
Structural Category

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

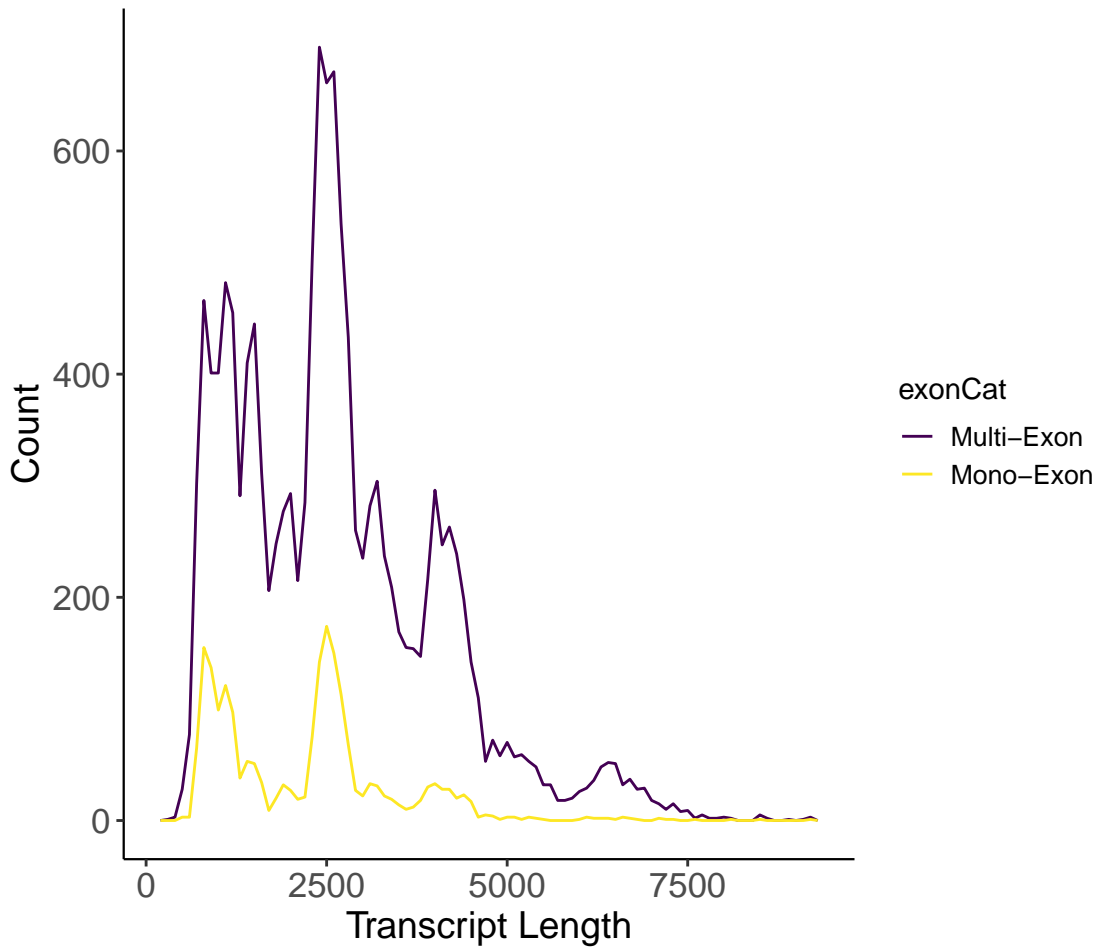
Transcript Lengths, all transcripts



Transcript Lengths, by structural category

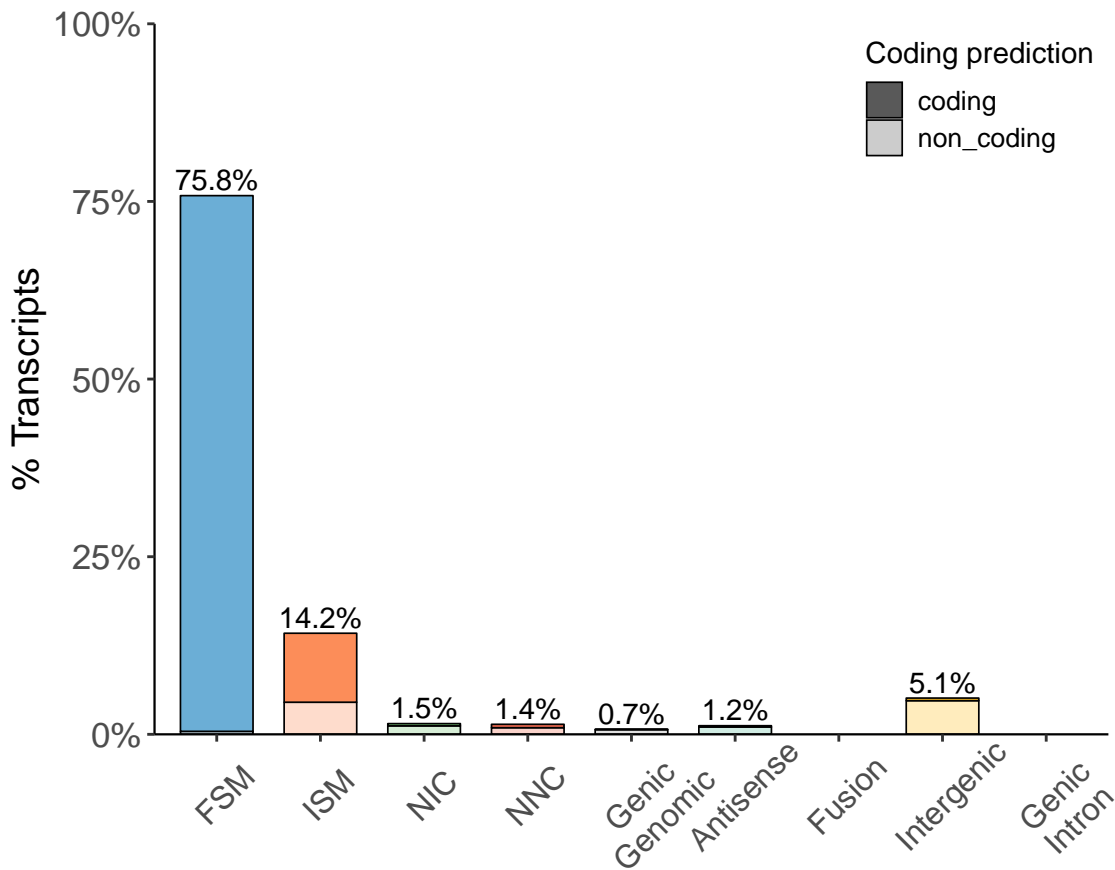


Transcript Lengths, Mono- vs Multi-Exons

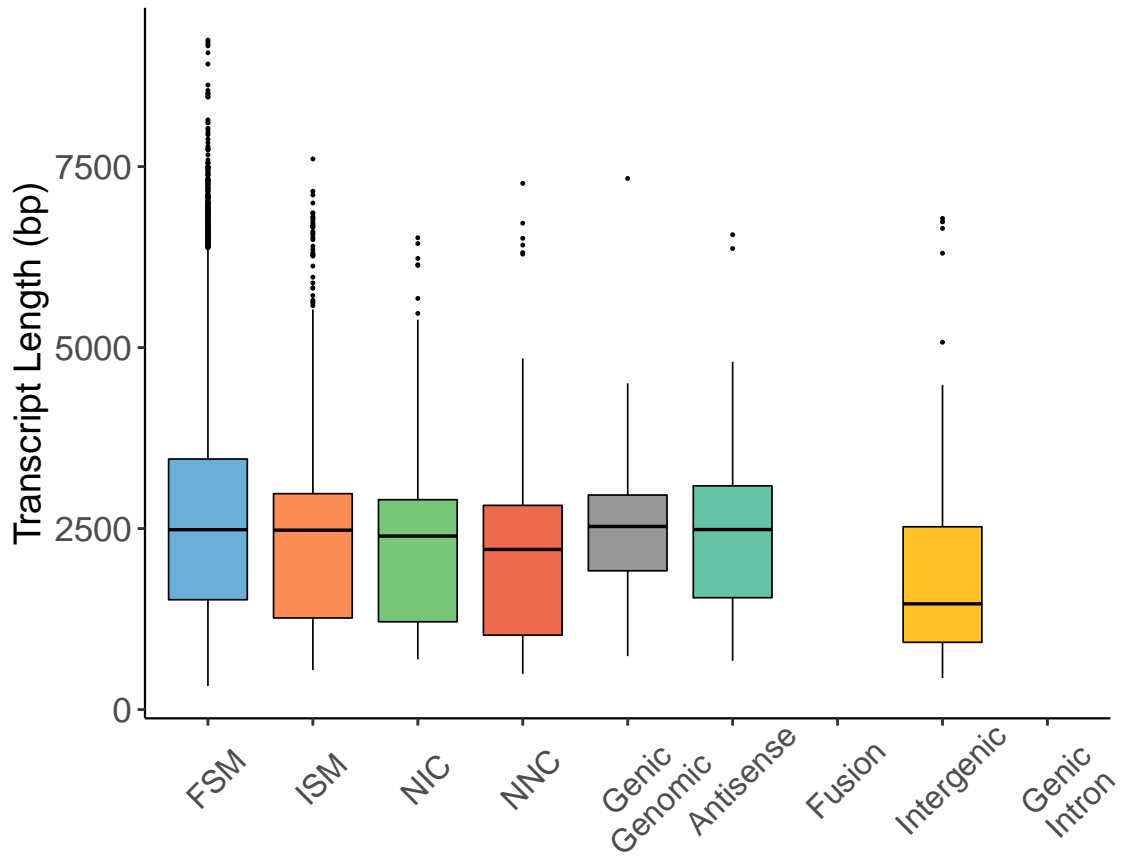


*Structural Isoform Characterization
by Splice Junctions*

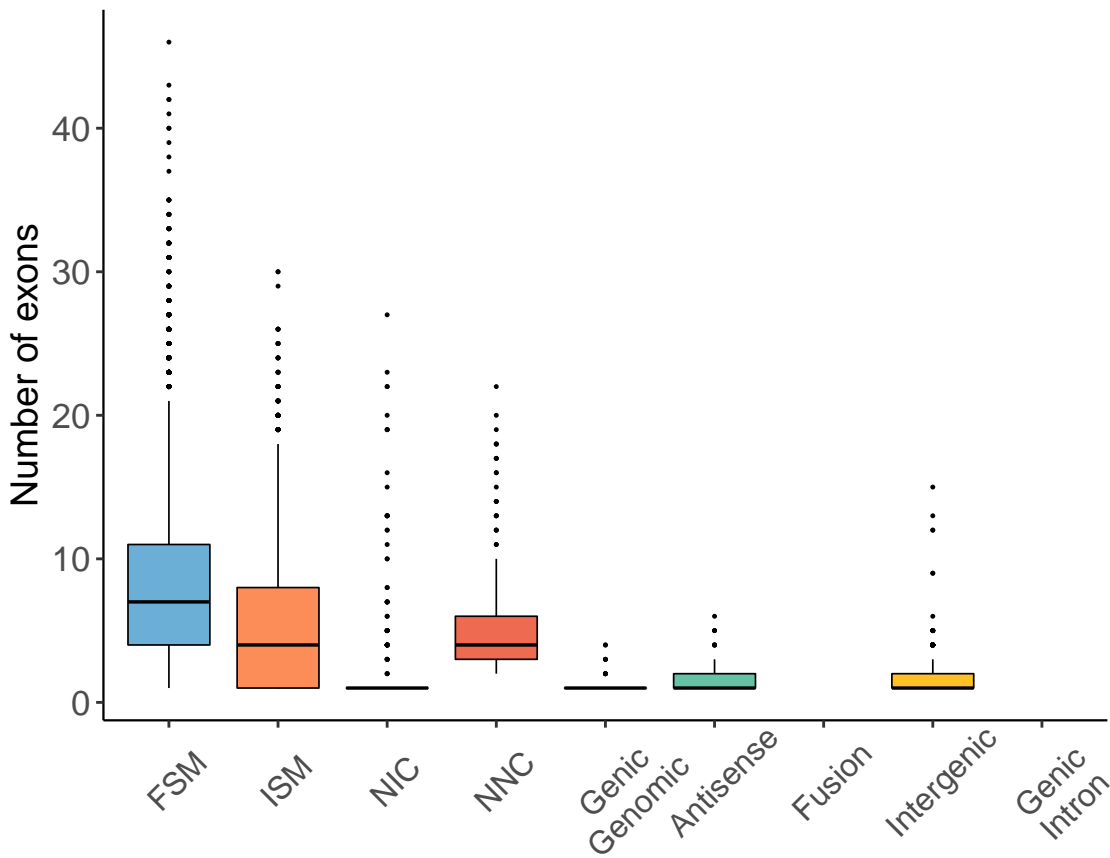
Isoform distribution across structural categories



Transcript Lengths by Structural Classification

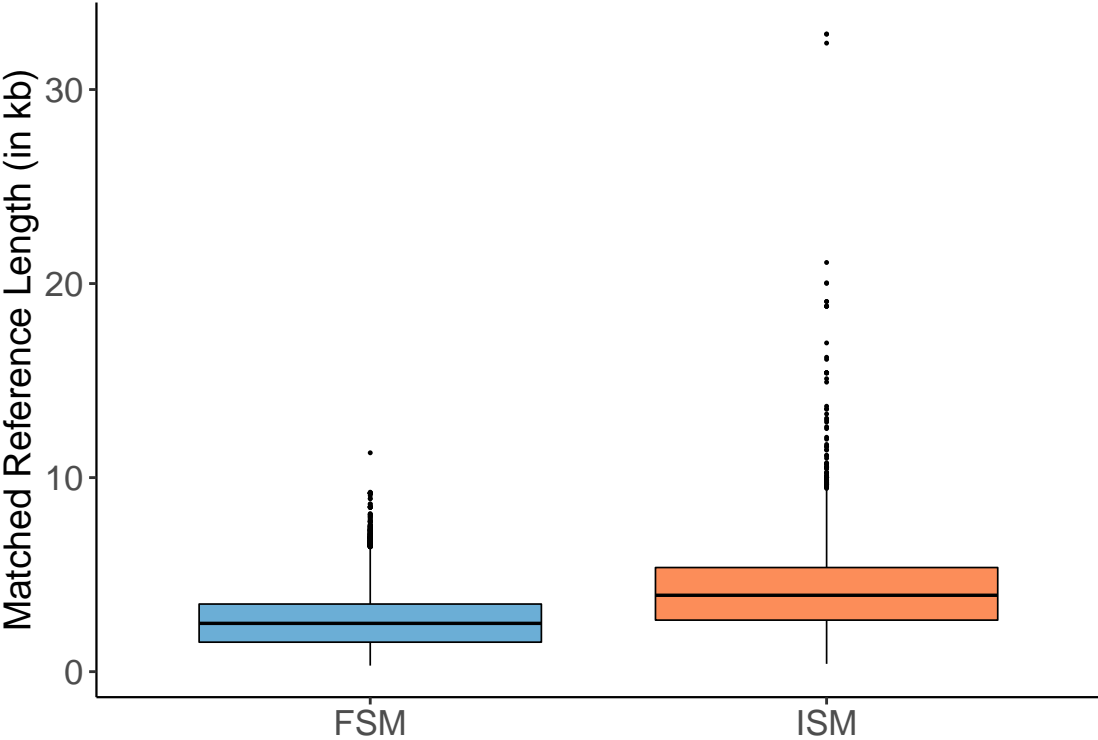


Exon Counts by Structural Classification



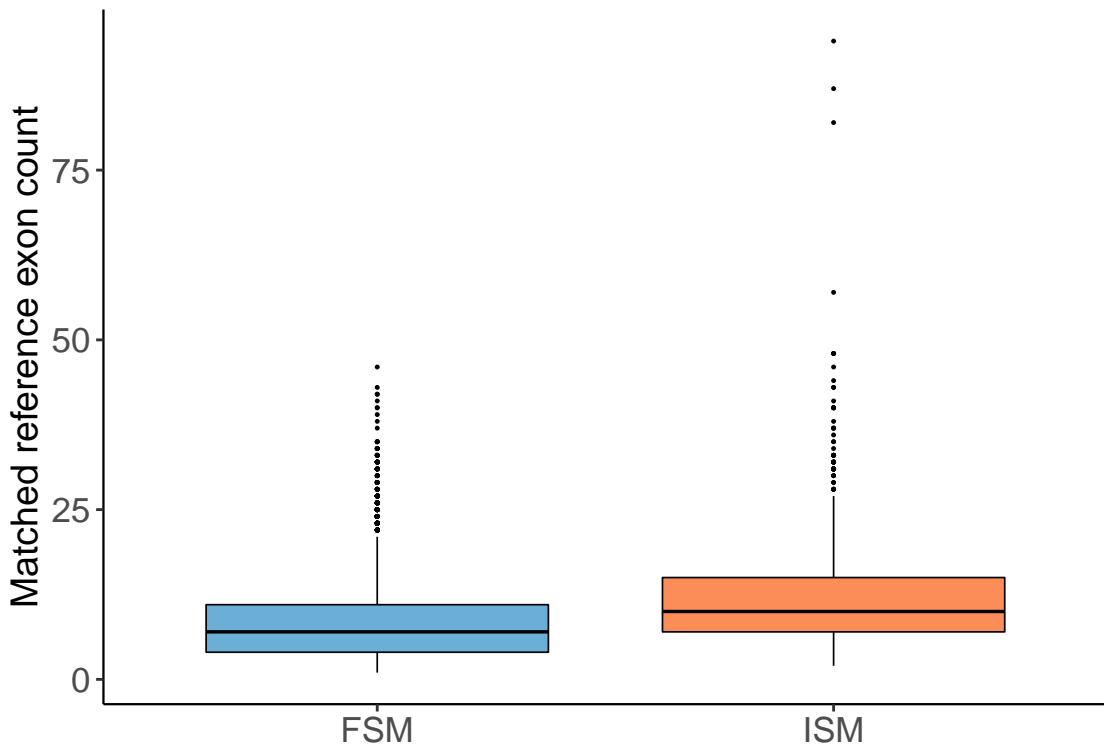
Length Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories



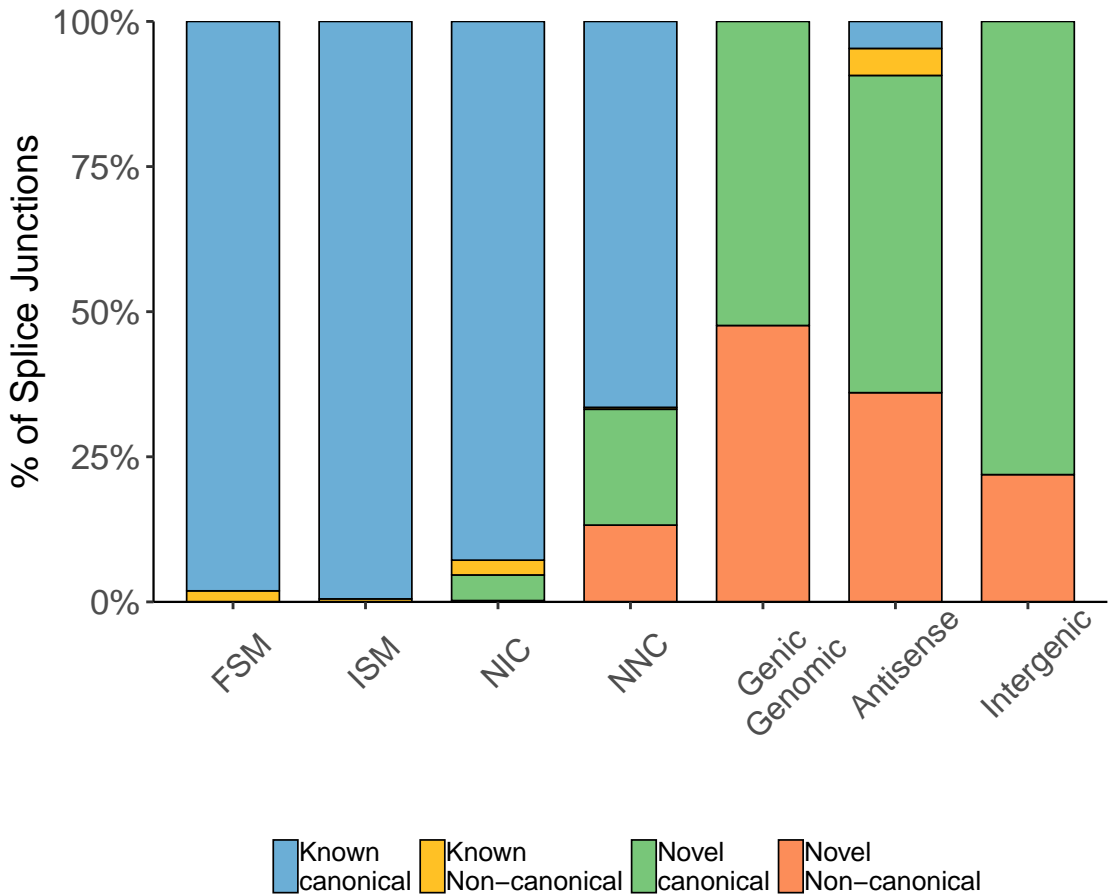
Exon Count Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories

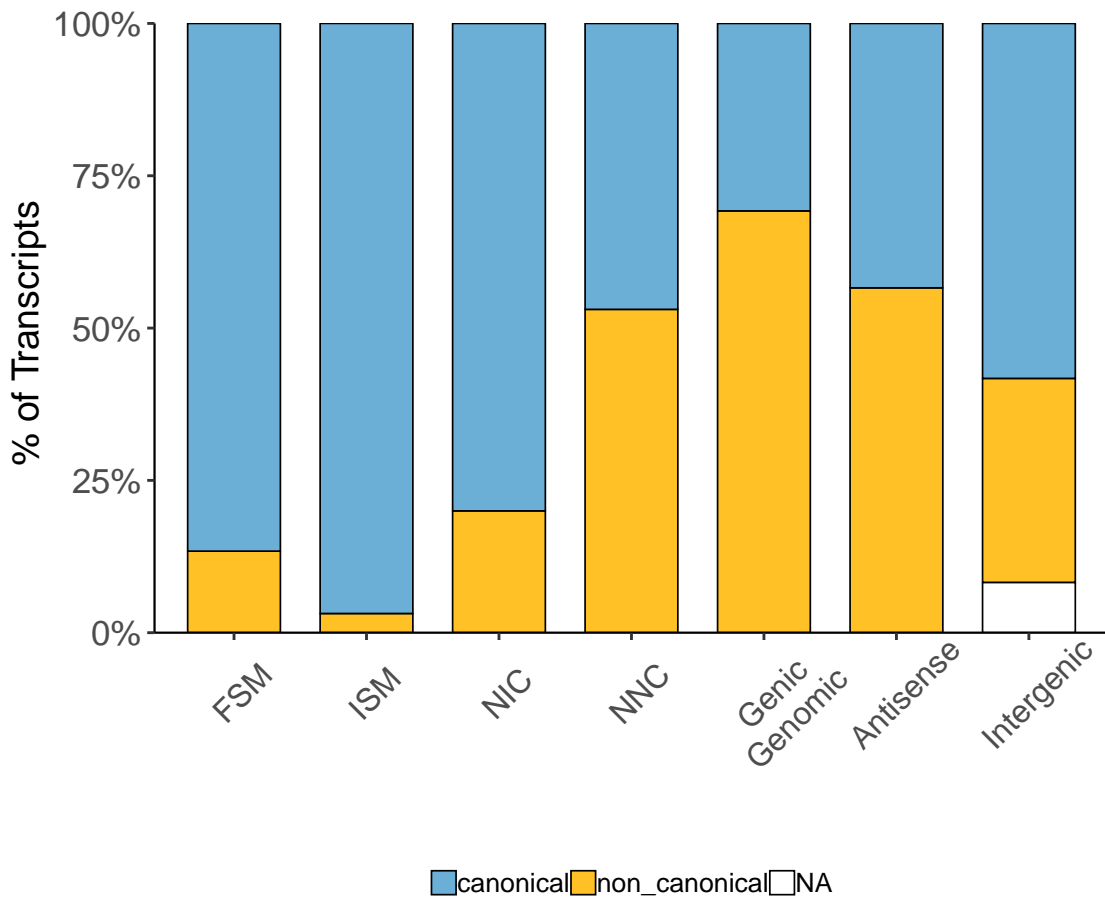


Splice Junction Characterization

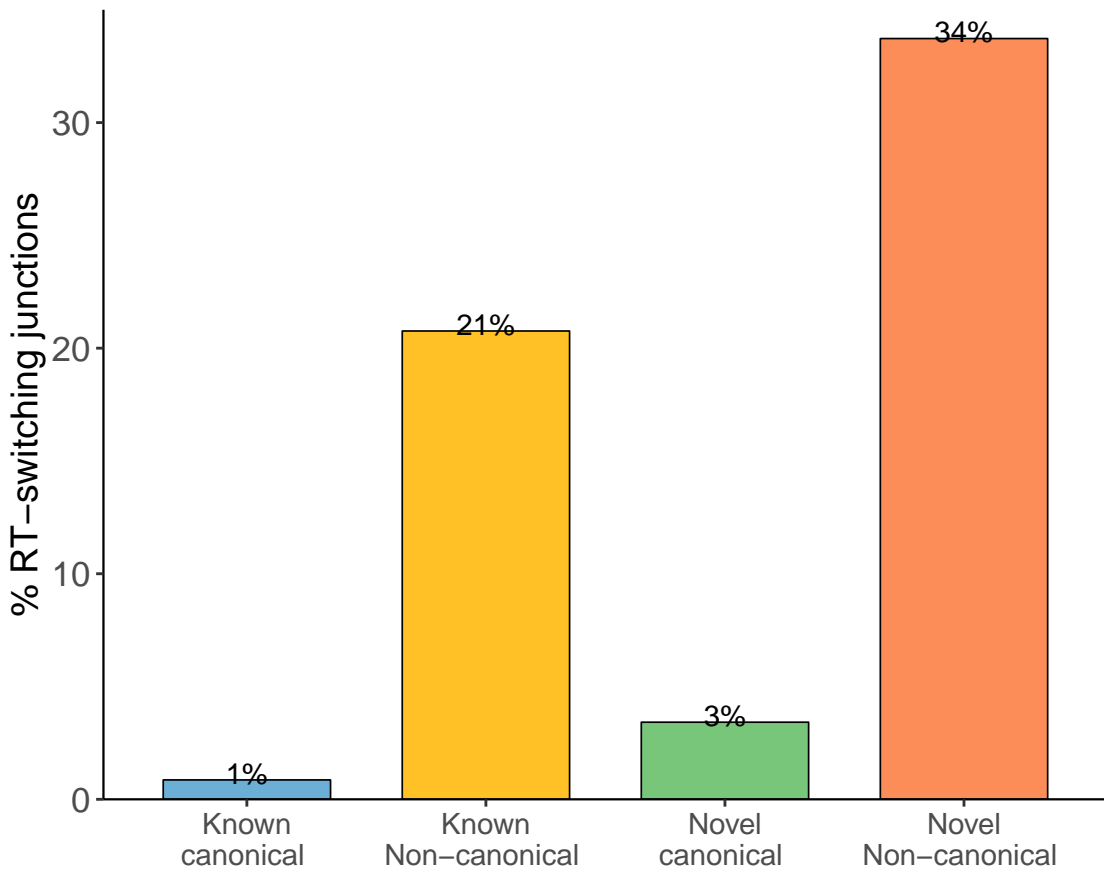
Distribution of Splice Junctions by Structural Classification



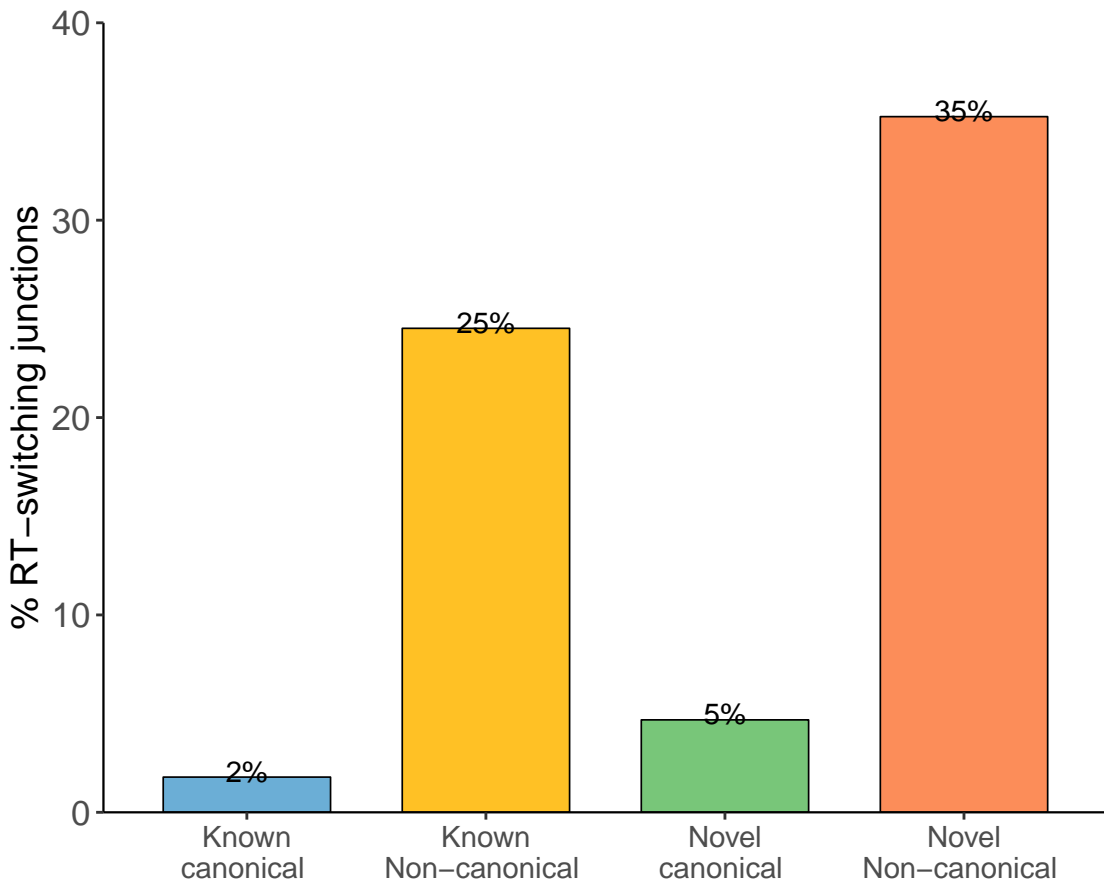
Distribution of Transcripts by Splice Junctions



RT-switching, all junctions



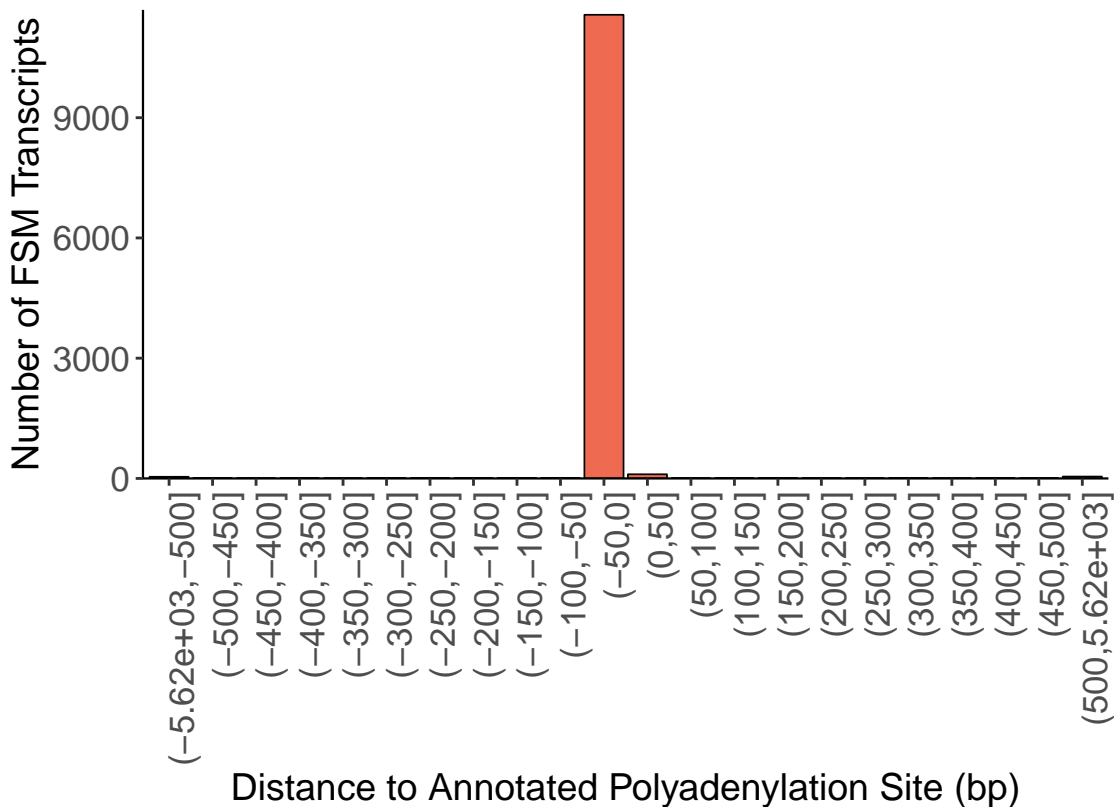
RT-switching, unique junctions



Comparison with Annotated TSS and PolyA Sites

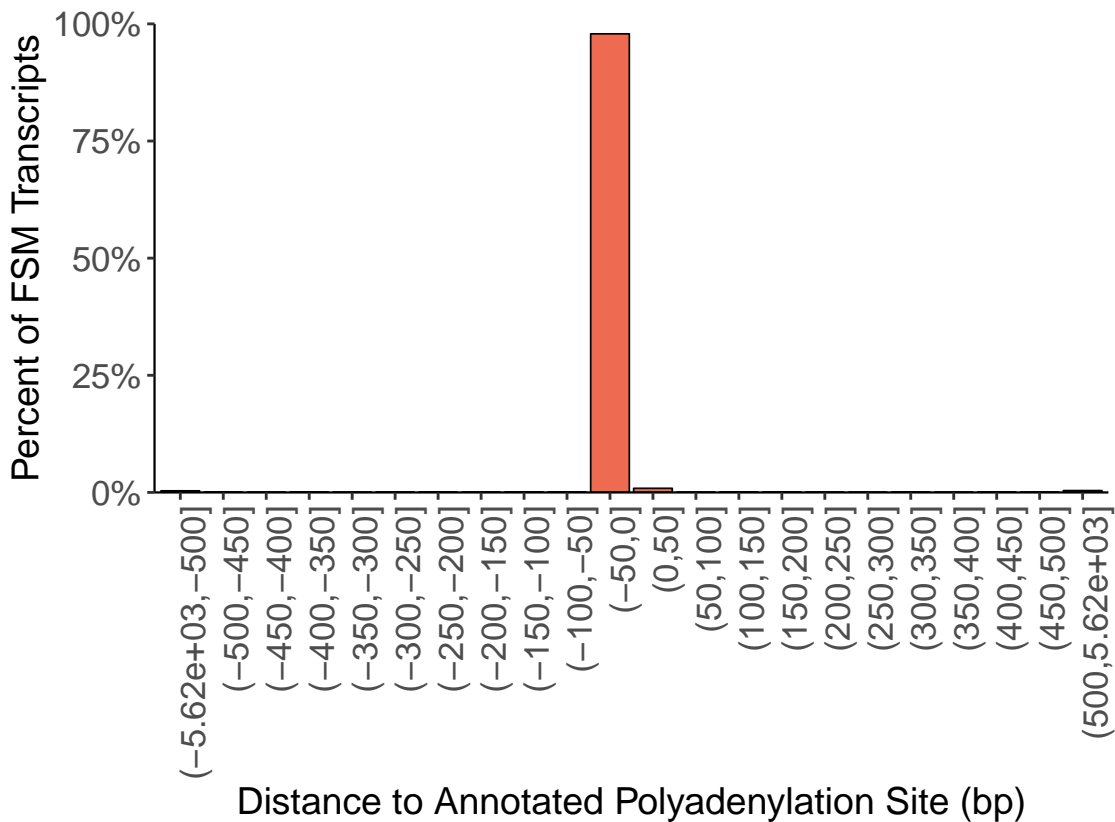
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



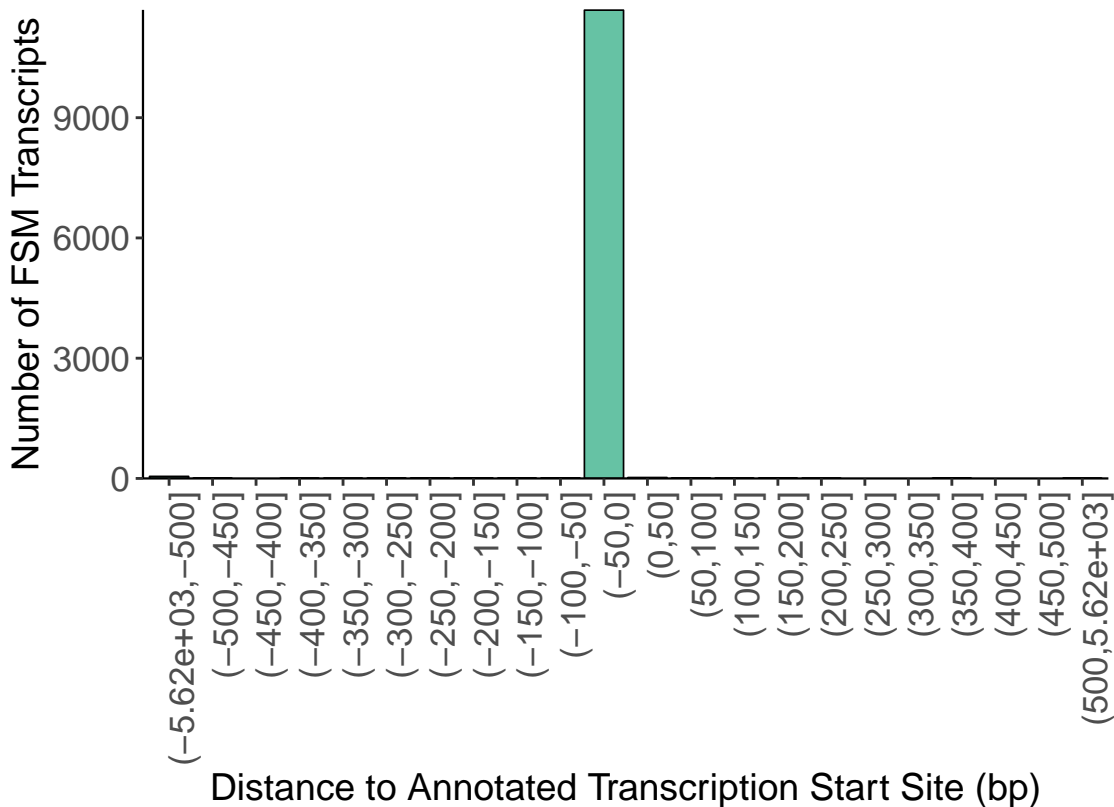
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



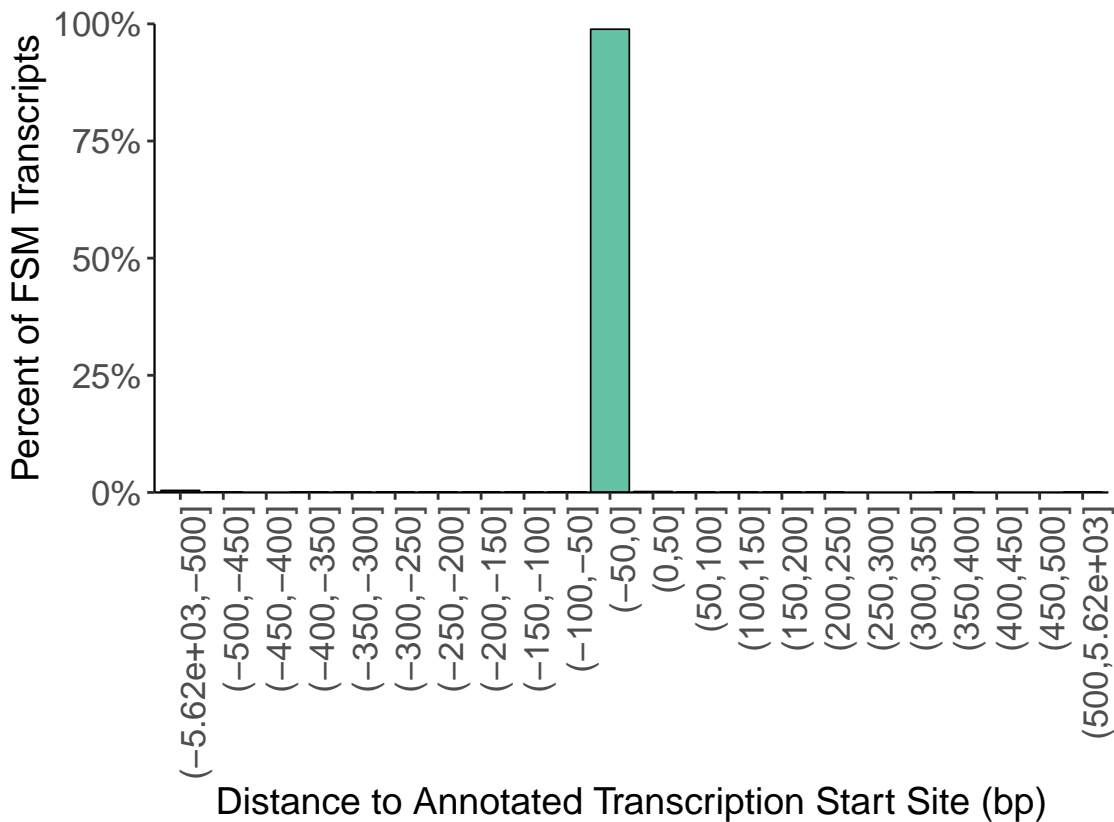
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



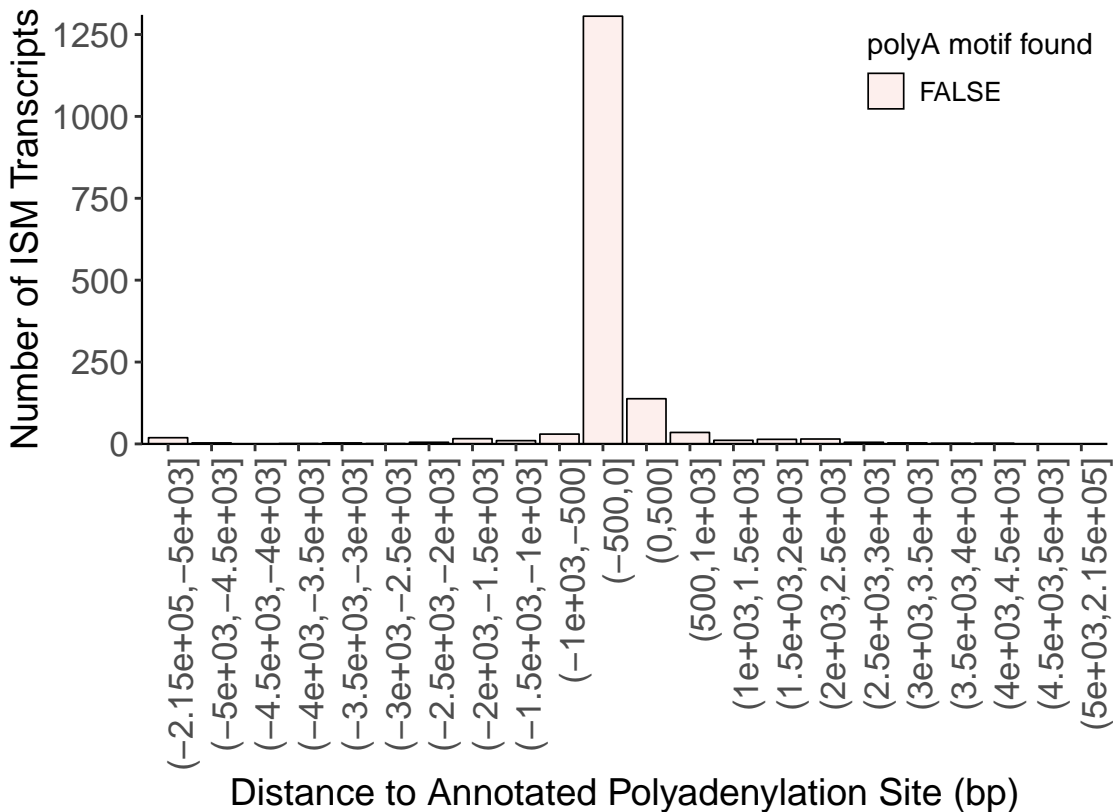
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



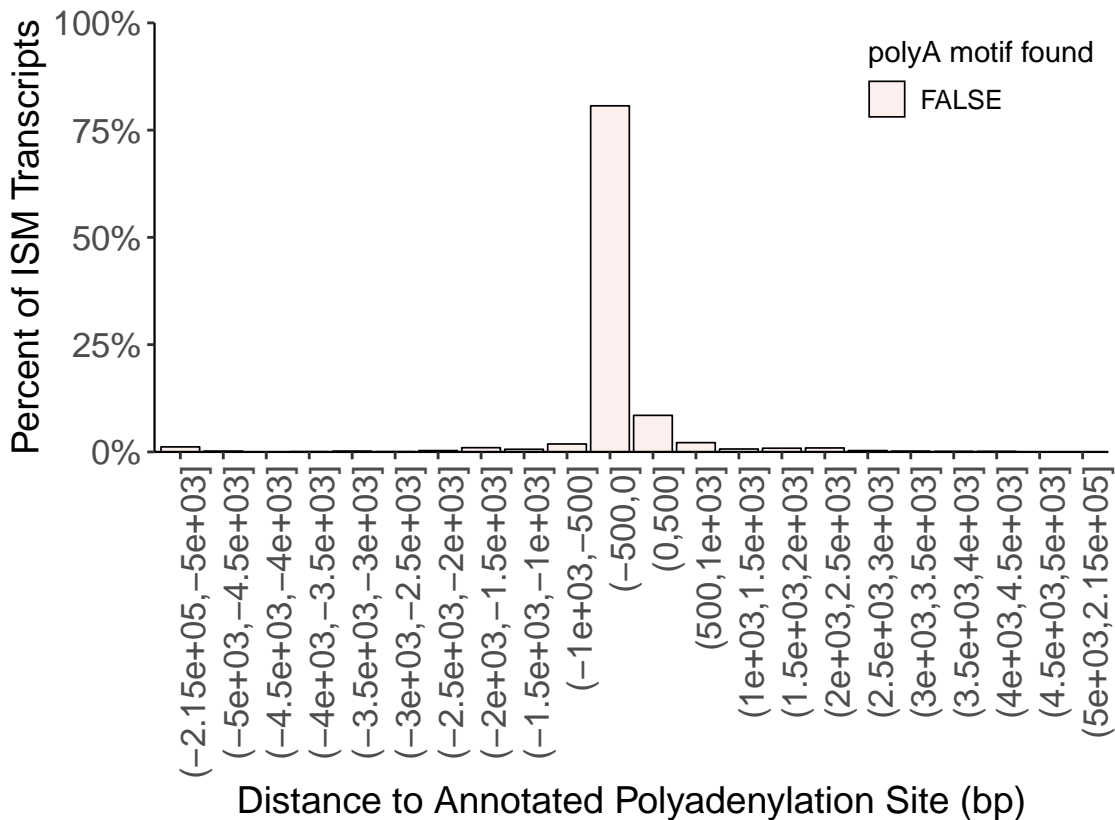
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



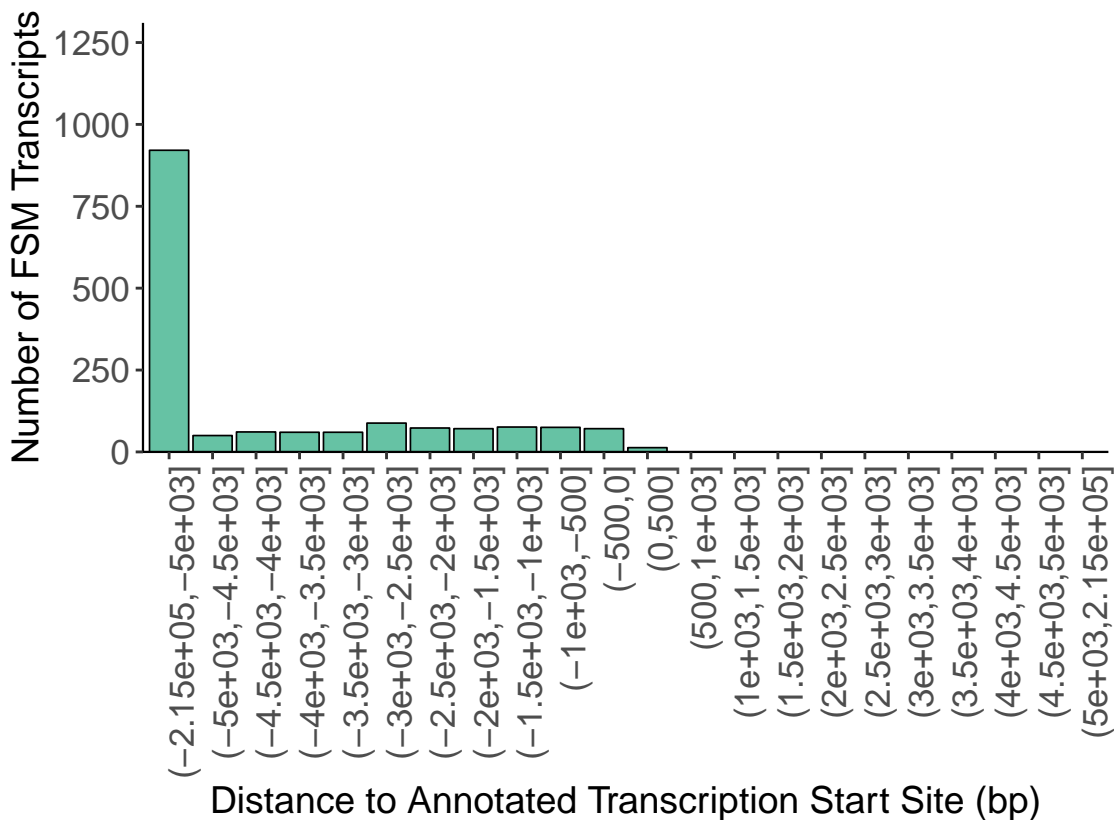
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



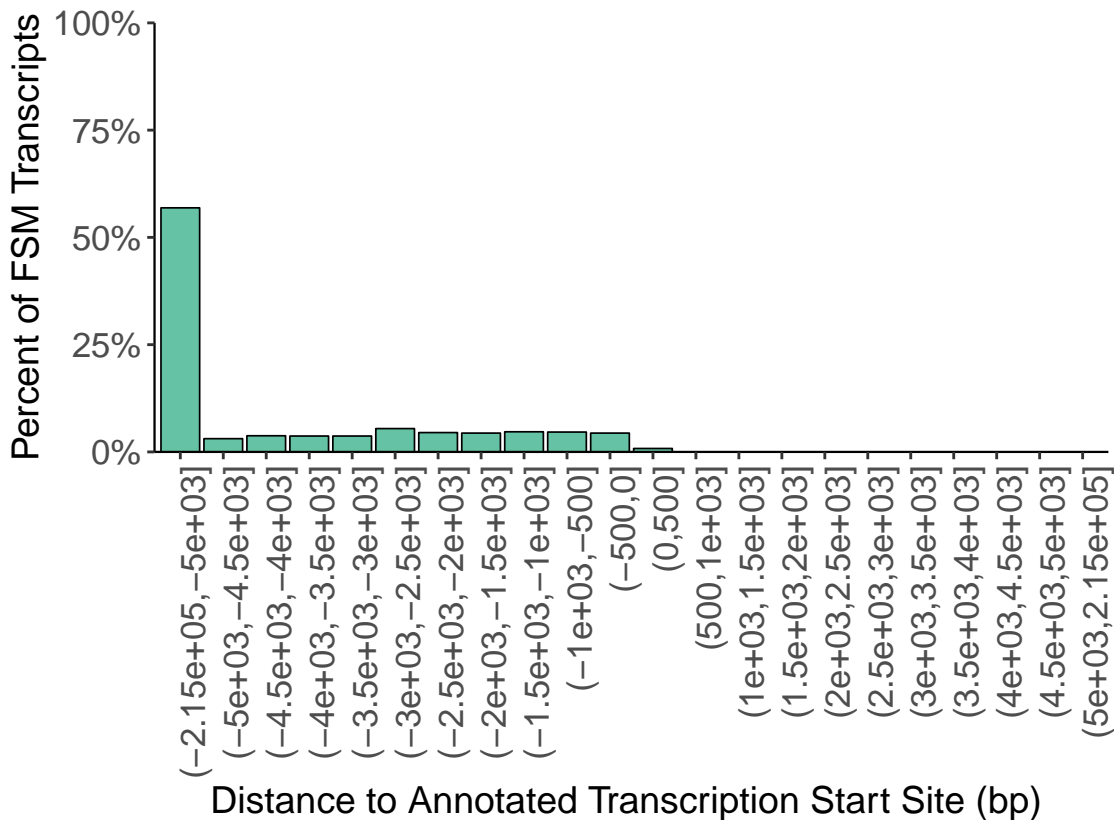
Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site, ISM only

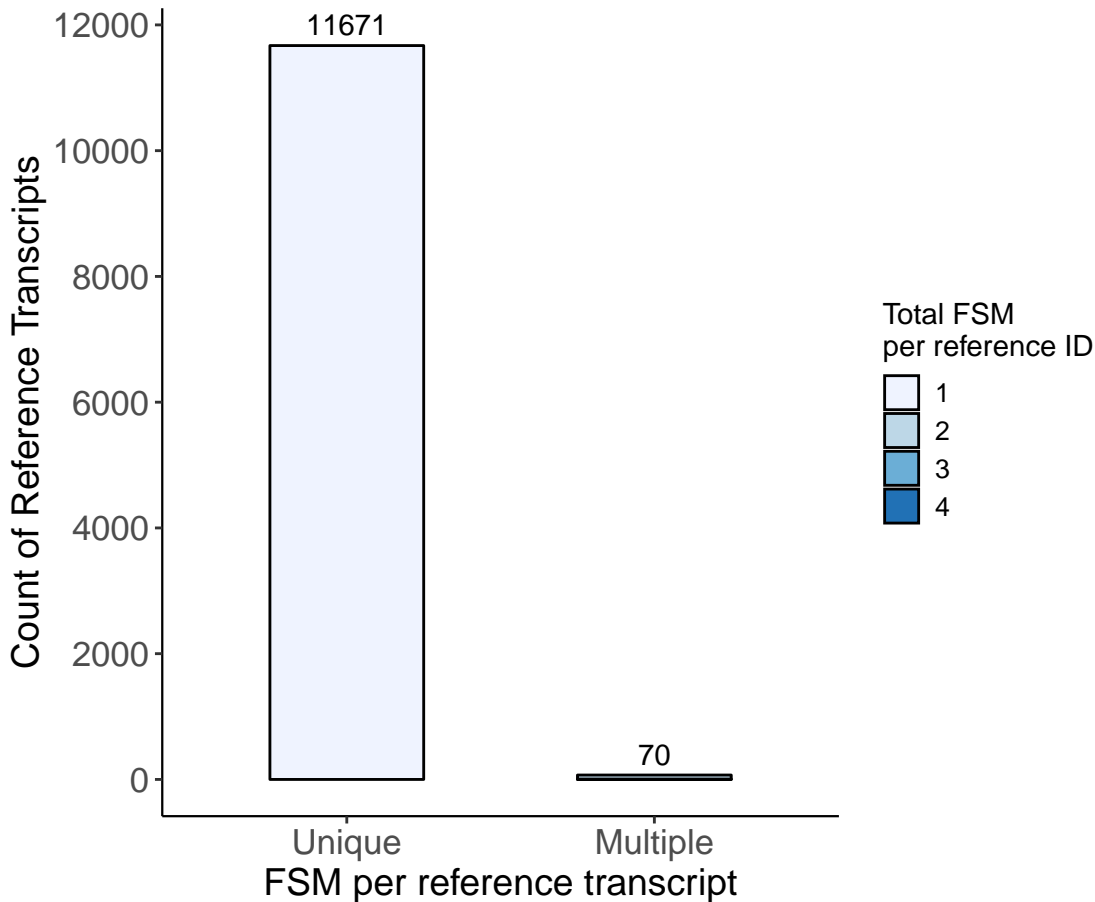
Negative values indicate downstream of annotated TSS



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

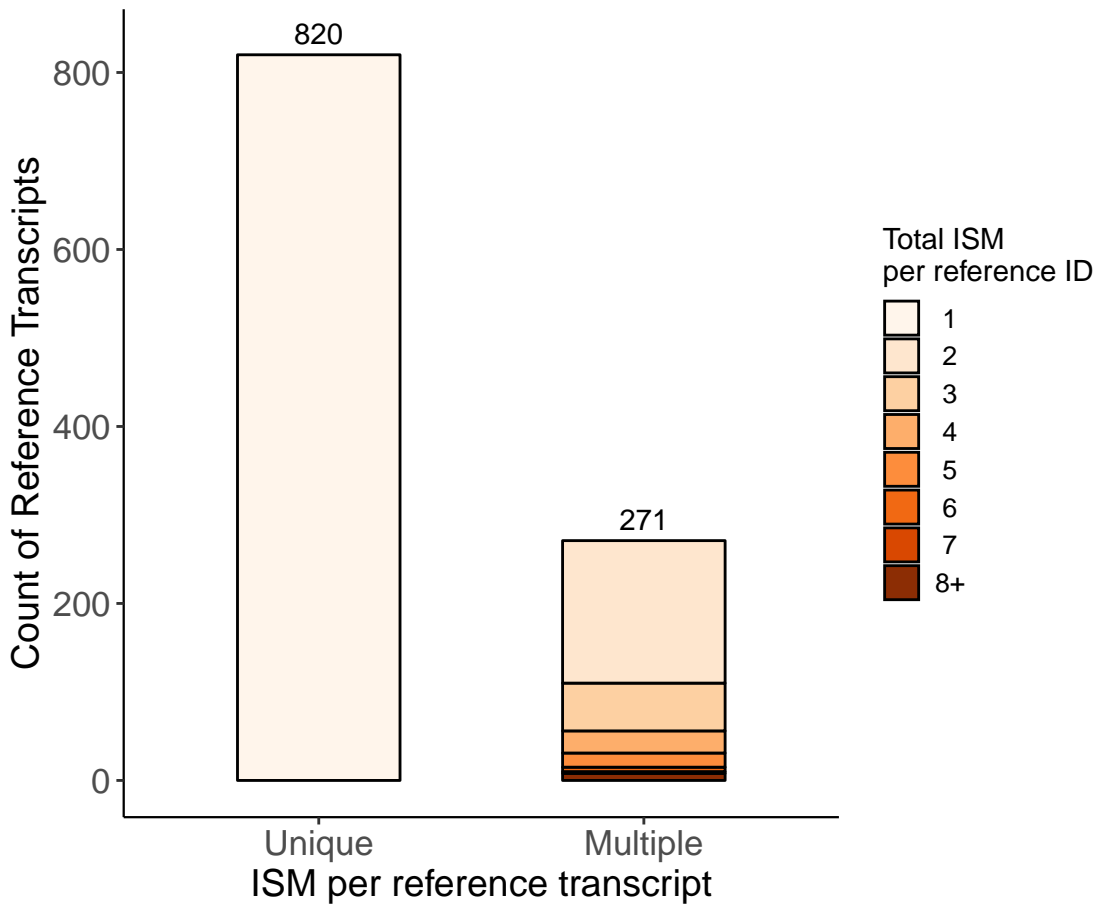
Reference transcript redundance

Only FSM



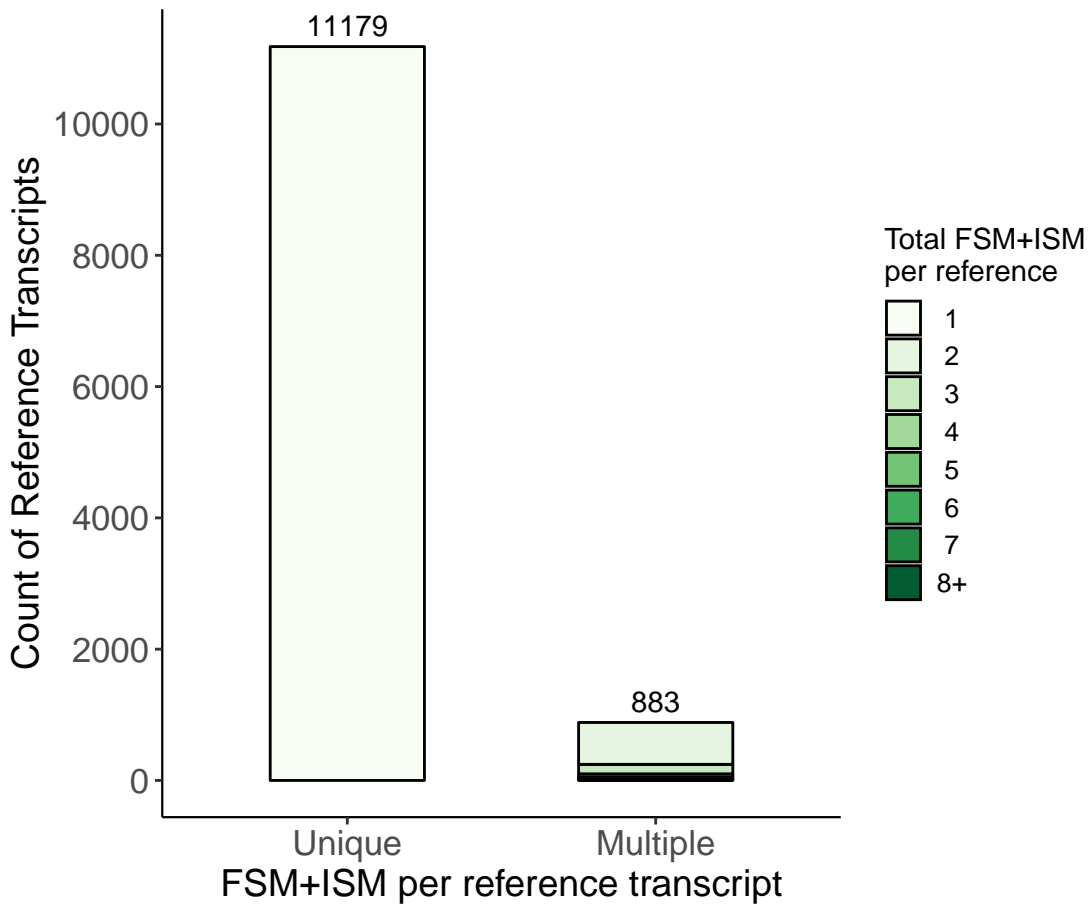
Reference transcript redundance

Only ISM



Reference transcript redundance

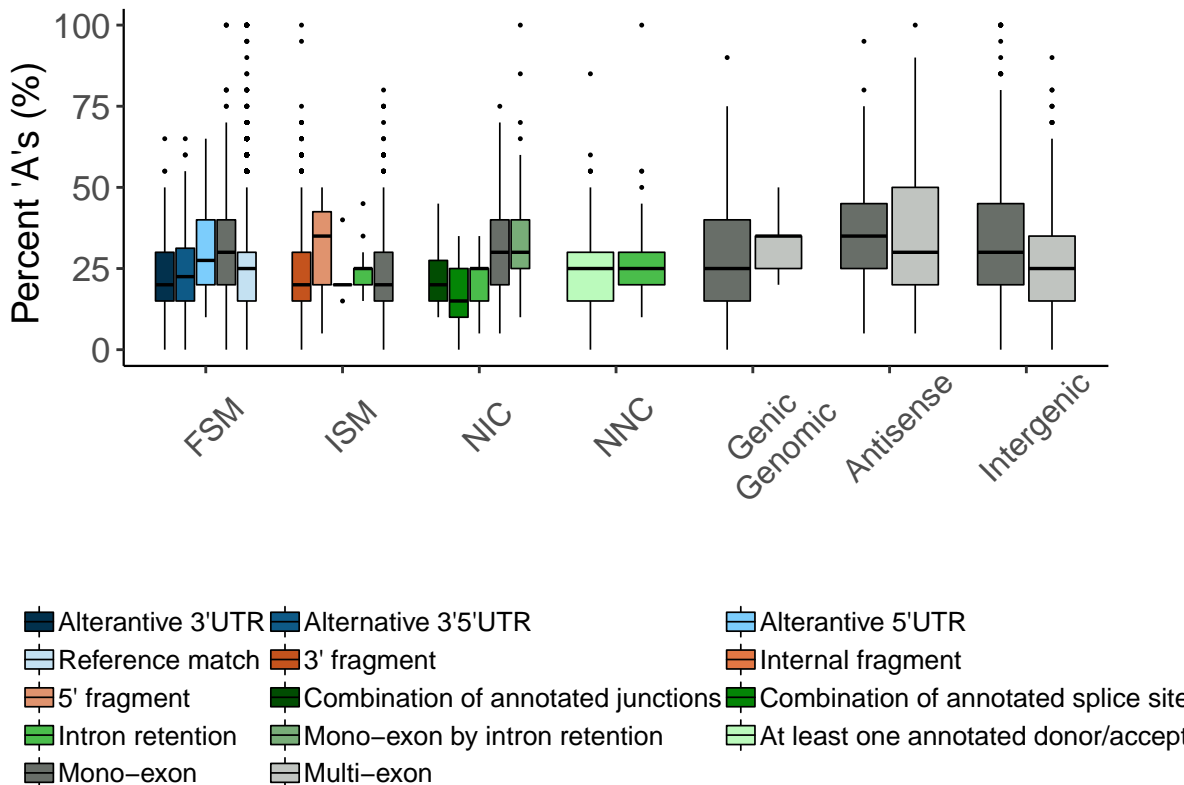
FSM+ISM



Intra-Priming Quality Check

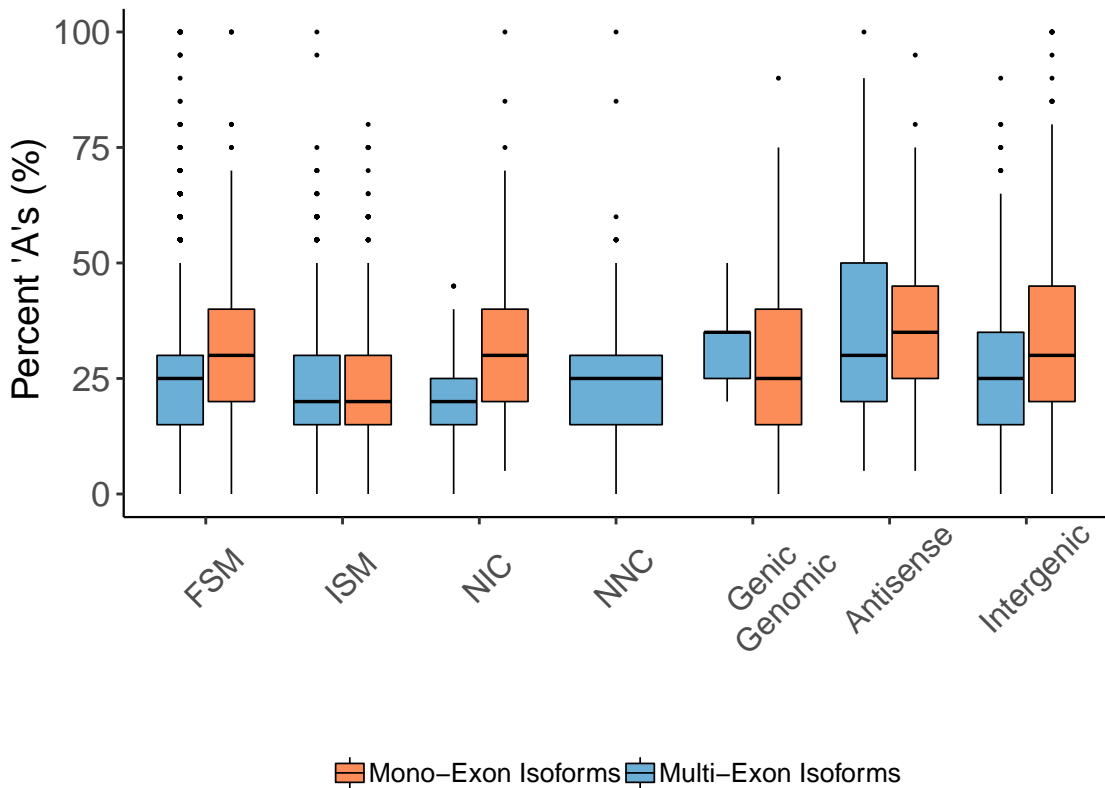
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



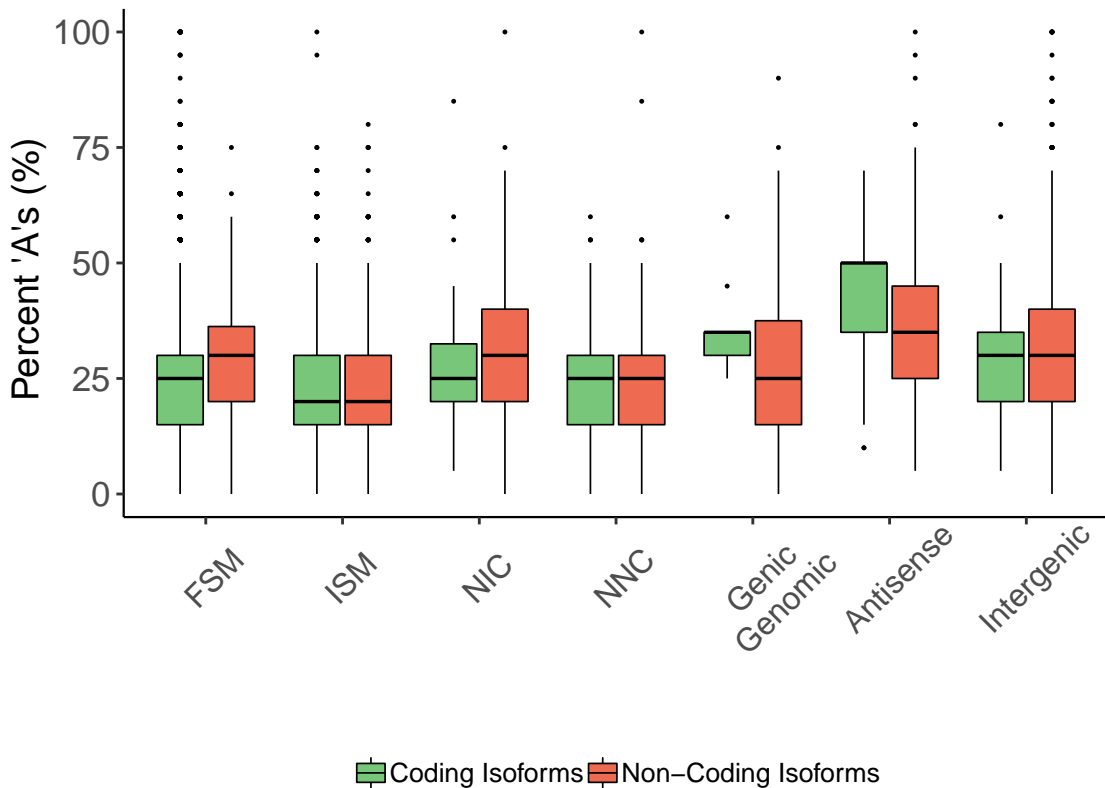
Possible Intra-Priming, Mono- vs Multi-Exon

Percent of genomic 'A's in downstream 20 bp



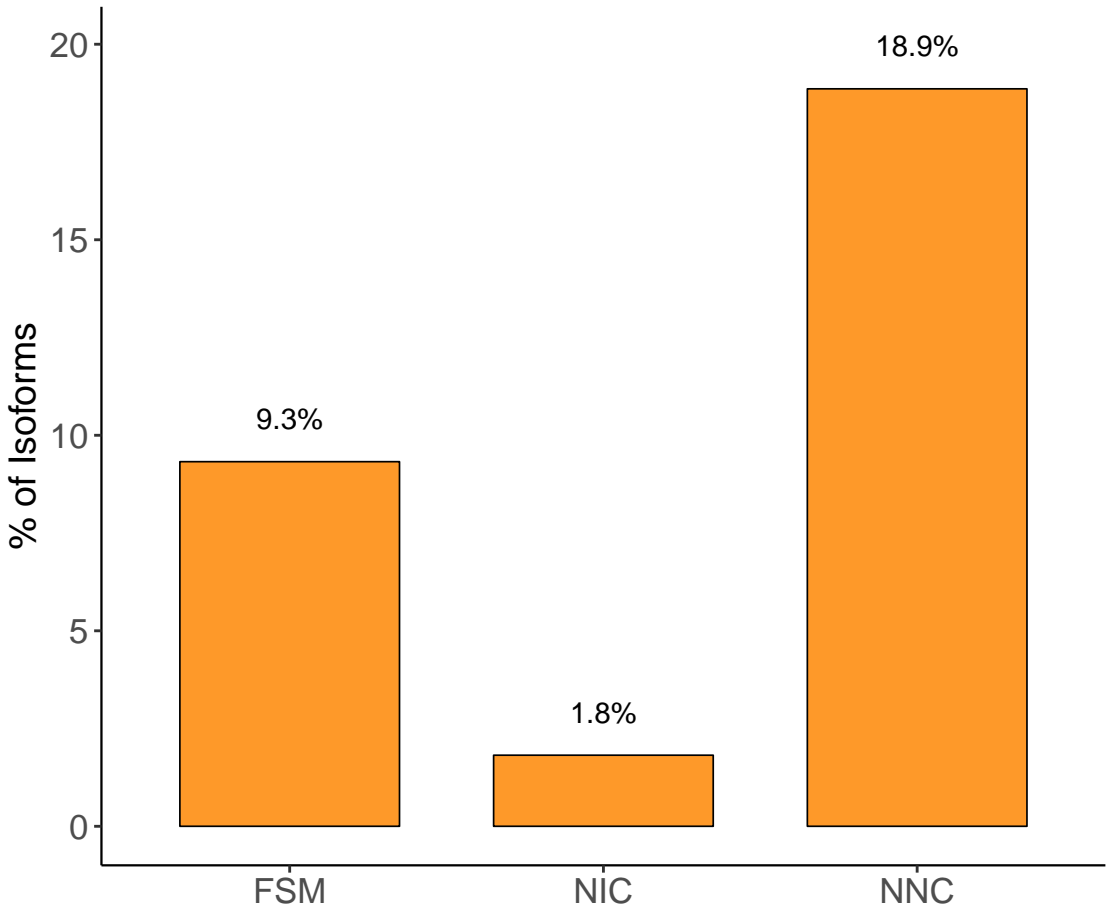
Possible Intra-Priming, Coding vs Non-Coding

Percent of genomic 'A's in downstream 20 bp

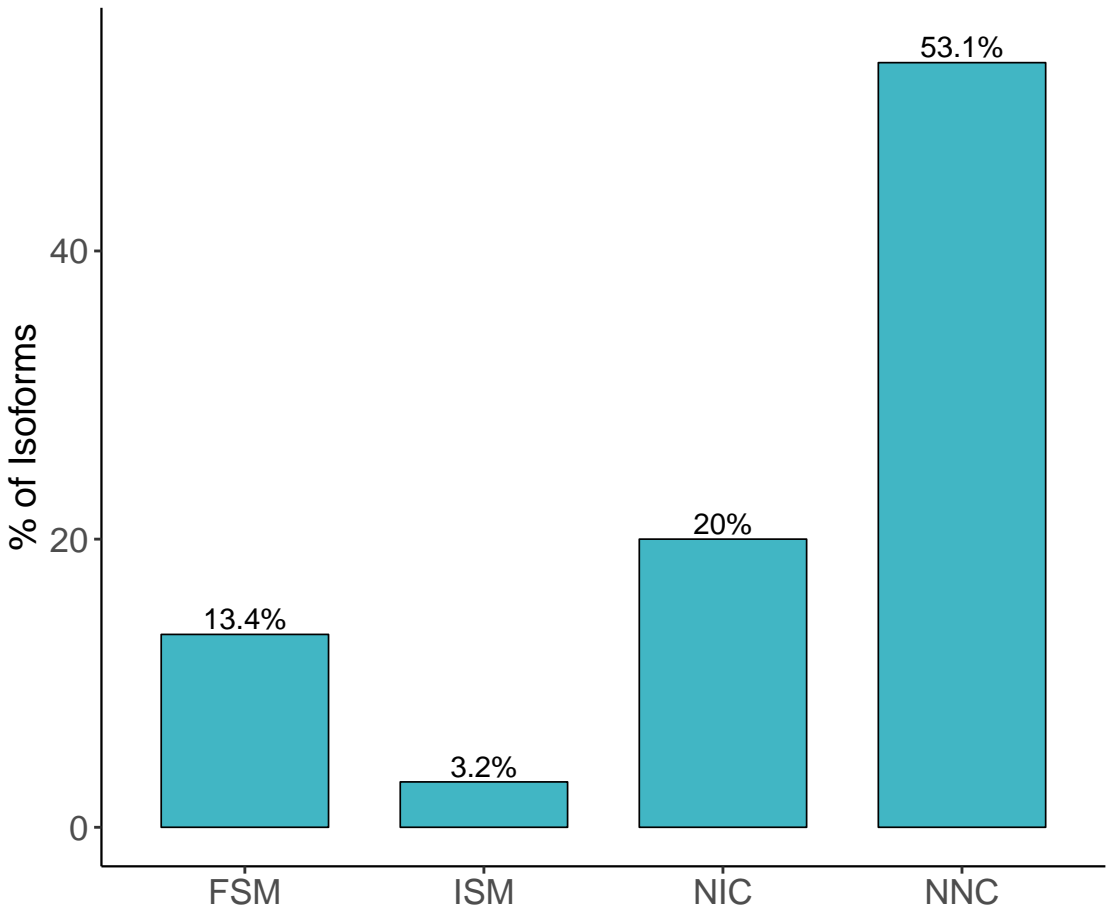


Quality Controls

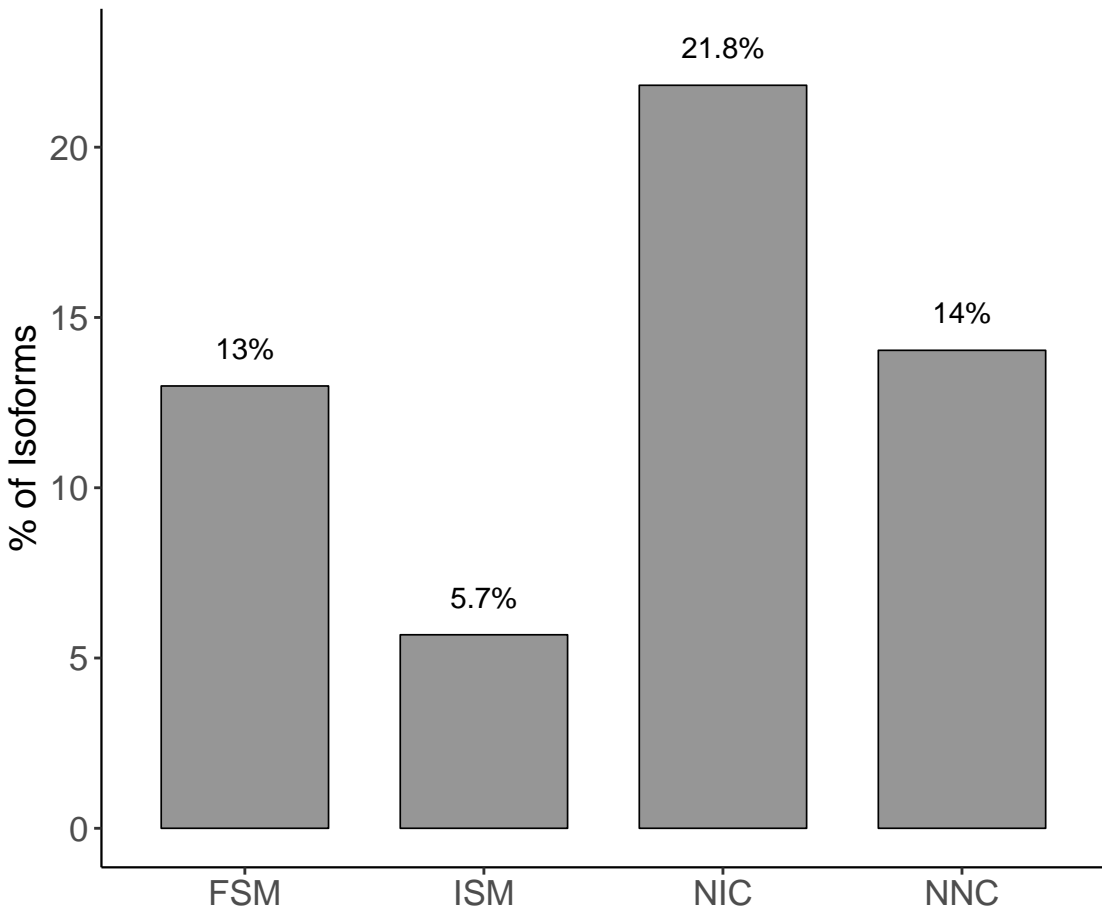
Incidence of RT-switching



Incidence of Non-Canonical Junctions



Incidence of NMD by structural category



Quality control attributes across structural categories

