

SQANTI3 report

Unique Genes: 652
Unique Isoforms: 3925

Transcript Classification

Gene Classification

Category	Genes, count
Annotated Genes	436
Novel Genes	216

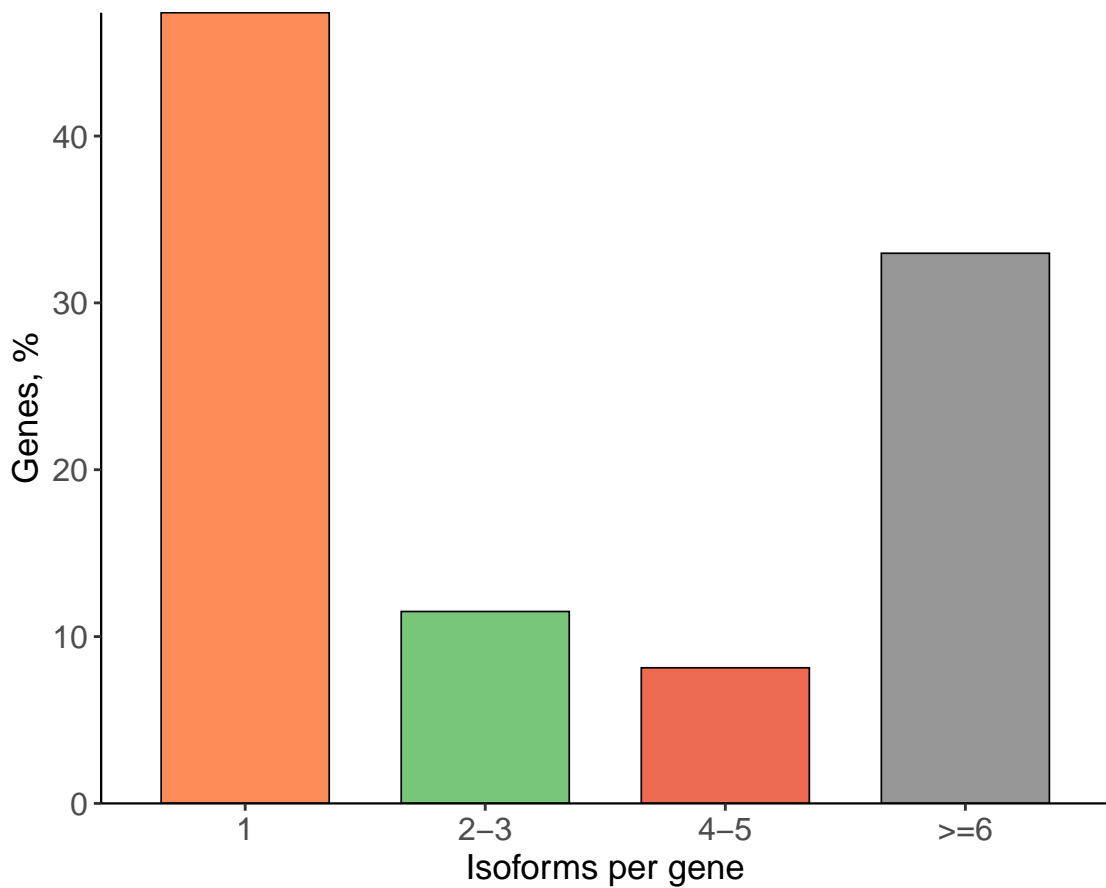
Category	Isoforms, count
FSM	534
ISM	1134
NIC	806
NNC	1139
Genic Genomic	56
Antisense	28
Fusion	38
Intergenic	190
Genic Intron	0

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

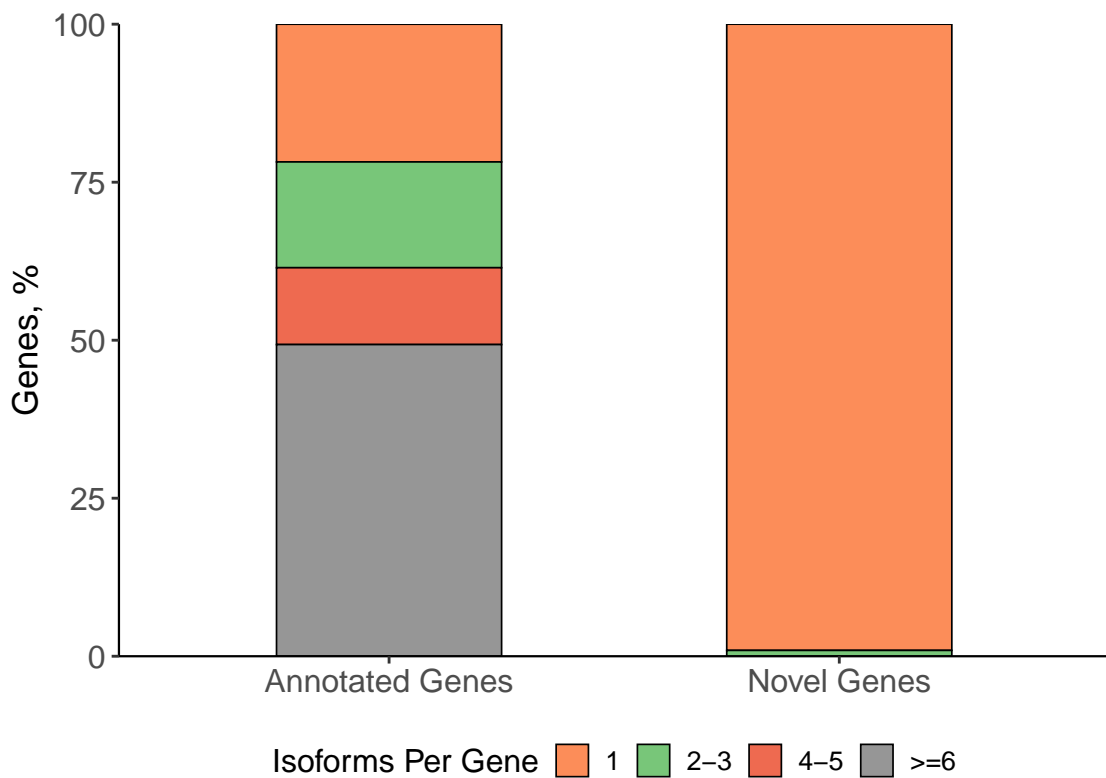
Gene Characterization

Number of Isoforms per Gene

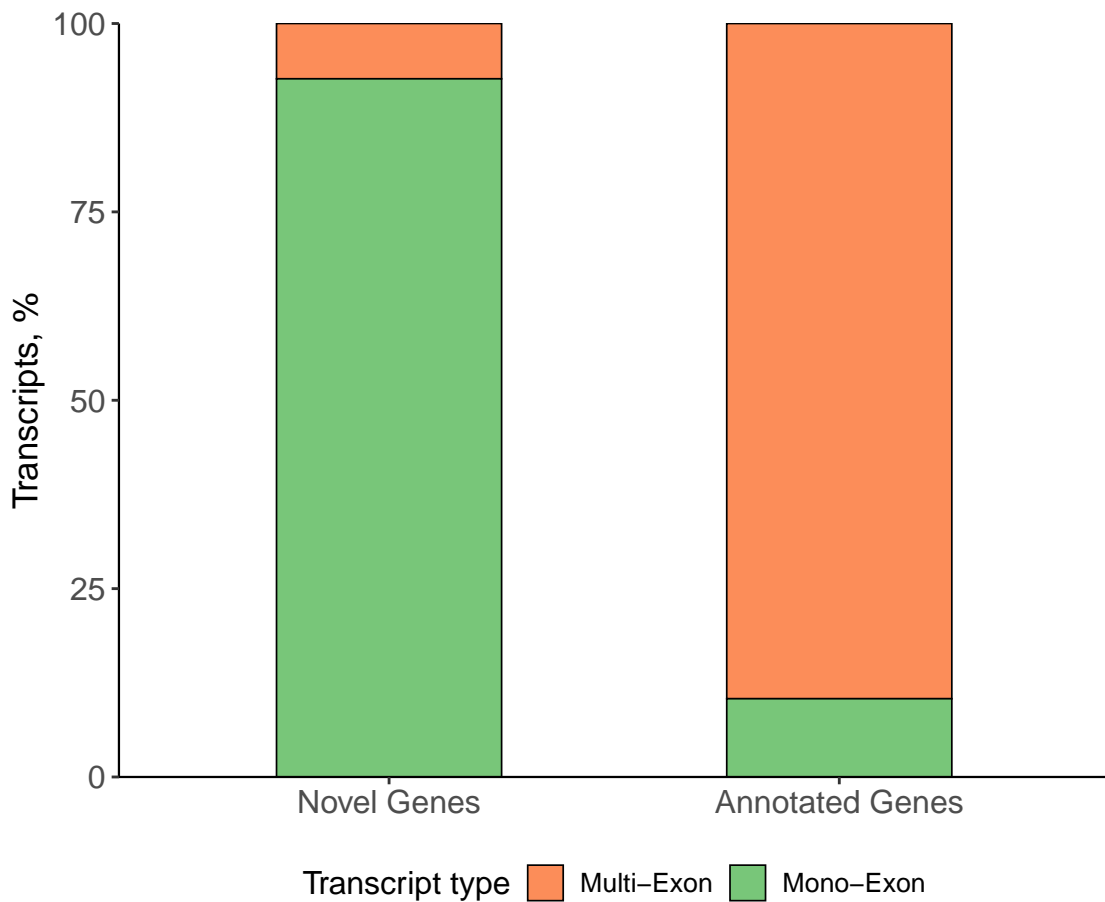


Number of Isoforms per Gene

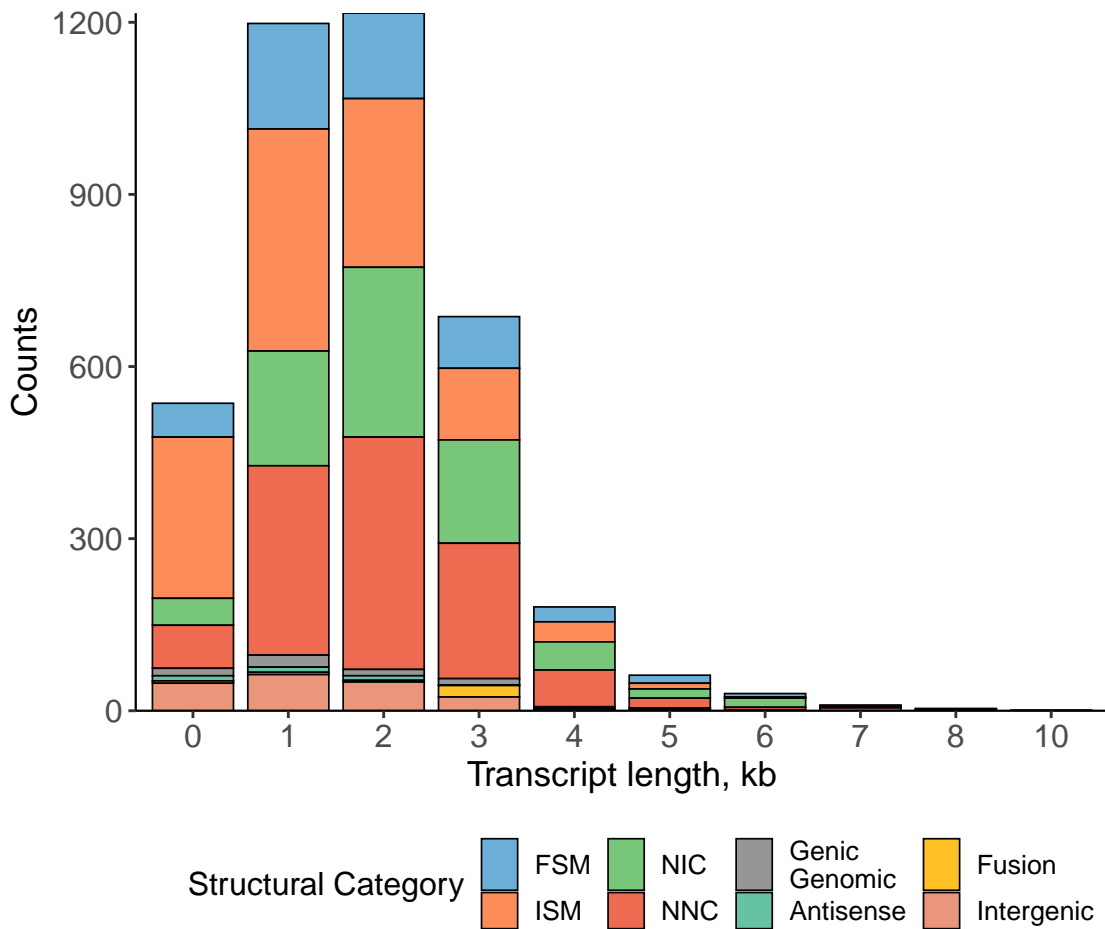
Known vs Novel Genes



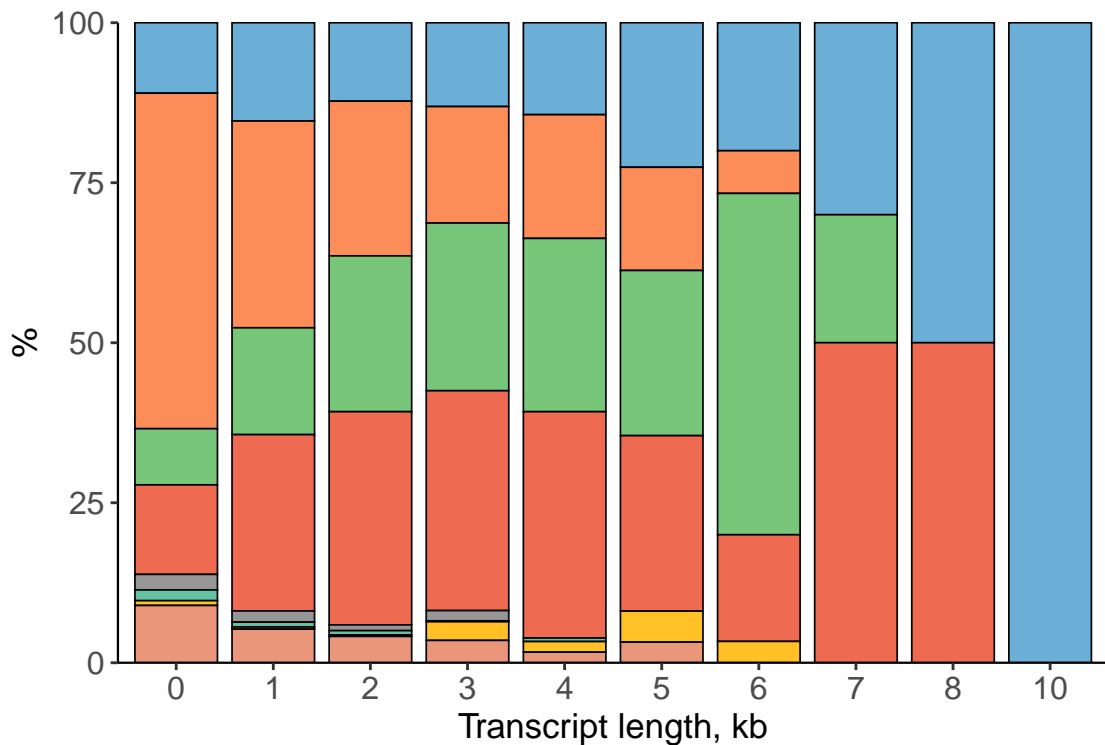
Distribution of Mono- vs Multi-Exon Transcripts



Structural Categories by Transcript Length



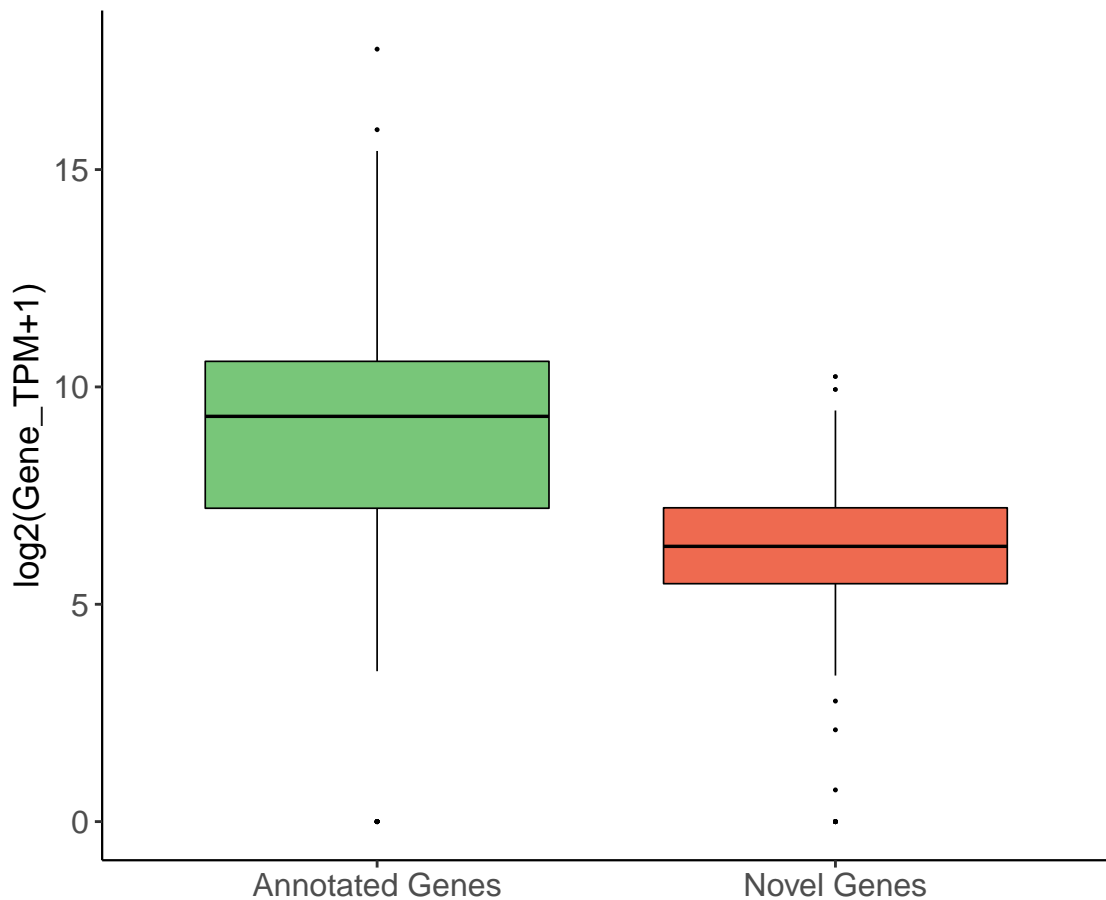
Structural Categories by Transcript Length



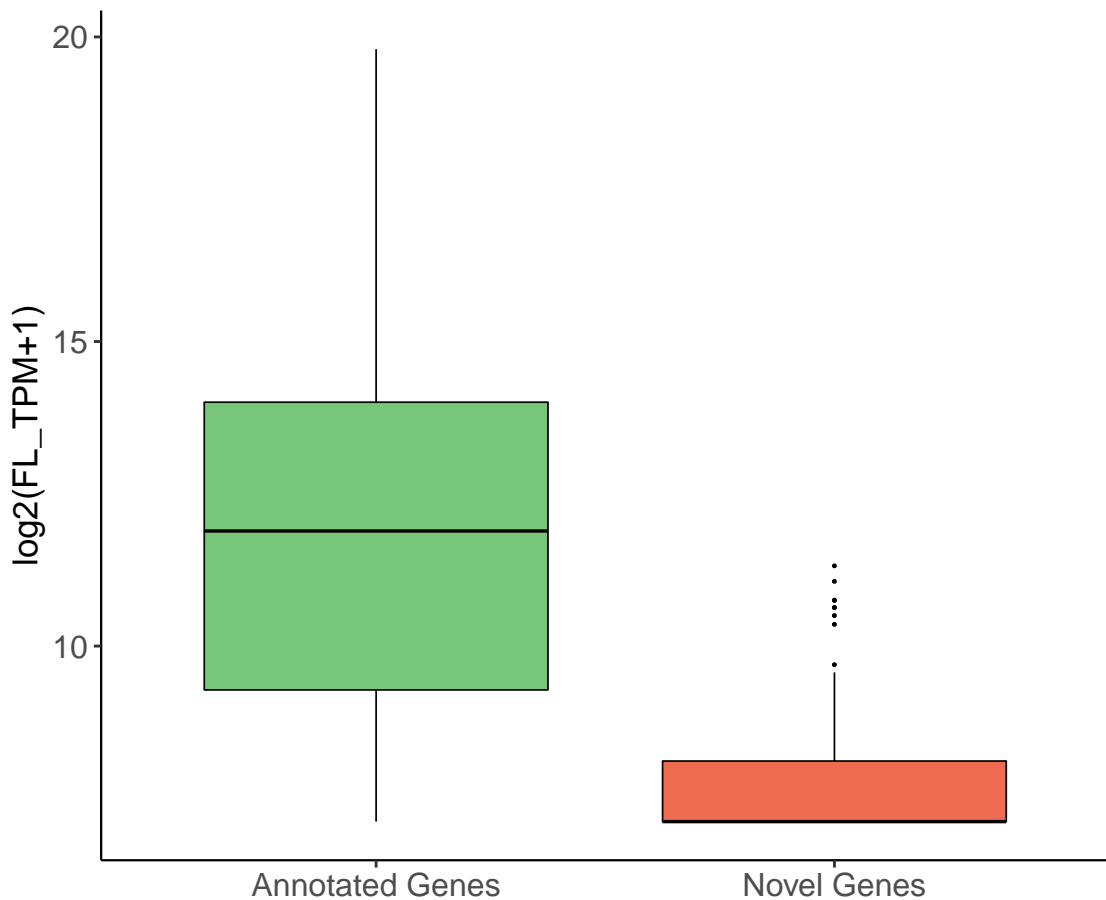
Structural Category

■ FSM	■ NIC	■ Genic Genomic	■ Fusion
■ ISM	■ NNC	■ Antisense	■ Intergenic

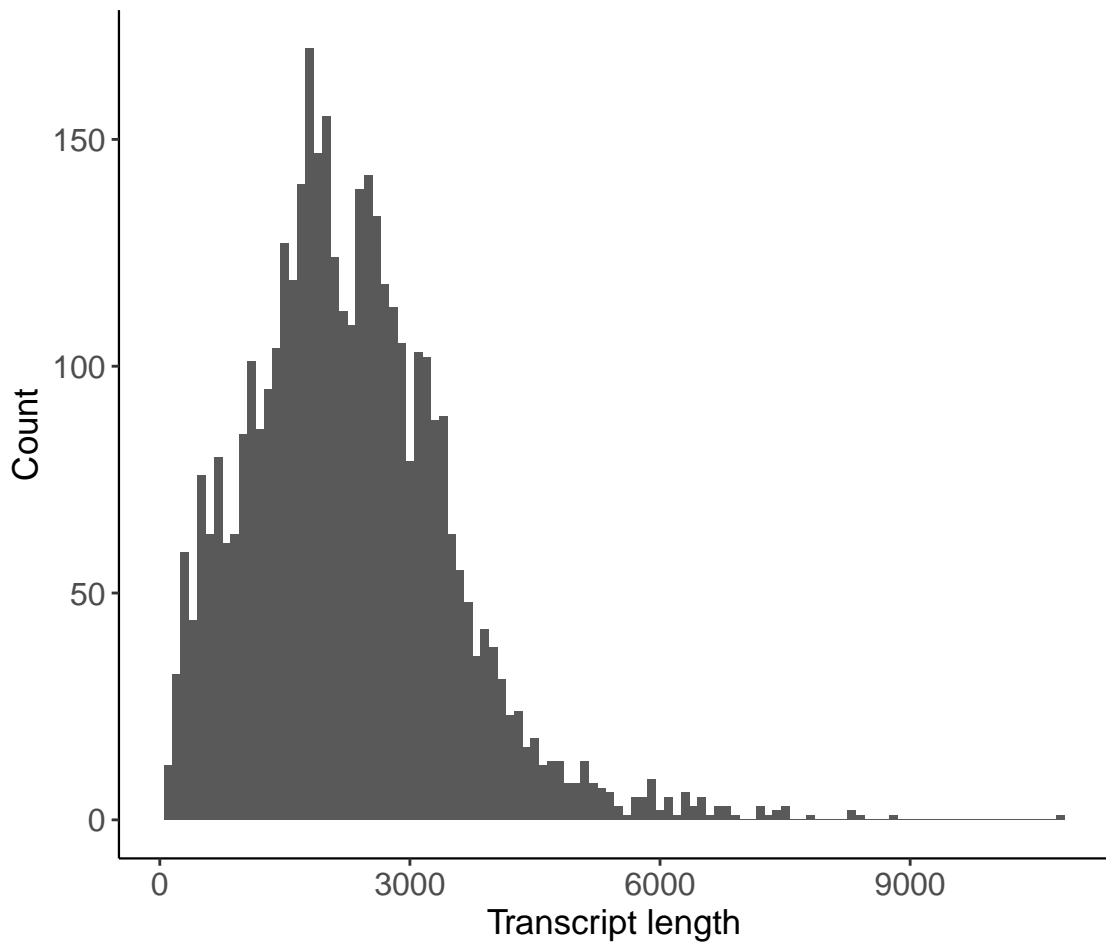
Annotated vs Novel Gene Expression



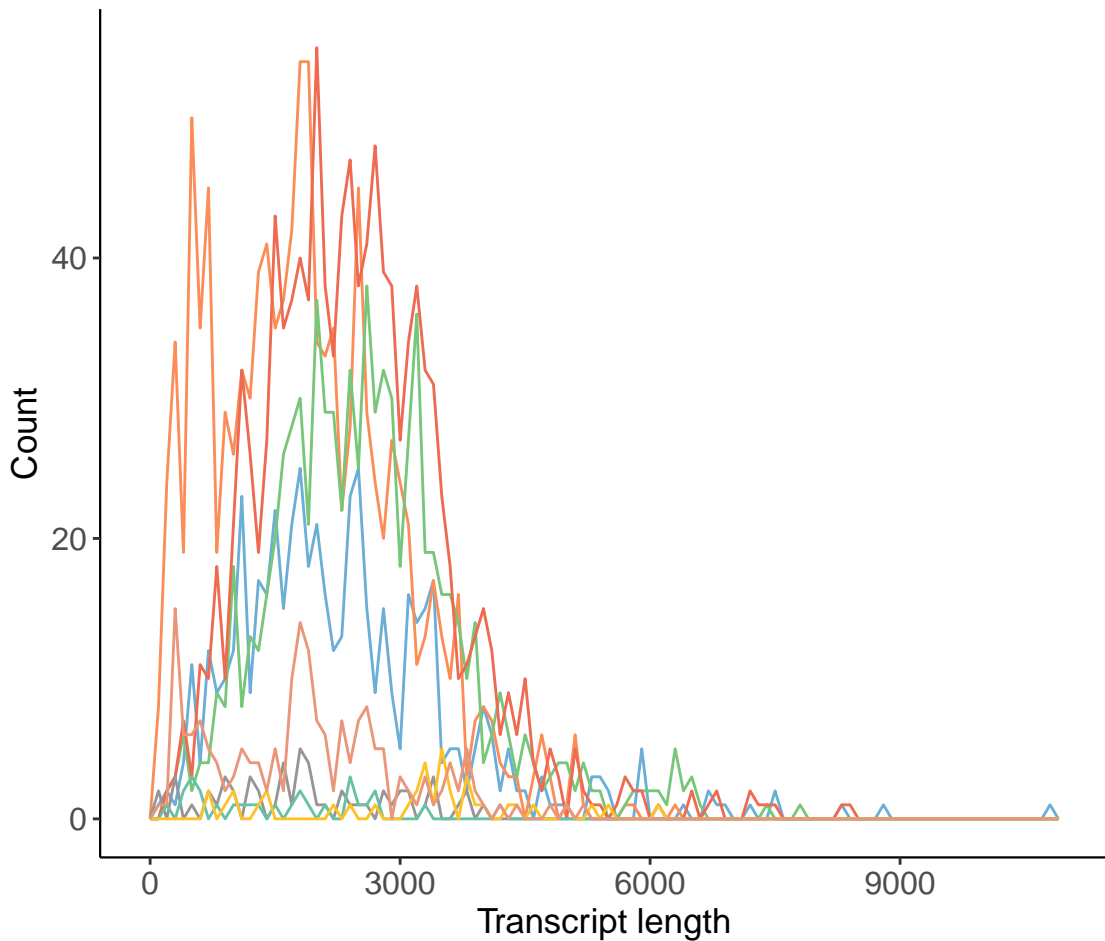
Number of FL reads per Gene by Type of Gene Annotation



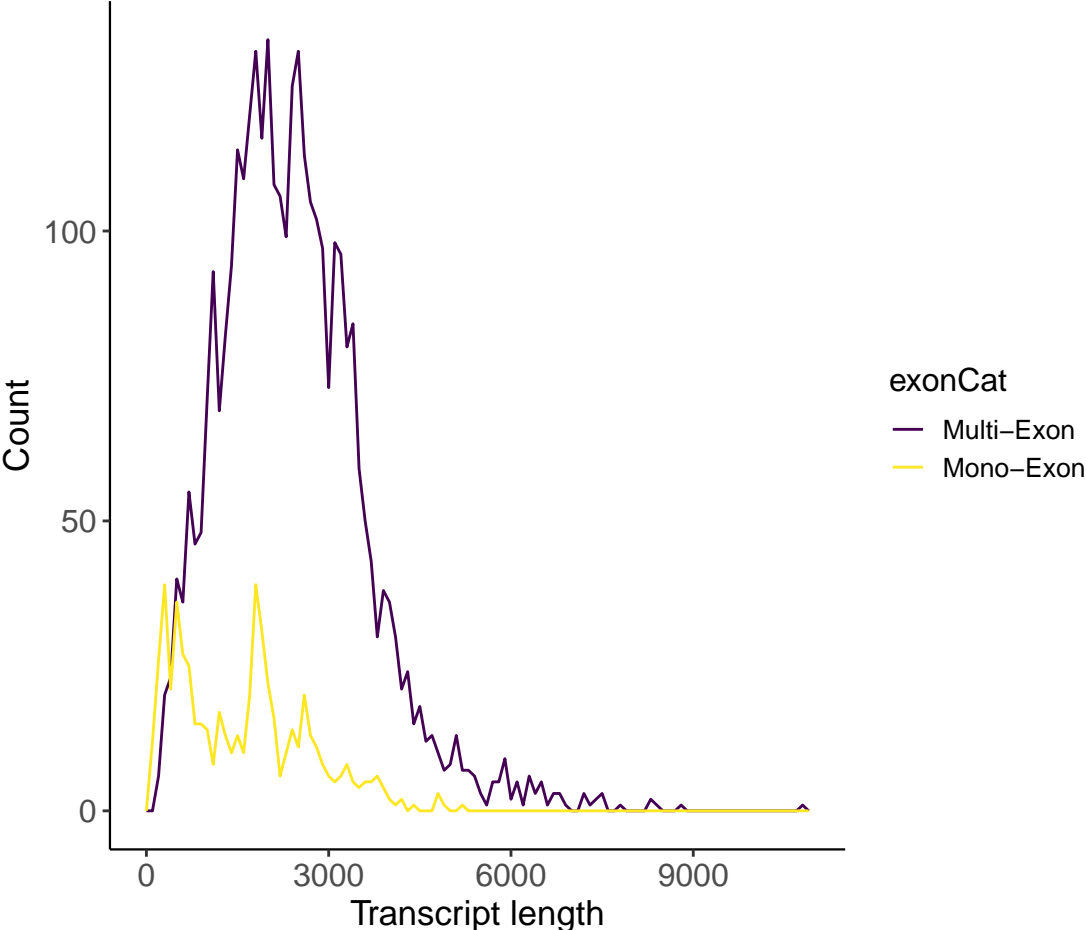
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

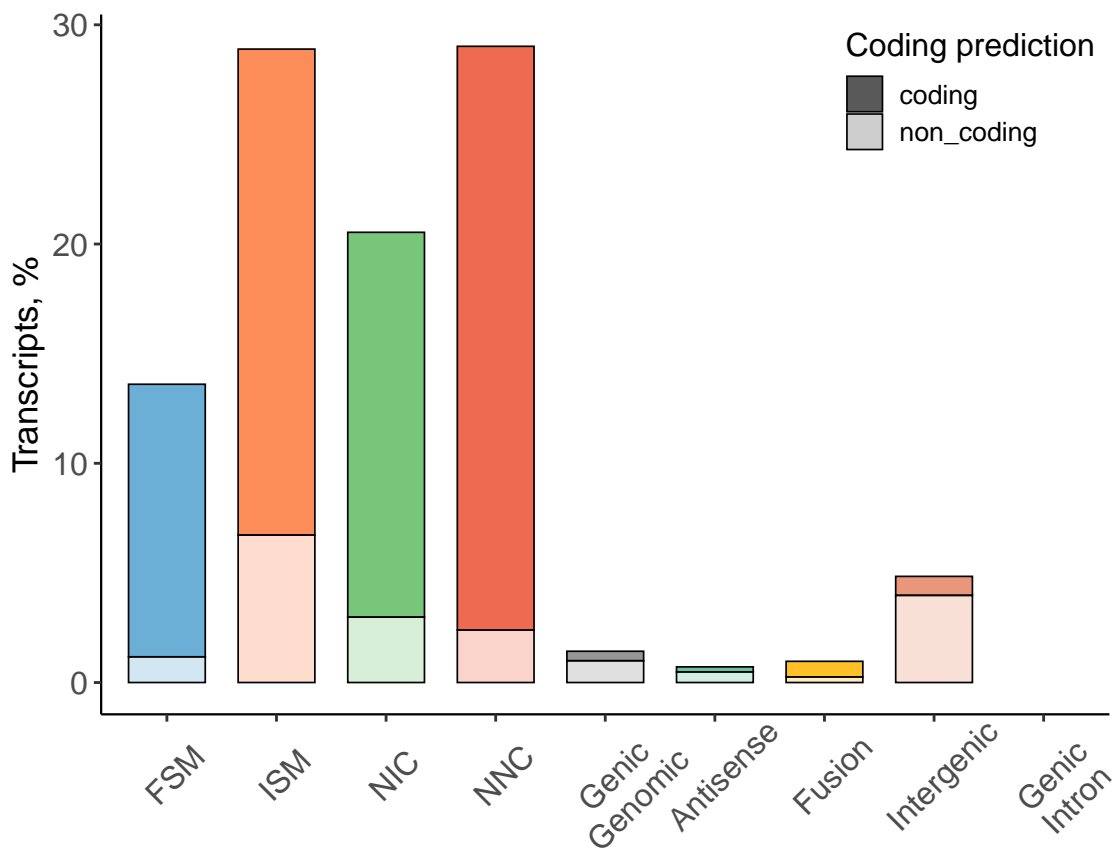


Mono- vs Multi- Exon Transcript Lengths Distribution

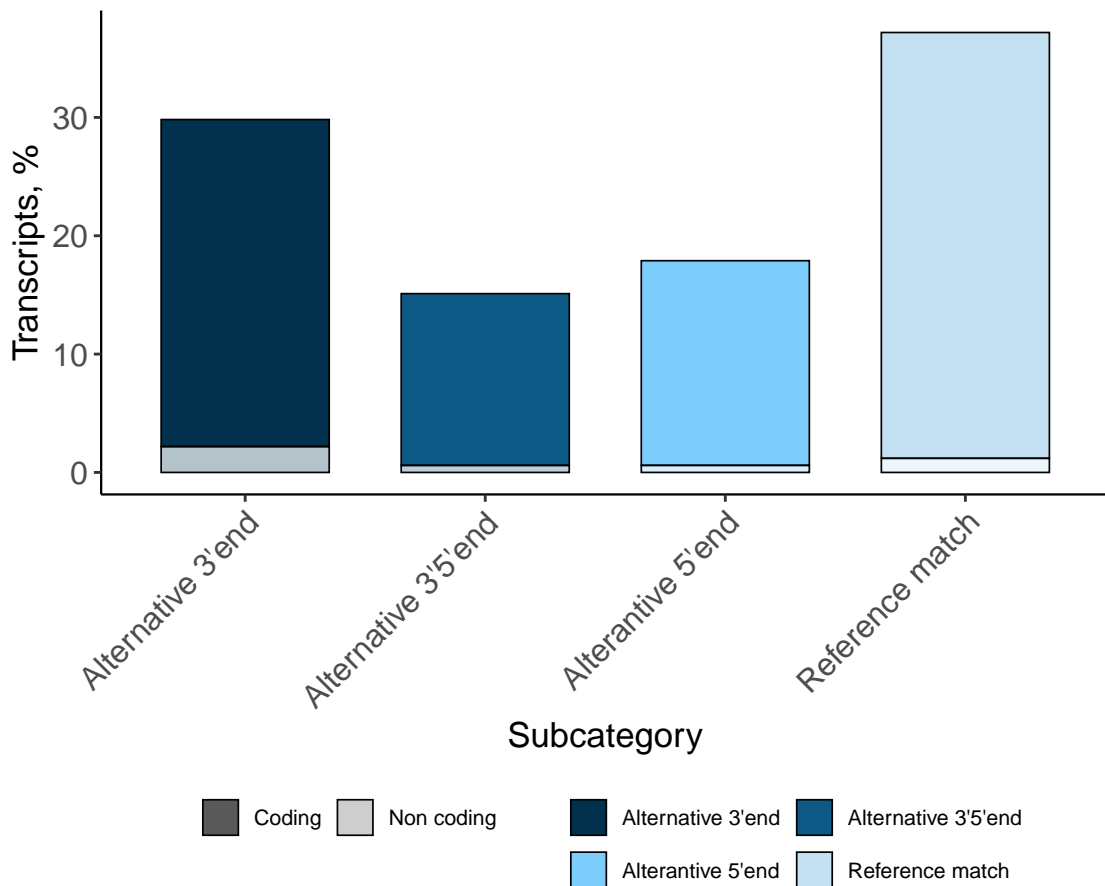


Structural Isoform Characterization

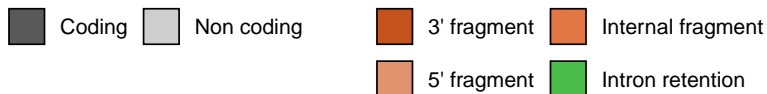
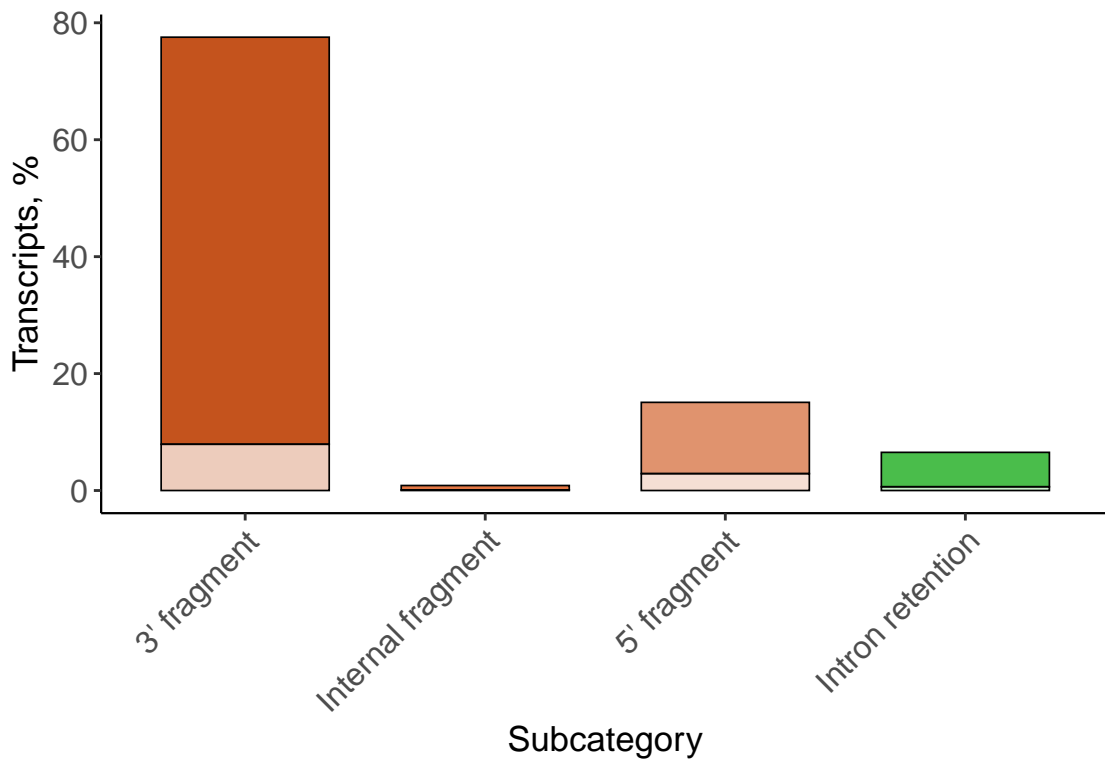
Isoform Distribution Across Structural Categories



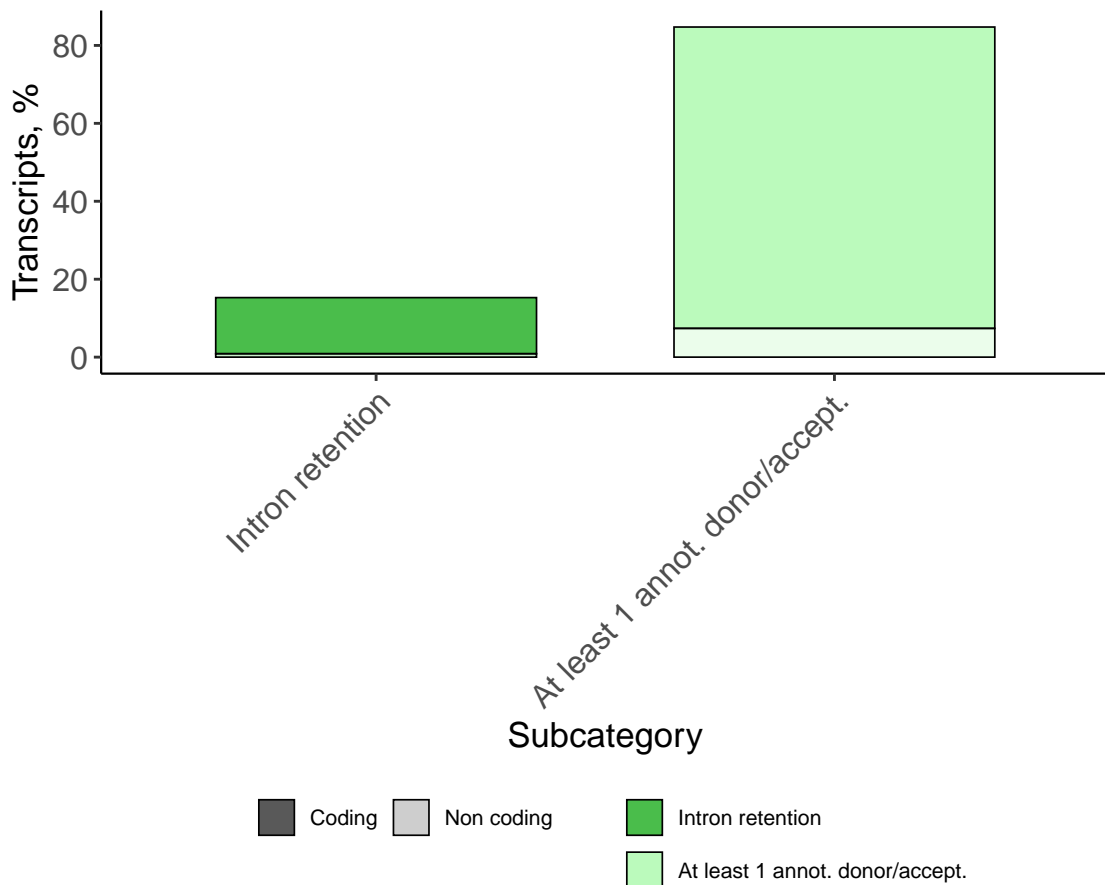
Isoform Distribution Across FSM



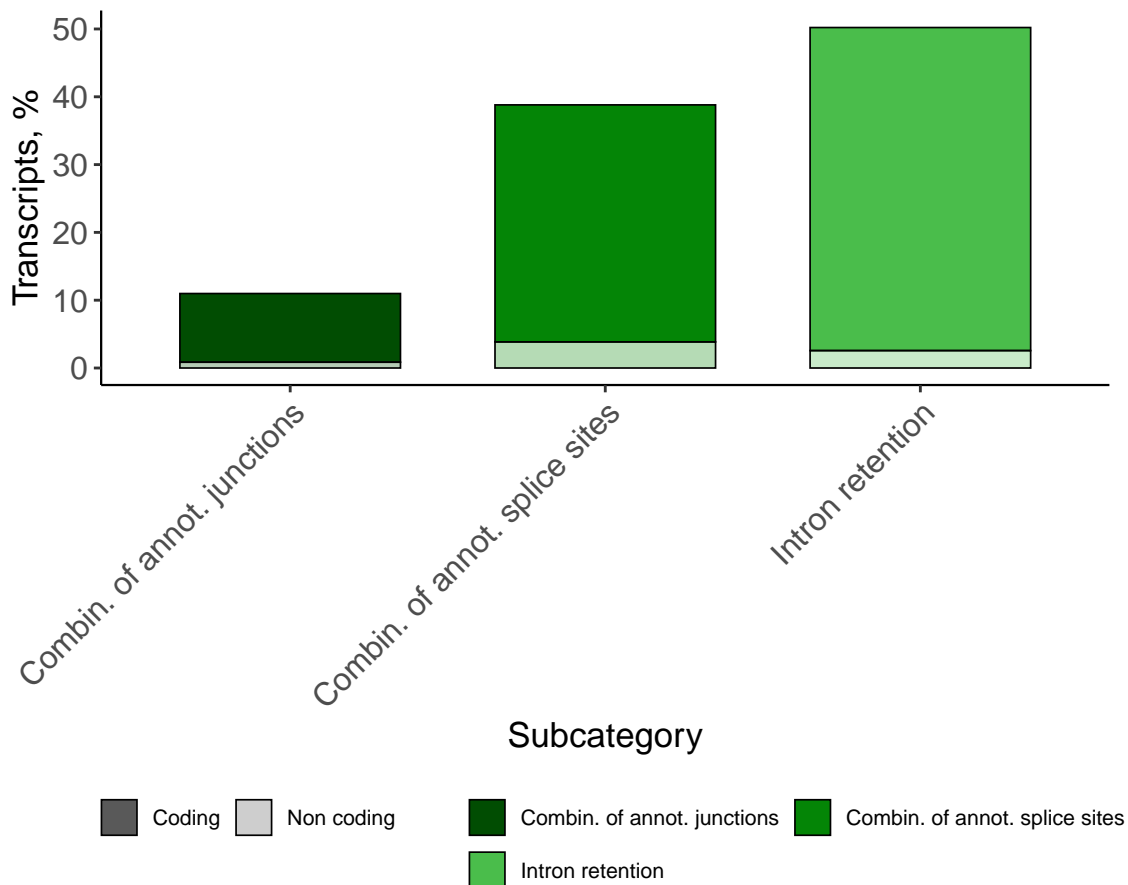
Isoform Distribution Across ISM



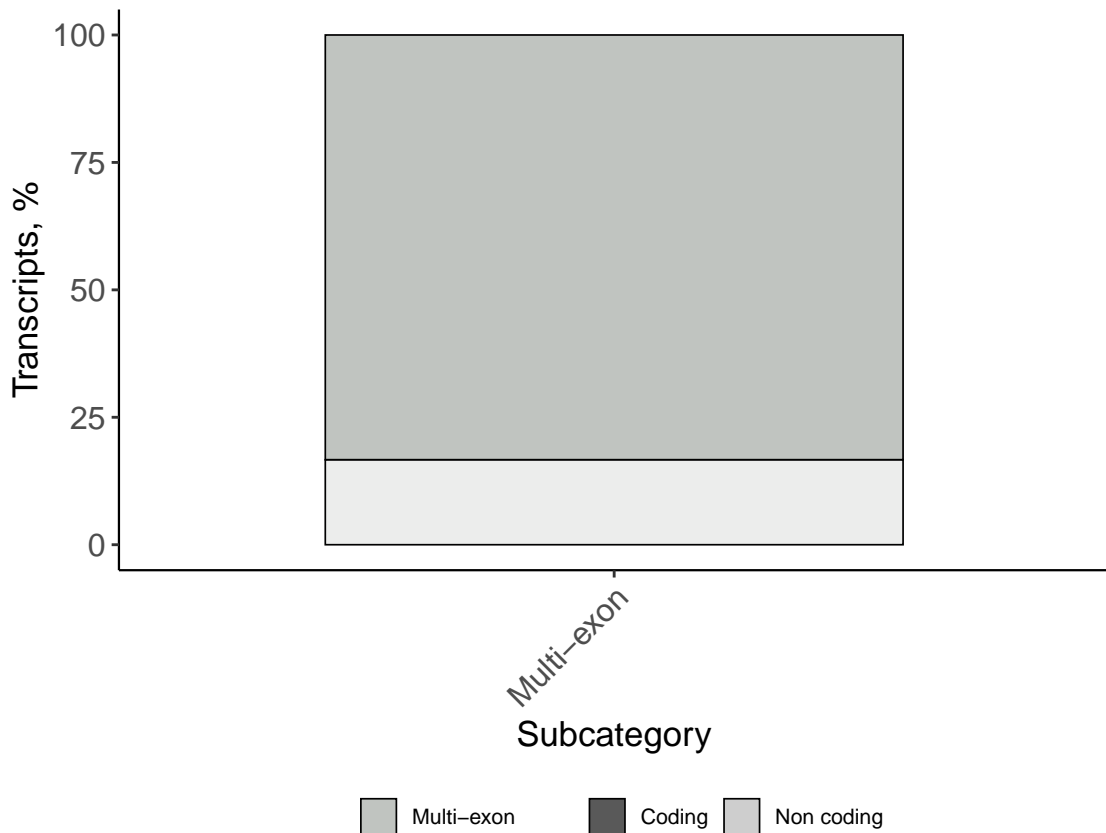
Isoform Distribution Across NNC



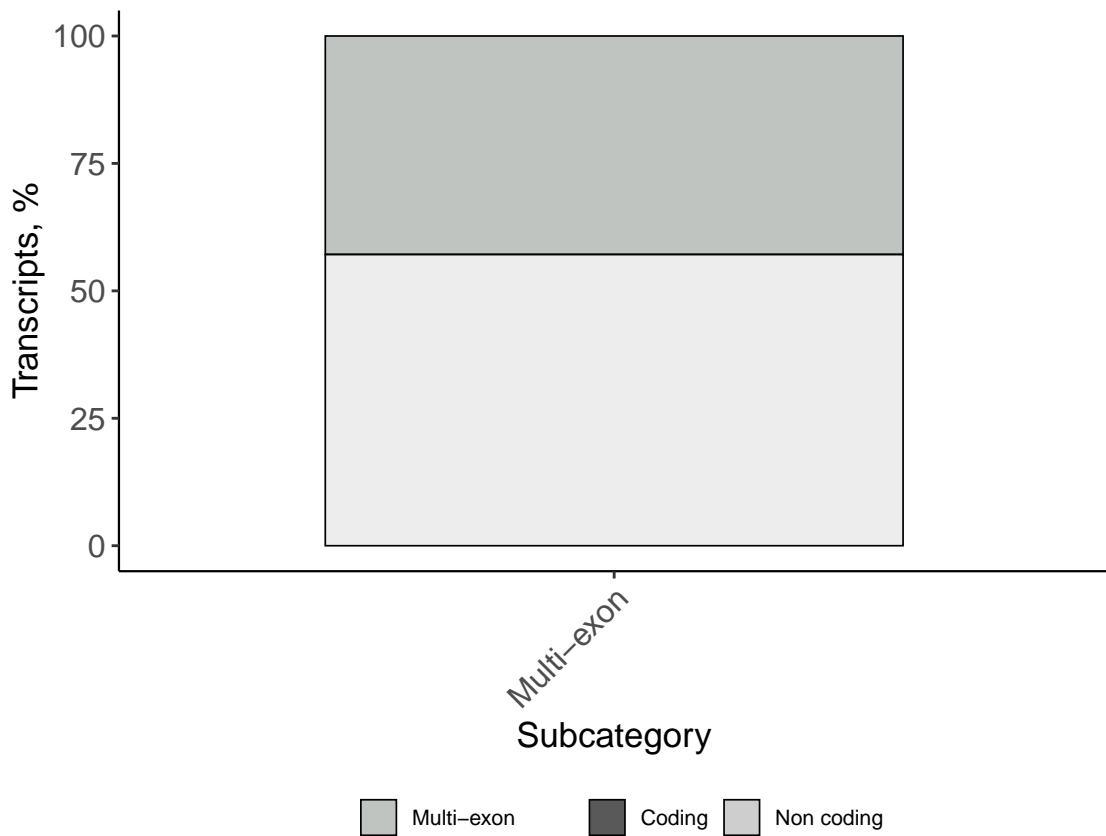
Isoform Distribution Across NIC



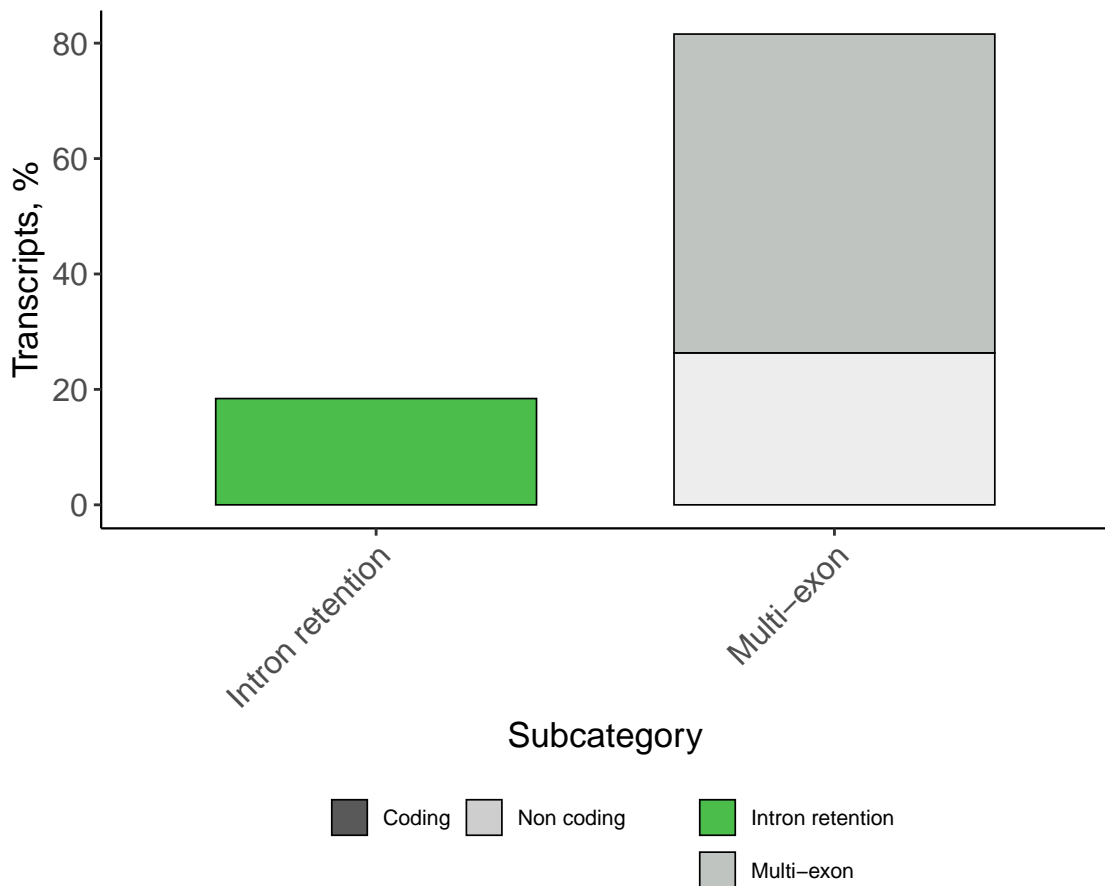
Isoform Distribution Across Genic Genomic



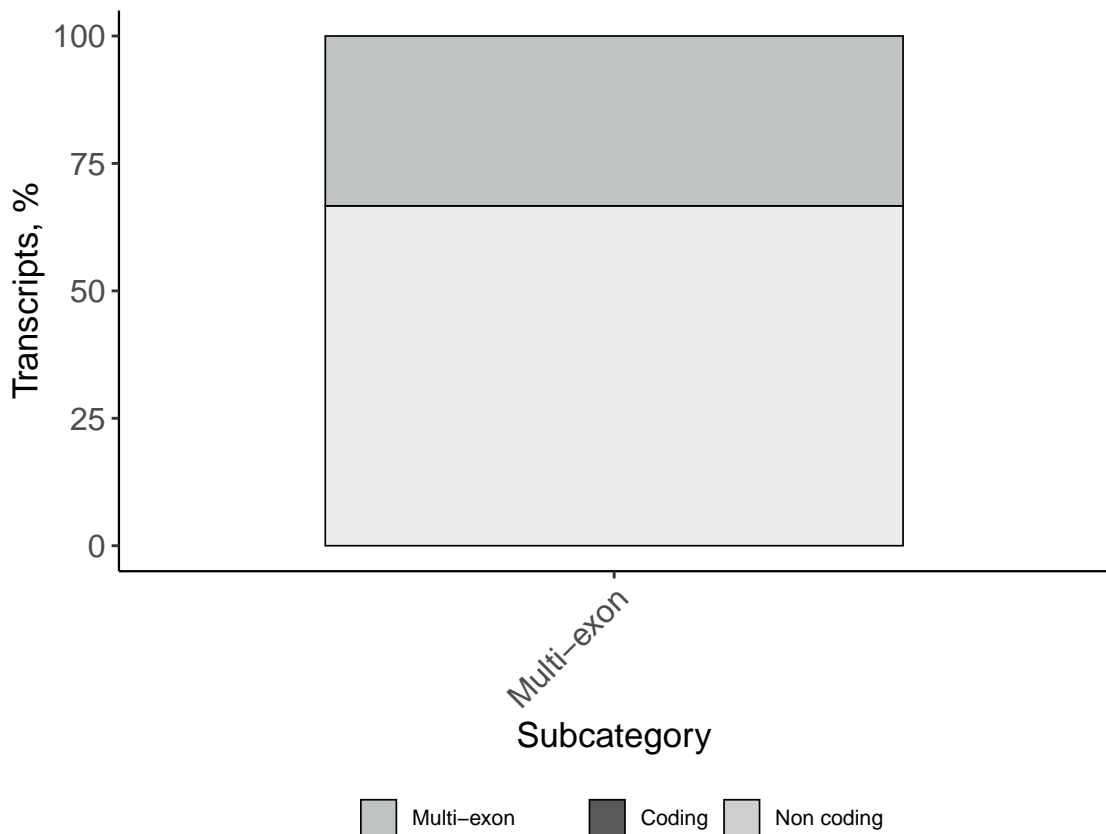
Isoform Distribution Across Antisense



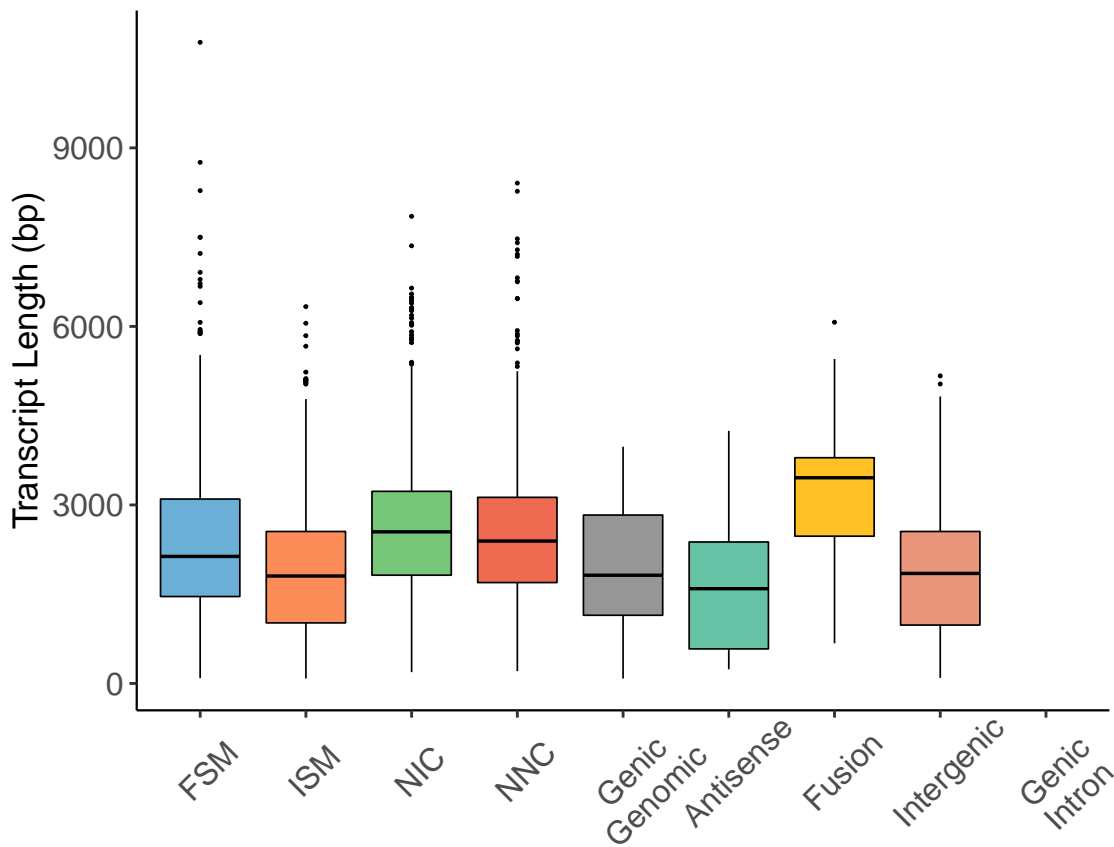
Isoform Distribution Across Fusion



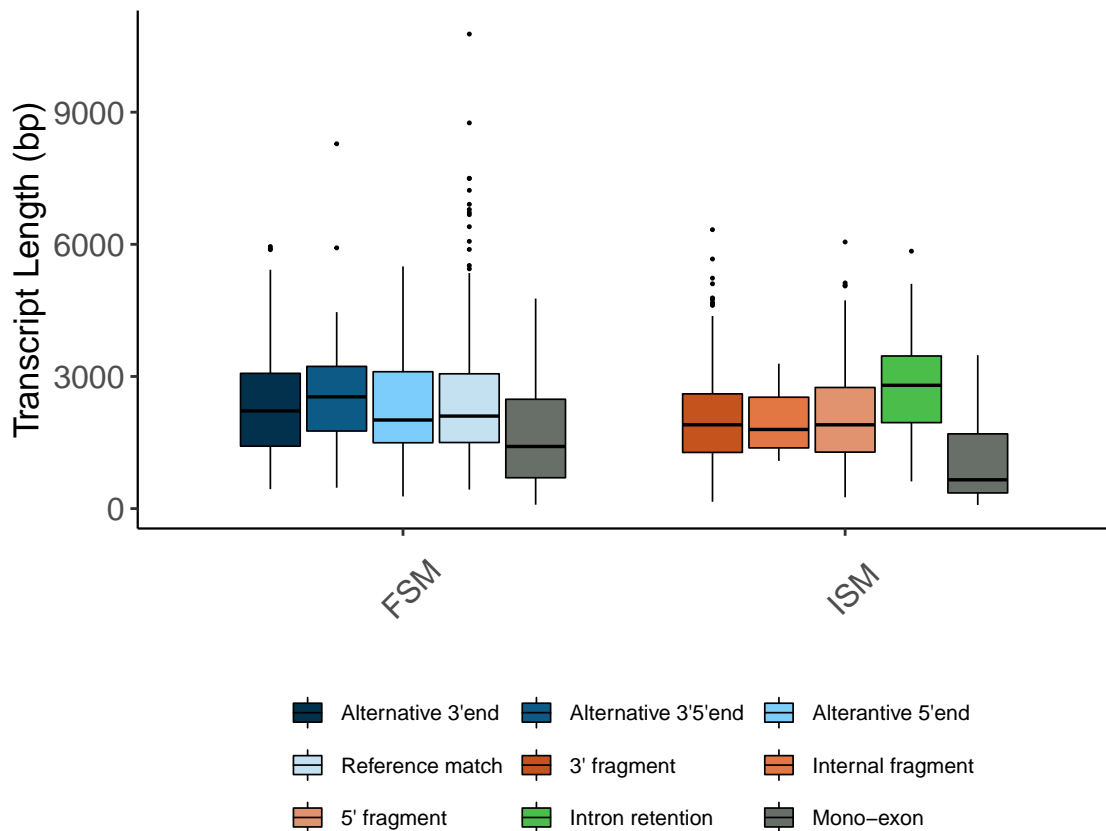
Isoform Distribution Across Intergenic



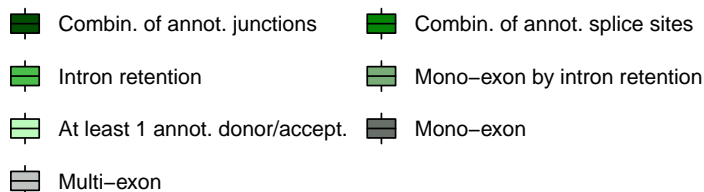
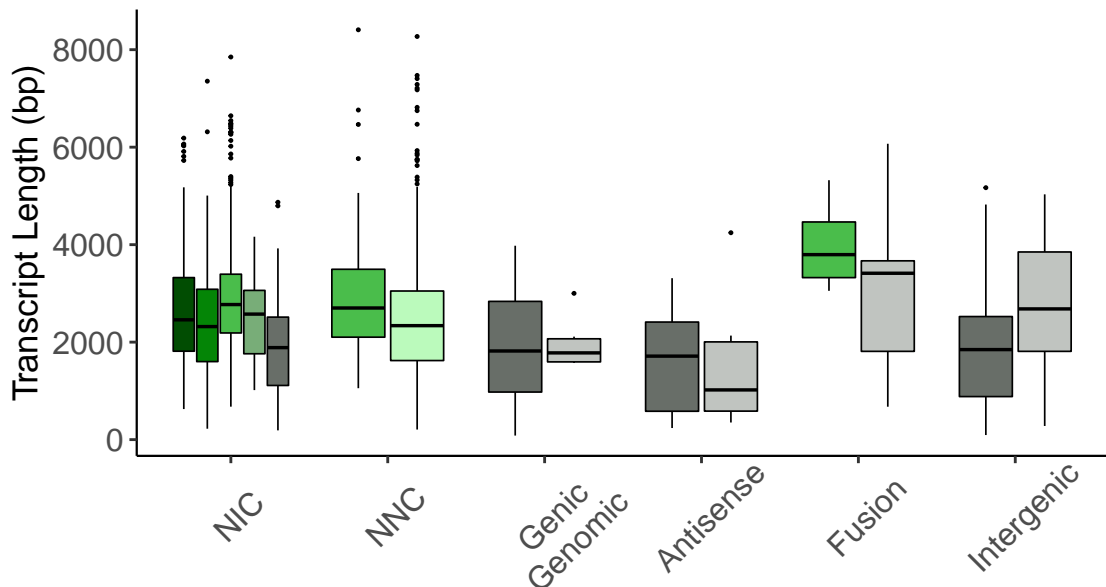
Transcript Lengths by Structural Classification



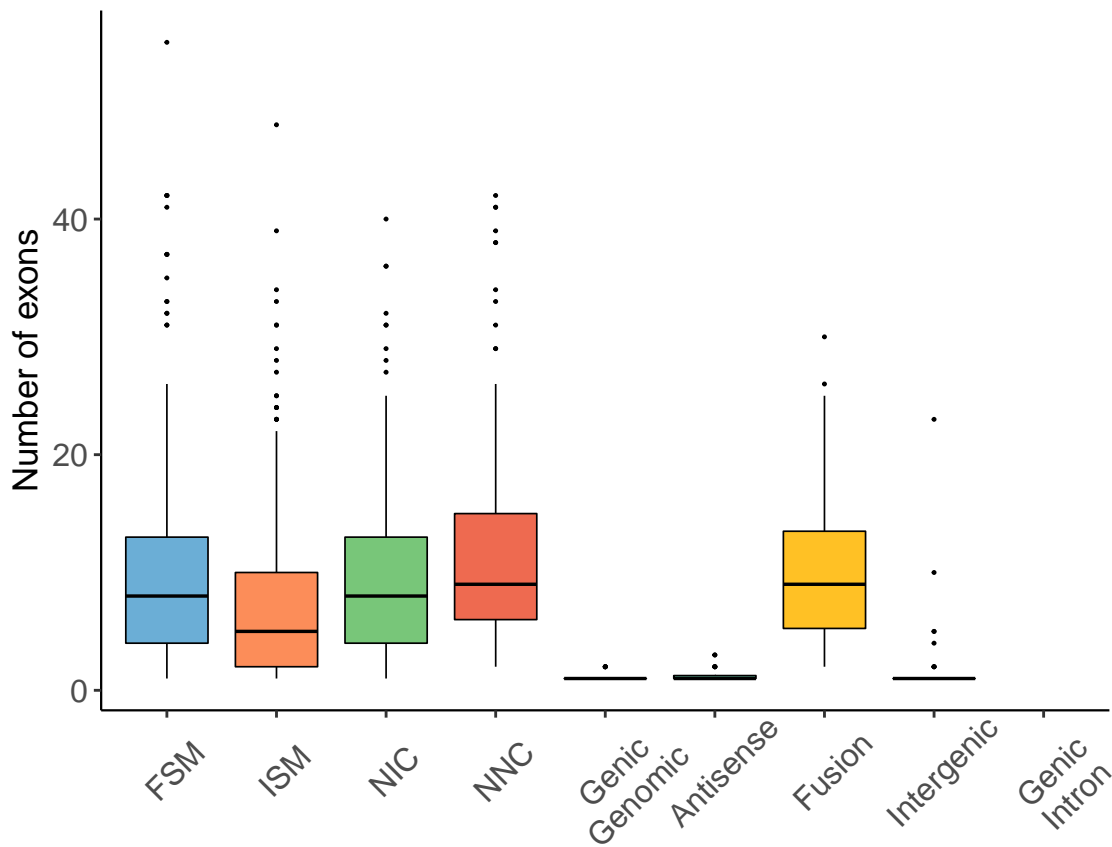
Transcript Lengths by Subcategory



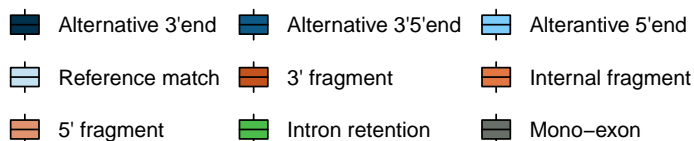
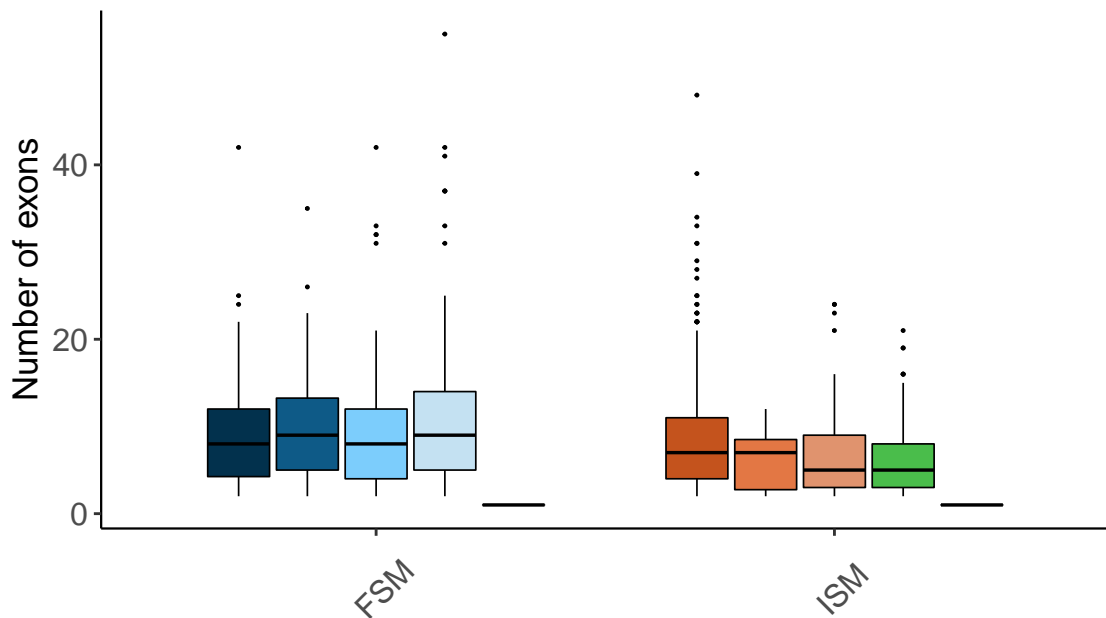
Transcript Lengths by Subcategory



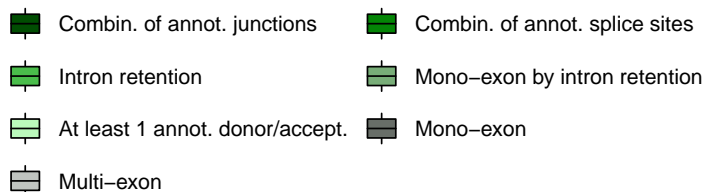
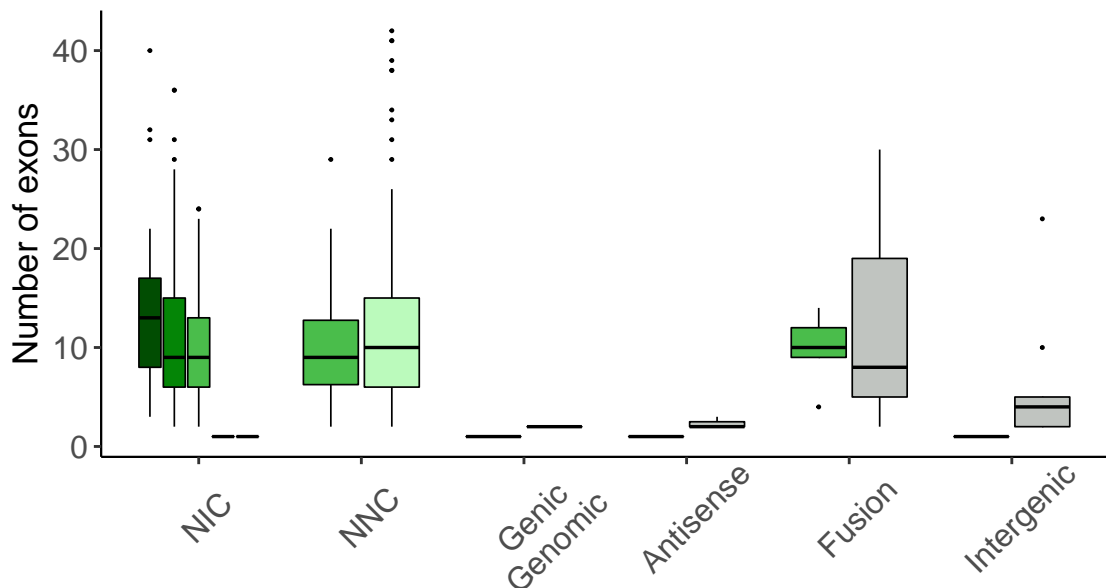
Exon Counts by Structural Classification



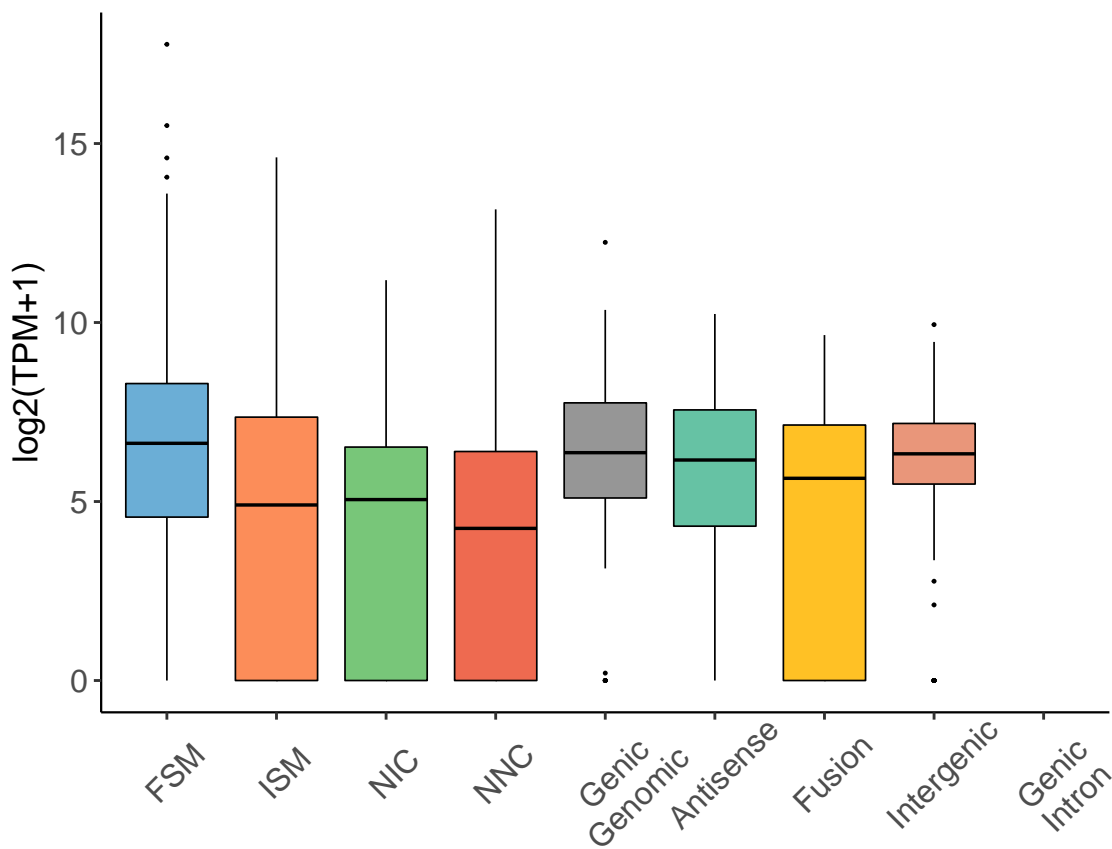
Exon Counts by Subcategory



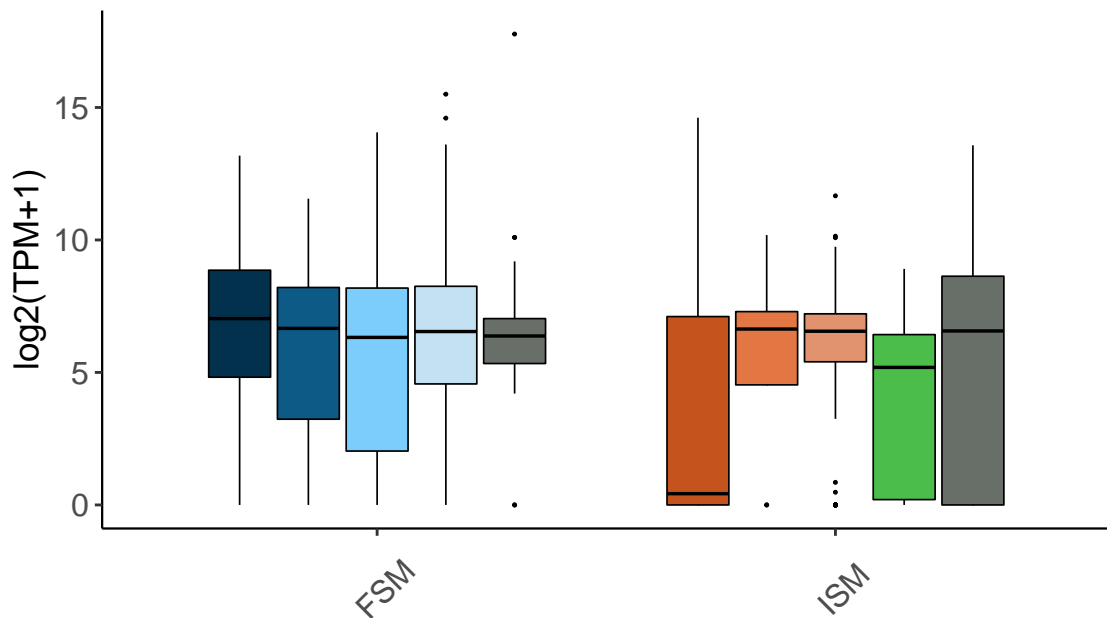
Exon Counts by Subcategory



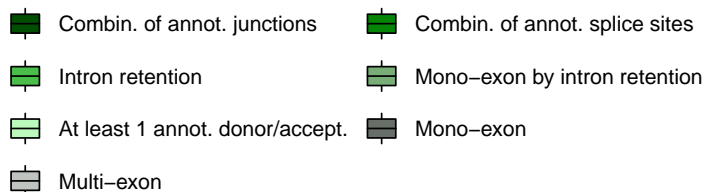
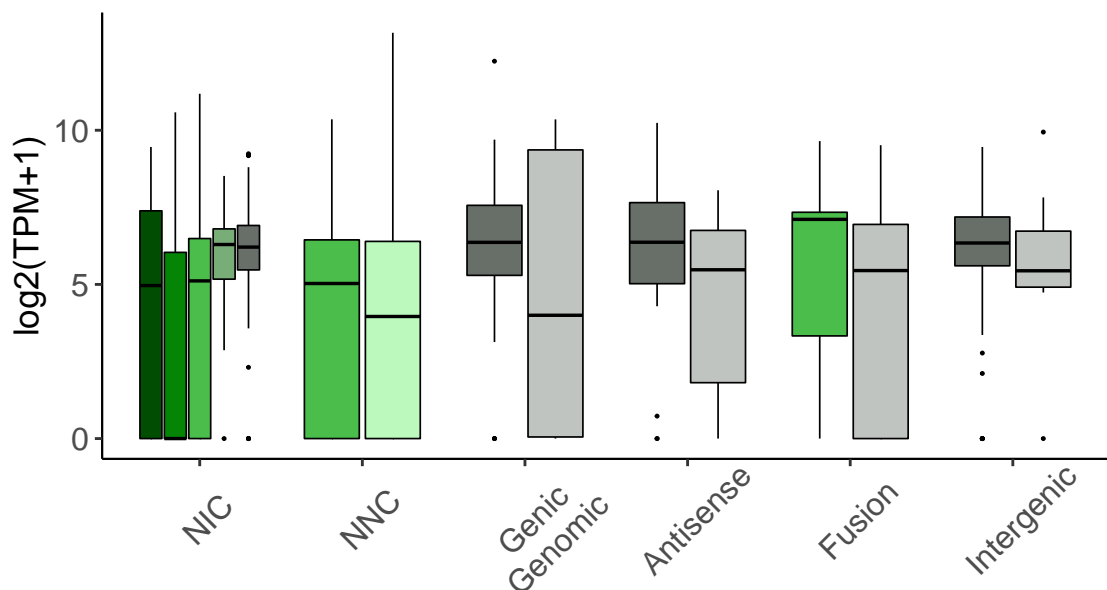
Transcript Expression by Structural Category



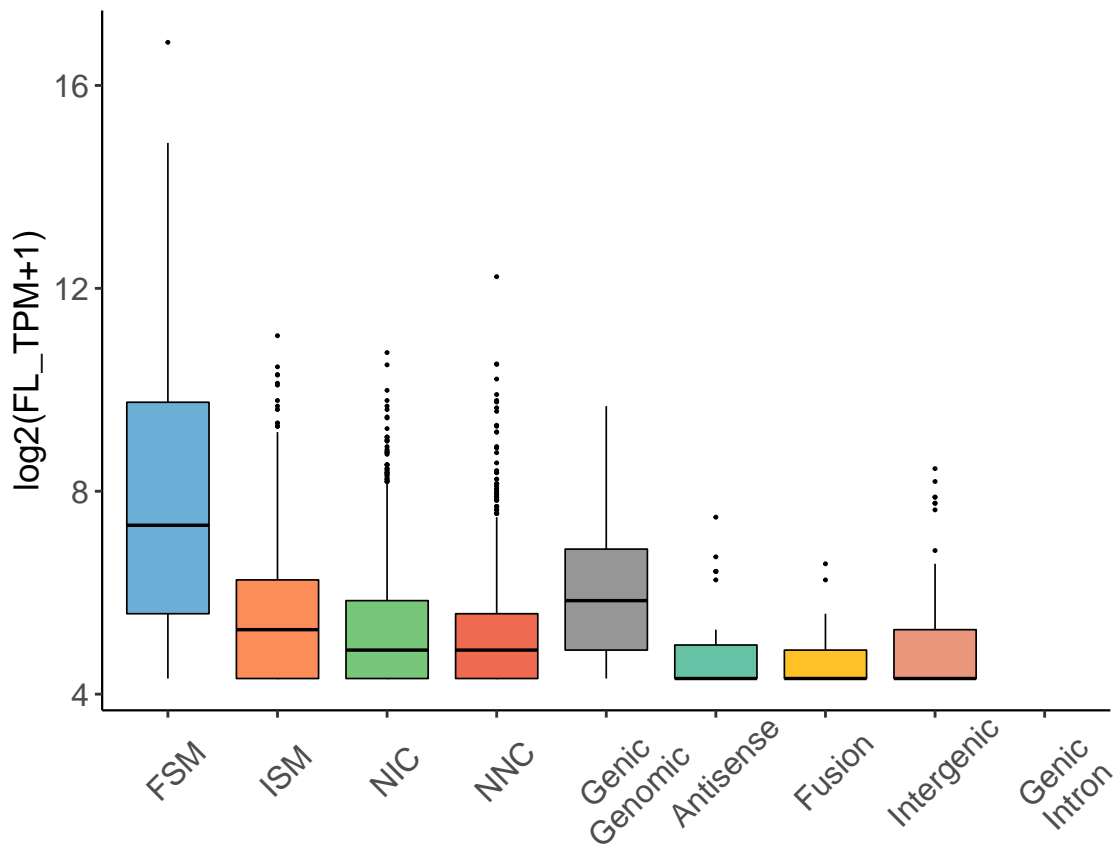
Transcript Expression by Subcategory



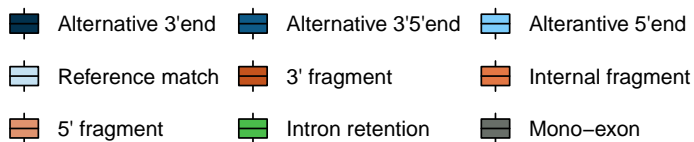
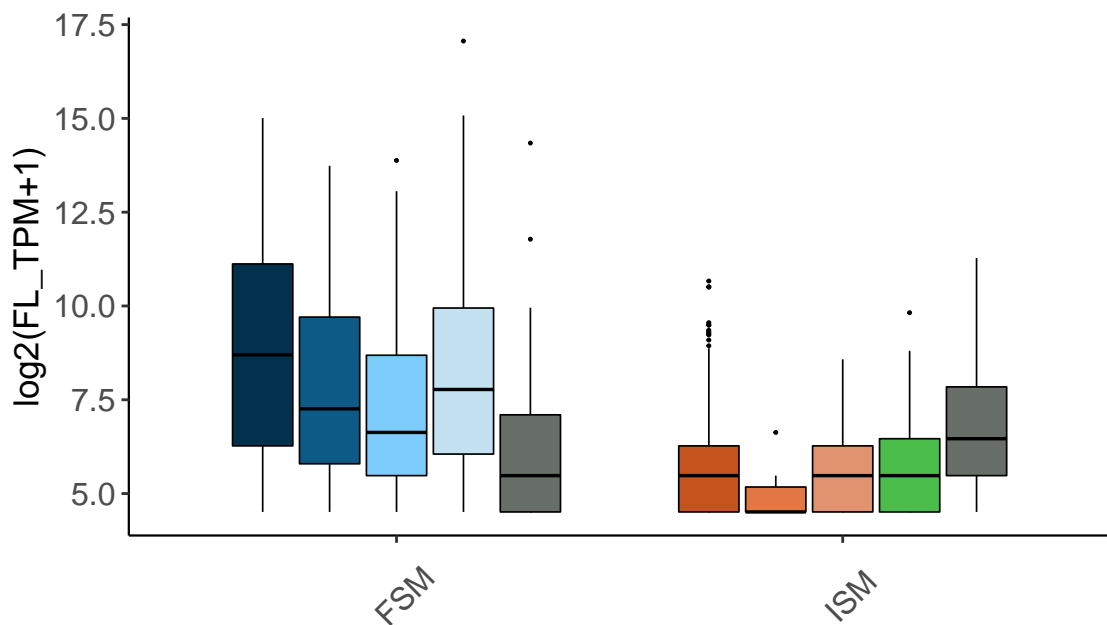
Transcript Expression by Subcategory



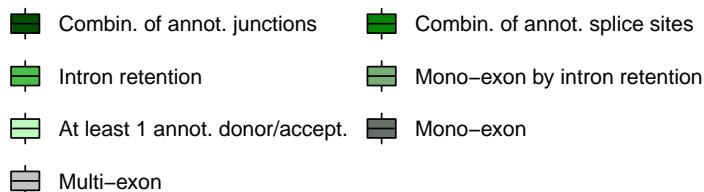
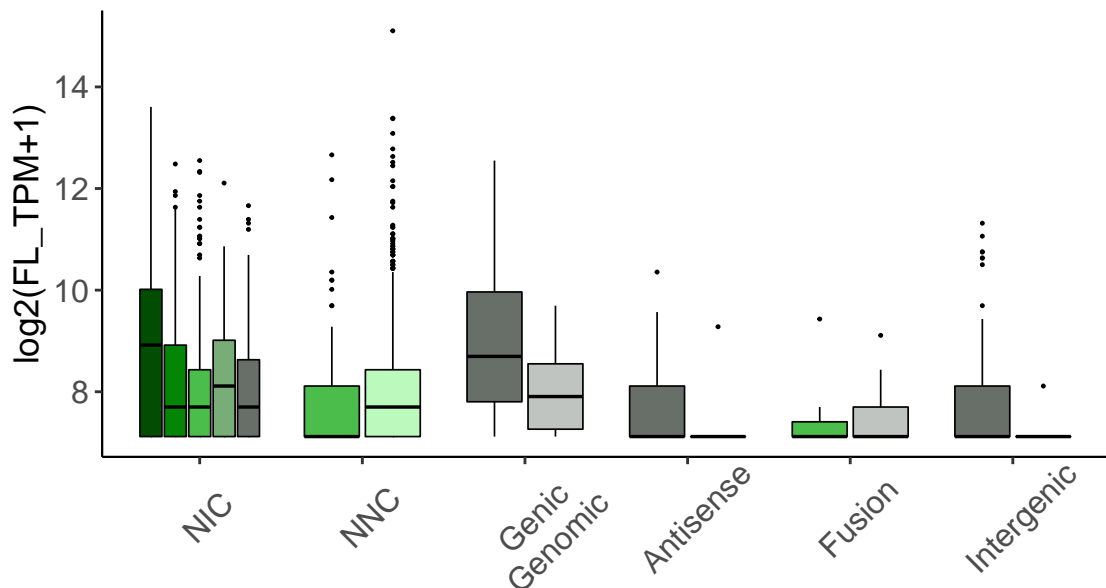
Long Reads Count by Structural Category



Long Reads Count by Subcategory

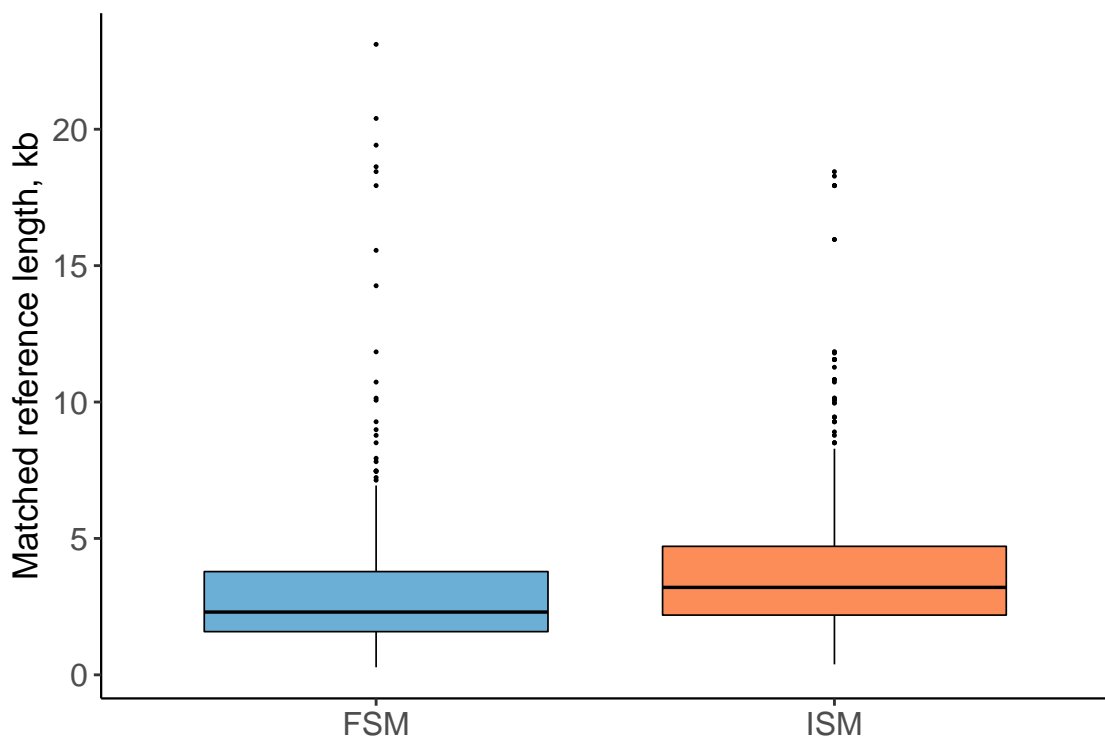


Long Reads Count by Subcategory



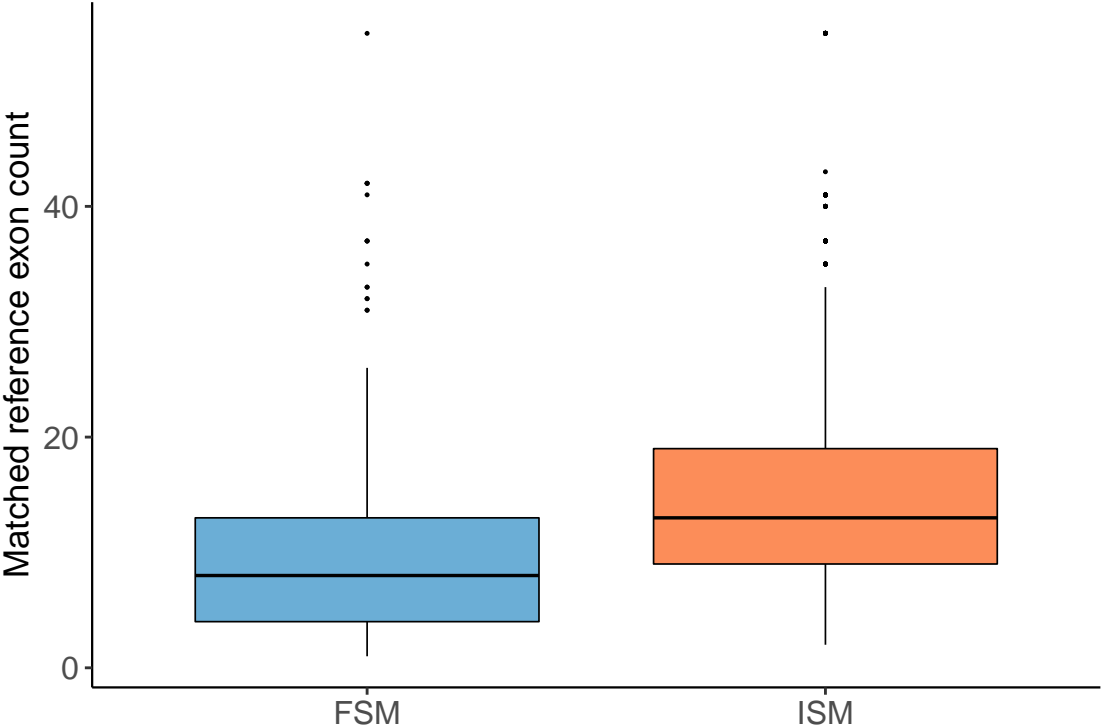
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

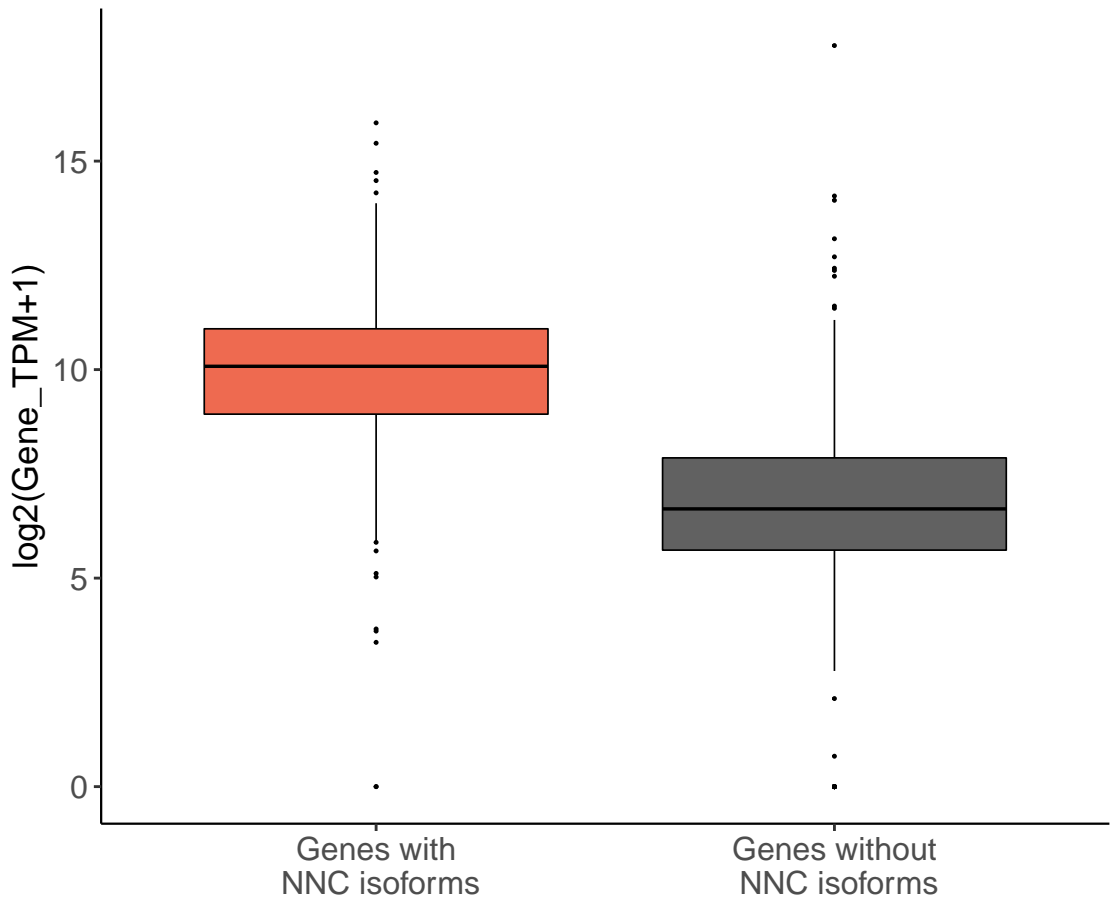


Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

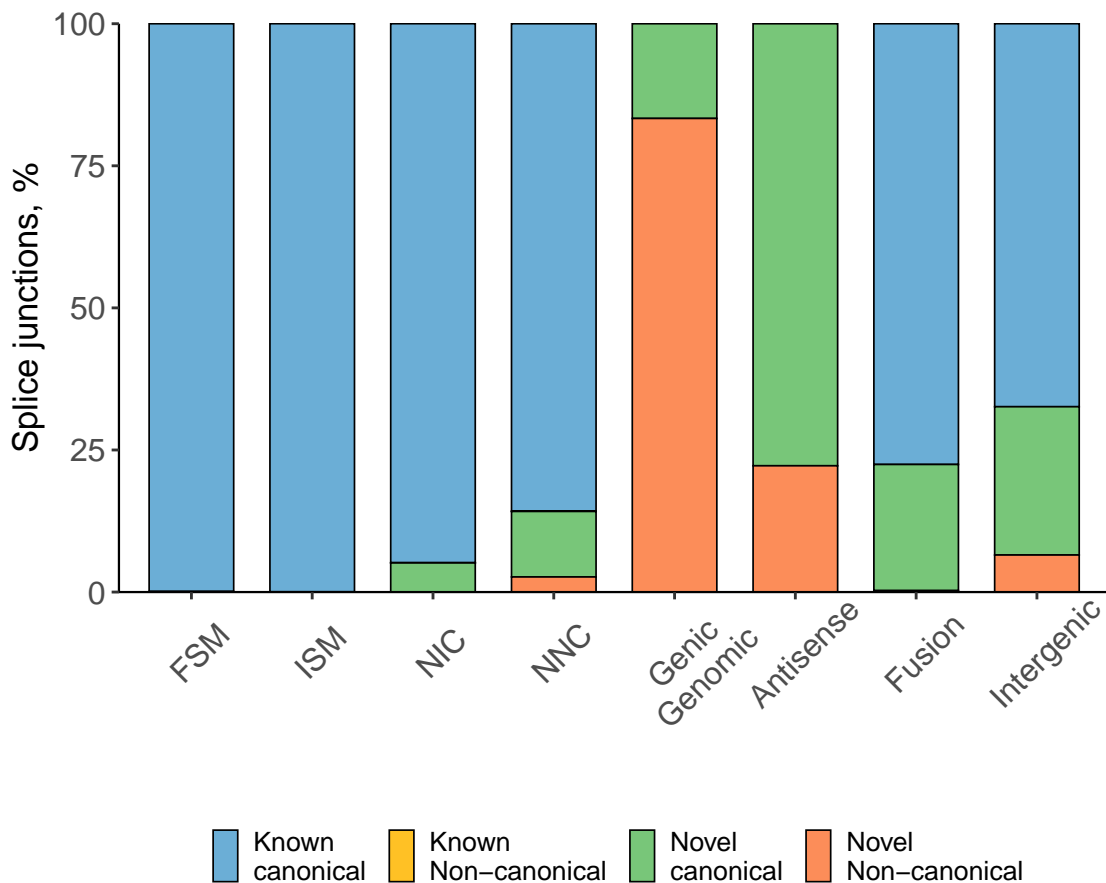


Gene Expression of NNC And Not NNC Containing Genes

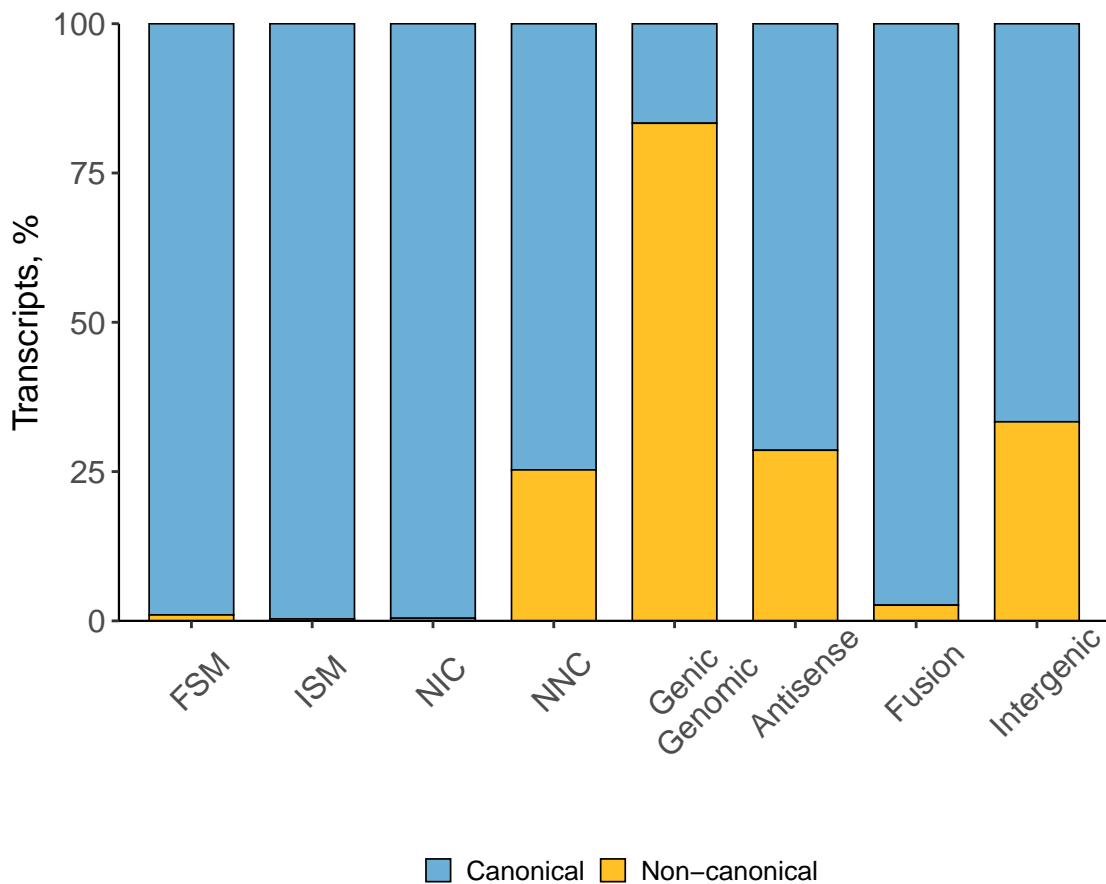


Splice Junction Characterization

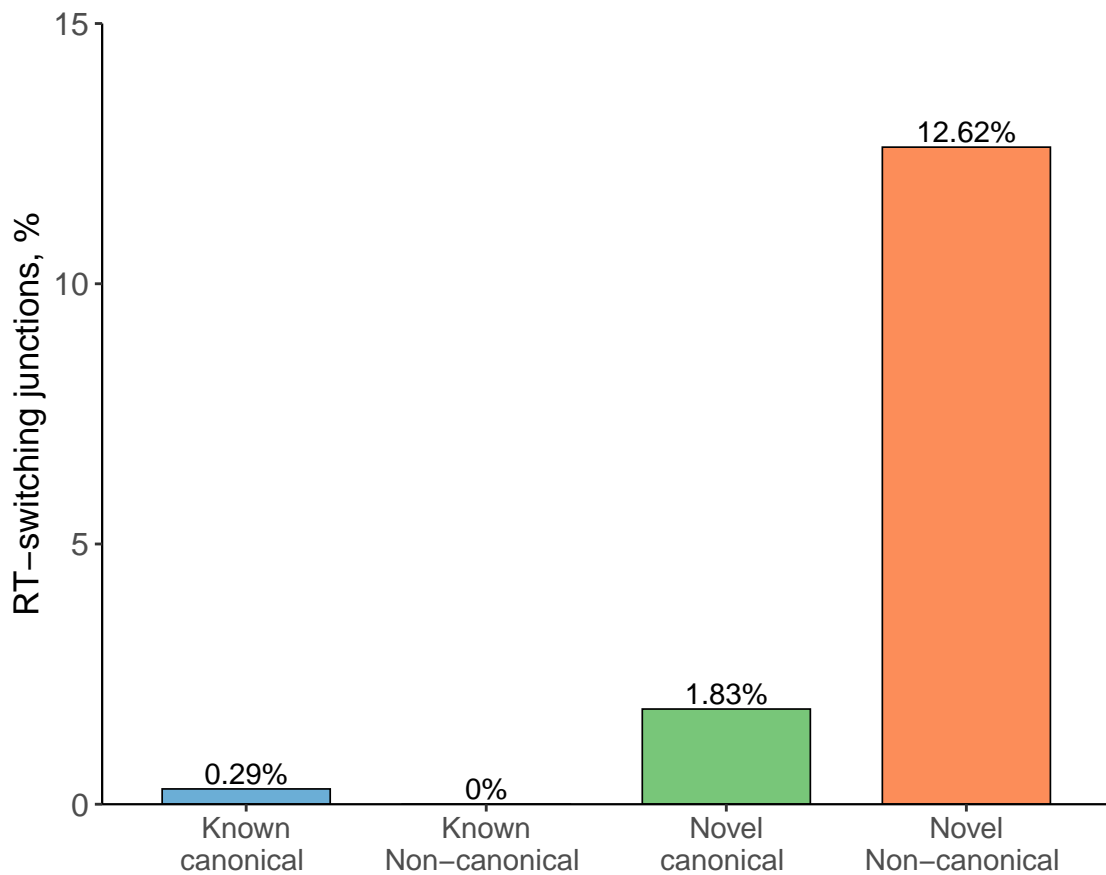
Distribution of Splice Junctions by Structural Classification



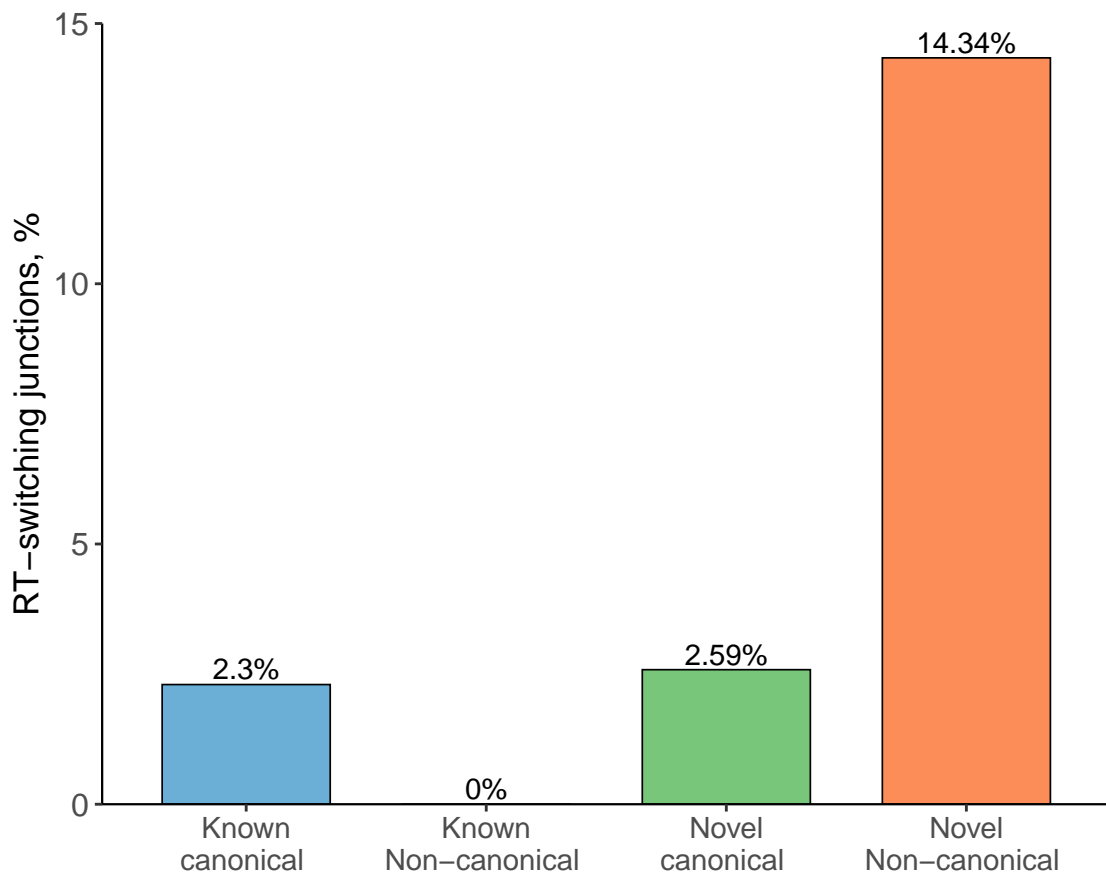
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



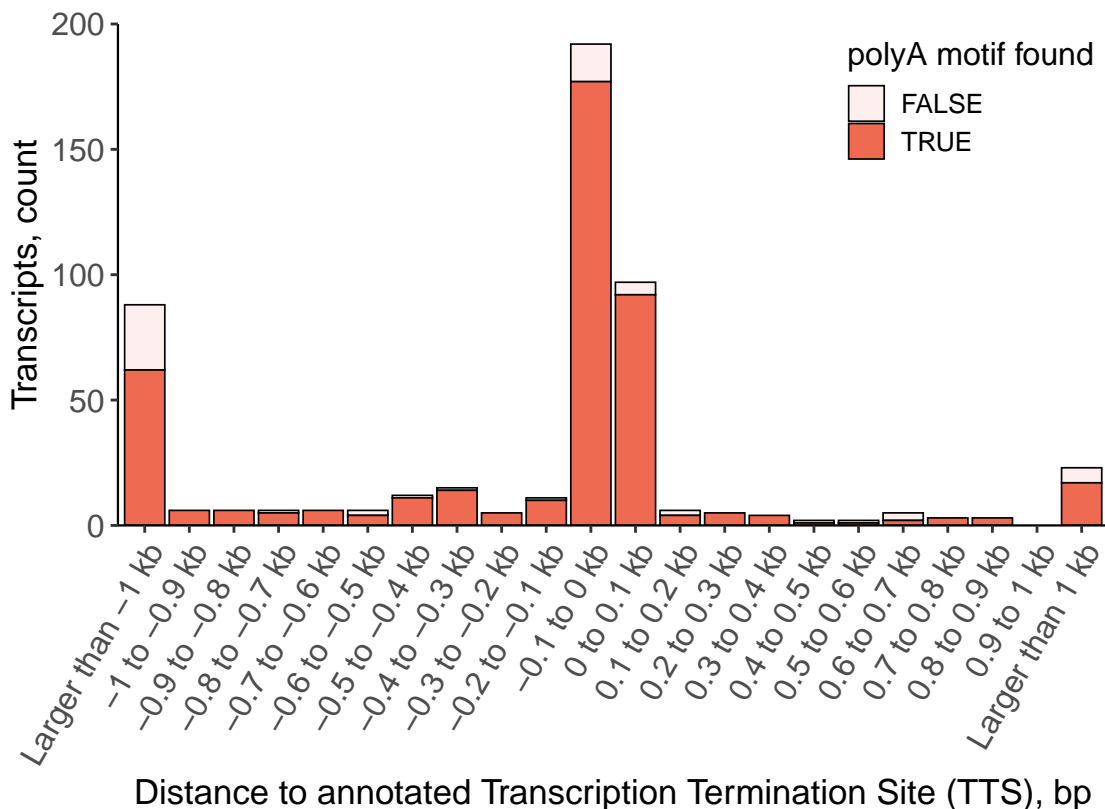
Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

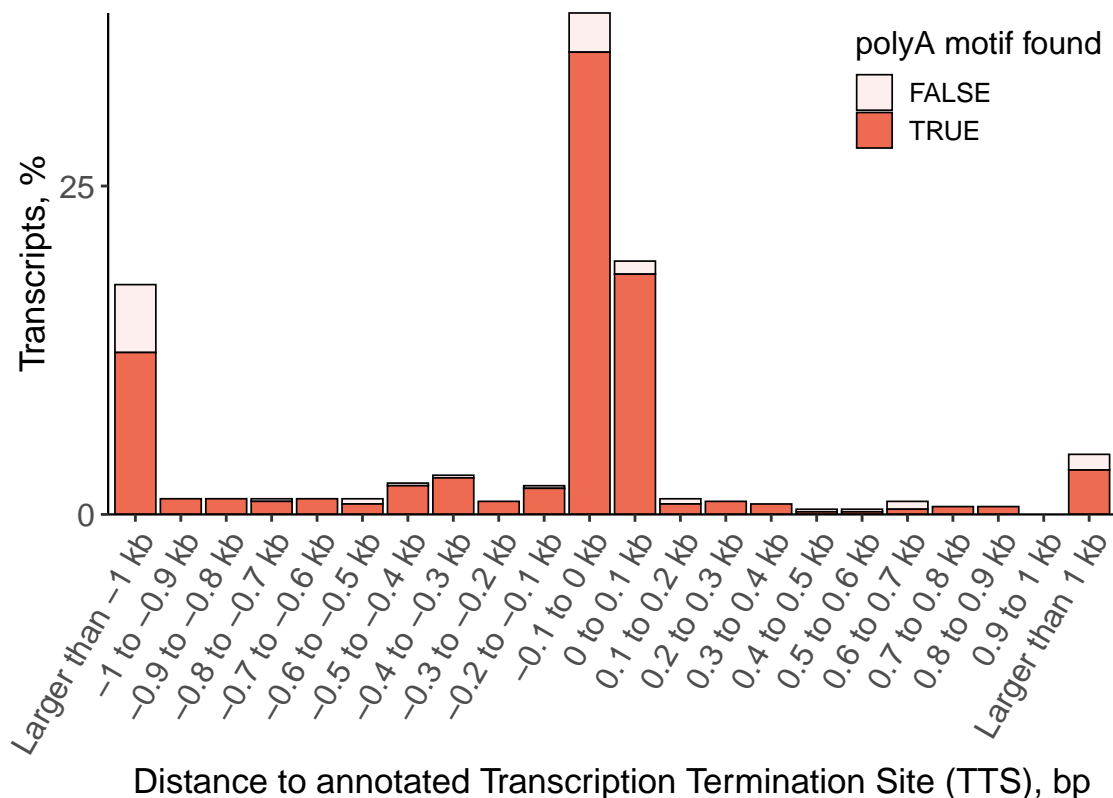
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



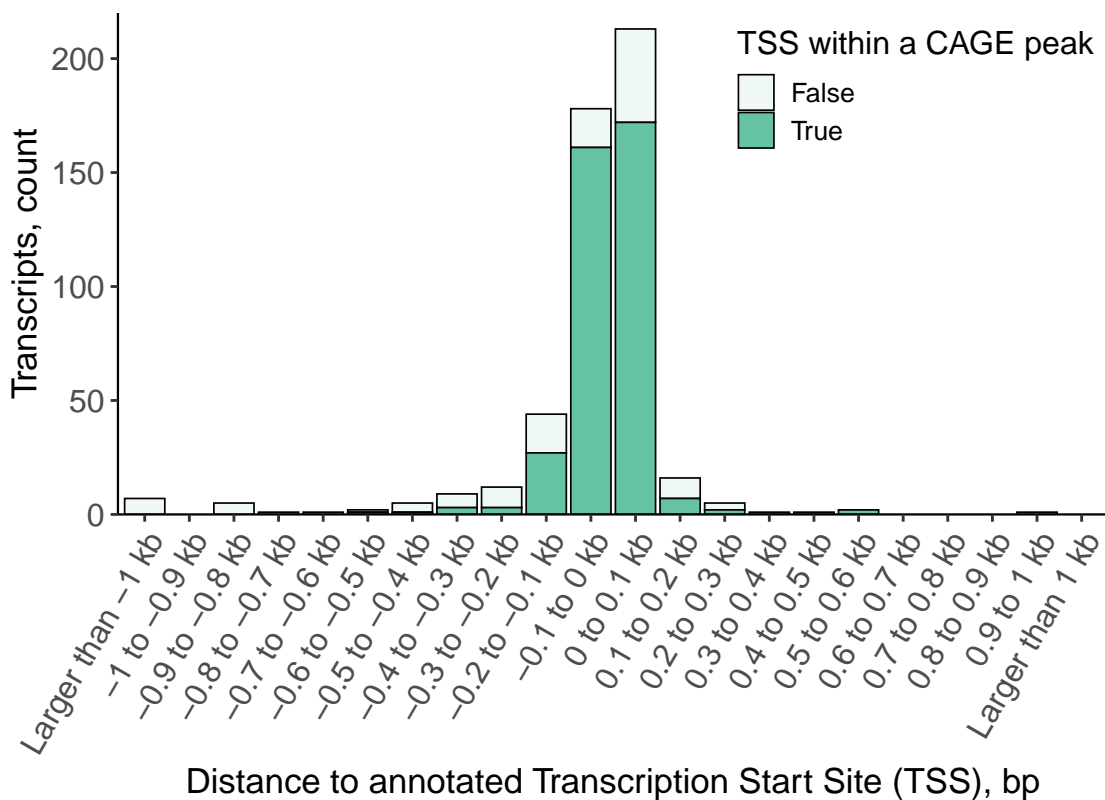
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



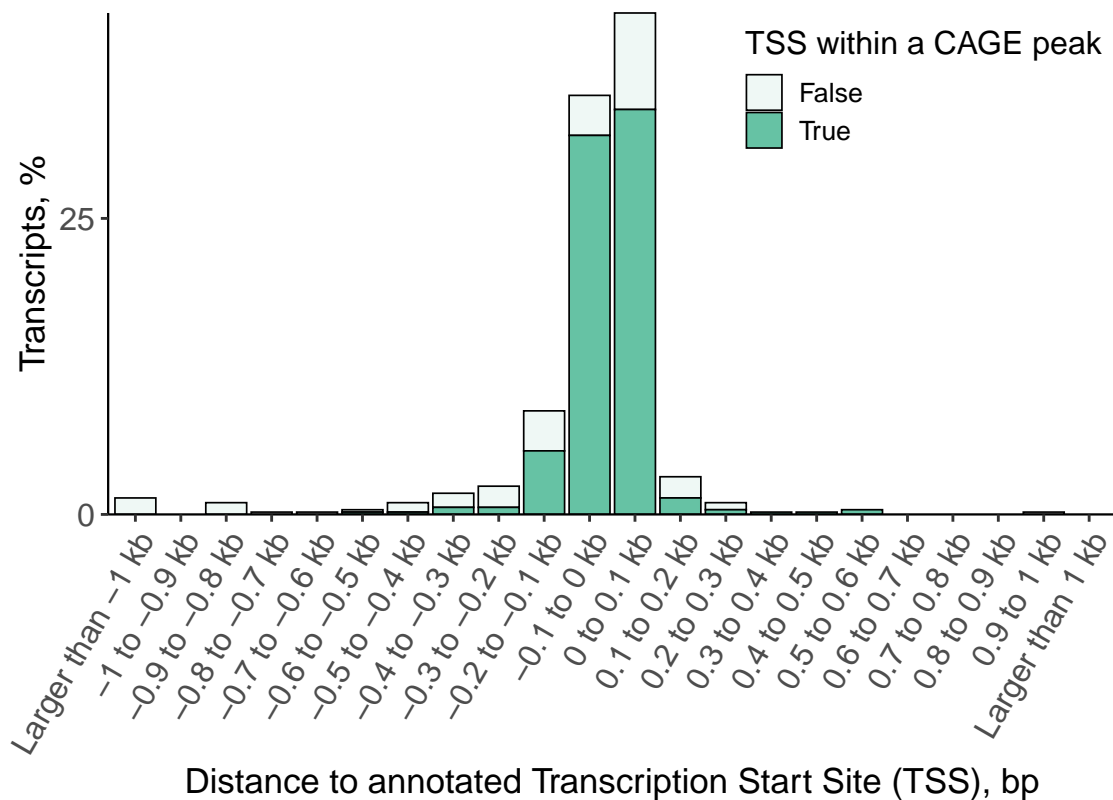
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



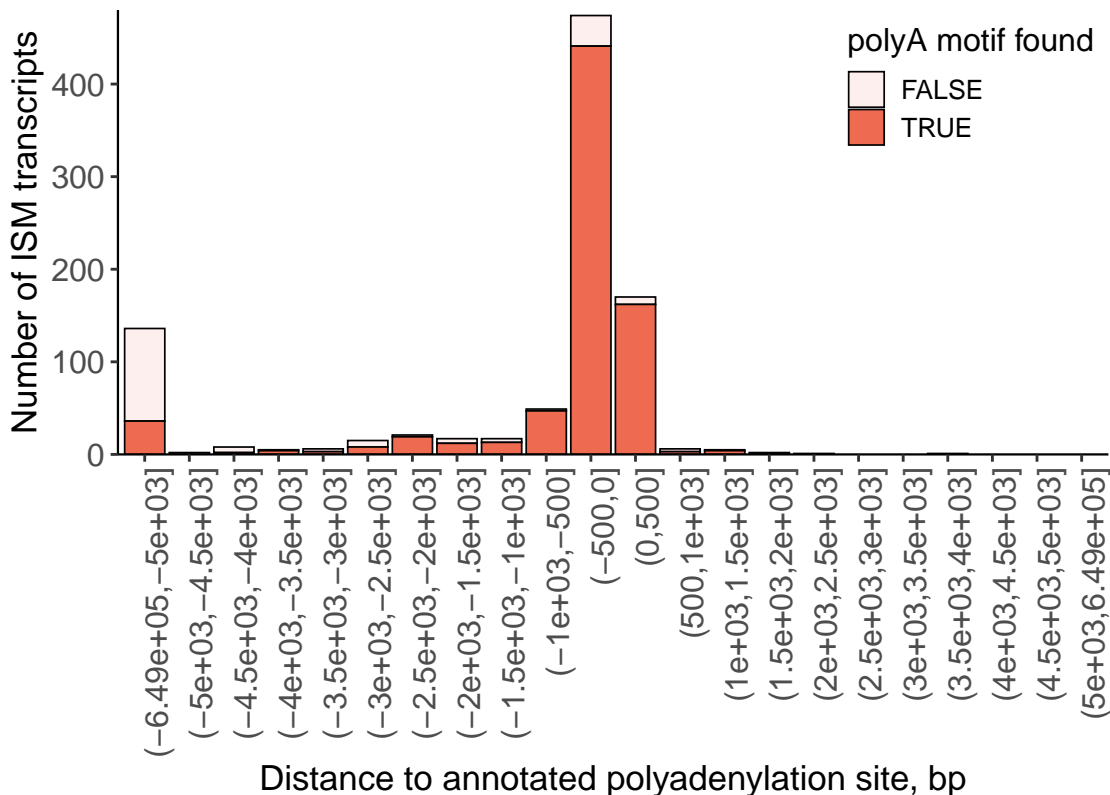
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



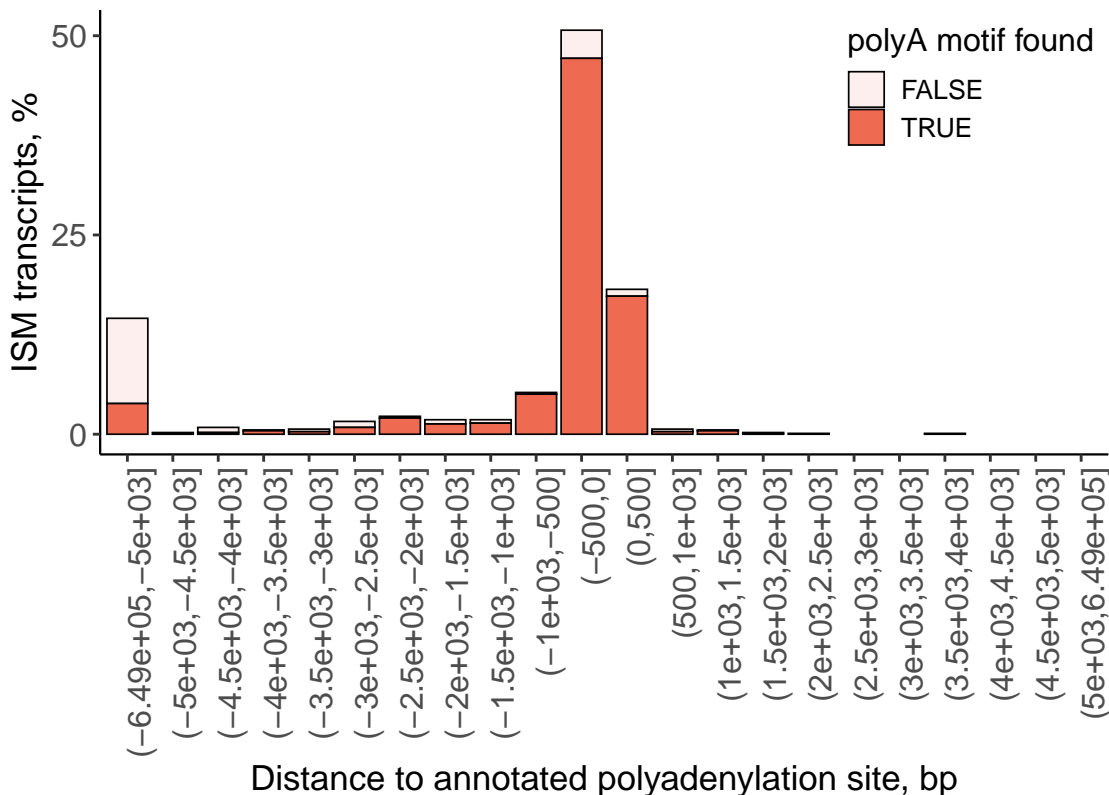
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



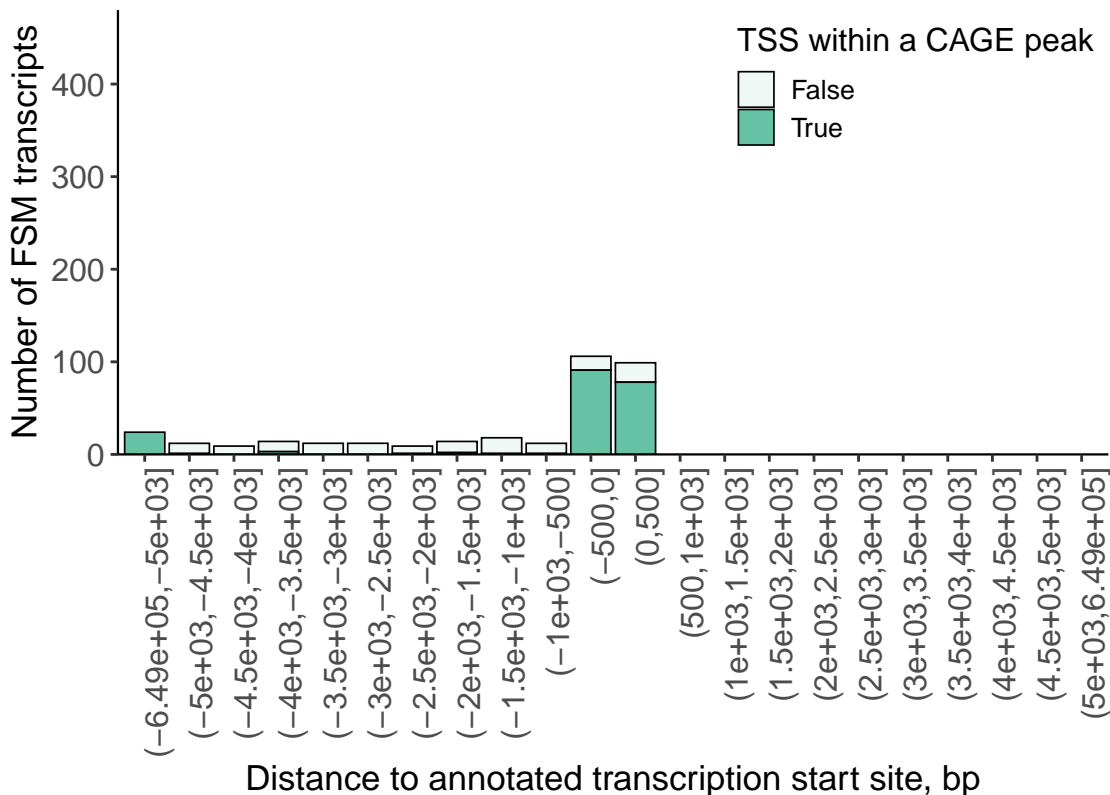
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



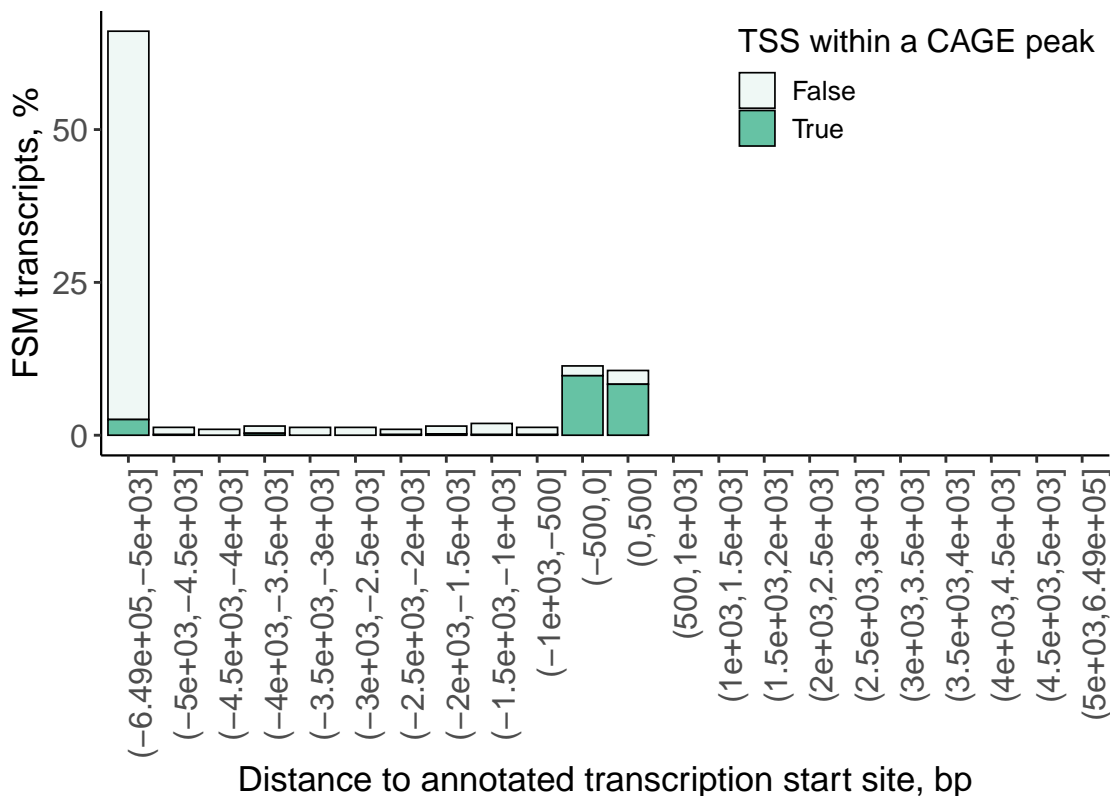
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

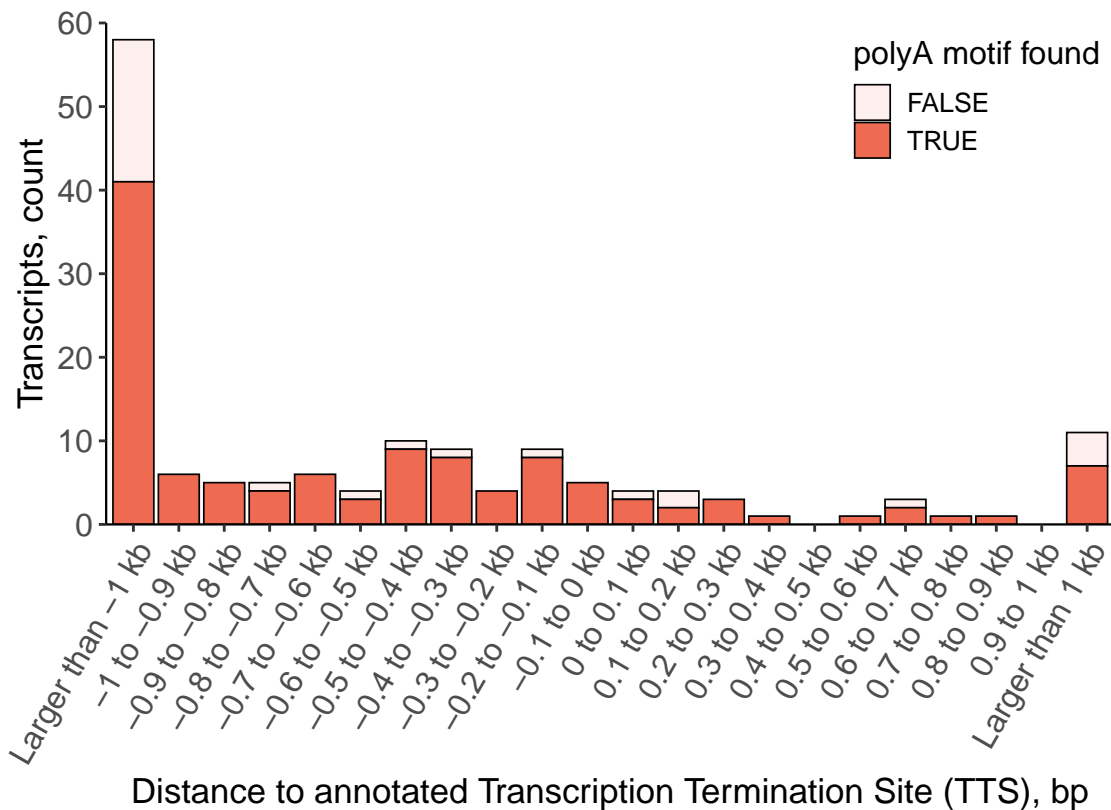
Negative values indicate downstream of annotated TSS



*Comparison With Annotated TSS and TTS
by Subcategories*

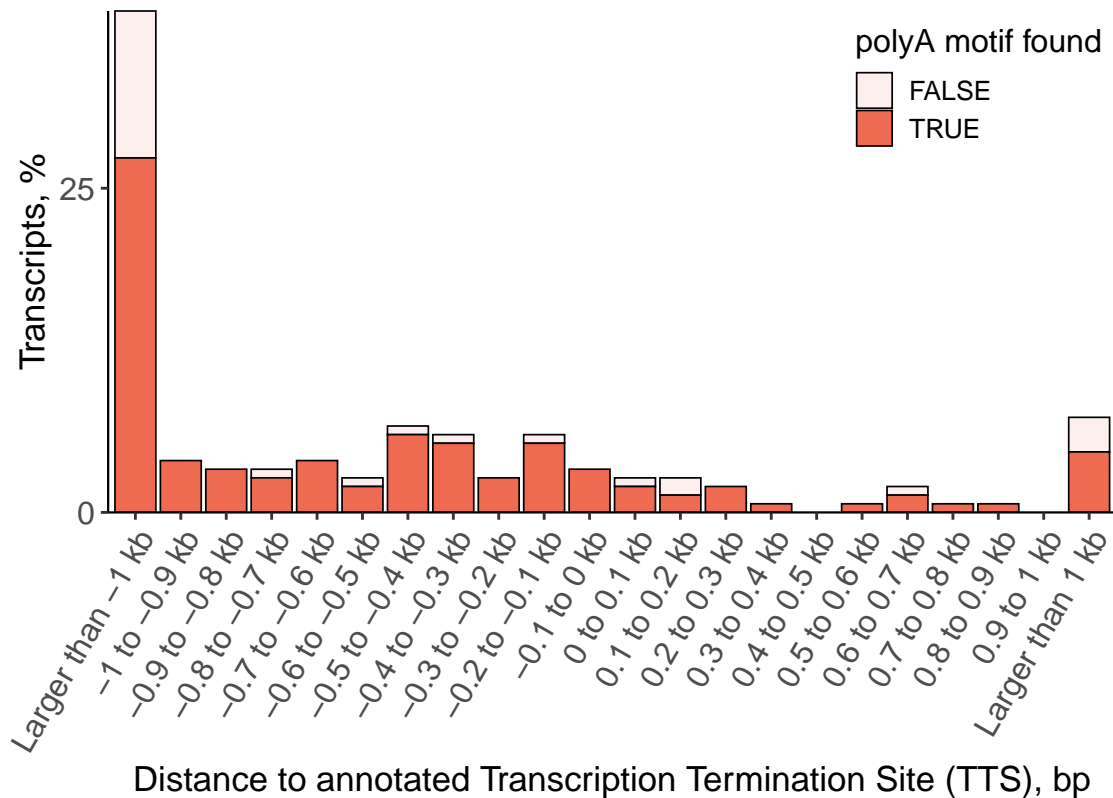
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



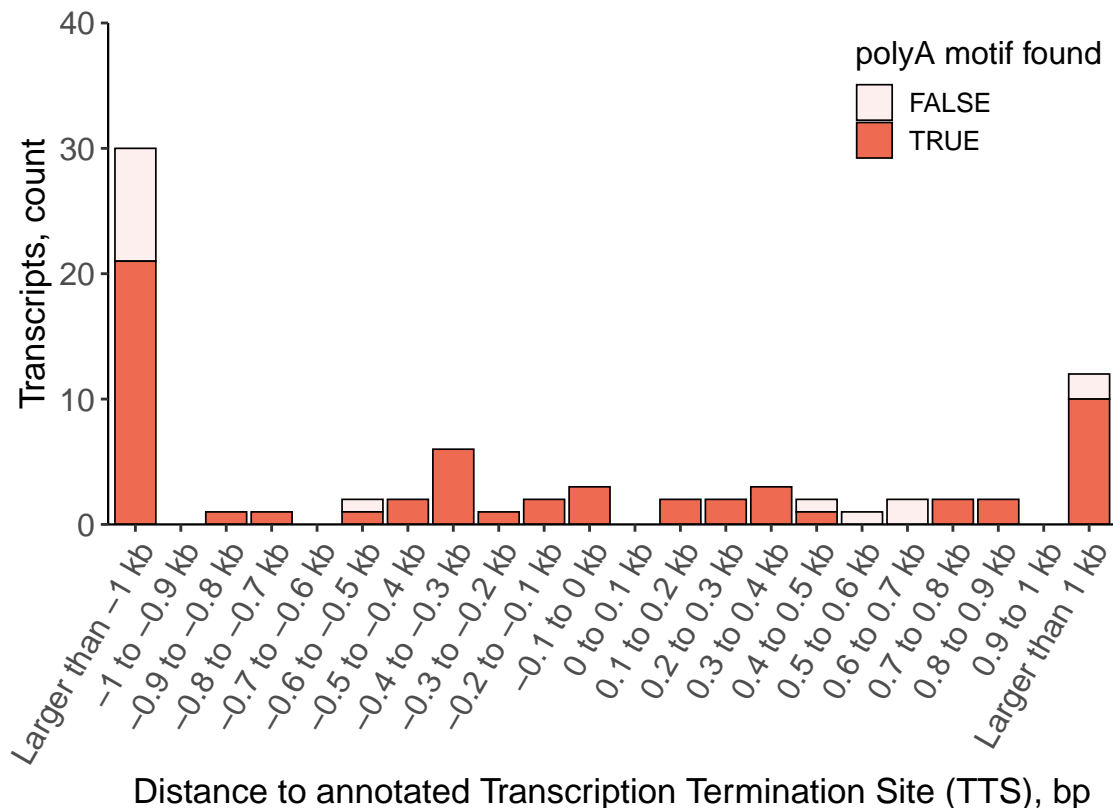
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



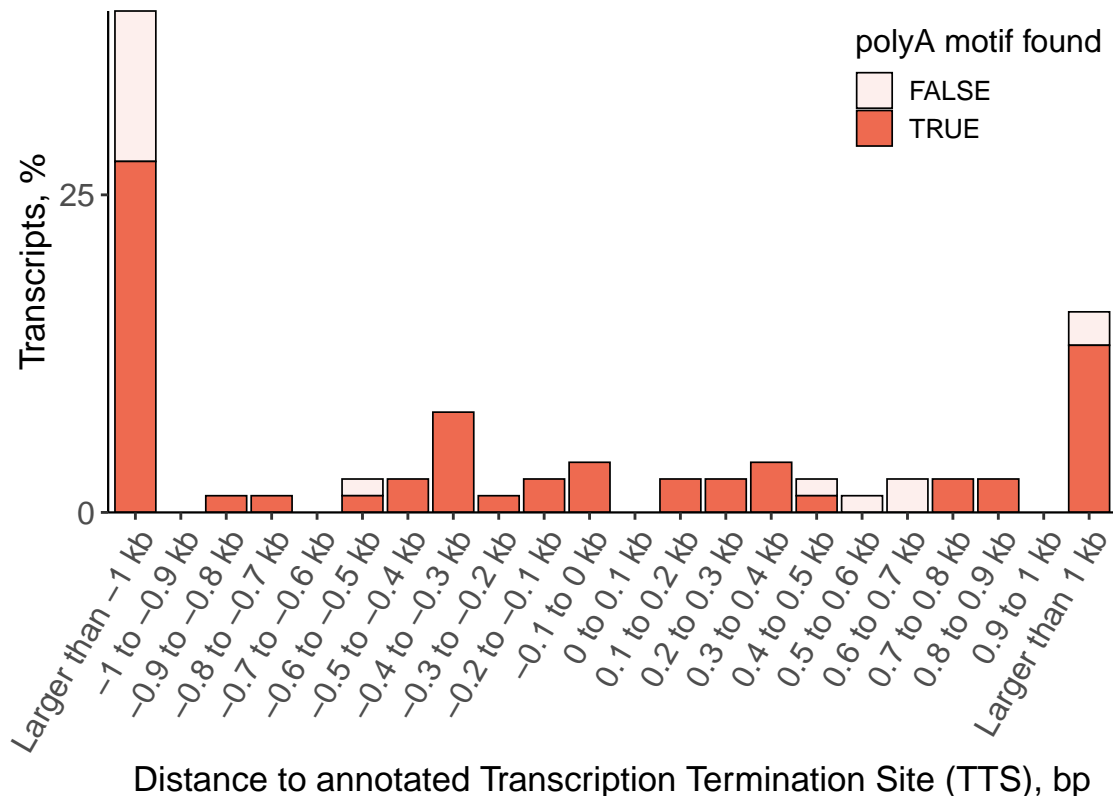
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



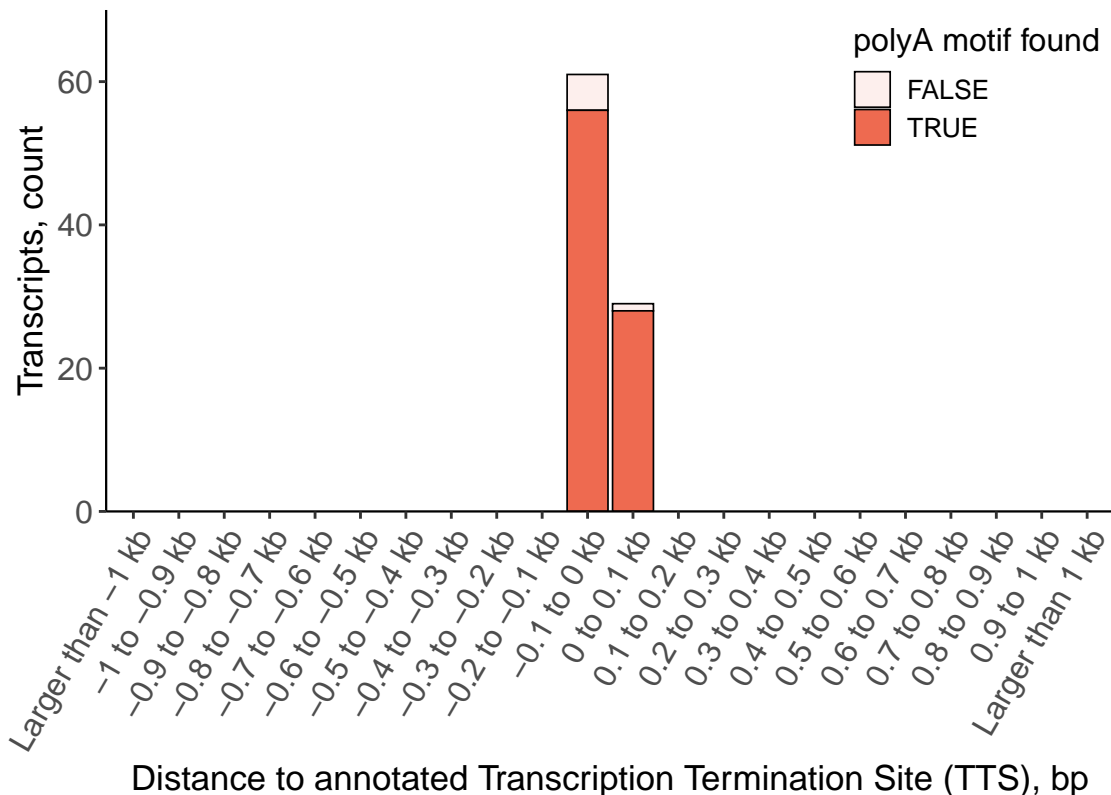
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



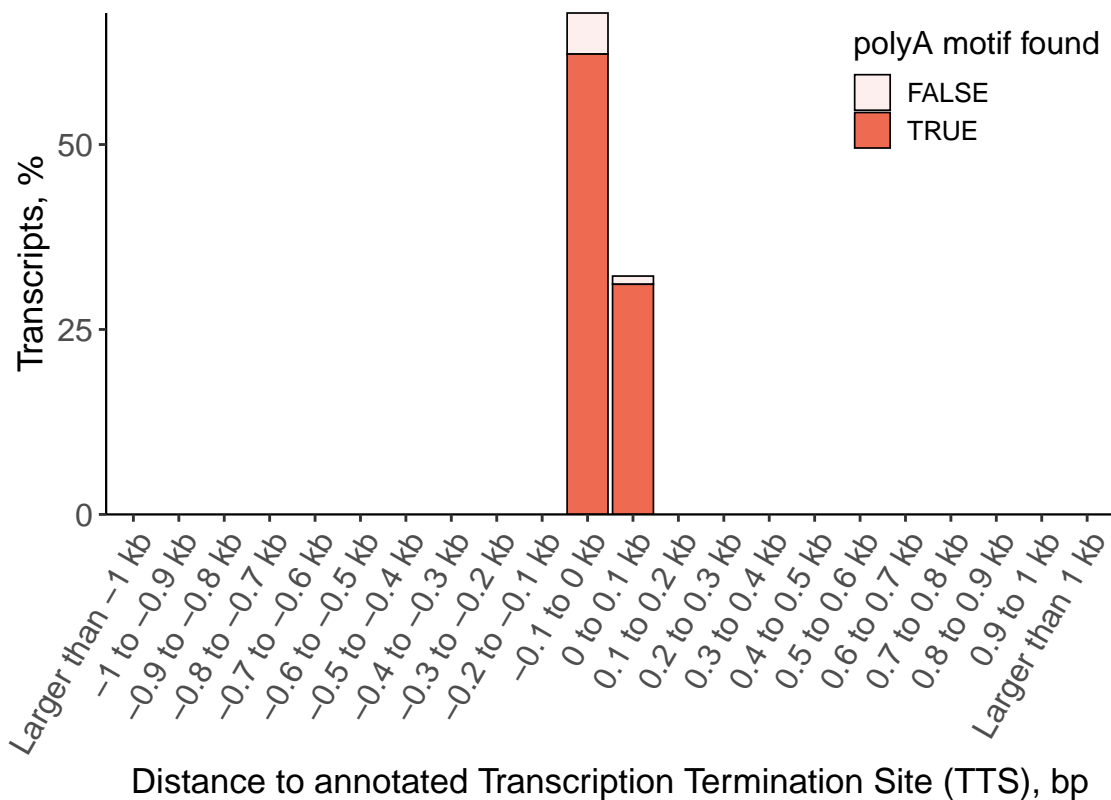
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



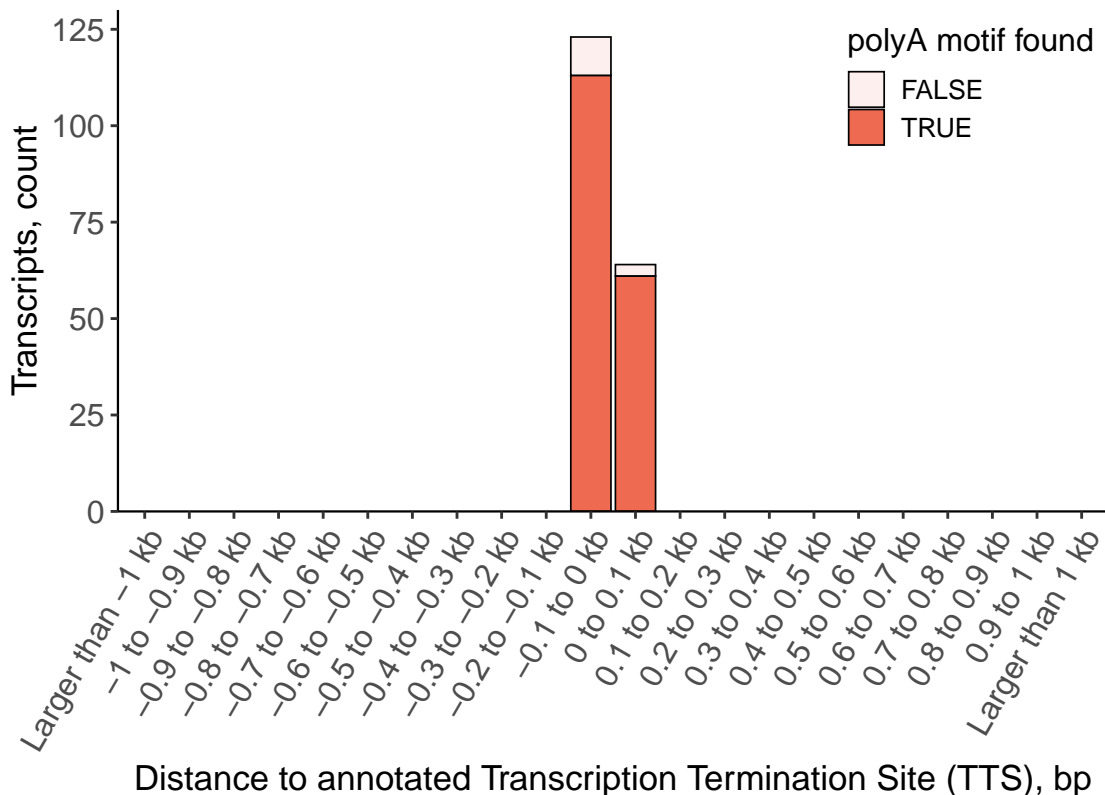
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



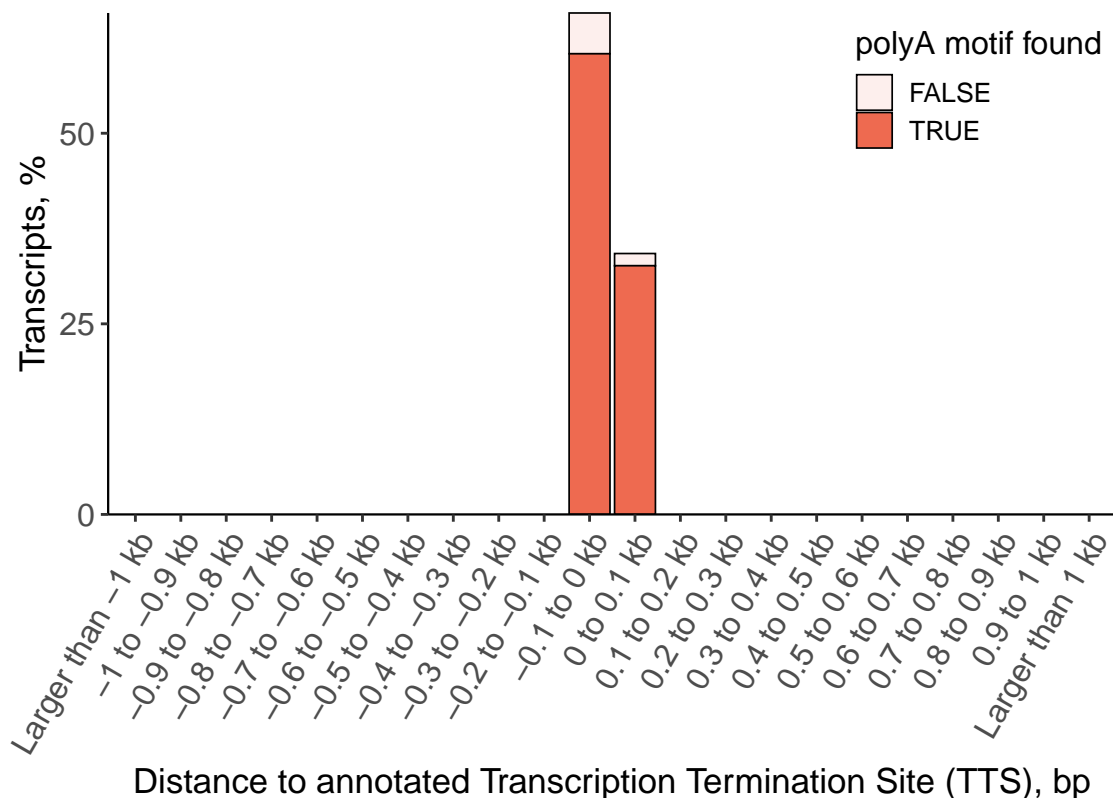
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



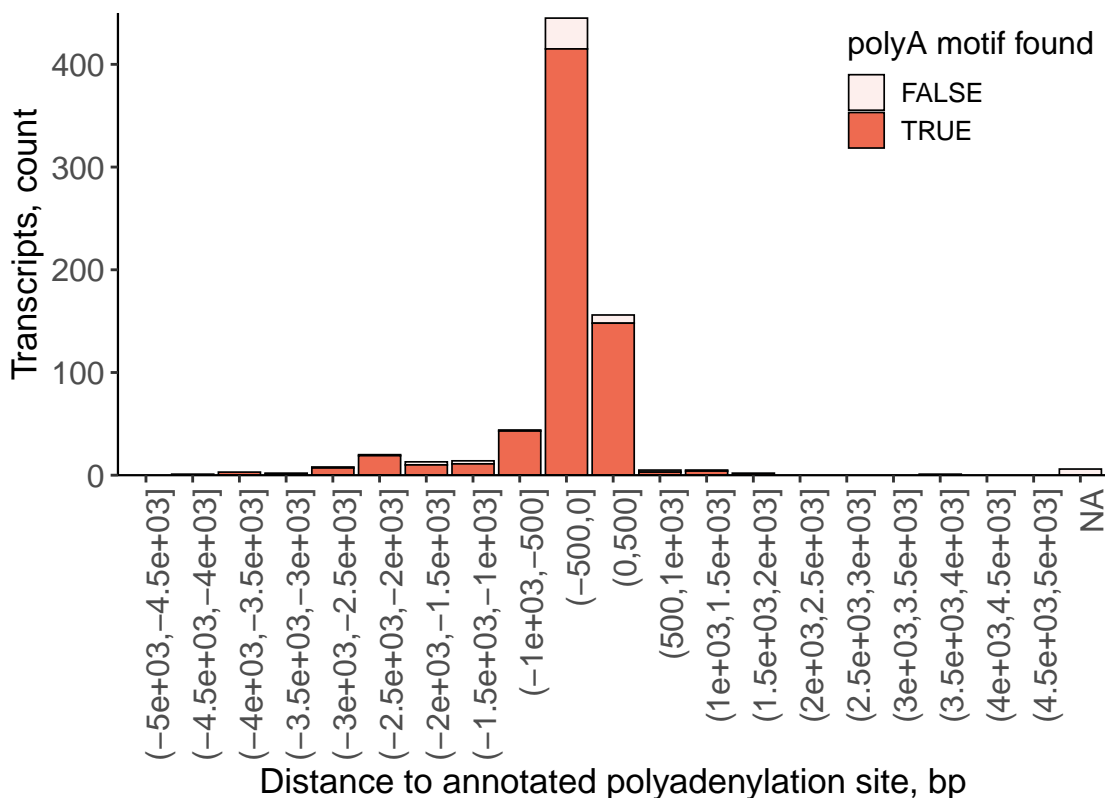
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



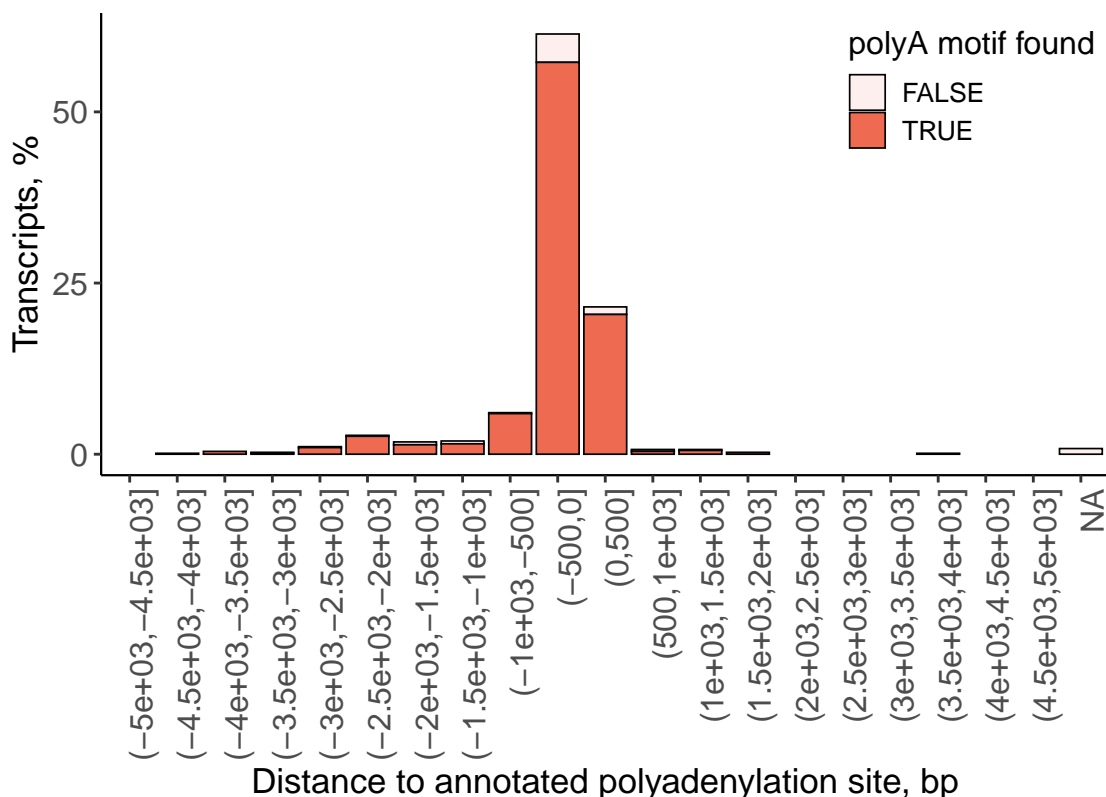
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



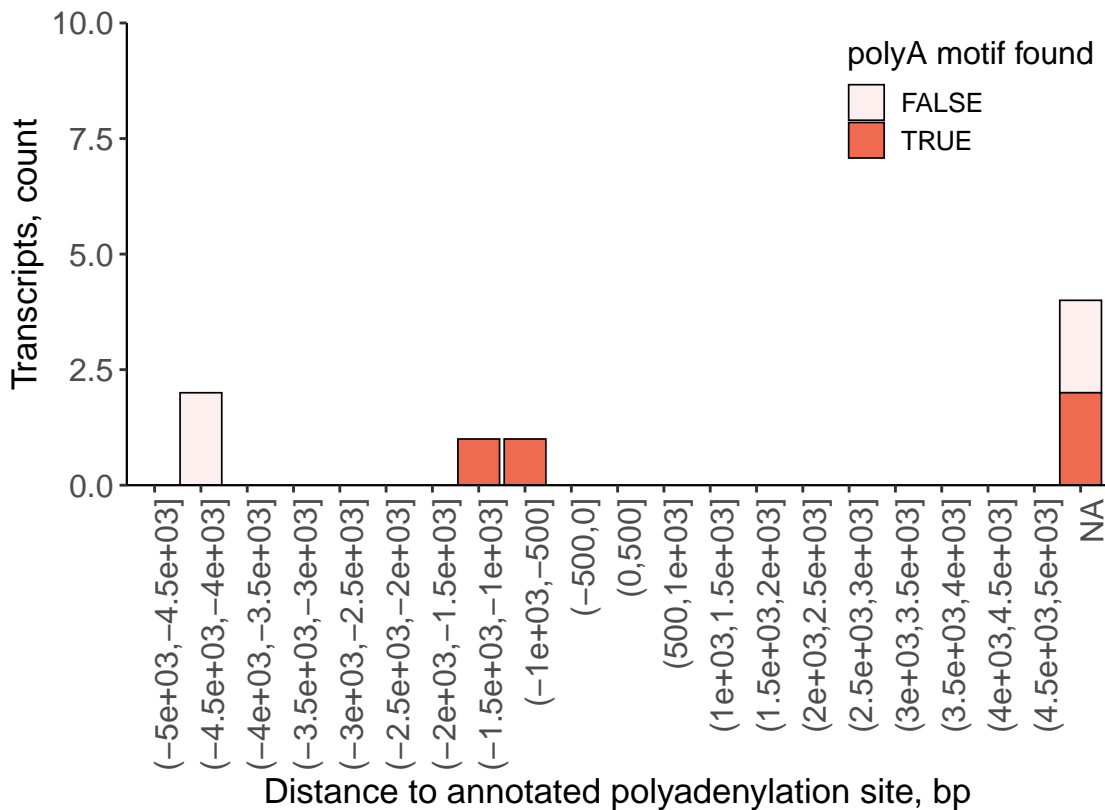
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



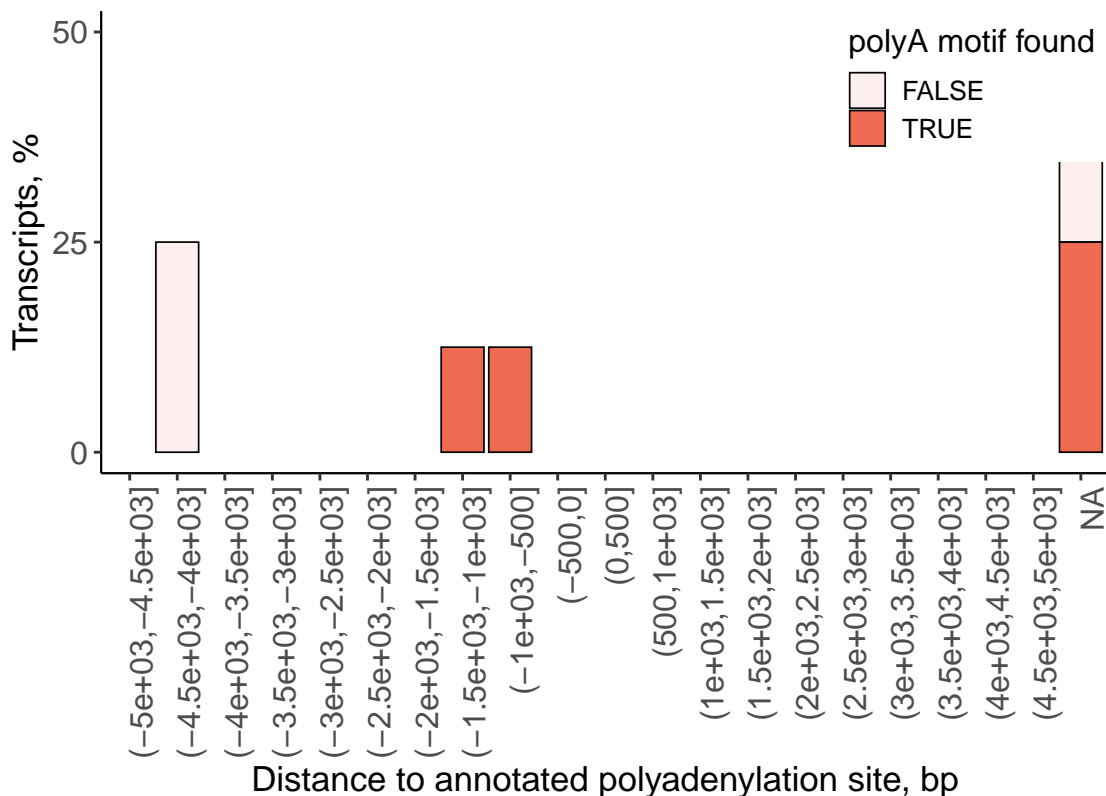
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



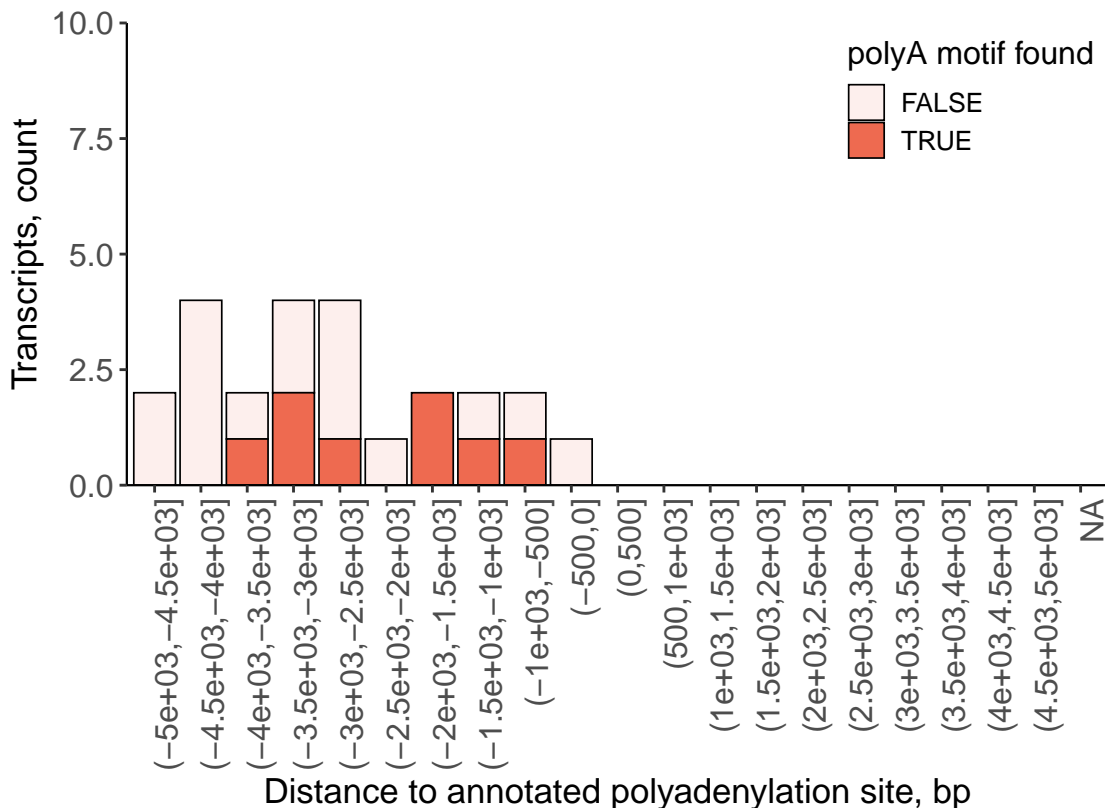
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



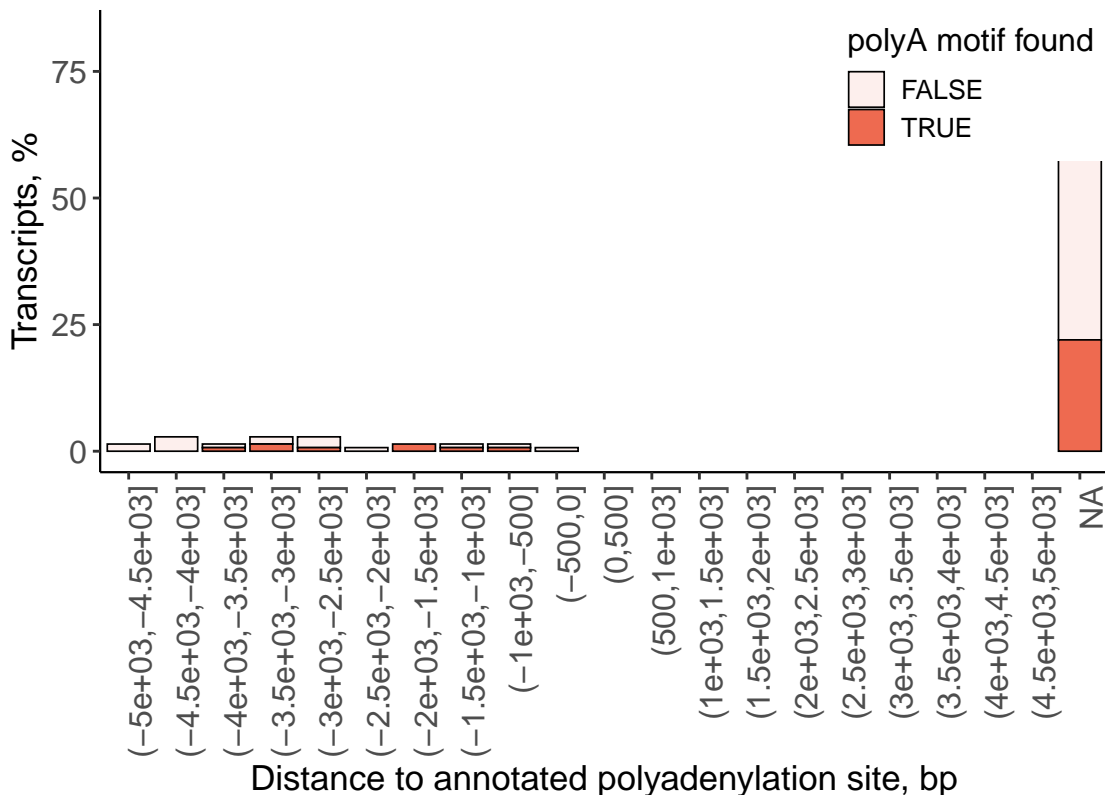
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



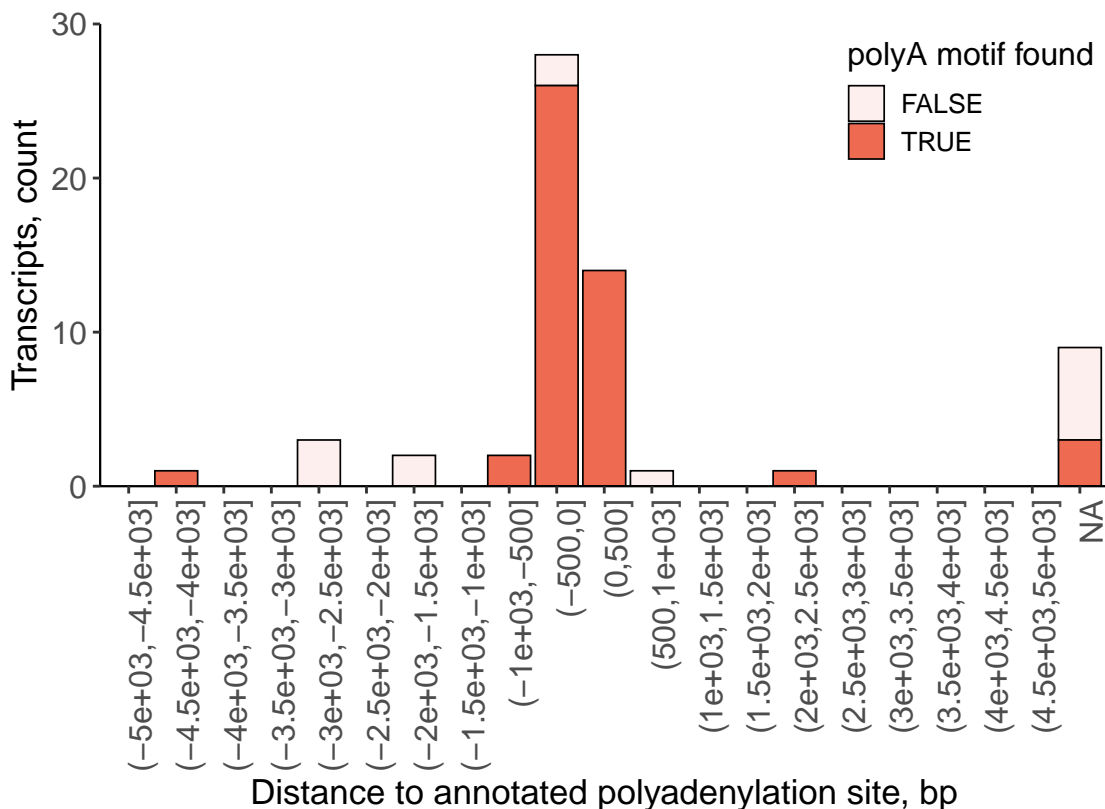
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



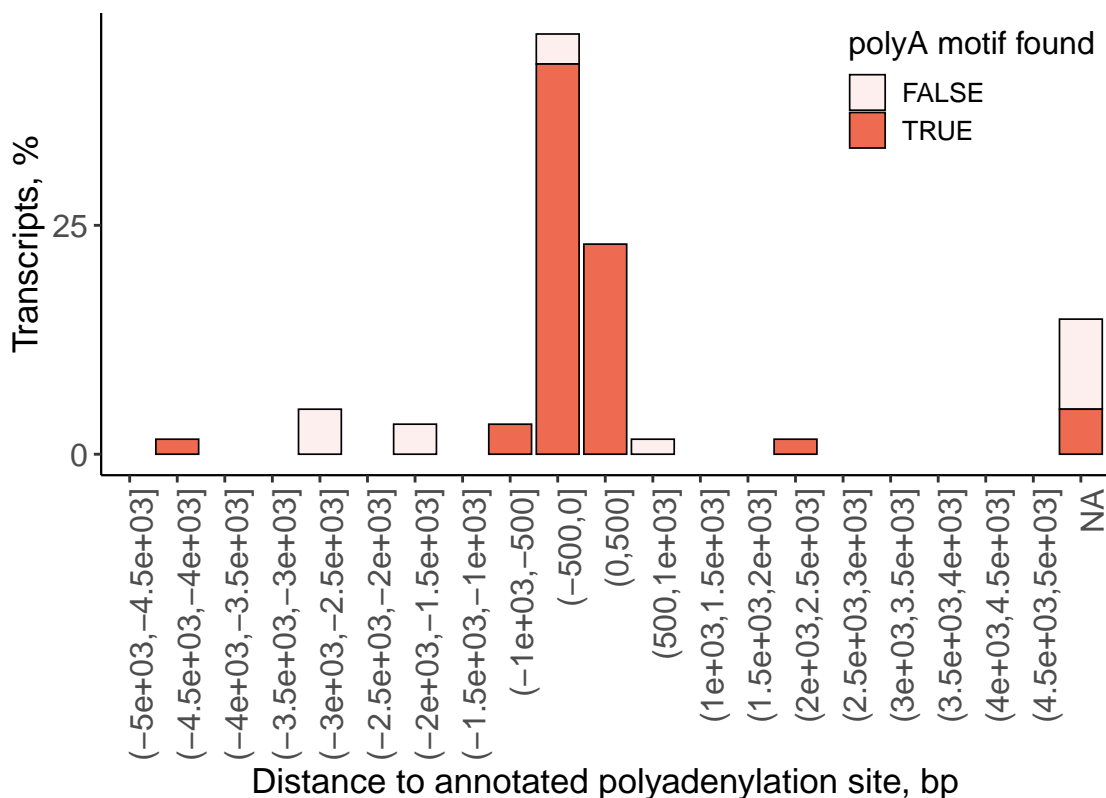
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



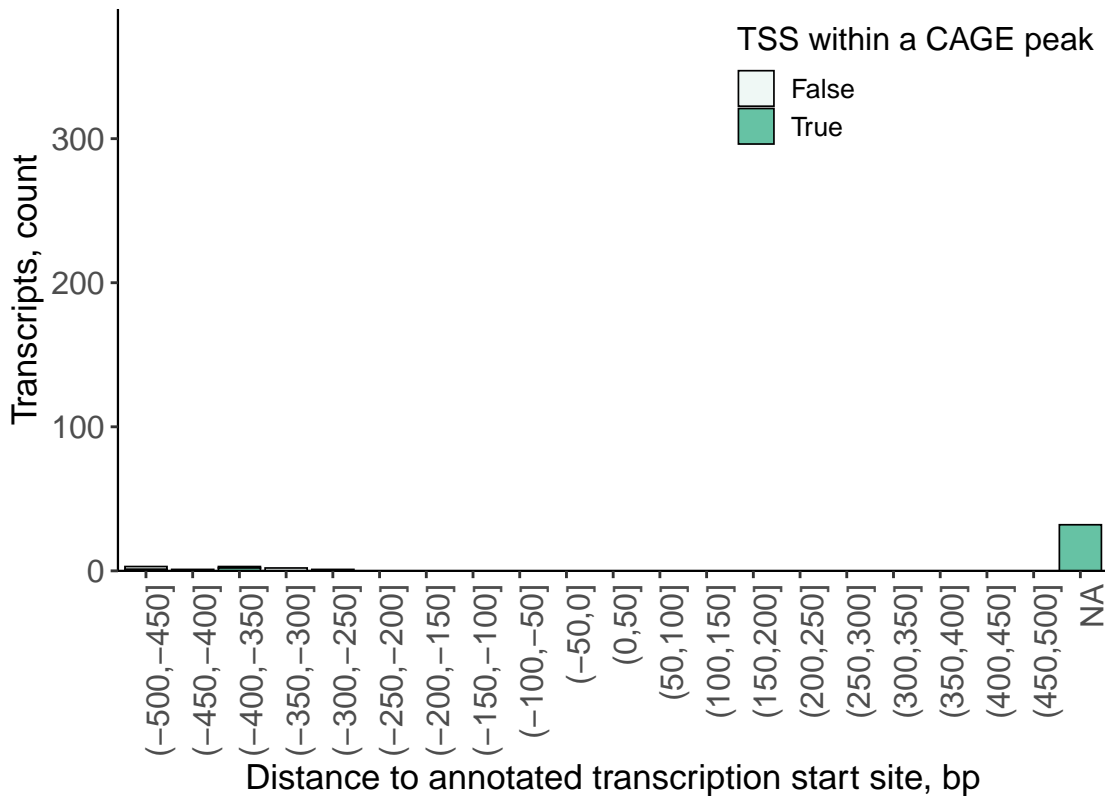
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



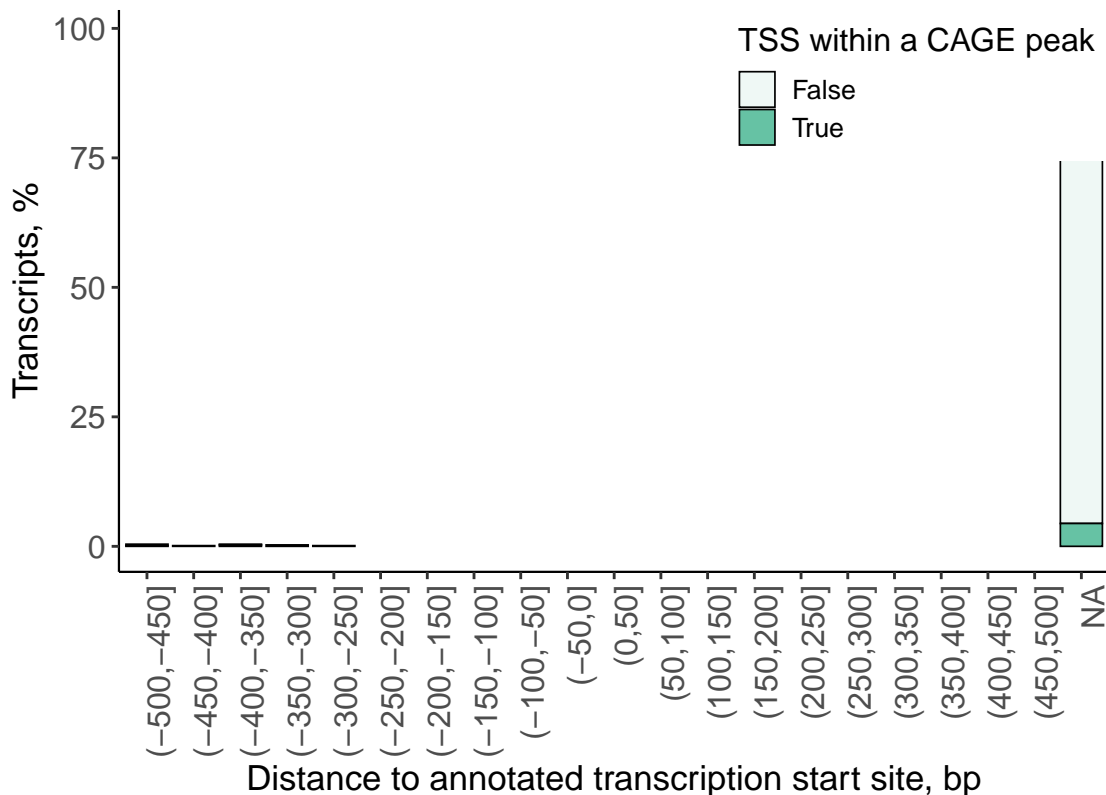
Distance to Annotated Transcription Start Site for ISM 3' Fragment

Negative values indicate downstream of annotated TSS



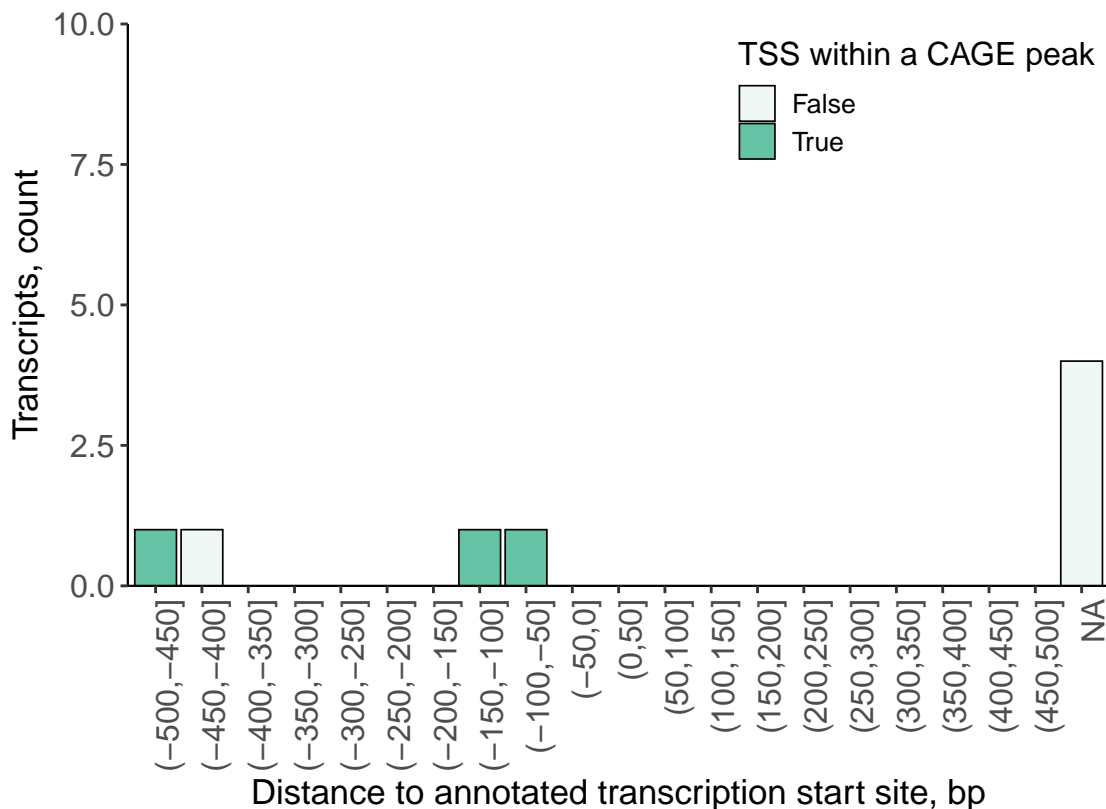
Distance to Annotated Transcription Start Site for ISM 3' Fragment

Negative values indicate downstream of annotated TSS



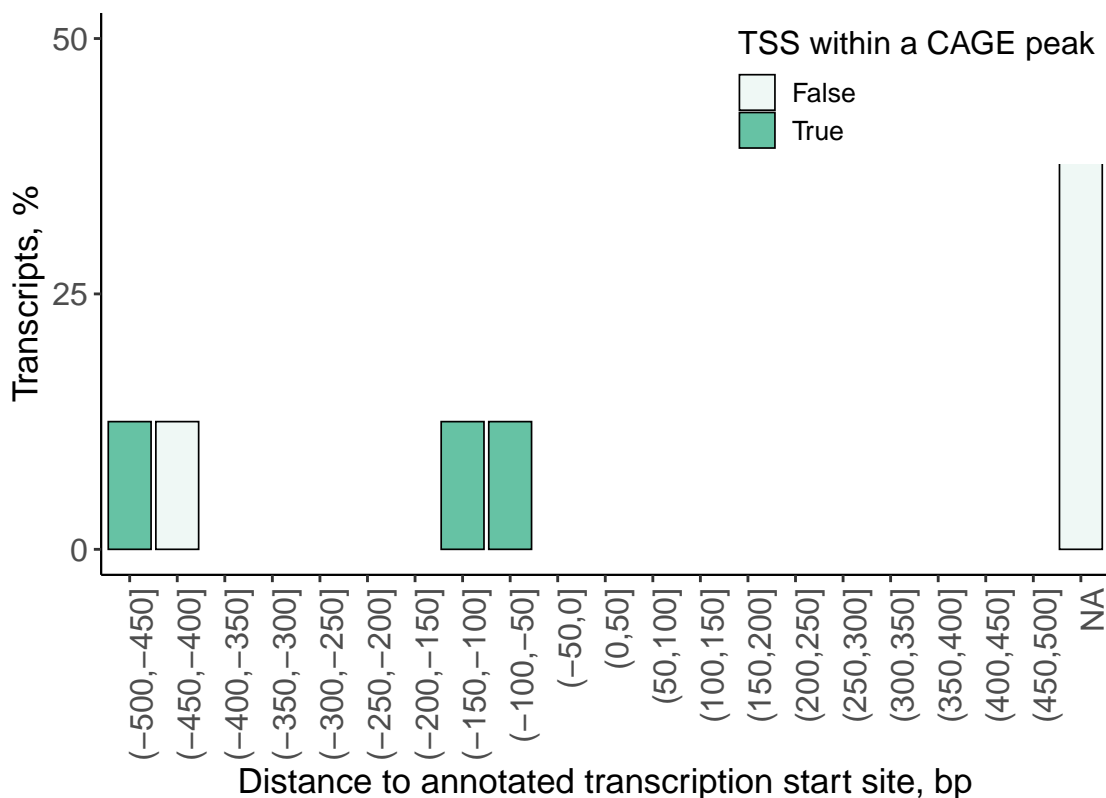
Distance to Annotated Transcription Start Site for ISM Internal Fragment

Negative values indicate downstream of annotated TSS



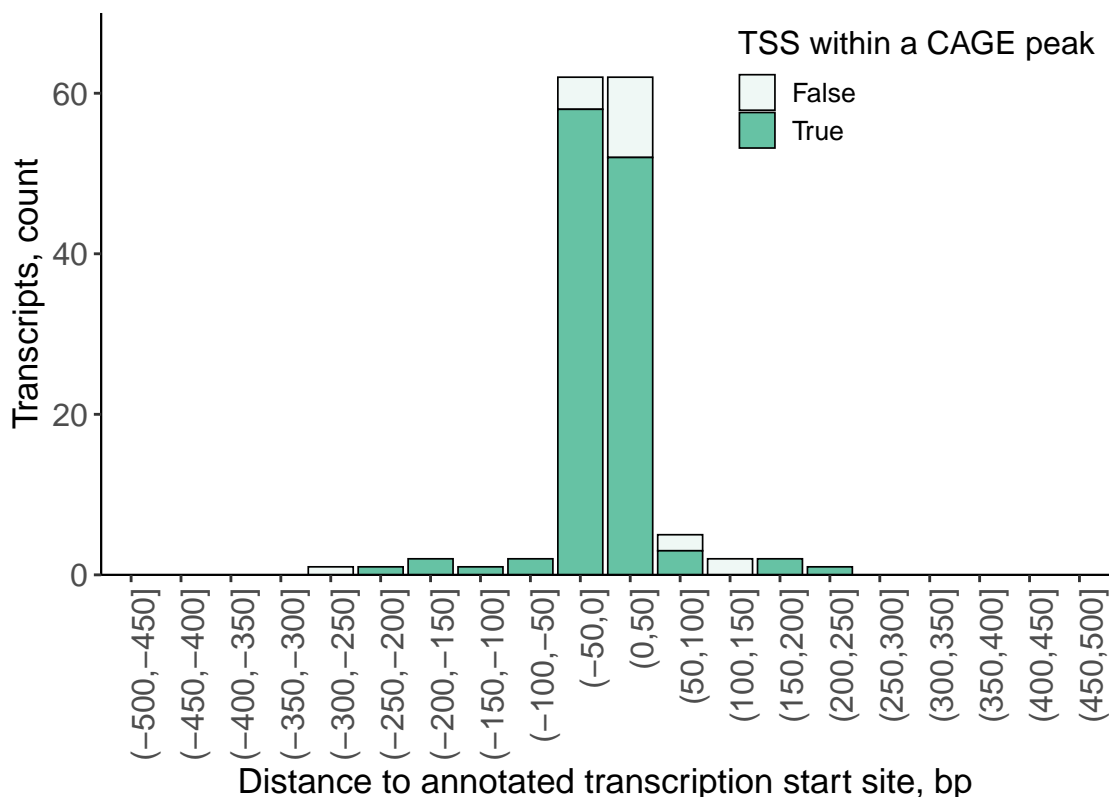
Distance to Annotated Transcription Start Site for ISM Internal Fragment

Negative values indicate downstream of annotated TSS



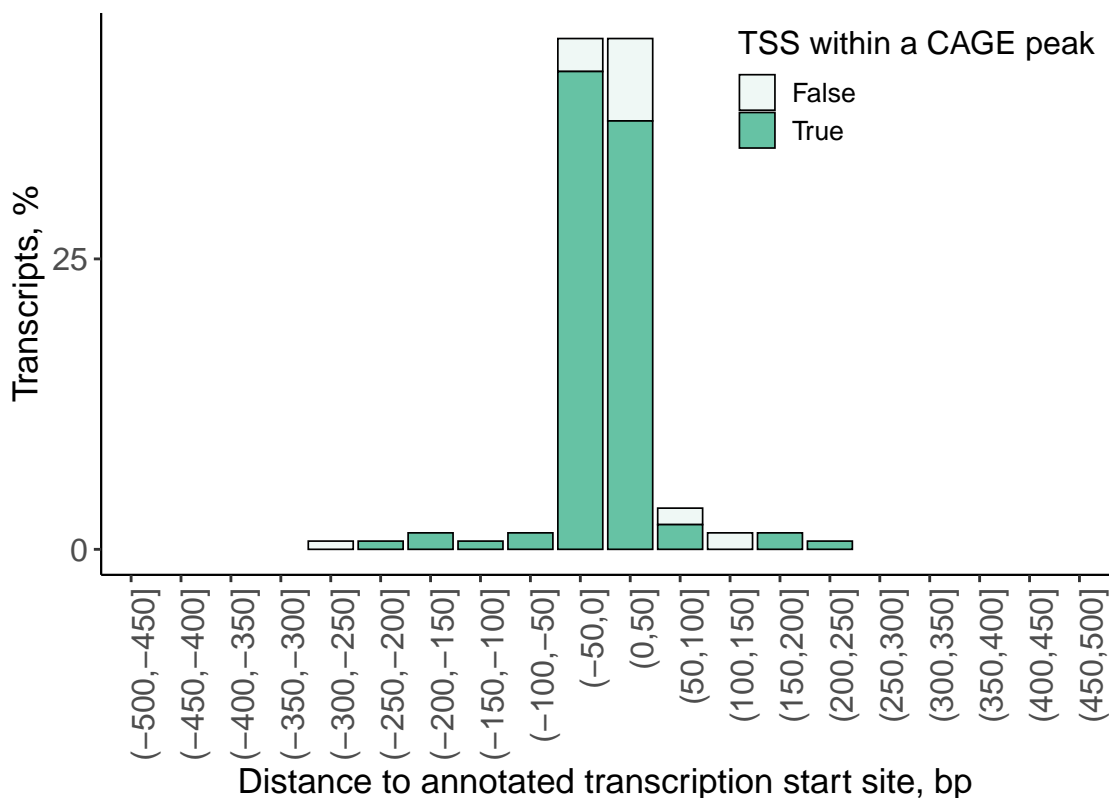
Distance to Annotated Transcription Start Site for ISM A5' Fragment

Negative values indicate downstream of annotated TSS



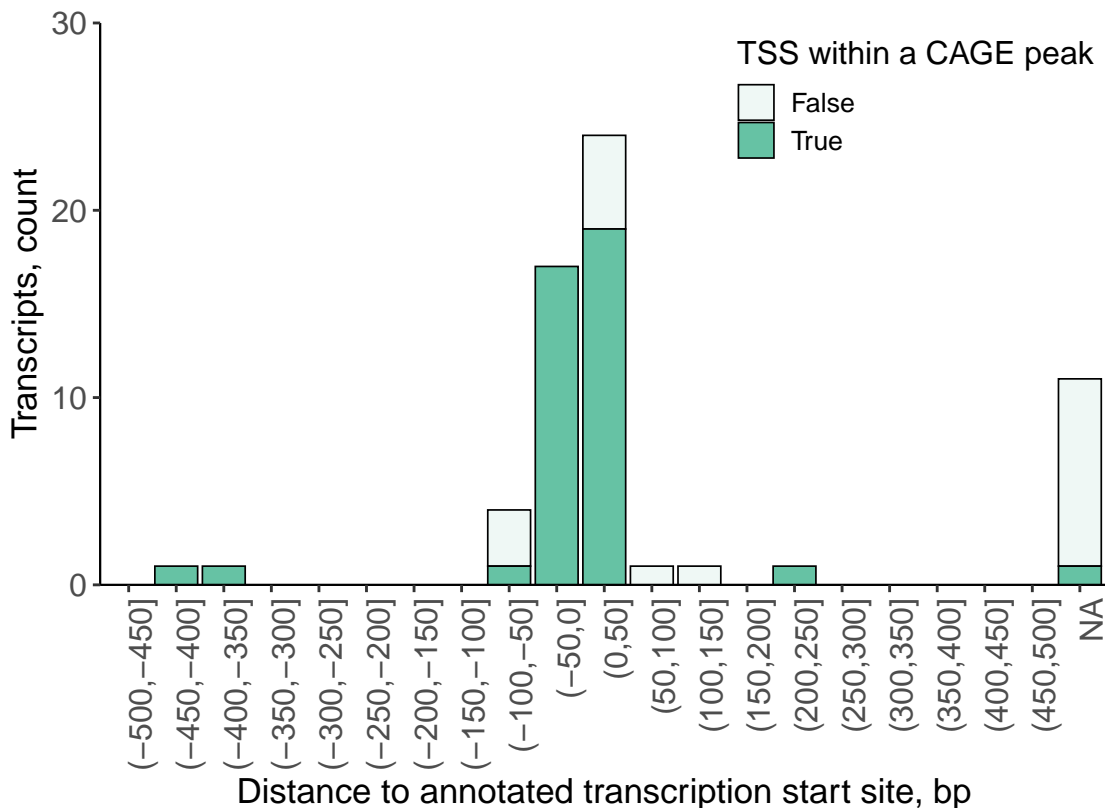
Distance to Annotated Transcription Start Site for ISM A5' Fragment

Negative values indicate downstream of annotated TSS



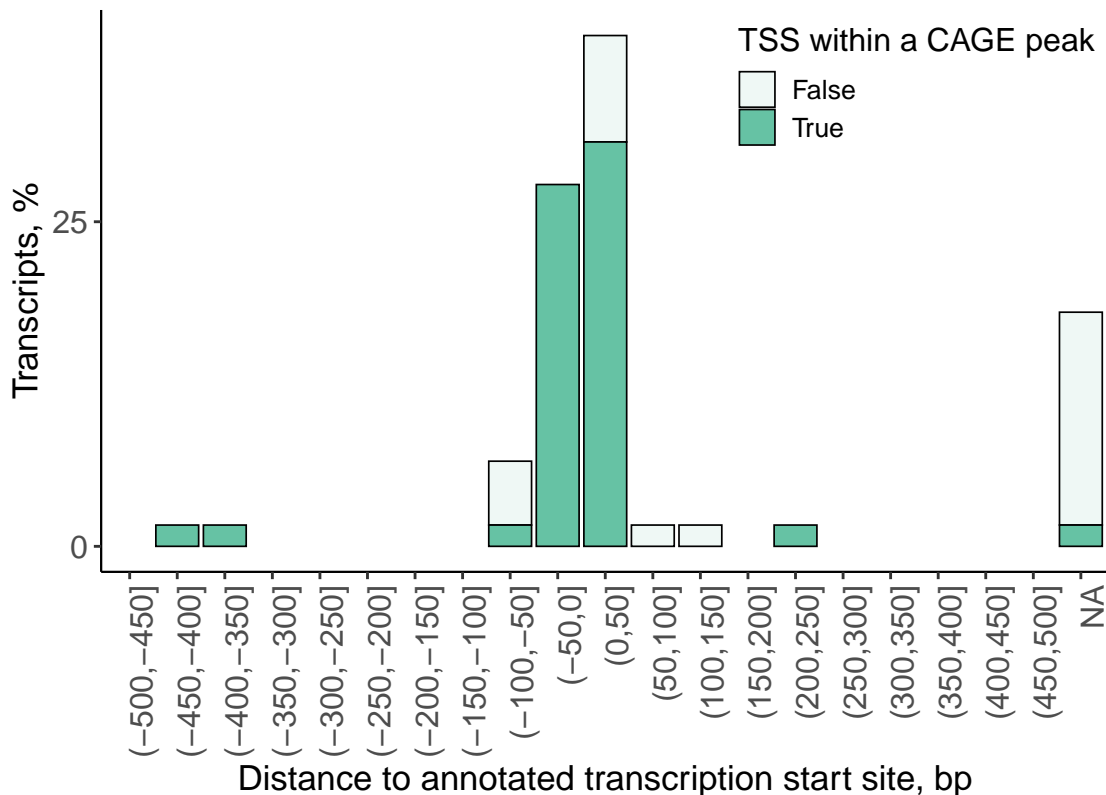
Distance to Annotated Transcription Start Site for ISM Intron Retention

Negative values indicate downstream of annotated TSS



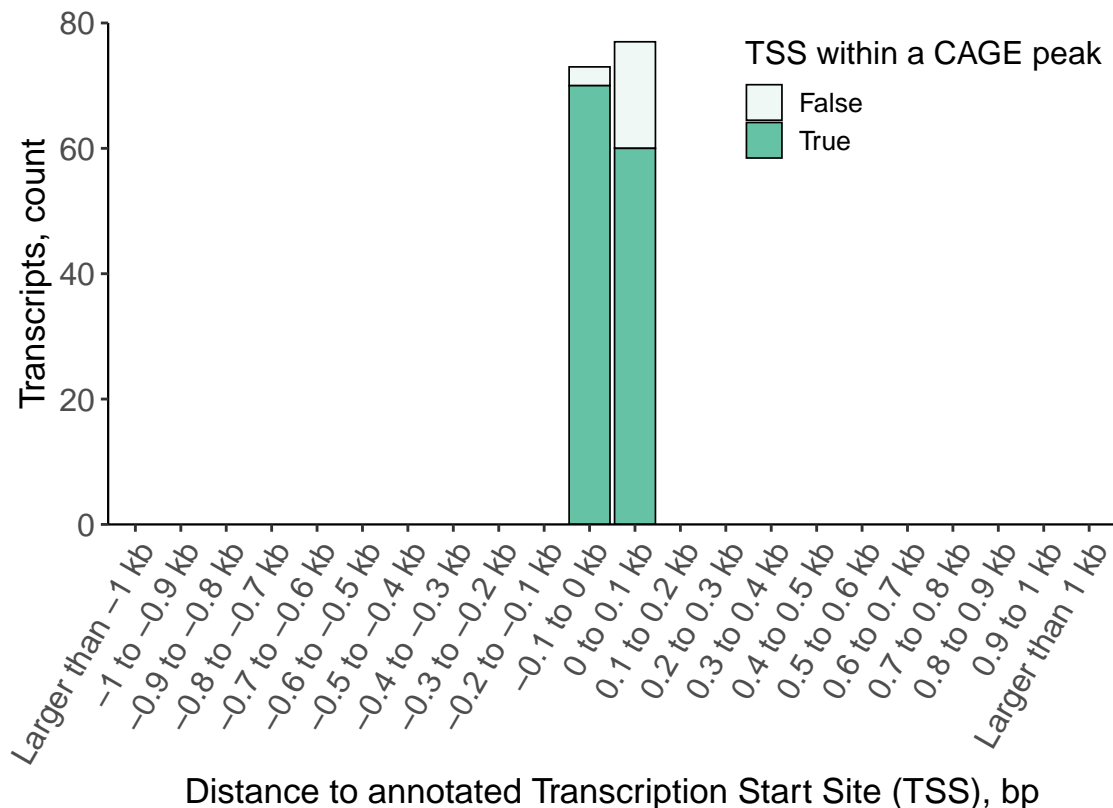
Distance to Annotated Transcription Start Site for ISM Intron Retention

Negative values indicate downstream of annotated TSS



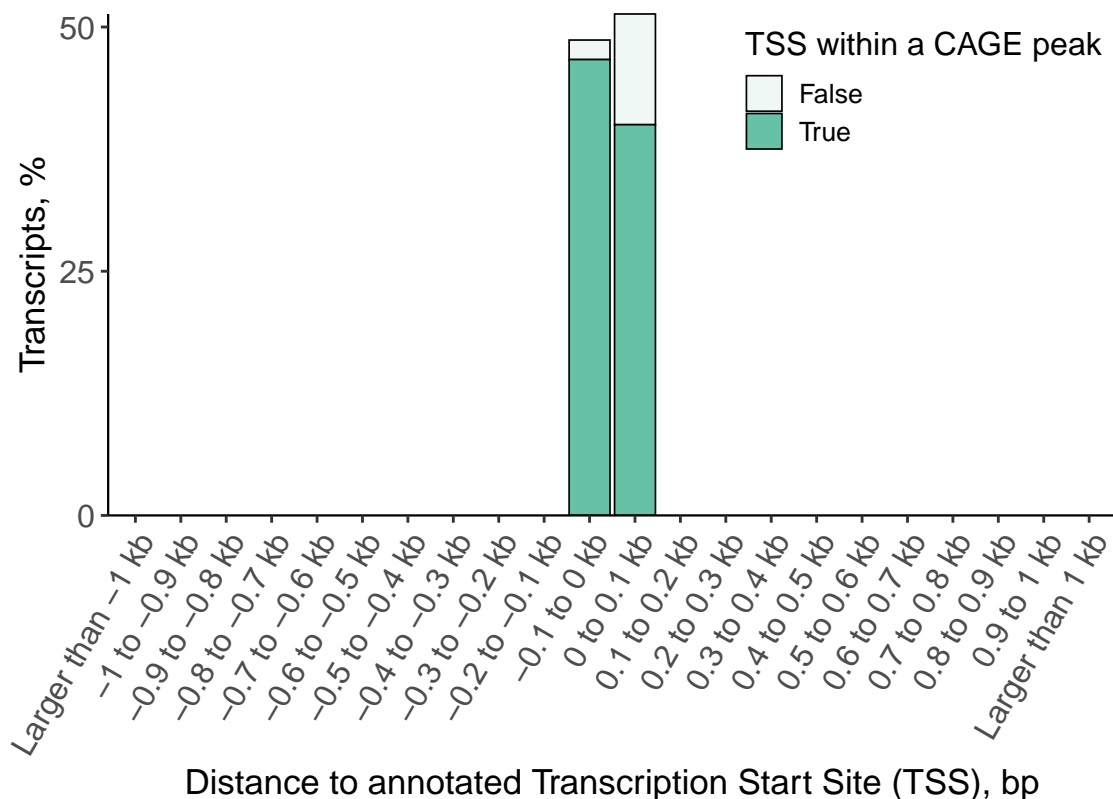
Distance to Annotated Transcription Start Site FSM Alternative 3' End

Negative values indicate downstream of annotated TSS



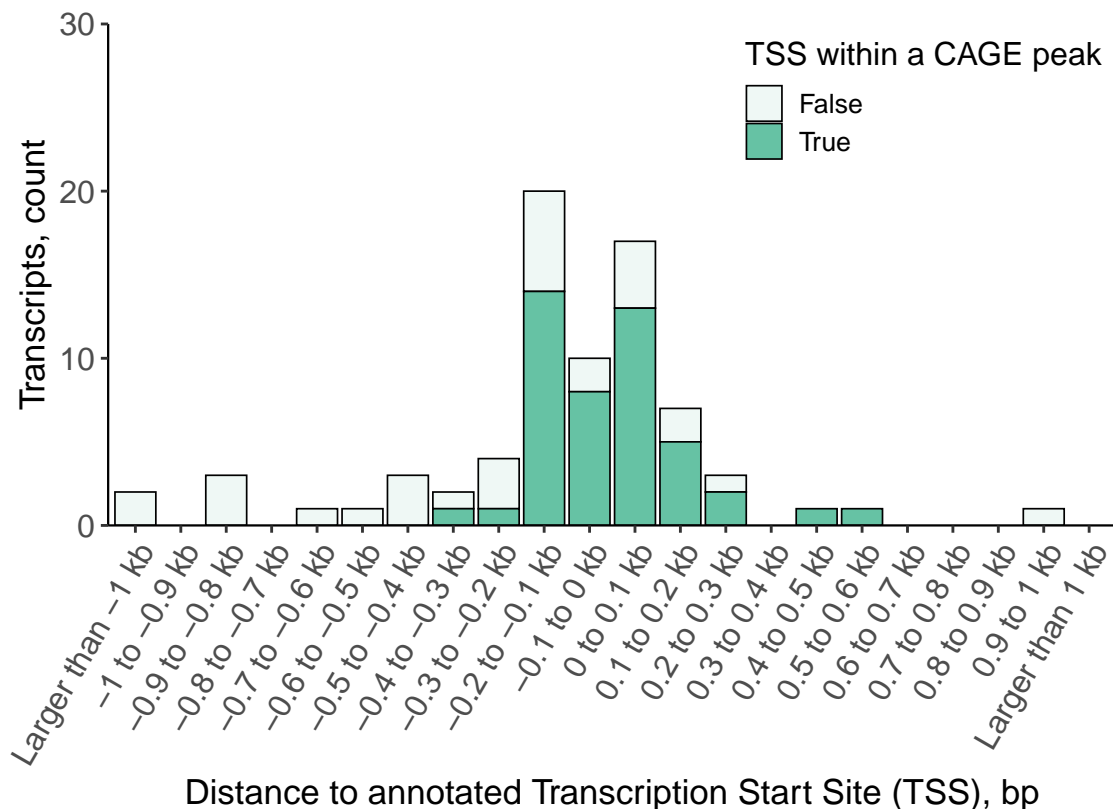
Distance to Annotated Transcription Start Site FSM Alternative 3' End

Negative values indicate downstream of annotated TSS



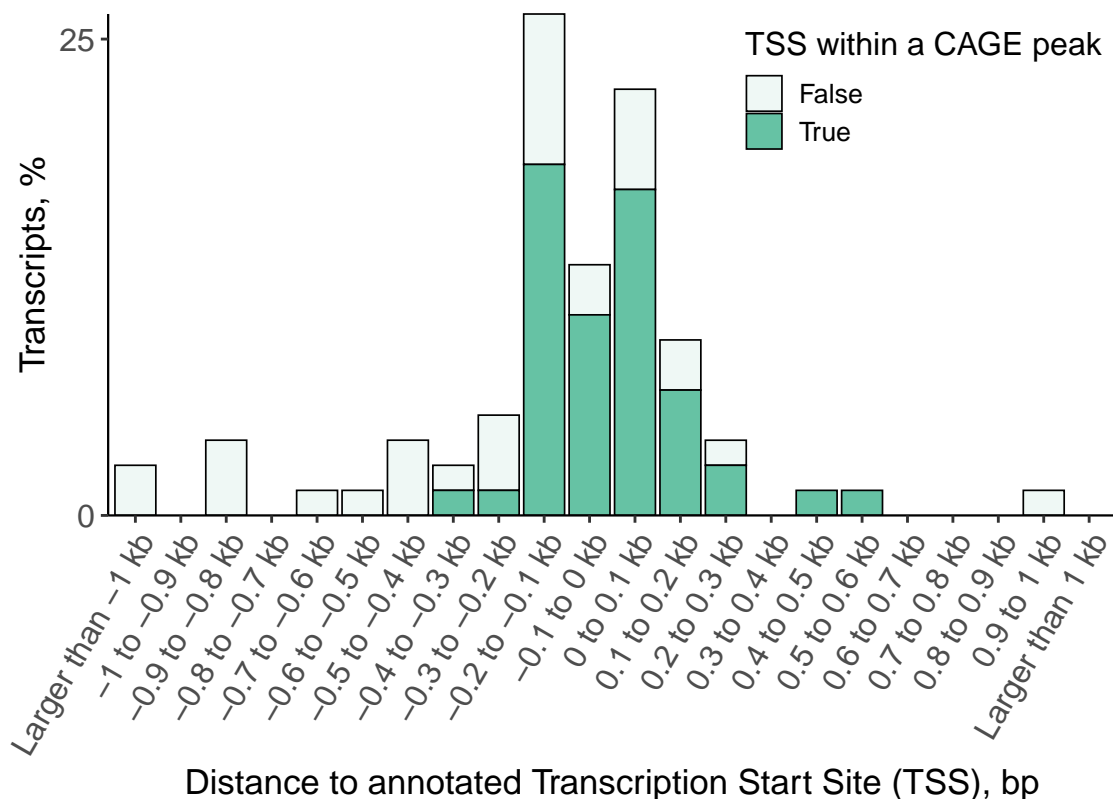
Distance to Annotated Transcription Start Site FSM Alternative 3'5' End

Negative values indicate downstream of annotated TSS



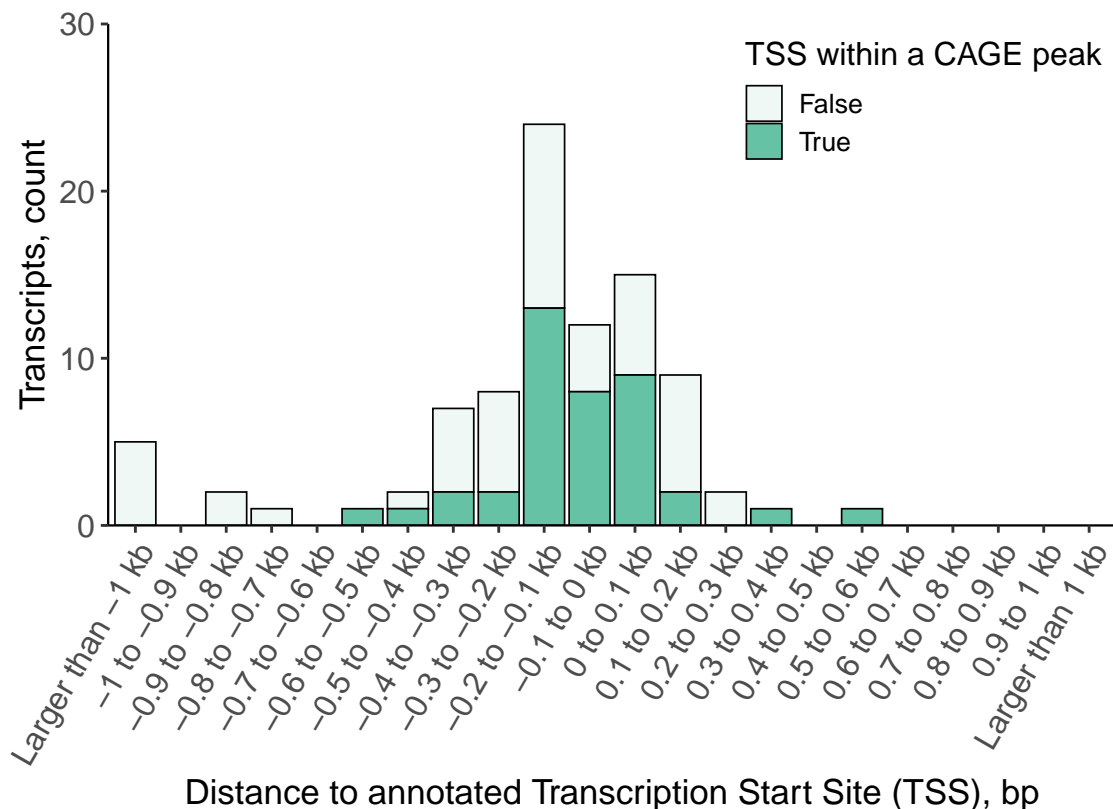
Distance to Annotated Transcription Start Site FSM Alternative 3'5' End

Negative values indicate downstream of annotated TSS



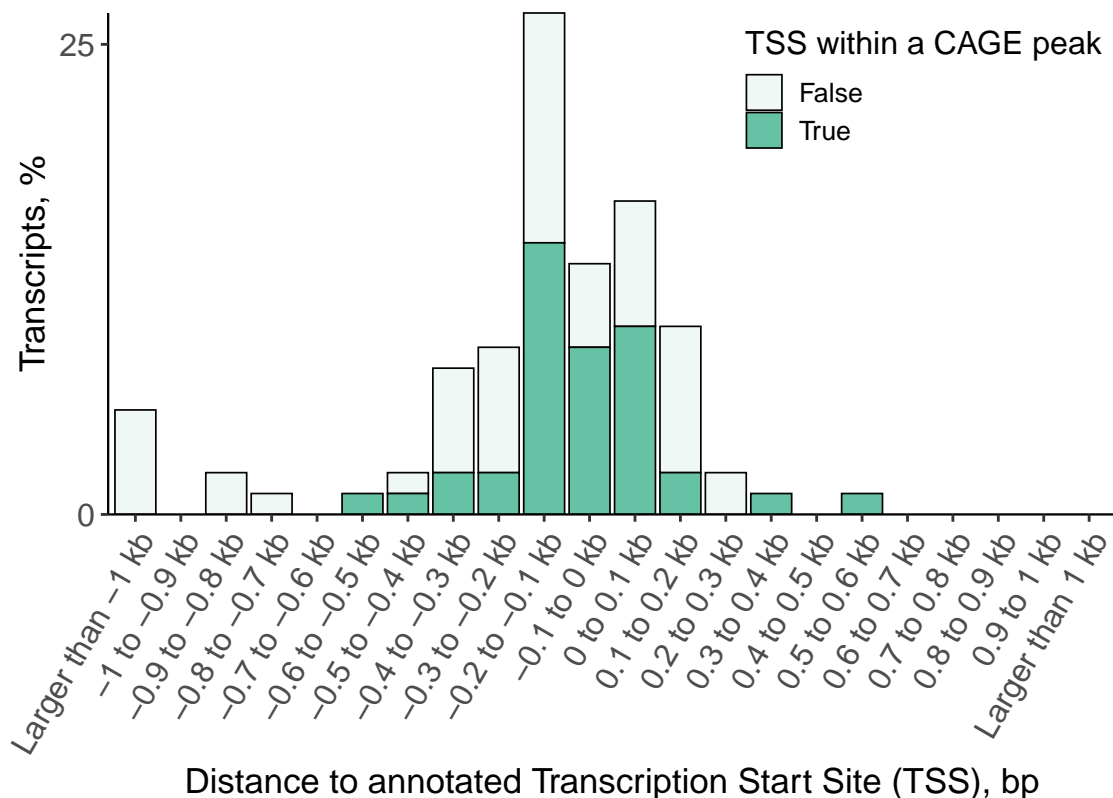
Distance to Annotated Transcription Start Site FSM Alternative 5' End

Negative values indicate downstream of annotated TSS



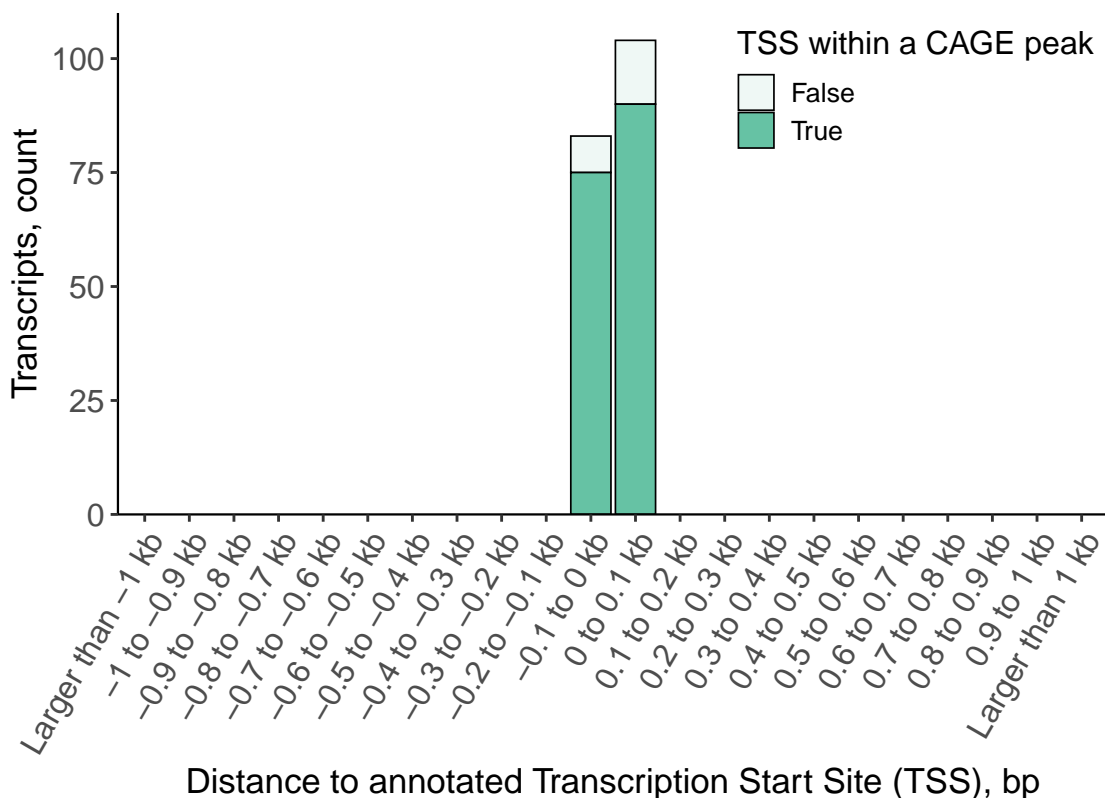
Distance to Annotated Transcription Start Site FSM Alternative 5' End

Negative values indicate downstream of annotated TSS



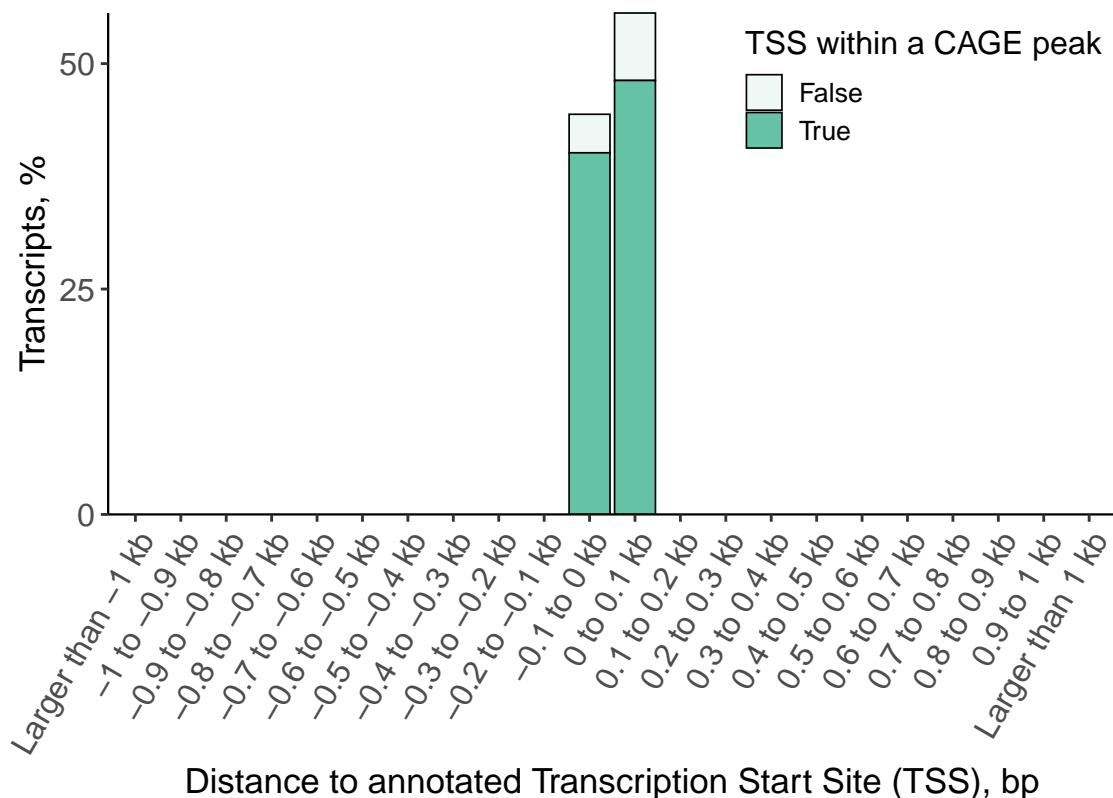
Distance to Annotated Transcription Start Site FSM Reference Match

Negative values indicate downstream of annotated TSS



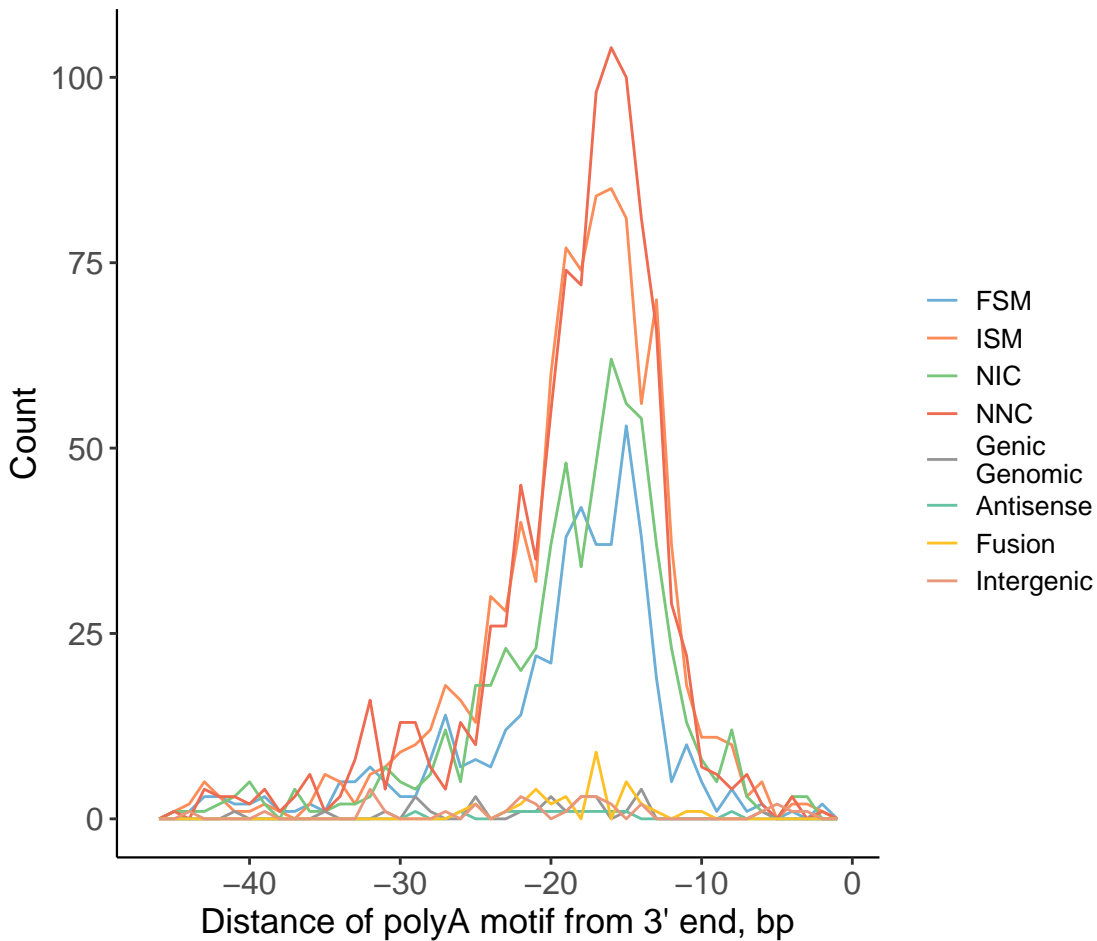
Distance to Annotated Transcription Start Site FSM Reference Match

Negative values indicate downstream of annotated TSS



PolyA Distance Analysis

Distance of Detected PolyA Motif From 3' end



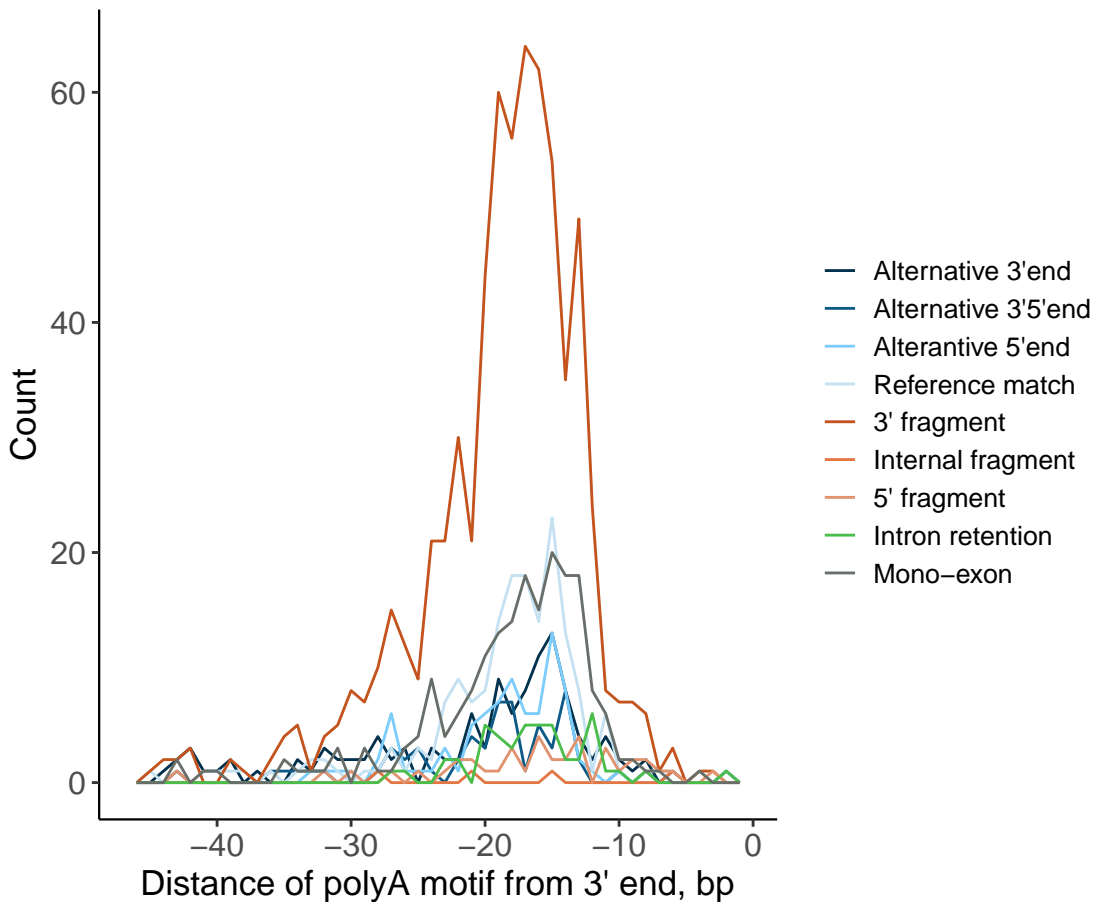
Frequency of PolyA Motifs

Number of polyA Motifs Detected

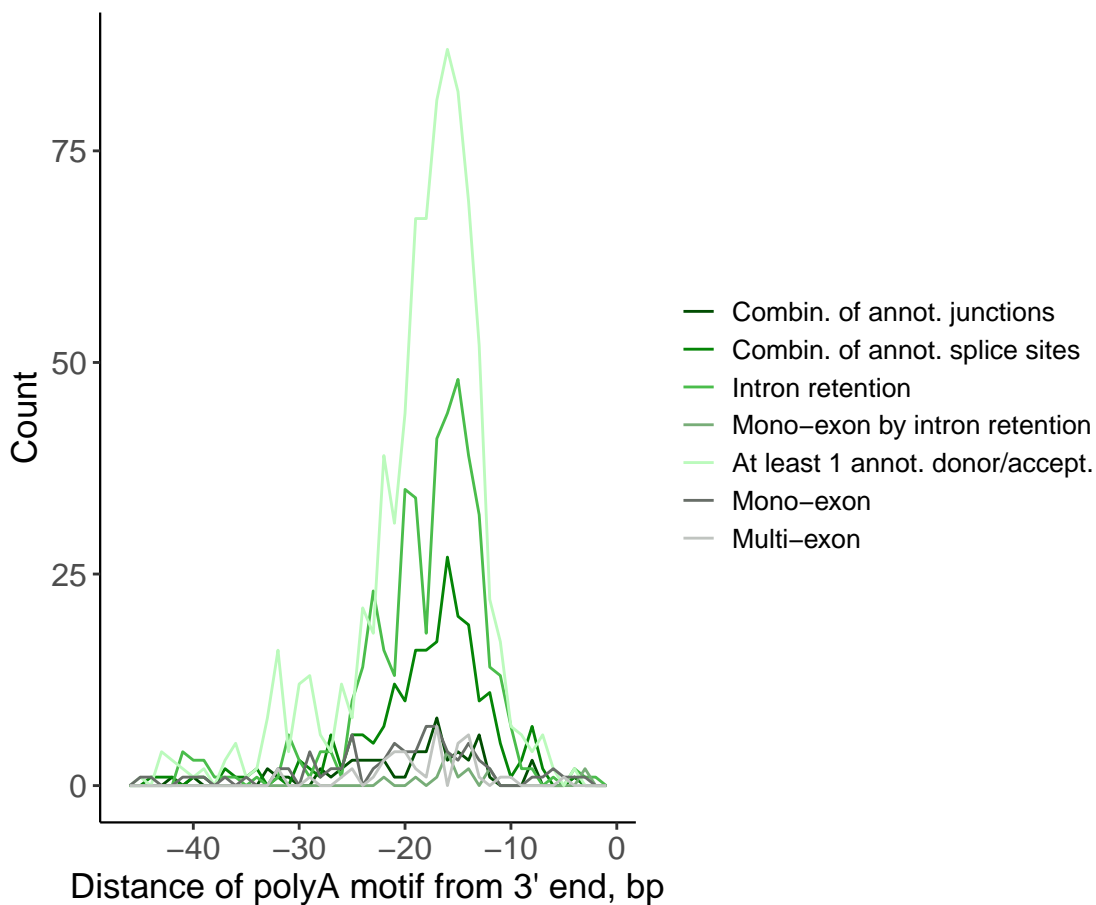
Category	Count	polyA Detected	%
FSM	534	456	85
ISM	1134	939	83
NIC	806	616	76
NNC	1139	981	86
Genic Genomic	56	28	50
Antisense	28	12	43
Fusion	38	34	89
Intergenic	190	32	17

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	150	120	80
Alternative 3'5'end	76	60	79
Alterantive 5'end	90	84	93
Reference match	187	174	93
3' fragment	725	668	92
Internal fragment	8	4	50
5' fragment	141	39	28
Combin. of annot. junctions	77	62	81
Combin. of annot. splice sites	272	227	83
Intron retention	594	491	83
Mono-exon by intron retention	31	14	45
At least 1 annot. donor/accept.	965	831	86
Mono-exon	556	281	51
Multi-exon	53	43	81

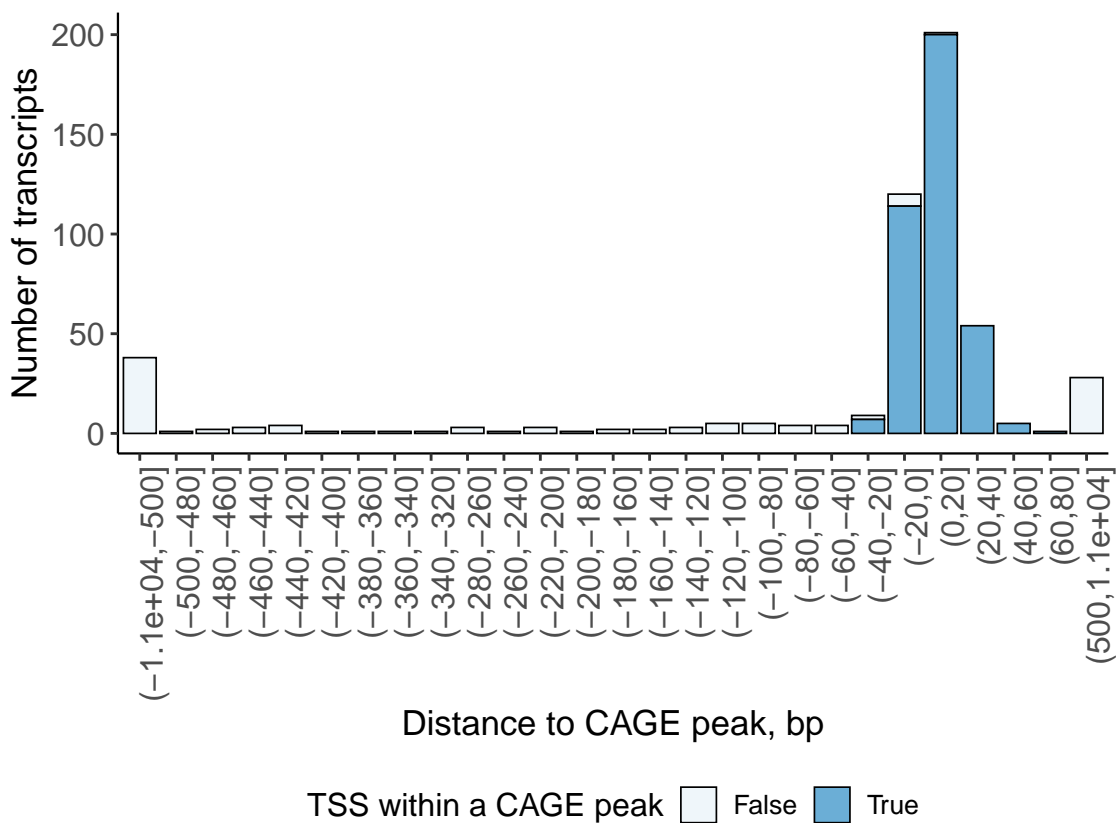
Frequency of PolyA Motifs

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

CAGE Distances Analysis

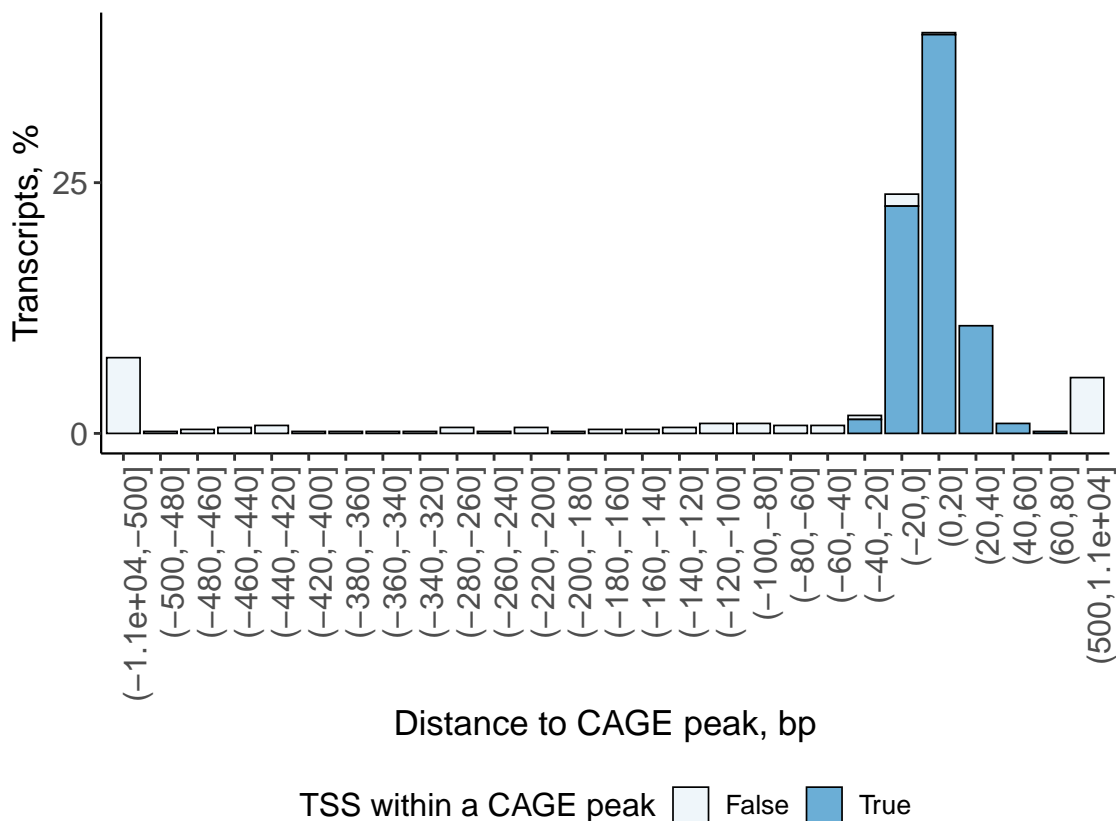
Distance to CAGE Peak of Multi-Exonic FSM

Negative values indicate downstream of annotated CAGE peak



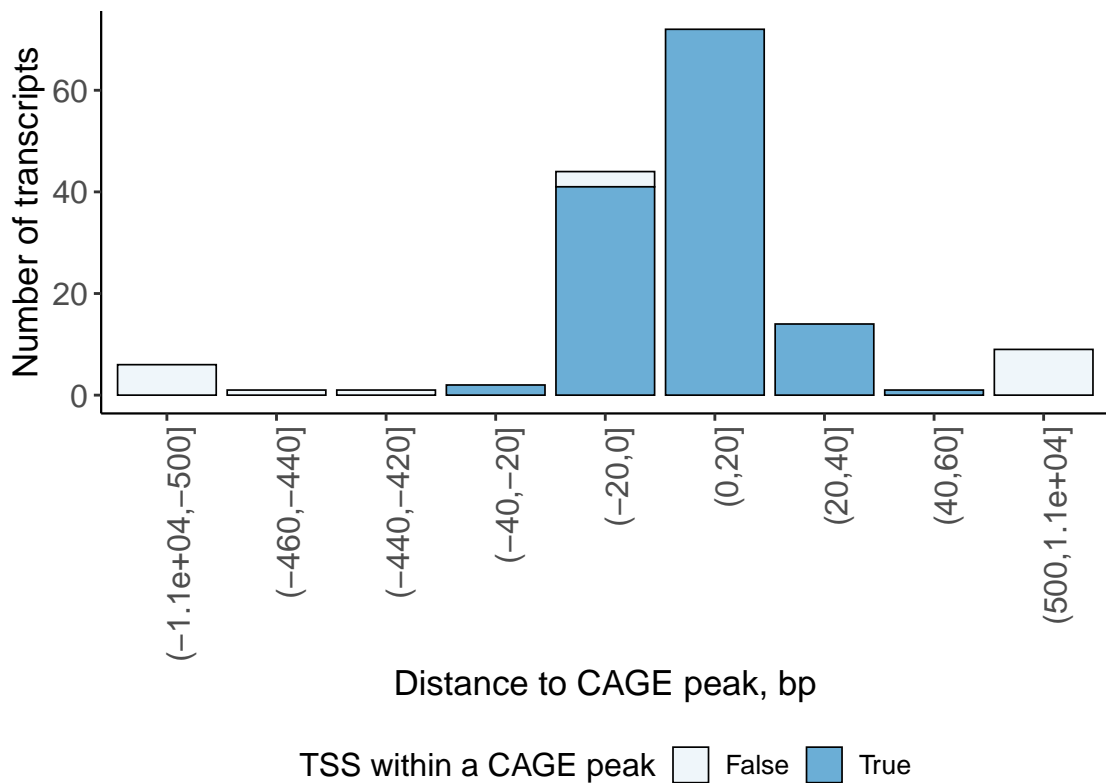
Distance to CAGE Peak of Multi-Exonic FSM

Negative values indicate downstream of annotated CAGE peak



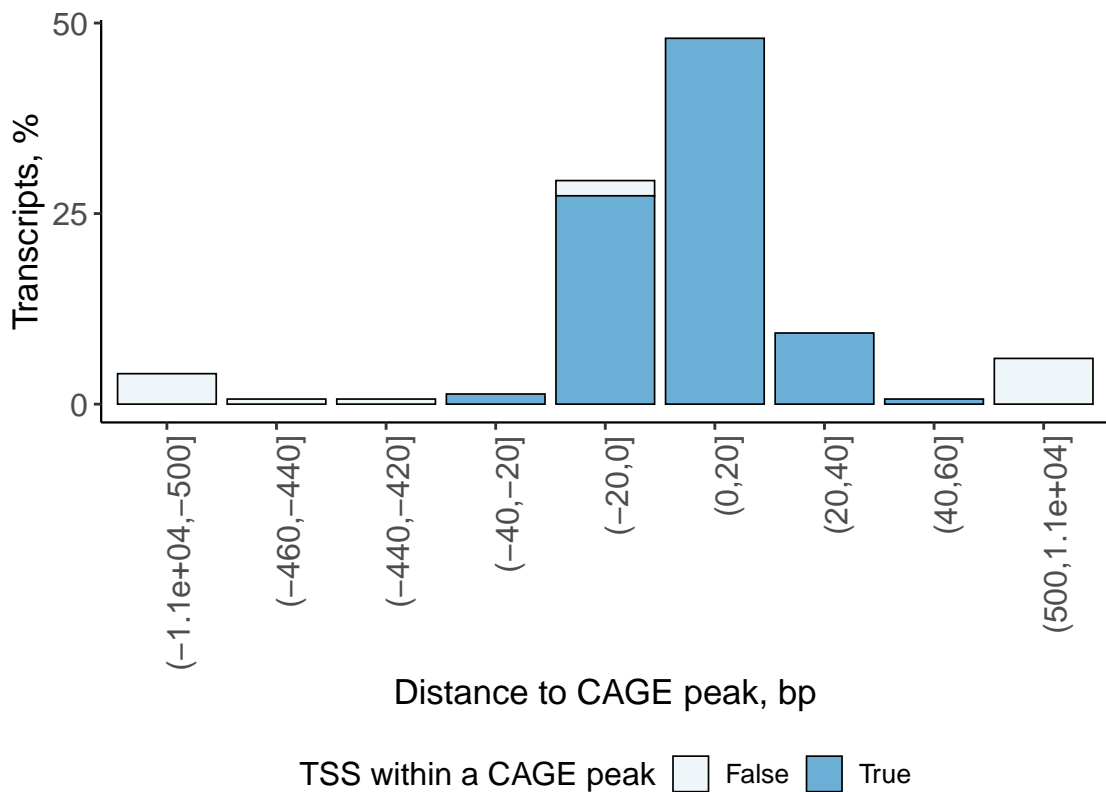
Distance to CAGE Peak of Multi-Exonic FSM Alternative 3' End

Negative values indicate downstream of annotated CAGE peak



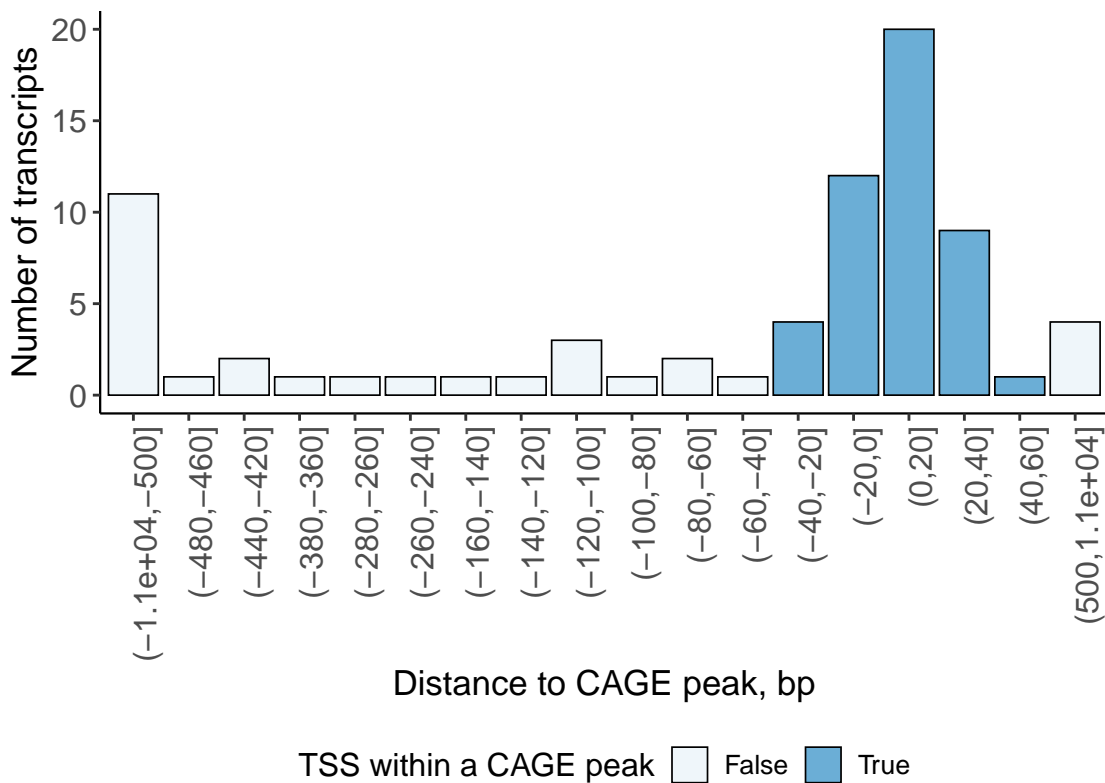
Distance to CAGE Peak of Multi-Exonic FSM Alternative 3' End

Negative values indicate downstream of annotated CAGE peak



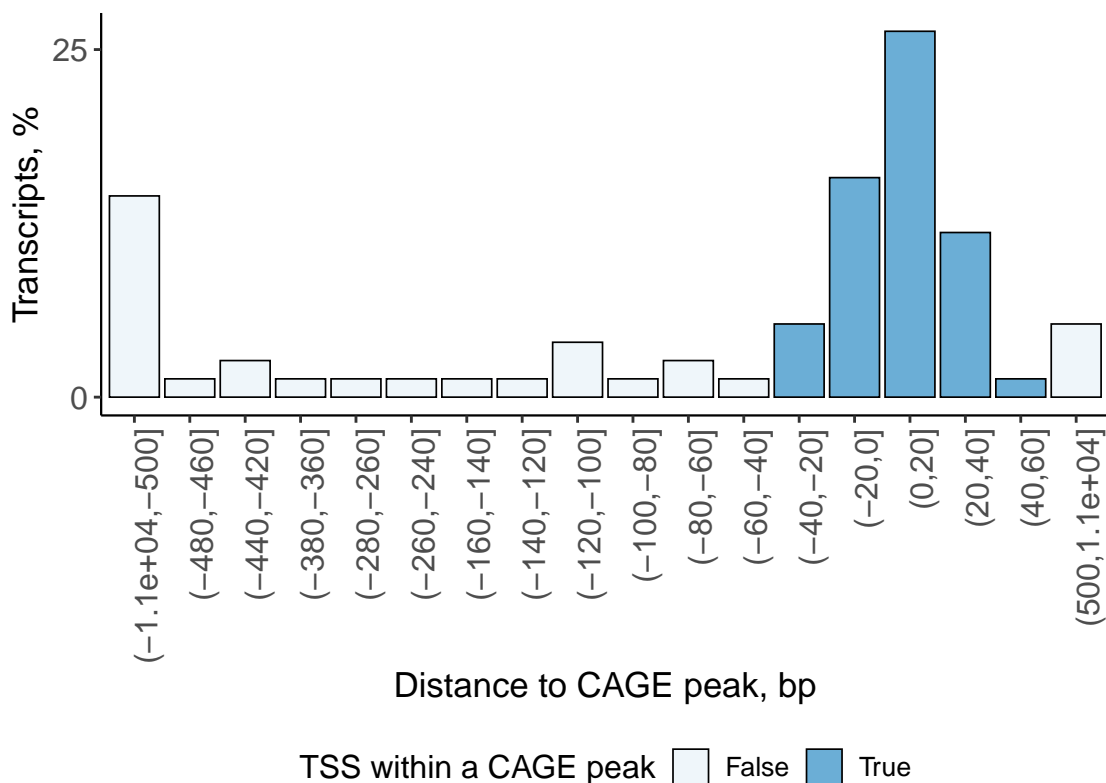
Distance to CAGE Peak of Multi-Exonic FSM Alternative 3'5' End

Negative values indicate downstream of annotated CAGE peak



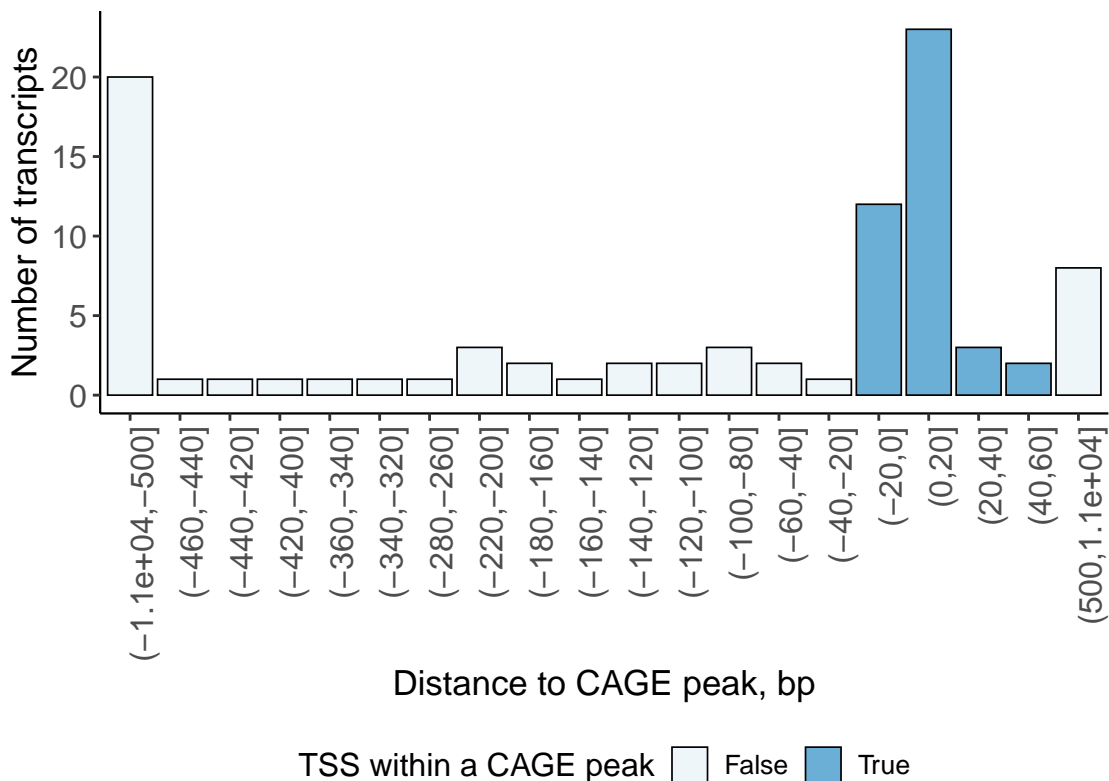
Distance to CAGE Peak of Multi-Exonic FSM Alternative 3'5' End

Negative values indicate downstream of annotated CAGE peak



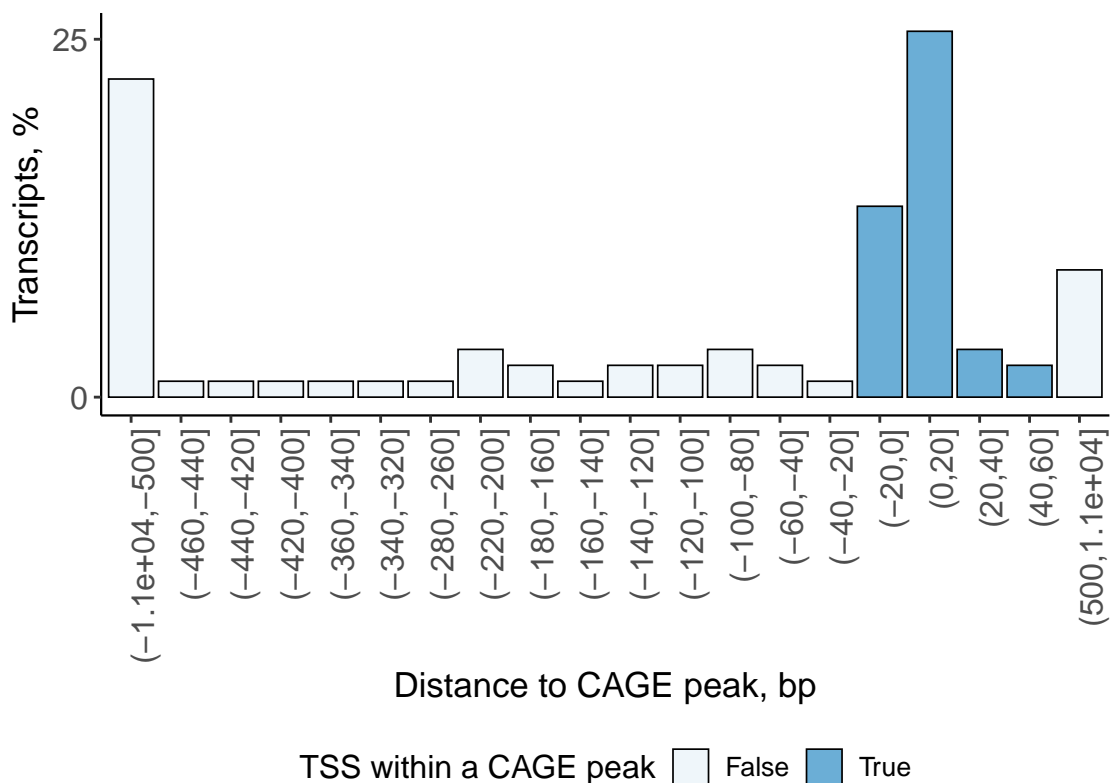
Distance to CAGE Peak of Multi-Exonic FSM Alternative 5' End

Negative values indicate downstream of annotated CAGE peak



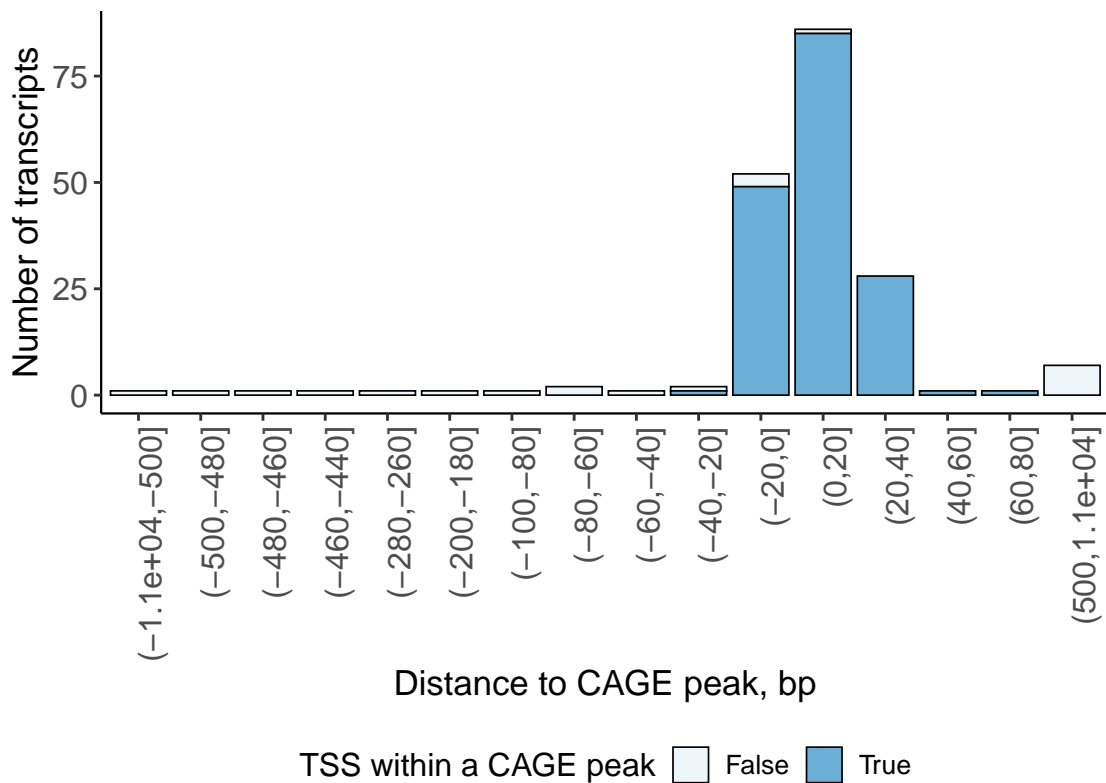
Distance to CAGE Peak of Multi-Exonic FSM Alternative 5' End

Negative values indicate downstream of annotated CAGE peak



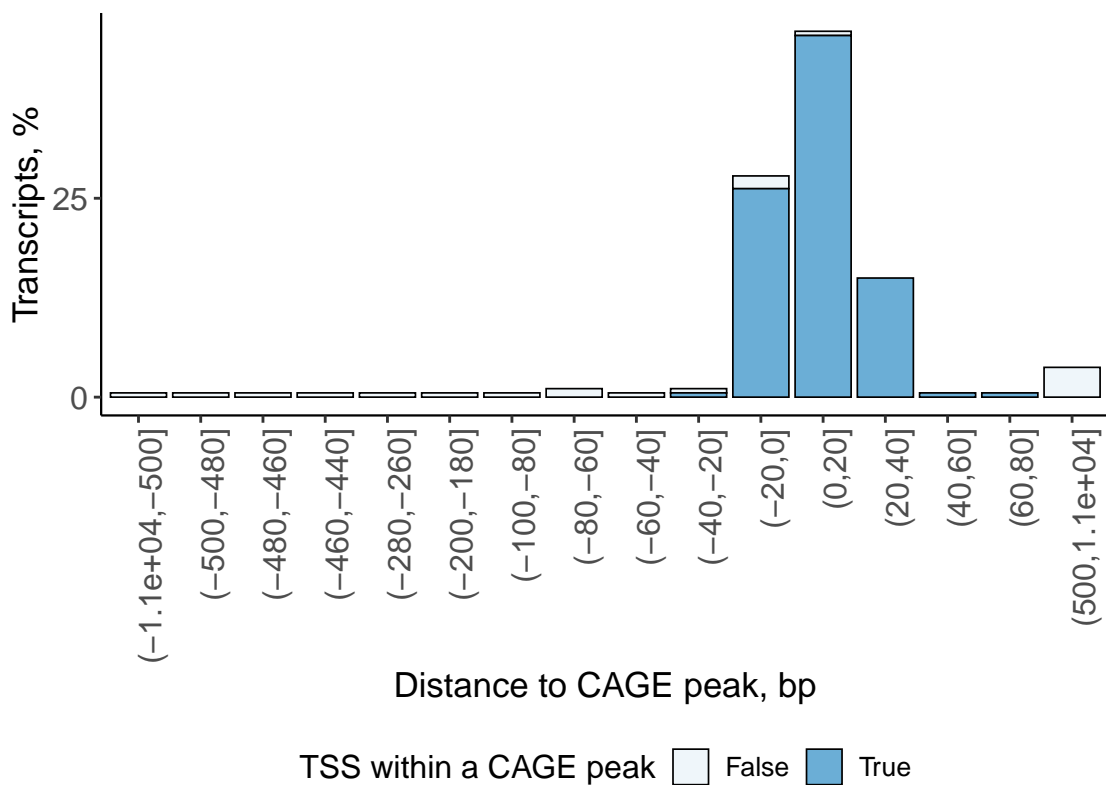
Distance to CAGE Peak of Multi-Exonic FSM Reference Match

Negative values indicate downstream of annotated CAGE peak



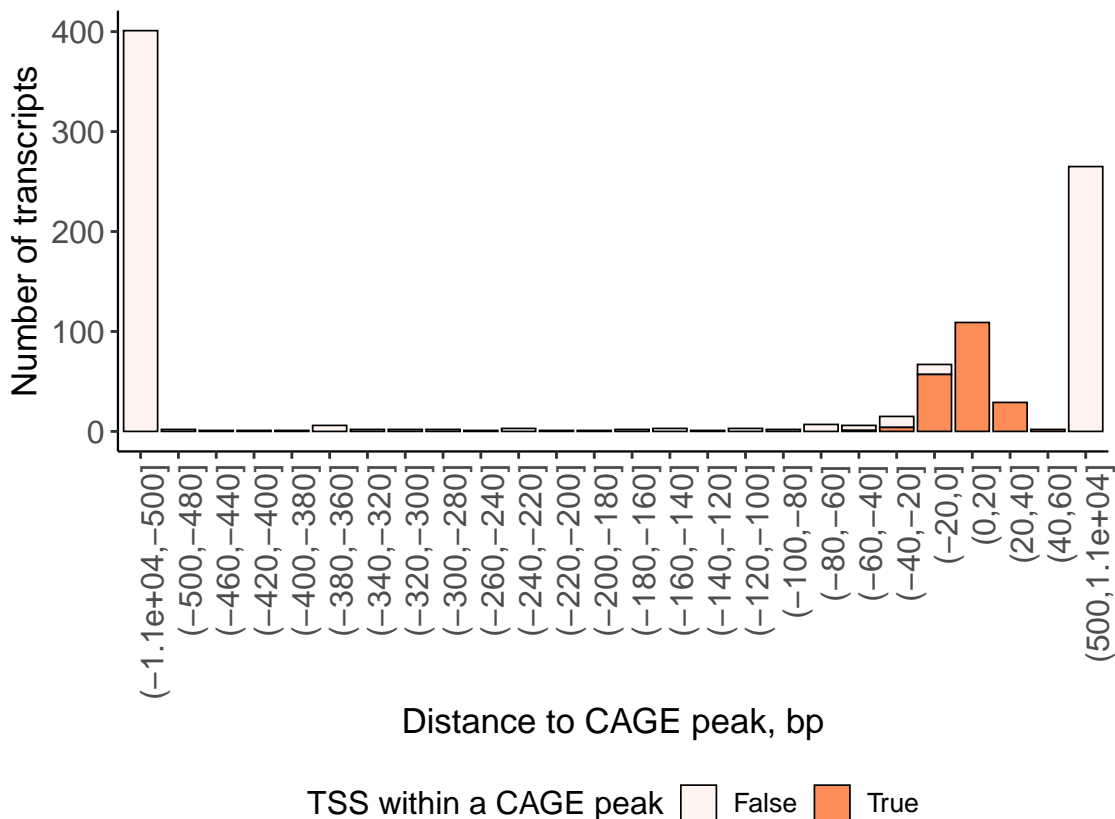
Distance to CAGE Peak of Multi-Exonic FSM Reference Match

Negative values indicate downstream of annotated CAGE peak



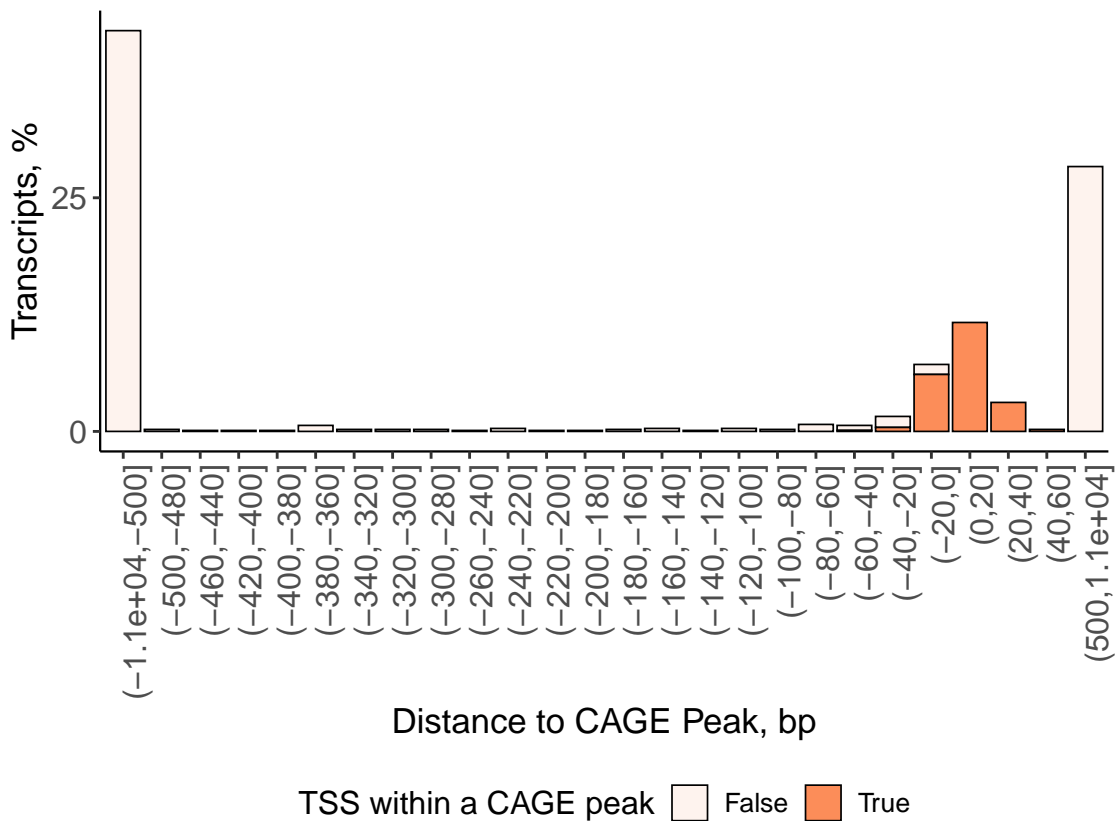
Distance to CAGE Peak of Multi-Exonic ISM

Negative values indicate downstream of annotated CAGE peak



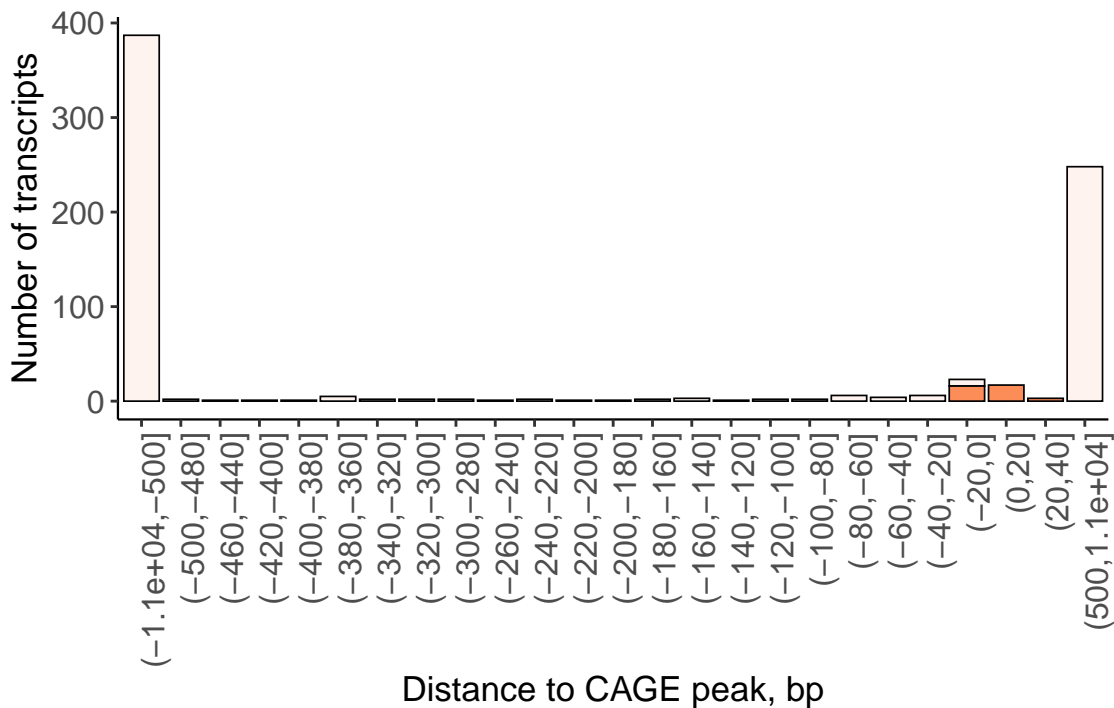
Distance to CAGE Peak of Multi-Exonic ISM

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic ISM 3' Fragment

Negative values indicate downstream of annotated CAGE peak



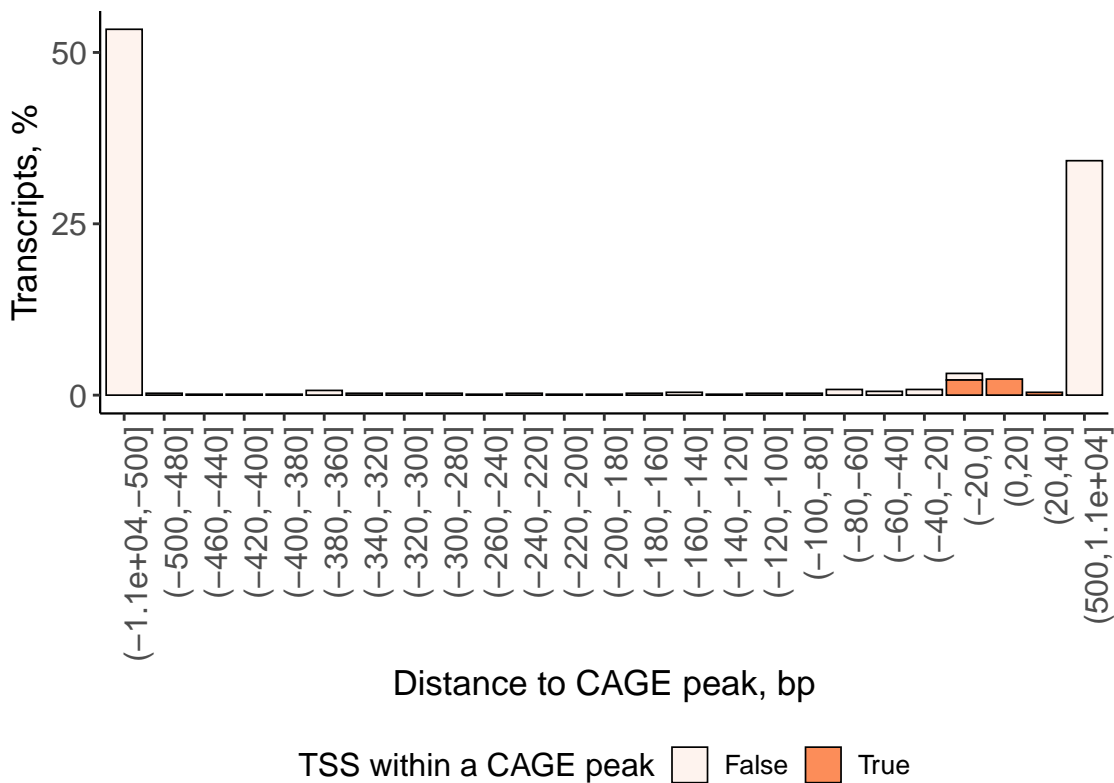
TSS within a CAGE peak



False True

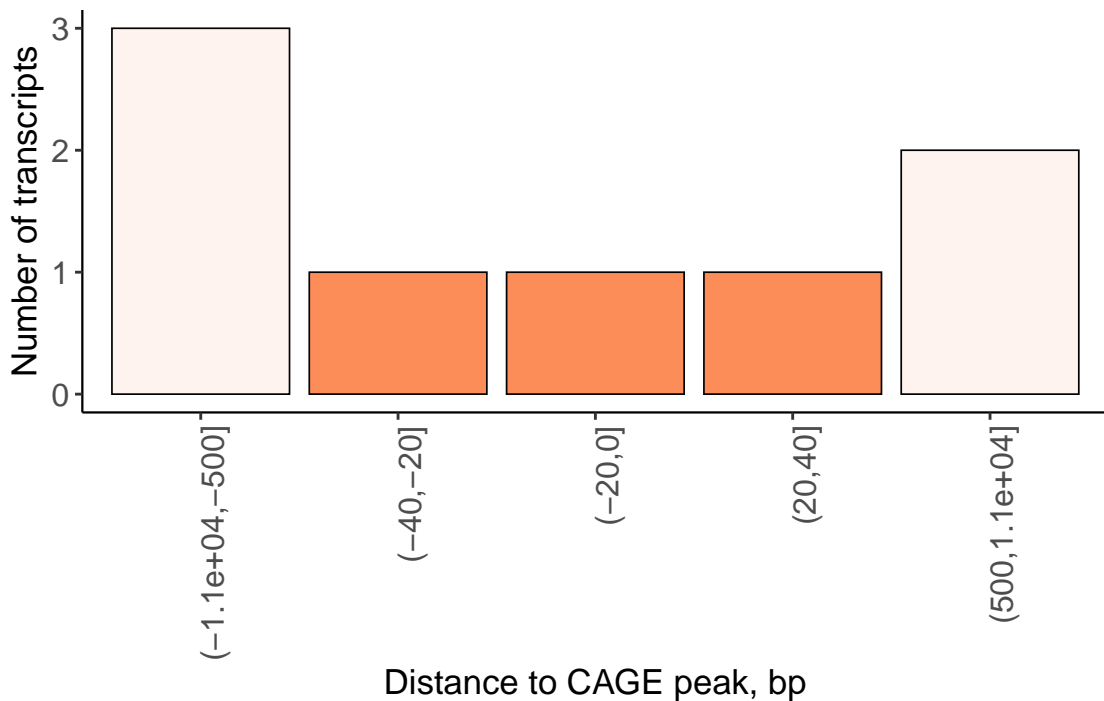
Distance to CAGE Peak of Multi-Exonic ISM 3' Fragment

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic ISM Internal Fragment

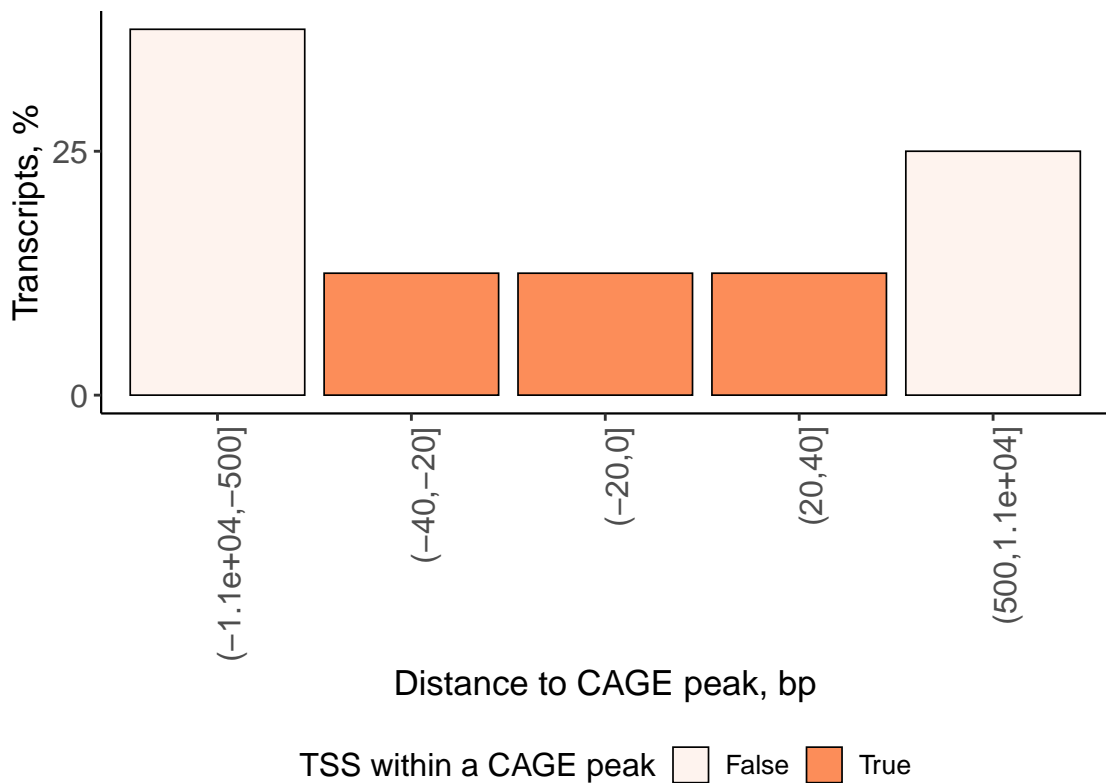
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

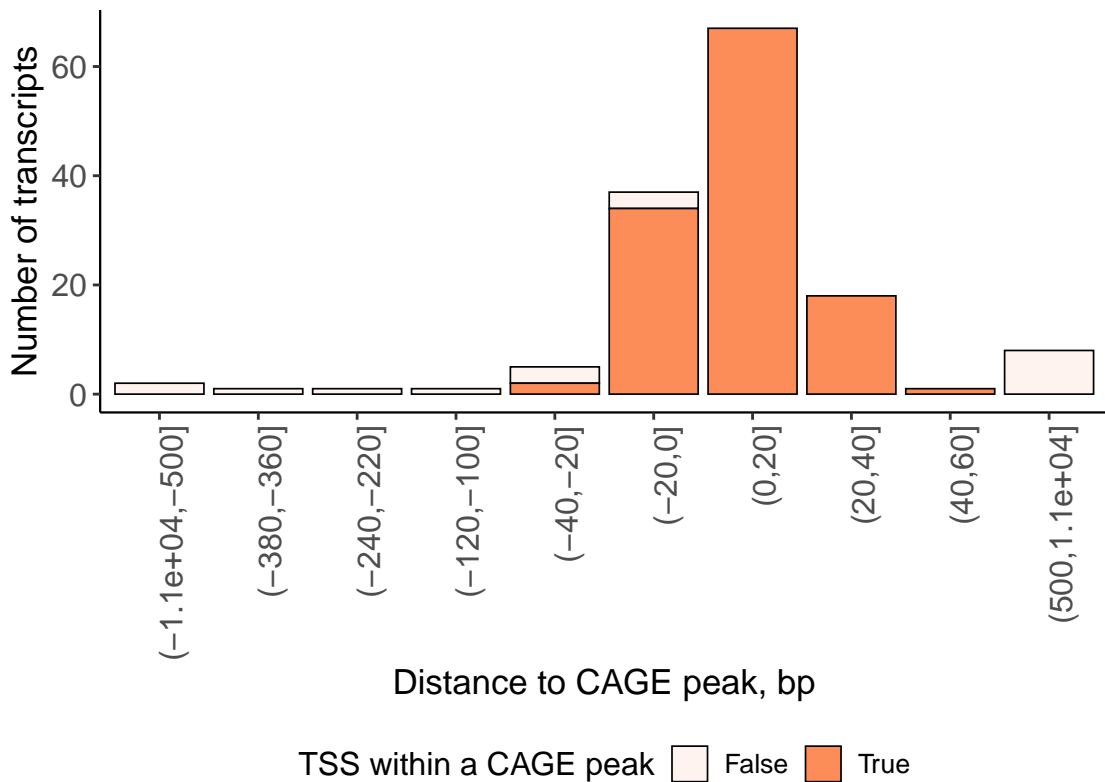
Distance to CAGE Peak of Multi-Exonic ISM Internal Fragment

Negative values indicate downstream of annotated CAGE peak



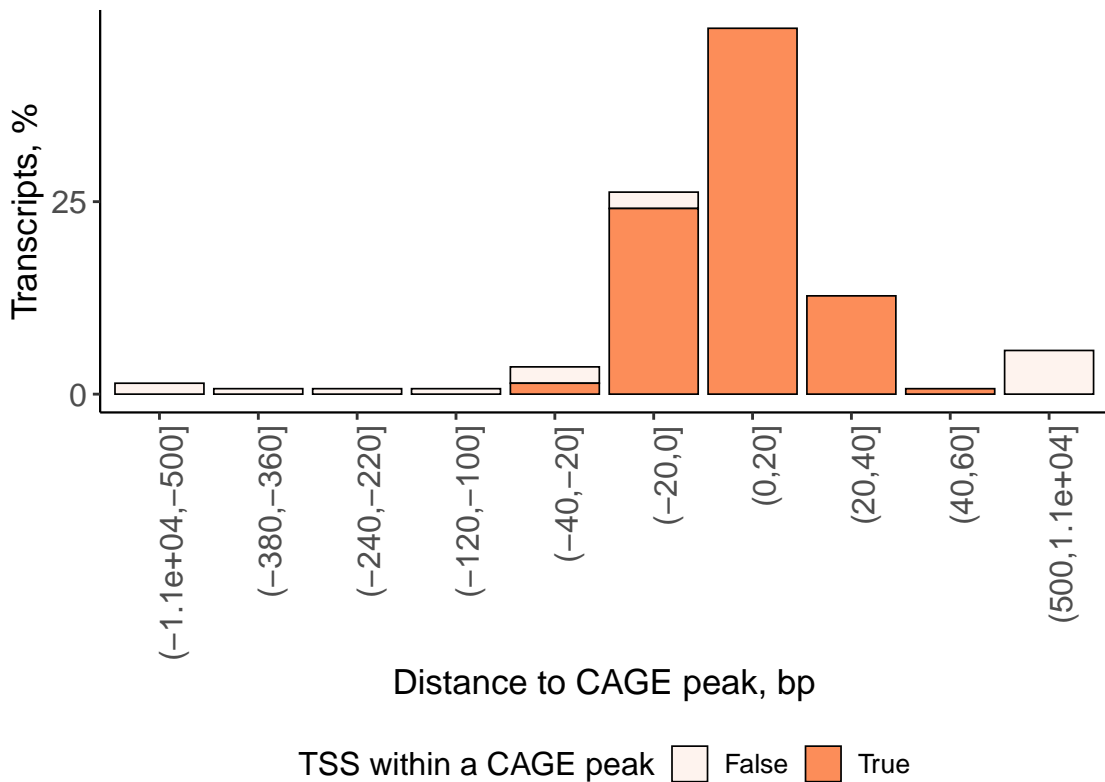
Distance to CAGE Peak of Multi-Exonic ISM 5' Fragment

Negative values indicate downstream of annotated CAGE peak



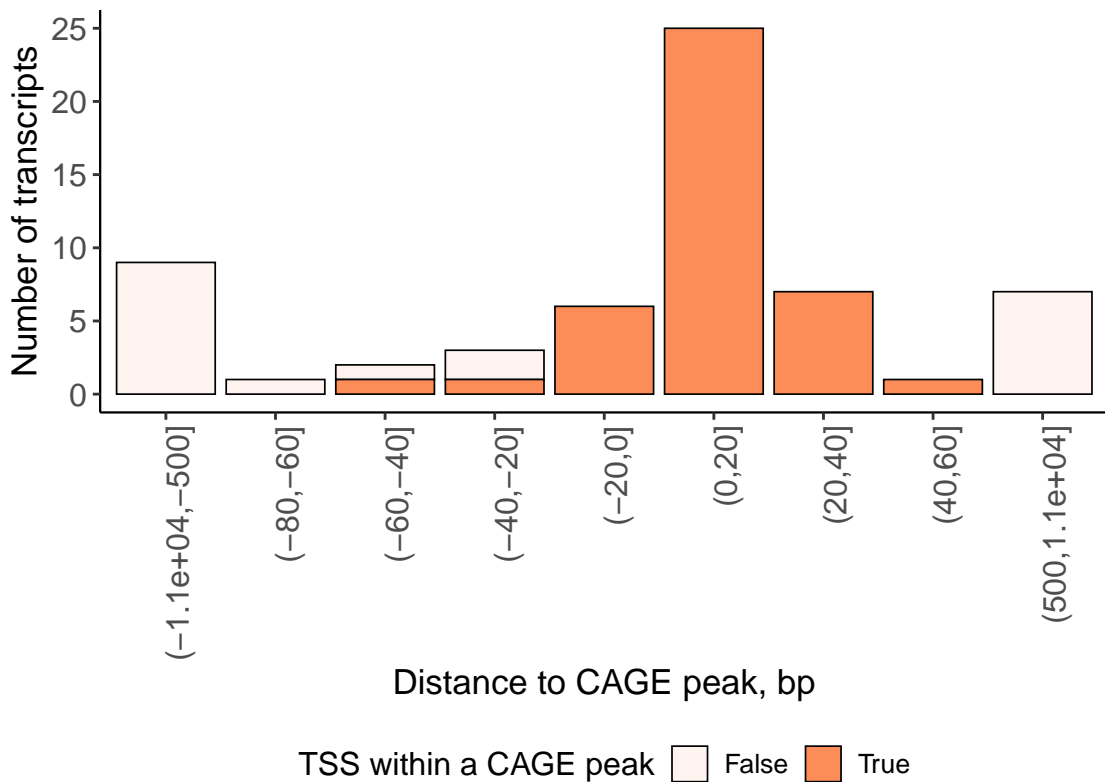
Distance to CAGE Peak of Multi-Exonic ISM 5' Fragment

Negative values indicate downstream of annotated CAGE peak



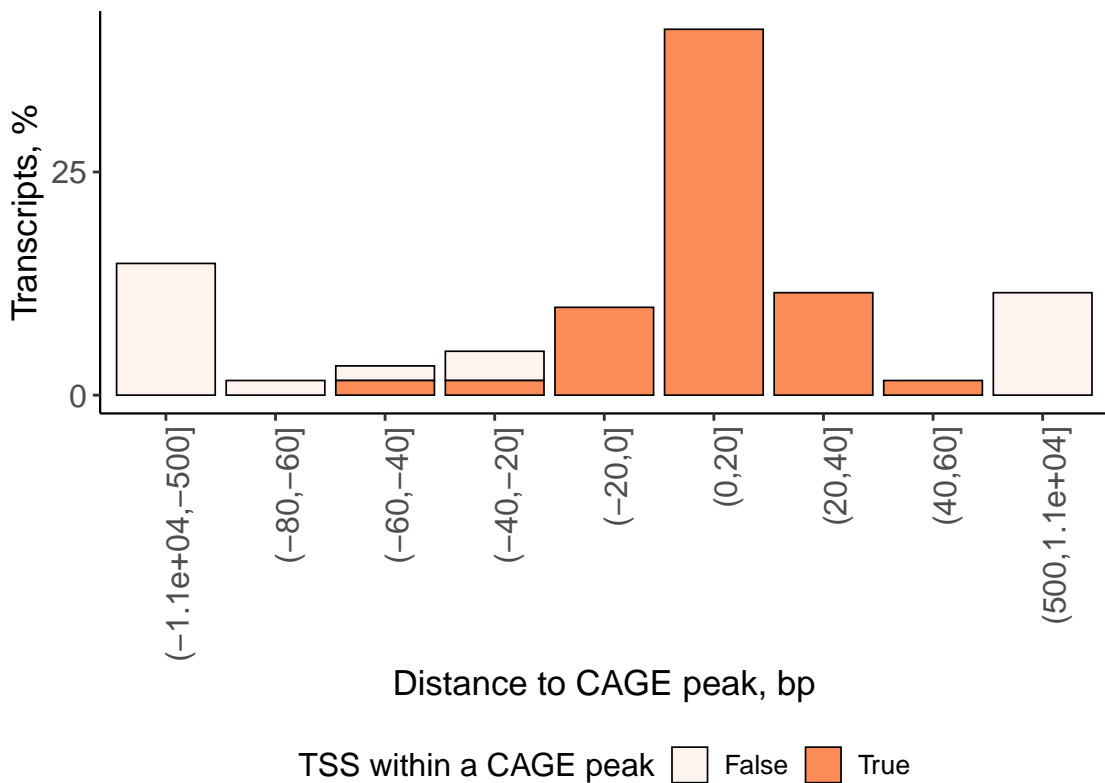
Distance to CAGE Peak of Multi-Exonic ISM Intron Retention

Negative values indicate downstream of annotated CAGE peak



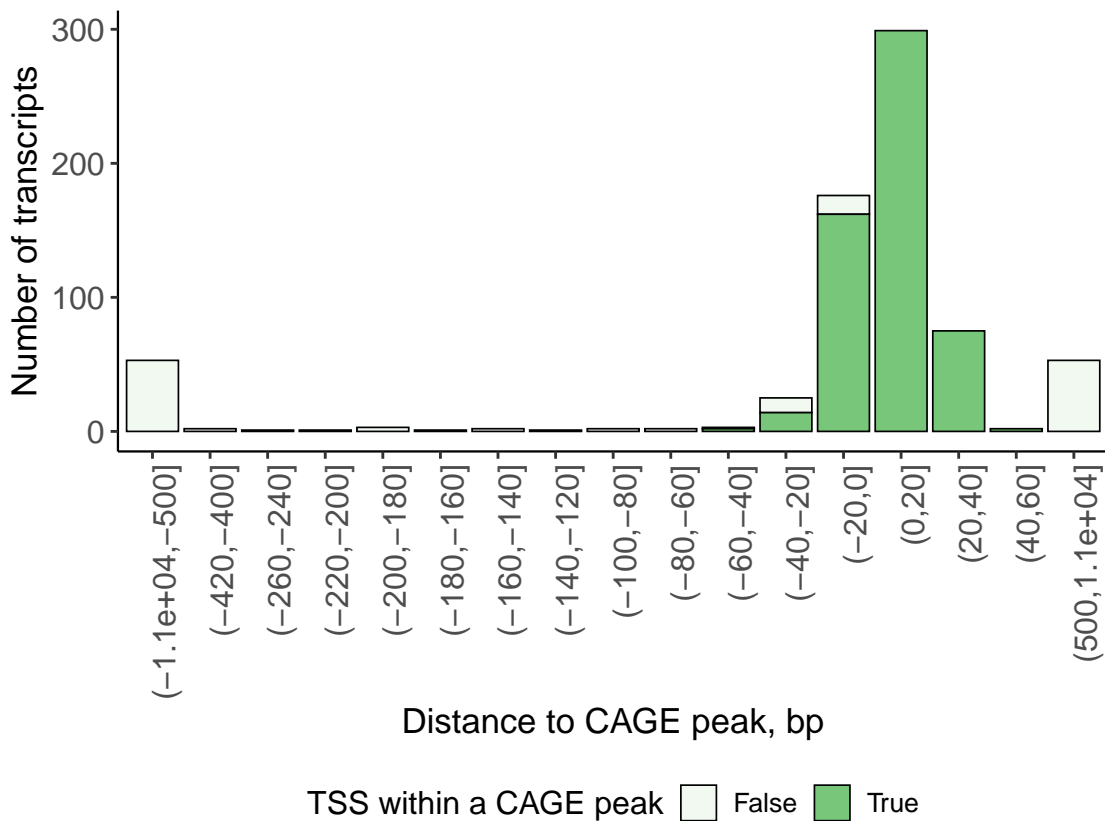
Distance to CAGE Peak of Multi-Exonic ISM Intron Retention

Negative values indicate downstream of annotated CAGE peak



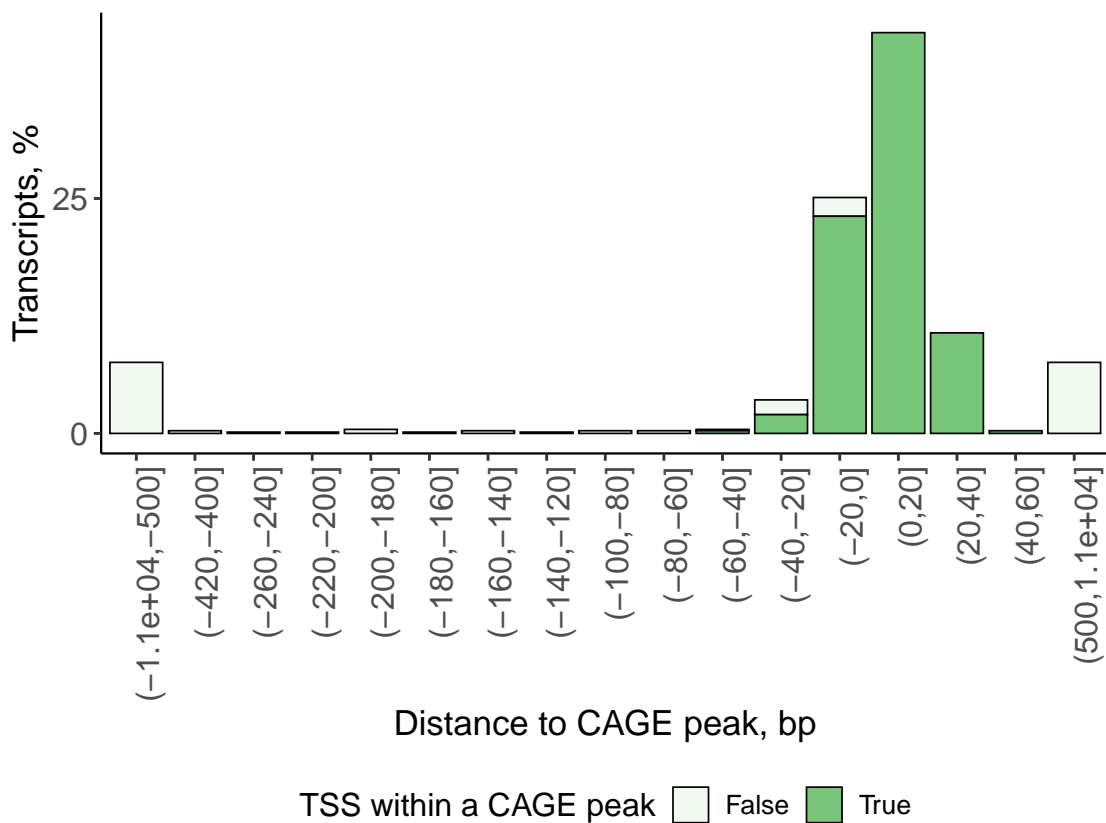
Distance to CAGE Peak of Multi-Exonic NIC

Negative values indicate downstream of annotated CAGE peak



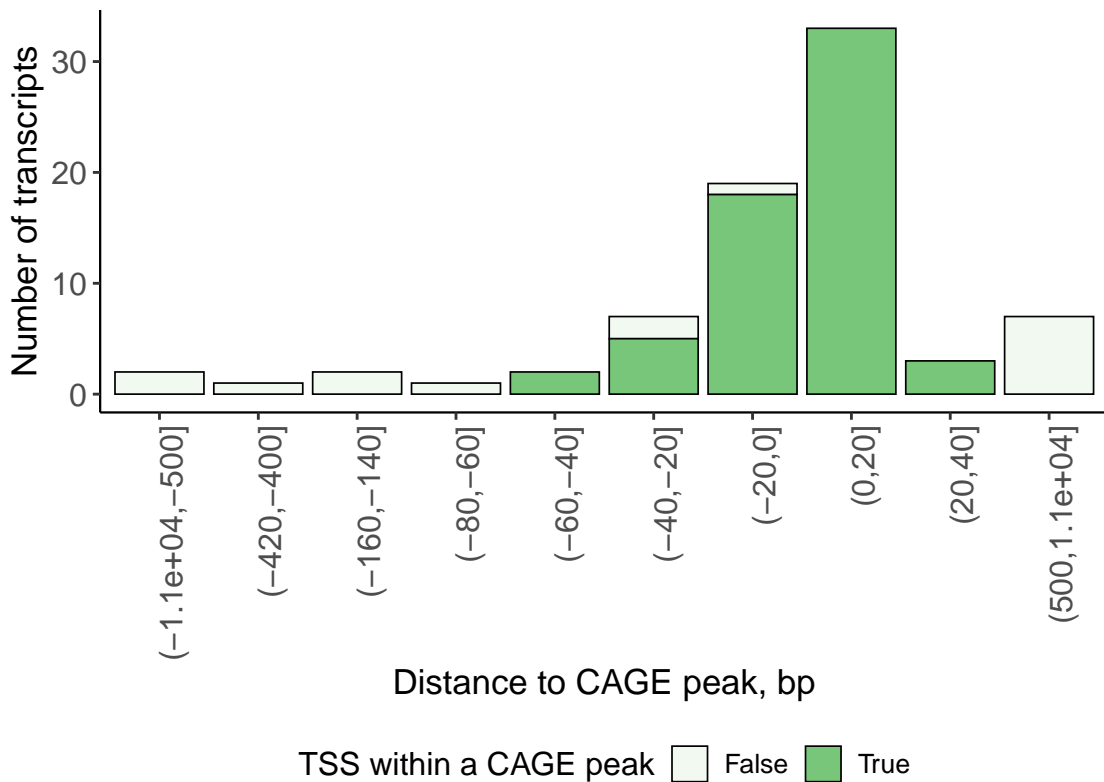
Distance to CAGE Peak of Multi-Exonic NIC

Negative values indicate downstream of annotated CAGE peak



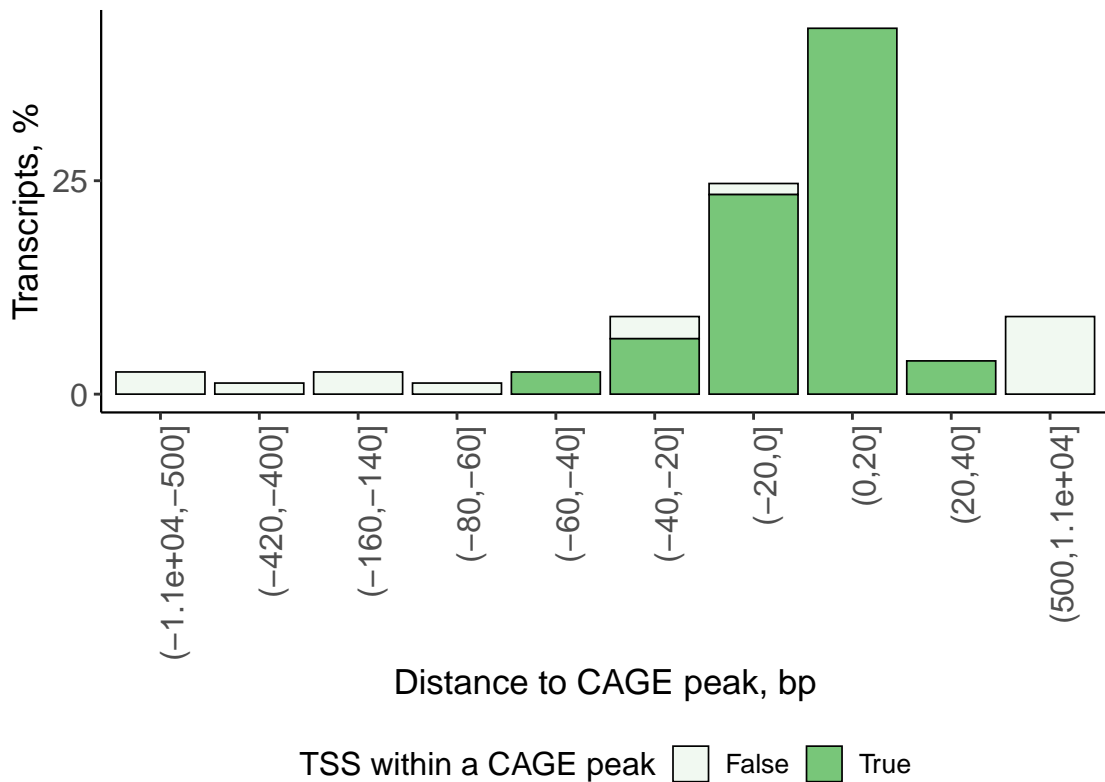
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Junctions

Negative values indicate downstream of annotated CAGE peak



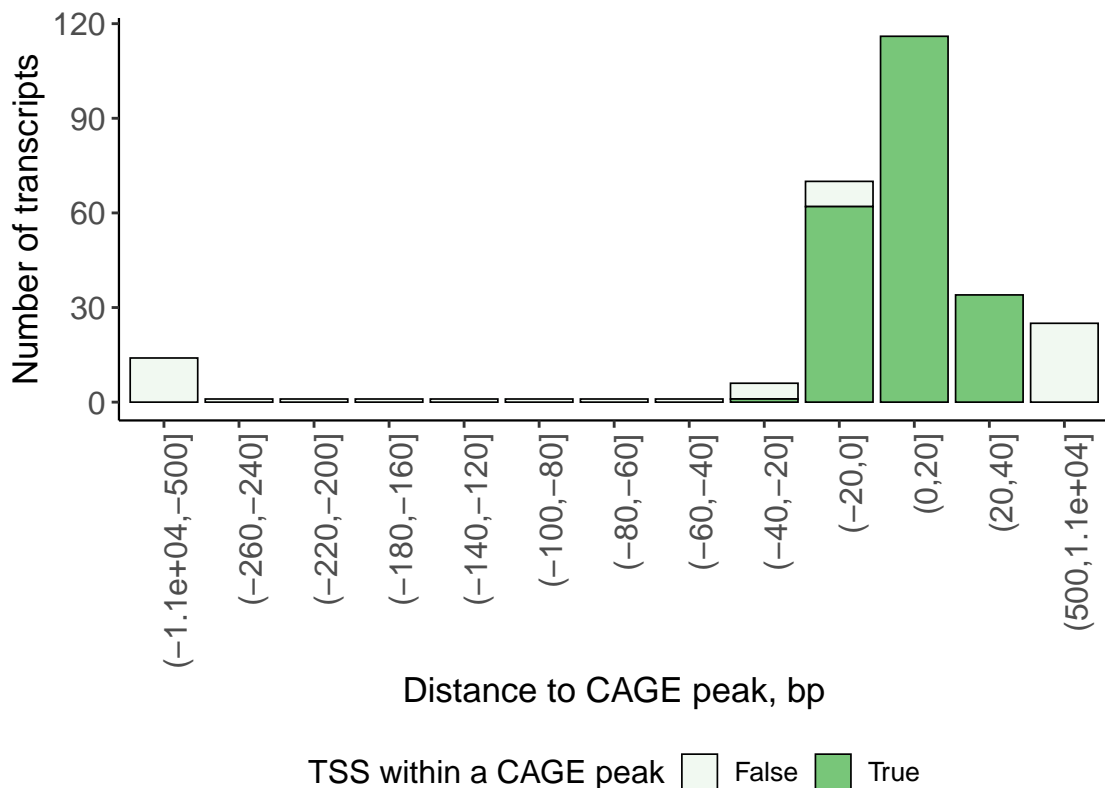
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Junctions

Negative values indicate downstream of annotated CAGE peak



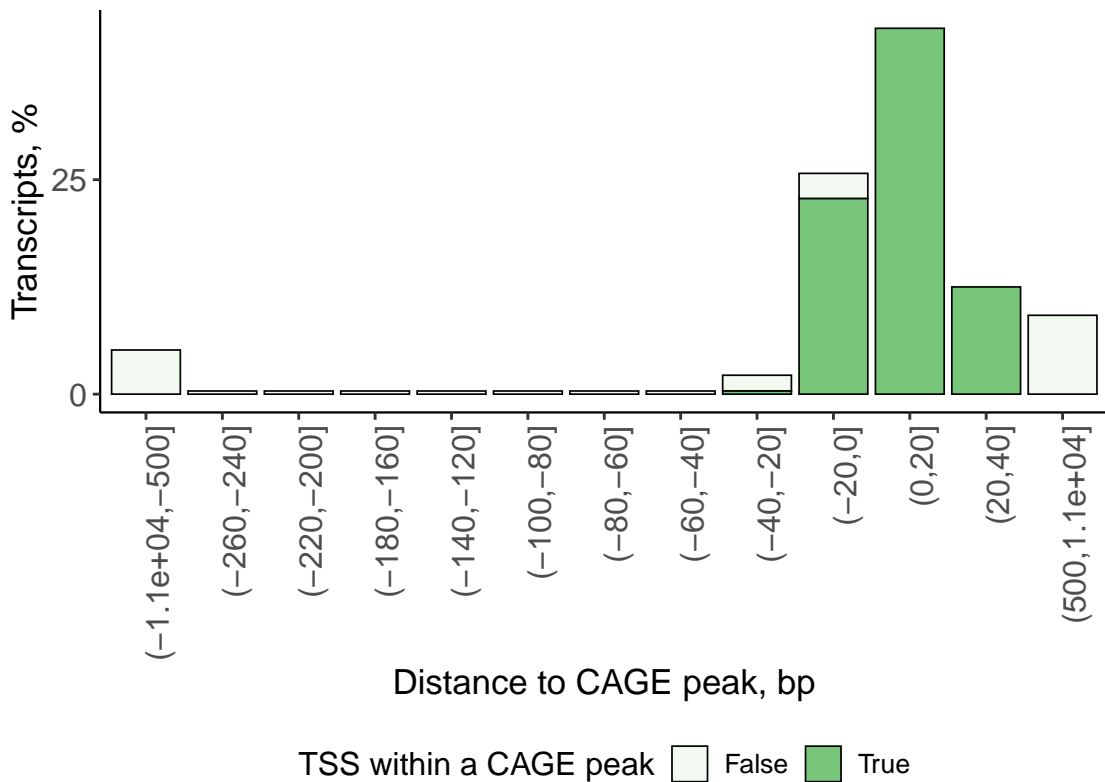
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Splice Sites

Negative values indicate downstream of annotated CAGE peak



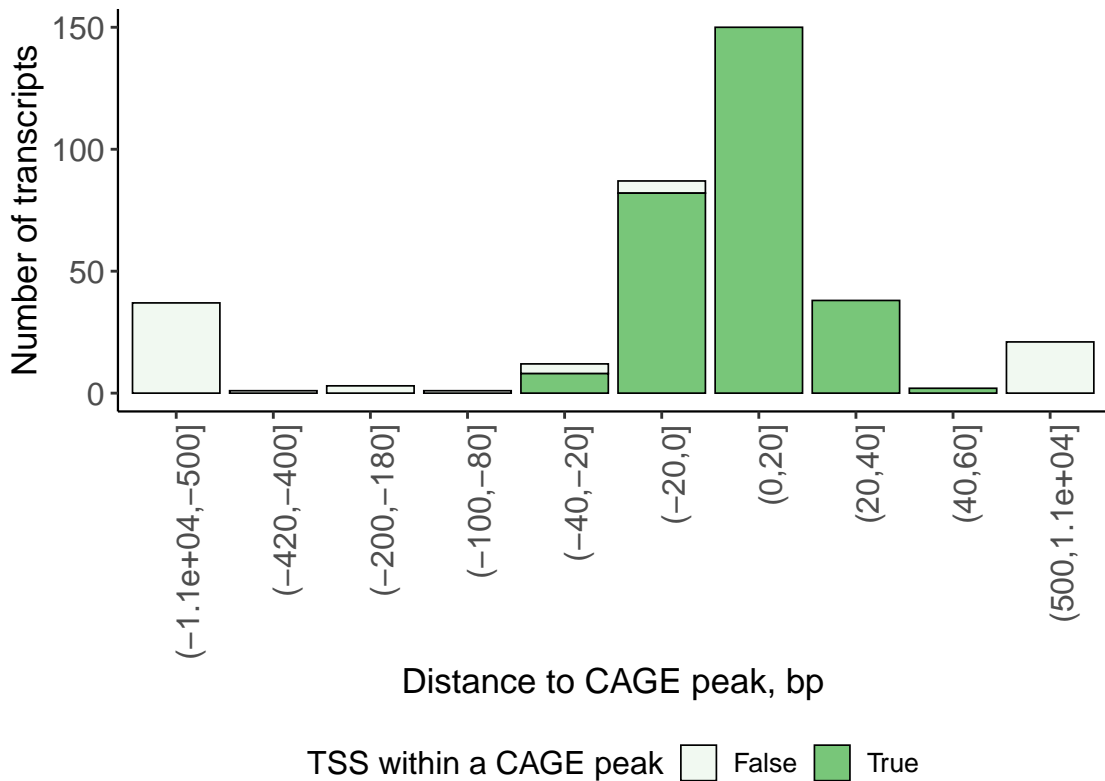
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Splice Sites

Negative values indicate downstream of annotated CAGE peak



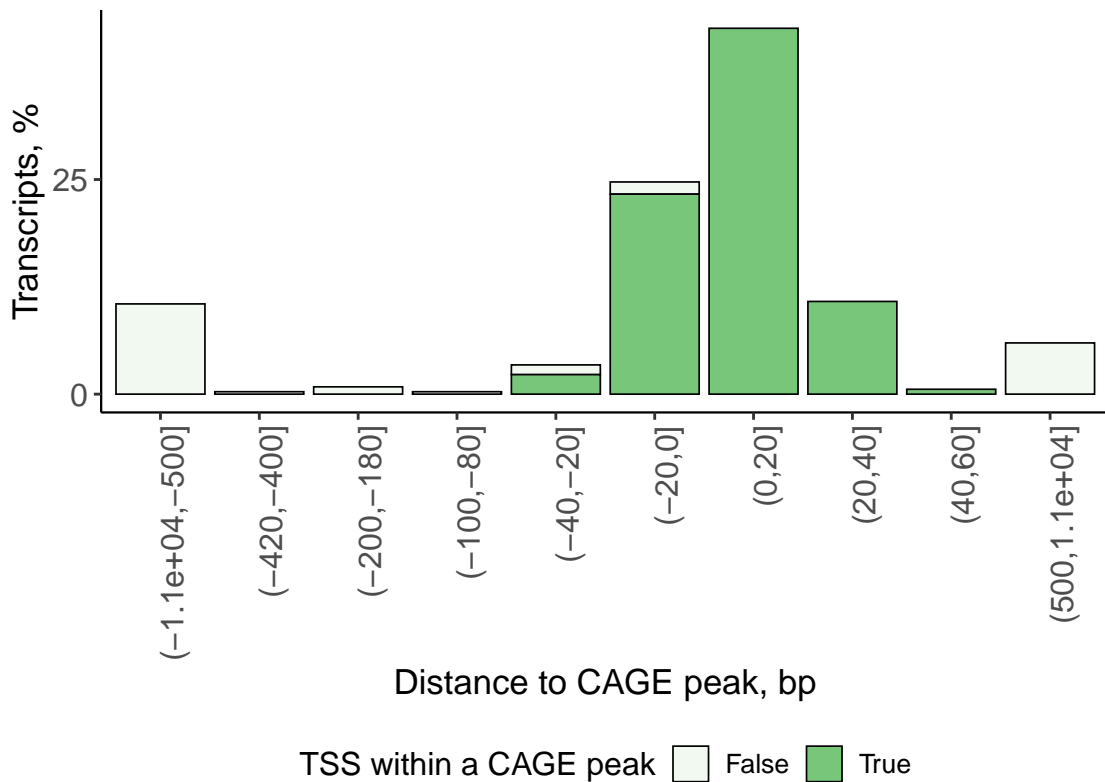
Distance to CAGE Peak of Multi-Exonic NIC Intron Retention

Negative values indicate downstream of annotated CAGE peak



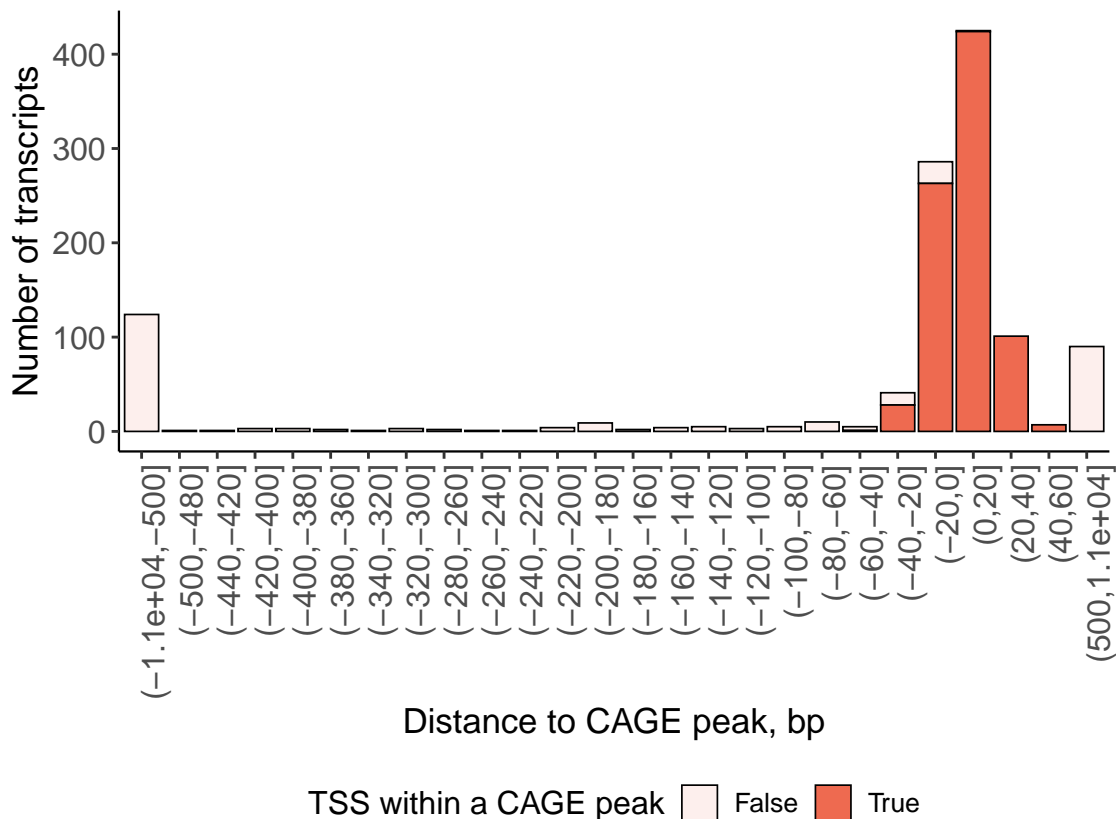
Distance to CAGE Peak of Multi-Exonic NIC Intron Retention

Negative values indicate downstream of annotated CAGE peak



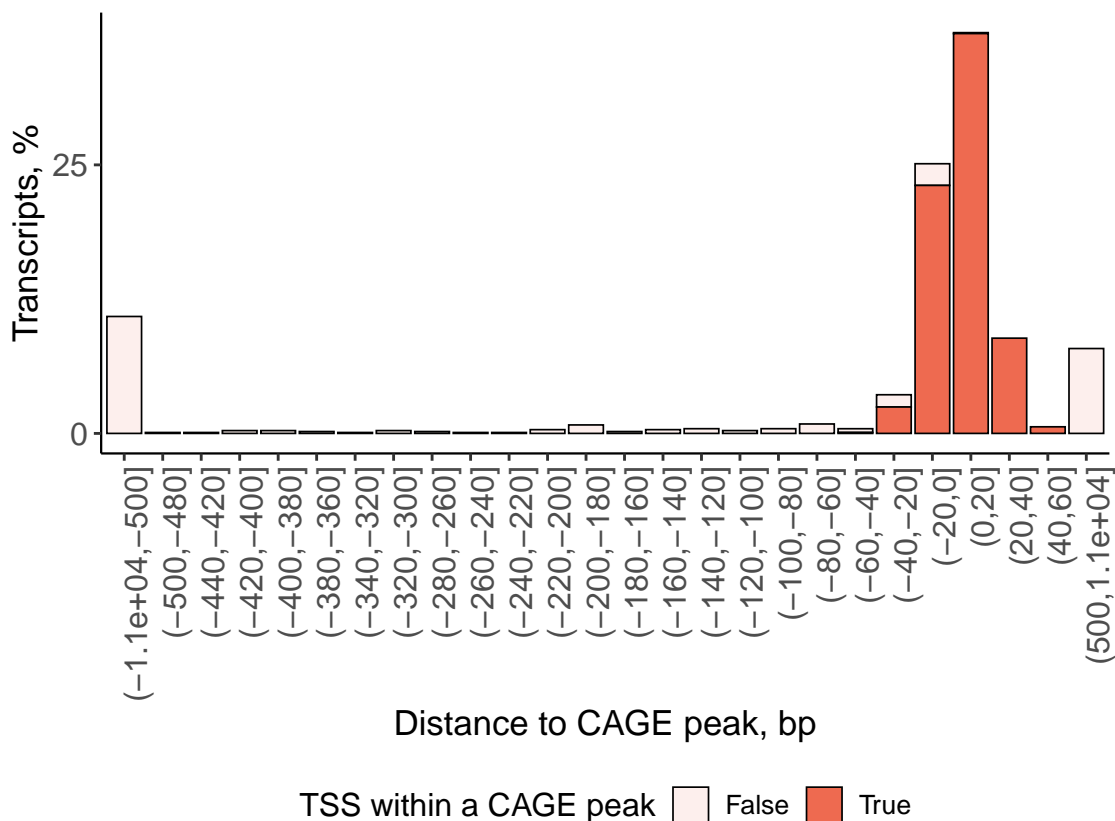
Distance to CAGE Peak of Multi-Exonic NNC

Negative values indicate downstream of annotated CAGE peak



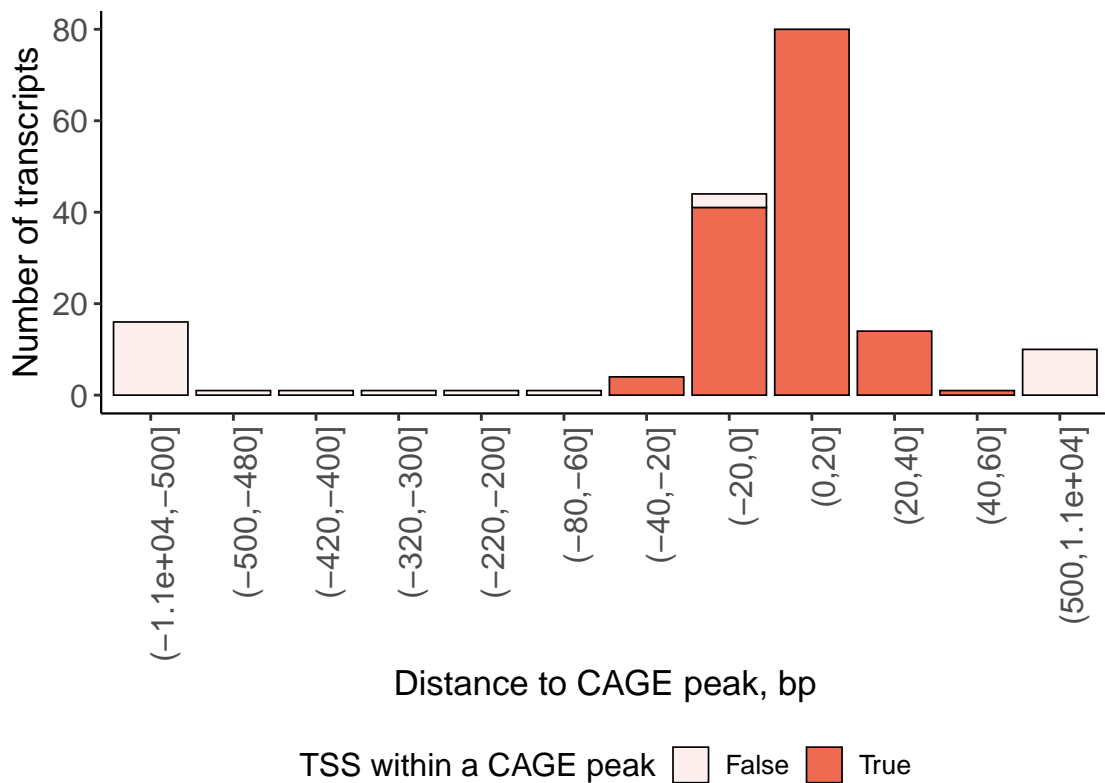
Distance to CAGE Peak of Multi-Exonic NNC

Negative values indicate downstream of annotated CAGE peak



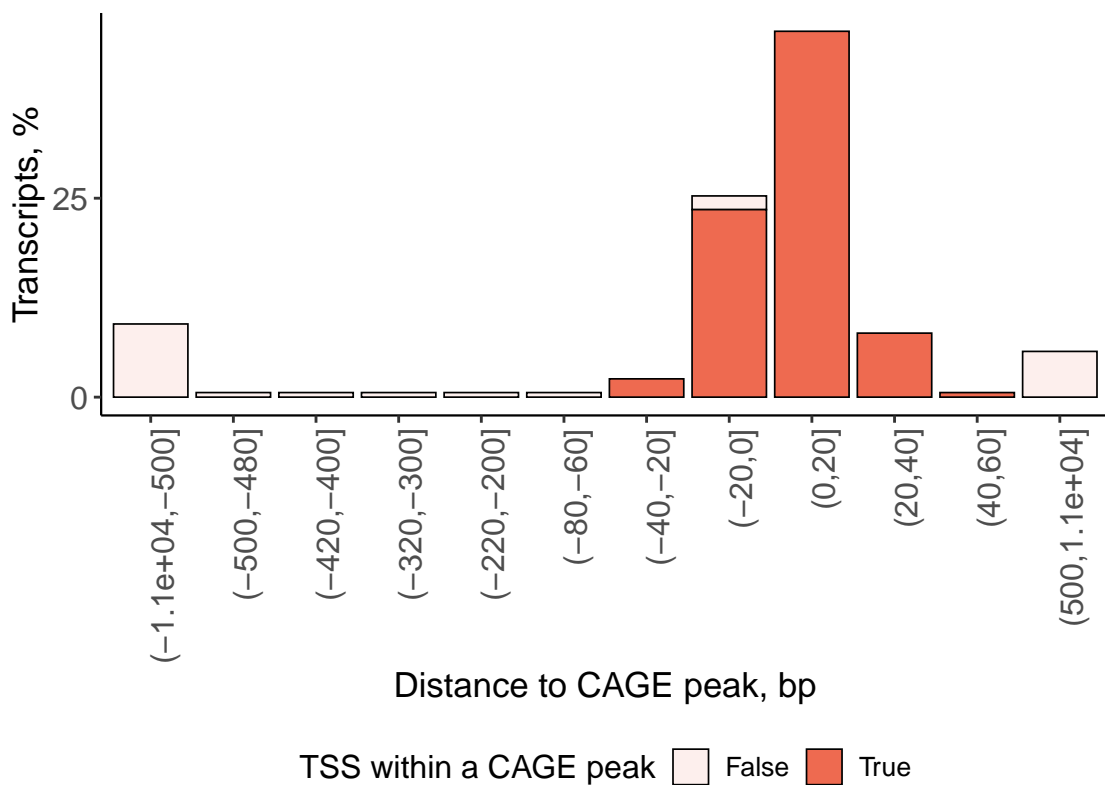
Distance to CAGE Peak of Multi-Exonic NNC Intron Retention

Negative values indicate downstream of annotated CAGE peak



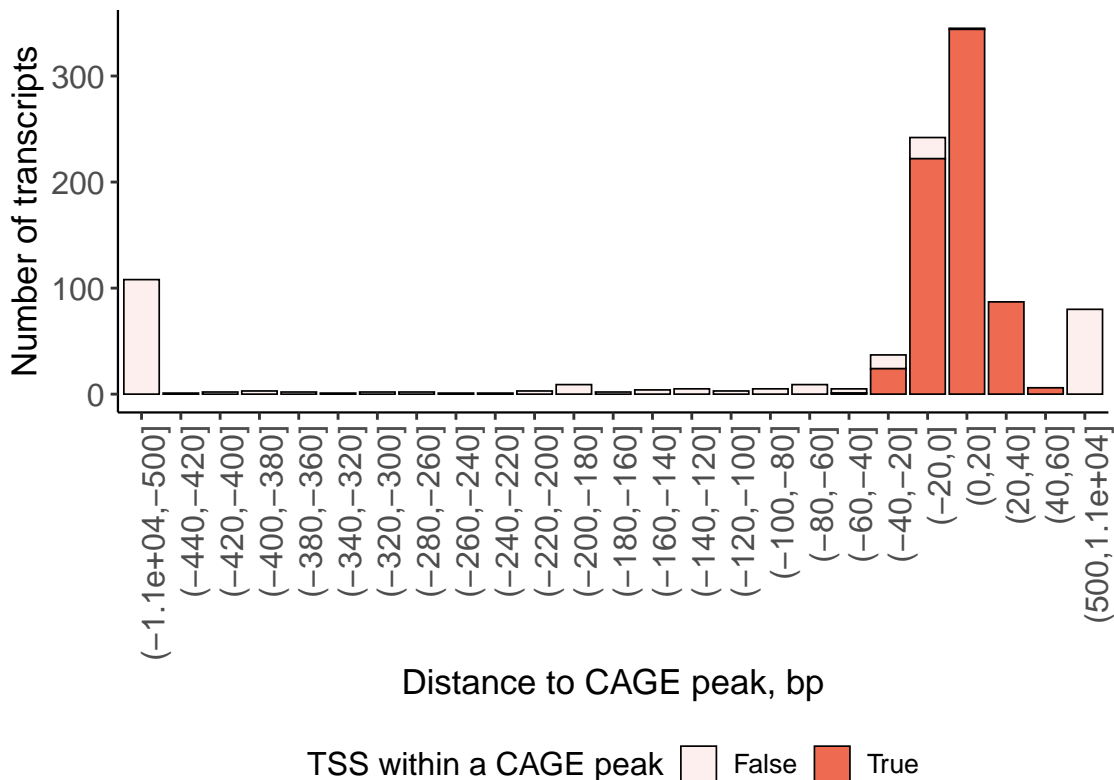
Distance to CAGE Peak of Multi-Exonic NNC Intron Retention

Negative values indicate downstream of annotated CAGE peak



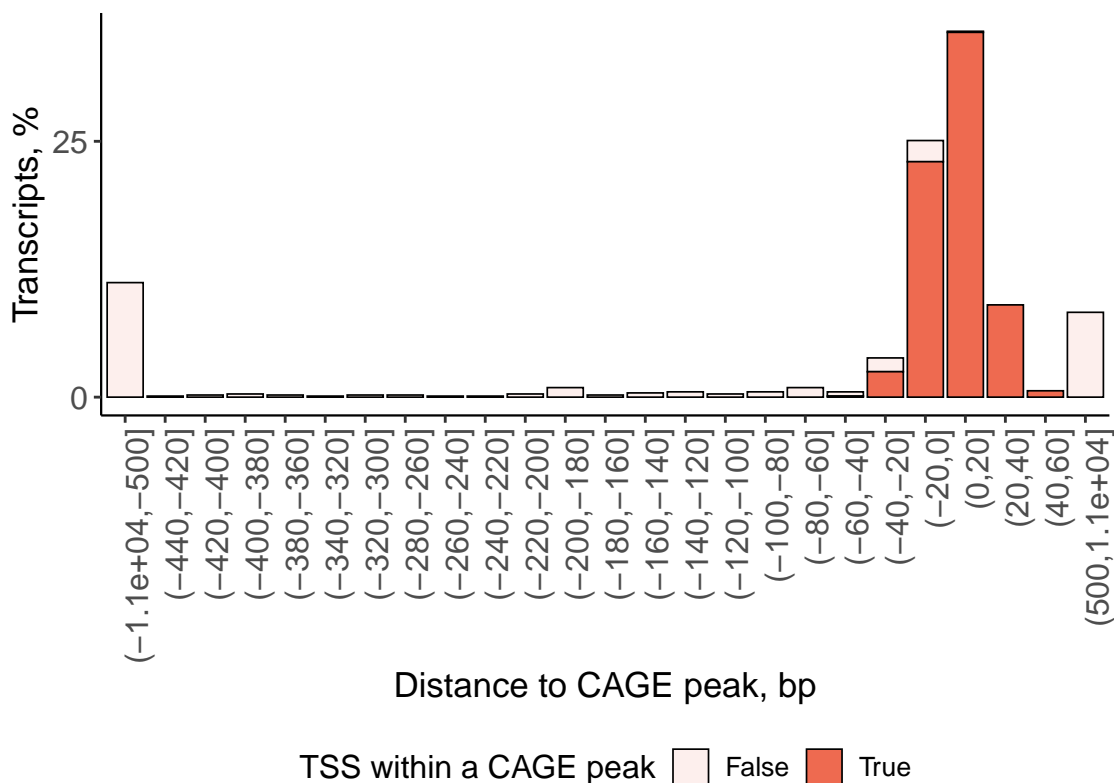
Distance to CAGE Peak of Multi-Exonic NNC At Least One Annotated Donor/Acceptor

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic NNC At Least One Annotated Donor/Acceptor

Negative values indicate downstream of annotated CAGE peak



Number of CAGE Detected

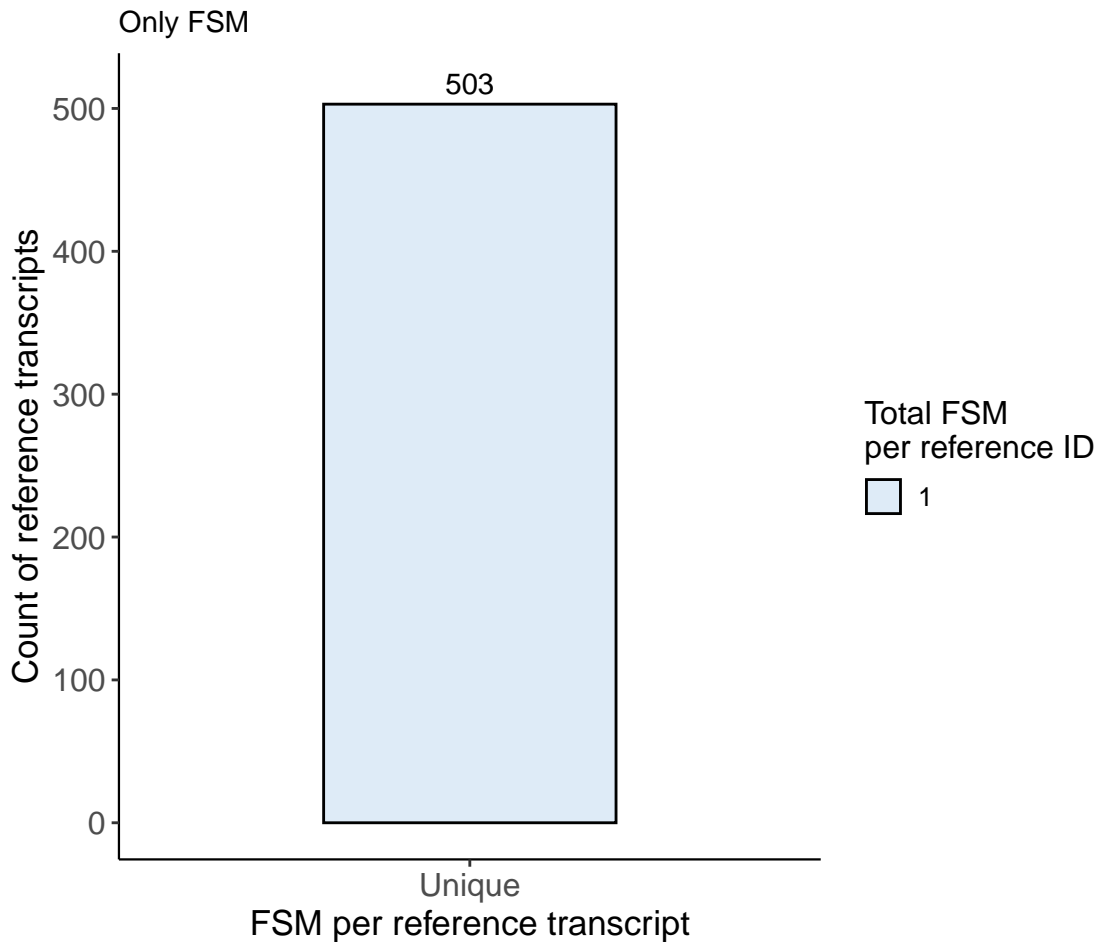
Category	Count	CAGE Detected	%
FSM	534	388	73
ISM	1134	211	19
NIC	806	598	74
NNC	1139	824	72
Genic Genomic	56	22	39
Antisense	28	1	4
Fusion	38	24	63
Intergenic	190	10	5

Number of CAGE Detected

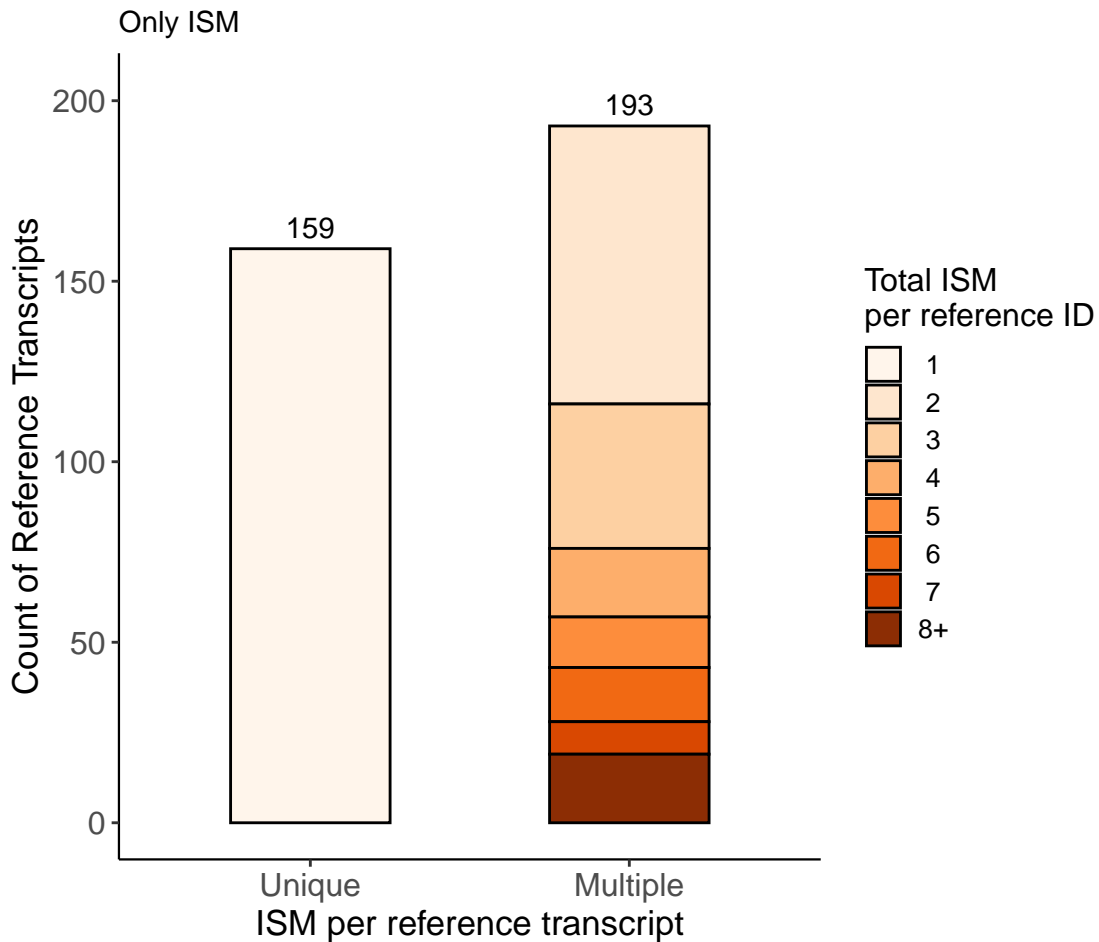
Subcategory	Count	CAGE Detected	%
Alternative 3'end	150	130	87
Alternative 3'5'end	76	46	61
Alterantive 5'end	90	40	44
Reference match	187	165	88
3' fragment	725	36	5
Internal fragment	8	3	38
5' fragment	141	122	87
Combin. of annot. junctions	77	61	79
Combin. of annot. splice sites	272	213	78
Intron retention	594	467	79
Mono-exon by intron retention	31	14	45
At least 1 annot. donor/accept.	965	684	71
Mono-exon	556	67	12
Multi-exon	53	30	57

Redundancy Analysis

Reference Transcript Redundancy

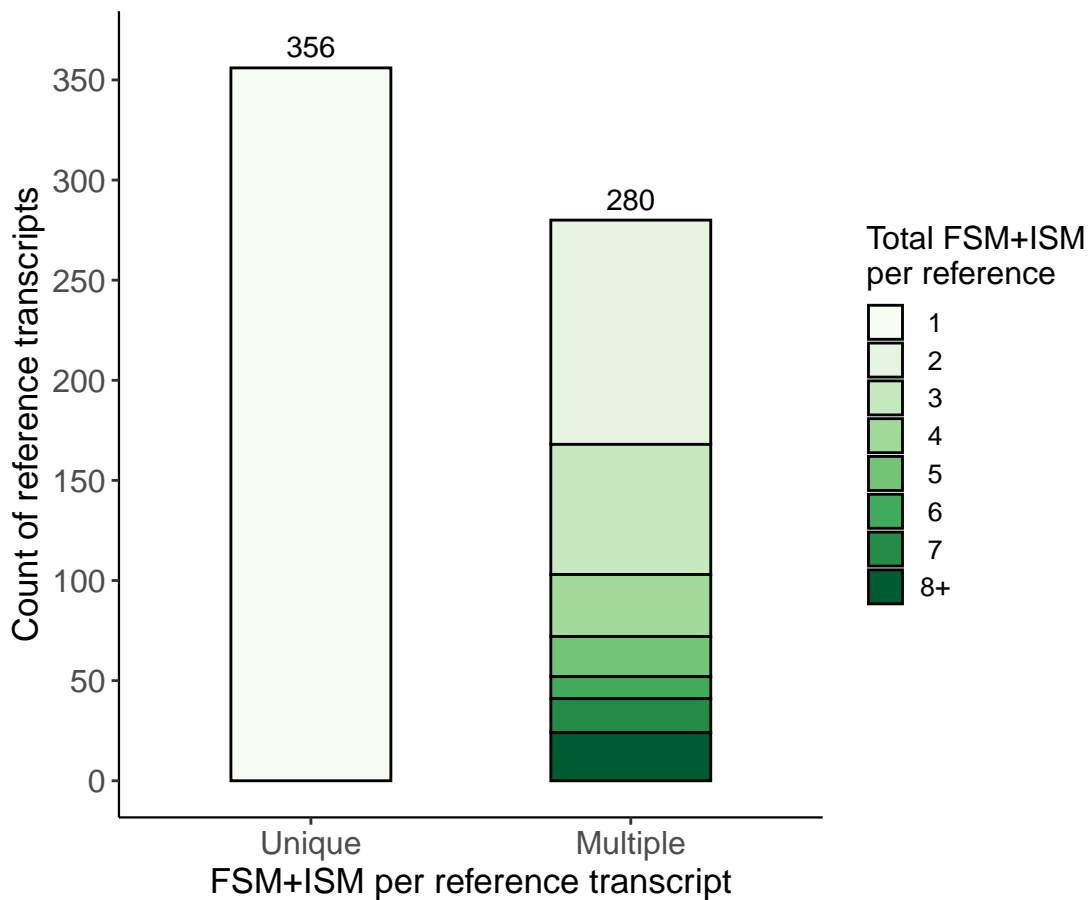


Reference Transcript Redundancy



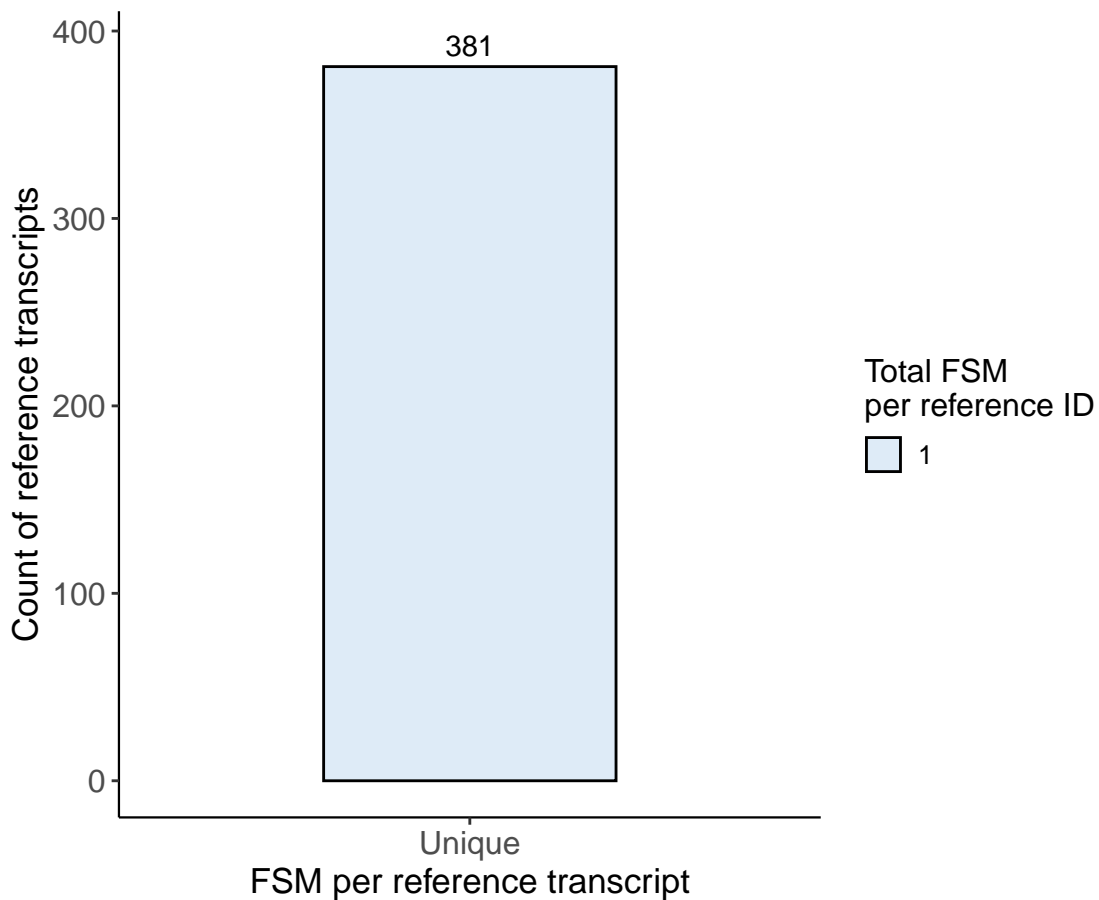
Reference Transcript Redundancy

FSM+ISM



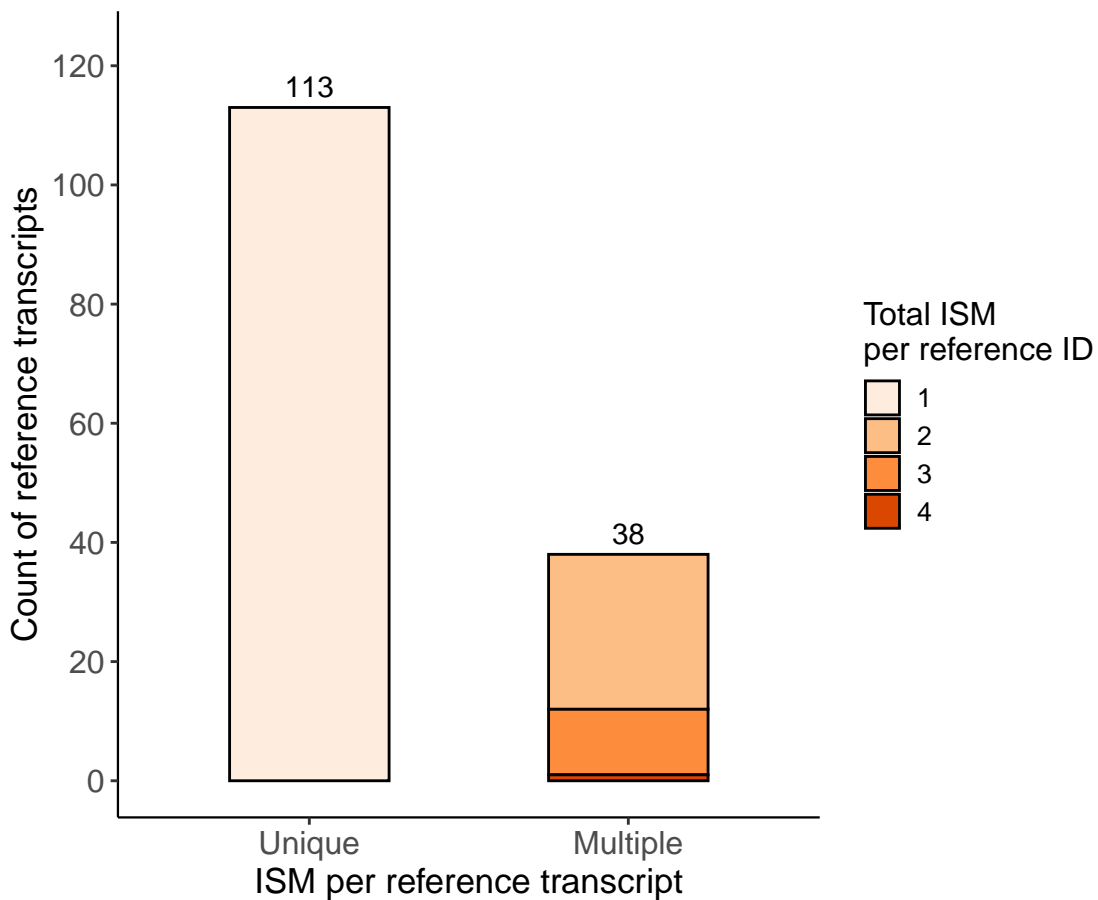
Reference Transcript Redundancy

Only FSM with CAGE support



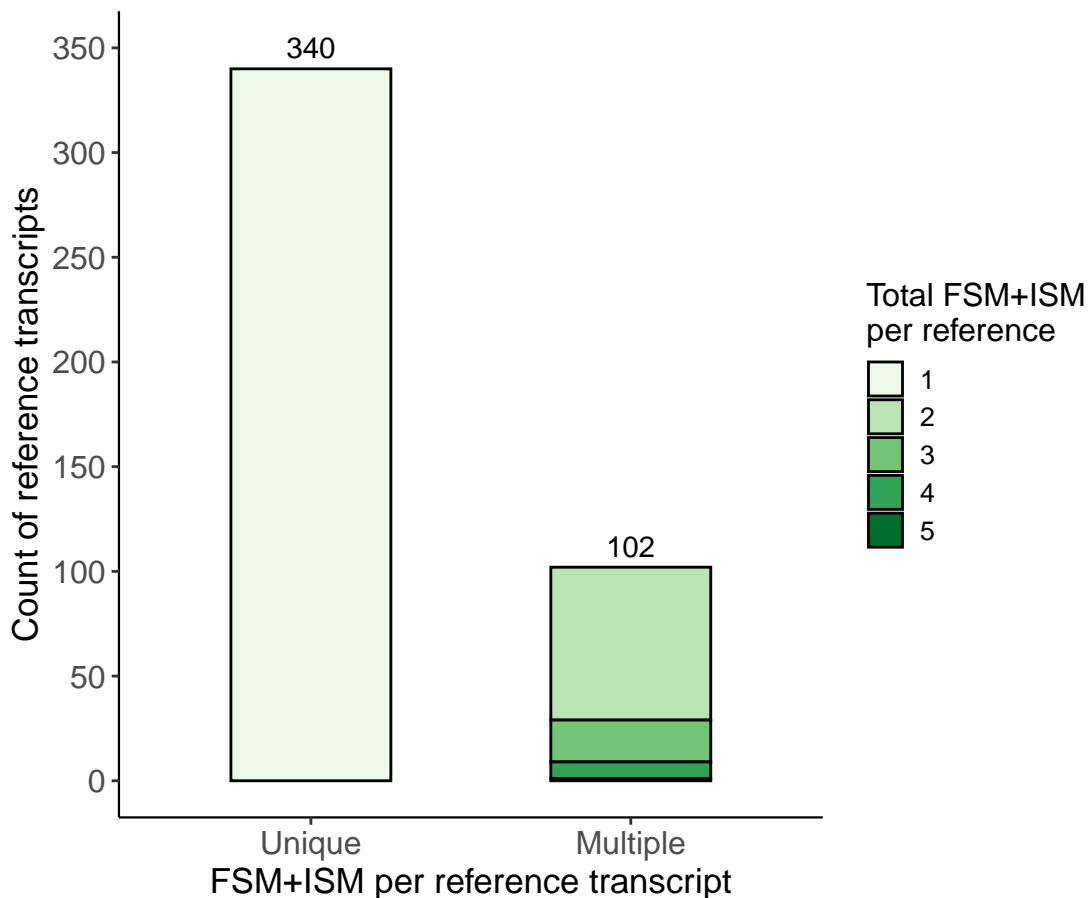
Reference Transcript Redundancy

Only ISM with CAGE support



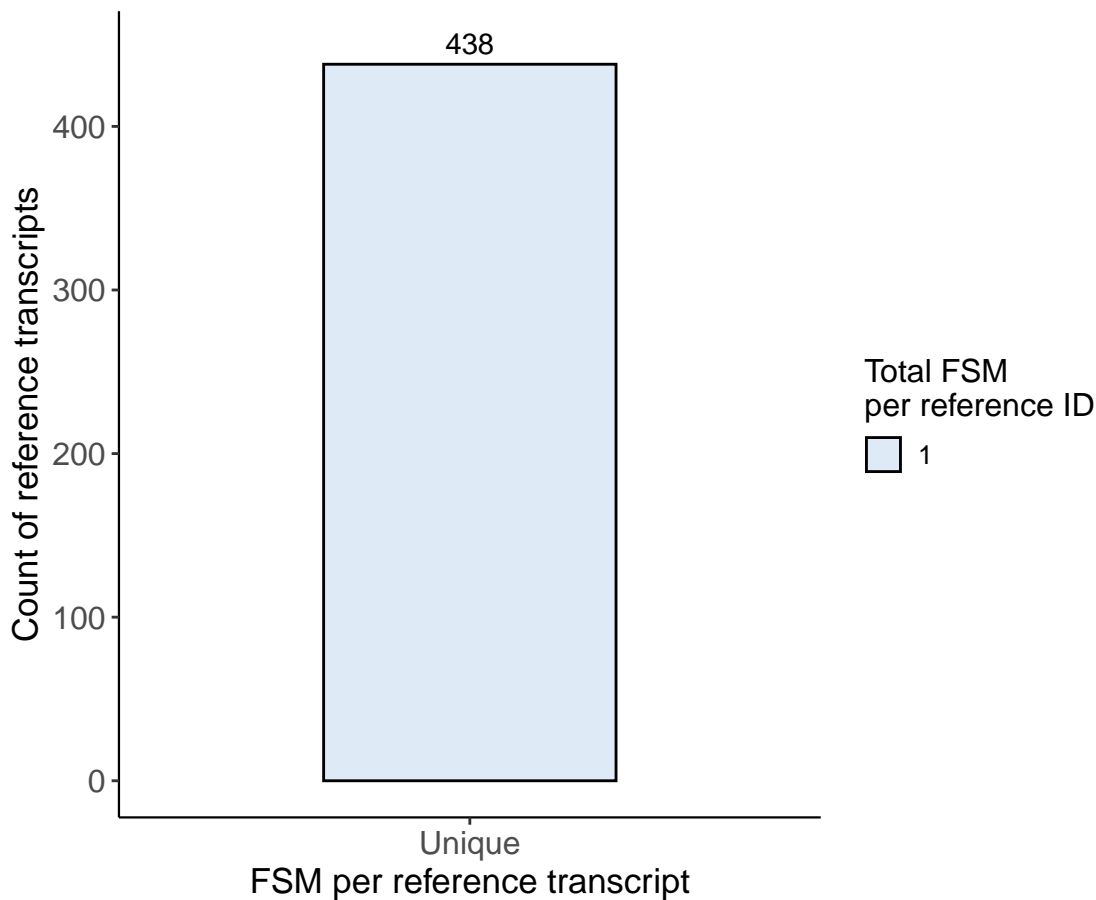
Reference Transcript Redundancy

FSM+ISM with CAGE support



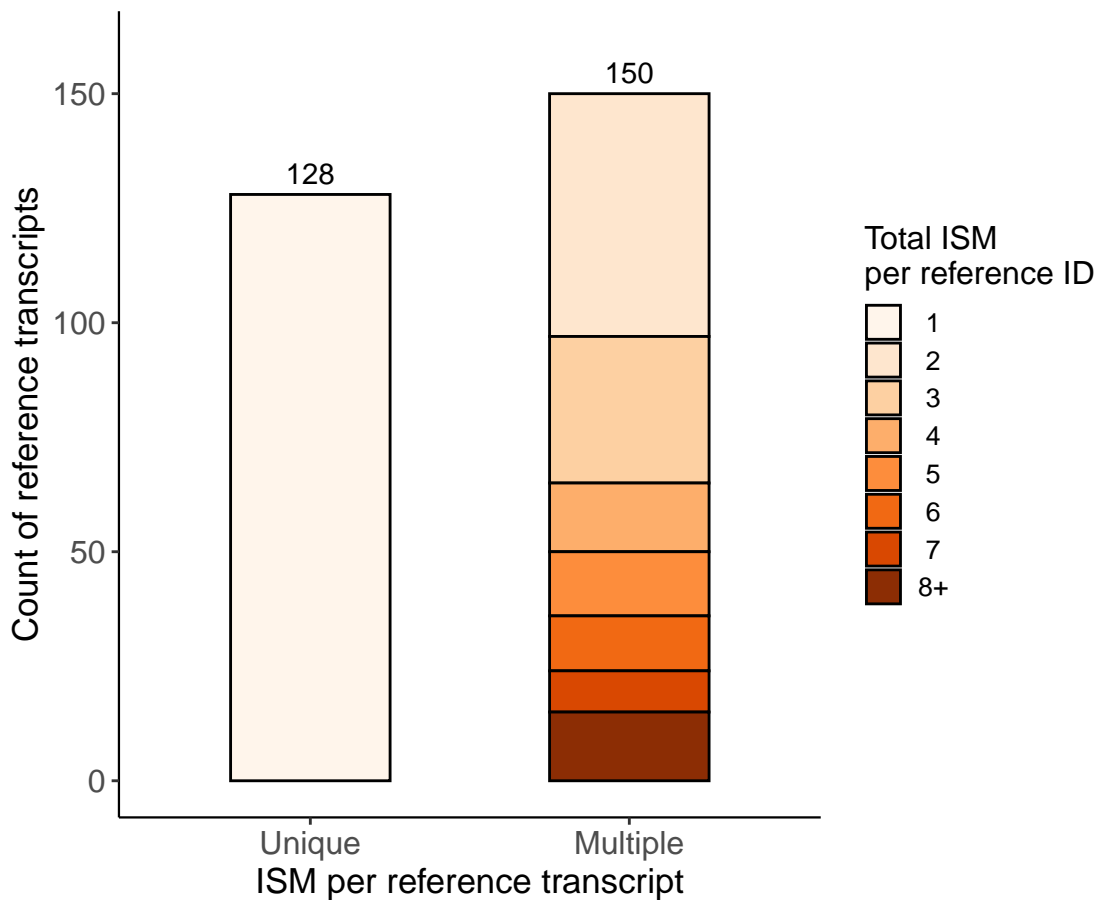
Reference Transcript Redundancy

Only FSM with a polyA motif found



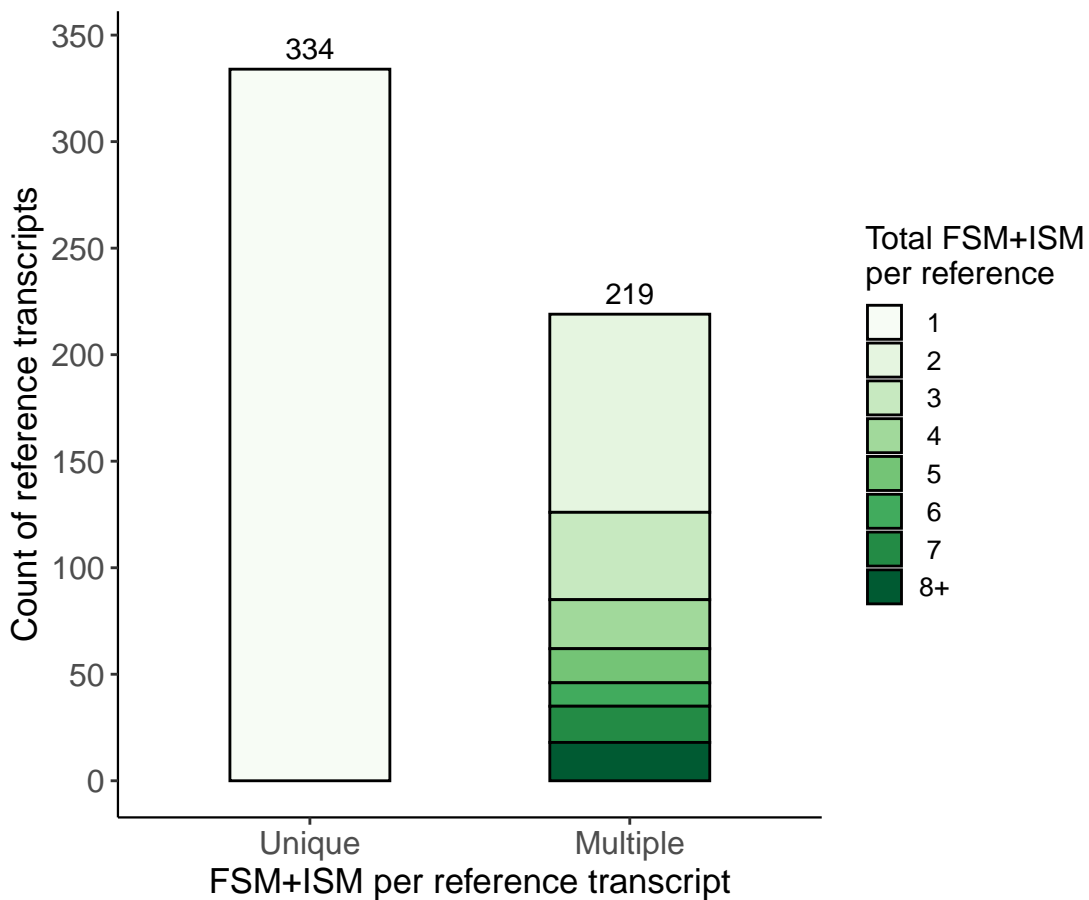
Reference Transcript Redundancy

Only ISM with a polyA motif found



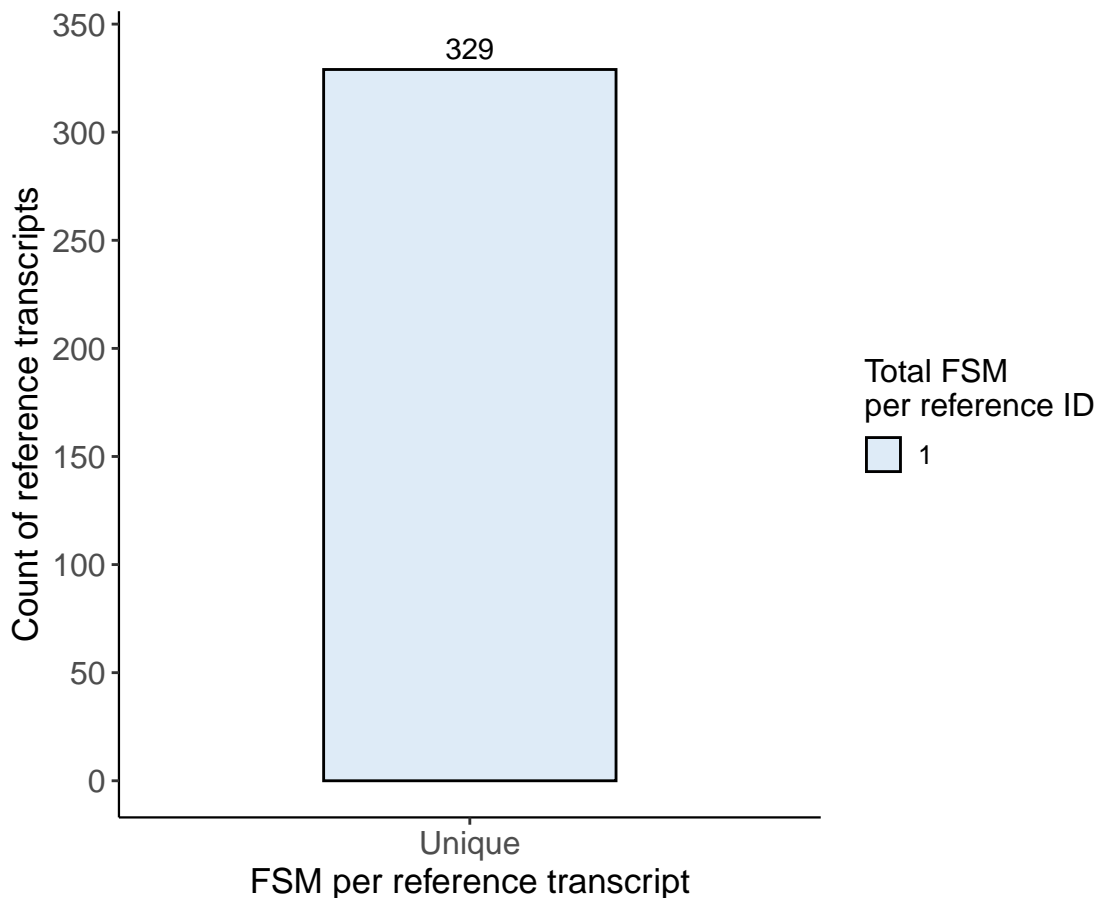
Reference Transcript Redundancy

FSM+ISM with a polyA motif found



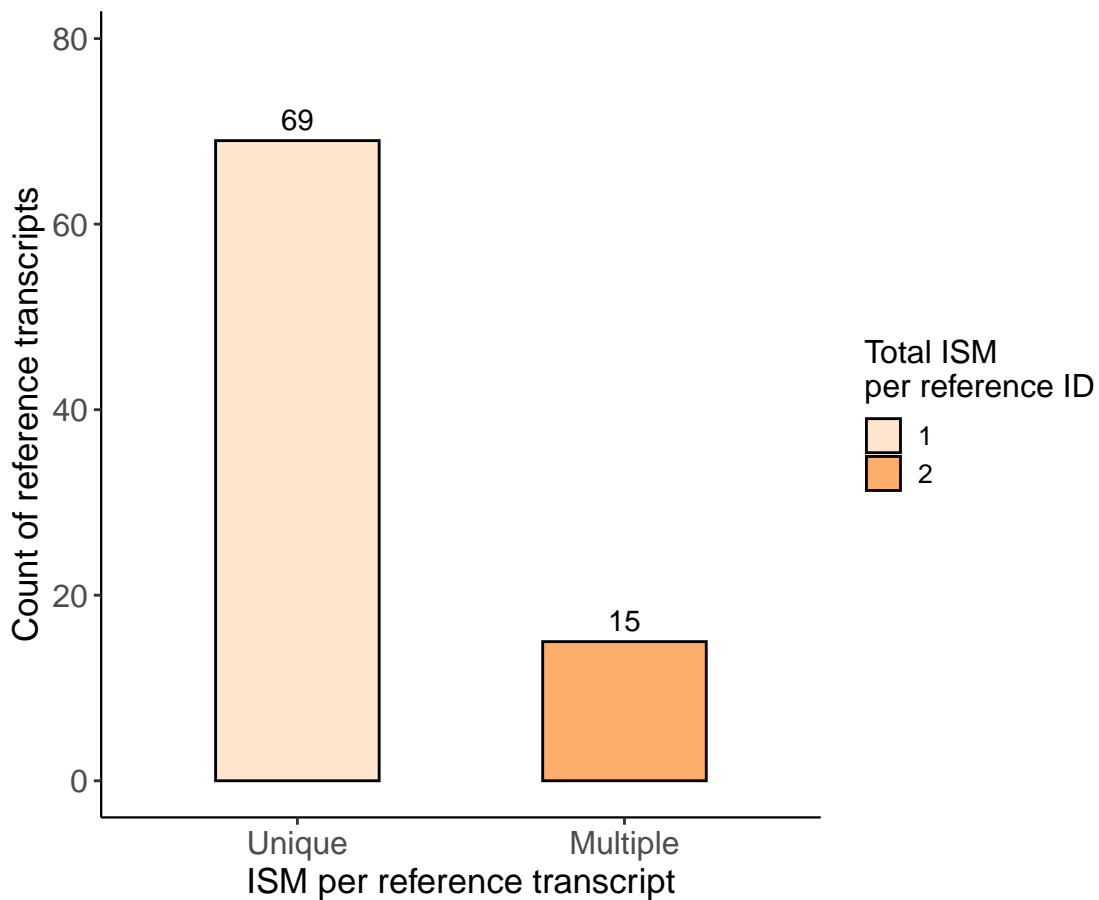
Reference Transcript Redundancy

Only FSM with CAGE support and polyA motif



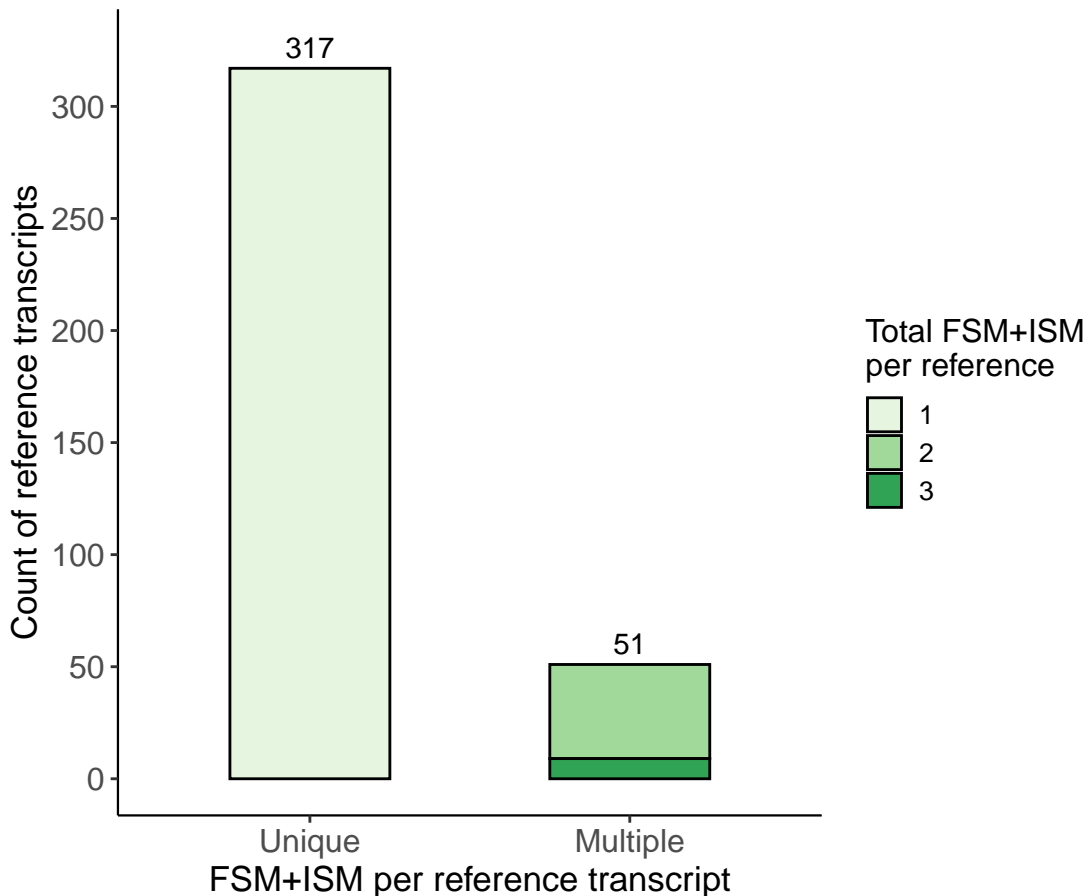
Reference Transcript Redundancy

Only ISM with CAGE support and polyA motif



Reference Transcript Redundancy

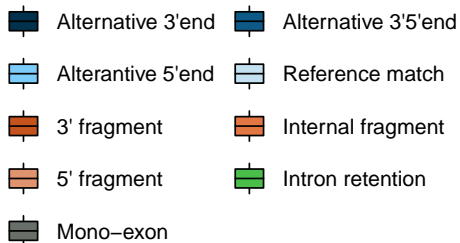
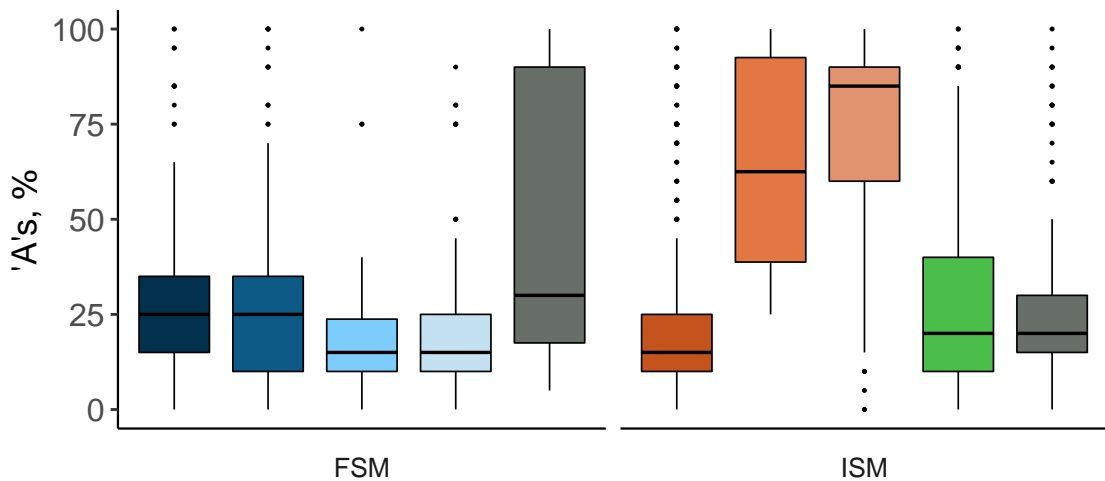
FSM+ISM with CAGE support and polyA motif



Intra-Priming Quality Check

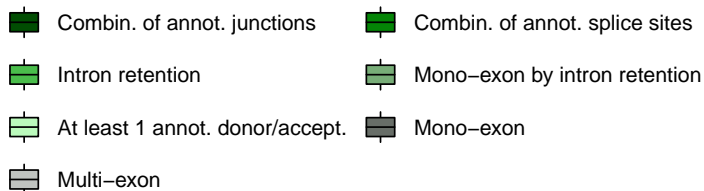
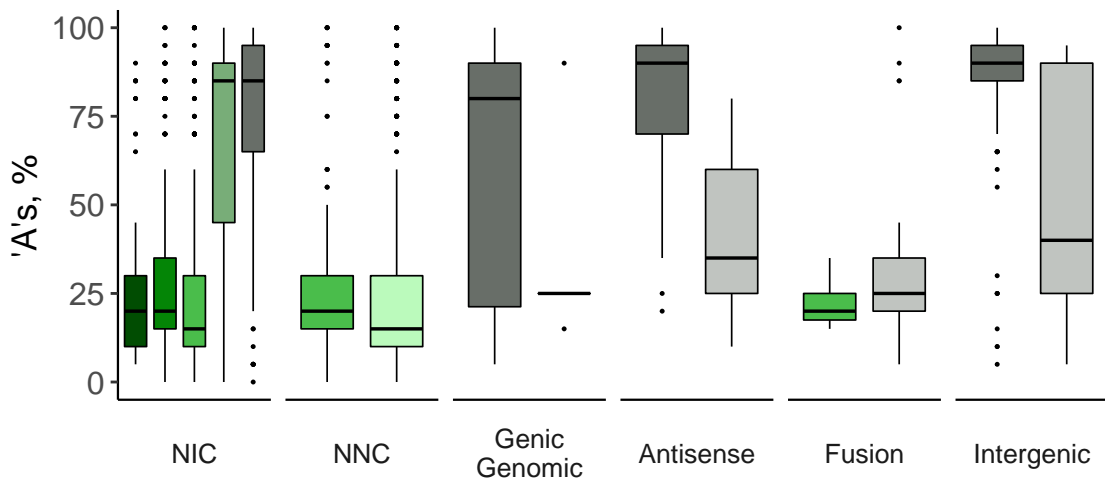
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



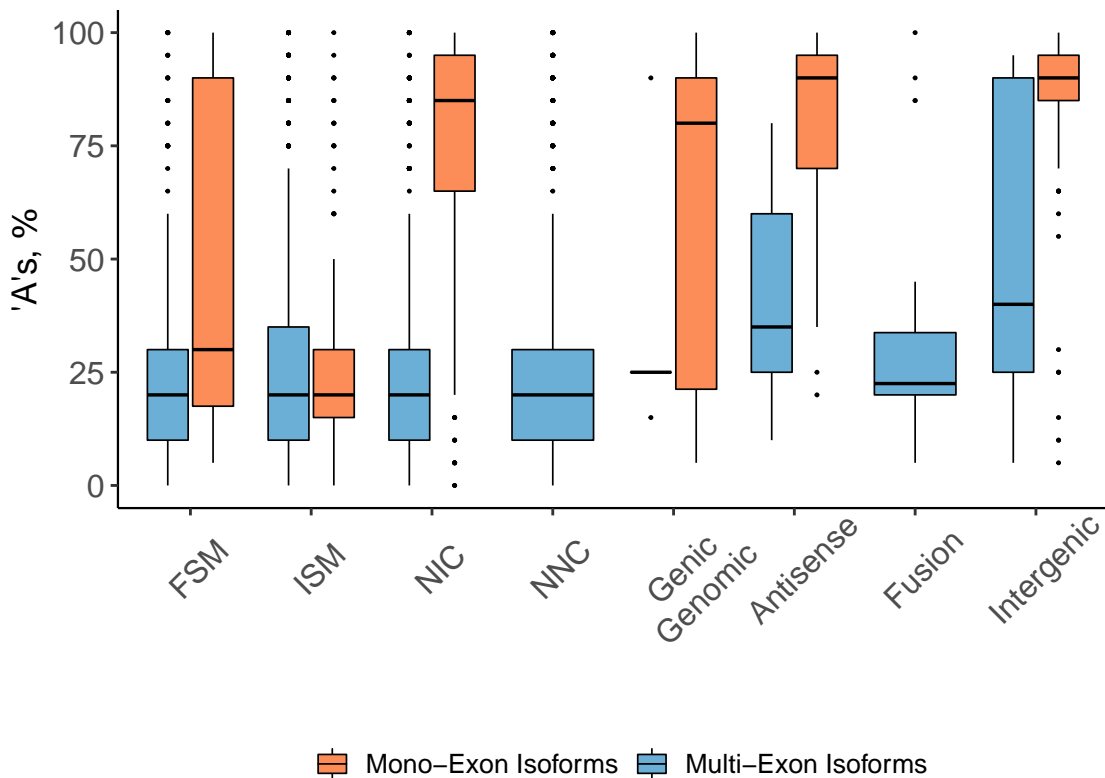
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



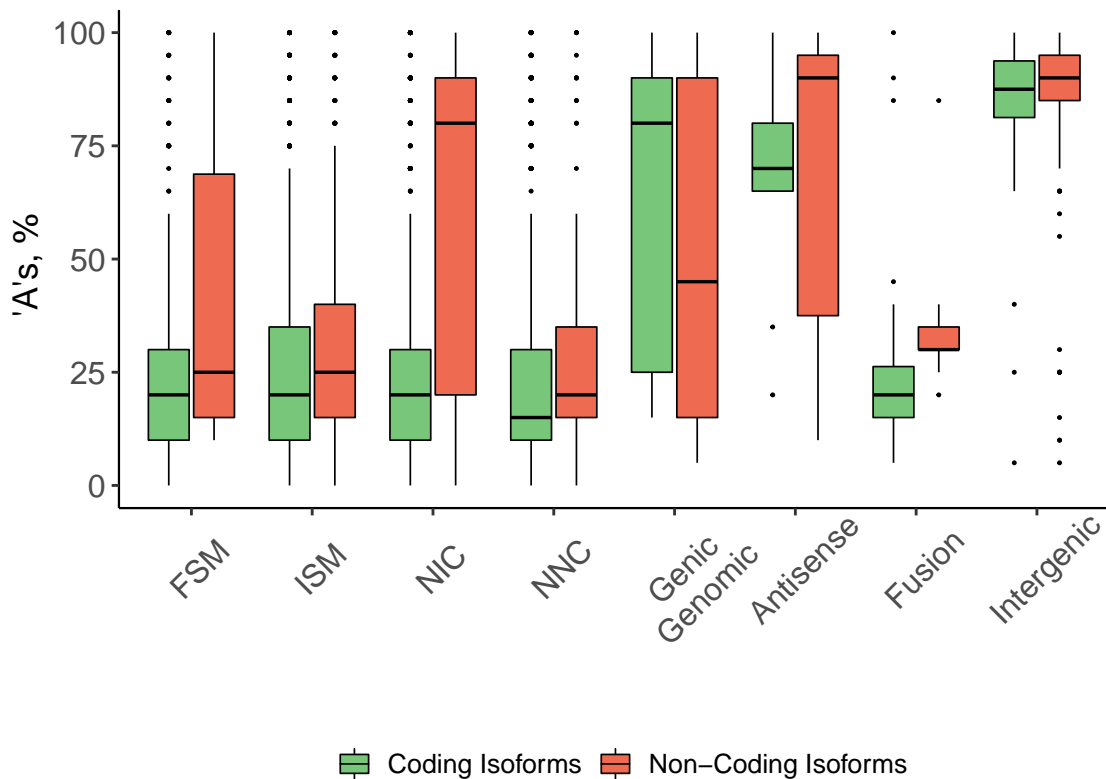
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



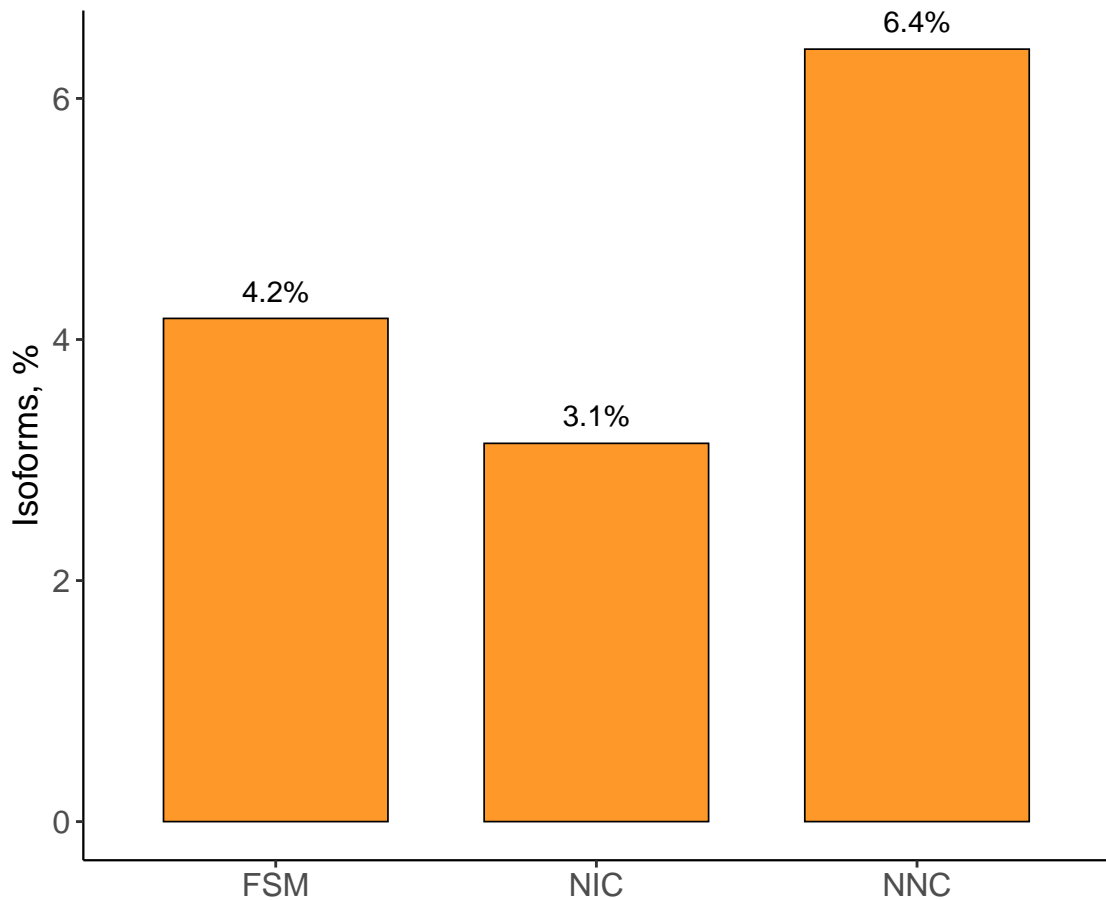
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp

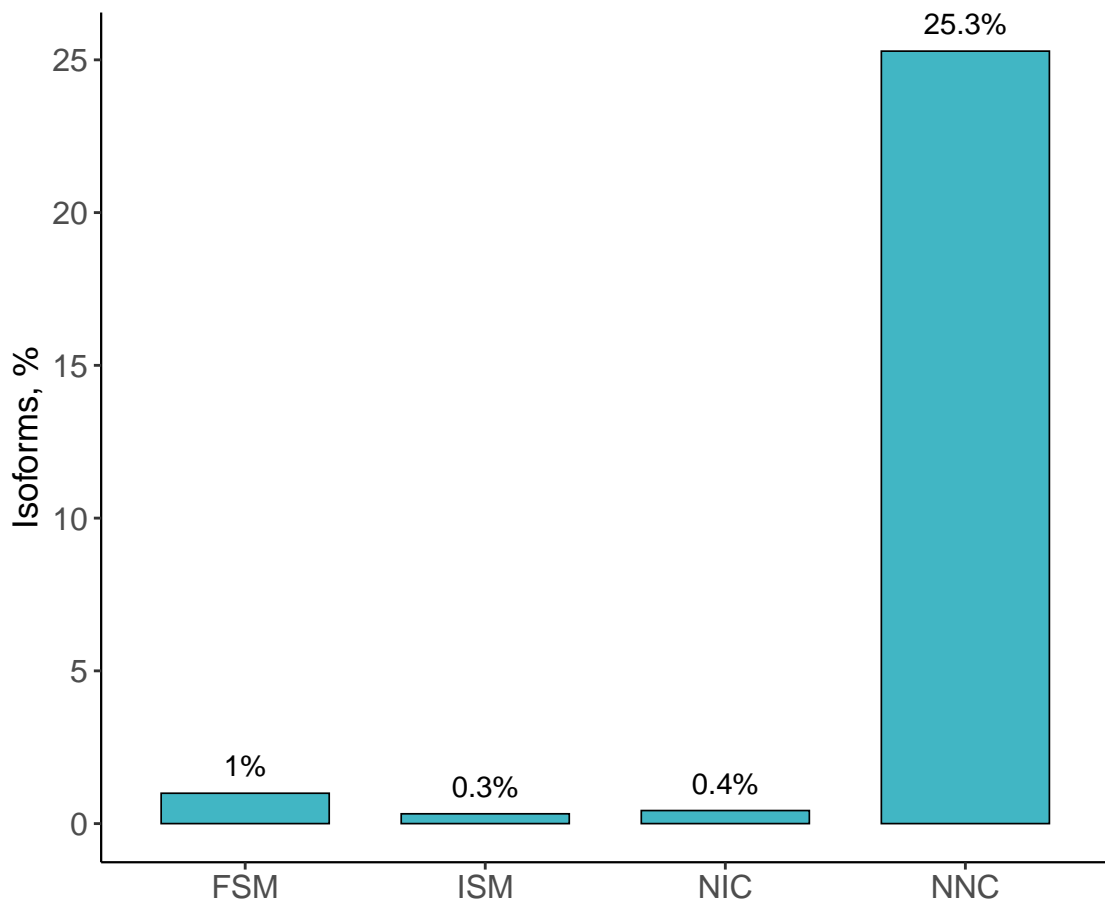


Features of Bad Quality

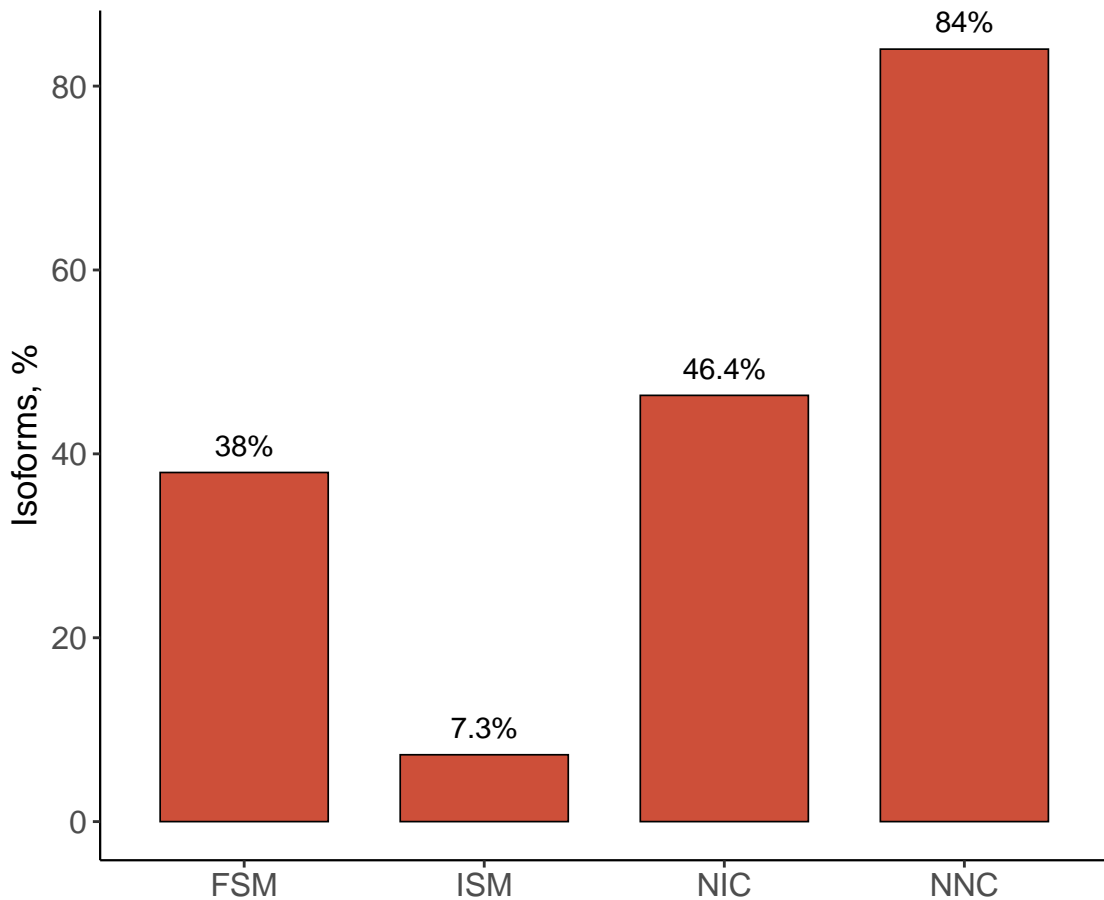
RT-switching



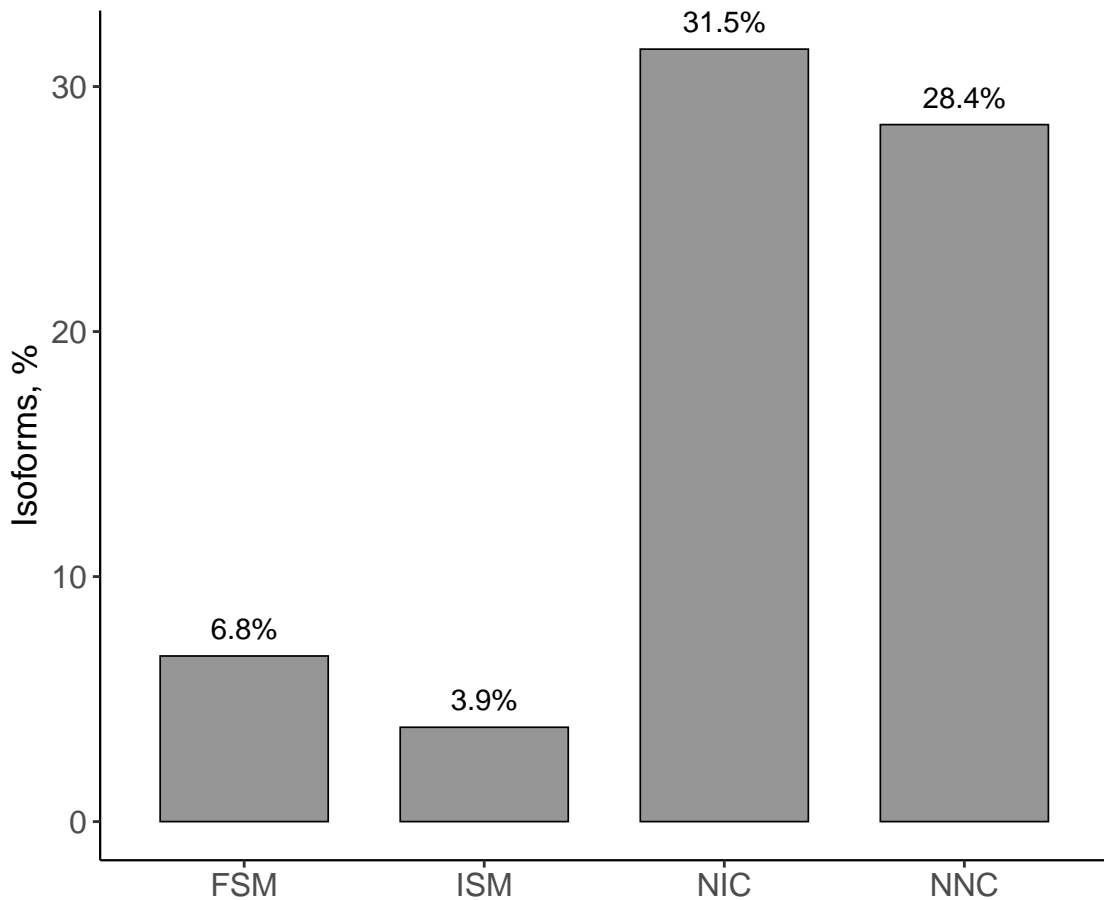
Non-Canonical Junctions



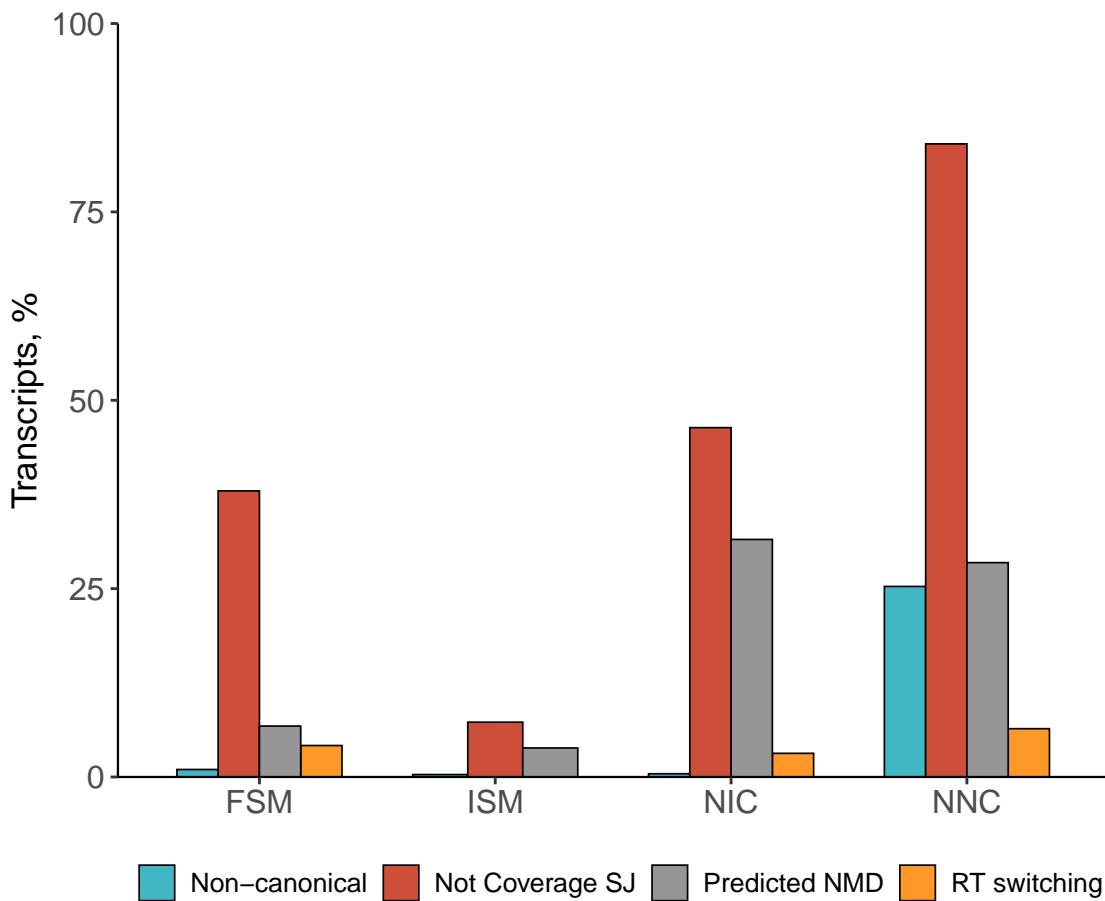
Splice Junctions Without Short Read Coverage



Nonsense-Mediated Decay by Structural Category

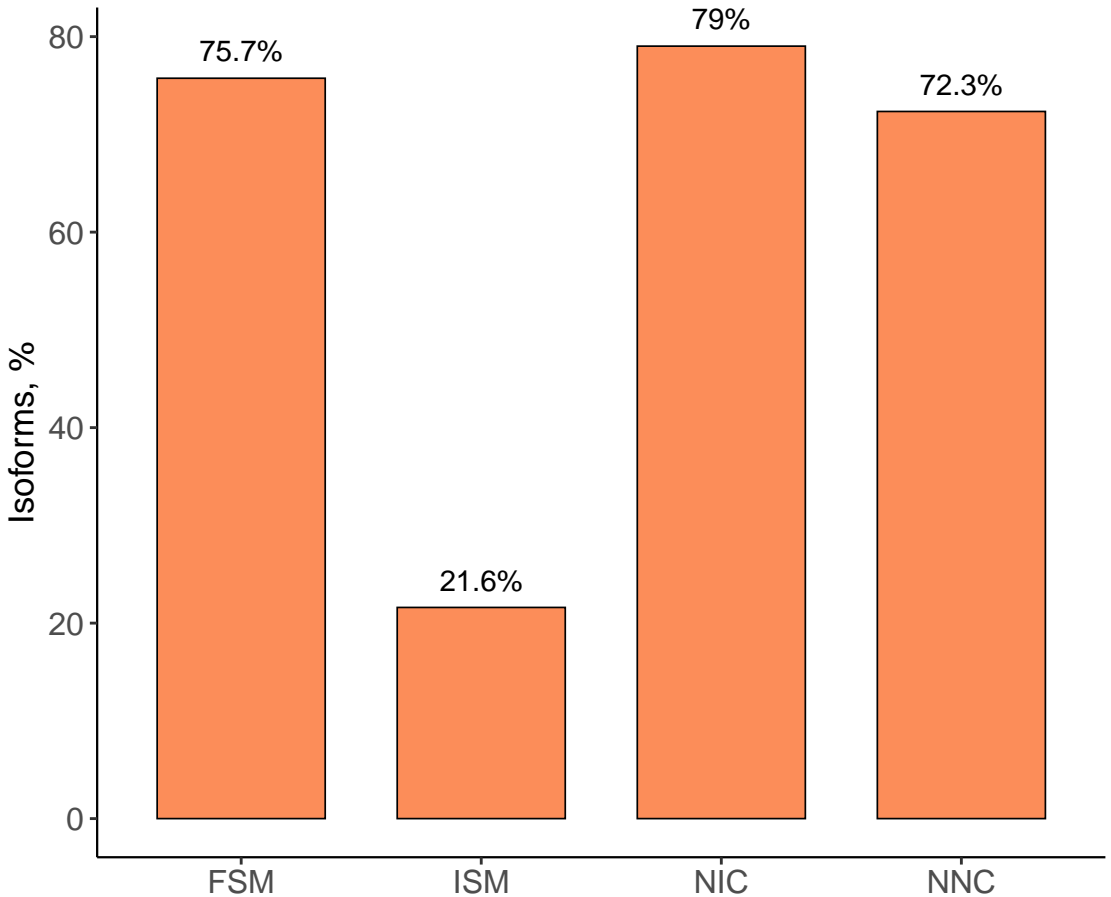


Quality Control Attributes Across Structural Categories

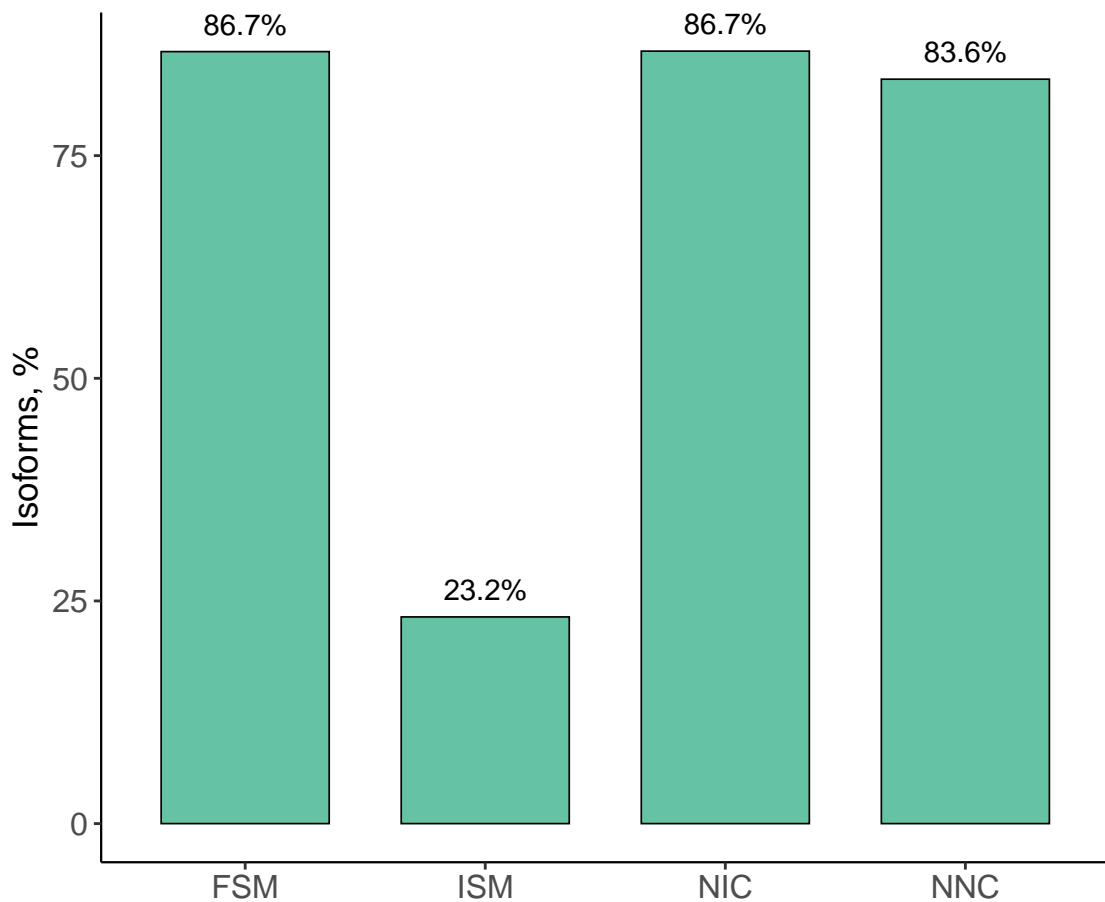


Features of Good Quality

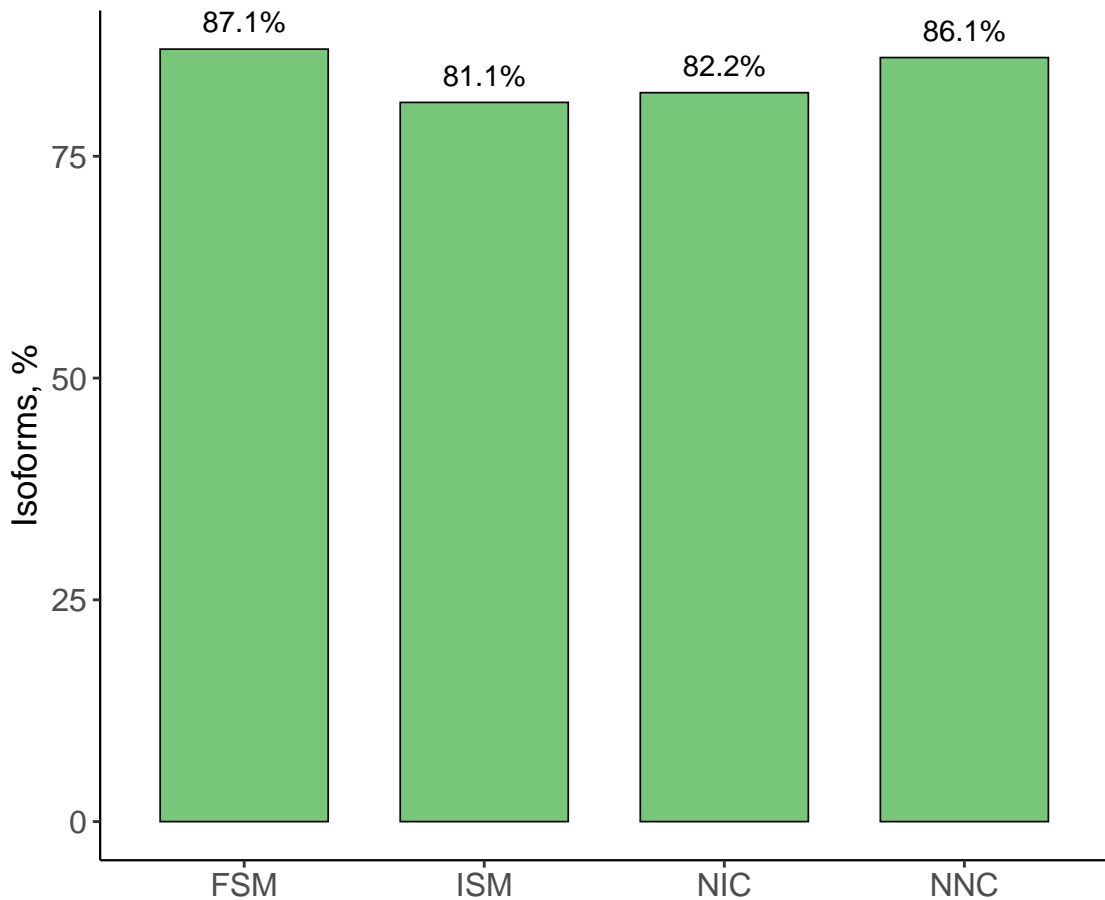
CAGE Support



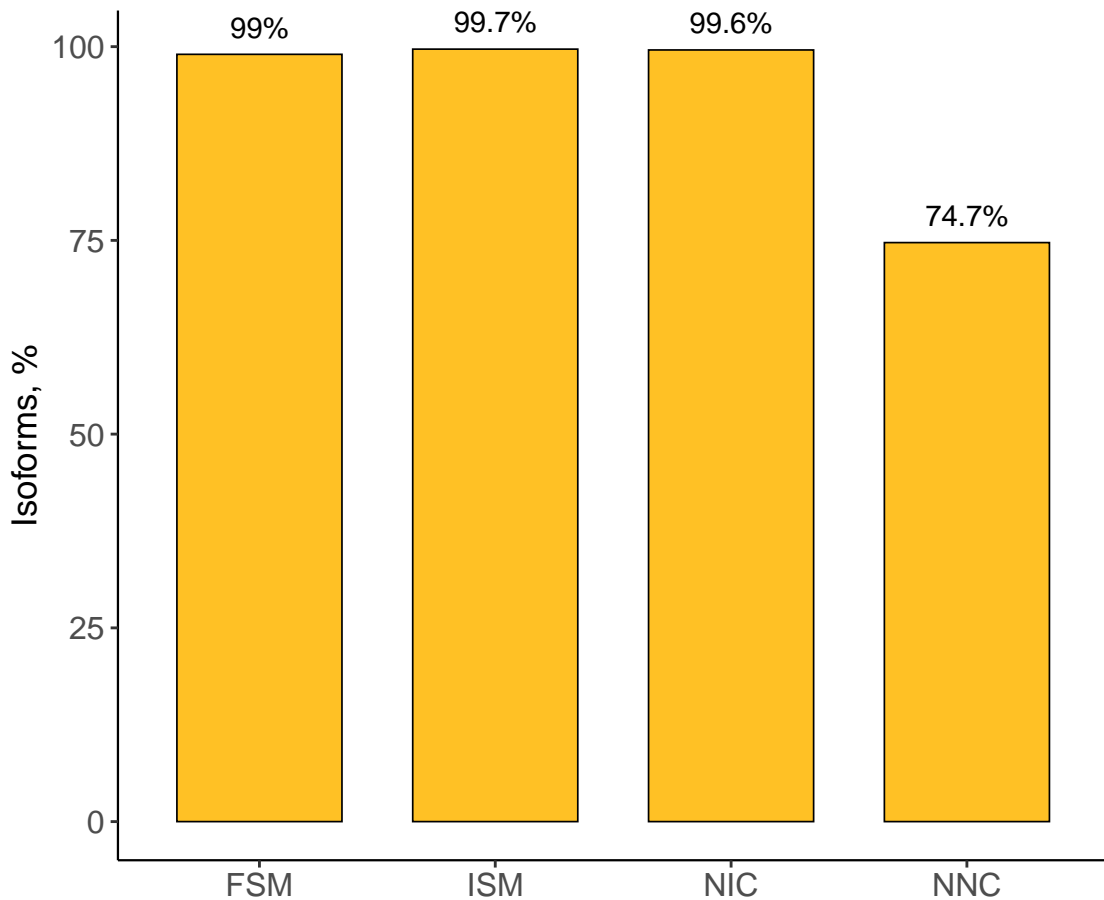
Annotation Support



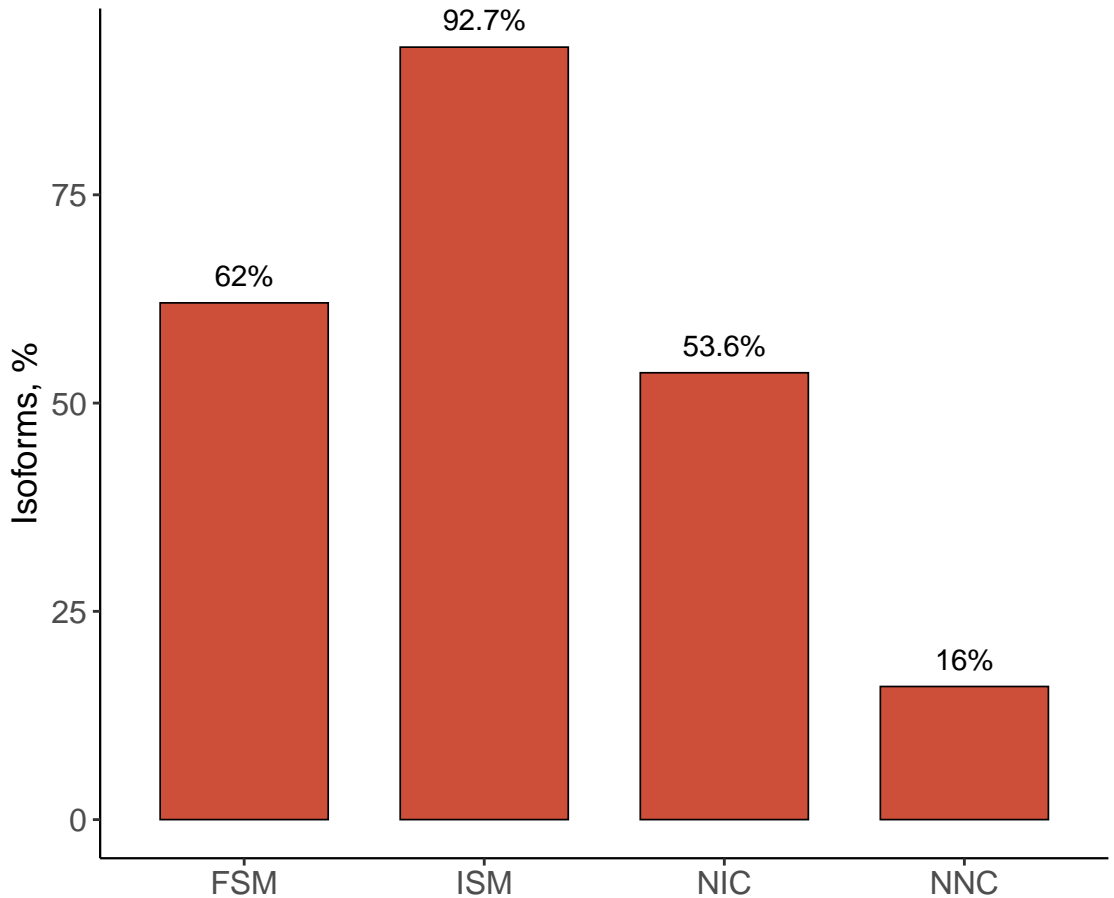
PolyA Support



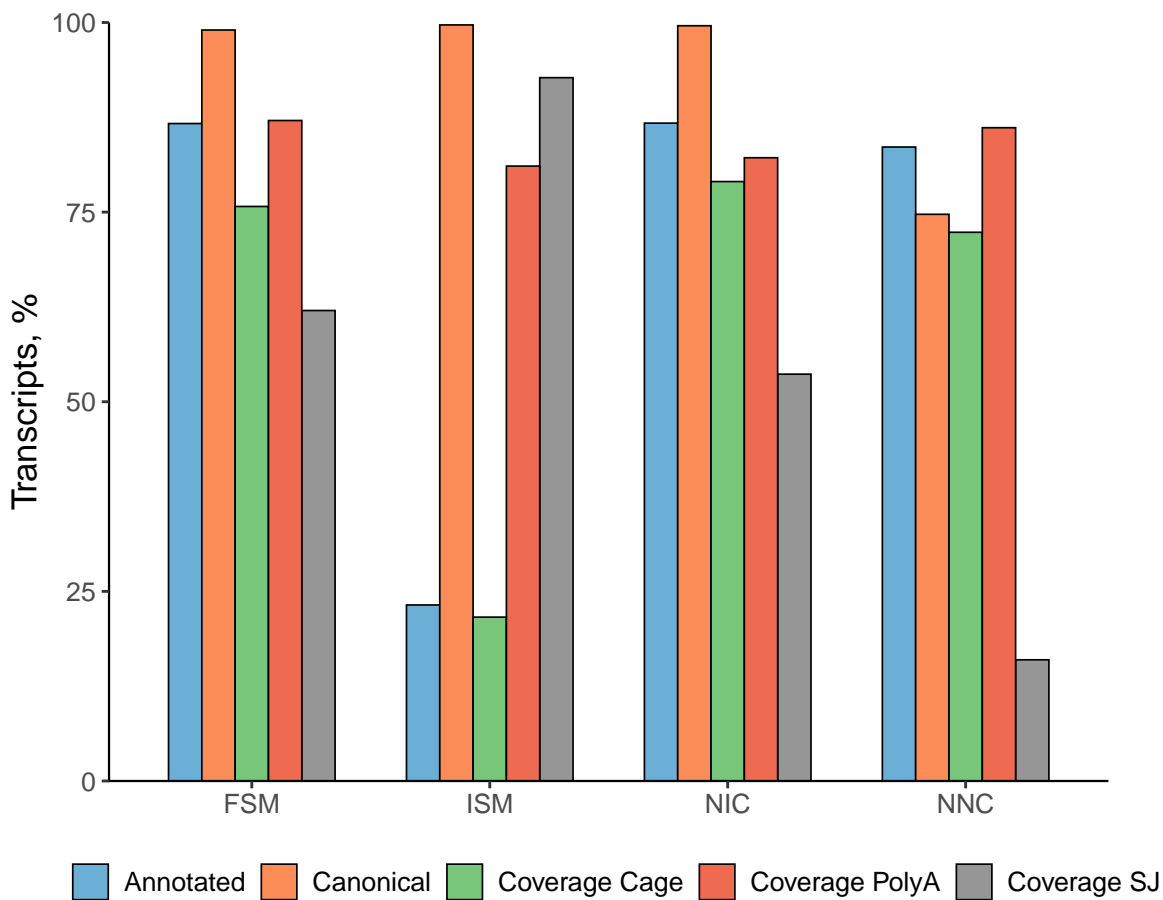
All Canonical Junctions



Splice Junctions With Short Read Coverage



Good Quality Control Attributes Across Structural Categories



TSS Ratio FSM Reference Match vs ISM

