

SQANTI3 report

Unique Genes: 656
Unique Isoforms: 3925

Transcript Classification

Category	Isoforms, count
FSM	539
ISM	1138
NIC	744
NNC	1139
Genic Genomic	113
Antisense	26
Fusion	38
Intergenic	41
Genic Intron	147

Gene Classification

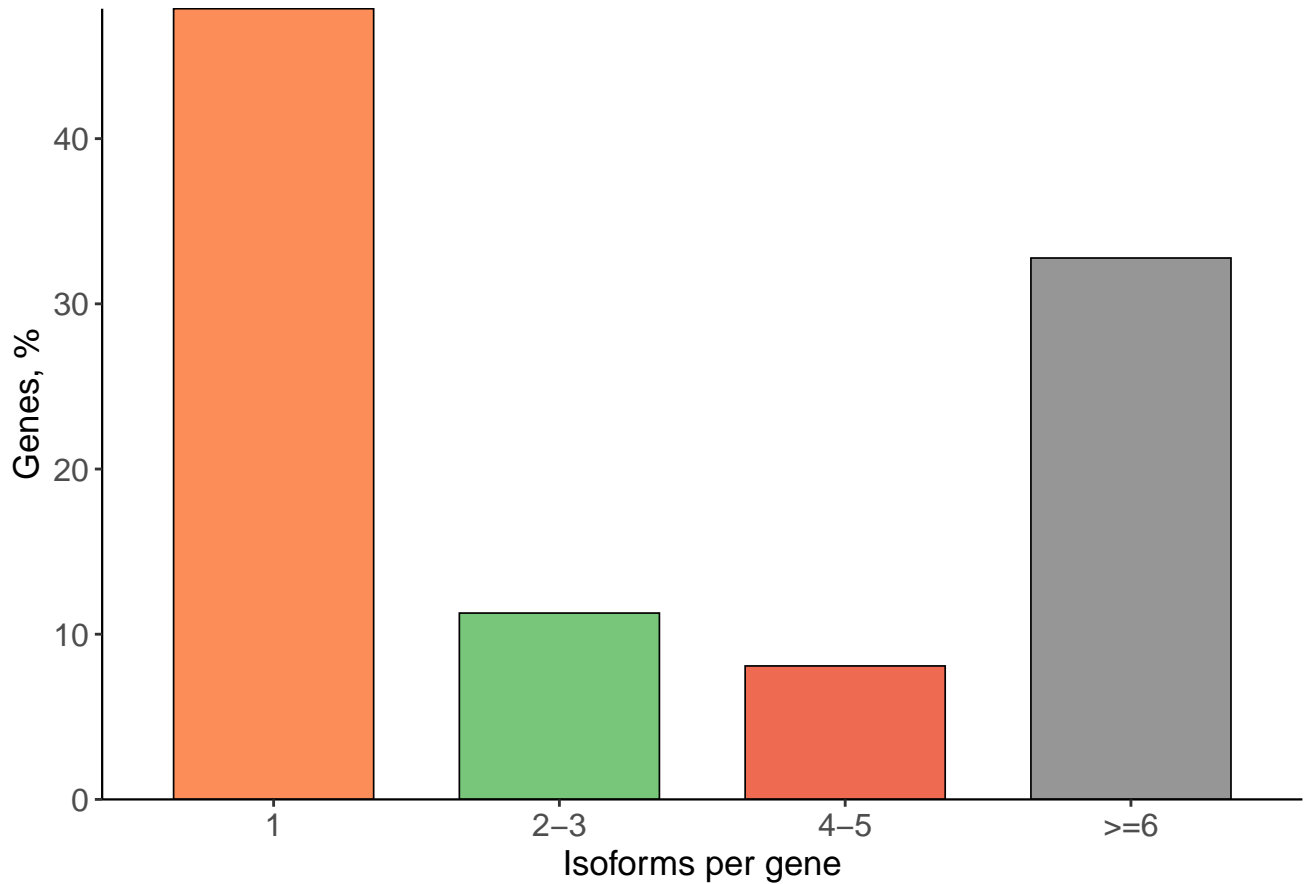
Category	Genes, count
Annotated Genes	443
Novel Genes	213

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	0	0.00
Known Non-canonical	0	0.00
Novel canonical	4569	94.44
Novel Non-canonical	269	5.56

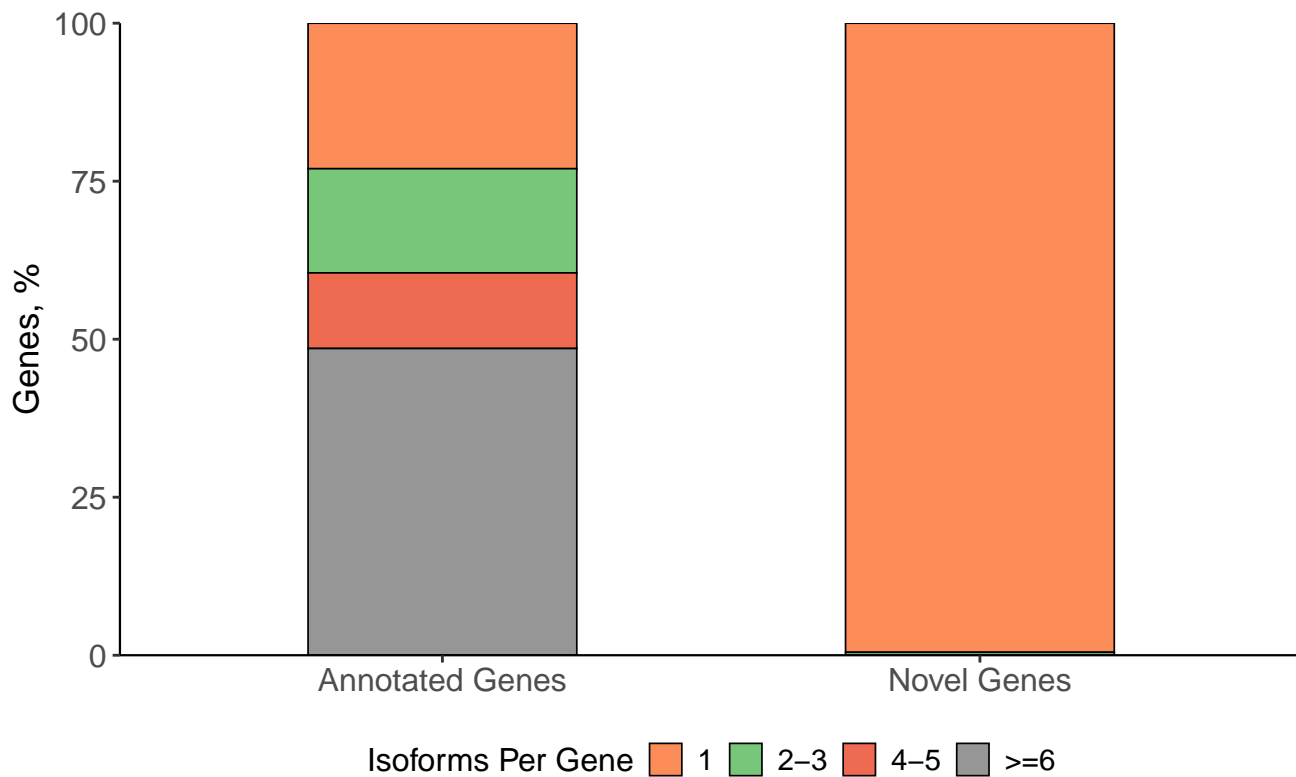
Gene Characterization

Number of Isoforms per Gene

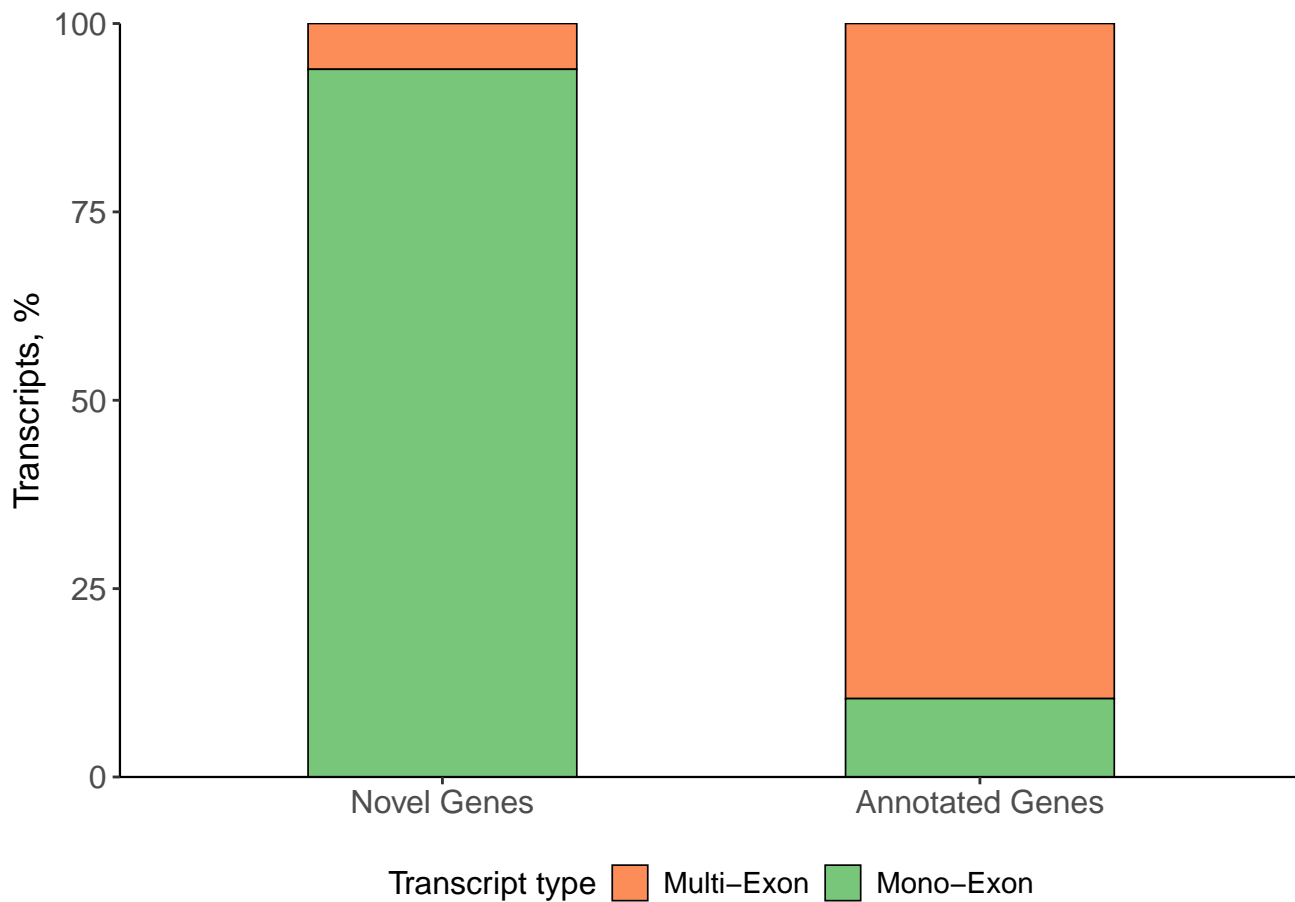


Number of Isoforms per Gene

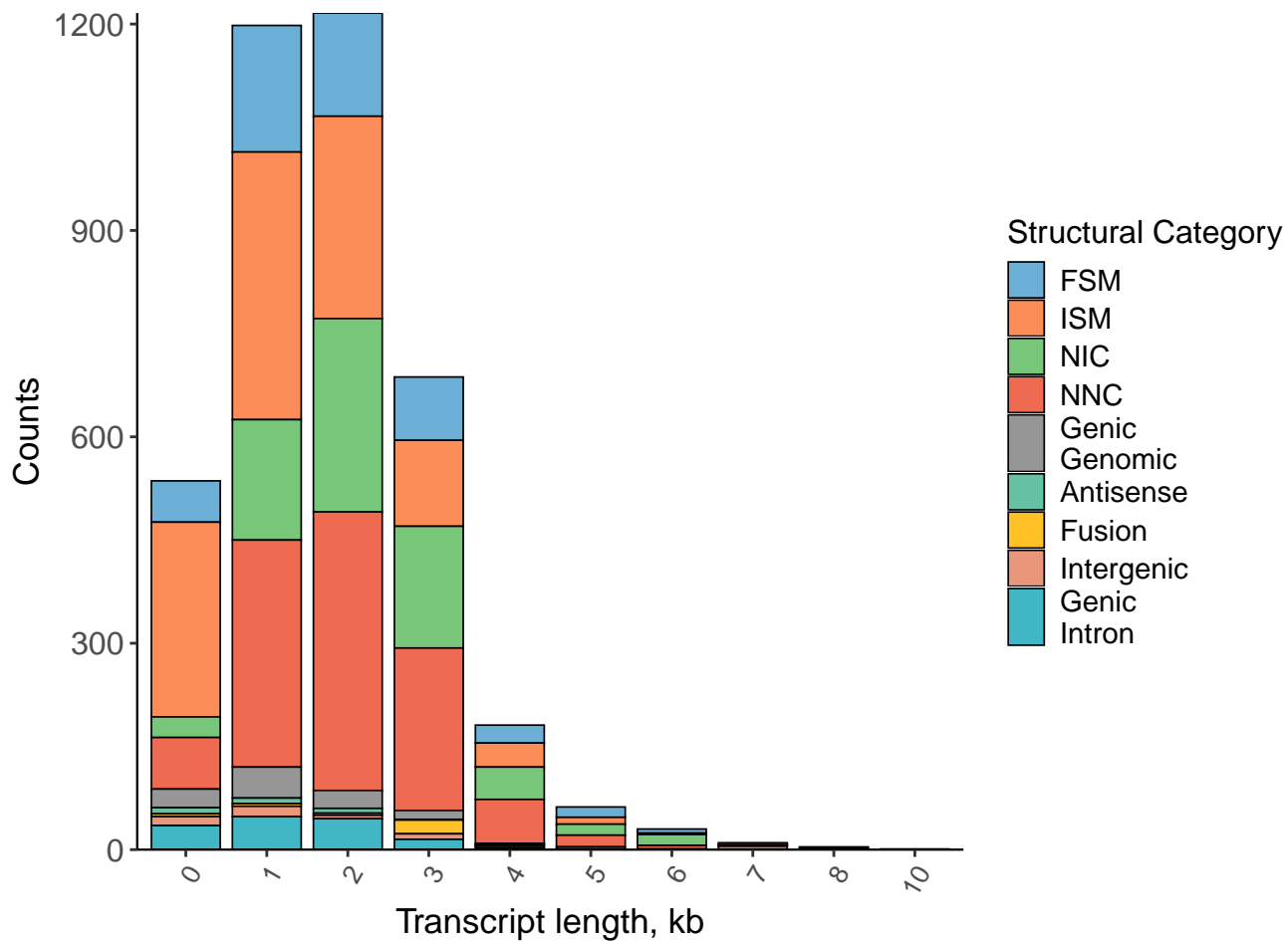
Known vs Novel Genes



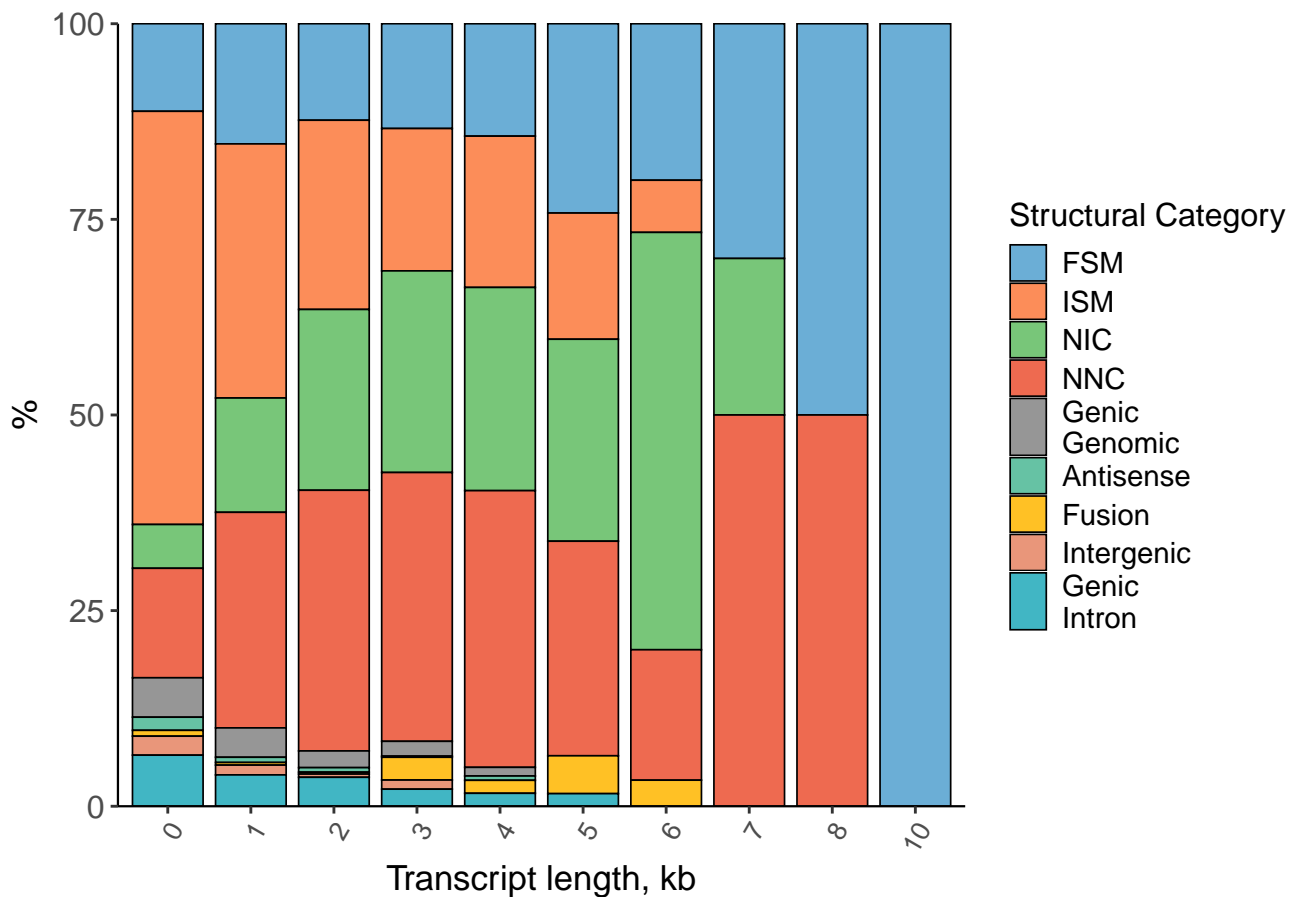
Distribution of Mono- vs Multi-Exon Transcripts



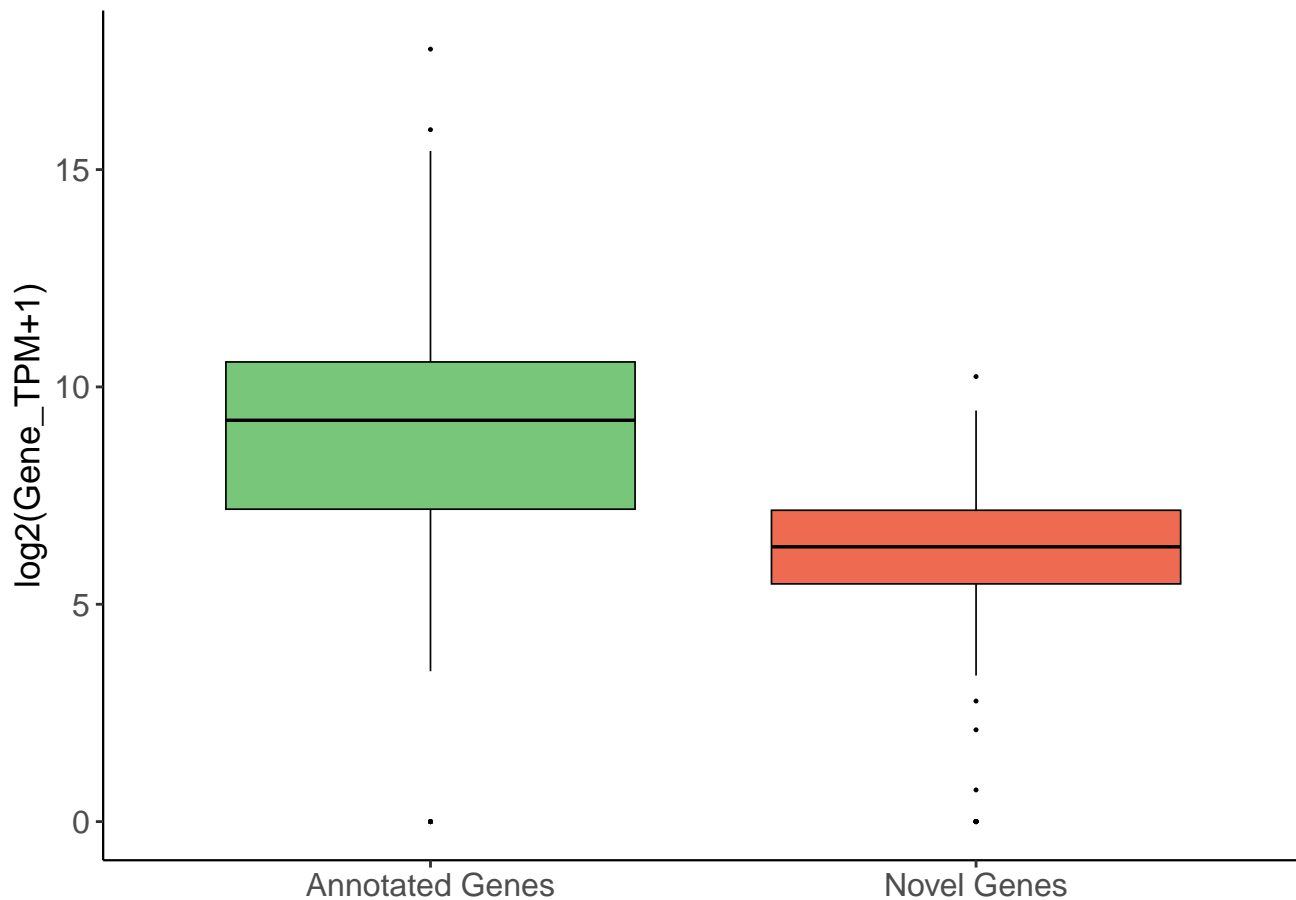
Structural Categories by Transcript Length



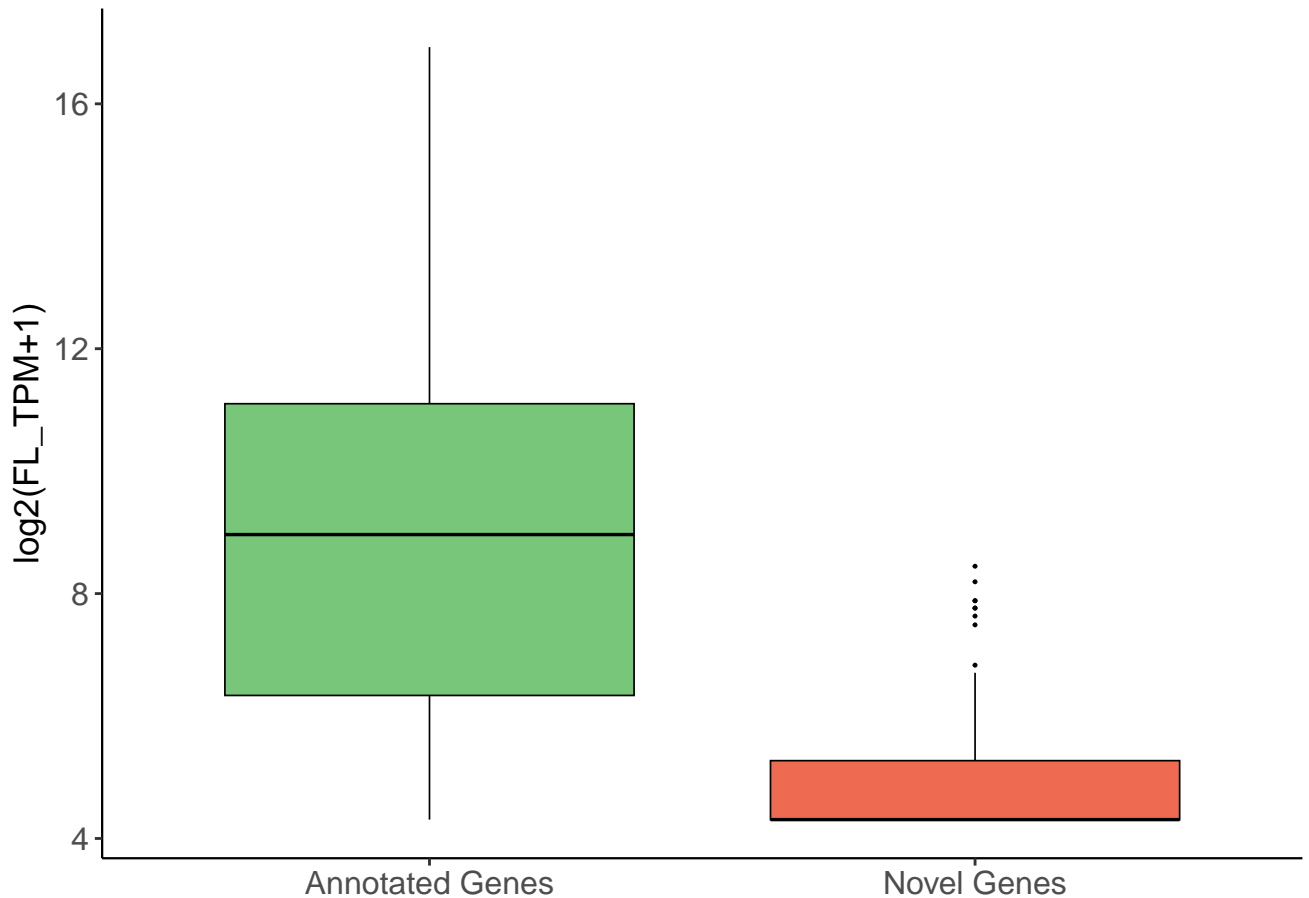
Structural Categories by Transcript Length



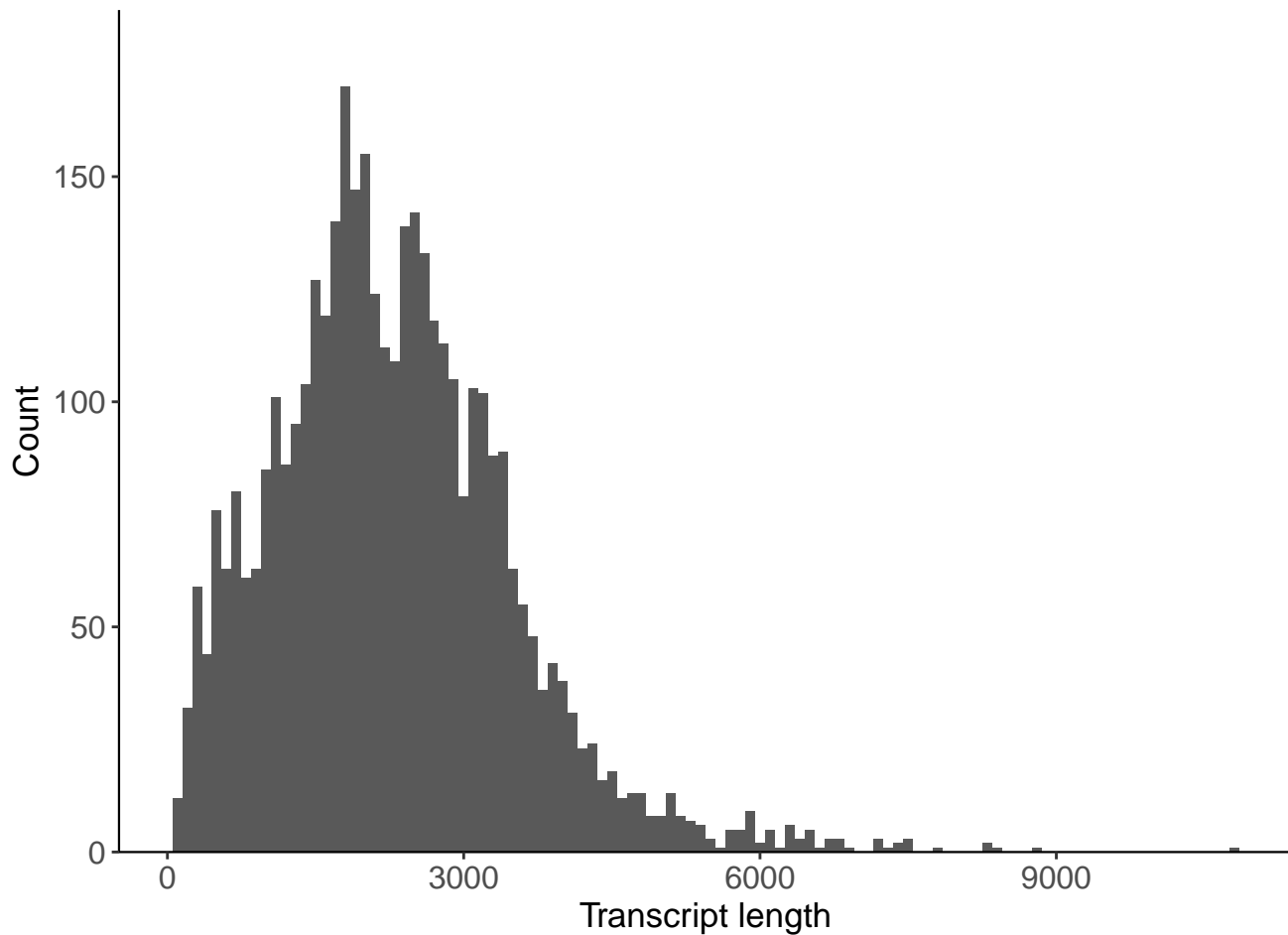
Annotated vs Novel Gene Expression



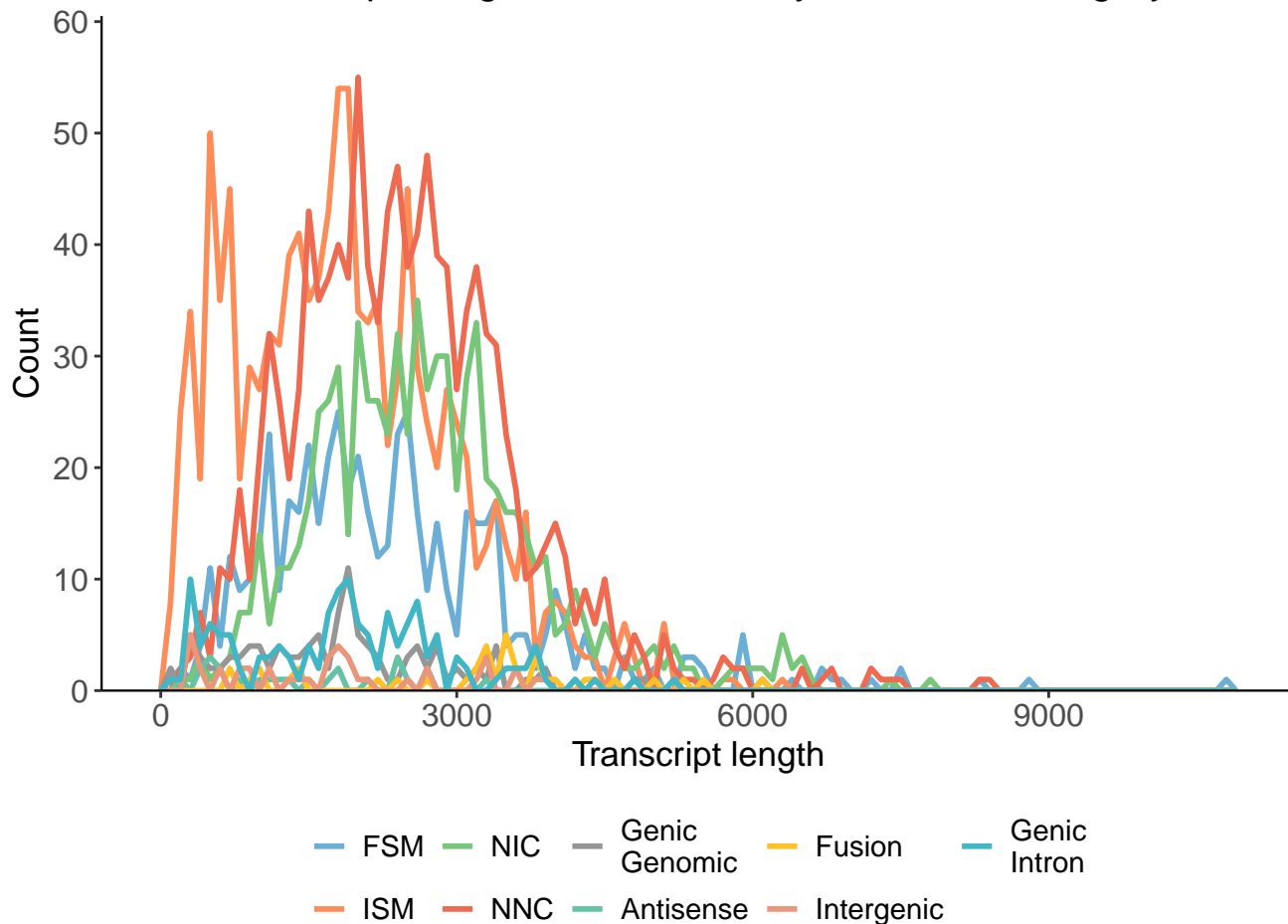
Number of FL reads per Gene by Type of Gene Annotation



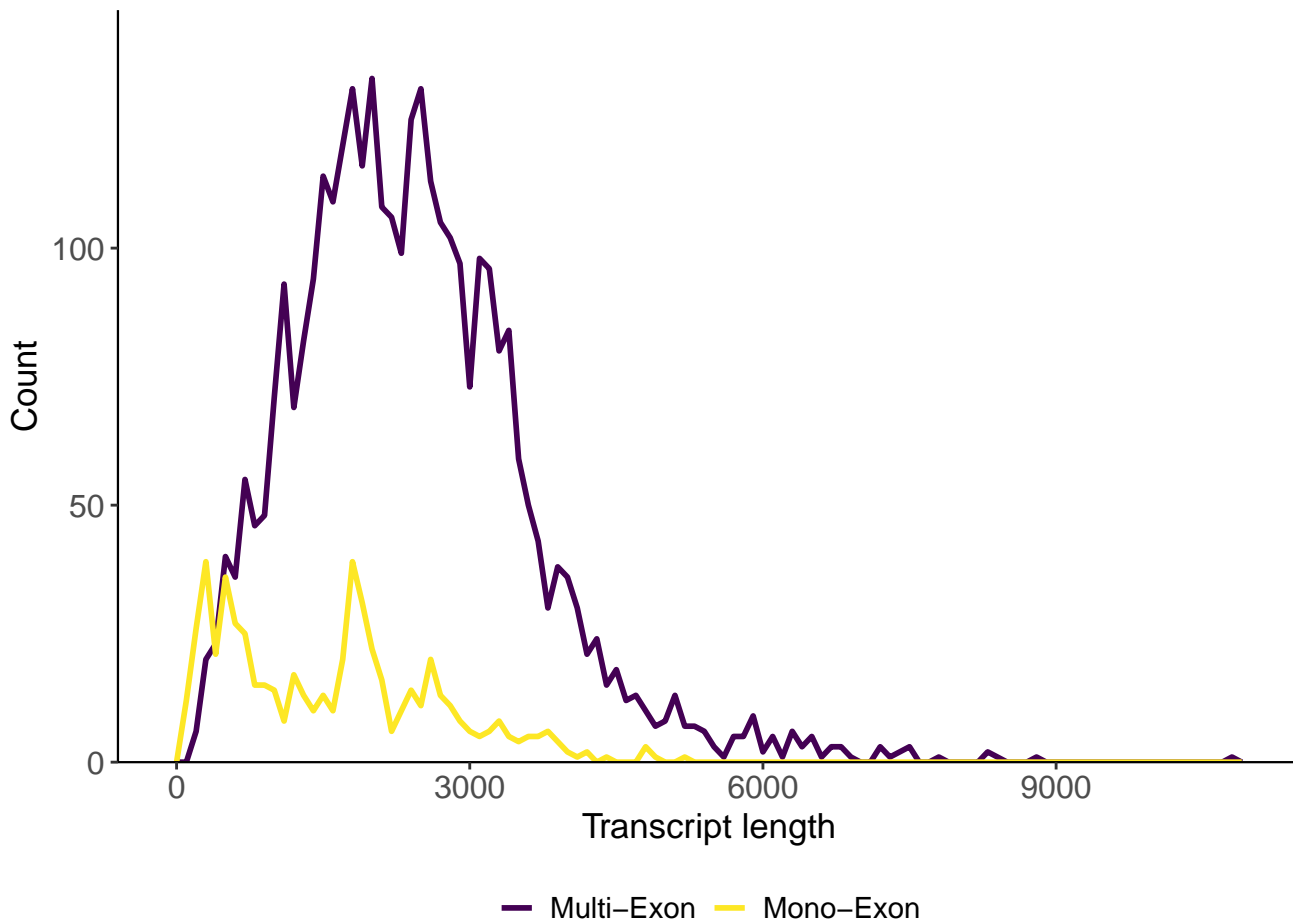
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

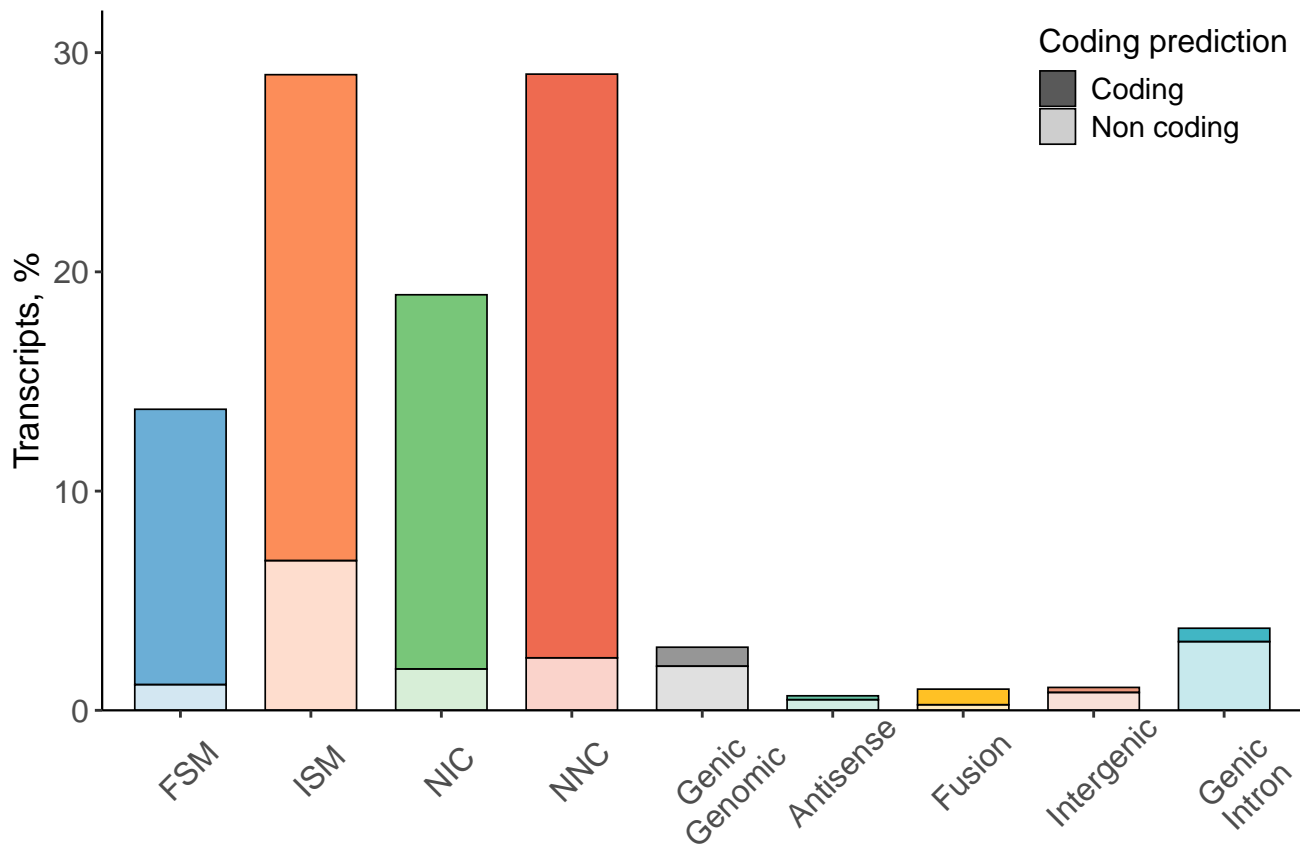


Mono- vs Multi- Exon Transcript Lengths Distribution

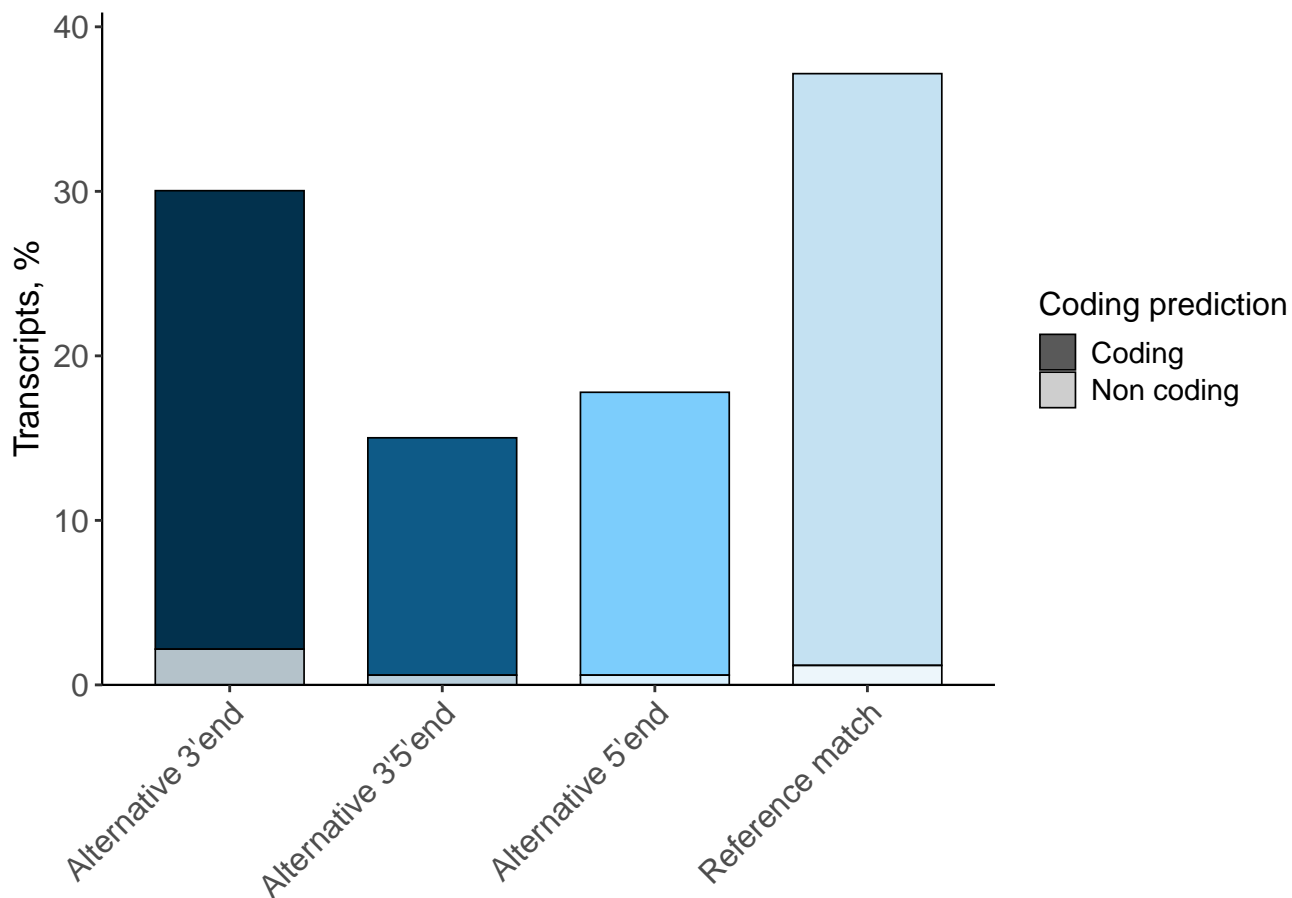


Structural Isoform Characterization

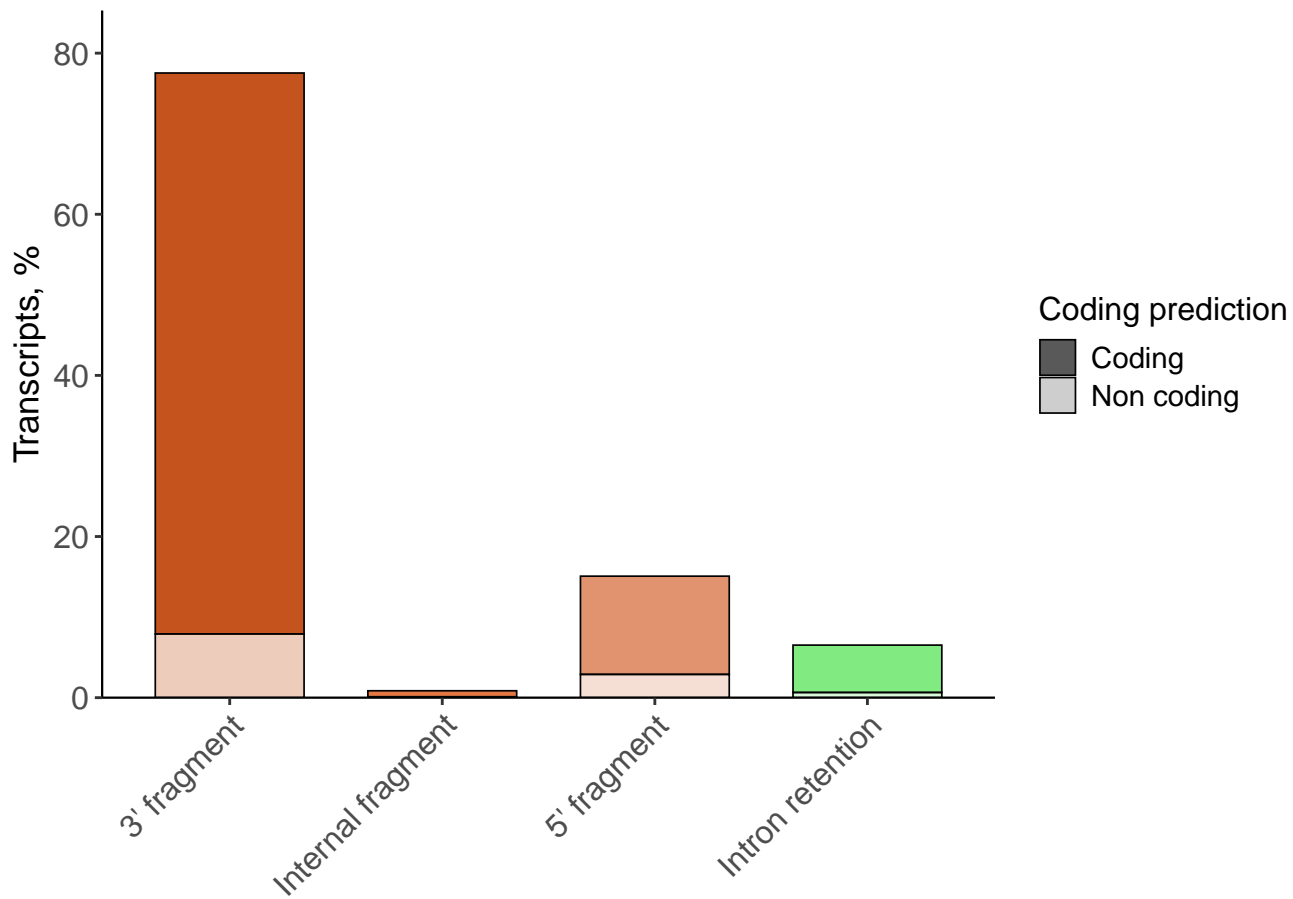
Isoform Distribution Across Structural Categories



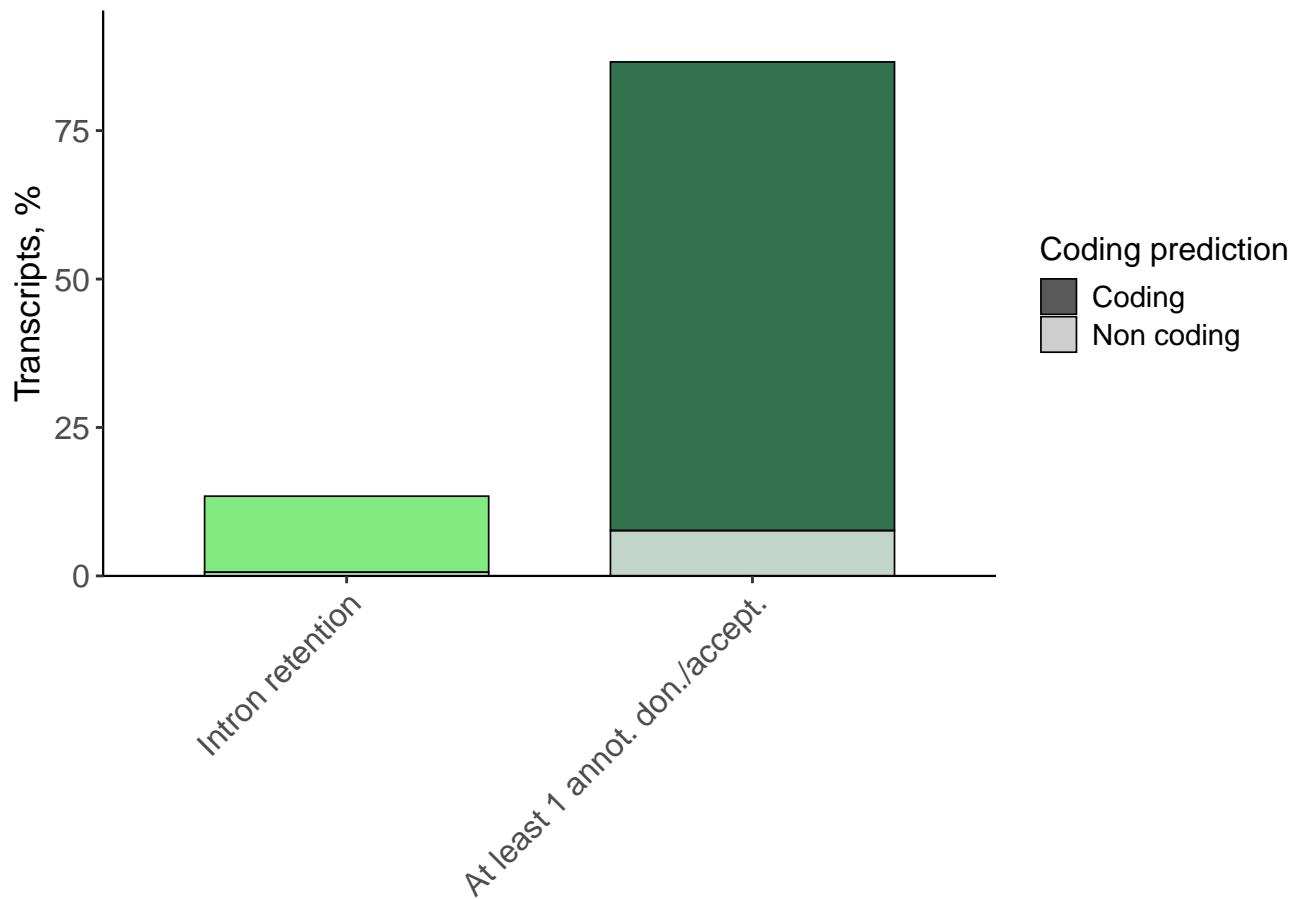
Isoform Distribution Across FSM



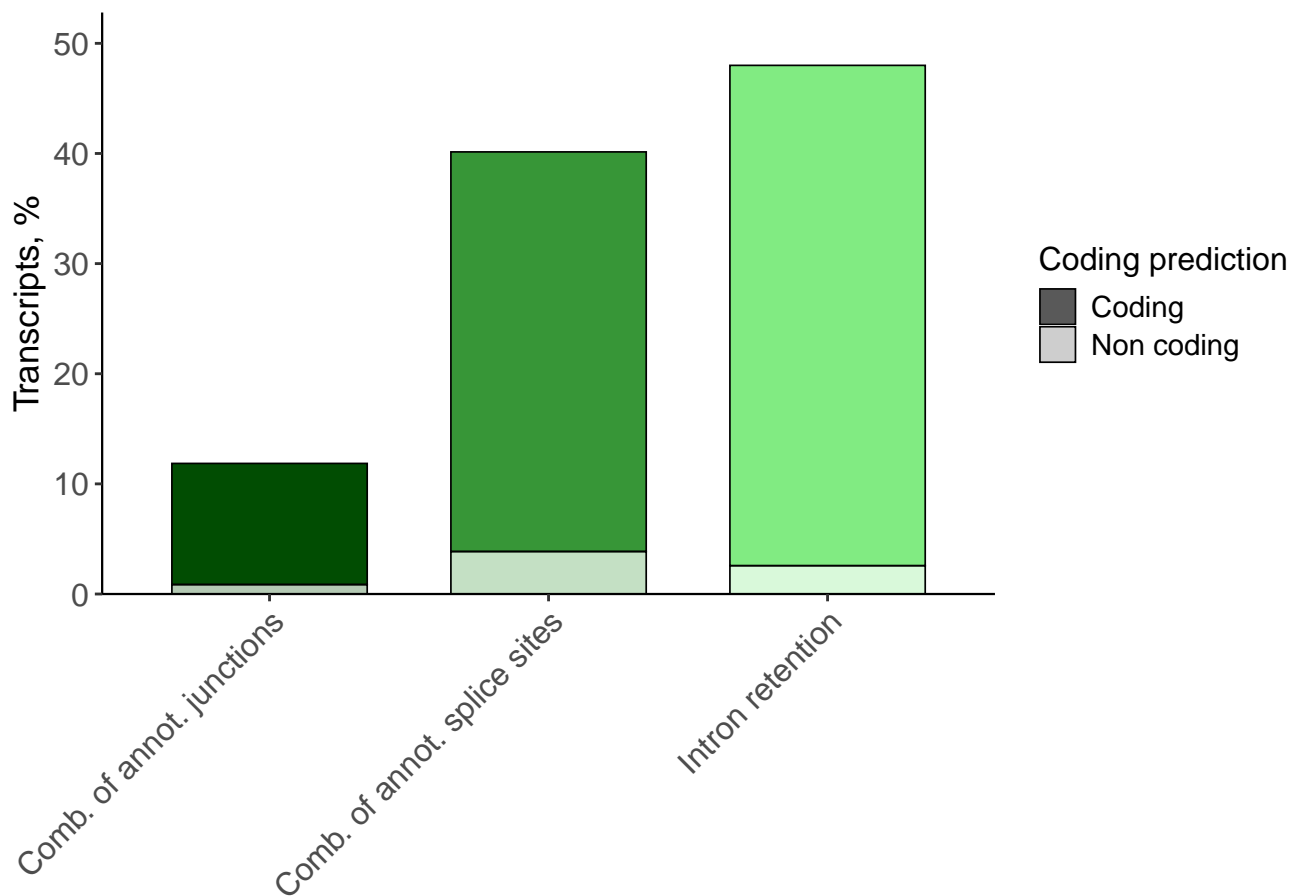
Isoform Distribution Across ISM



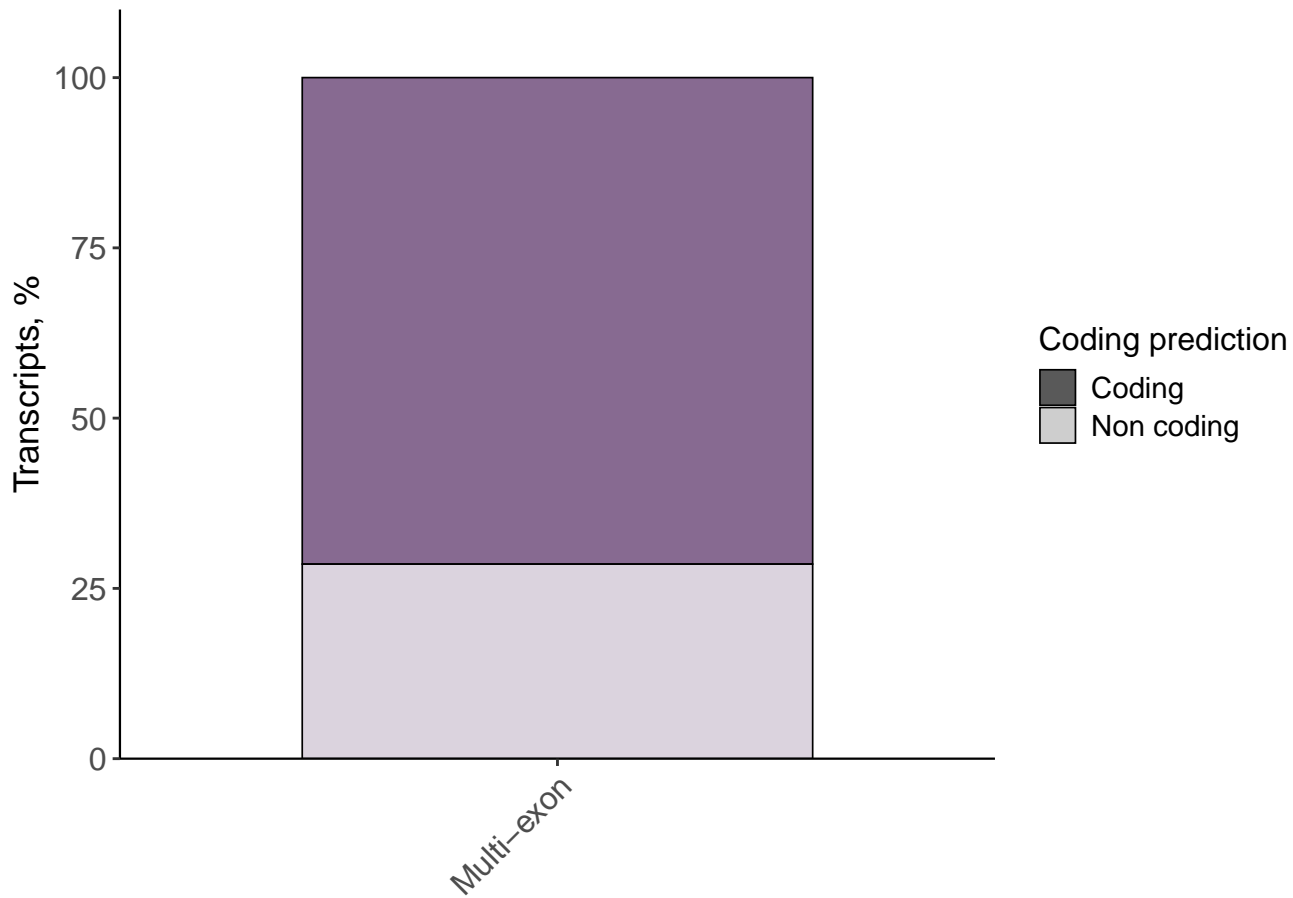
Isoform Distribution Across NNC



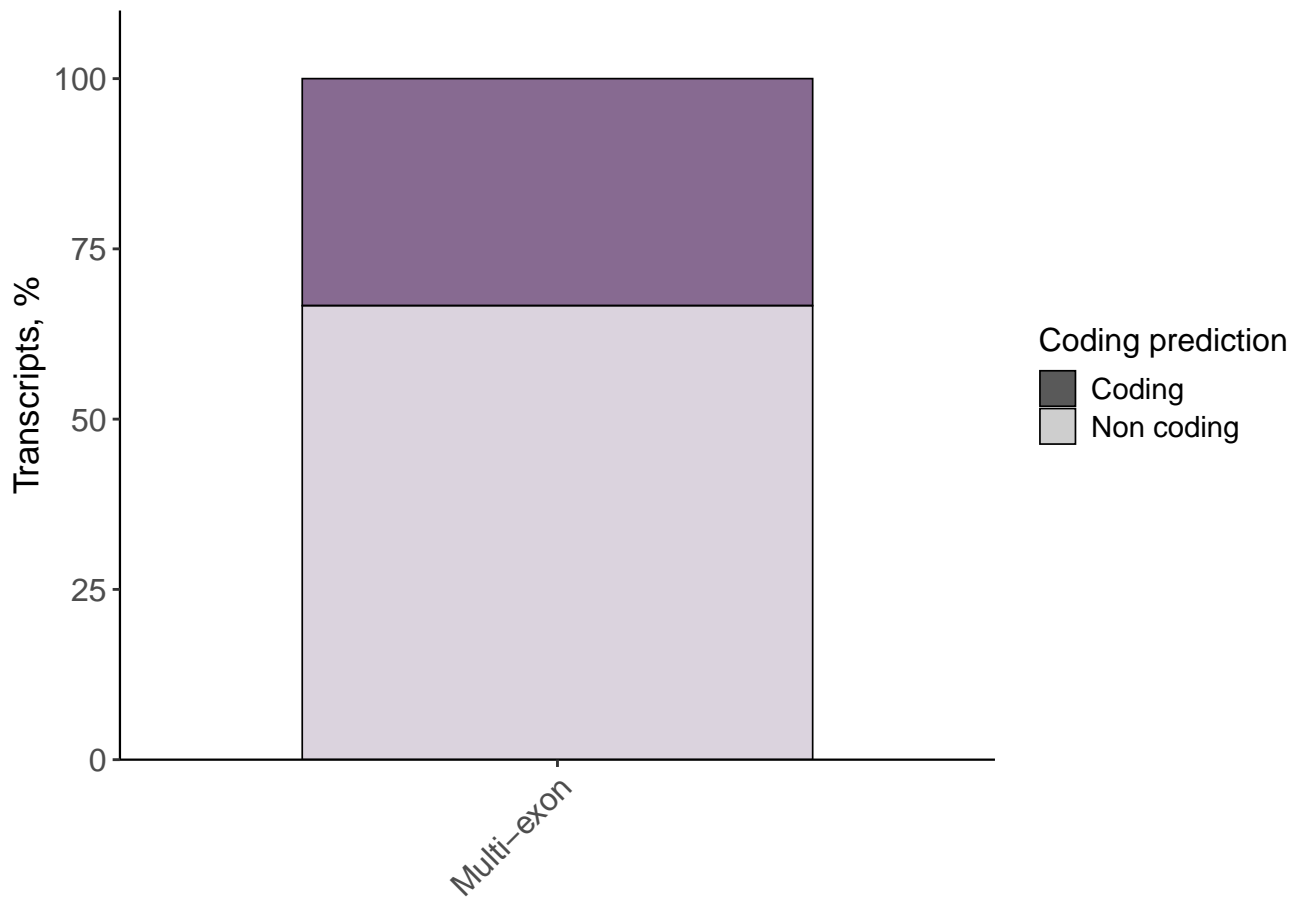
Isoform Distribution Across NIC



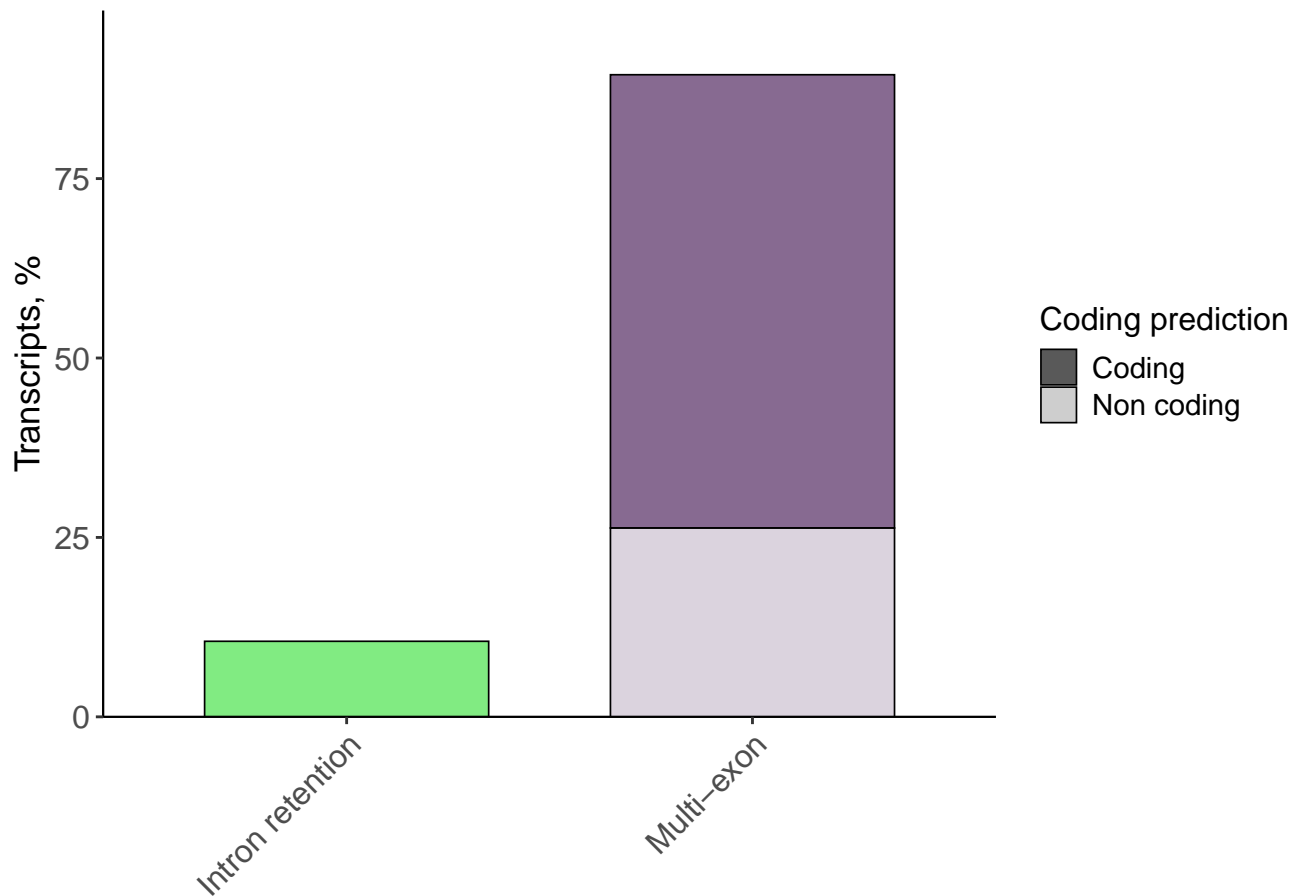
Isoform Distribution Across Genic Genomic



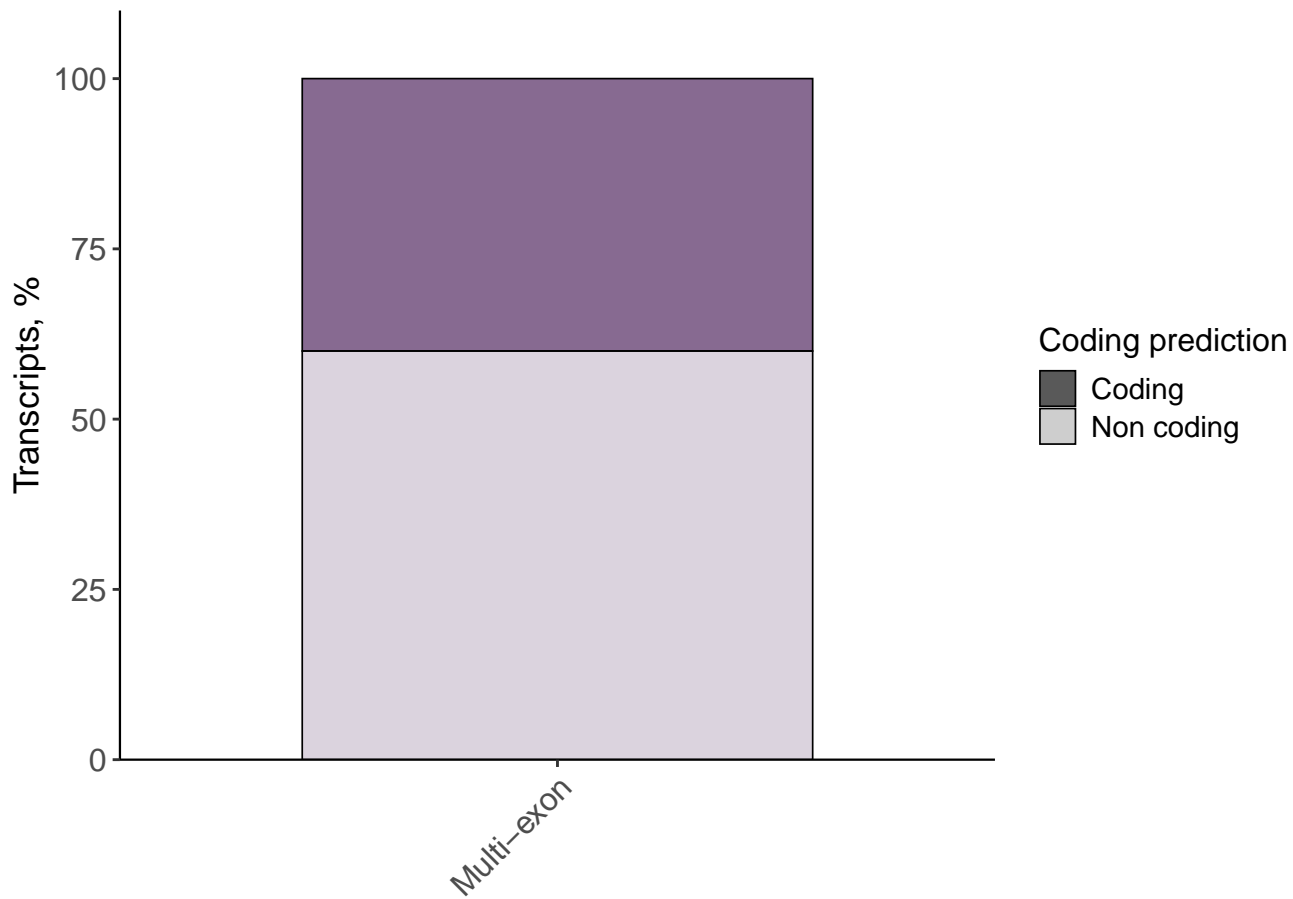
Isoform Distribution Across Antisense



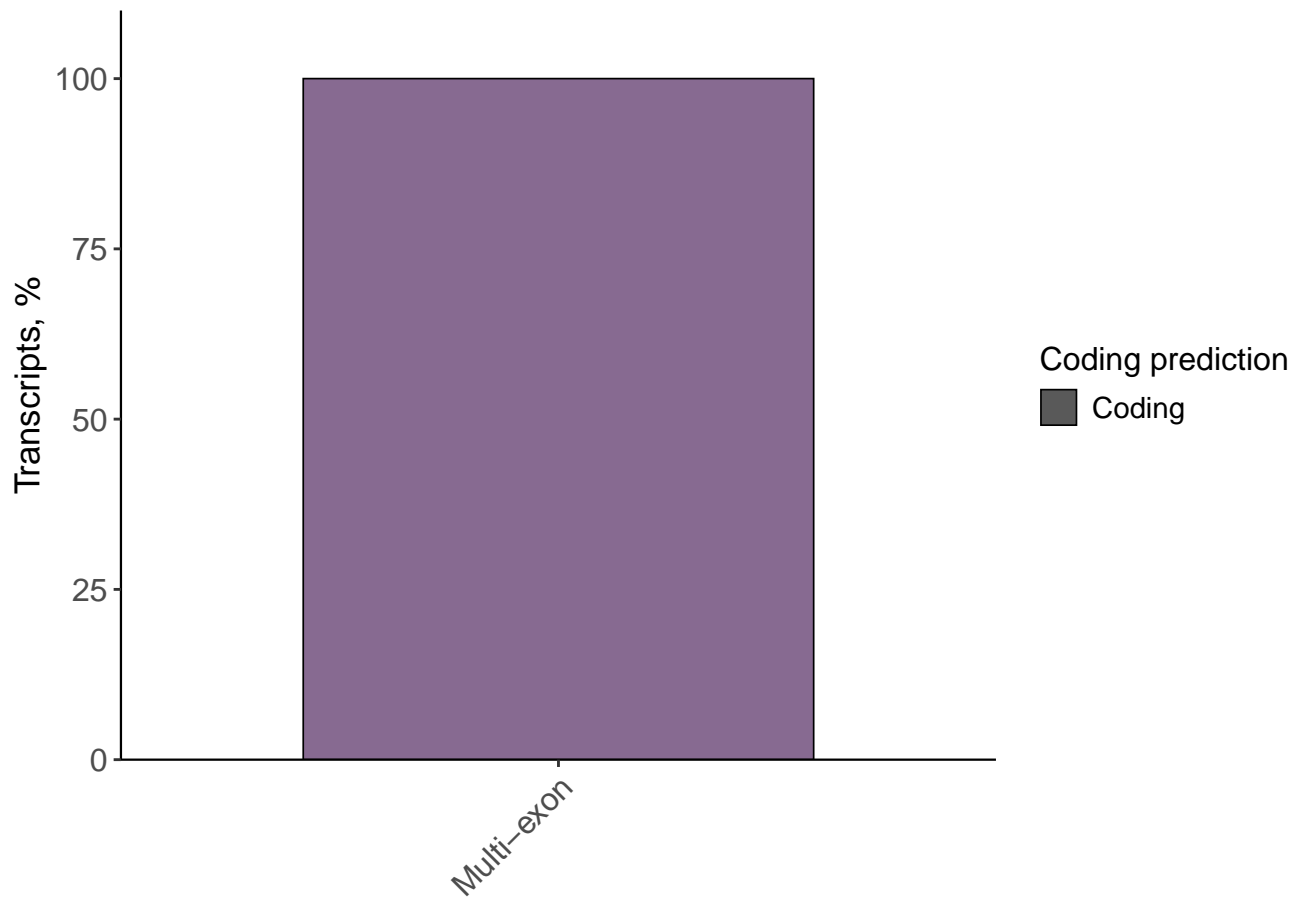
Isoform Distribution Across Fusion



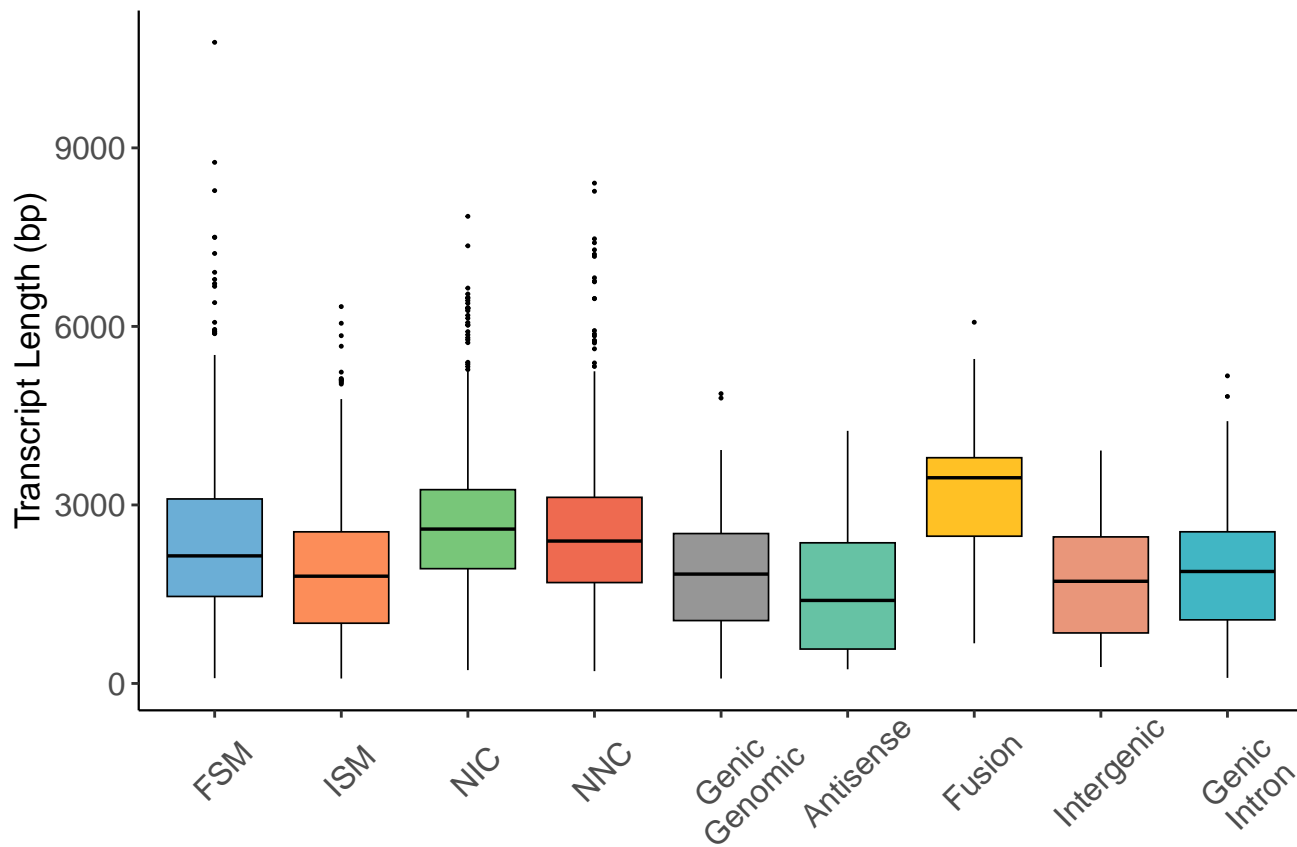
Isoform Distribution Across Intergenic



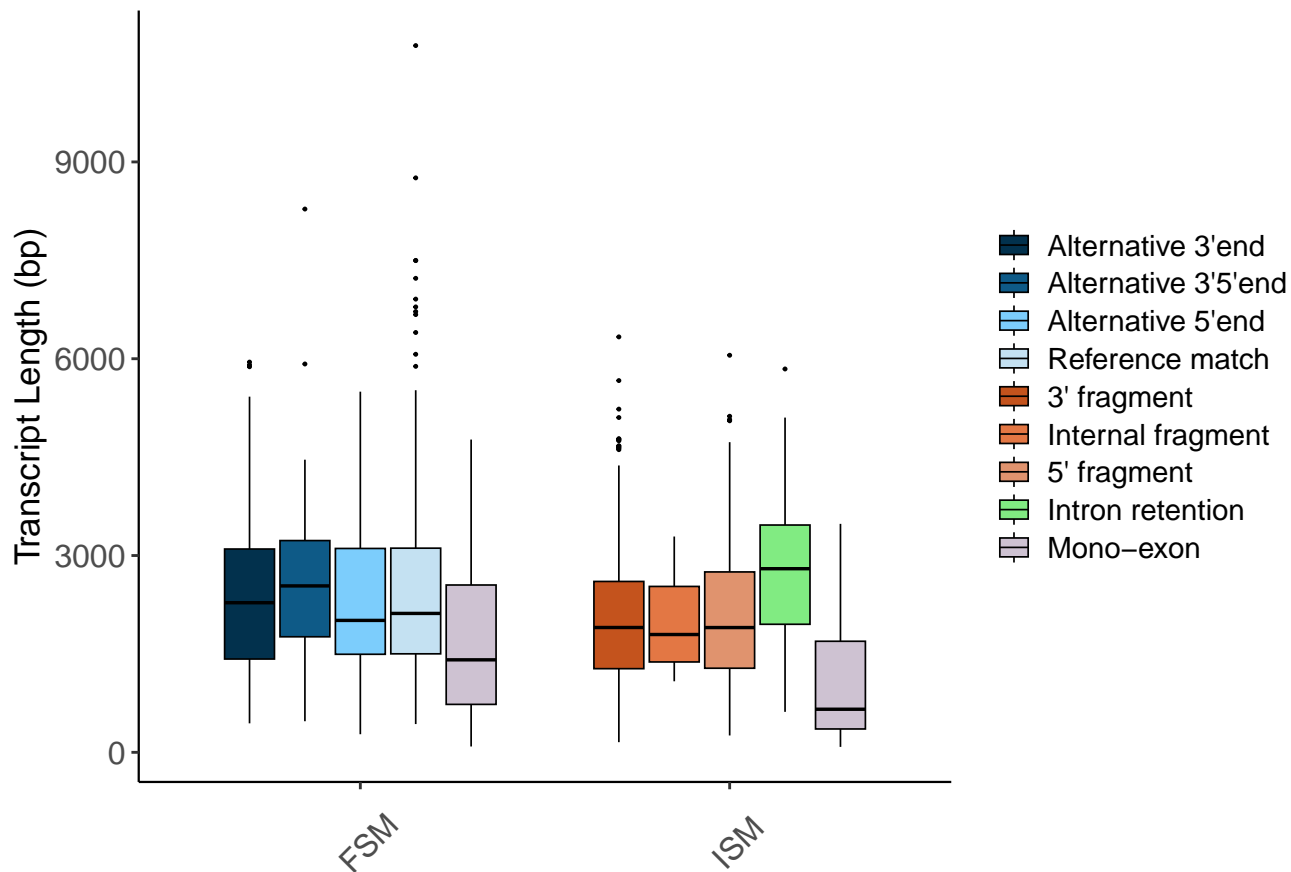
Isoform Distribution Across Genic Intron



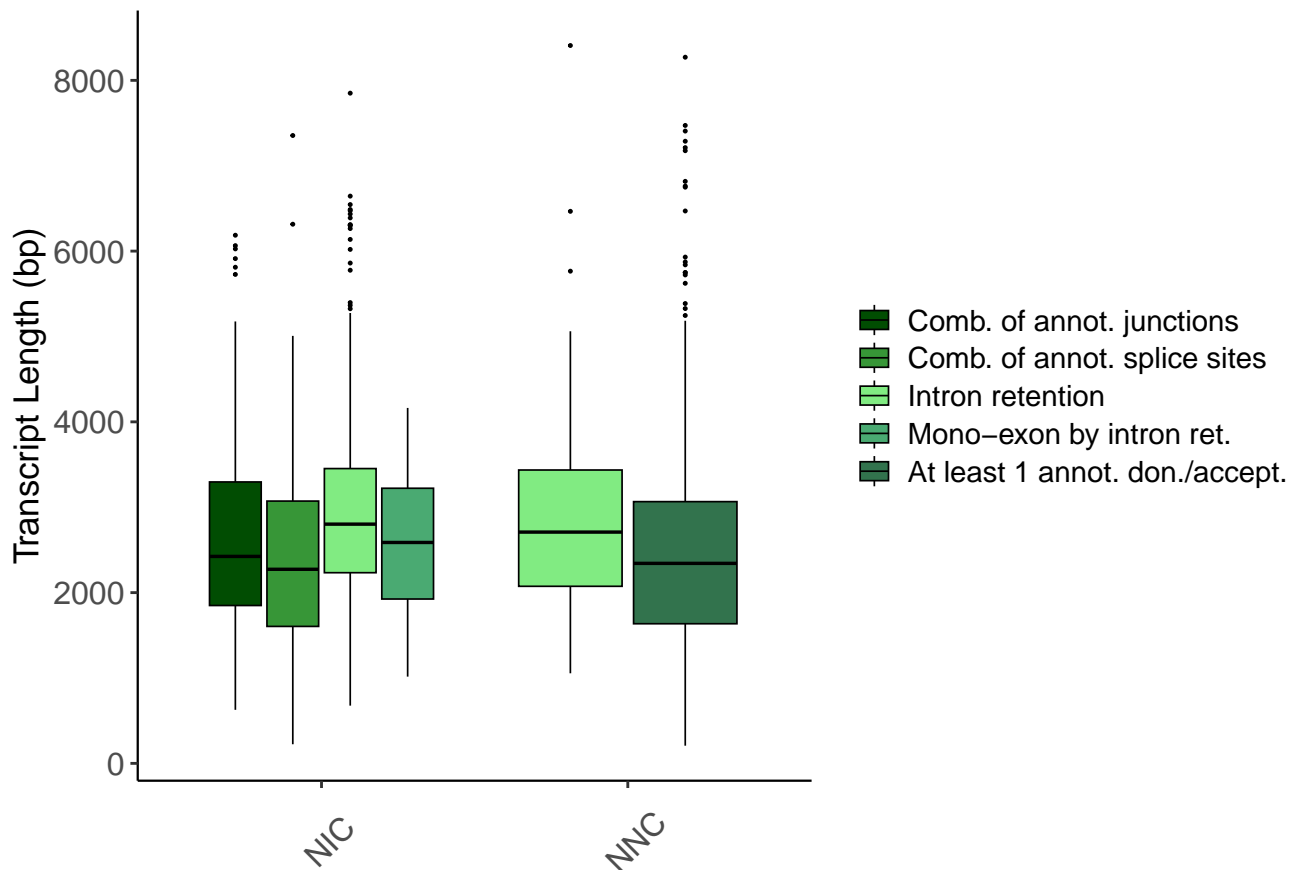
Transcript Lengths by Structural Classification



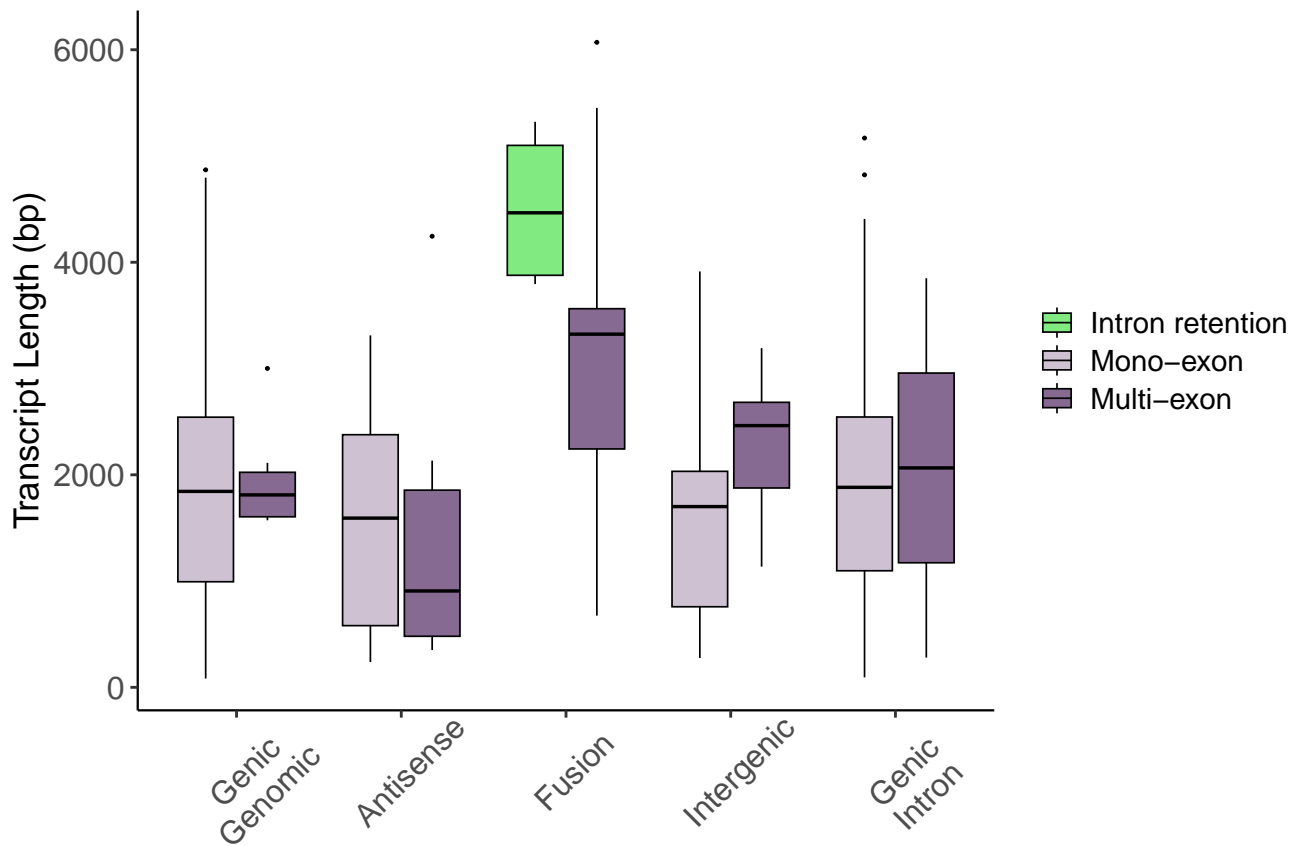
Transcript Lengths by Subcategory



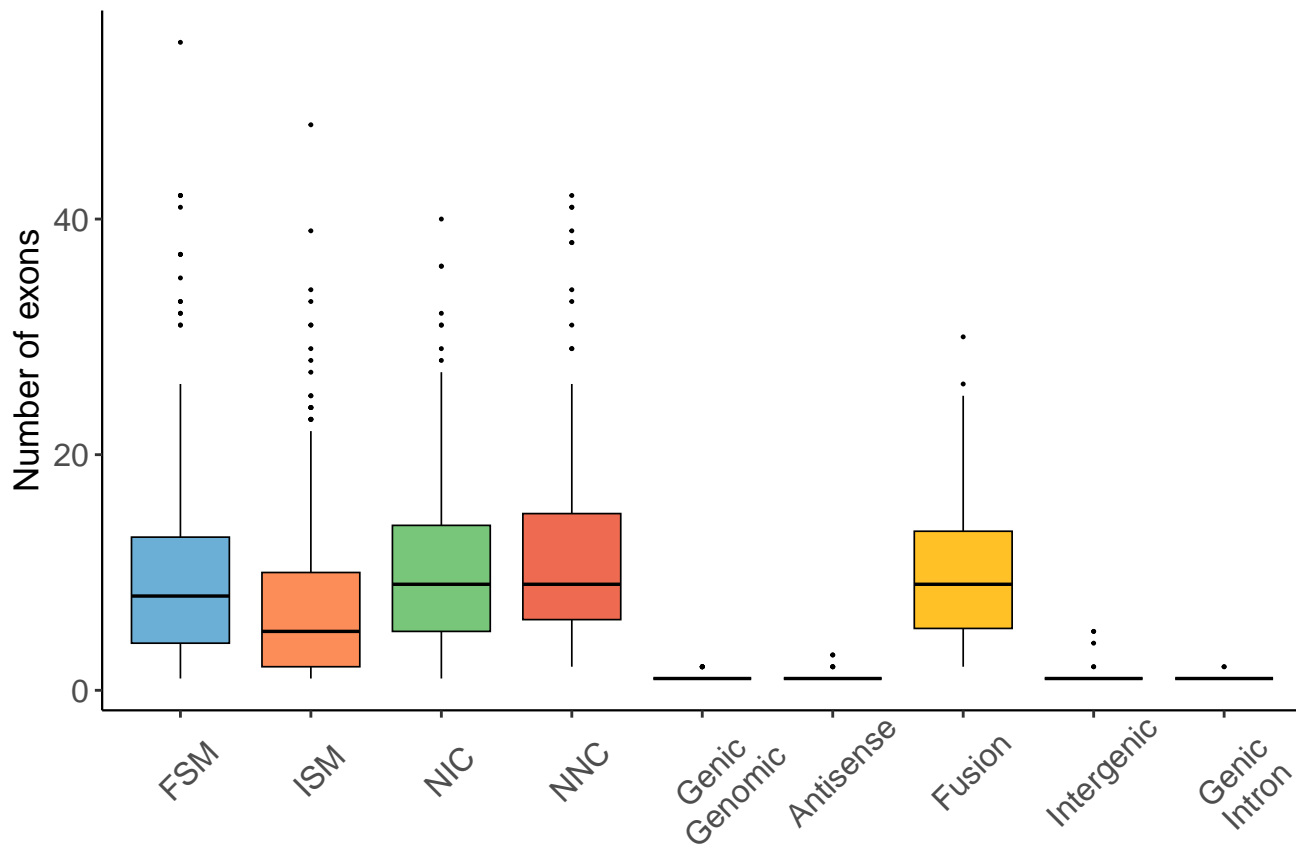
Transcript Lengths by Subcategory



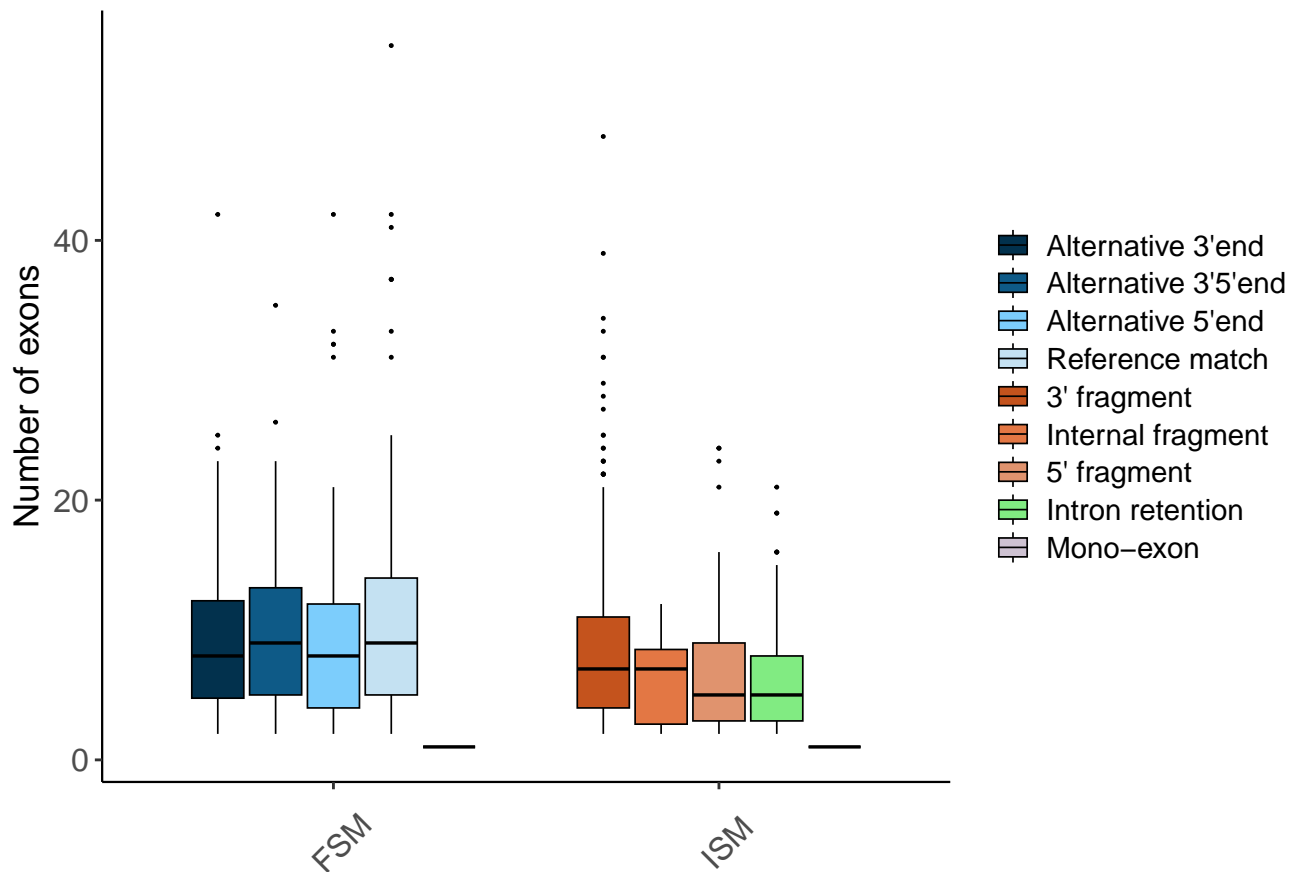
Transcript Lengths by Subcategory



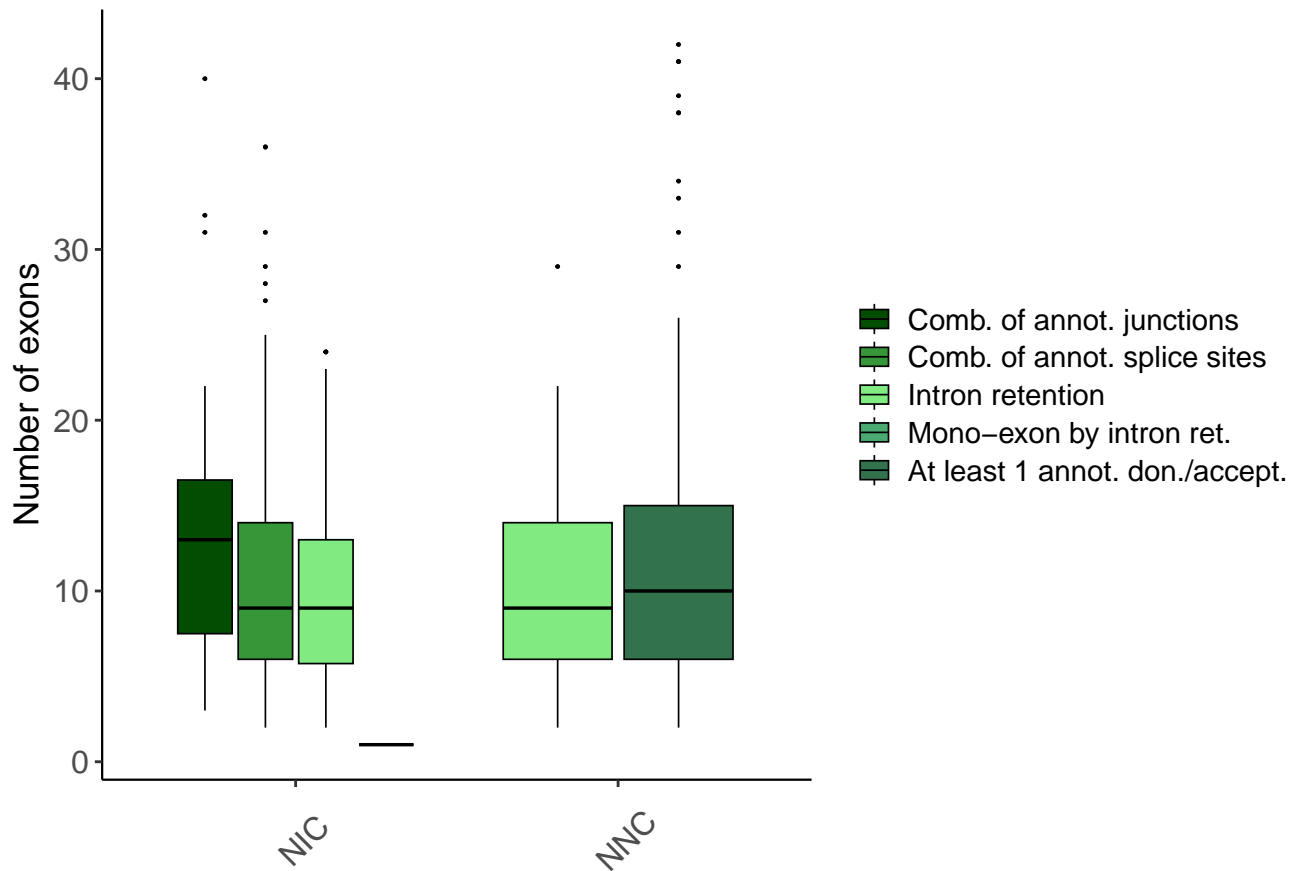
Exon Counts by Structural Classification



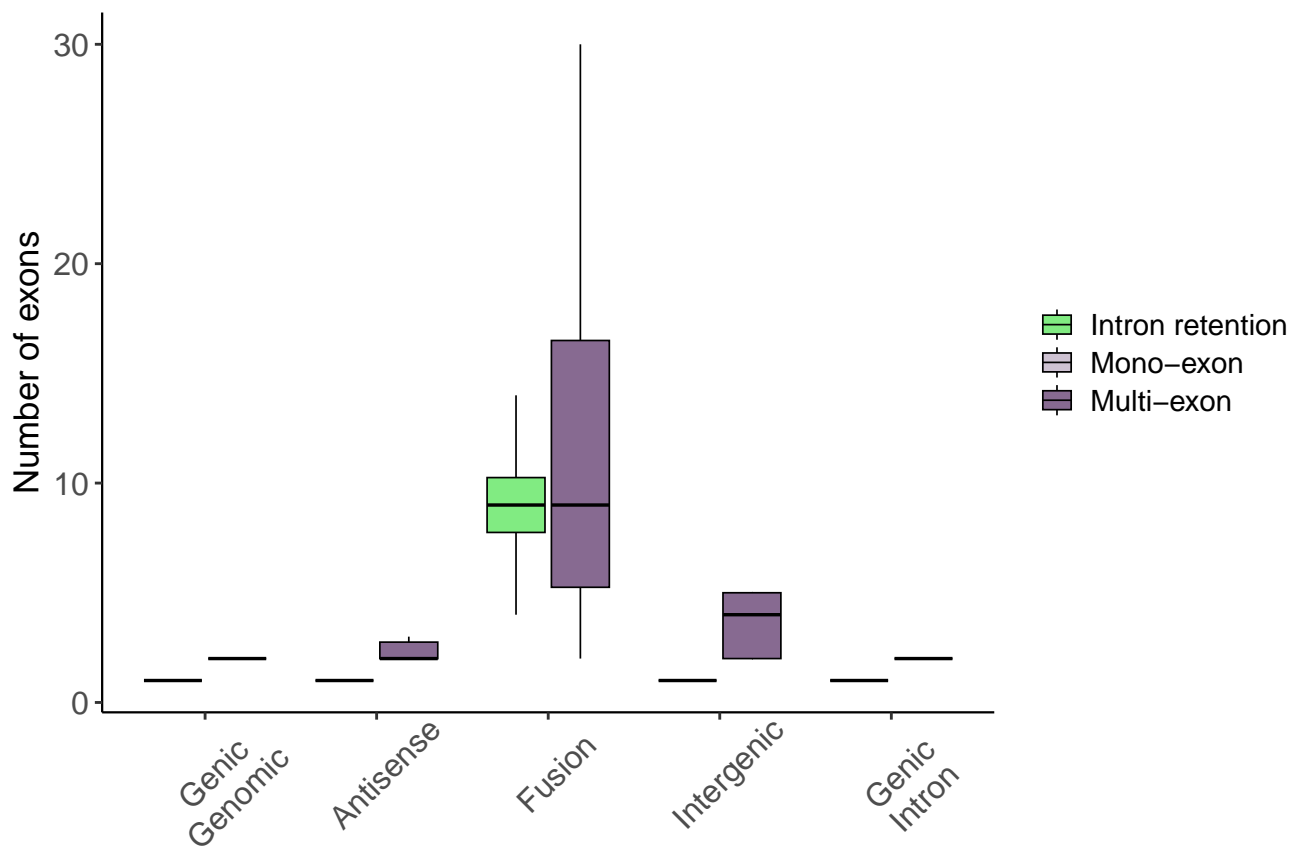
Exon Counts by Subcategory



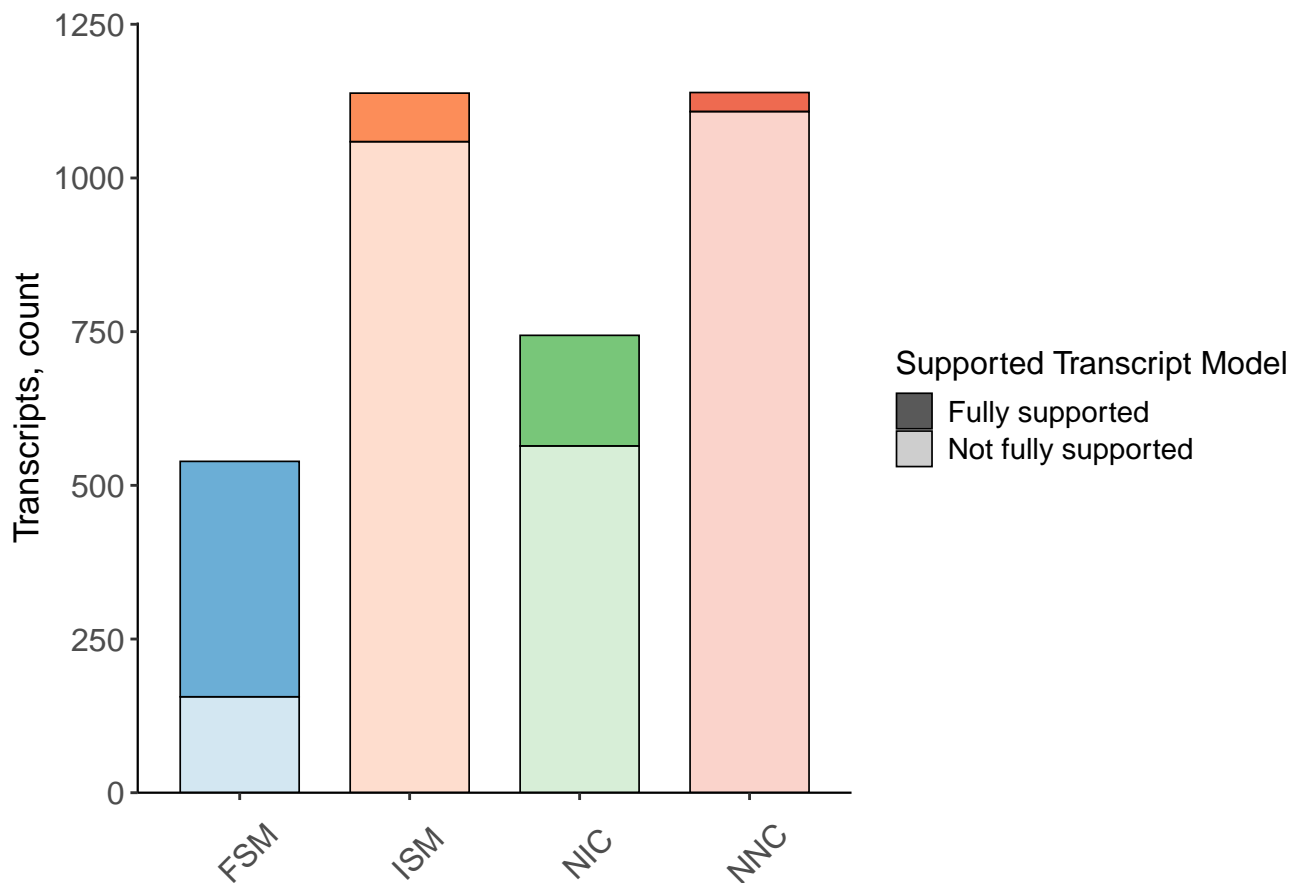
Exon Counts by Subcategory



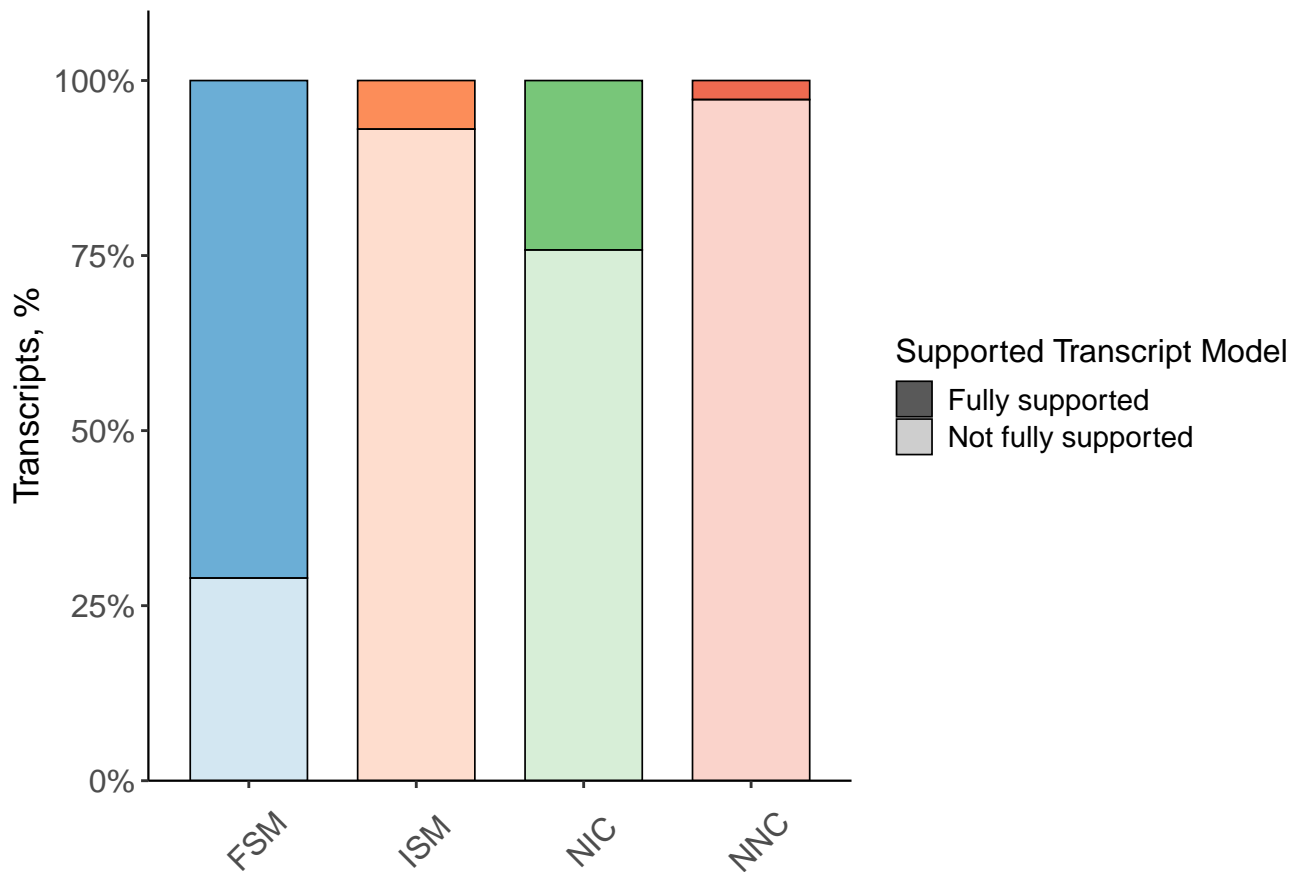
Exon Counts by Subcategory



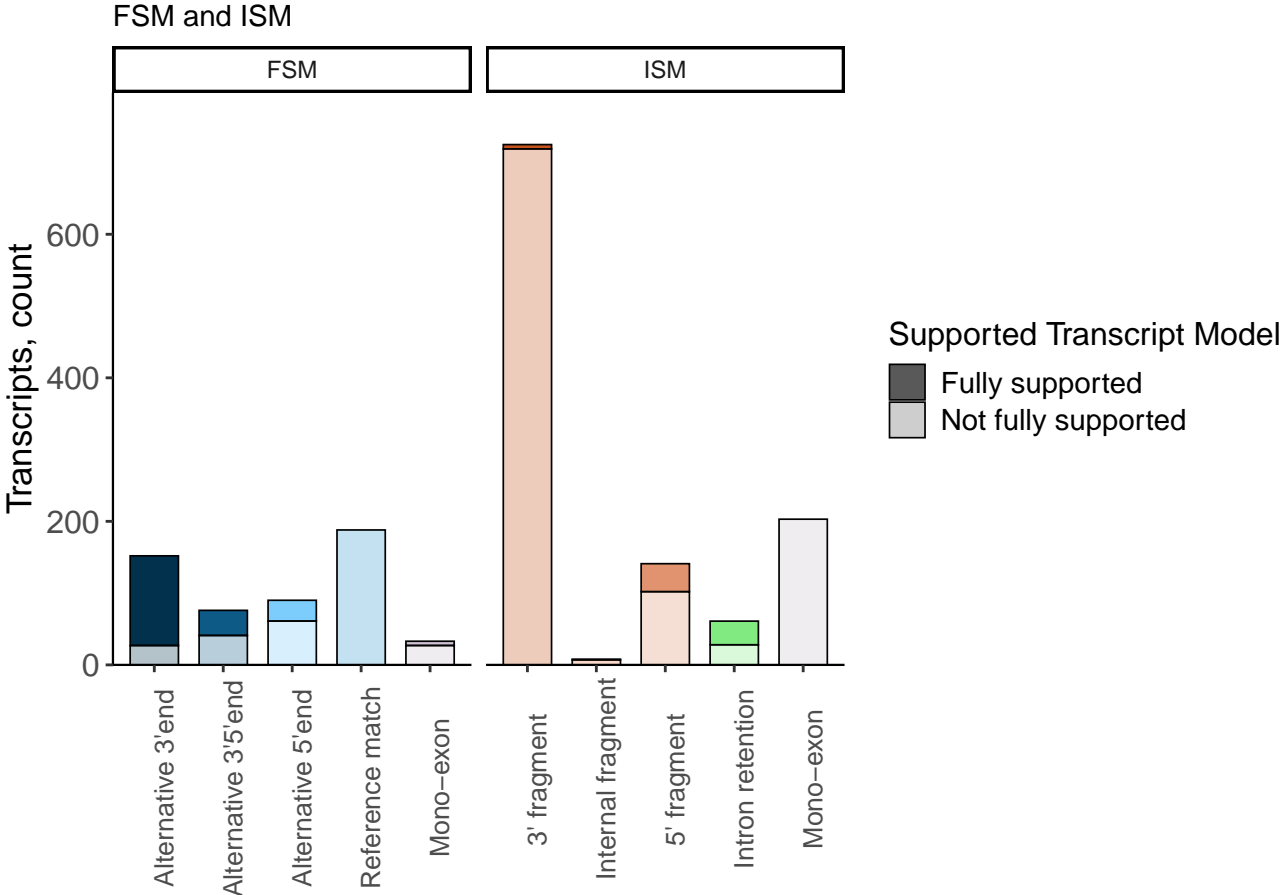
Isoform Distribution Across Structural Categories



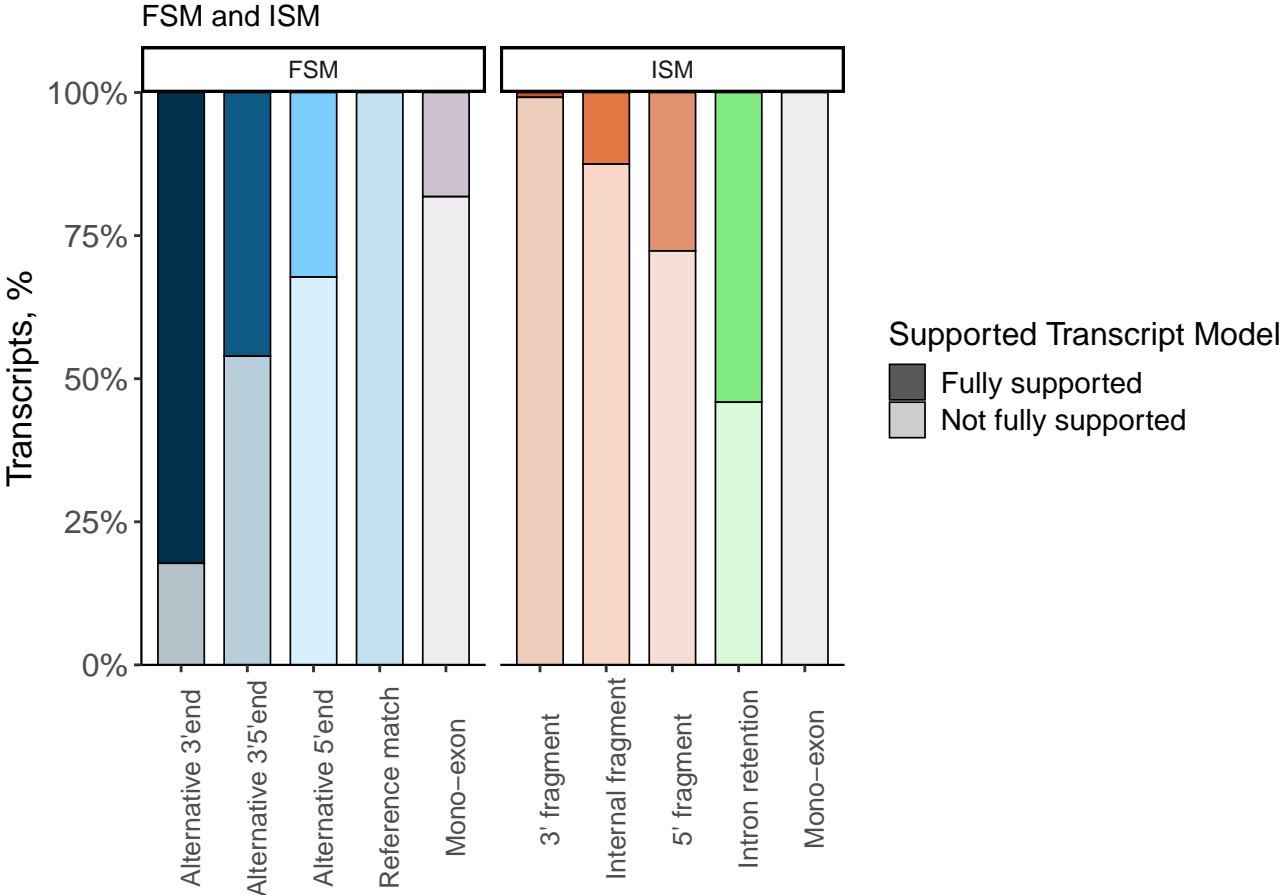
Isoform Distribution Across Structural Categories



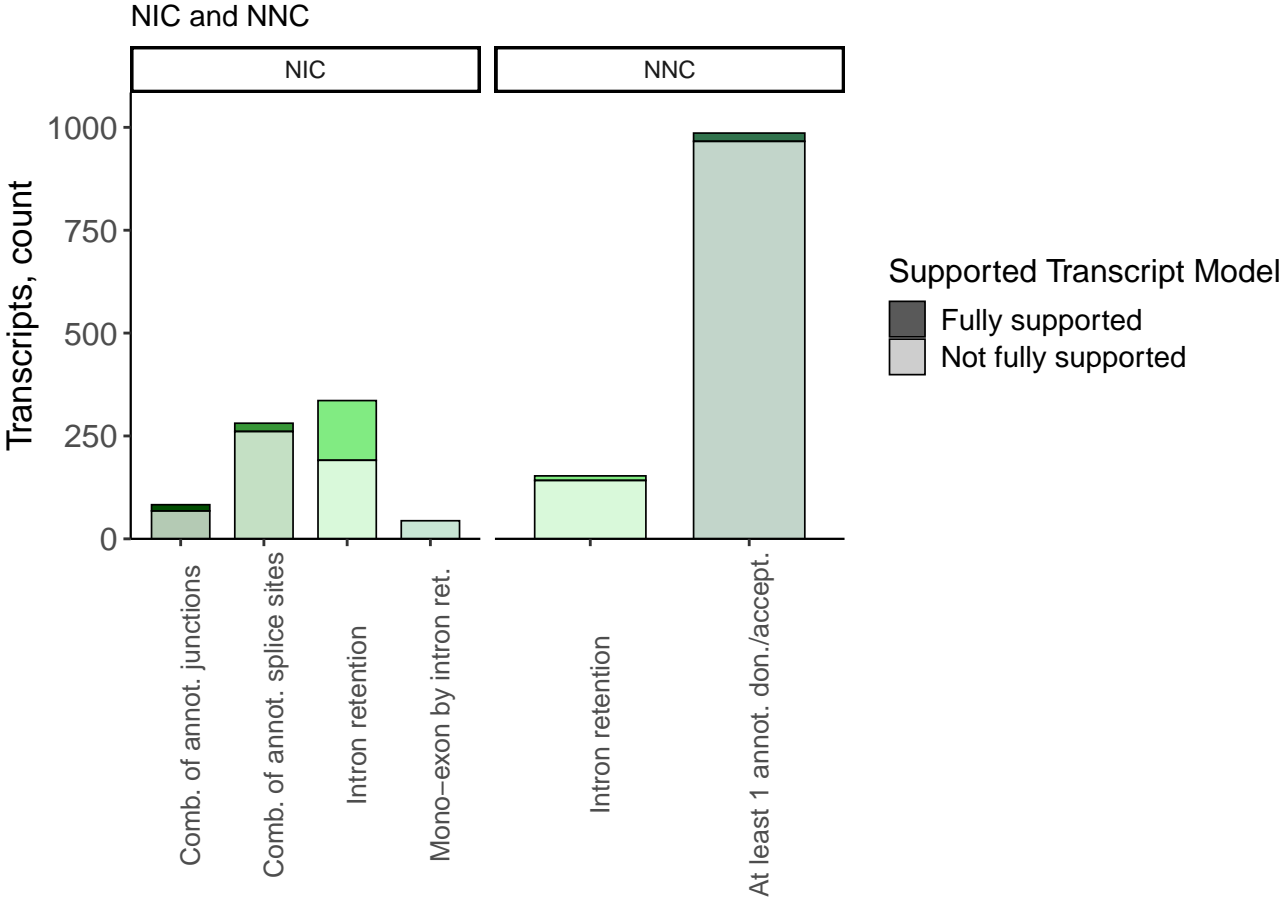
Isoform Distribution Across Structural Subcategories



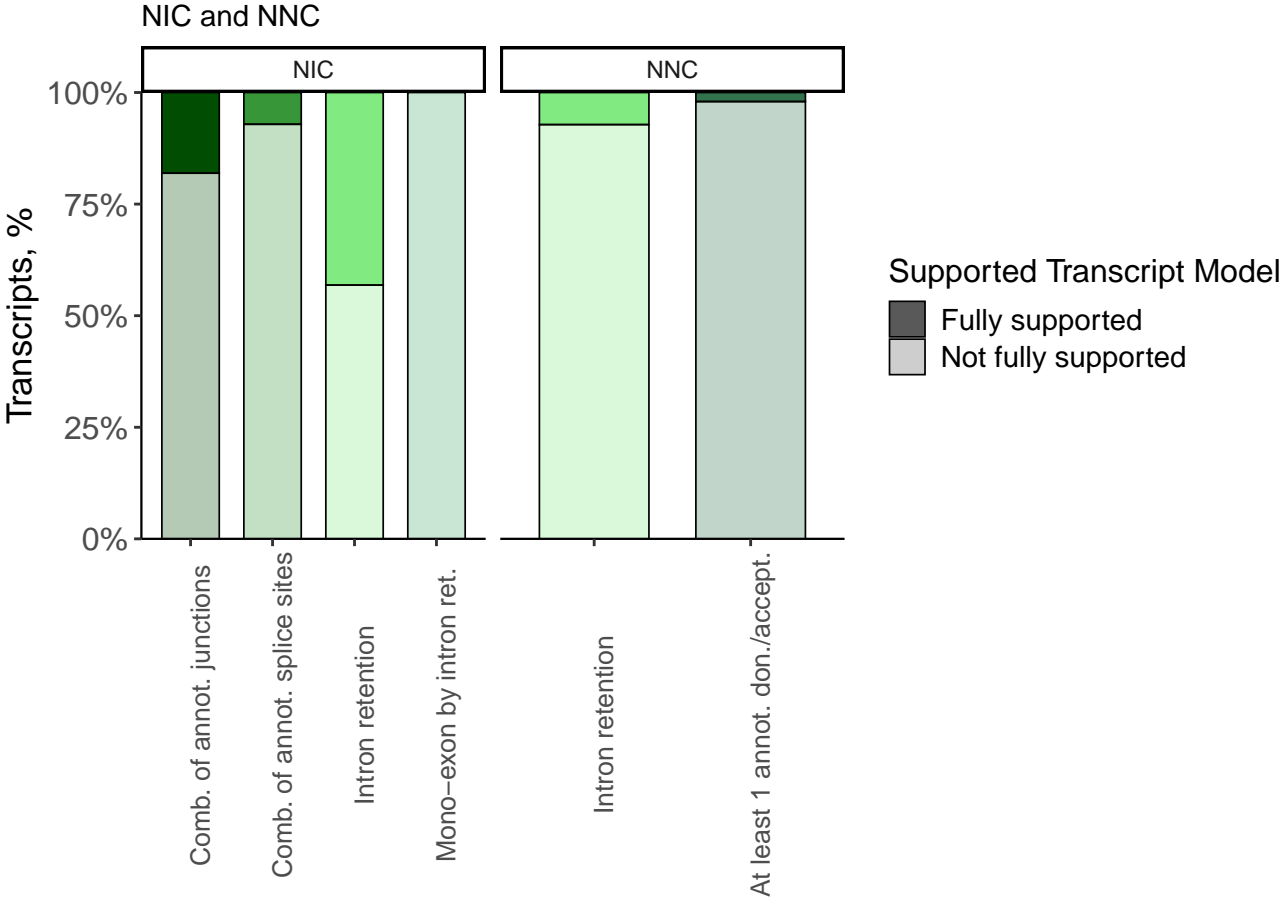
Isoform Distribution Across Structural Subcategories



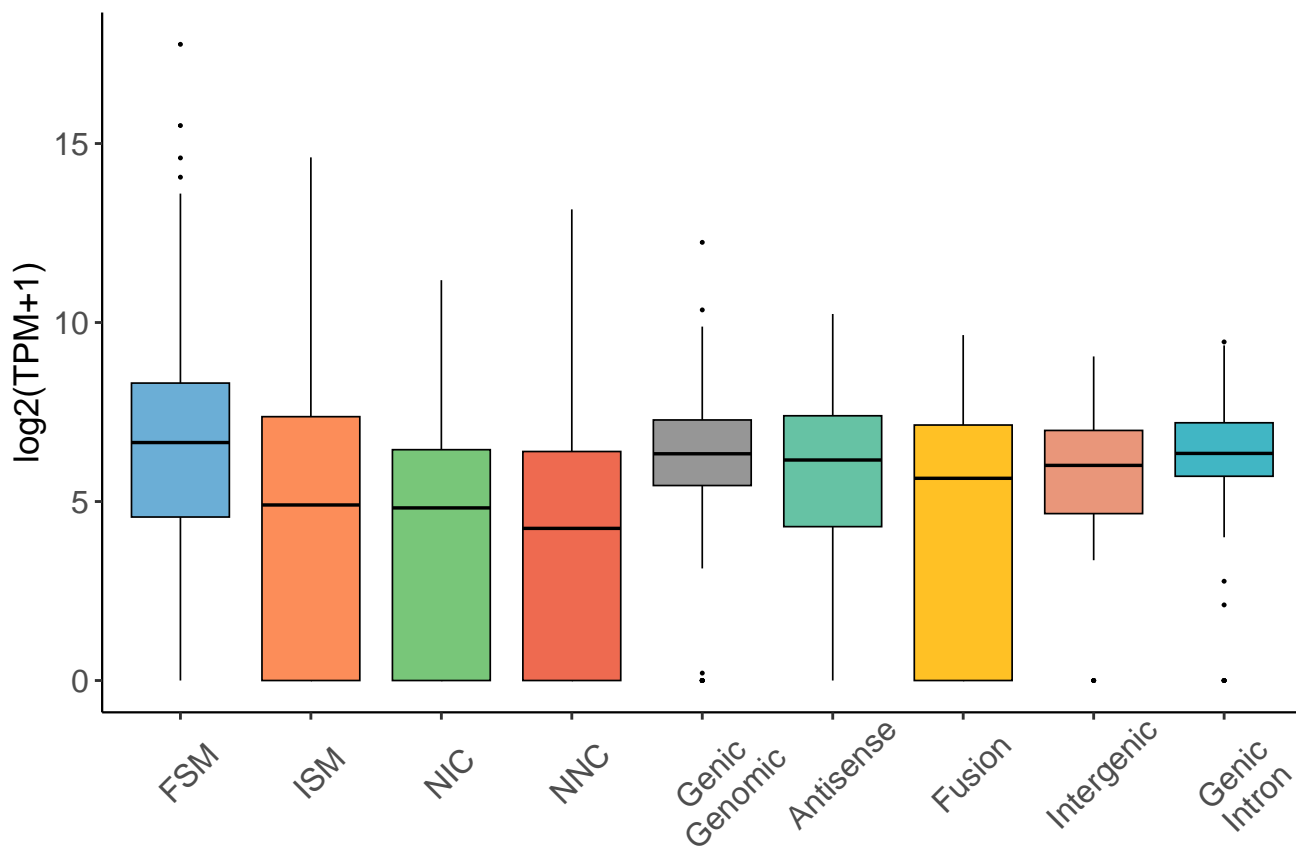
Isoform Distribution Across Structural Subcategories



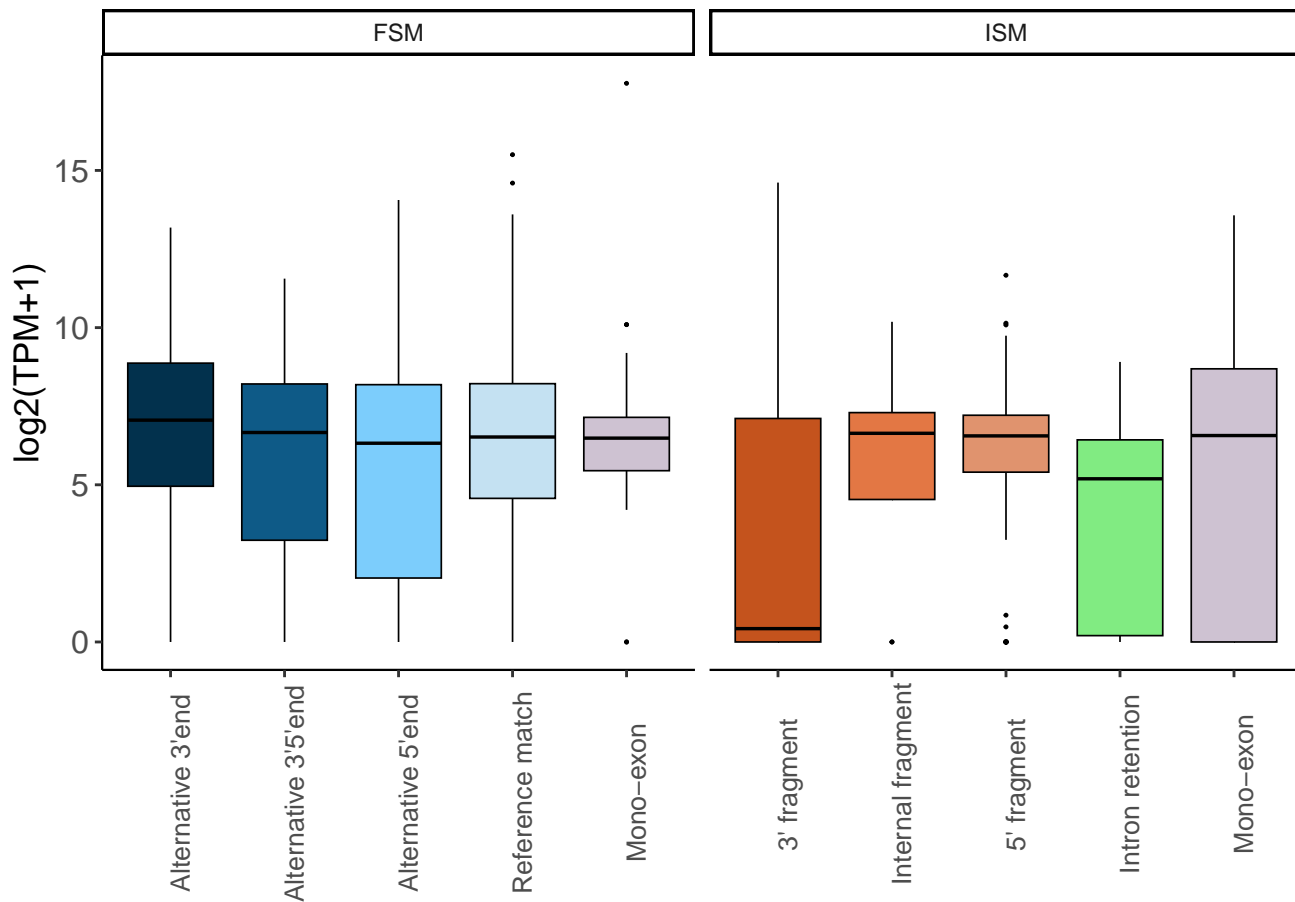
Isoform Distribution Across Structural Subcategories



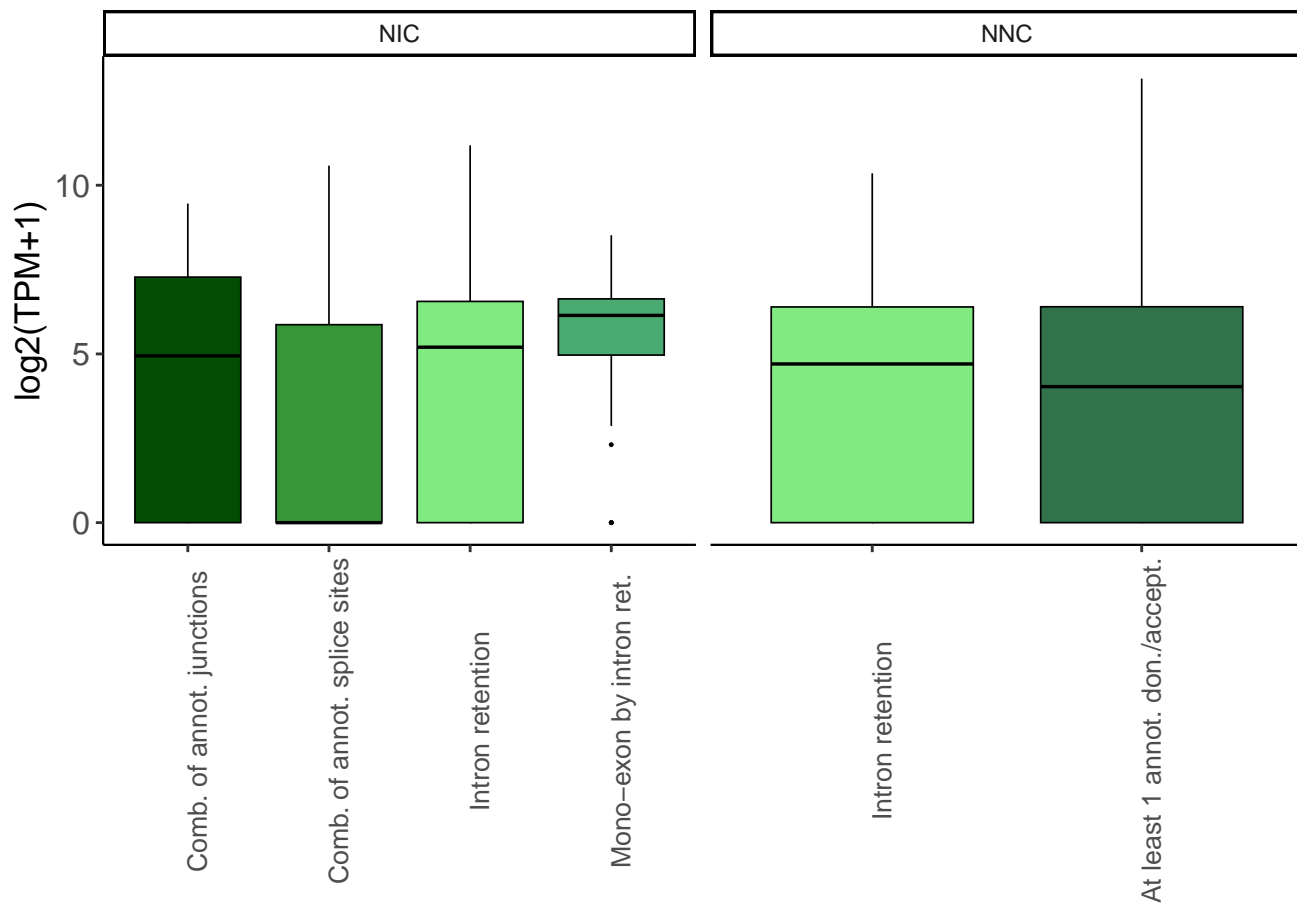
Transcript Expression by Structural Category



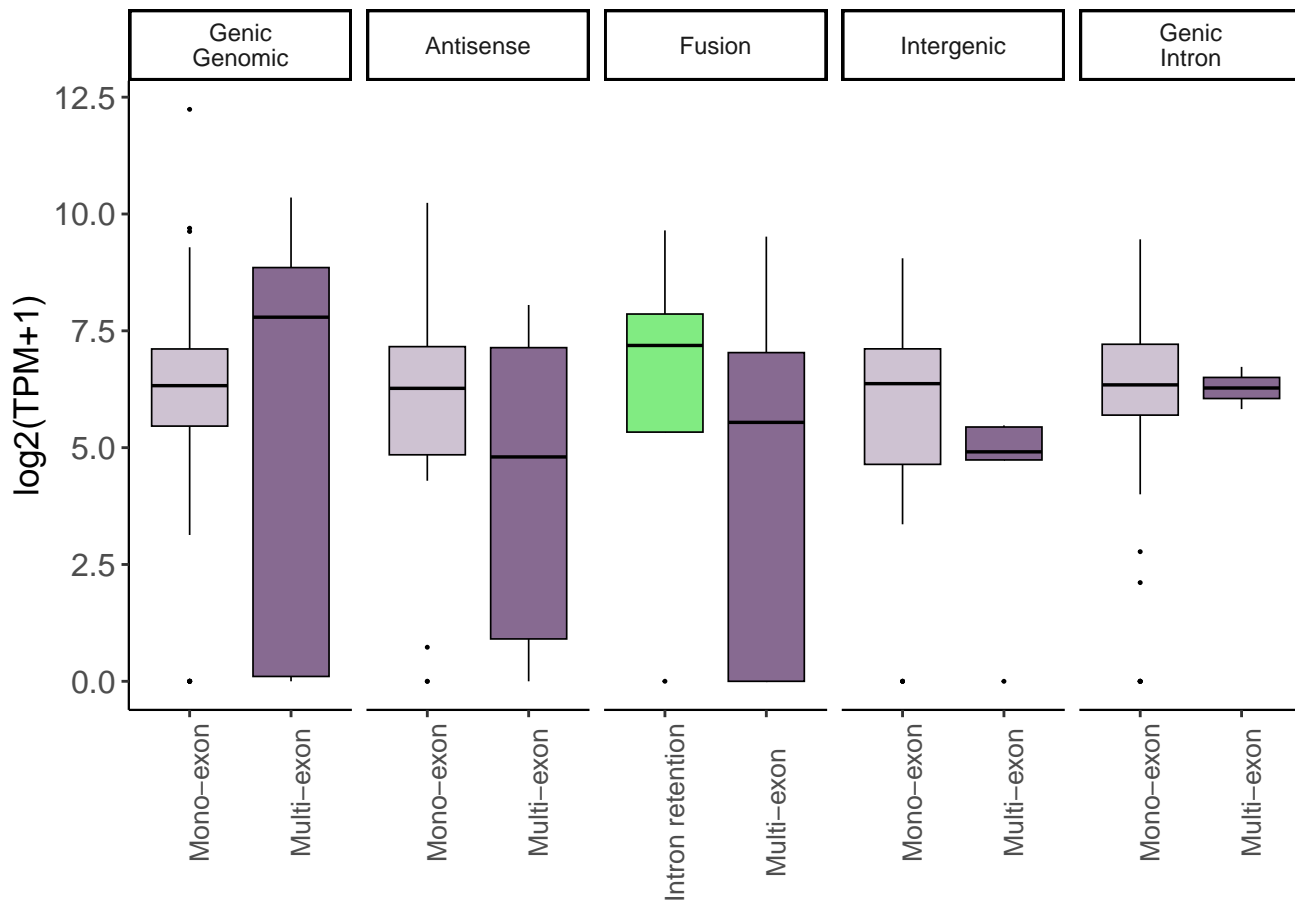
Transcript Expression by Subcategory



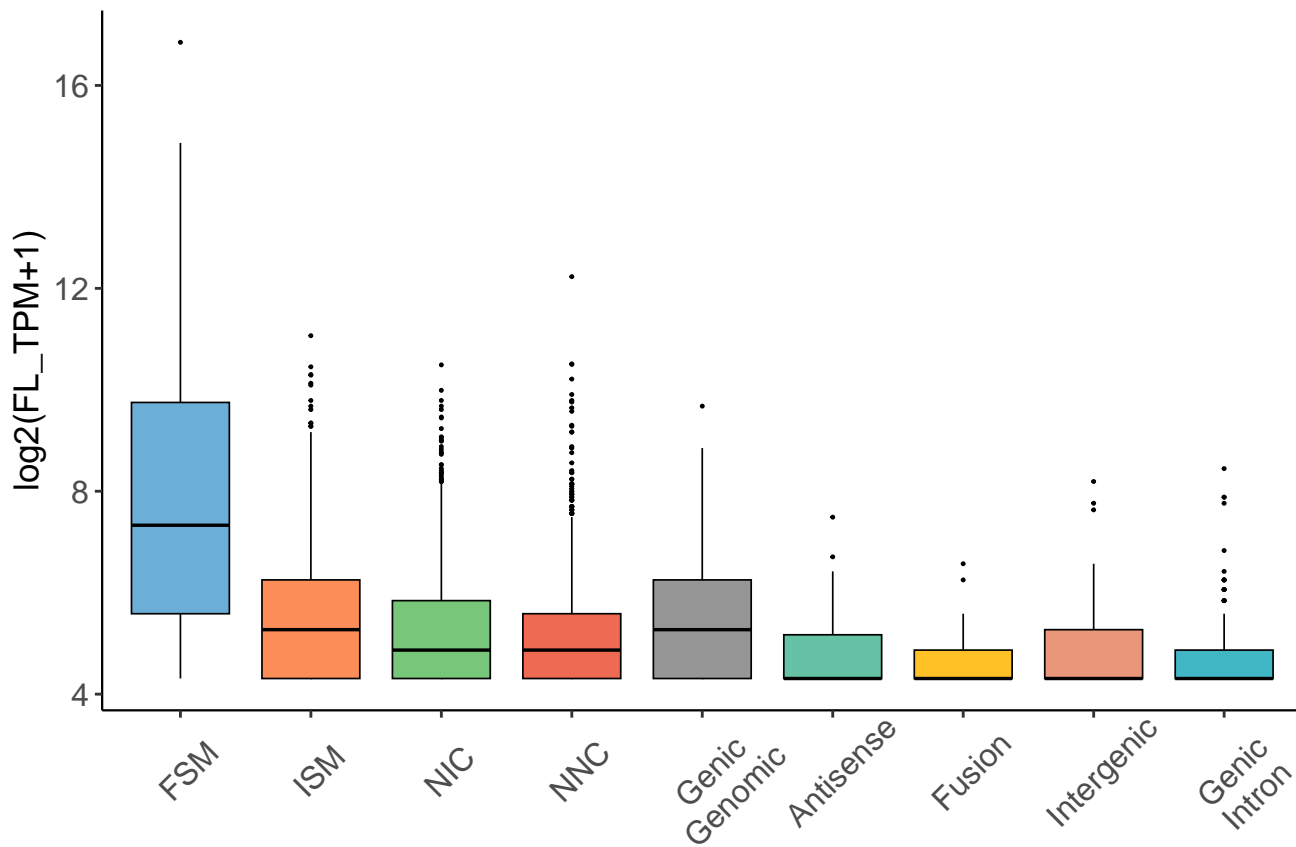
Transcript Expression by Subcategory



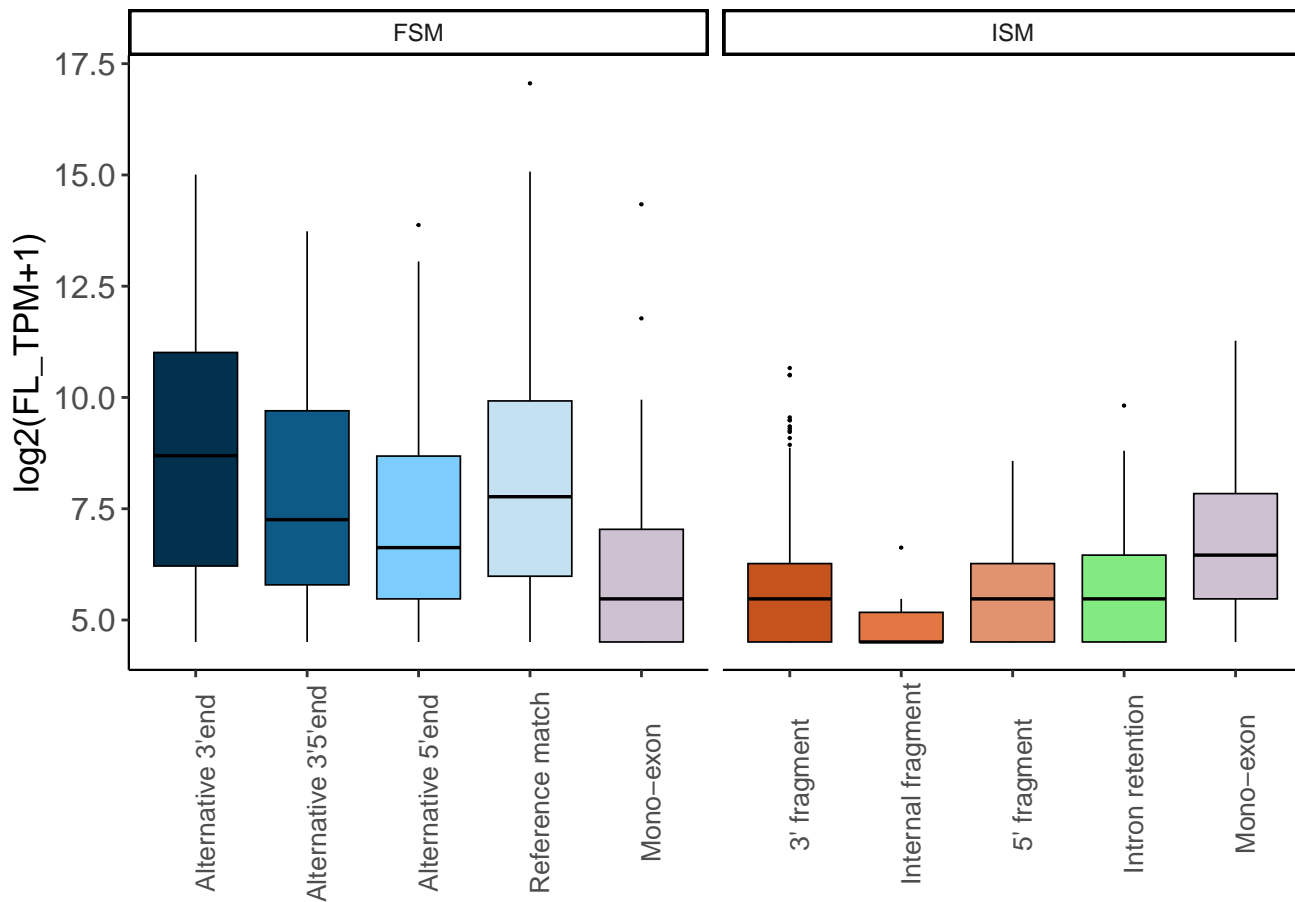
Transcript Expression by Subcategory



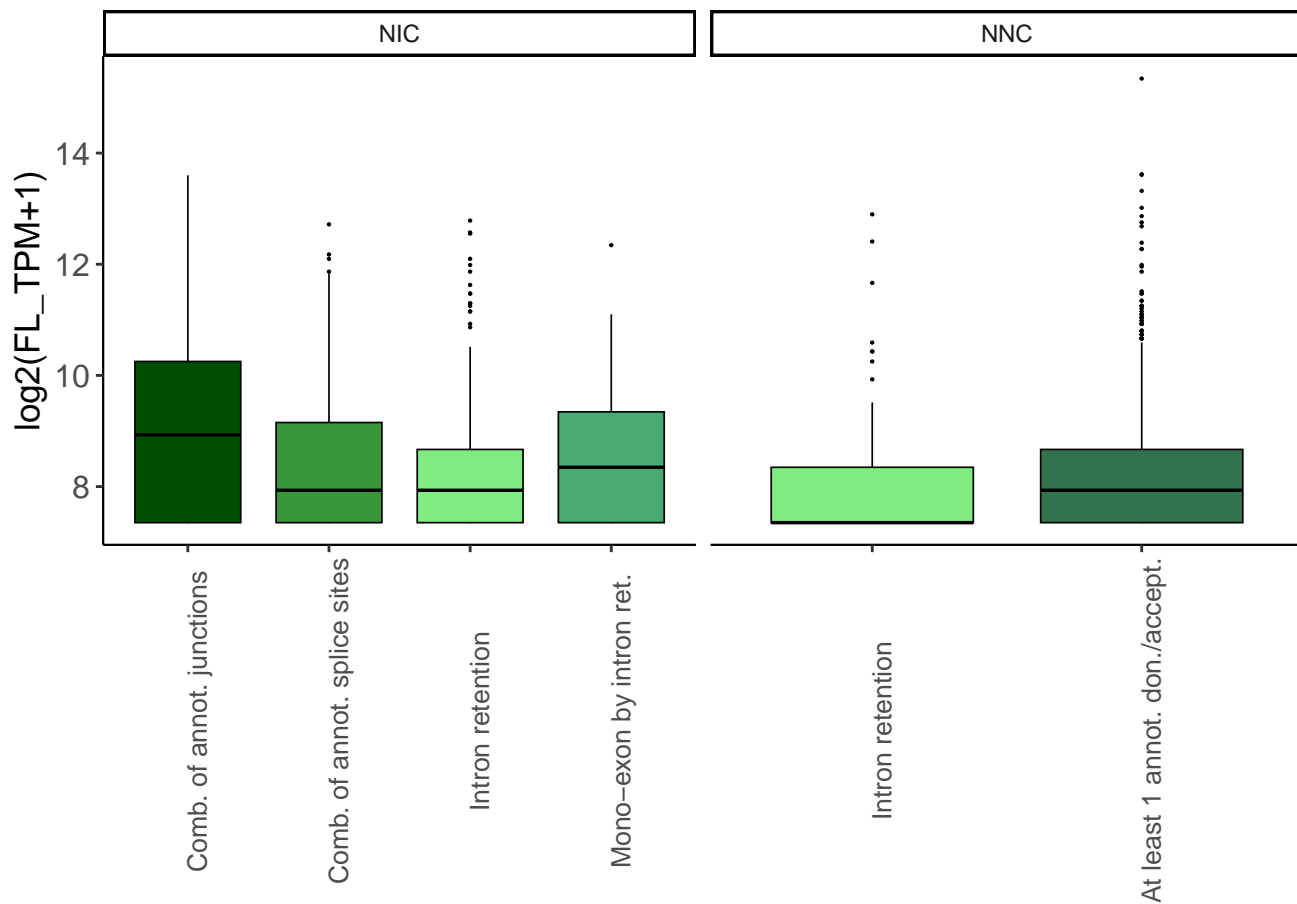
Long Reads Count by Structural Category



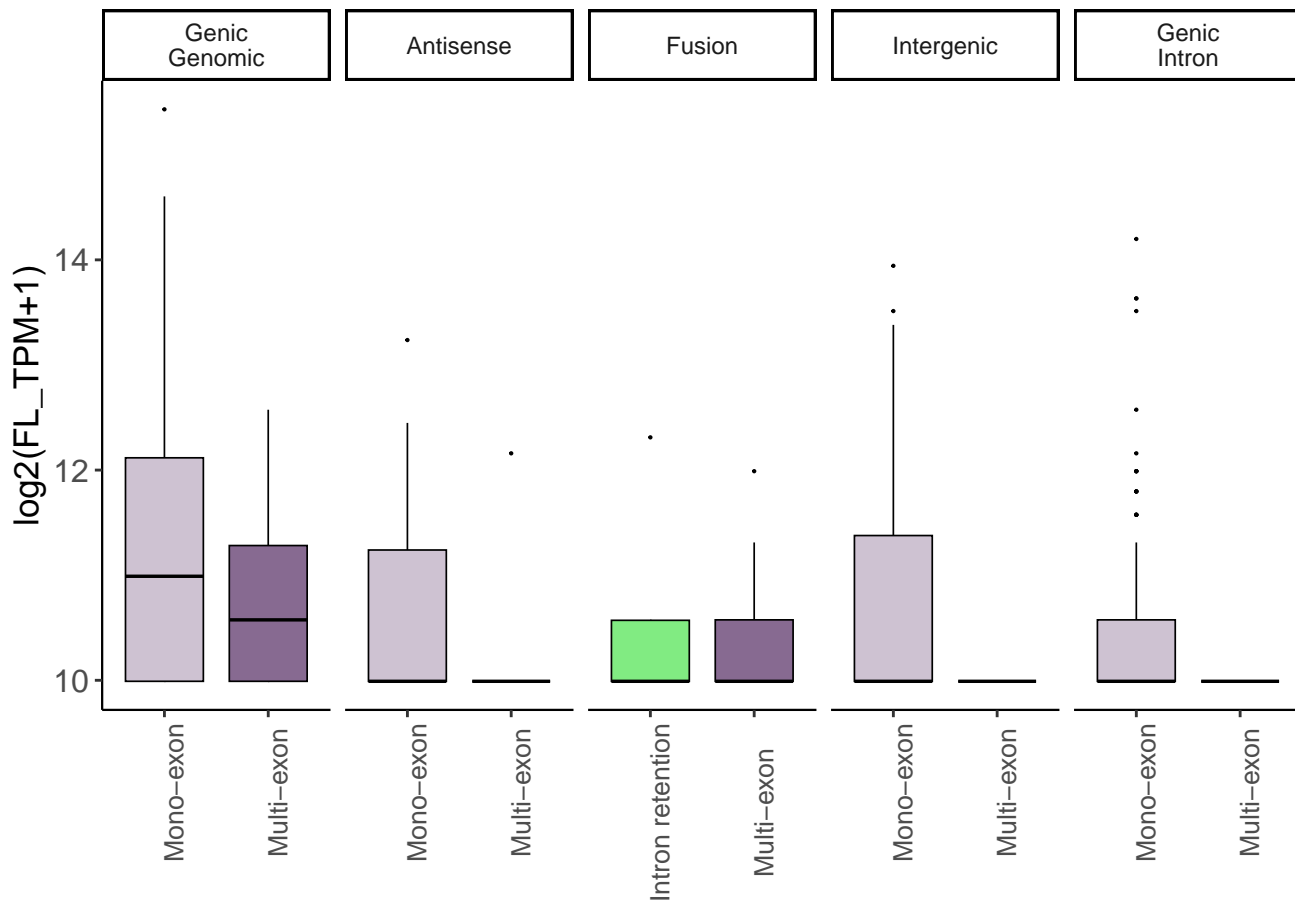
Long Reads Count by Subcategory



Long Reads Count by Subcategory

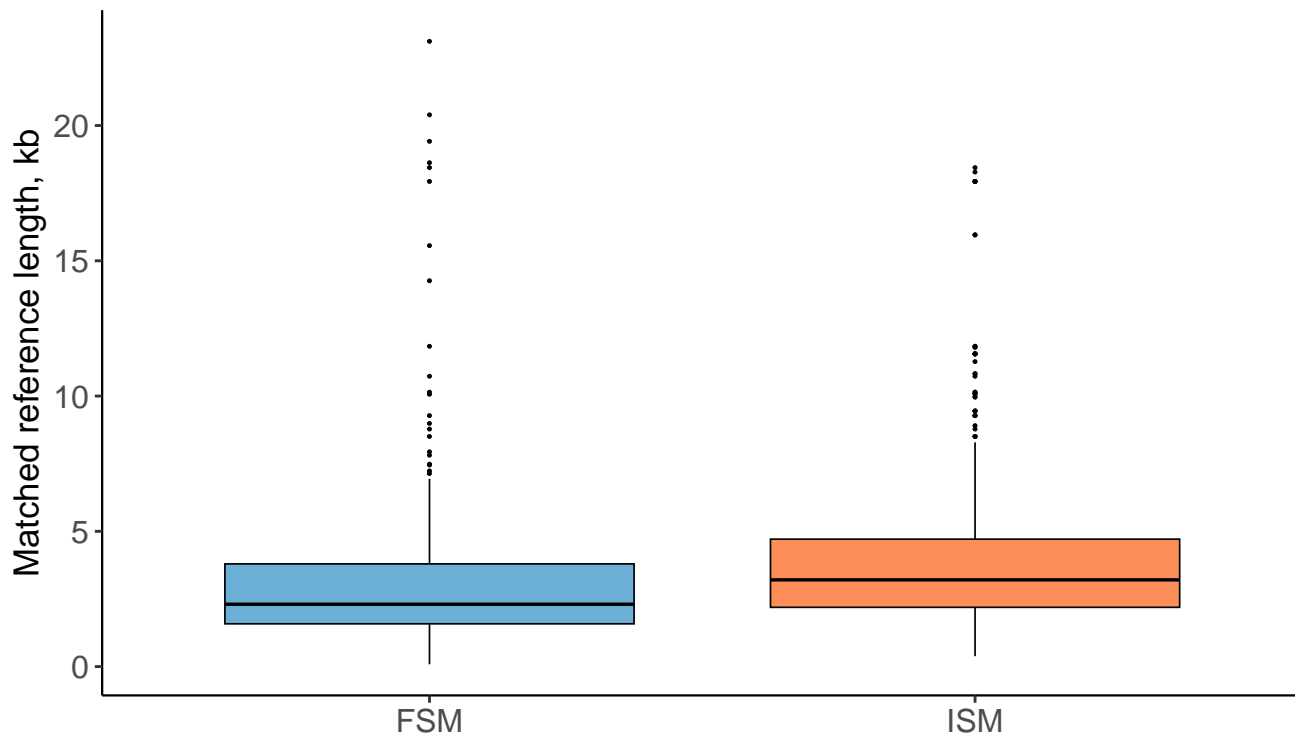


Long Reads Count by Subcategory



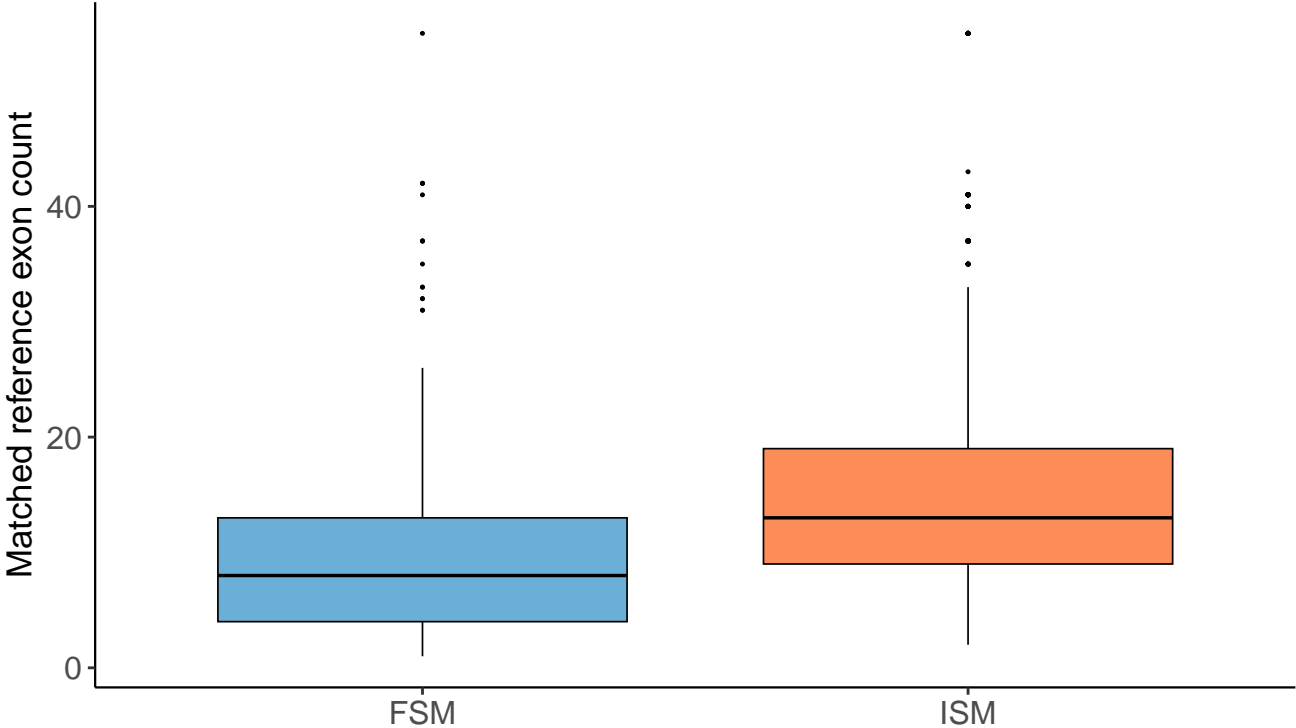
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

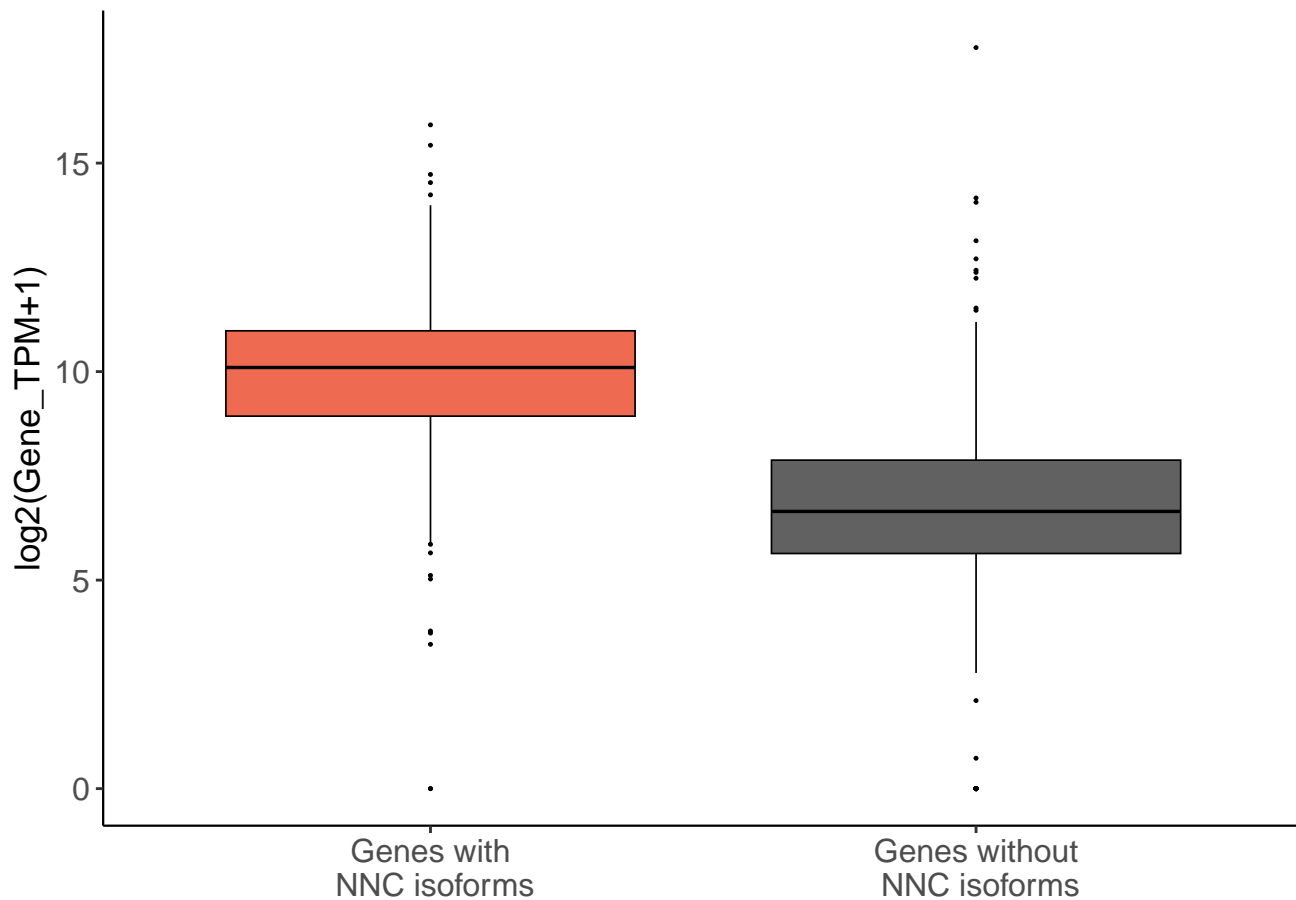


Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

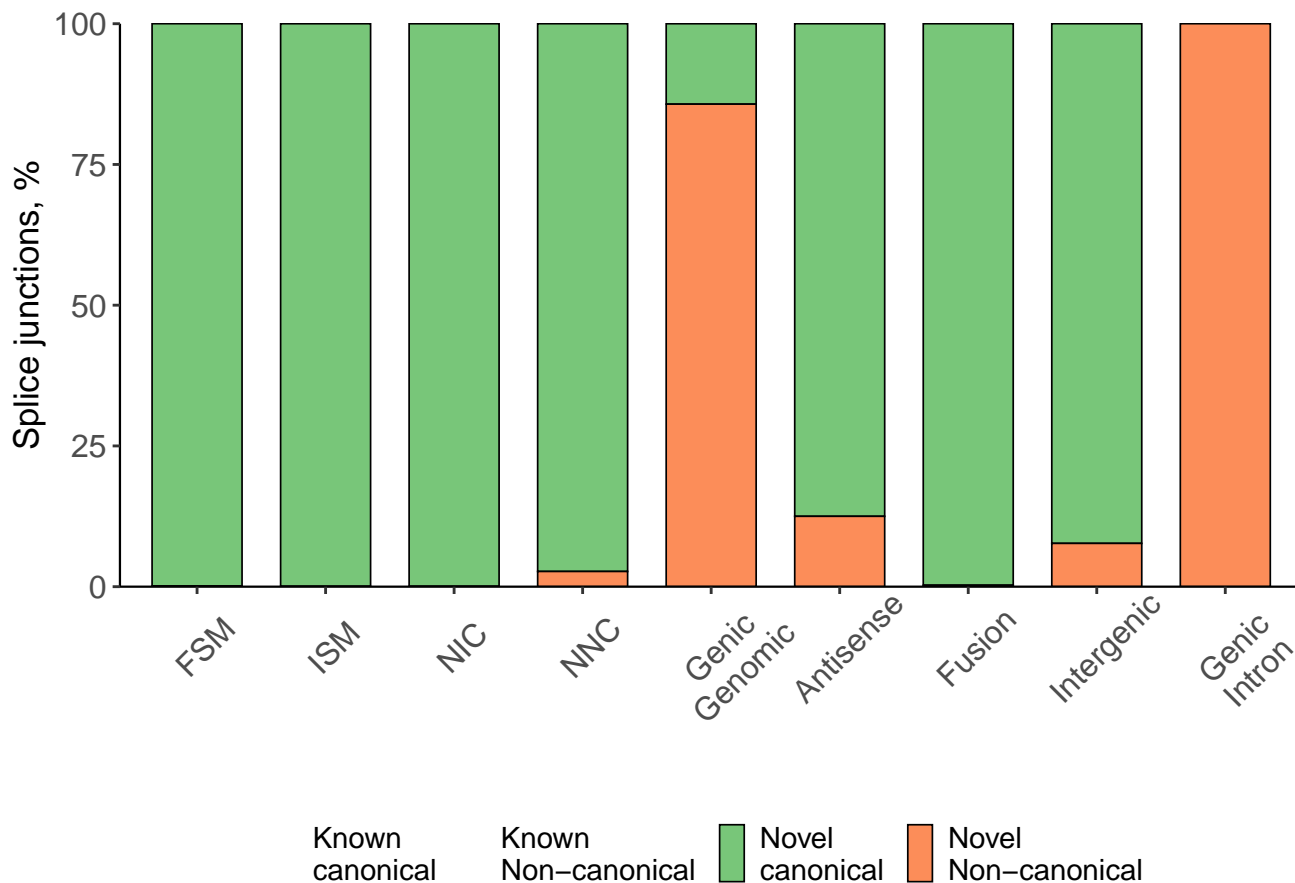


Gene Expression of NNC And Not NNC Containing Genes

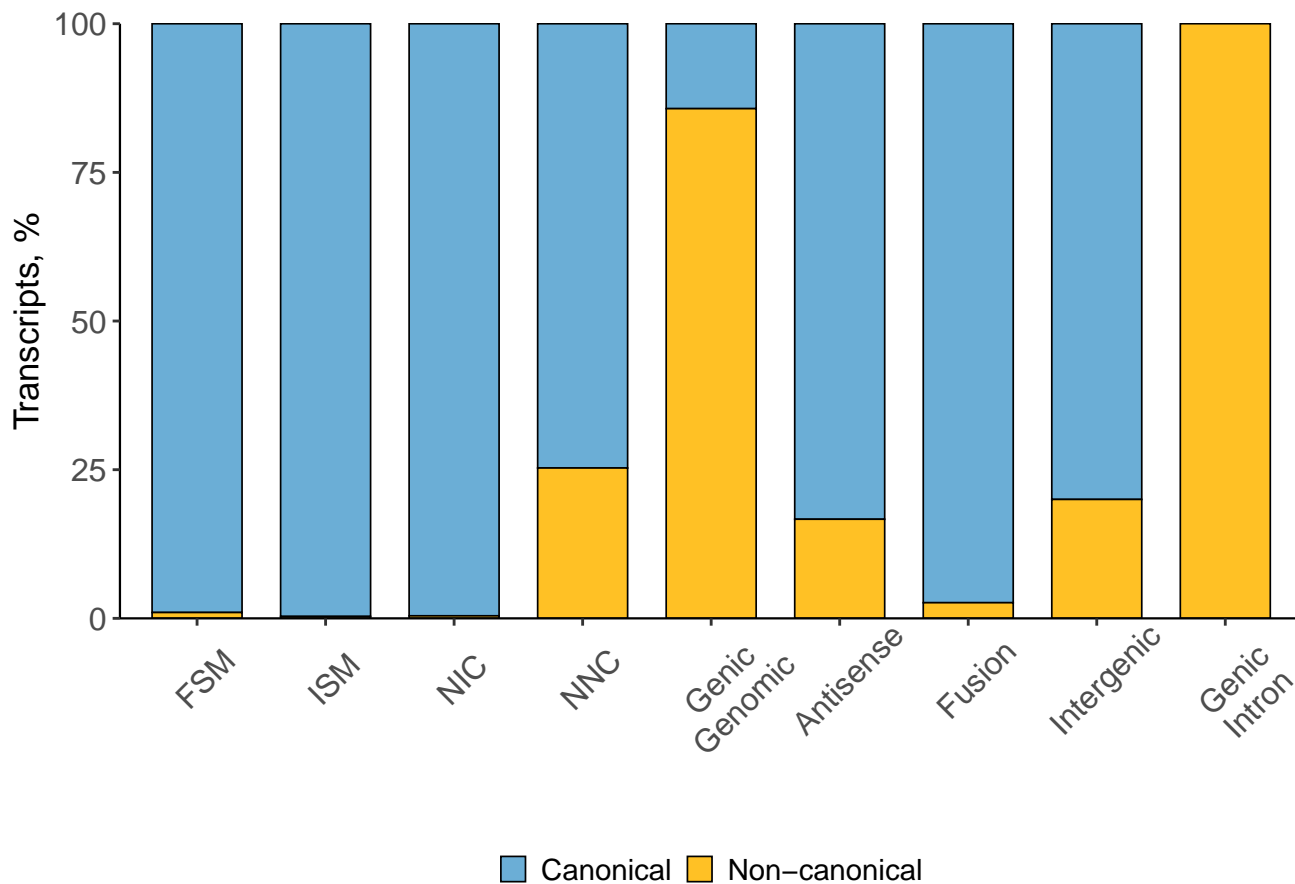


Splice Junction Characterization

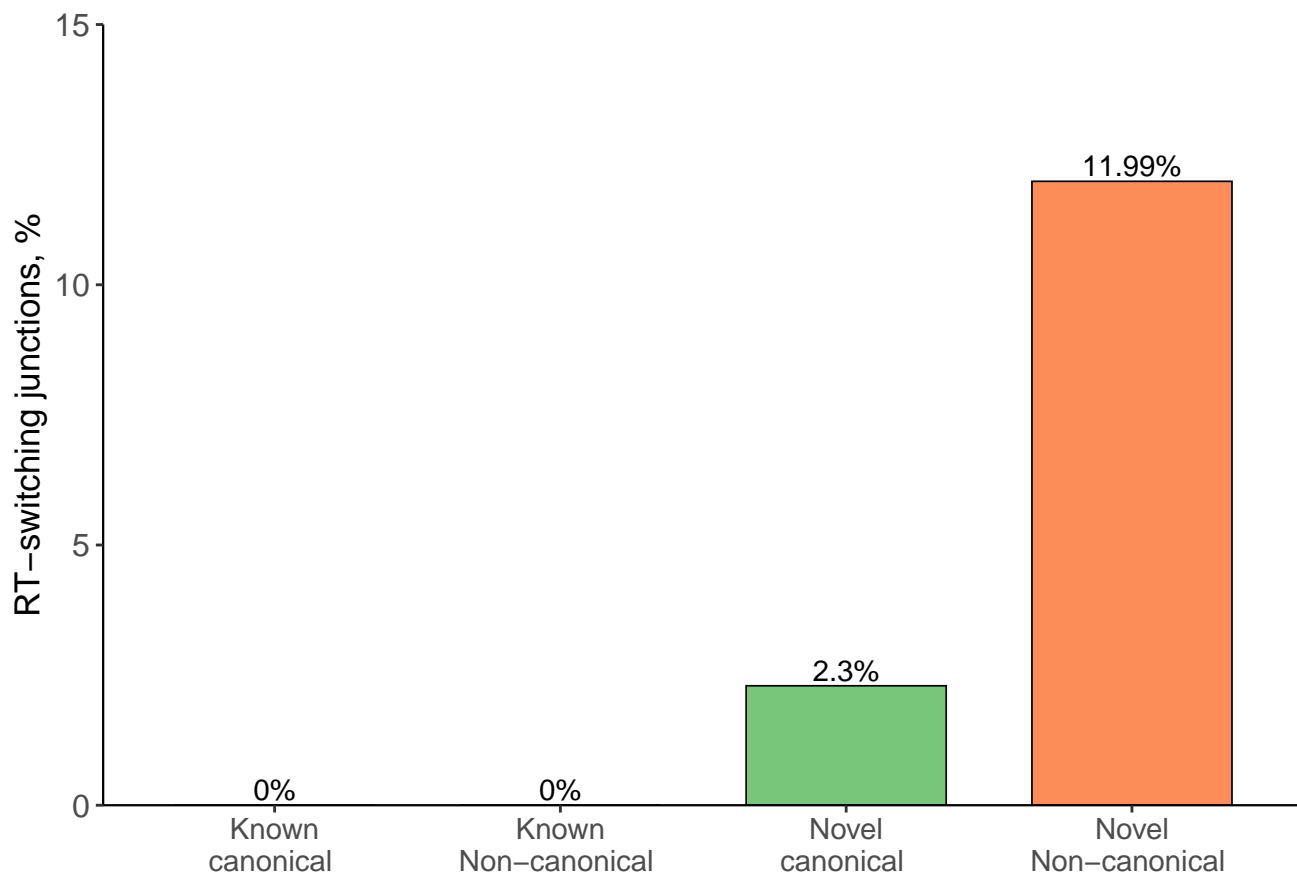
Distribution of Splice Junctions by Structural Classification



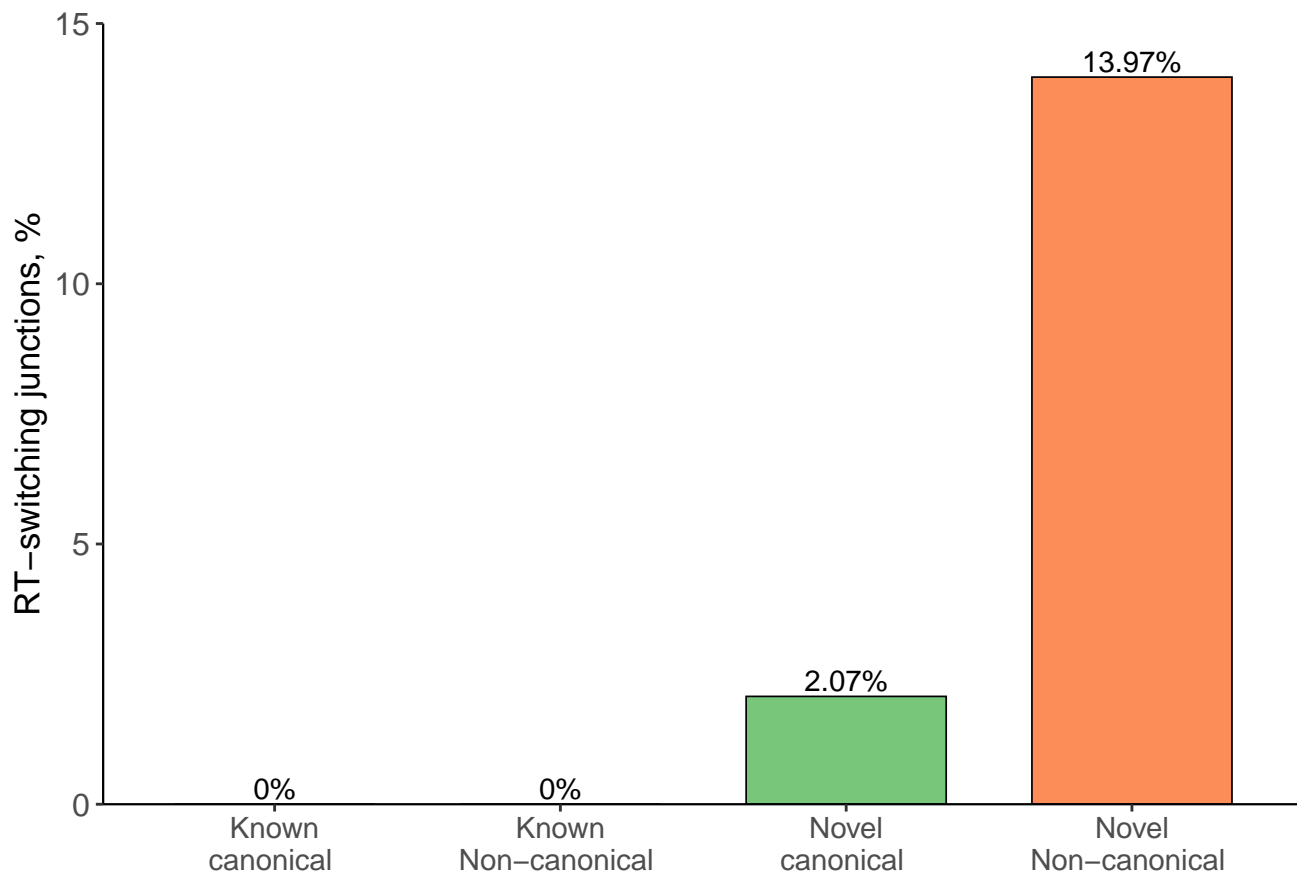
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



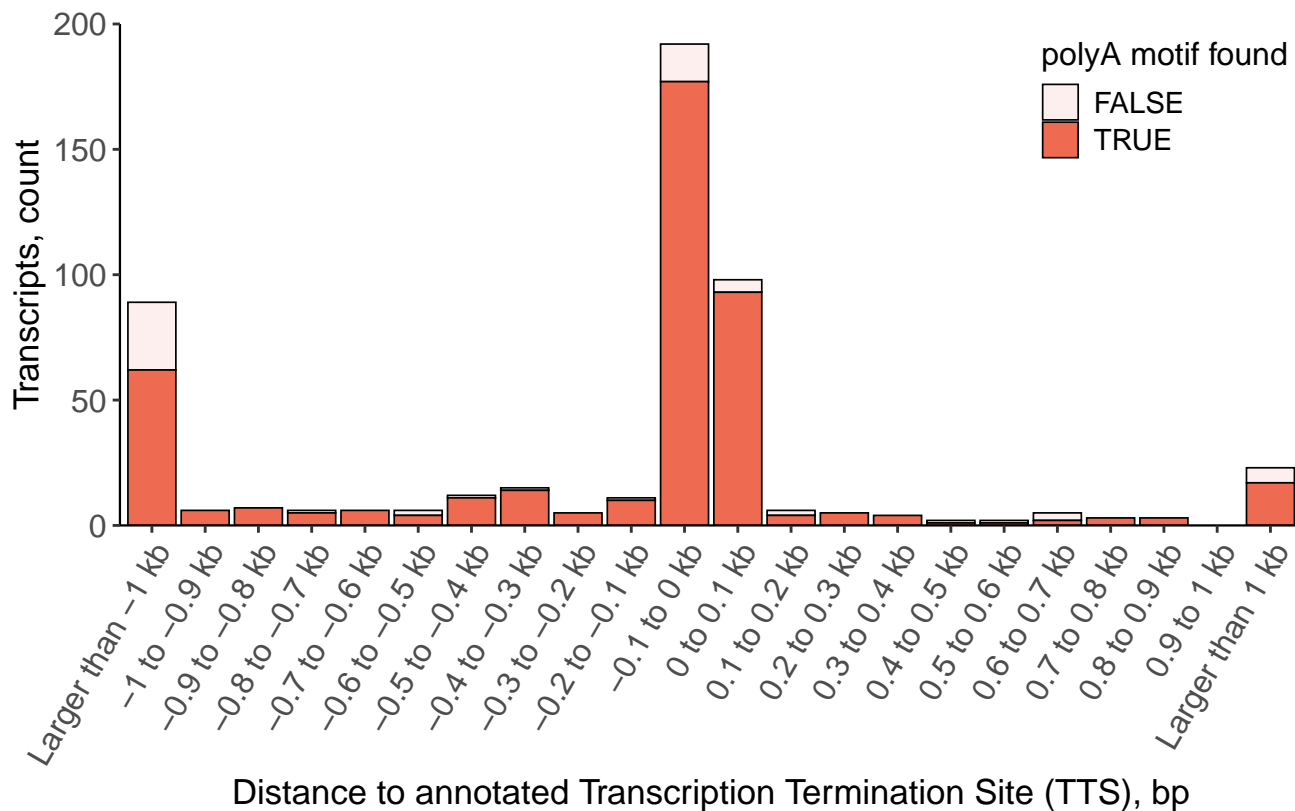
Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

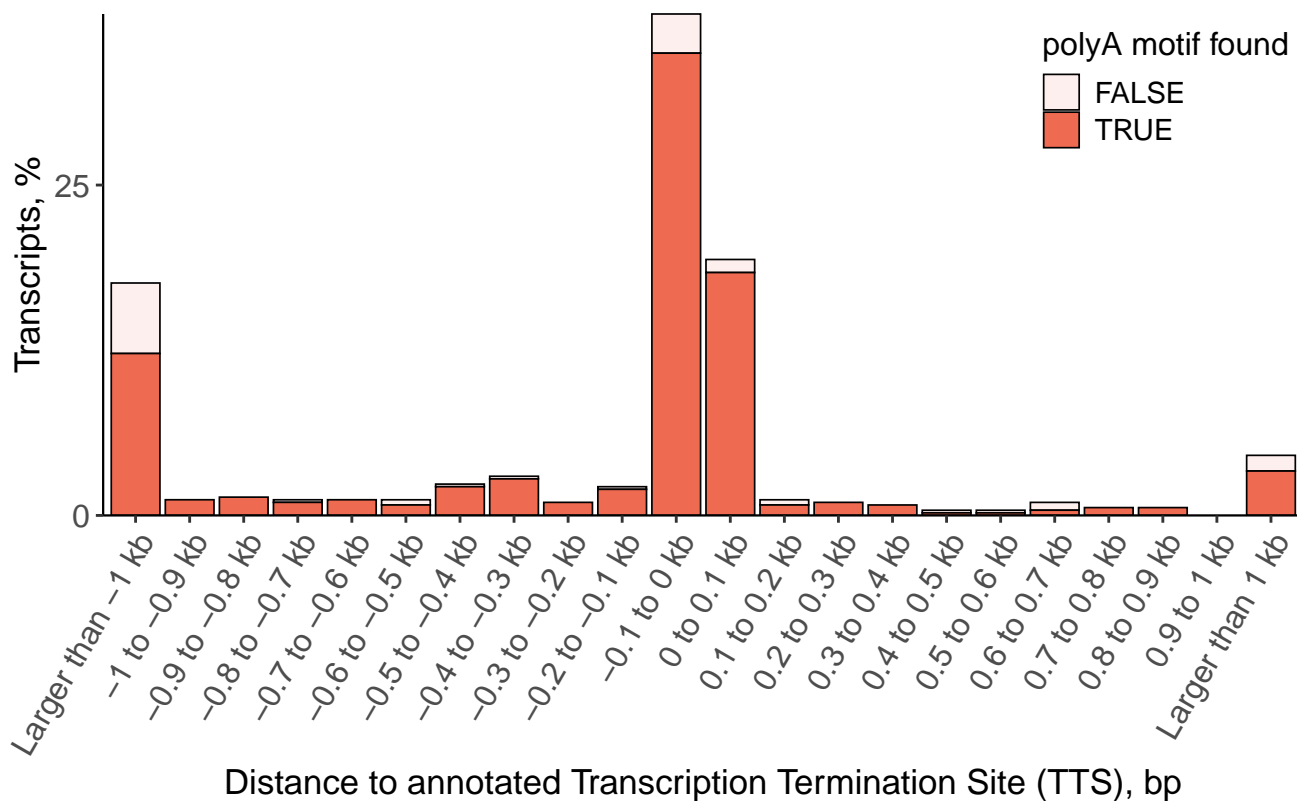
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



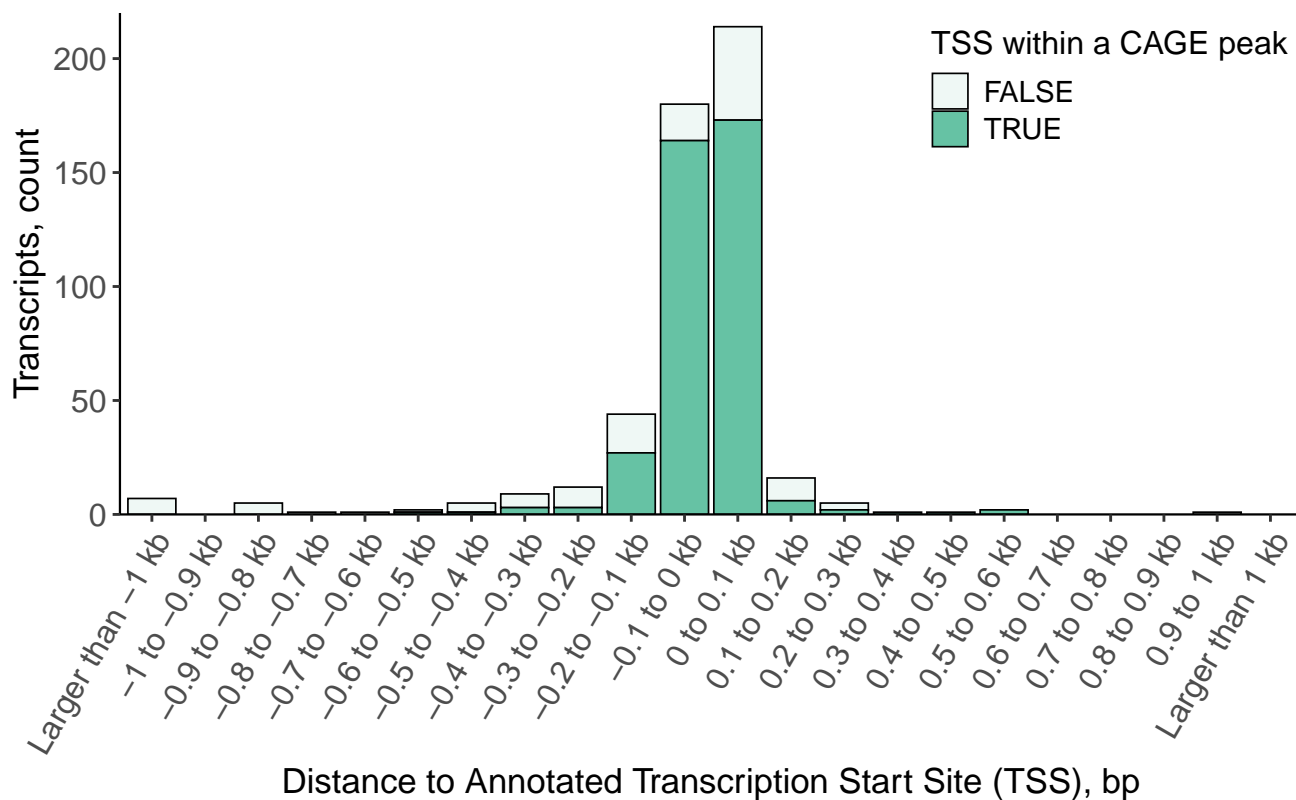
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



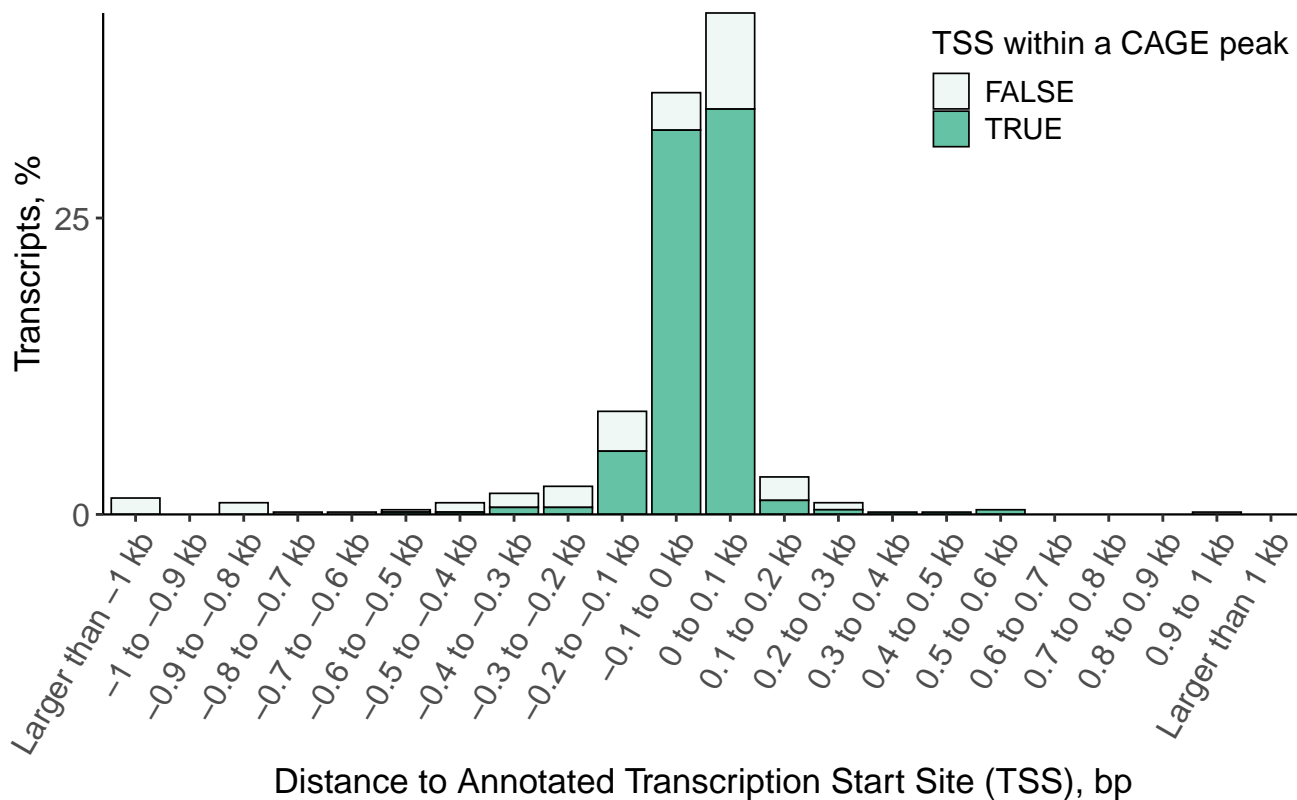
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



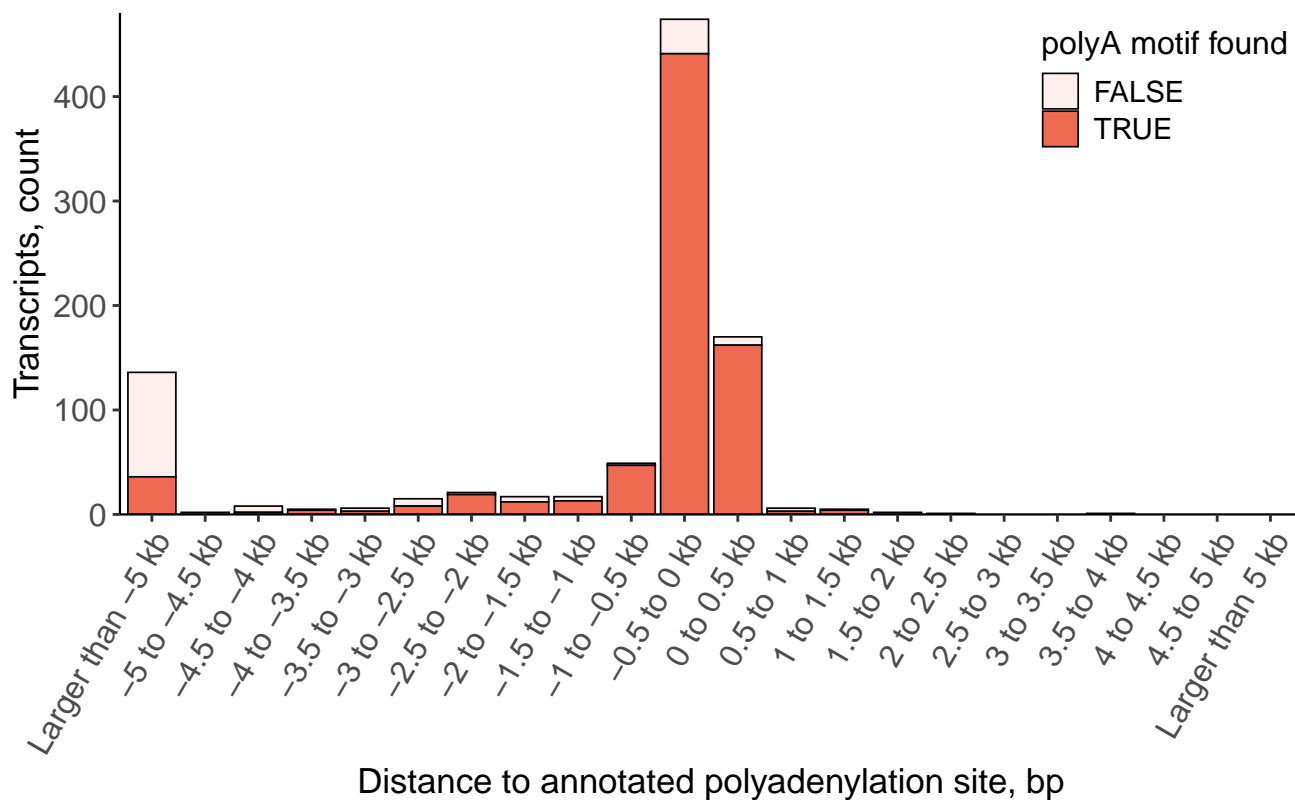
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



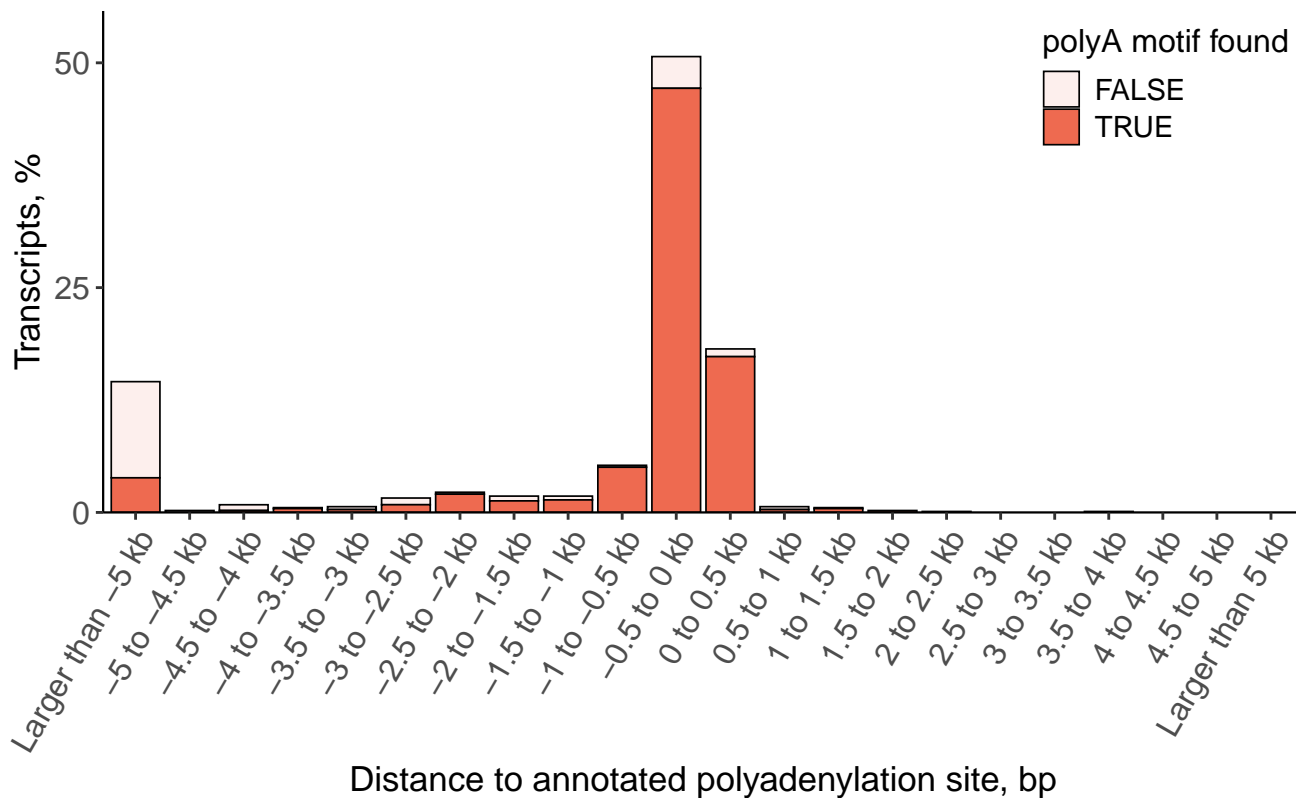
Distance to Annotated Transcription Termination Site (TTS)

Negative values indicate upstream of annotated TTS



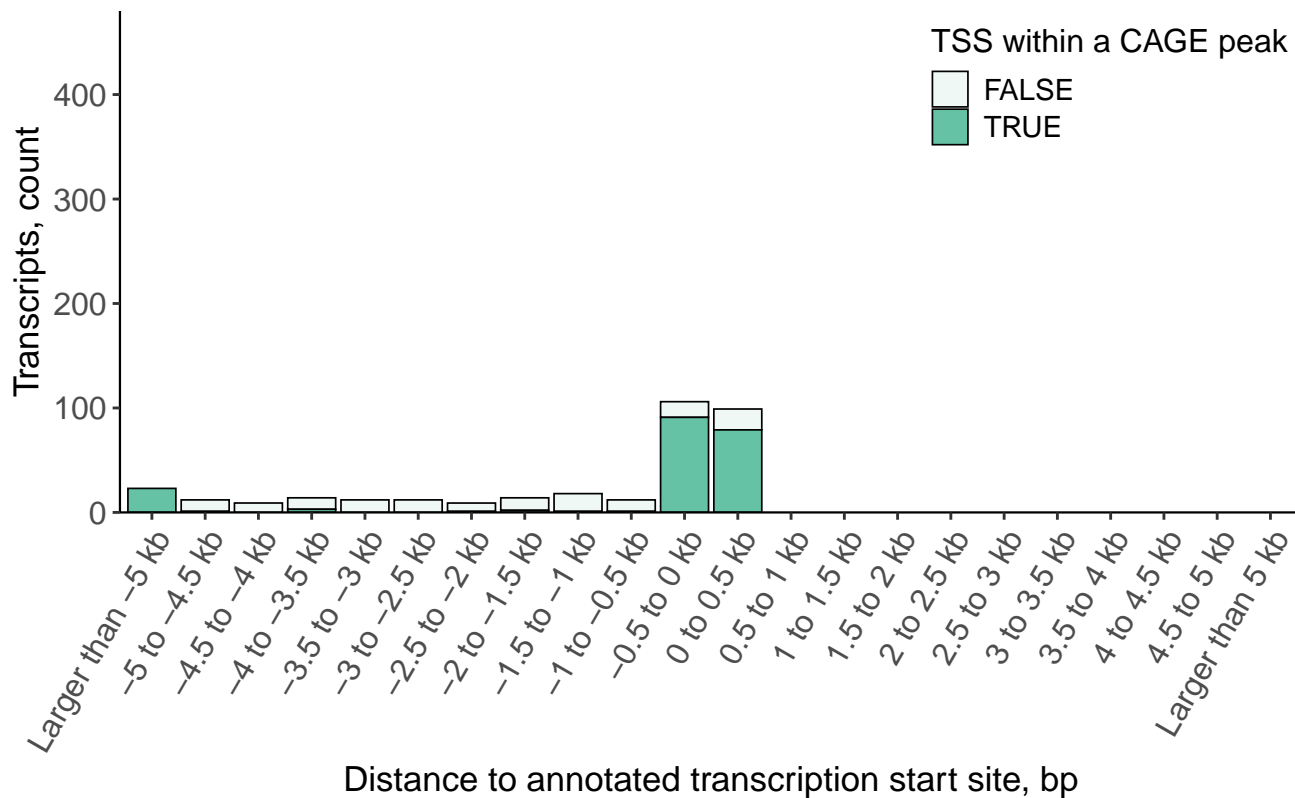
Distance to Annotated Transcription Termination Site (TTS)

Negative values indicate upstream of annotated TTS



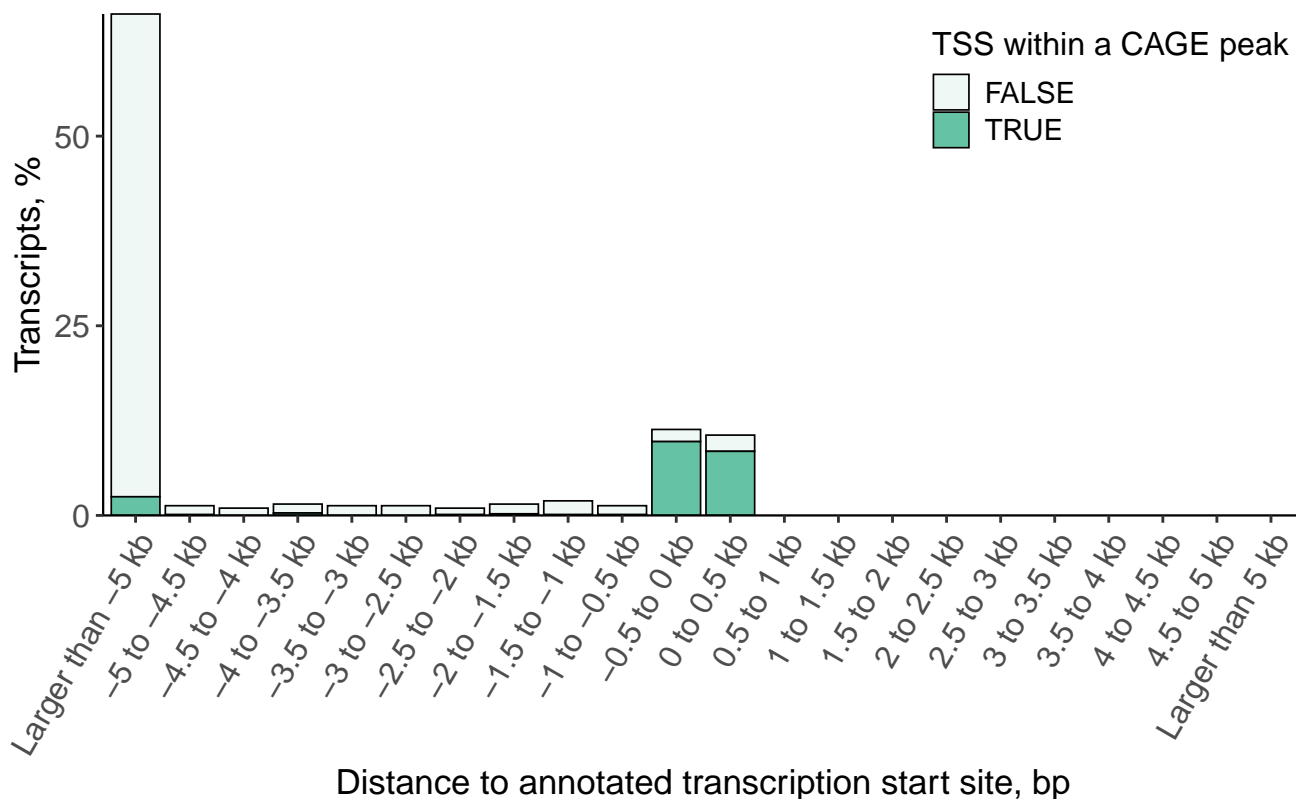
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

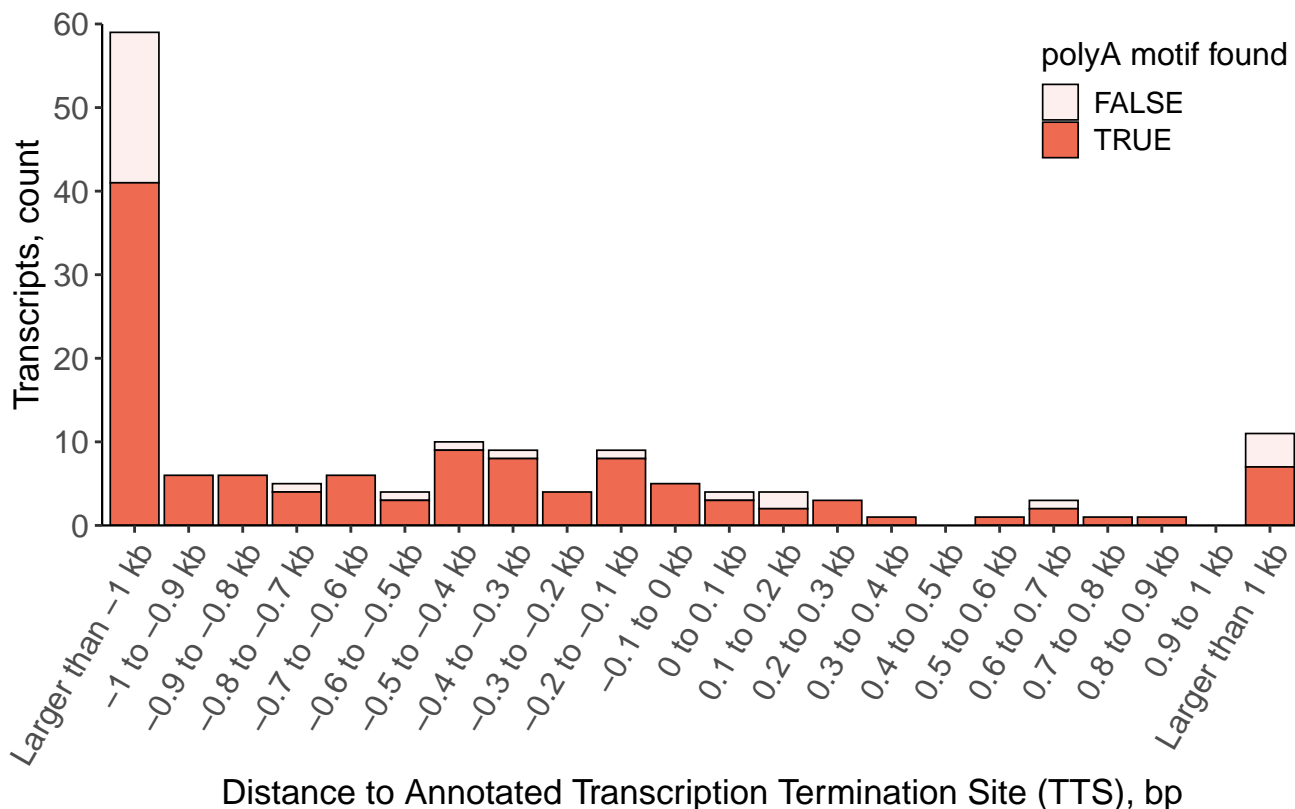
Negative values indicate downstream of annotated TSS



*Comparison With Annotated TSS and TTS
by Subcategories*

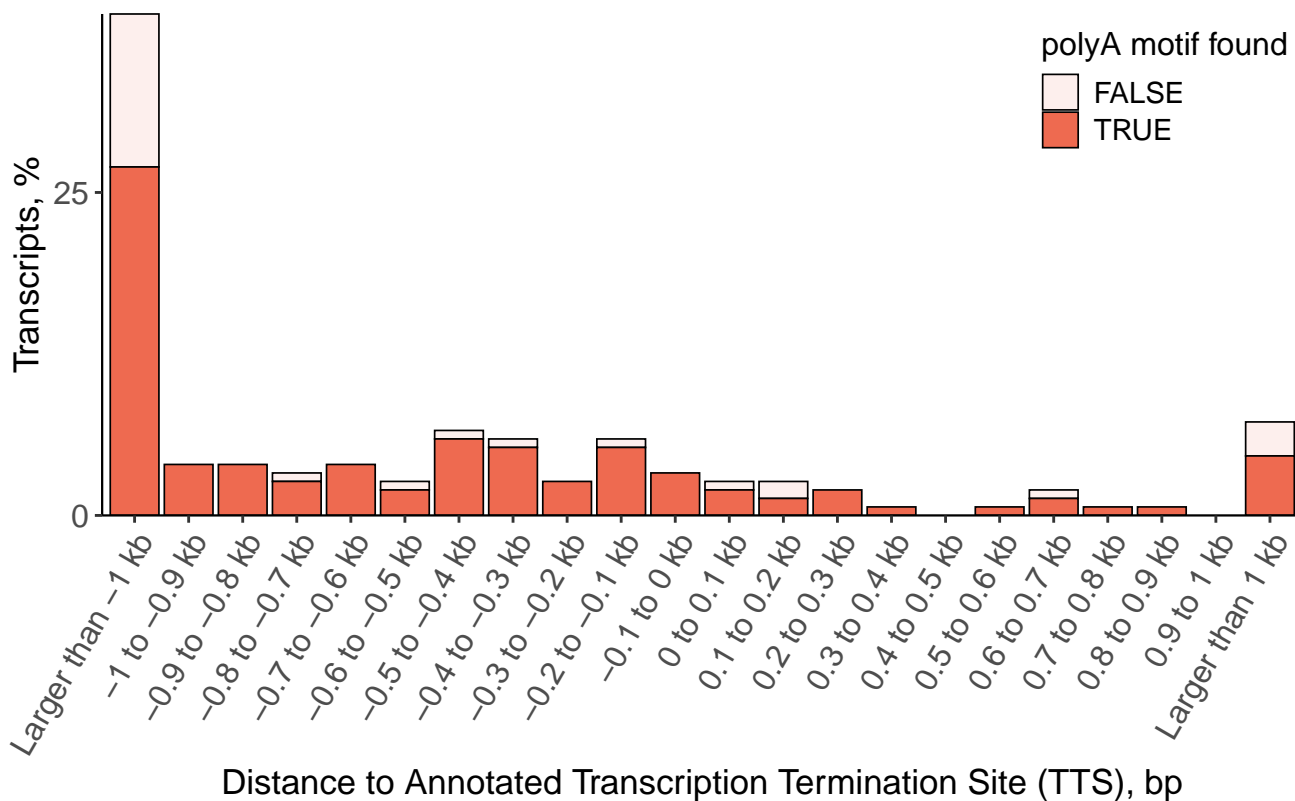
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



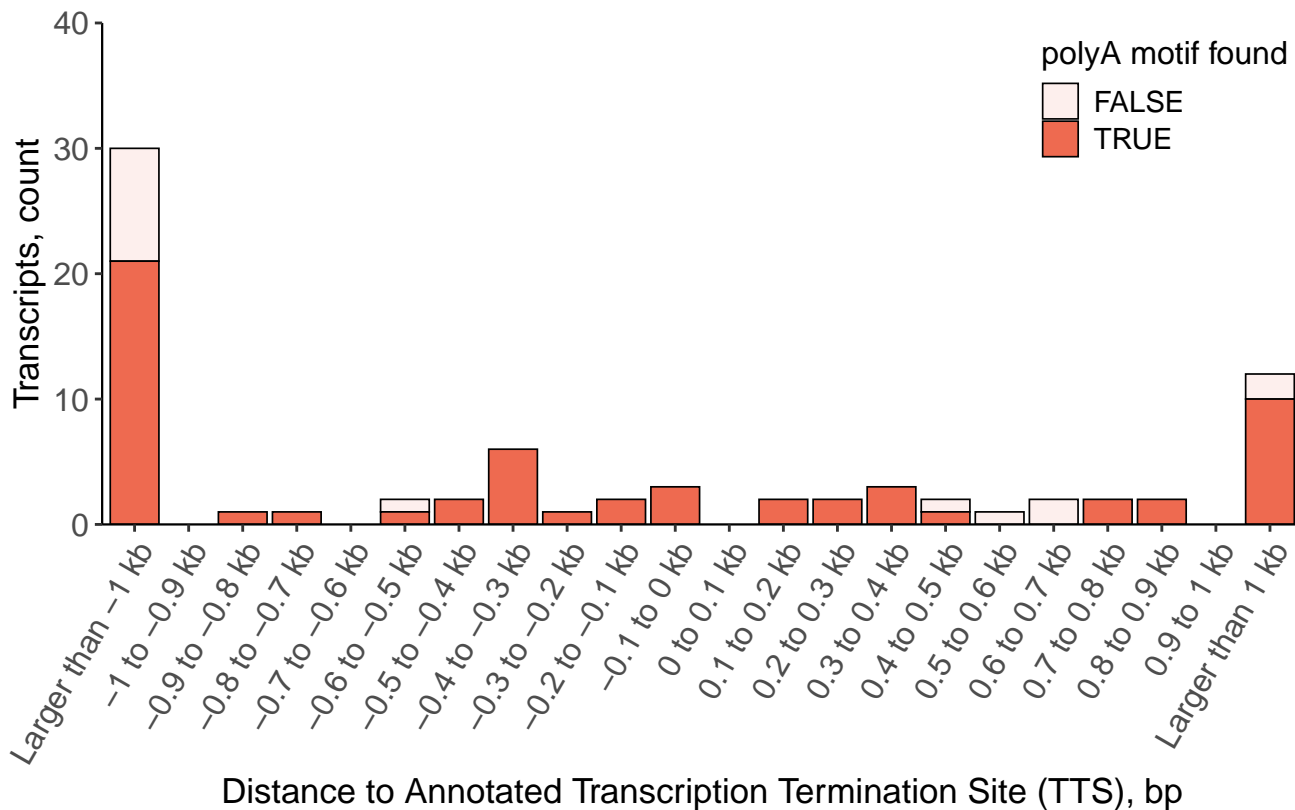
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



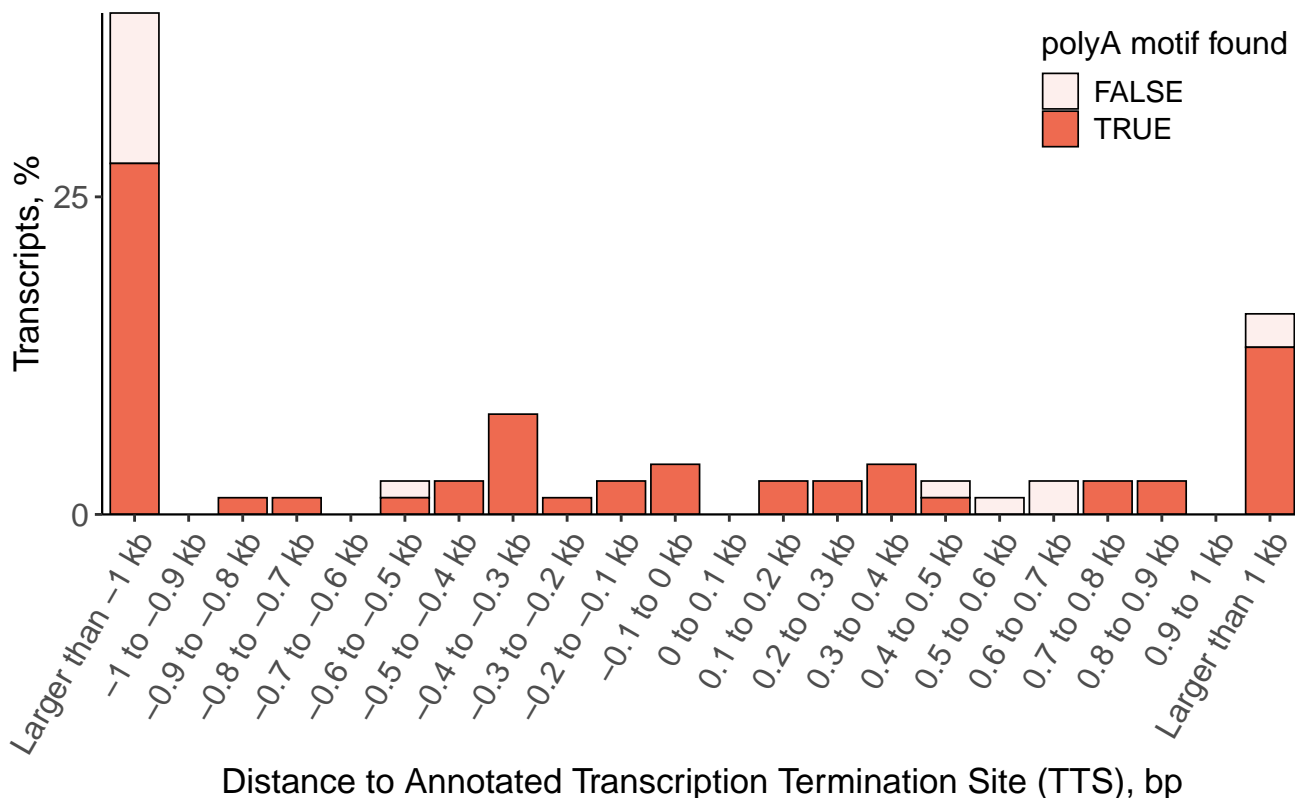
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



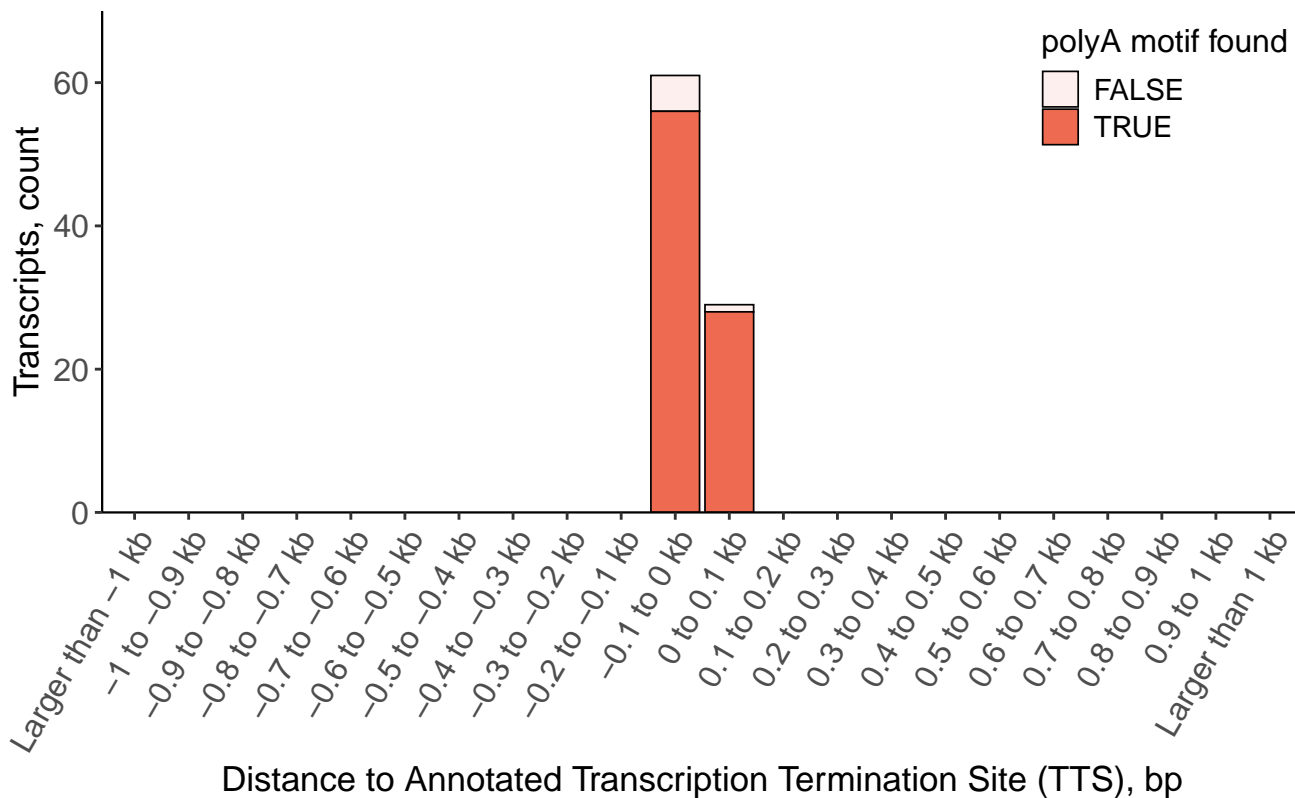
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



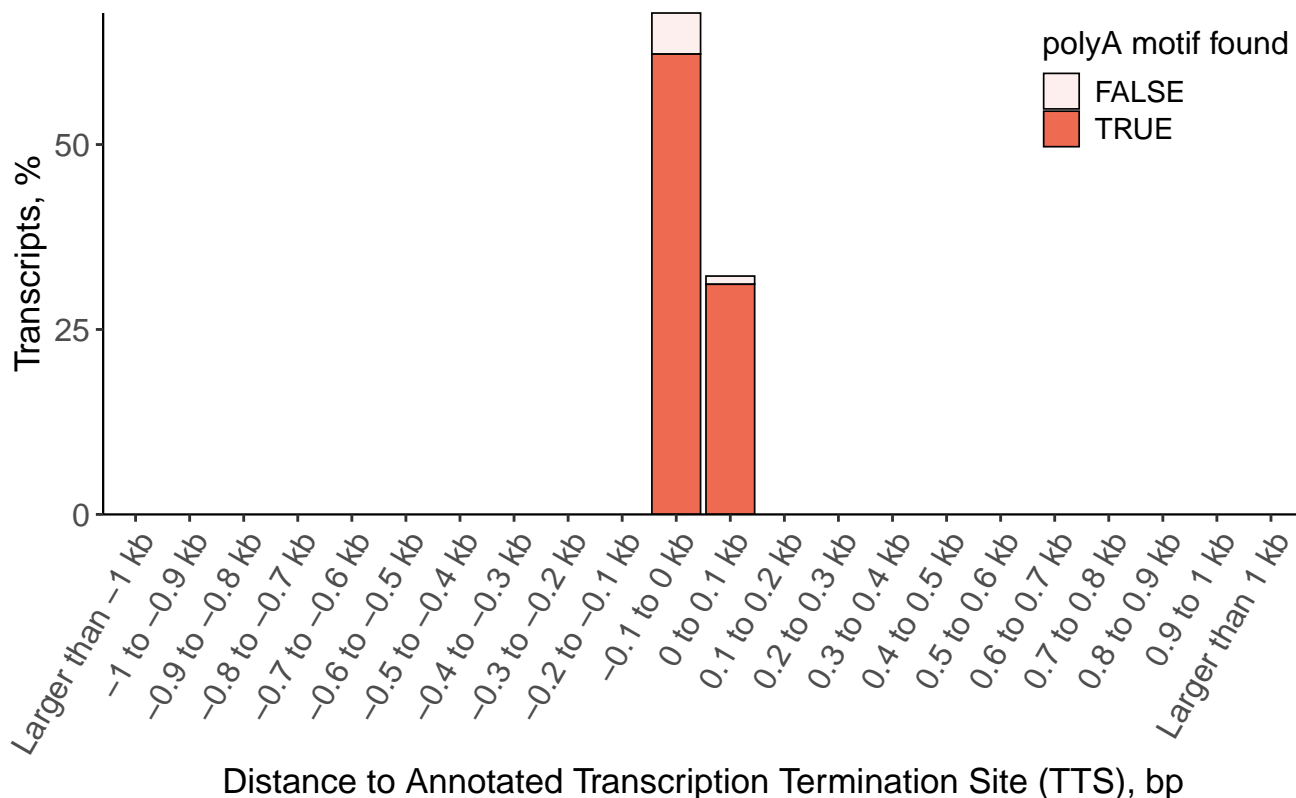
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



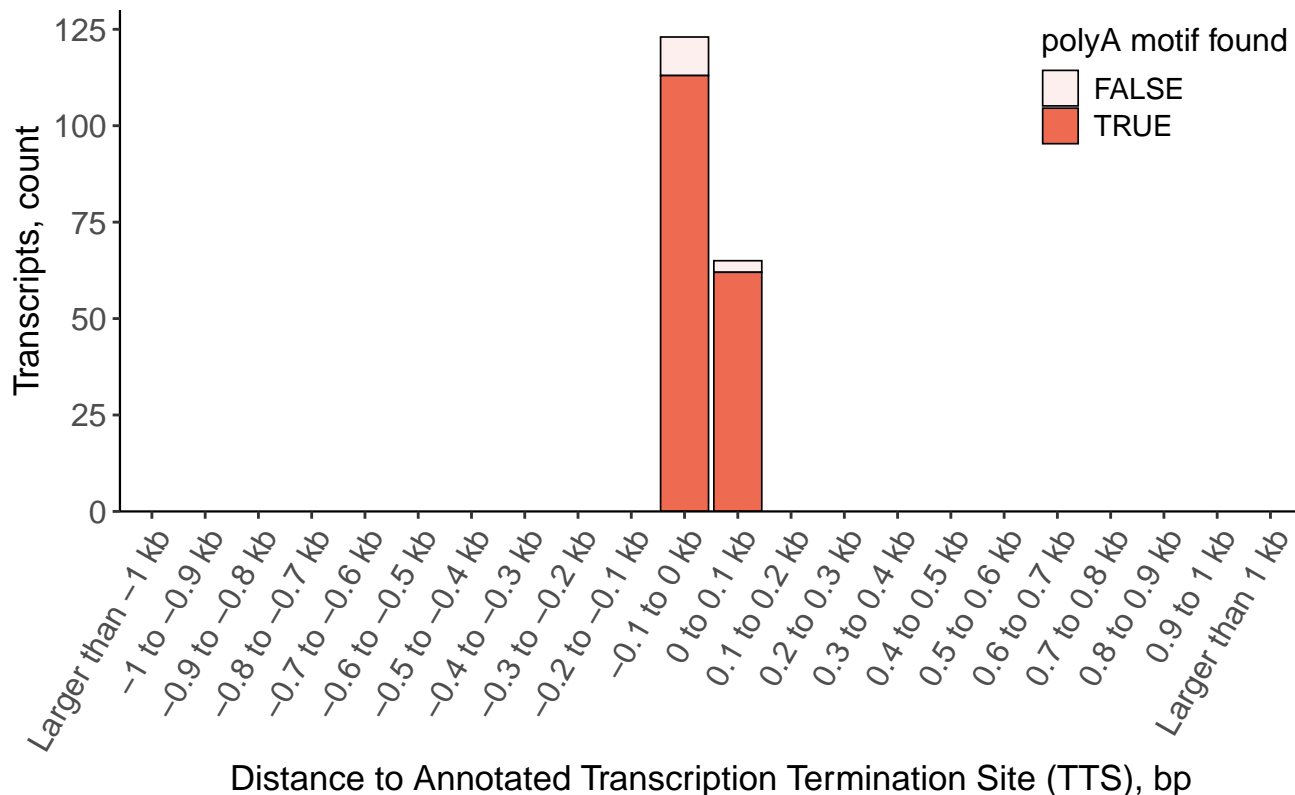
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



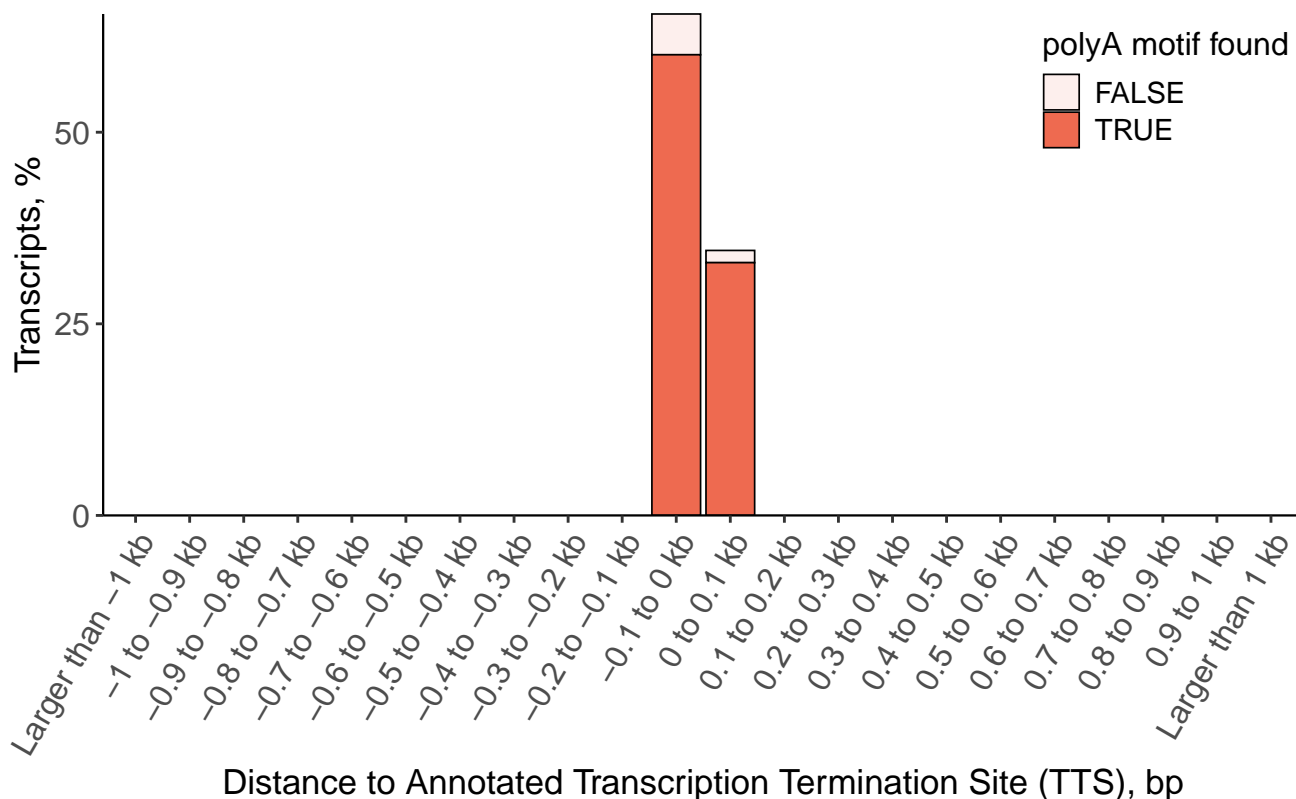
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



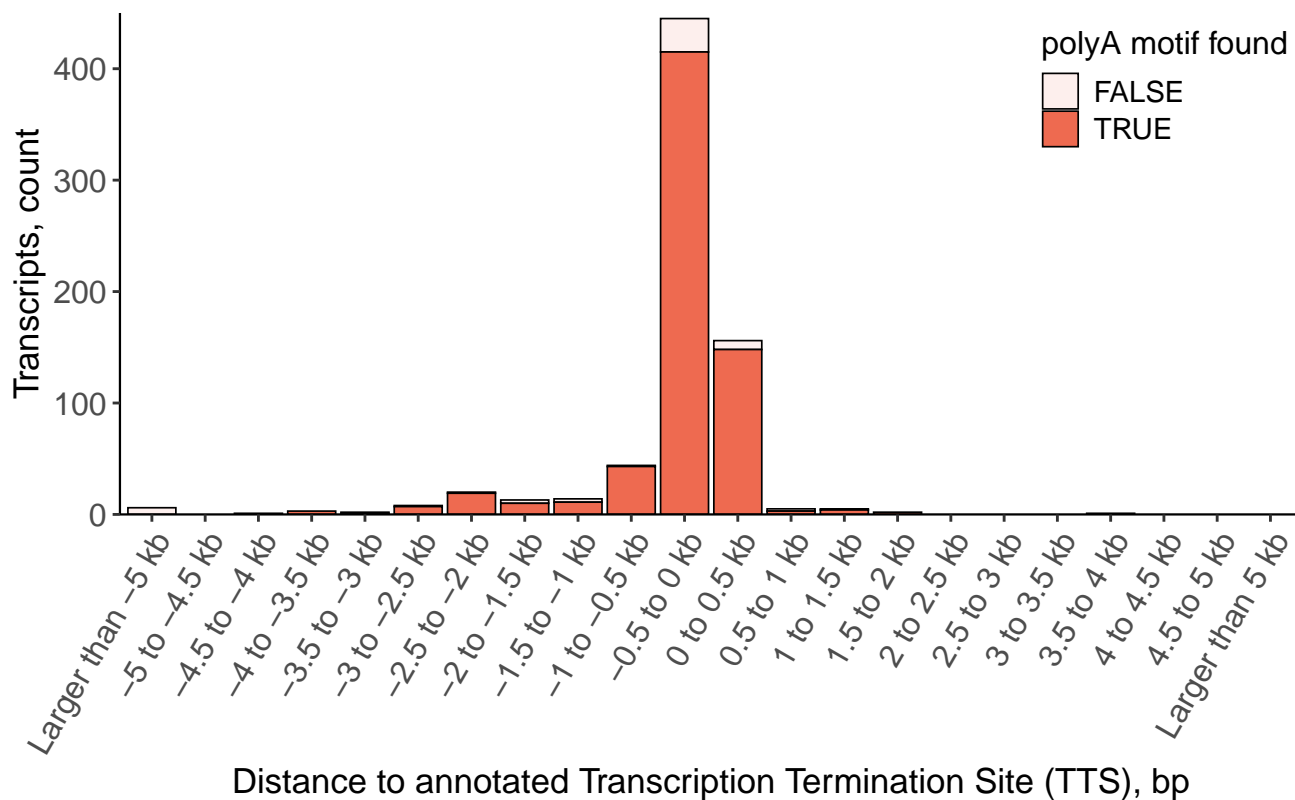
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



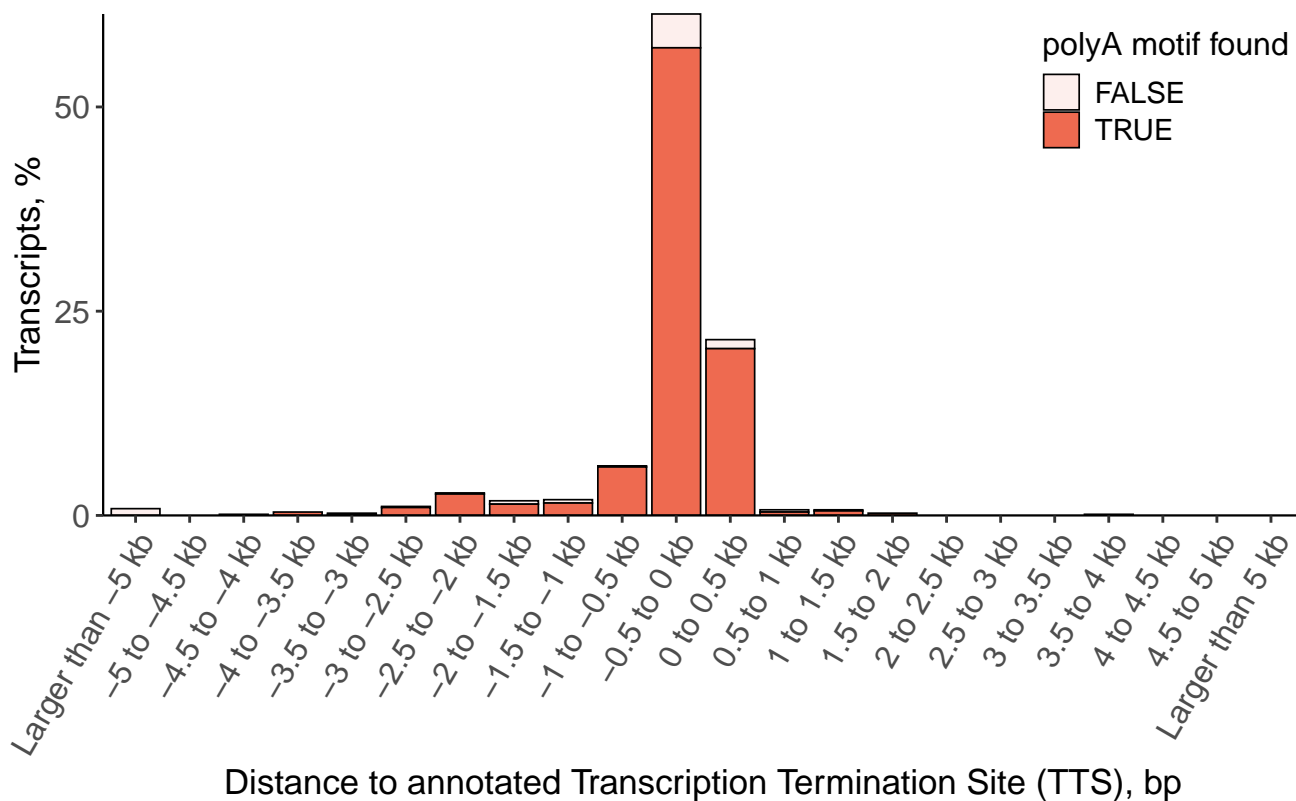
Distance to Annotated Transcription Termination Site for ISM 3' Fragment

Negative values indicate upstream of annotated TTS



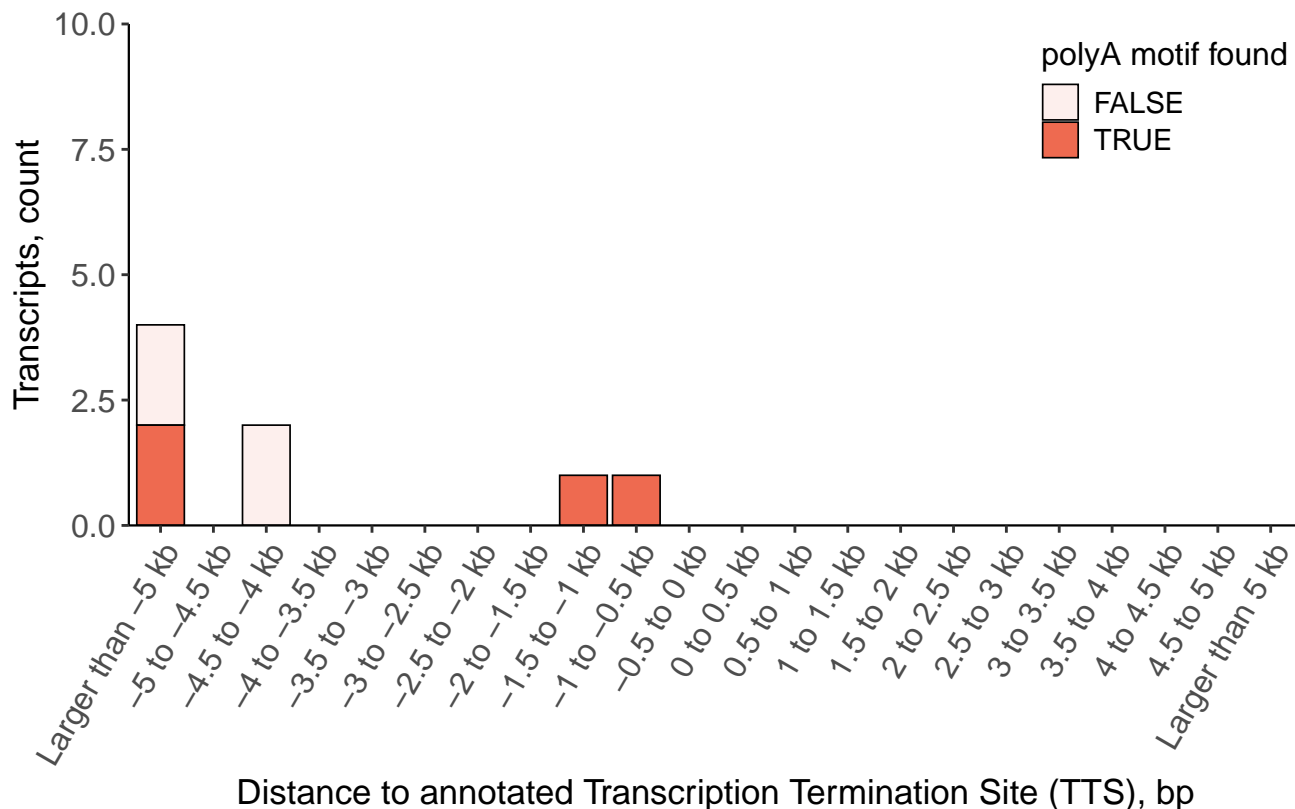
Distance to Annotated Transcription Termination Site for ISM 3' Fragment

Negative values indicate upstream of annotated TTS



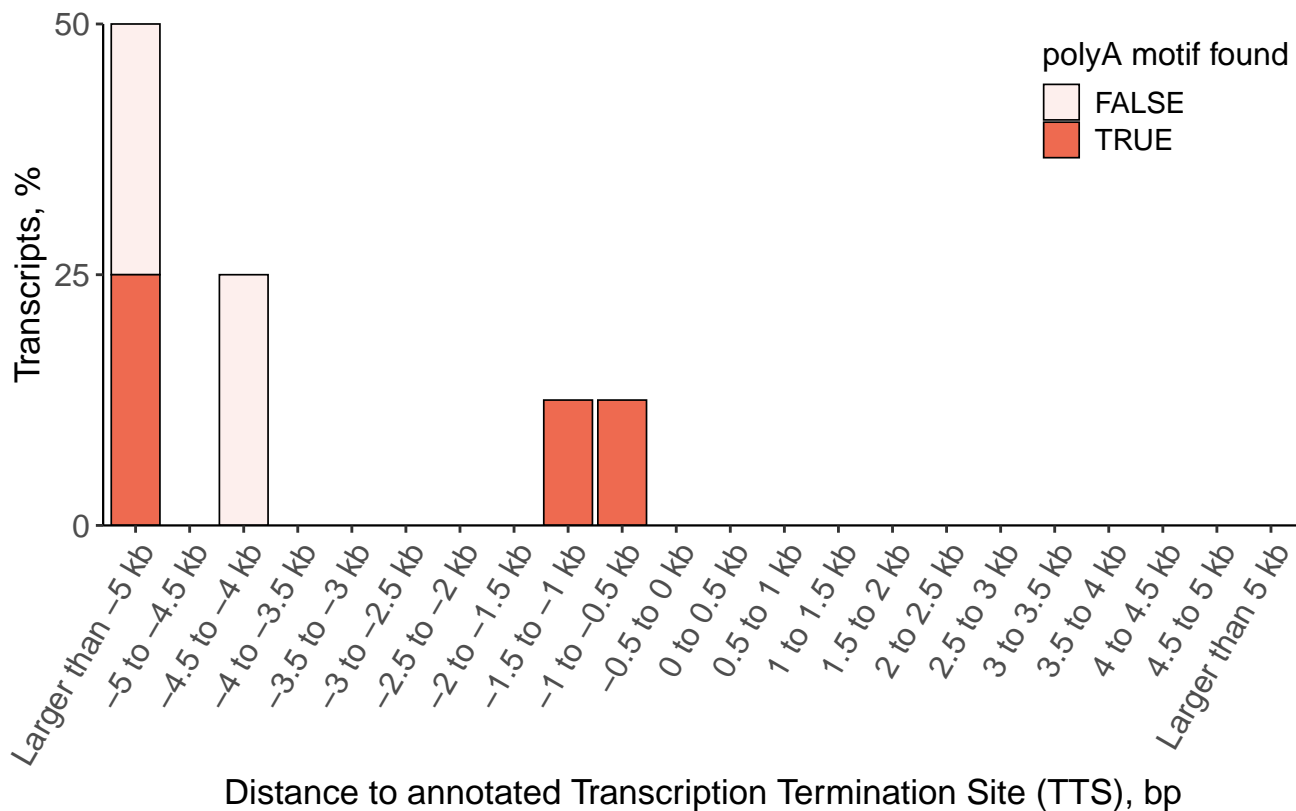
Distance to Annotated Transcription Termination Site for ISM Internal Fragment

Negative values indicate upstream of annotated TTS



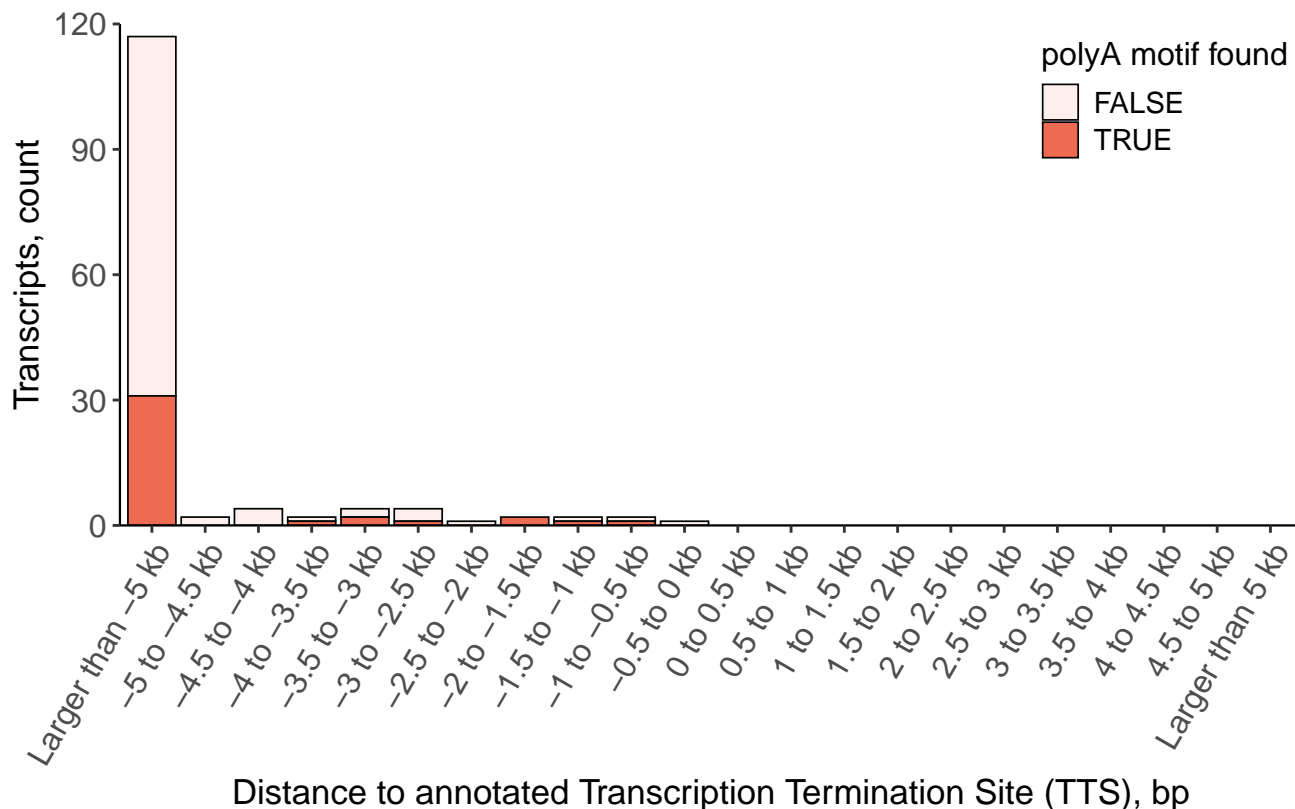
Distance to Annotated Transcription Termination Site for ISM Internal Fragment

Negative values indicate upstream of annotated TTS



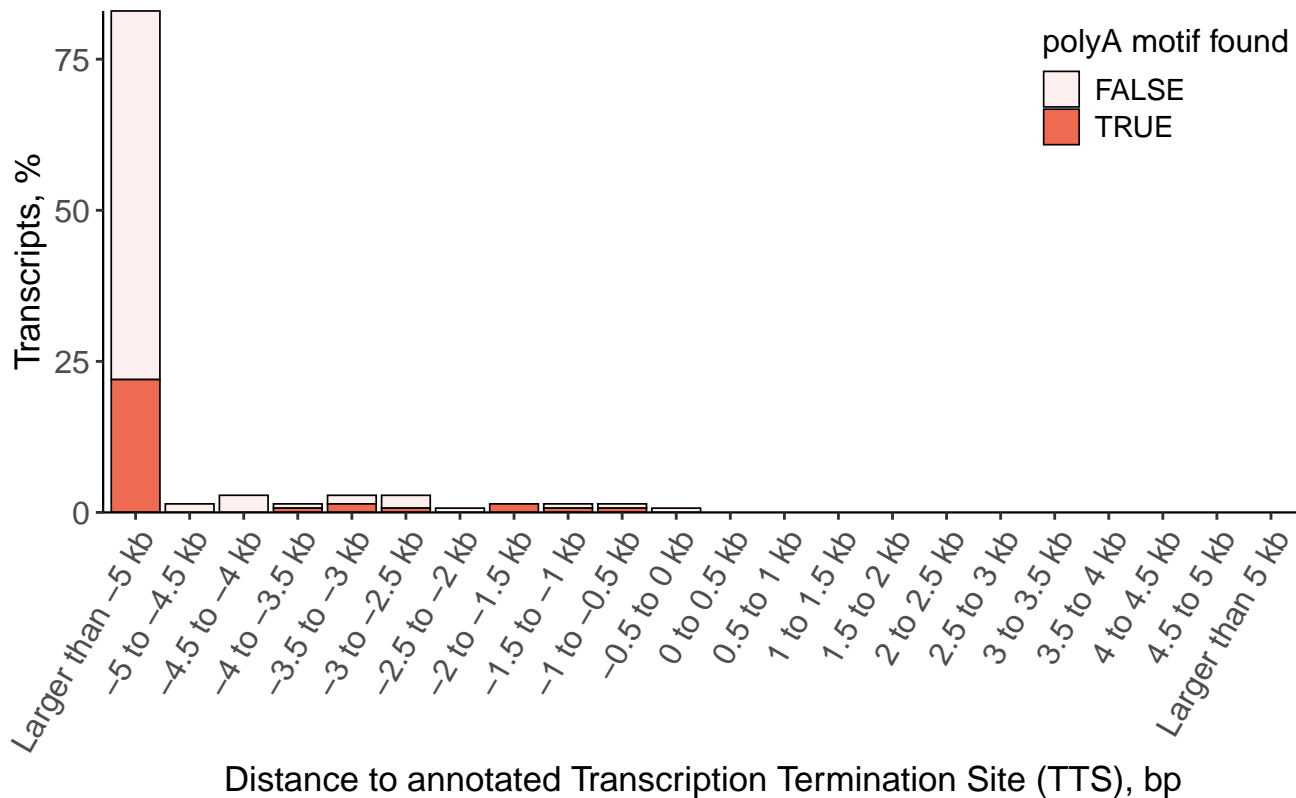
Distance to Annotated Transcription Termination Site for ISM A5' Fragment

Negative values indicate upstream of annotated TTS



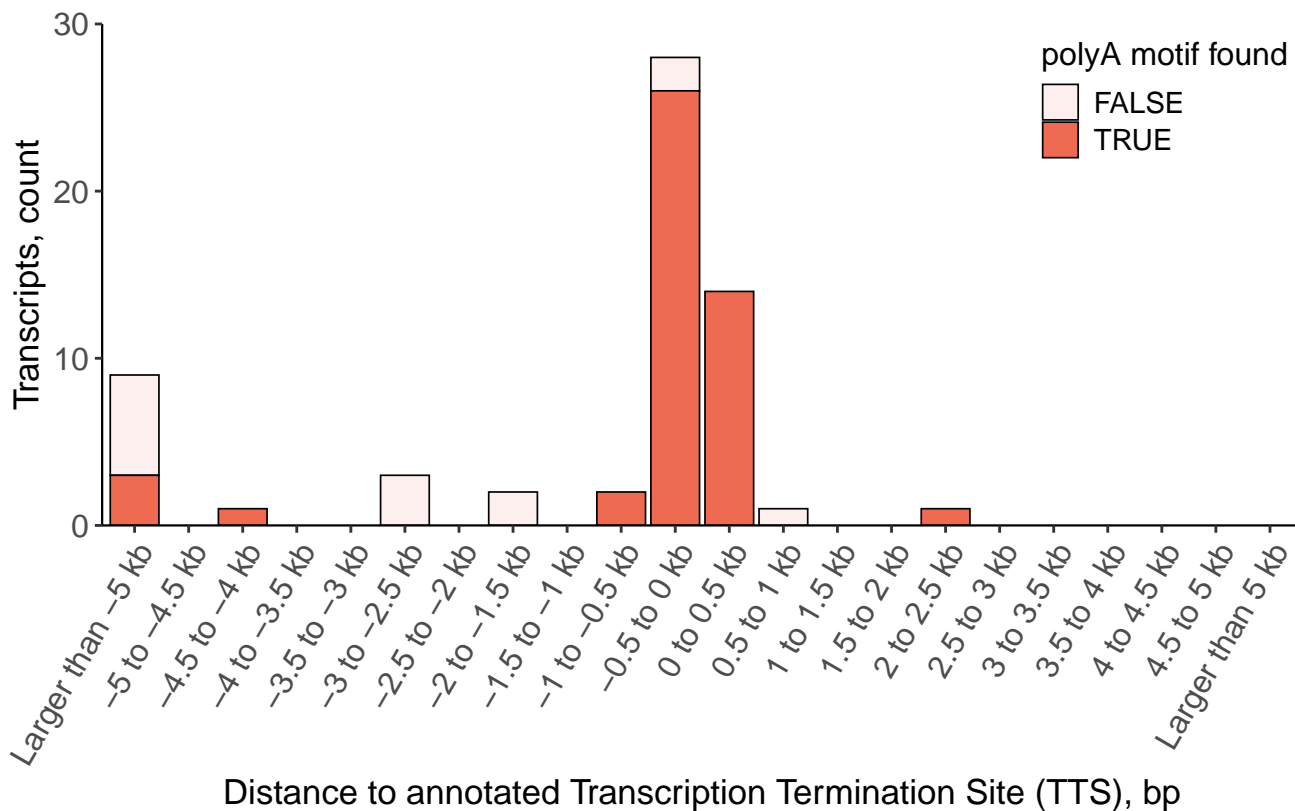
Distance to Annotated Transcription Termination Site for ISM A5' Fragment

Negative values indicate upstream of annotated TTS



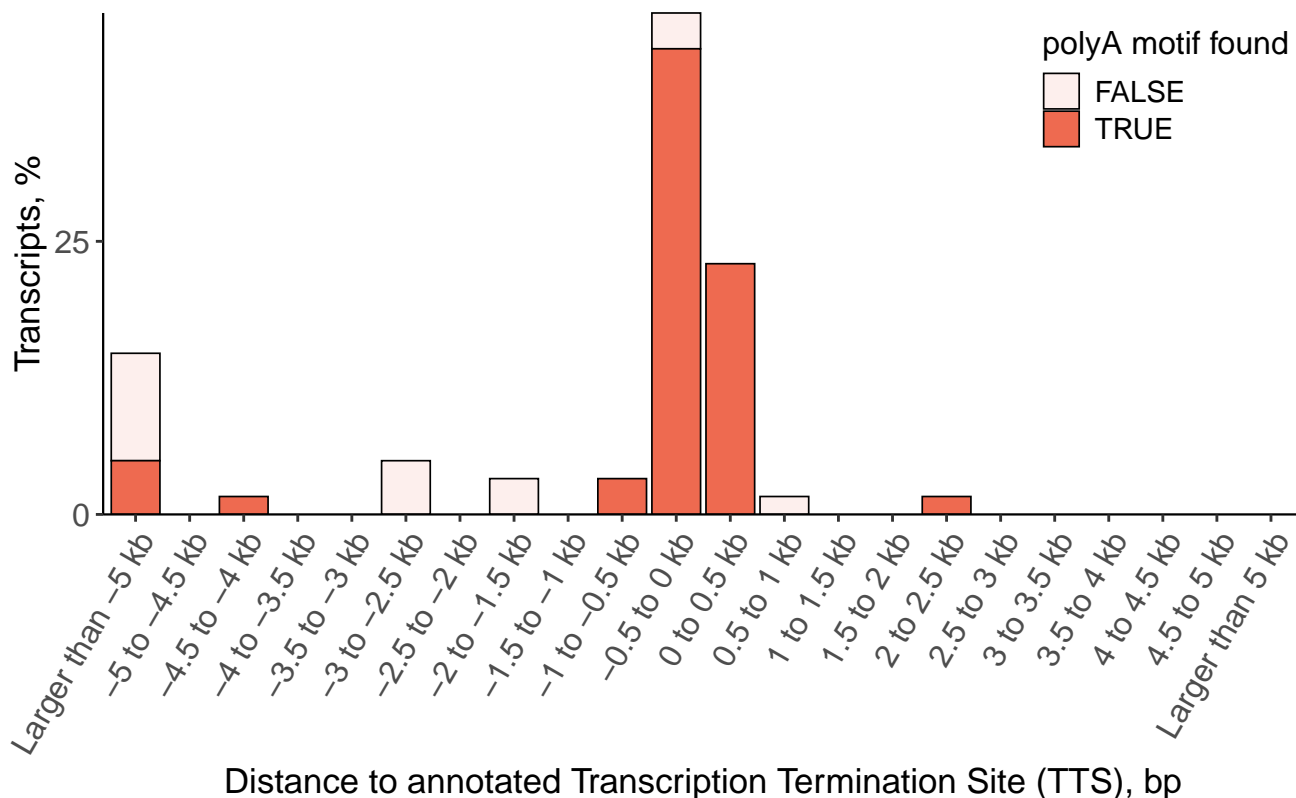
Distance to Annotated Transcription Termination Site for ISM Intron Retention

Negative values indicate upstream of annotated TTS



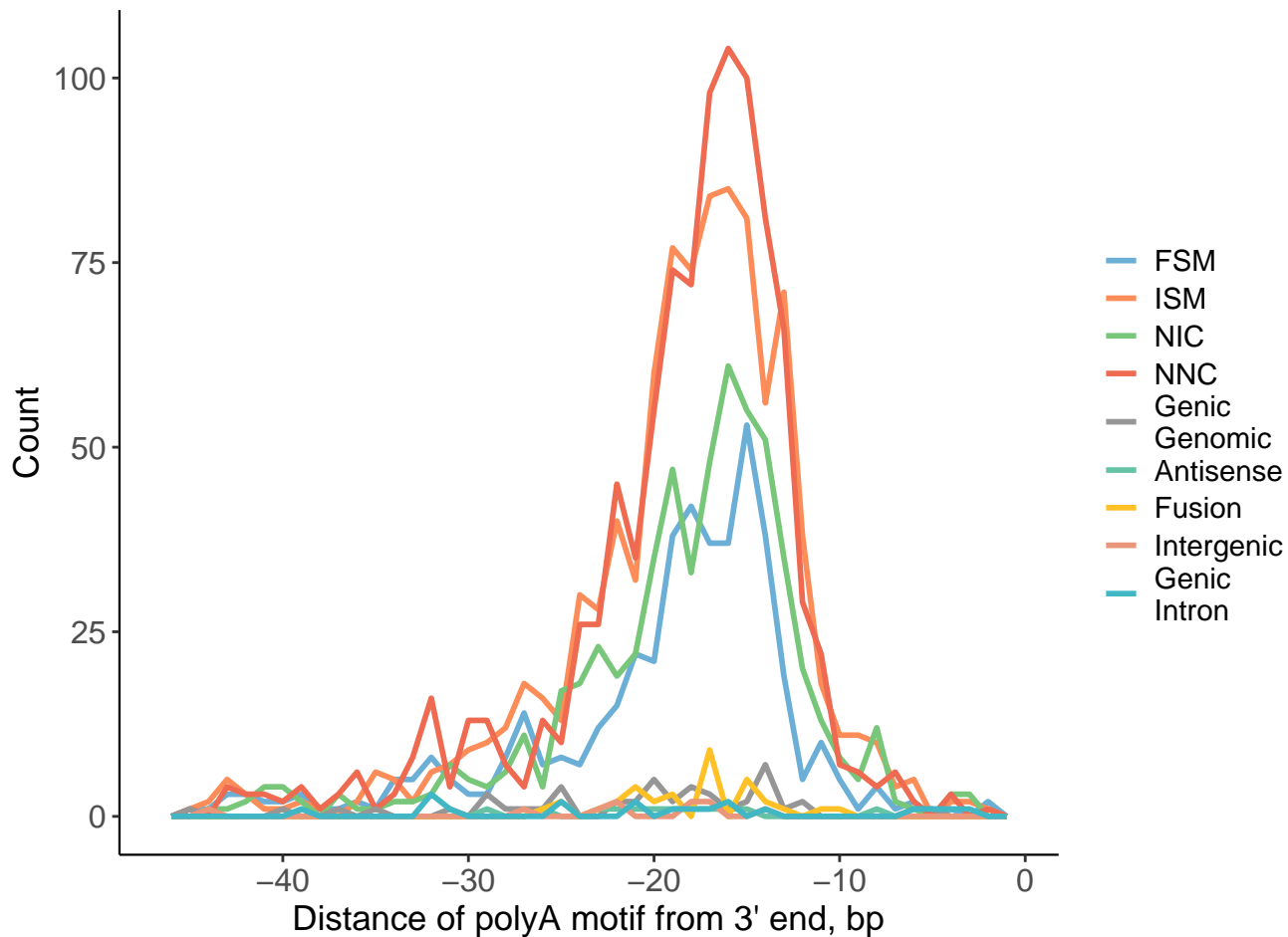
Distance to Annotated Transcription Termination Site for ISM Intron Retention

Negative values indicate upstream of annotated TTS



PolyA Distance Analysis

Distance of Detected PolyA Motif From 3' end



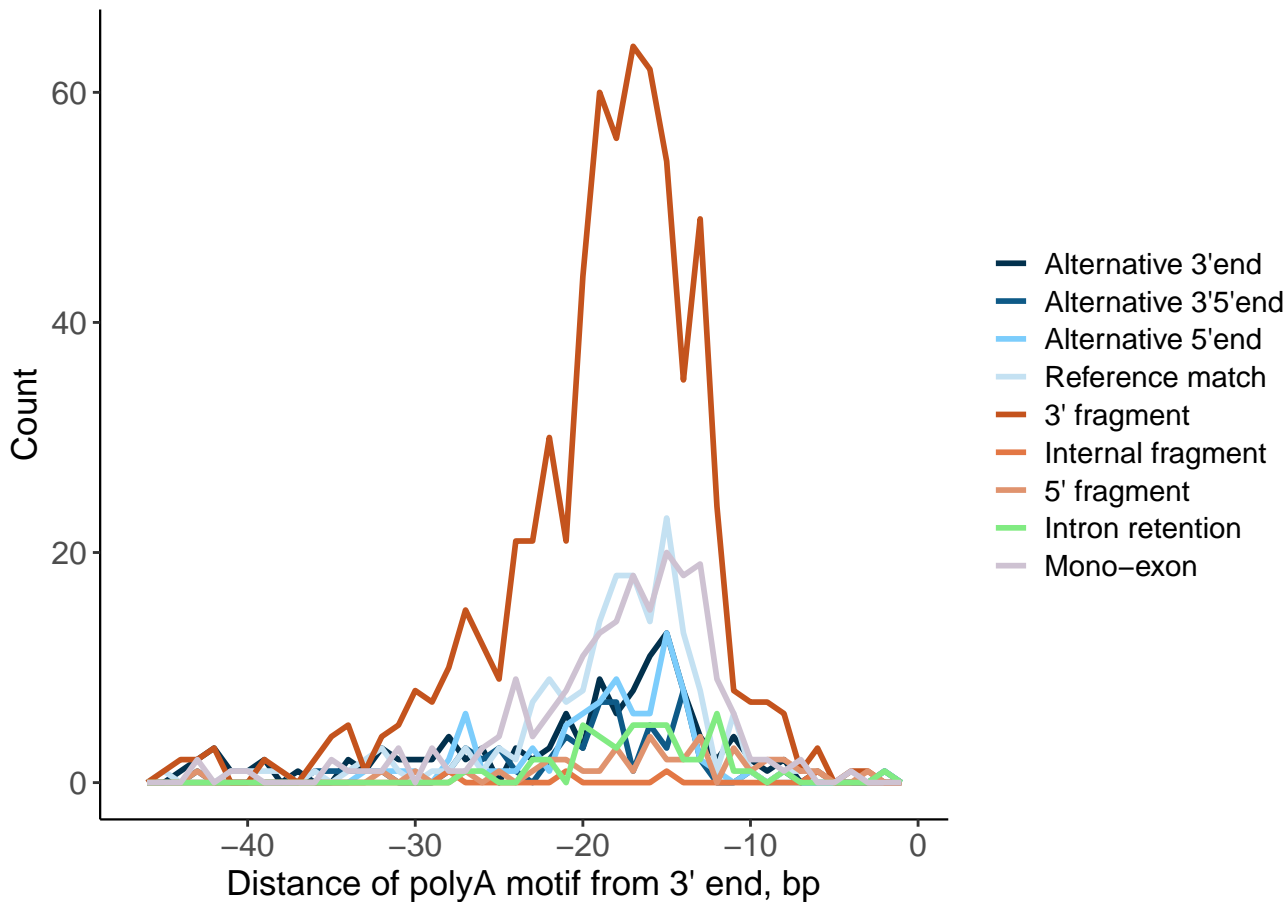
Frequency of PolyA Motifs

Number of polyA Motifs Detected

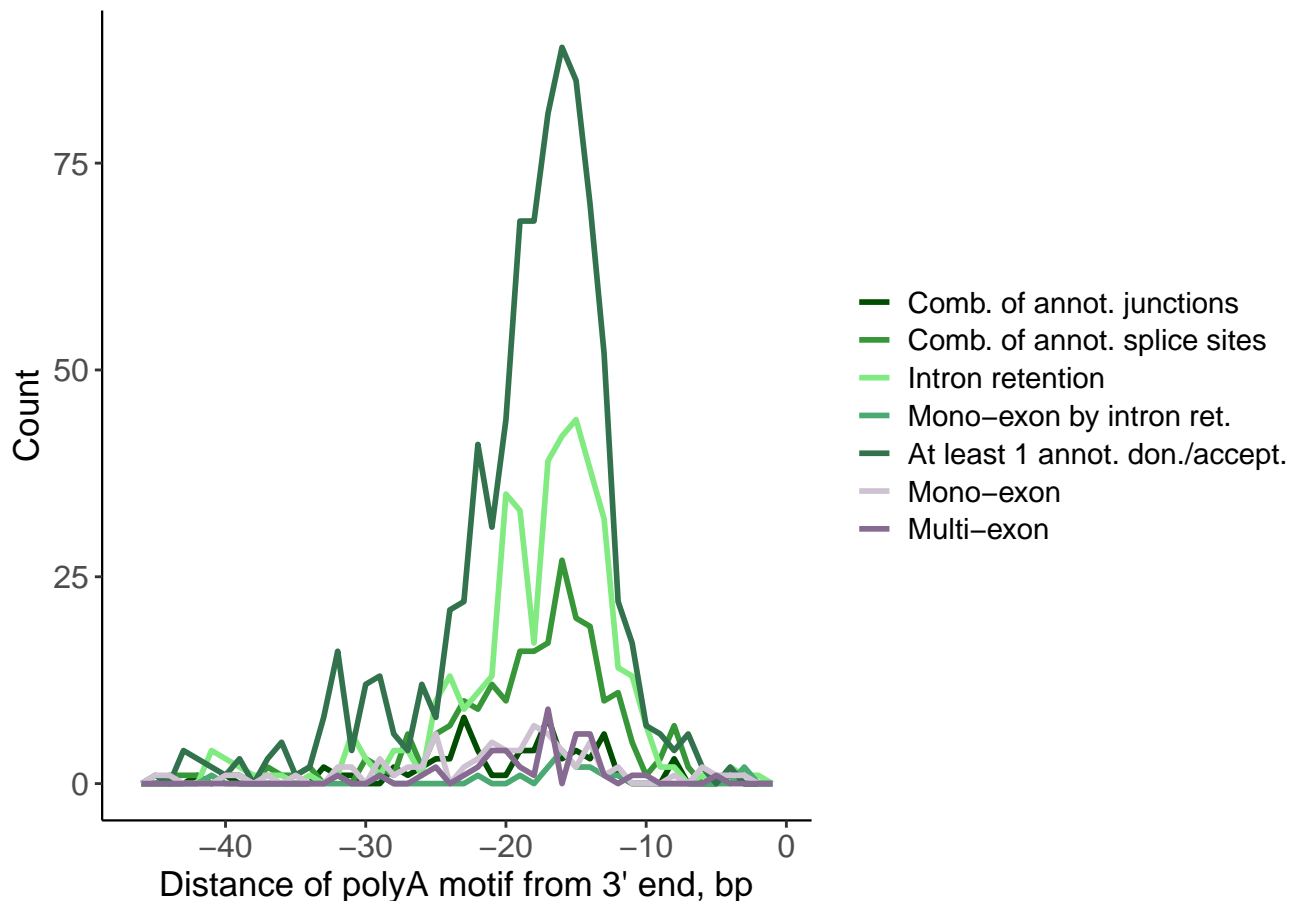
Category	Count	polyA Detected	%
FSM	539	458	85
ISM	1138	942	83
NIC	744	594	80
NNC	1139	981	86
Genic Genomic	113	48	42
Antisense	26	12	46
Fusion	38	34	89
Intergenic	41	10	24
Genic Intron	147	19	13

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

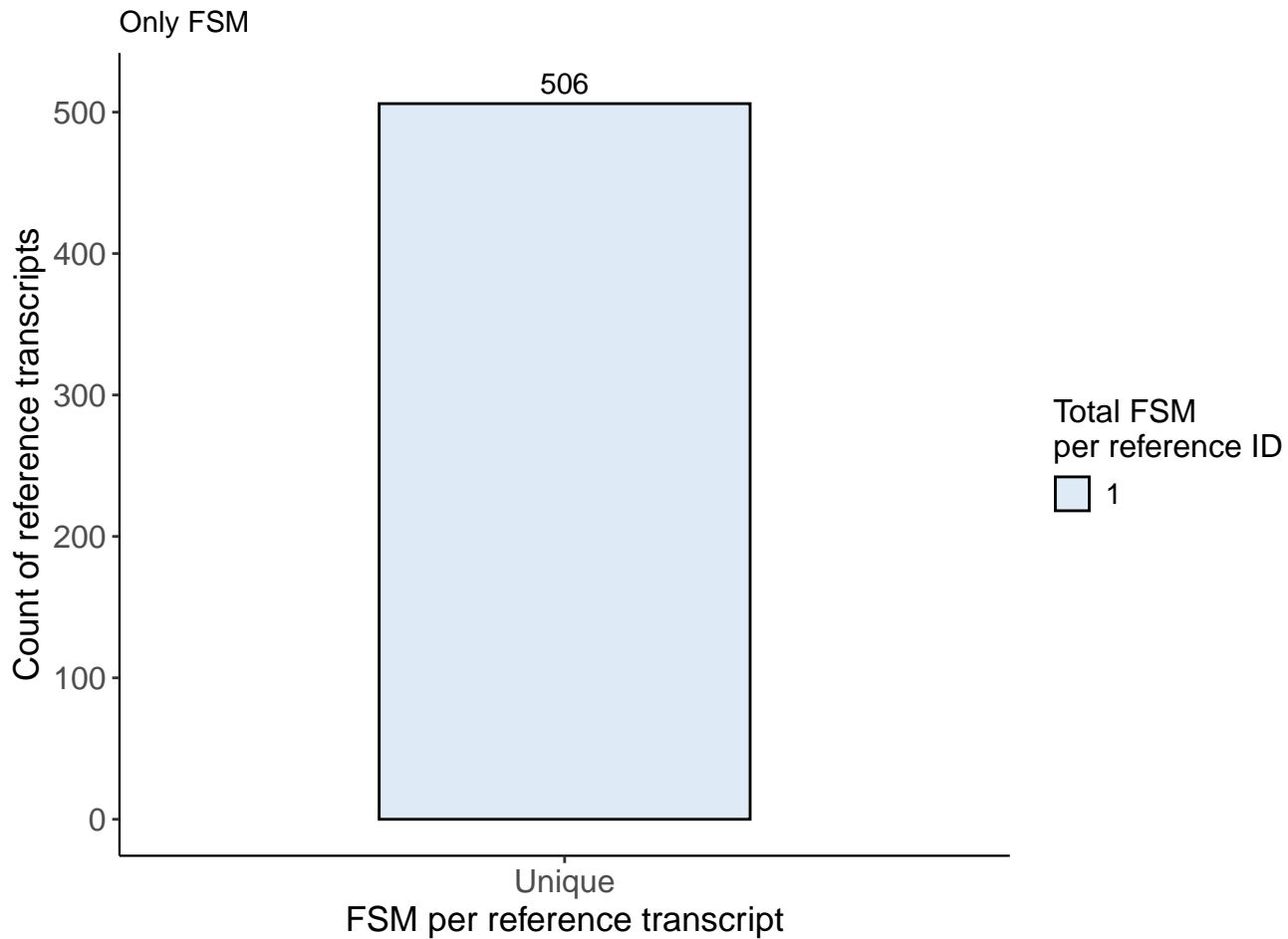
Subcategory	Count	polyA Detected	%
Alternative 3'end	152	121	80
Alternative 3'5'end	76	60	79
Alternative 5'end	90	84	93
Reference match	188	175	93
3' fragment	725	668	92
Internal fragment	8	4	50
5' fragment	141	39	28
Comb. of annot. junctions	83	68	82
Comb. of annot. splice sites	281	235	84
Intron retention	554	459	83
Mono-exon by intron ret.	44	18	41
At least 1 annot. don./accept.	986	846	86
Mono-exon	543	277	51
Multi-exon	54	44	81

Frequency of PolyA Motifs

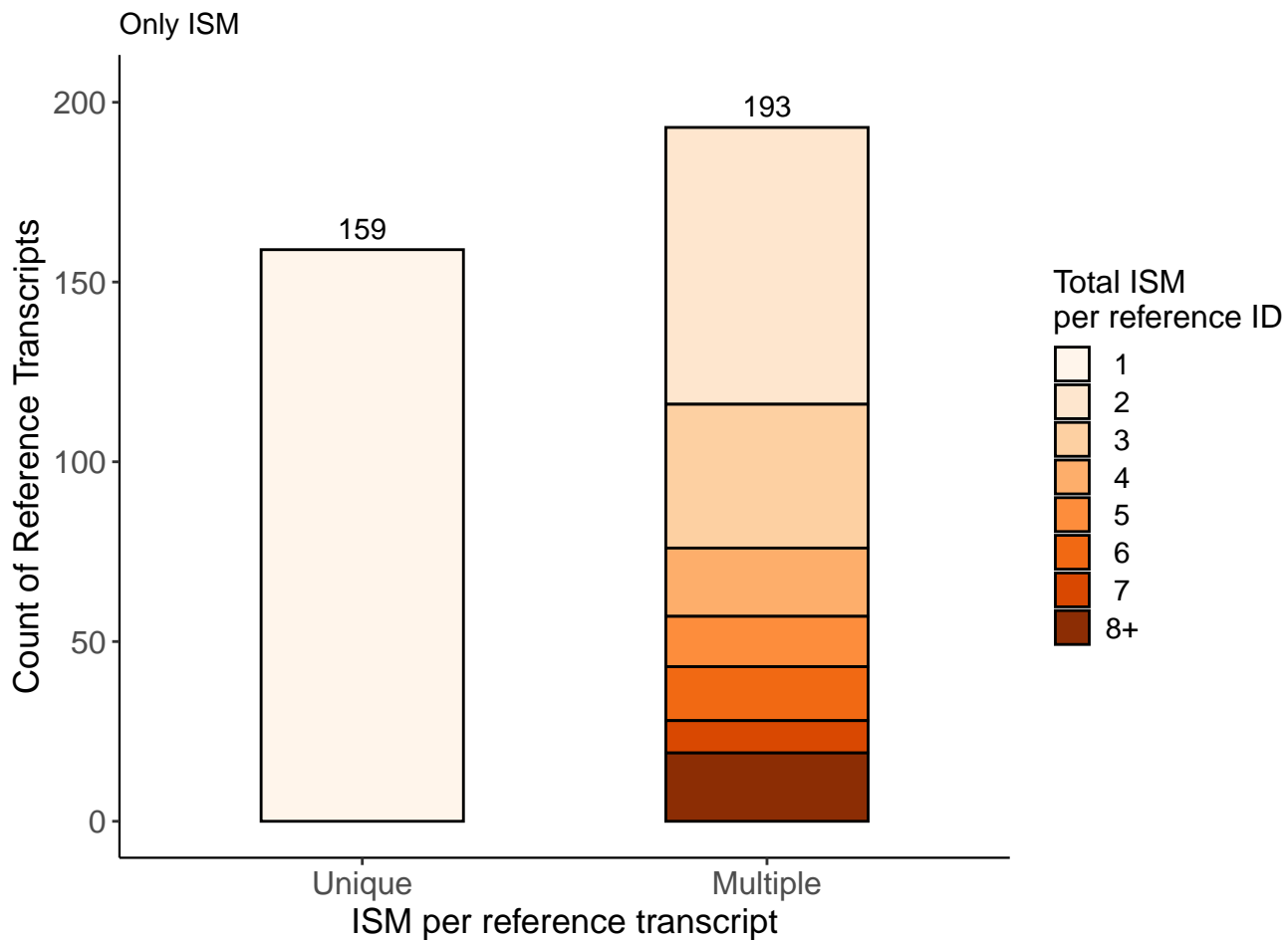
Motif	Count	%
AATAAA	2014	65.0
ATTAAA	529	17.1
AGTAAA	161	5.2
TATAAA	90	2.9
GATAAA	54	1.7
AAAACA	41	1.3
AATACA	38	1.2
AAAAAG	32	1.0
AATAGA	28	0.9
CATAAA	26	0.8
AAGAAA	24	0.8
AATATA	20	0.6
TTTAAA	16	0.5
AATGAA	13	0.4
ACTAAA	10	0.3
GGGGCT	2	0.1

Redundancy Analysis

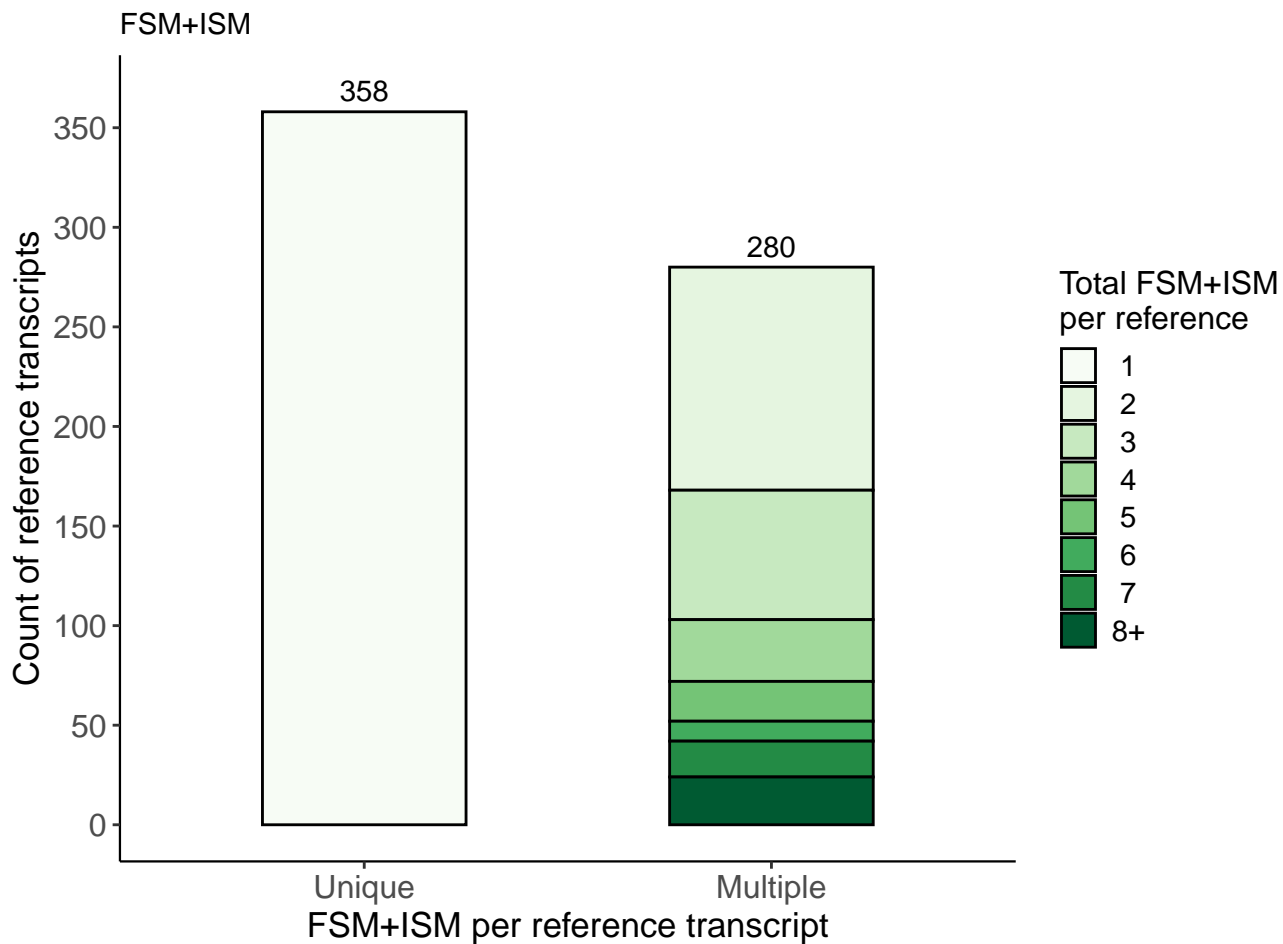
Reference Transcript Redundancy



Reference Transcript Redundancy

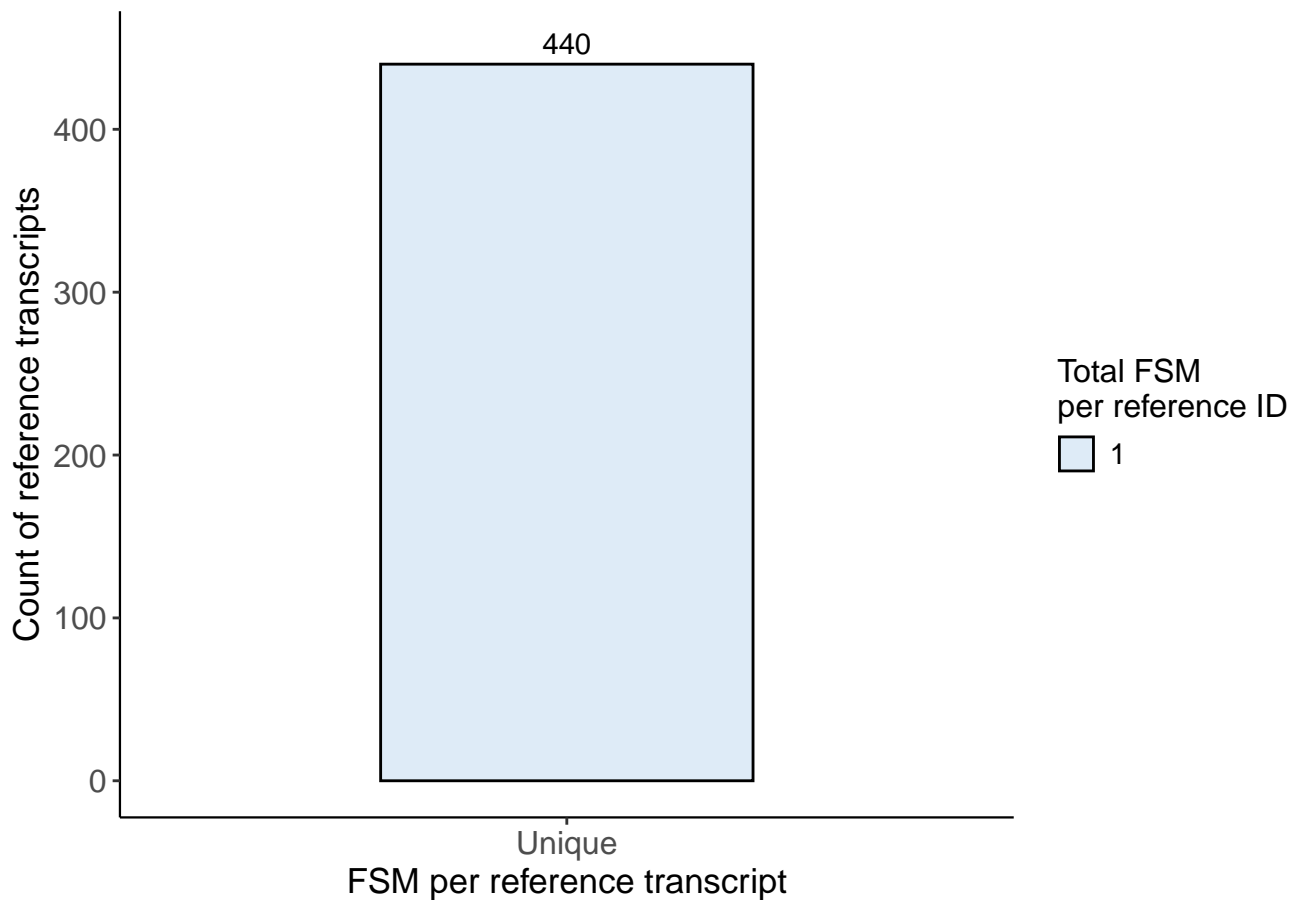


Reference Transcript Redundancy



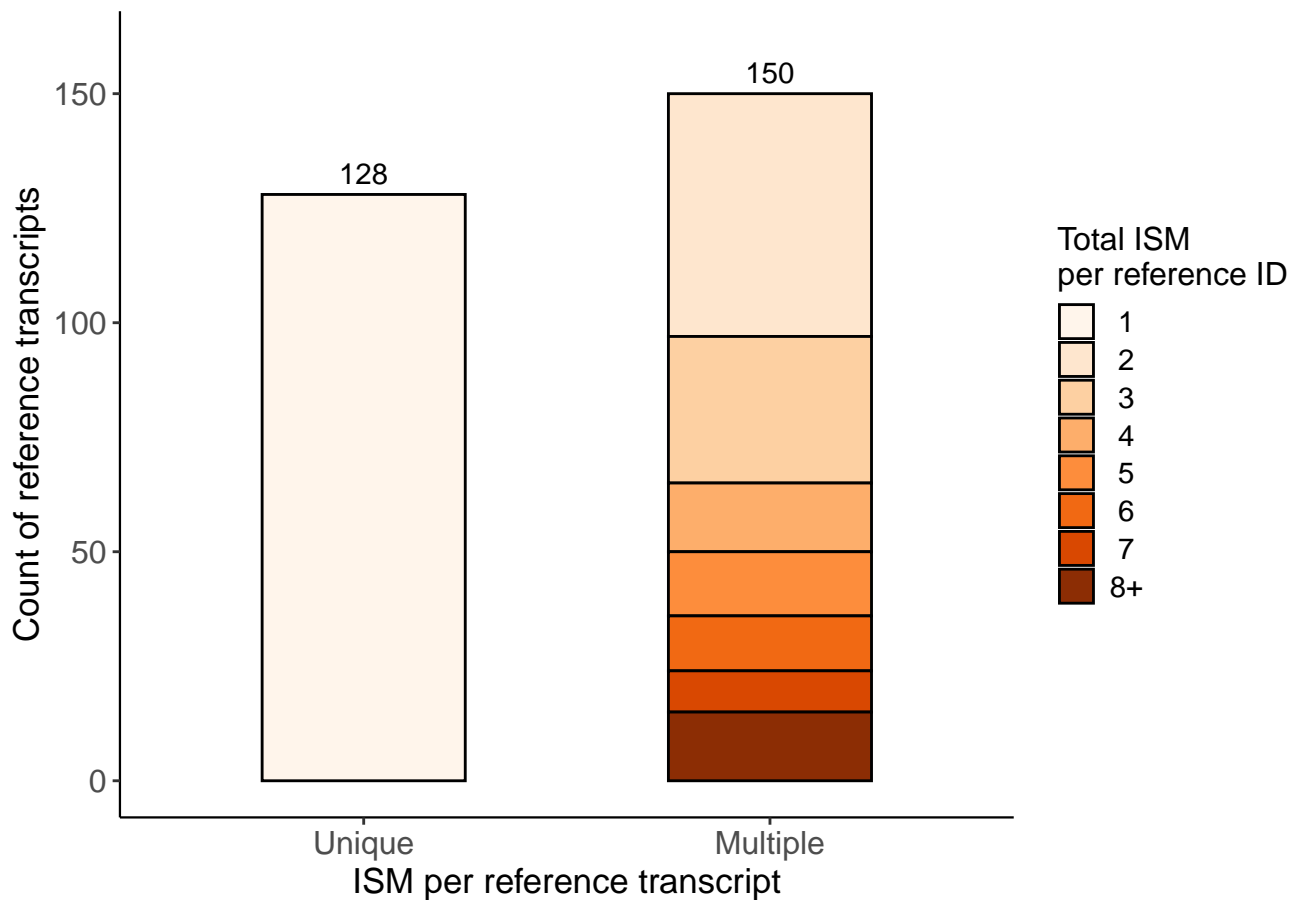
Reference Transcript Redundancy

Only FSM with a polyA motif found



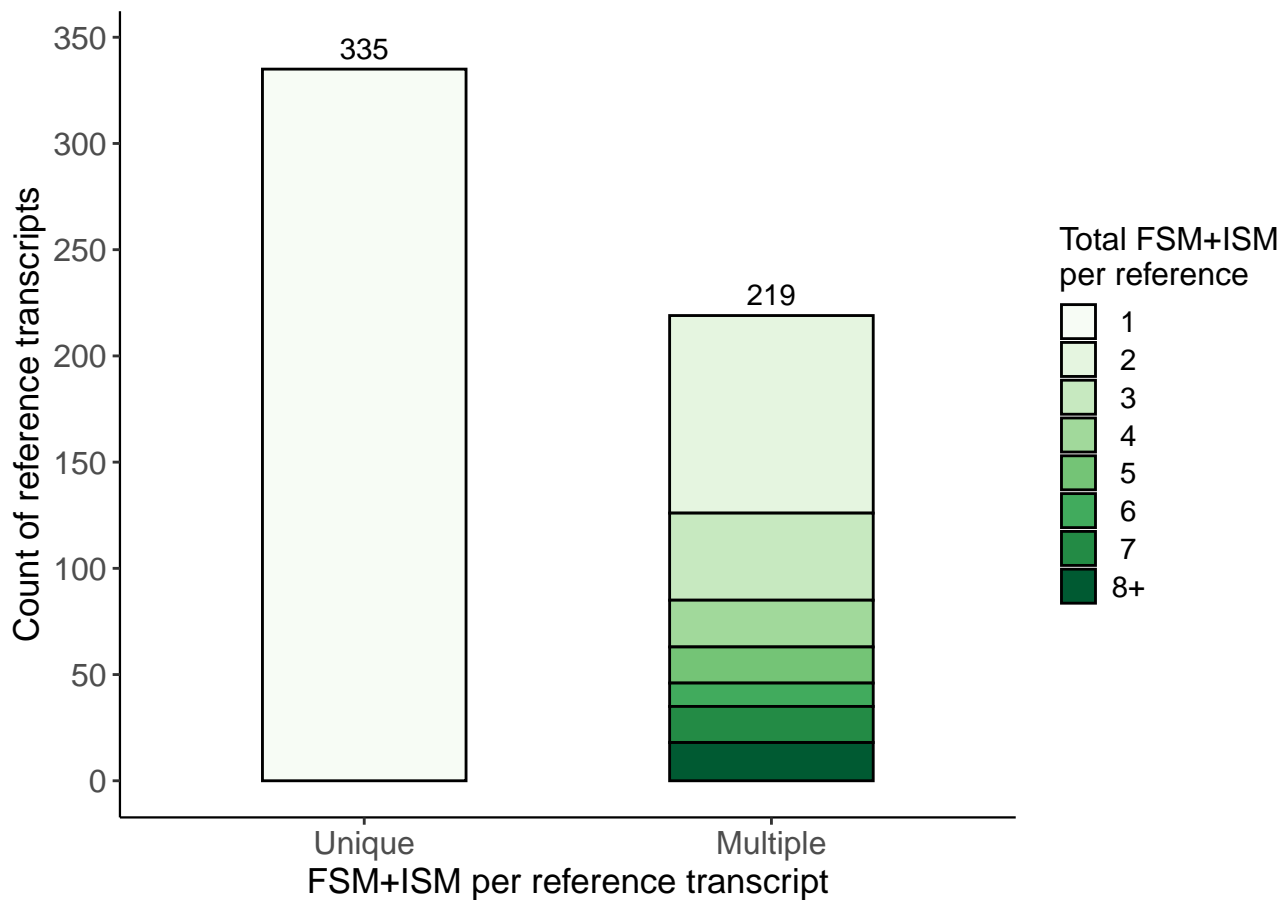
Reference Transcript Redundancy

Only ISM with a polyA motif found



Reference Transcript Redundancy

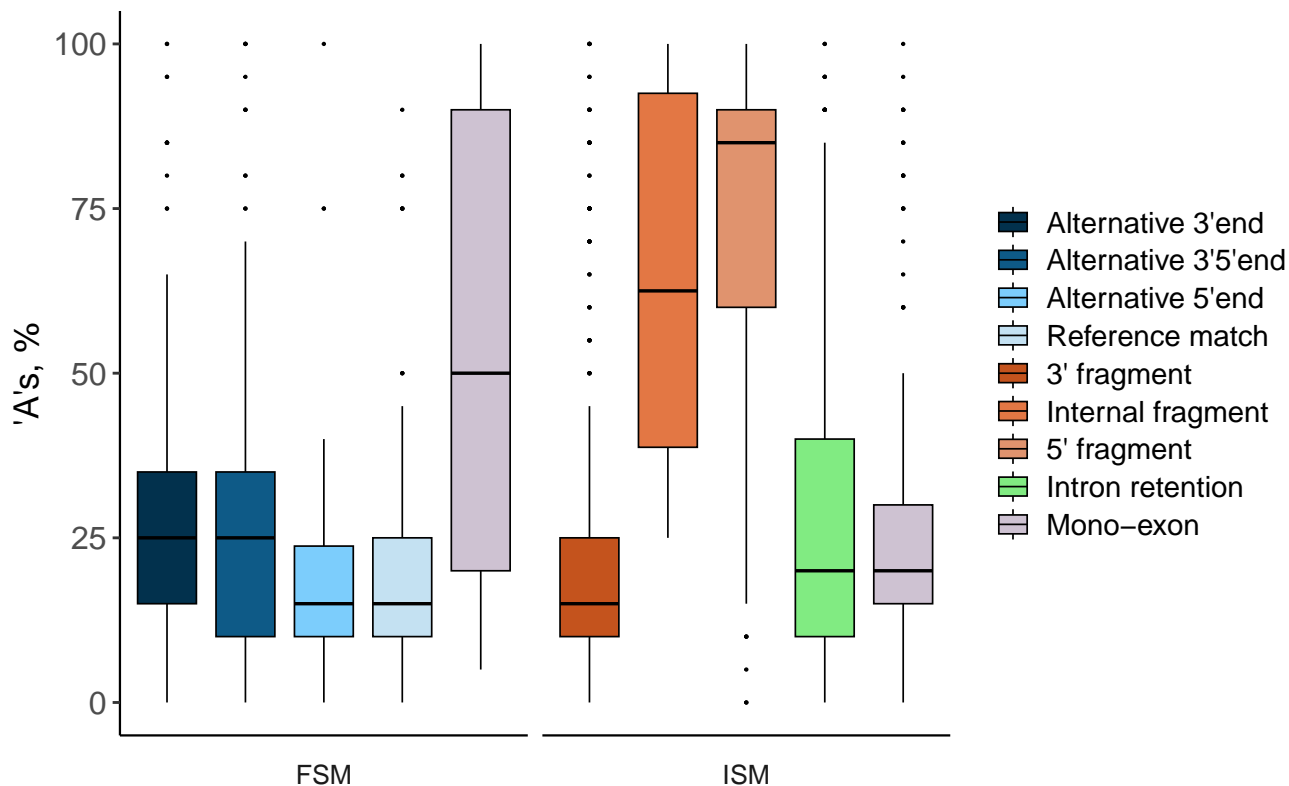
FSM+ISM with a polyA motif found



Intra-Priming Quality Check

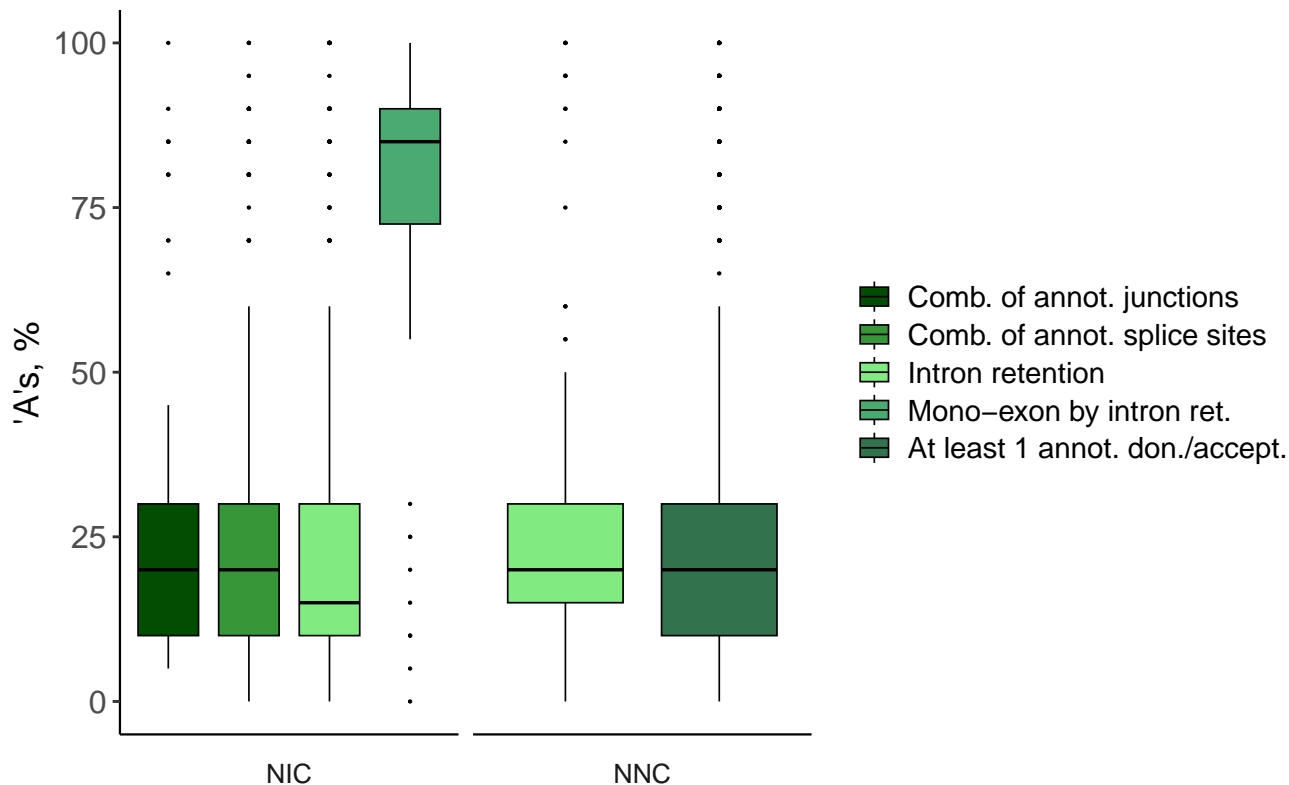
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



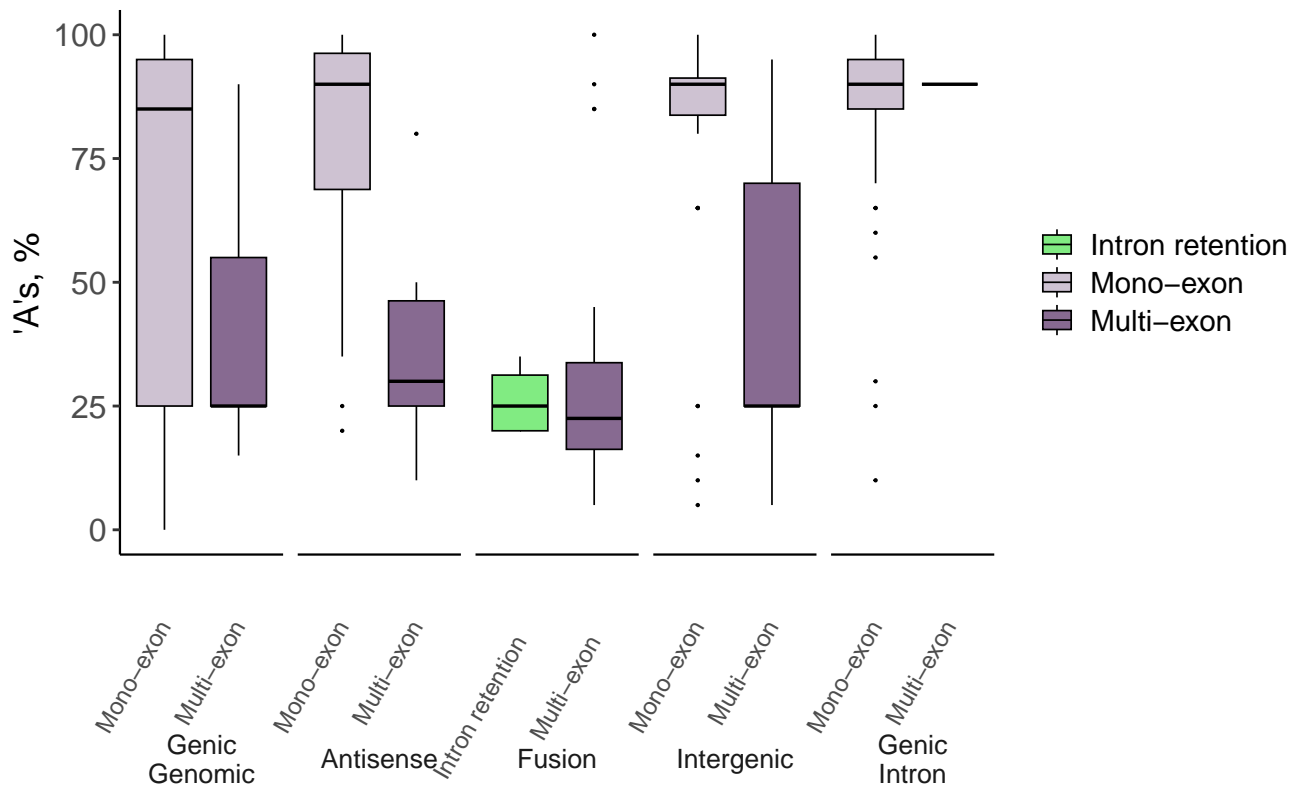
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



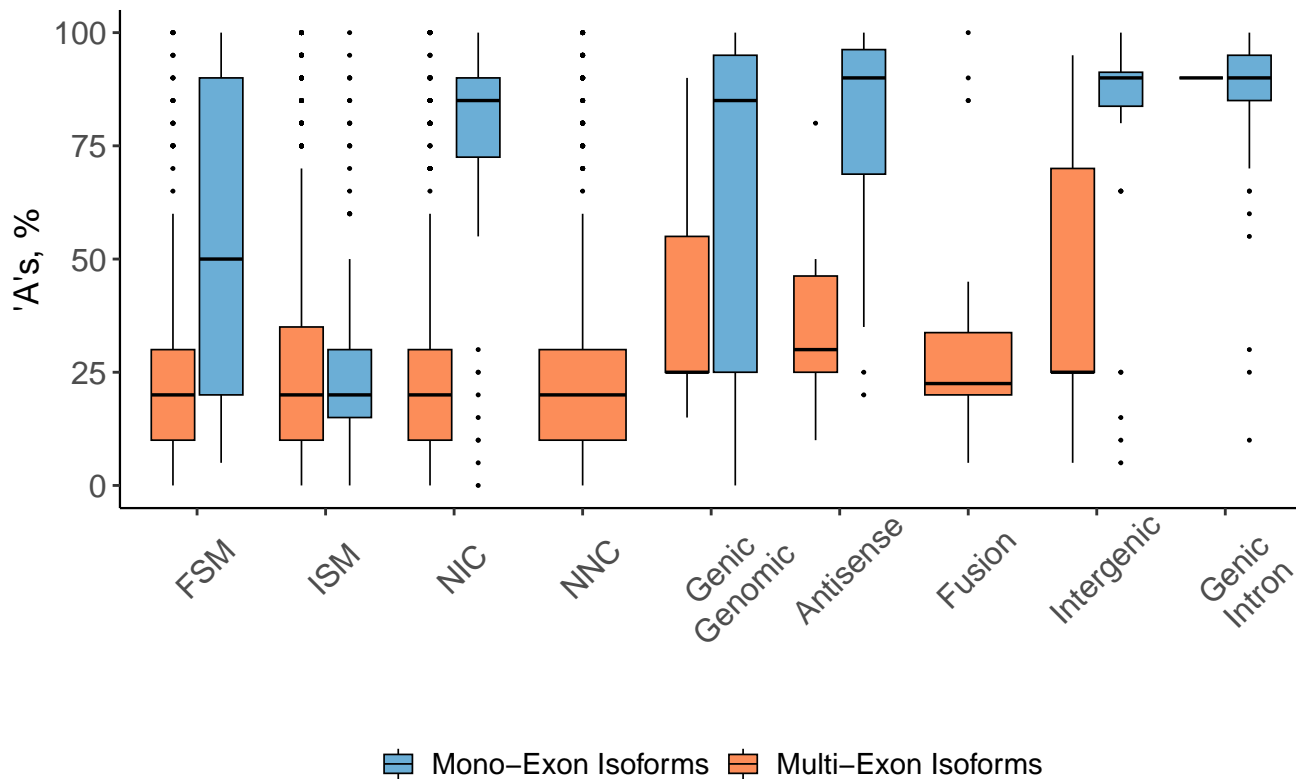
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



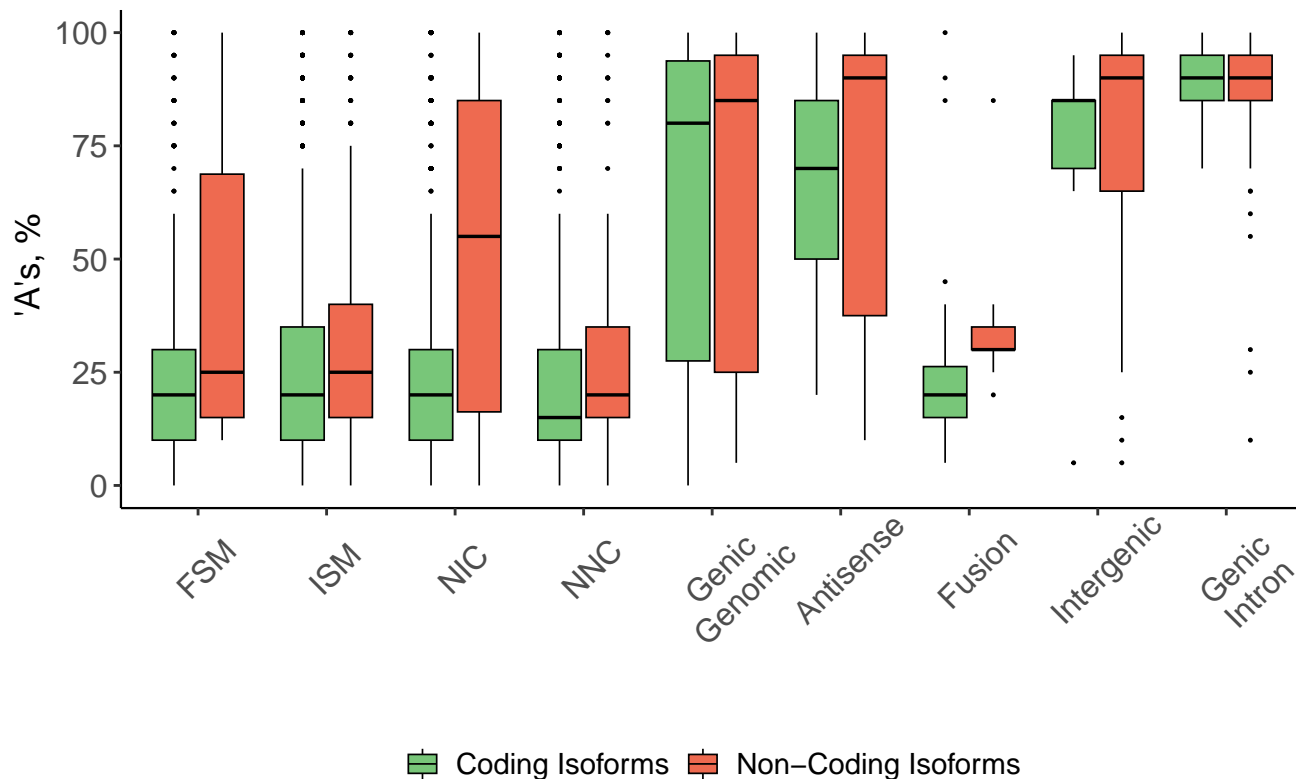
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



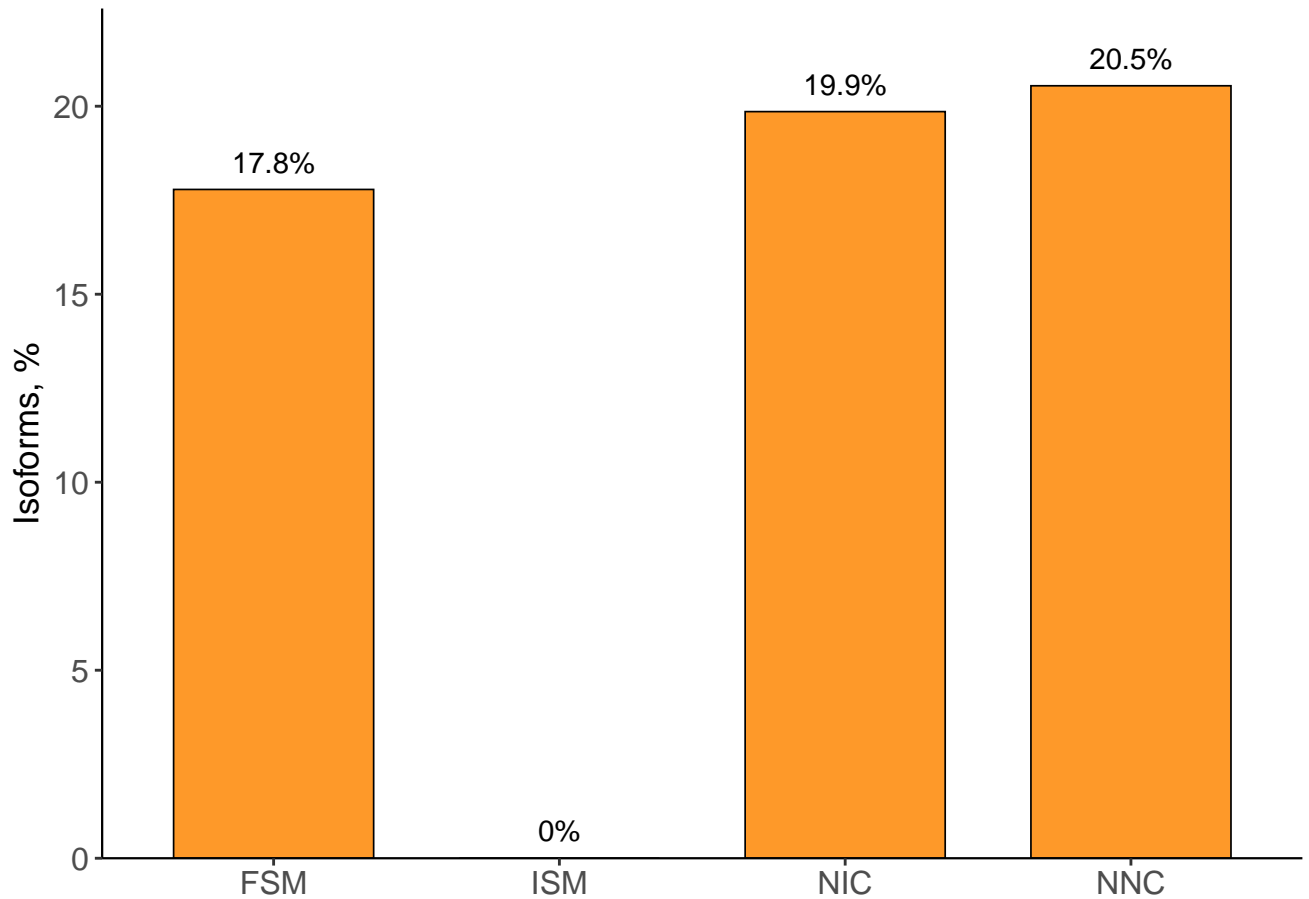
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp

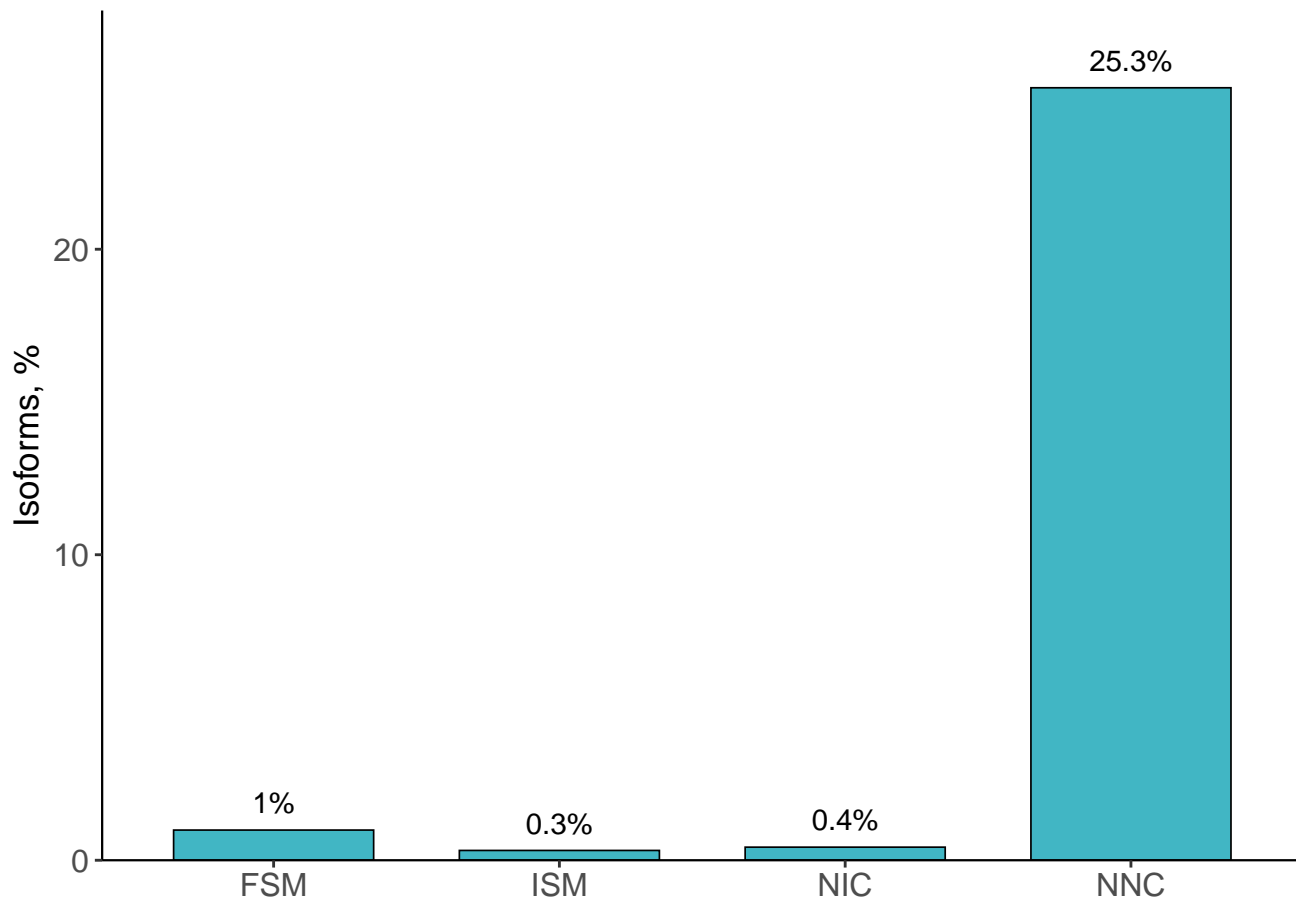


Features of Bad Quality

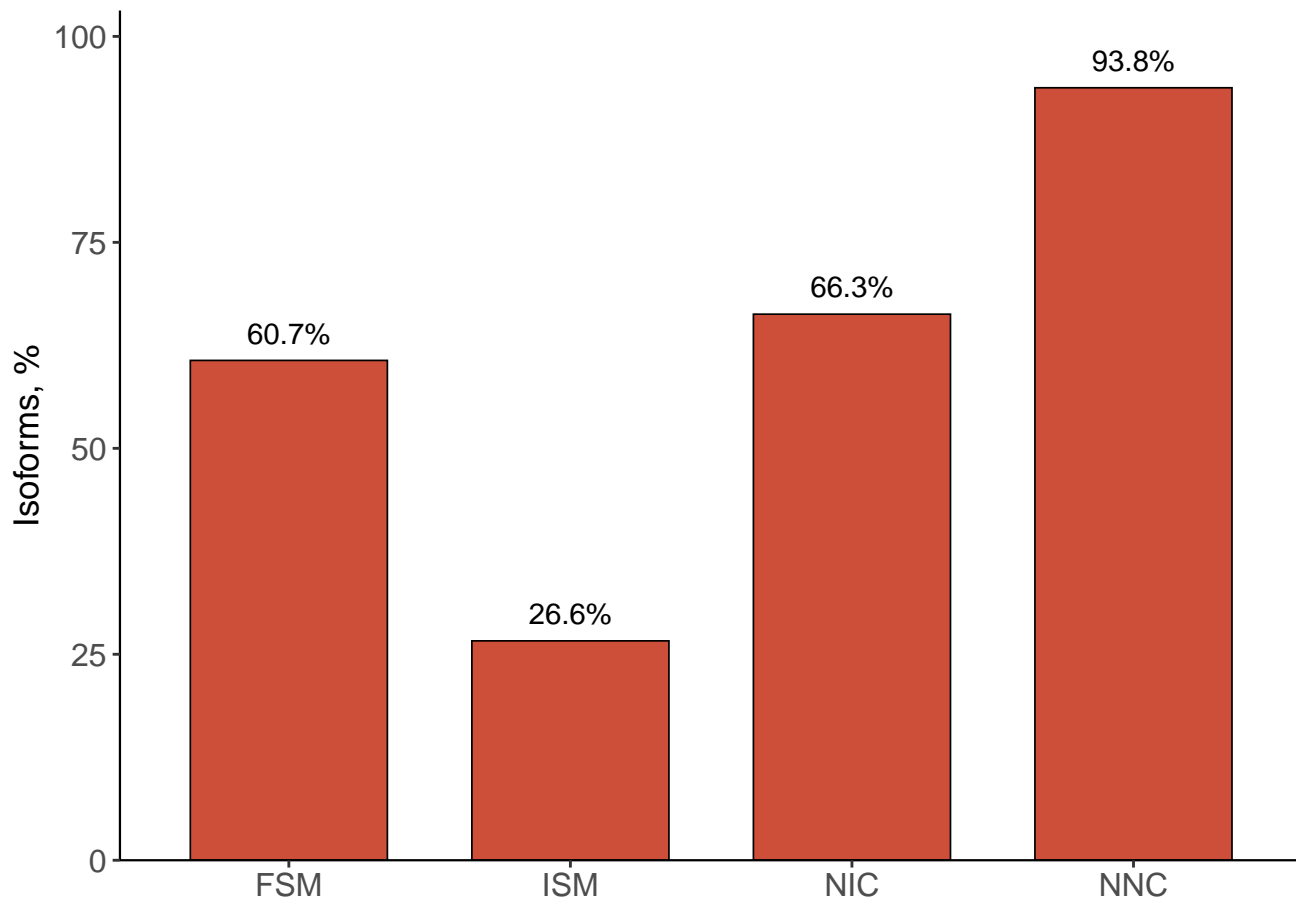
RT-switching



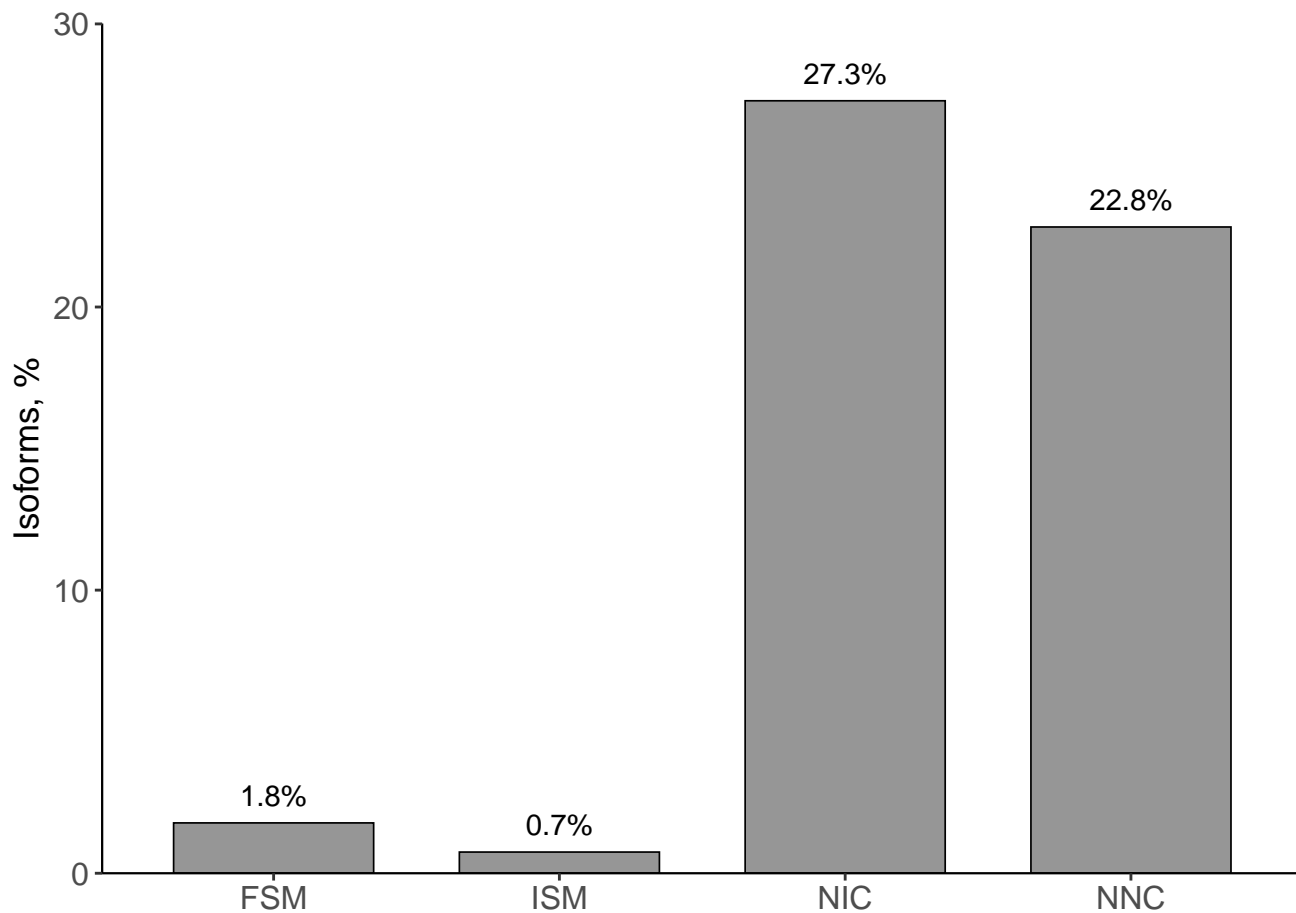
Non-Canonical Junctions



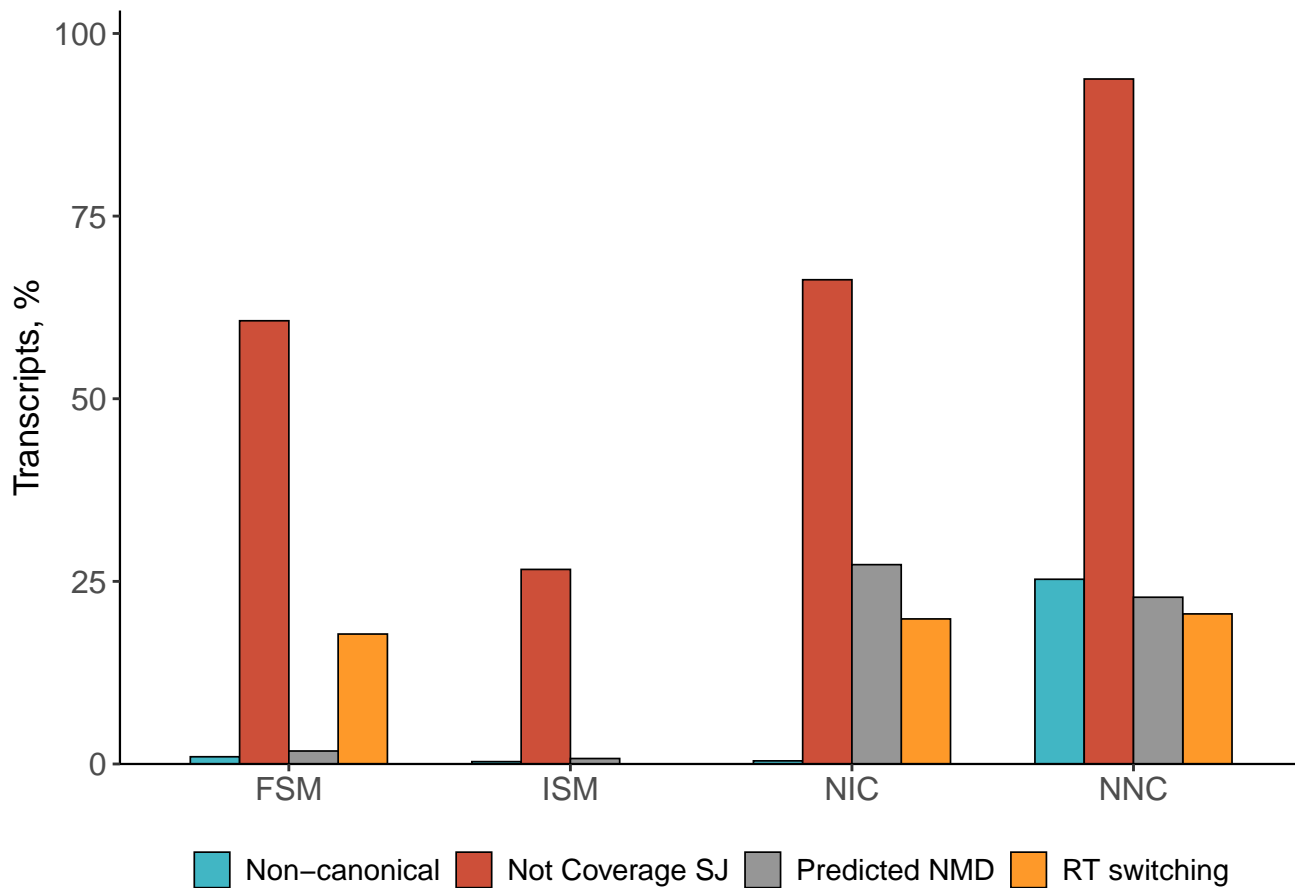
Splice Junctions Without Short Read Coverage



Nonsense-Mediated Decay by Structural Category

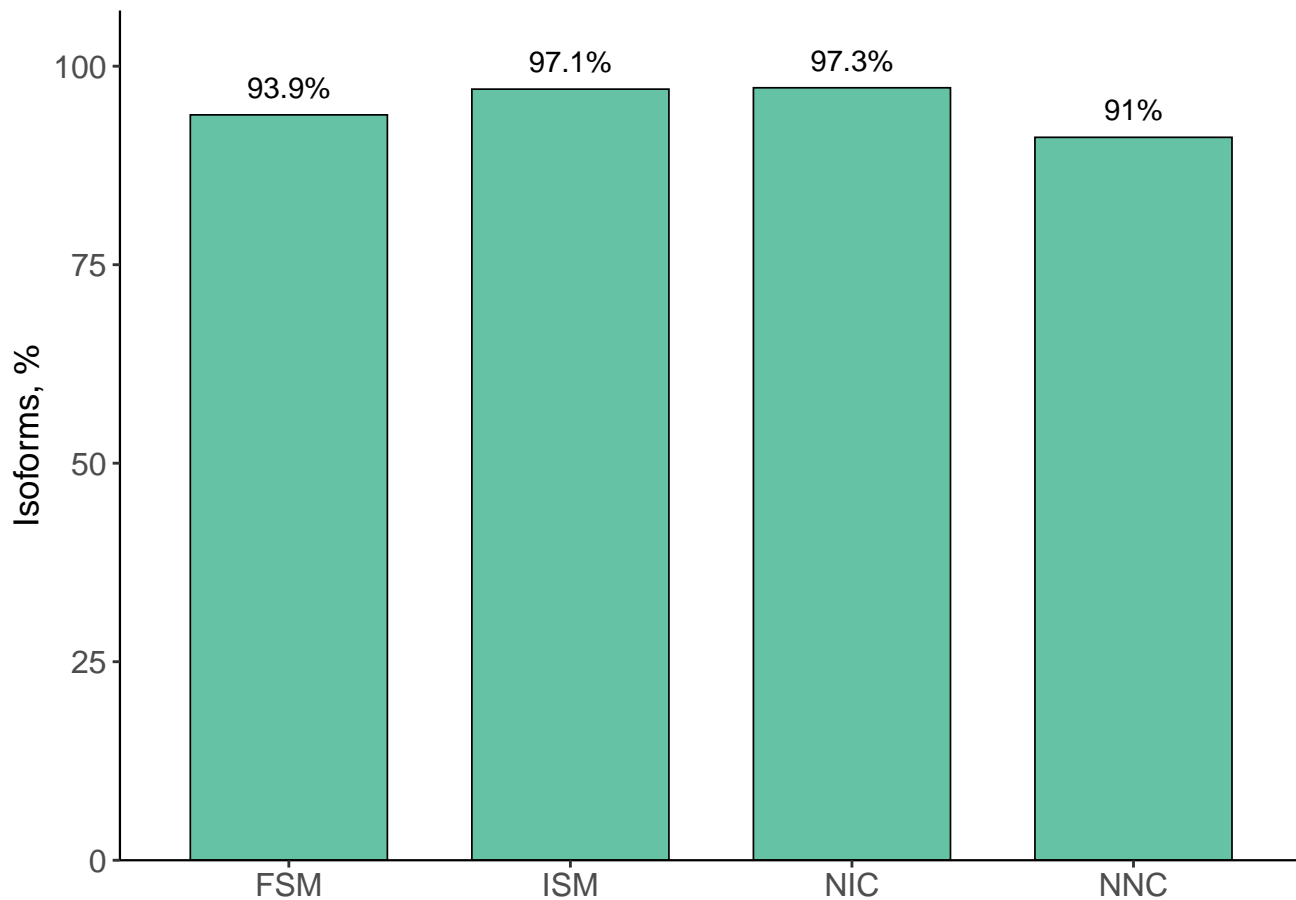


Quality Control Attributes Across Structural Categories

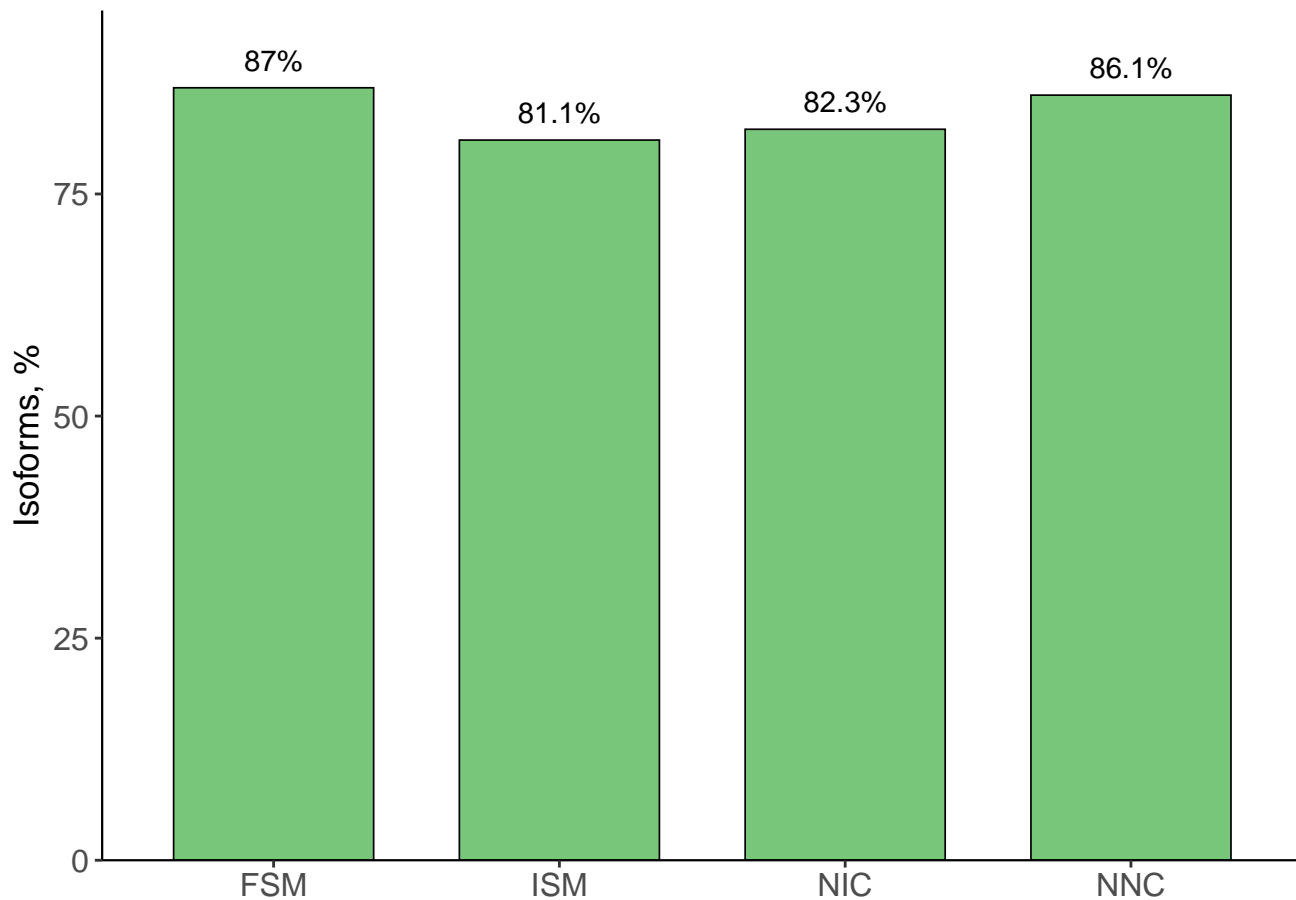


Features of Good Quality

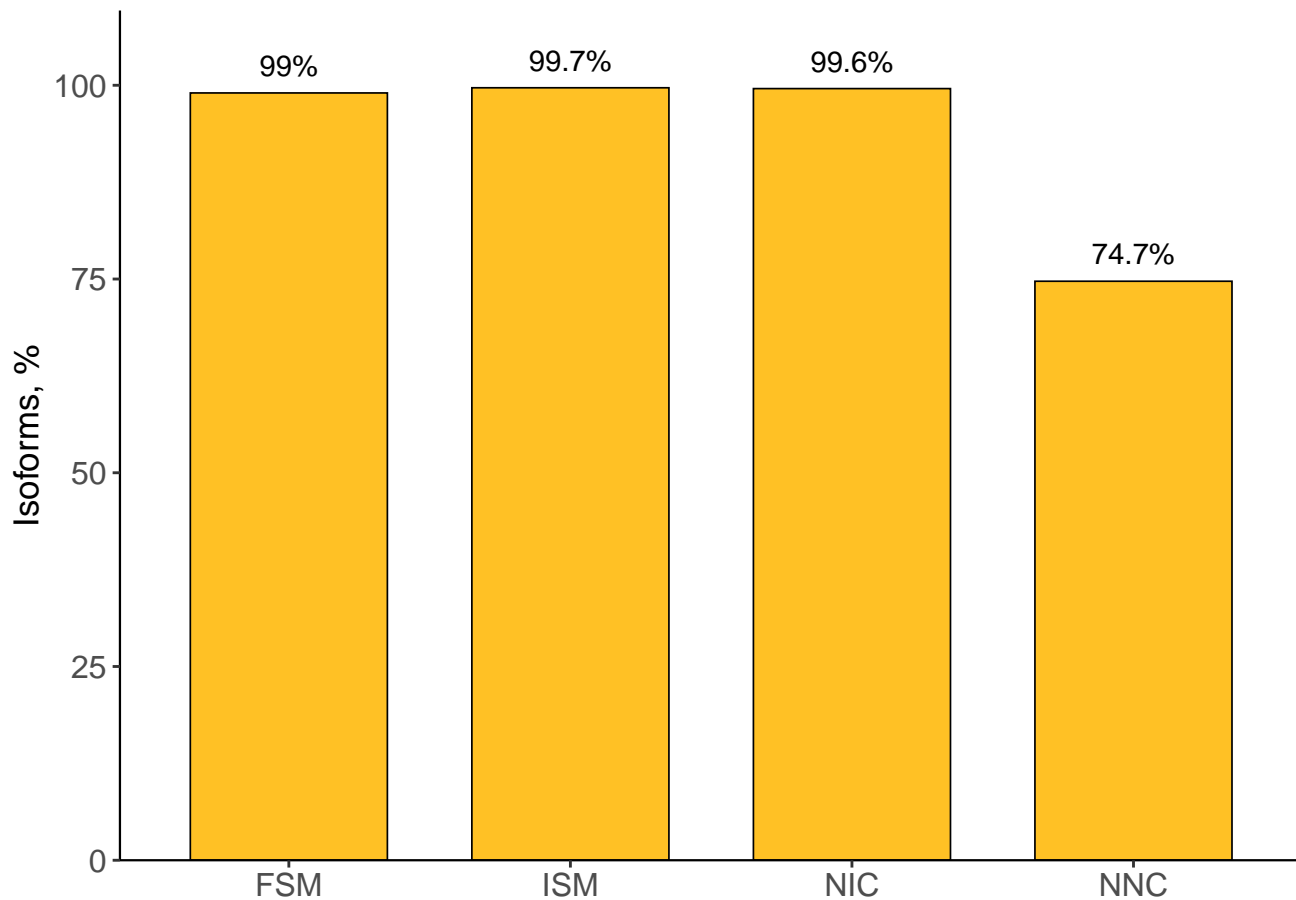
Annotation Support



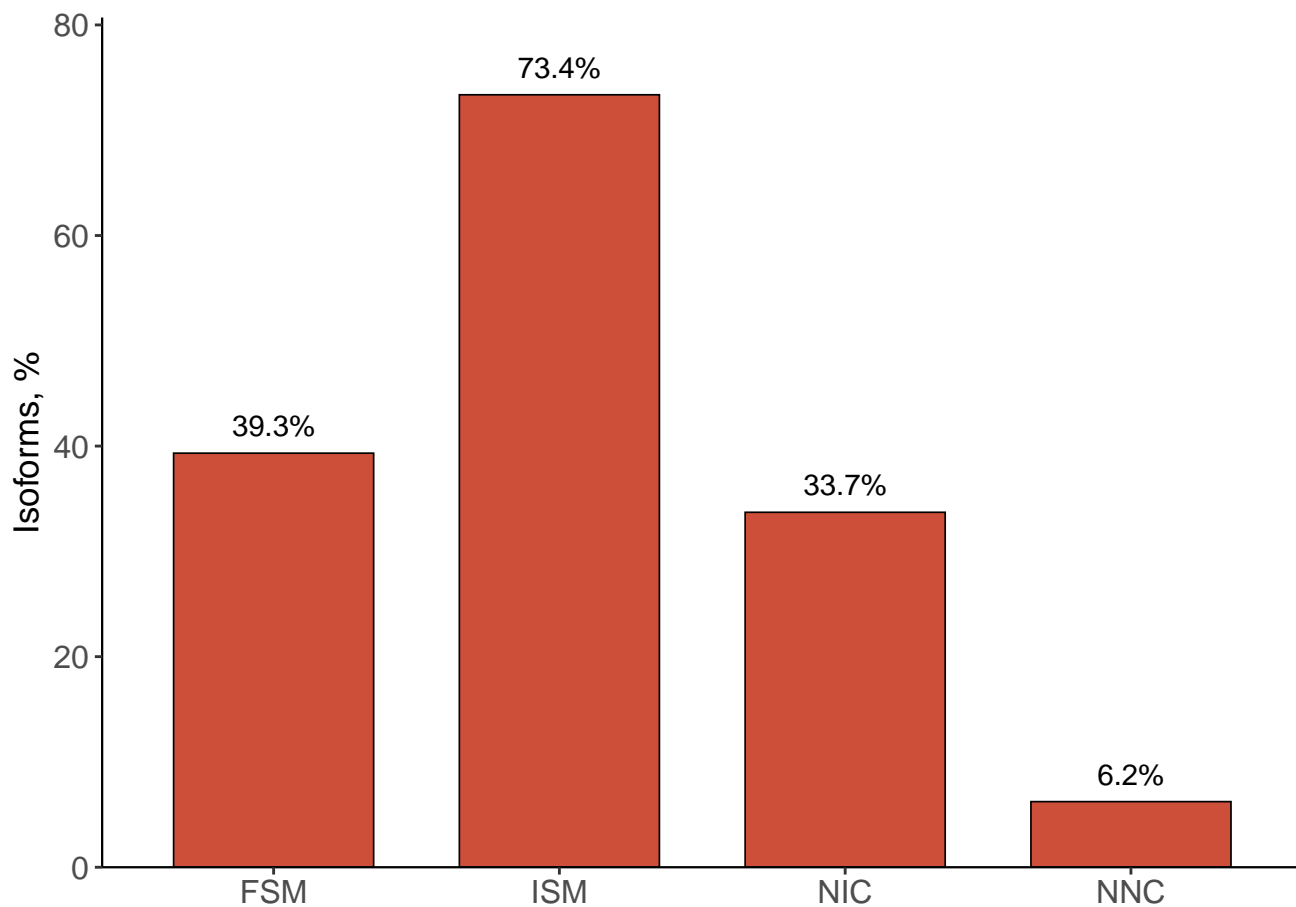
PolyA Support



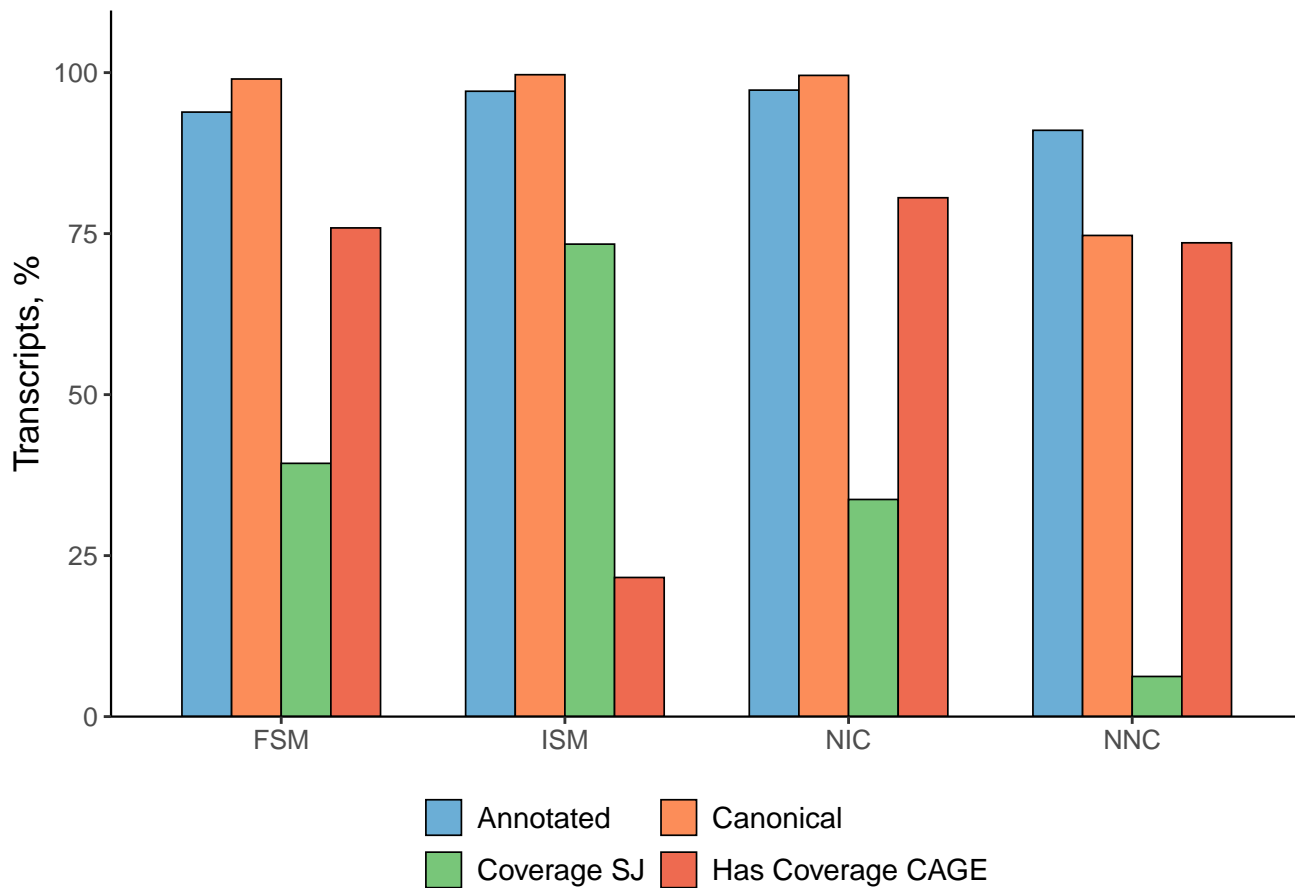
All Canonical Junctions



Splice Junctions With Short Read Coverage



Good Quality Control Attributes Across Structural Categories



TSS Ratio FSM Reference Match vs ISM

