

SQANTI3 report

Unique Genes: 31829
Unique Isoforms: 107649

Gene classification

Category	# Genes
Annotated Genes	28124
Novel Genes	3705

Splice Junction Classification

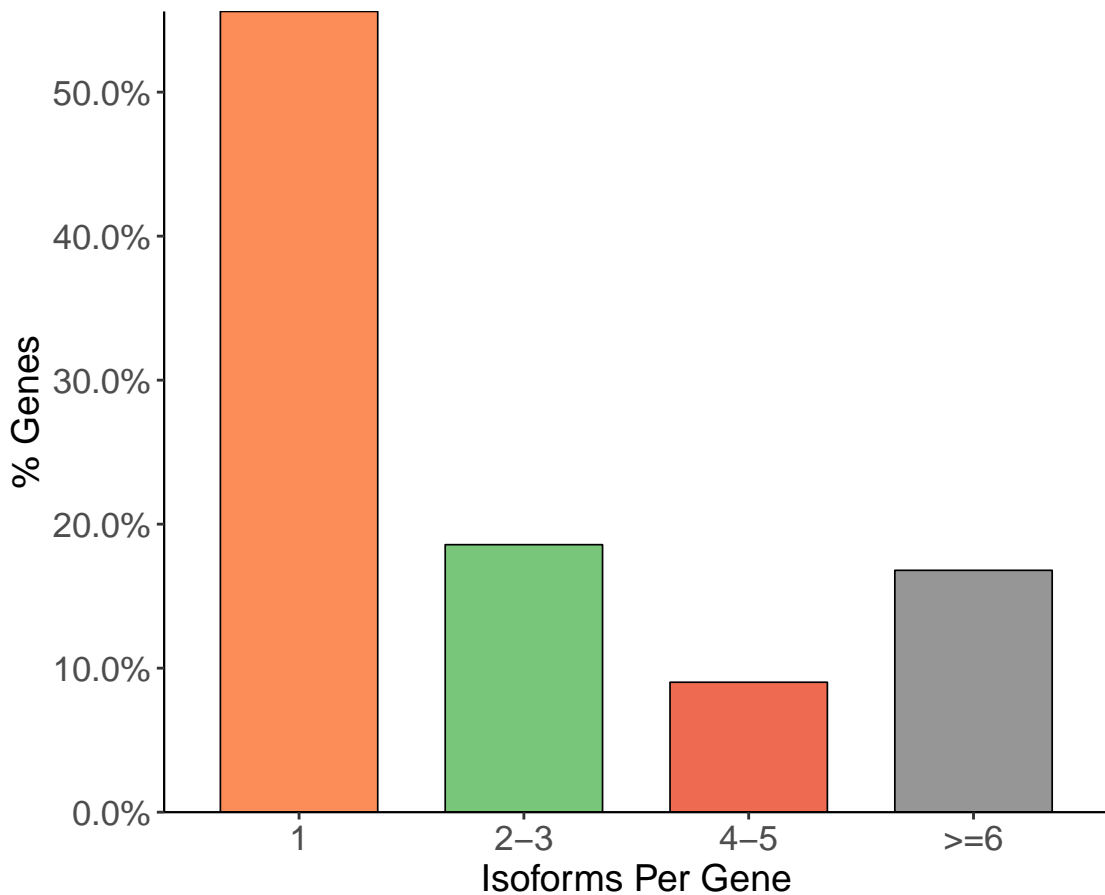
Category	# SJs	Percent
Known canonical	220195	88.47
Known Non–canonical	860	0.35
Novel canonical	27810	11.17
Novel Non–canonical	37	0.01

*Characterization of transcripts
based on splice junctions*

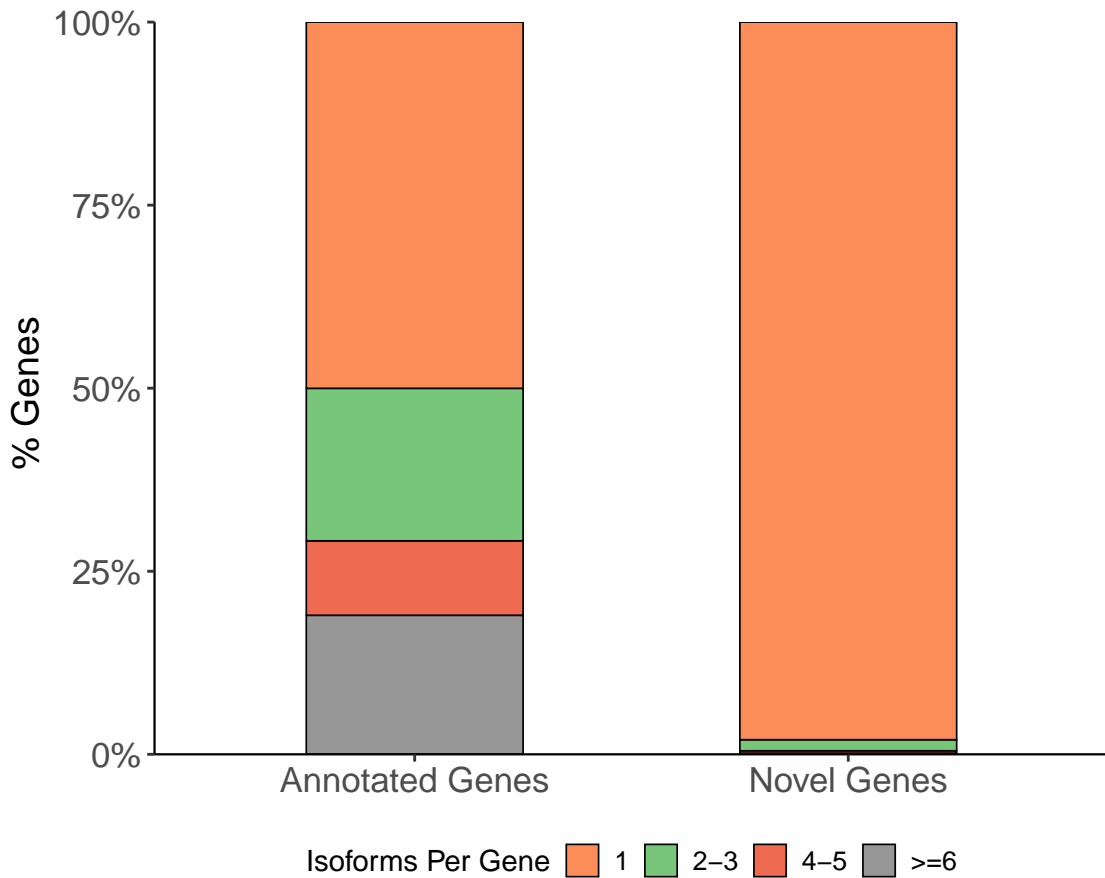
Category	# Isoforms
FSM	55043
ISM	7585
NIC	19082
NNC	21055
Genic Genomic	72
Antisense	575
Fusion	947
Intergenic	3290
Genic Intron	0

Gene Characterization

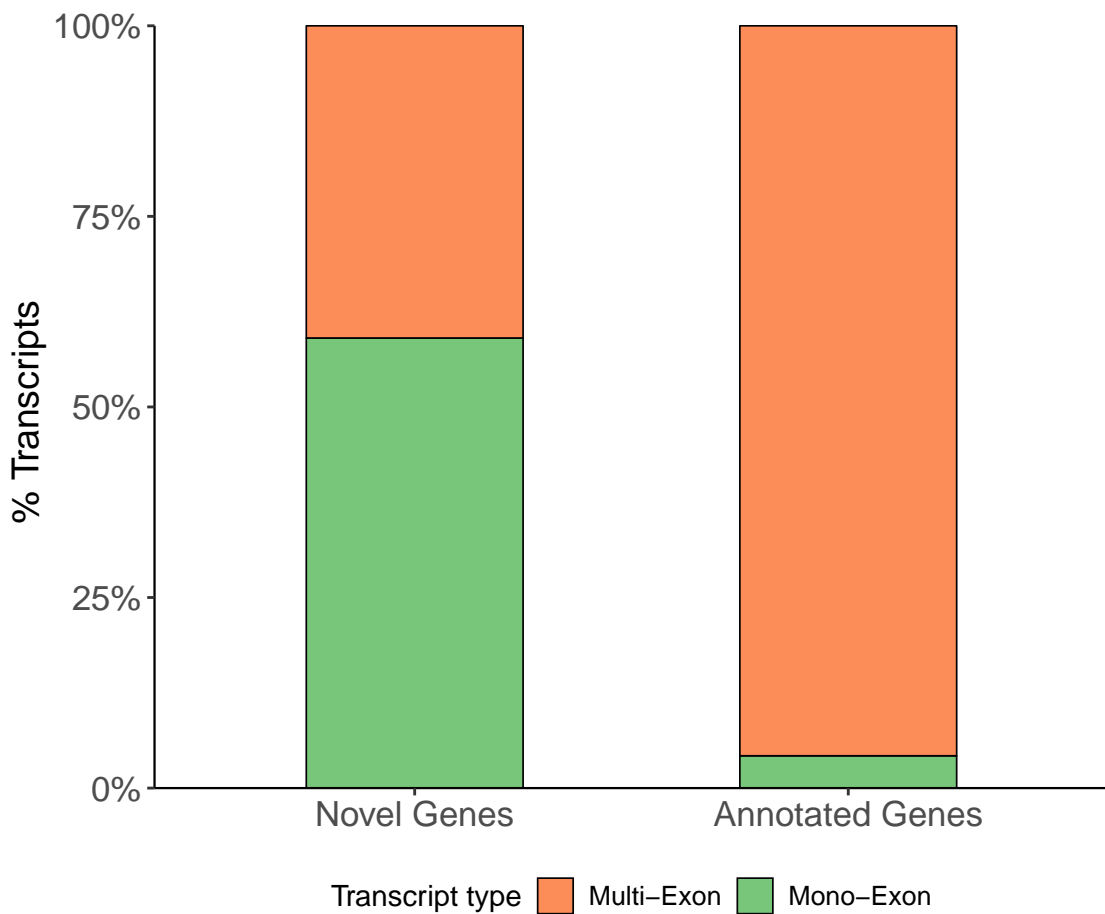
Number of Isoforms per Gene



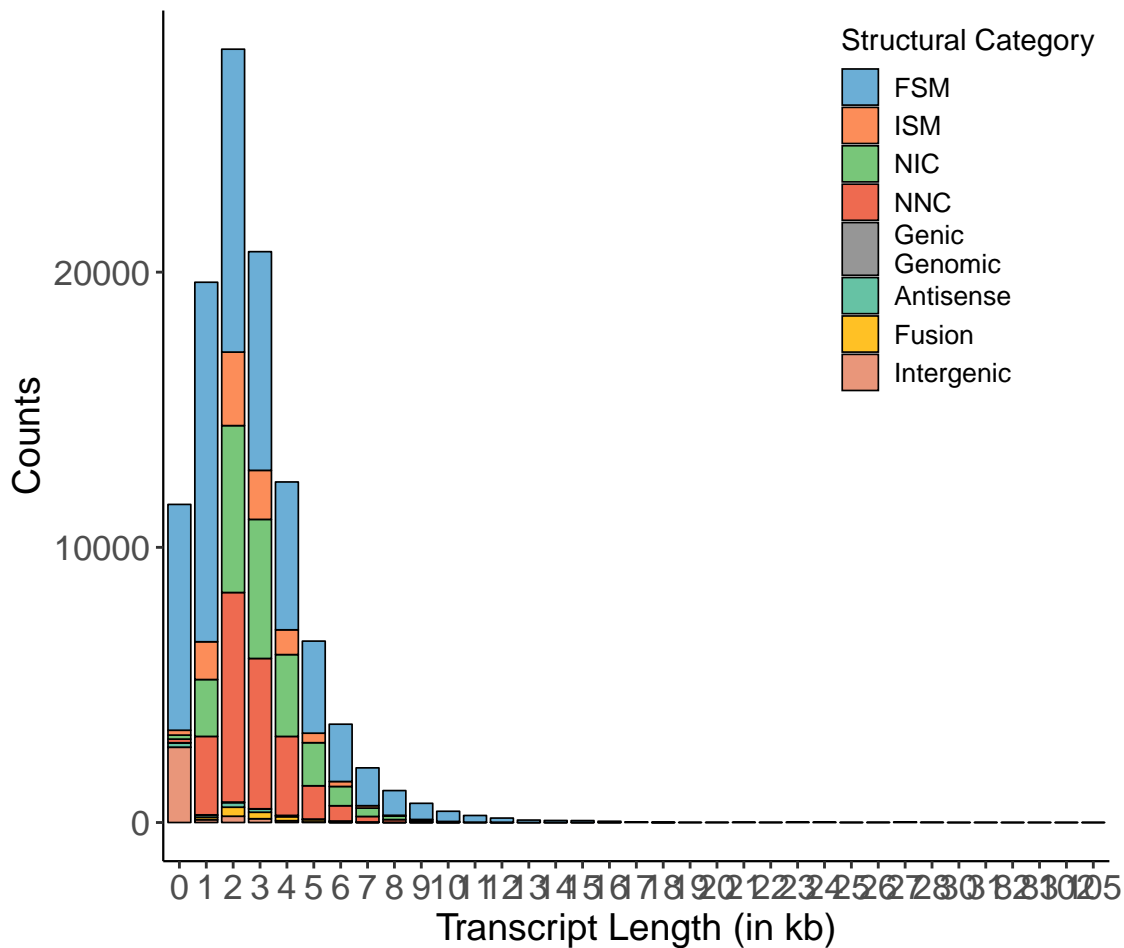
Number of Isoforms per Gene, Known vs Novel Genes



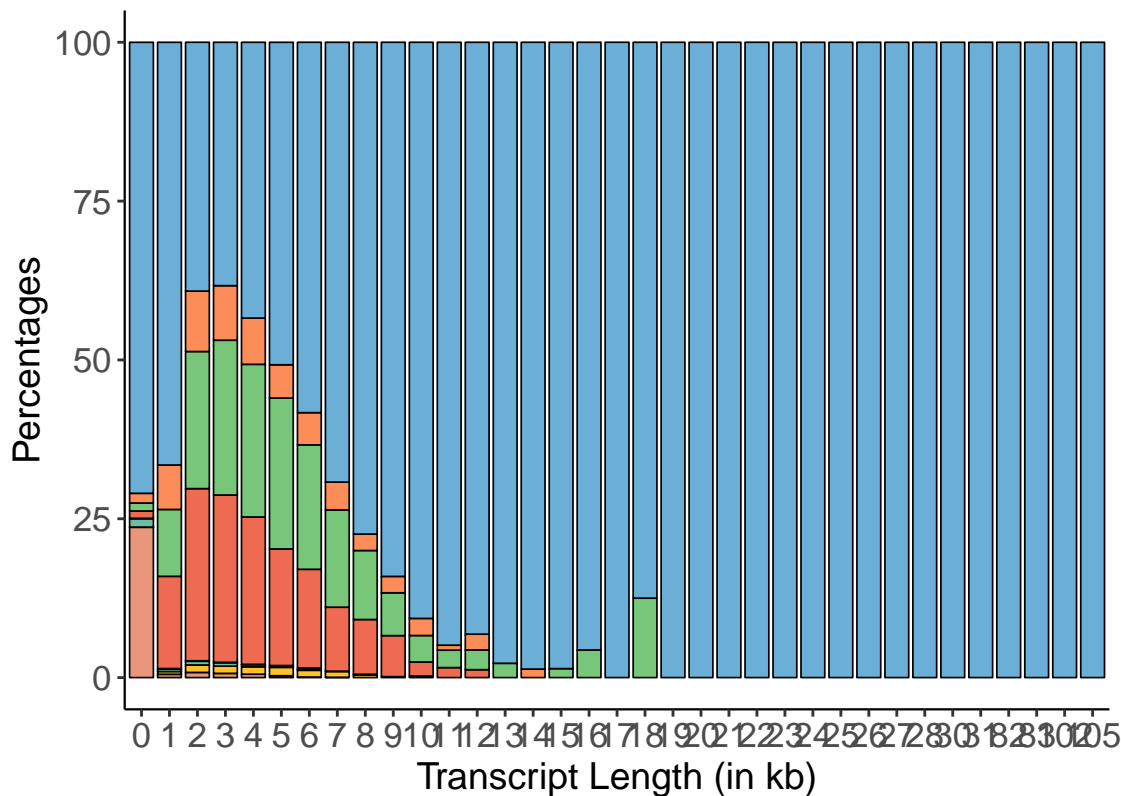
Distribution of Mono- vs Multi-Exon Transcripts



Classifications by Transcript Length



Classifications by Transcript Length, normalized



Structural Category

FSM	NIC	Genic Genomic	Fusion
ISM	NNC	Antisense	Intergenic

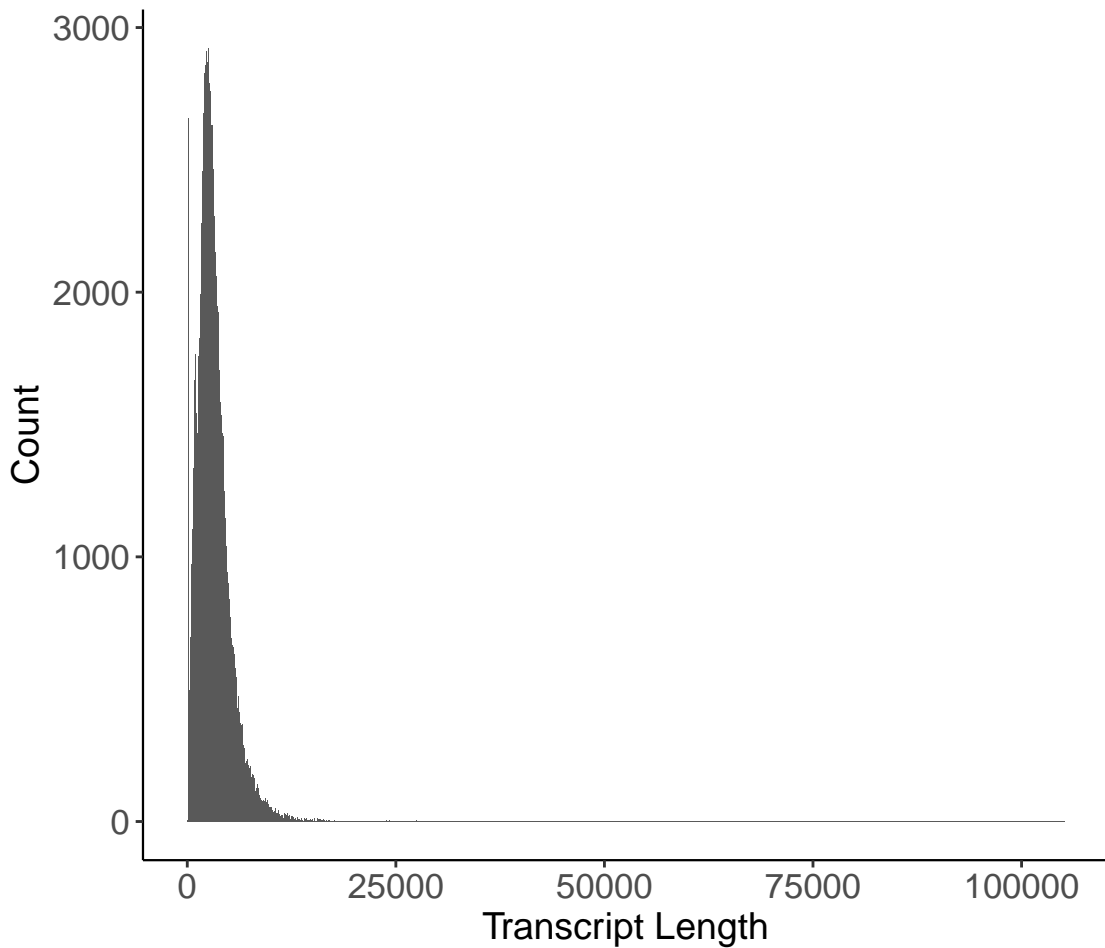
Number of FL reads per Gene by type of gene annotation

$\log_2(\text{FL_TPM}+1)$

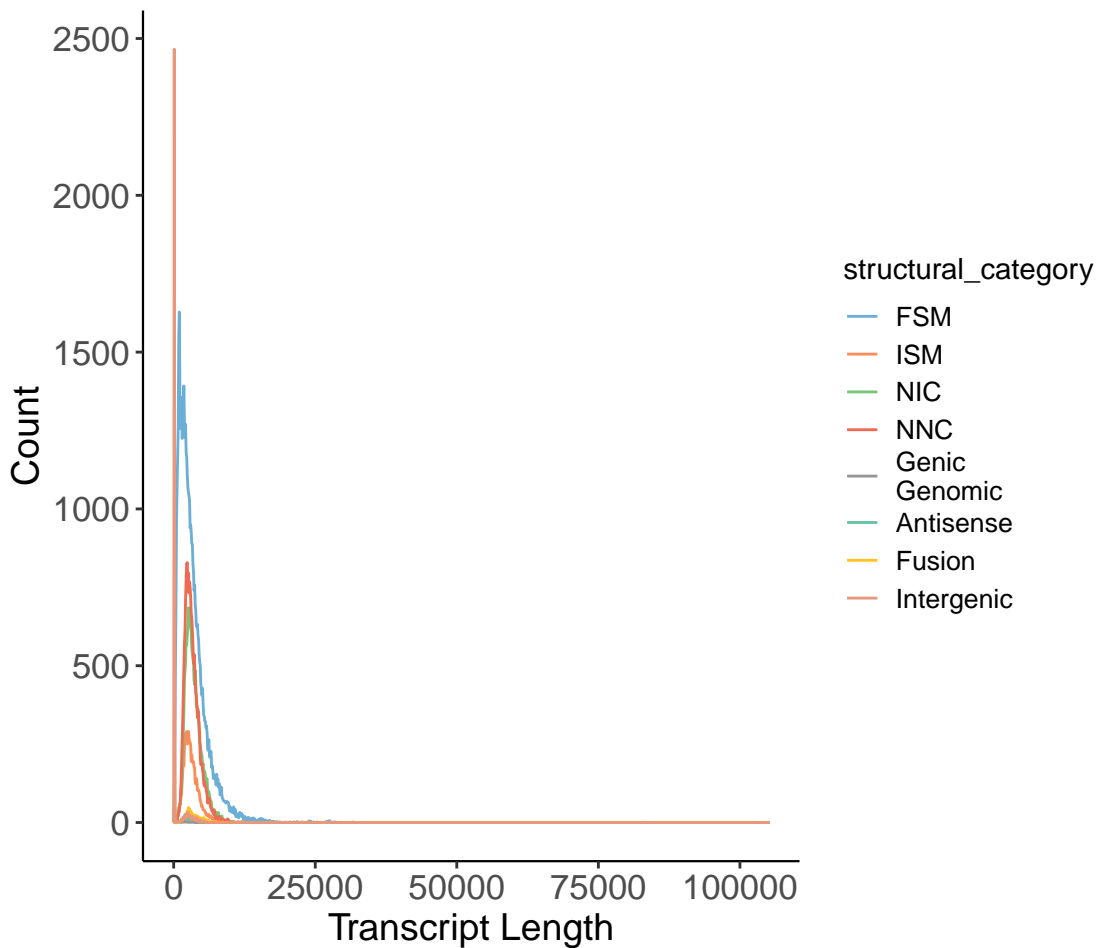
Annotated Genes

Novel Genes

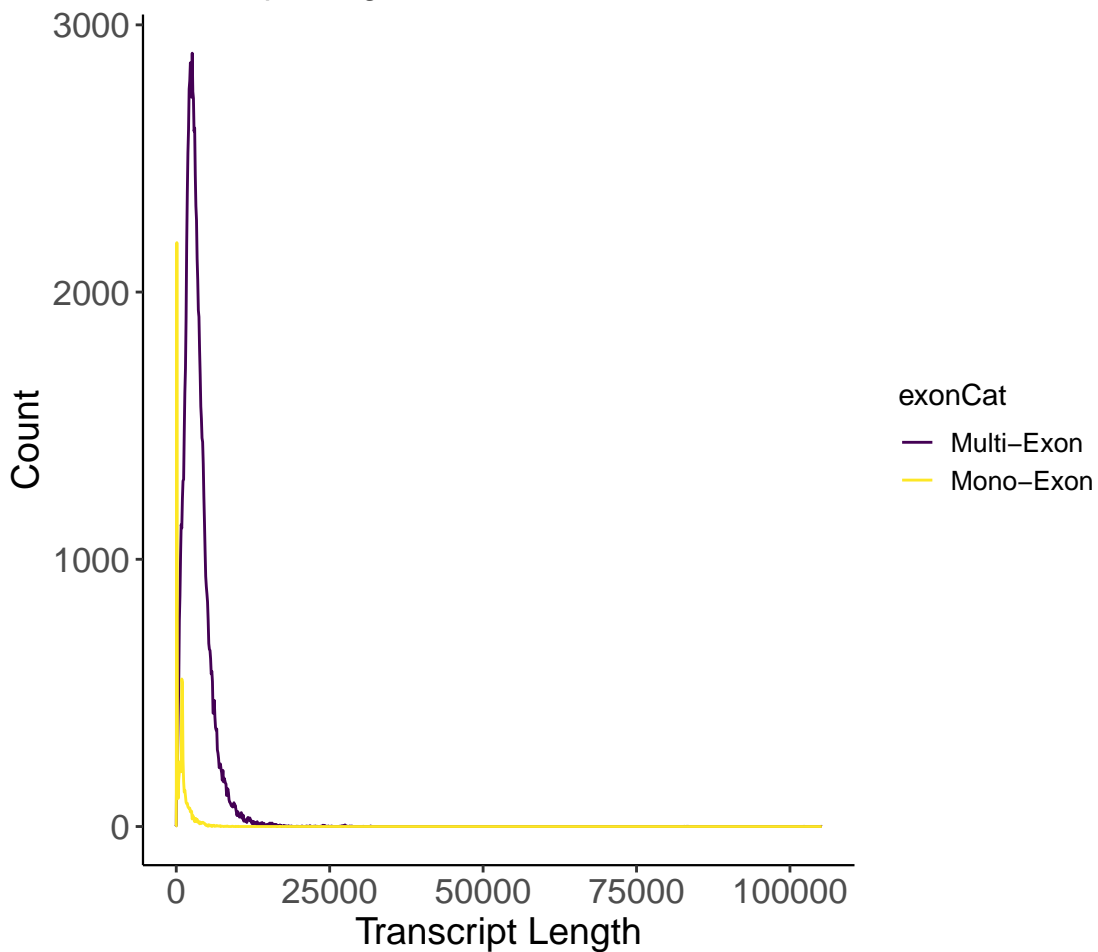
Transcript Lengths, all transcripts



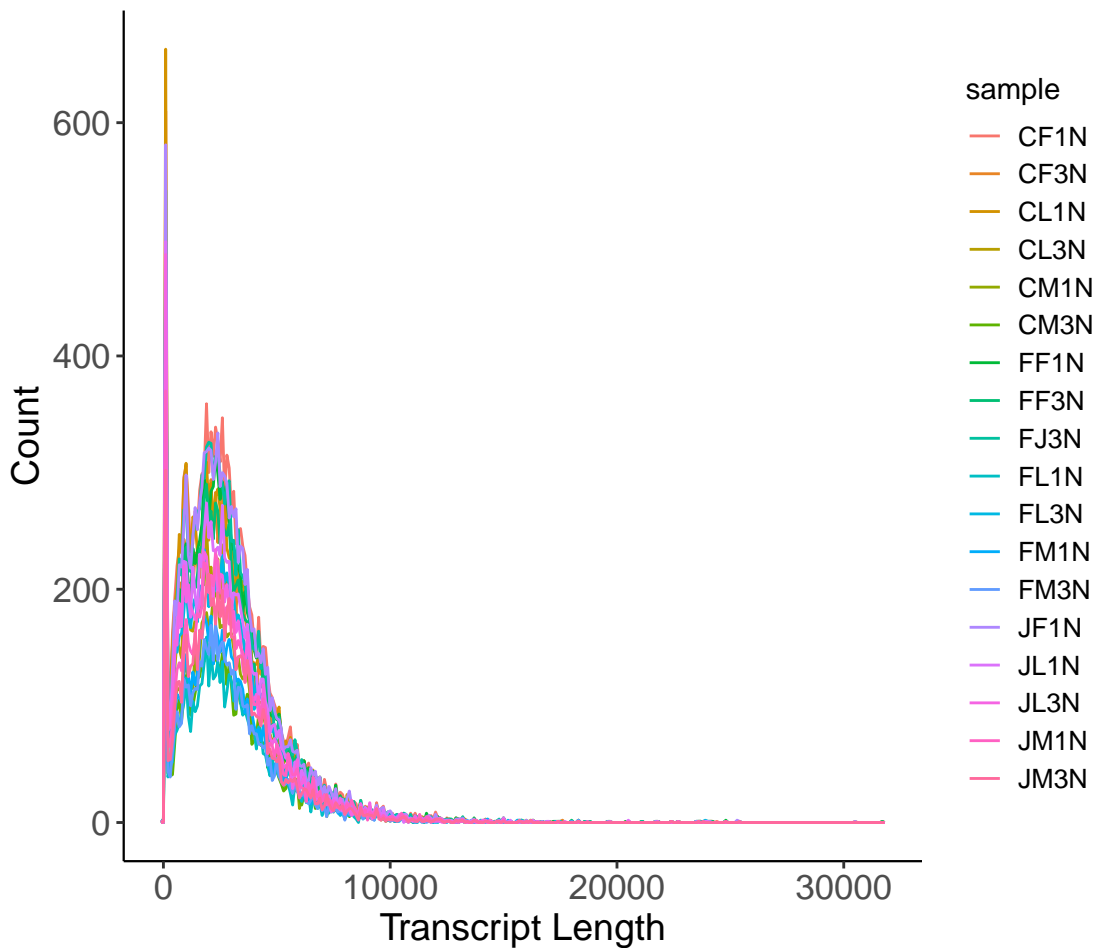
Transcript Lengths, by structural category



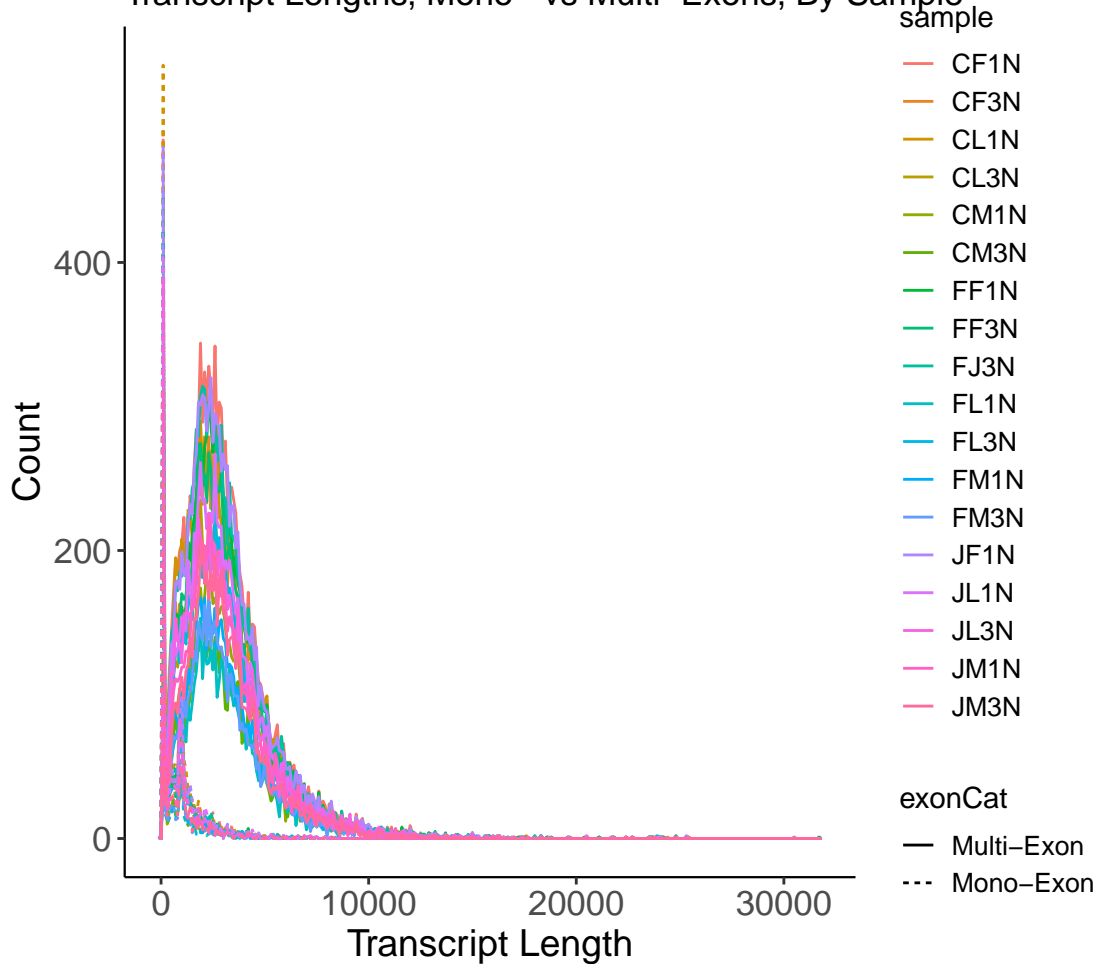
Transcript Lengths, Mono- vs Multi-Exons



Transcript Lengths, By Sample

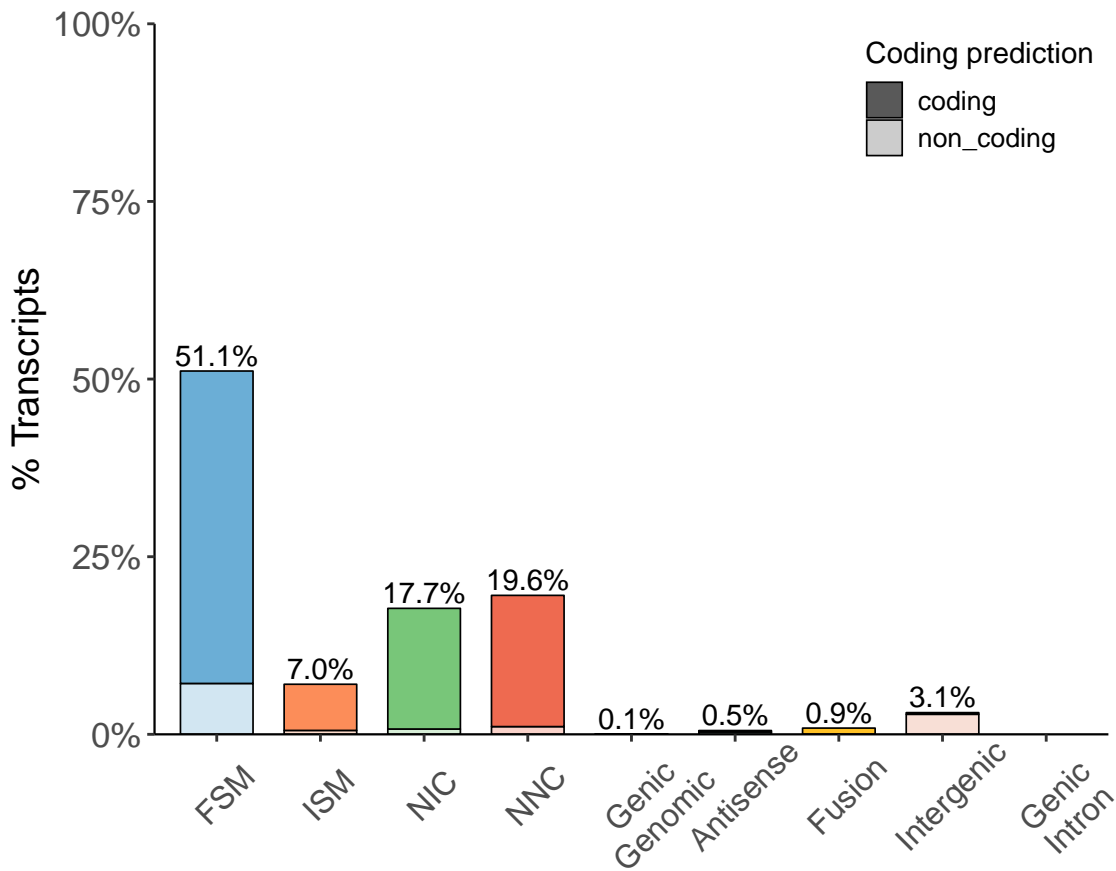


Transcript Lengths, Mono- vs Multi-Exons, By Sample

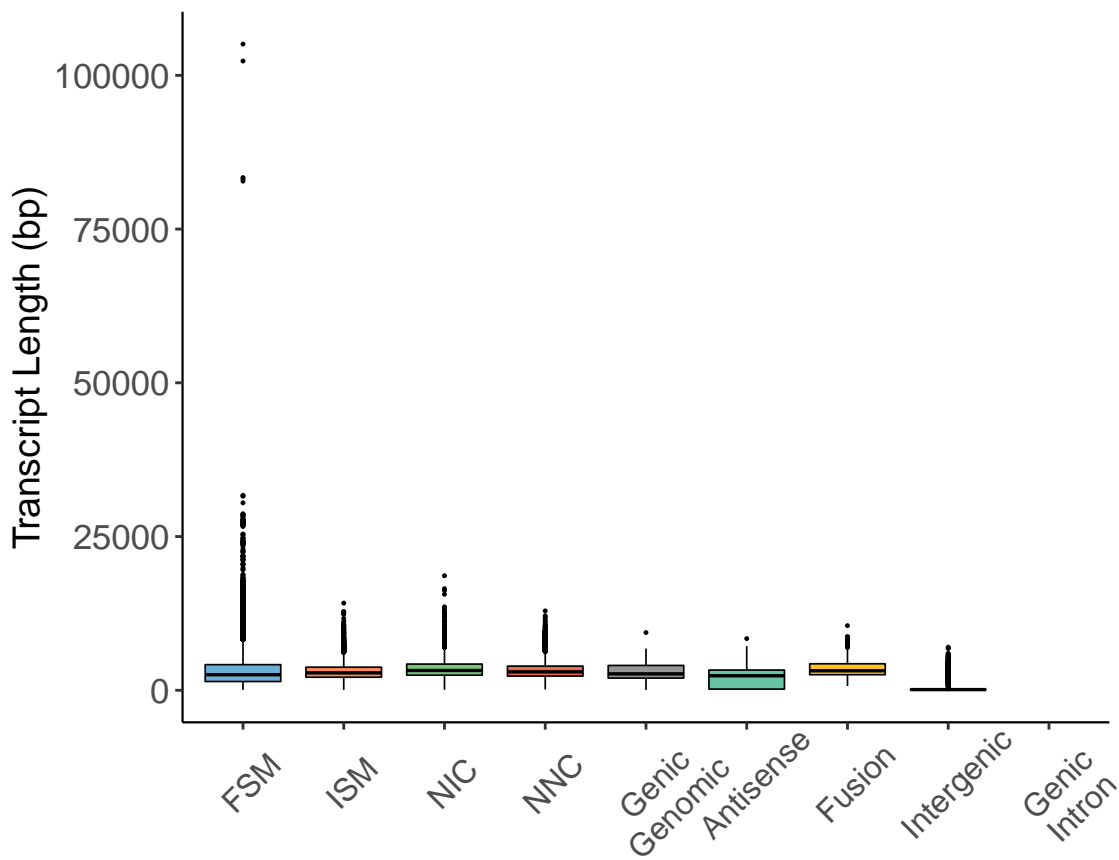


*Structural Isoform Characterization
by Splice Junctions*

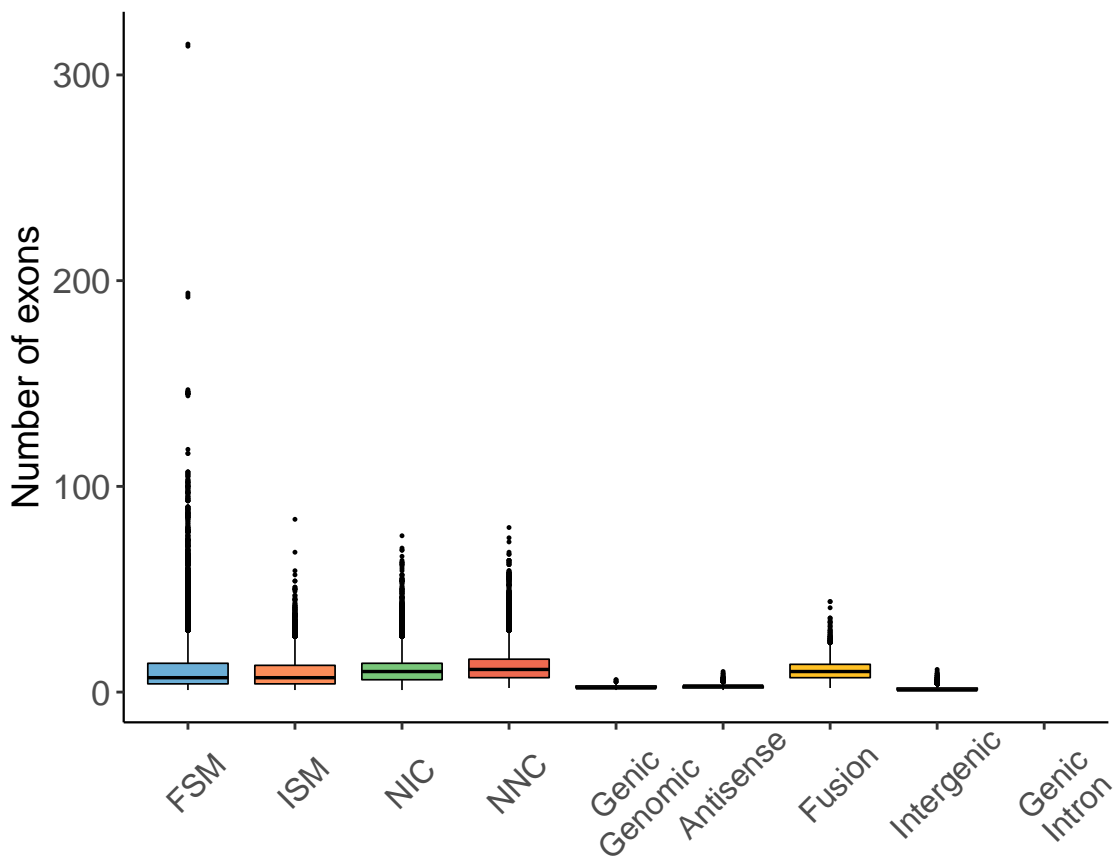
Isoform distribution across structural categories



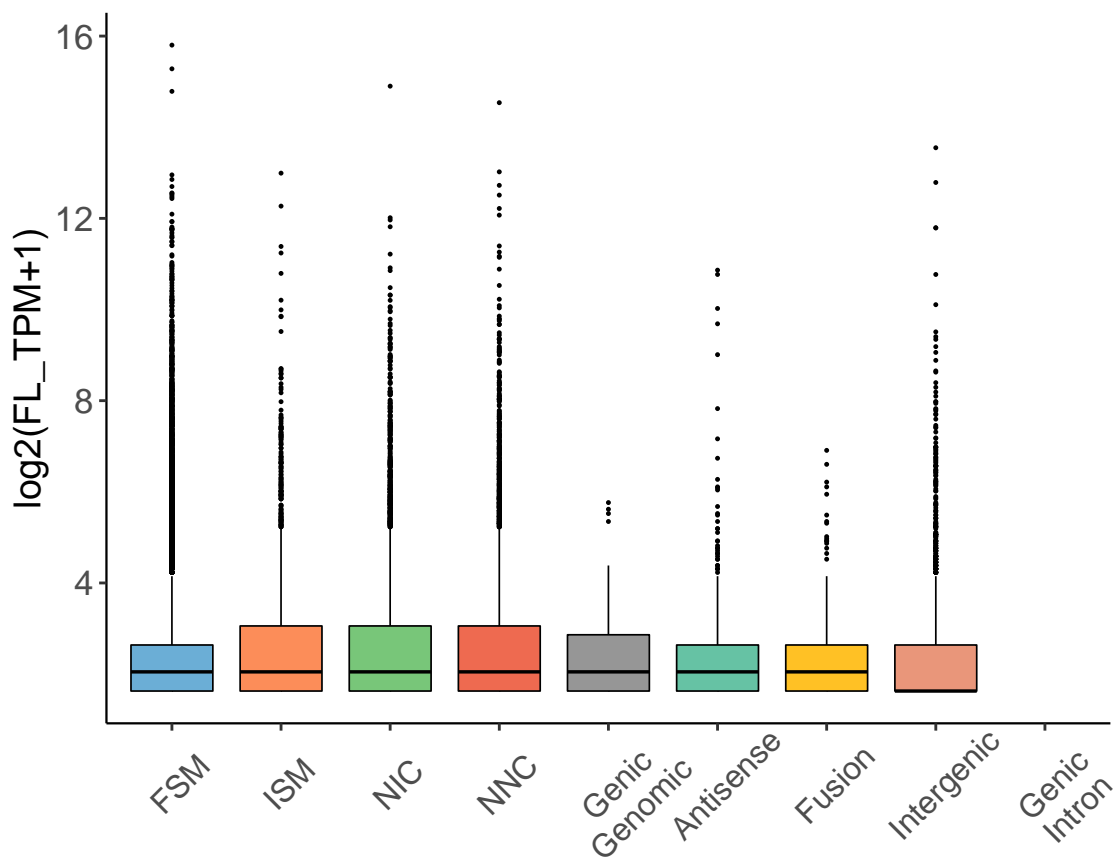
Transcript Lengths by Structural Classification



Exon Counts by Structural Classification

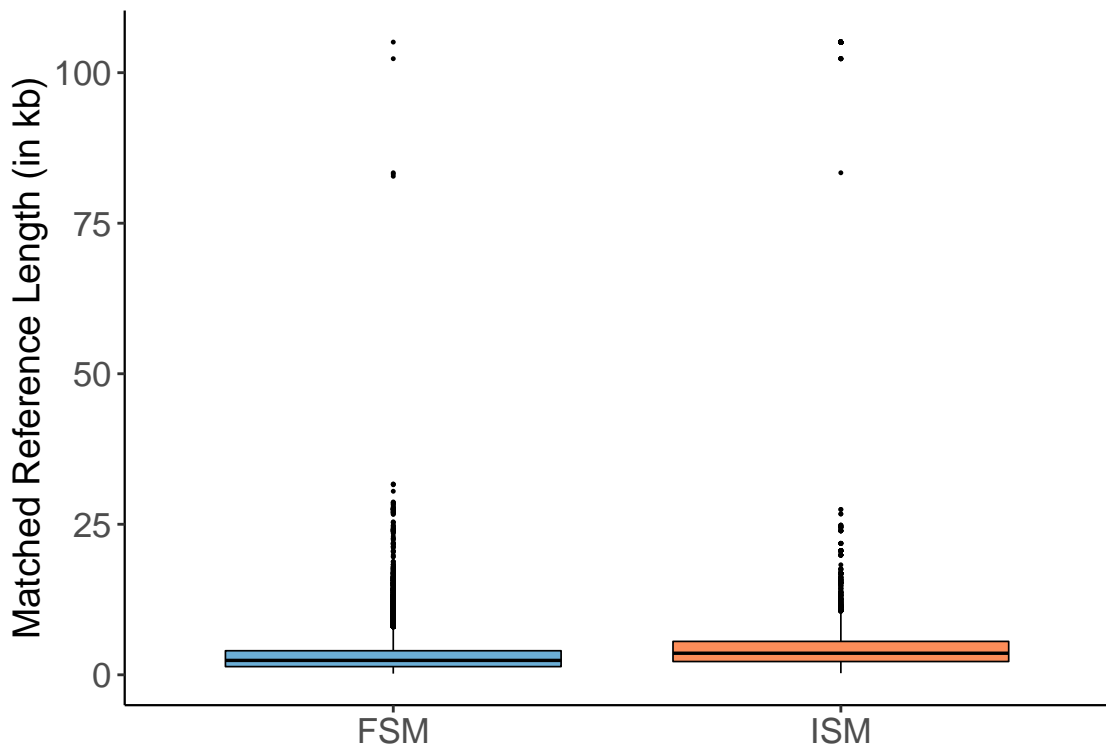


FL Count (normalized) by Structural Category



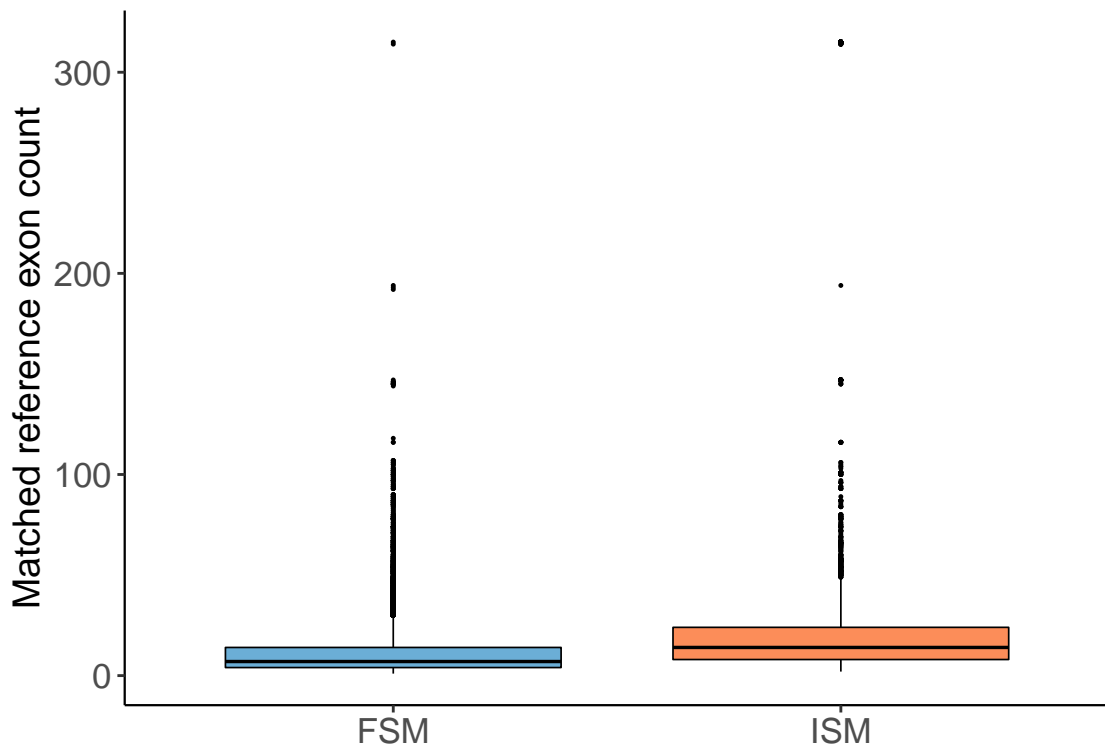
Length Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories



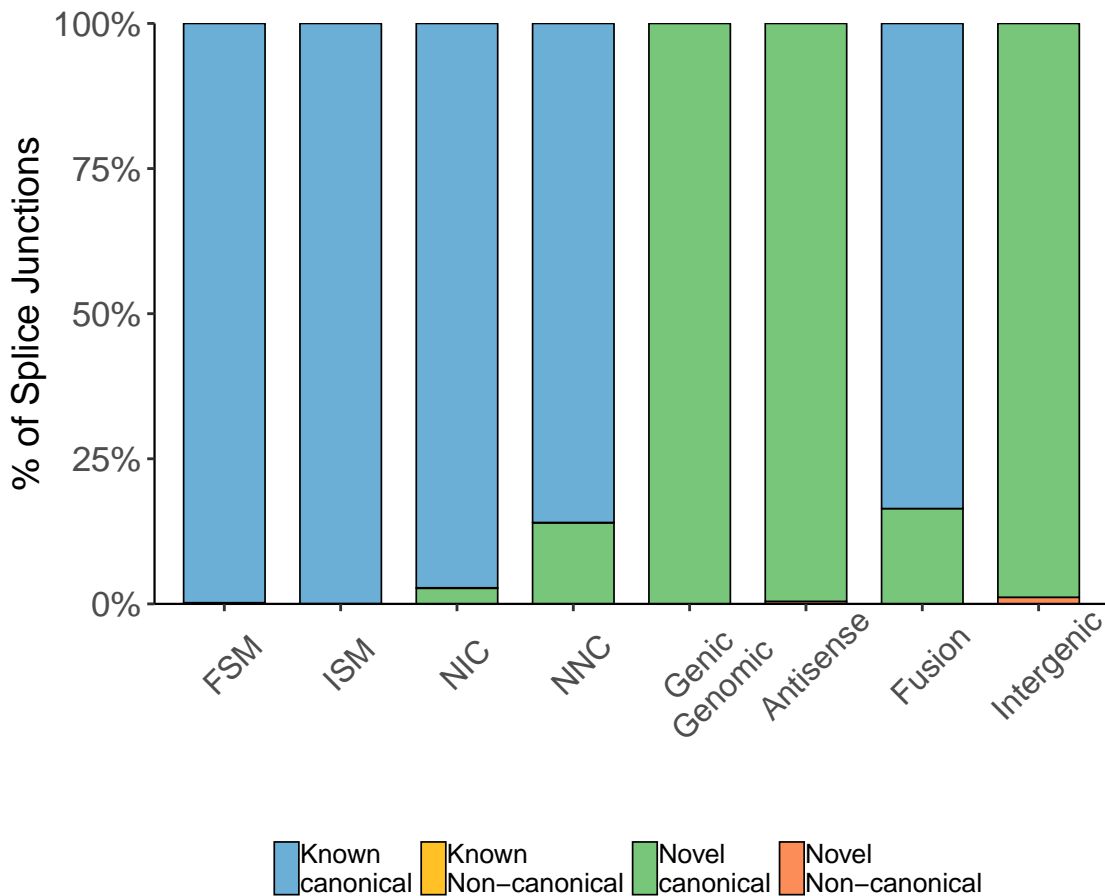
Exon Count Distribution of Matched Reference Transcripts

Applicable only to FSM and ISM categories

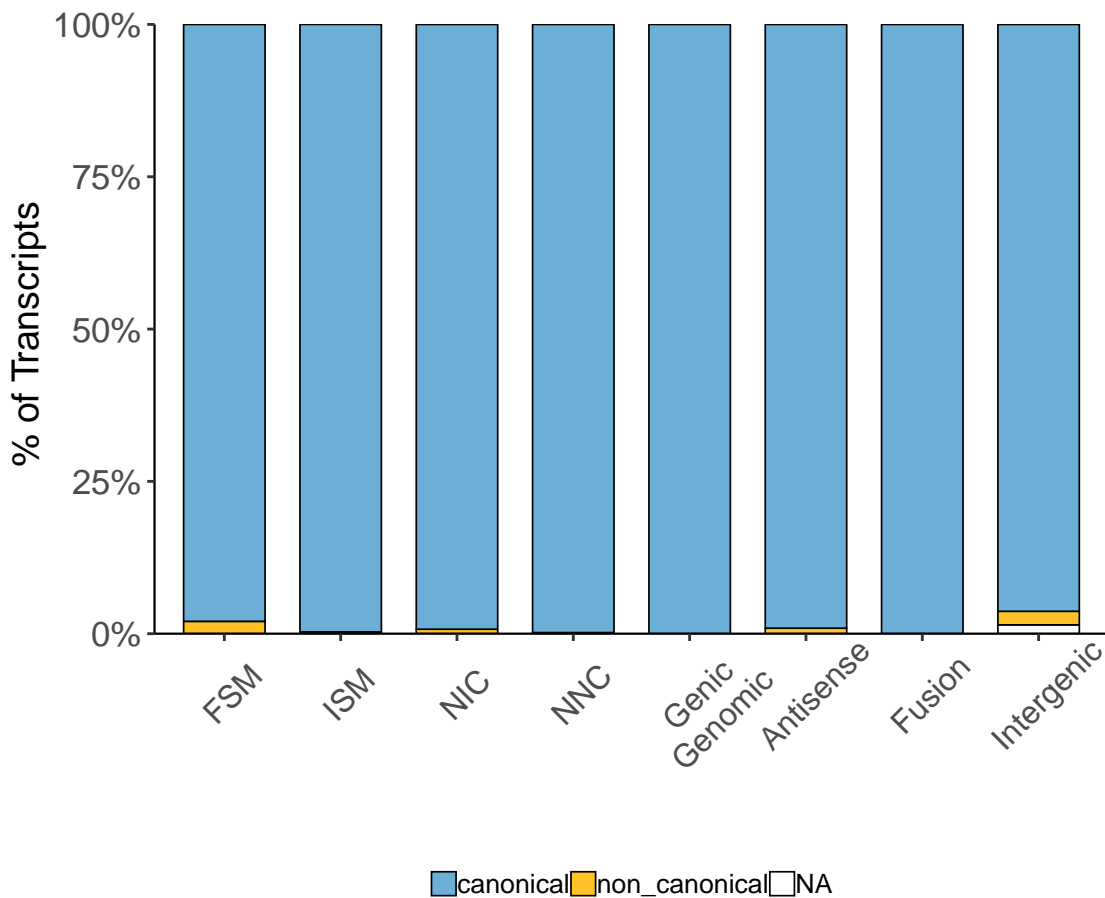


Splice Junction Characterization

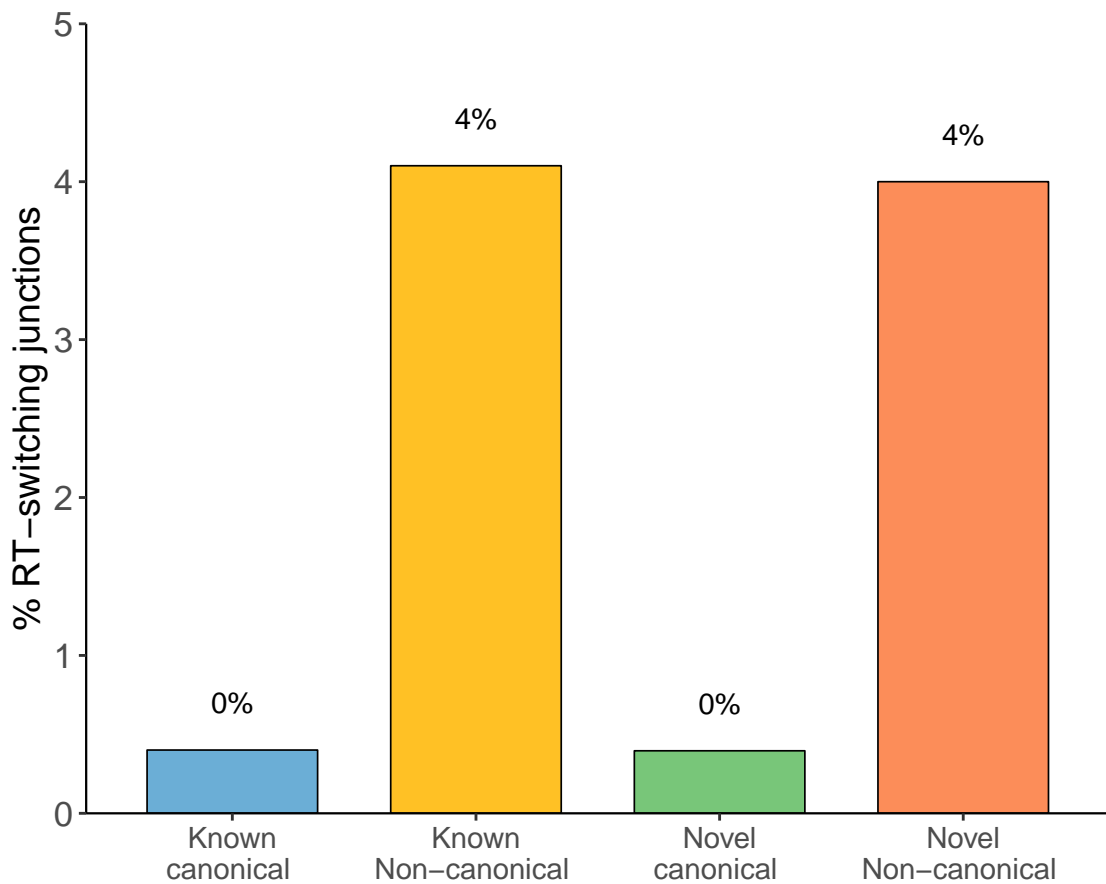
Distribution of Splice Junctions by Structural Classification



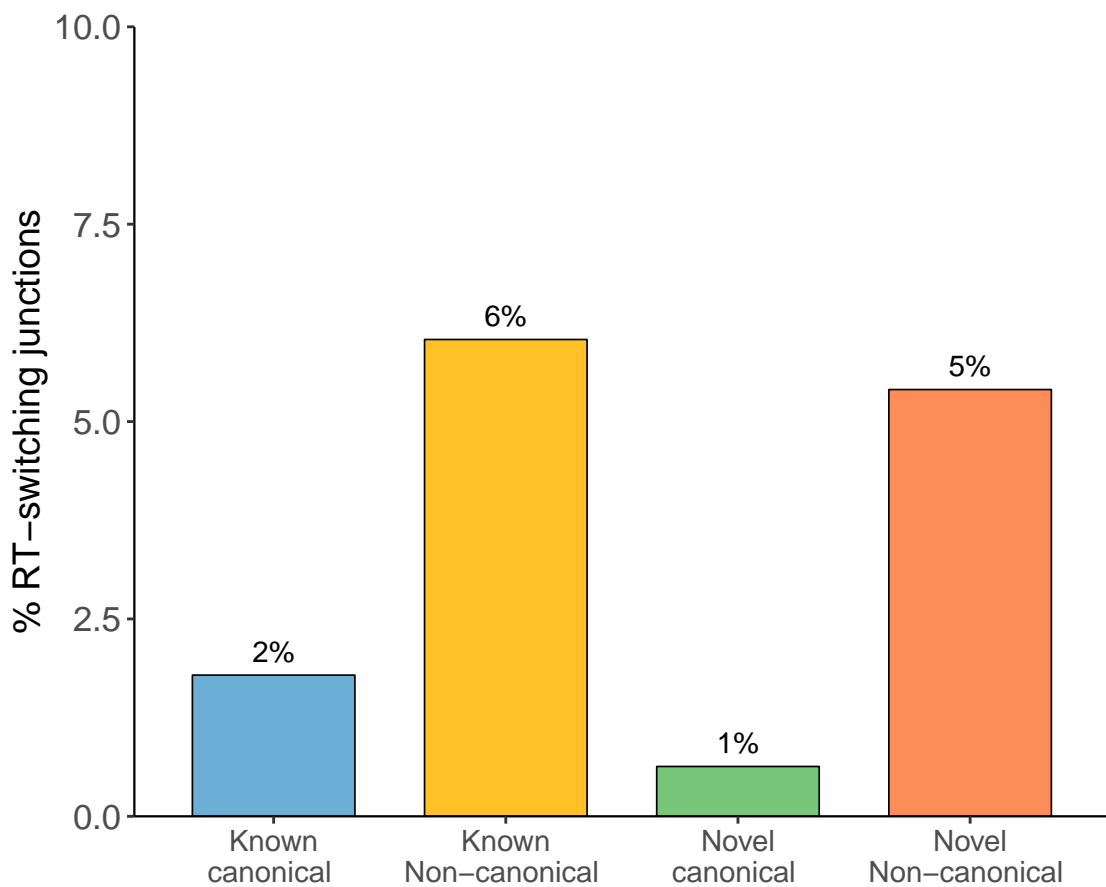
Distribution of Transcripts by Splice Junctions



RT-switching, all junctions



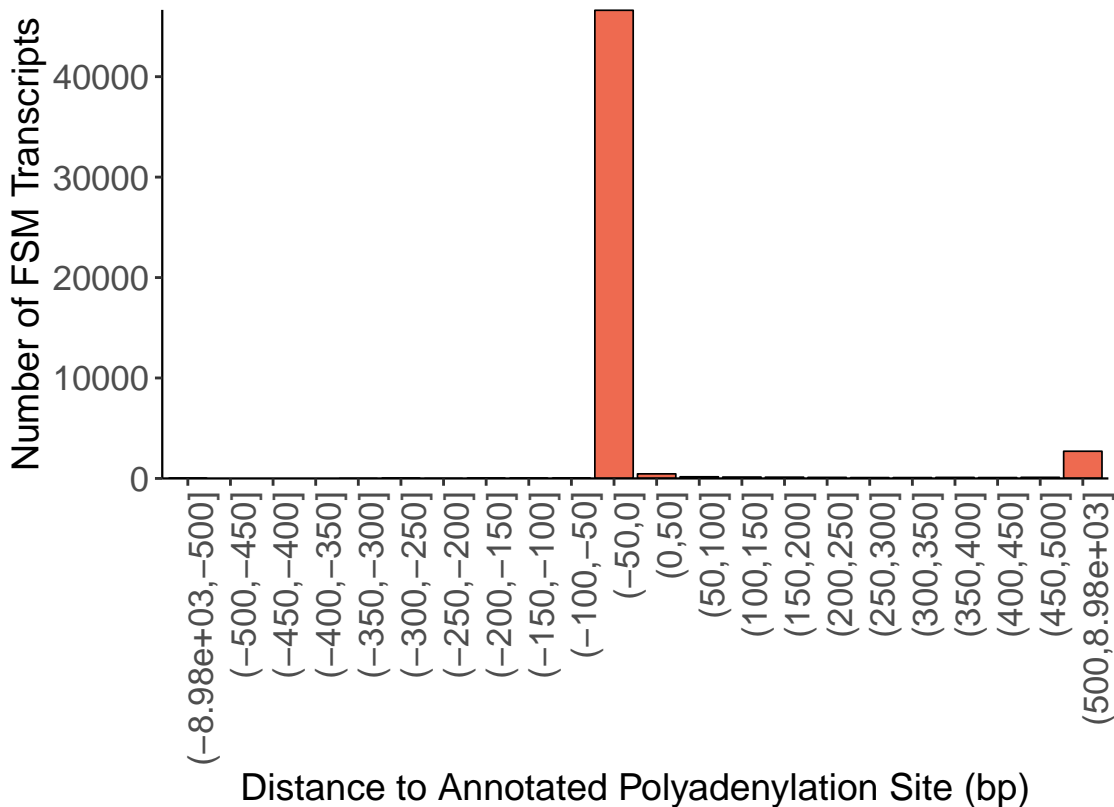
RT-switching, unique junctions



Comparison with Annotated TSS and PolyA Sites

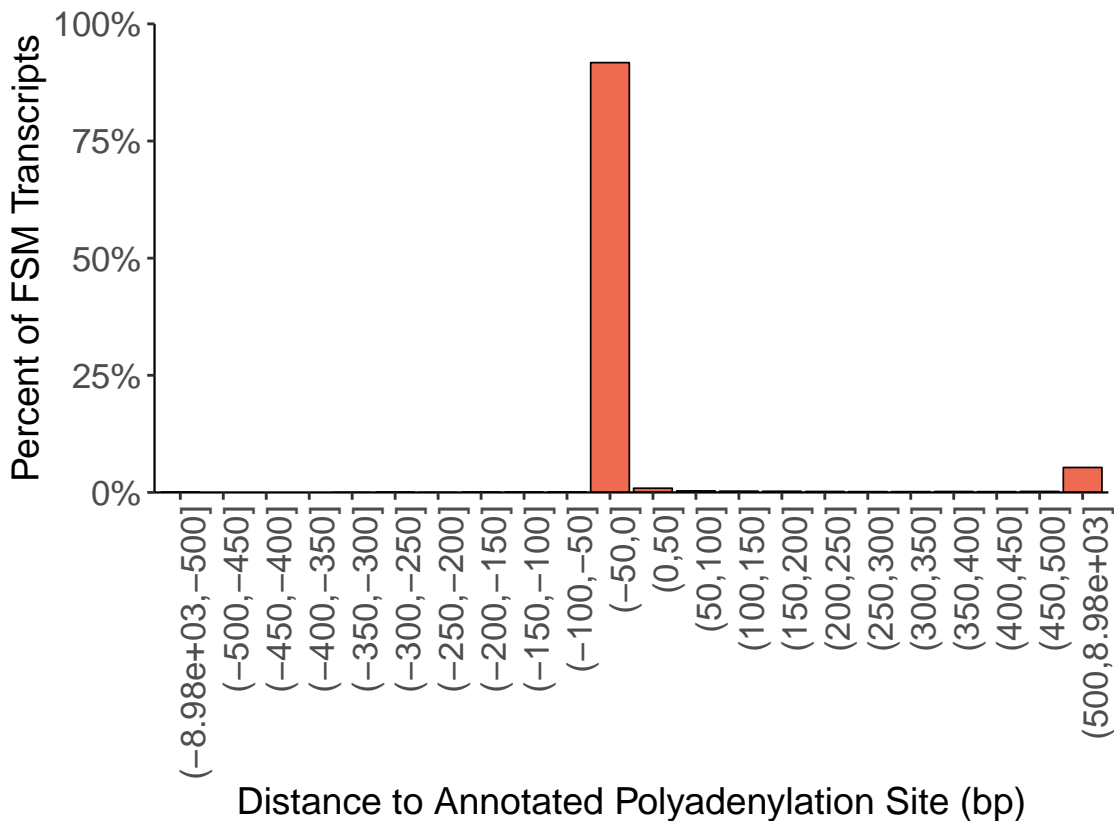
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



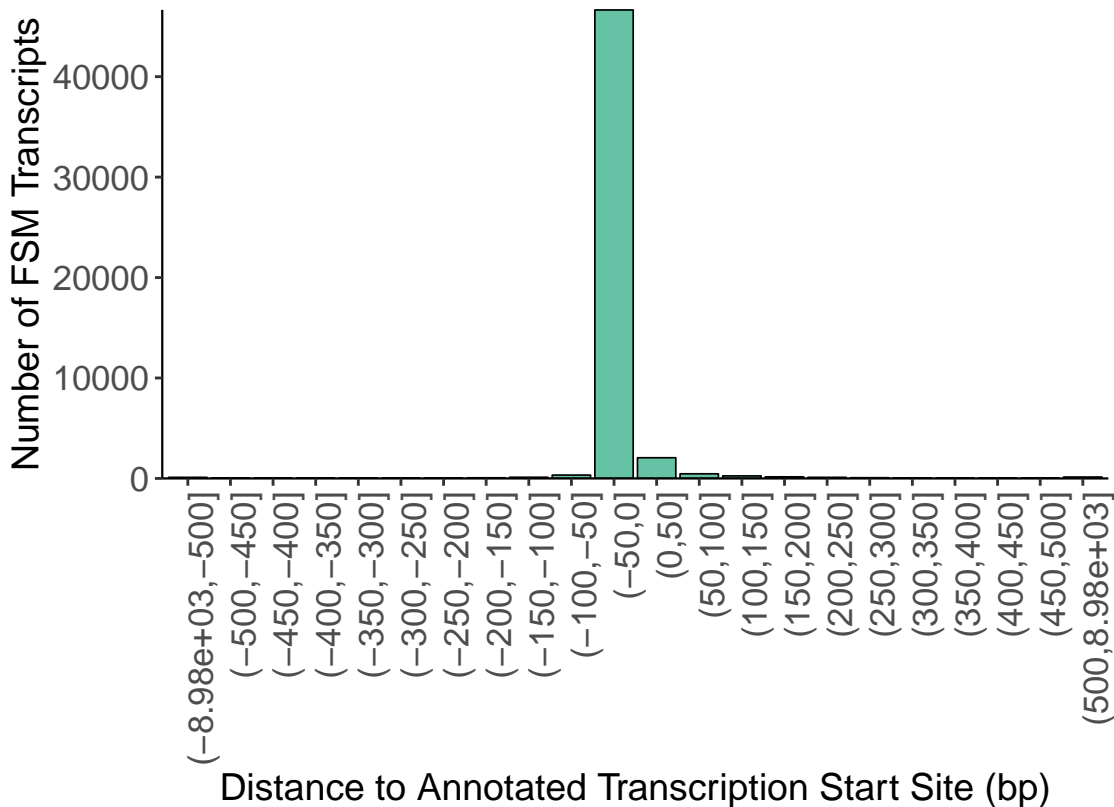
Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site



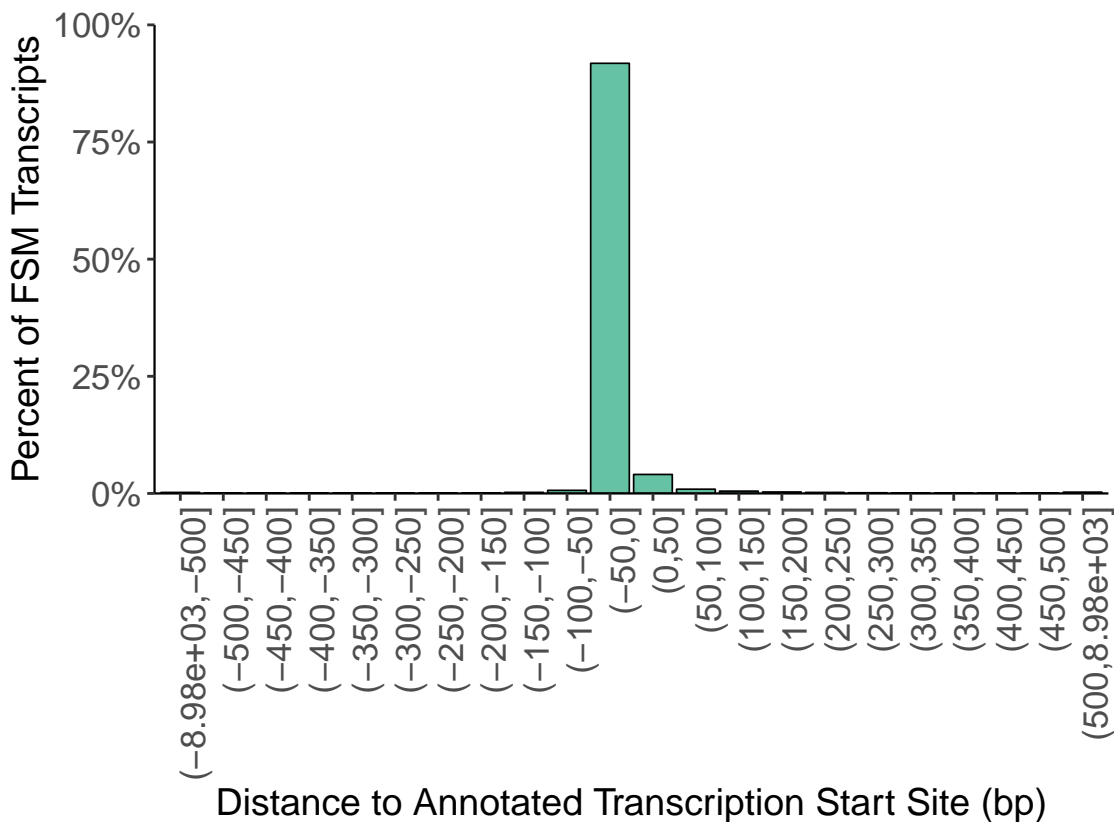
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



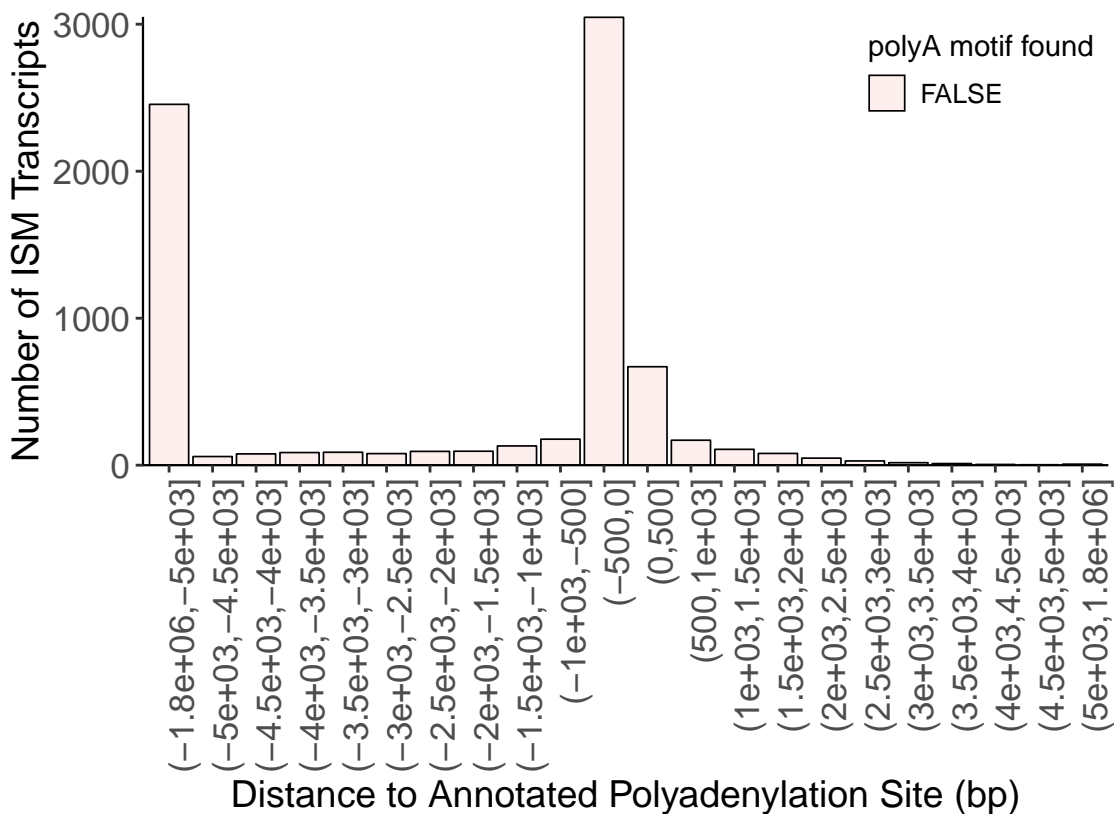
Distance to Annotated Transcription Start Site, FSM only

Negative values indicate downstream of annotated TSS



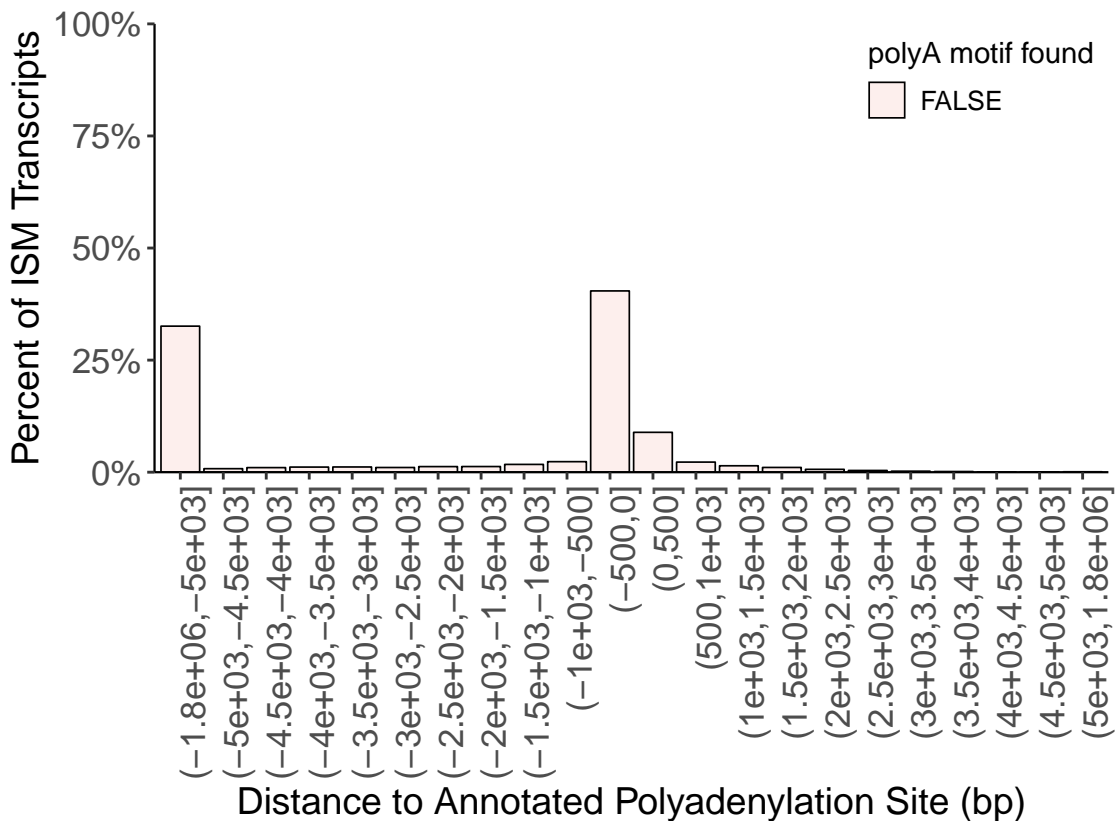
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



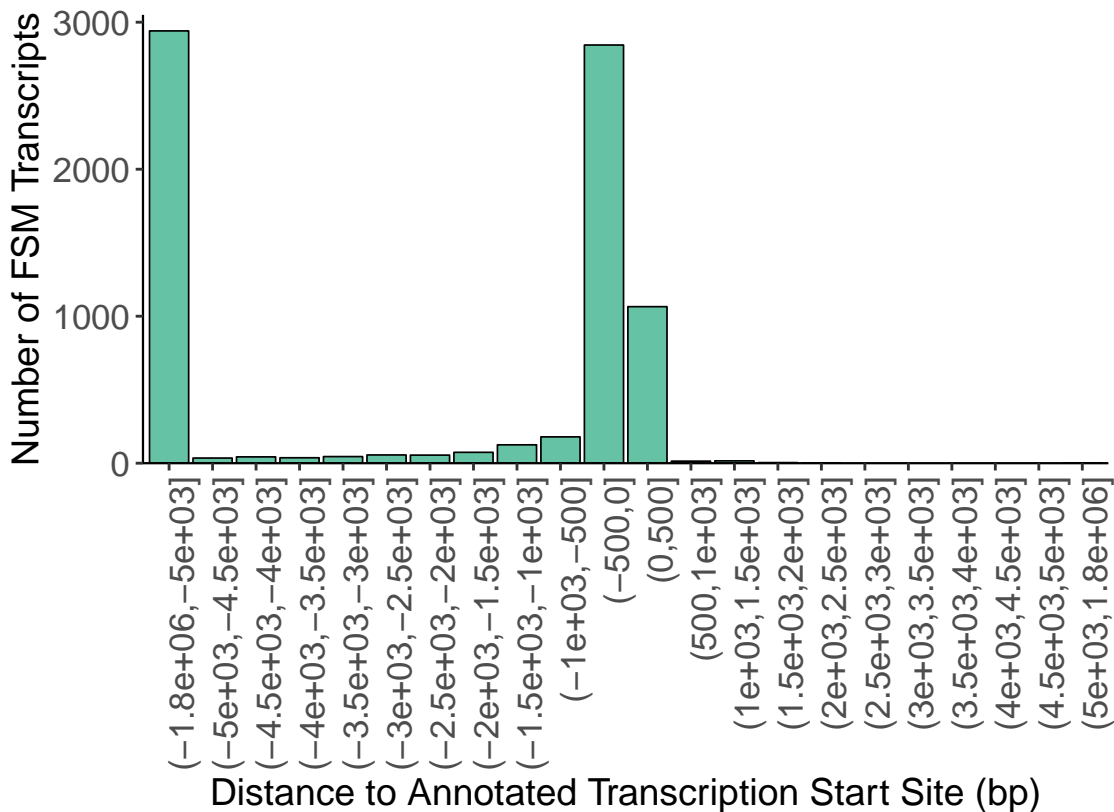
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



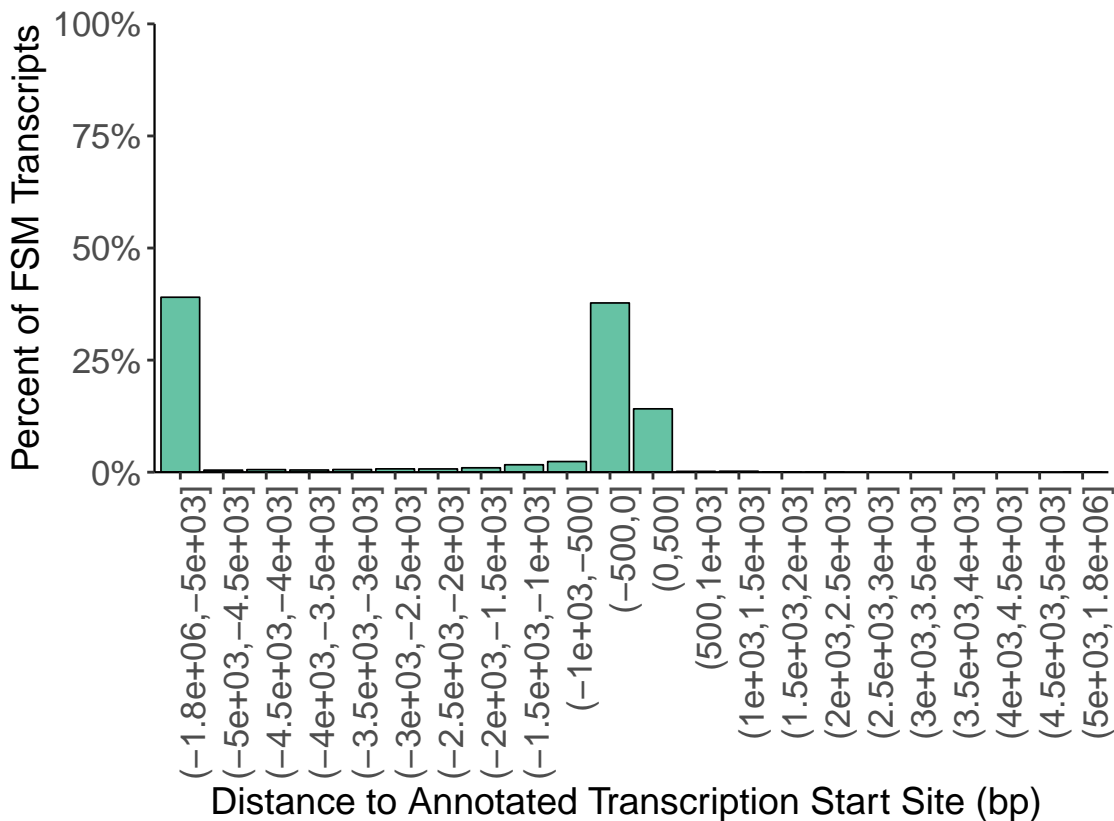
Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS

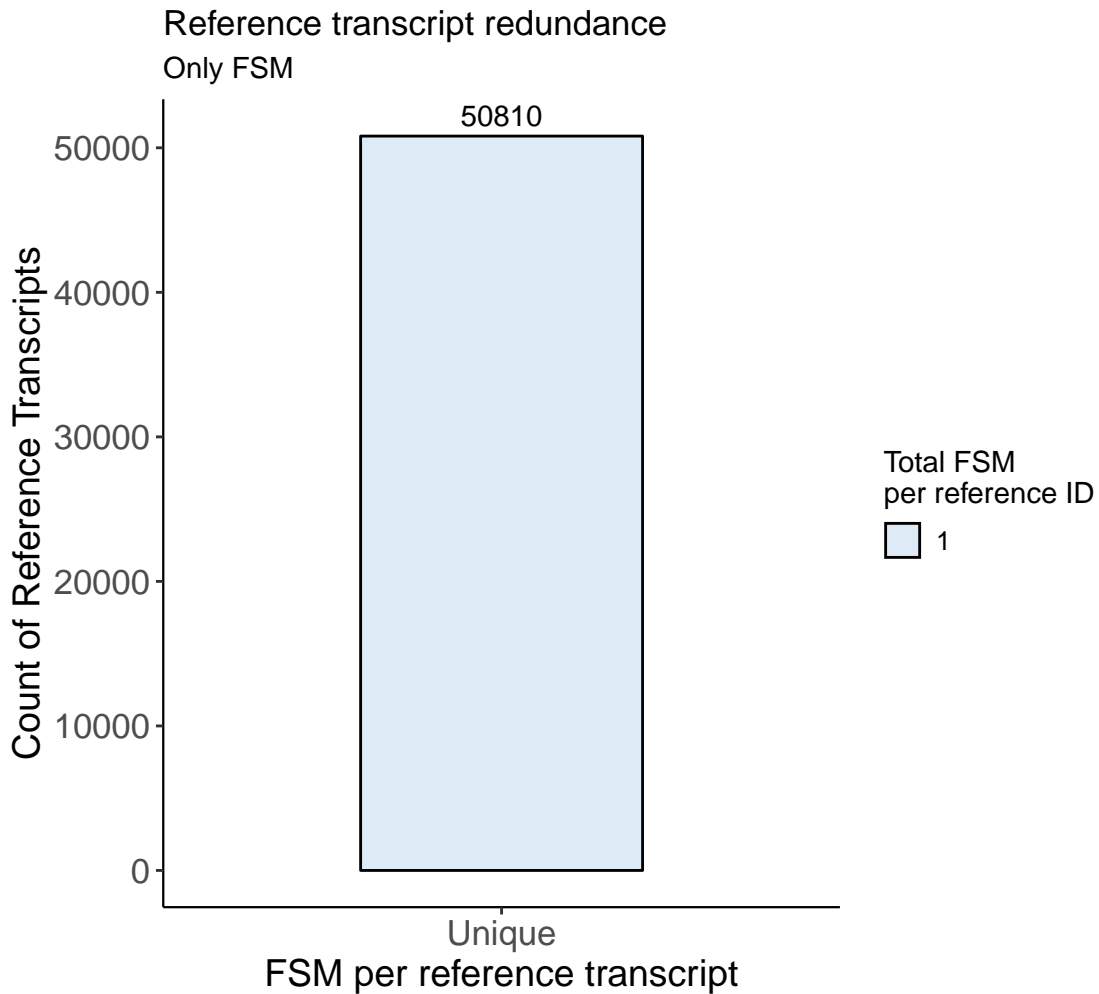


Distance to Annotated Transcription Start Site, ISM only

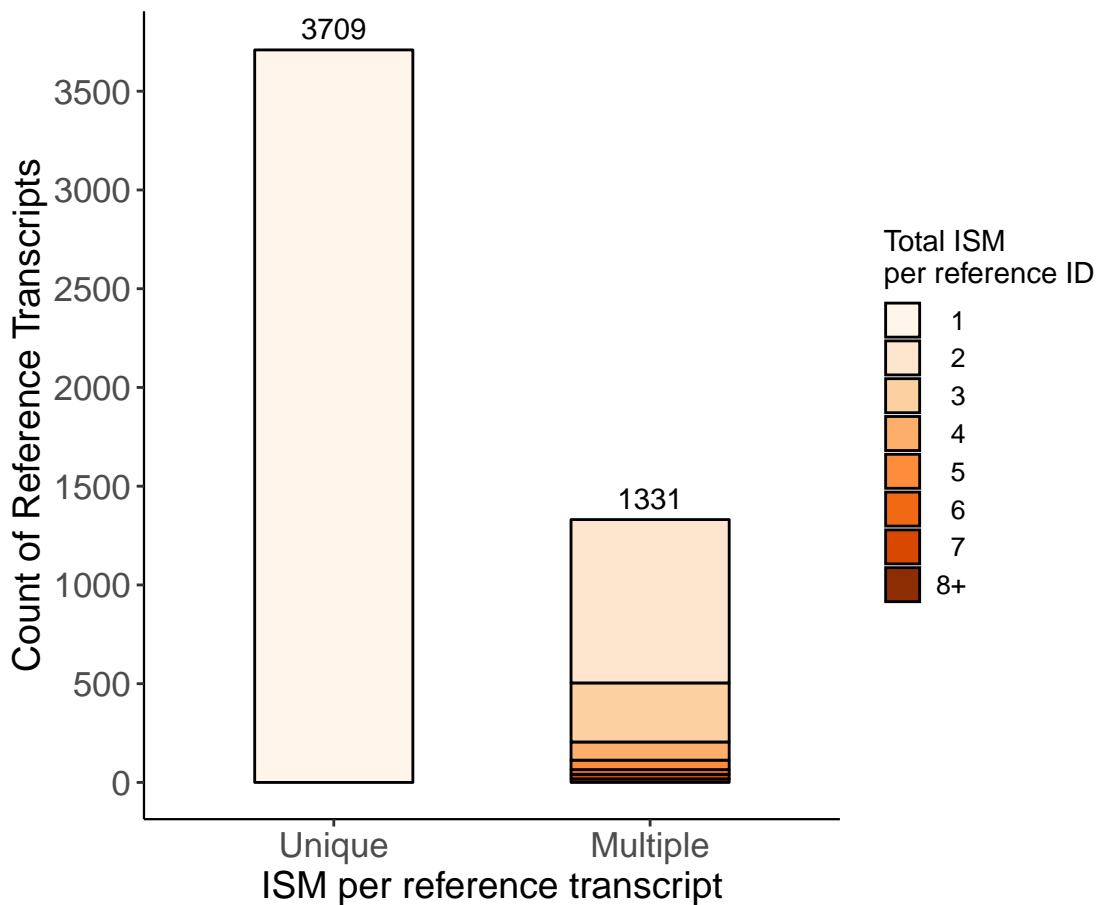
Negative values indicate downstream of annotated TSS

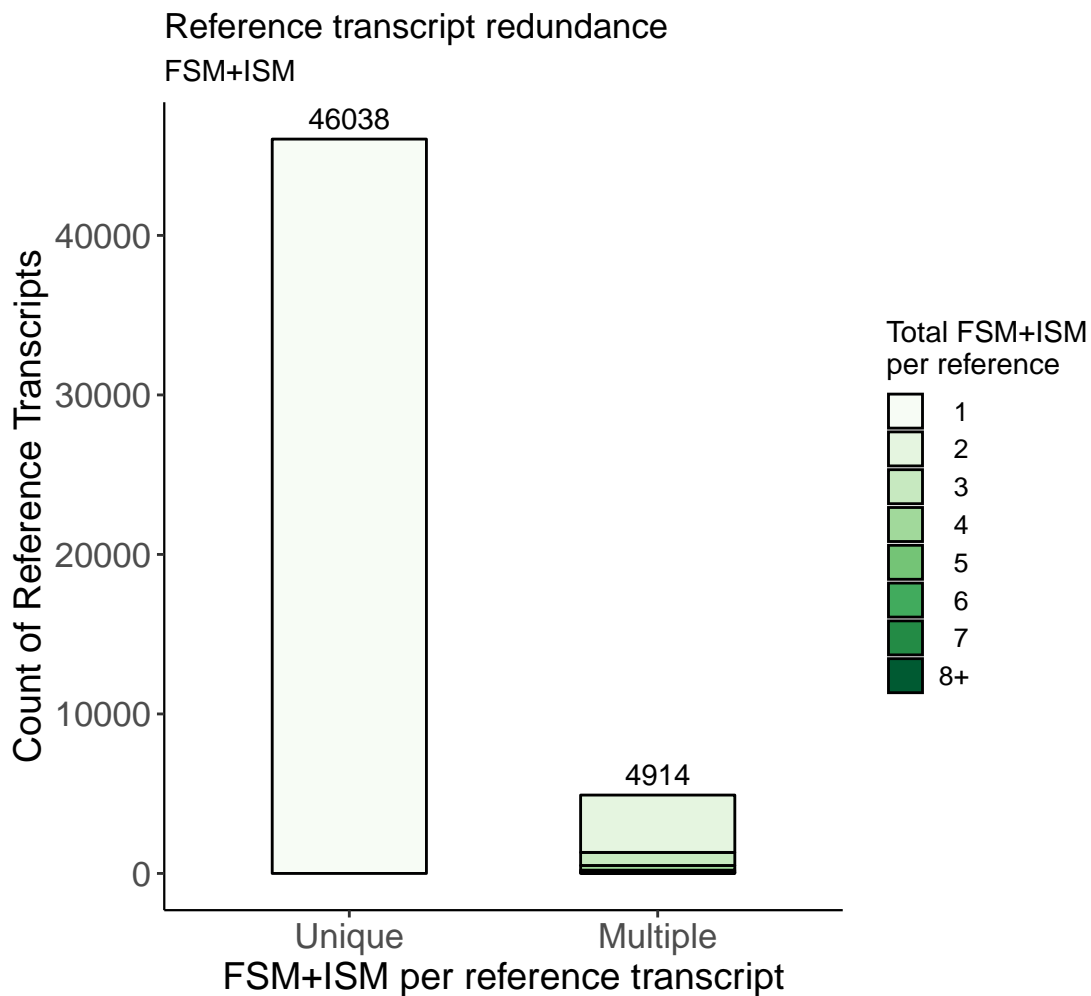


*Accumulation of FSM and ISM
to the same reference transcript*



Reference transcript redundance
Only ISM

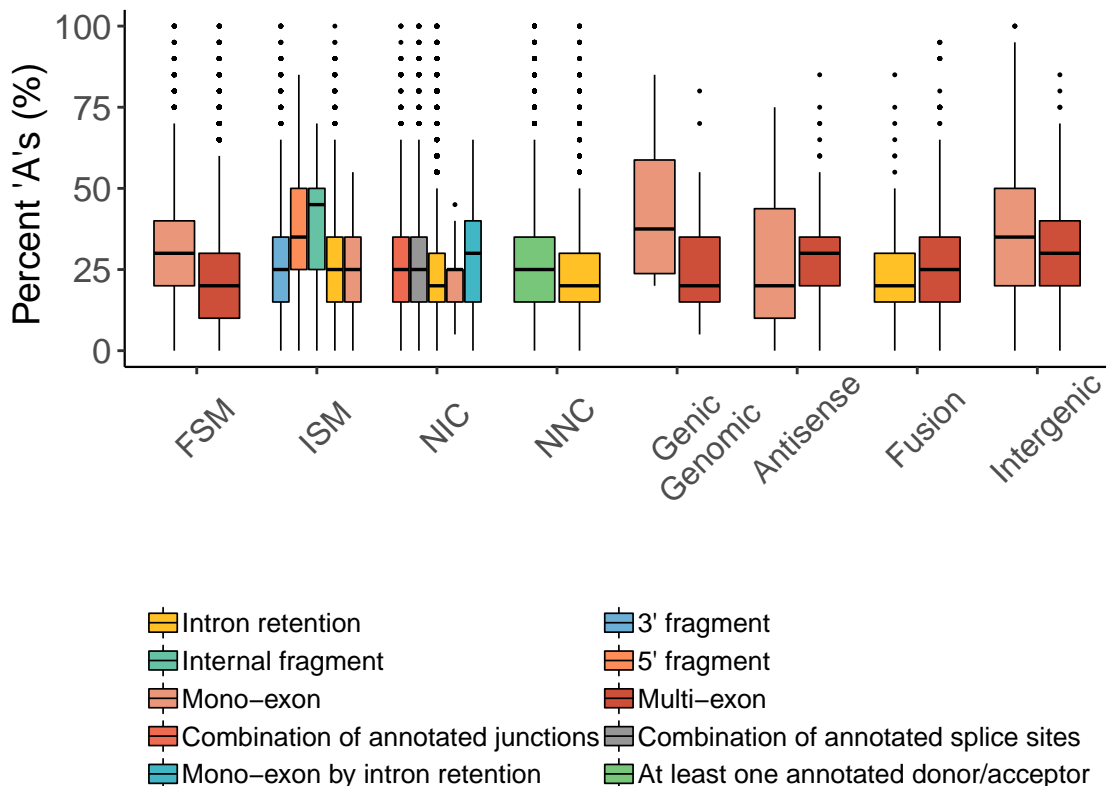




Intra-Priming Quality Check

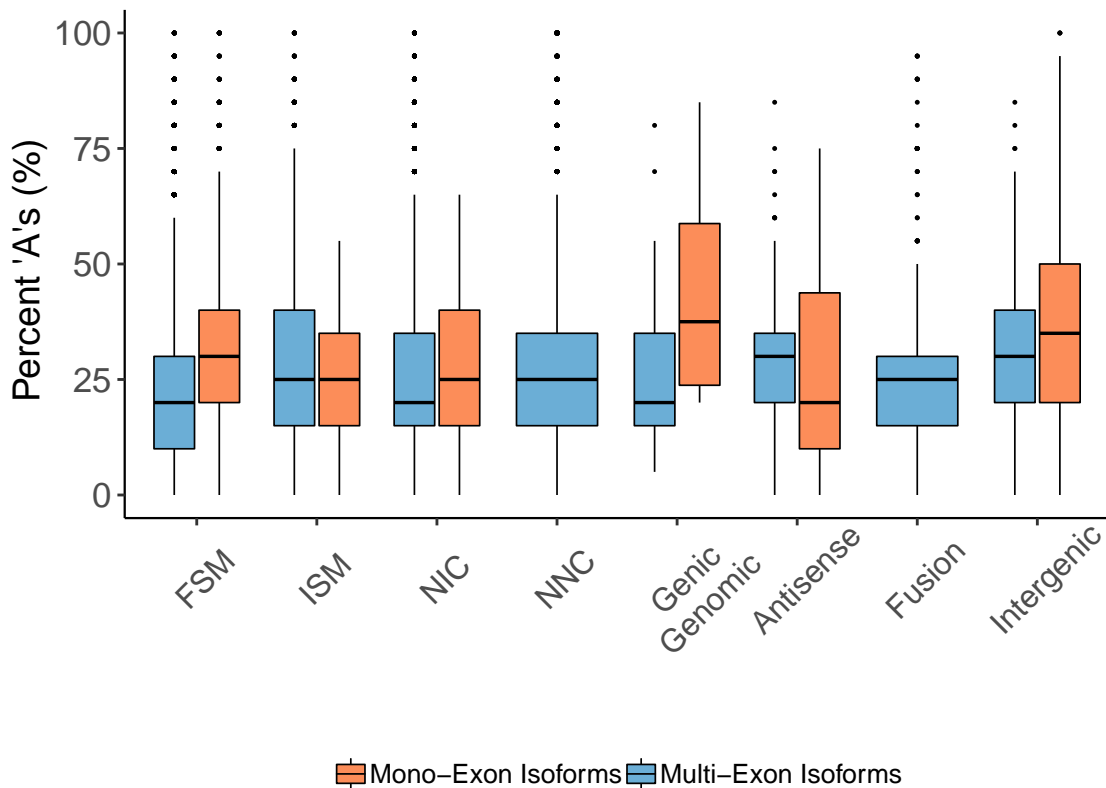
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



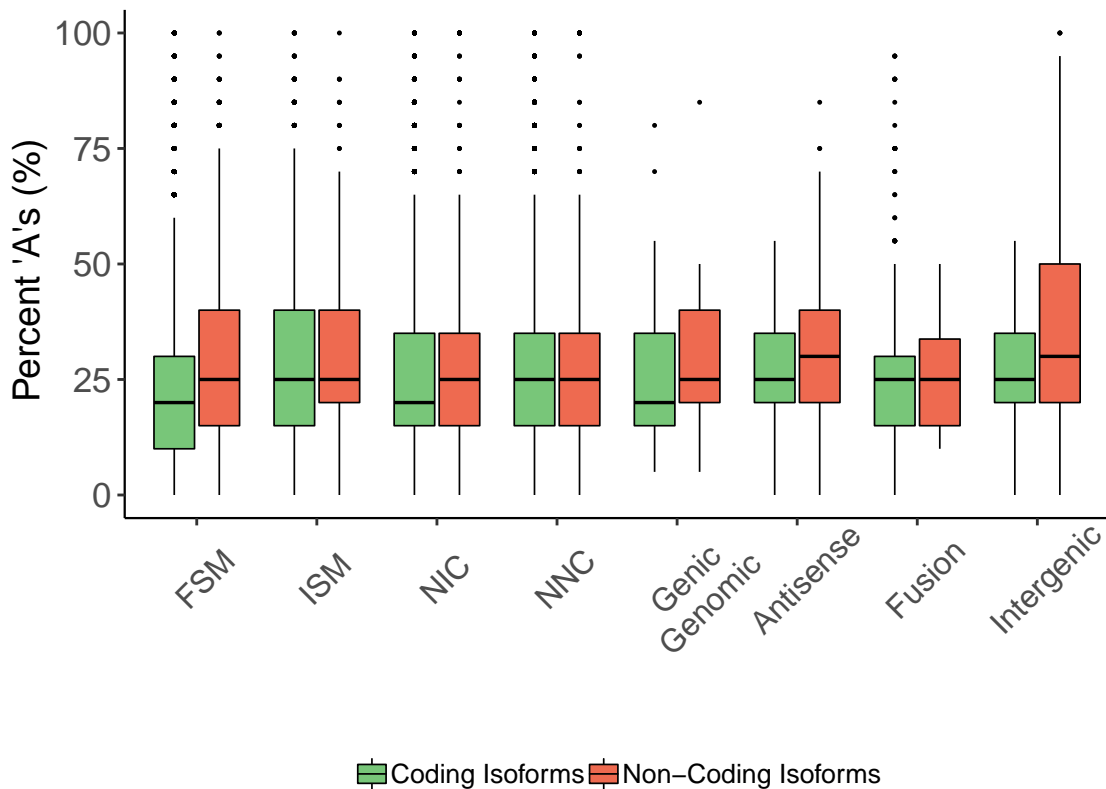
Possible Intra-Priming, Mono- vs Multi-Exon

Percent of genomic 'A's in downstream 20 bp



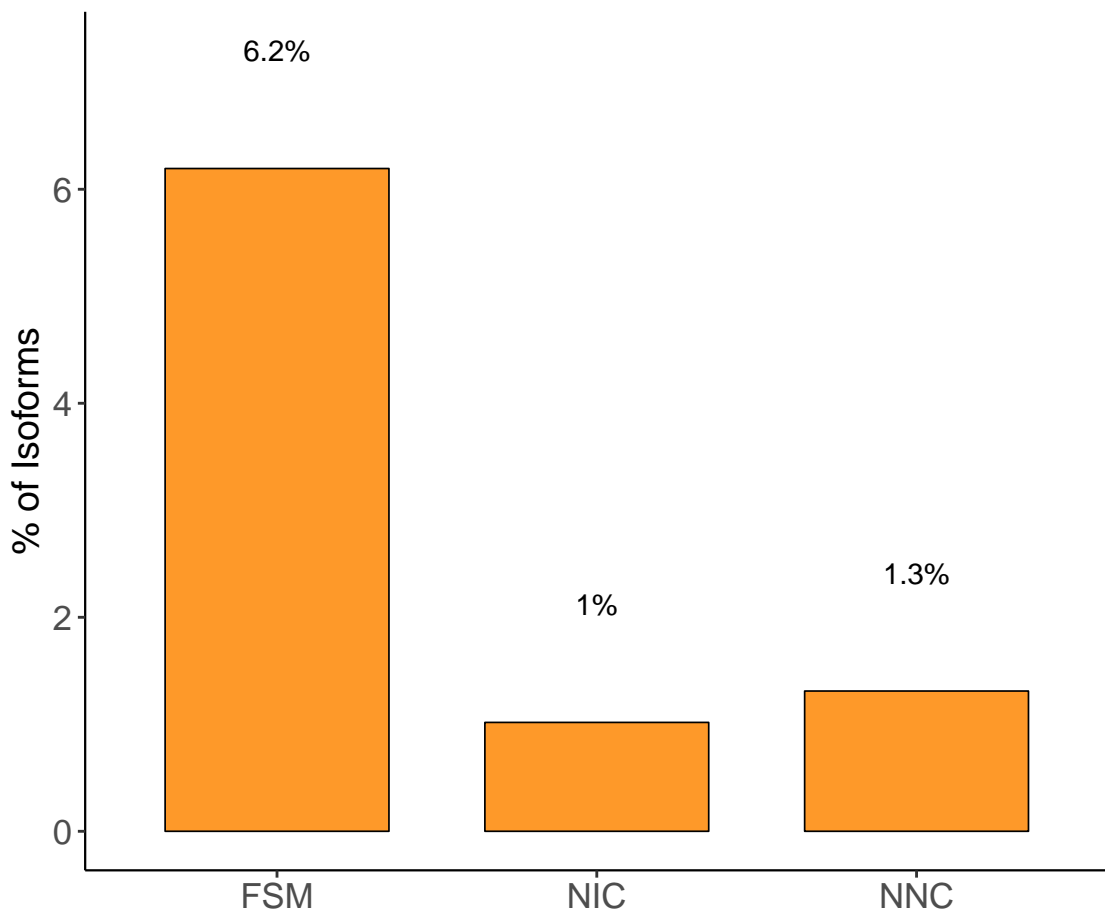
Possible Intra-Priming, Coding vs Non-Coding

Percent of genomic 'A's in downstream 20 bp

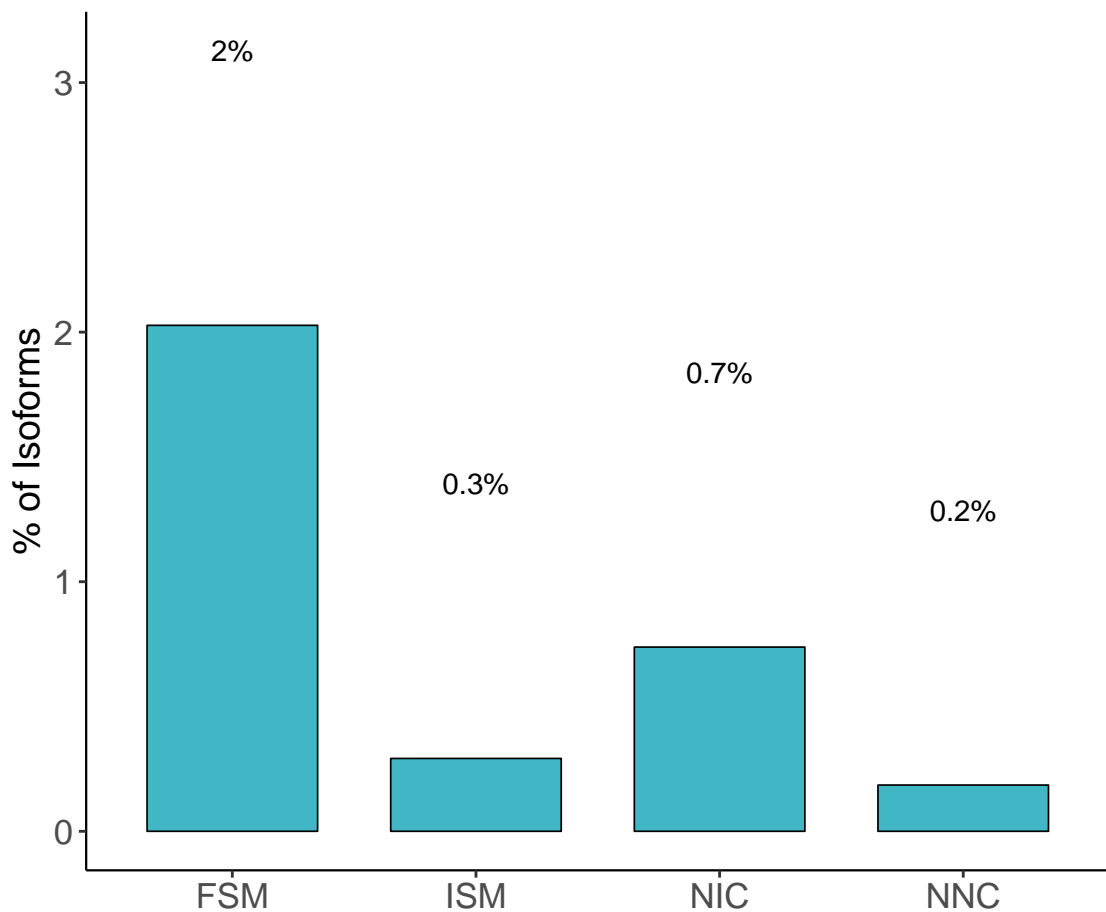


Quality Controls

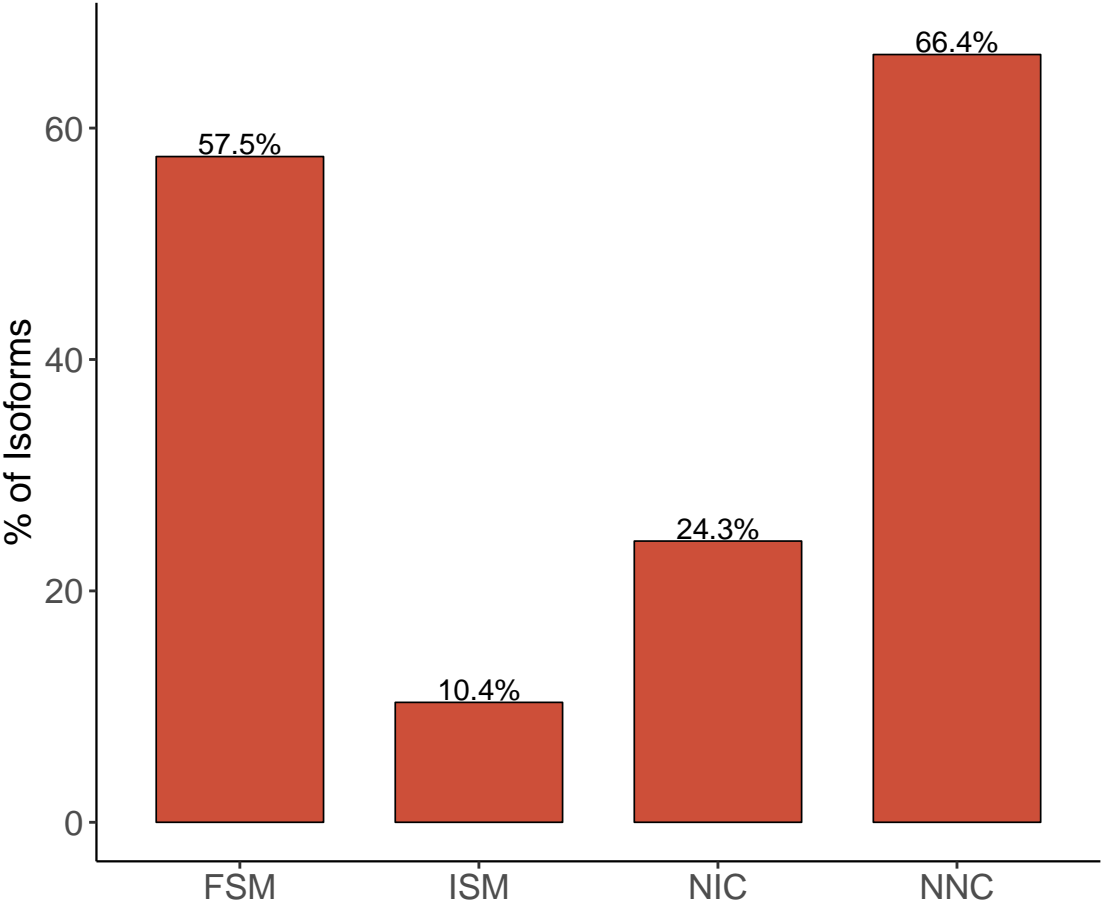
Incidence of RT-switching



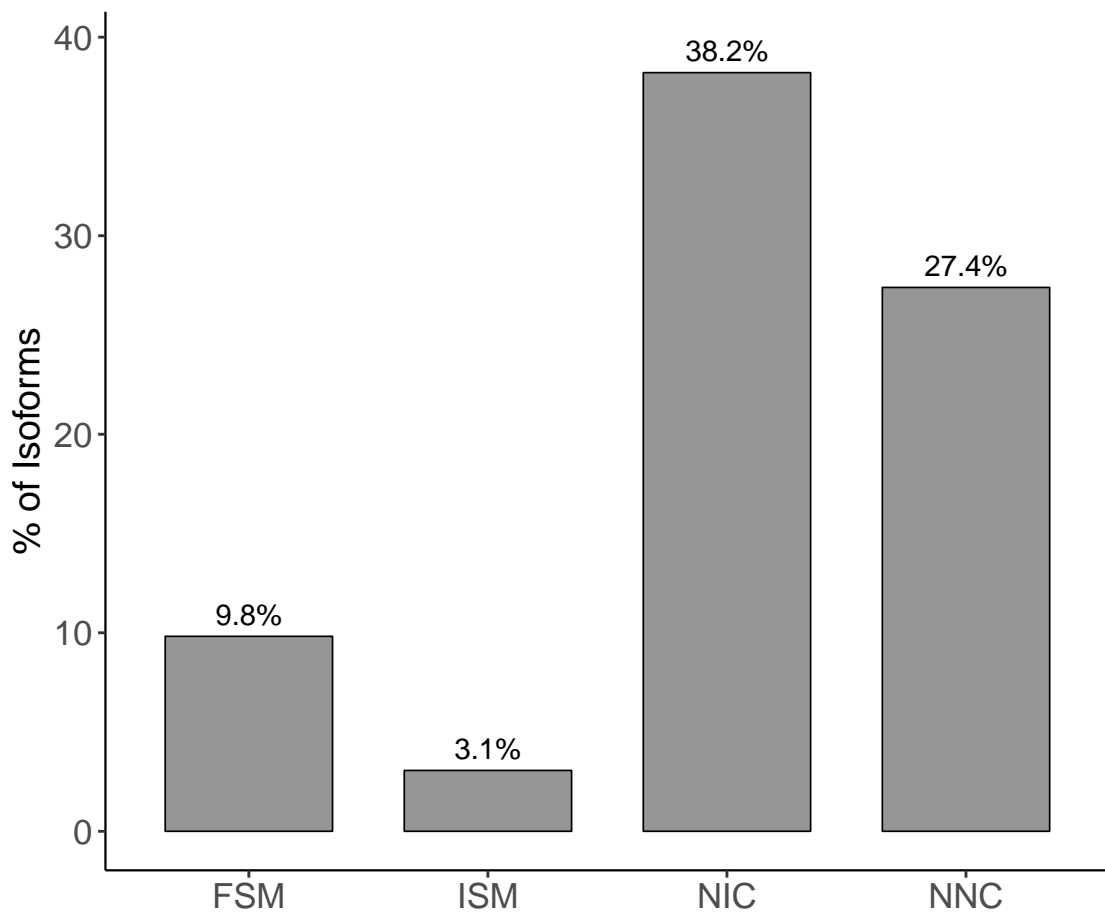
Incidence of Non-Canonical Junctions



Incidence of SJ without SR coverage Junctions



Incidence of NMD by structural category



Quality control attributes across structural categories

