SQANTI report

Unique Genes: 9264
Unique Isoforms: 19448

Characterization of transcripts
based on splice junctions

Category	# Isoforms
FSM	12713
ISM	1574
NIC	3122
NNC	1473
Genic Genomic	107
Antisense	396
Fusion	0
Intergenic	63
Genic Intron	0

Gene classification

Category	# Genes
Annotated Genes	9163
Novel Genes	101

Splice Junction Classification

Category	# SJs	Percent
Known canonical	85667	98.70
Known Non−canonical	130	0.15
Novel canonical	599	0.69
Novel Non−canonical	400	0.46

Gene Characterization

Number of Isoforms per Gene
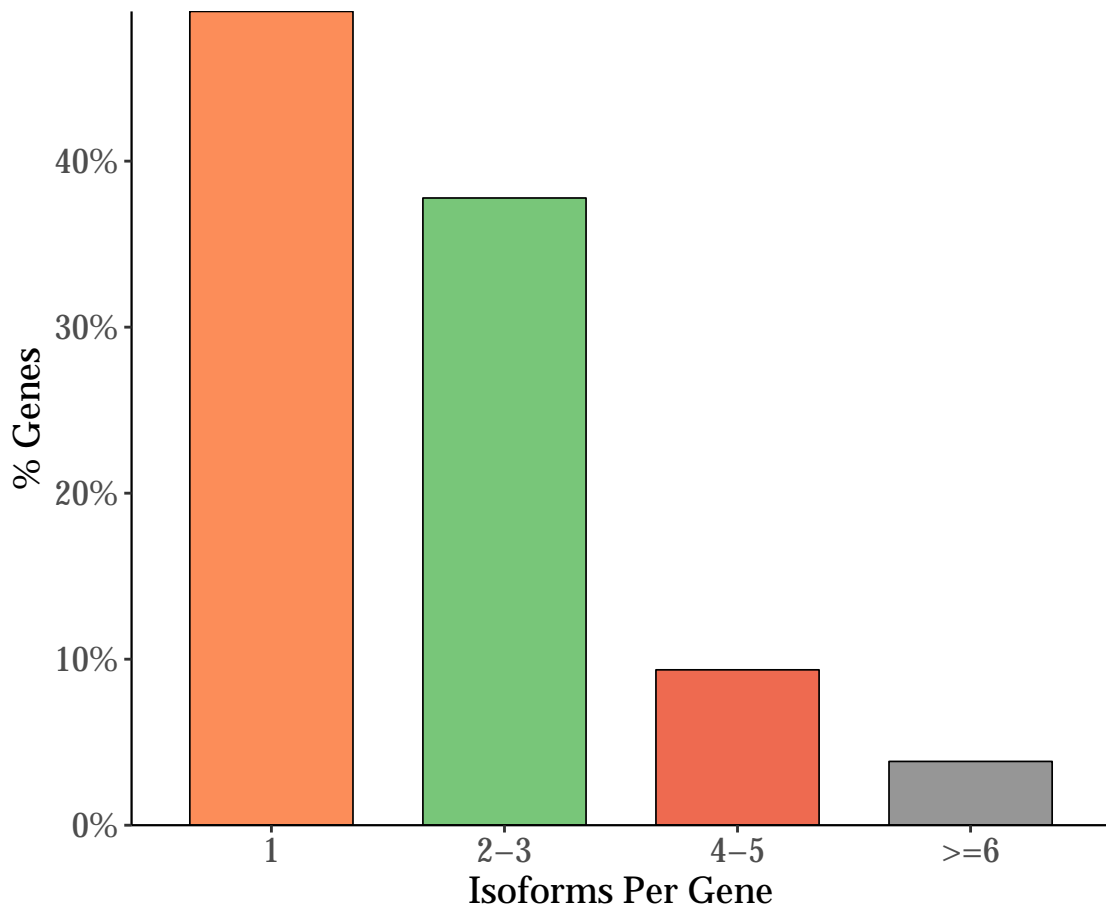
Number of Isoforms per Gene, Novel vs Known Geness

% Genes

Isoforms Per Gene ■ 1 ■ 2−3 ■ 4−5 ■ >=6
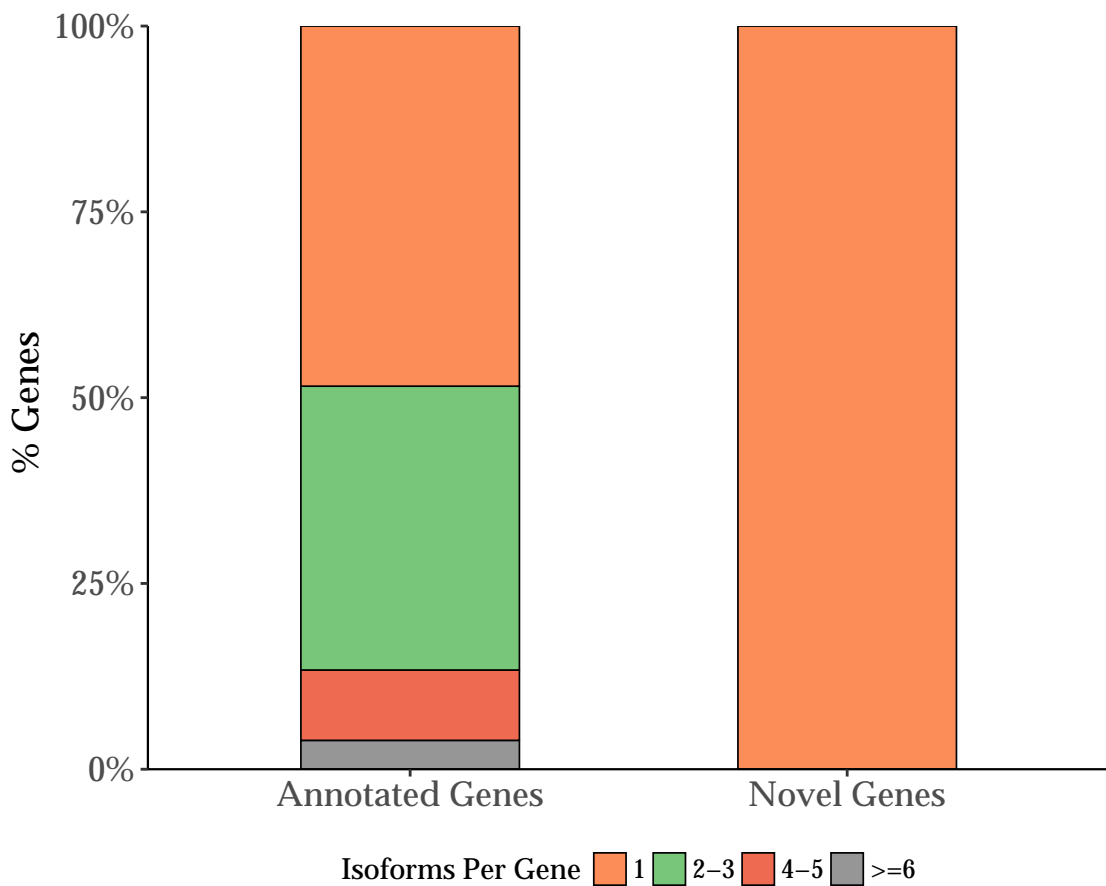
Distribution of Mono− vs Multi−Exon Transcripts

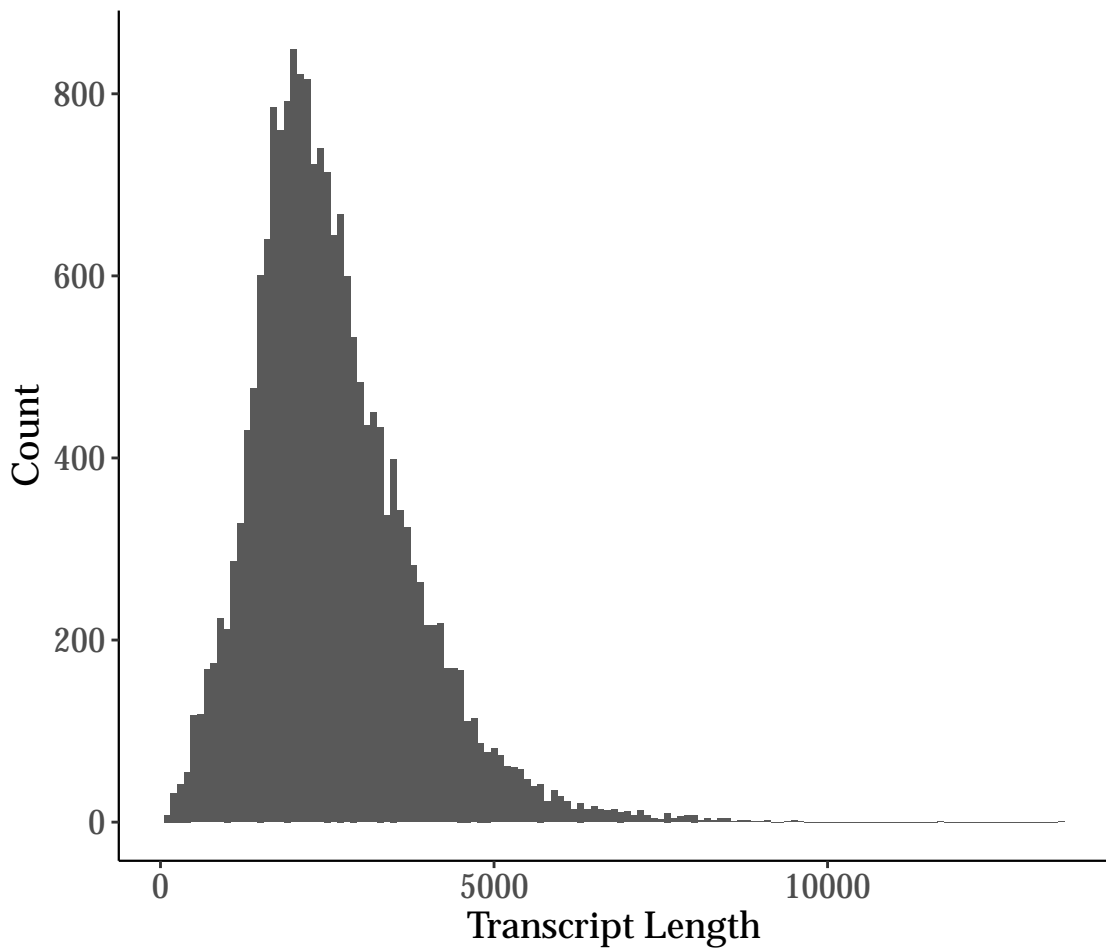Classifications by Transcript Length
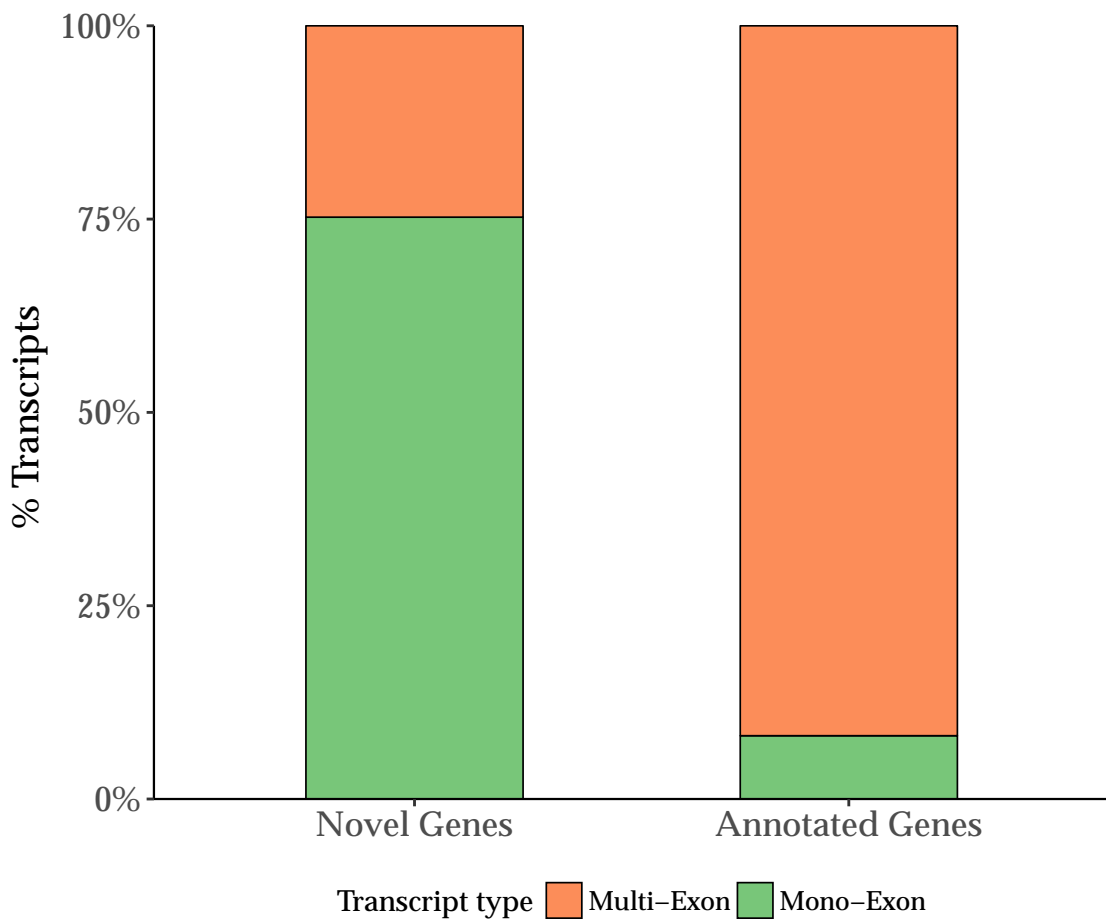
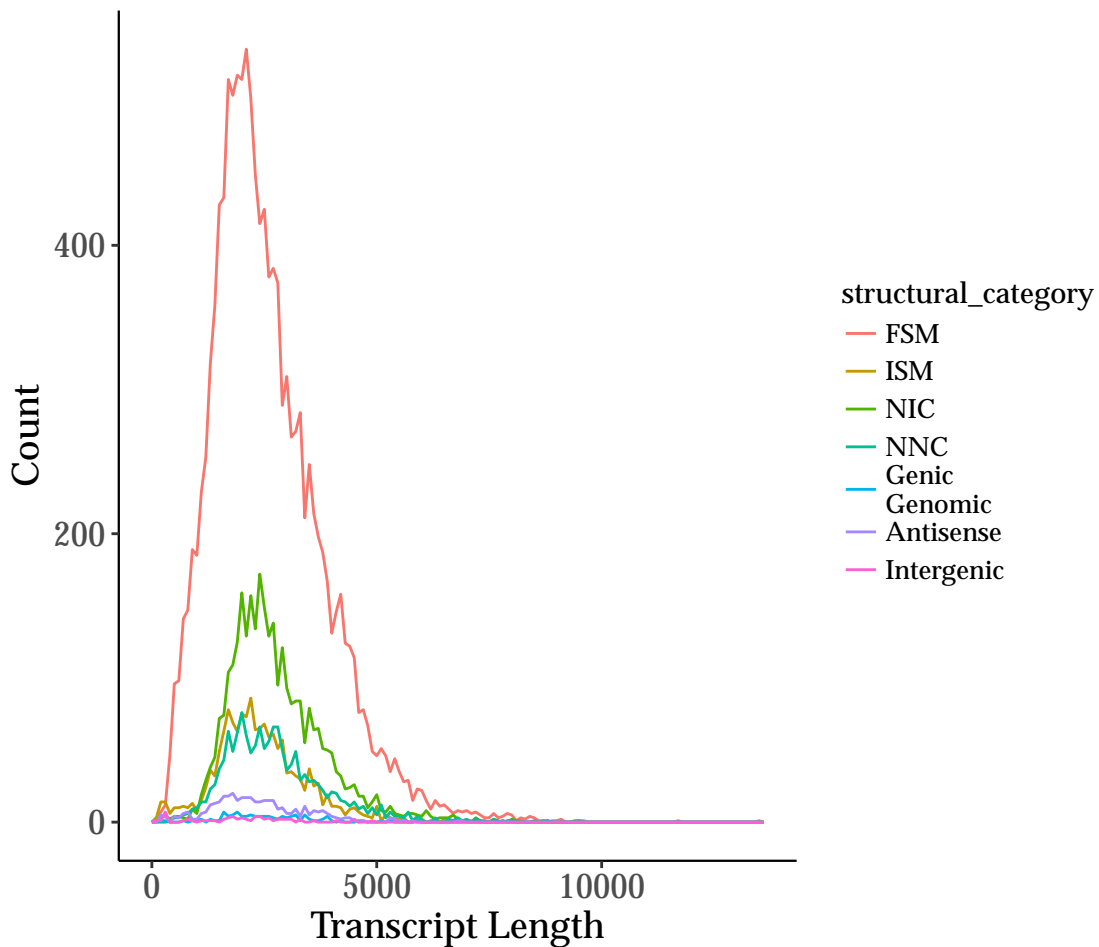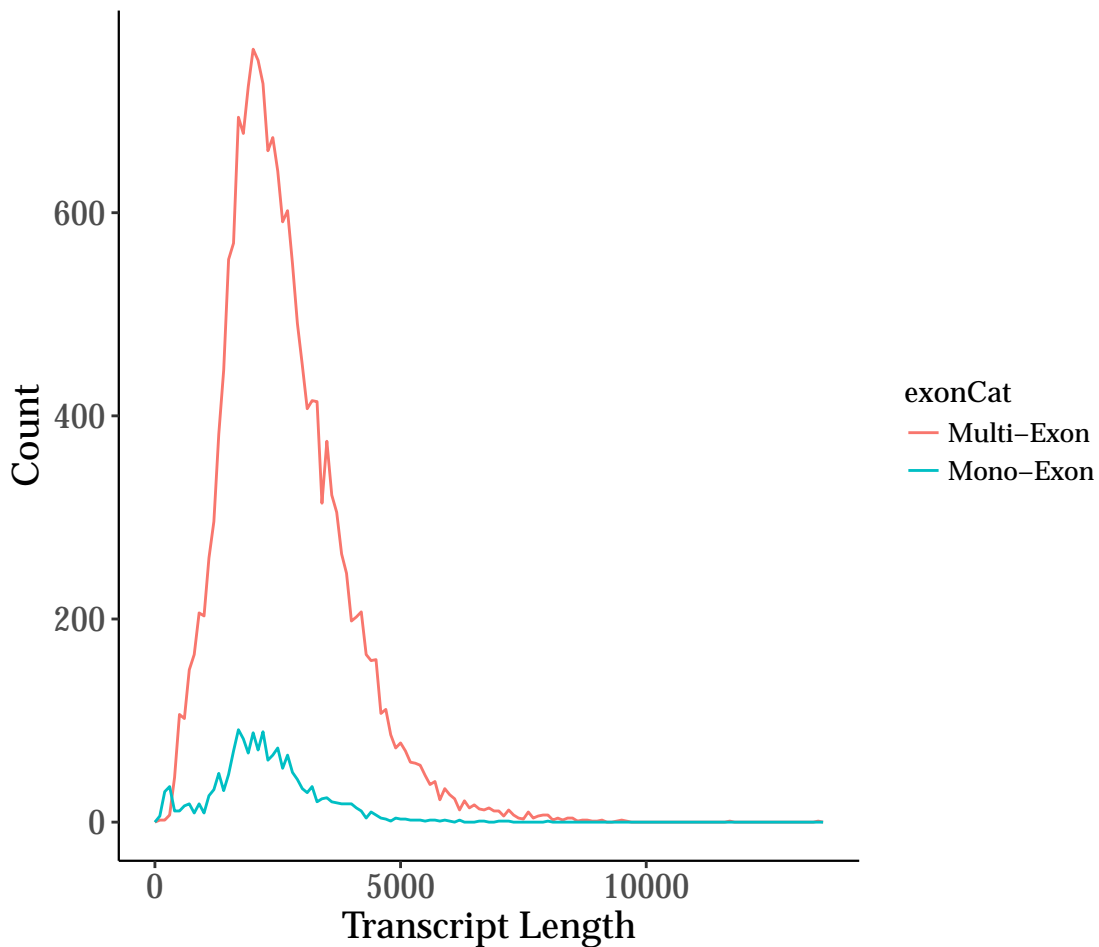Classifications by Transcript Length, normalized
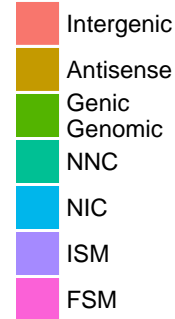
Transcript Lengths, all transcripts
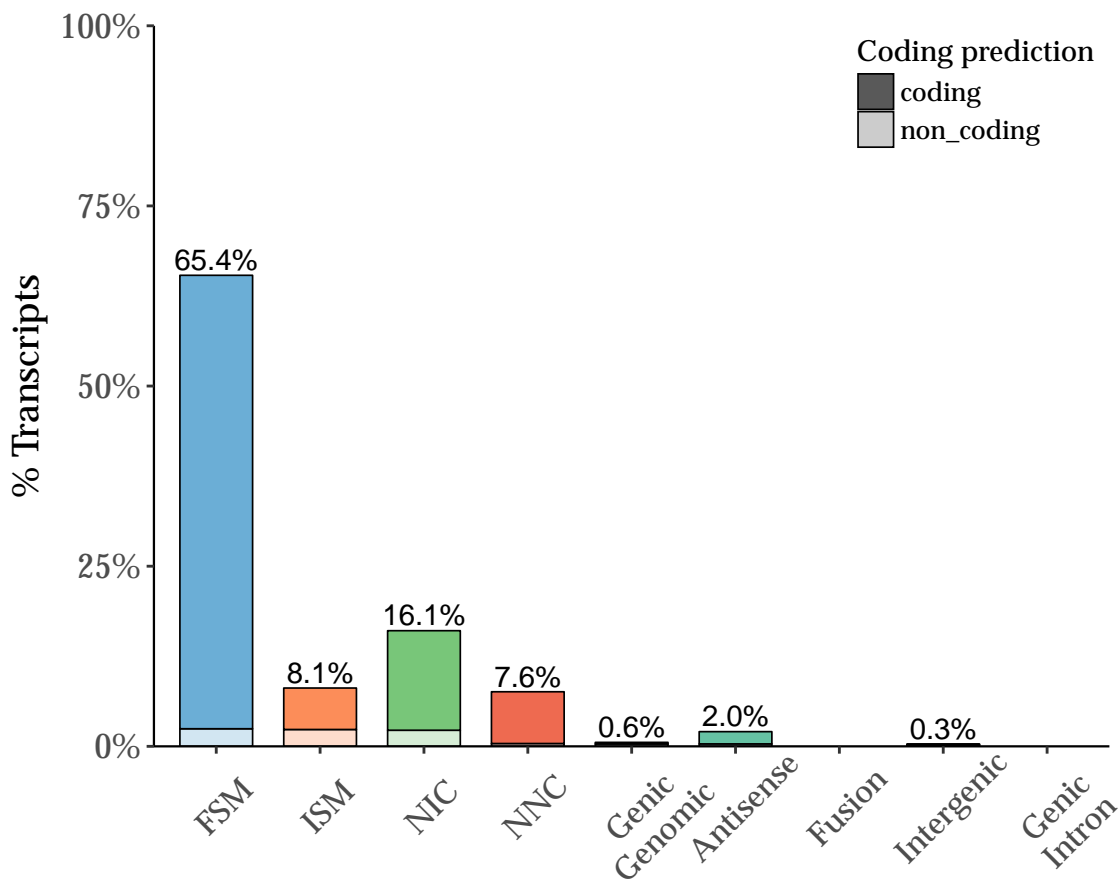
Transcript Lengths, by structural category
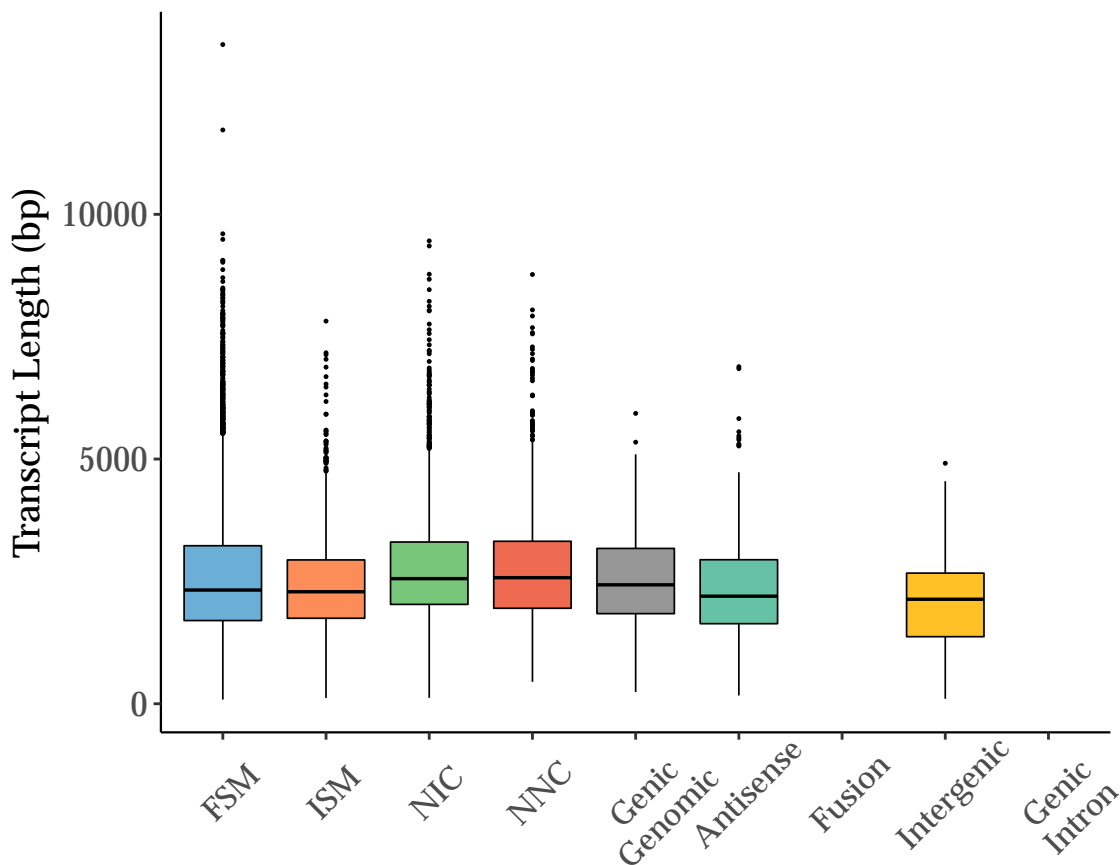
Transcript Lengths, Mono− vs Multi−Exons
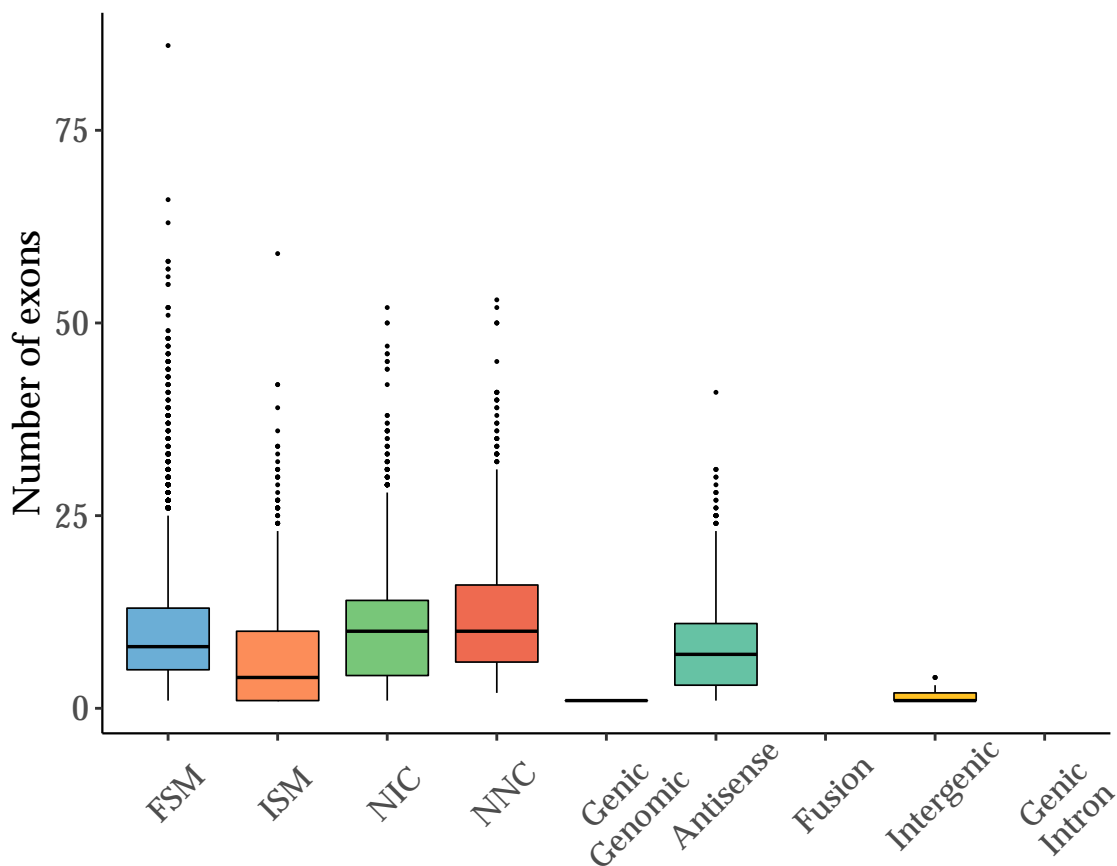
*Structrual Isoform Characterization
by Splice Junctions*

Isoform distribution across structural categories
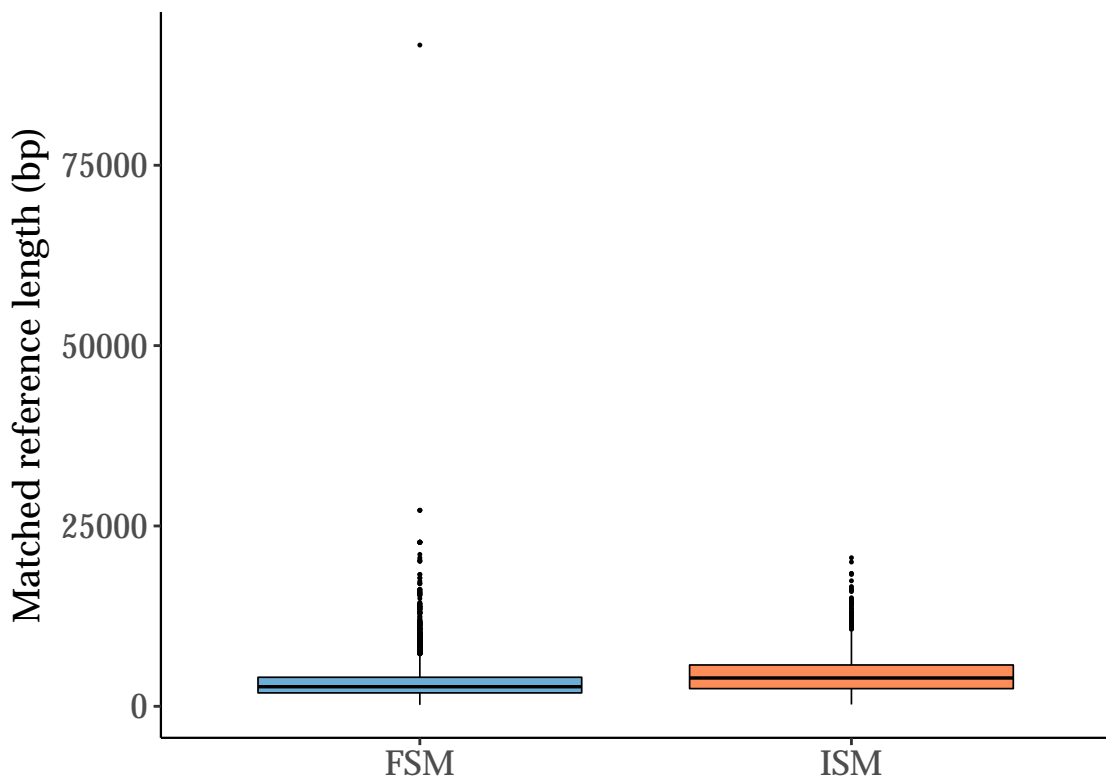
Transcript Lengths by Structural Classification

Exon Counts by Structural Classification
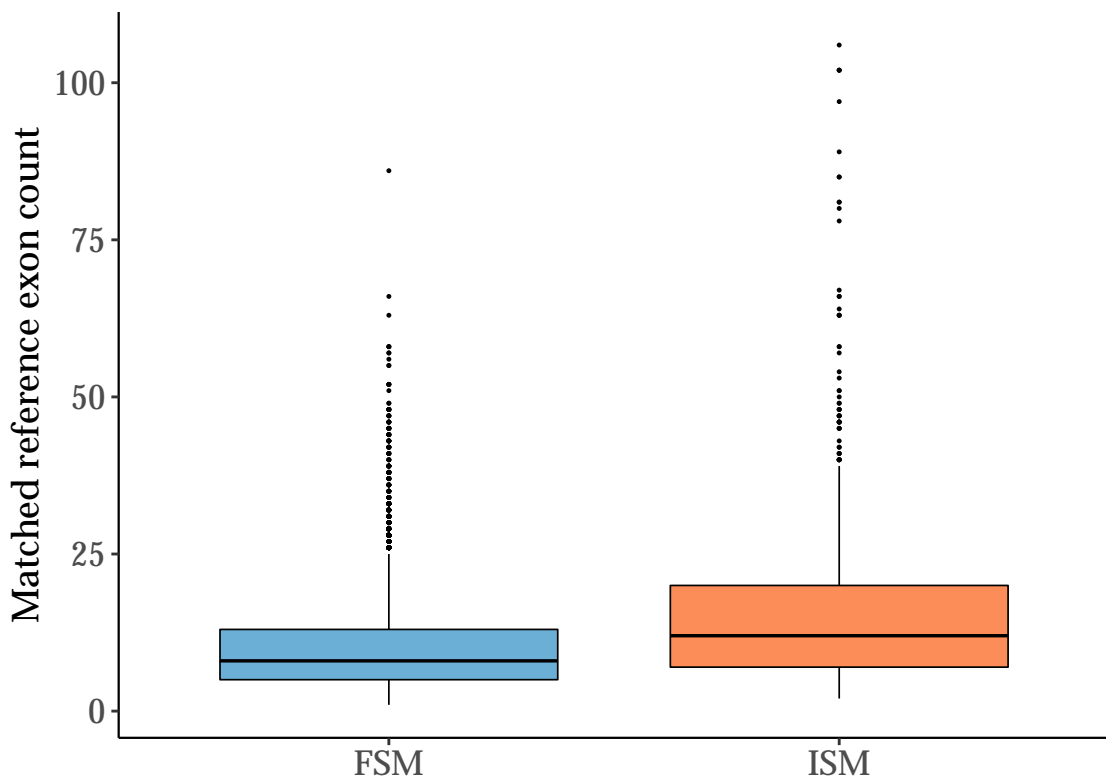
Length distribution of matched reference transcripts

Applicable only to FSM and ISM categories
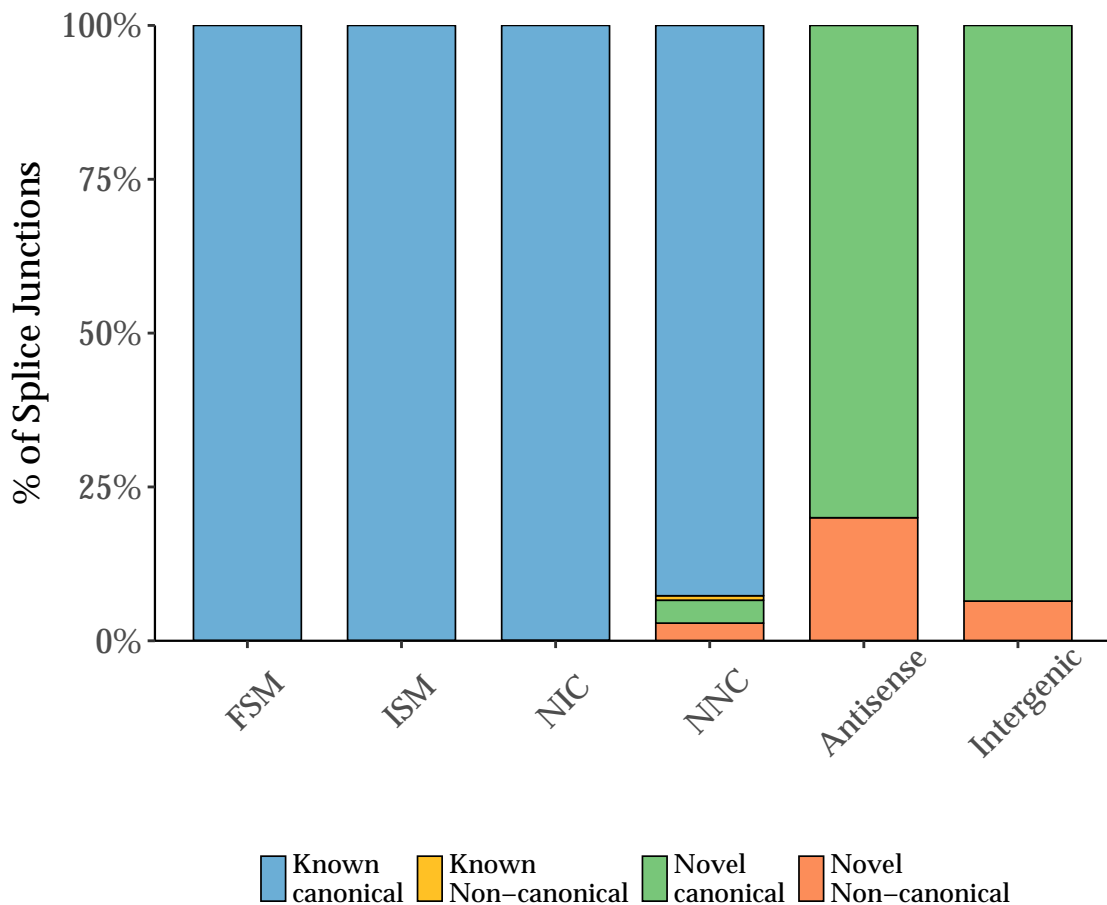
Exon number distribution of matched reference transcripts

Applicable only to FSM and ISM categories

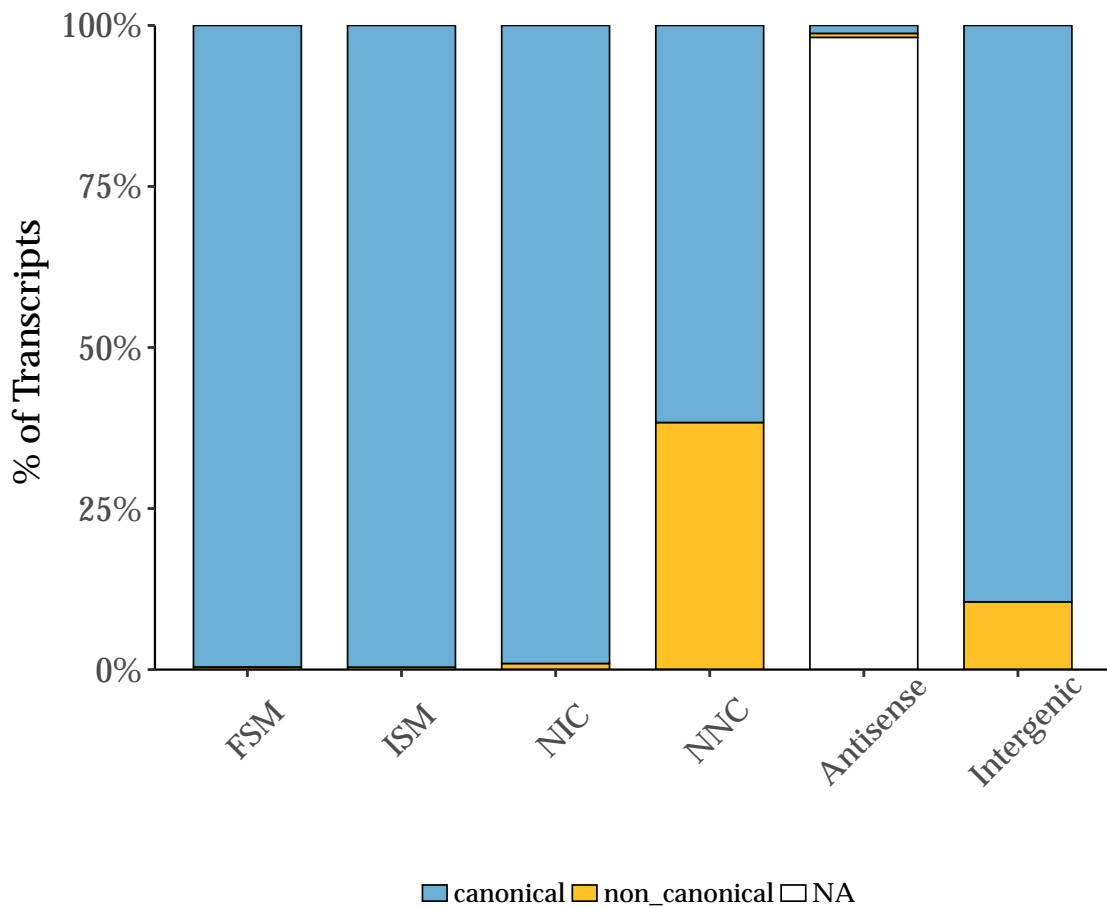*Splice Junction Characterization*

Distribution of Splice Junctions by Structural Classification

% of Splice Junctions

FSM ISM NIC NNC Antisense Intergenic

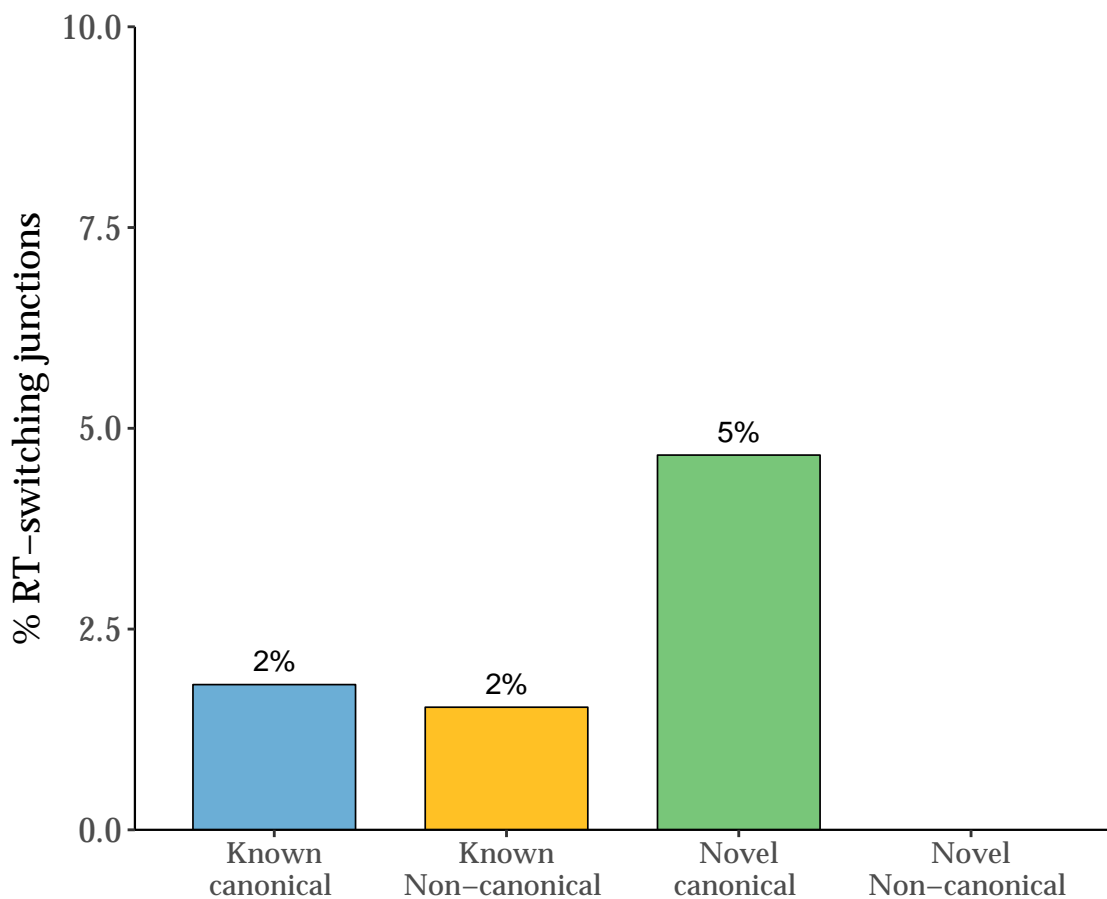Known canonical   Known Non−canonical   Novel canonical   Novel Non−canonical

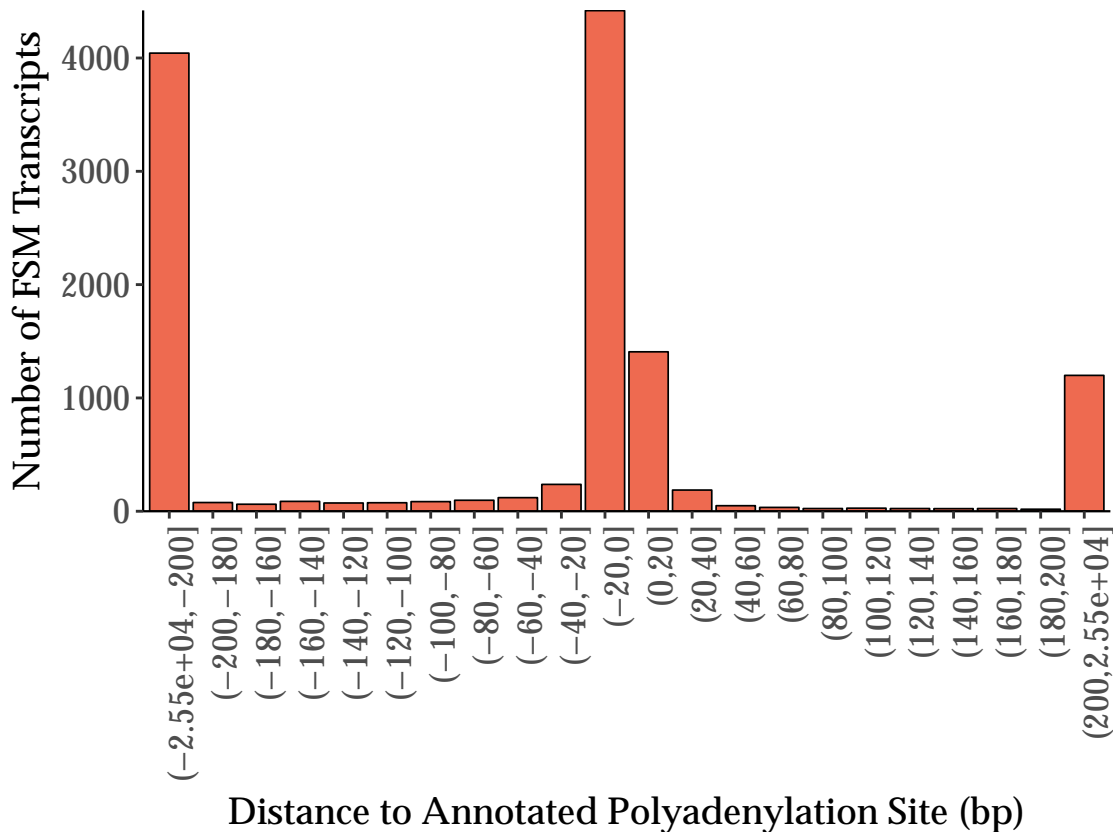Distribution of Transcripts by Splice Junctions

RT−switching, all junctions
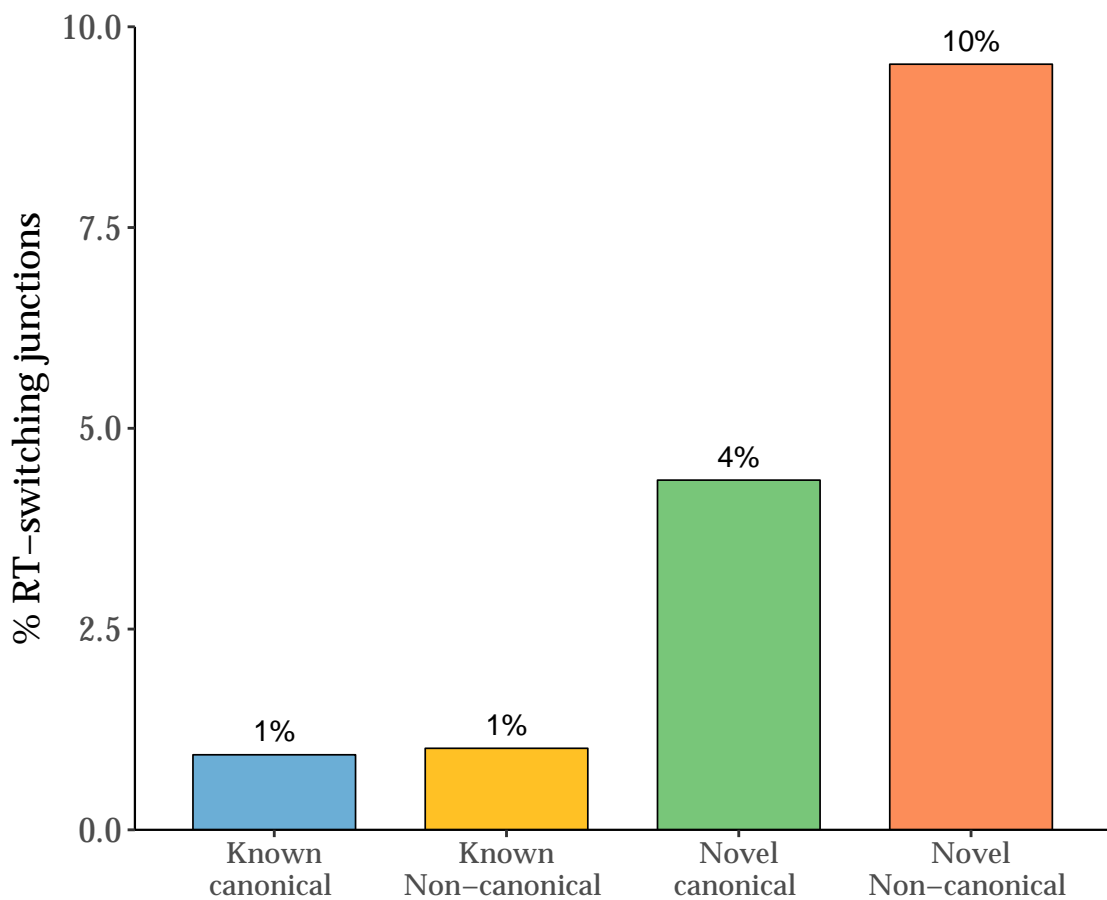
RT−switching, unique junctions

Comparison with Annotated TSS and PolyA Sites

Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site

Number of FSM Transcripts

Distance to Annotated Polyadenylation Site (bp)

x-axis labels:
(−2.55e+04,−200]
(−200,−180]
(−180,−160]
(−160,−140]
(−140,−120]
(−120,−100]
(−100,−80]
(−80,−60]
(−60,−40]
(−40,−20]
(−20,0]
(0,20]
(20,40]
(40,60]
(60,80]
(80,100]
(100,120]
(120,140]
(140,160]
(160,180]
(180,200]
(200,2.55e+04]

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
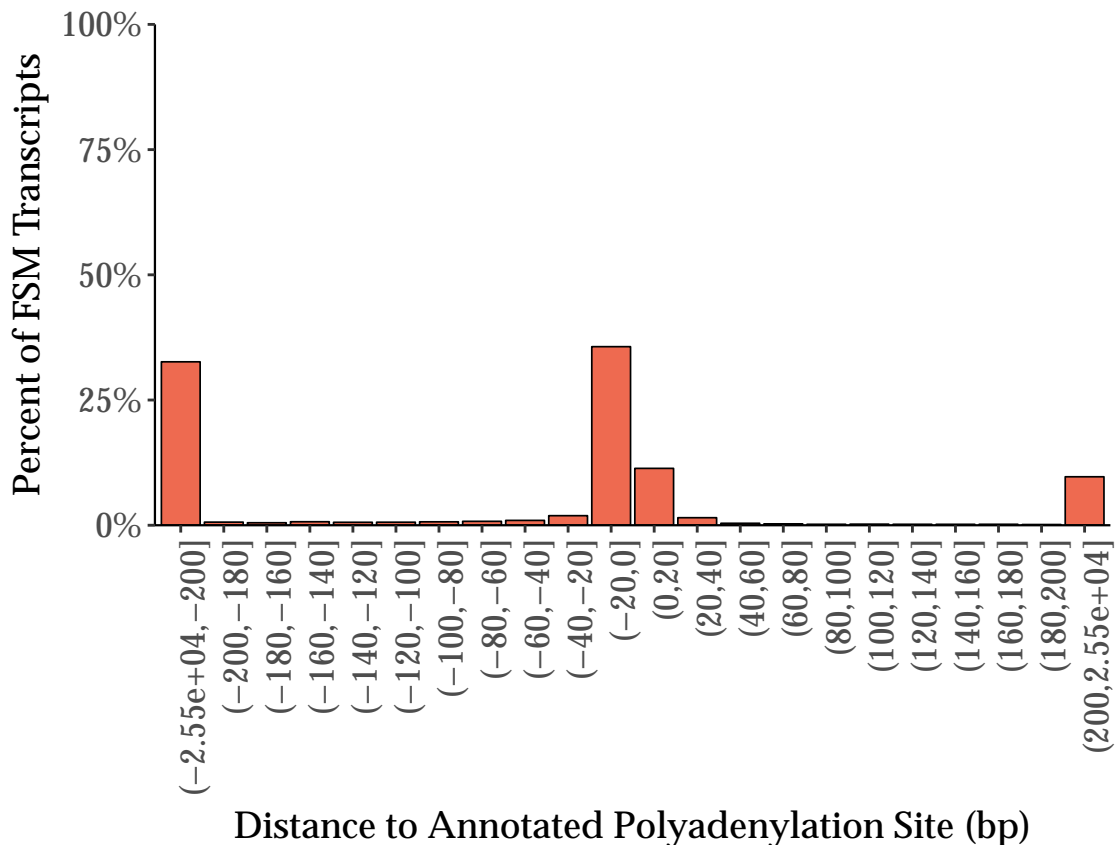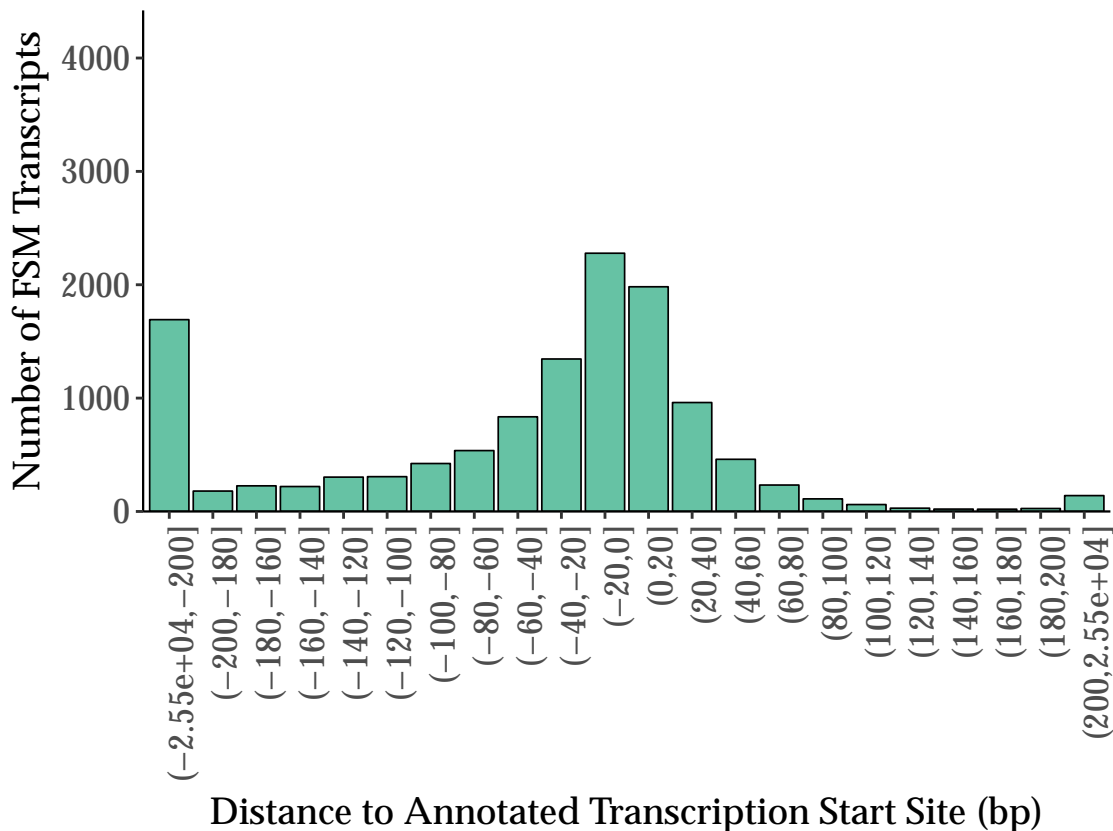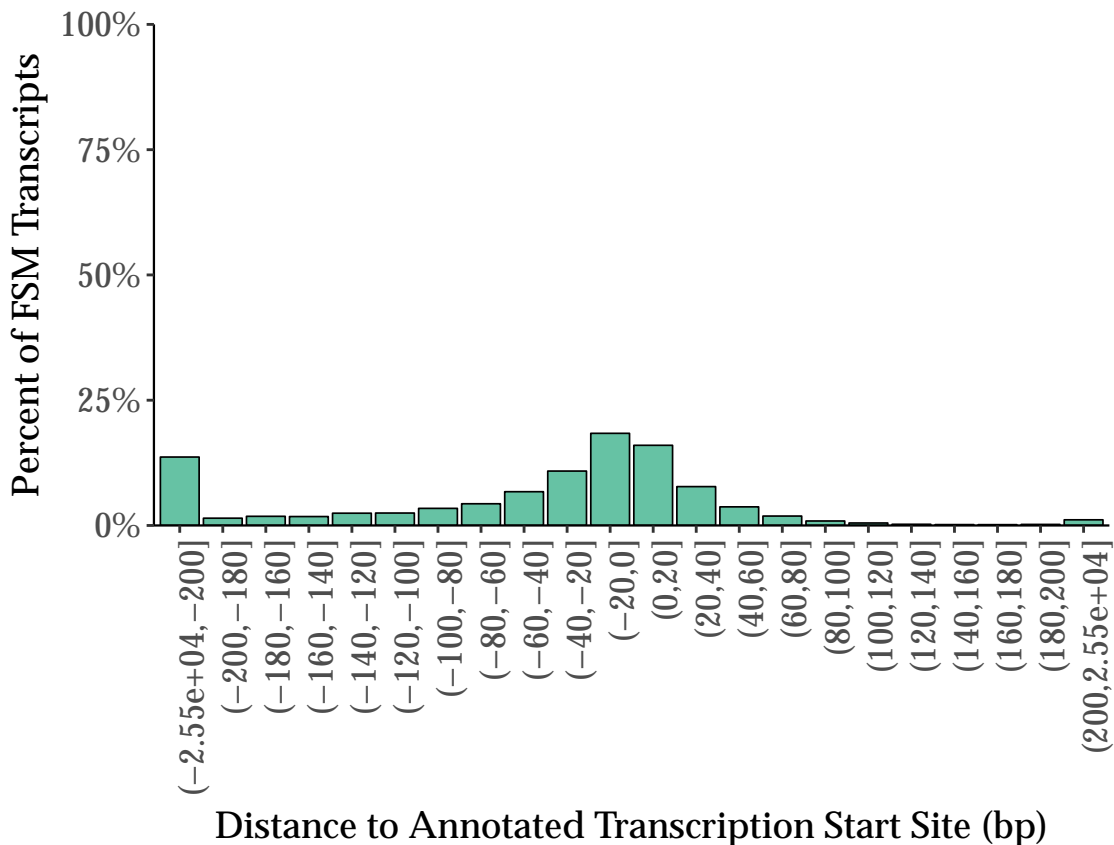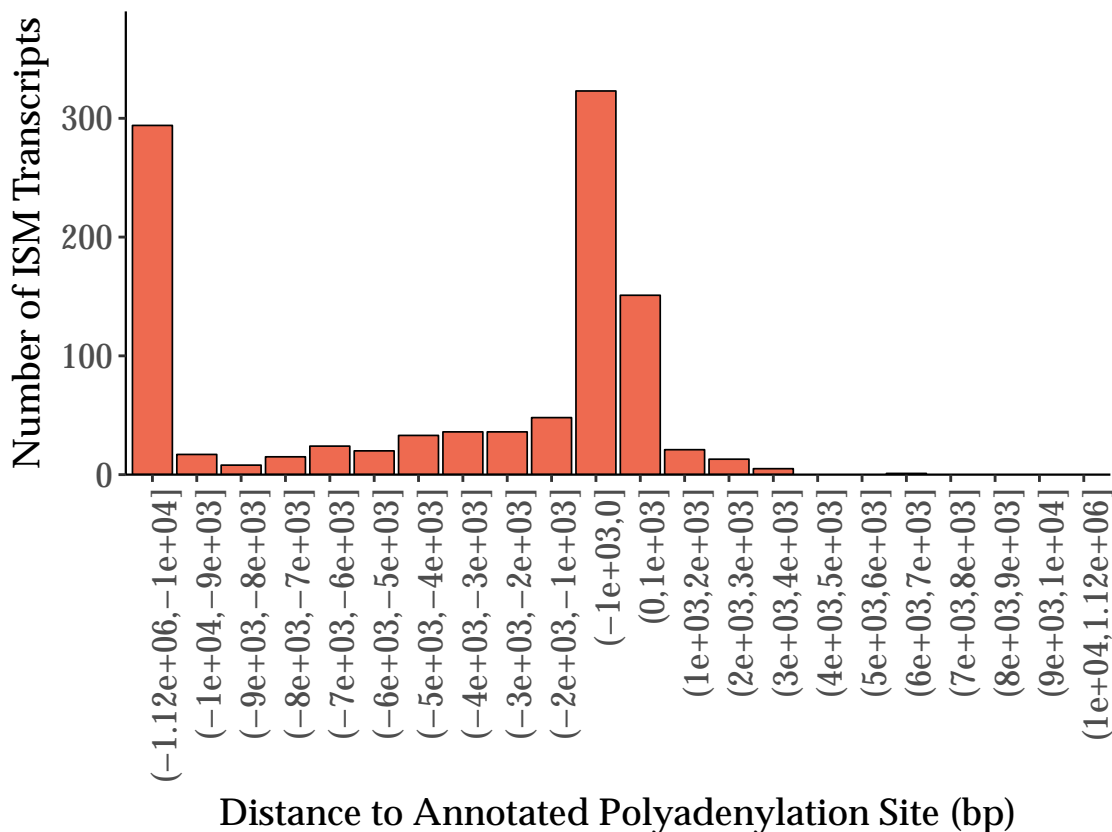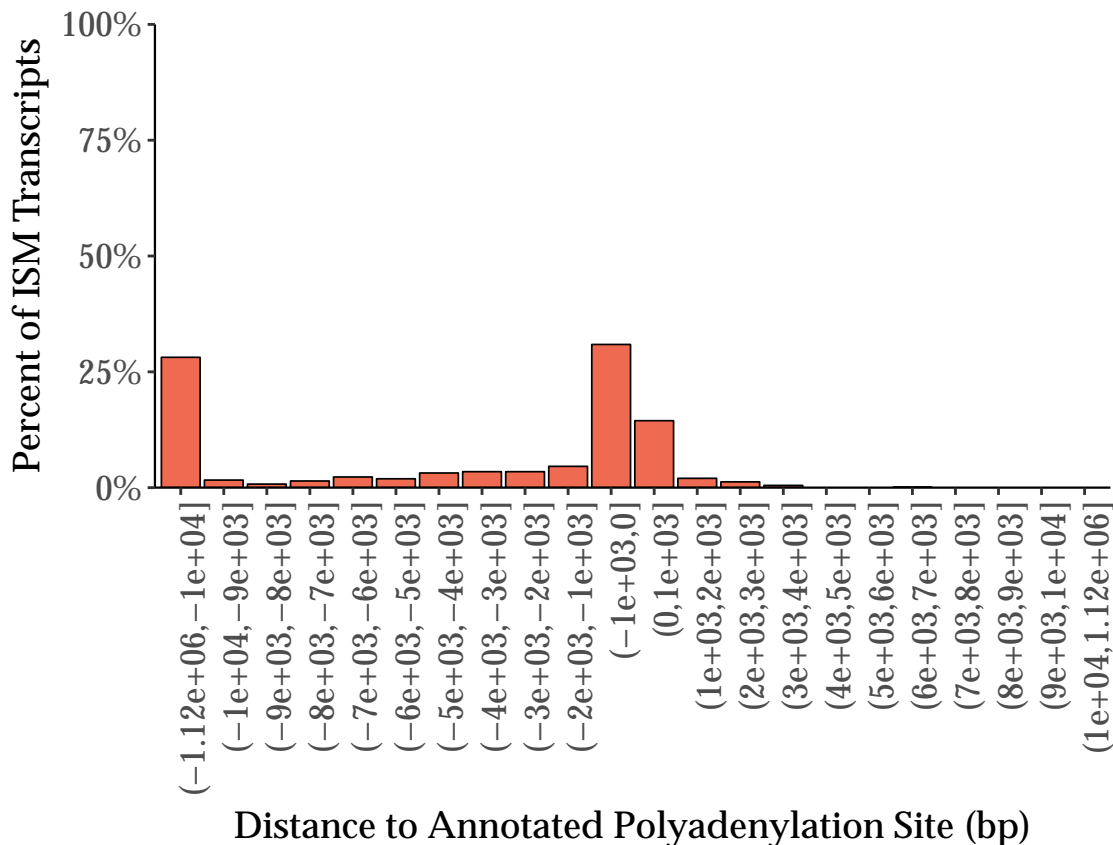
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site
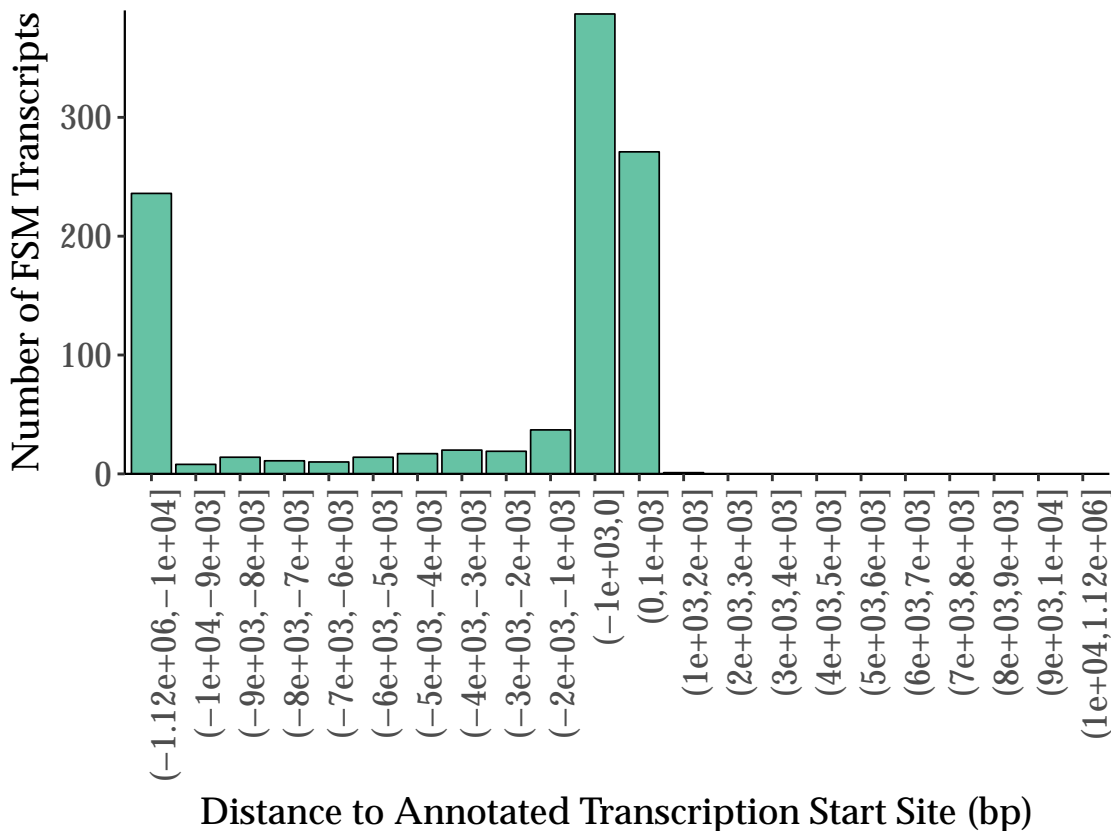
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site

Percent of ISM Transcripts

Distance to Annotated Polyadenylation Site (bp)
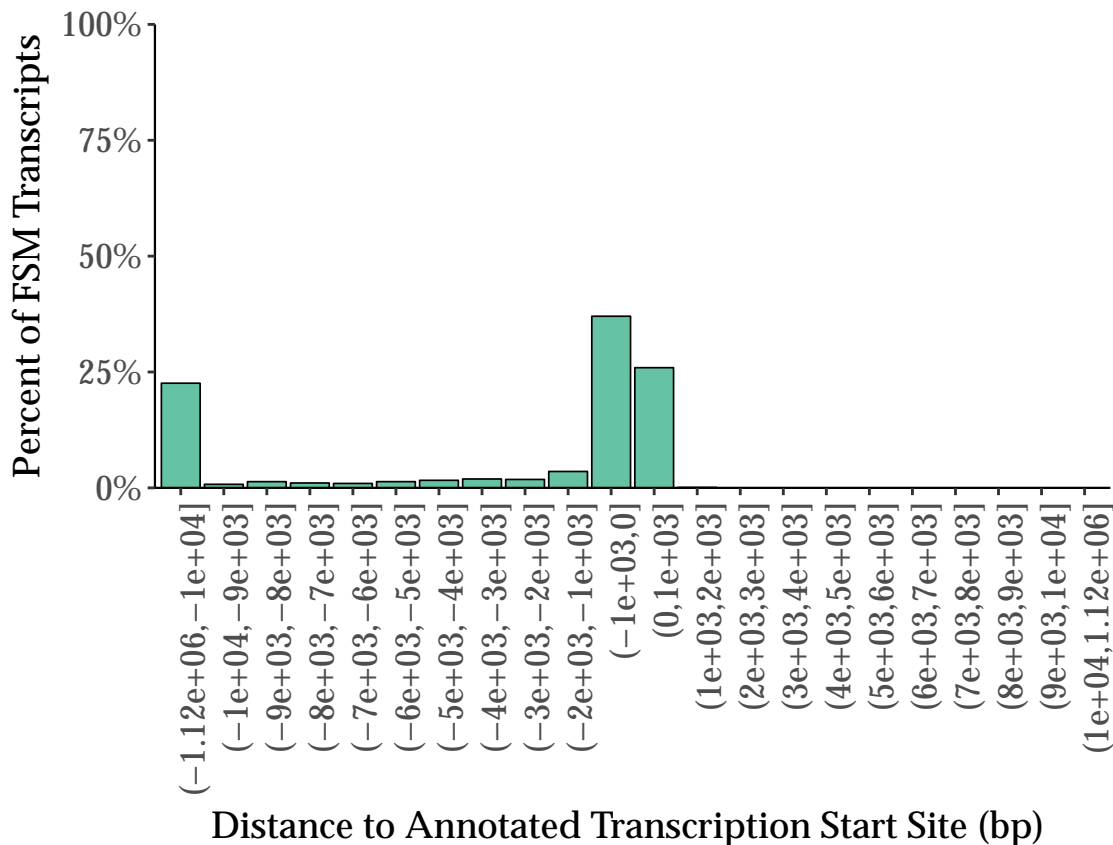
Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS

Number of FSM Transcripts

Distance to Annotated Transcription Start Site (bp)

Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS
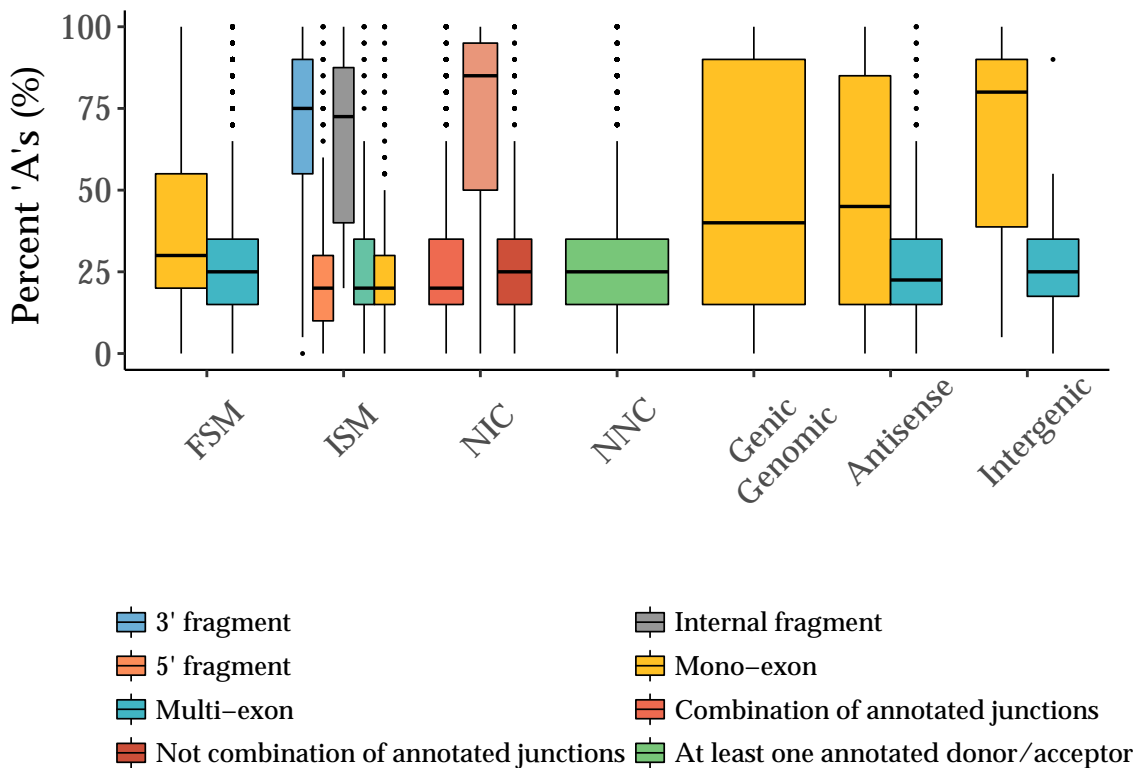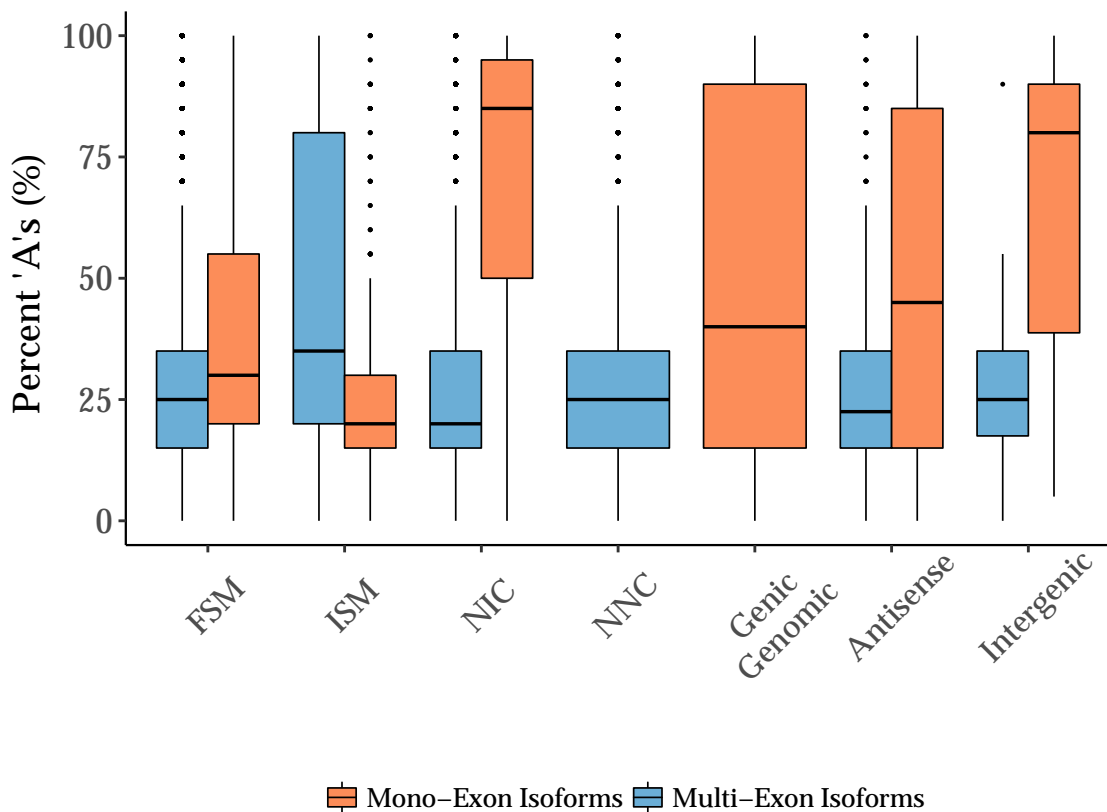
Intra–Priming Quality Check

Possible Intra−Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp

Percent 'A's (%)
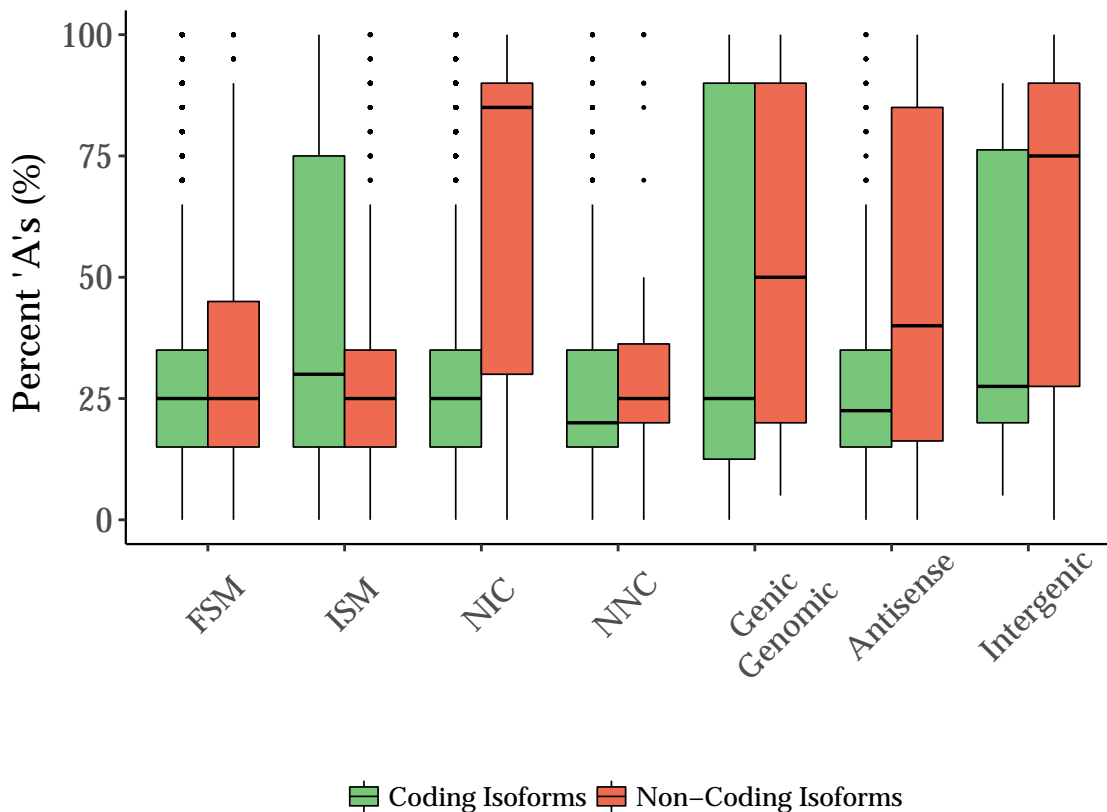
FSM   ISM   NIC   NNC   Genic Genomic   Antisense   Intergenic

3' fragment
5' fragment
Multi−exon
Not combination of annotated junctions
Internal fragment
Mono−exon
Combination of annotated junctions
At least one annotated donor/acceptor

Possible Intra−Priming, Mono− vs Multi−Exon

Percent of genomic 'A's in downstream 20 bp

Mono−Exon Isoforms   Multi−Exon Isoforms

Possible Intra−Priming, Coding vs Non−Coding

Percent of genomic 'A's in downstream 20 bp

Percent 'A's (%)

FSM   ISM   NIC   NNC   Genic Genomic   Antisense   Intergenic

Coding Isoforms   Non−Coding Isoforms

Quality Controls

Incidence of RT−switching
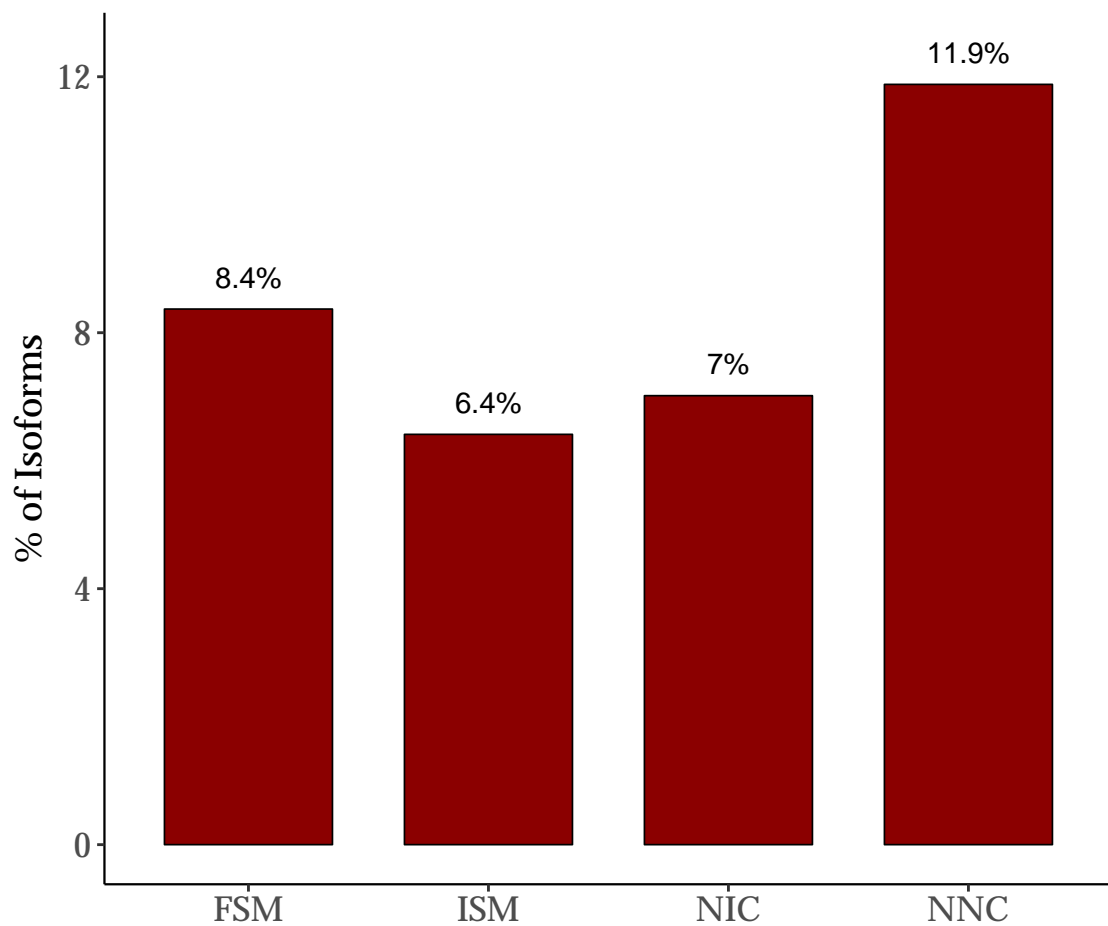
Incidence of Non−Canonical Junctions