

SQANTI3 report

Unique Genes: 8939
Unique Isoforms: 23906

Transcript Classification

Category	Isoforms, count
FSM	18039
ISM	3458
NIC	2047
NNC	305
Genic Genomic	3
Antisense	13
Fusion	19
Intergenic	22
Genic Intron	0

Gene Classification

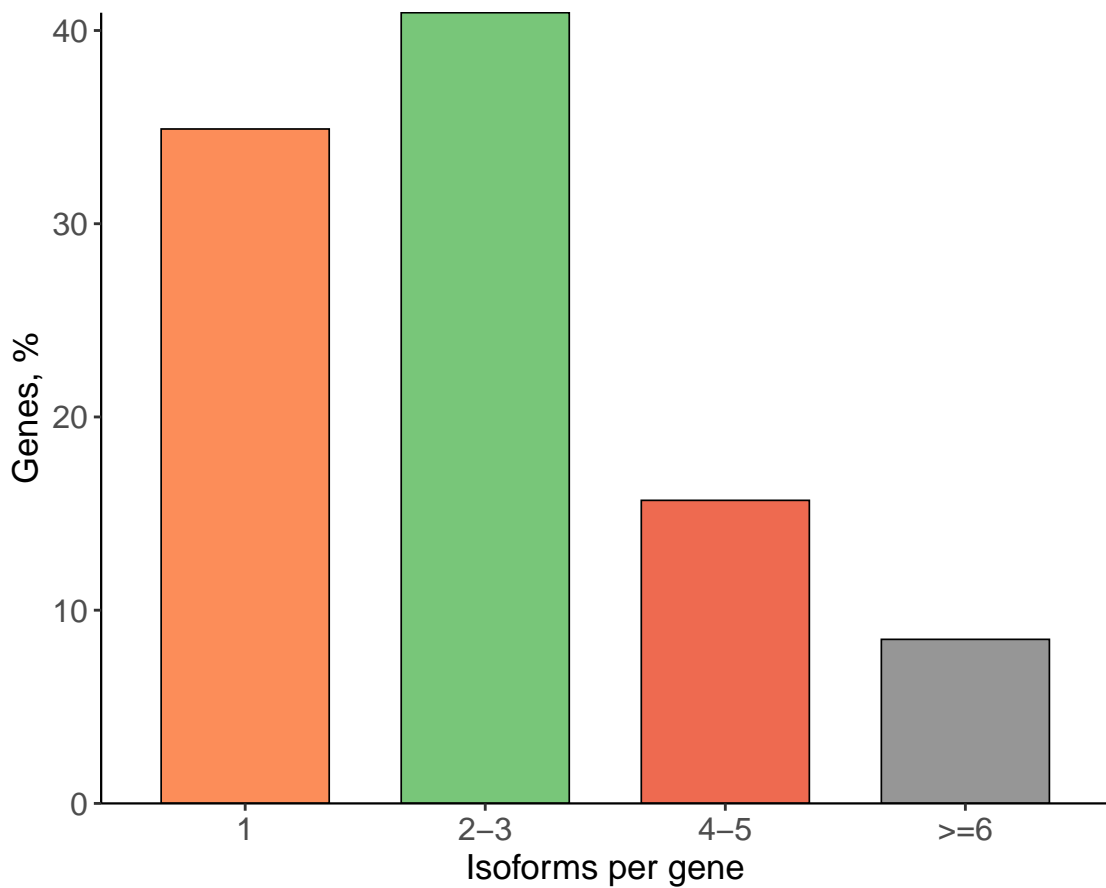
Category	Genes, count
Annotated Genes	8907
Novel Genes	32

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	72067	99.15
Known Non-canonical	32	0.04
Novel canonical	586	0.81
Novel Non-canonical	0	0.00

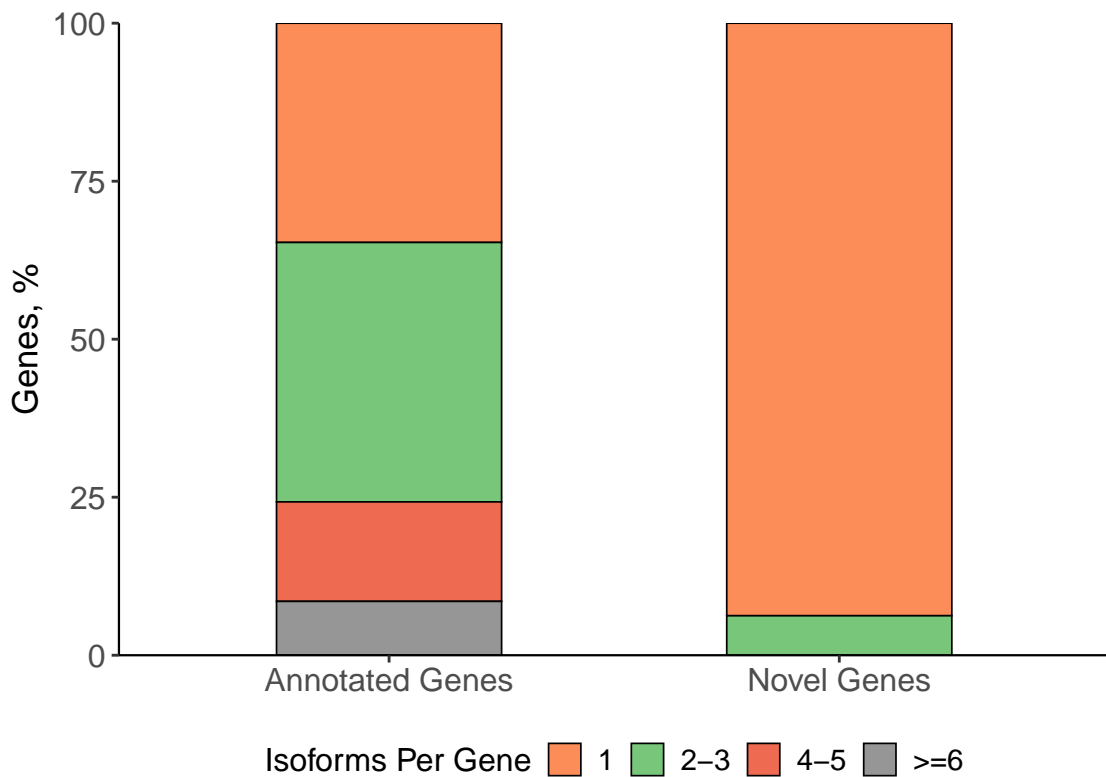
Gene Characterization

Number of Isoforms per Gene

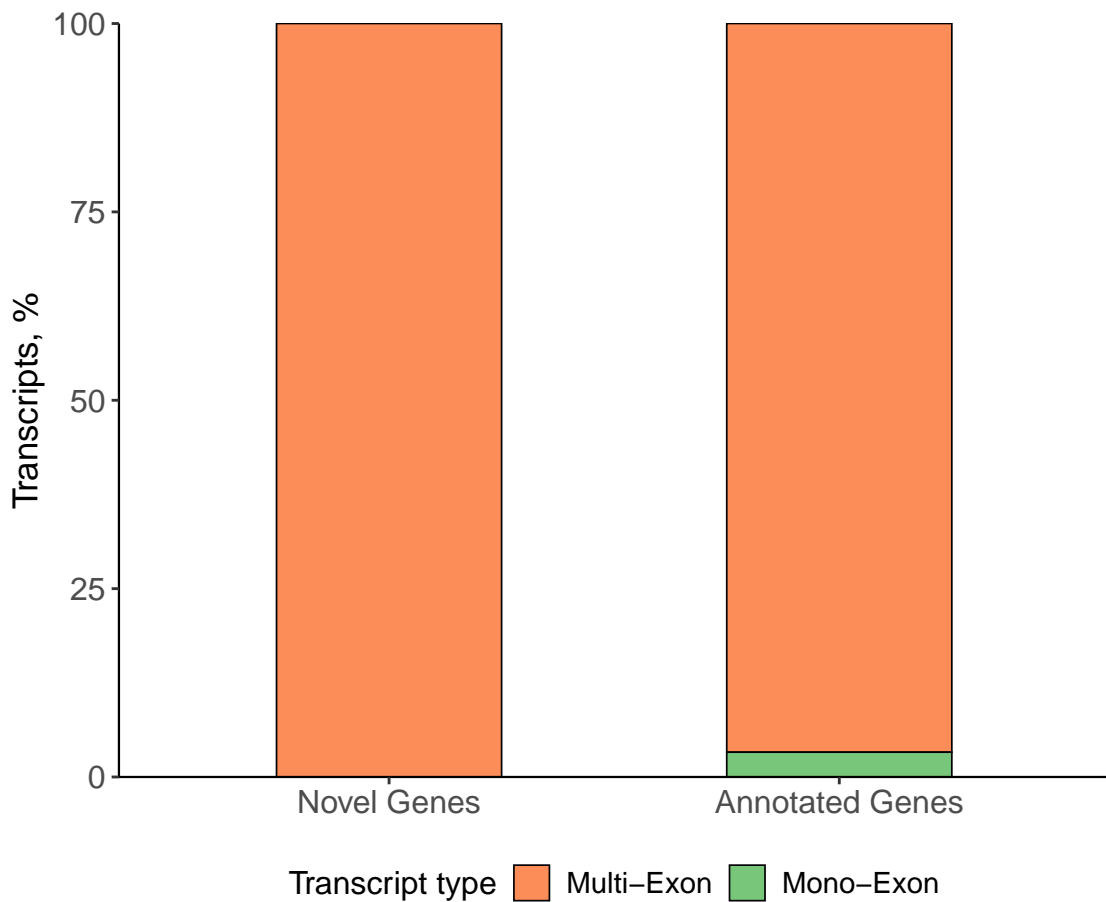


Number of Isoforms per Gene

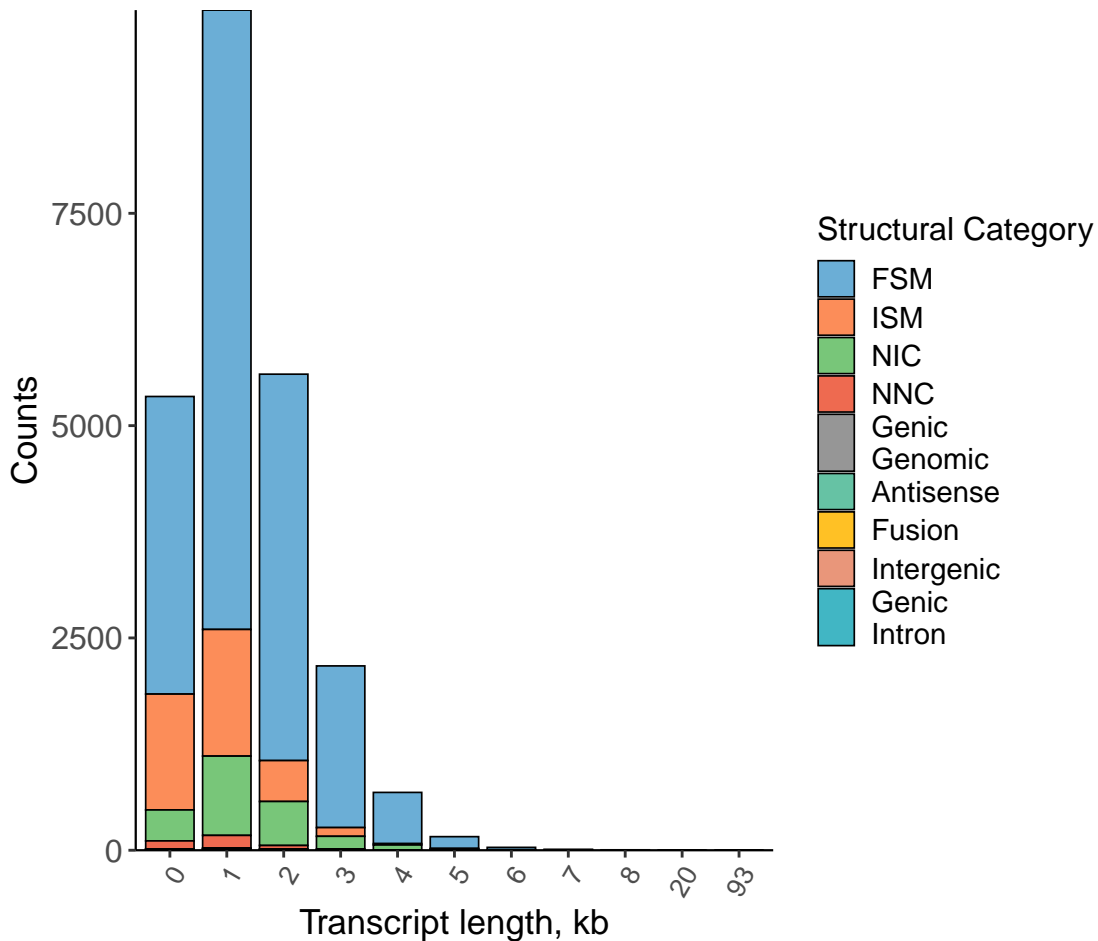
Known vs Novel Genes



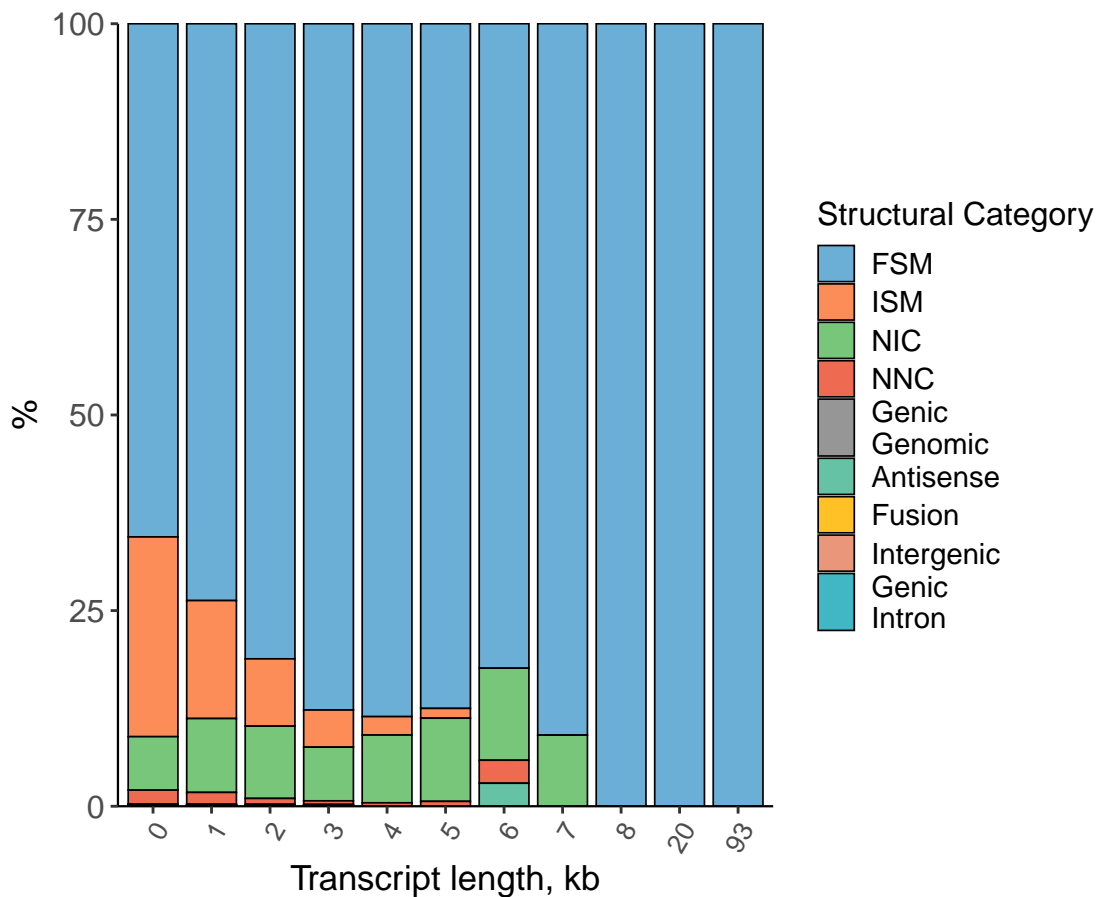
Distribution of Mono- vs Multi-Exon Transcripts



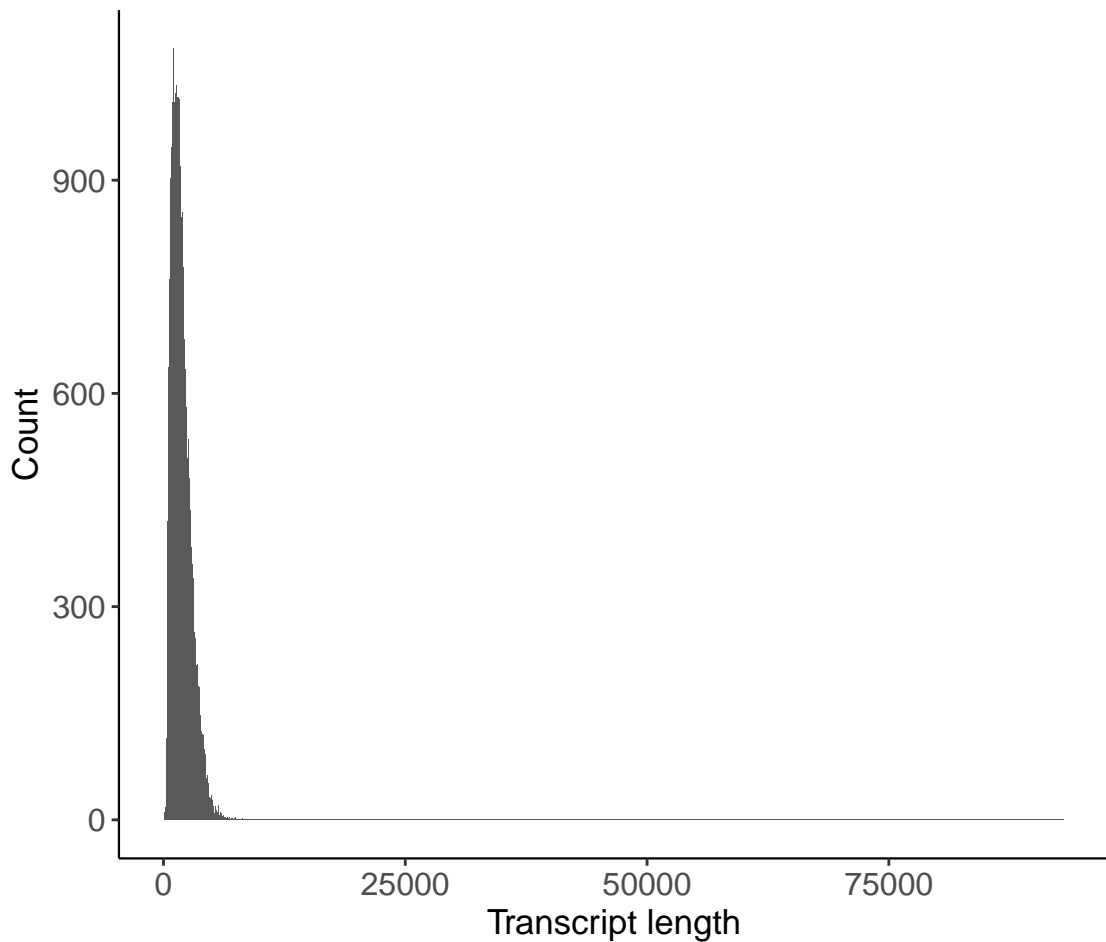
Structural Categories by Transcript Length



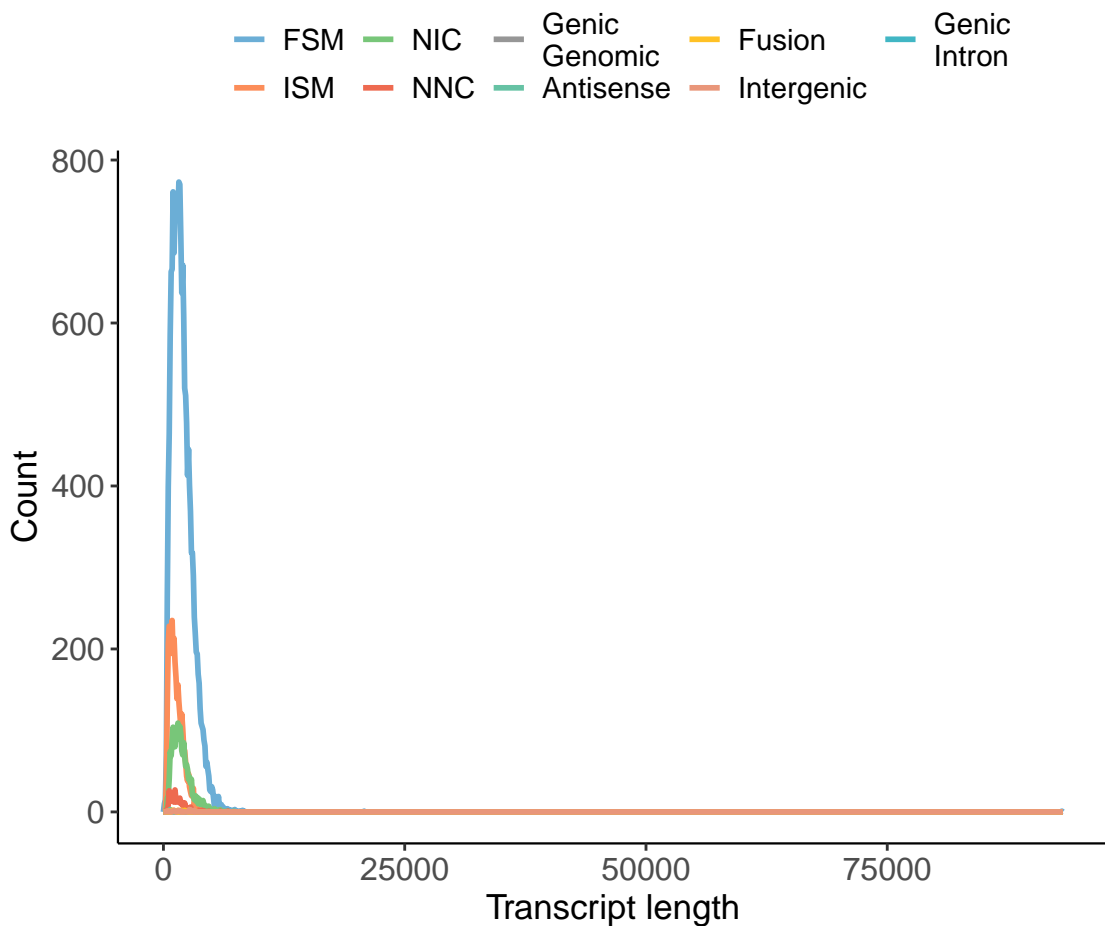
Structural Categories by Transcript Length



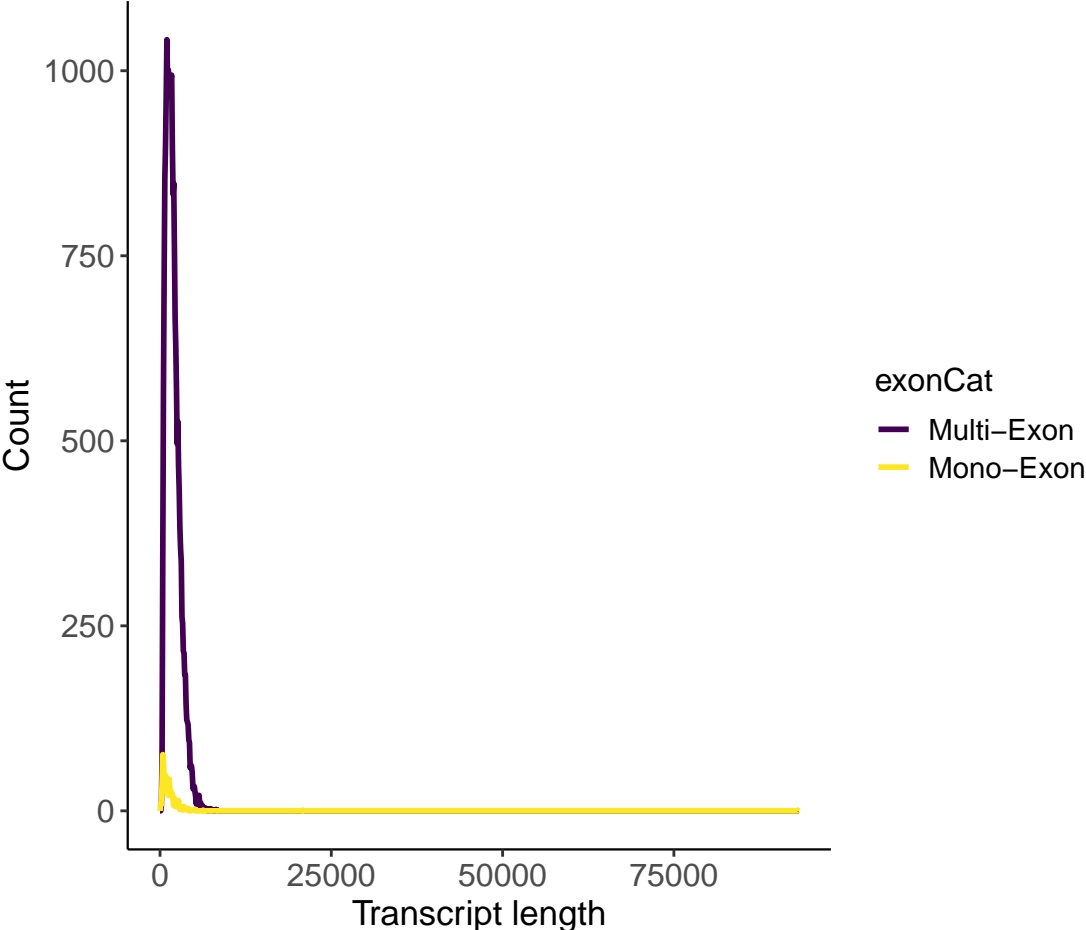
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

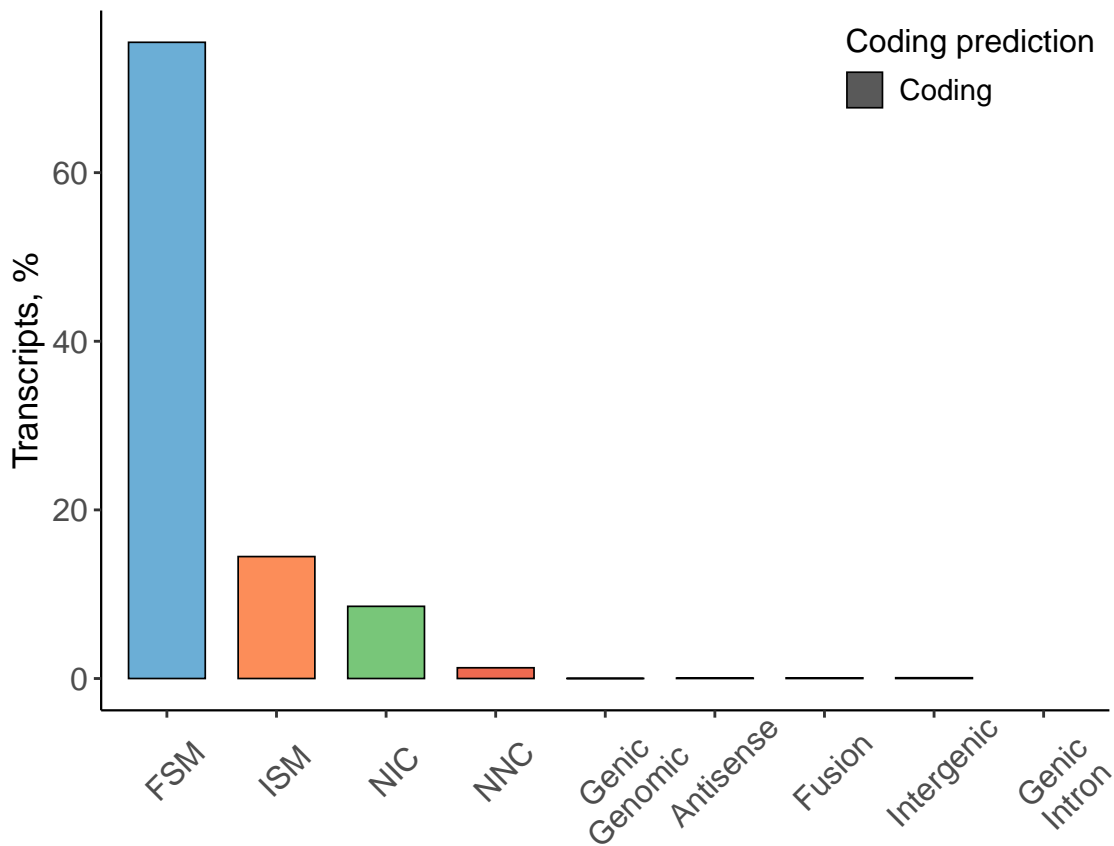


Mono- vs Multi- Exon Transcript Lengths Distribution

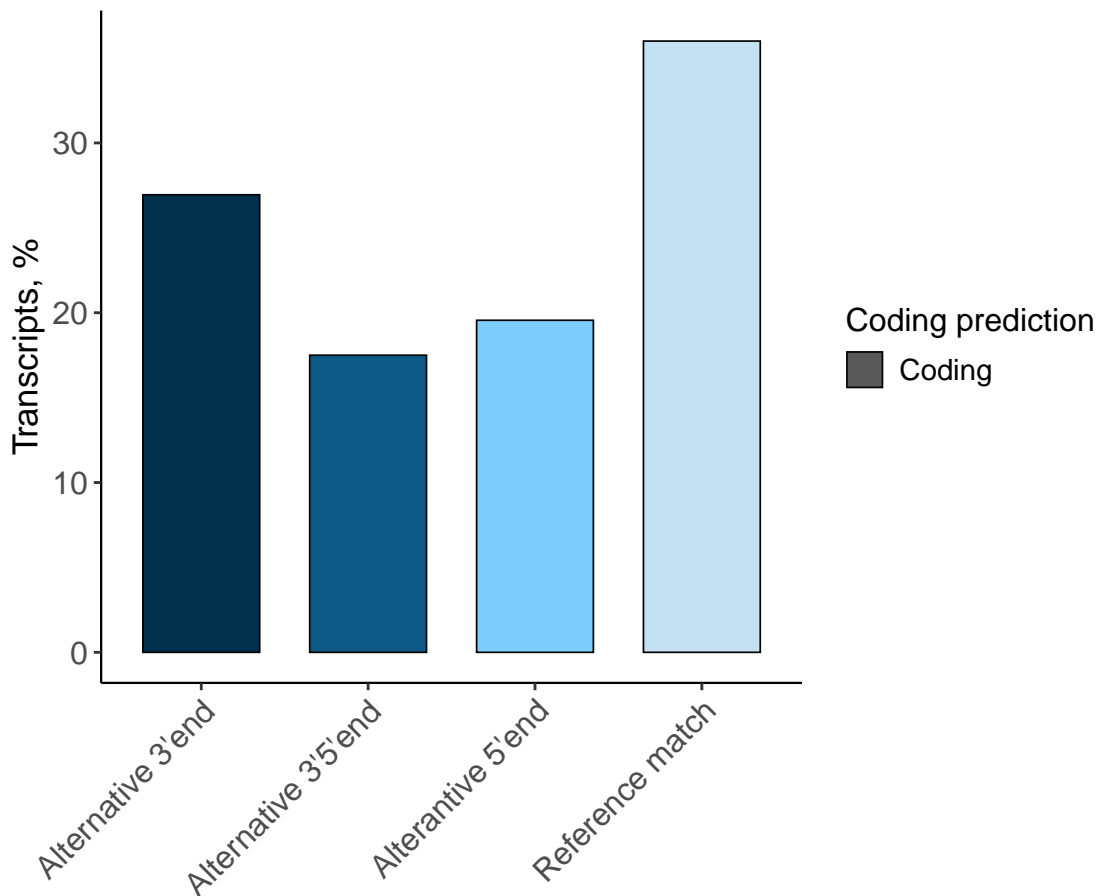


Structural Isoform Characterization

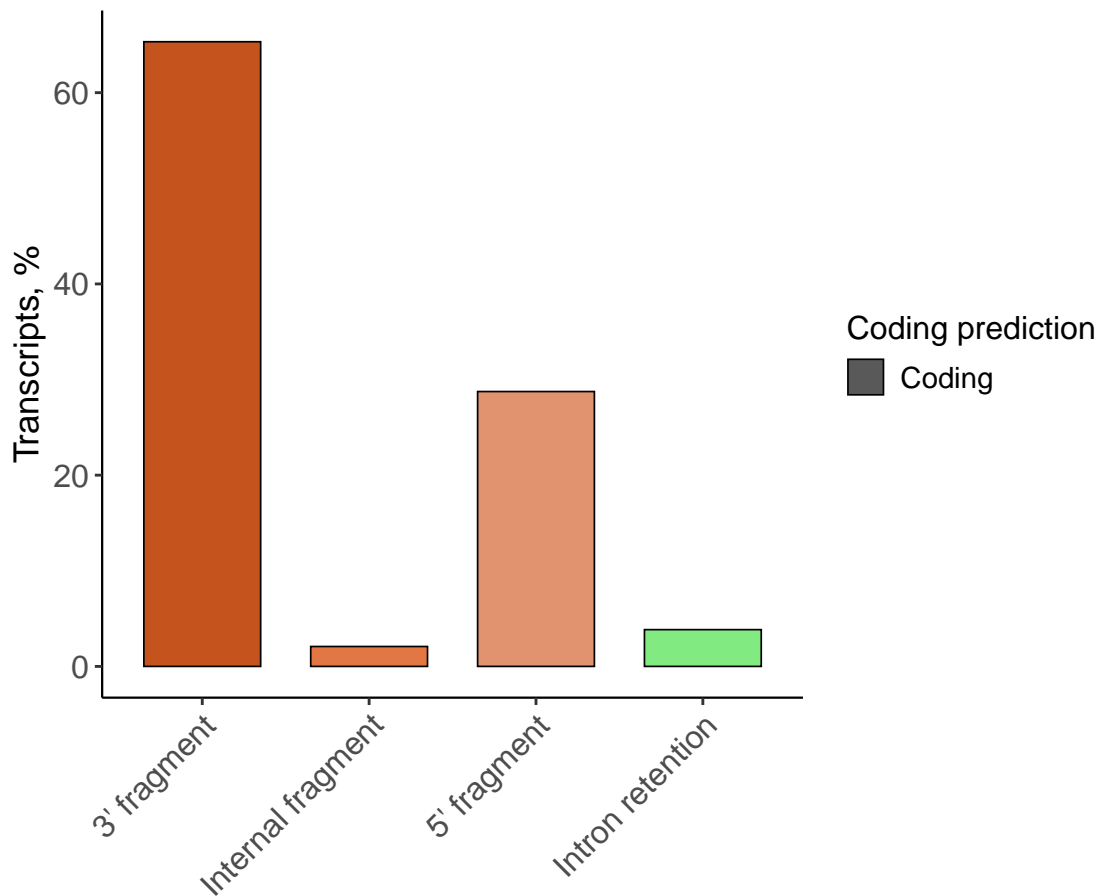
Isoform Distribution Across Structural Categories



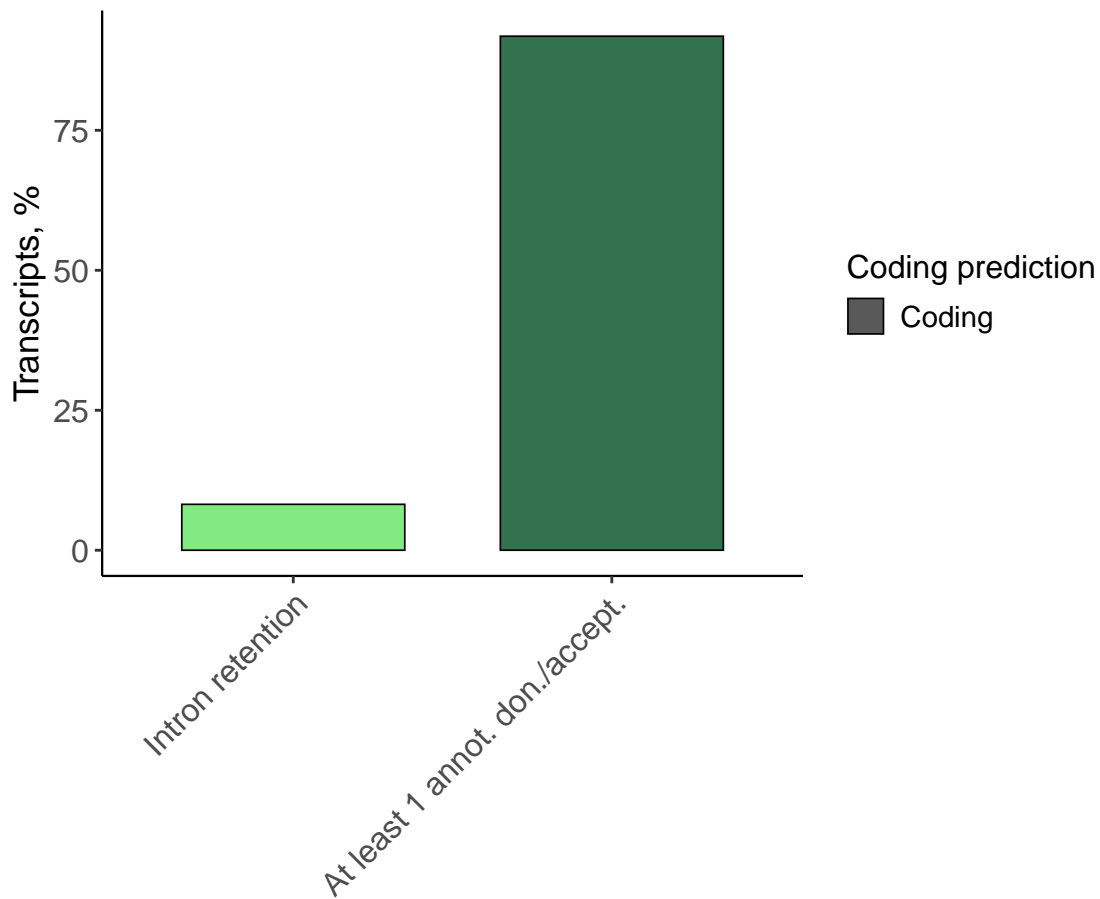
Isoform Distribution Across FSM



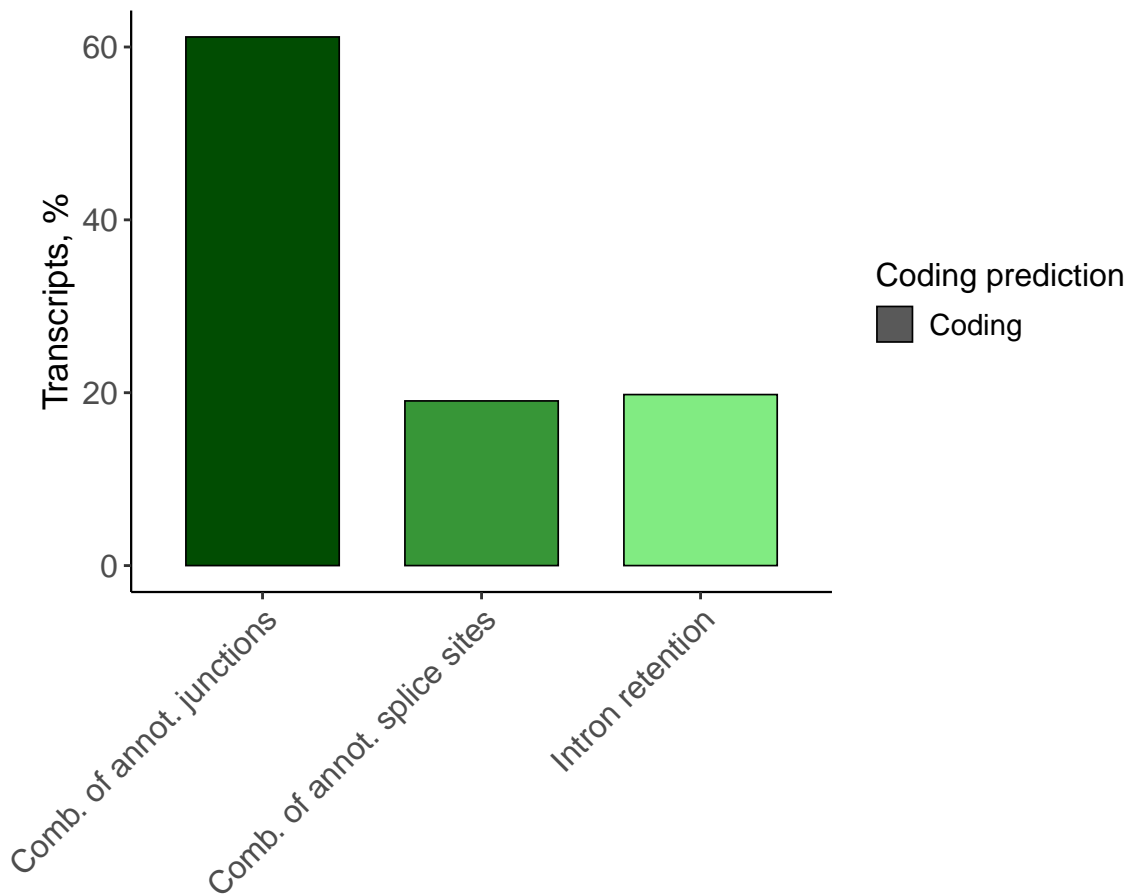
Isoform Distribution Across ISM



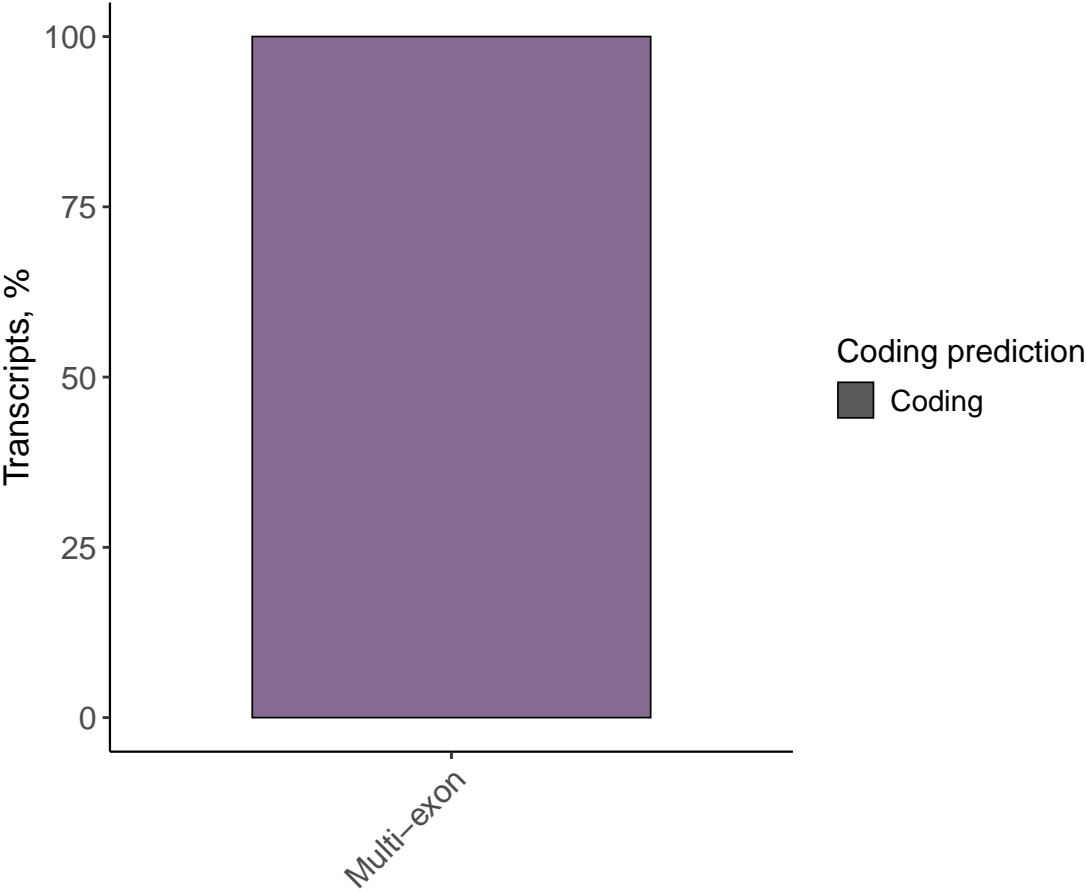
Isoform Distribution Across NNC



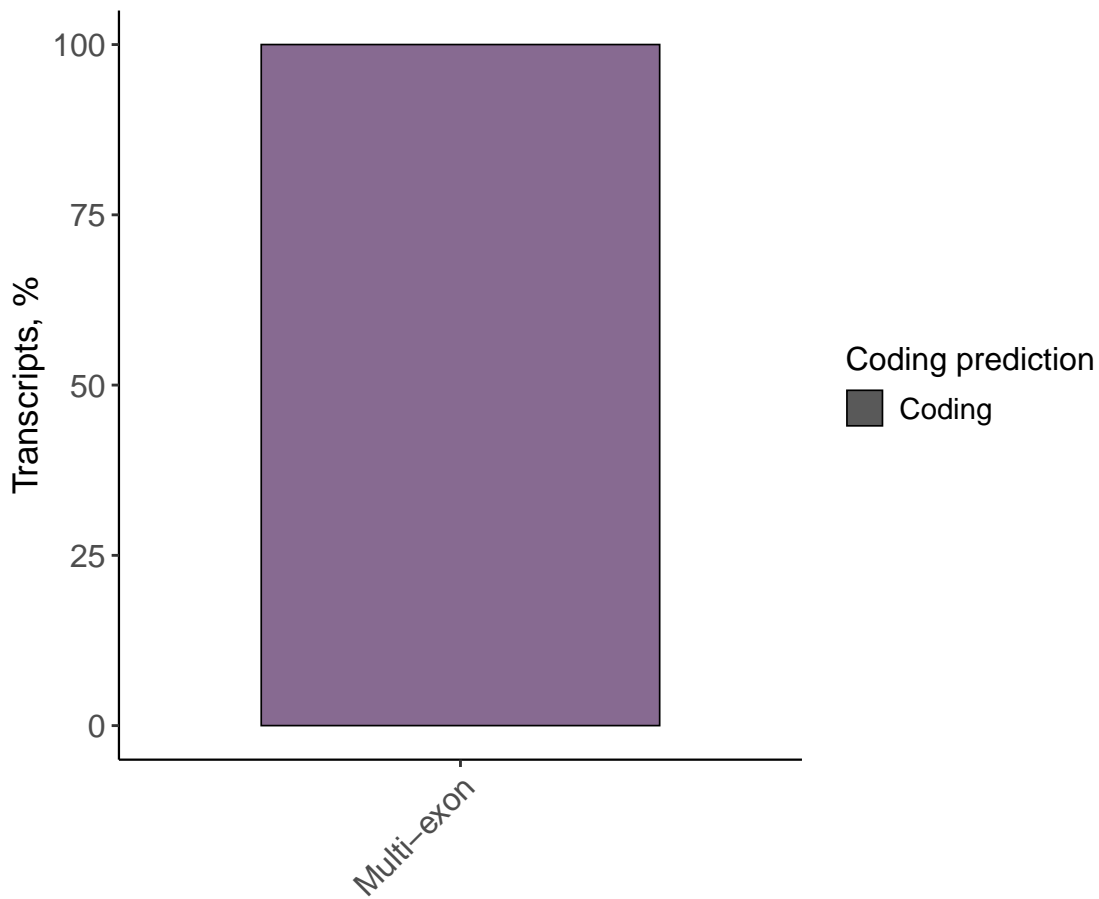
Isoform Distribution Across NIC



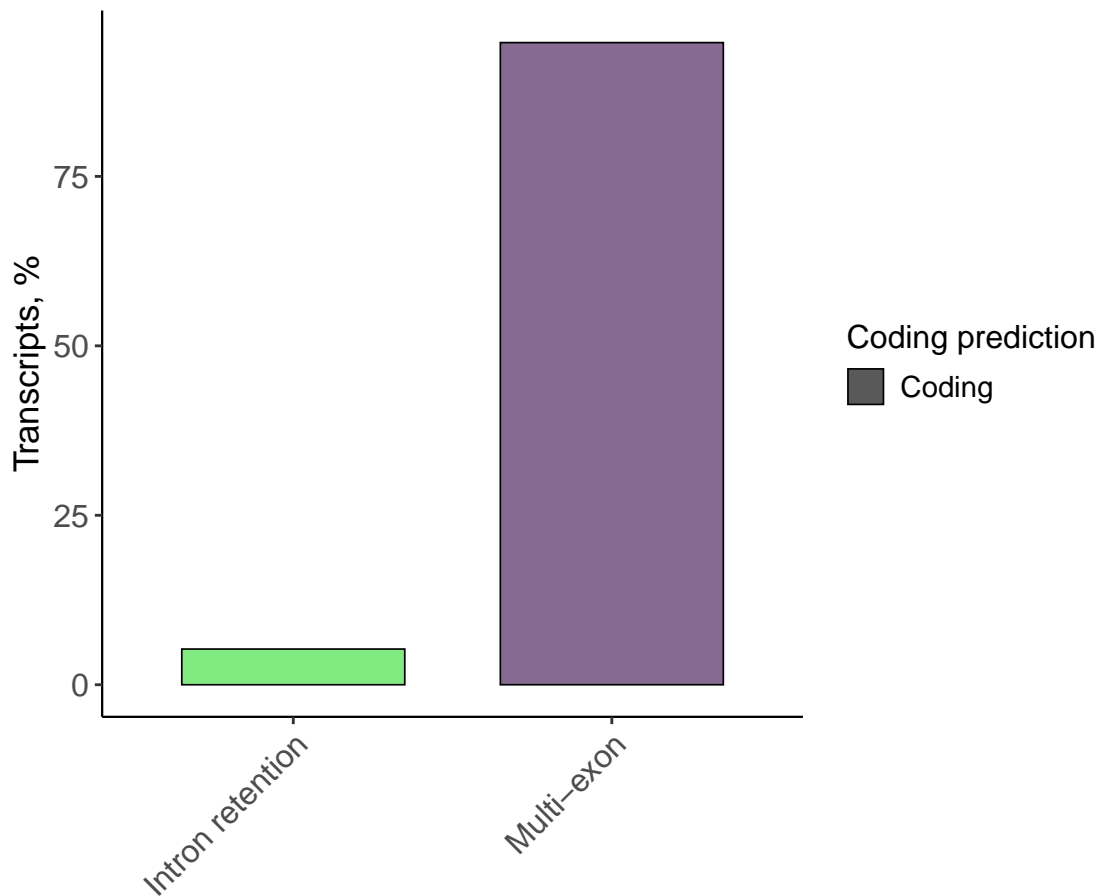
Isoform Distribution Across Genic Genomic



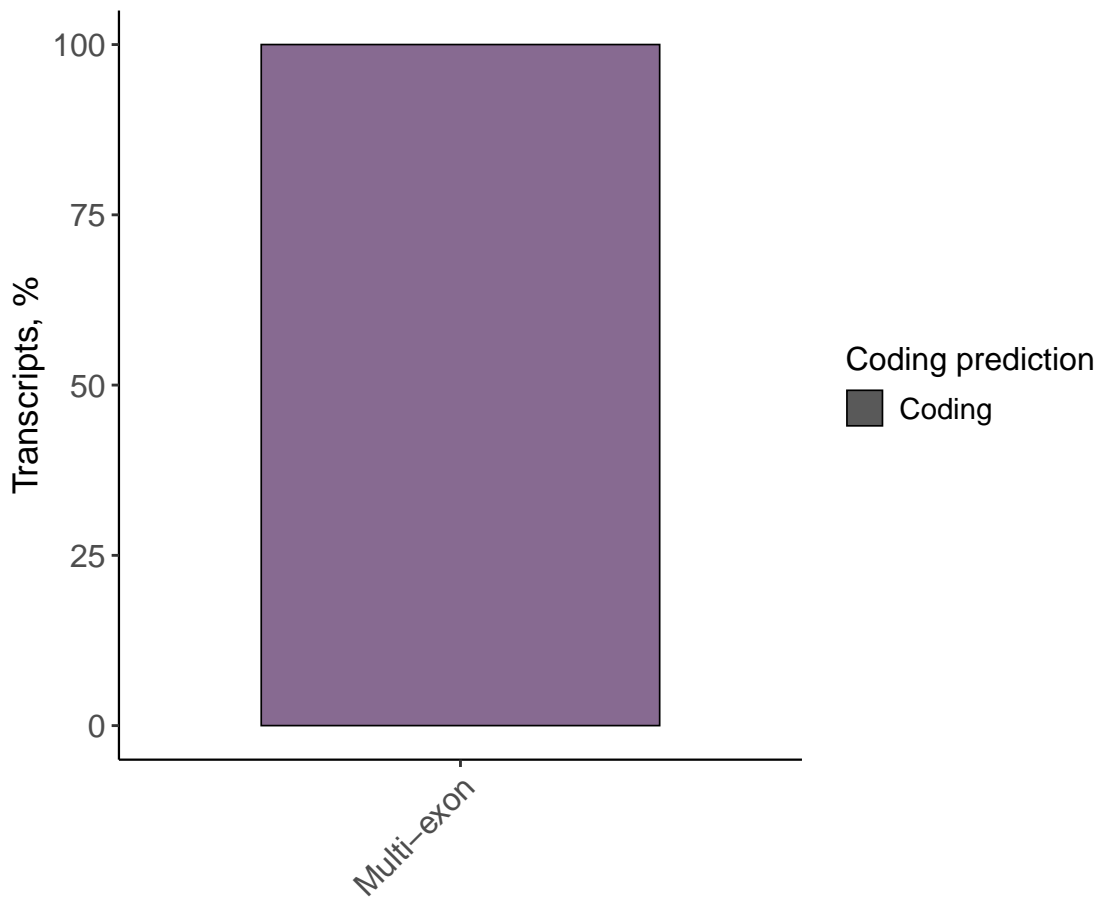
Isoform Distribution Across Antisense



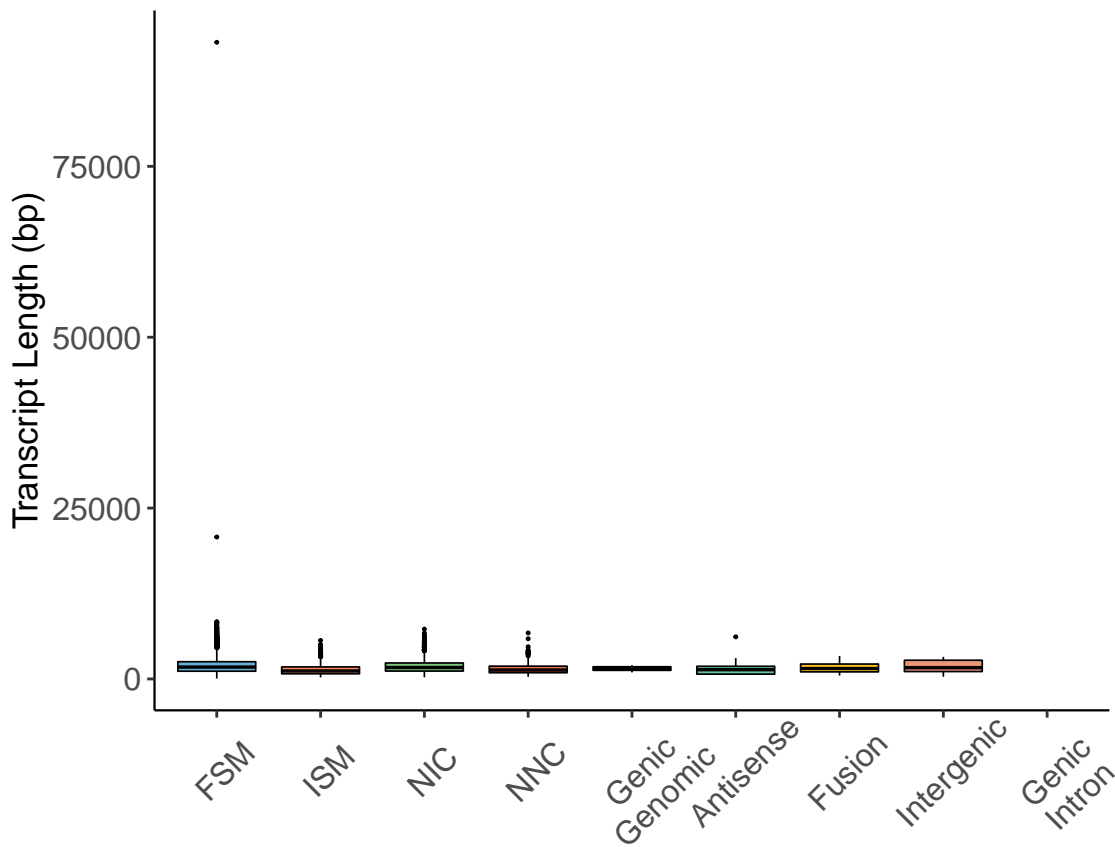
Isoform Distribution Across Fusion



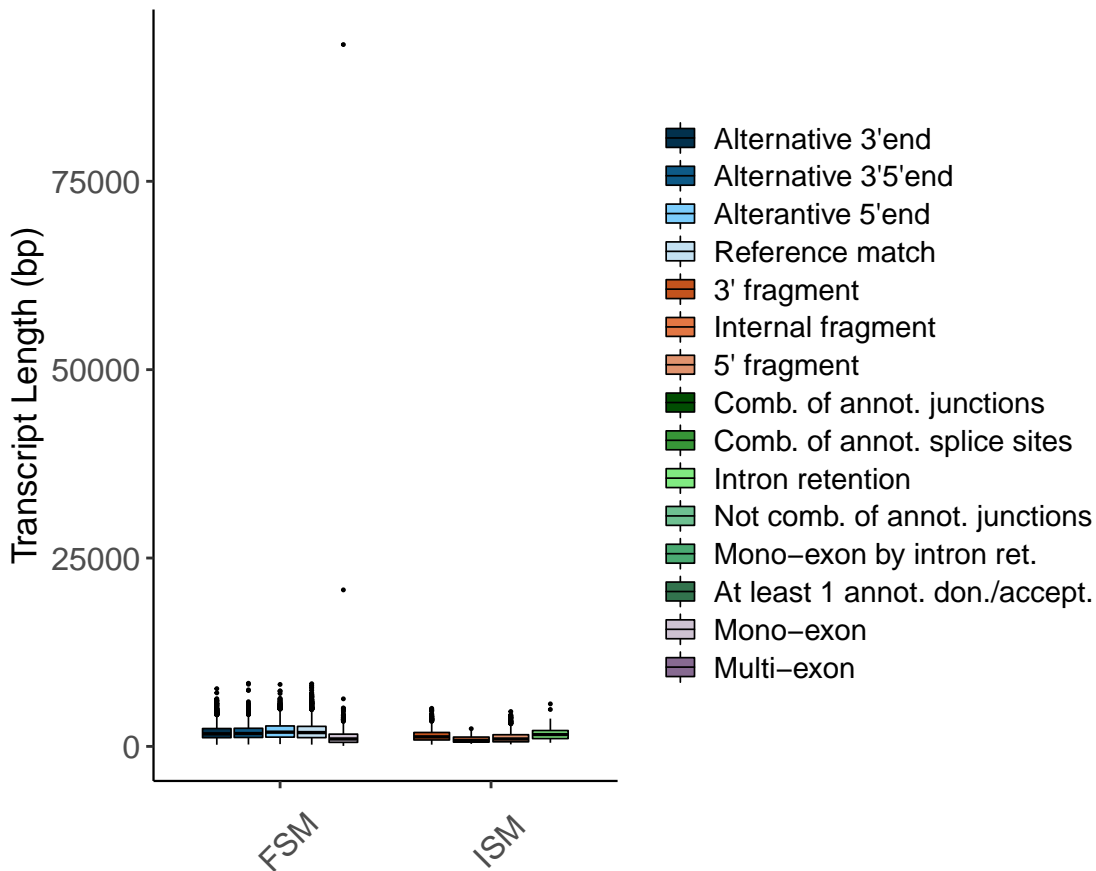
Isoform Distribution Across Intergenic



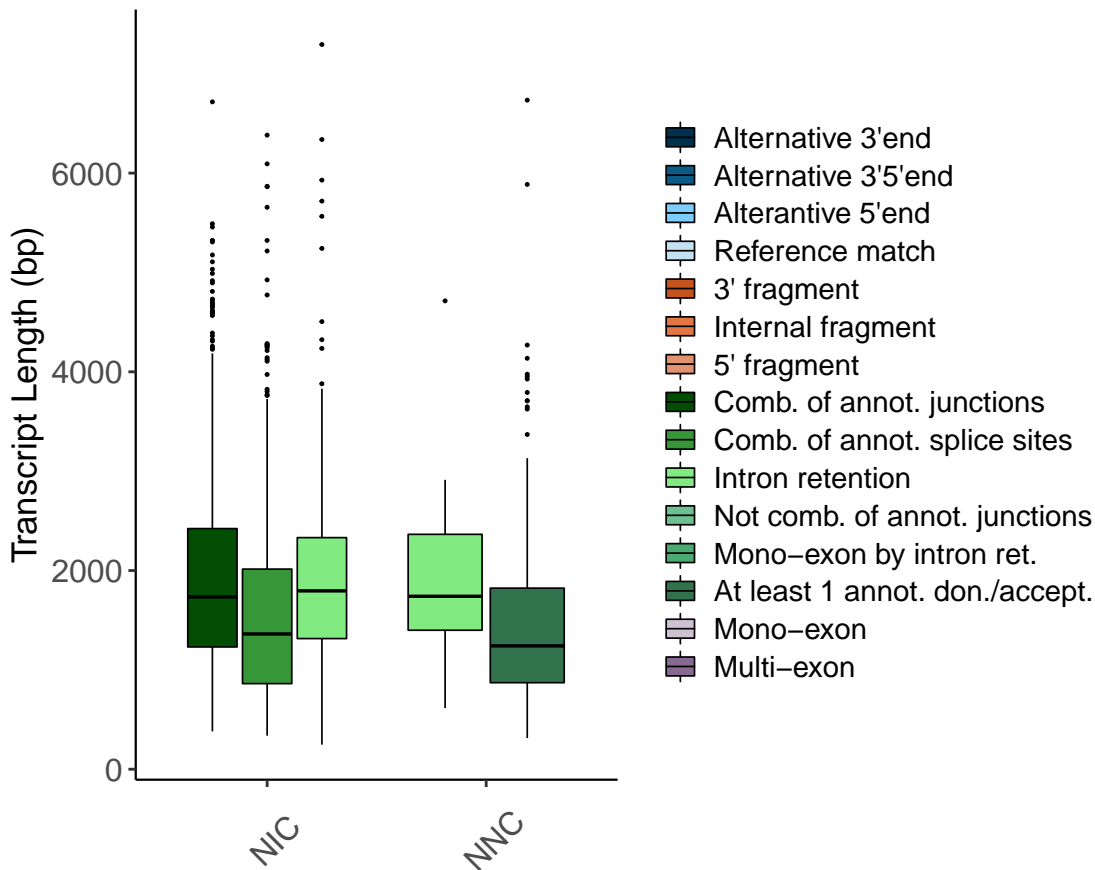
Transcript Lengths by Structural Classification



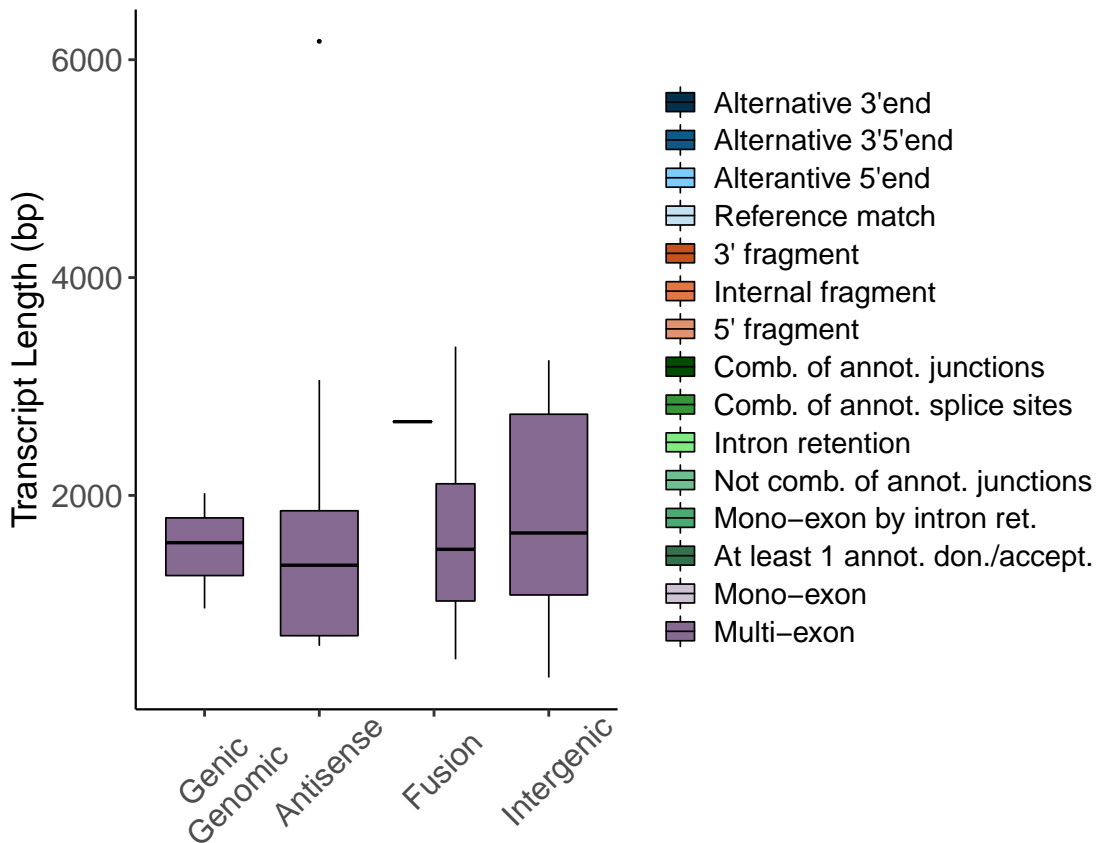
Transcript Lengths by Subcategory



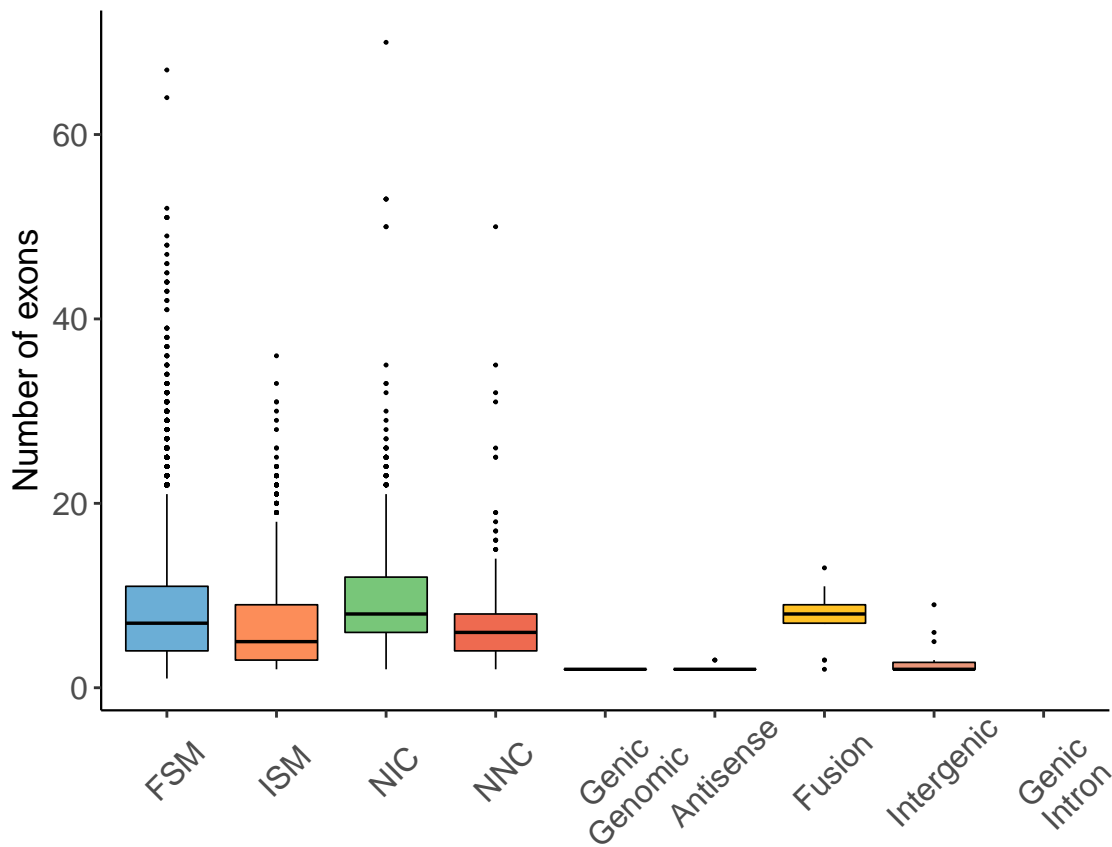
Transcript Lengths by Subcategory



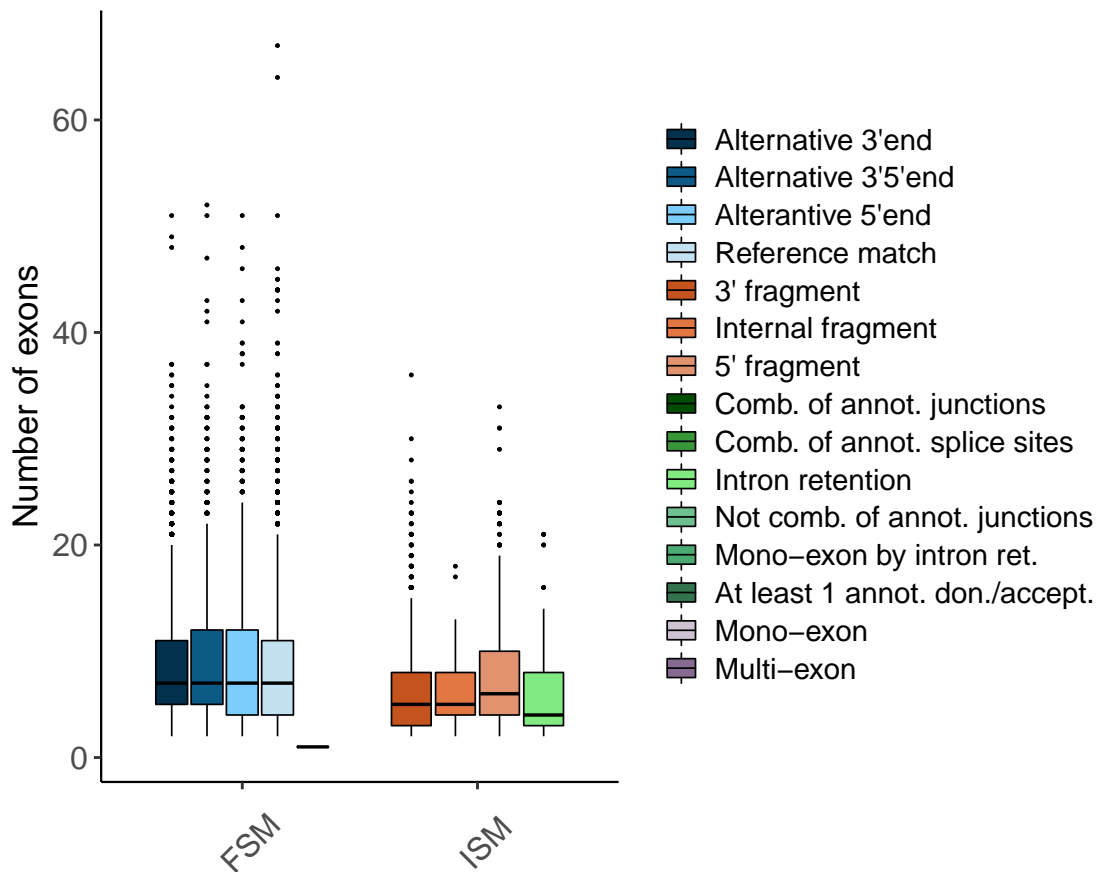
Transcript Lengths by Subcategory



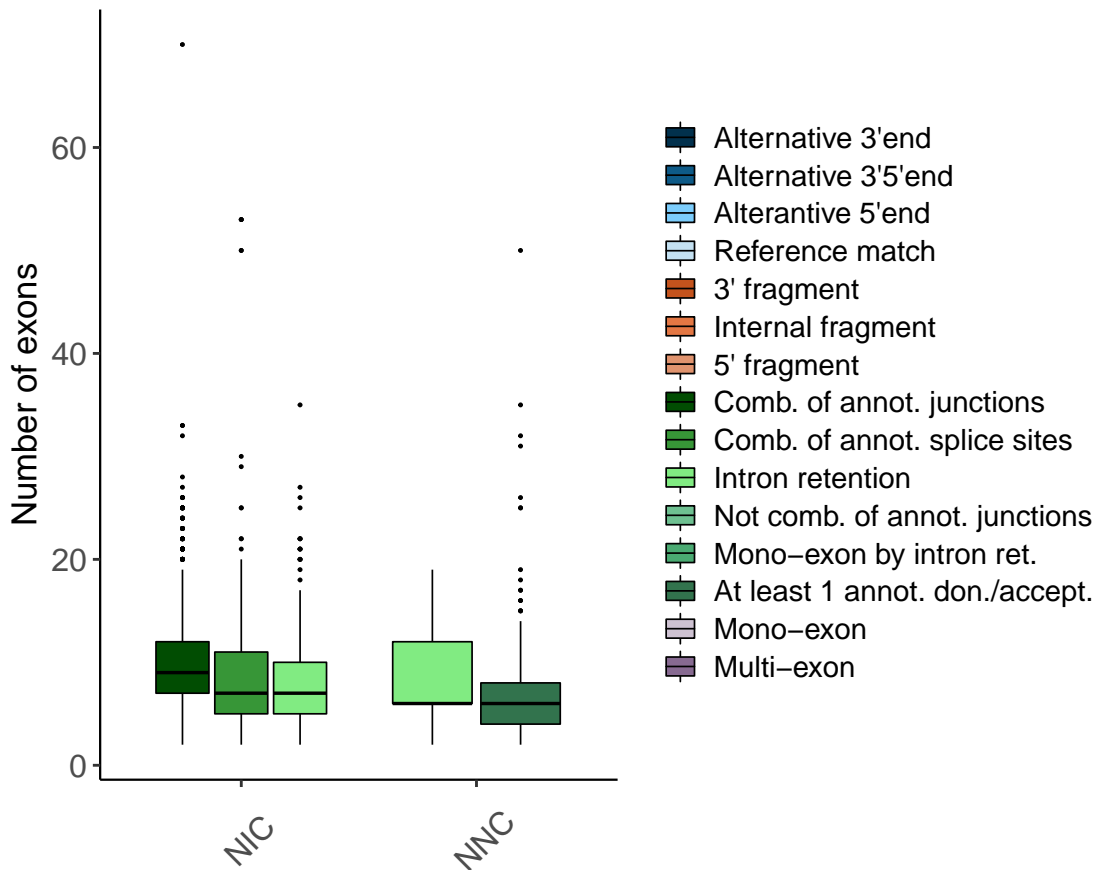
Exon Counts by Structural Classification



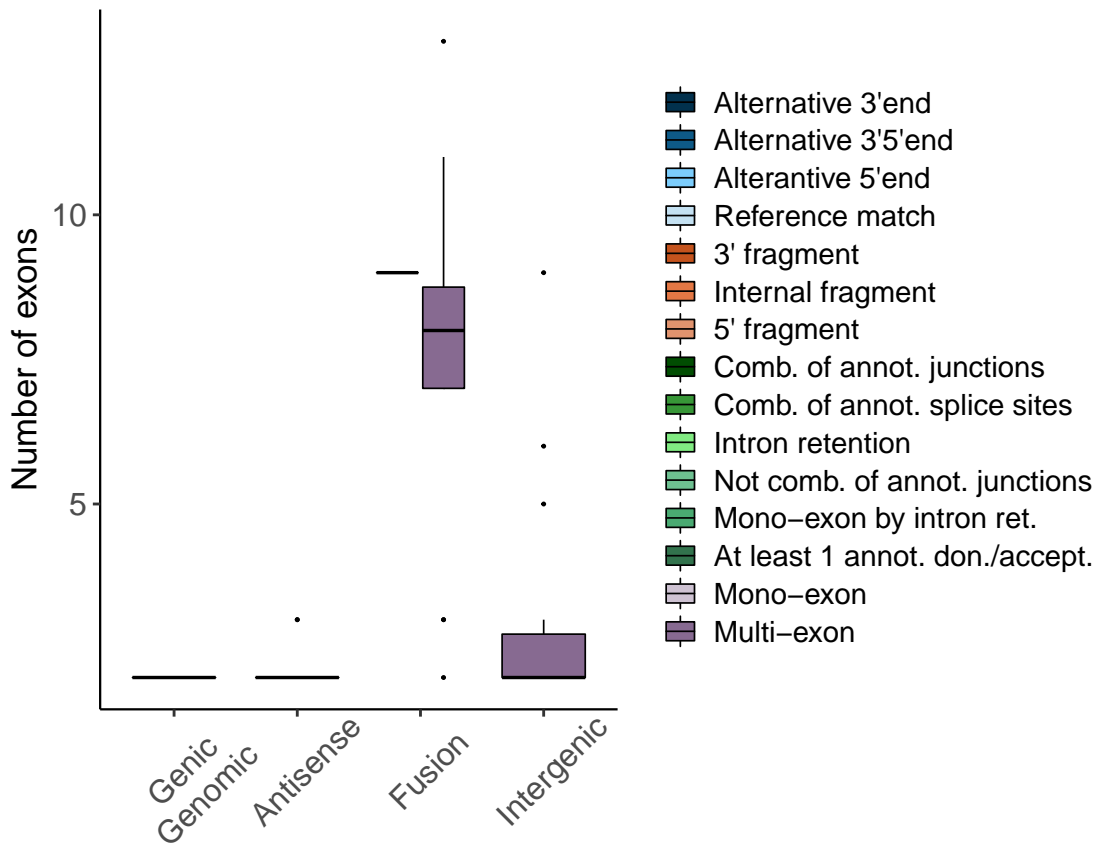
Exon Counts by Subcategory



Exon Counts by Subcategory

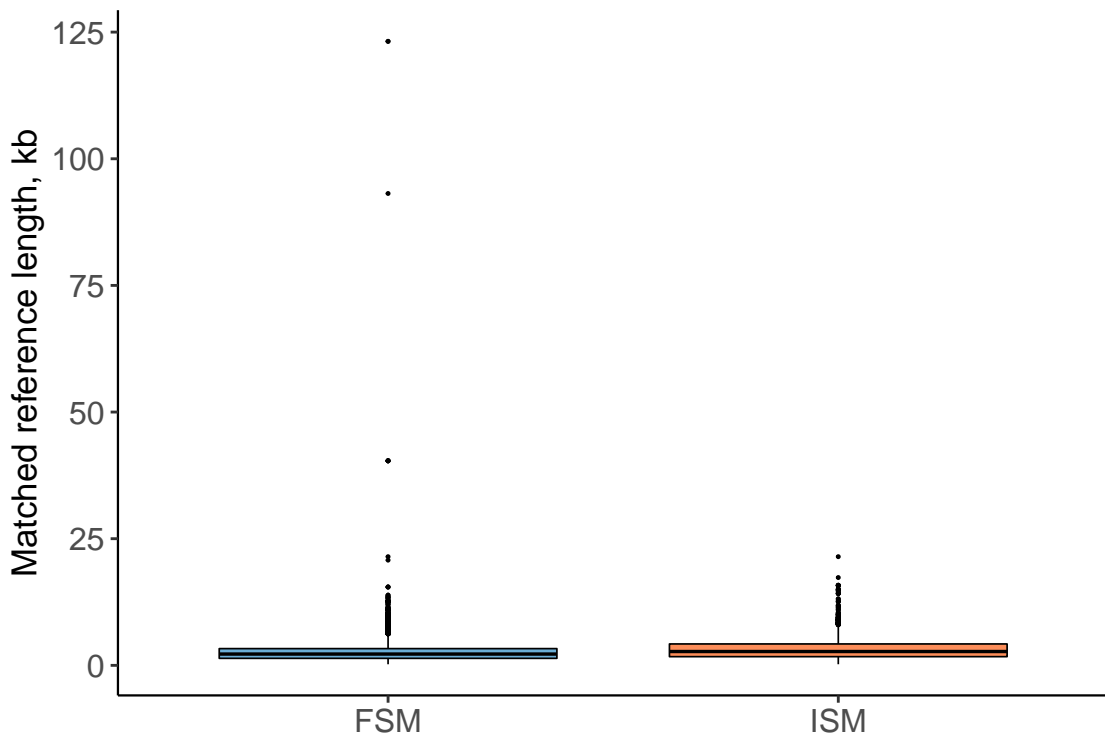


Exon Counts by Subcategory



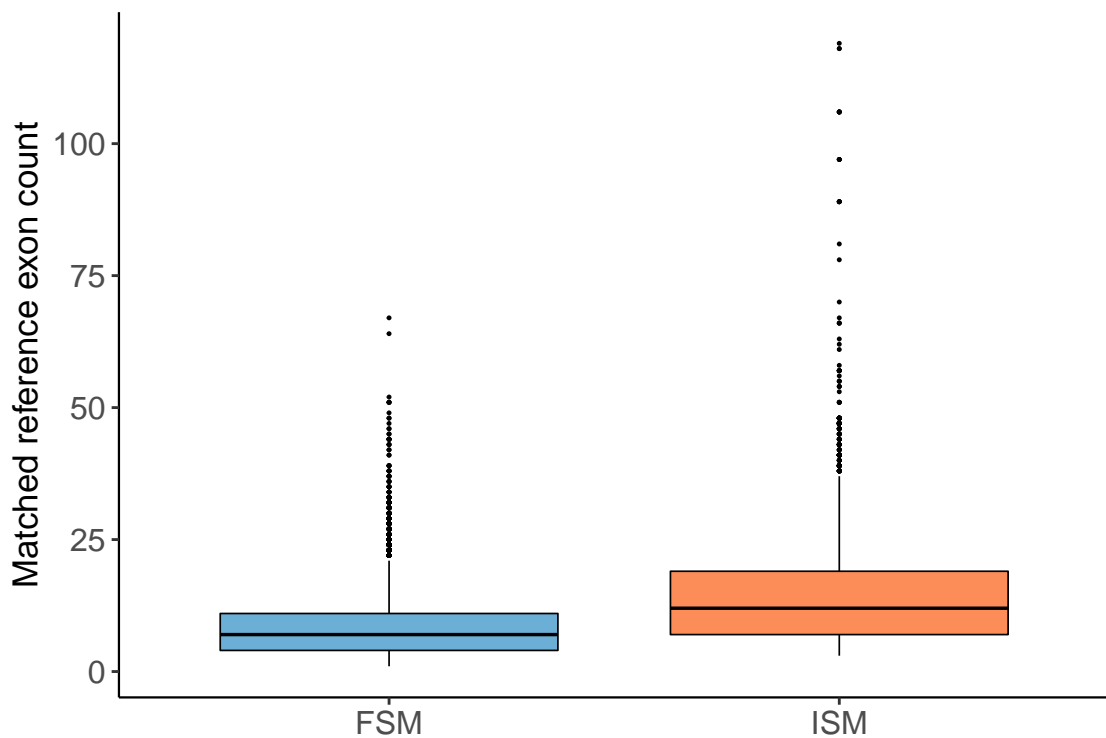
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories



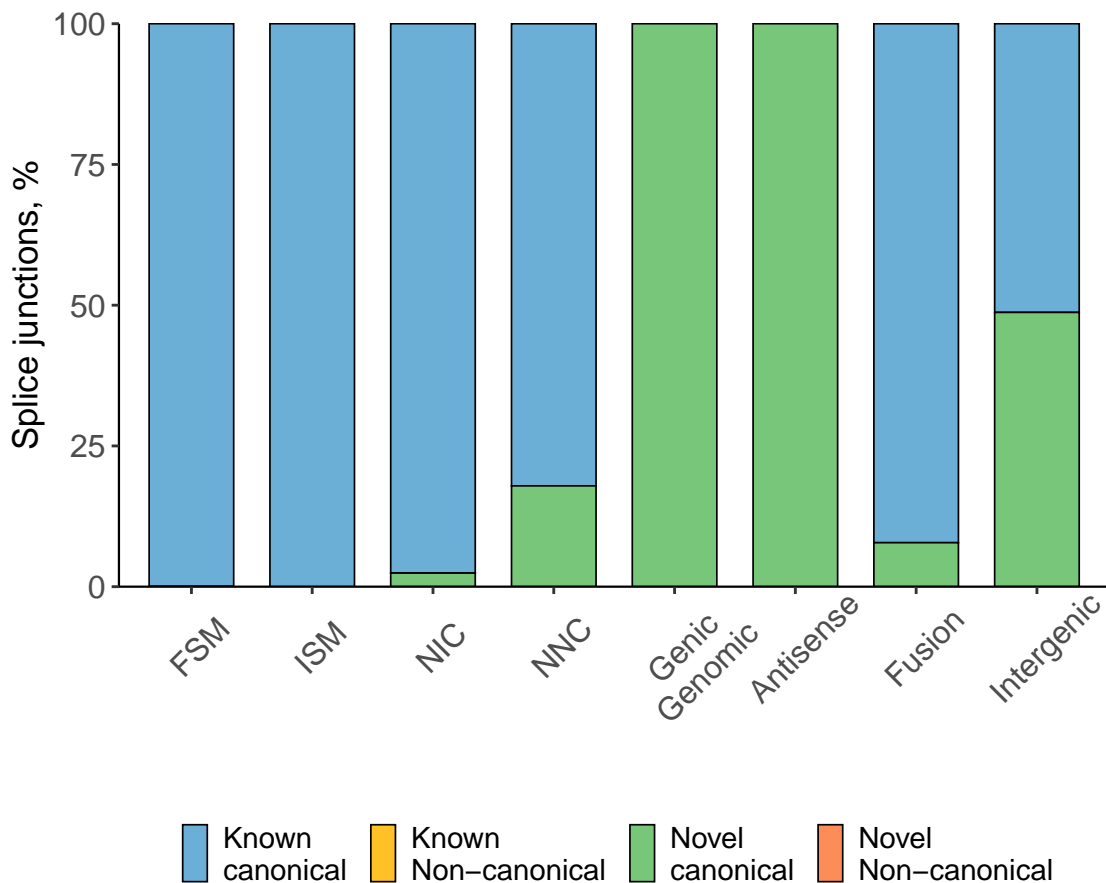
Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

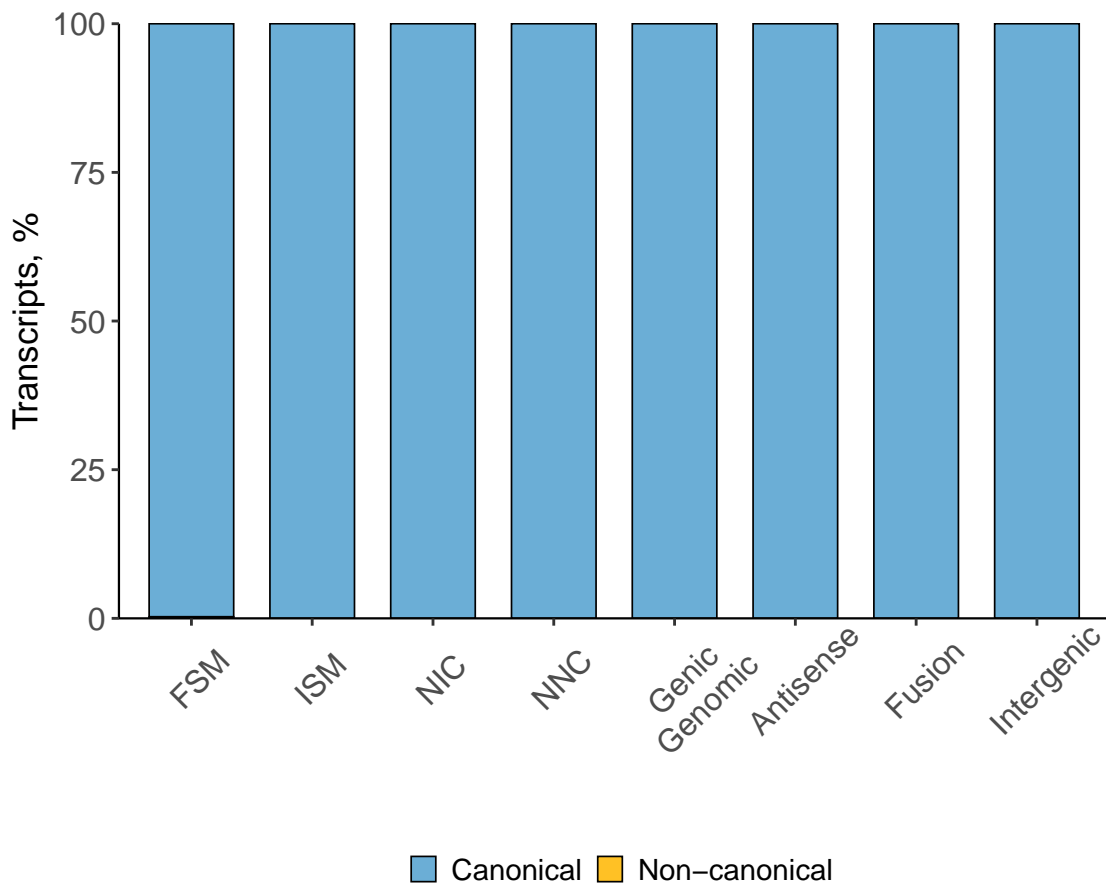


Splice Junction Characterization

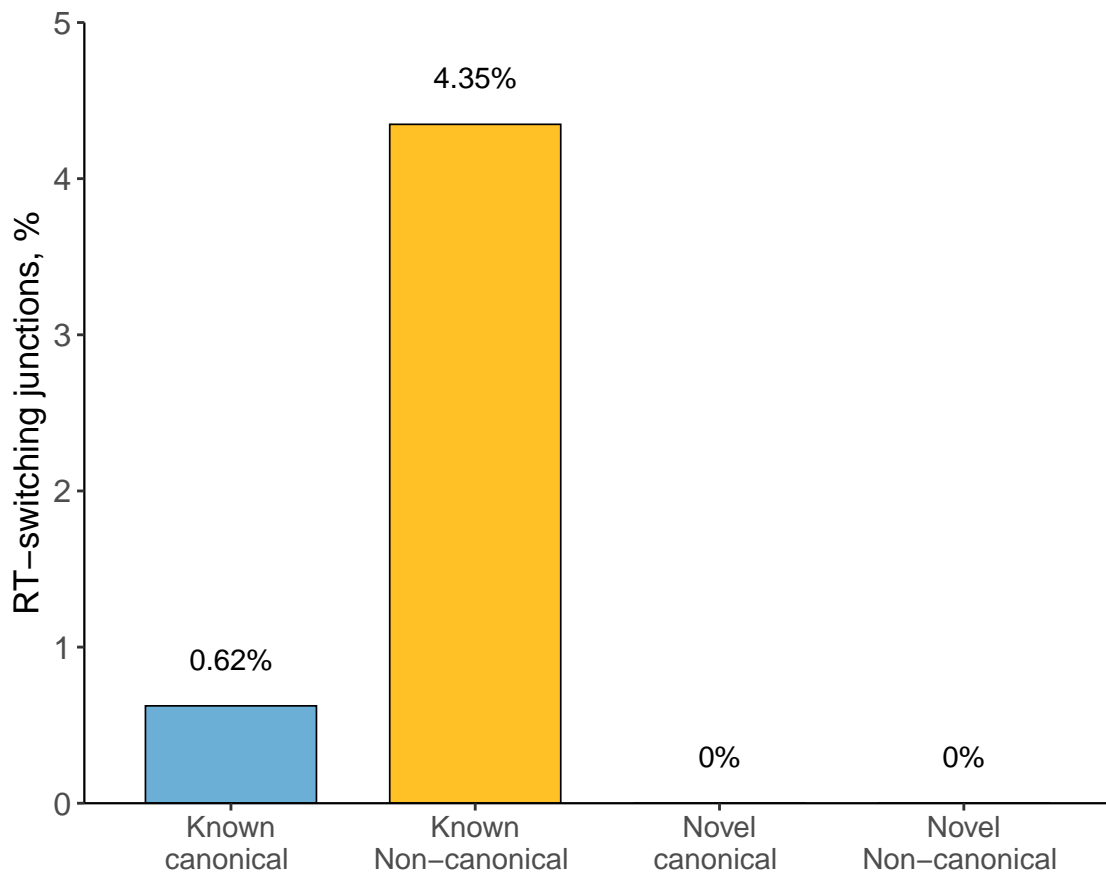
Distribution of Splice Junctions by Structural Classification



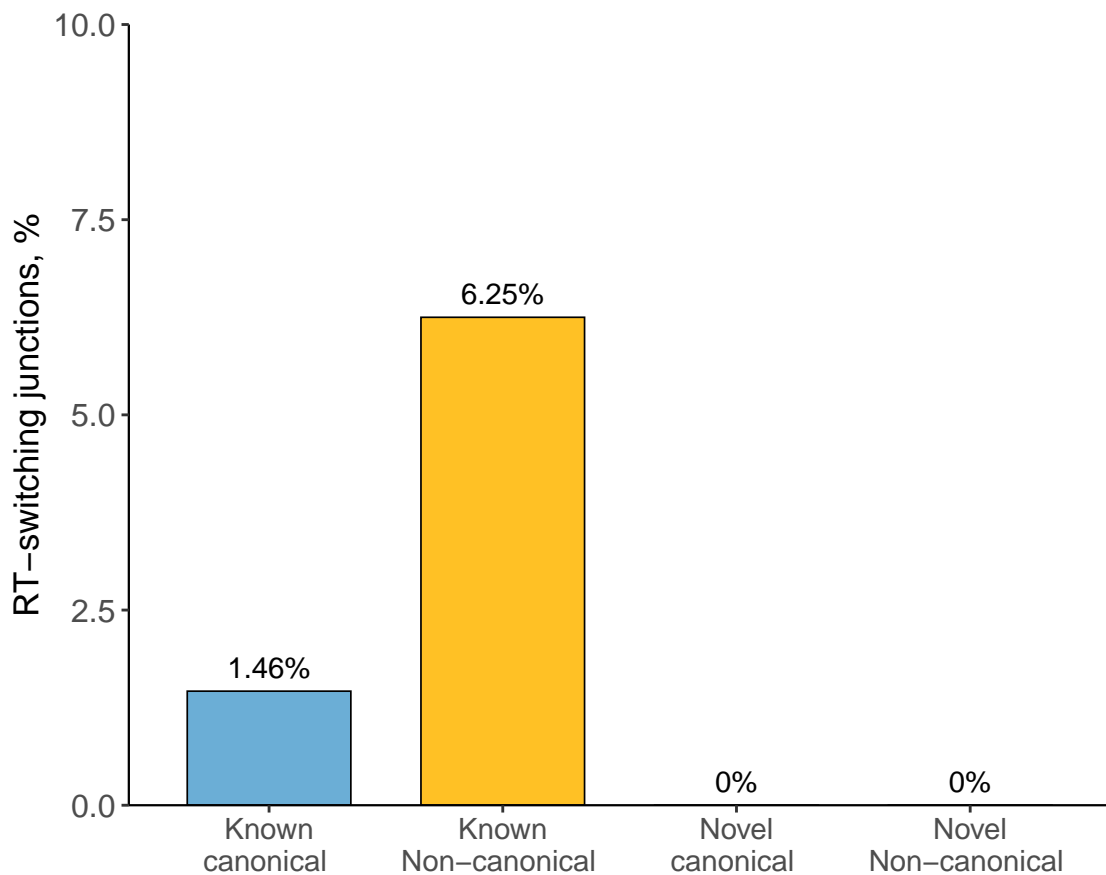
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



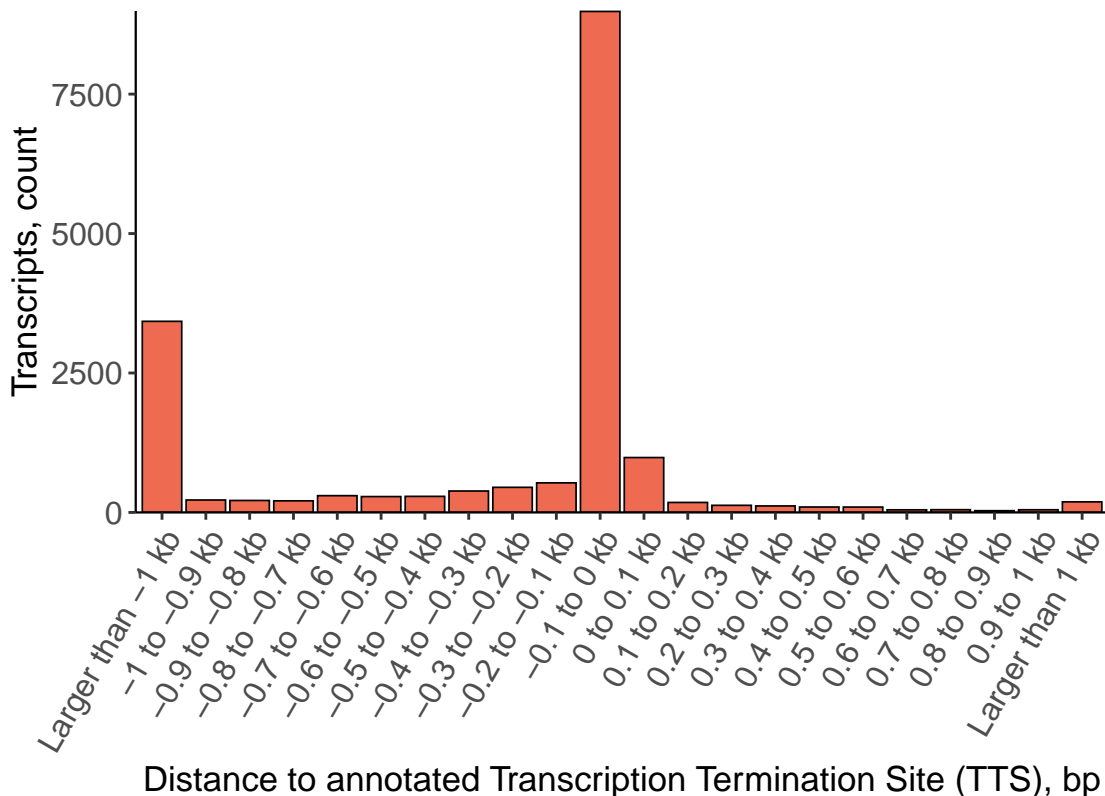
Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

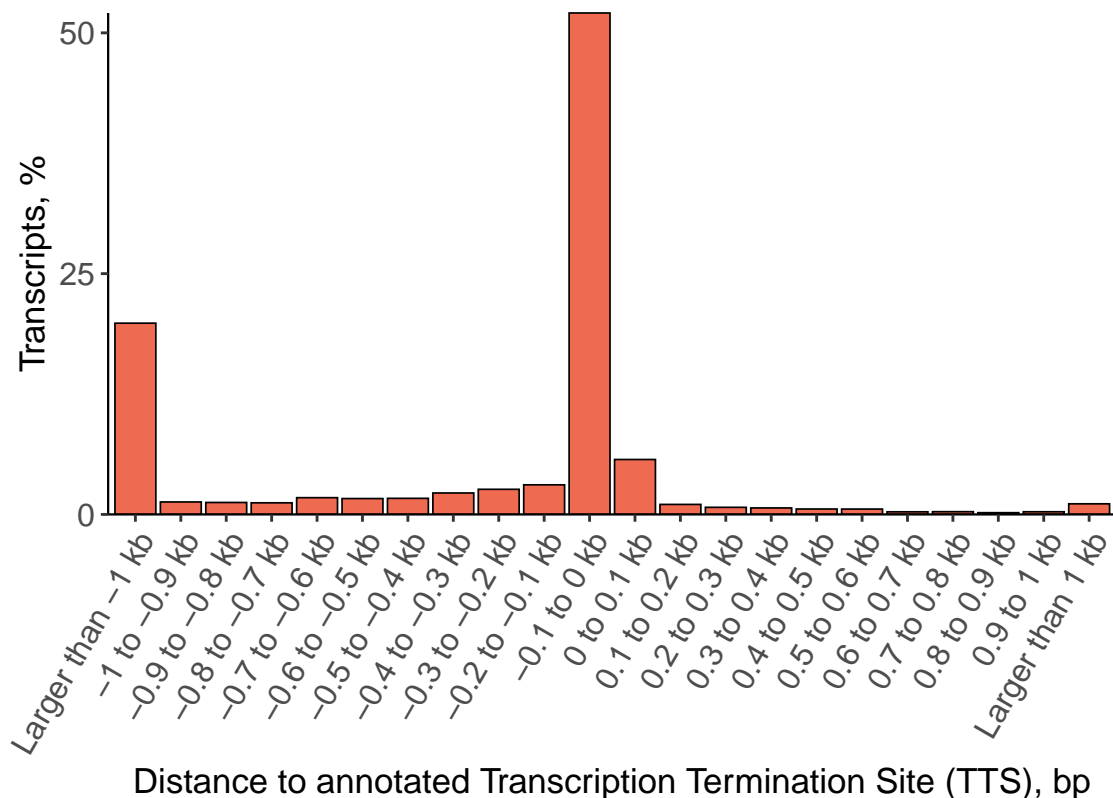
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



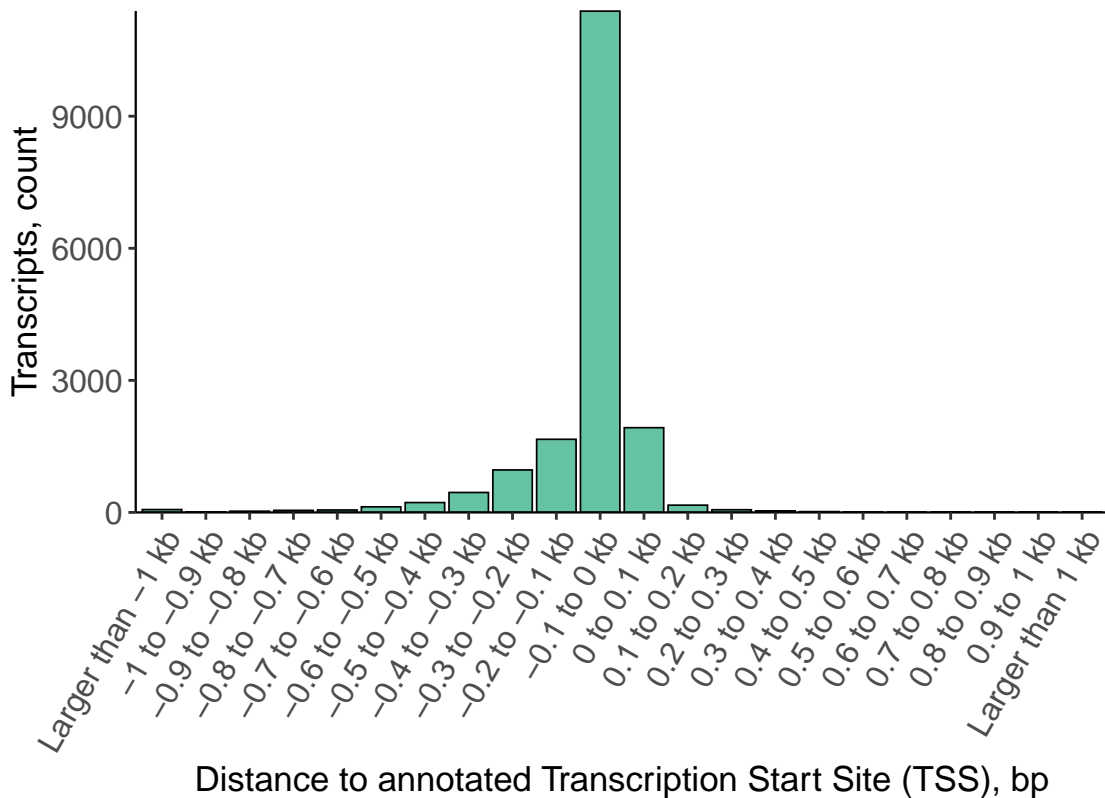
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



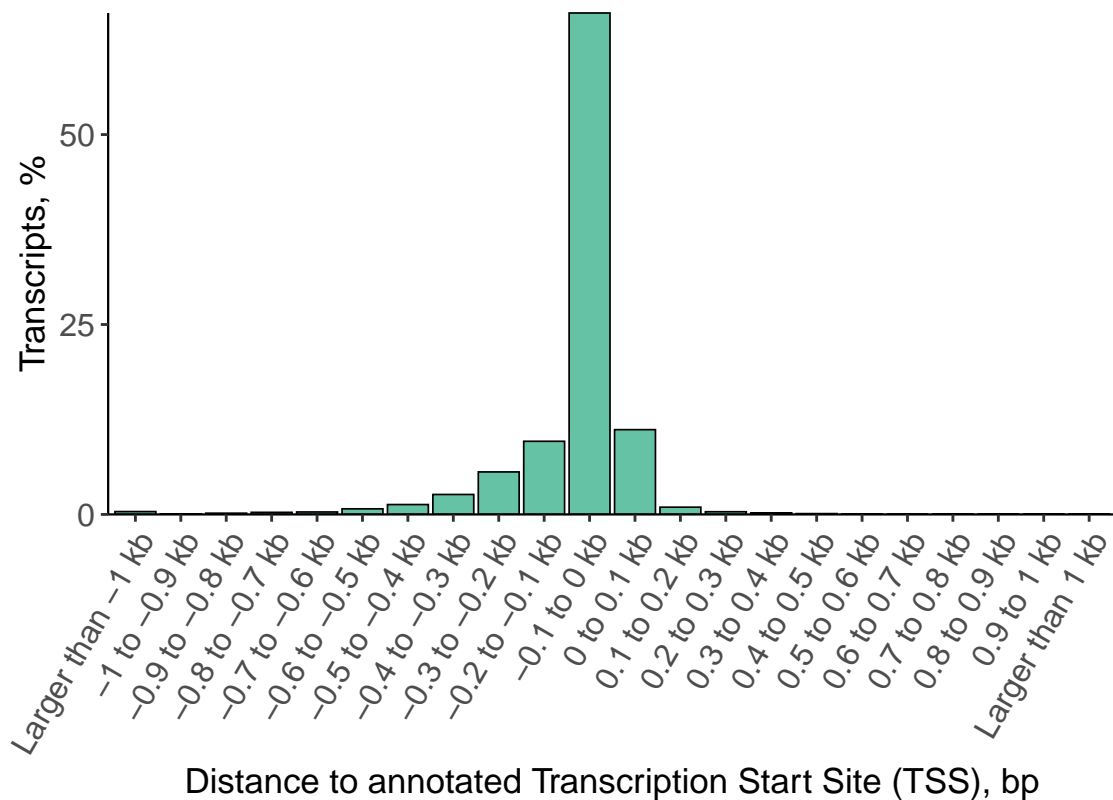
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



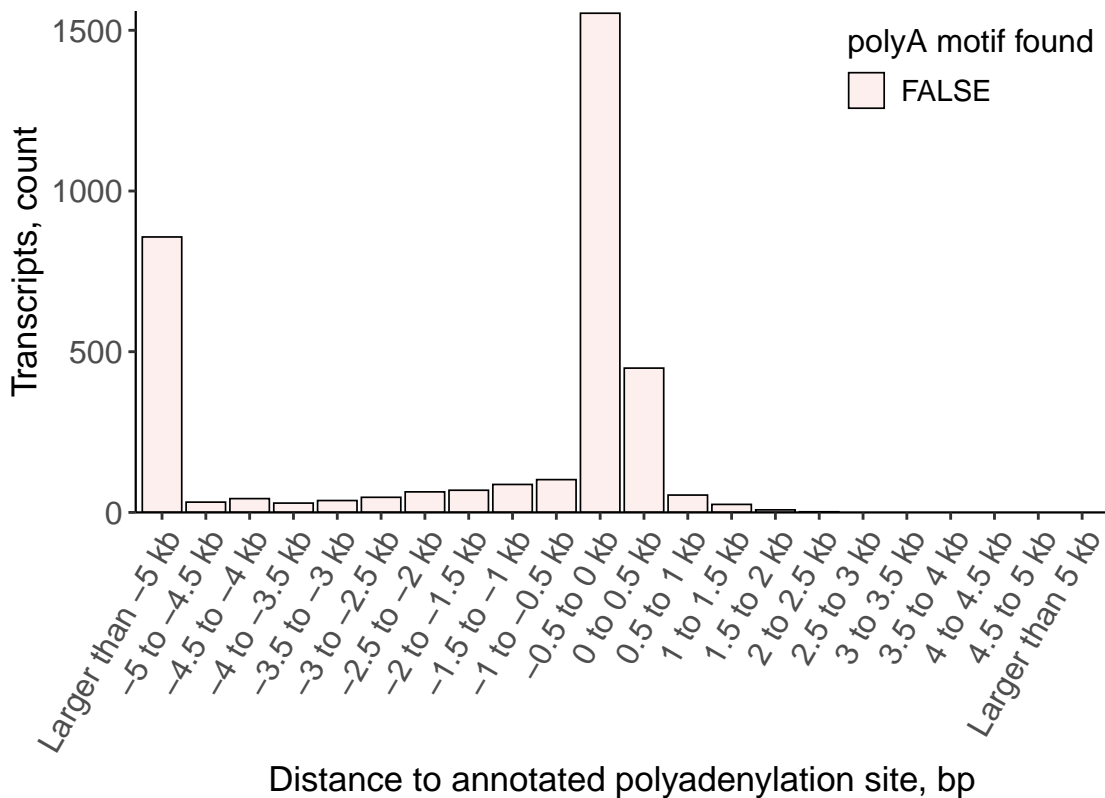
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



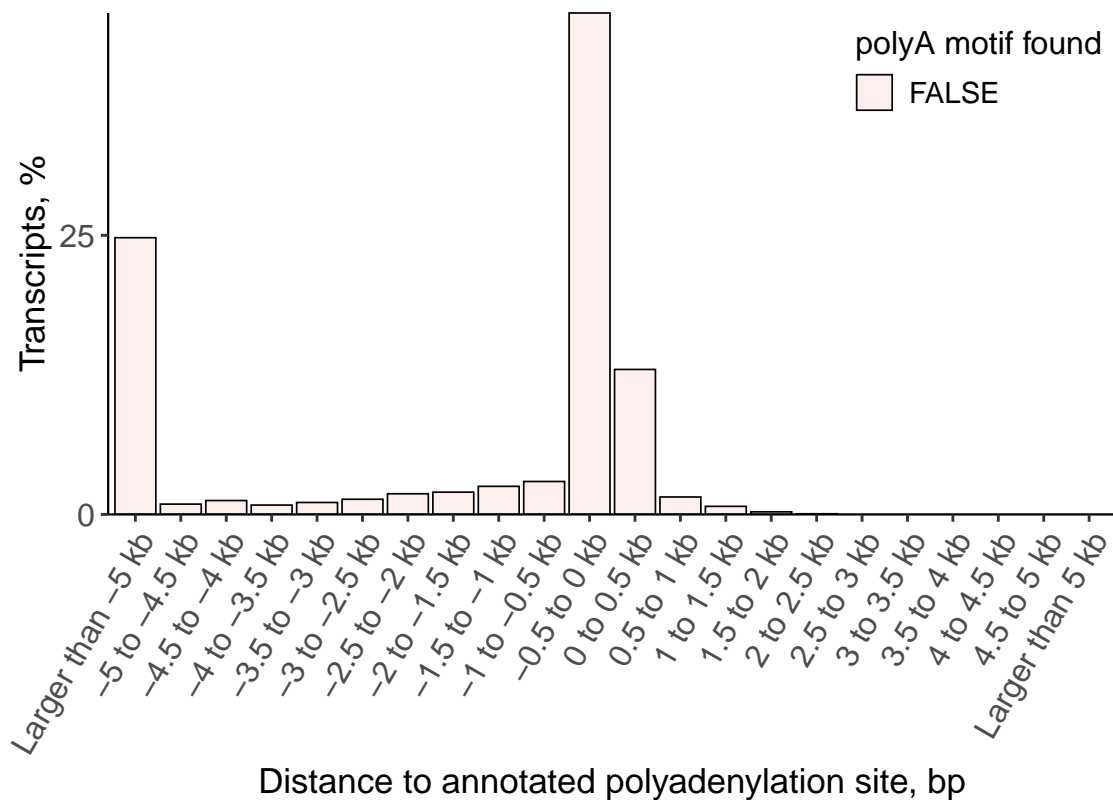
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



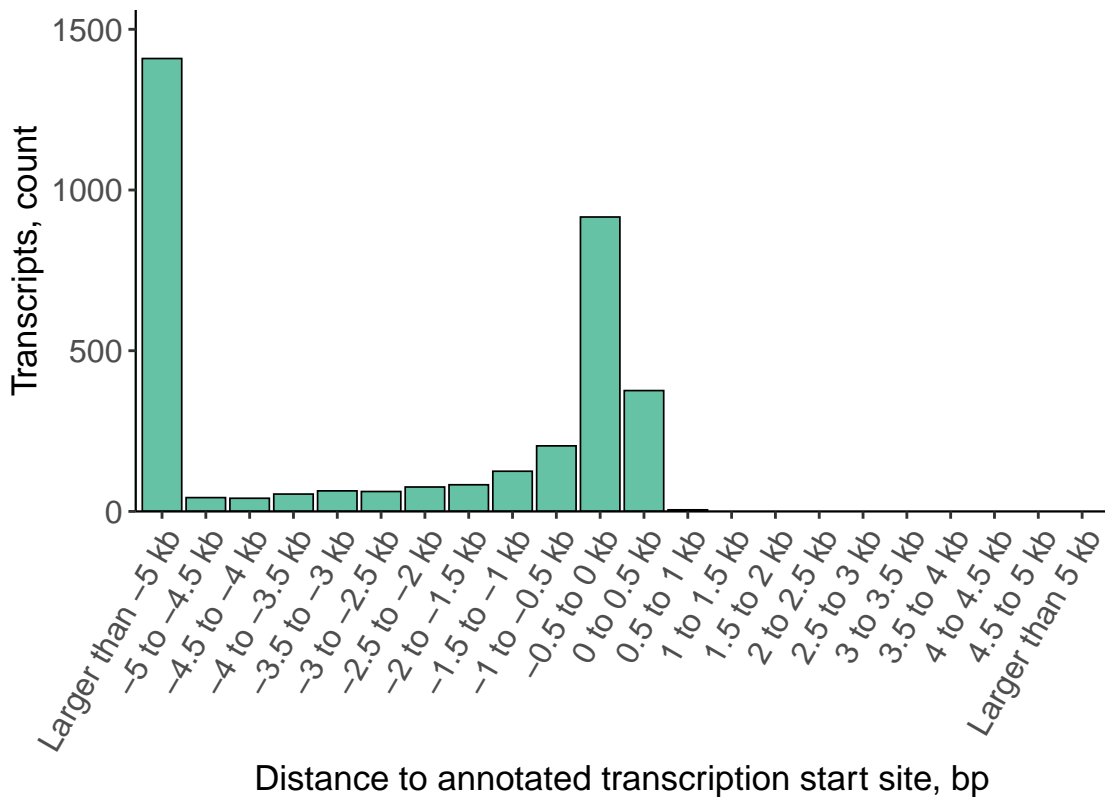
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



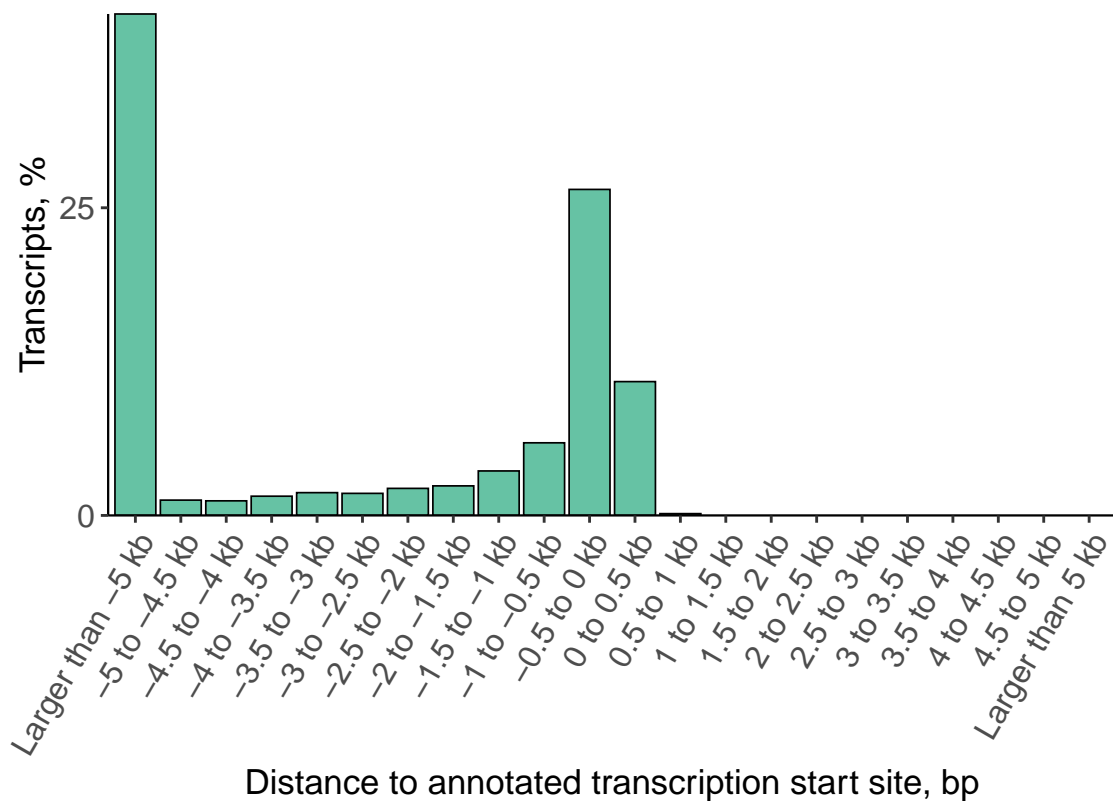
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



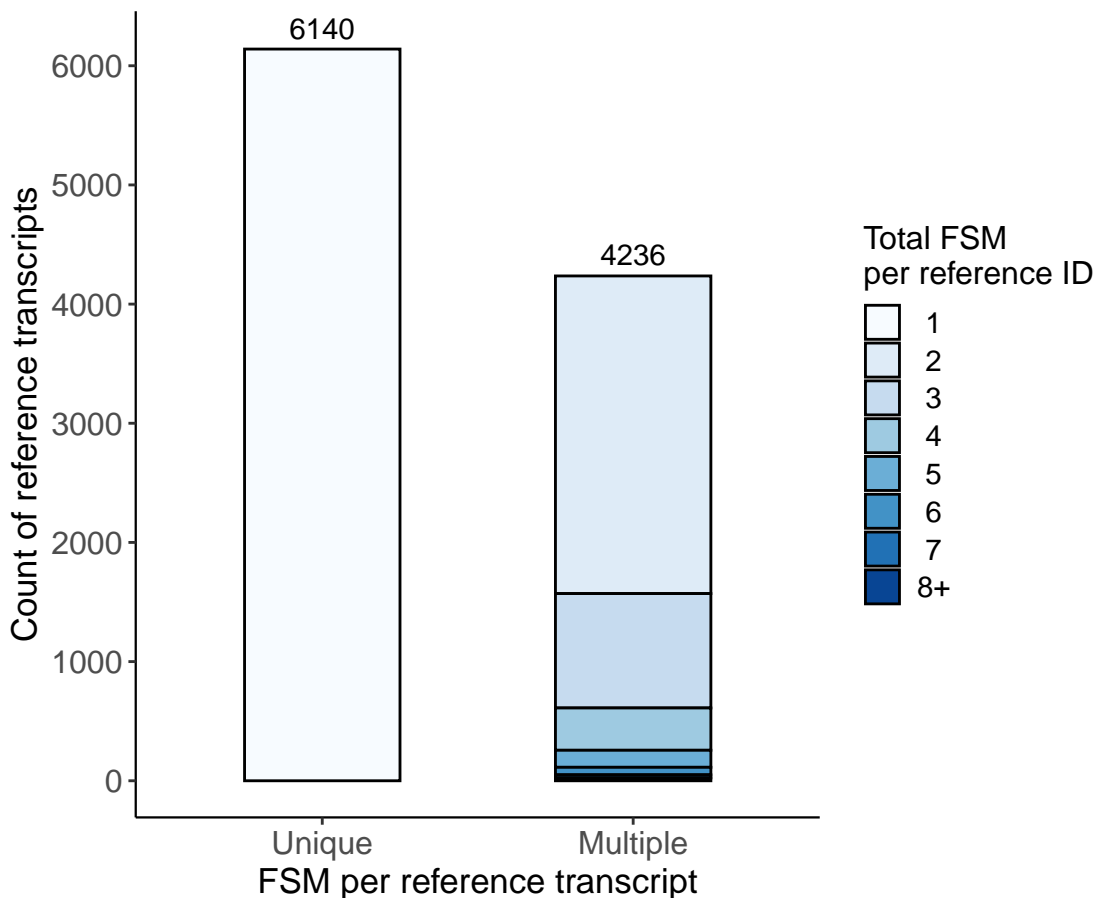
*Comparison With Annotated TSS and TTS
by Subcategories*

PolyA Distance Analysis

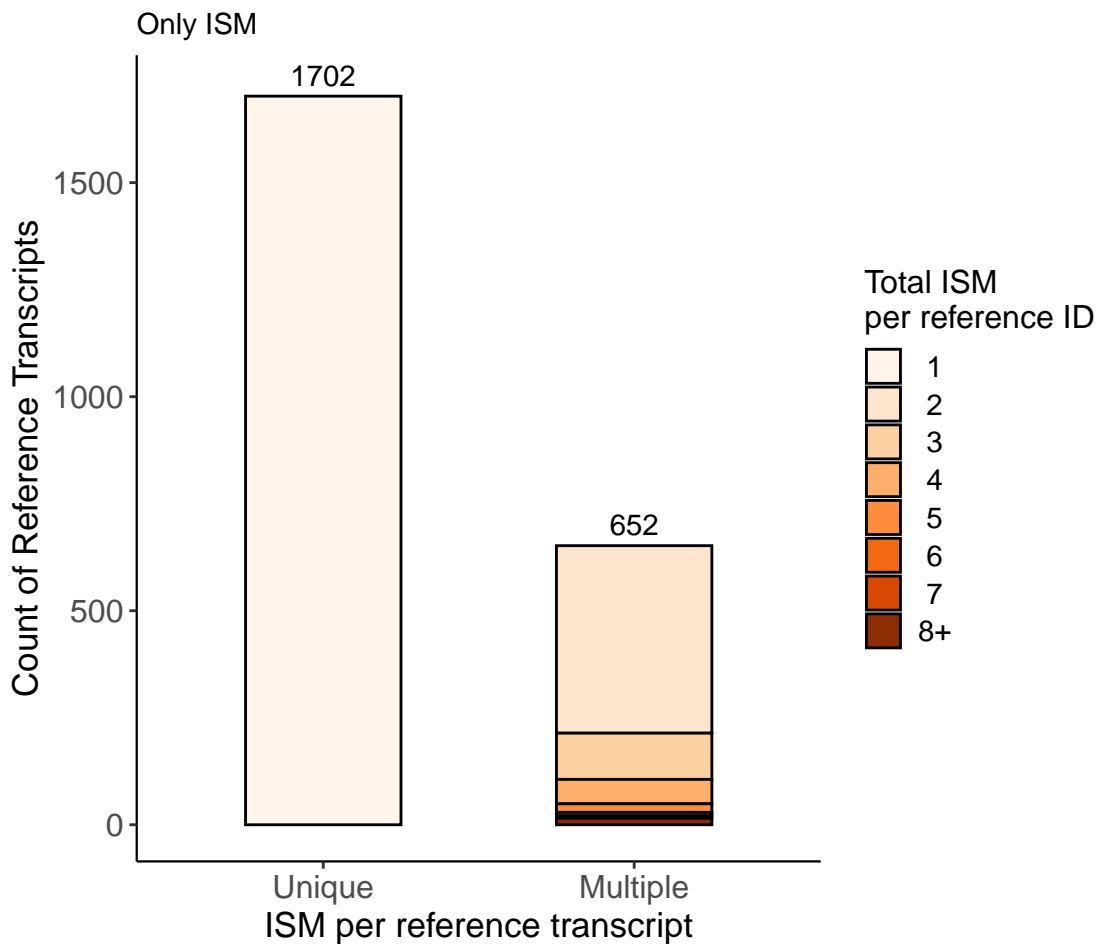
Redundancy Analysis

Reference Transcript Redundancy

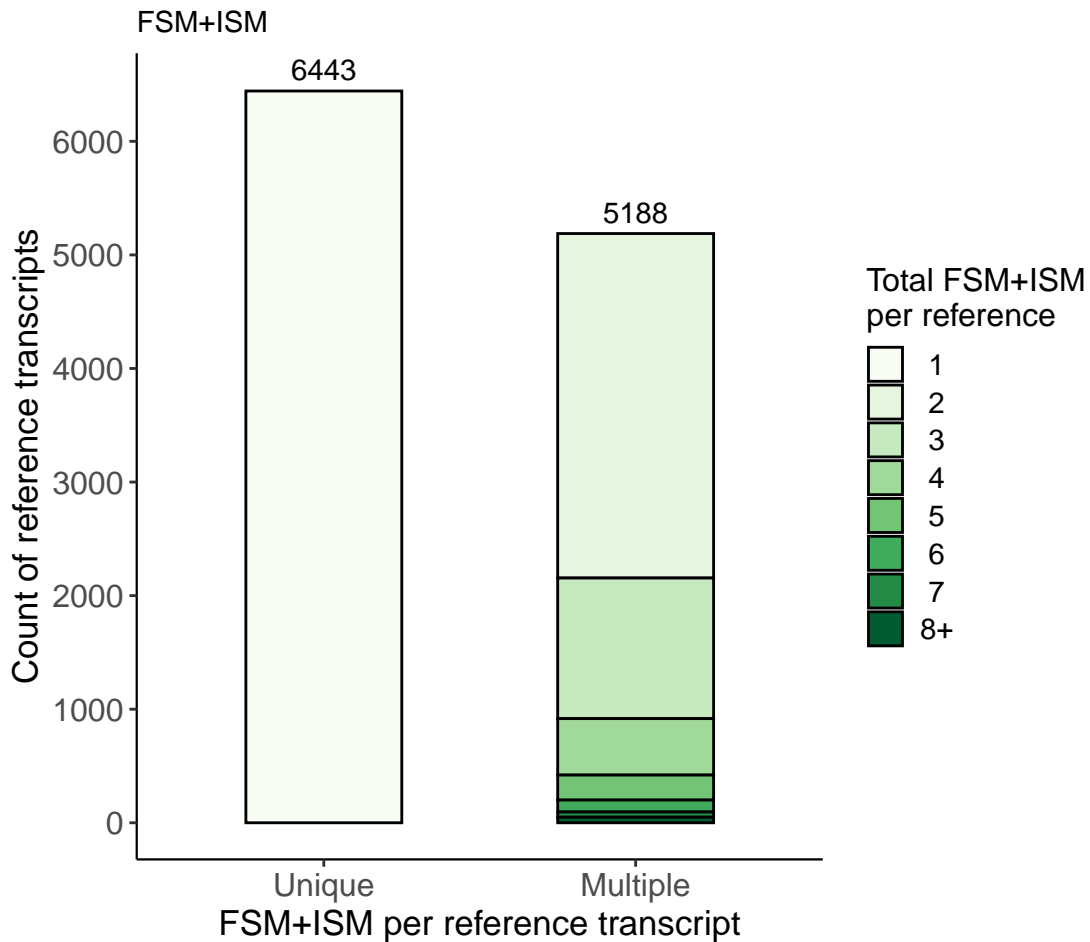
Only FSM



Reference Transcript Redundancy

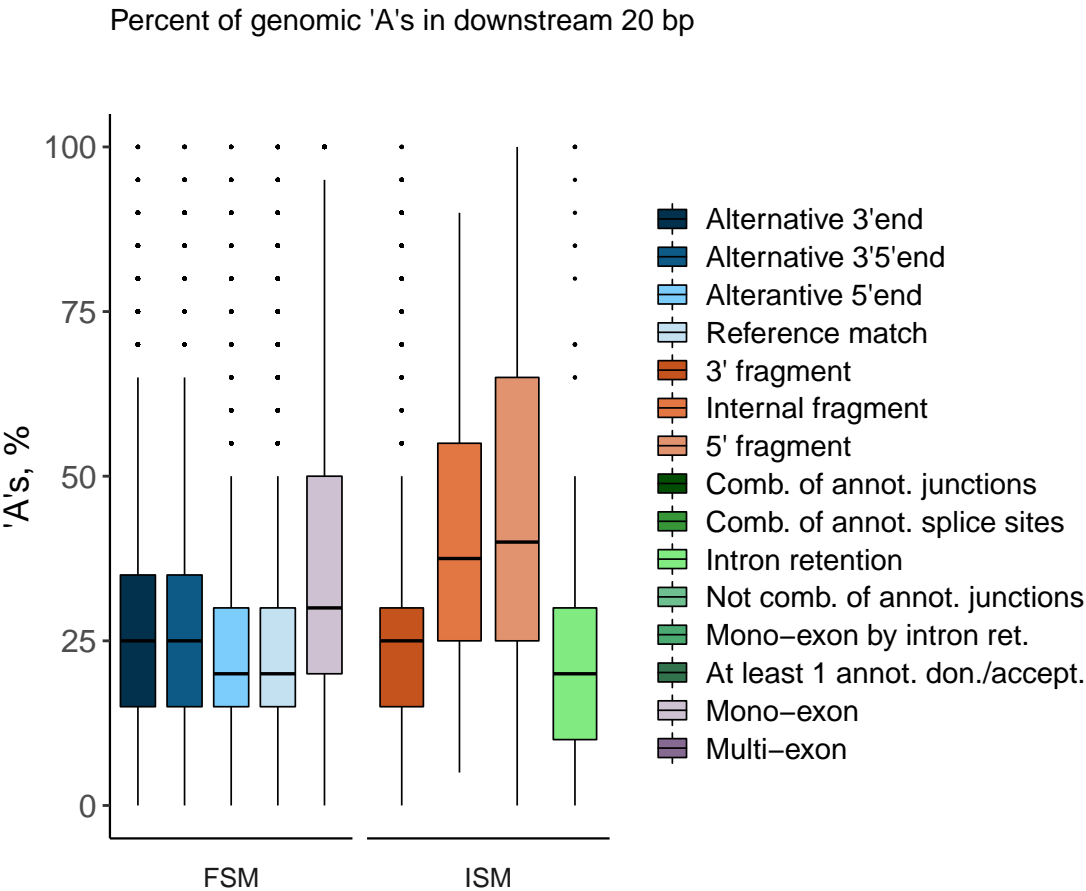


Reference Transcript Redundancy



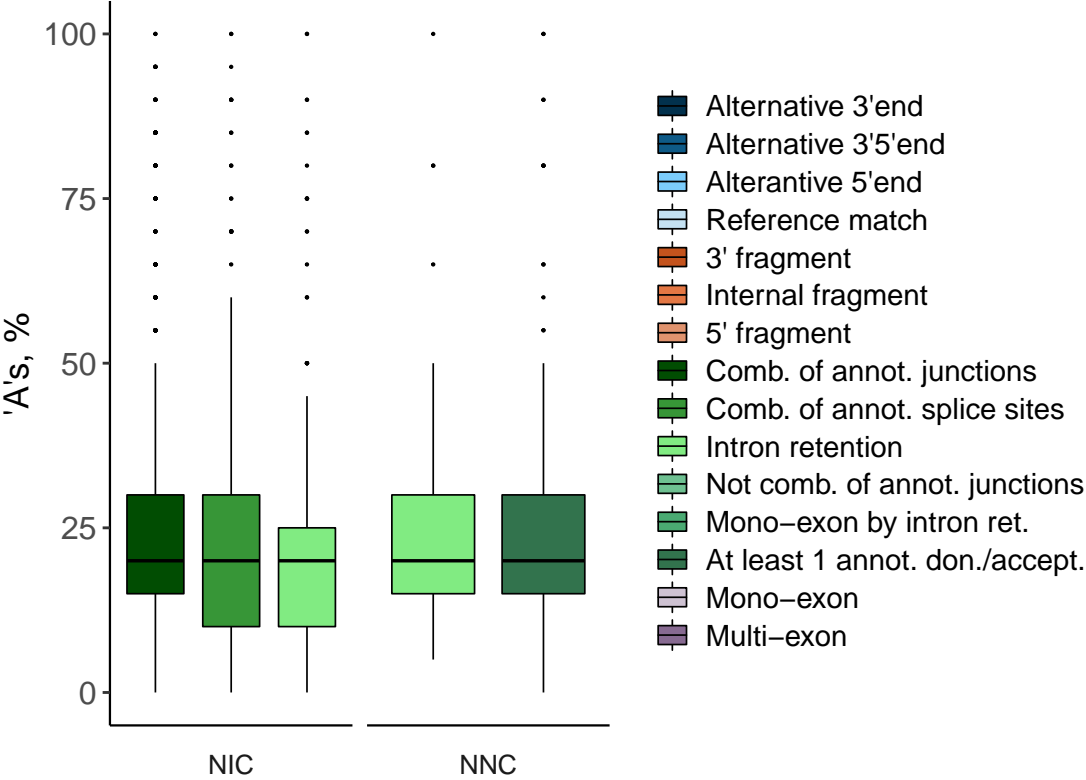
Intra-Priming Quality Check

Possible Intra-Priming by Structural Category



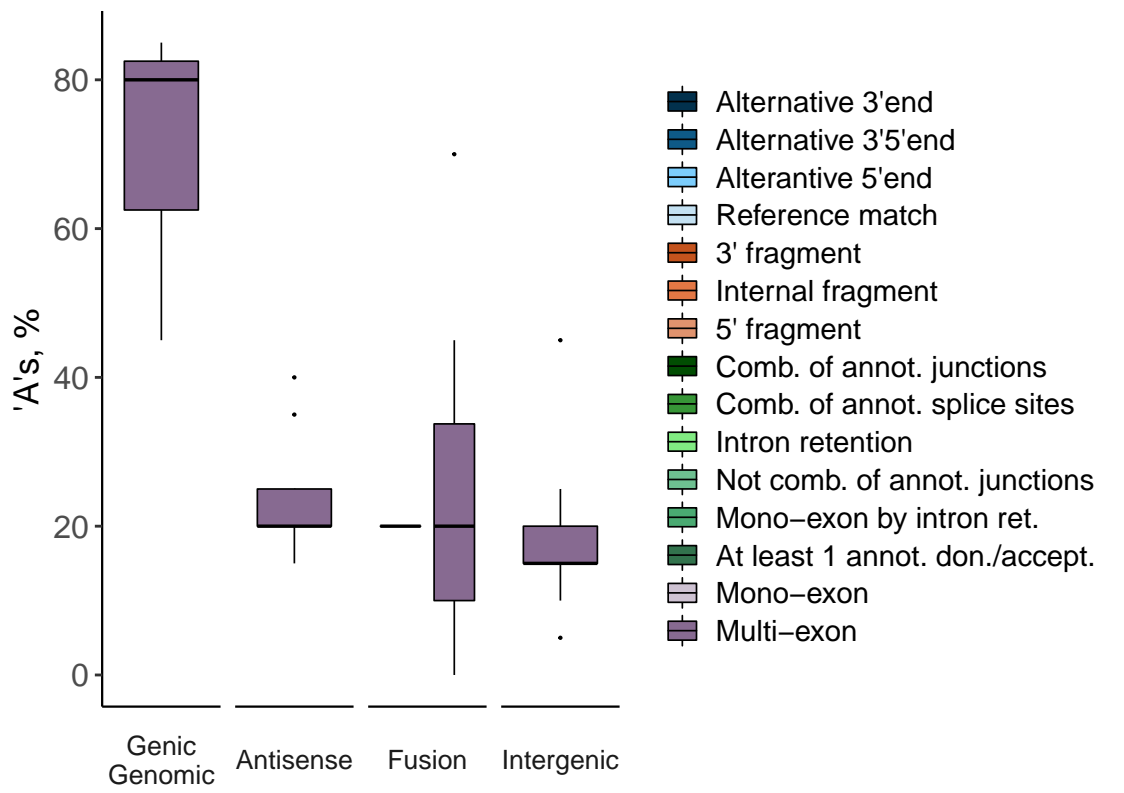
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



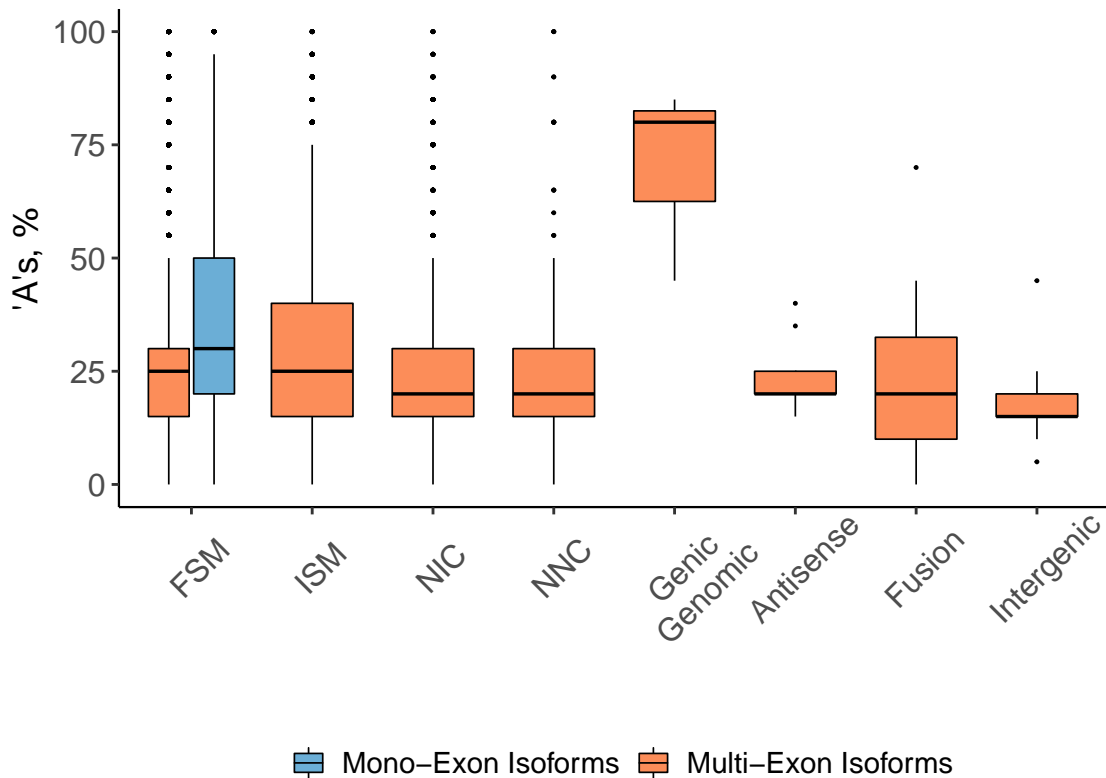
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



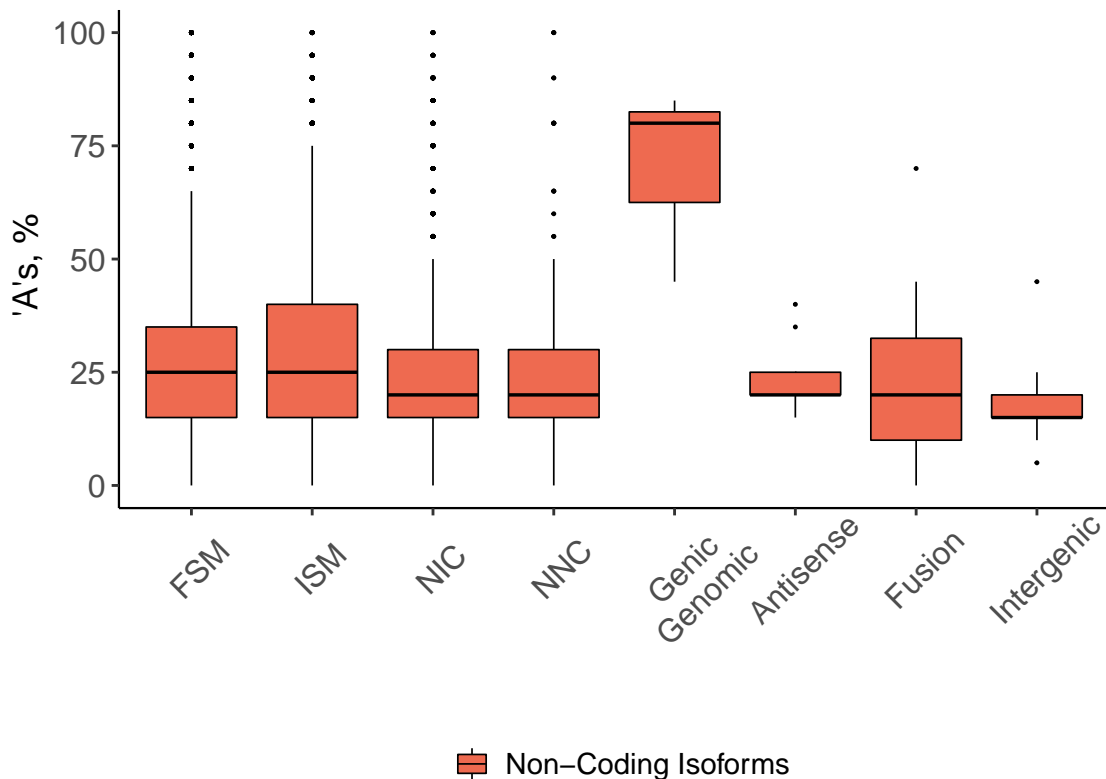
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



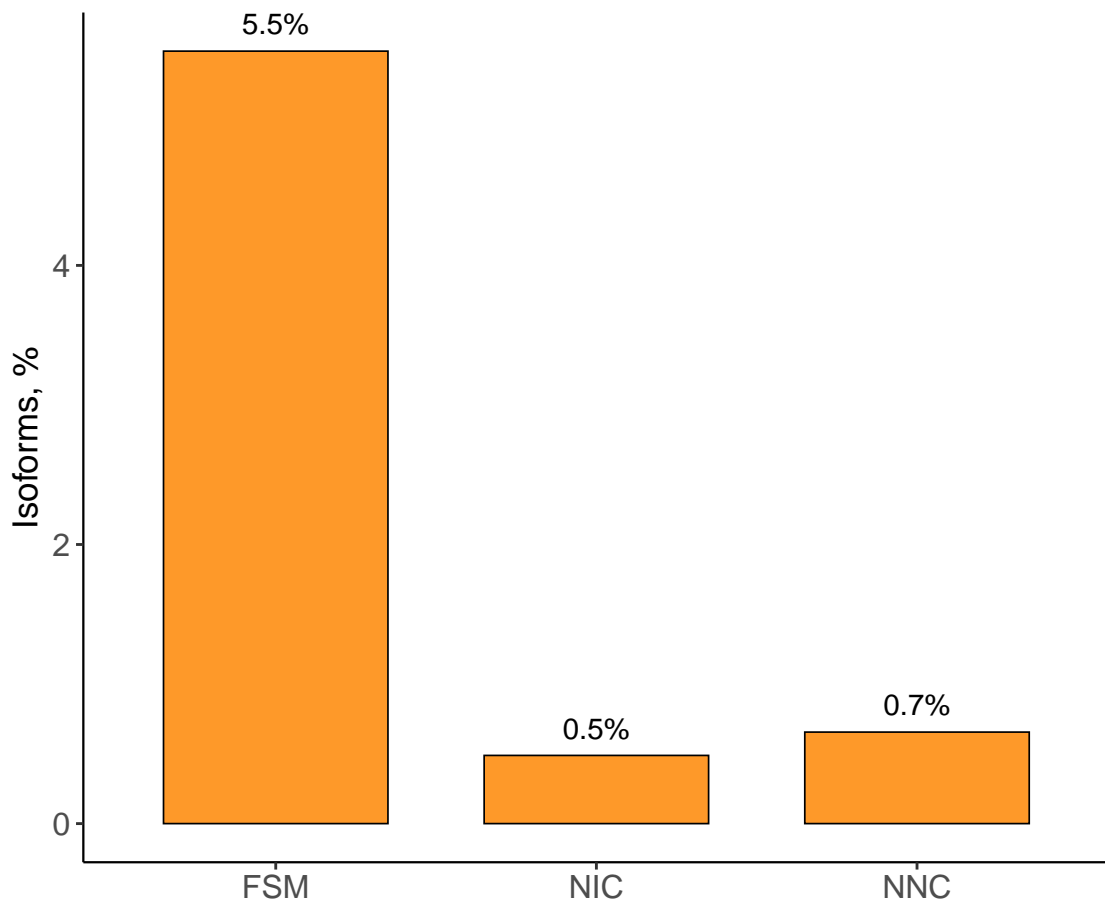
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



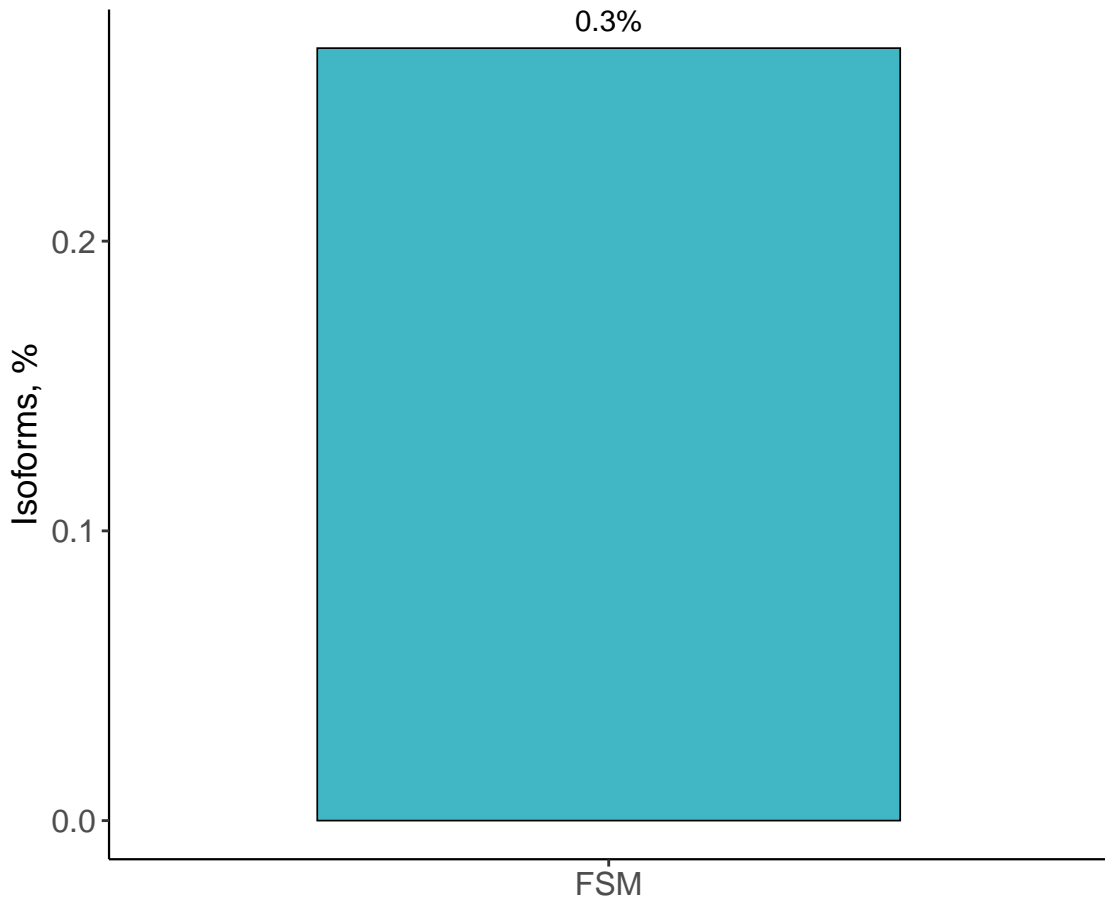
Features of Bad Quality

RT-switching

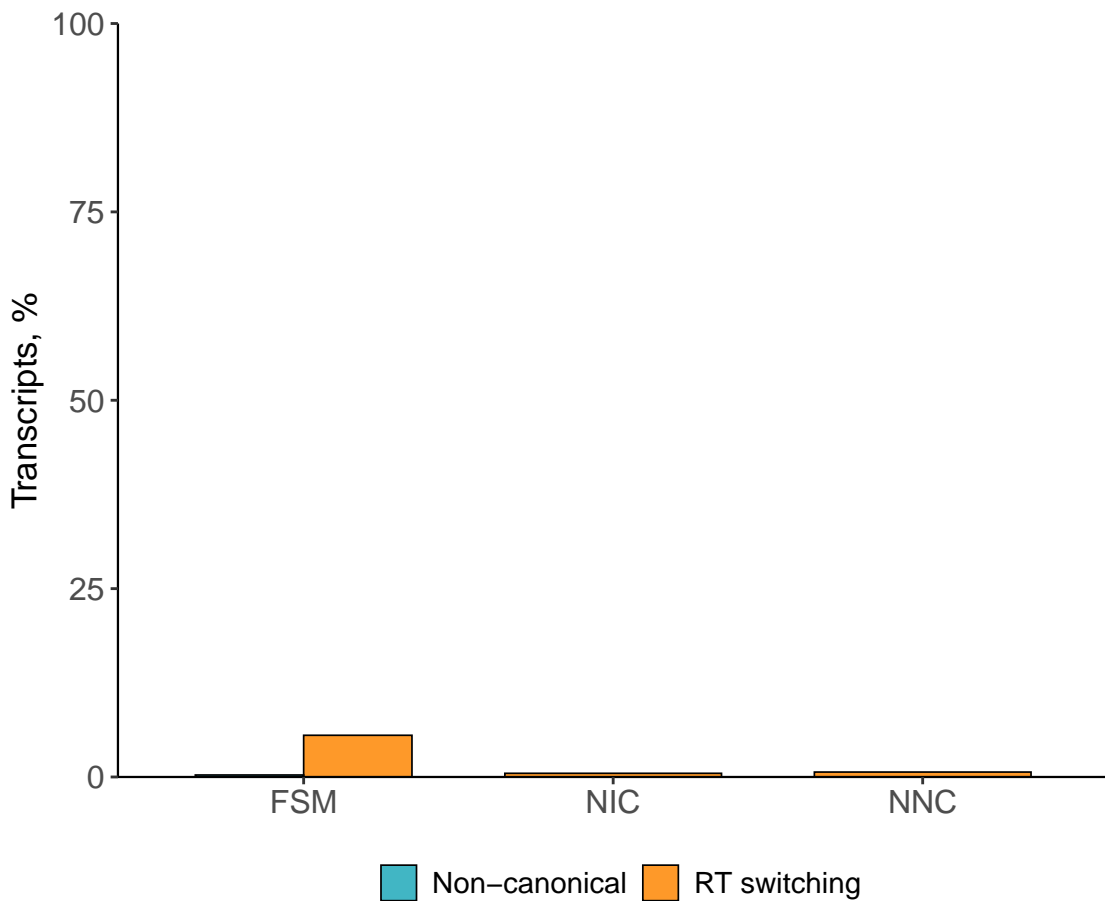


Non-Canonical Junctions

0.3%

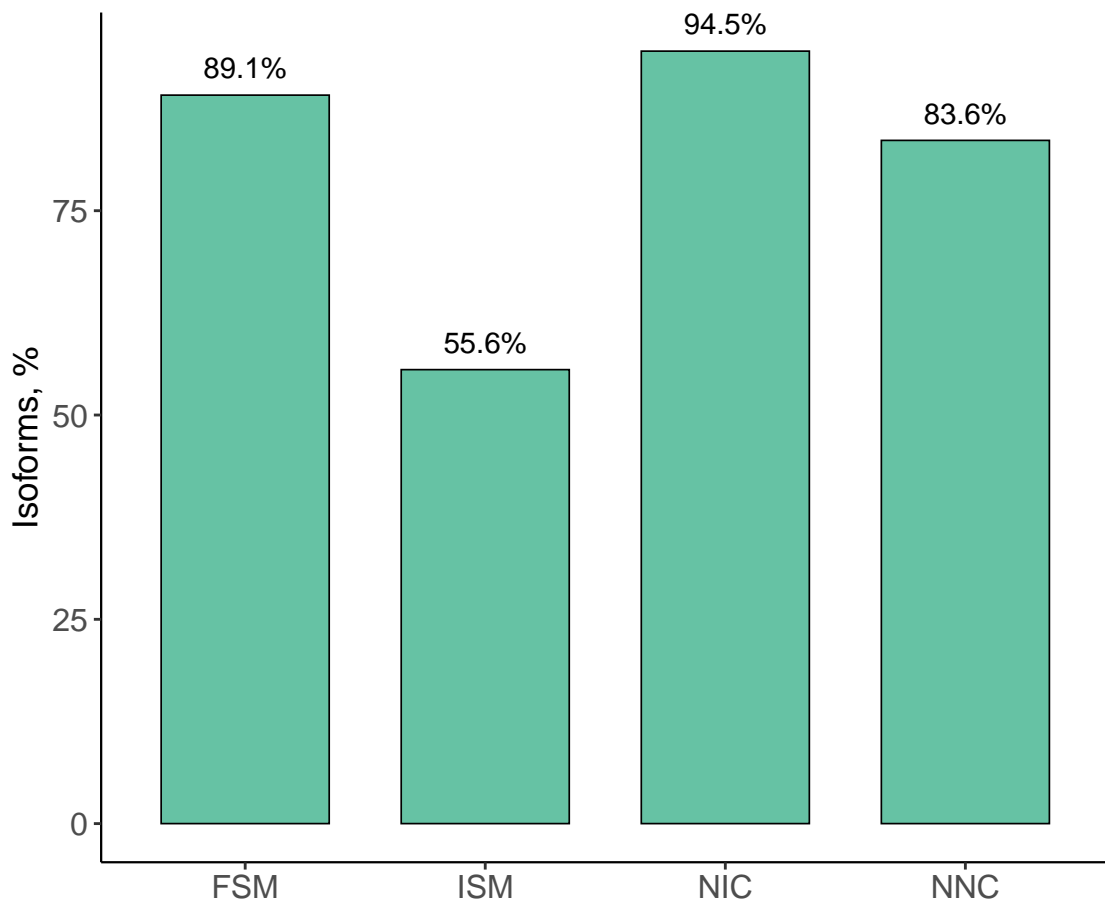


Quality Control Attributes Across Structural Categories

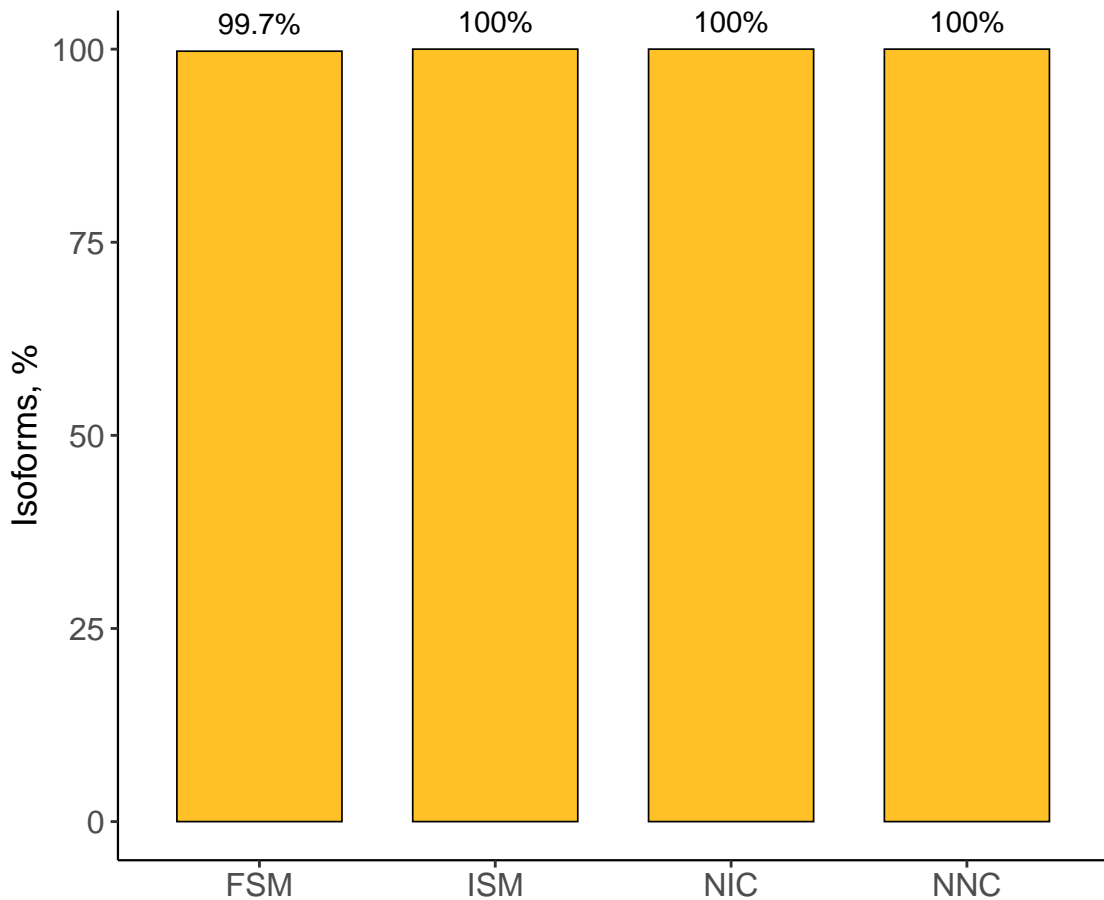


Features of Good Quality

Annotation Support



All Canonical Junctions



Good Quality Control Attributes Across Structural Categories

