SQANTI3 report

Unique Genes: 9526
Unique Isoforms: 36934

Characterization of transcripts based on splice junctions

Gene classification

Category	# Genes
Annotated Genes	9362
Novel Genes	164

Category	# Isoforms
FSM	13978
ISM	8407
NIC	12453
NNC	1080
Genic Genomic	522
Antisense	285
Fusion	97
Intergenic	112
Genic Intron	0

Splice Junction Classification

Category	# SJs	Percent
Known canonical	64543	98.84
Known Non−canonical	109	0.17
Novel canonical	347	0.53
Novel Non−canonical	301	0.46

Gene Characterization

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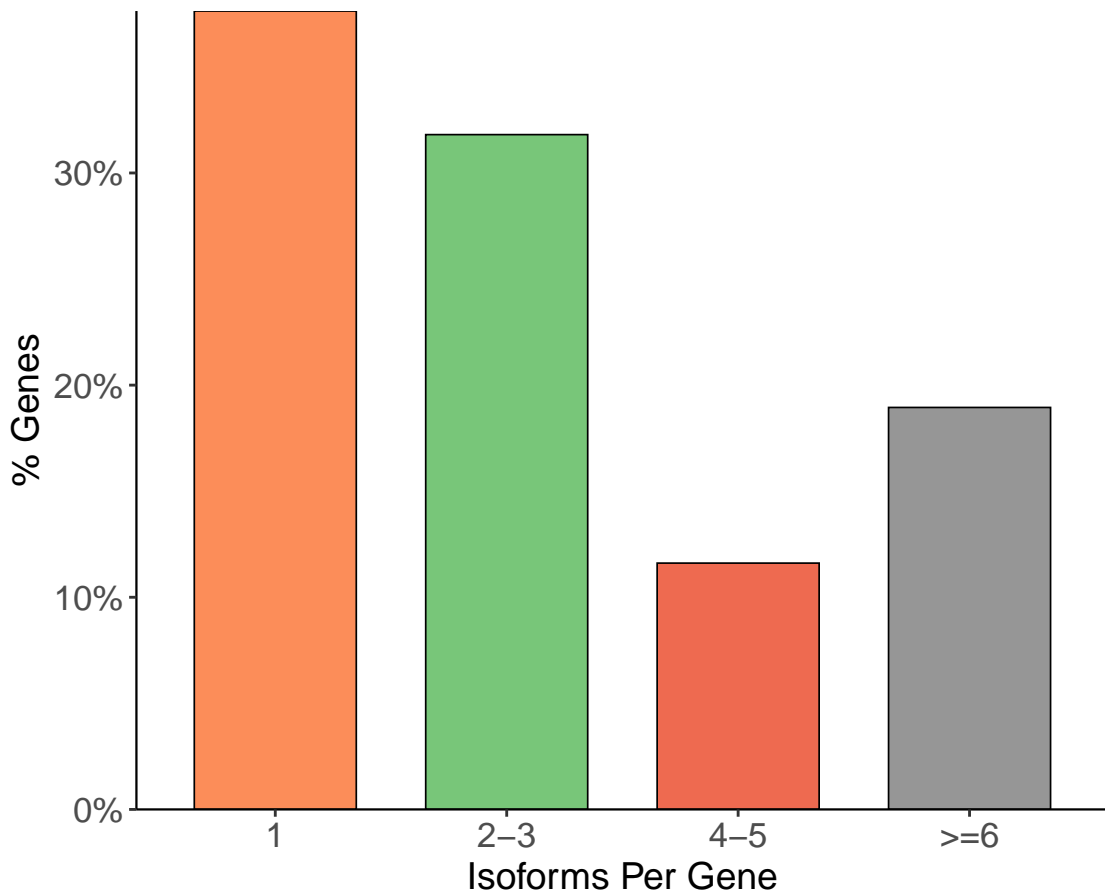
Number of Isoforms per Gene, Known vs Novel Genes

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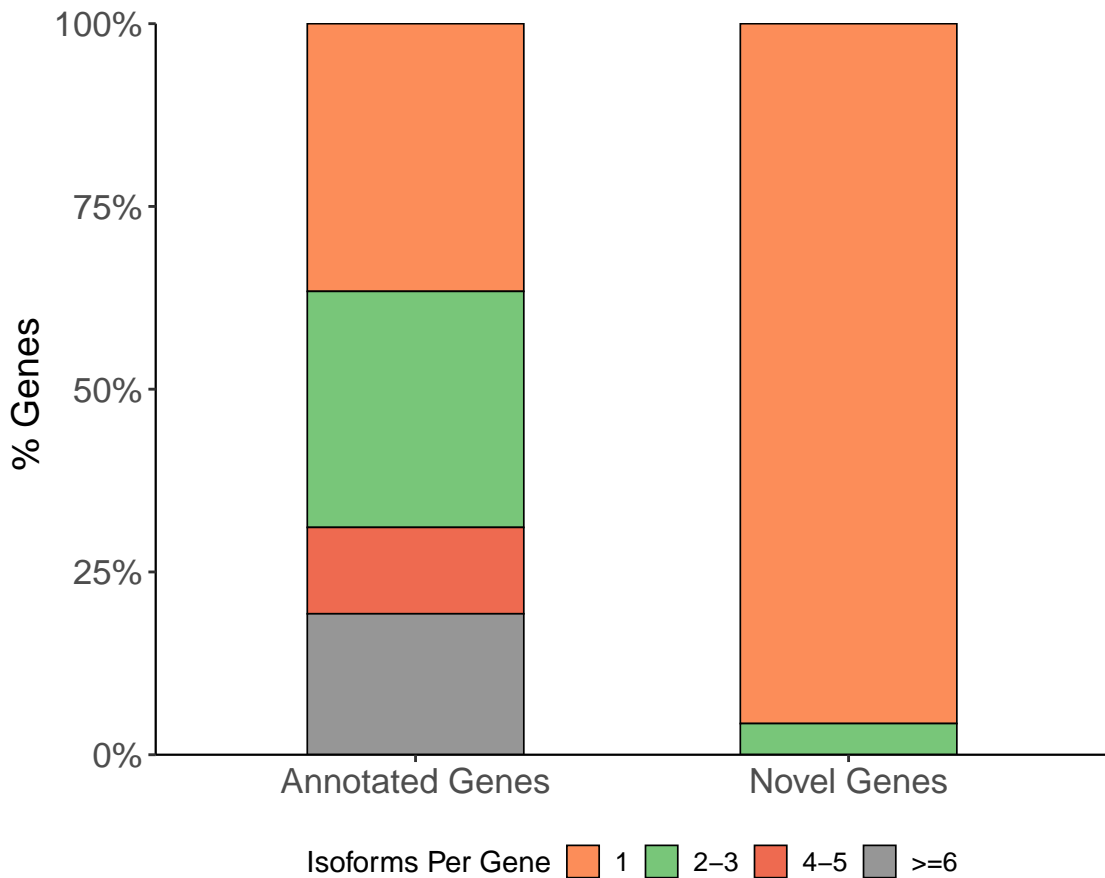
Distribution of Mono− vs Multi−Exon Transcripts

Transcript type ■ Multi−Exon ■ Mono−Exon
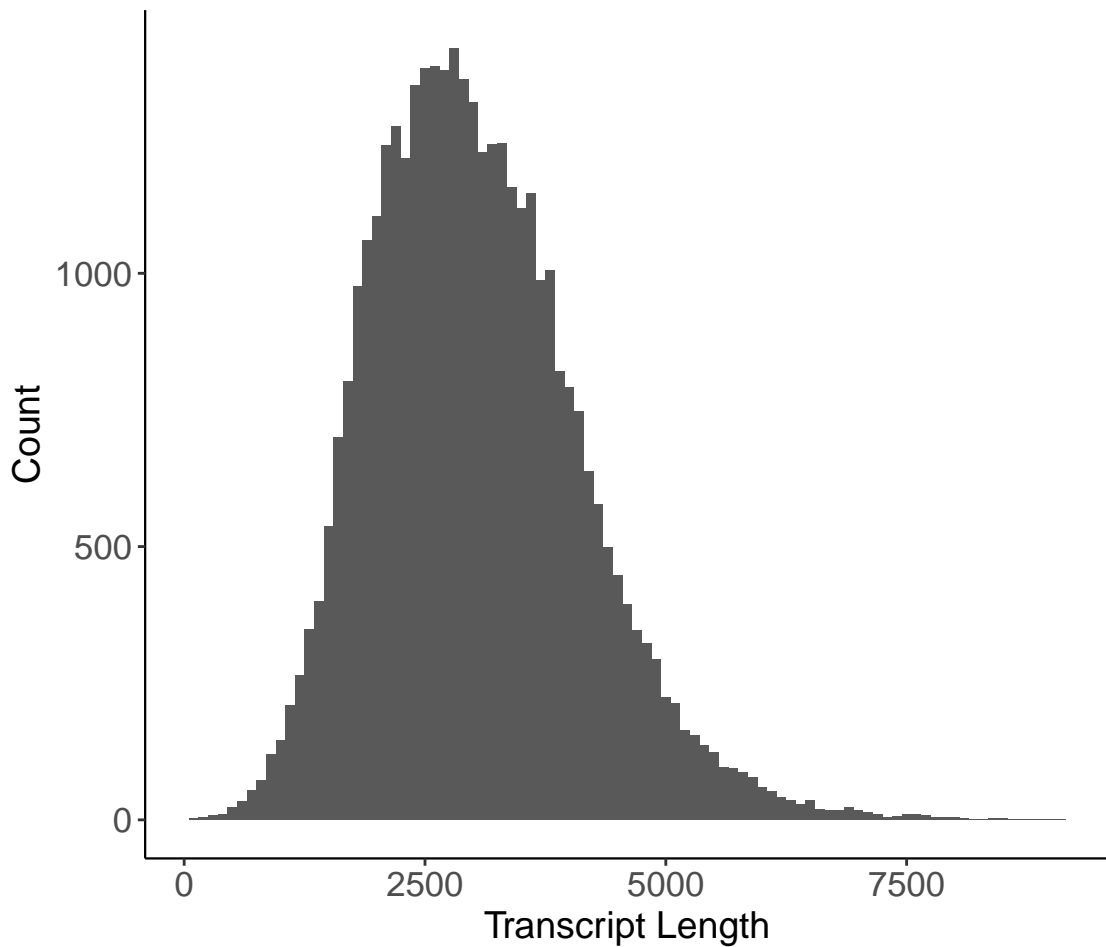
Classifications by Transcript Length
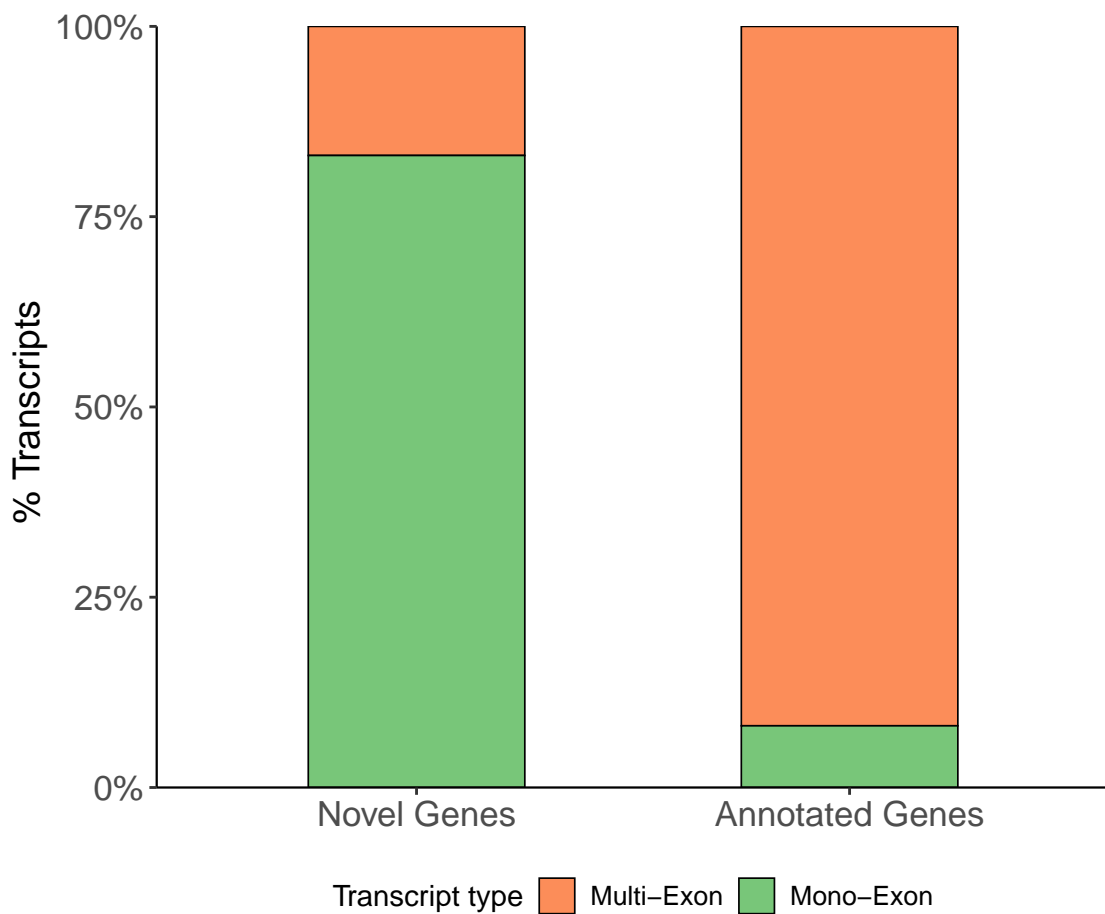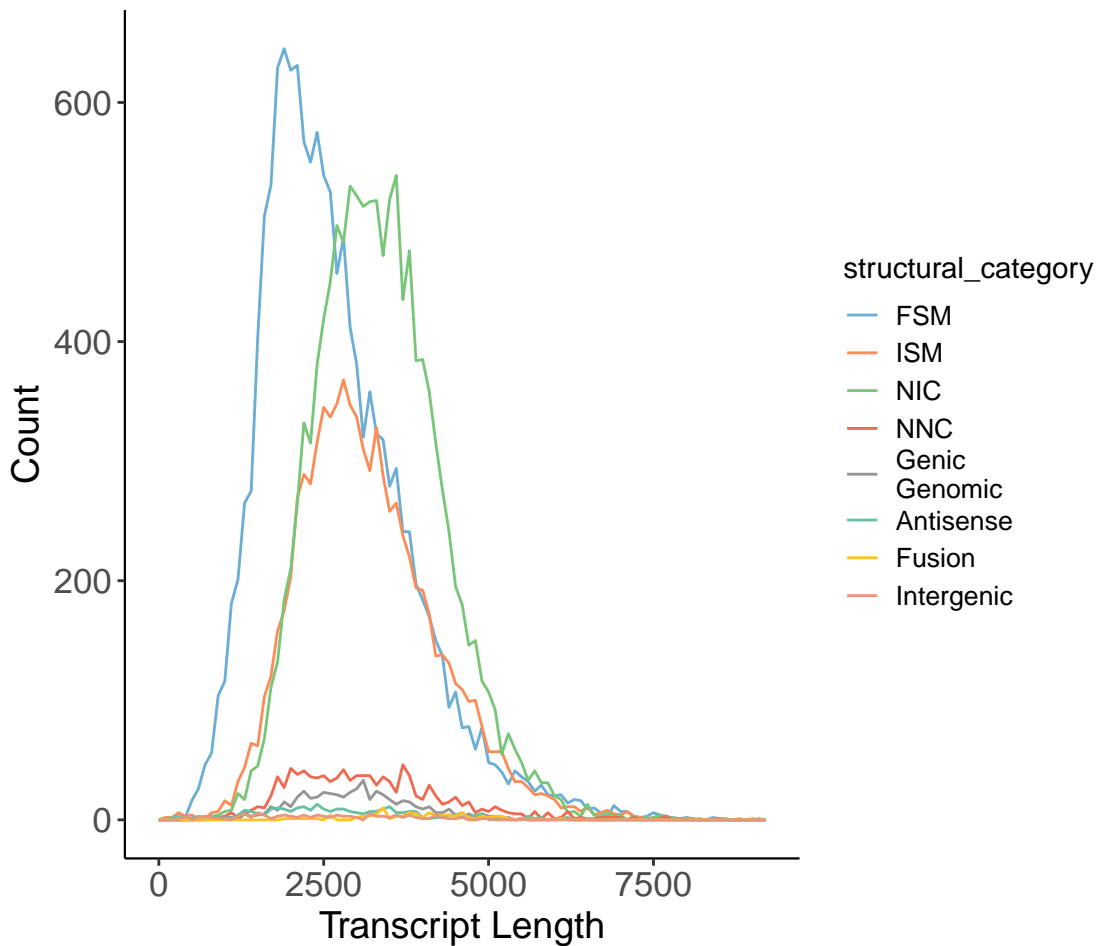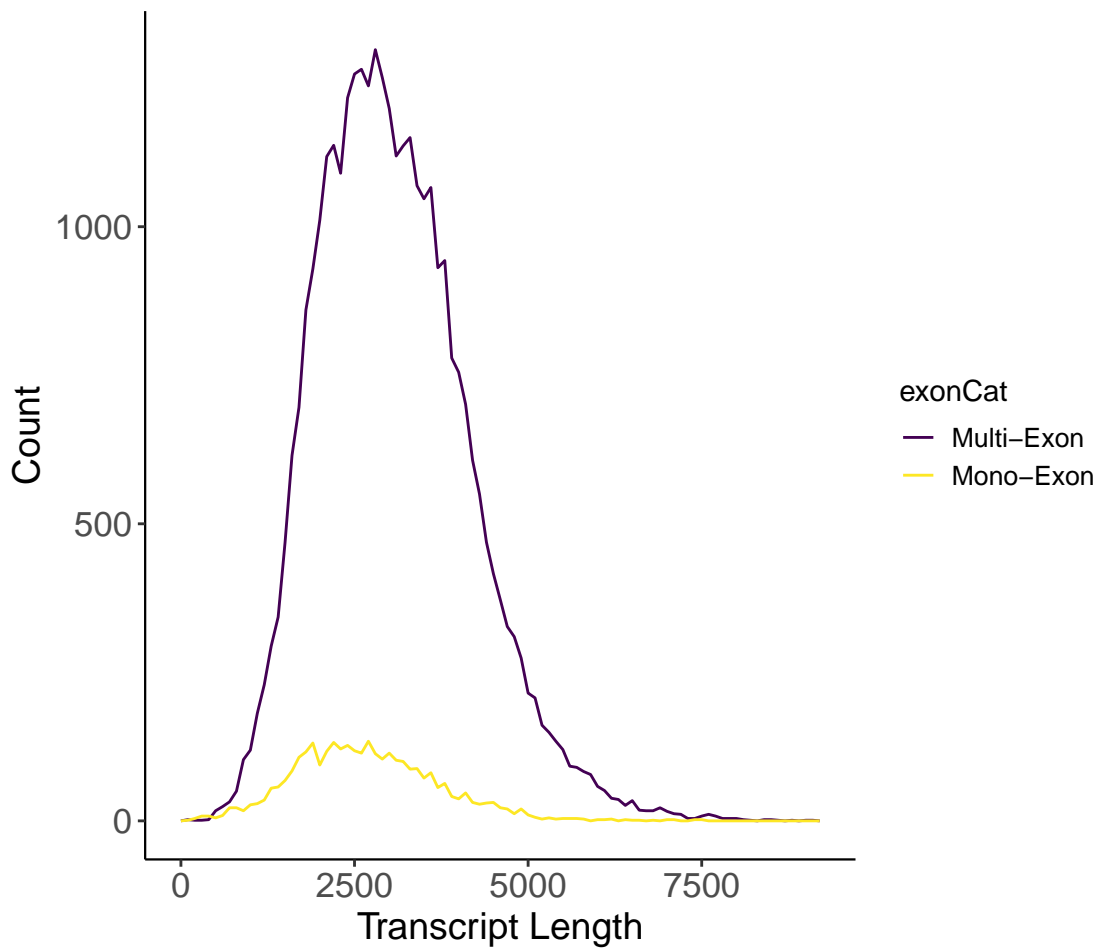
Classifications by Transcript Length, normalized
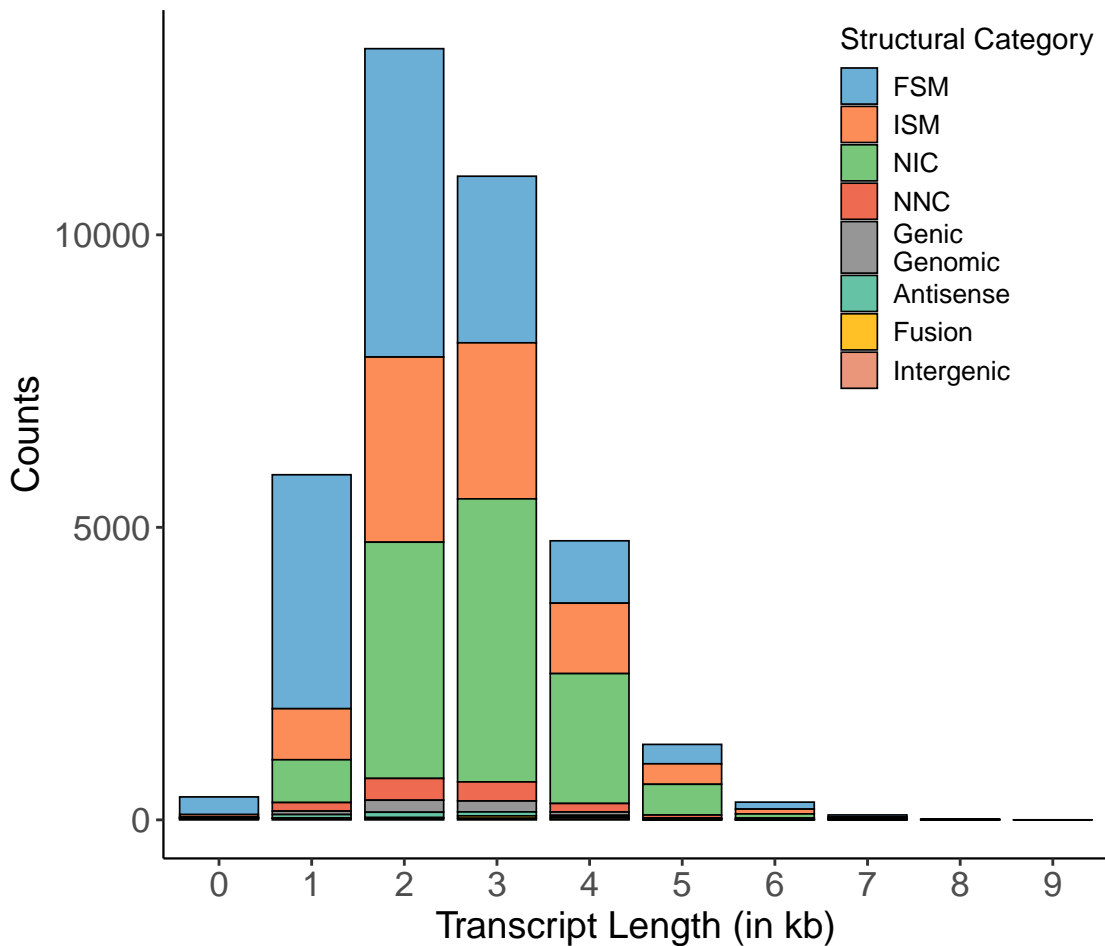
Transcript Lengths, all transcripts

Transcript Lengths, by structural category

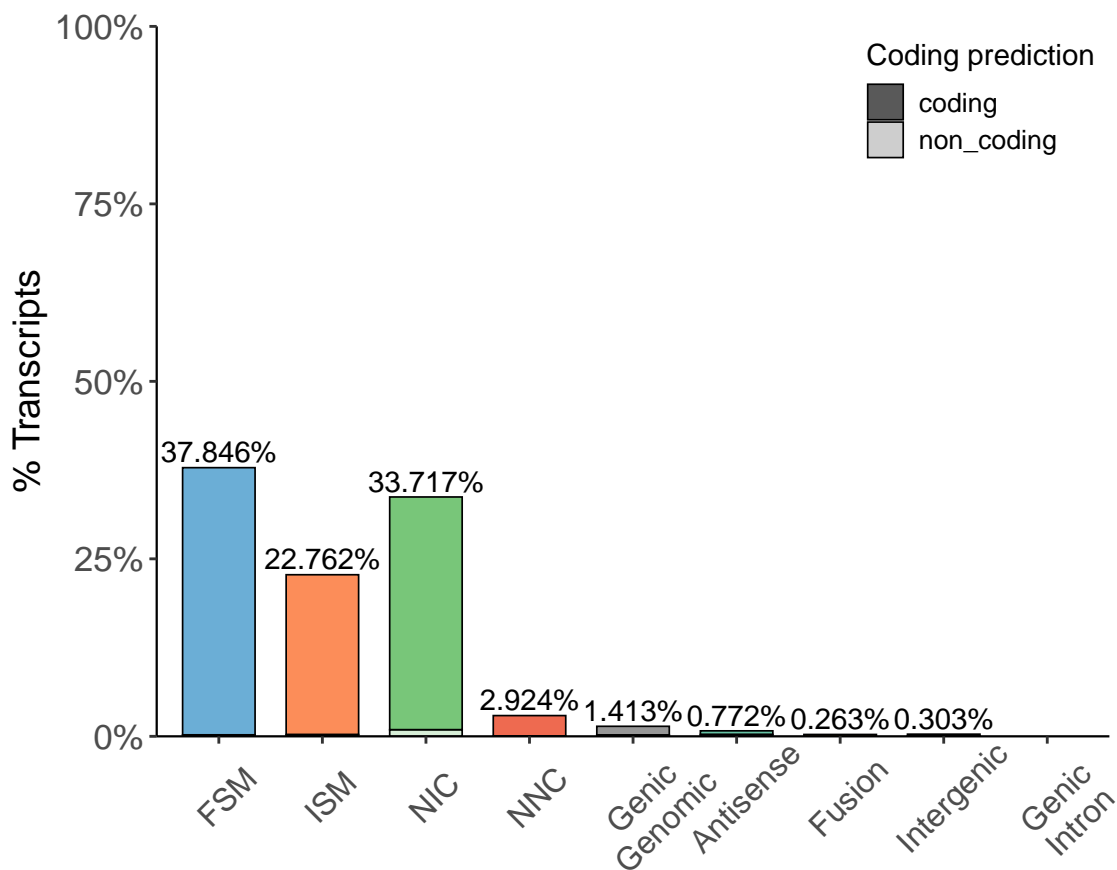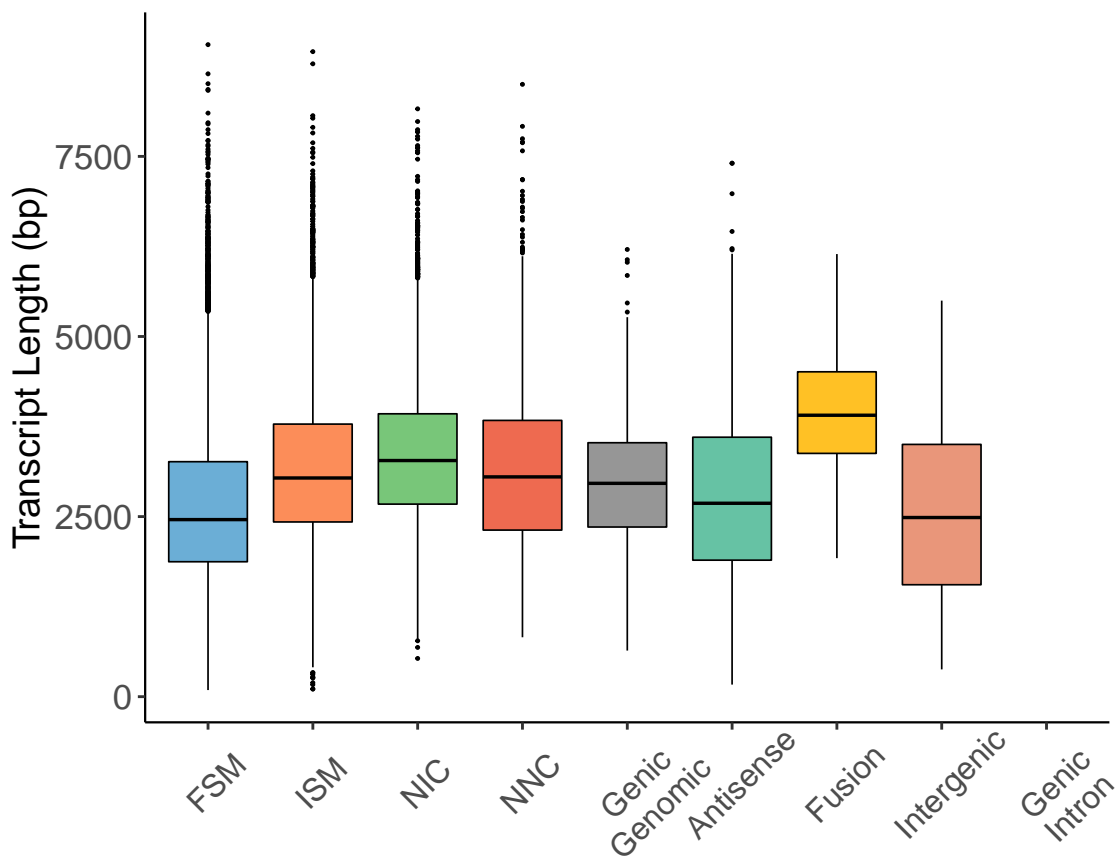Transcript Lengths, Mono− vs Multi−Exons
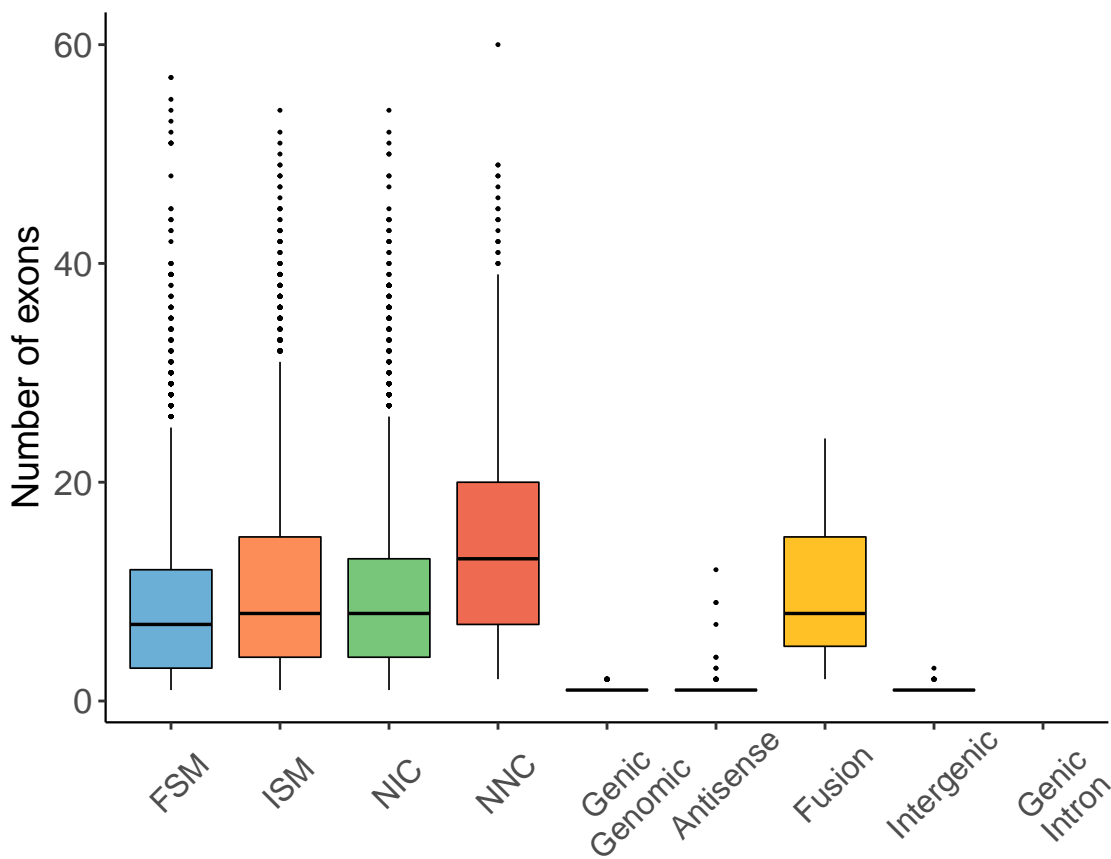
*Structural Isoform Characterization
by Splice Junctions*

Isoform distribution across structural categories
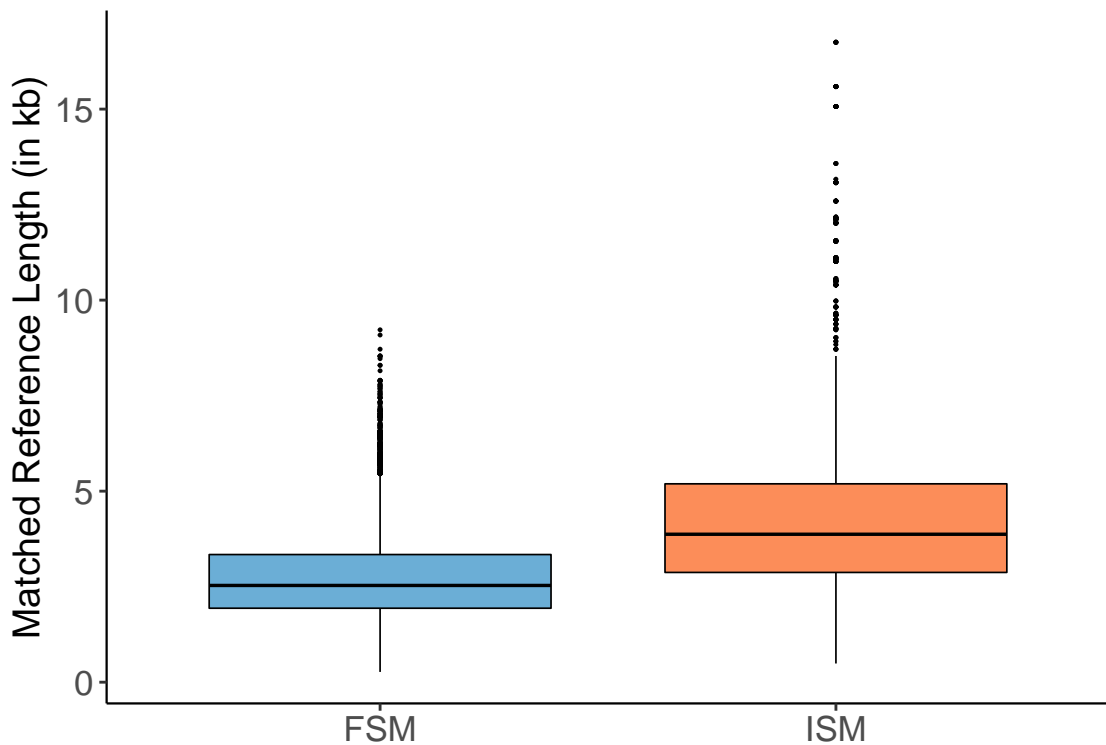
Transcript Lengths by Structural Classification

Exon Counts by Structural Classification
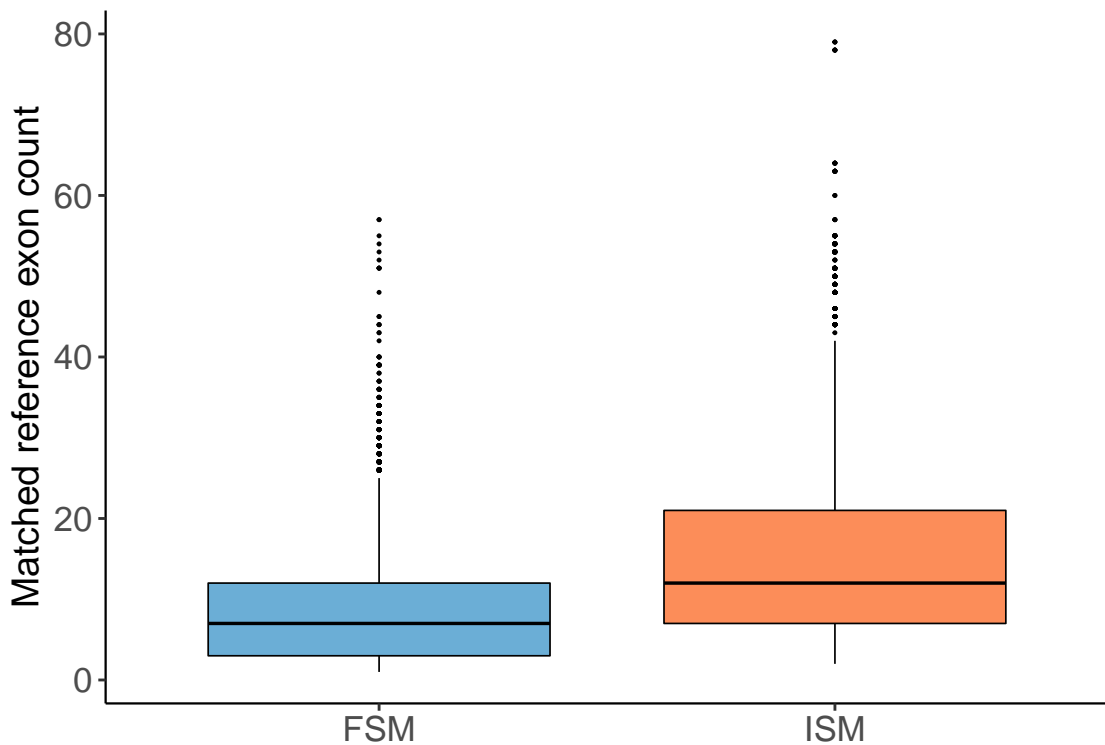
Length Distribution of Matched Reference Transcripts
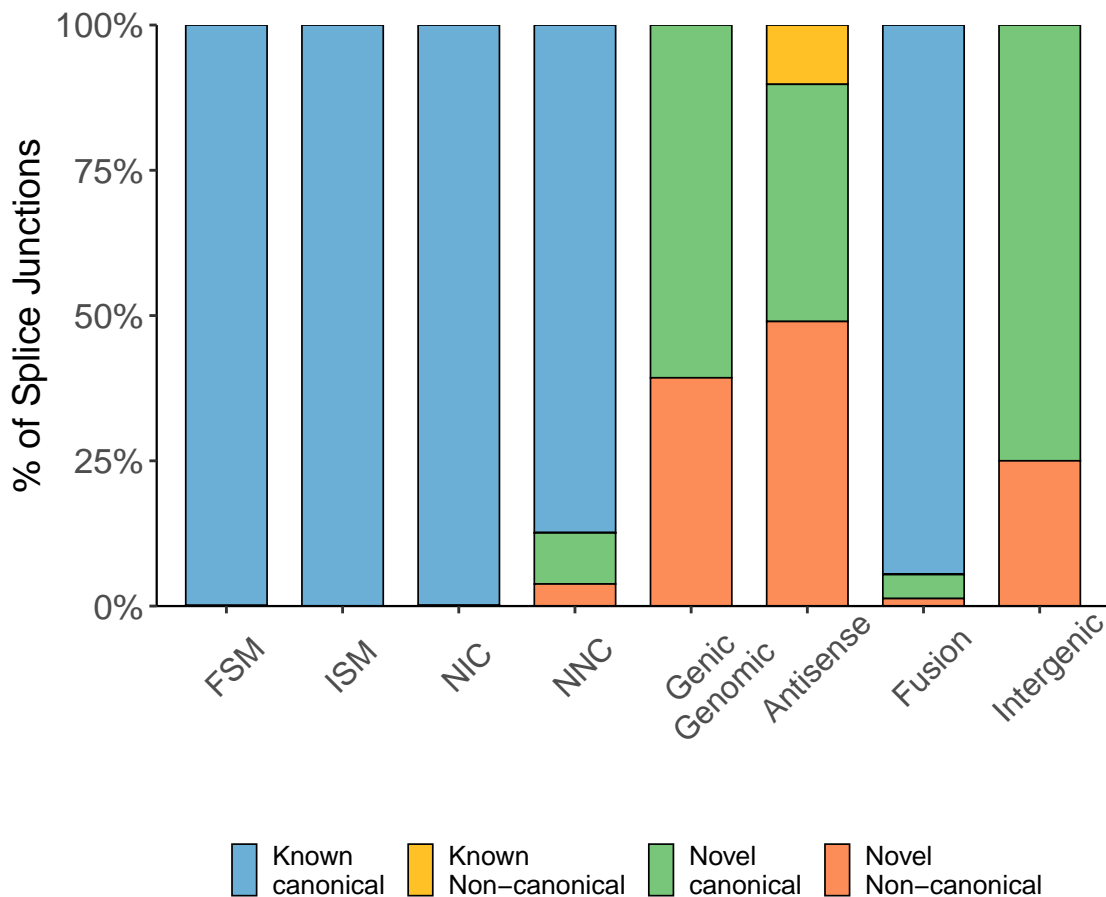
Applicable only to FSM and ISM categories

Exon Count Distribution of Matched Reference Transcripts
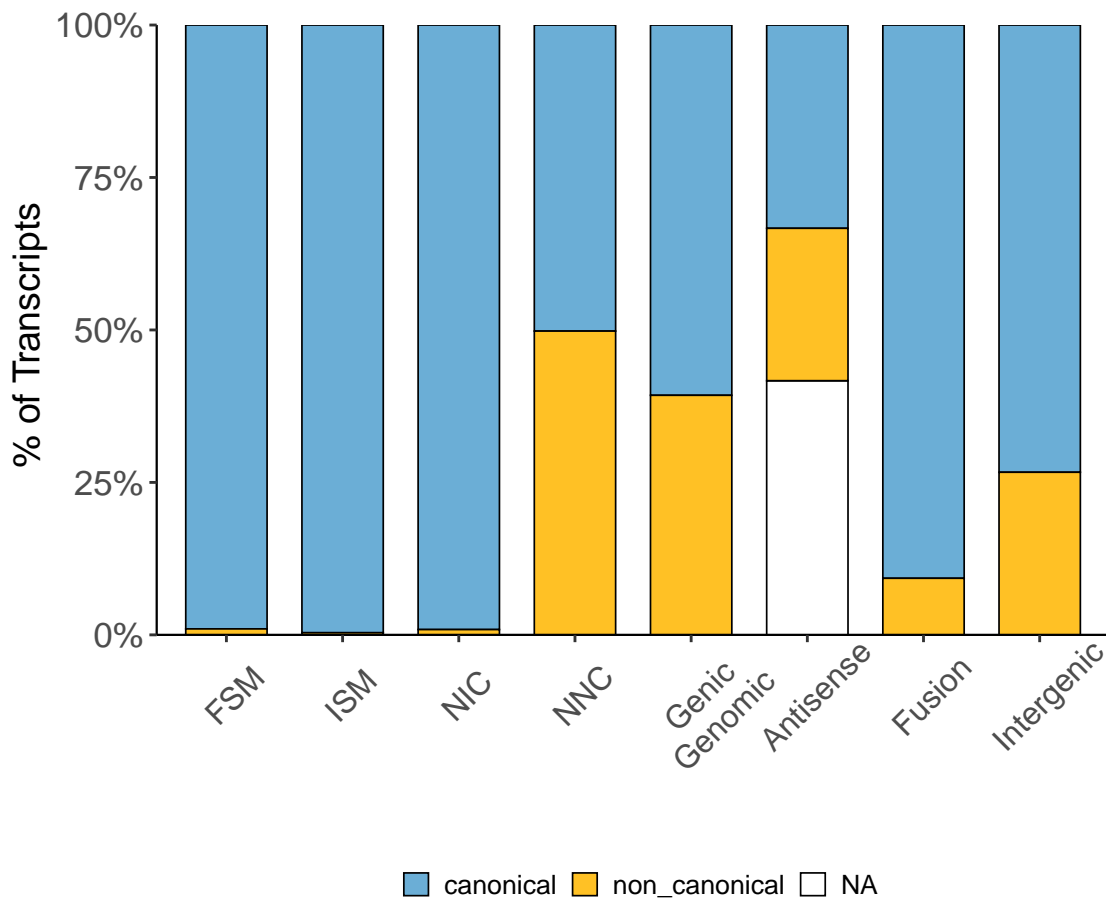
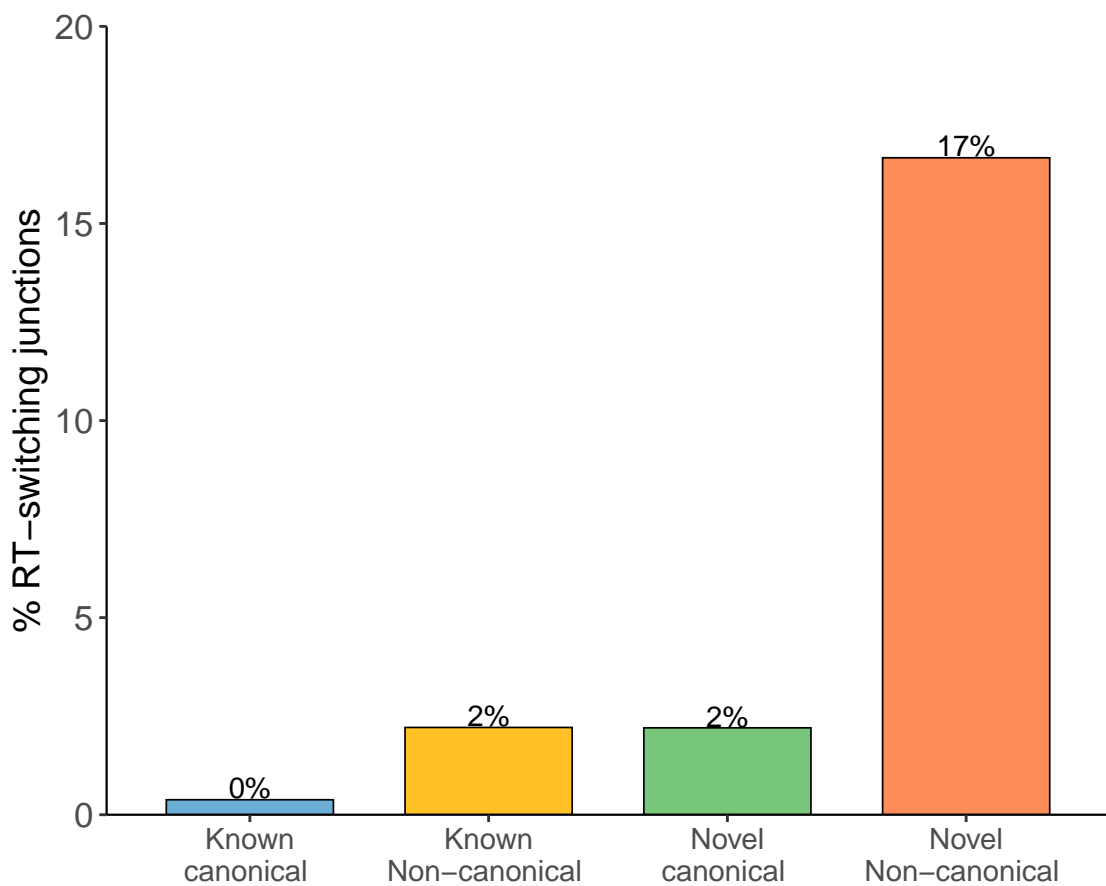Applicable only to FSM and ISM categories

Splice Junction Characterization

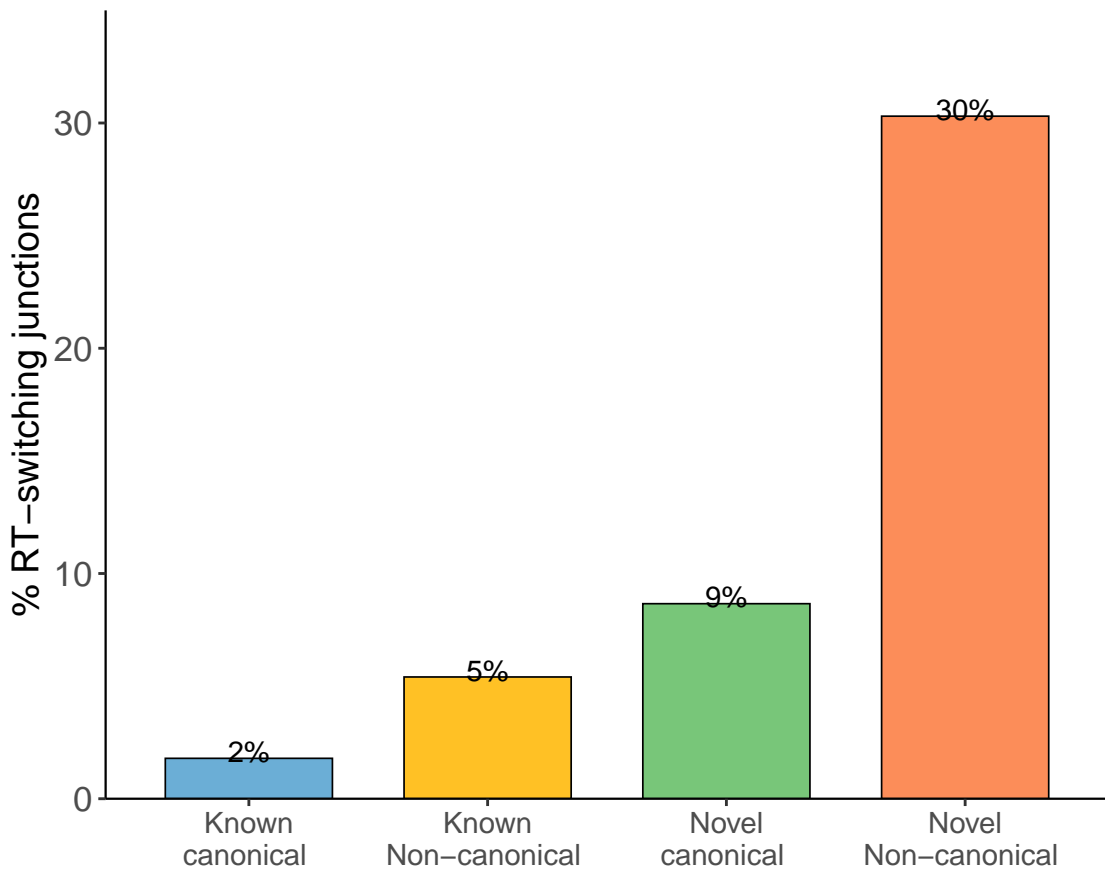Distribution of Splice Junctions by Structural Classification

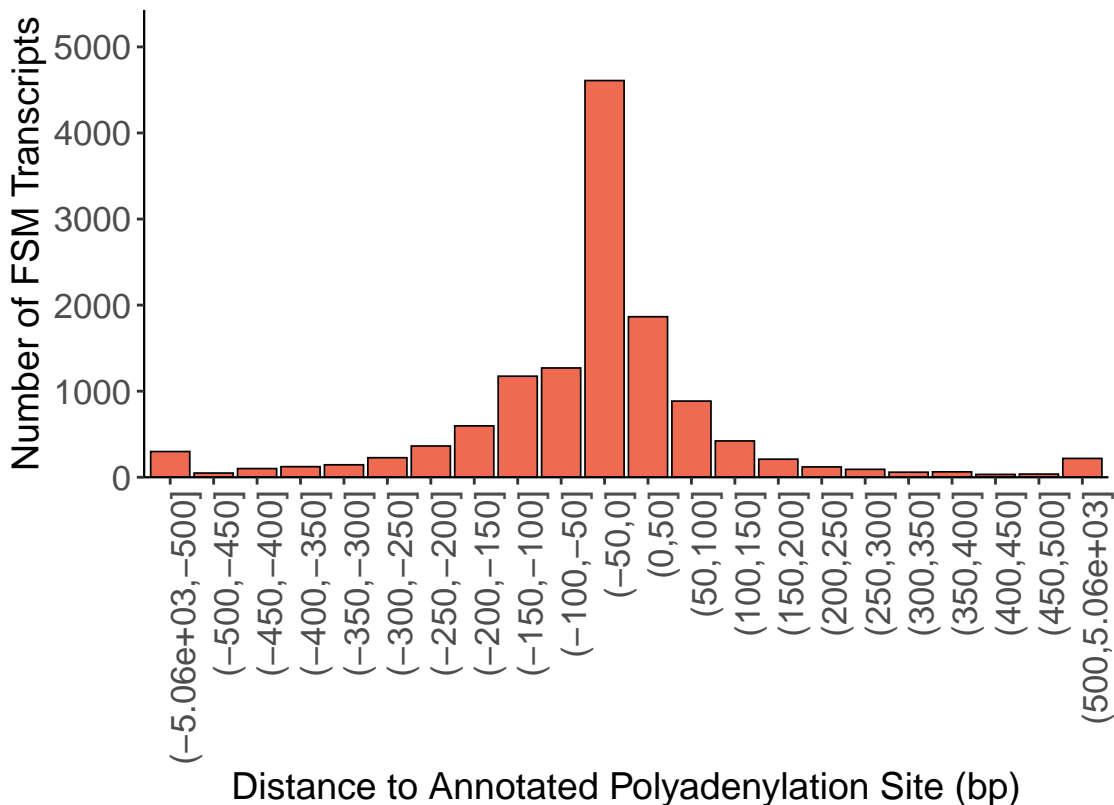Distribution of Transcripts by Splice Junctions

RT−switching, all junctions

RT−switching, unique junctions

Comparison with Annotated TSS and PolyA Sites
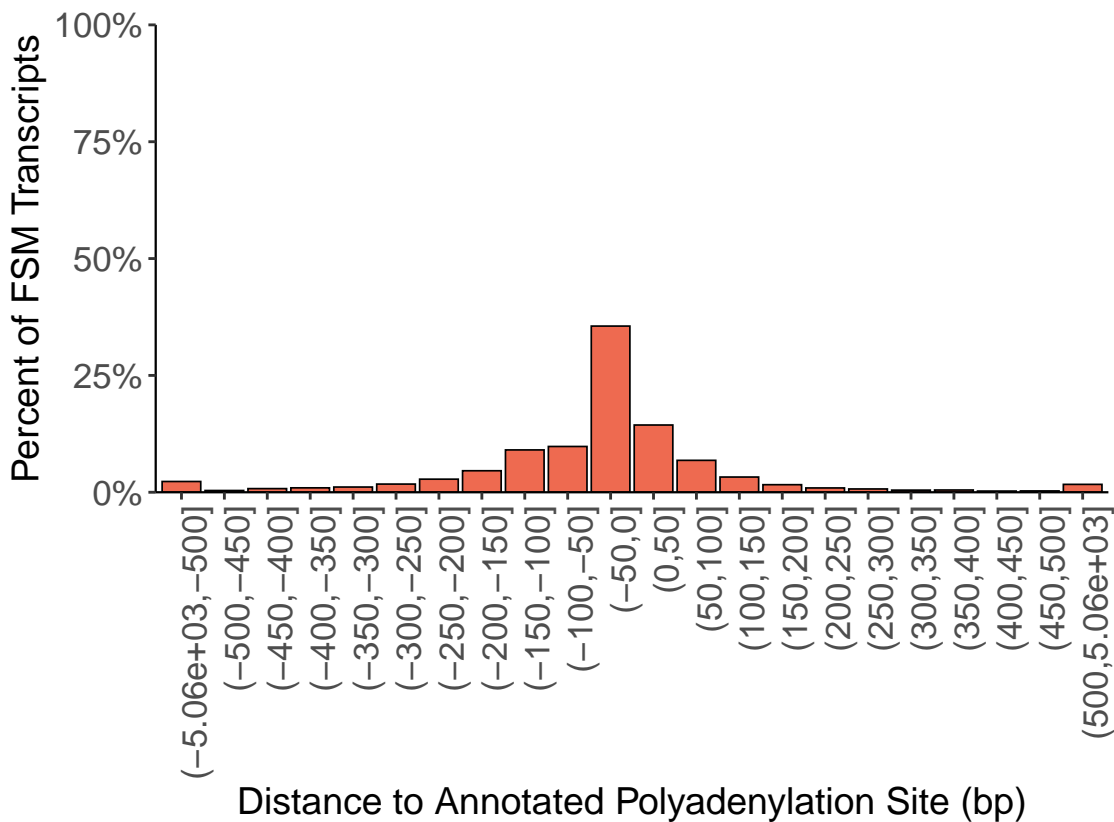
Distance to Annotated Polyadenylation Site, FSM only
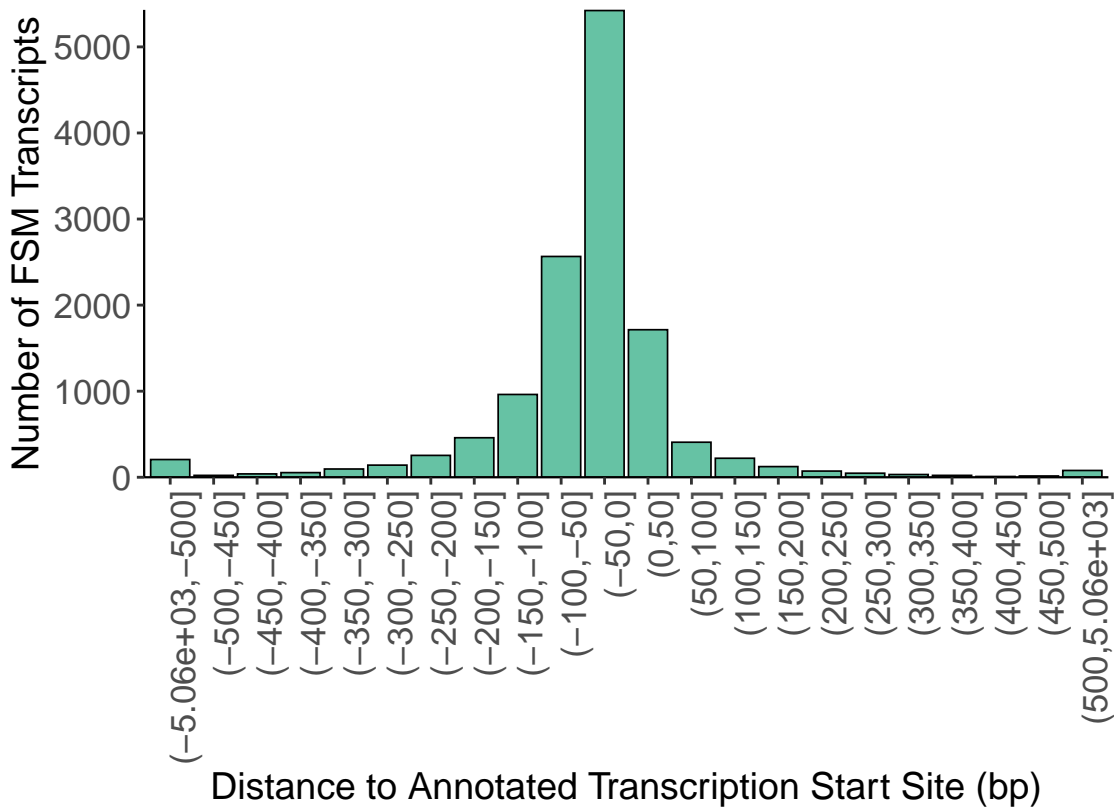
Negative values indicate upstream of annotated polyA site

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
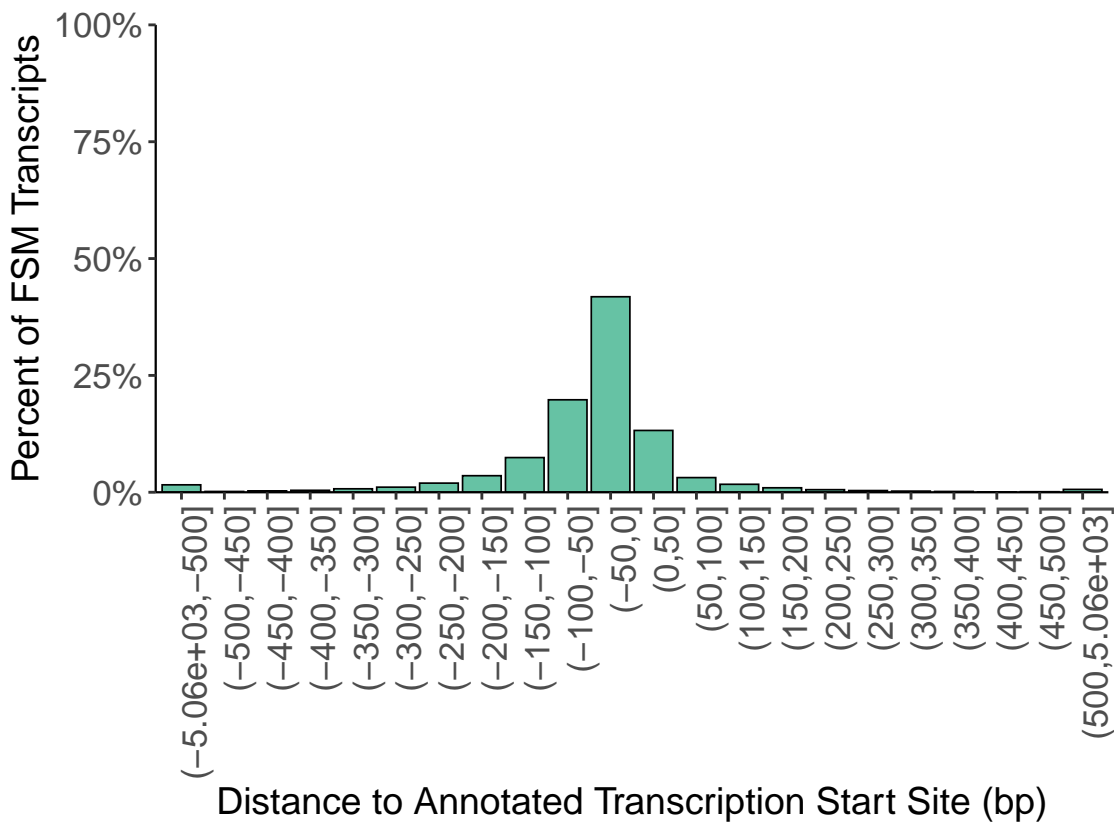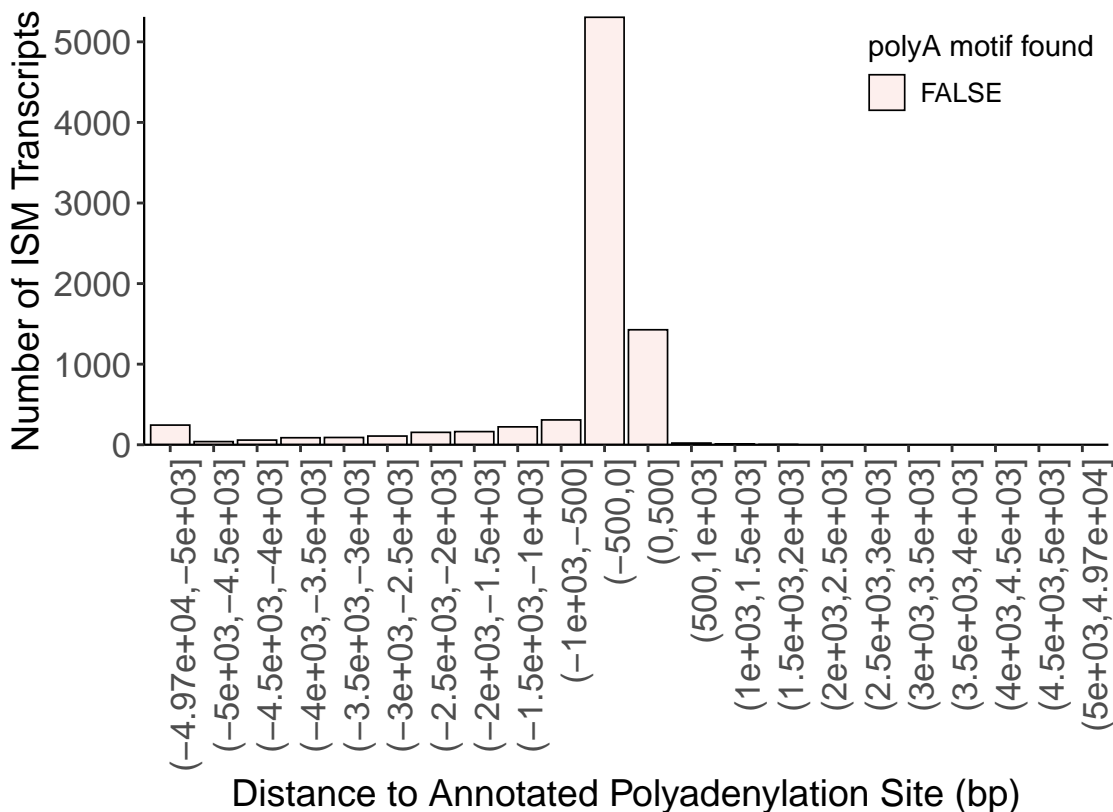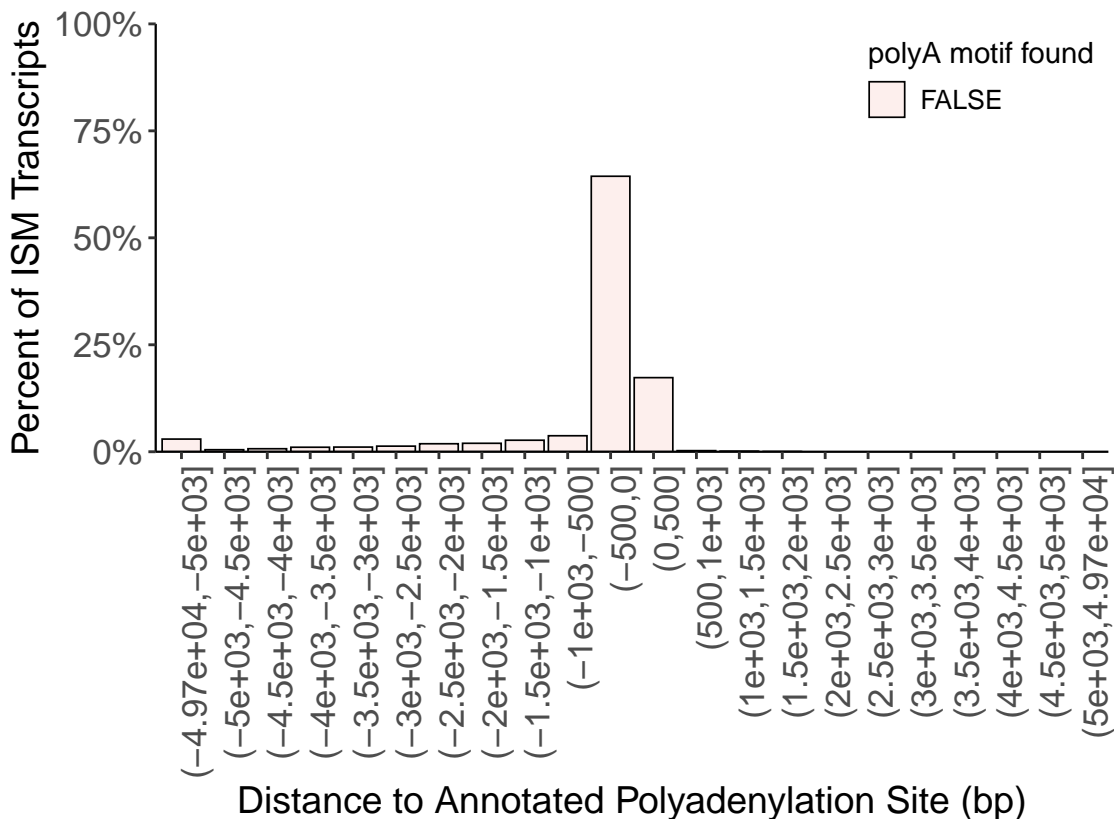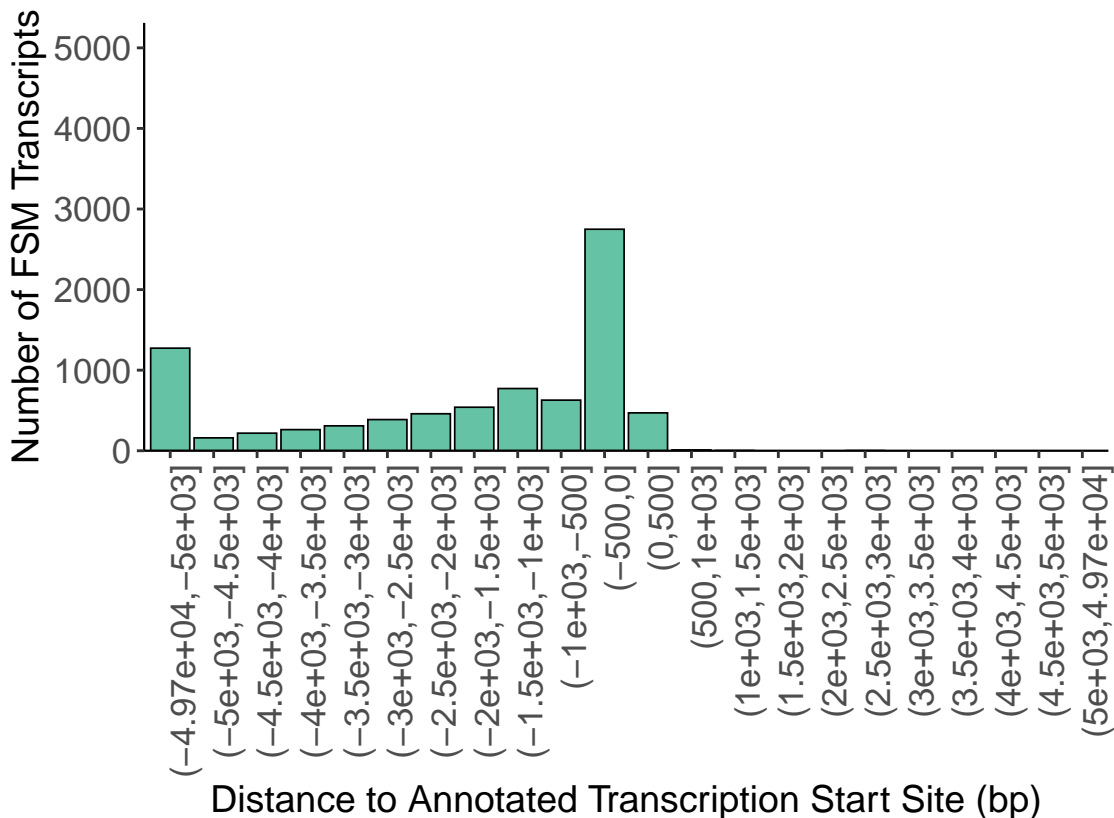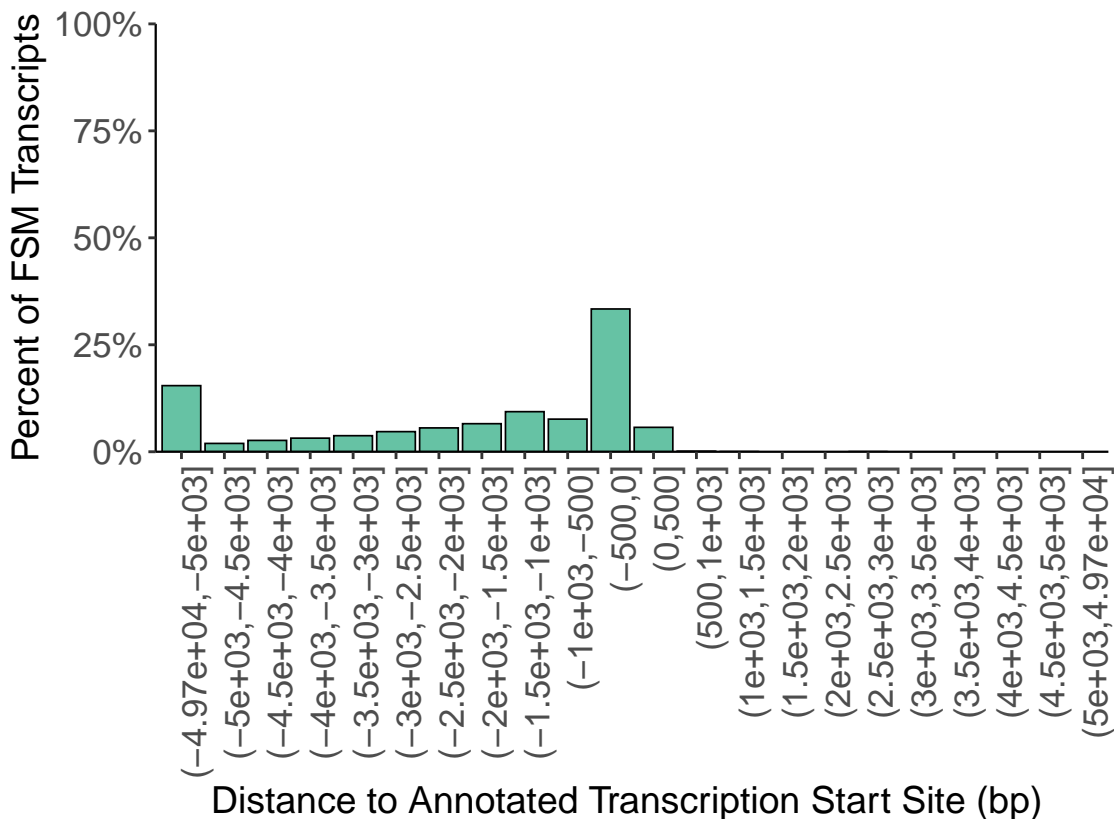
Negative values indicate upstream of annotated polyA site

polyA motif found
FALSE

Distance to Annotated Transcription Start Site, ISM only

Negative values indicate downstream of annotated TSS

Distance to Annotated Transcription Start Site, ISM only
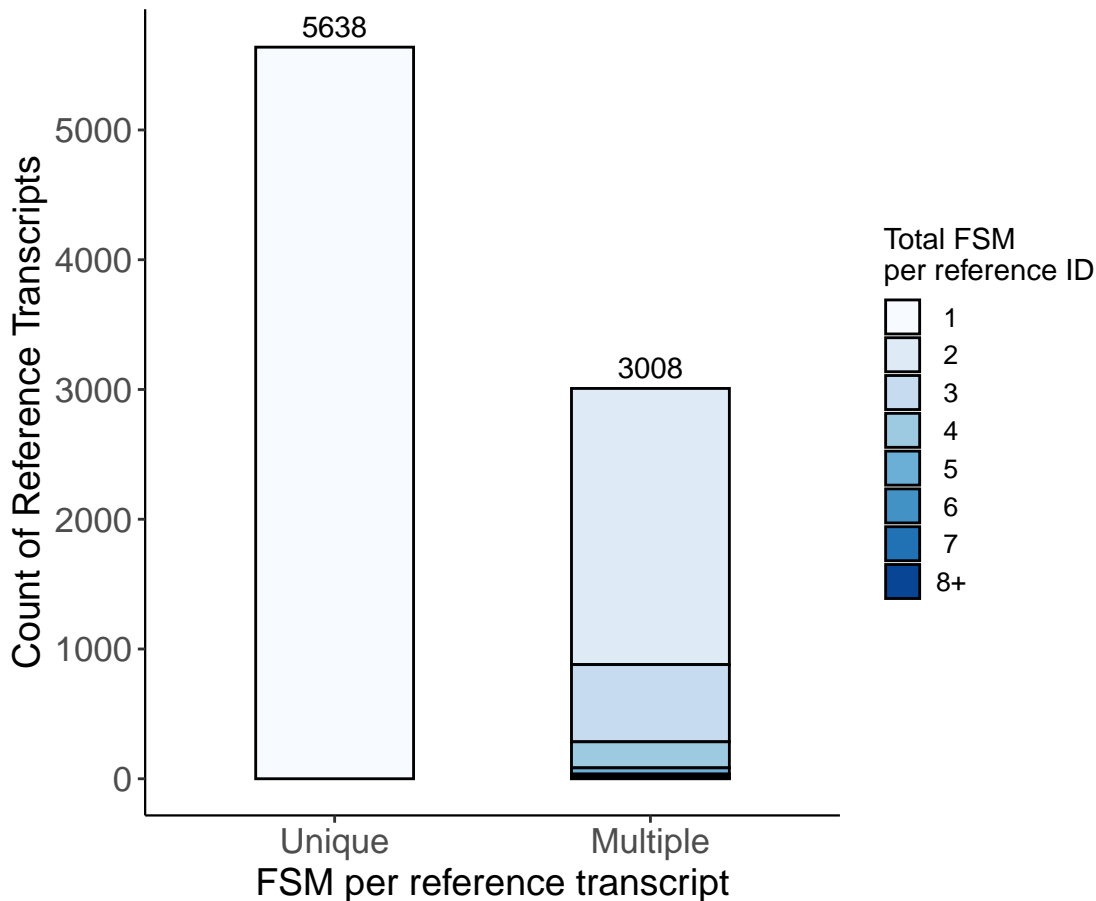
Negative values indicate downstream of annotated TSS

*Accumulation of FSM and ISM
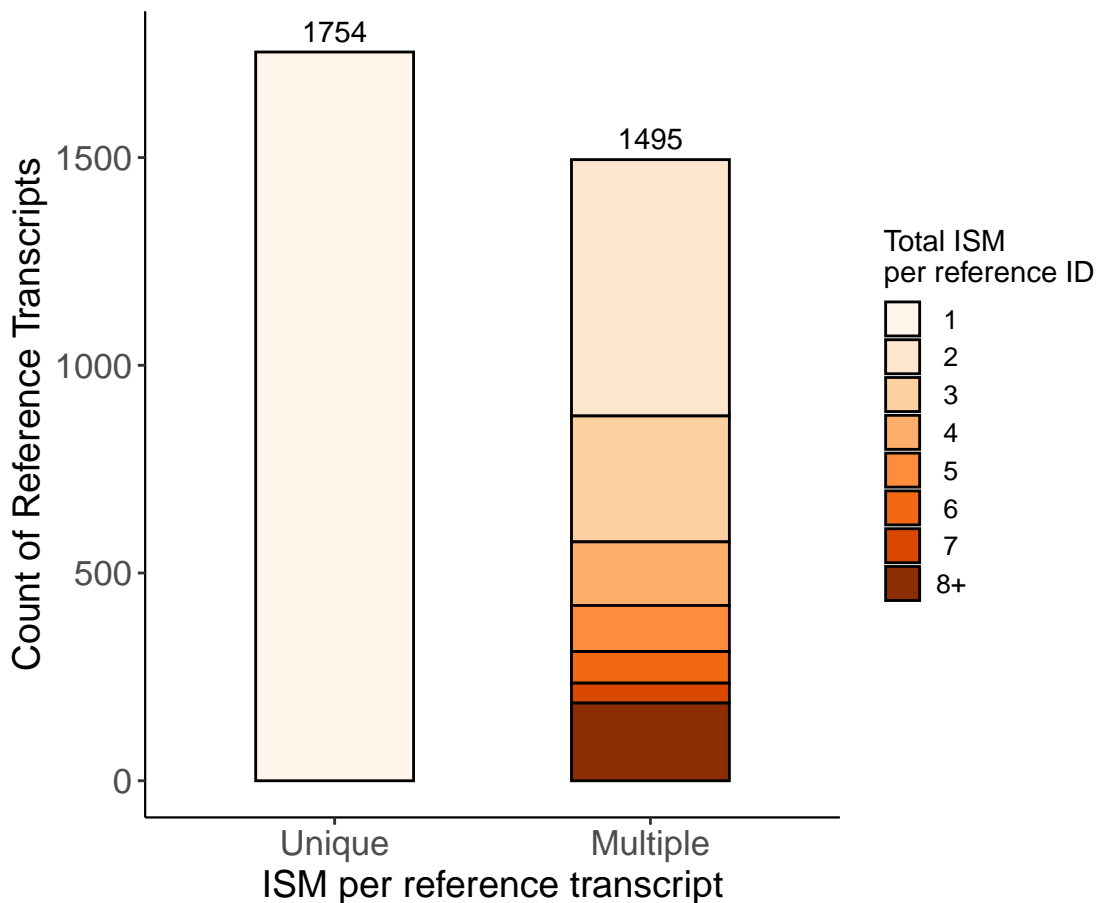to the same reference transcript*
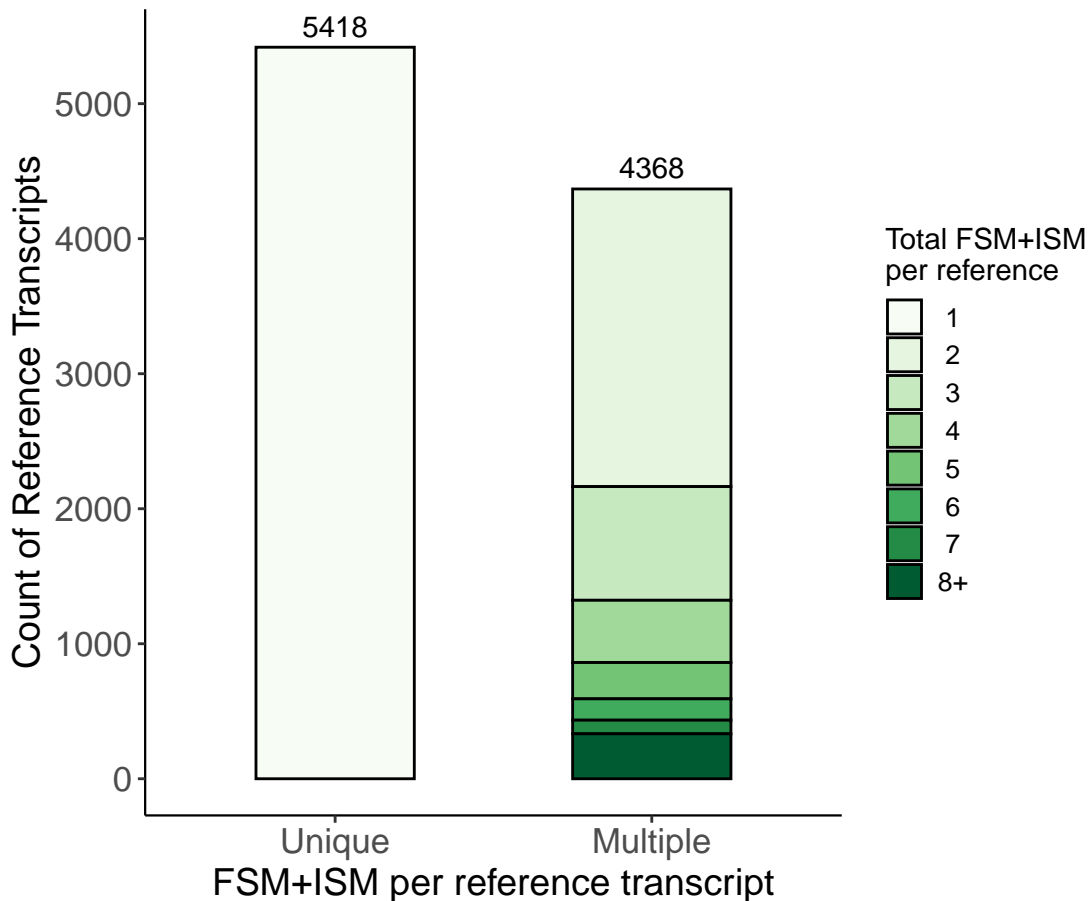
Reference transcript redundance
Only FSM

Reference transcript redundance
Only ISM
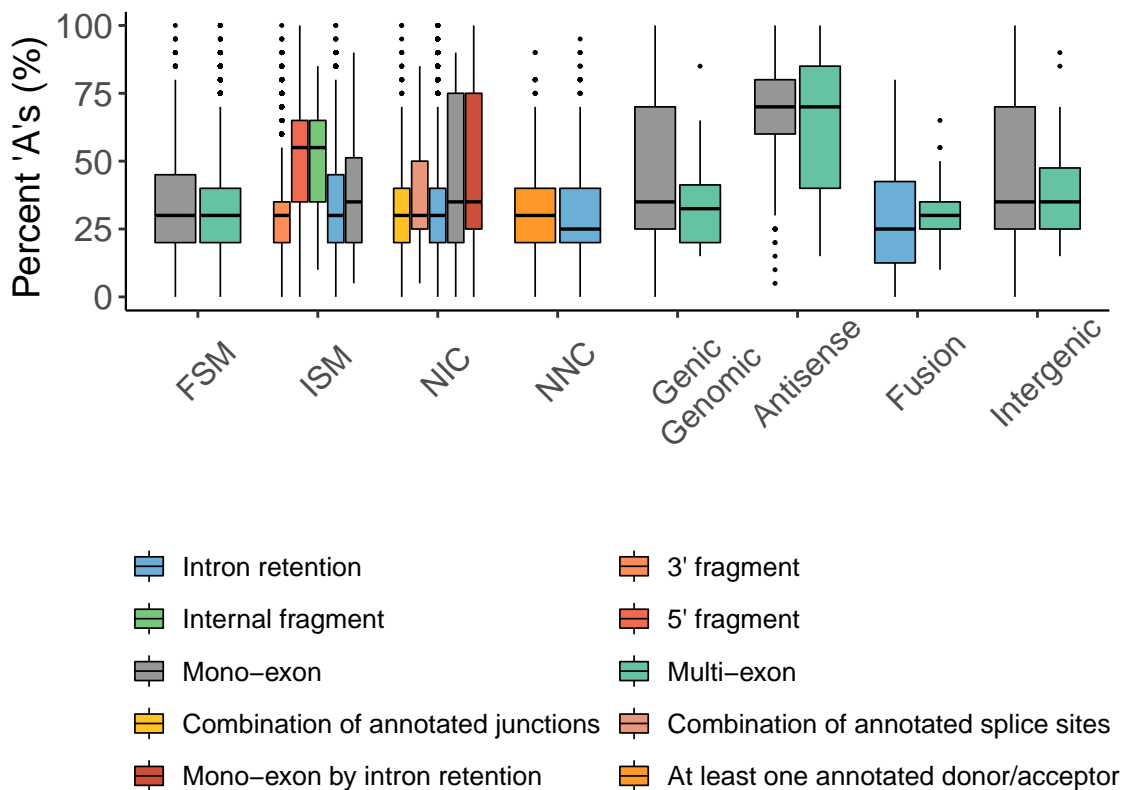
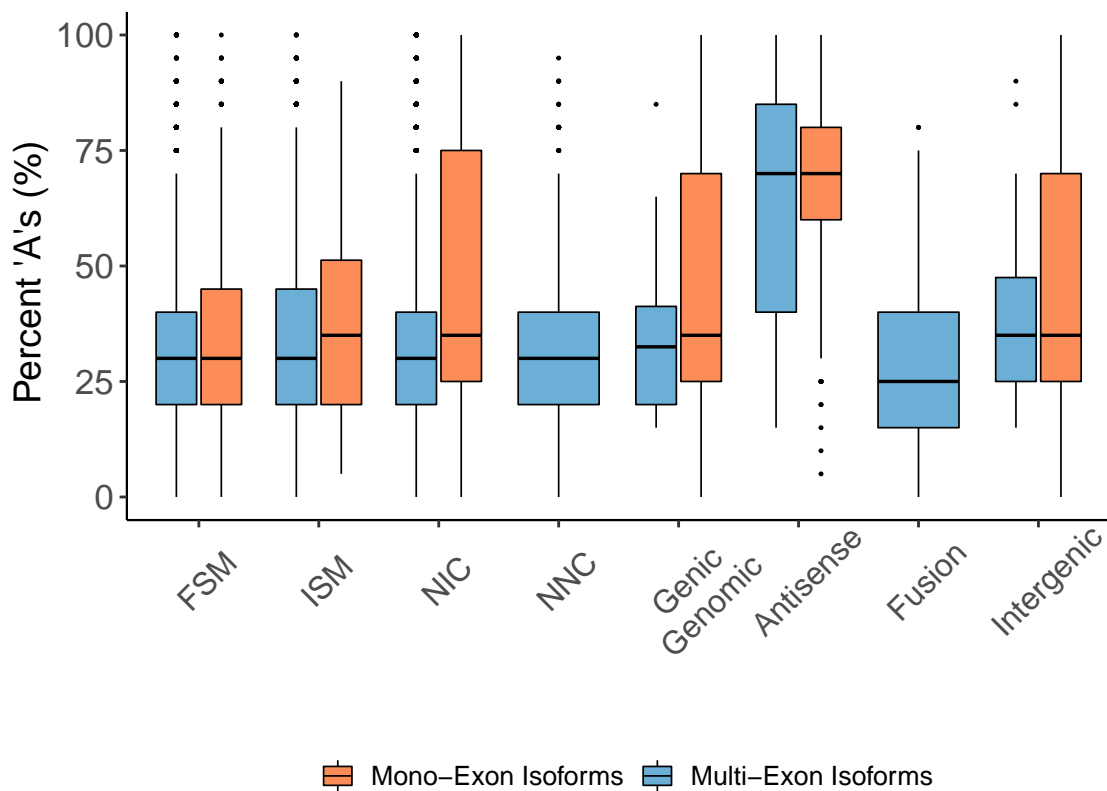Reference transcript redundance
FSM+ISM

Intra−Priming Quality Check

Possible Intra−Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp

Legend:
- Intron retention
- Internal fragment
- Mono−exon
- Combination of annotated junctions
- Mono−exon by intron retention
- 3' fragment
- 5' fragment
- Multi−exon
- Combination of annotated splice sites
- 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

Coding Isoforms   Non−Coding Isoforms
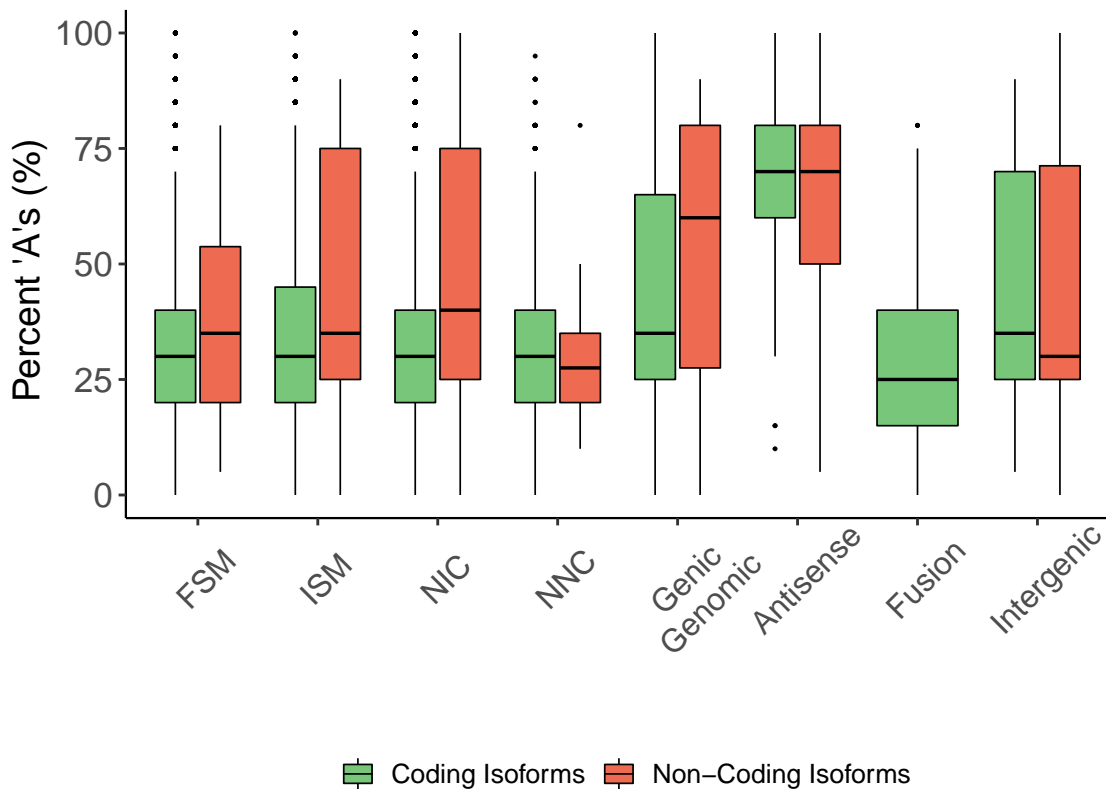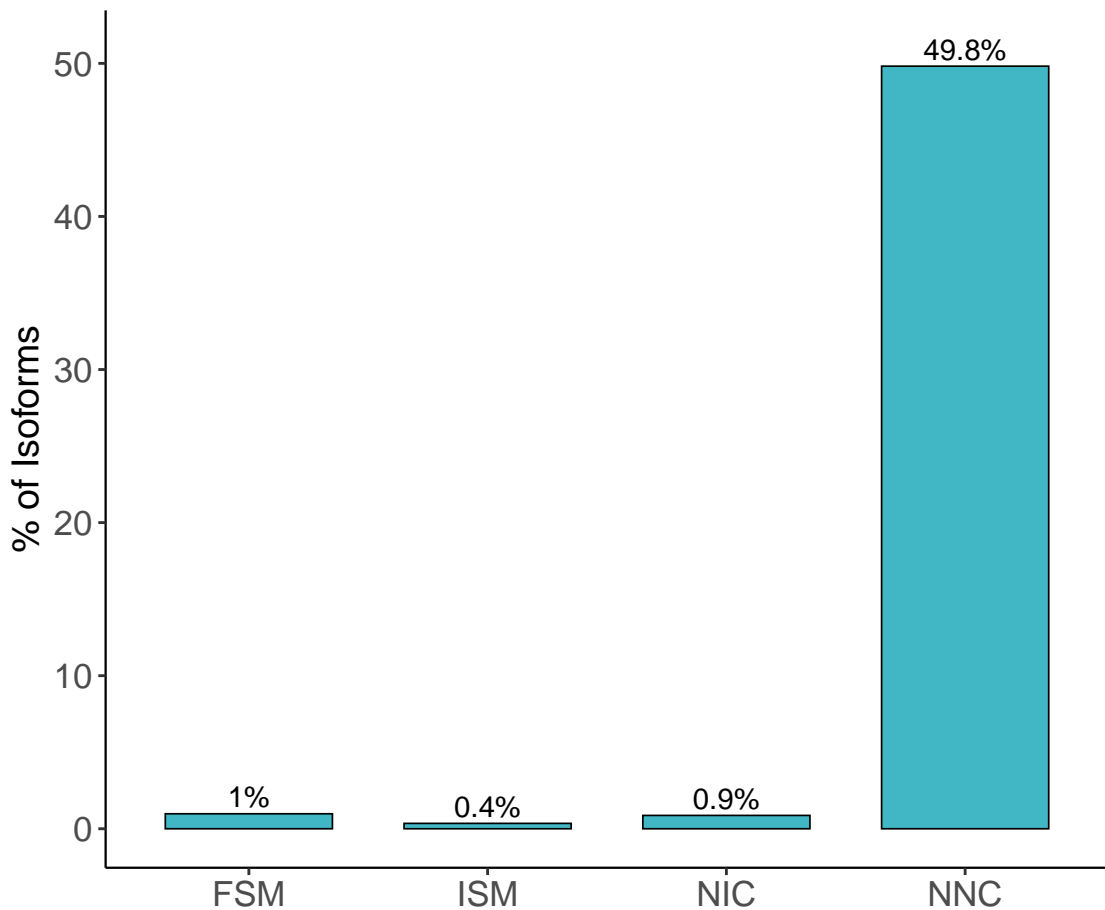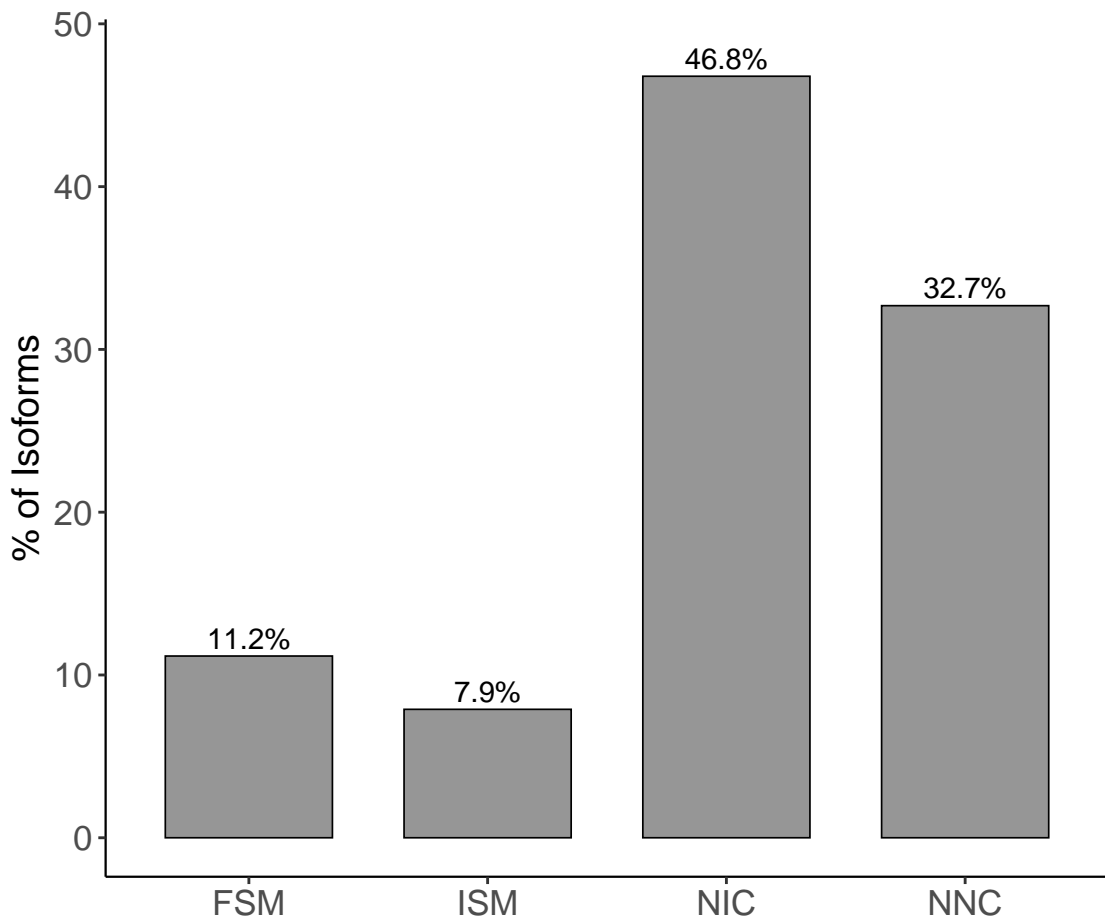
Quality Controls

Incidence of RT−switching
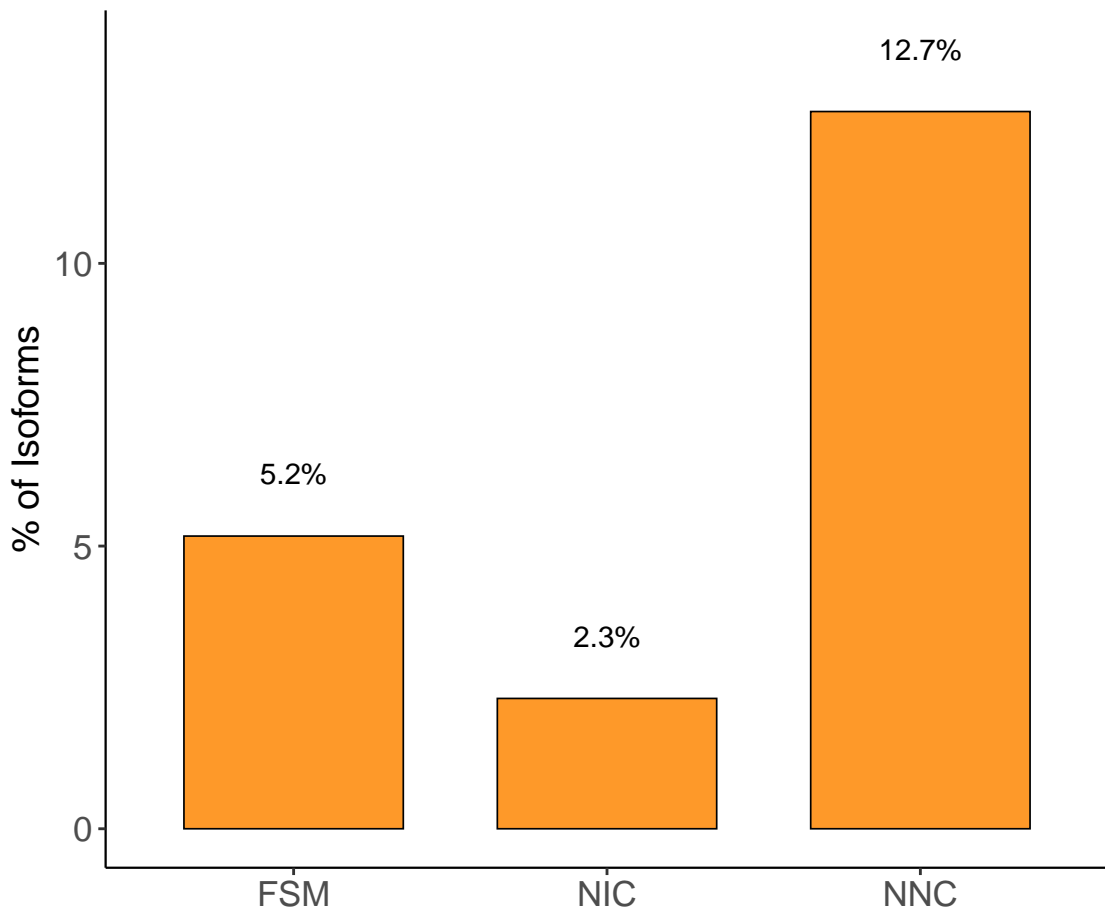
Incidence of Non−Canonical Junctions

Incidence of NMD by structural category

Quality control attributes across structural categories