

SQANTI3 report

Unique Genes: 650
Unique Isoforms: 3925

Transcript Classification

Category	Isoforms, count
FSM	537
ISM	1134
NIC	805
NNC	1139
Genic Genomic	56
Antisense	29
Fusion	38
Intergenic	187
Genic Intron	0

Gene Classification

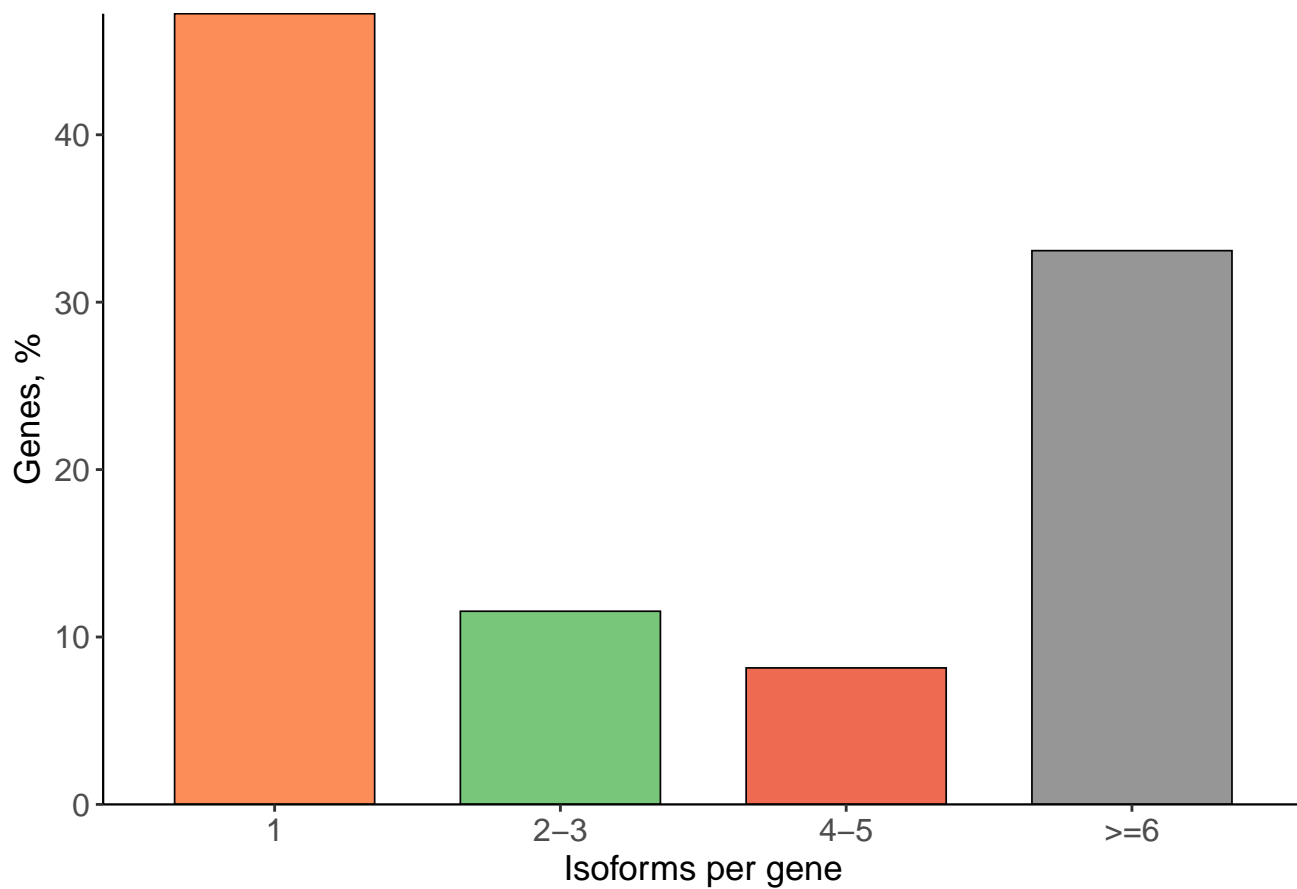
Category	Genes, count
Annotated Genes	437
Novel Genes	213

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	3373	69.72
Known Non–canonical	4	0.08
Novel canonical	1196	24.72
Novel Non–canonical	265	5.48

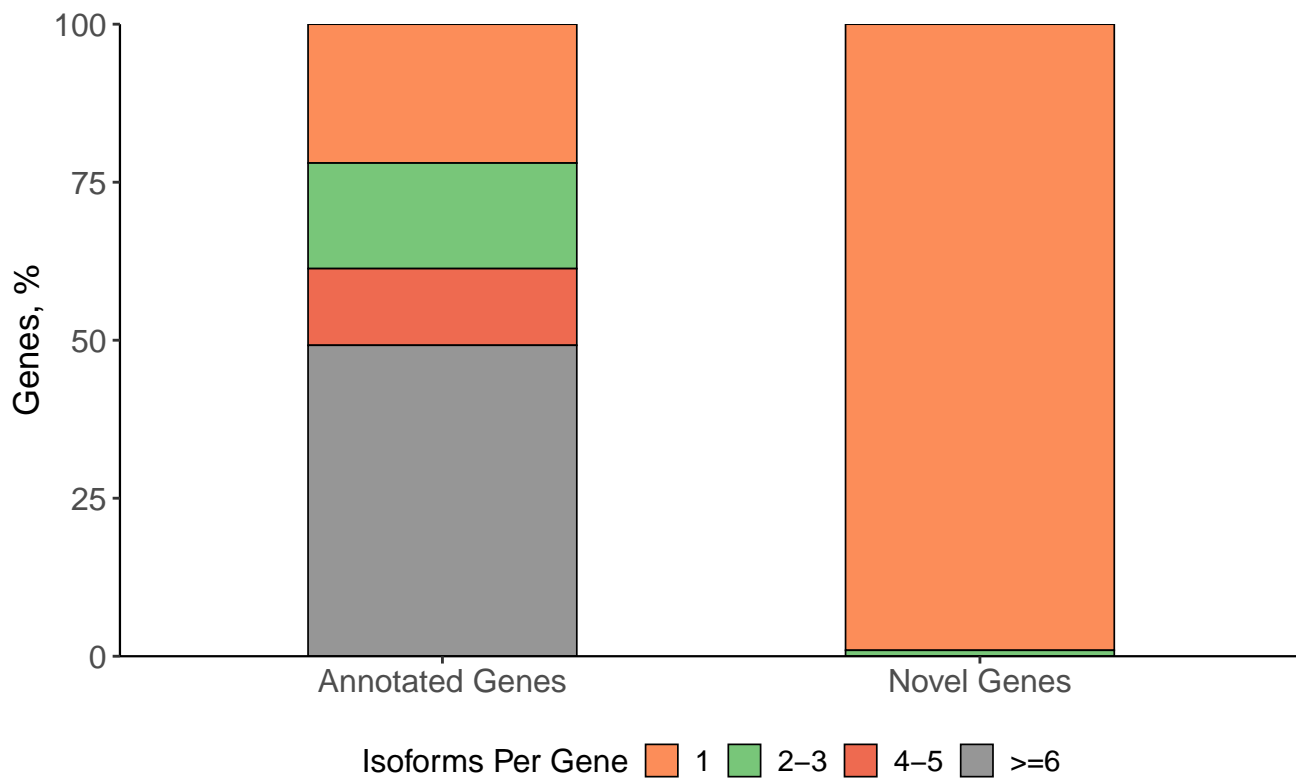
Gene Characterization

Number of Isoforms per Gene

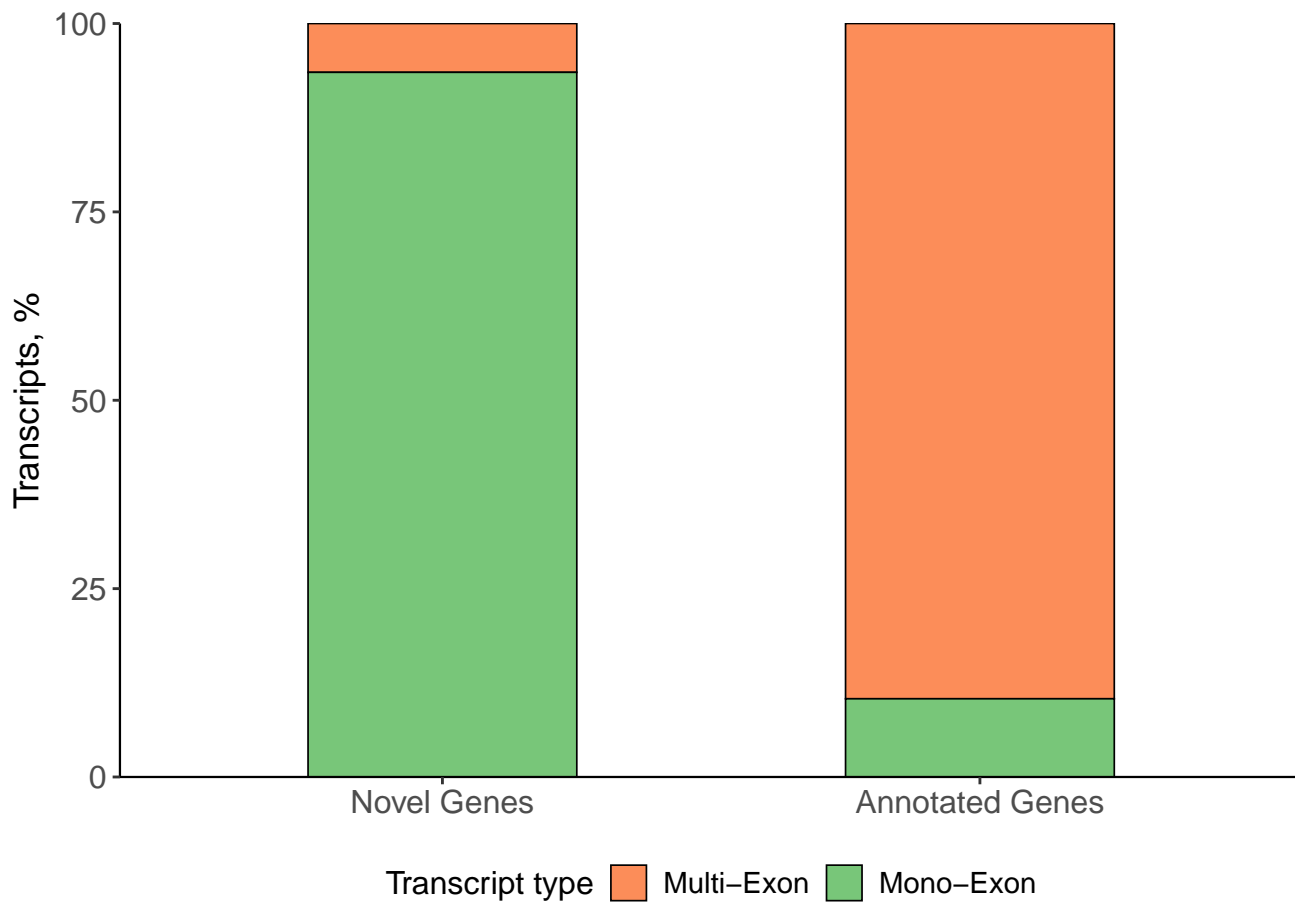


Number of Isoforms per Gene

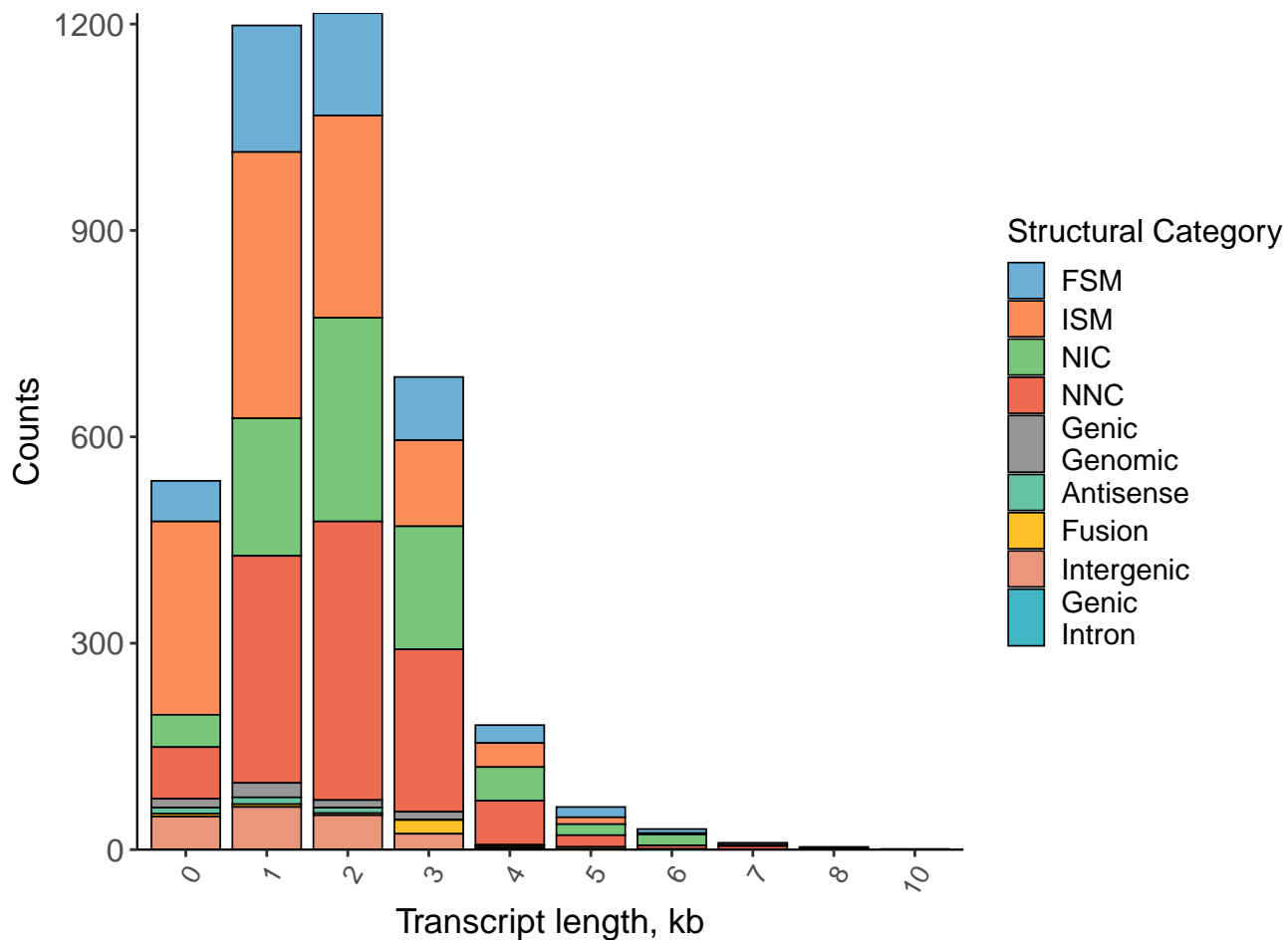
Known vs Novel Genes



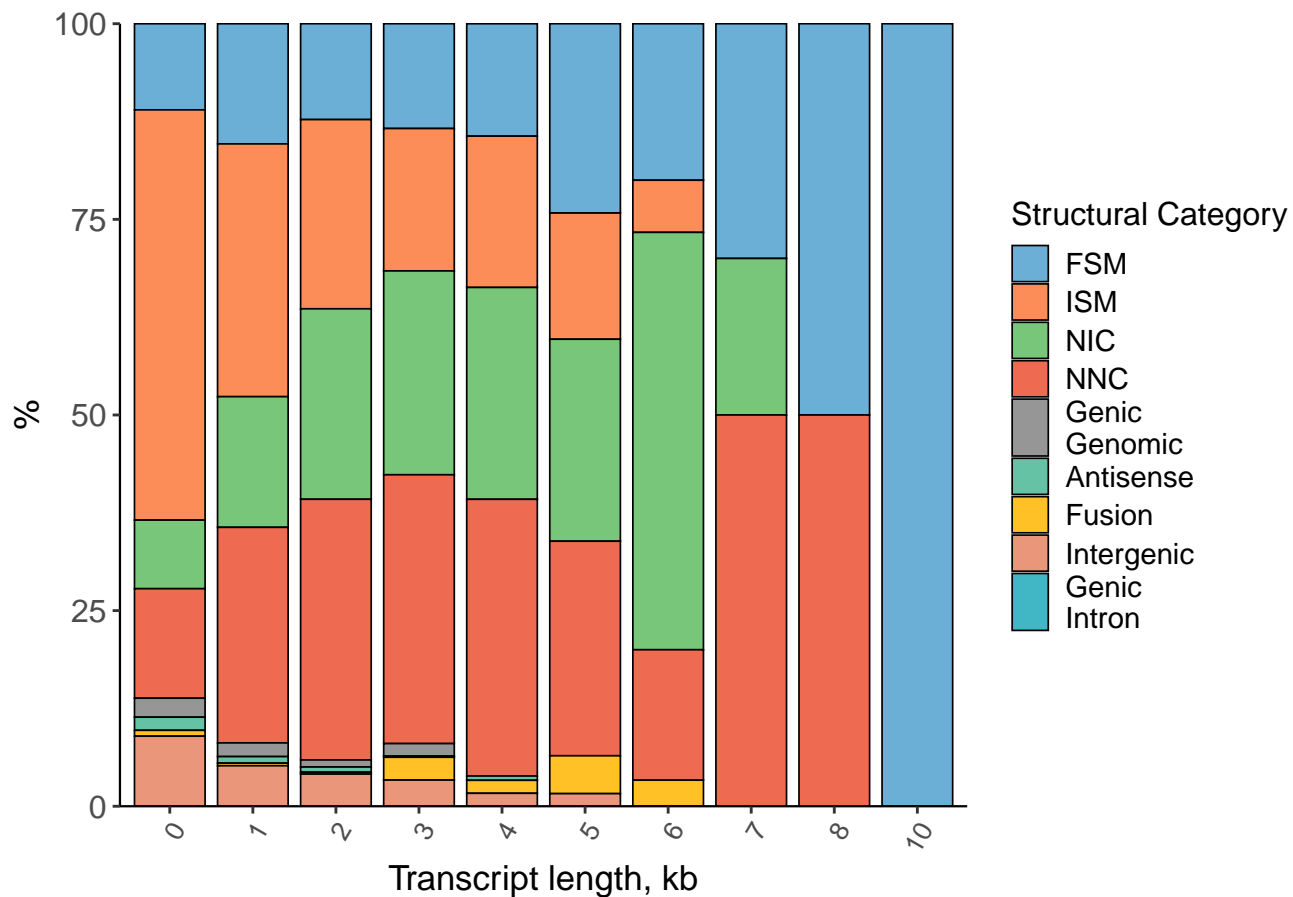
Distribution of Mono- vs Multi-Exon Transcripts



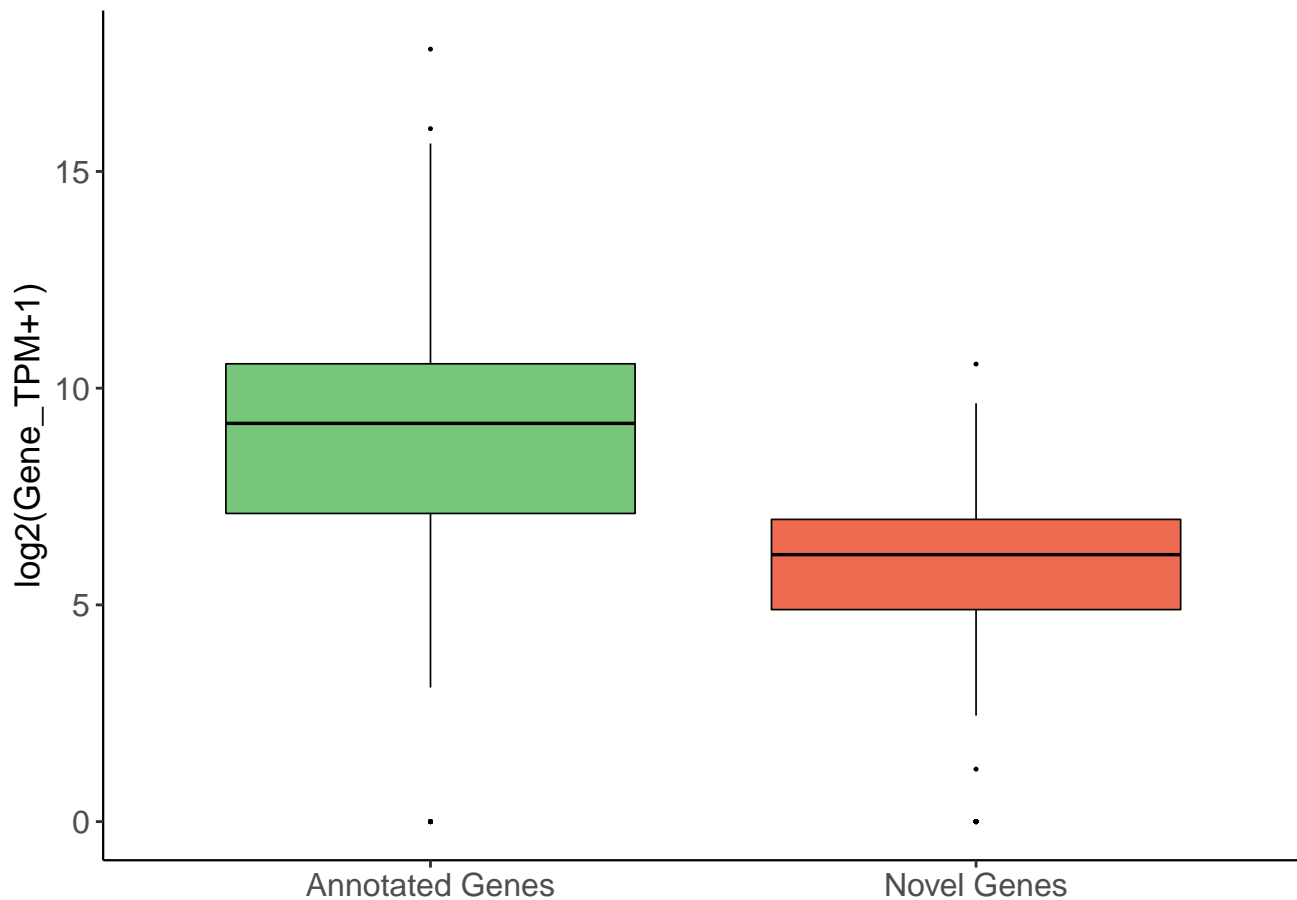
Structural Categories by Transcript Length



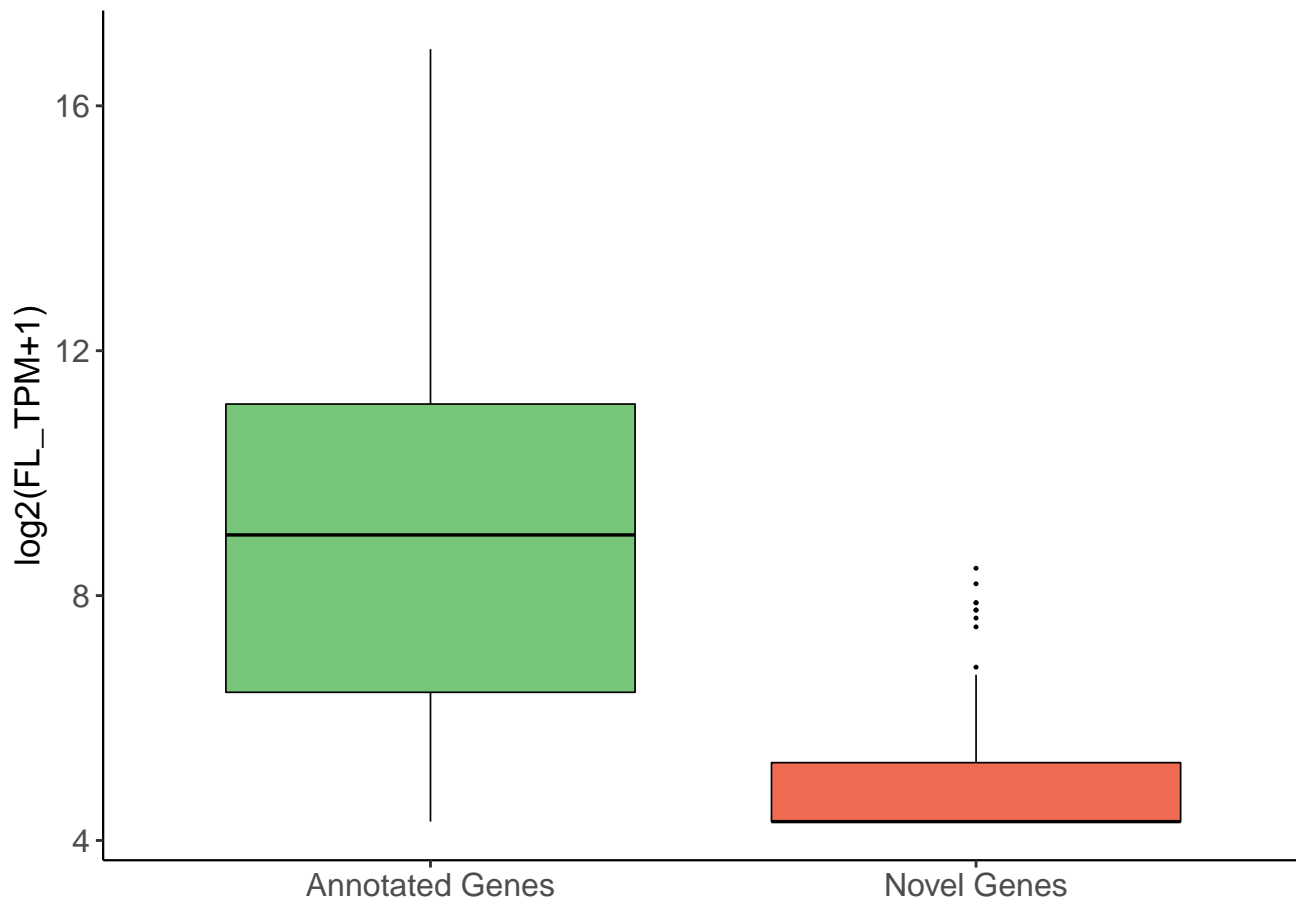
Structural Categories by Transcript Length



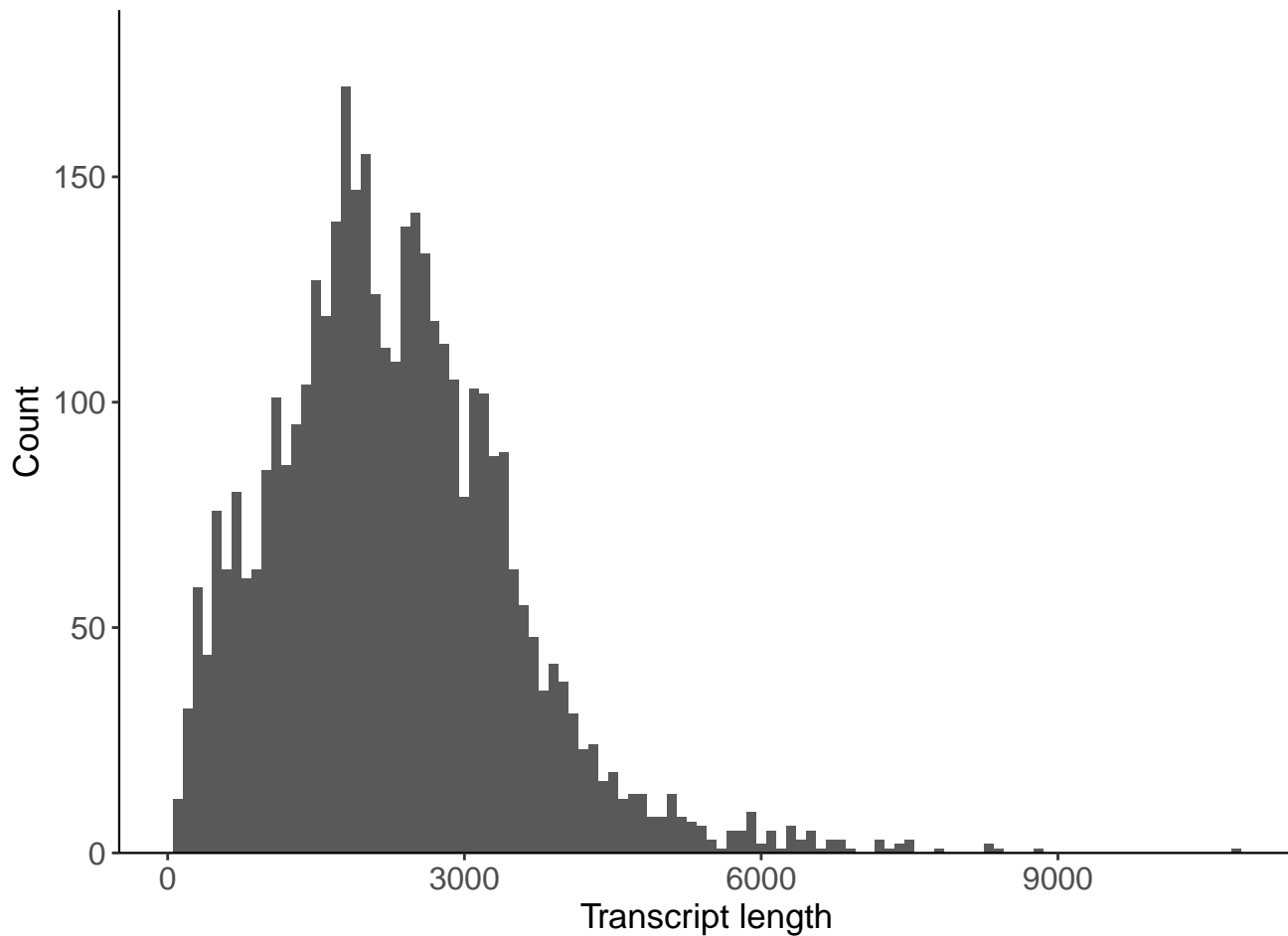
Annotated vs Novel Gene Expression



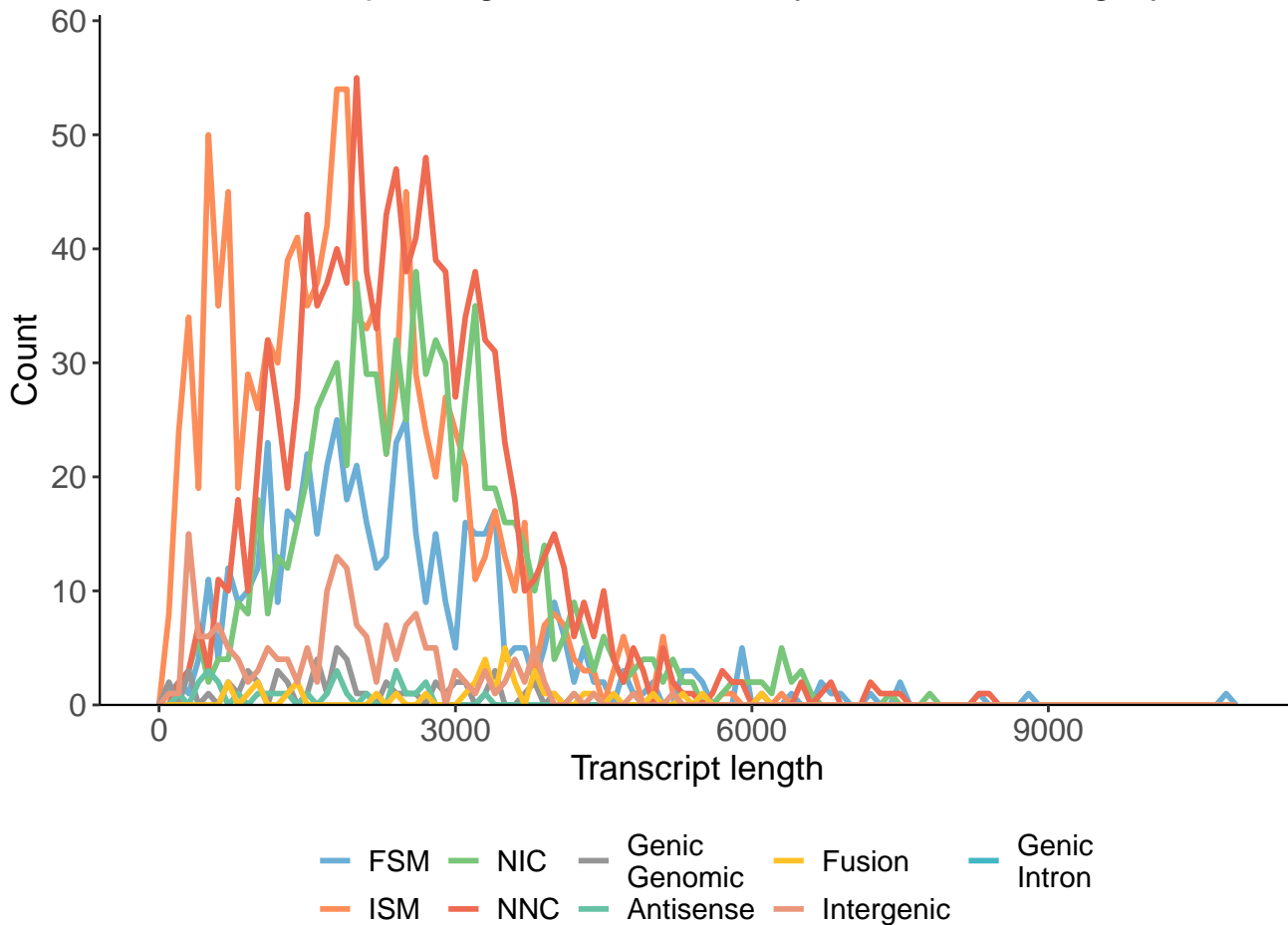
Number of FL reads per Gene by Type of Gene Annotation



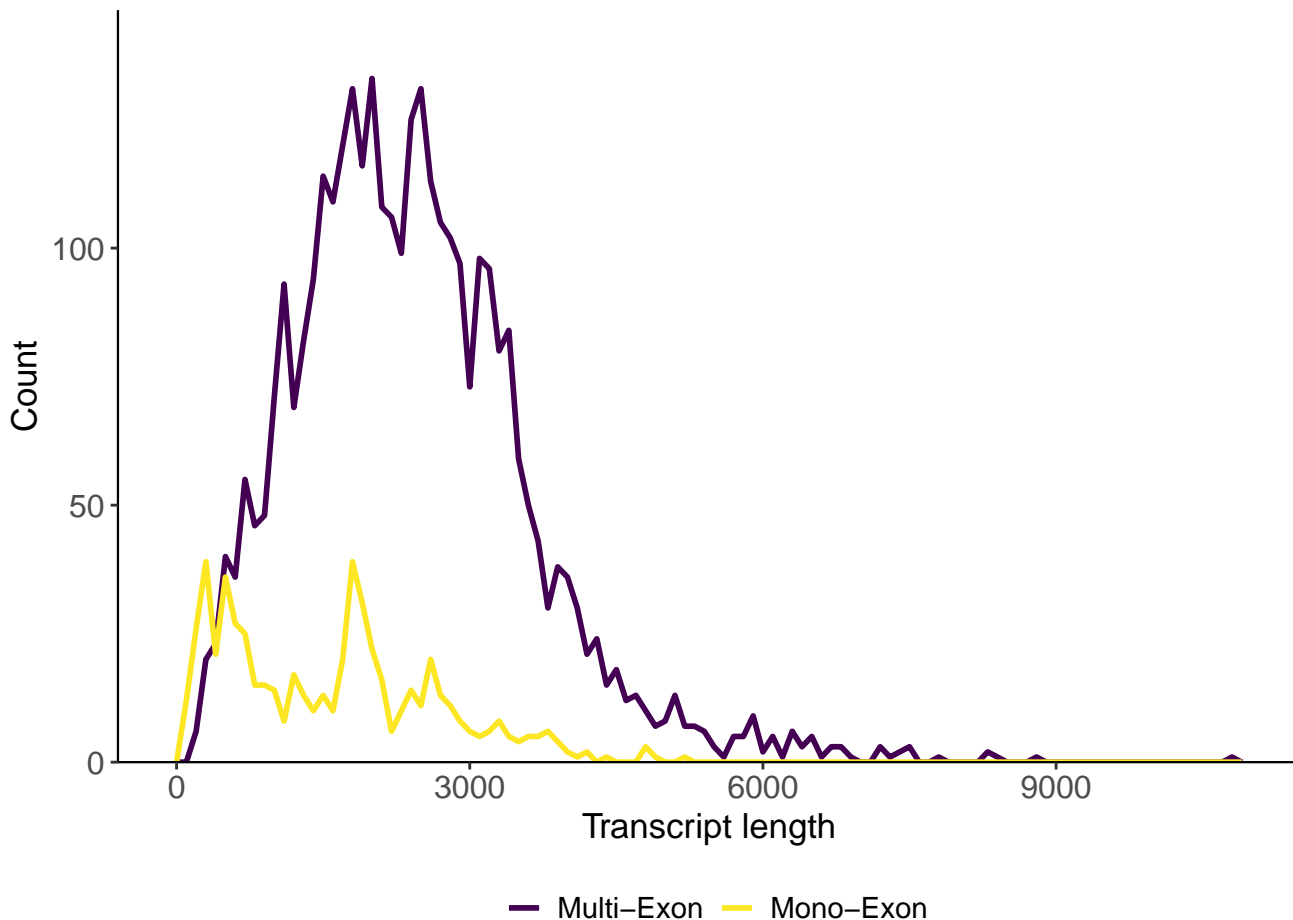
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

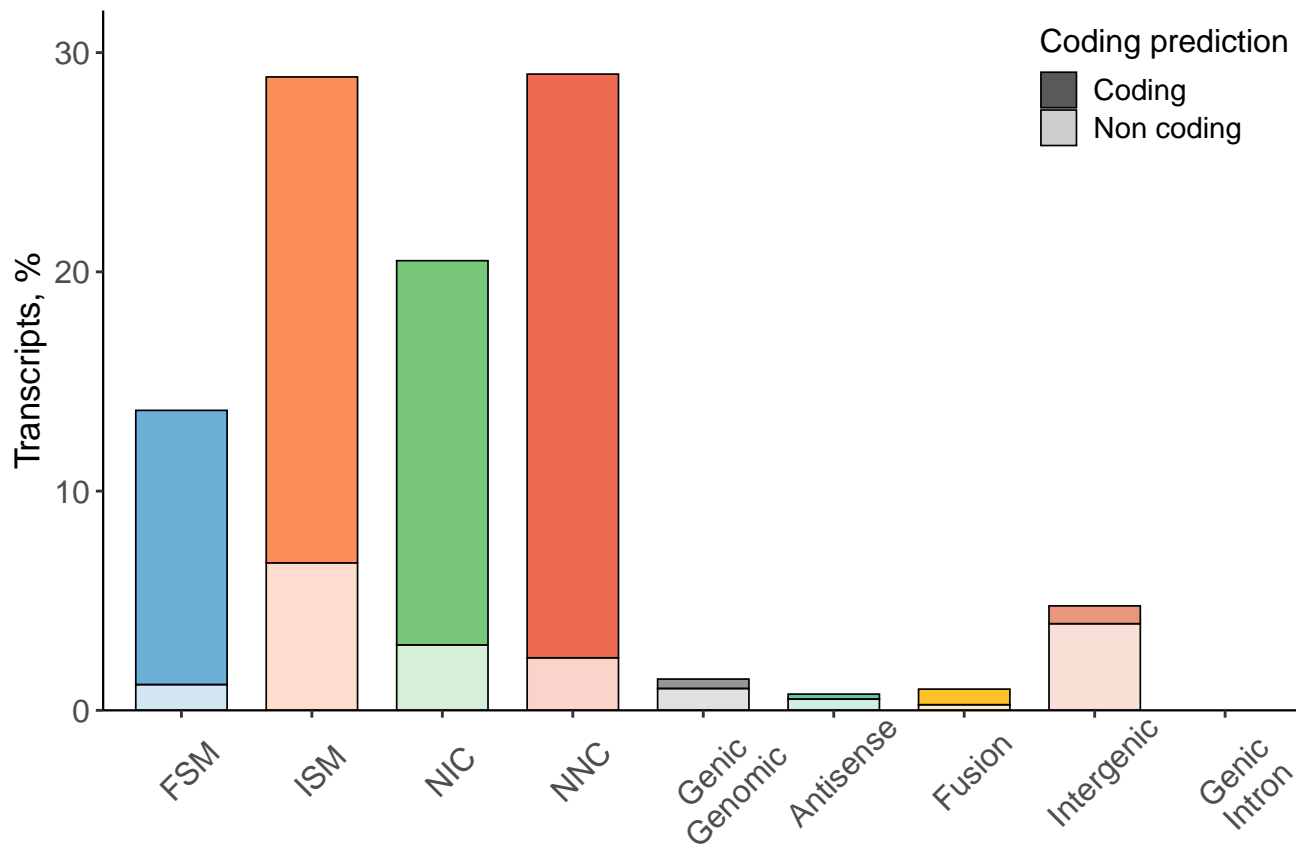


Mono- vs Multi- Exon Transcript Lengths Distribution

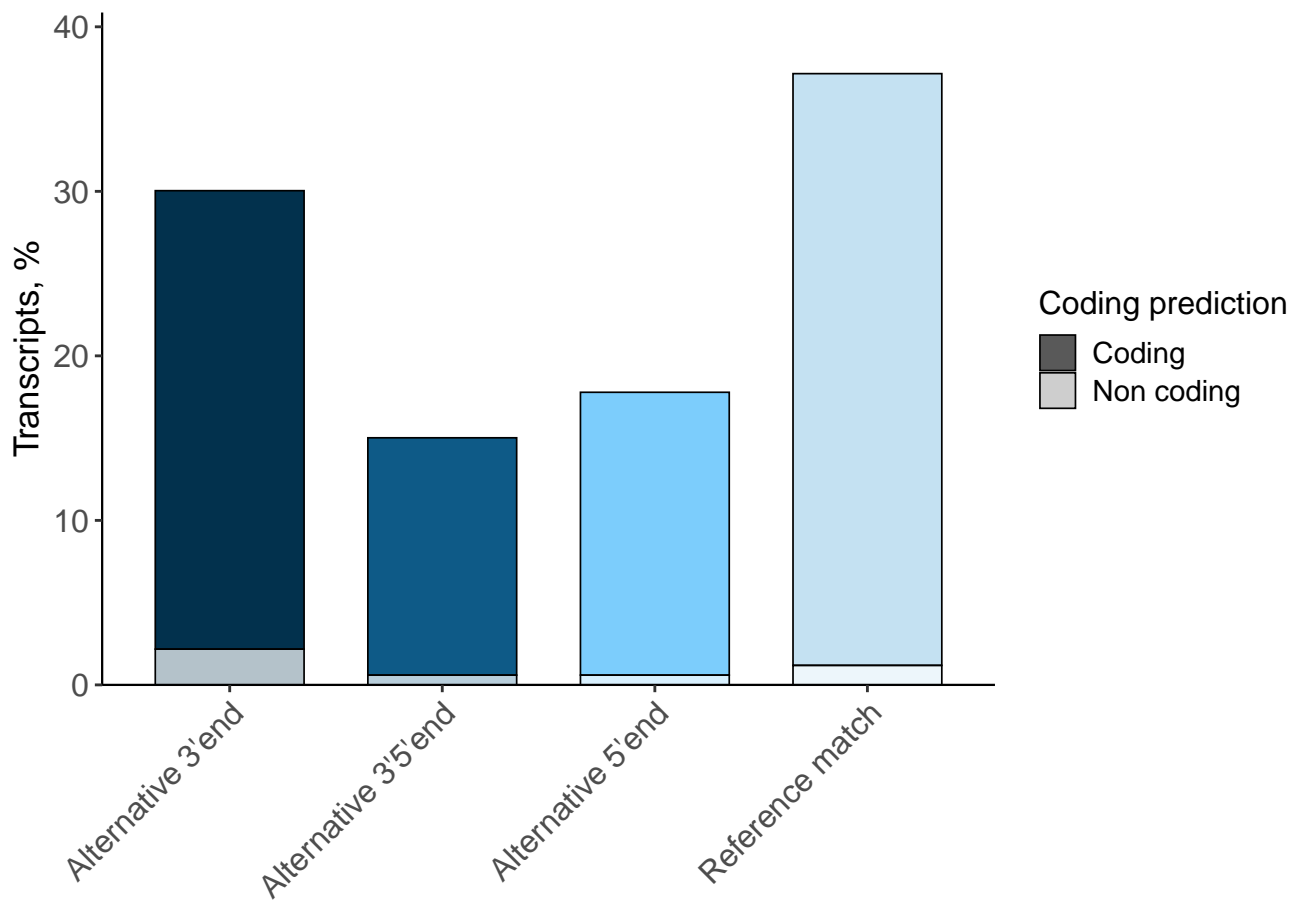


Structural Isoform Characterization

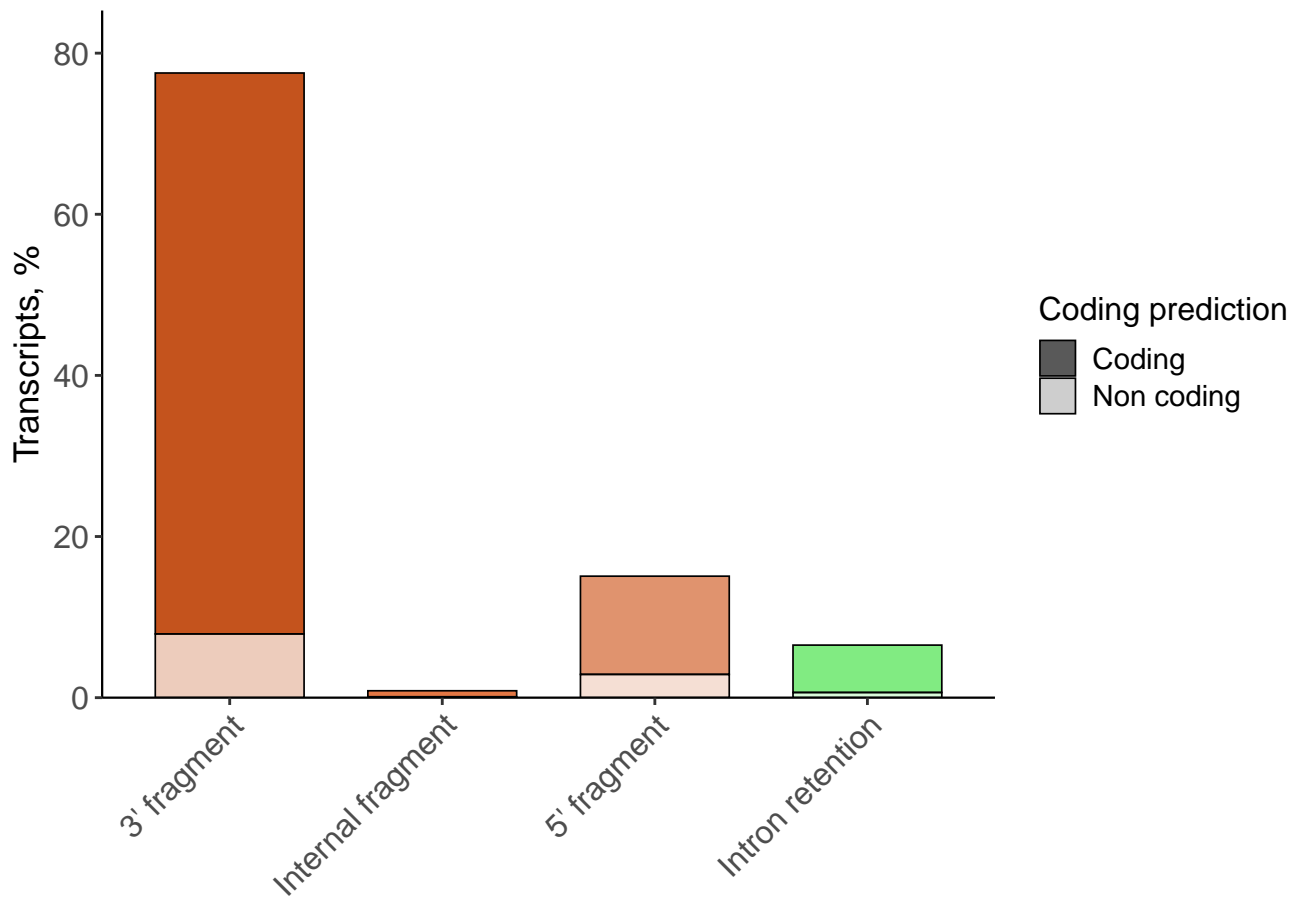
Isoform Distribution Across Structural Categories



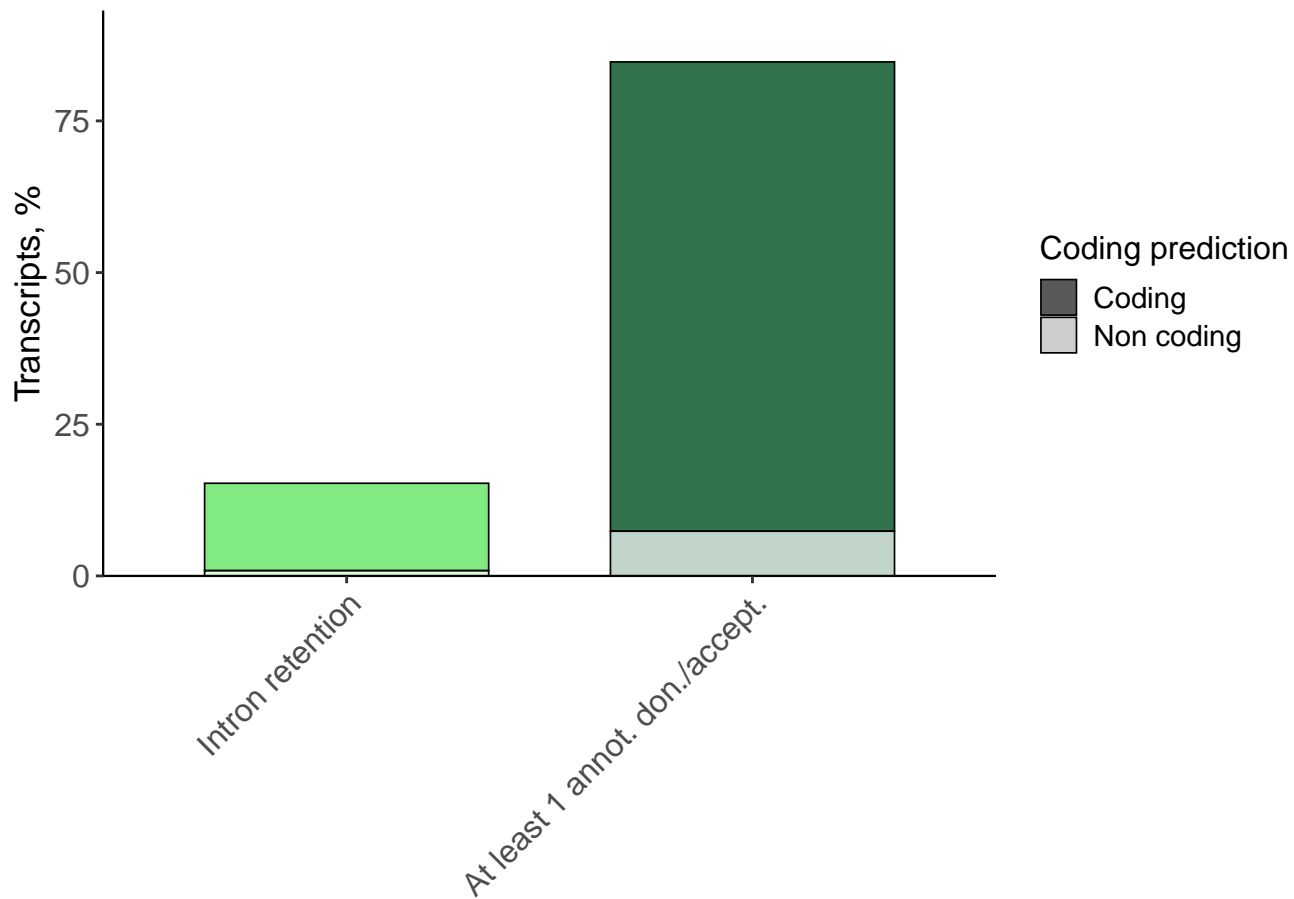
Isoform Distribution Across FSM



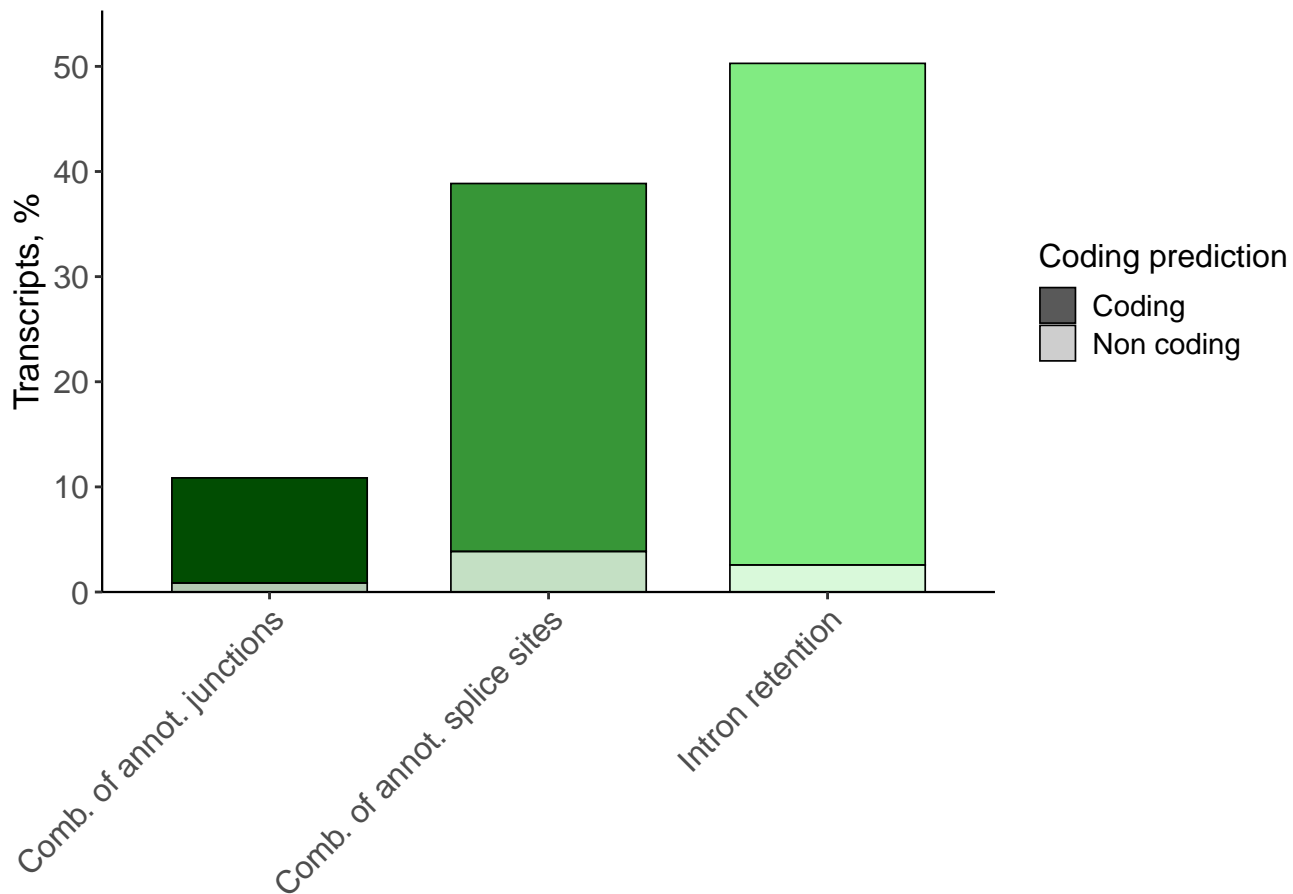
Isoform Distribution Across ISM



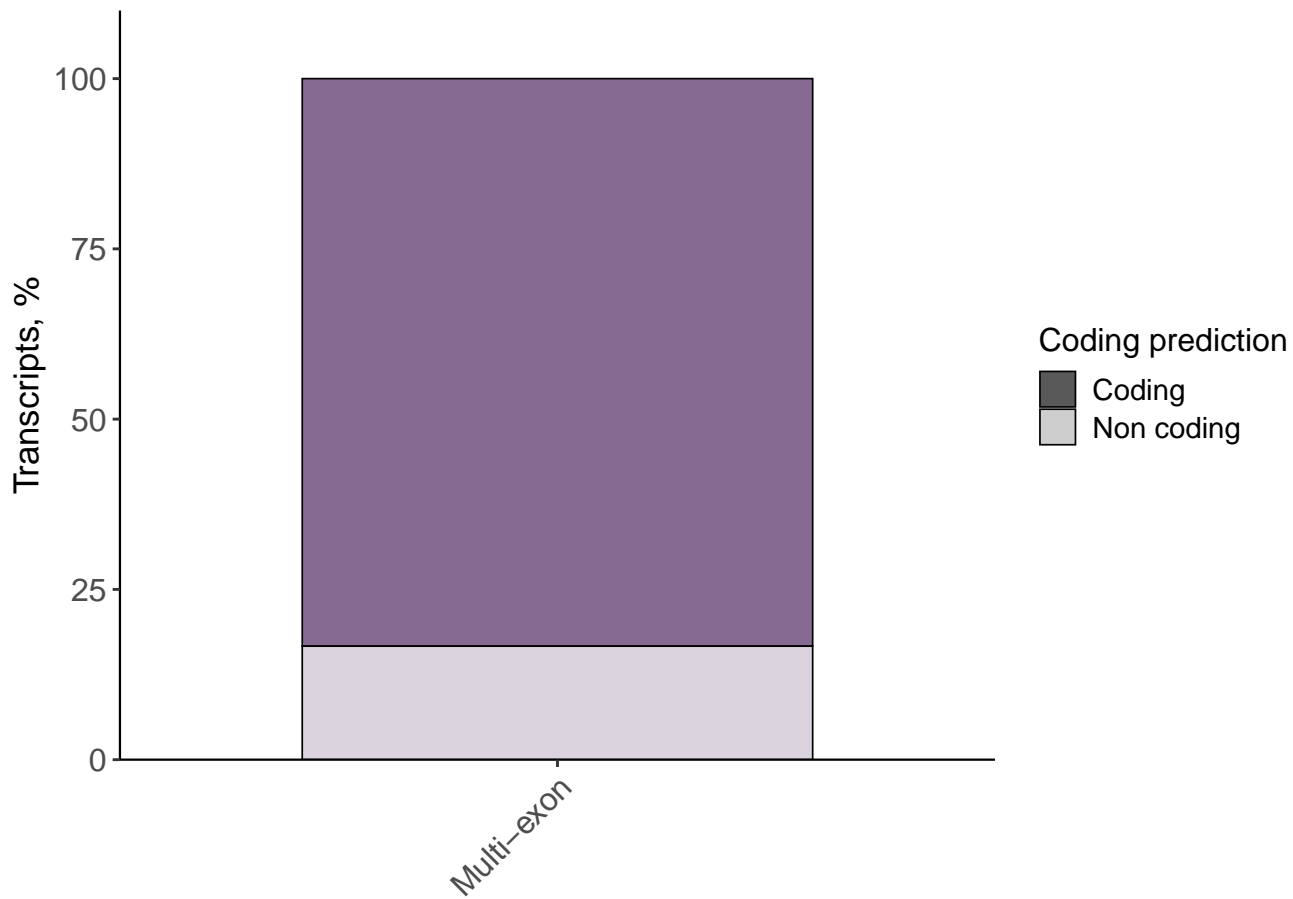
Isoform Distribution Across NNC



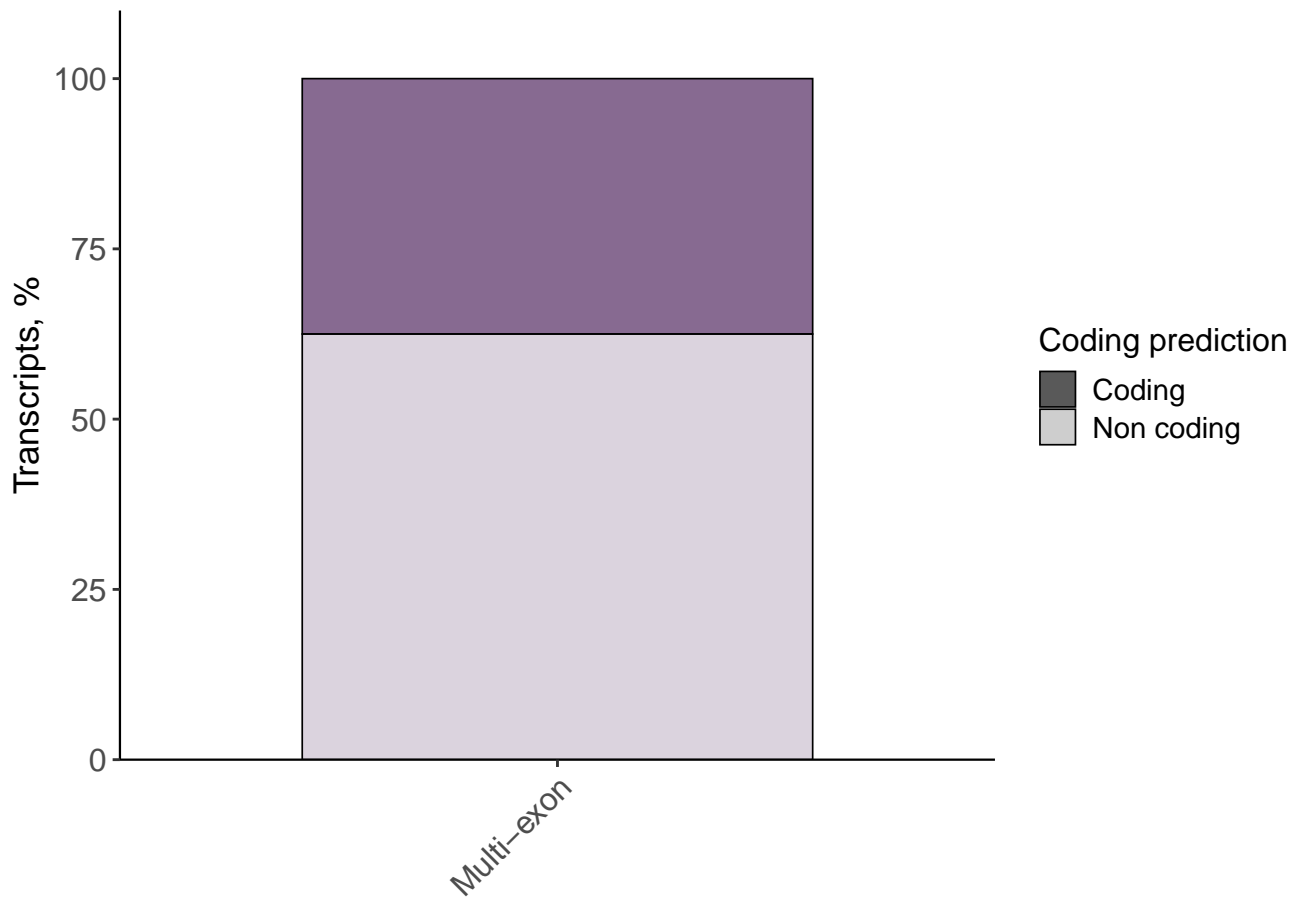
Isoform Distribution Across NIC



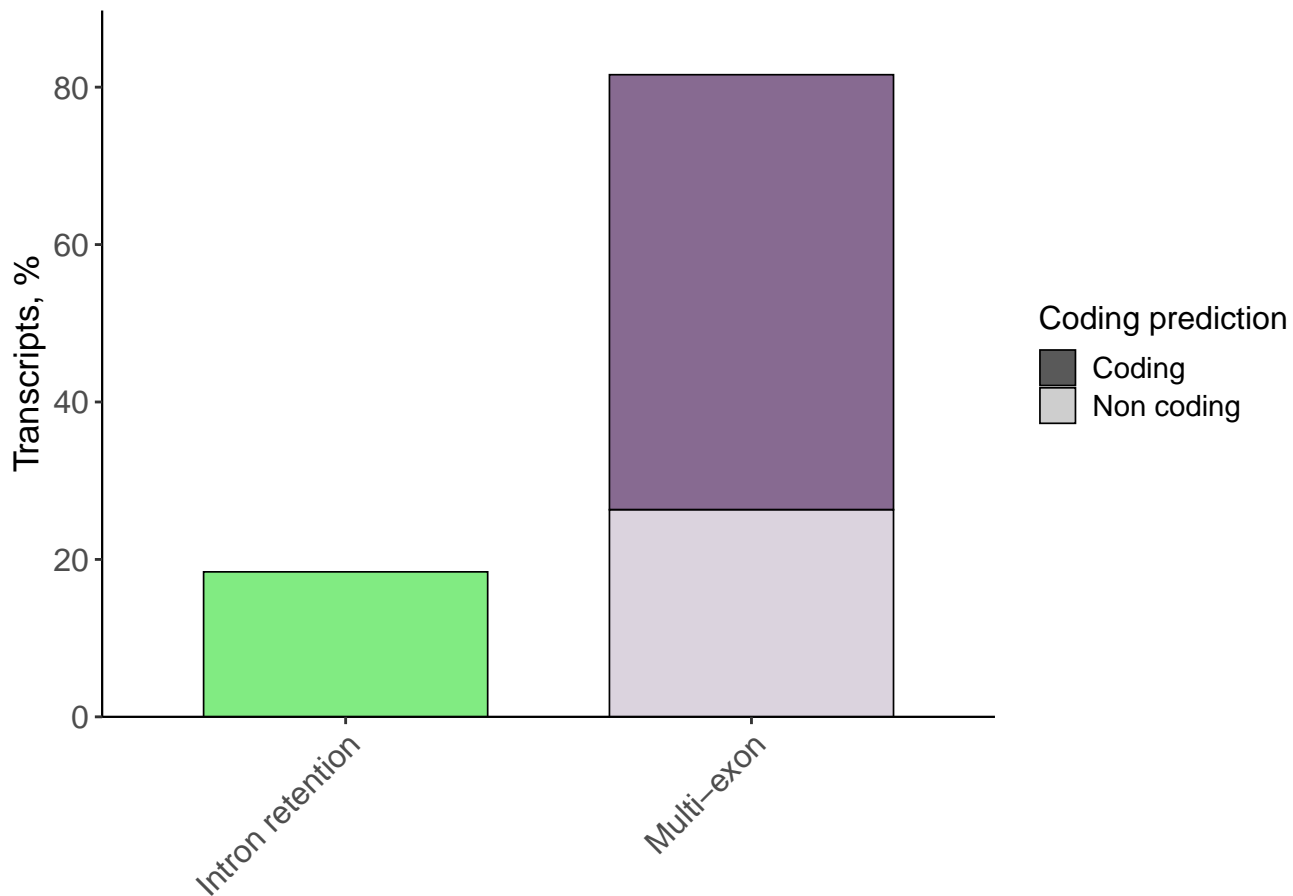
Isoform Distribution Across Genic Genomic



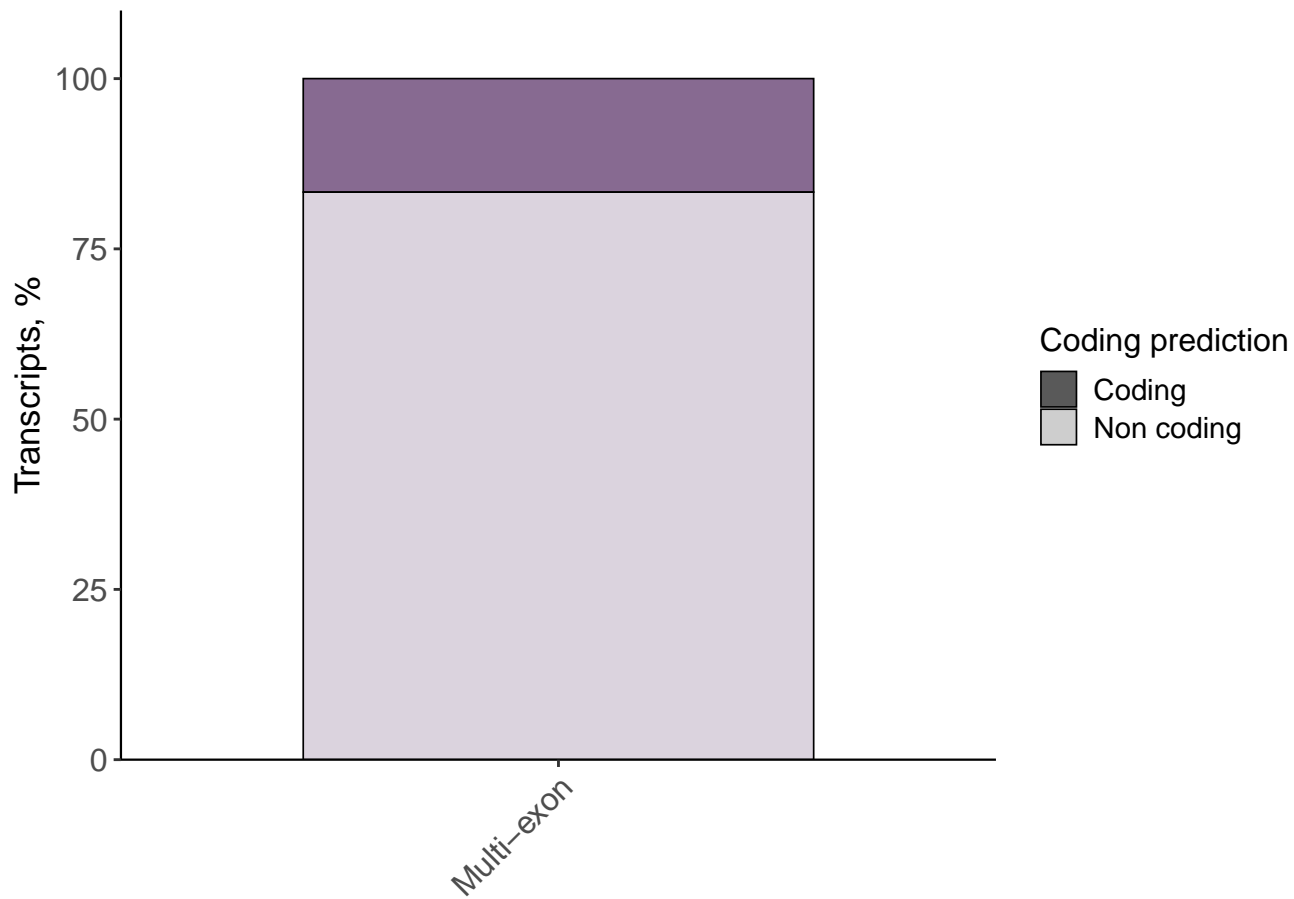
Isoform Distribution Across Antisense



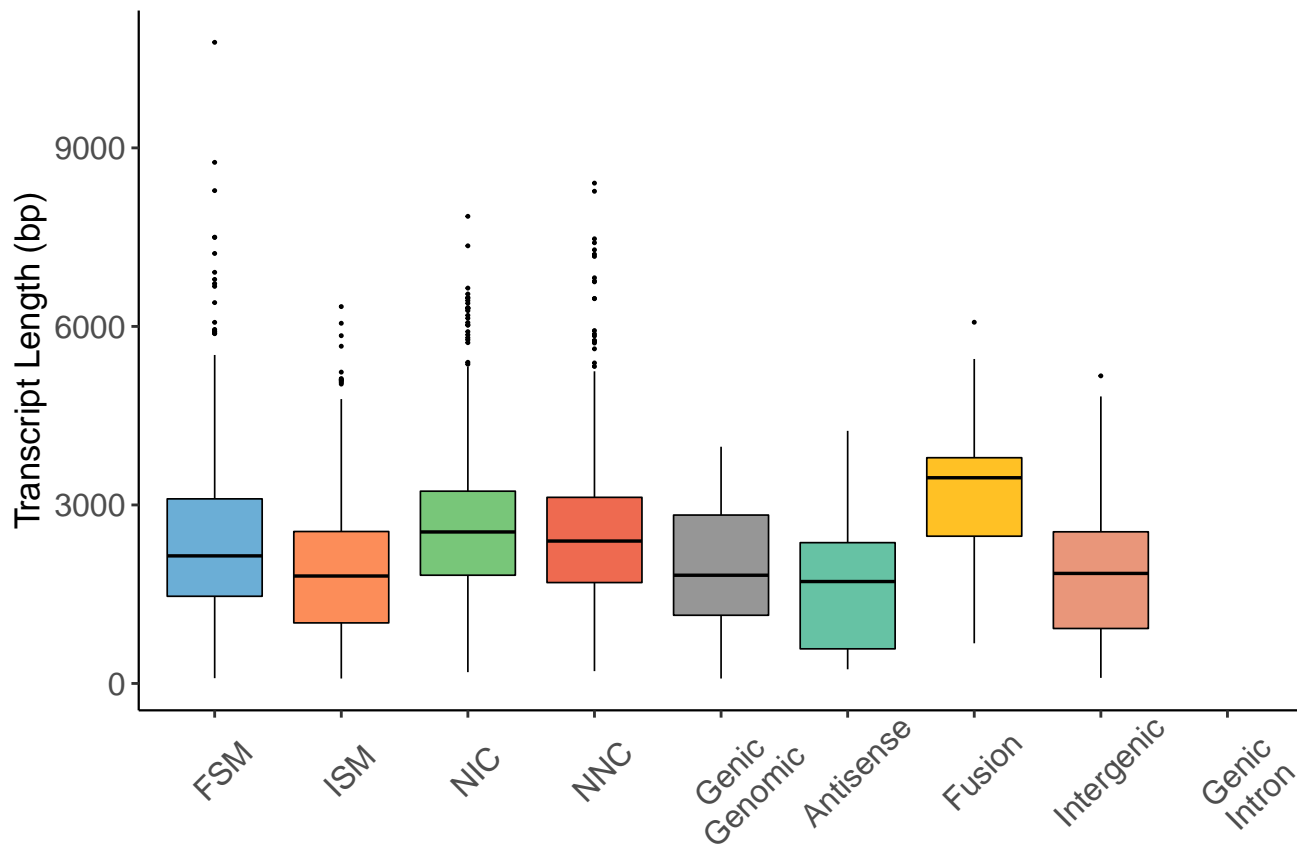
Isoform Distribution Across Fusion



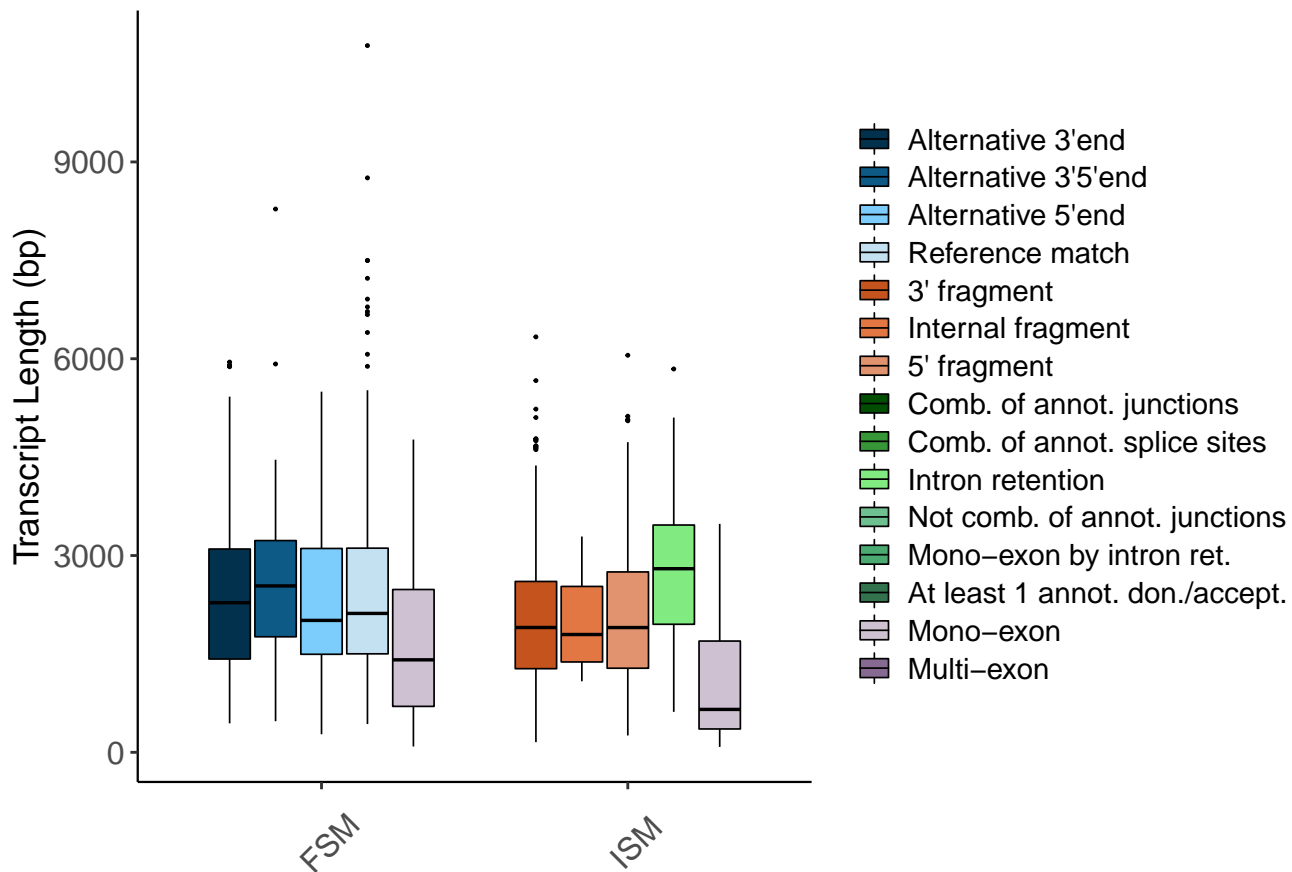
Isoform Distribution Across Intergenic



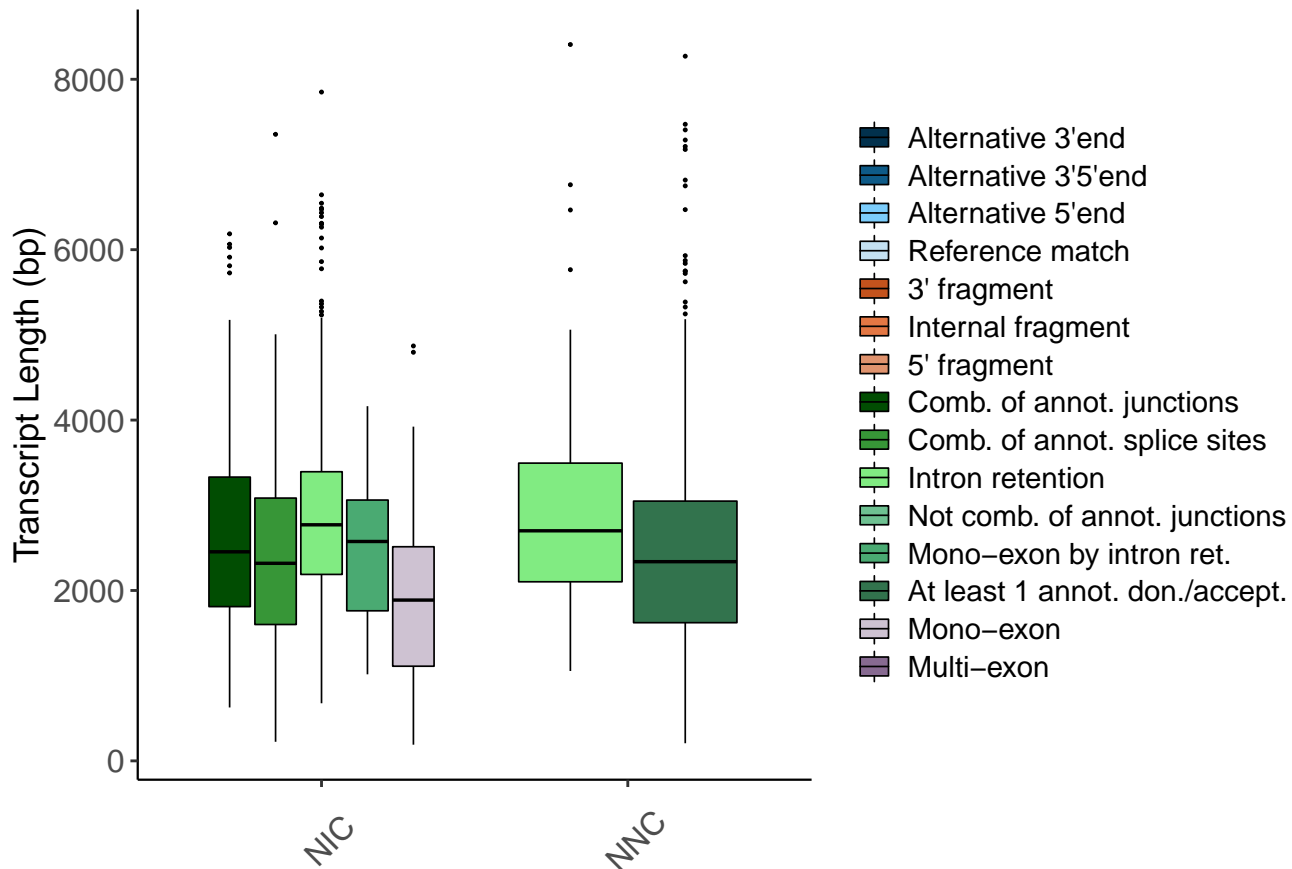
Transcript Lengths by Structural Classification



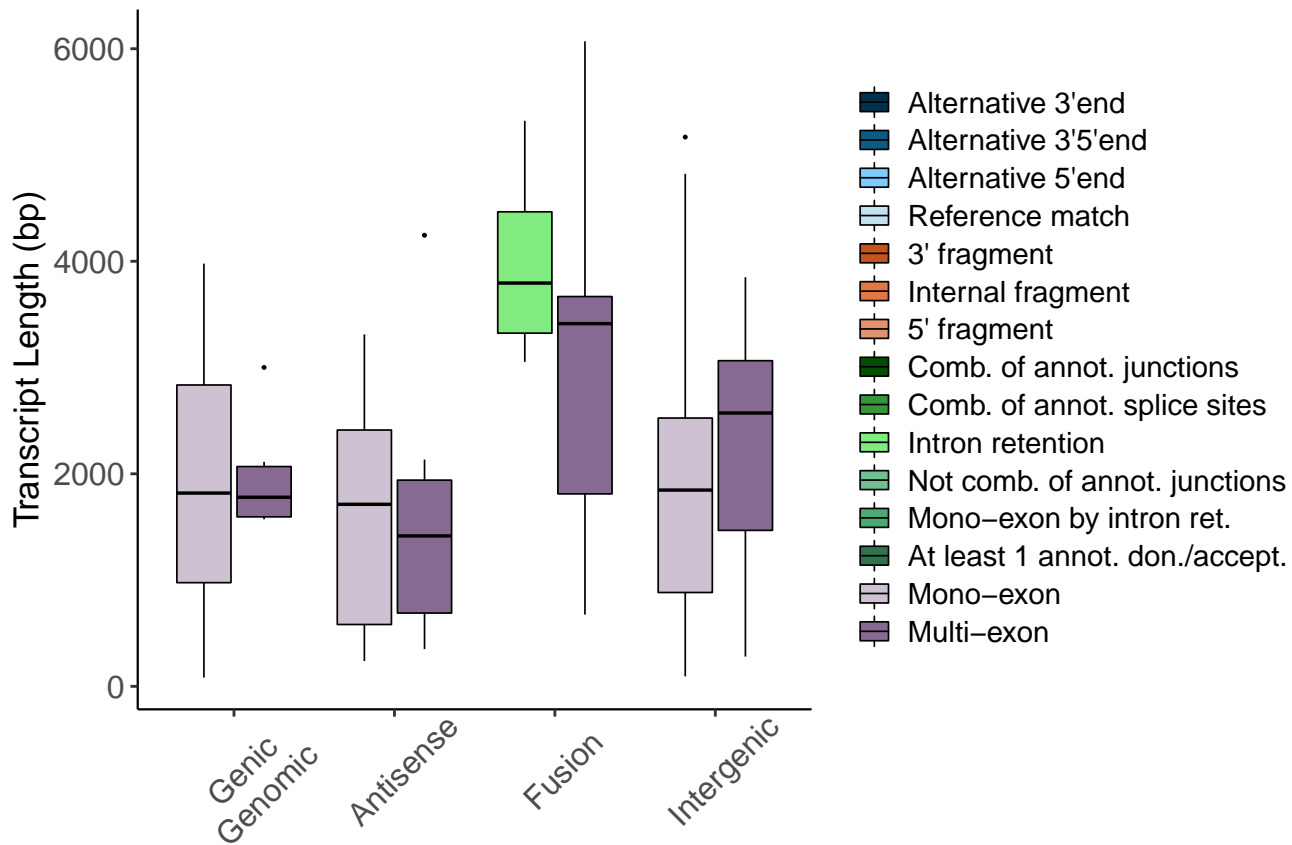
Transcript Lengths by Subcategory



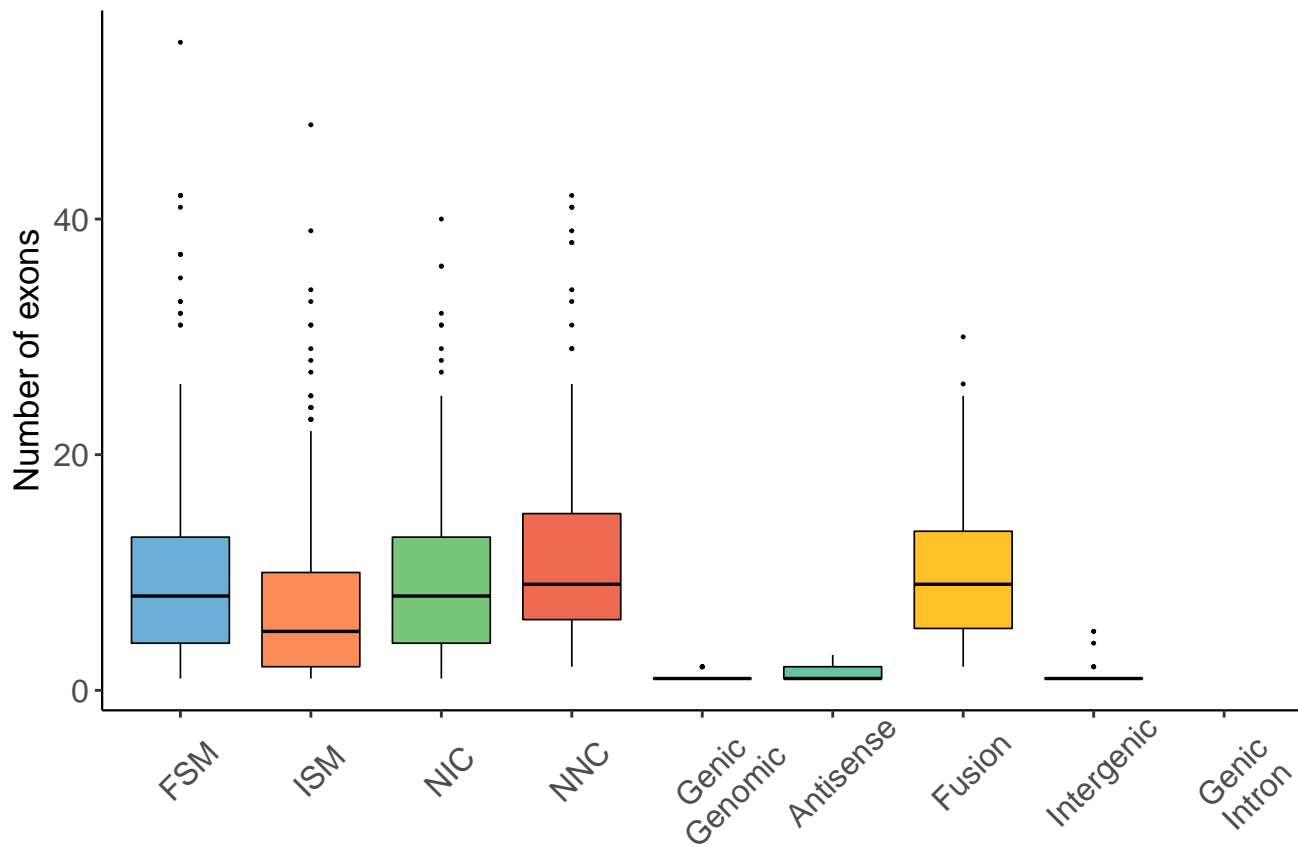
Transcript Lengths by Subcategory



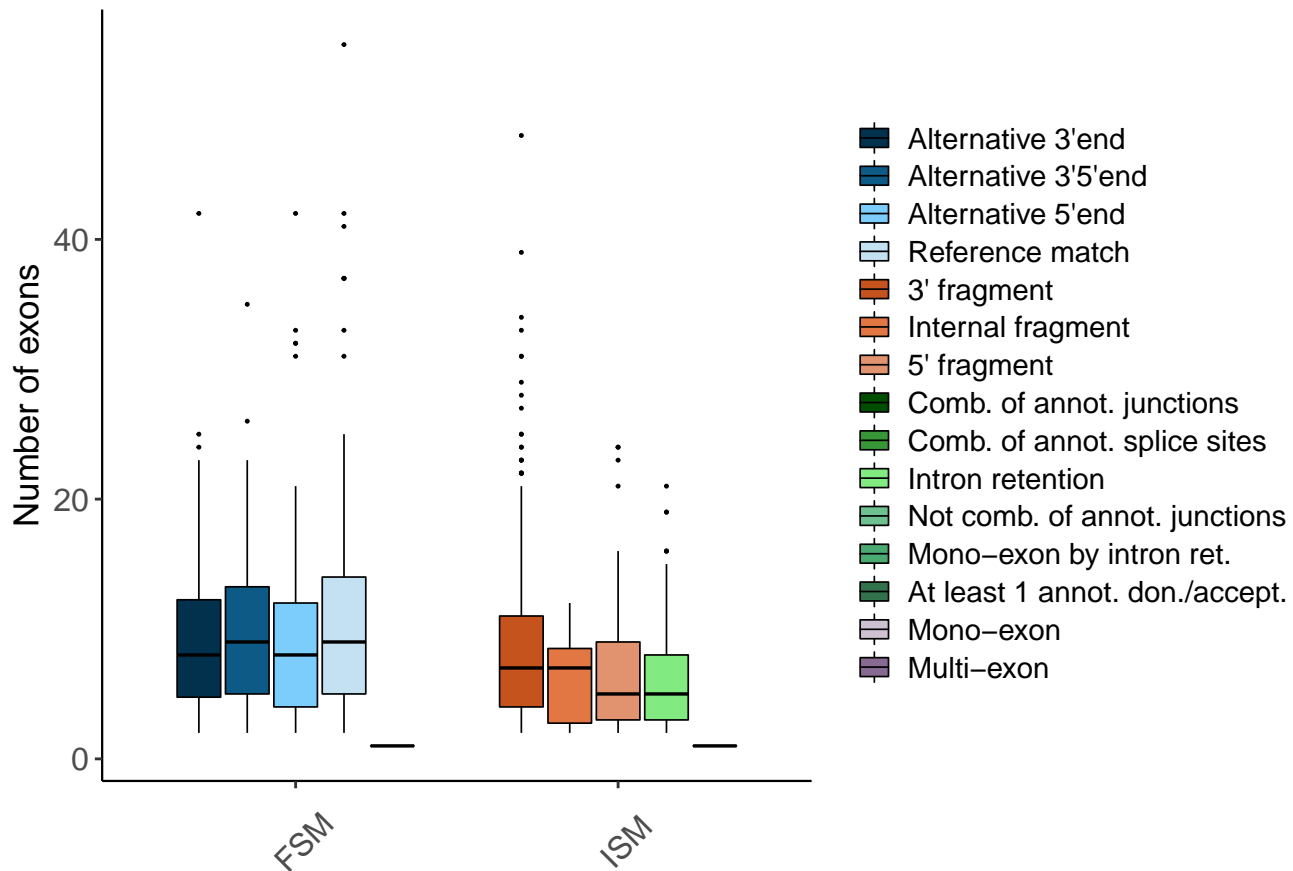
Transcript Lengths by Subcategory



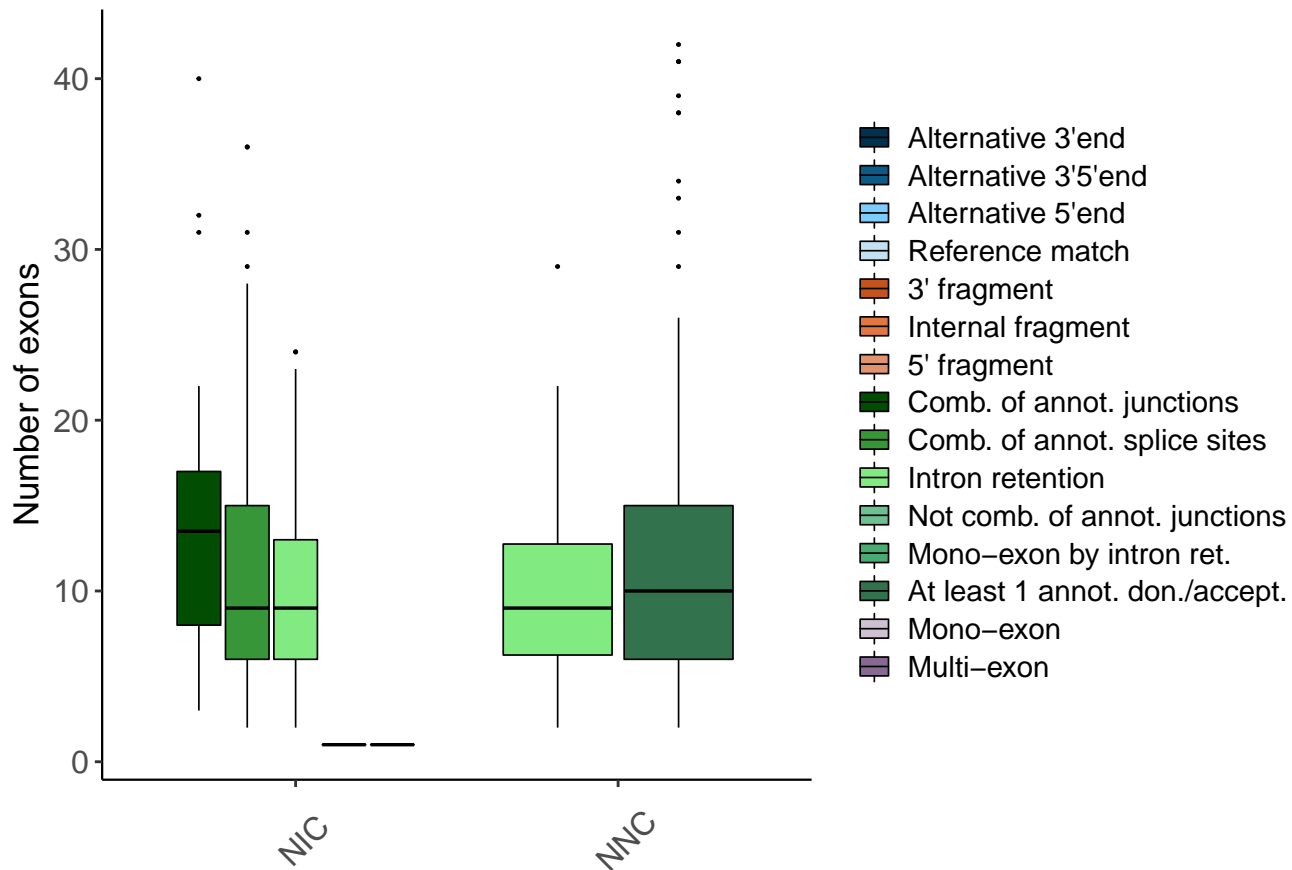
Exon Counts by Structural Classification



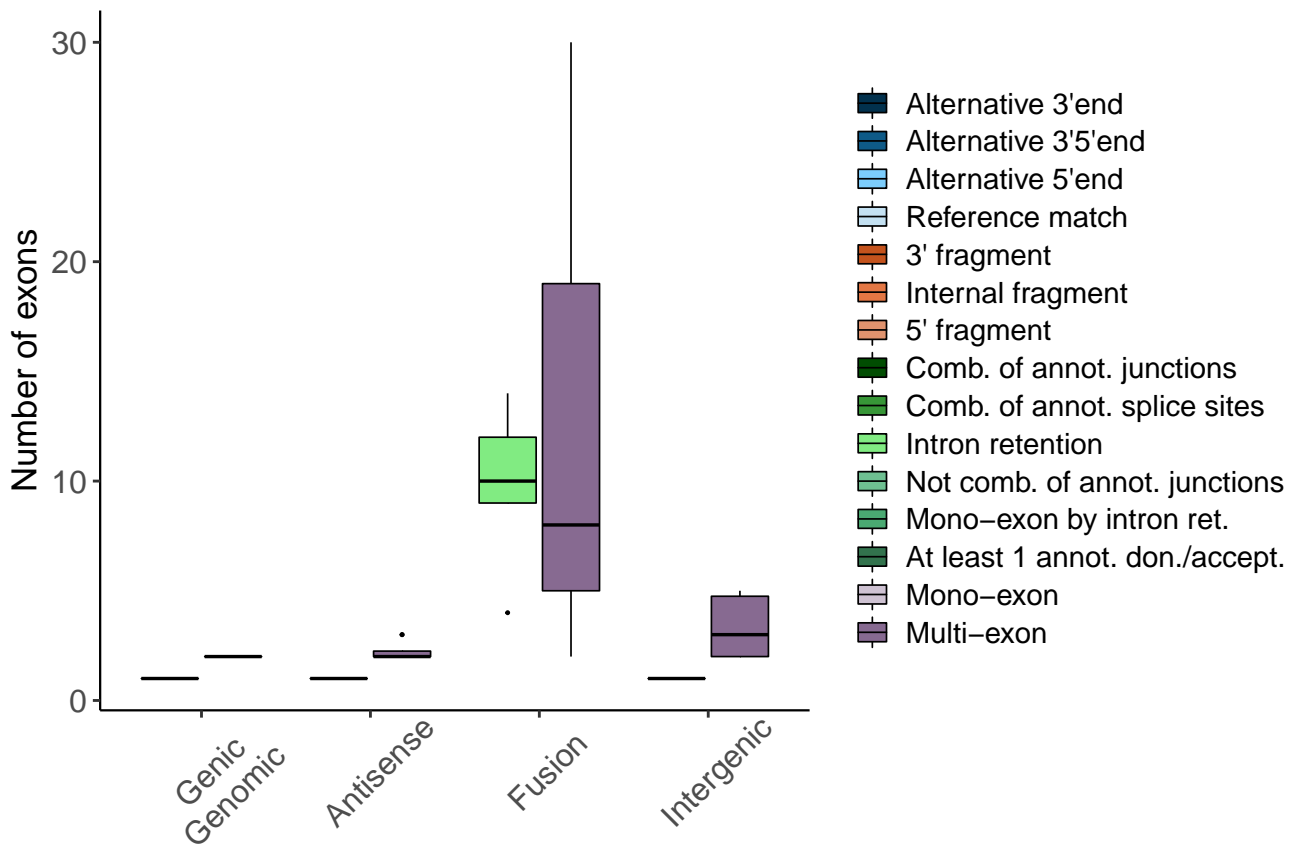
Exon Counts by Subcategory



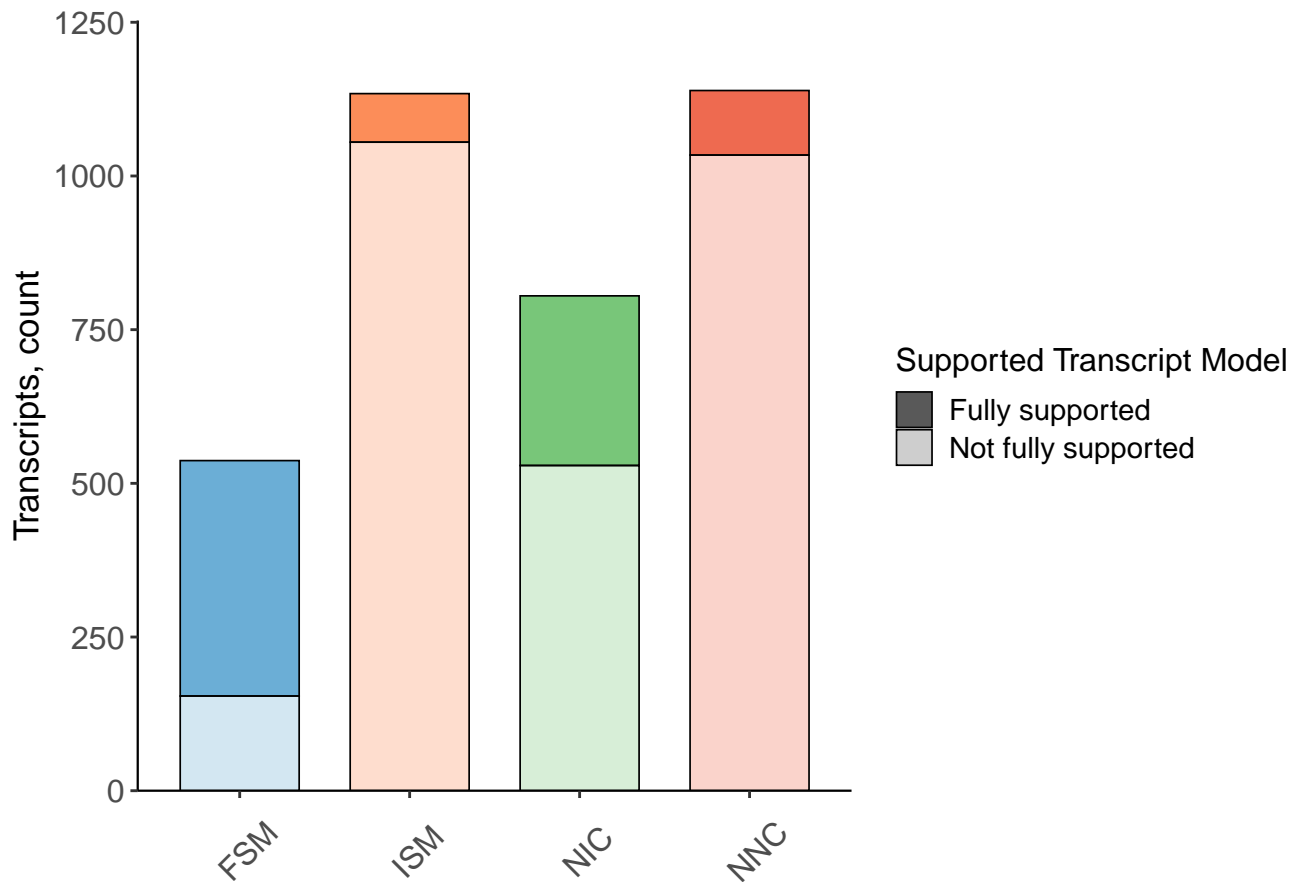
Exon Counts by Subcategory



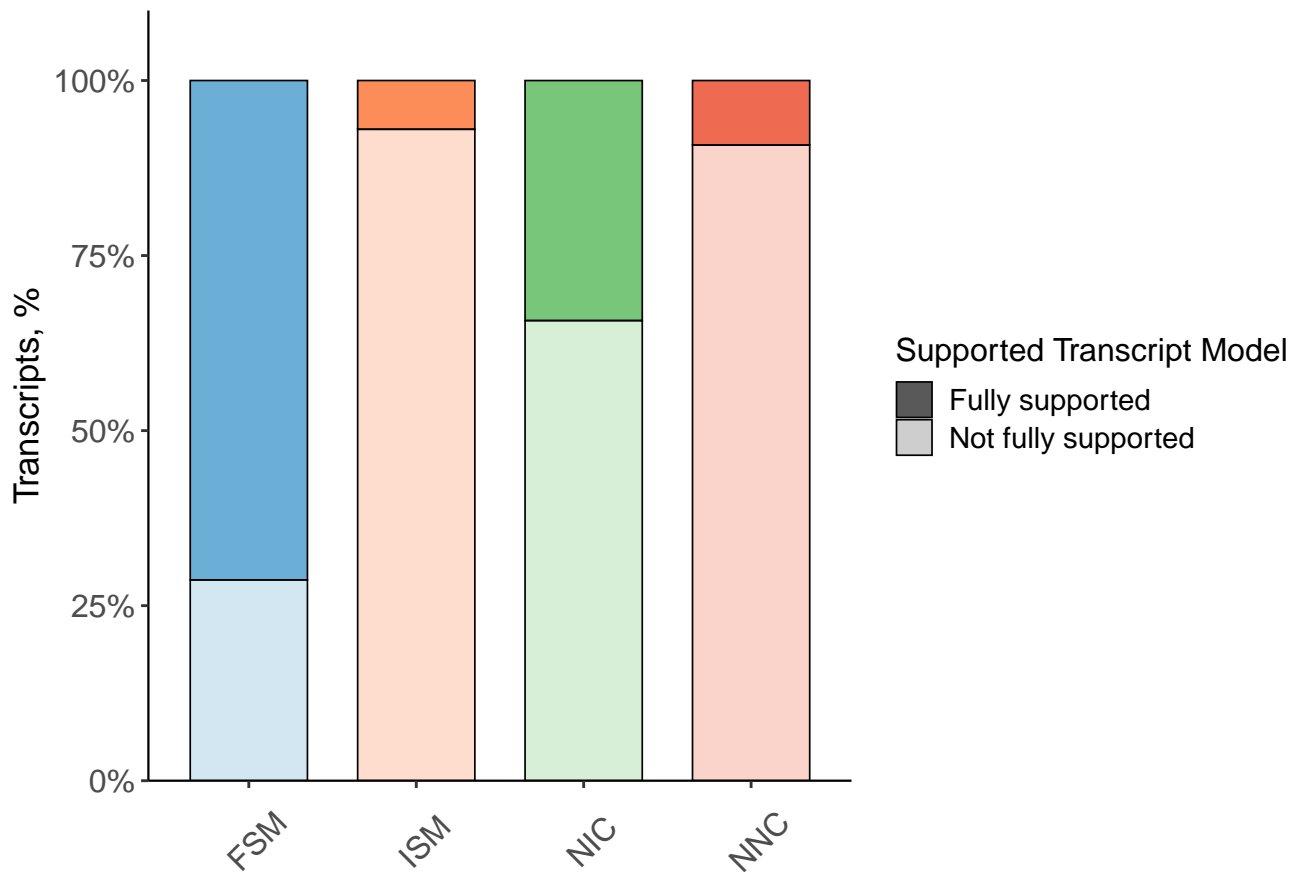
Exon Counts by Subcategory



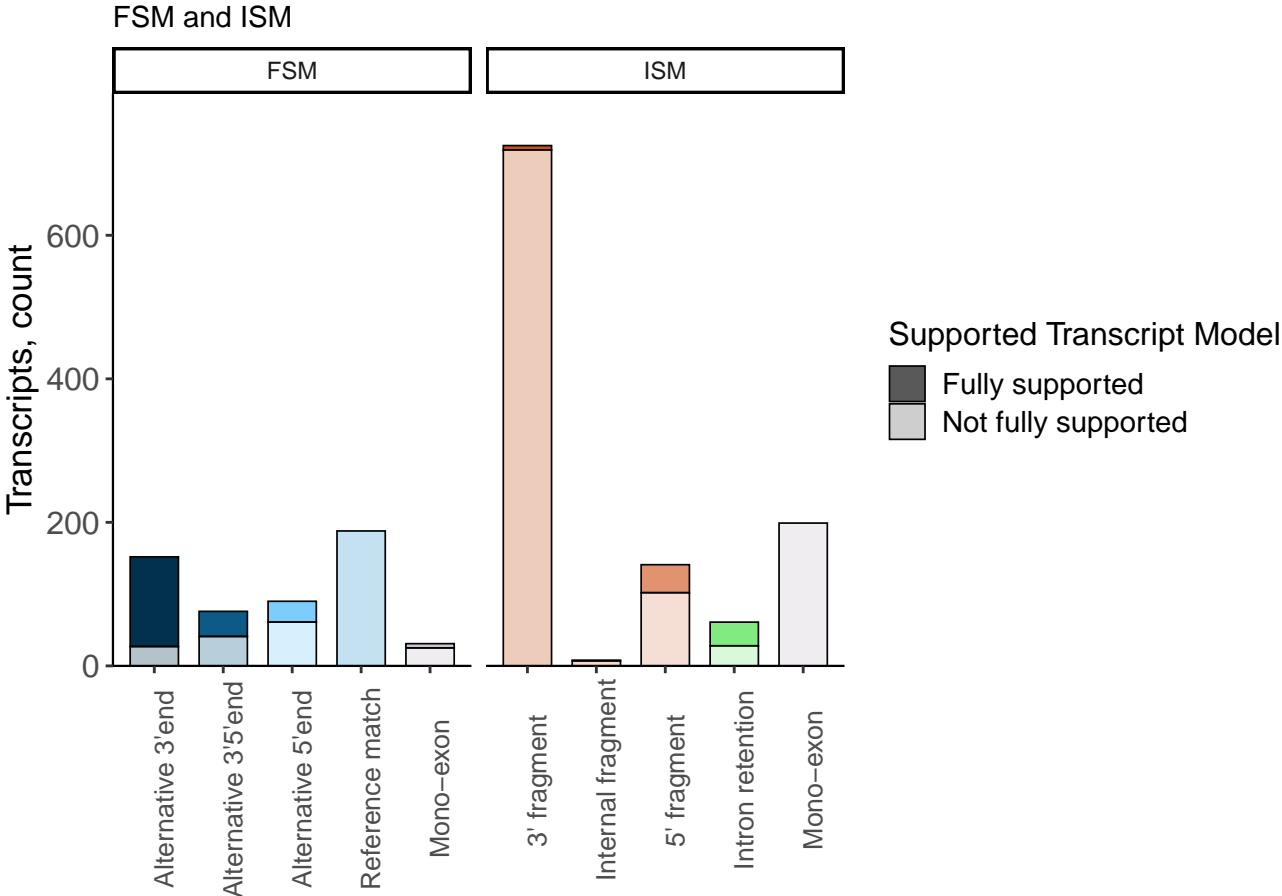
Isoform Distribution Across Structural Categories



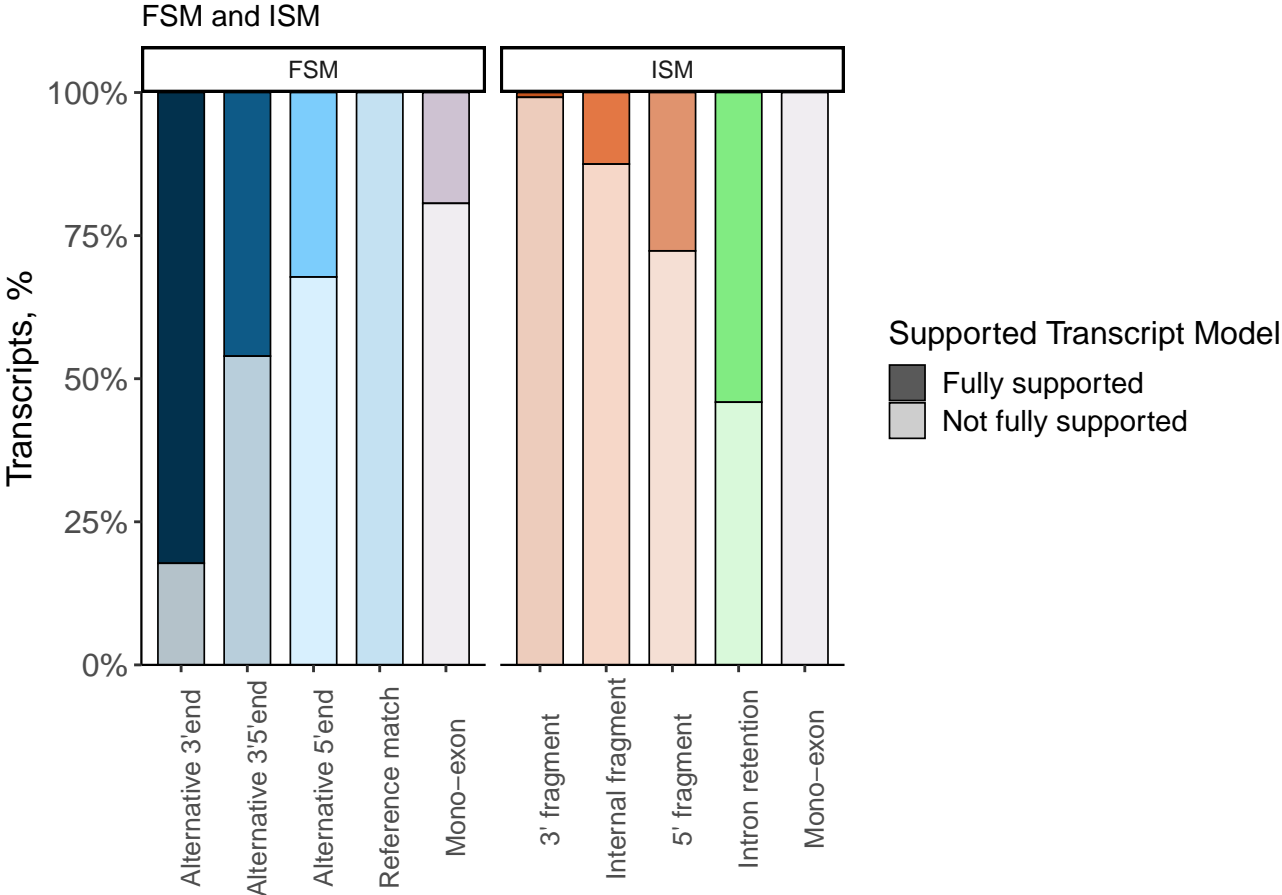
Isoform Distribution Across Structural Categories



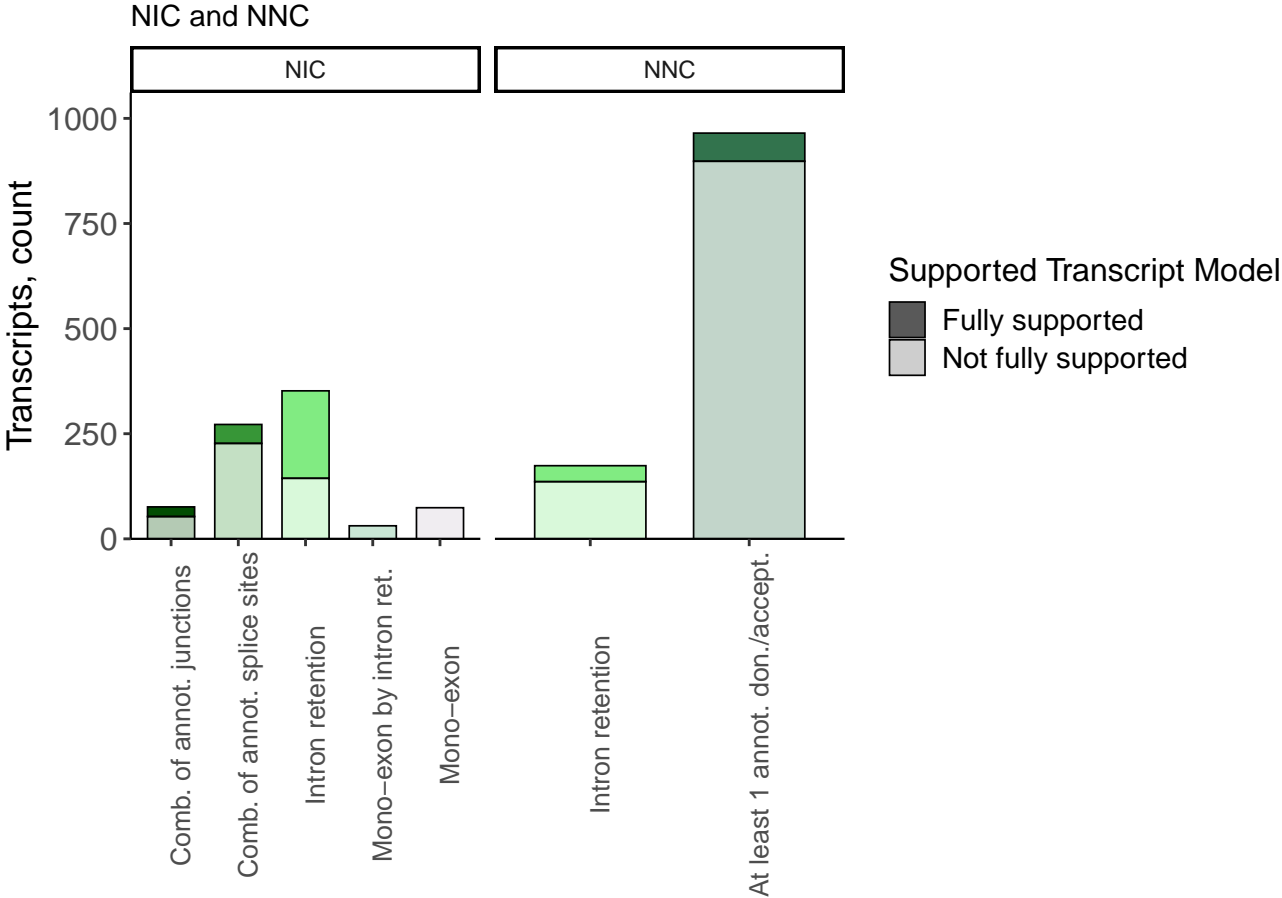
Isoform Distribution Across Structural Subcategories



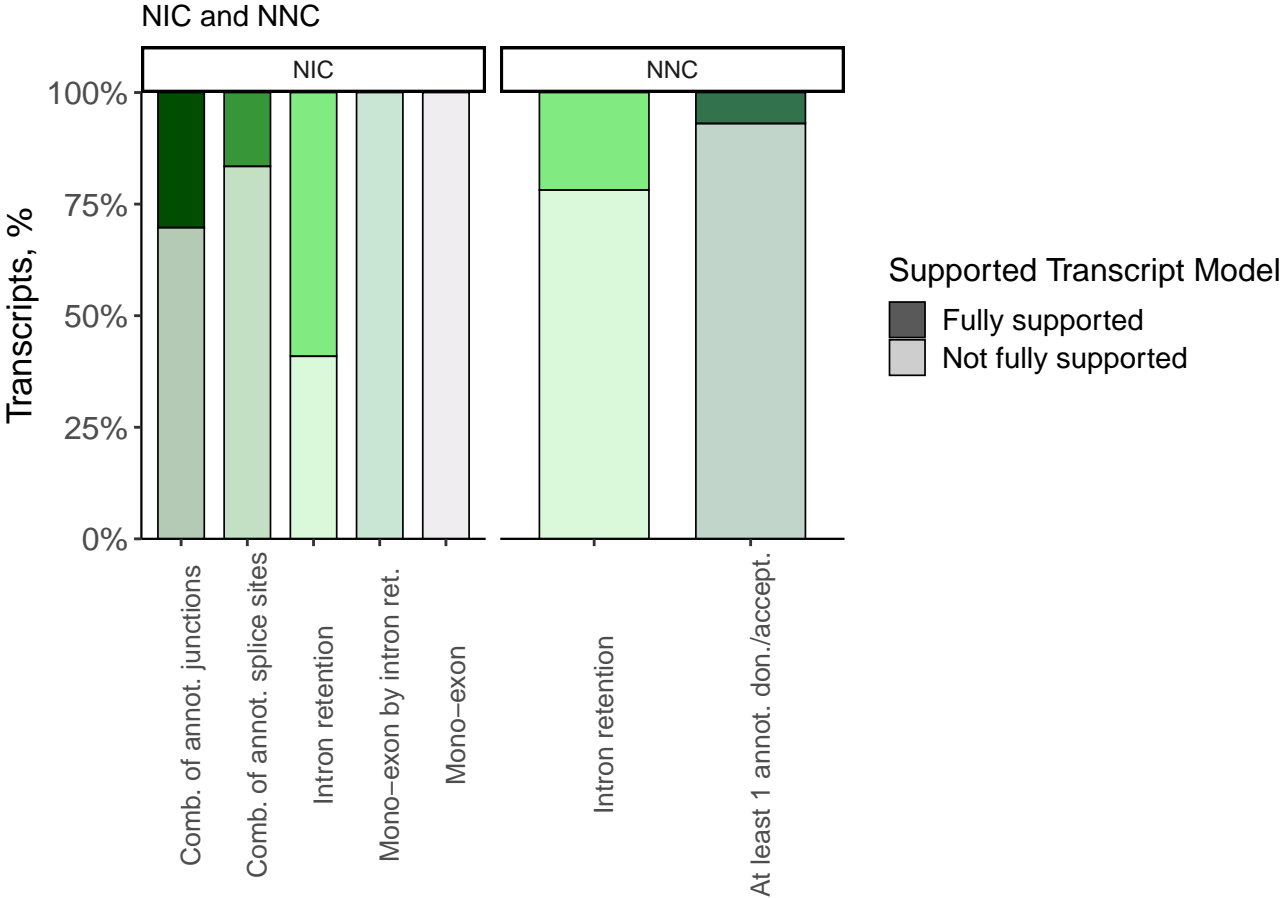
Isoform Distribution Across Structural Subcategories



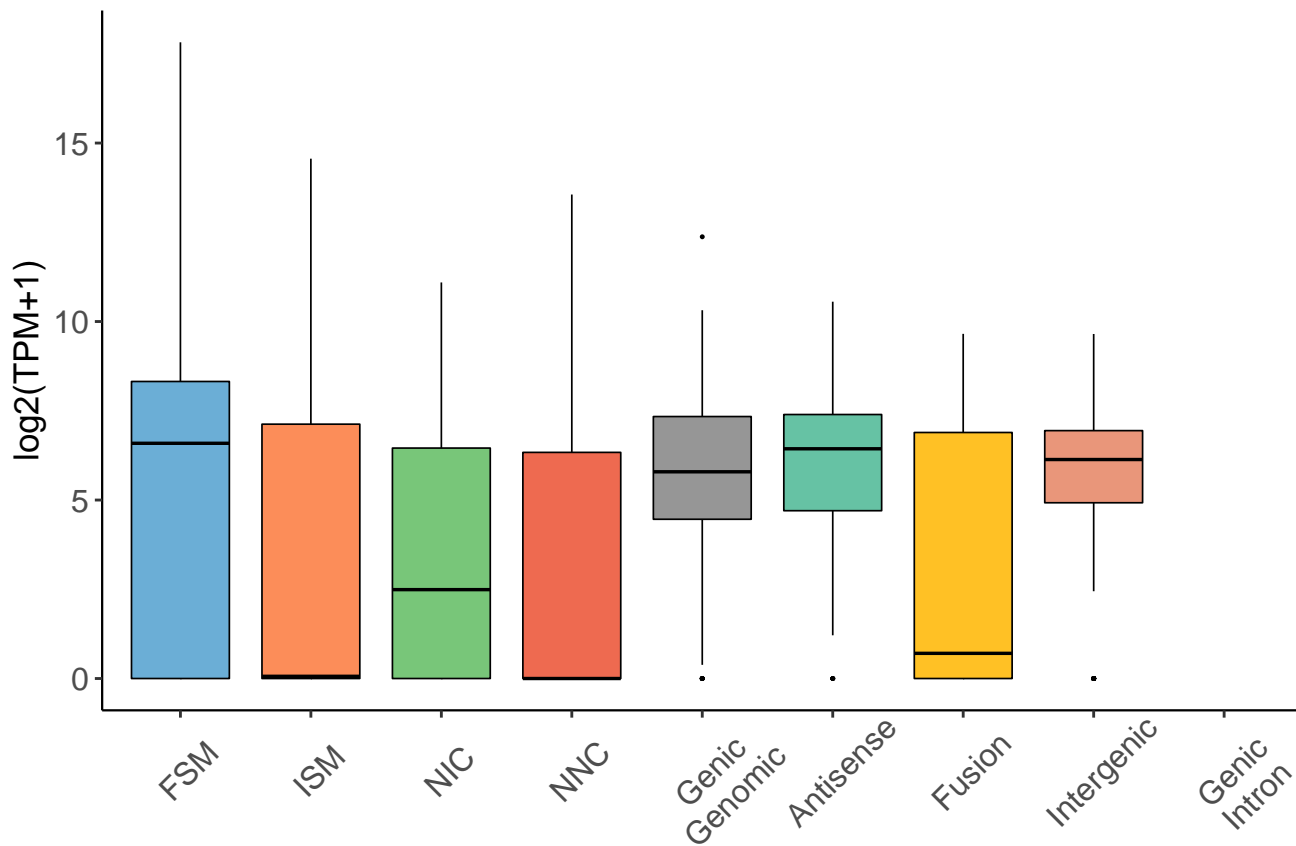
Isoform Distribution Across Structural Subcategories



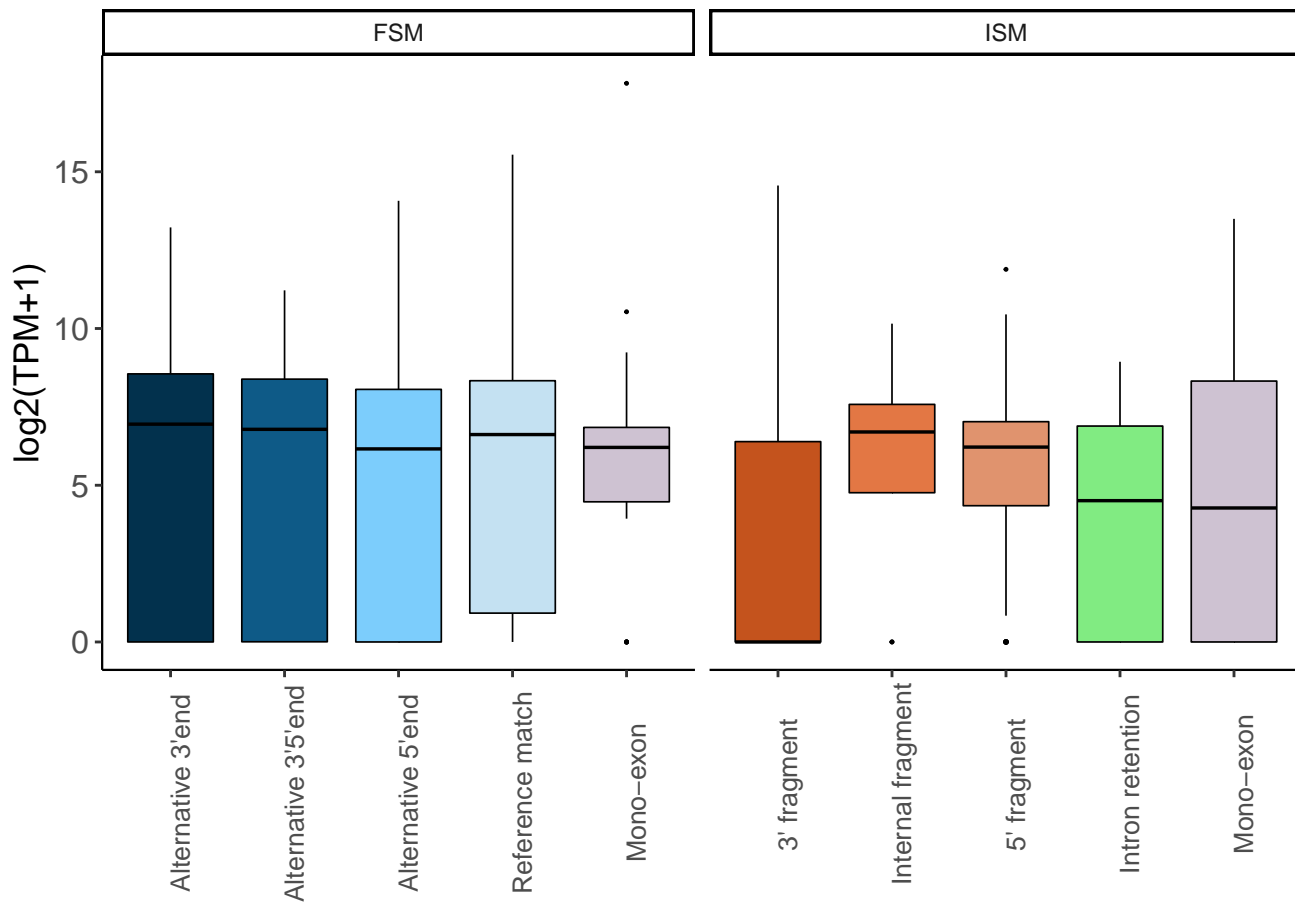
Isoform Distribution Across Structural Subcategories



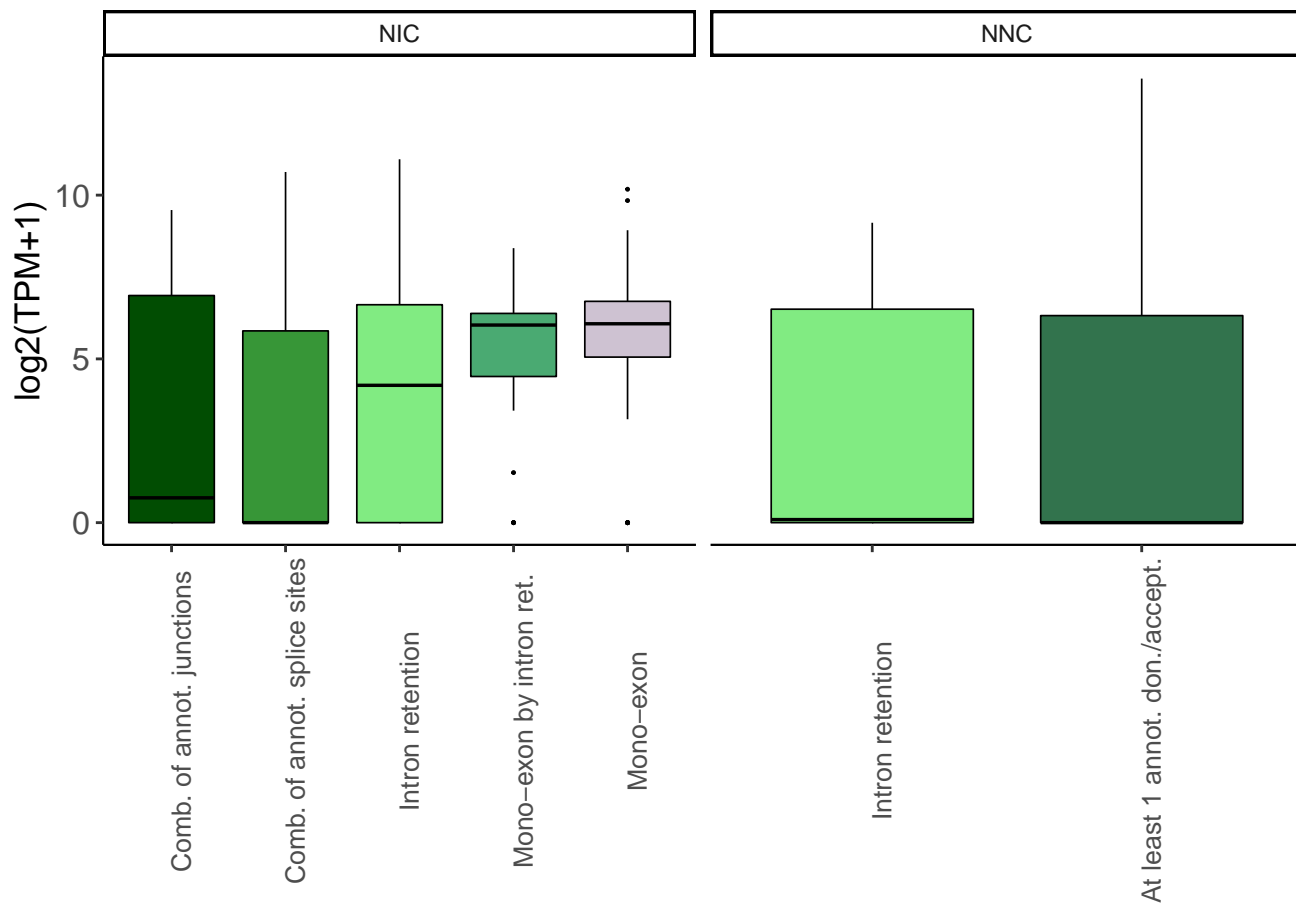
Transcript Expression by Structural Category



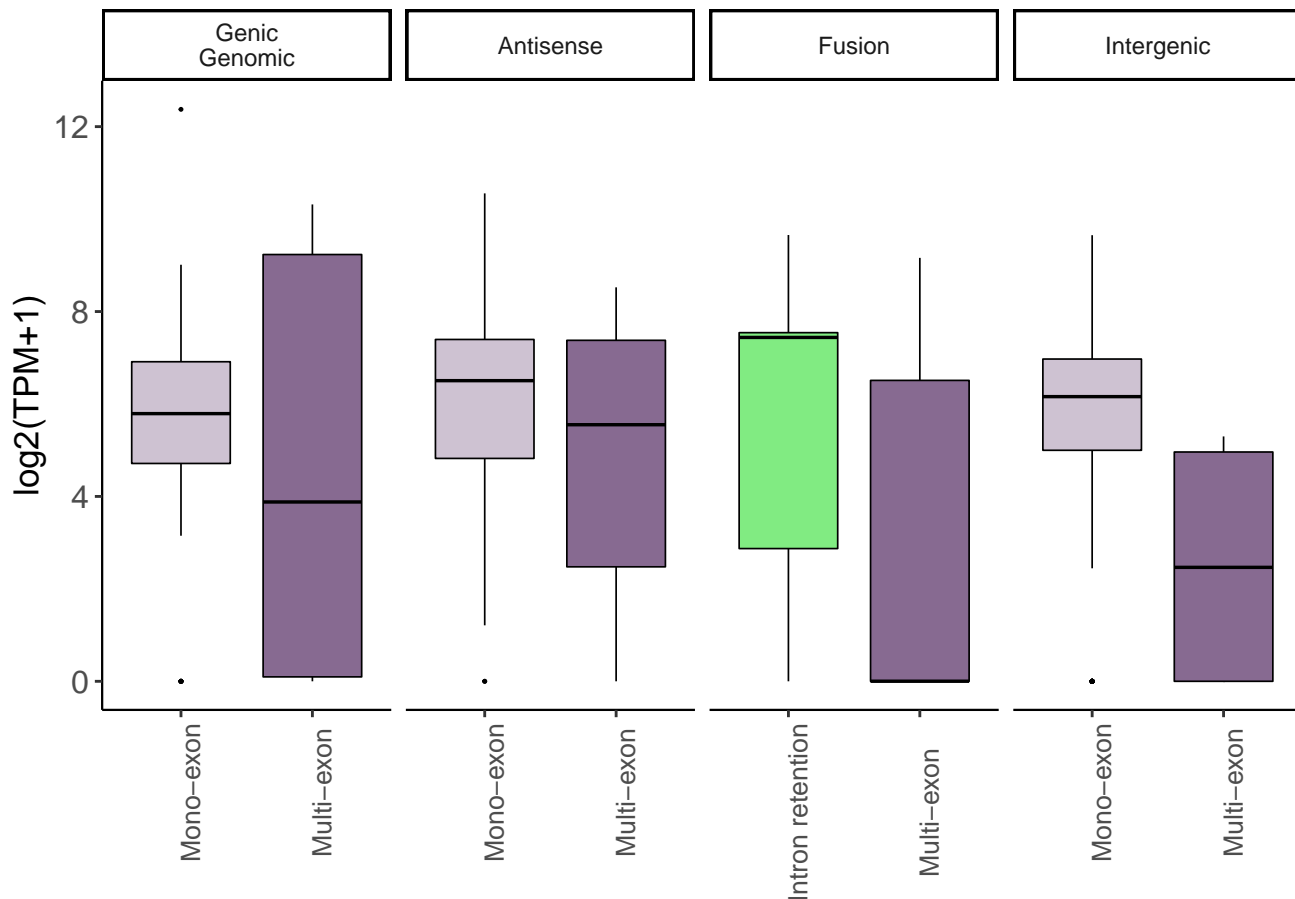
Transcript Expression by Subcategory



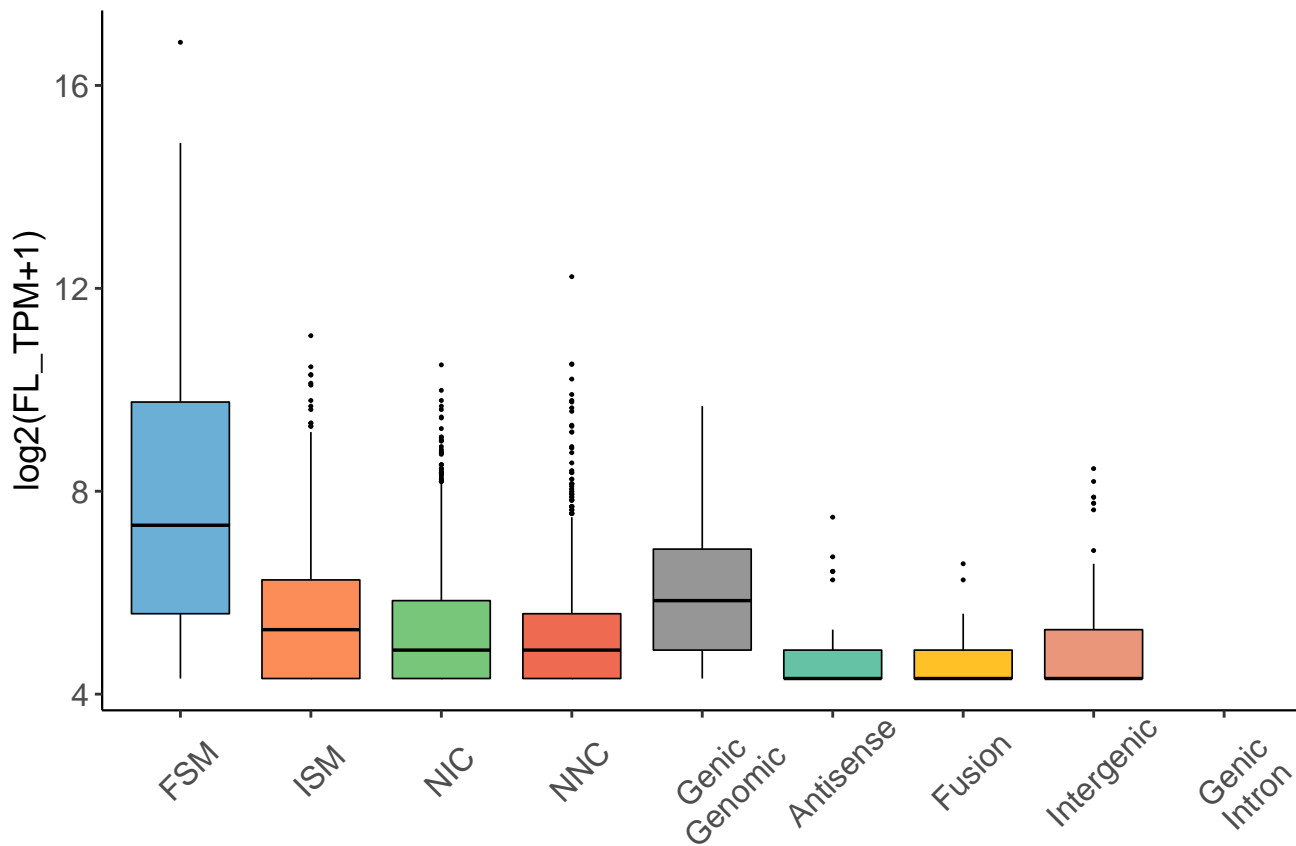
Transcript Expression by Subcategory



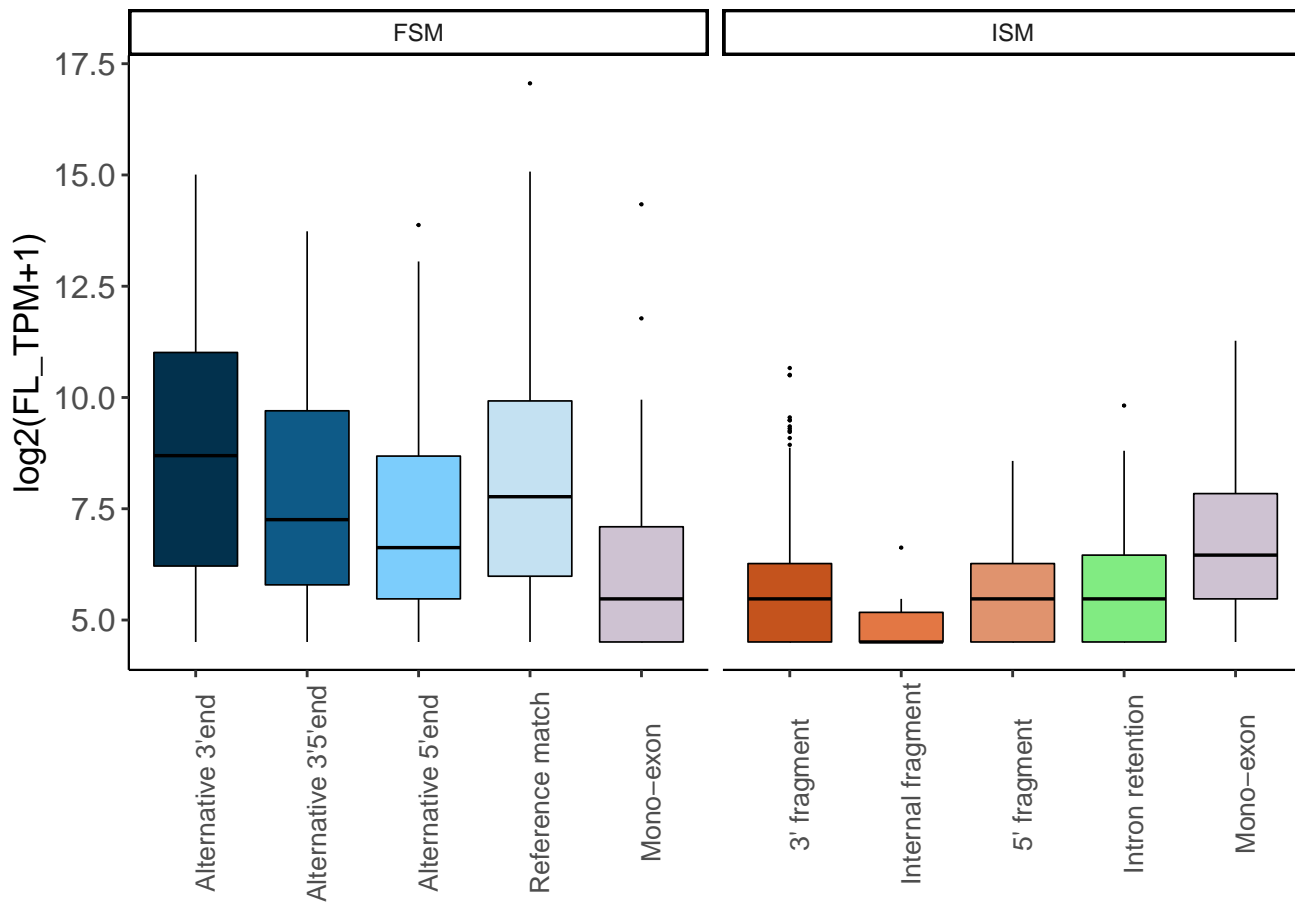
Transcript Expression by Subcategory



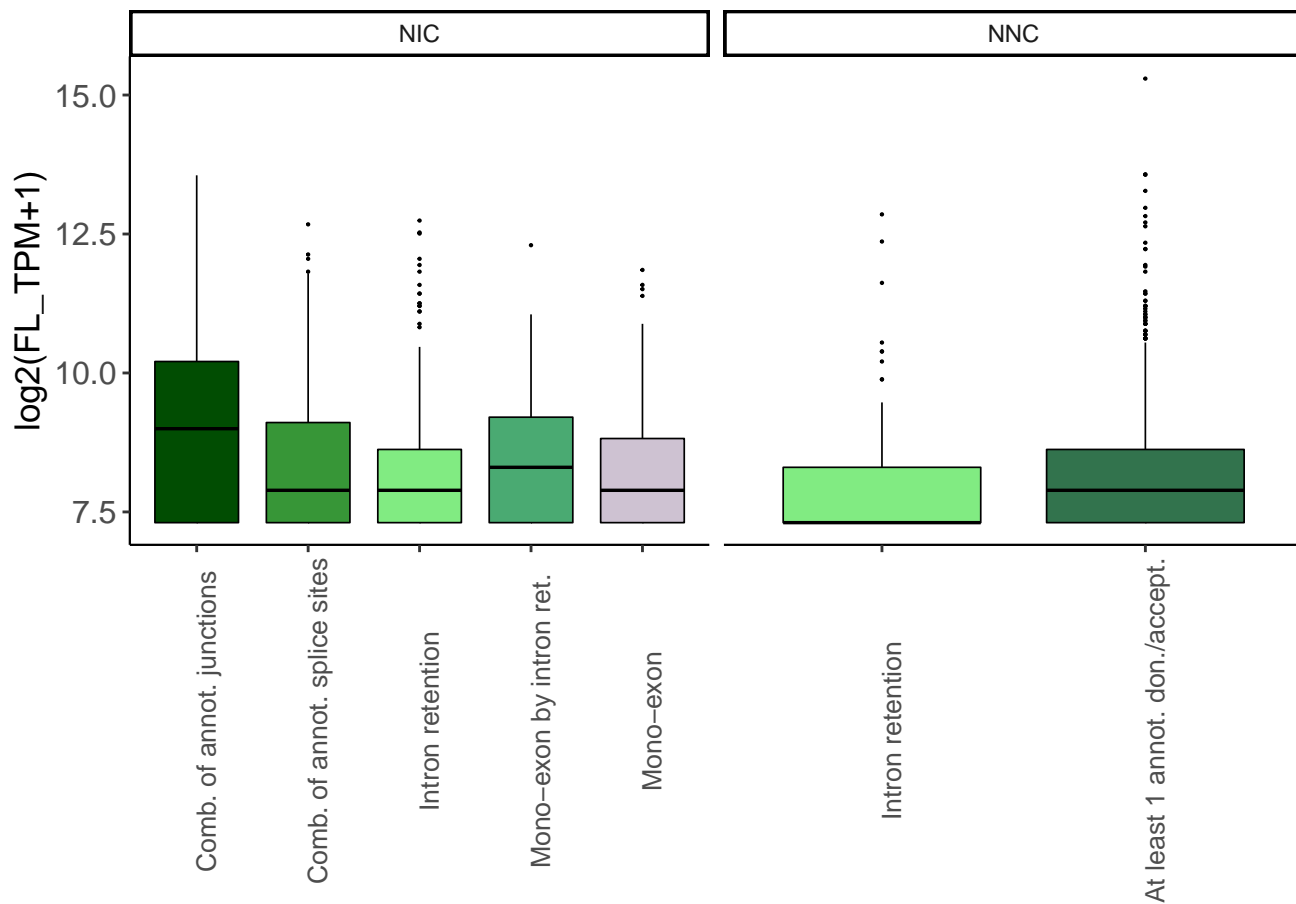
Long Reads Count by Structural Category



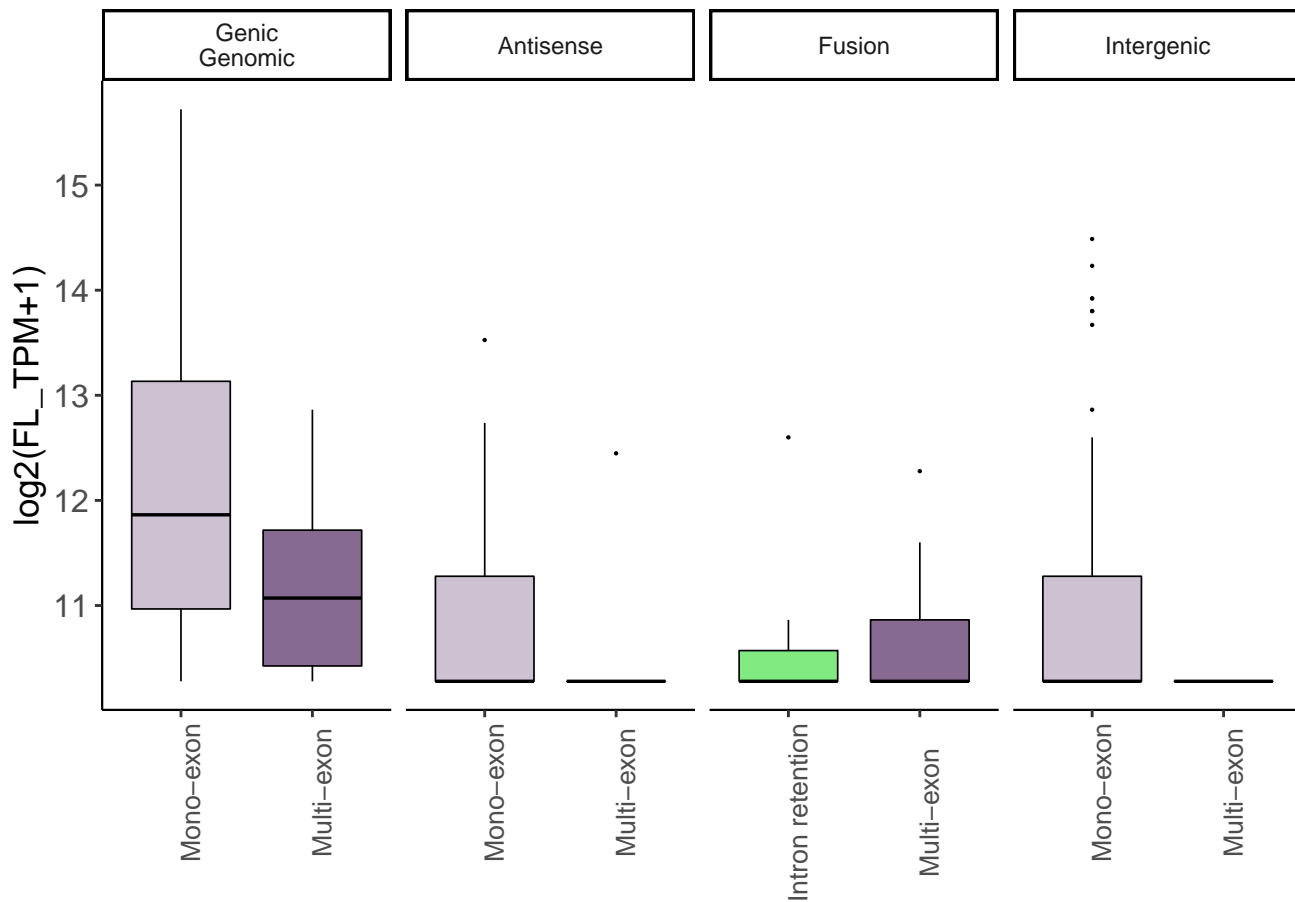
Long Reads Count by Subcategory



Long Reads Count by Subcategory

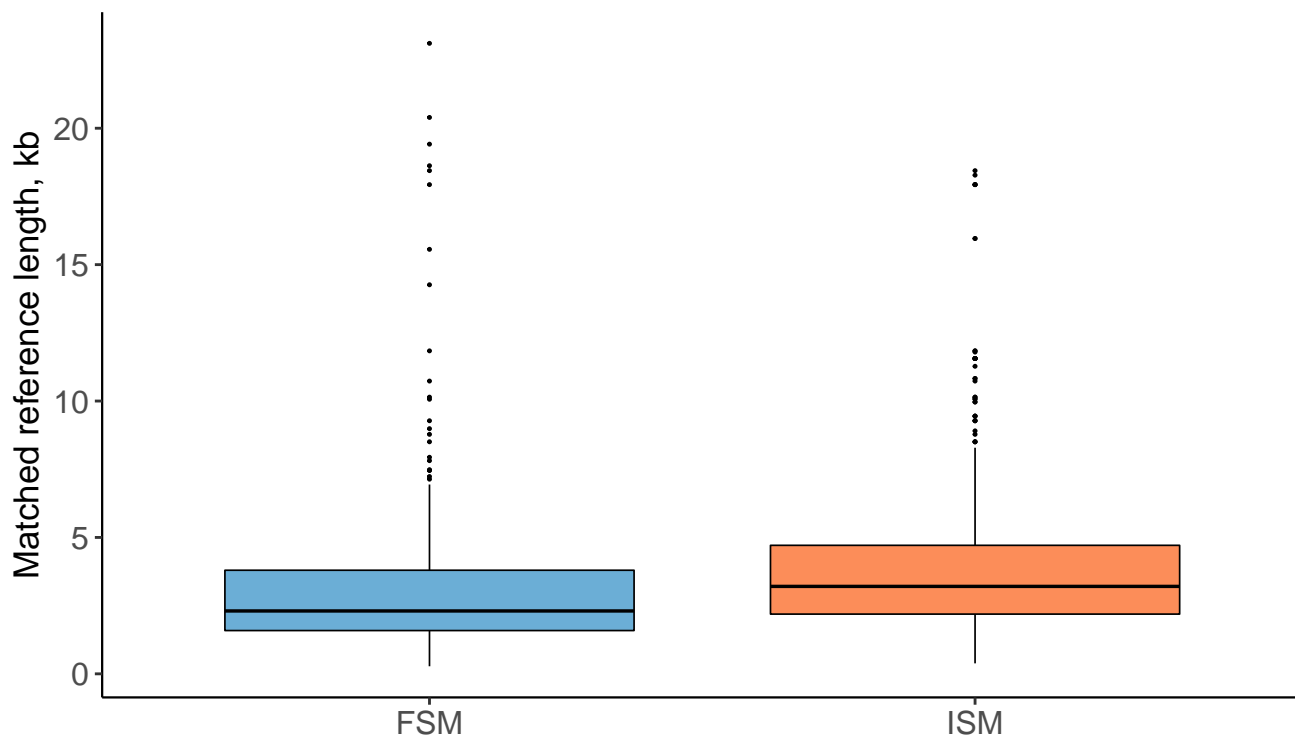


Long Reads Count by Subcategory



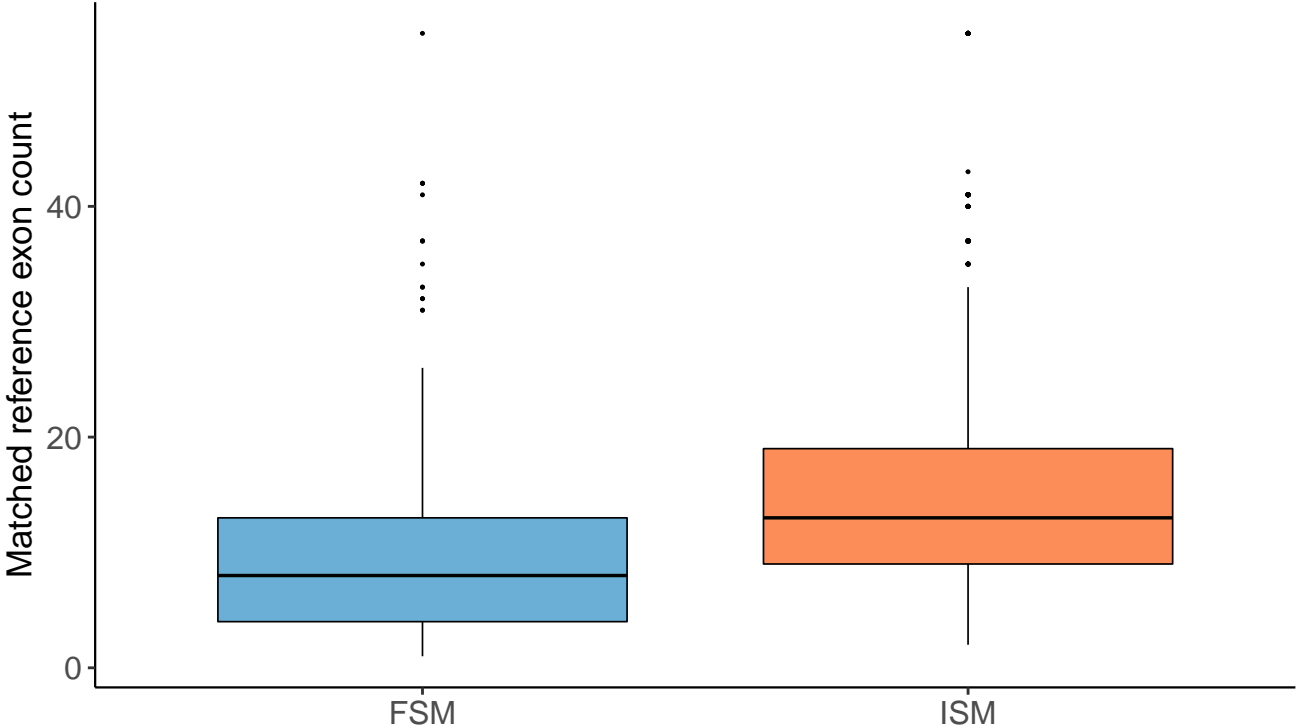
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

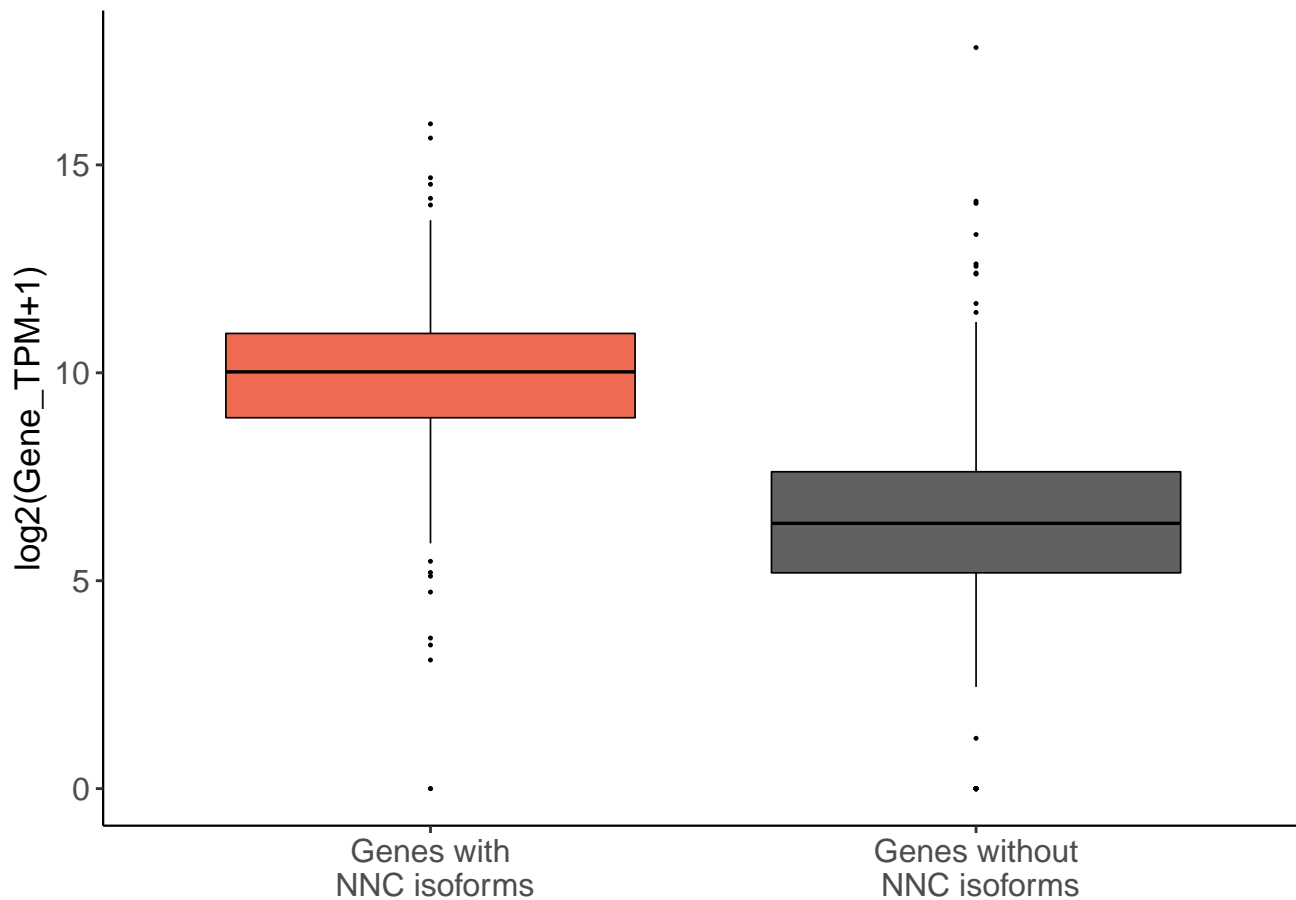


Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

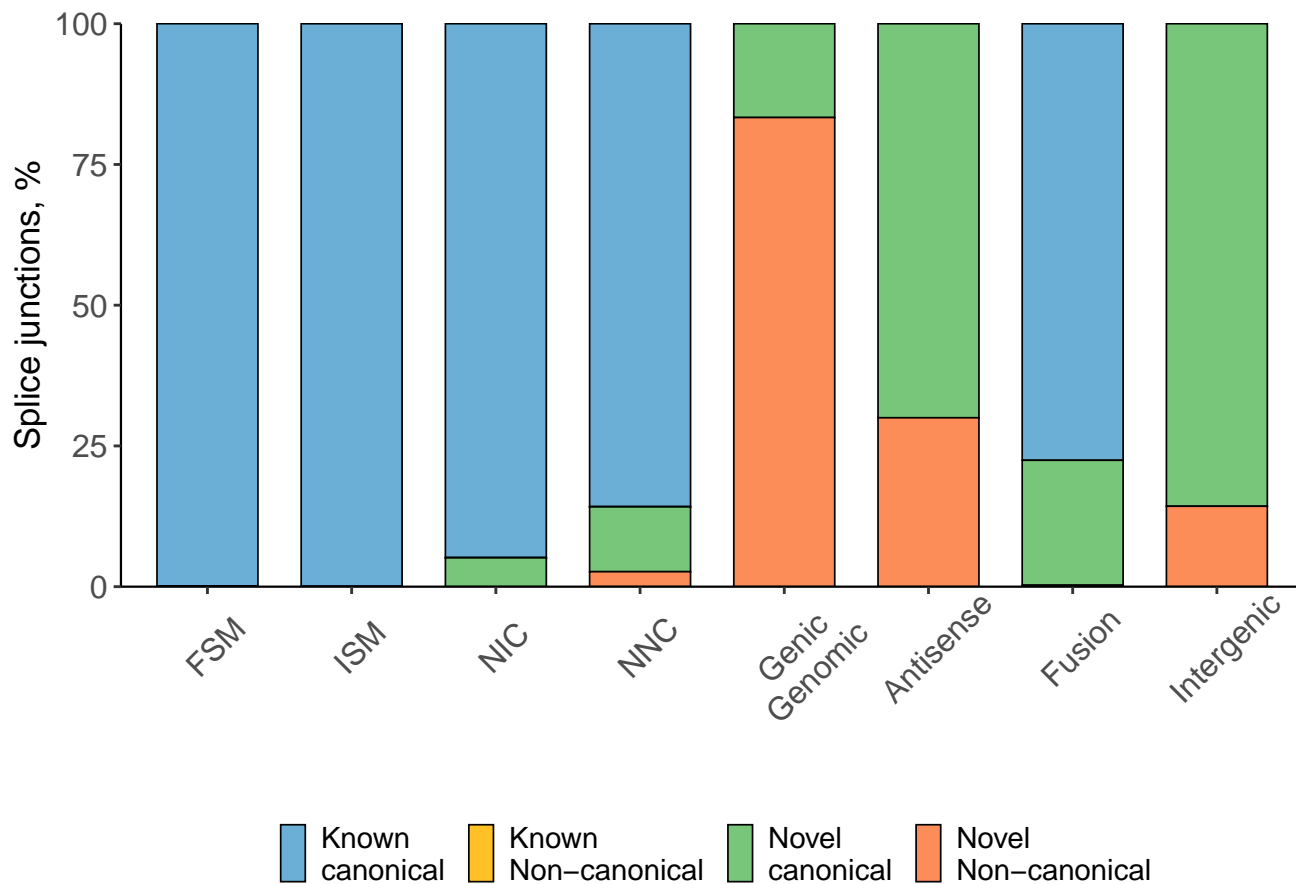


Gene Expression of NNC And Not NNC Containing Genes

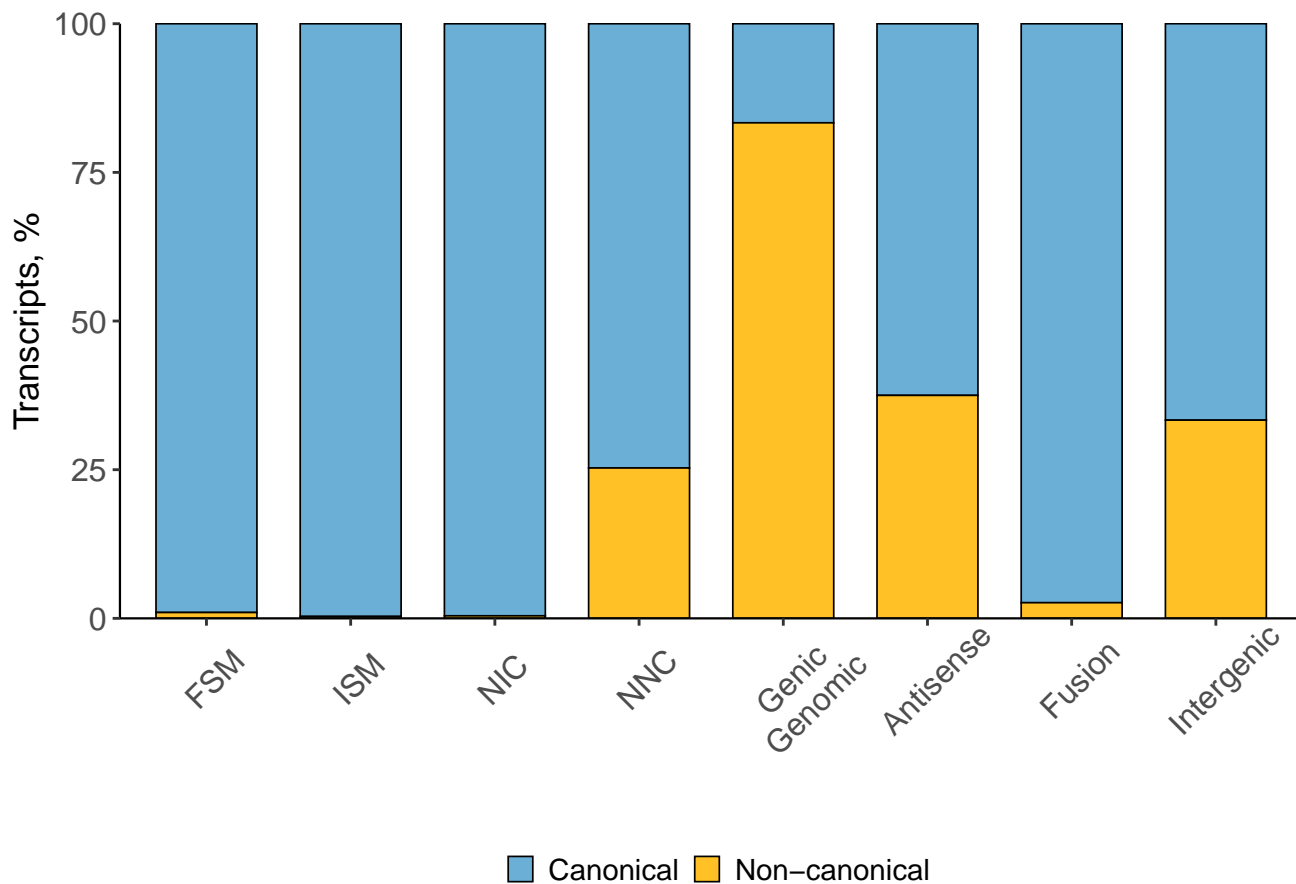


Splice Junction Characterization

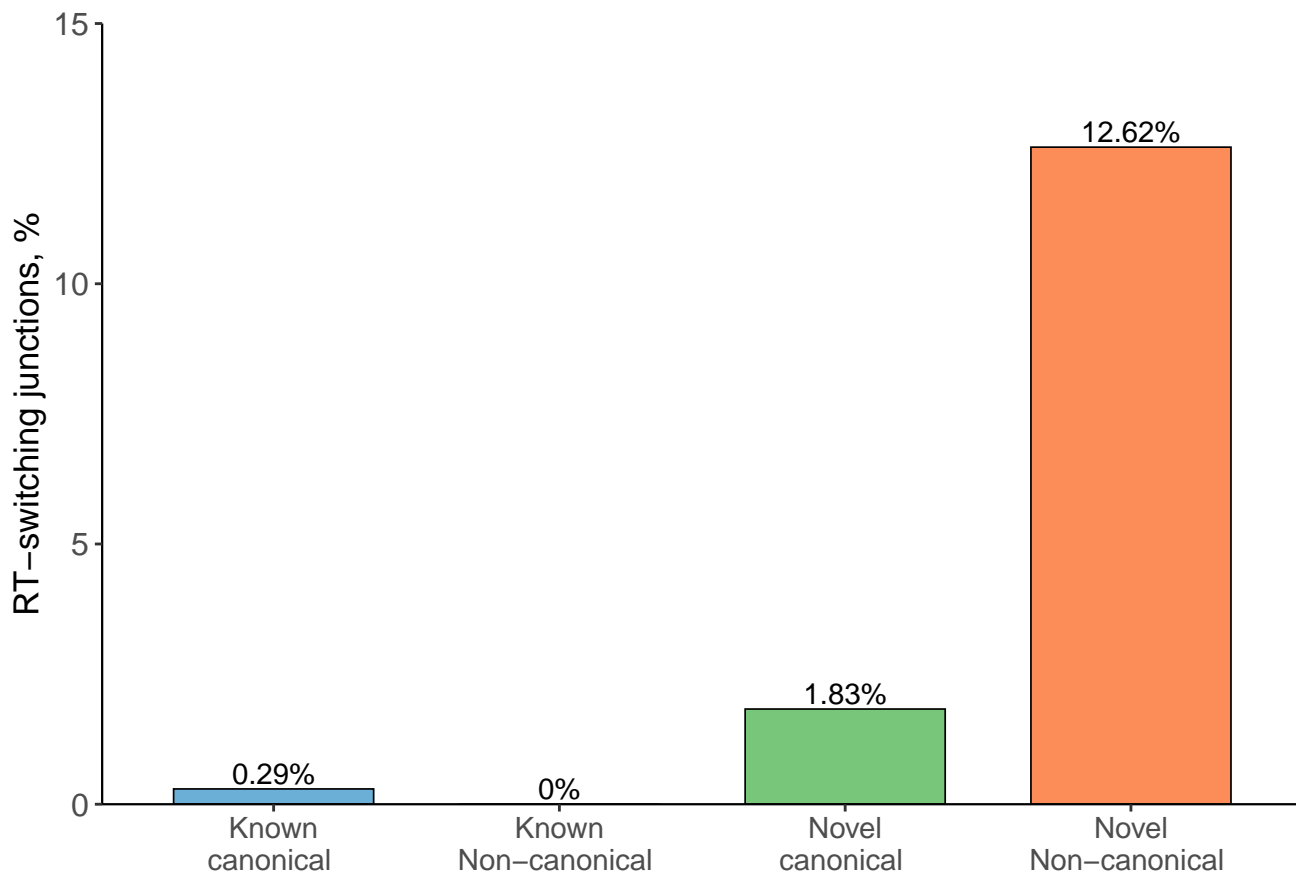
Distribution of Splice Junctions by Structural Classification



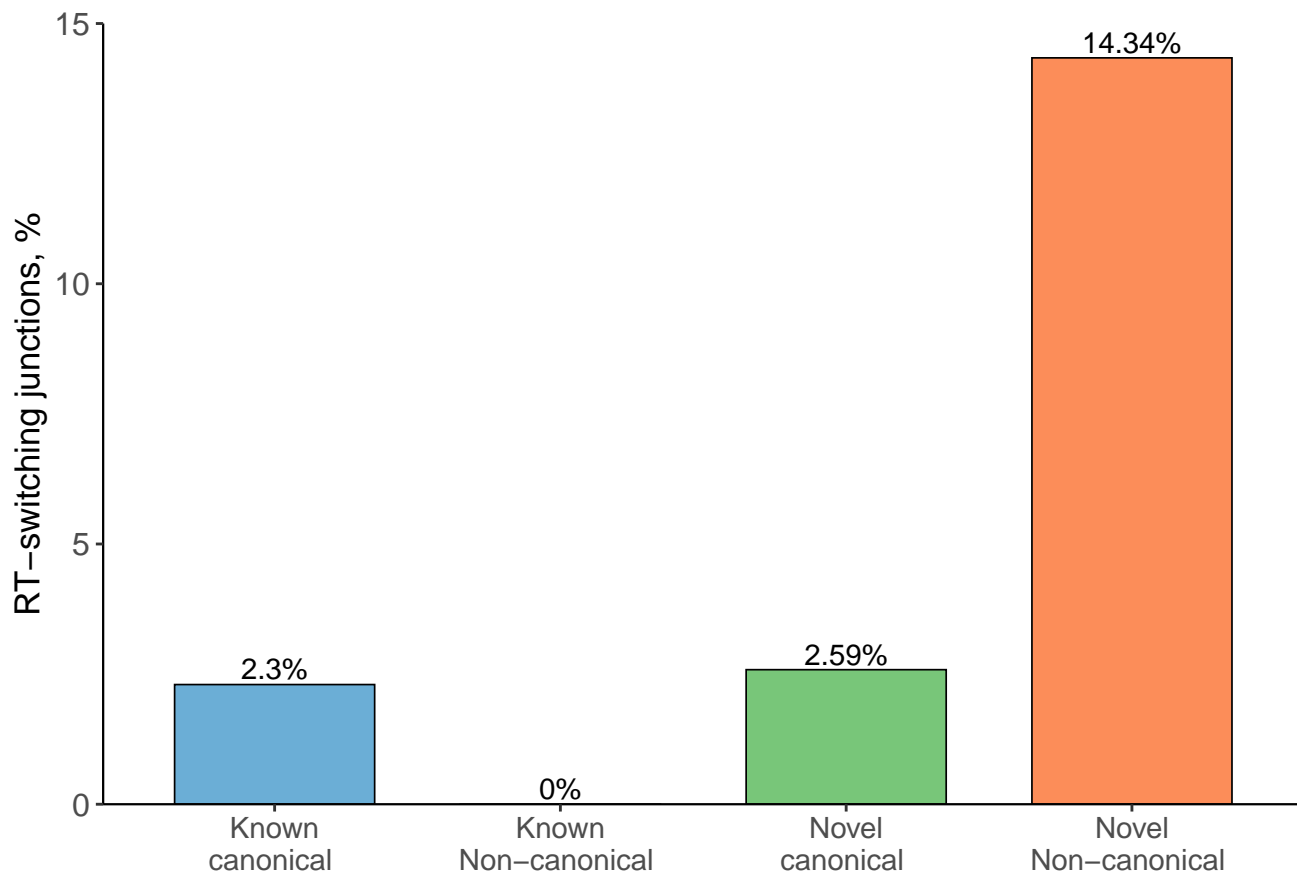
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

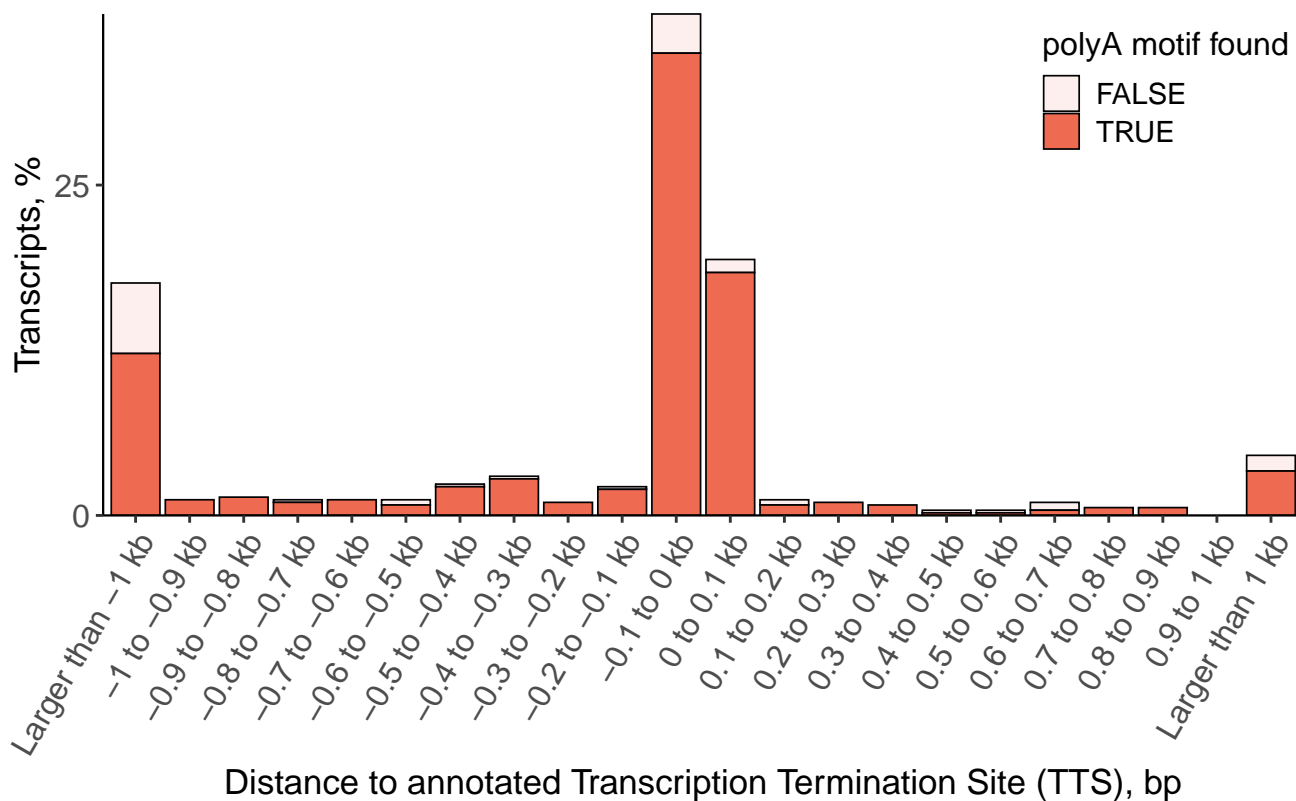
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



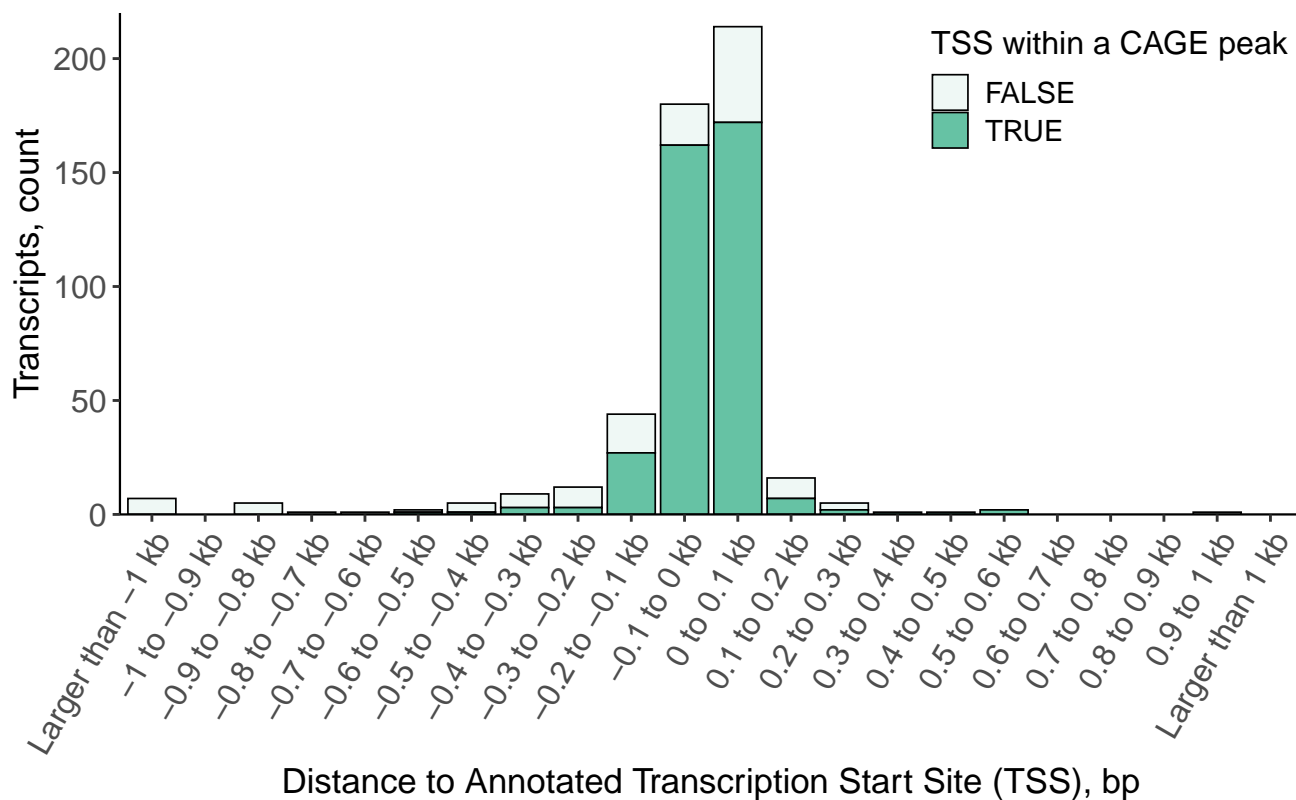
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



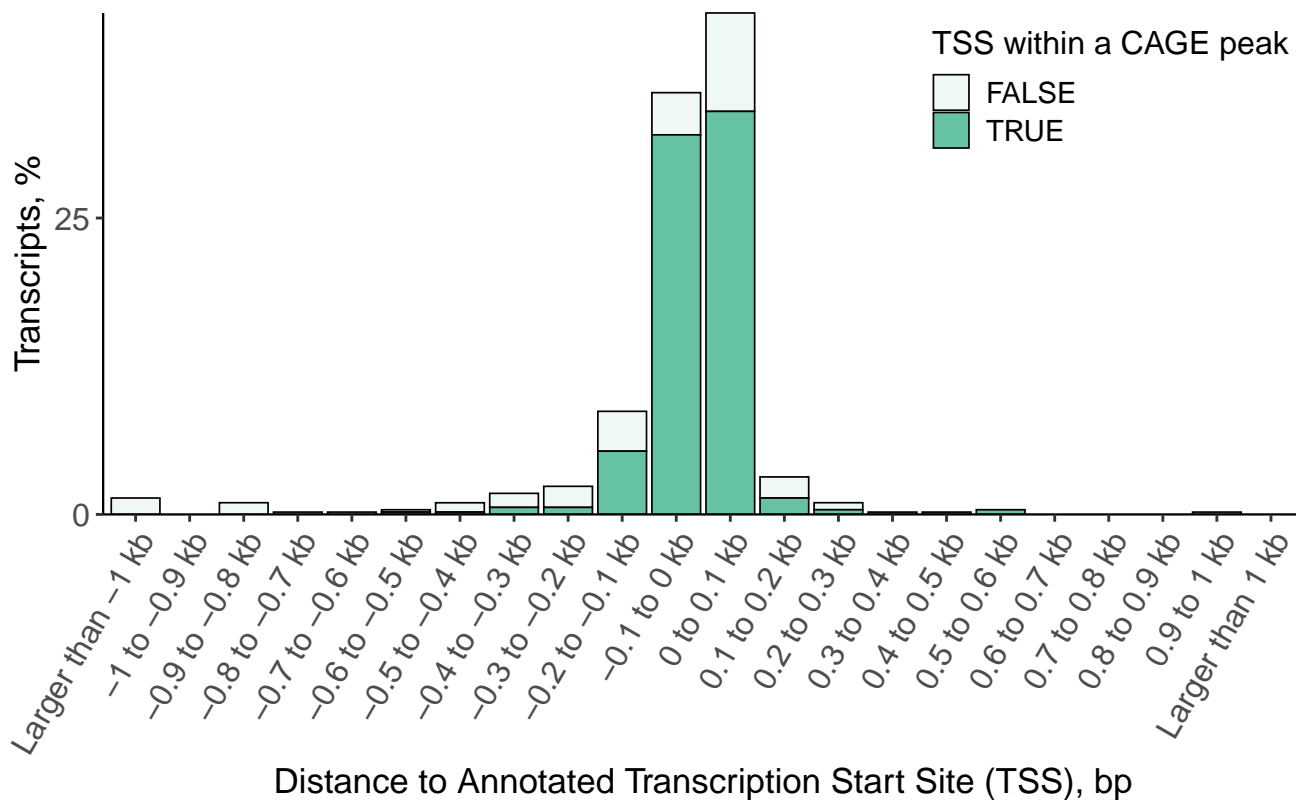
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



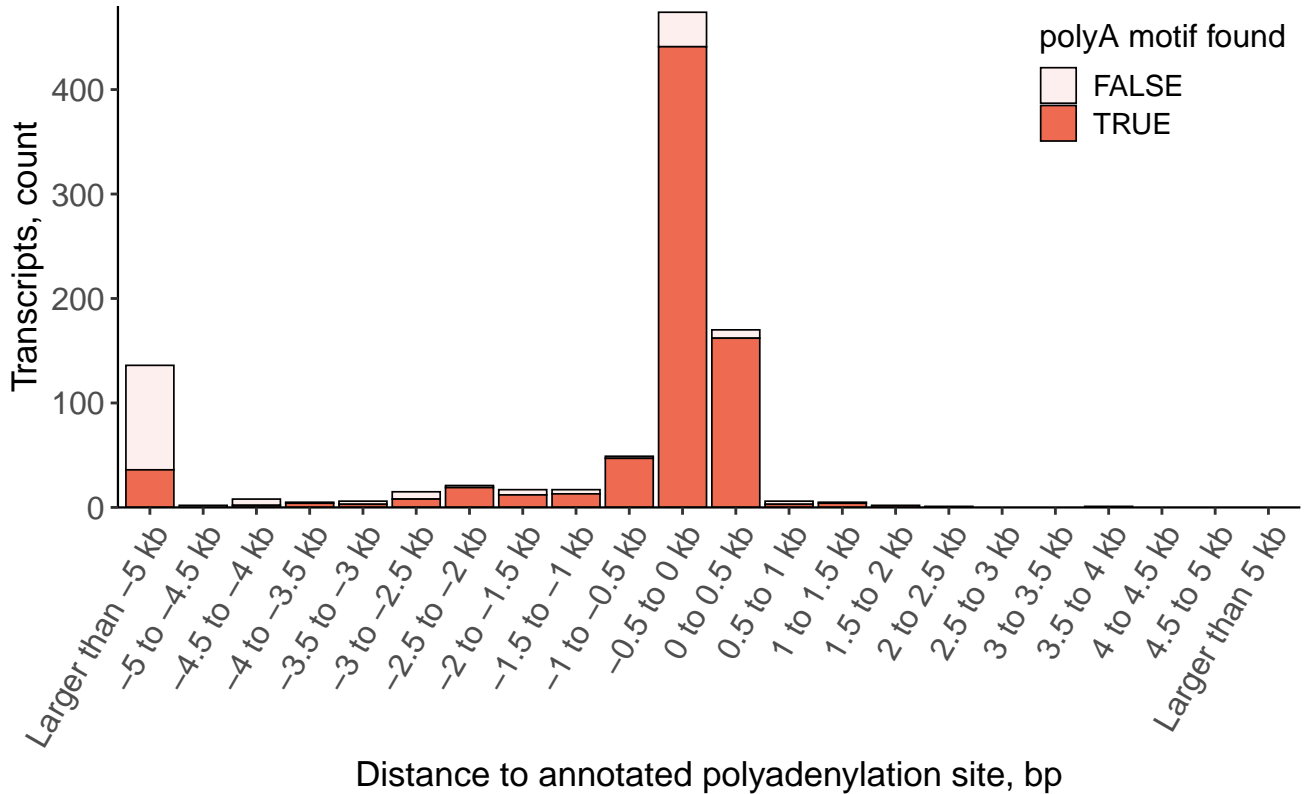
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



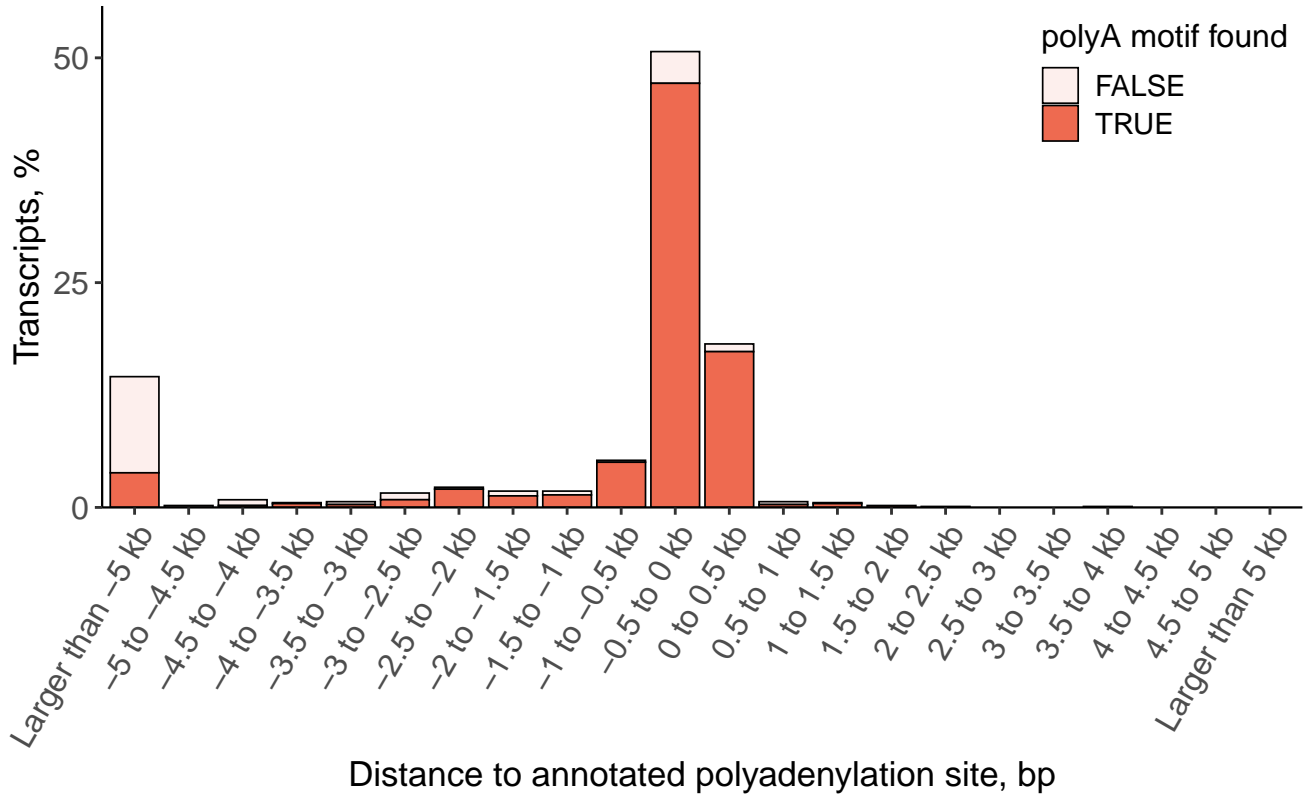
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



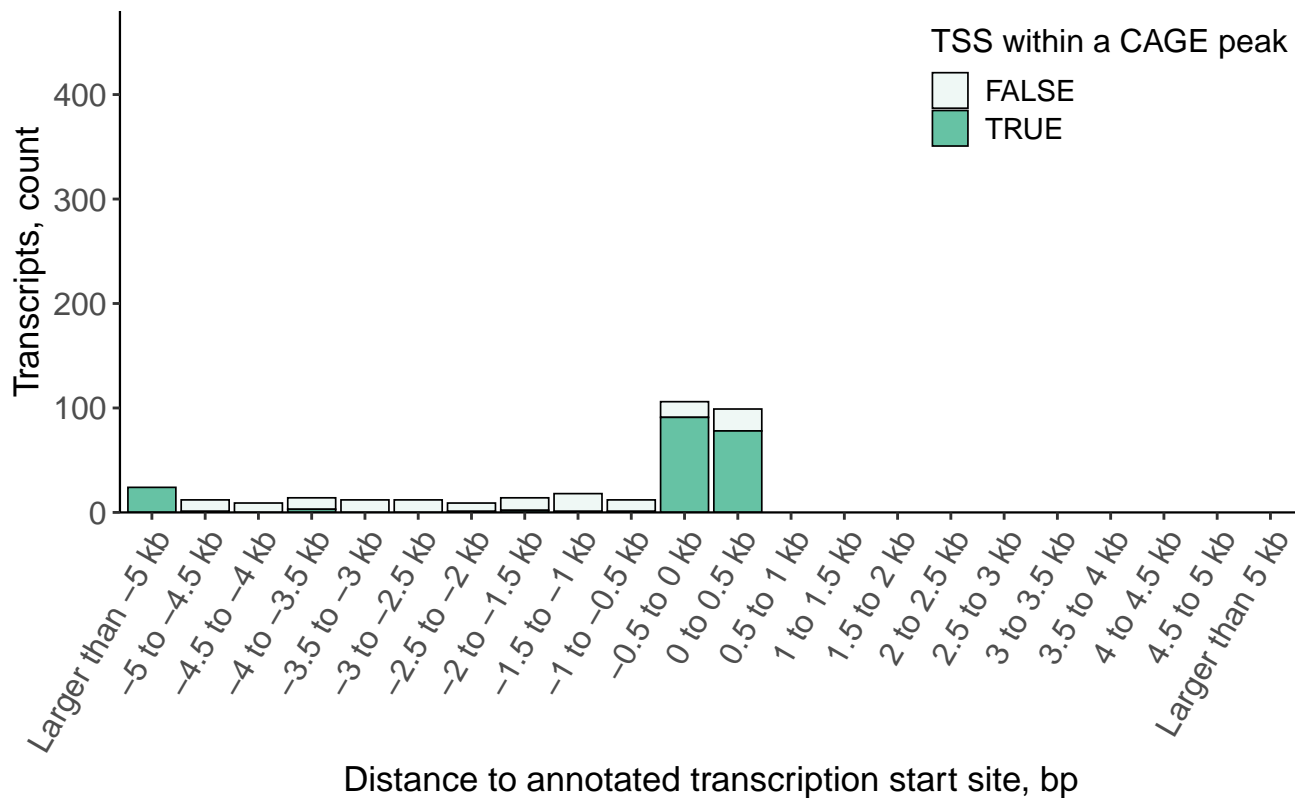
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



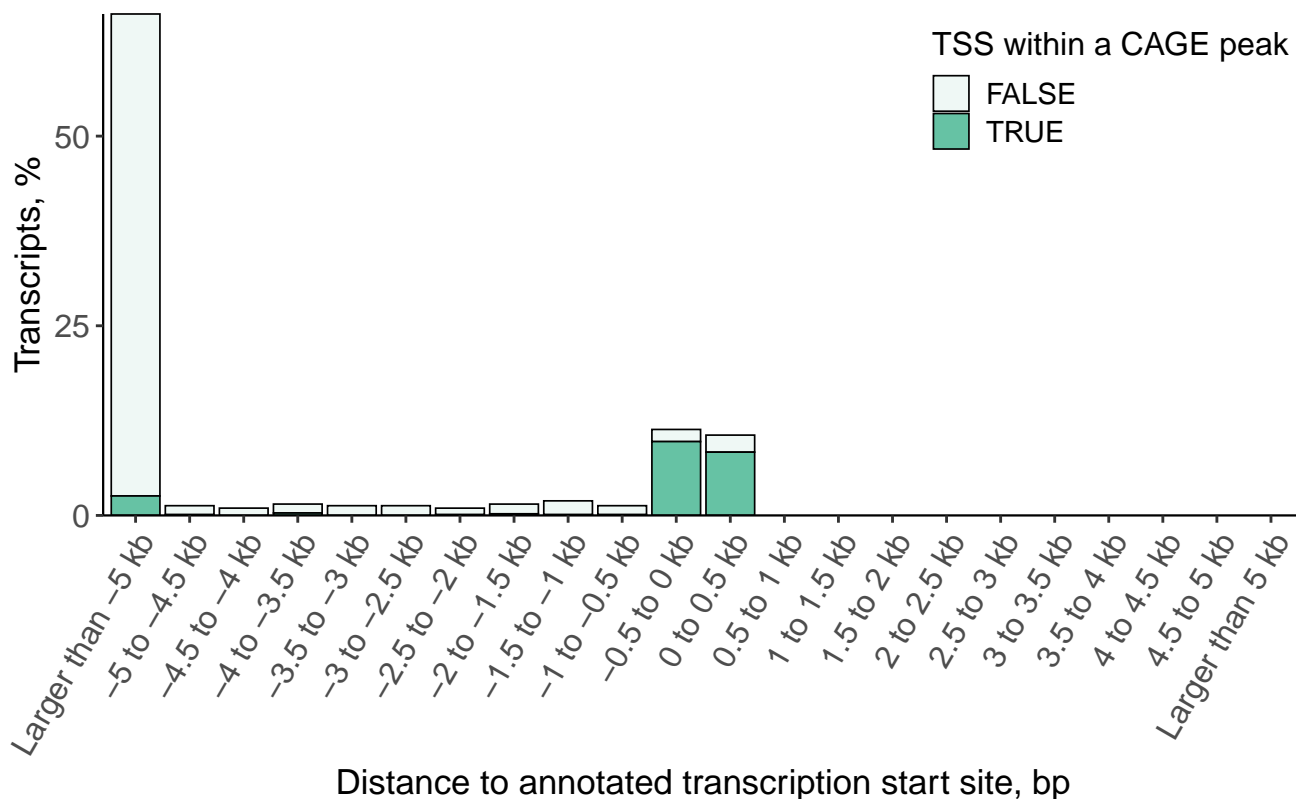
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

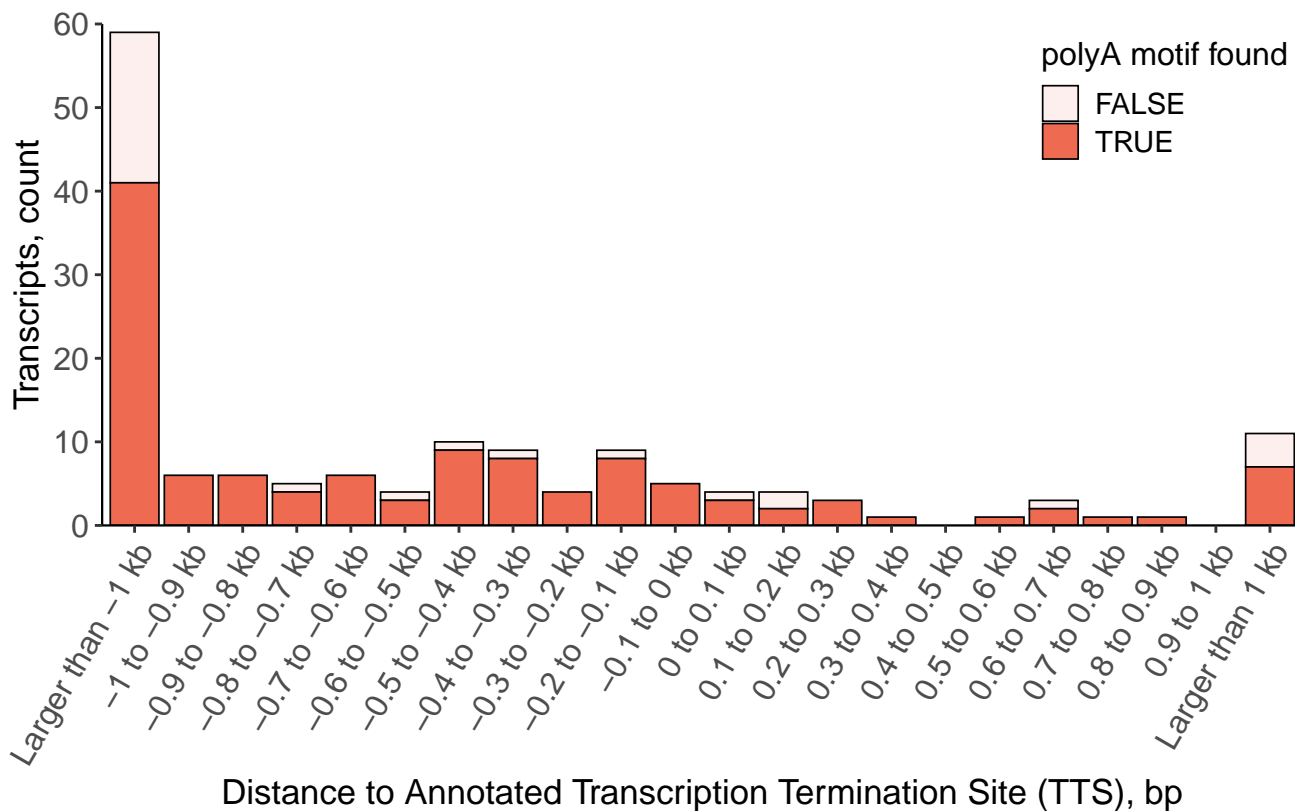
Negative values indicate downstream of annotated TSS



*Comparison With Annotated TSS and TTS
by Subcategories*

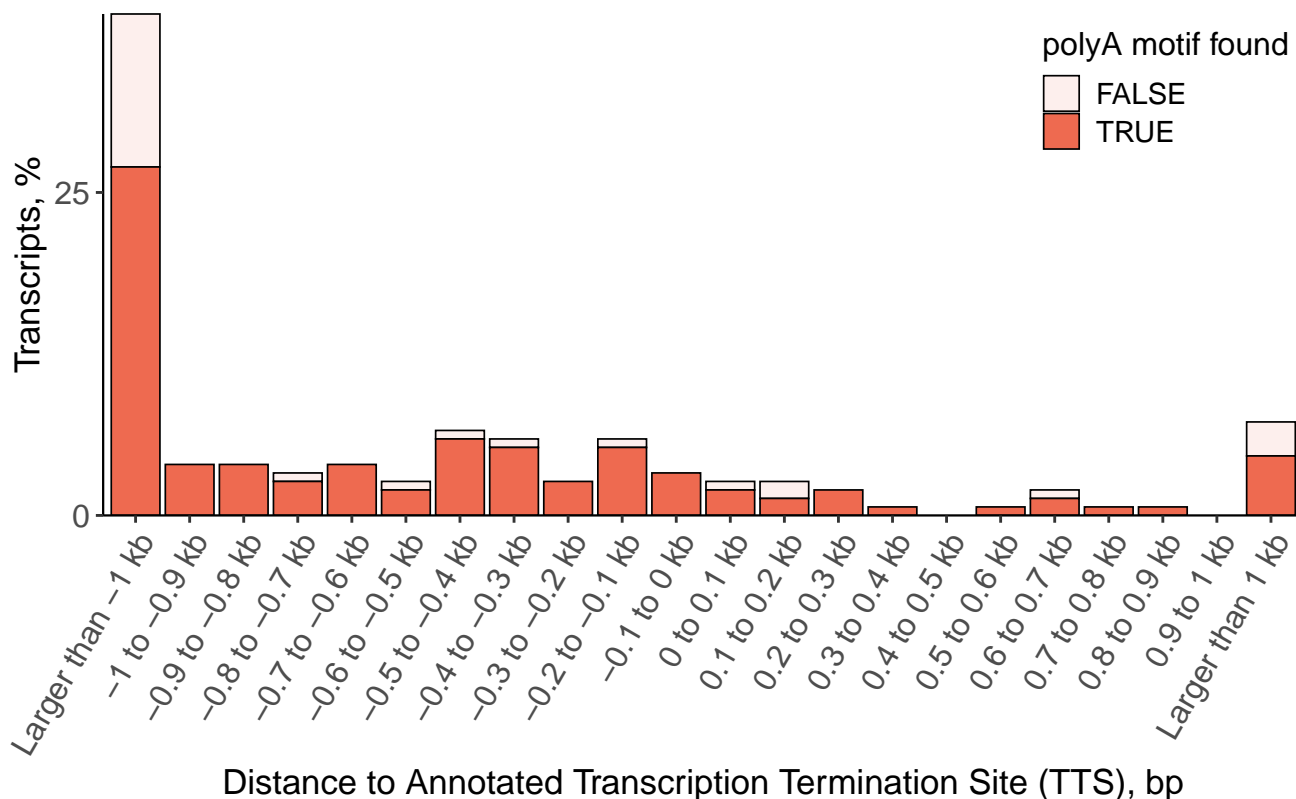
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



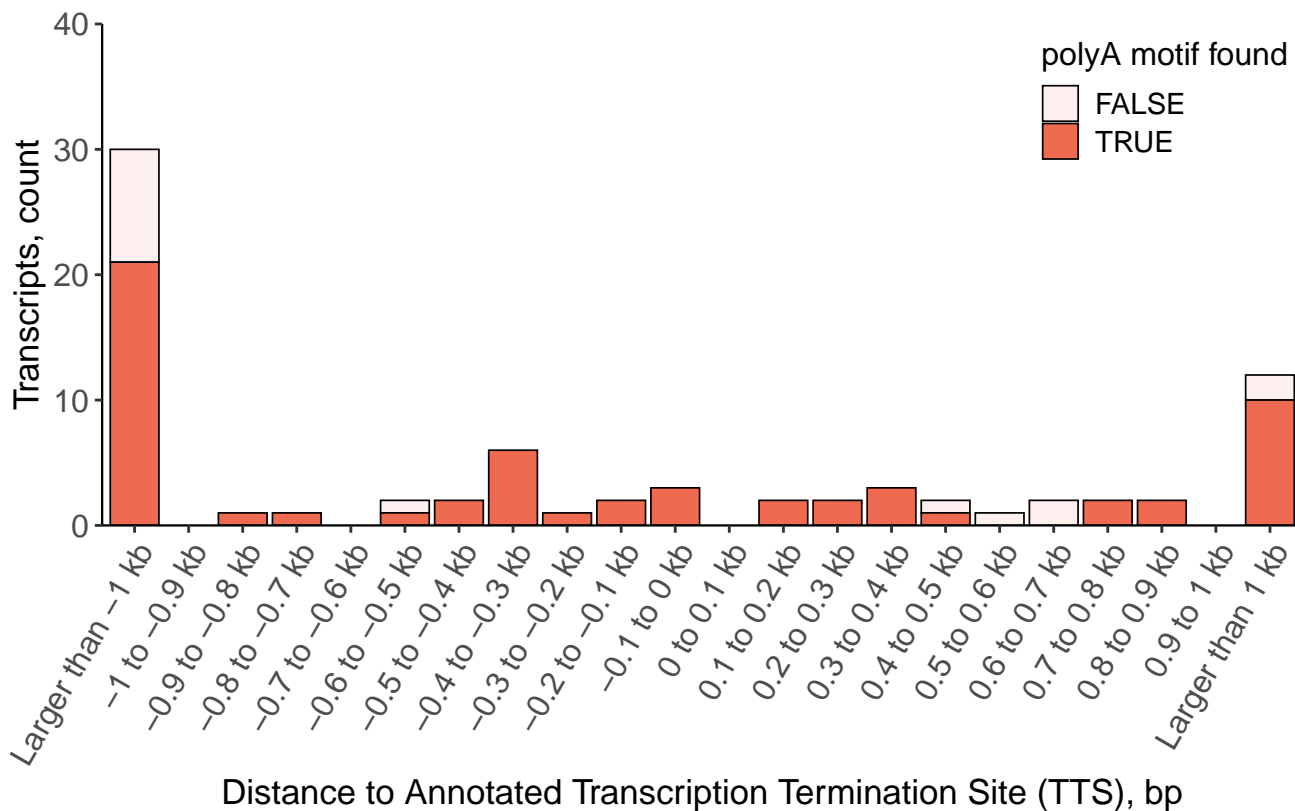
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



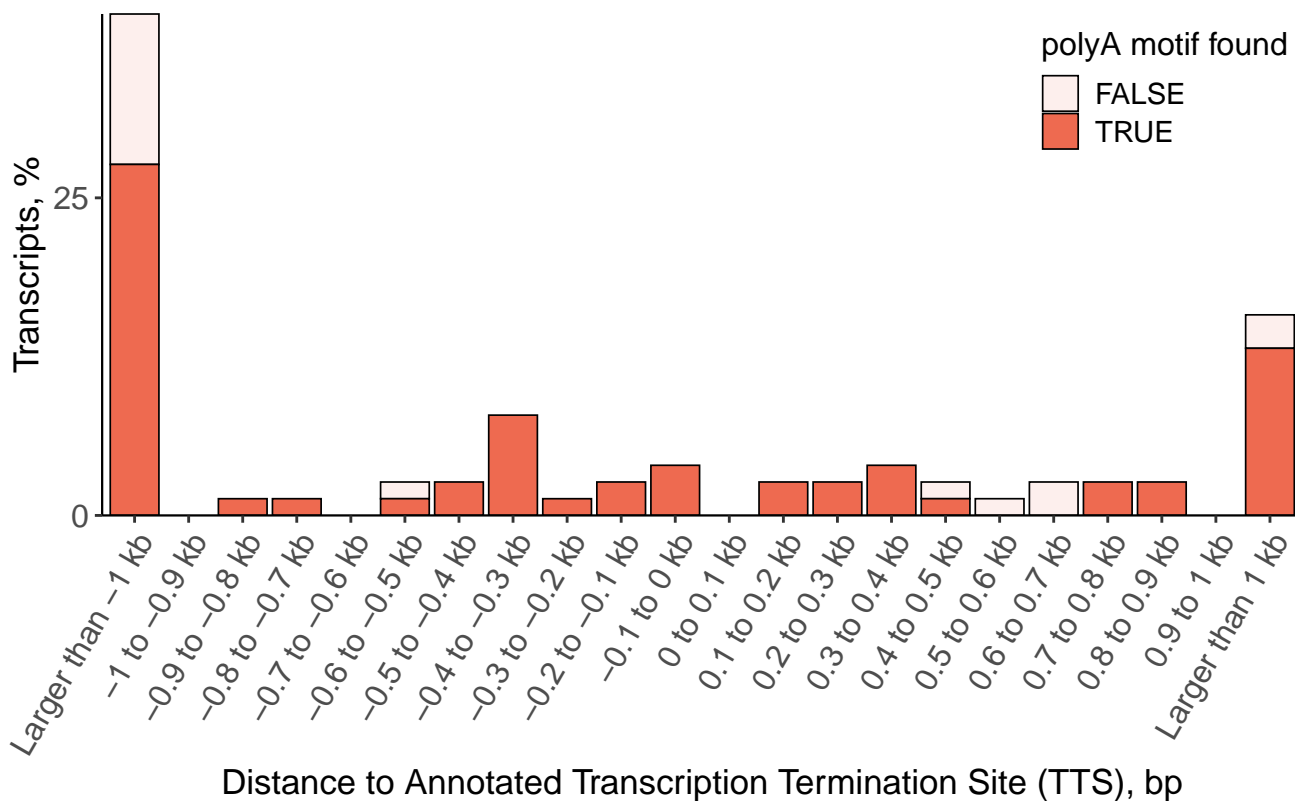
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



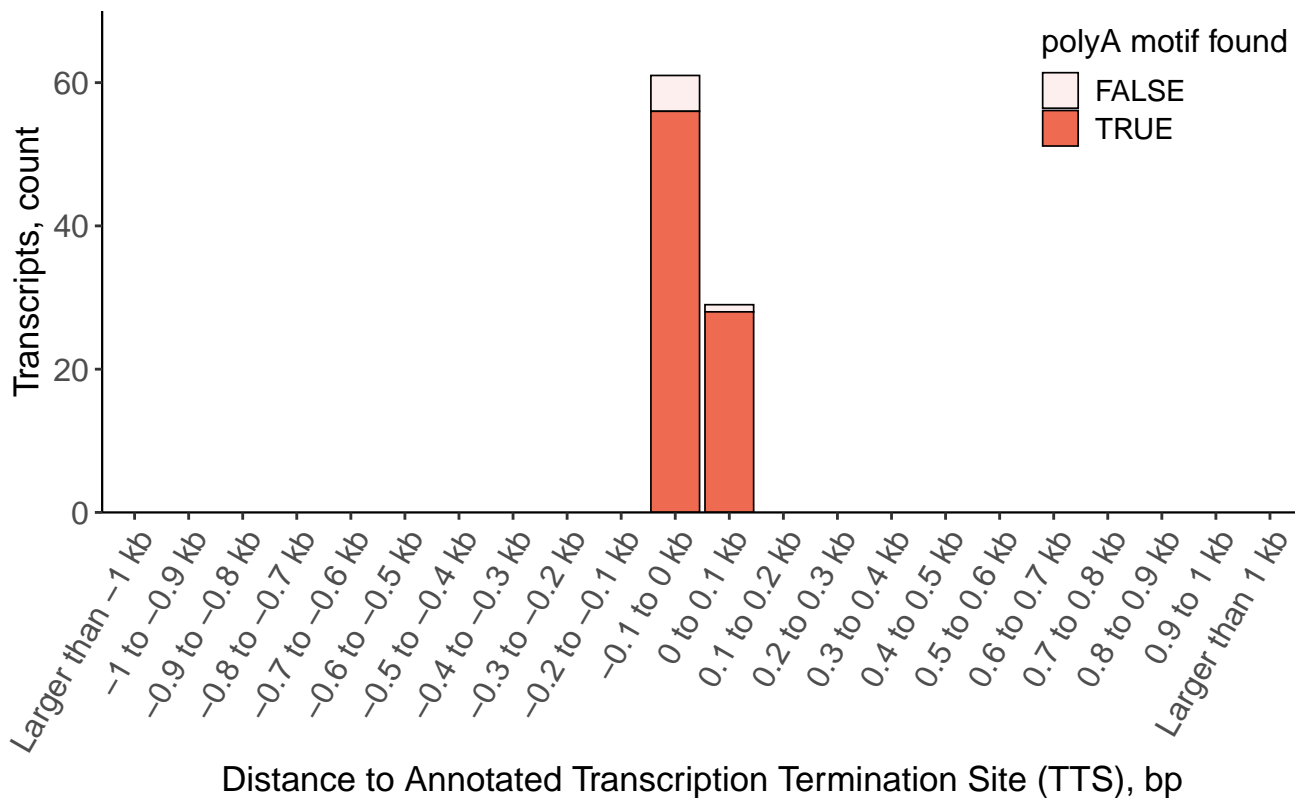
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



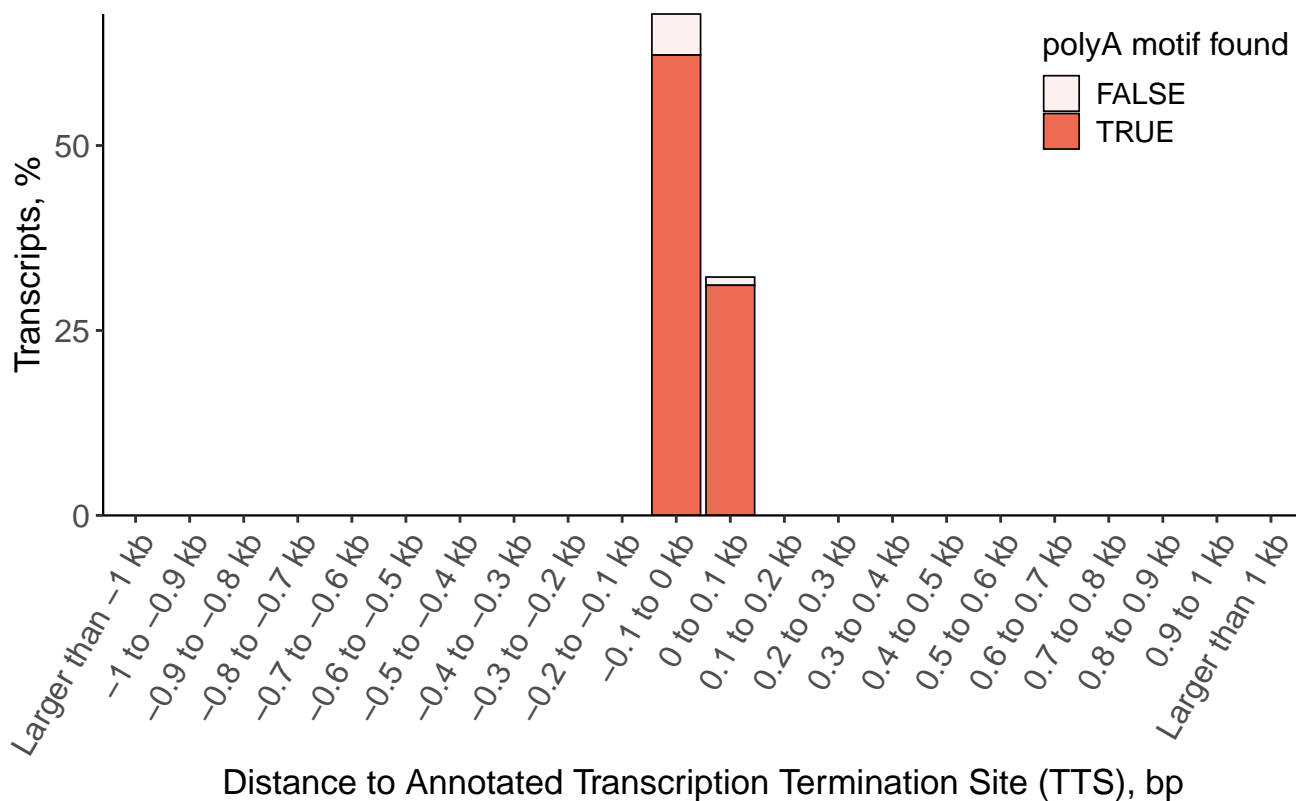
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



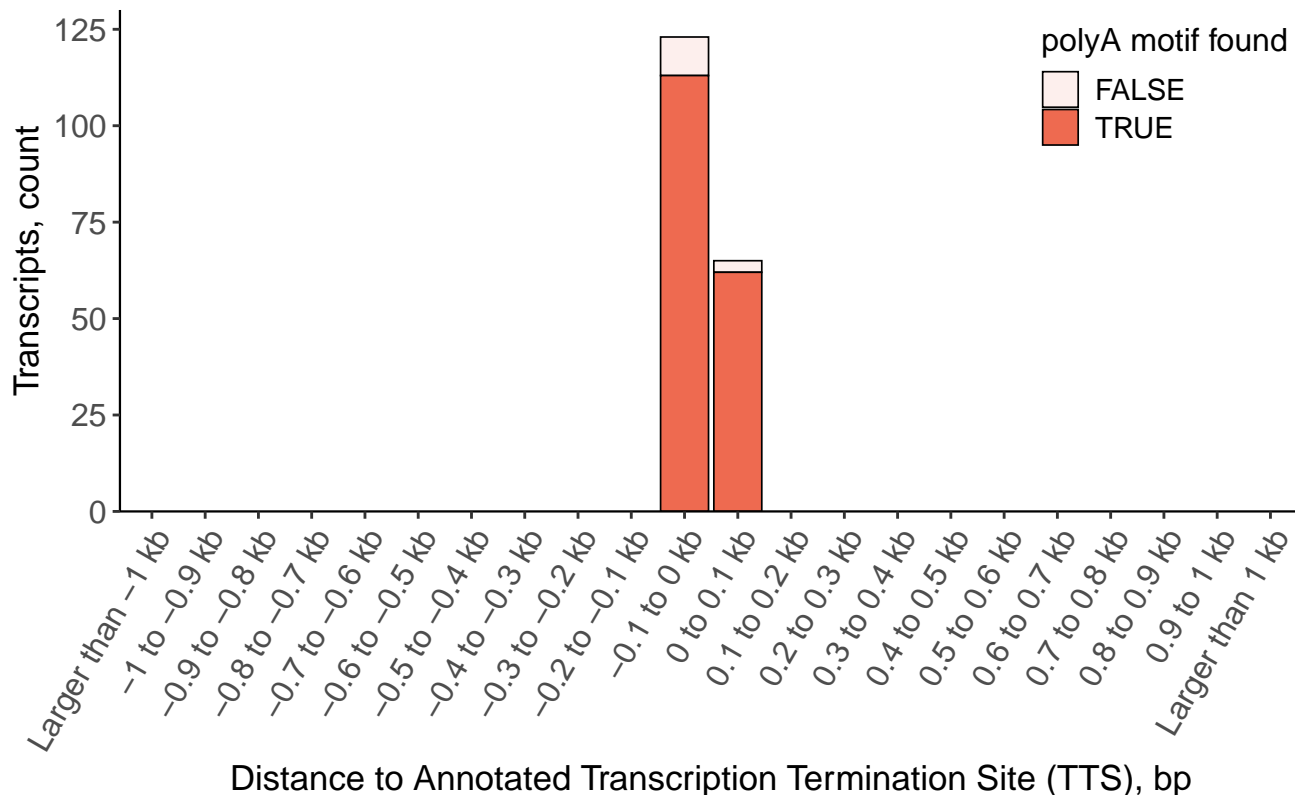
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



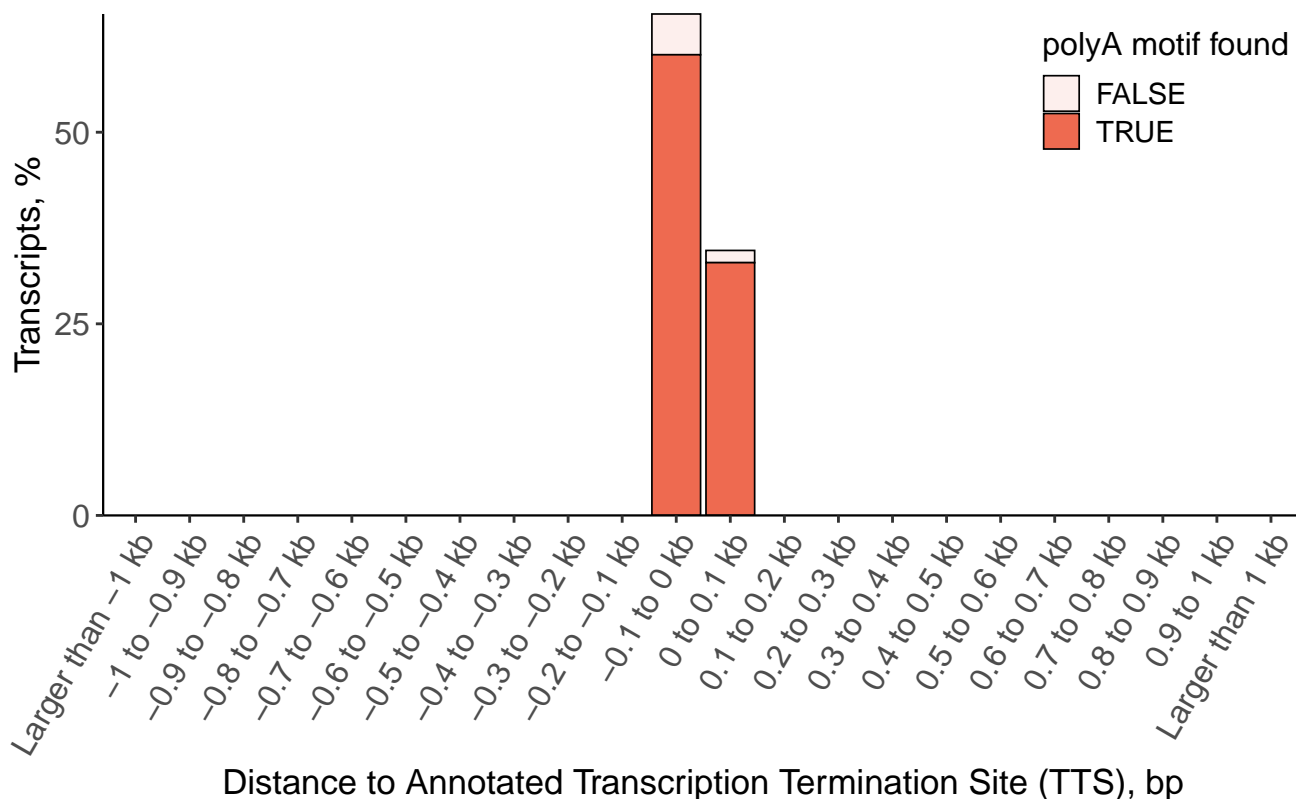
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



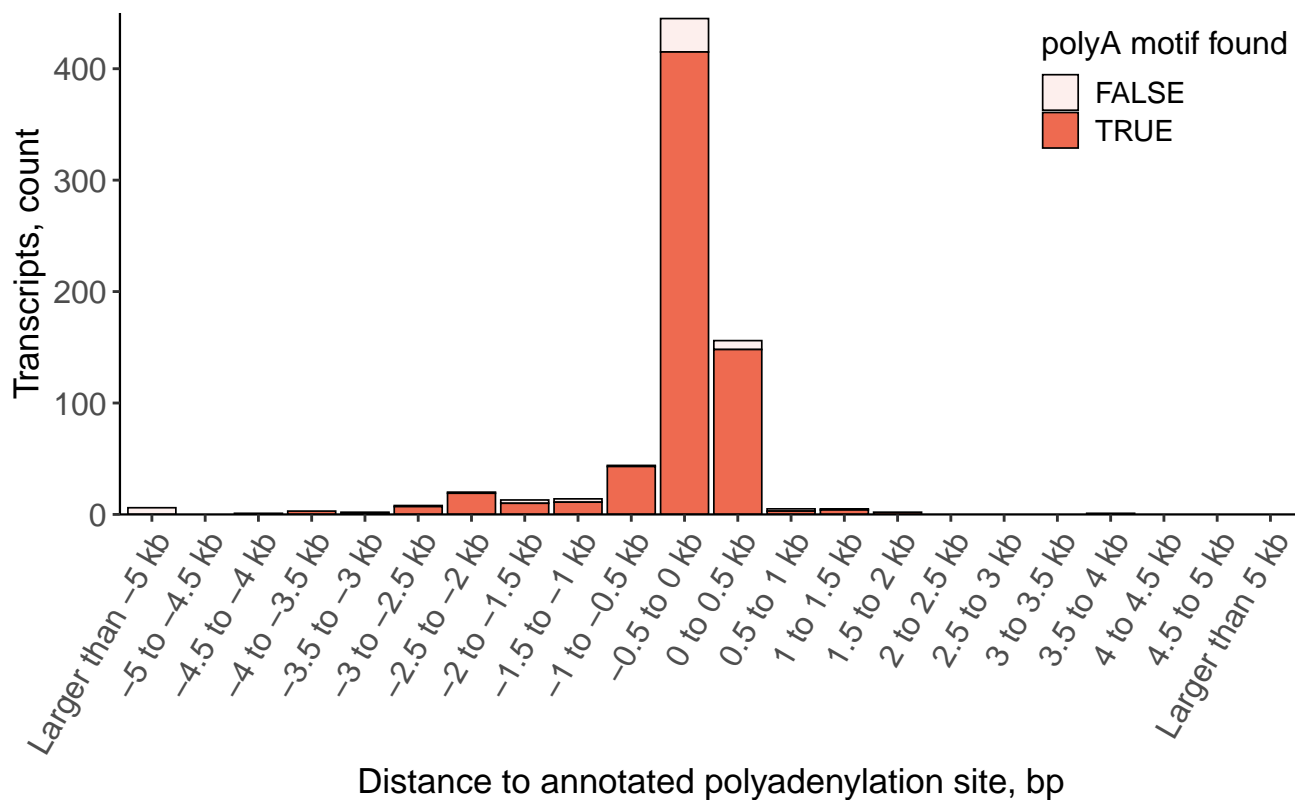
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



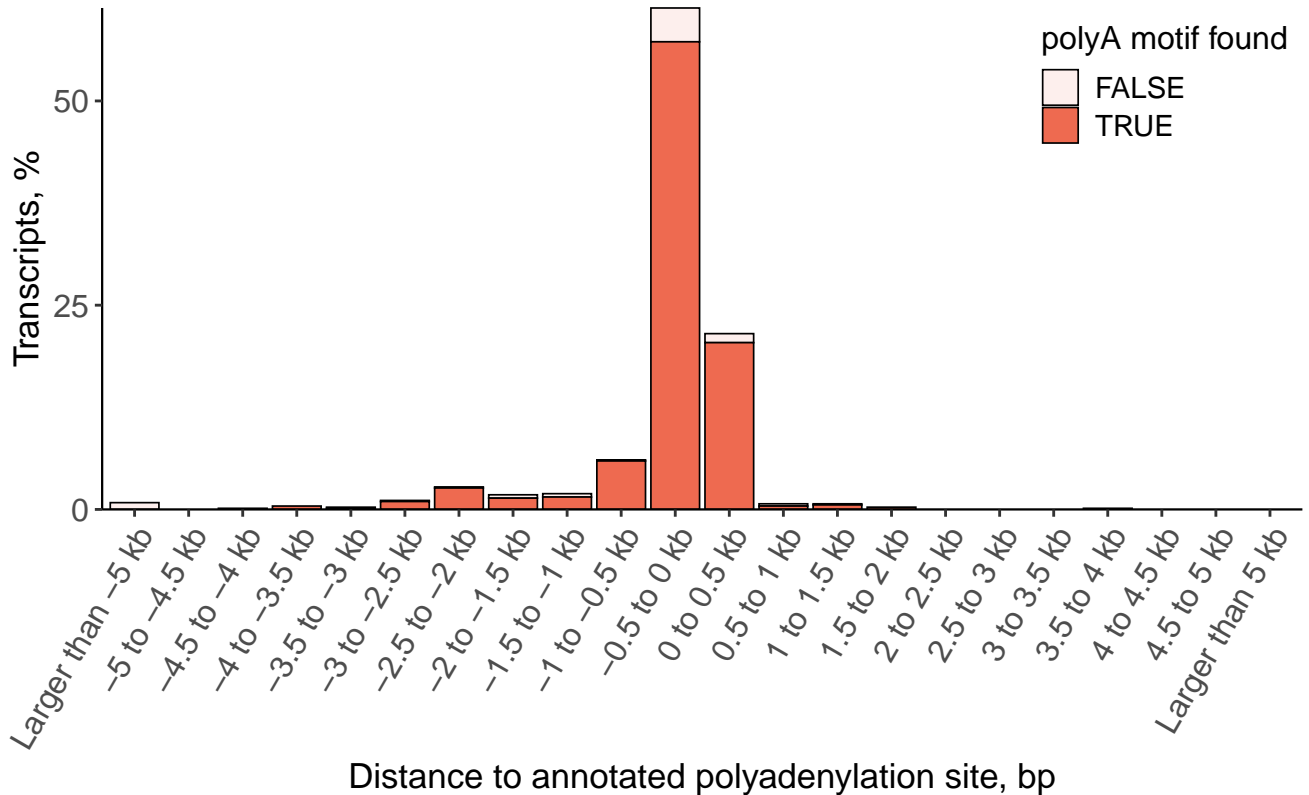
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



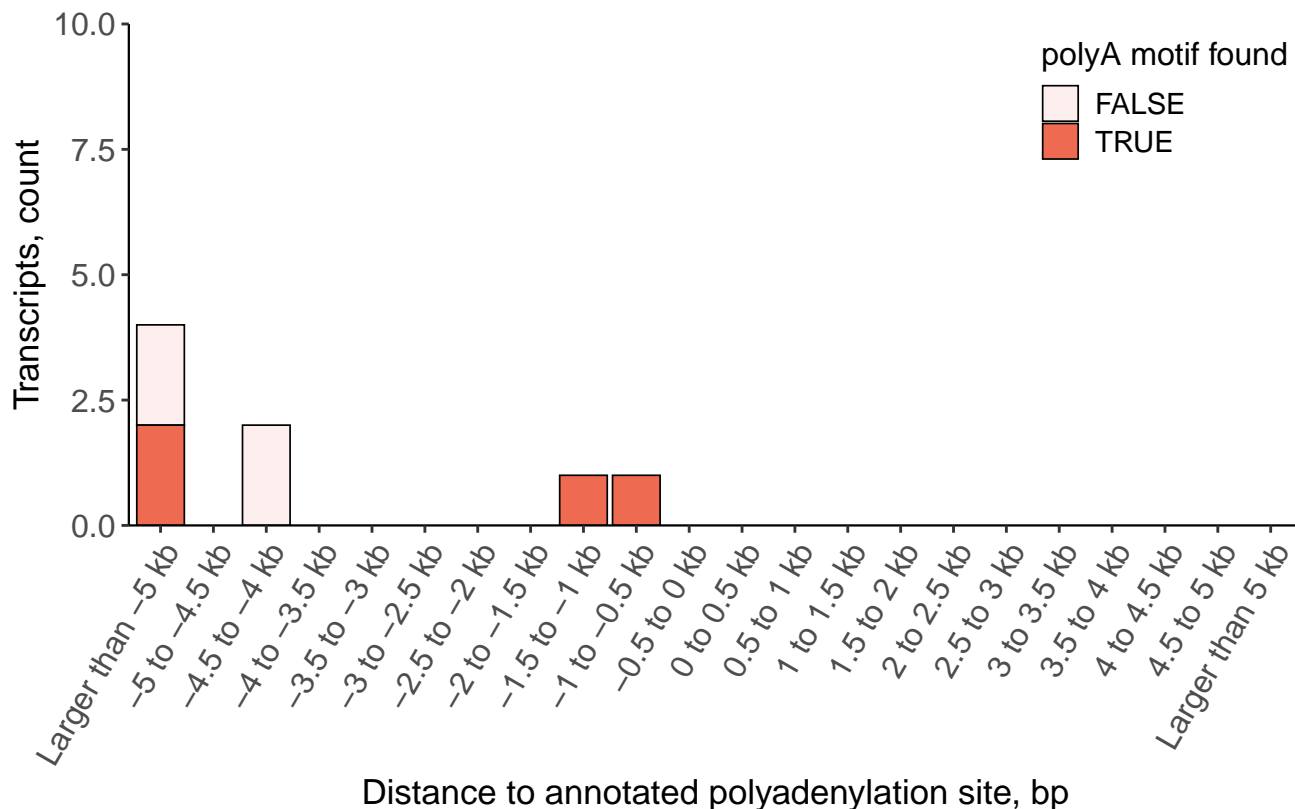
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



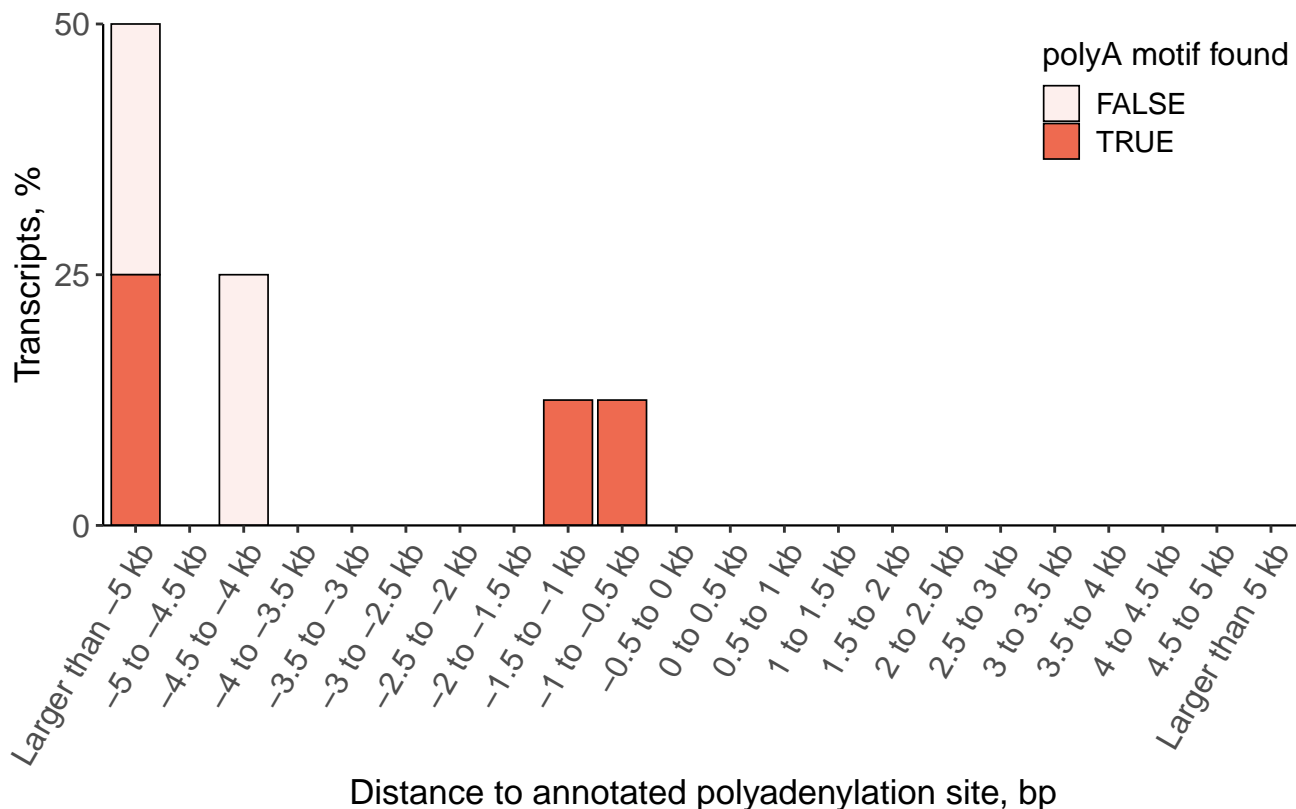
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



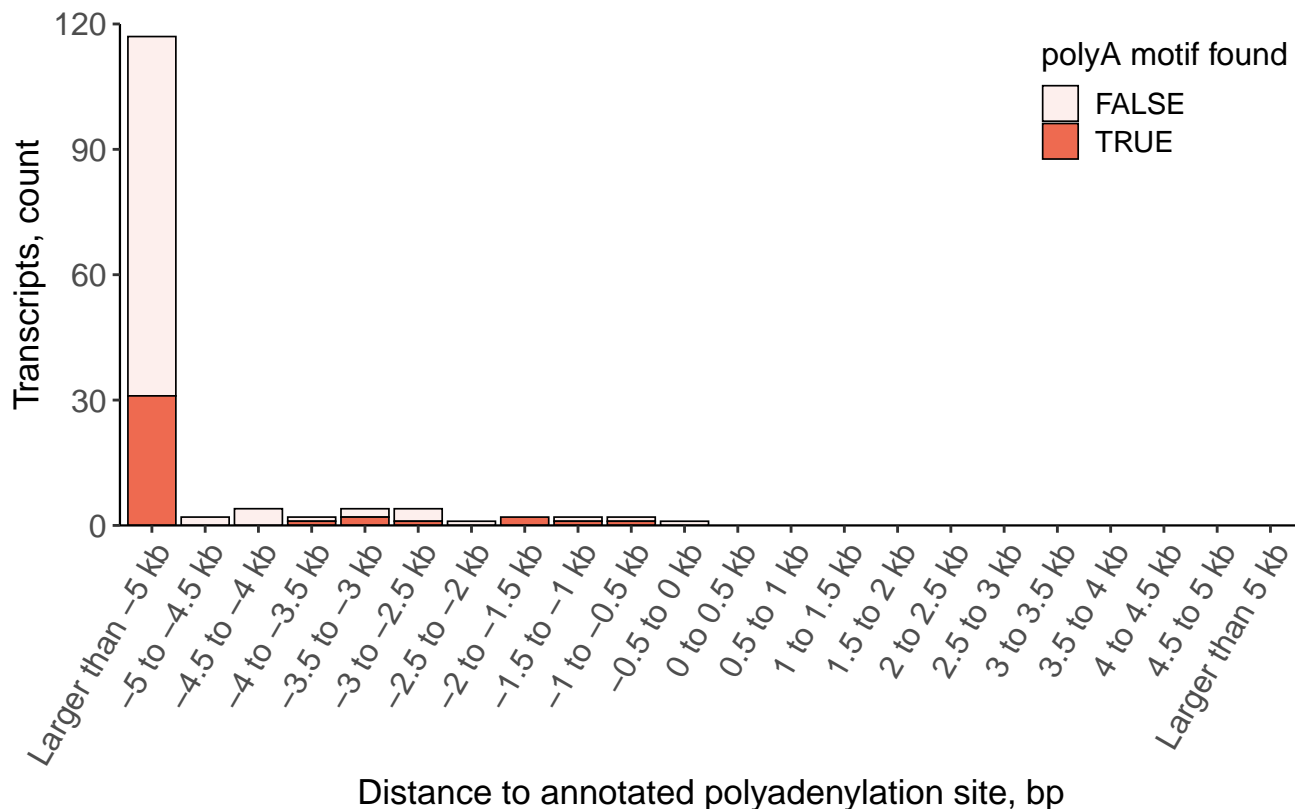
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



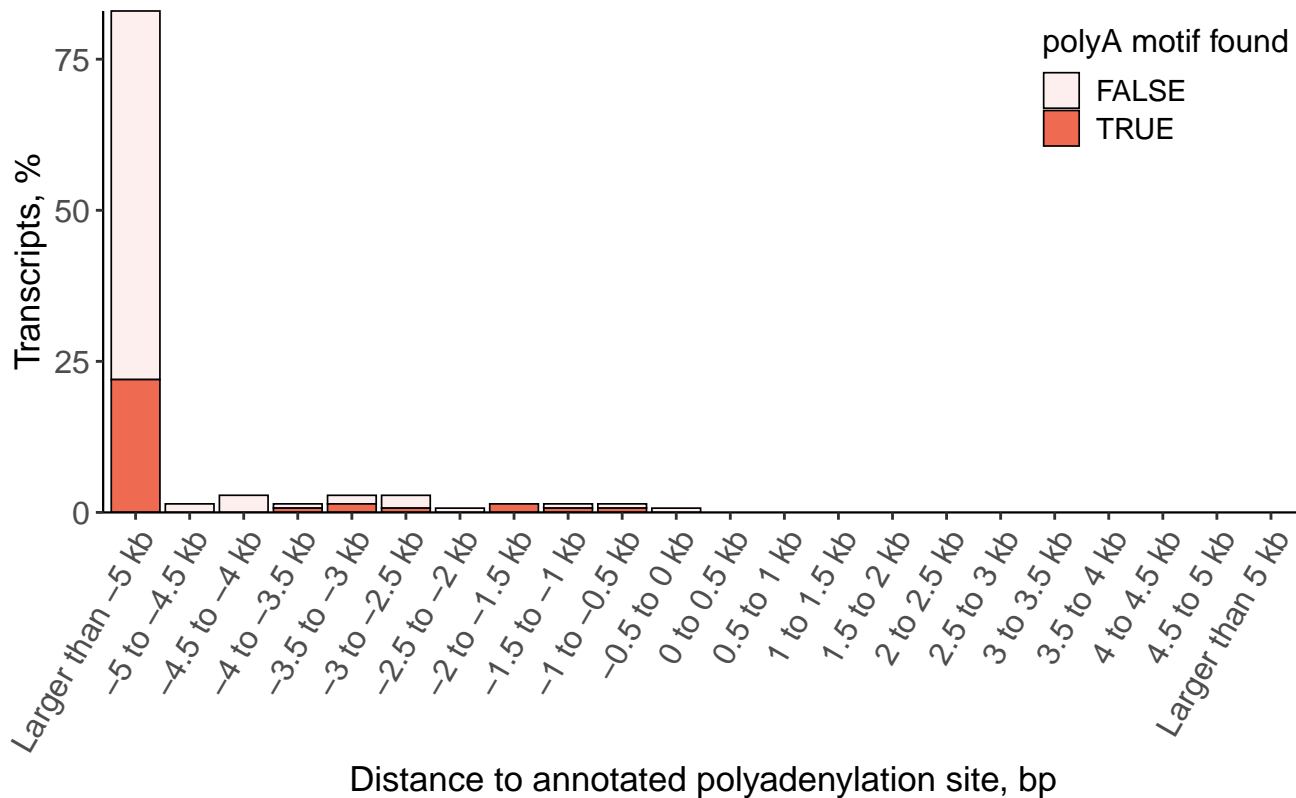
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



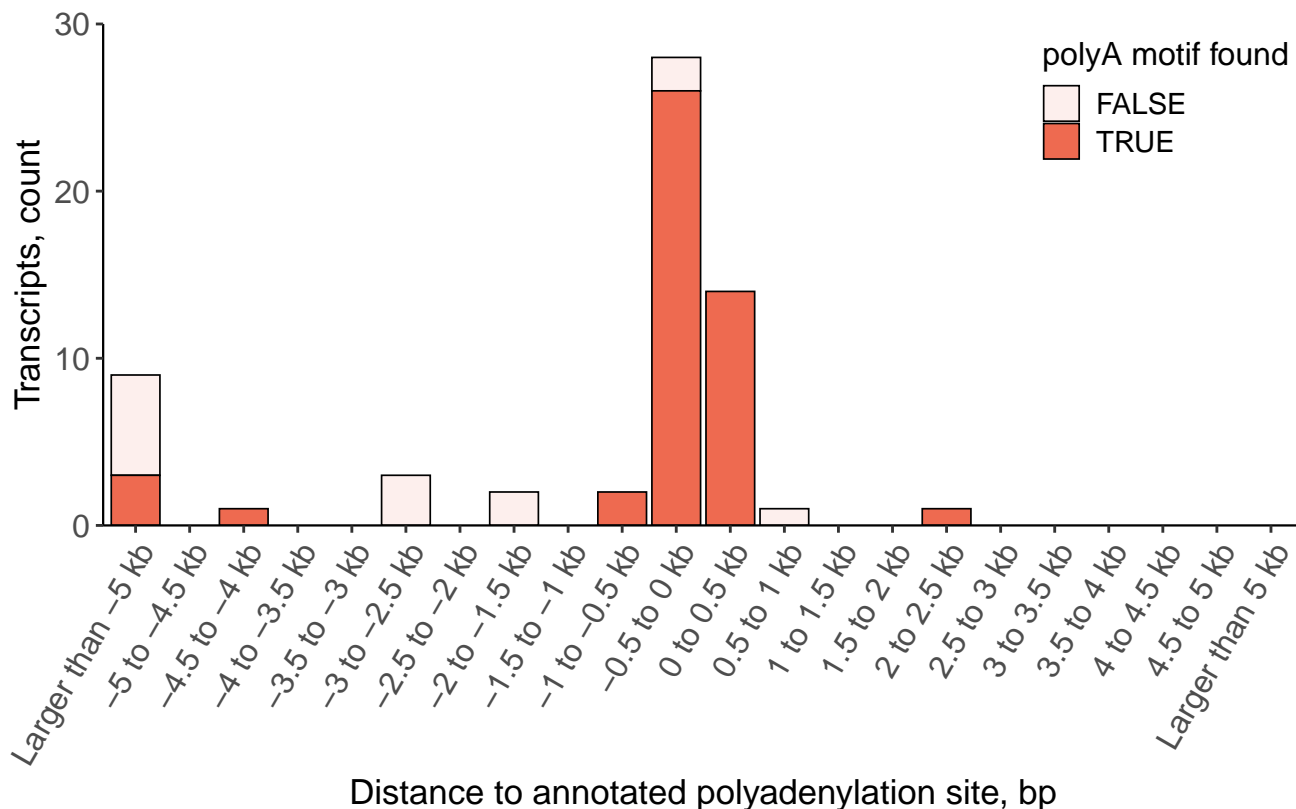
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



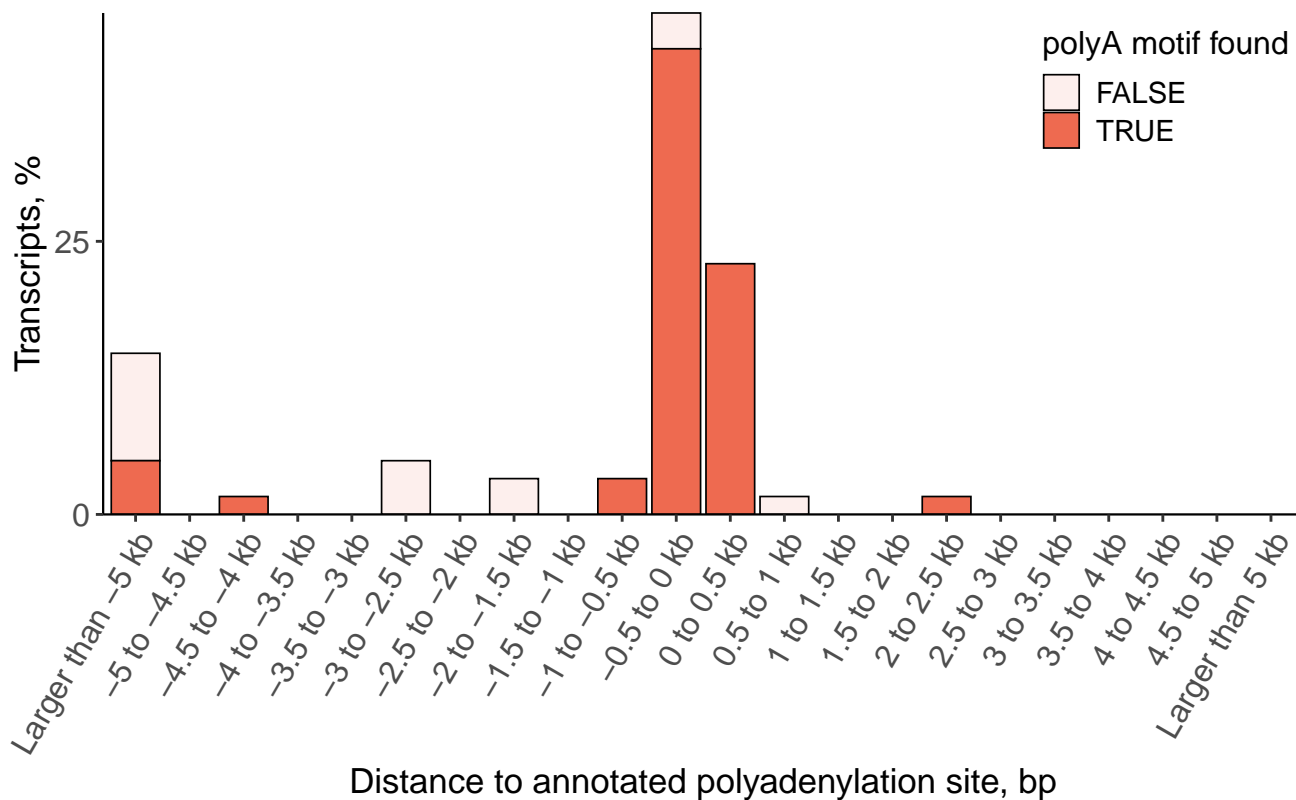
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



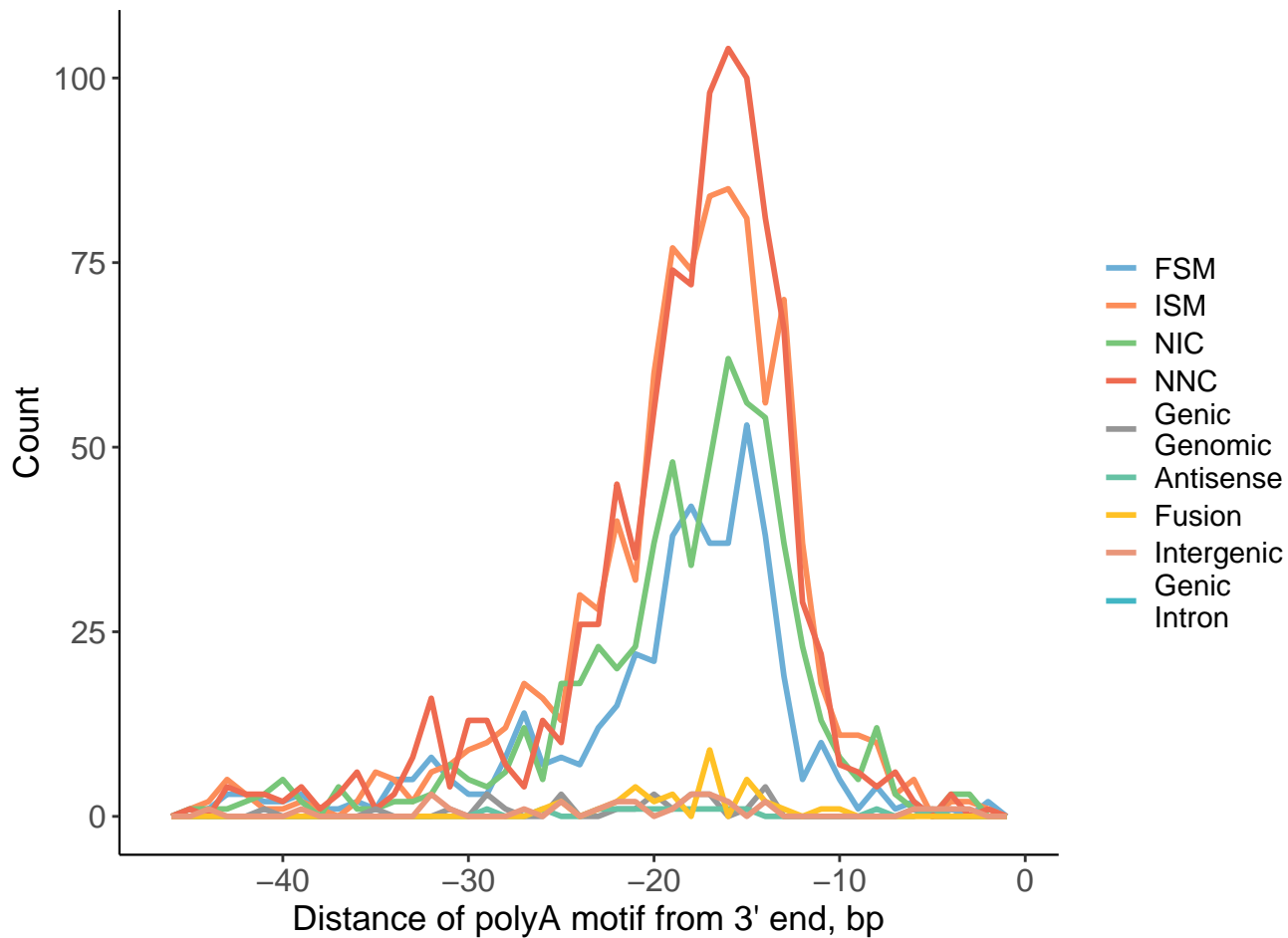
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



PolyA Distance Analysis

Distance of Detected PolyA Motif From 3' end



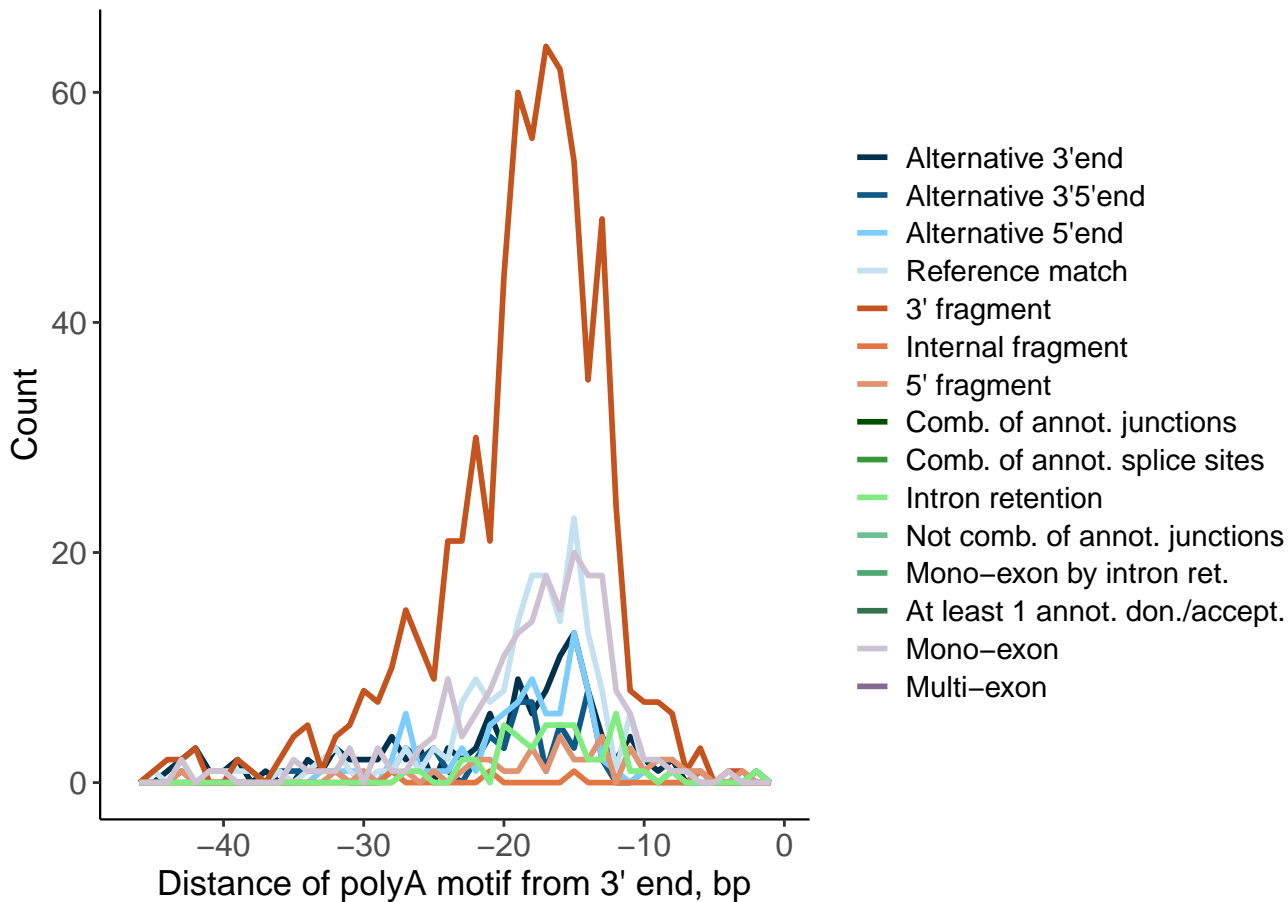
Frequency of PolyA Motifs

Number of polyA Motifs Detected

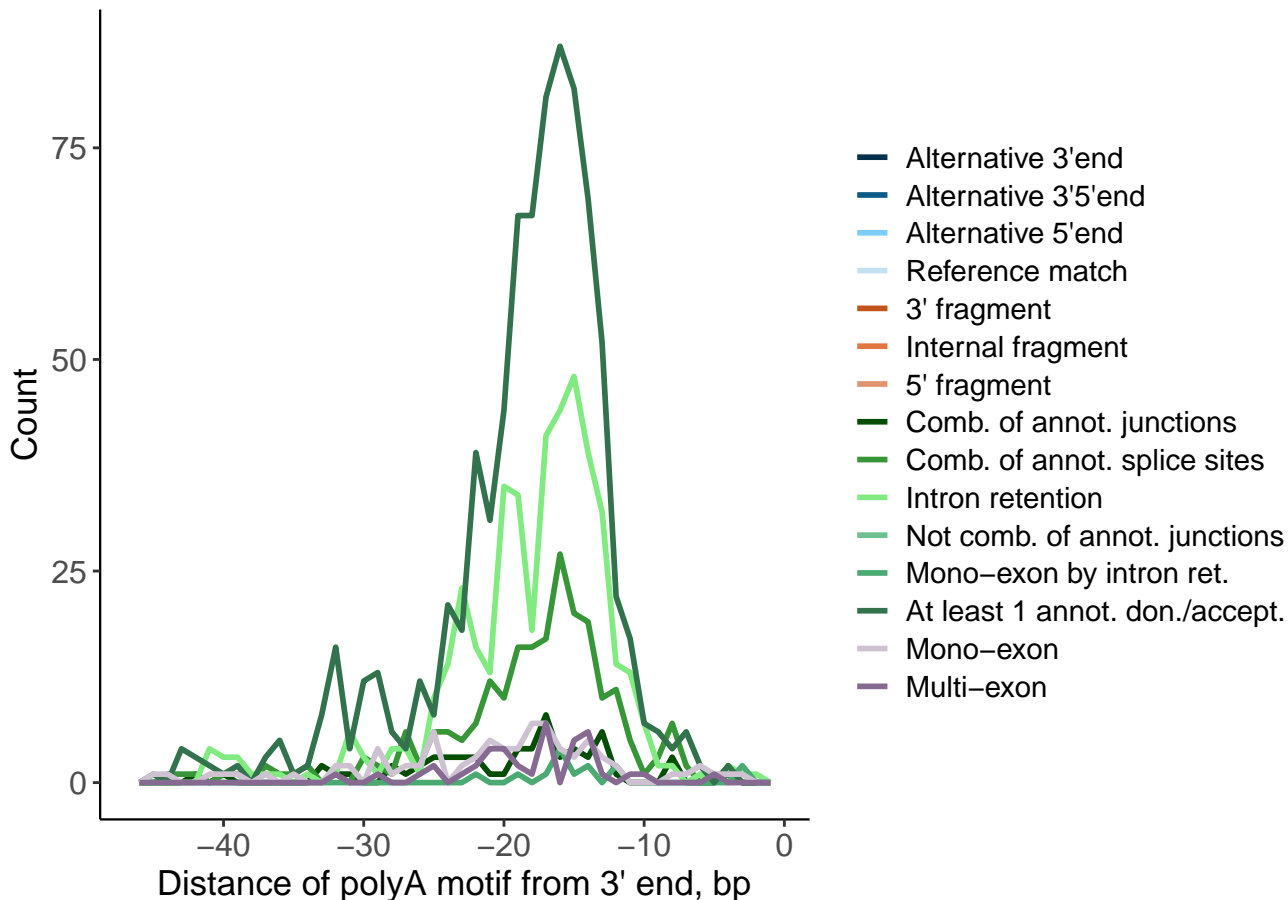
Category	Count	polyA Detected	%
FSM	537	458	85
ISM	1134	939	83
NIC	805	616	77
NNC	1139	981	86
Genic Genomic	56	28	50
Antisense	29	13	45
Fusion	38	34	89
Intergenic	187	29	16

Motif	Count	%
AATAAA	2014	65.0
ATTAAA	529	17.1
AGTAAA	161	5.2
TATAAA	90	2.9
GATAAA	54	1.7
AAAACA	41	1.3
AATACA	38	1.2
AAAAAG	32	1.0
AATAGA	28	0.9
CATAAA	26	0.8
AAGAAA	24	0.8
AATATA	20	0.6
TTTAAA	16	0.5
AATGAA	13	0.4
ACTAAA	10	0.3
GGGGCT	2	0.1

Distance of Detected PolyA Motif From 3'End by FSM and ISM Subcategories



Distance of Detected PolyA Motif From 3'End by Non-FSM/ISM Subcategories



Number of polyA Motifs Detected

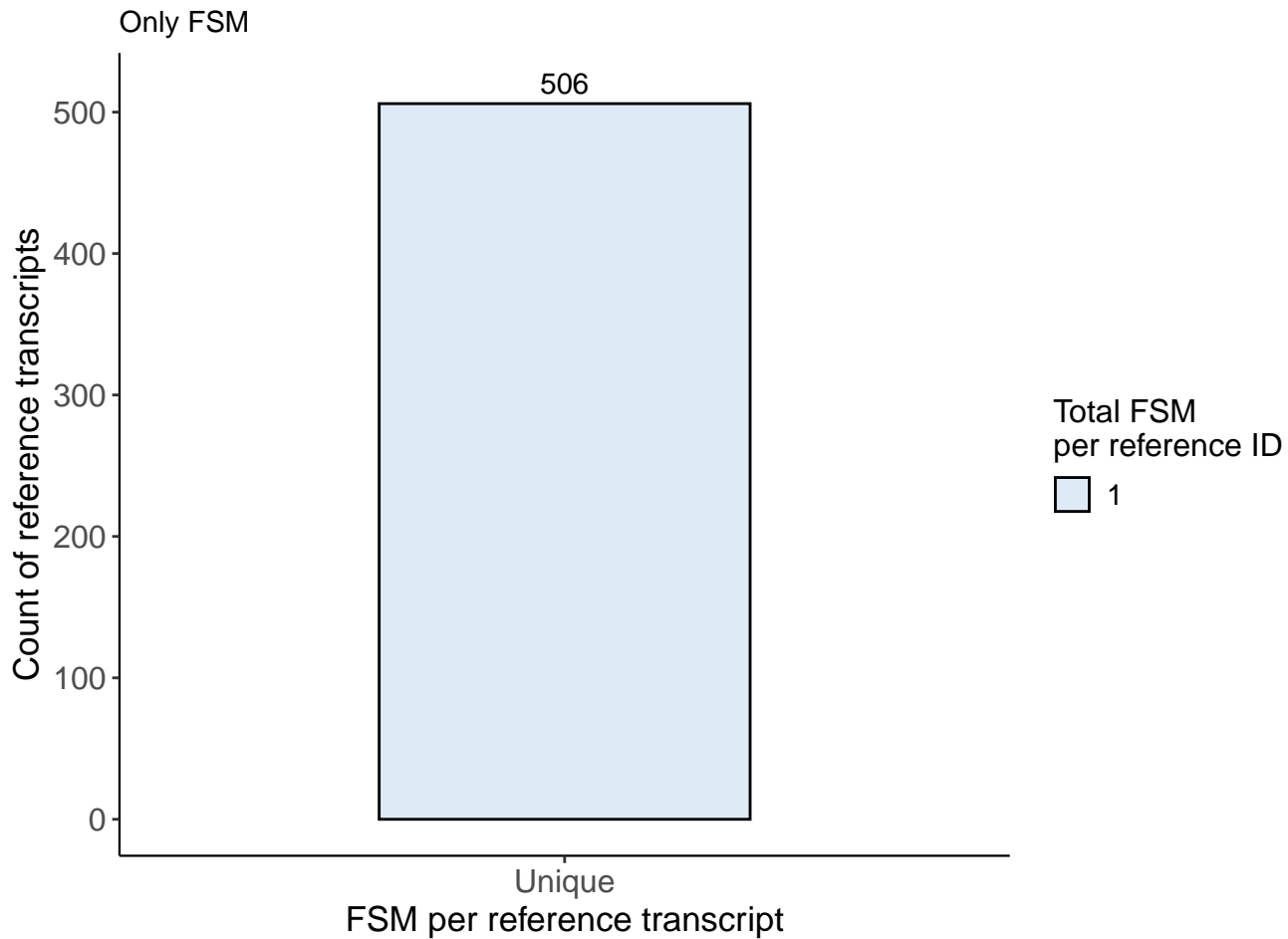
Subcategory	Count	polyA Detected	%
Alternative 3'end	152	121	80
Alternative 3'5'end	76	60	79
Alternative 5'end	90	84	93
Reference match	188	175	93
3' fragment	725	668	92
Internal fragment	8	4	50
5' fragment	141	39	28
Comb. of annot. junctions	76	62	82
Comb. of annot. splice sites	272	227	83
Intron retention	594	491	83
Mono-exon by intron ret.	31	14	45
At least 1 annot. don./accept.	965	831	86
Mono-exon	556	281	51
Multi-exon	51	41	80

Frequency of PolyA Motifs

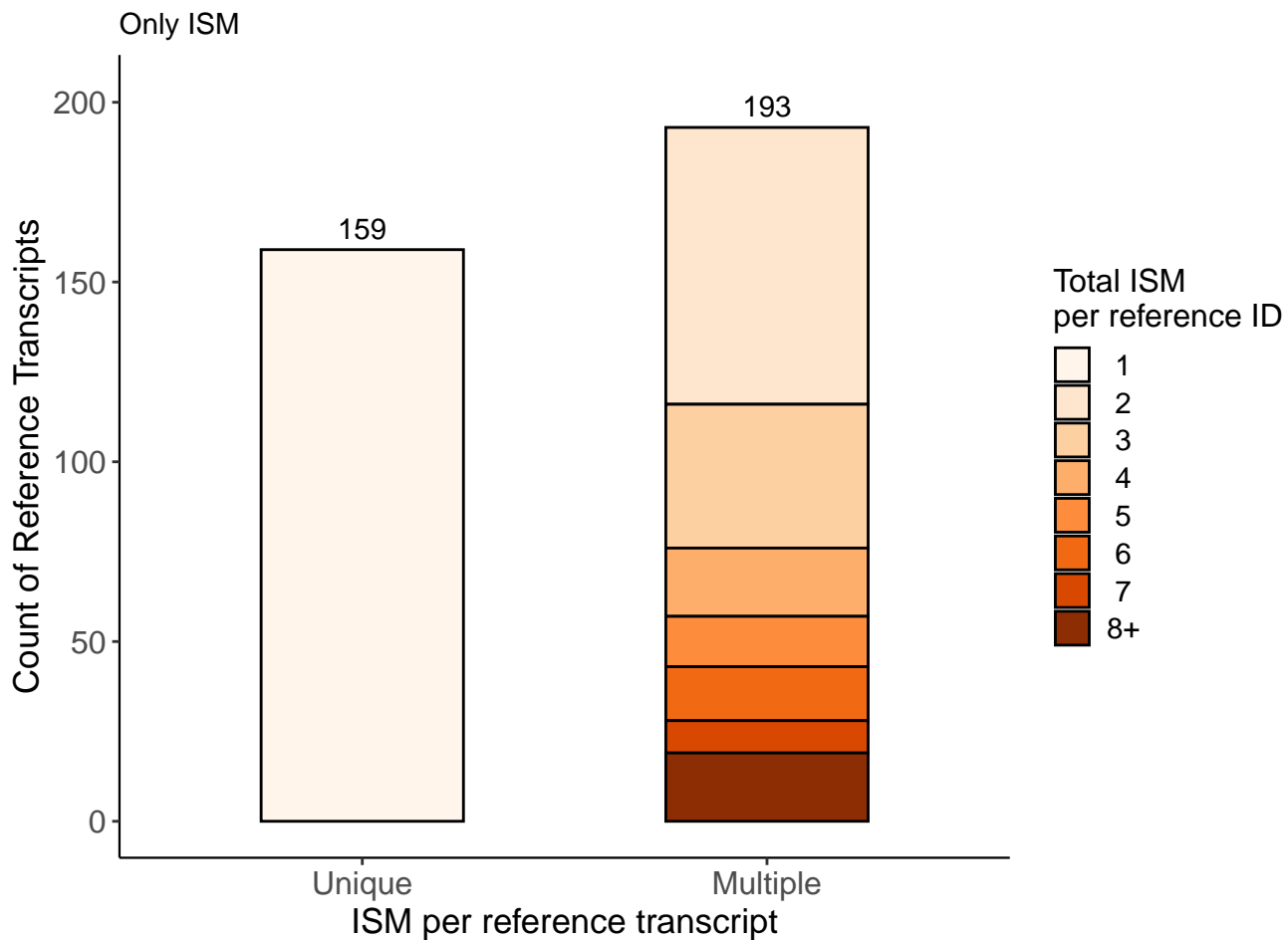
Motif	Count	%
AATAAA	2014	65.0
ATTAAA	529	17.1
AGTAAA	161	5.2
TATAAA	90	2.9
GATAAA	54	1.7
AAAACA	41	1.3
AATACA	38	1.2
AAAAAG	32	1.0
AATAGA	28	0.9
CATAAA	26	0.8
AAGAAA	24	0.8
AATATA	20	0.6
TTTAAA	16	0.5
AATGAA	13	0.4
ACTAAA	10	0.3
GGGGCT	2	0.1

Redundancy Analysis

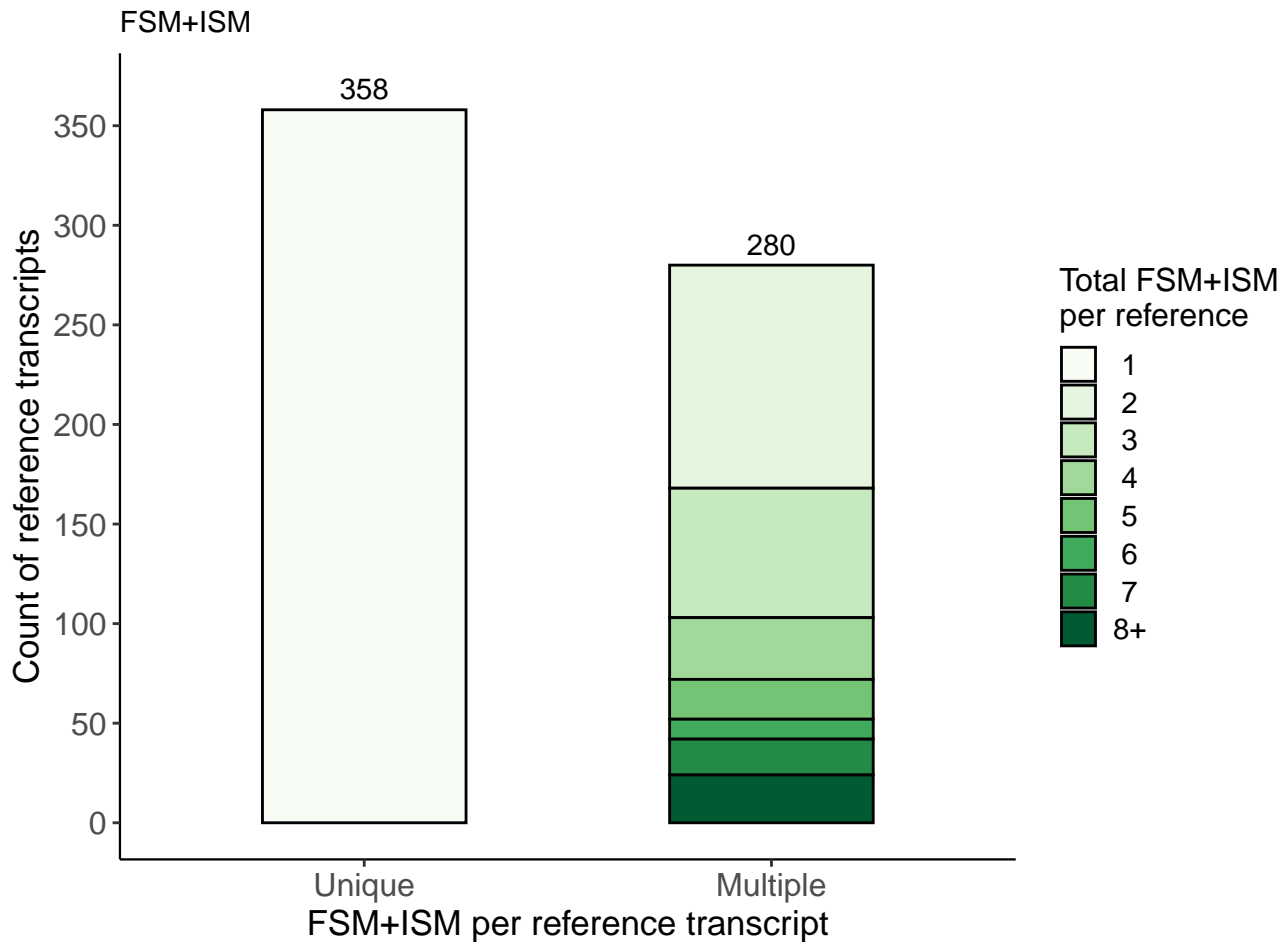
Reference Transcript Redundancy



Reference Transcript Redundancy

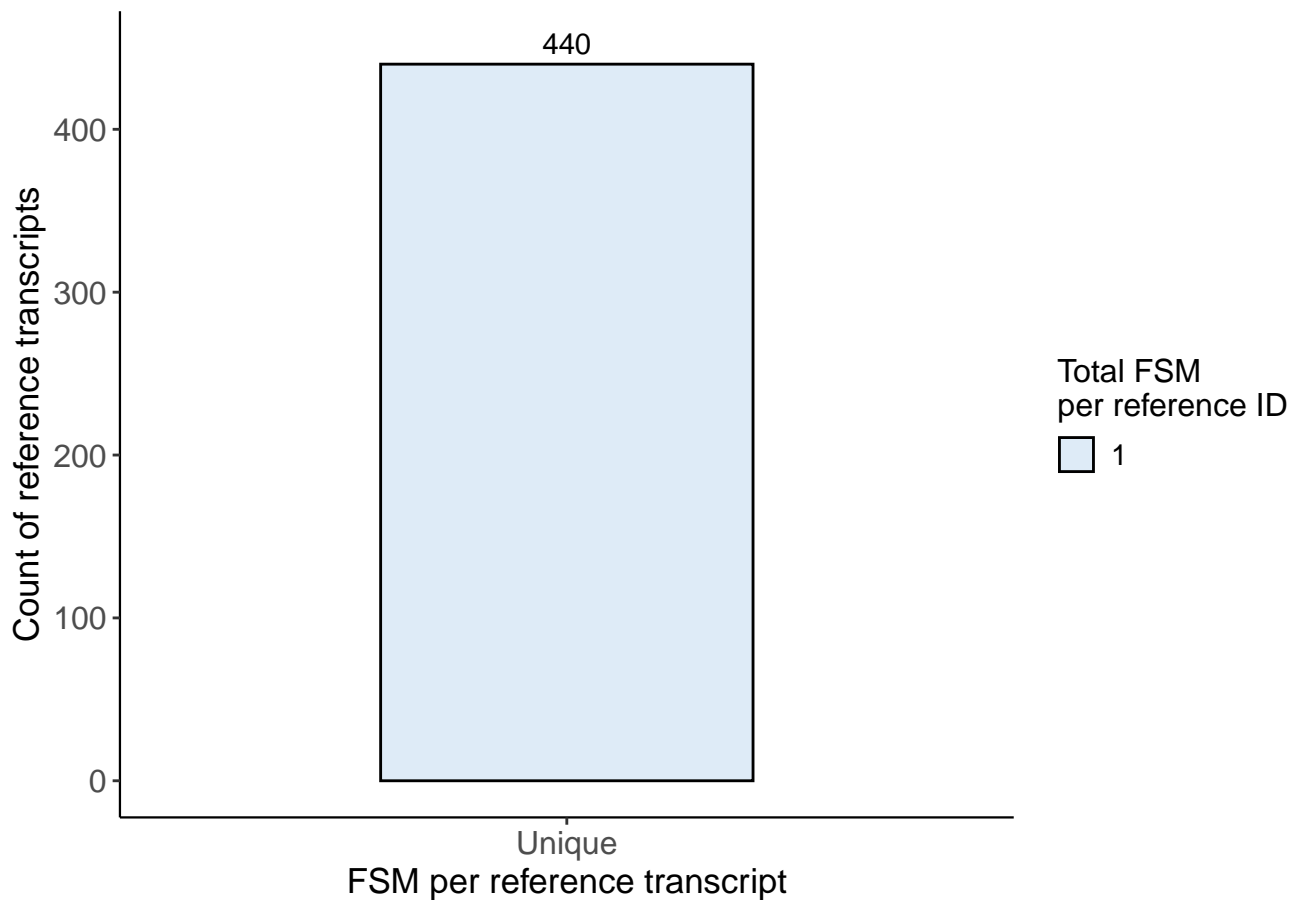


Reference Transcript Redundancy



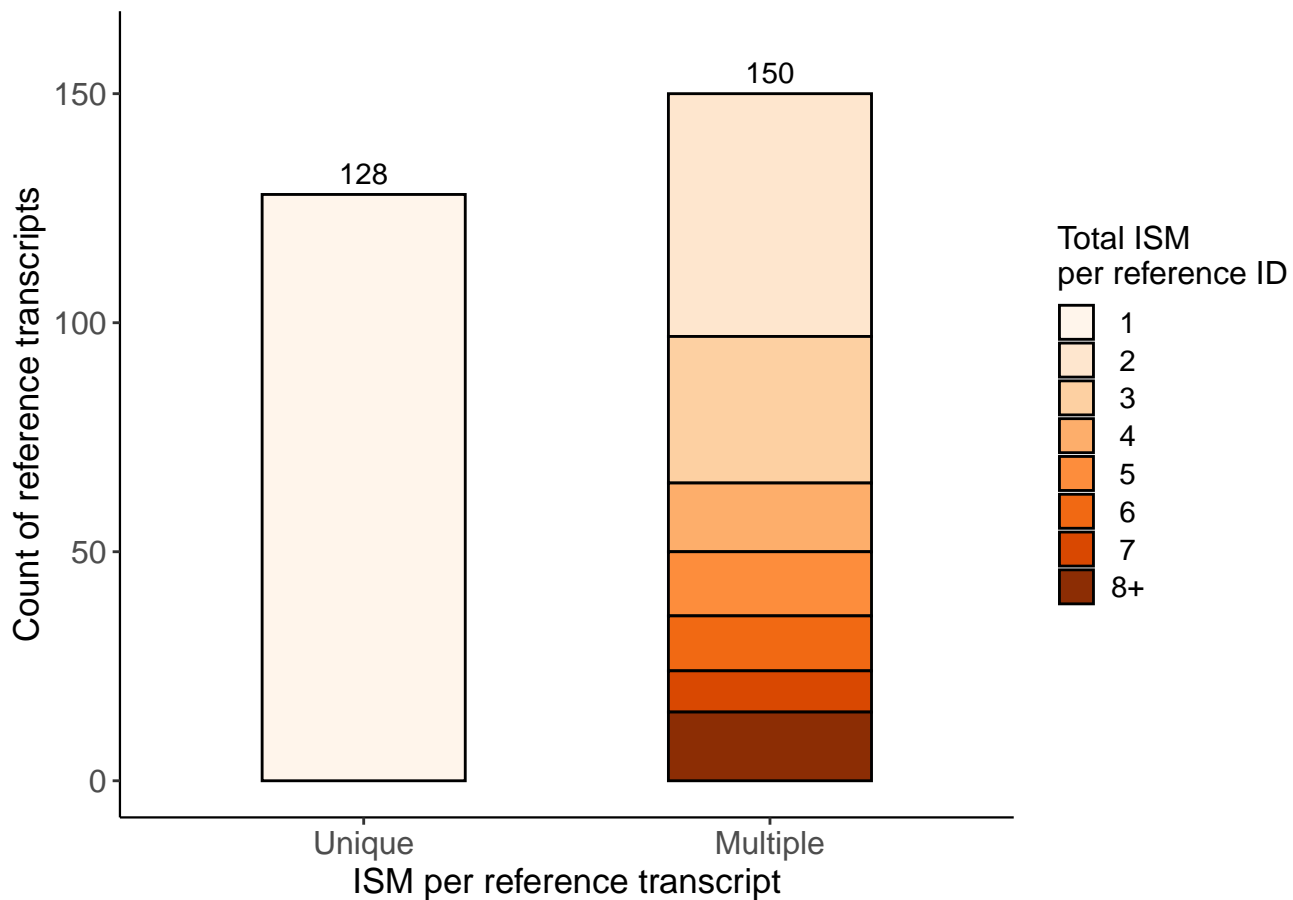
Reference Transcript Redundancy

Only FSM with a polyA motif found



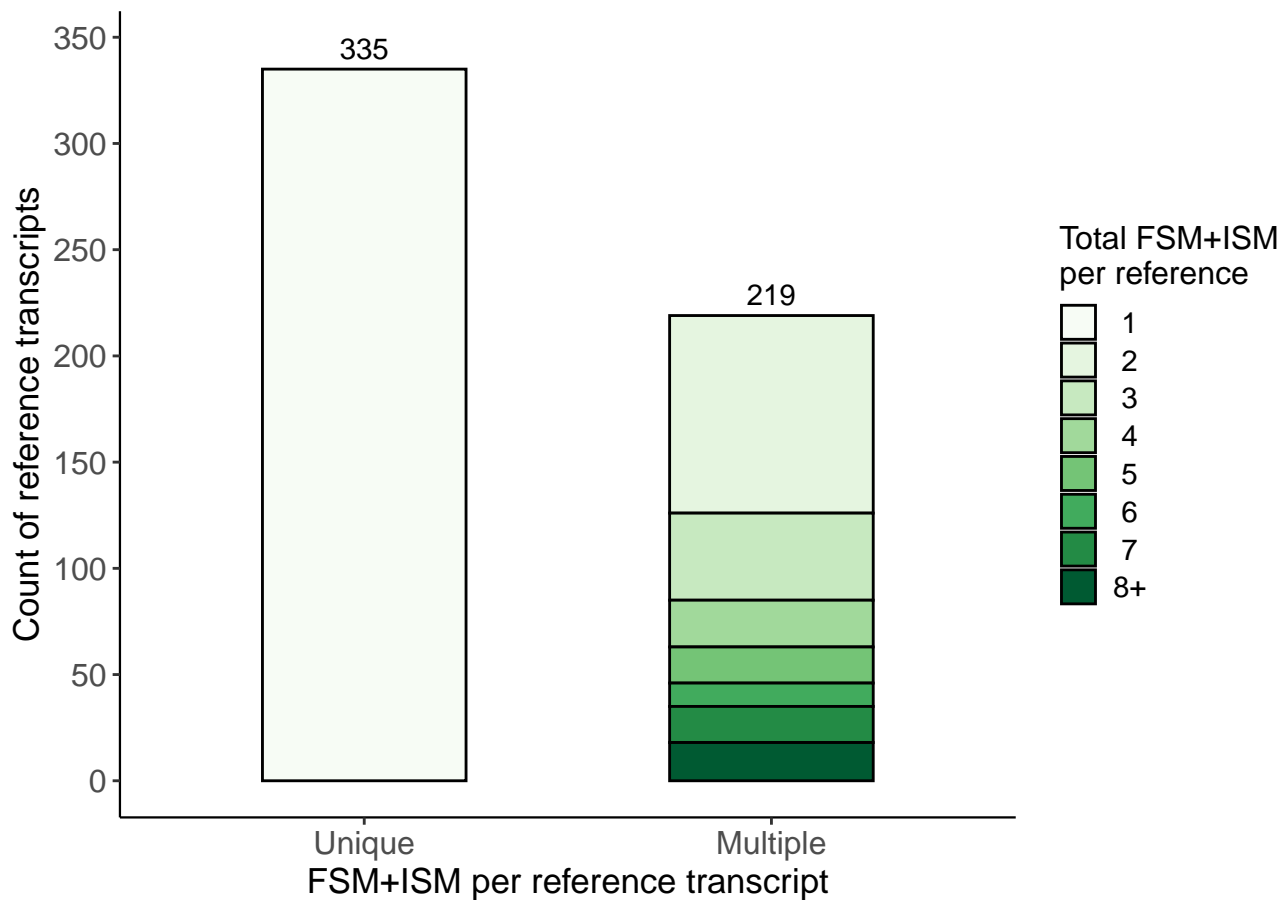
Reference Transcript Redundancy

Only ISM with a polyA motif found



Reference Transcript Redundancy

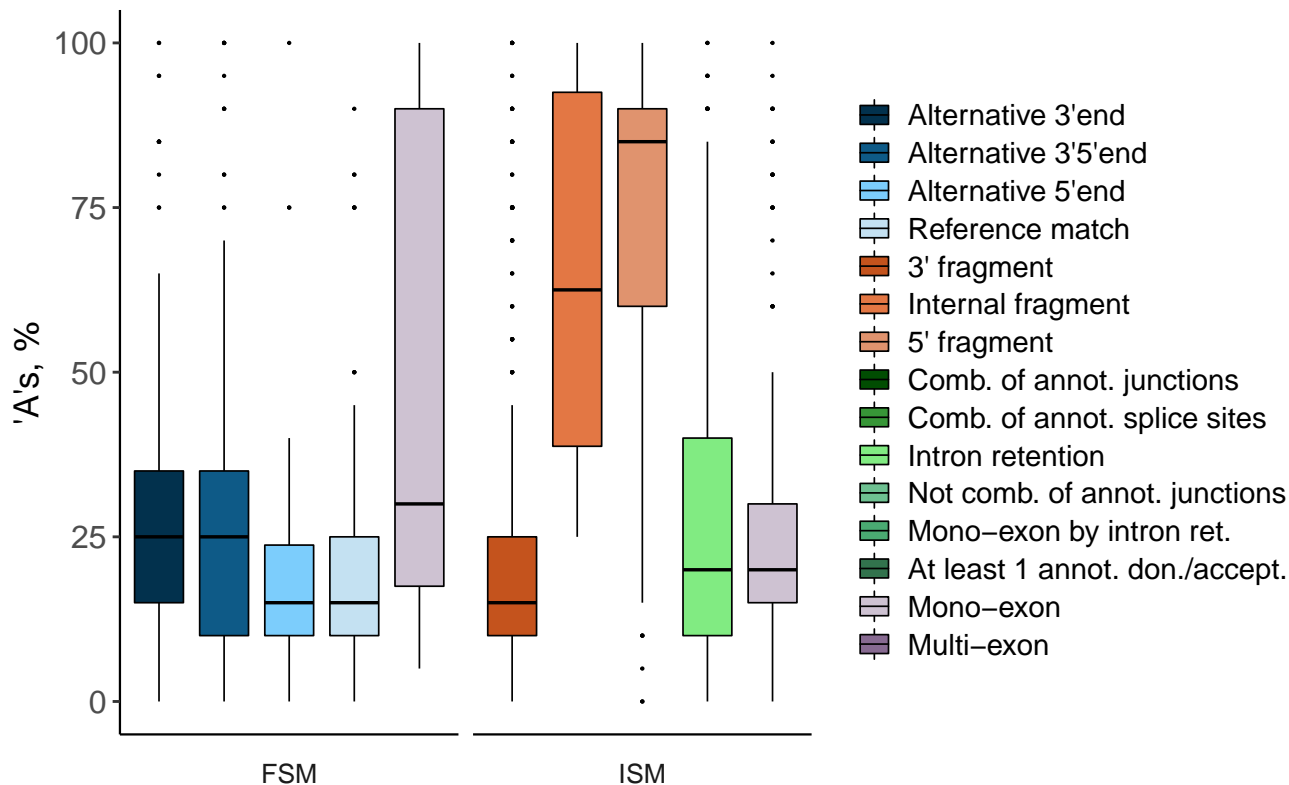
FSM+ISM with a polyA motif found



Intra-Priming Quality Check

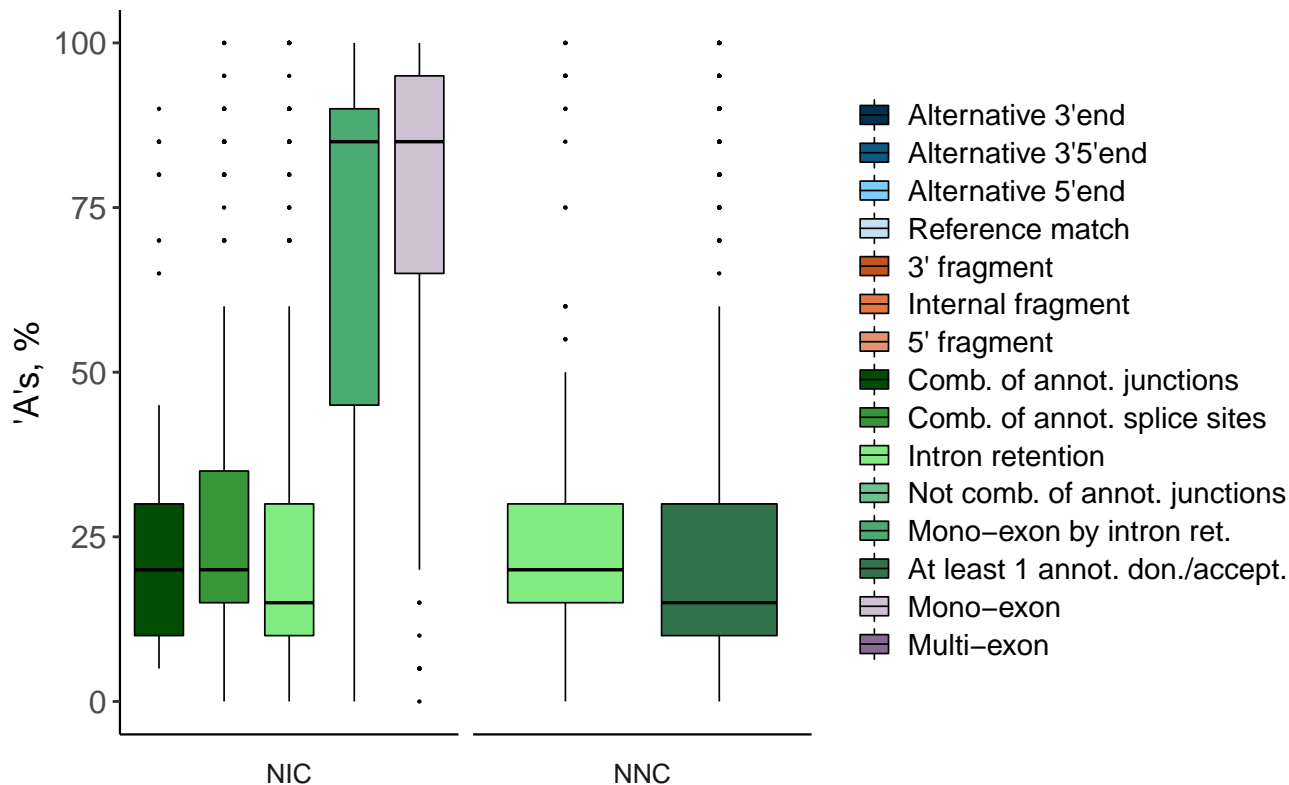
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



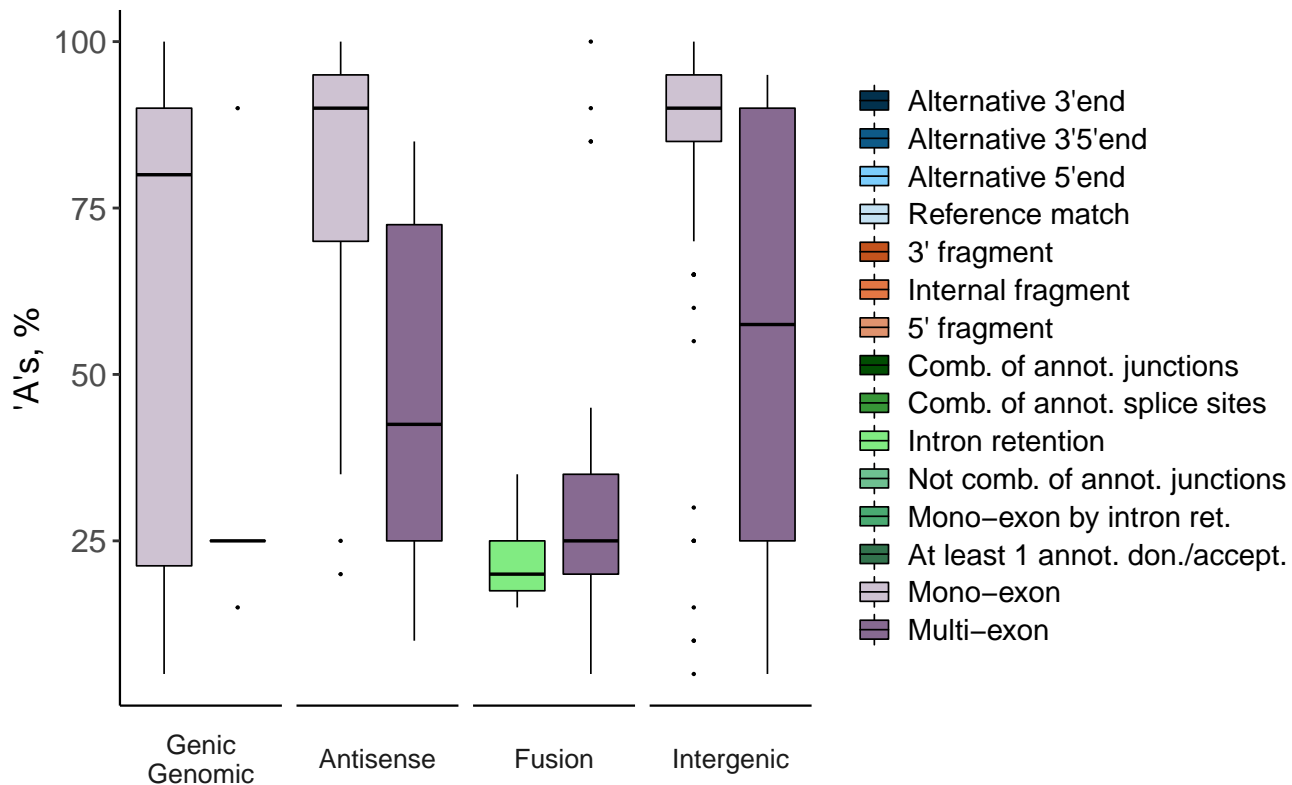
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



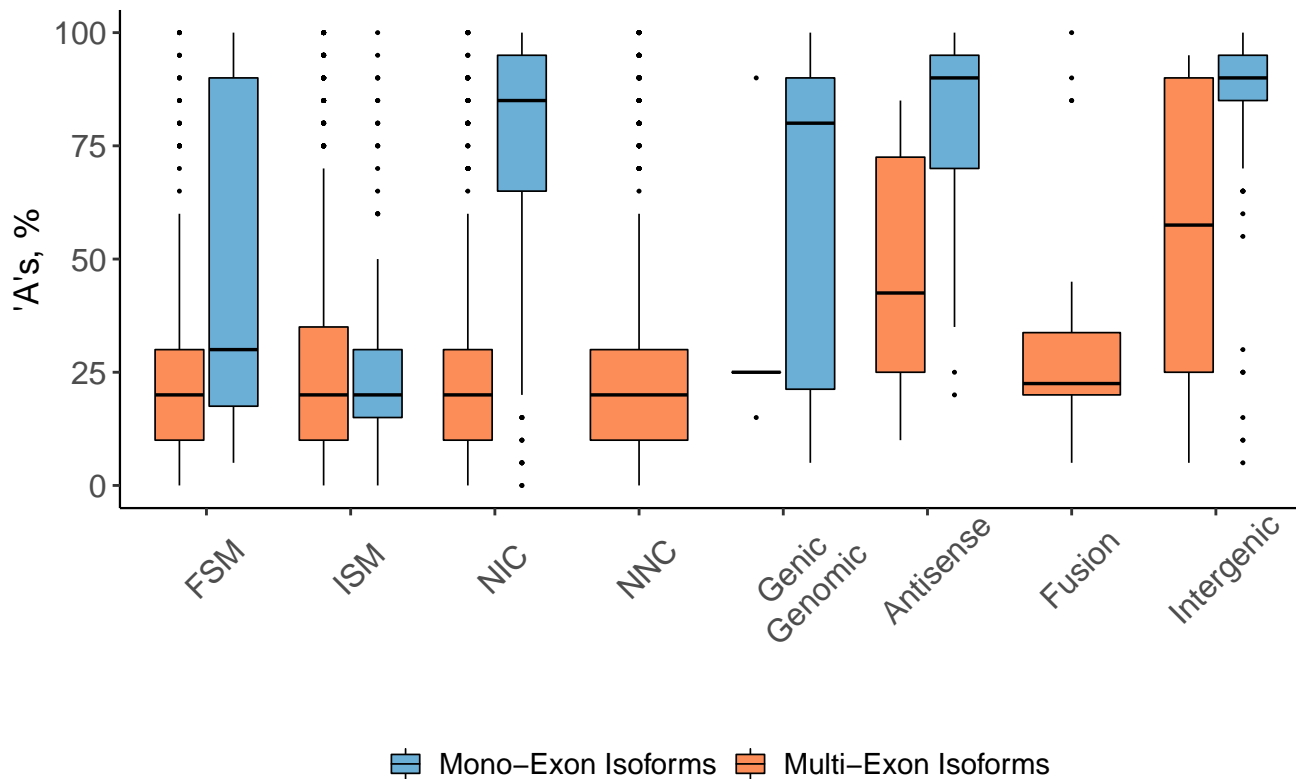
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



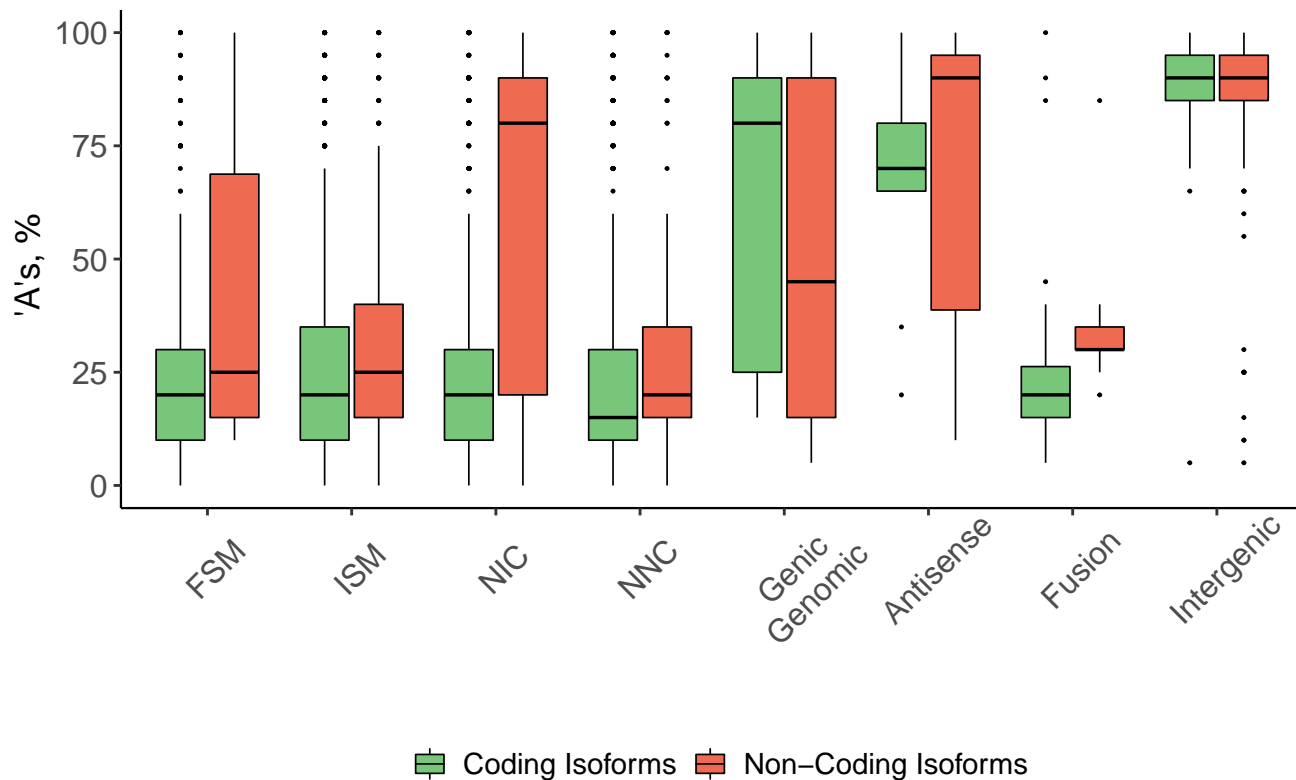
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



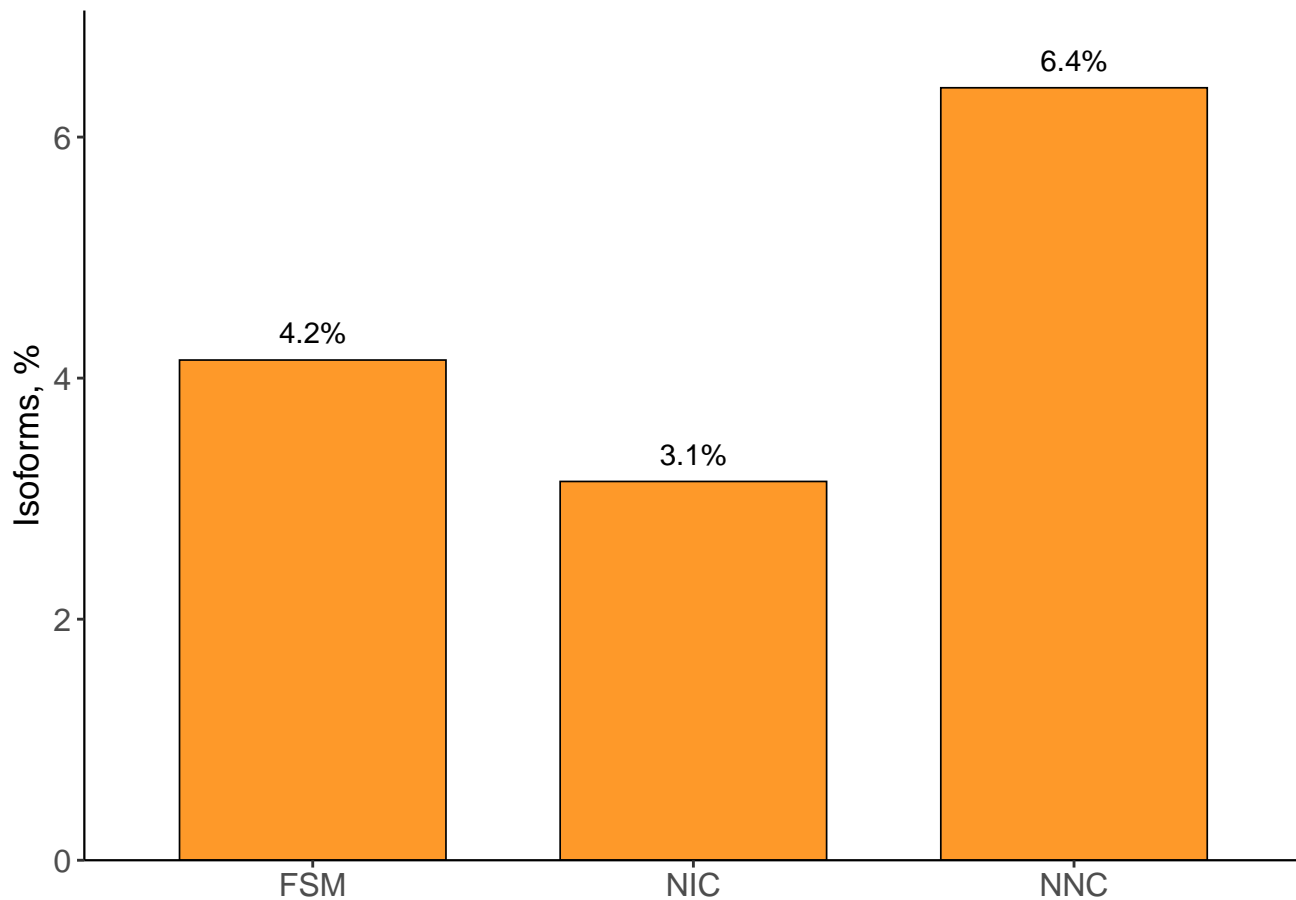
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp

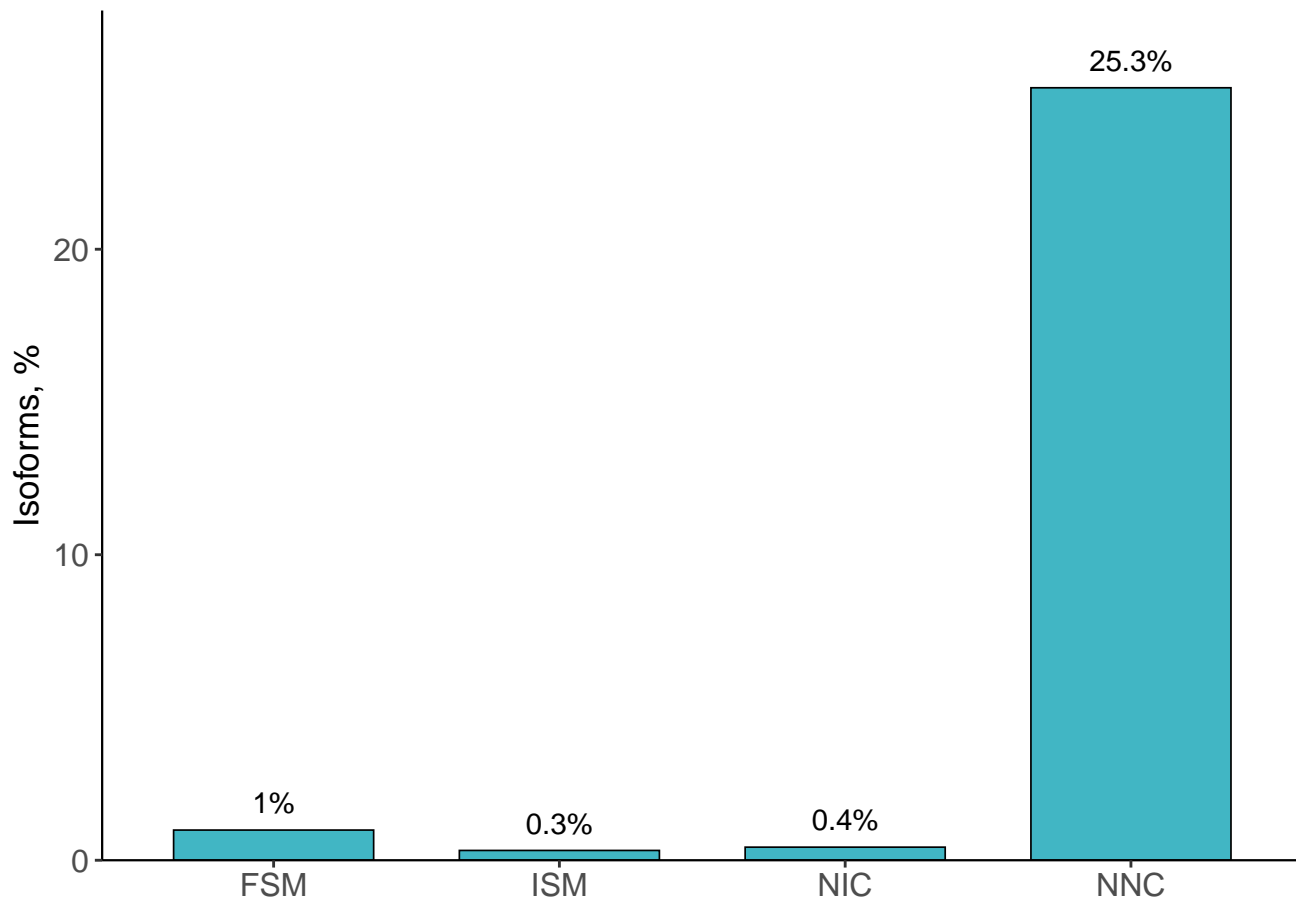


Features of Bad Quality

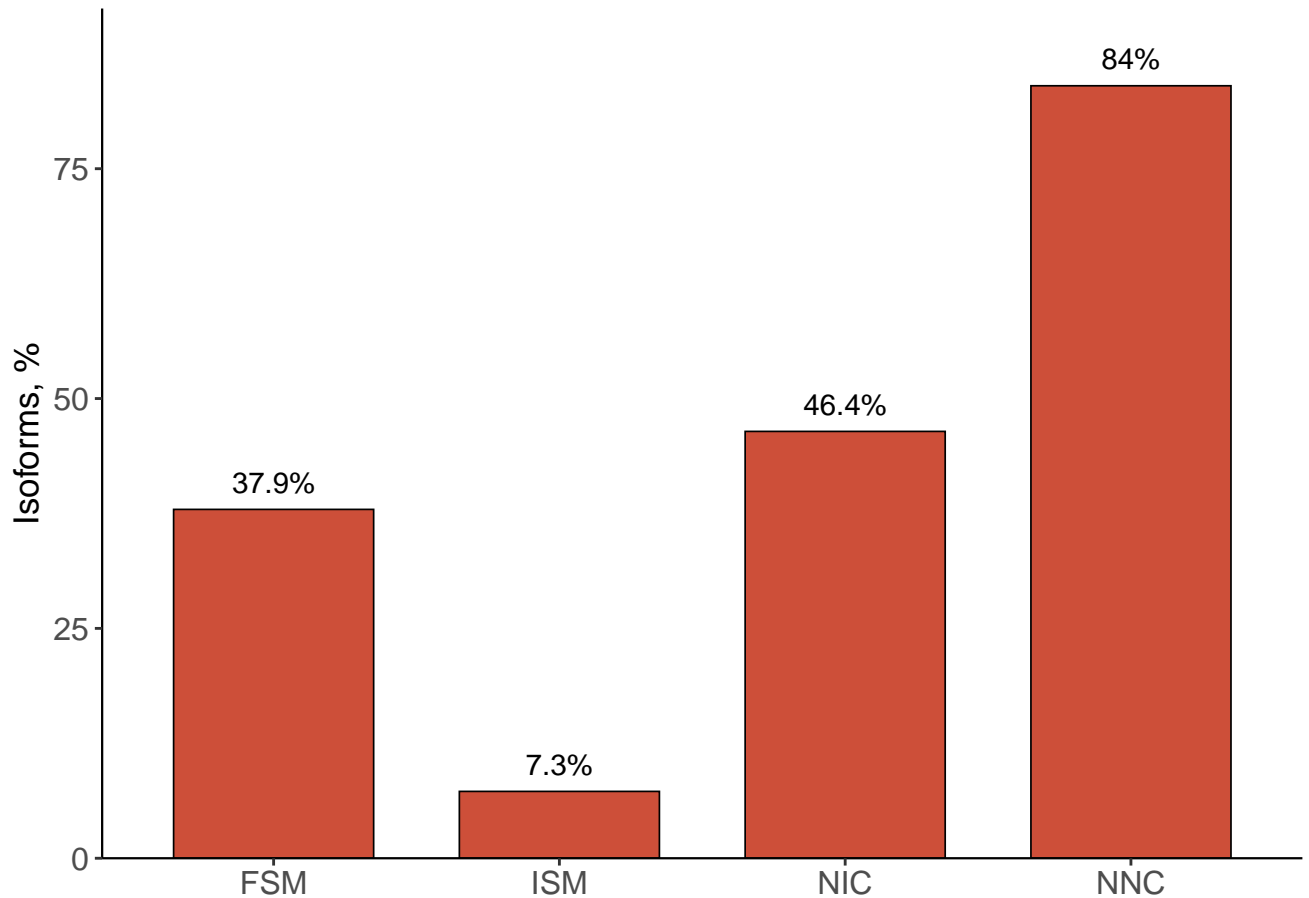
RT-switching



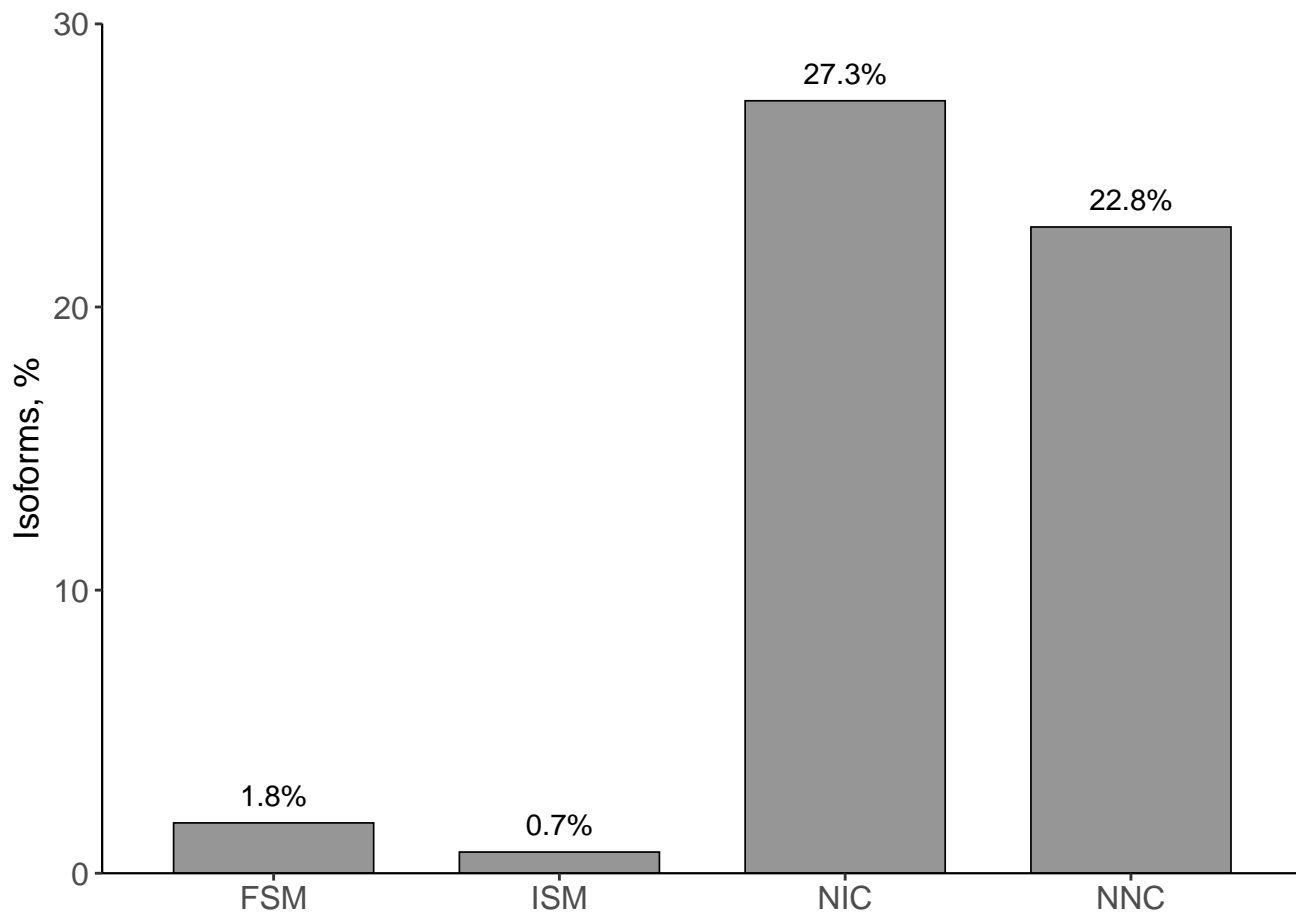
Non-Canonical Junctions



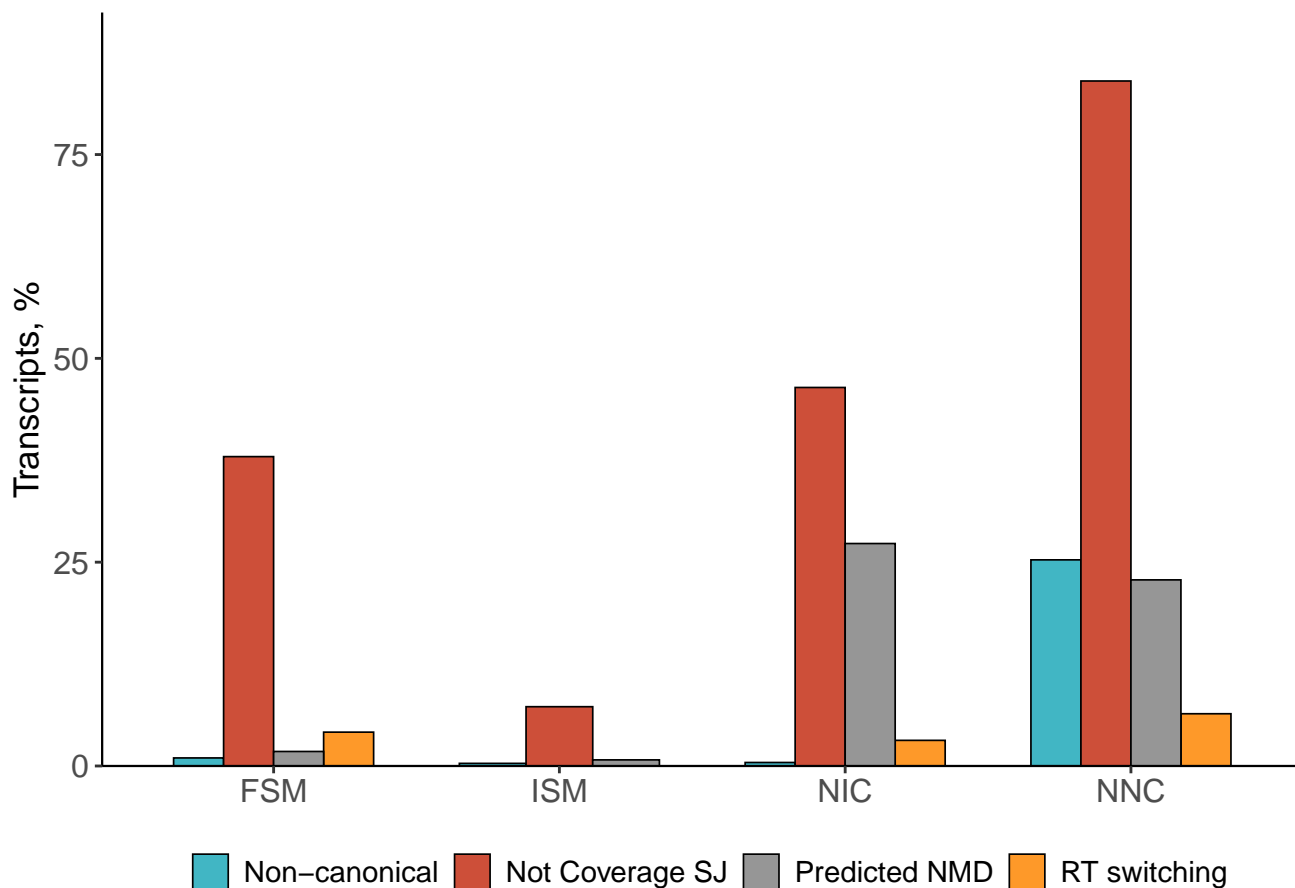
Splice Junctions Without Short Read Coverage



Nonsense-Mediated Decay by Structural Category

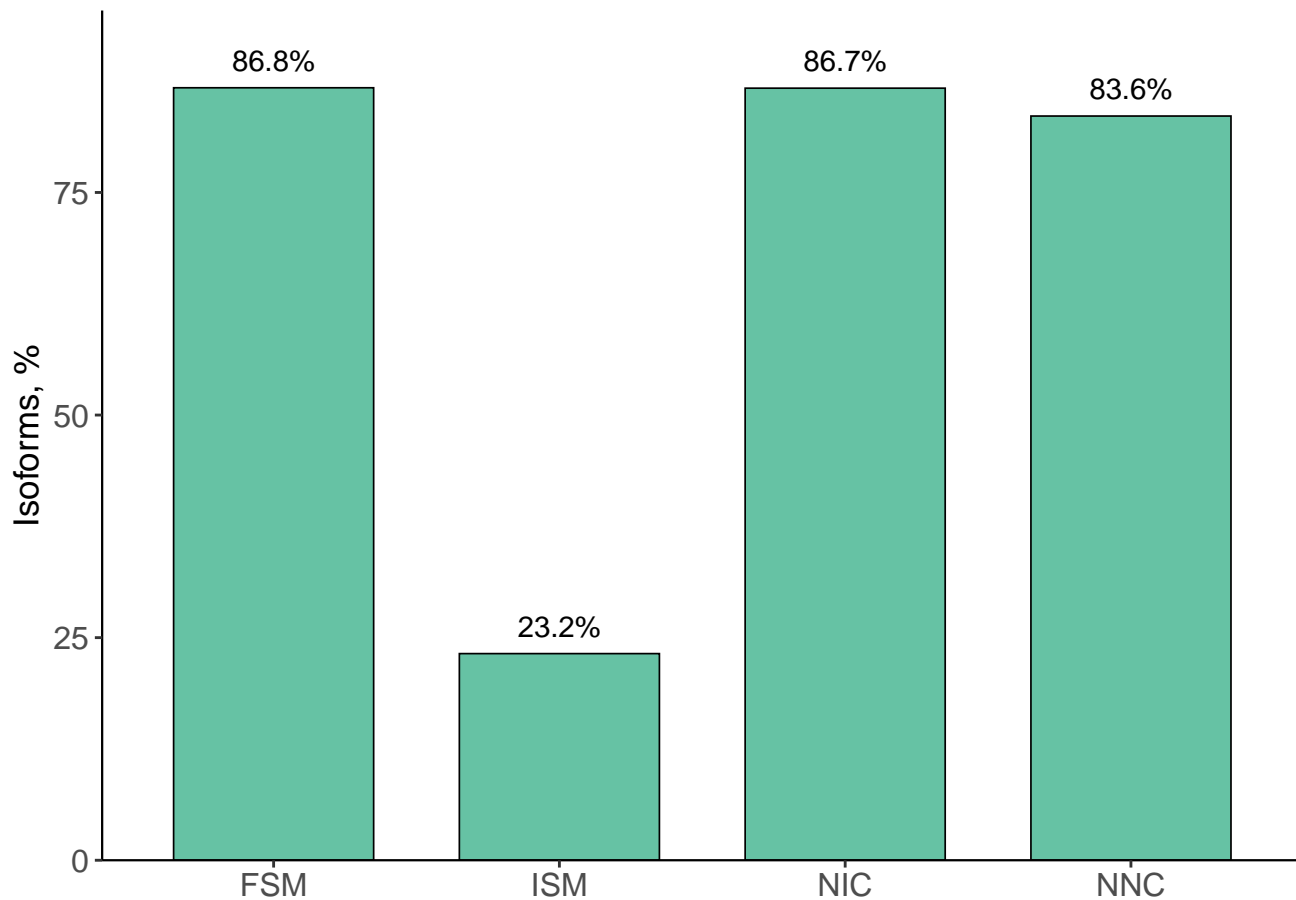


Quality Control Attributes Across Structural Categories

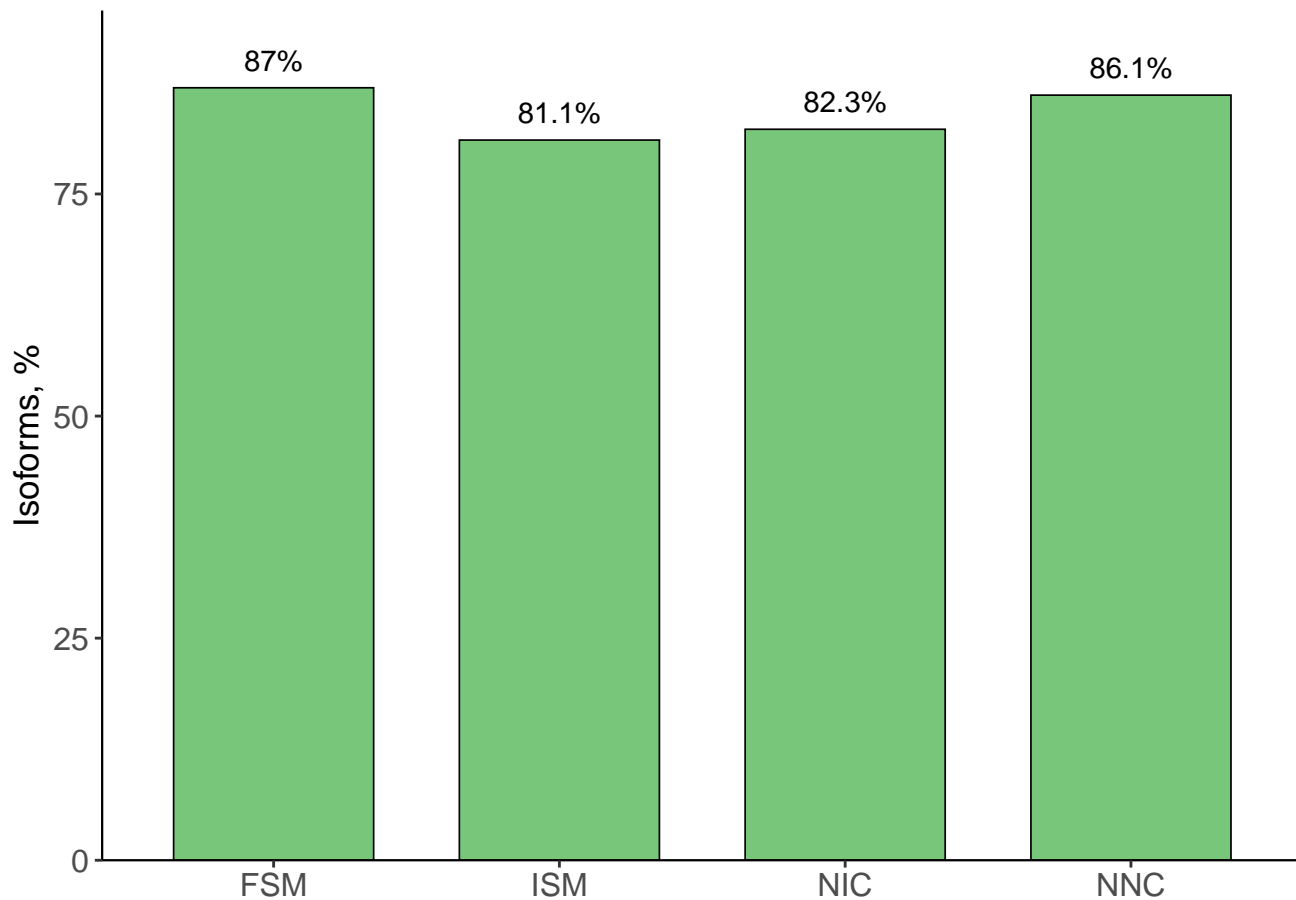


Features of Good Quality

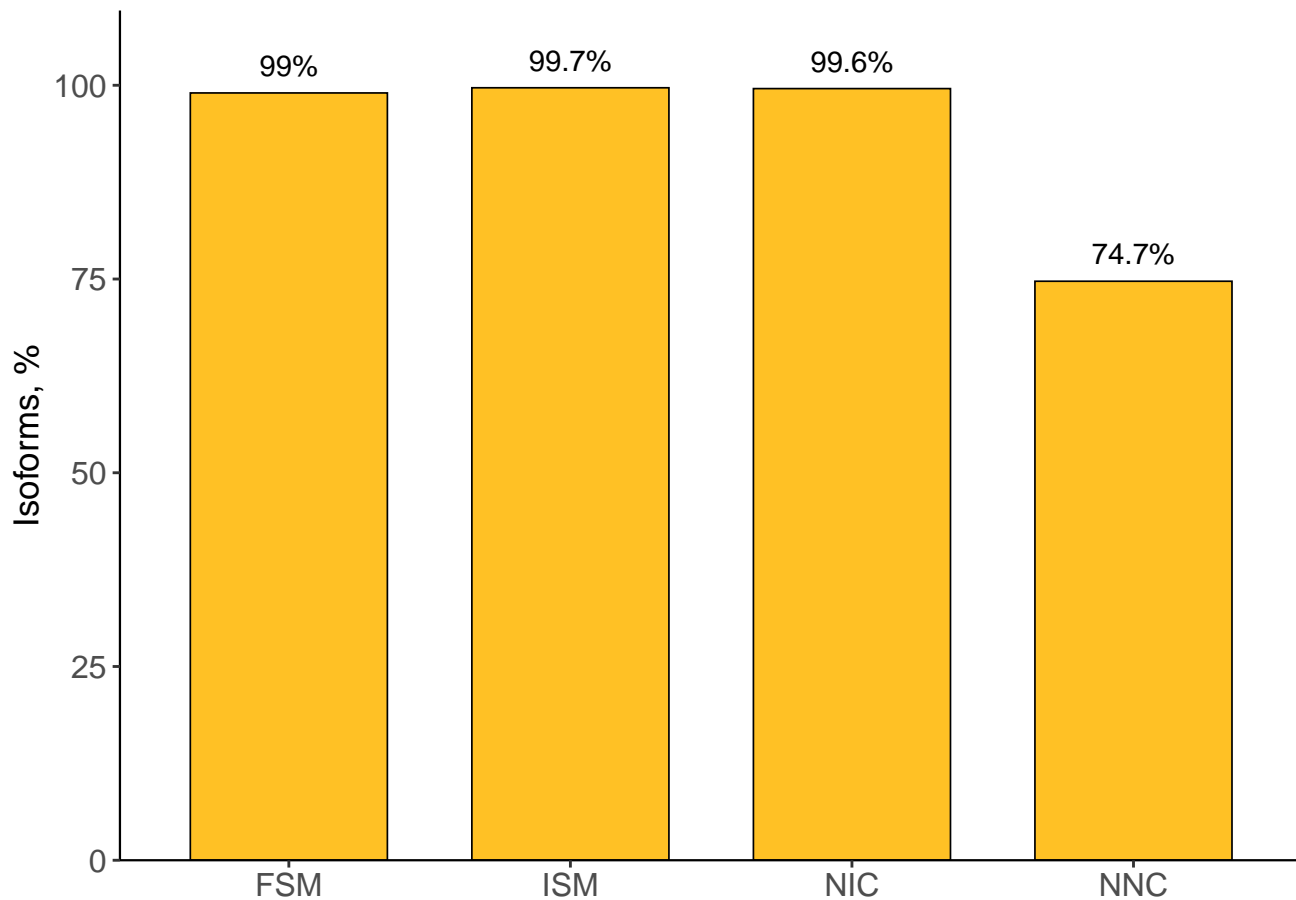
Annotation Support



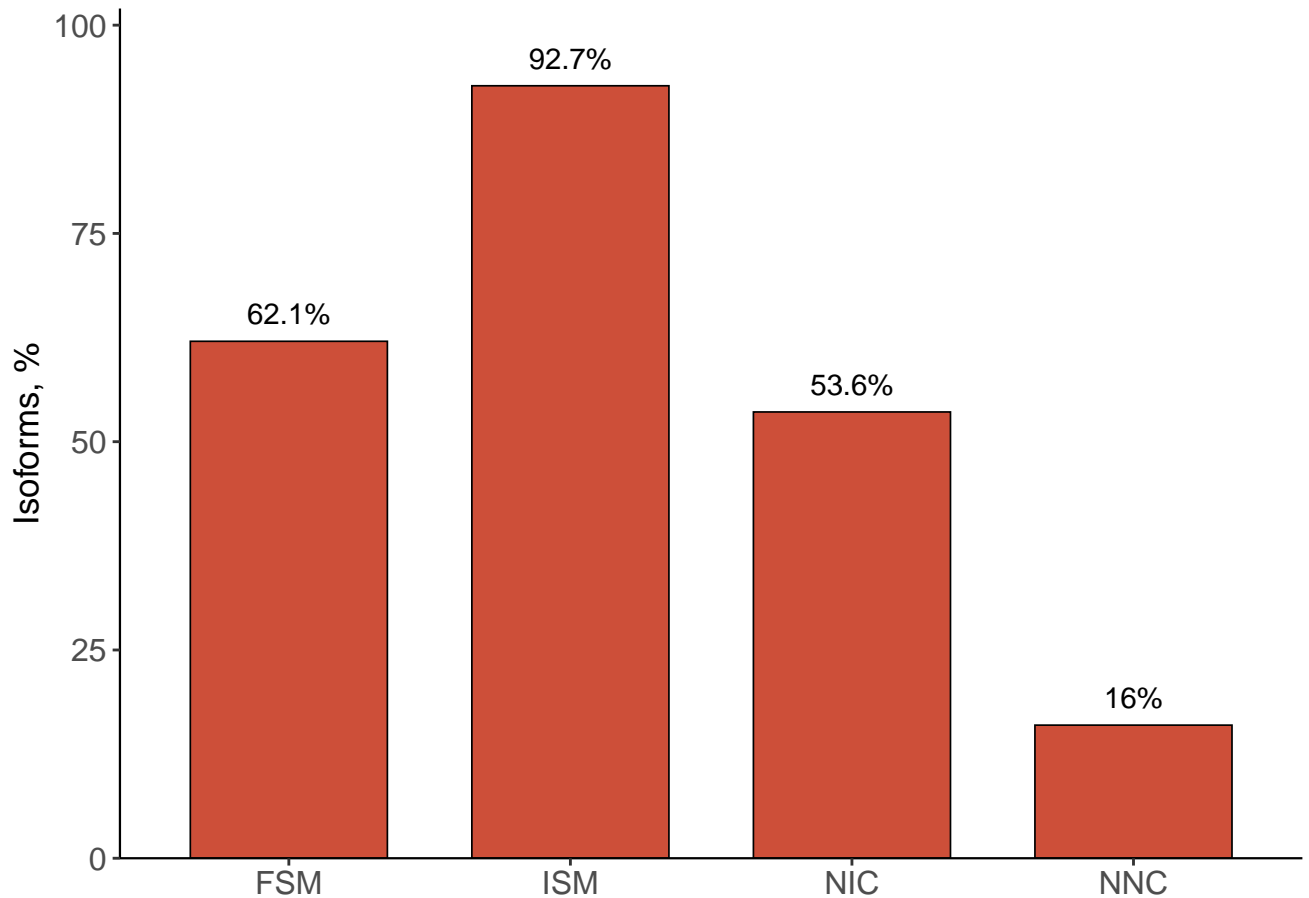
PolyA Support



All Canonical Junctions



Splice Junctions With Short Read Coverage



Good Quality Control Attributes Across Structural Categories

