

SQANTI3 report

Unique Genes: 23247
Unique Isoforms: 375649

Gene classification

Category	# Genes
Annotated Genes	15323
Novel Genes	7924

Splice Junction Classification

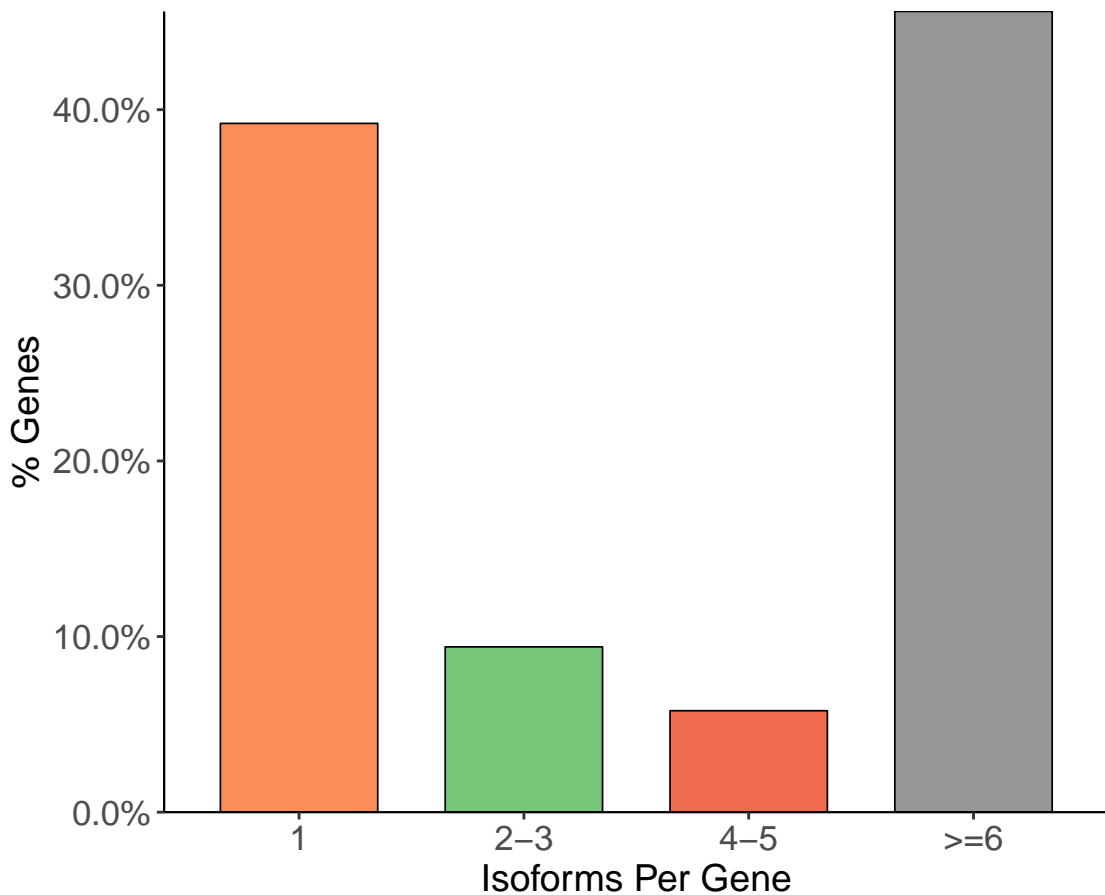
Category	# SJs	Percent
Known canonical	152849	51.43
Known Non-canonical	46	0.02
Novel canonical	144317	48.56
Novel Non-canonical	0	0.00

*Characterization of transcripts
based on splice junctions*

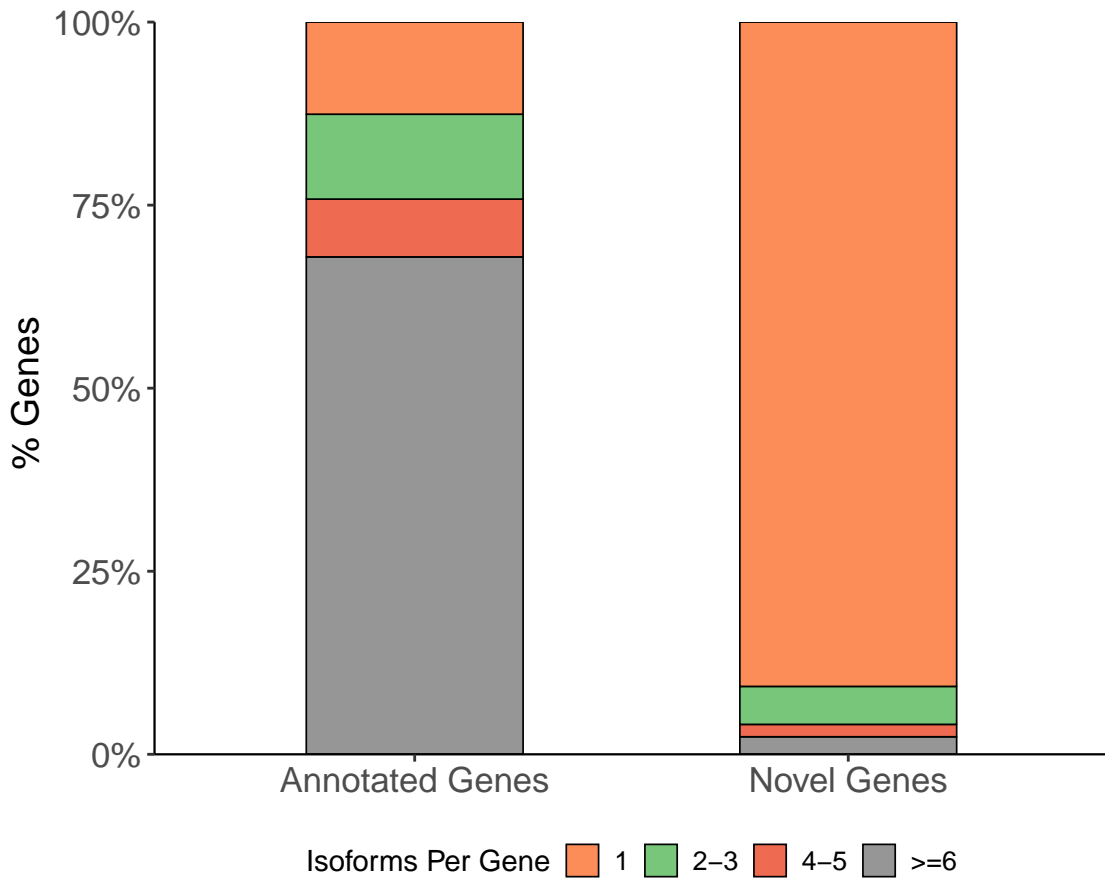
Category	# Isoforms
FSM	30385
ISM	38116
NIC	105395
NNC	186125
Genic Genomic	1192
Antisense	4760
Fusion	3304
Intergenic	6372
Genic Intron	0

Gene Characterization

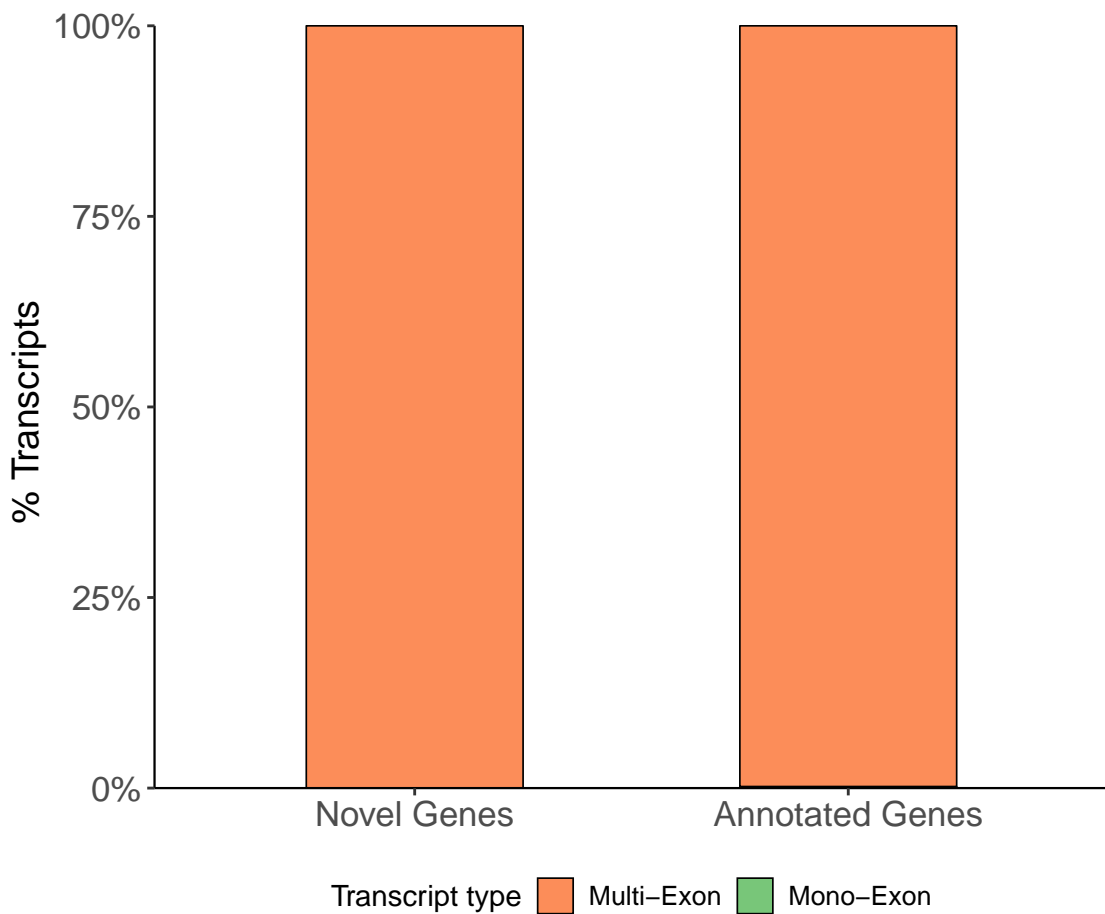
Number of Isoforms per Gene



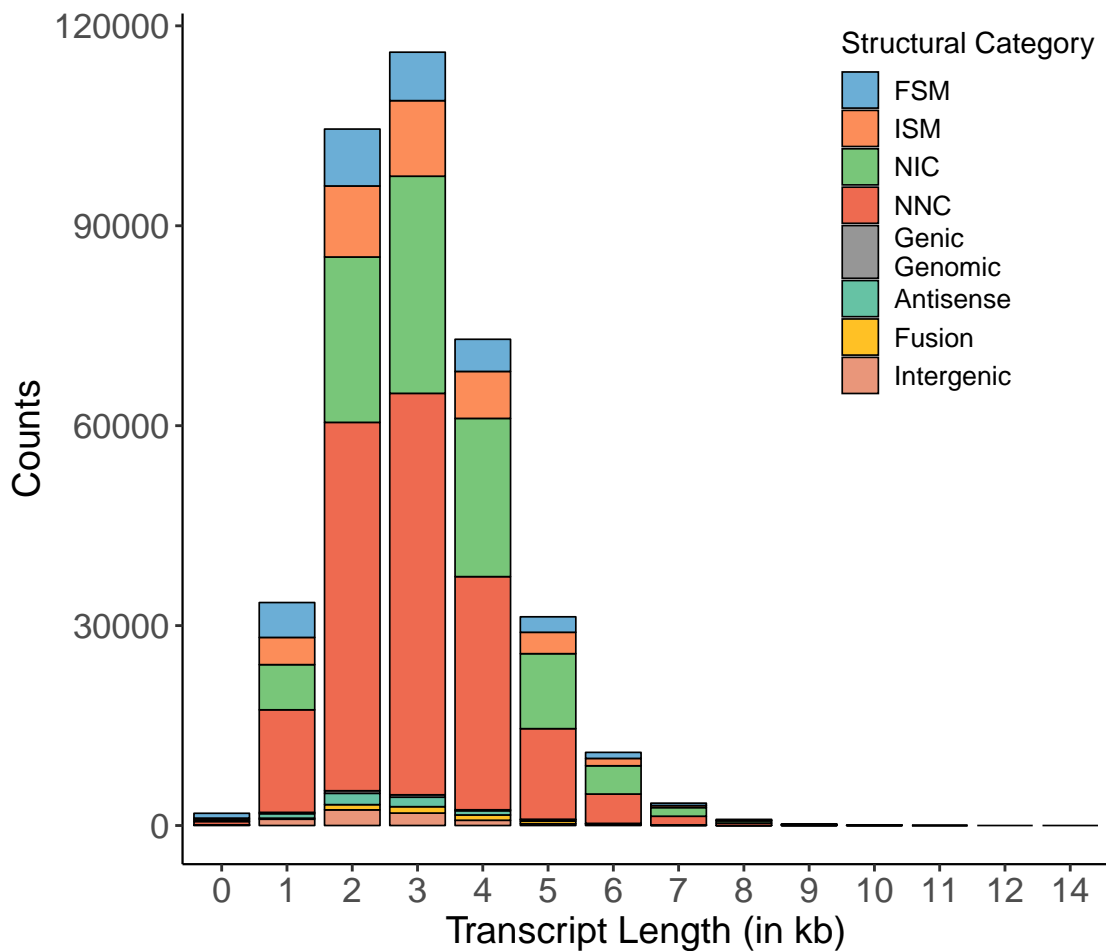
Number of Isoforms per Gene, Known vs Novel Genes



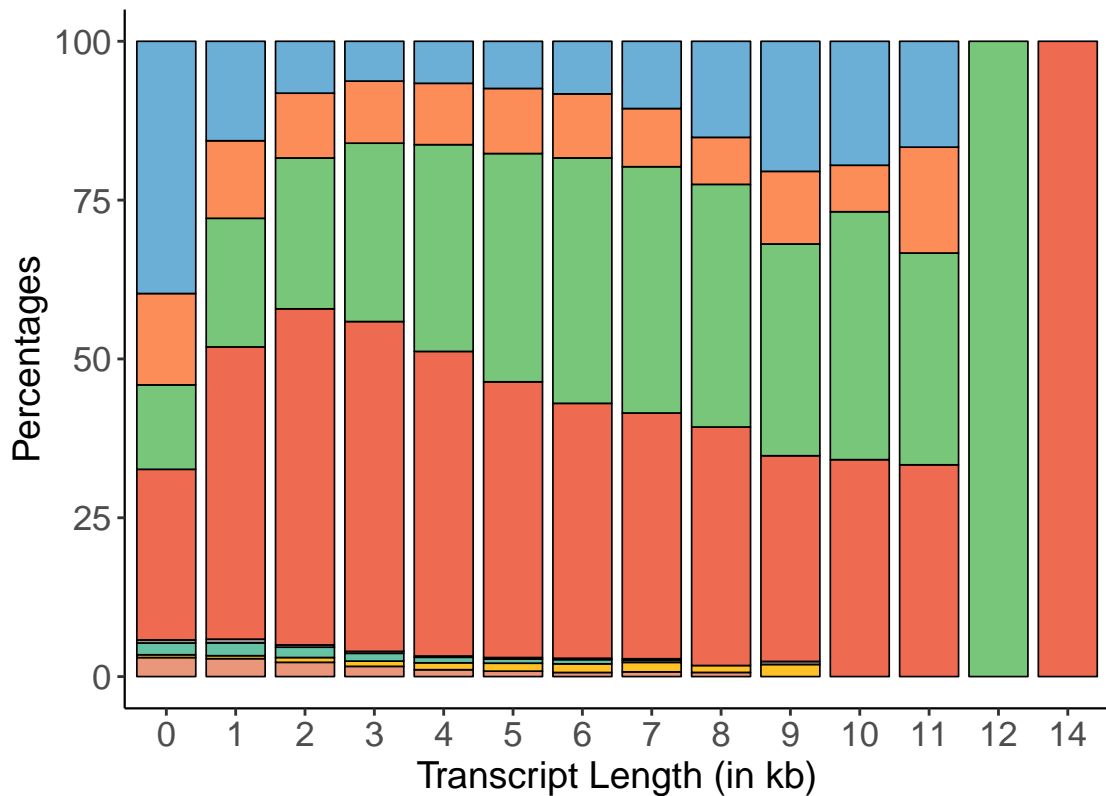
Distribution of Mono- vs Multi-Exon Transcripts



Classifications by Transcript Length



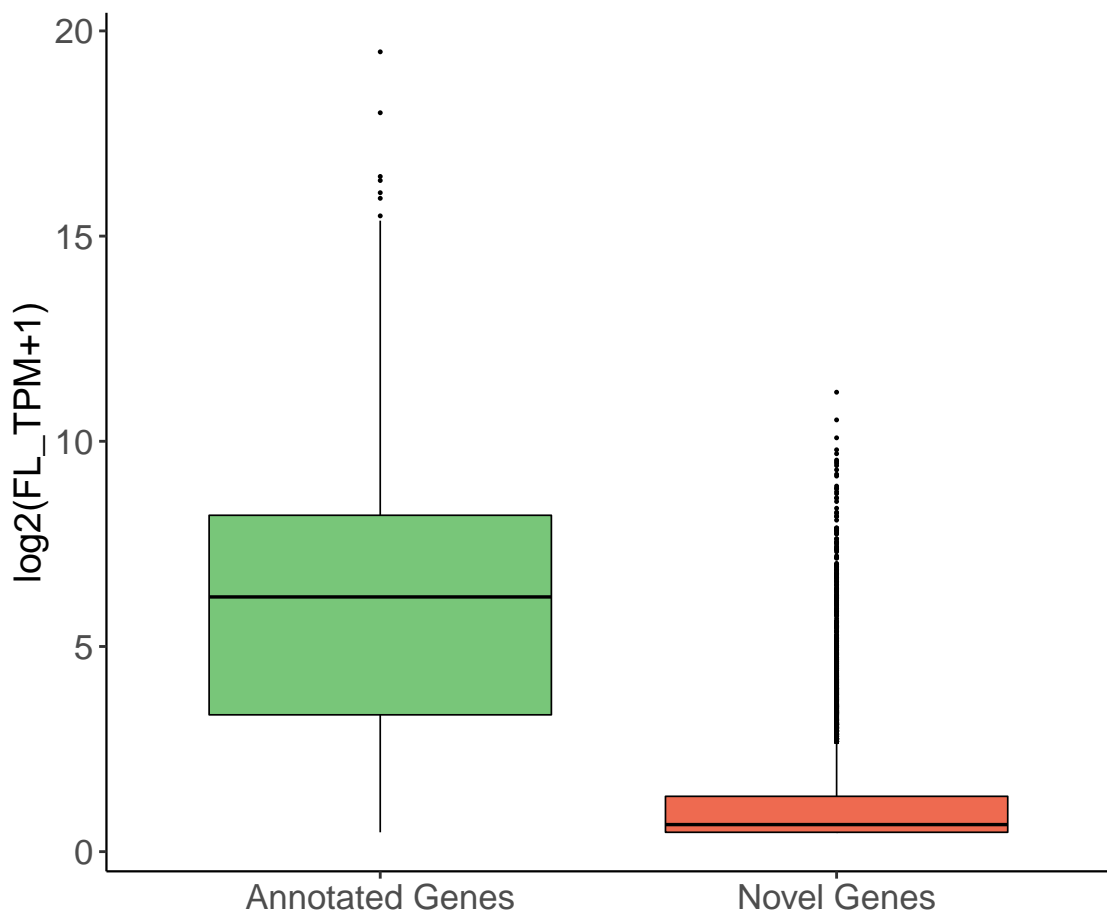
Classifications by Transcript Length, normalized



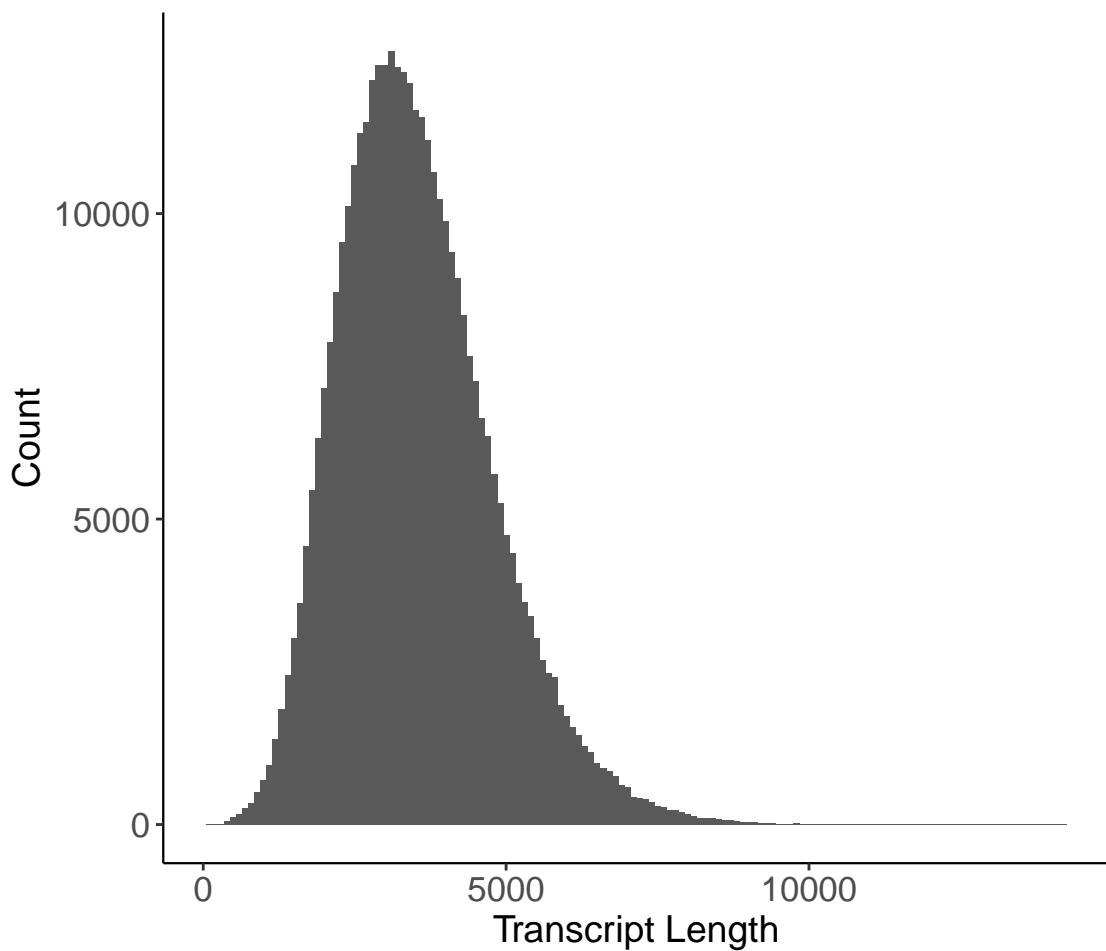
Structural Category

FSM	NIC	Genic	Fusion
ISM	NNC	Genomic	Intergenic
		Antisense	

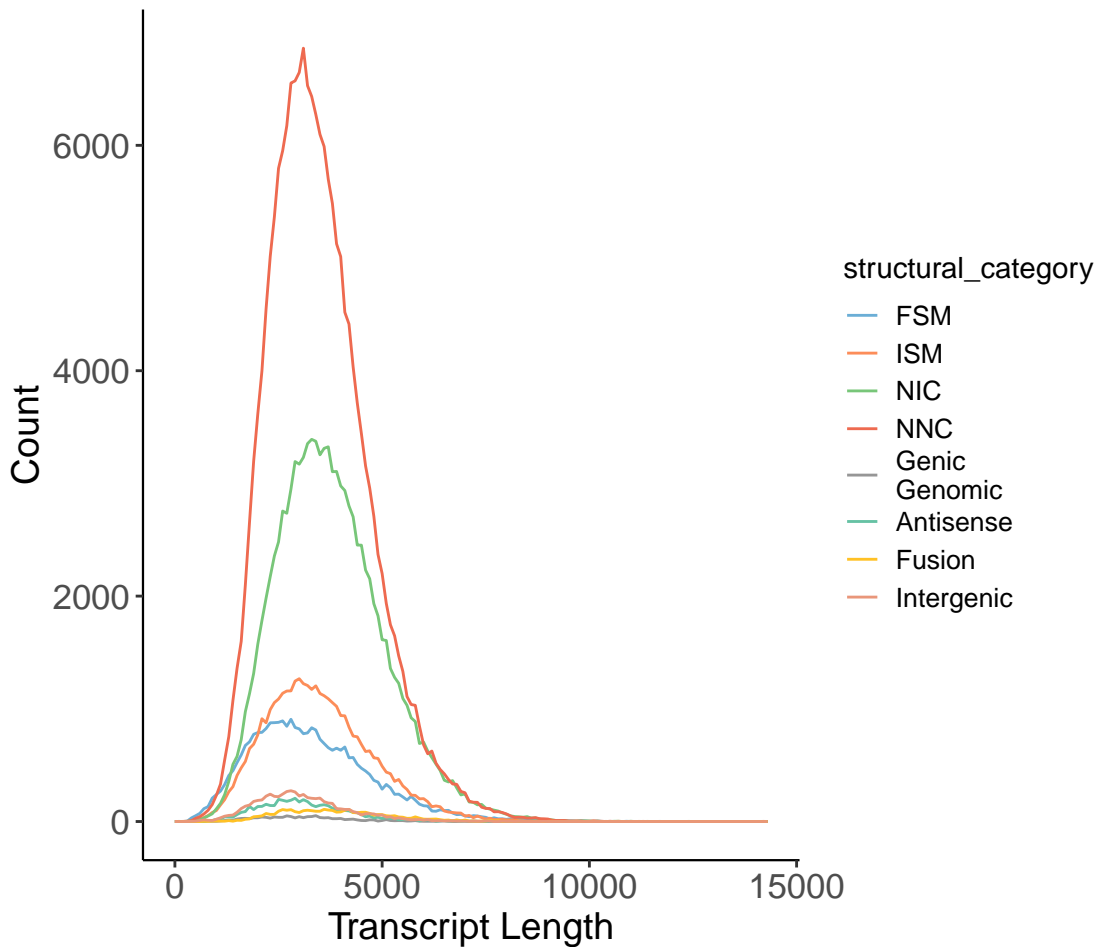
Number of FL reads per Gene by type of gene annotation



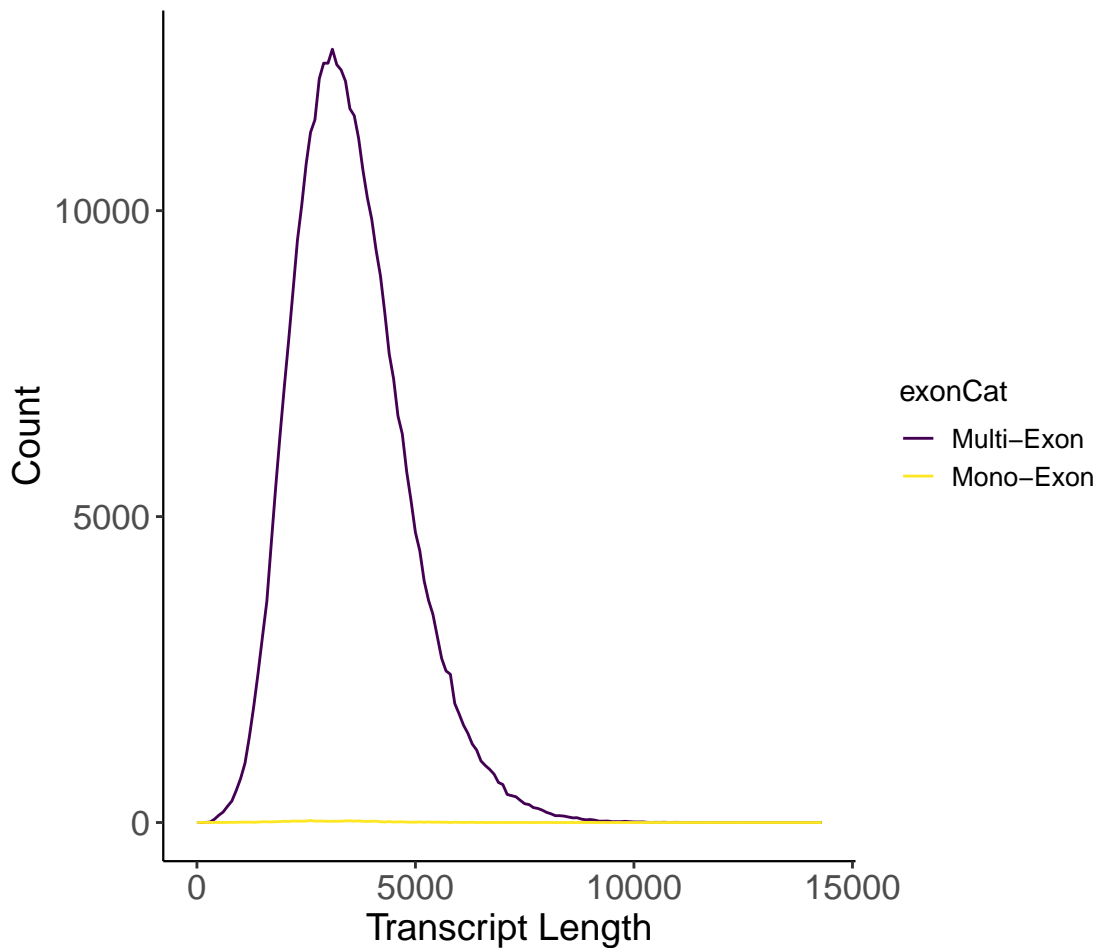
Transcript Lengths, all transcripts



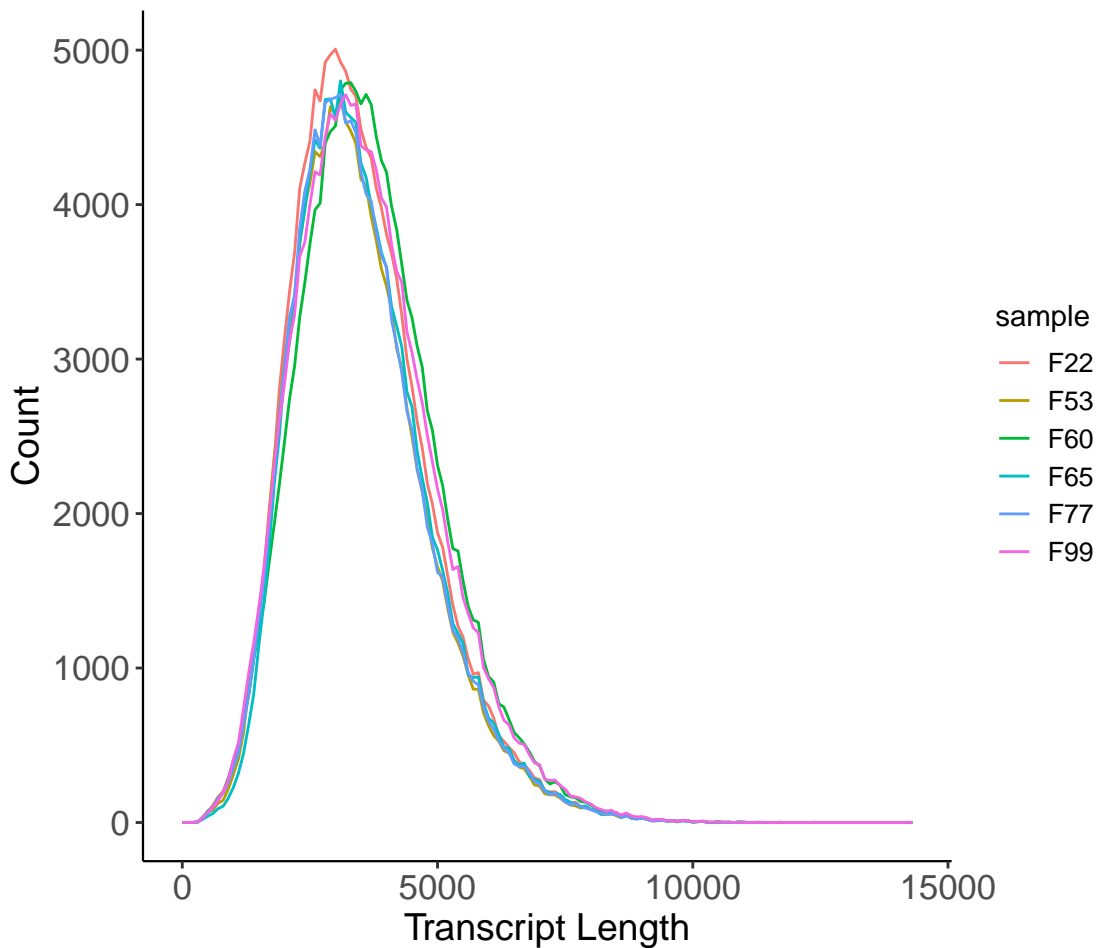
Transcript Lengths, by structural category



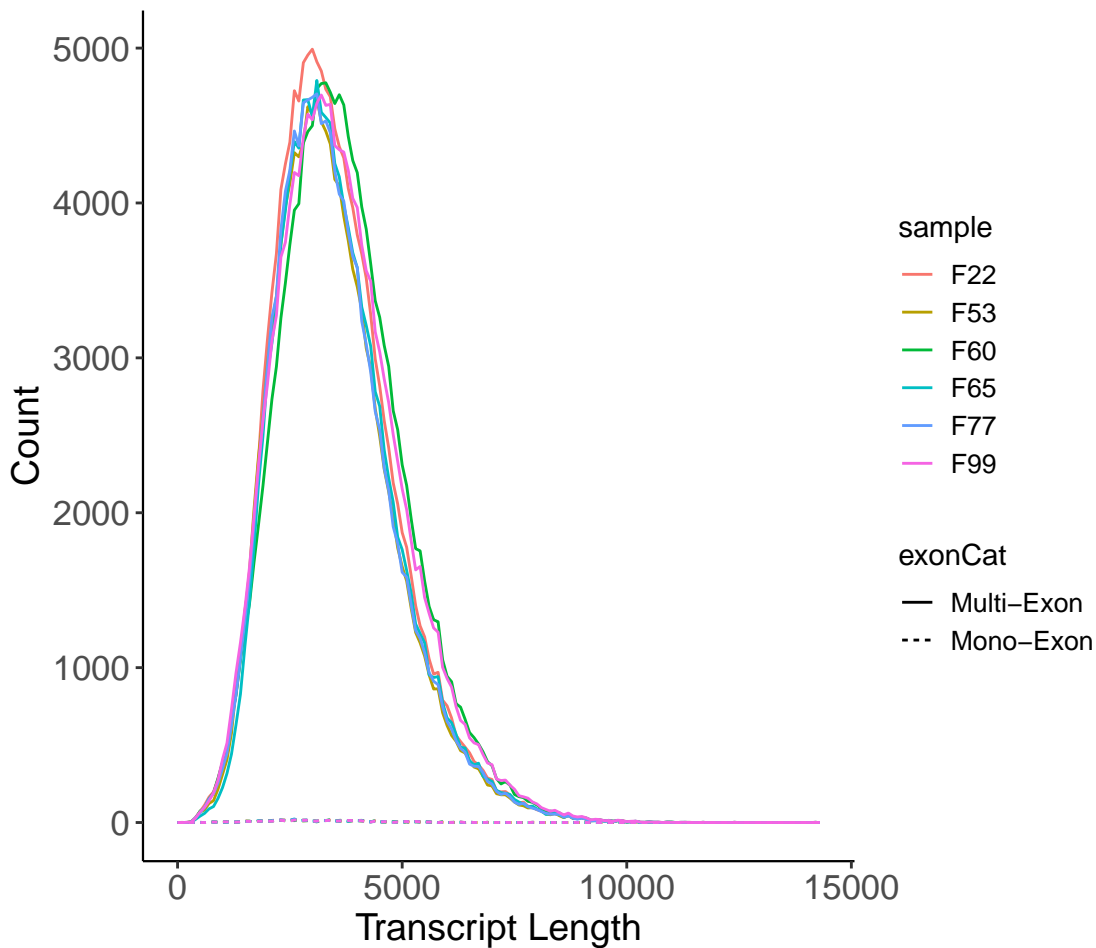
Transcript Lengths, Mono- vs Multi-Exons



Transcript Lengths, By Sample

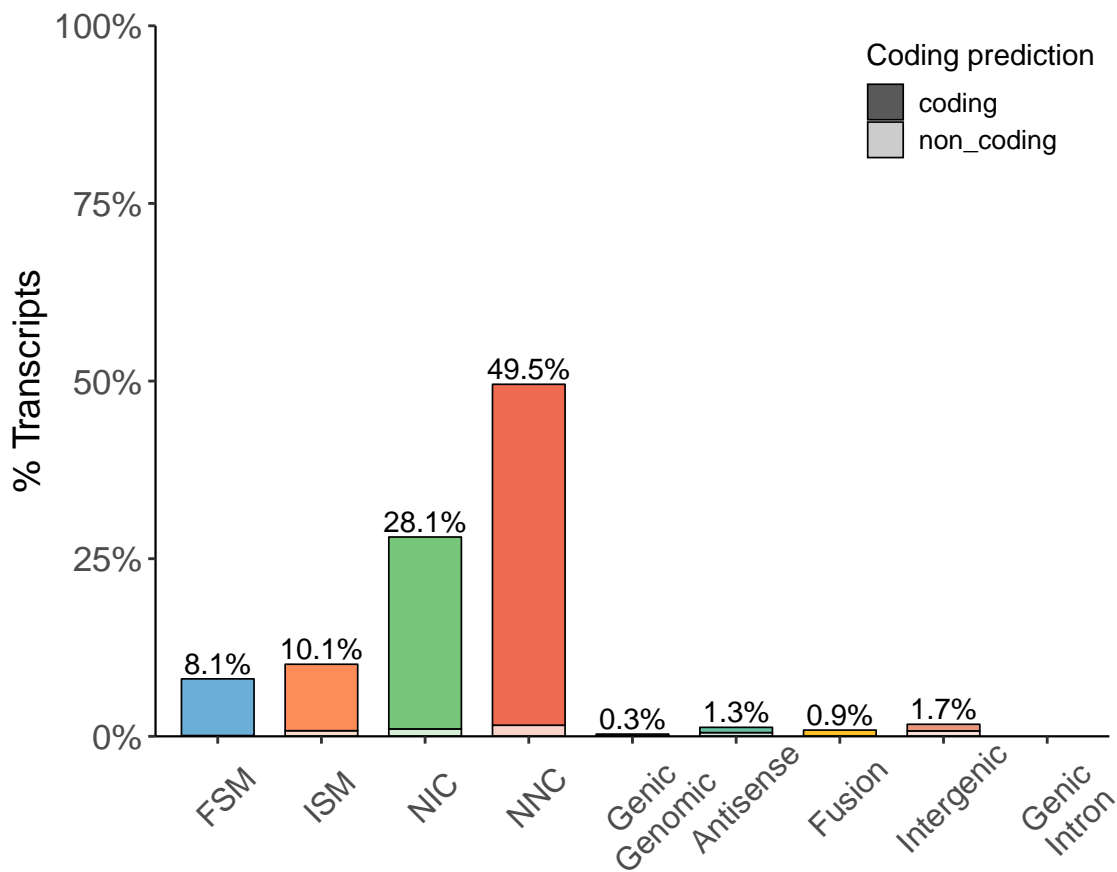


Transcript Lengths, Mono- vs Multi-Exons, By Sample

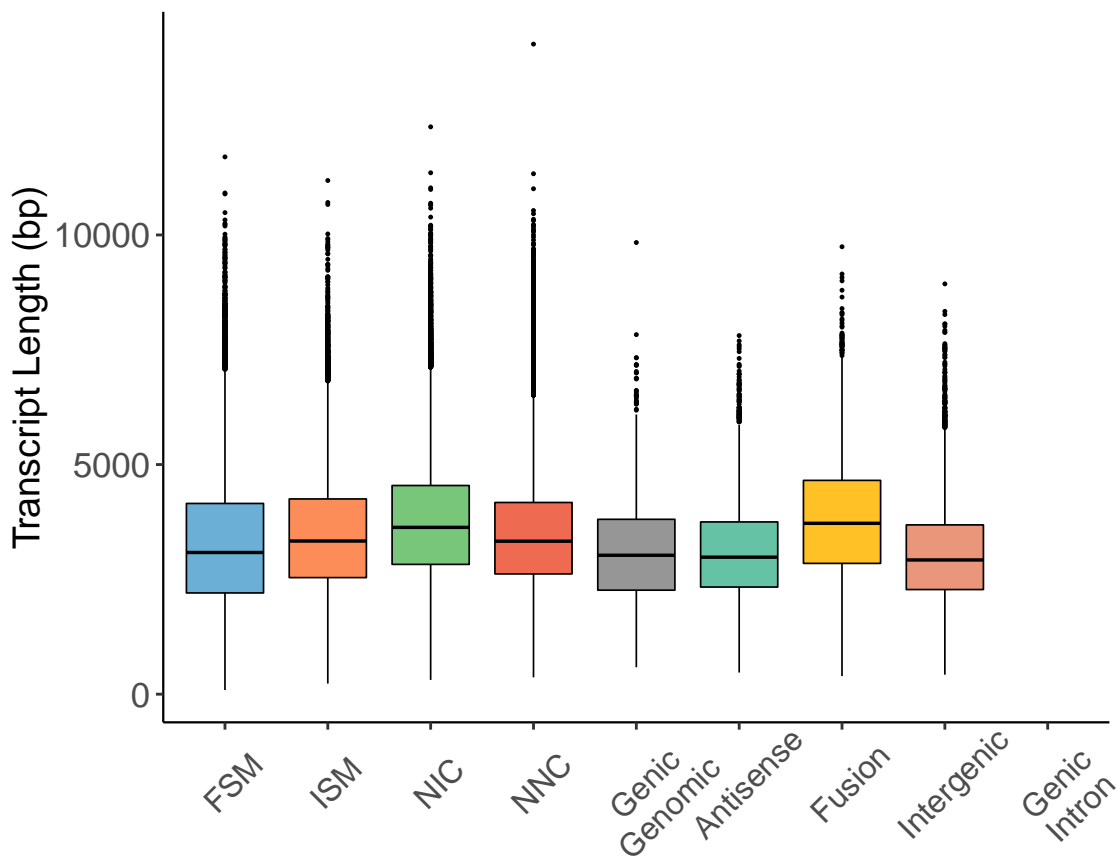


*Structural Isoform Characterization
by Splice Junctions*

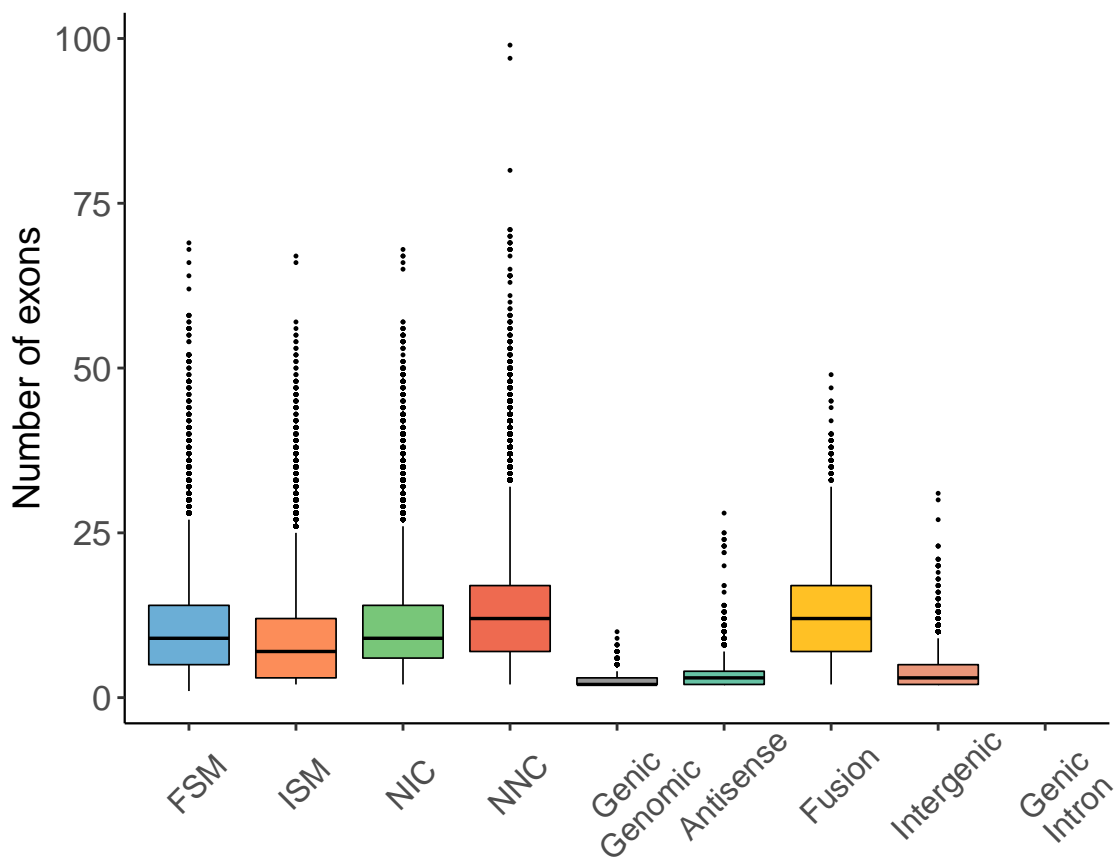
Isoform distribution across structural categories



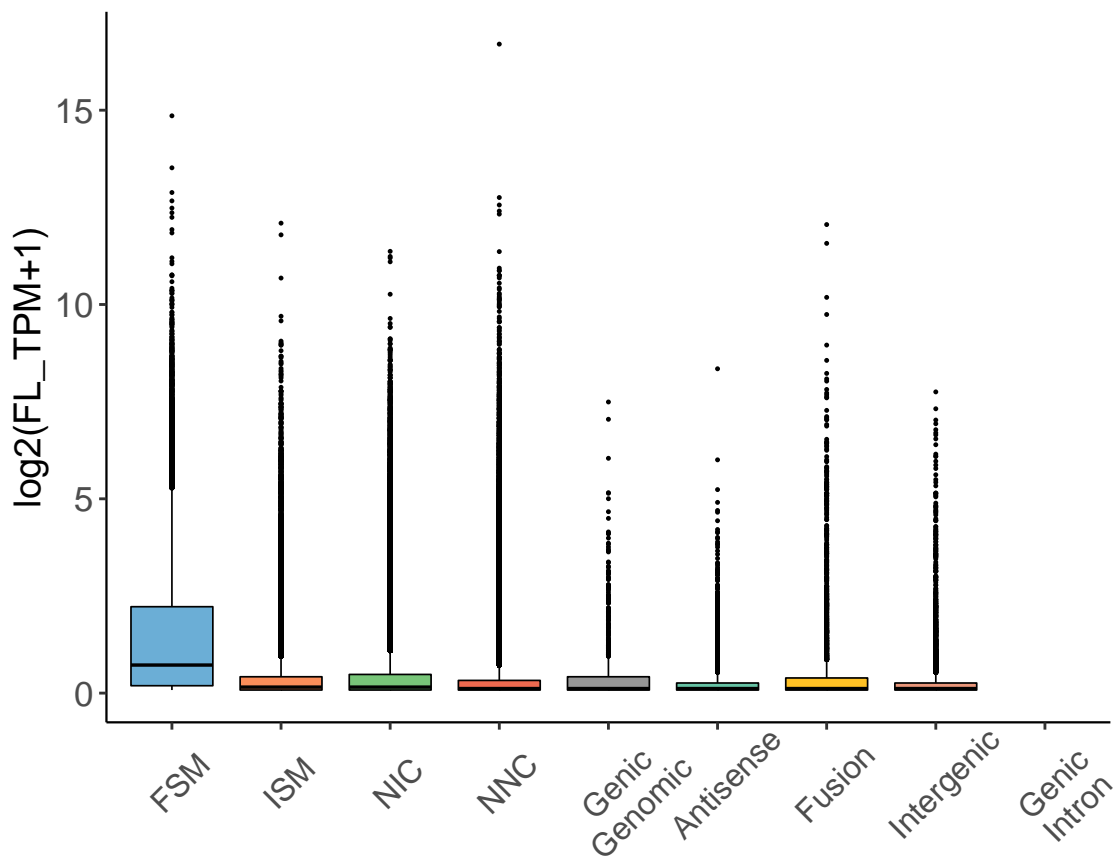
Transcript Lengths by Structural Classification



Exon Counts by Structural Classification

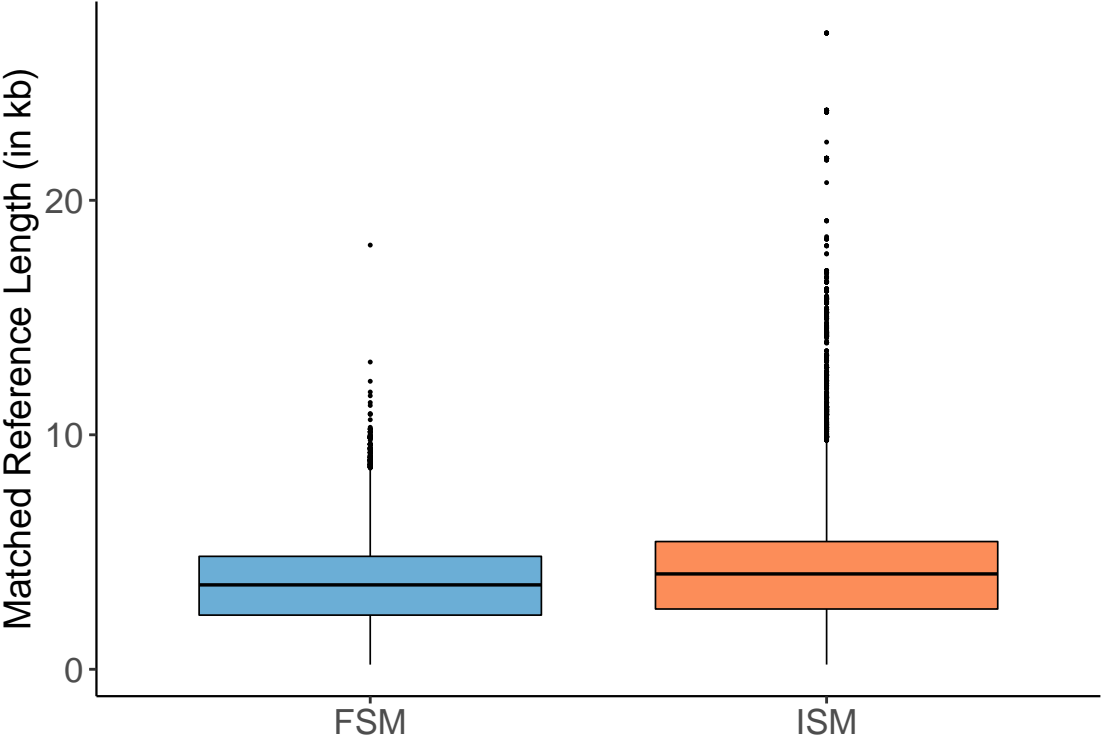


FL Count (normalized) by Structural Category



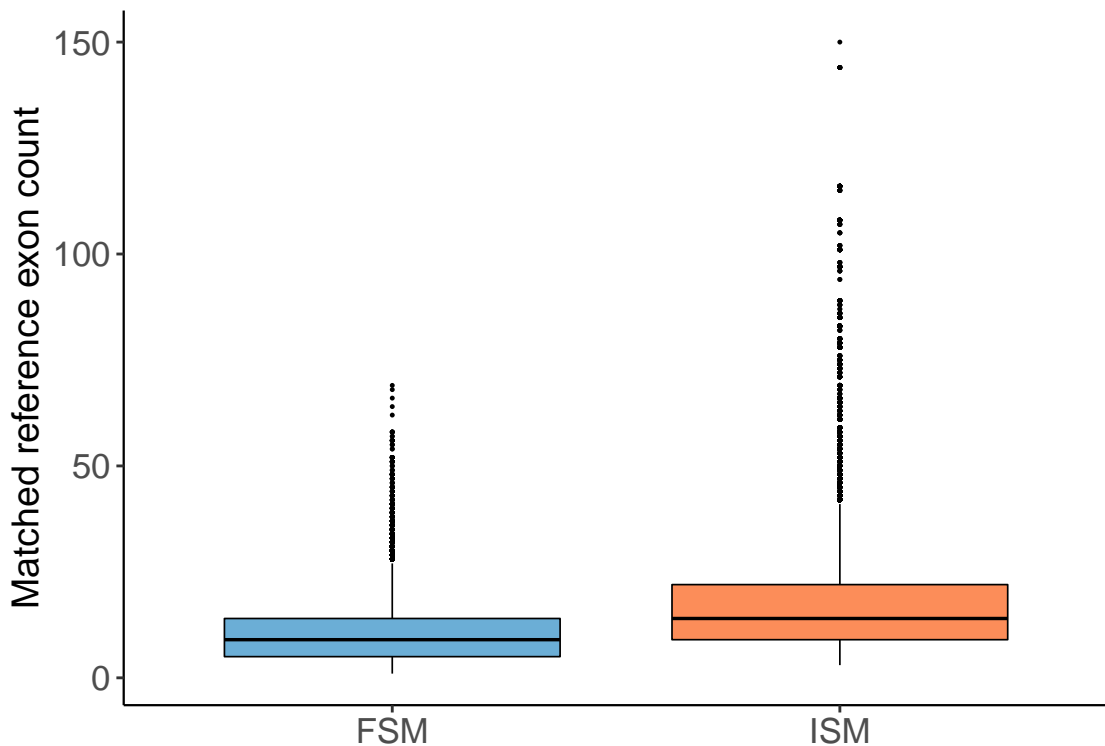
Length Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories



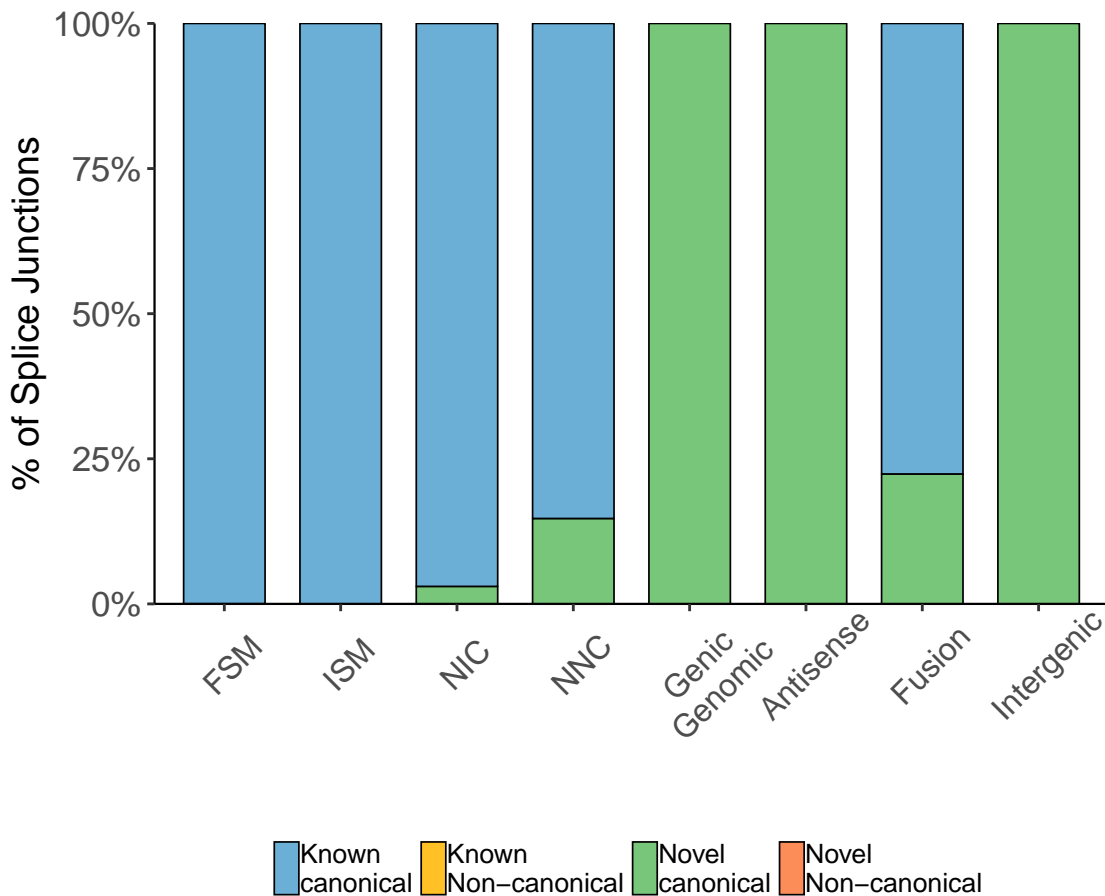
Exon Count Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories

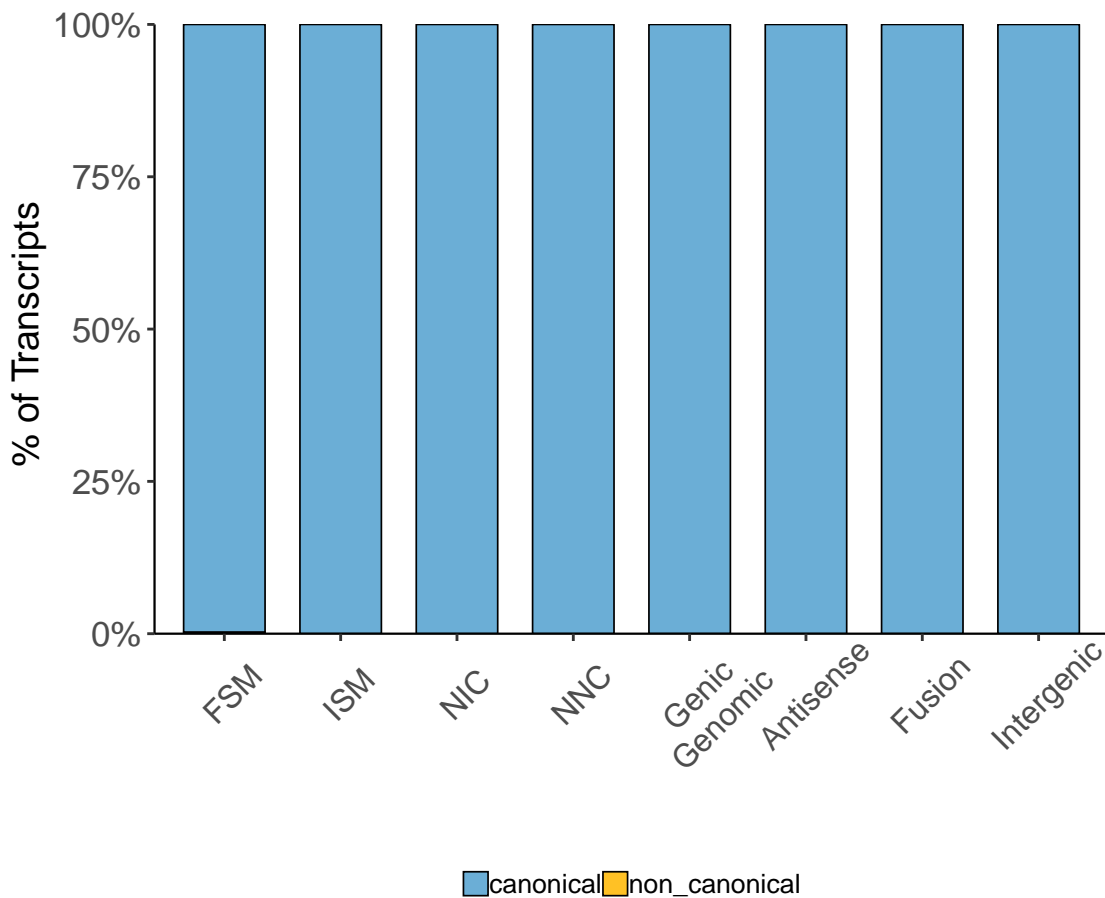


Splice Junction Characterization

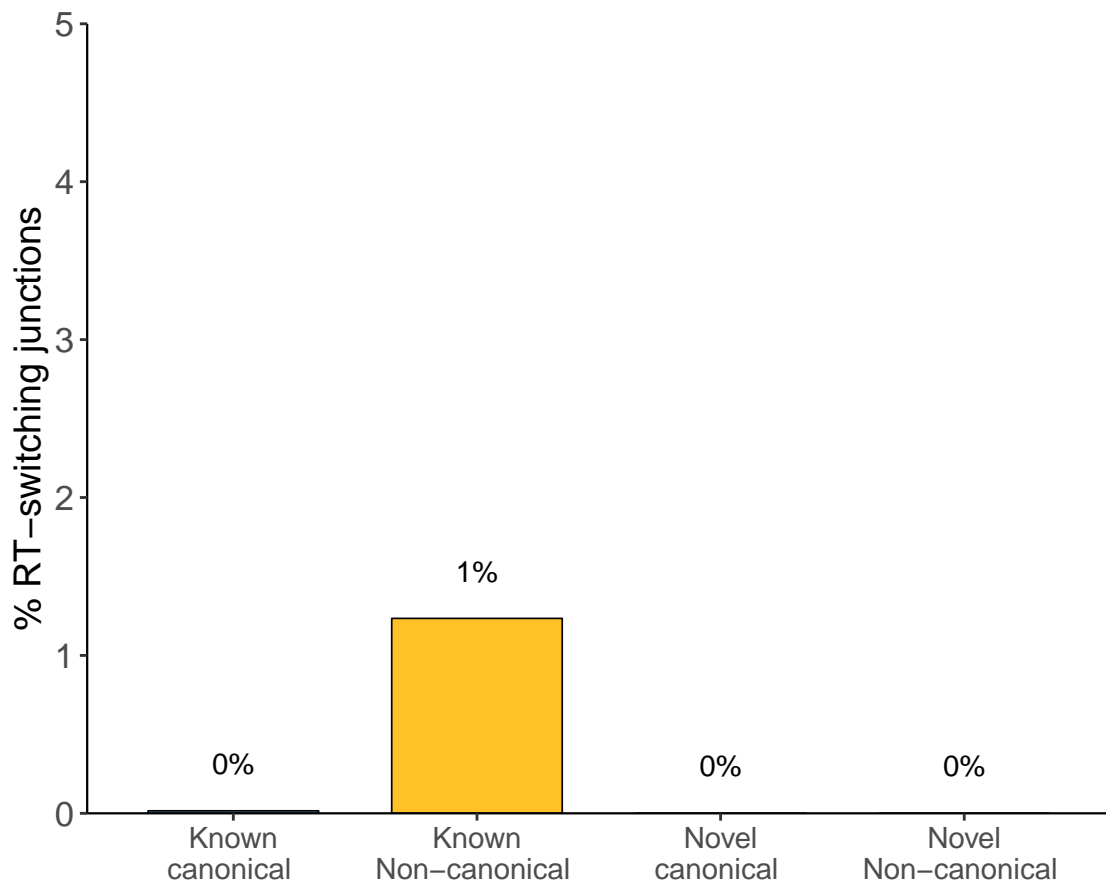
Distribution of Splice Junctions by Structural Classification



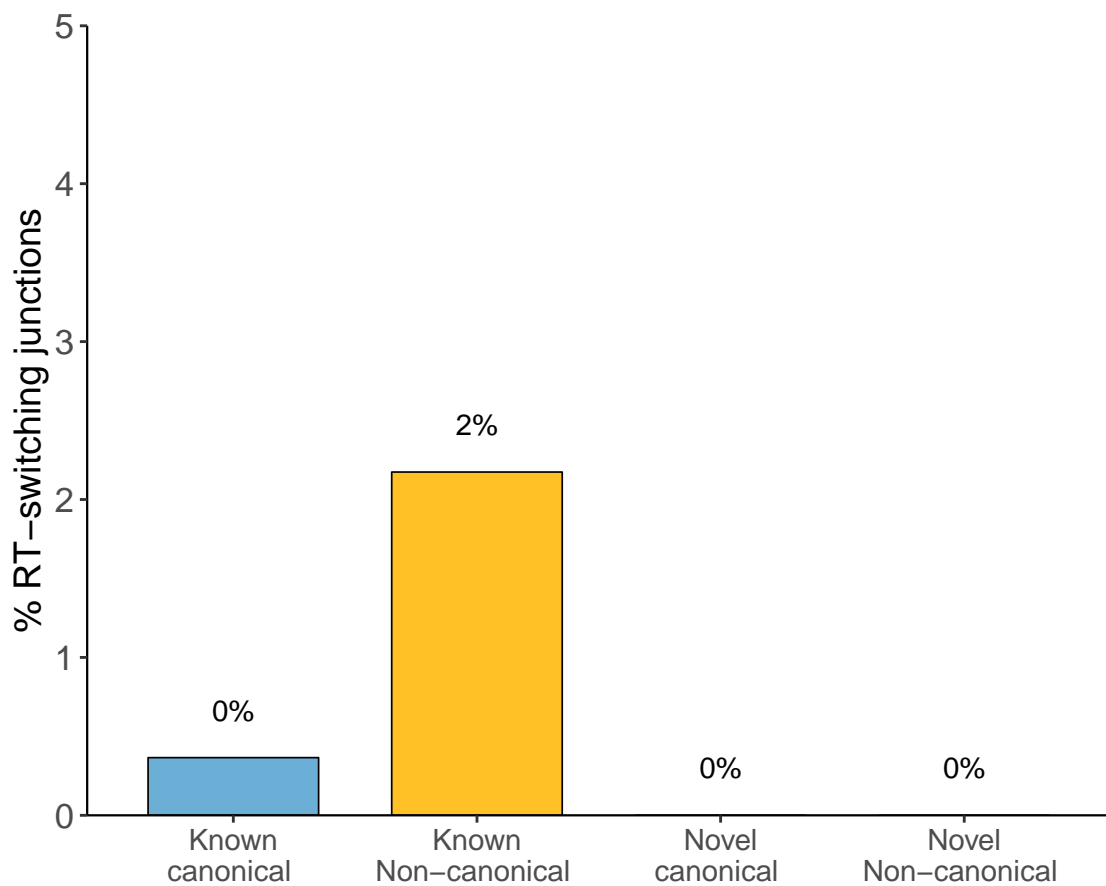
Distribution of Transcripts by Splice Junctions



RT-switching, all junctions



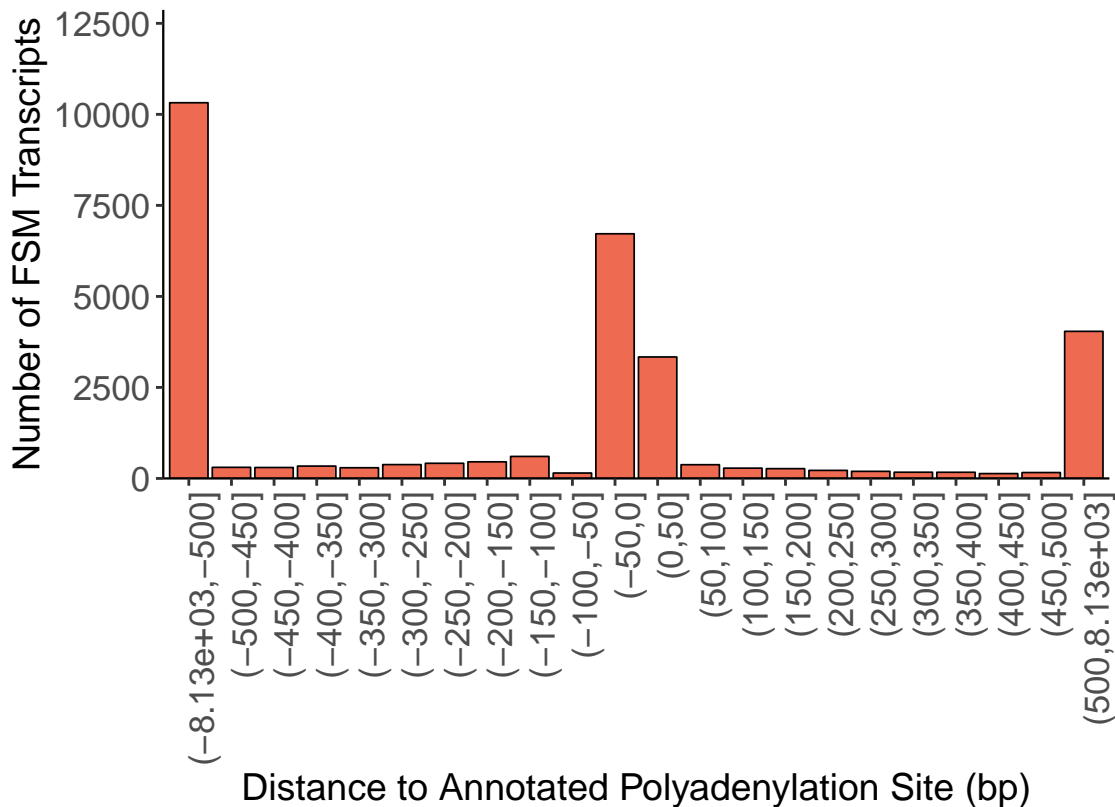
RT-switching, unique junctions



Comparison with Annotated TSS and PolyA Sites

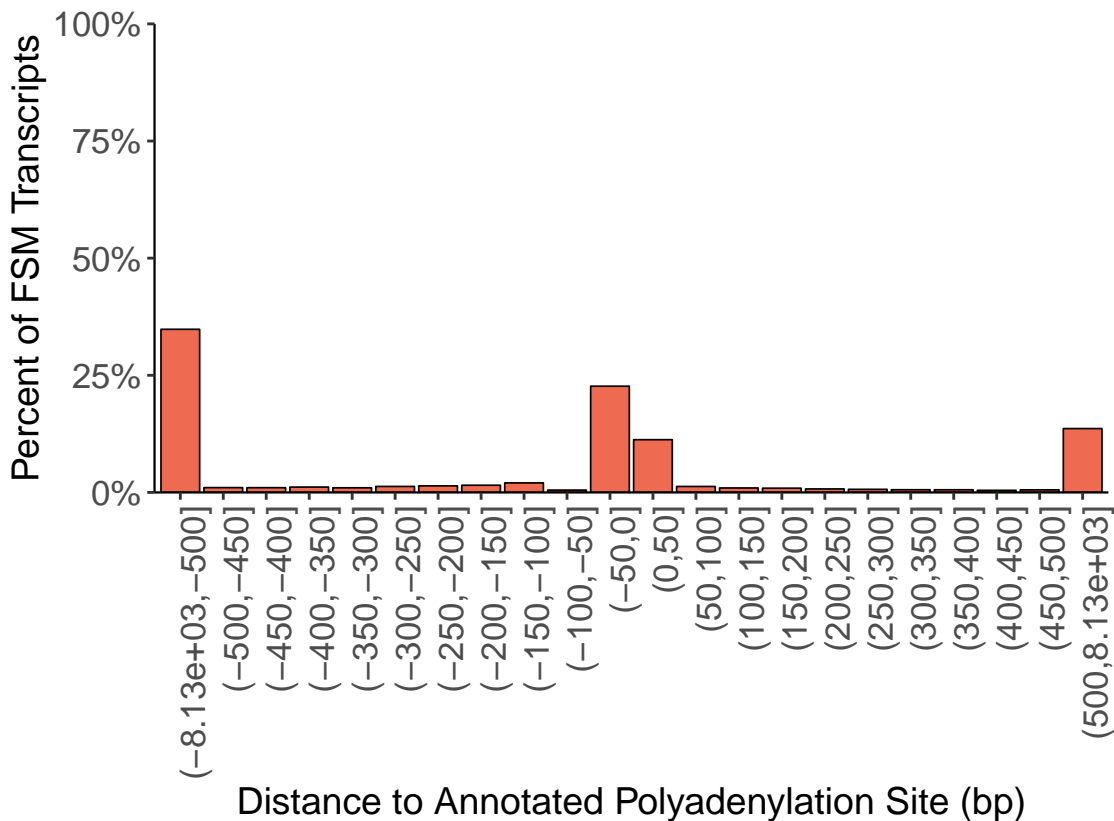
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



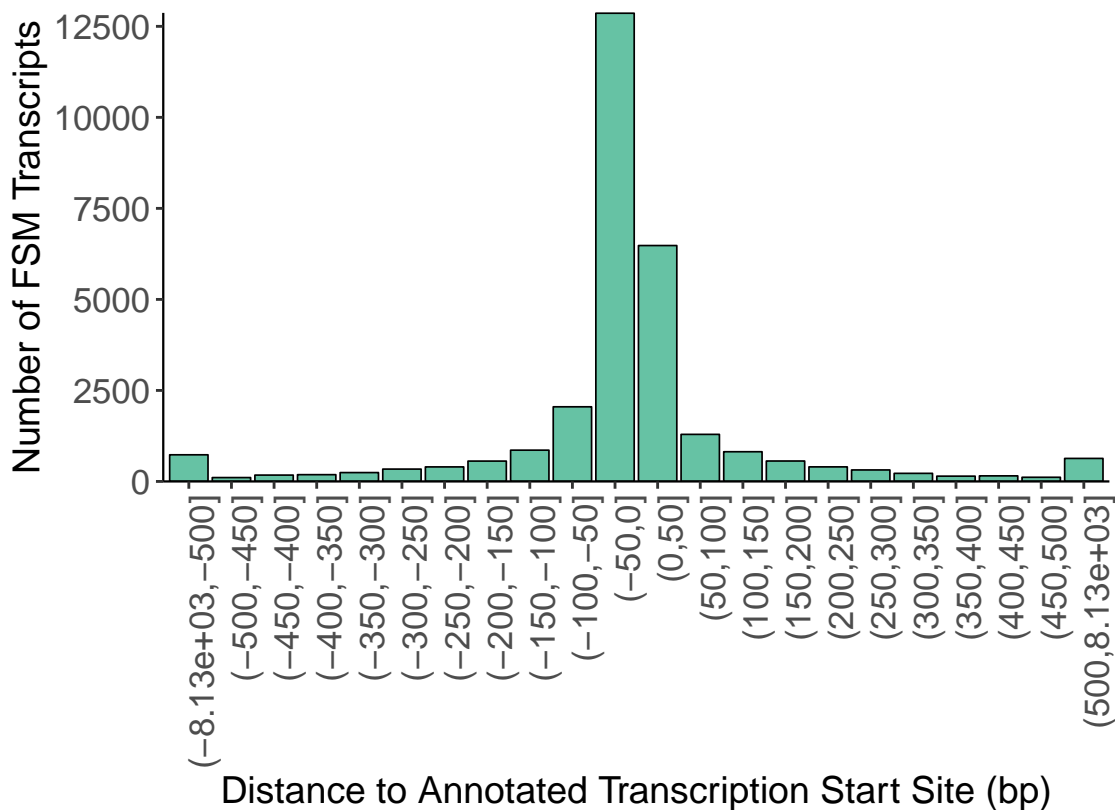
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



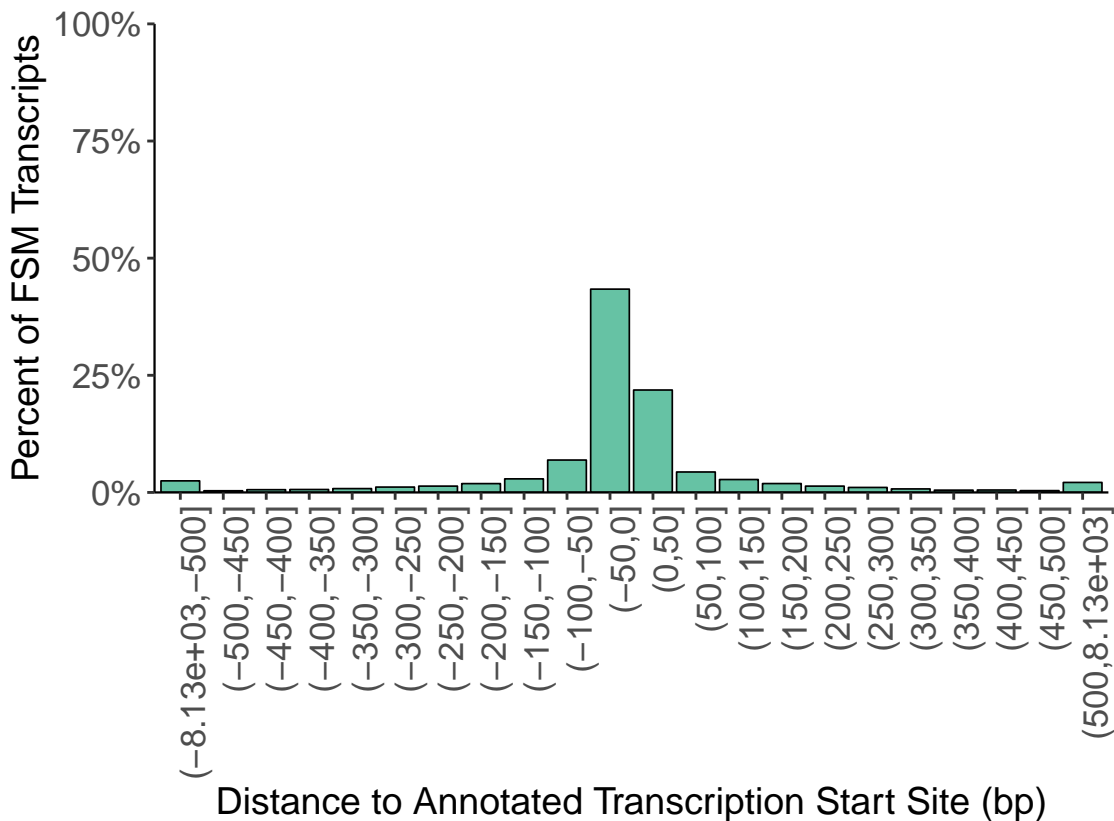
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



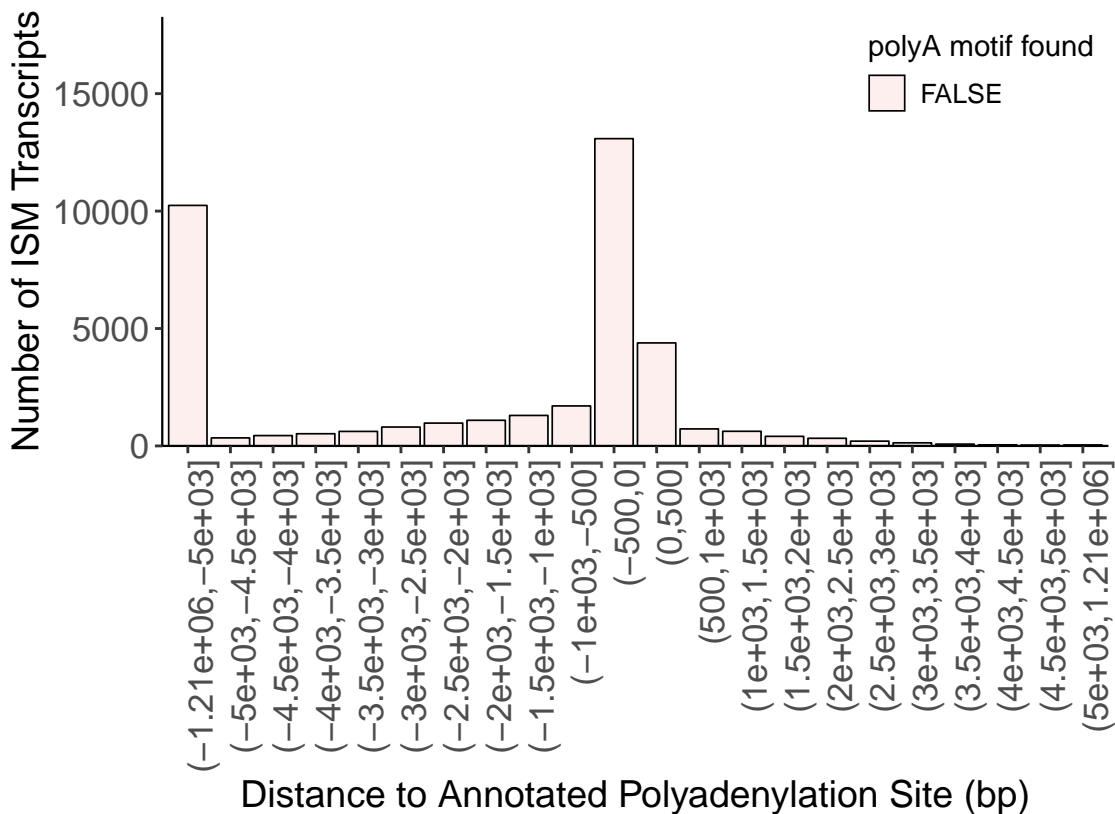
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



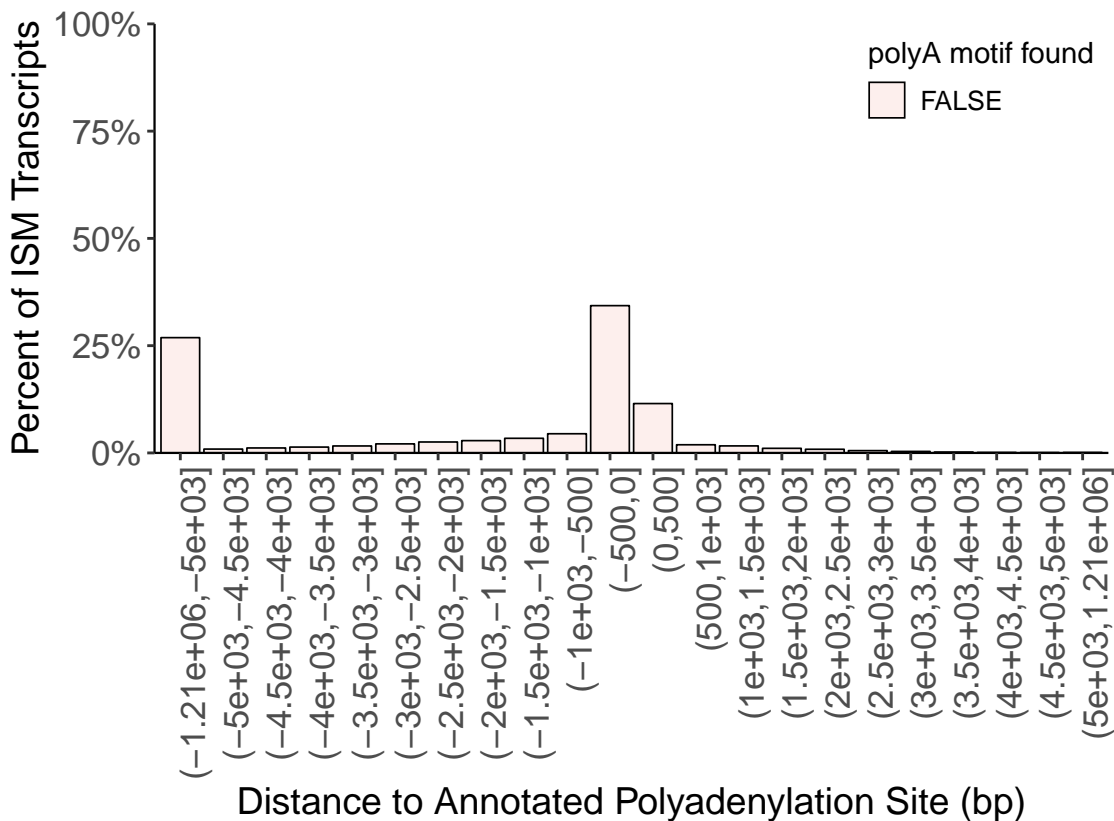
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



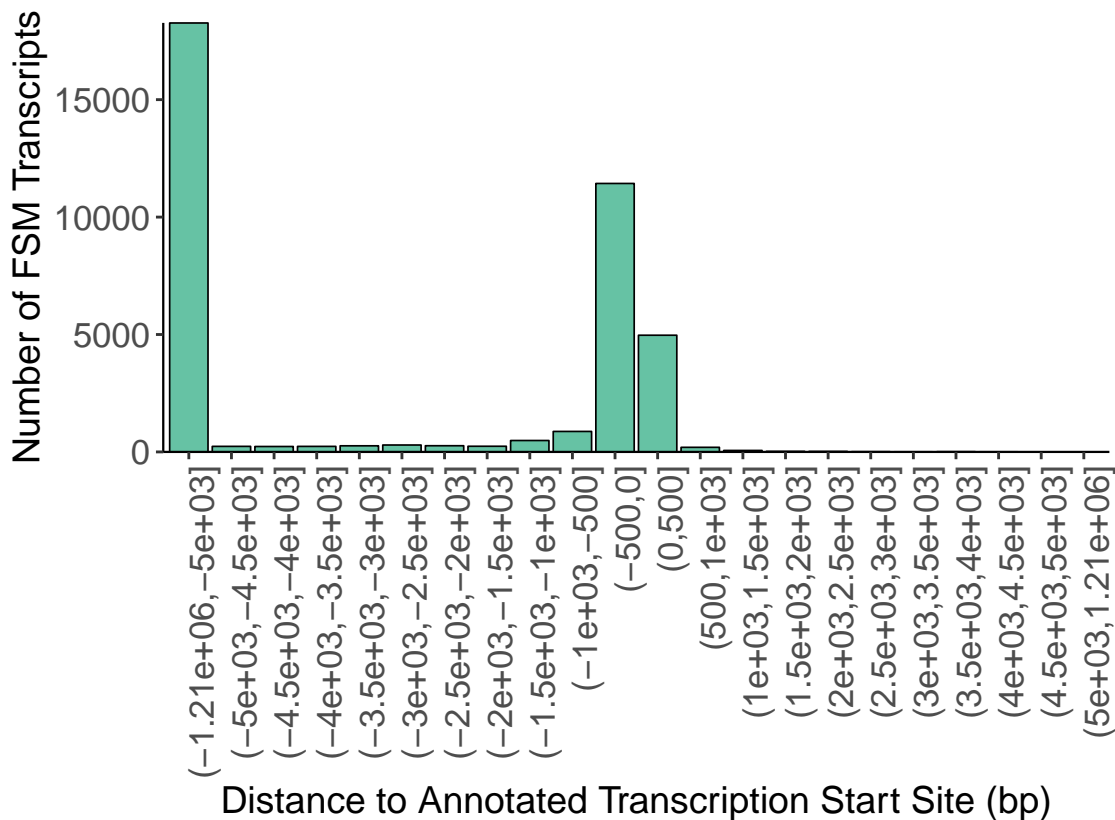
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



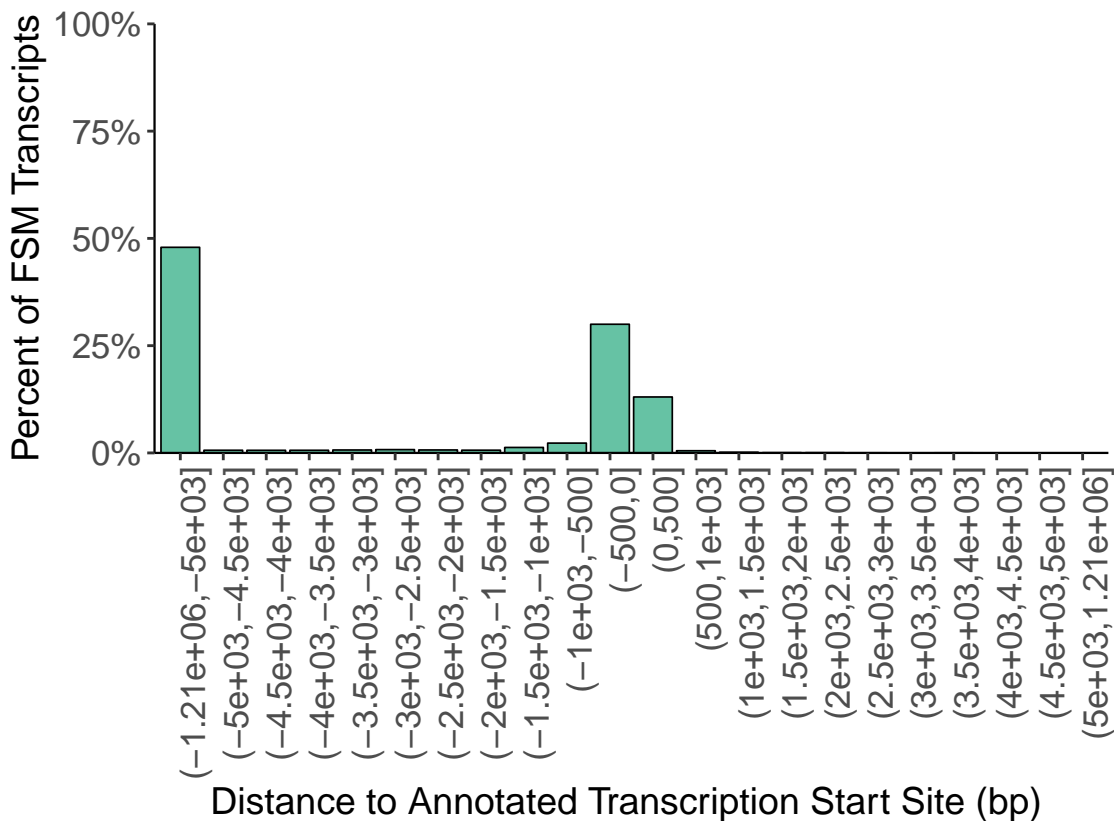
Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site, ISM only

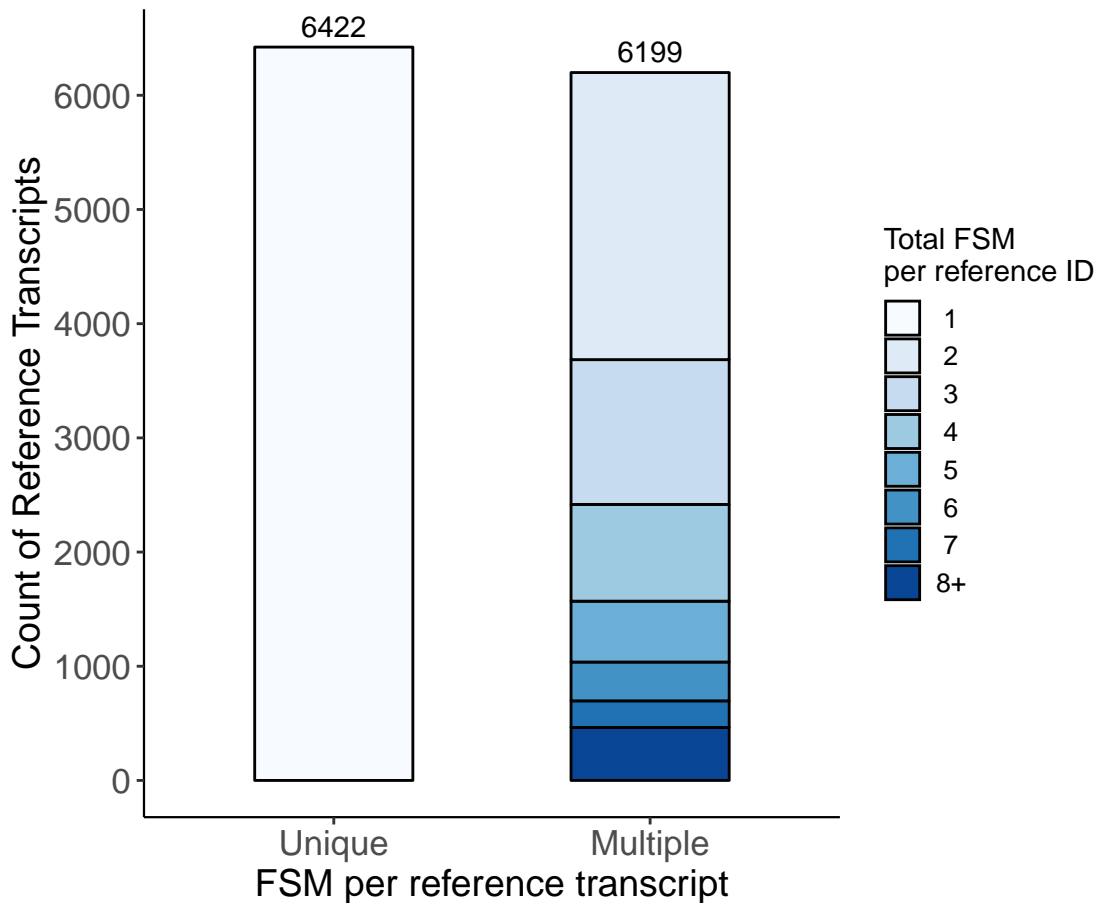
Negative values indicate downstream of annotated TSS



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

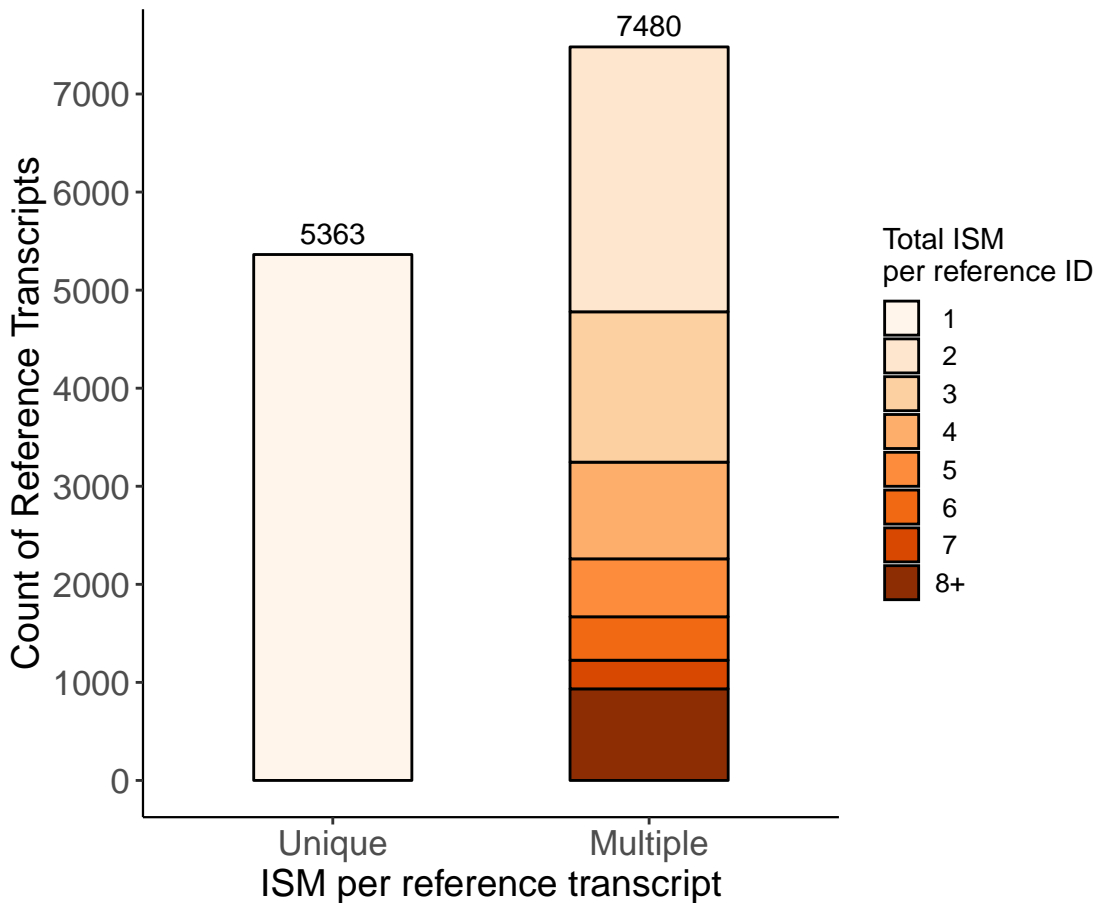
Reference transcript redundance

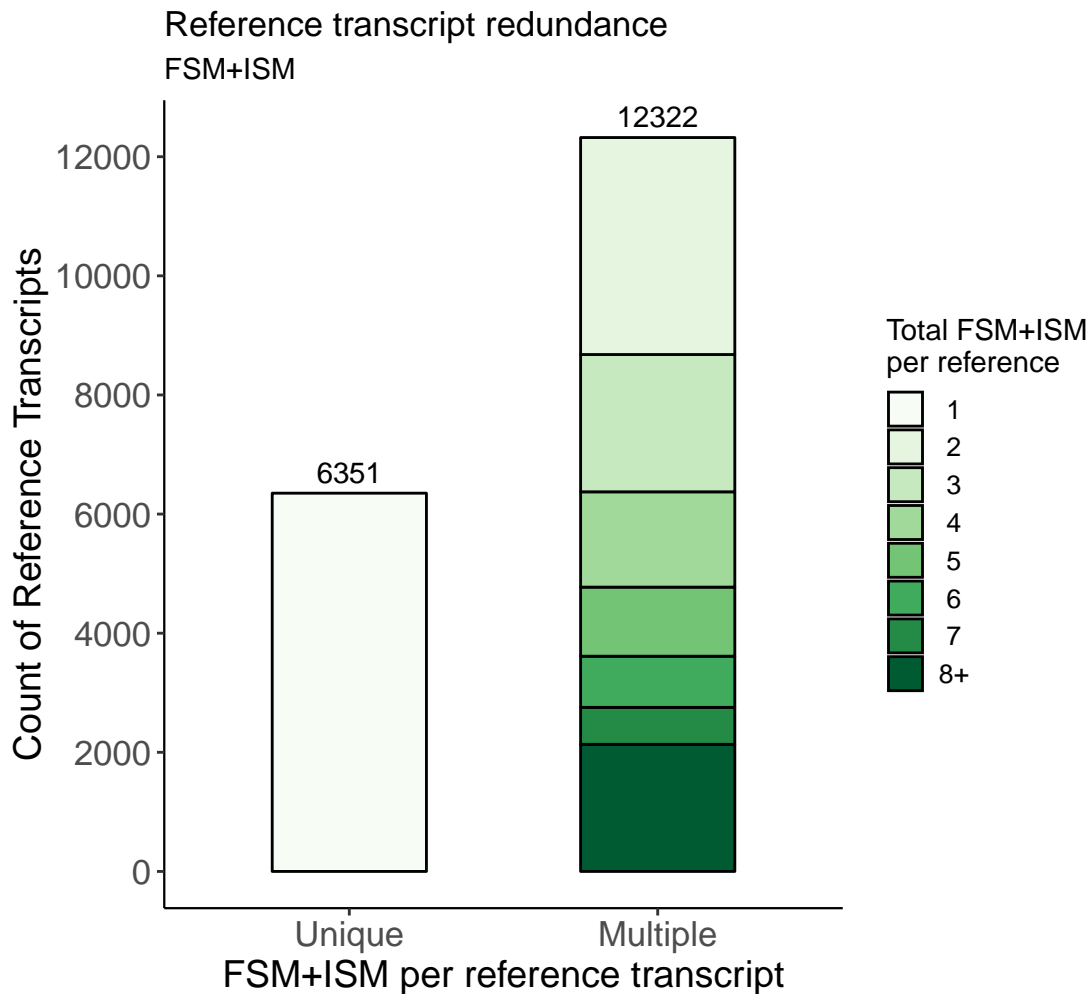
Only FSM



Reference transcript redundance

Only ISM

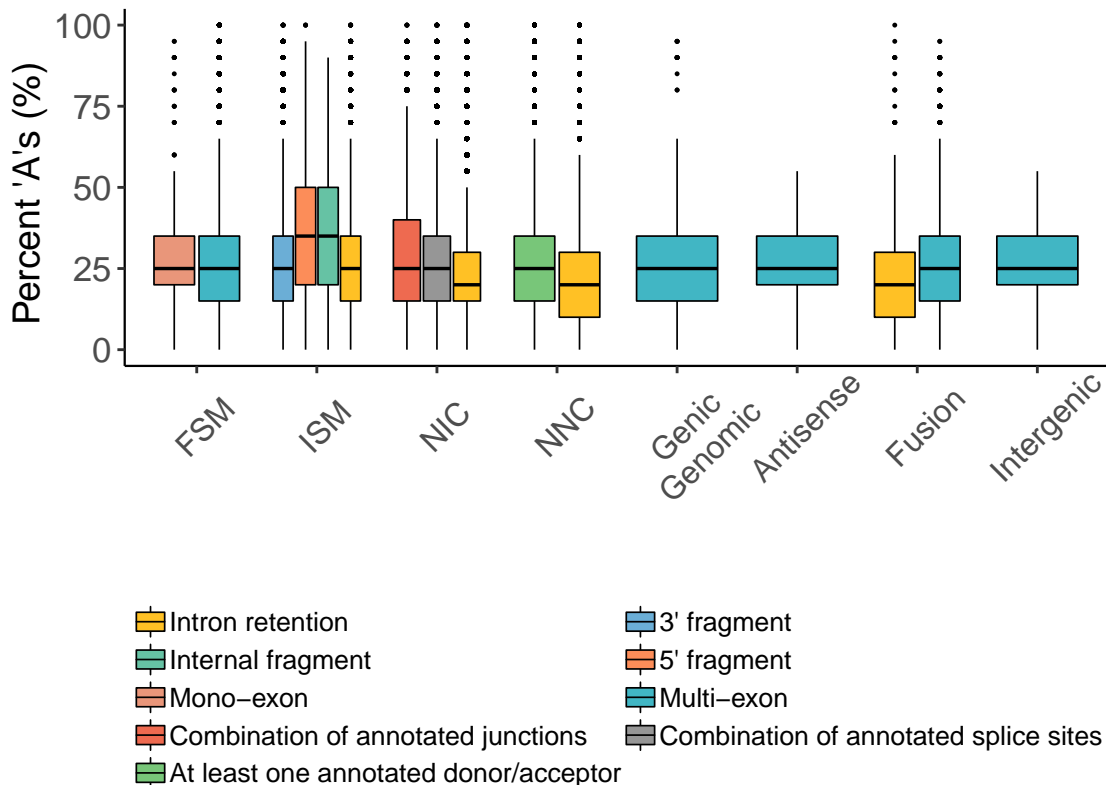




Intra-Priming Quality Check

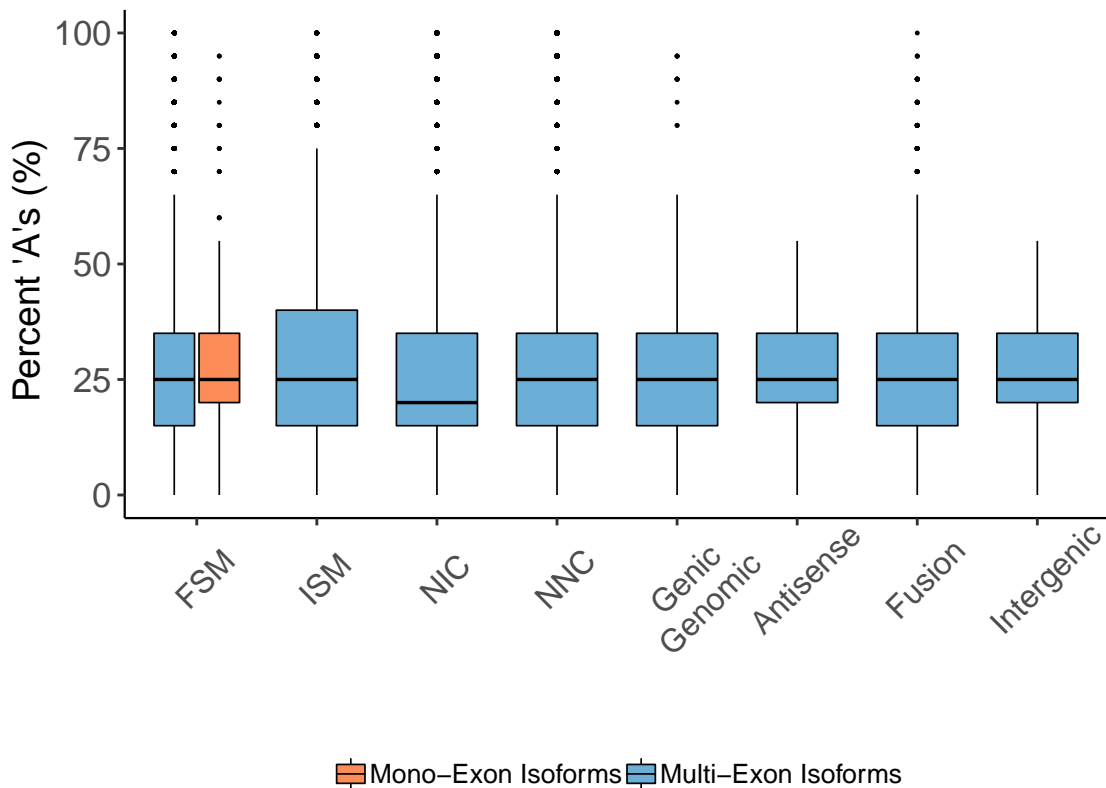
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



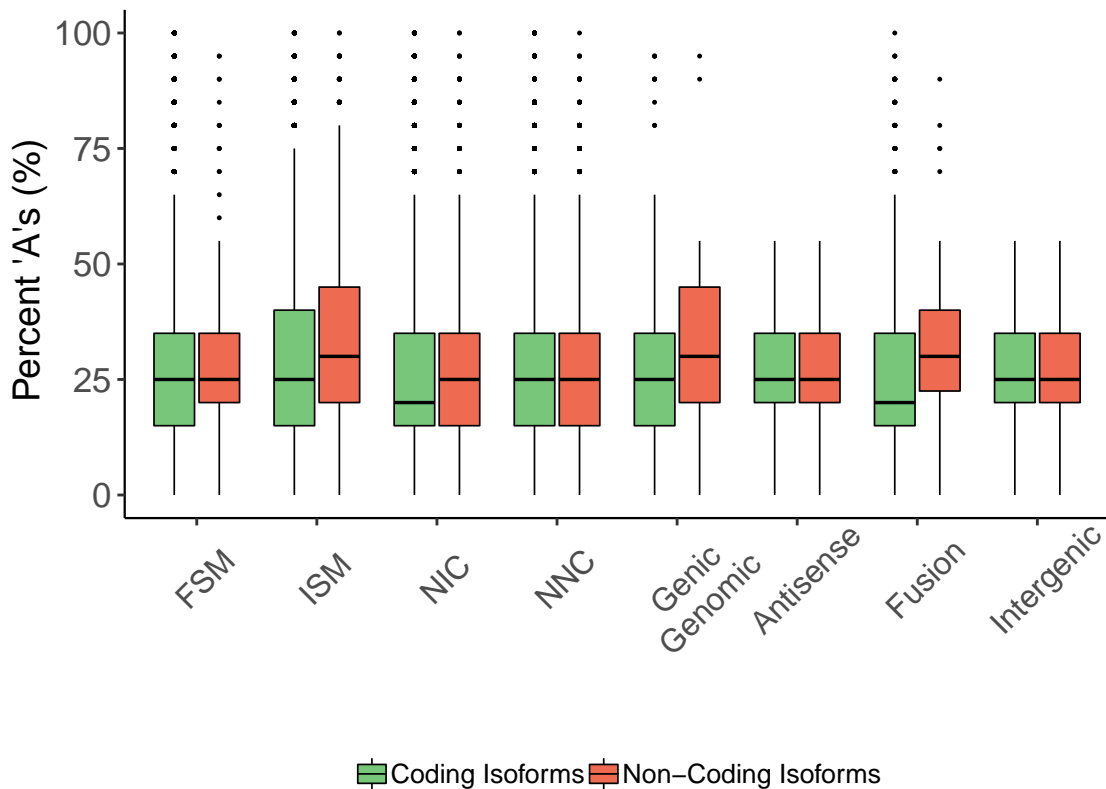
Possible Intra-Priming, Mono- vs Multi-Exon

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

1.7%

% of Isoforms

2

1

0

FSM



Incidence of Non-Canonical Junctions

0.3%

% of Isoforms

1.0

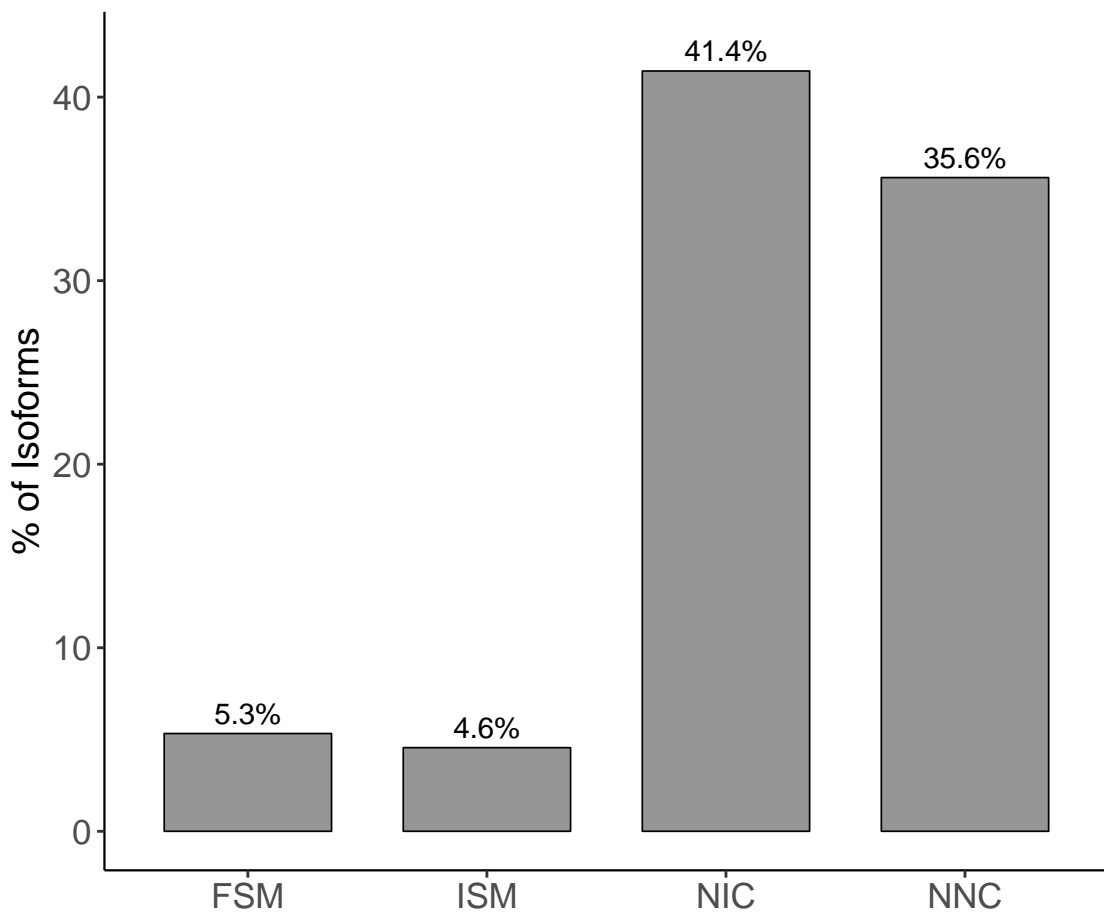
0.5

0.0

FSM



Incidence of NMD by structural category



Quality control attributes across structural categories

