

SQANTI3 report

Unique Genes: 50702
Unique Isoforms: 149434

Transcript Classification

Category	Isoforms, count
FSM	41311
ISM	10079
NIC	30369
NNC	29119
Genic Genomic	5913
Antisense	9243
Fusion	891
Intergenic	21252
Genic Intron	1257

Gene Classification

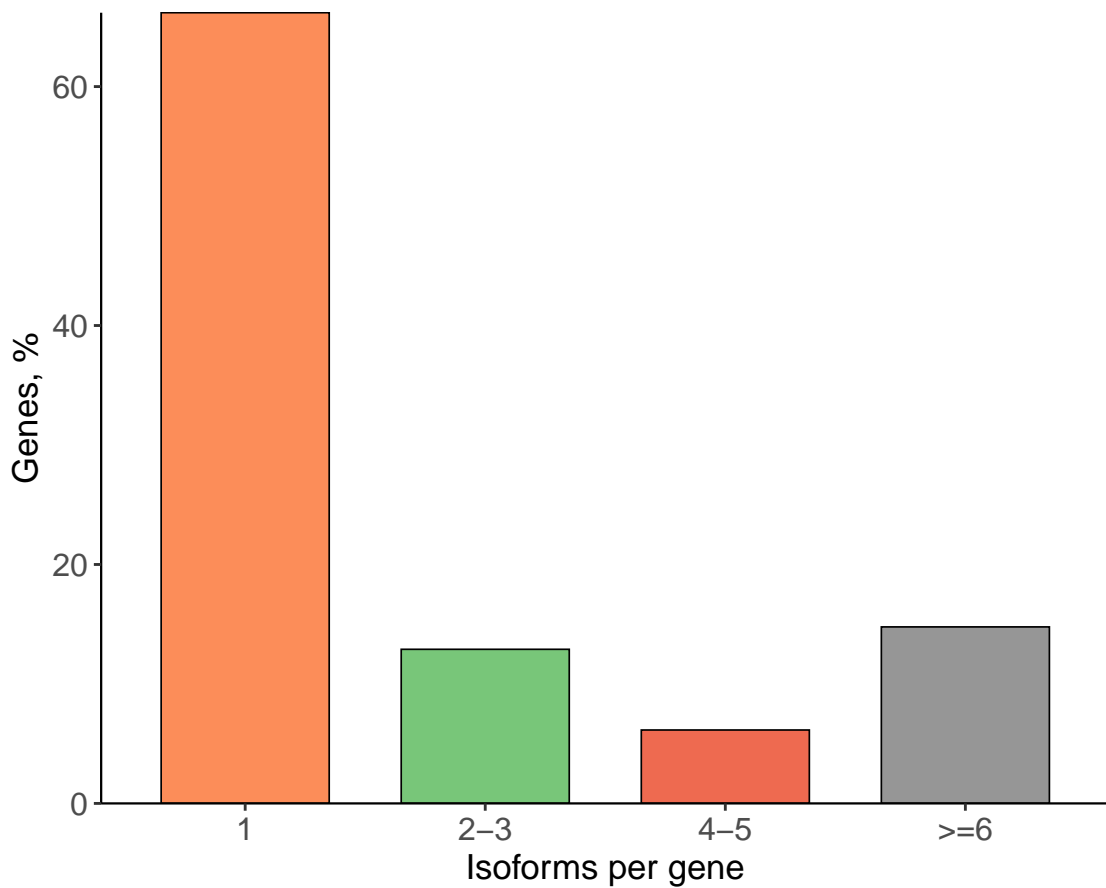
Category	Genes, count
Annotated Genes	24022
Novel Genes	26680

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	157767	73.20
Known Non-canonical	329	0.15
Novel canonical	46417	21.54
Novel Non-canonical	11022	5.11

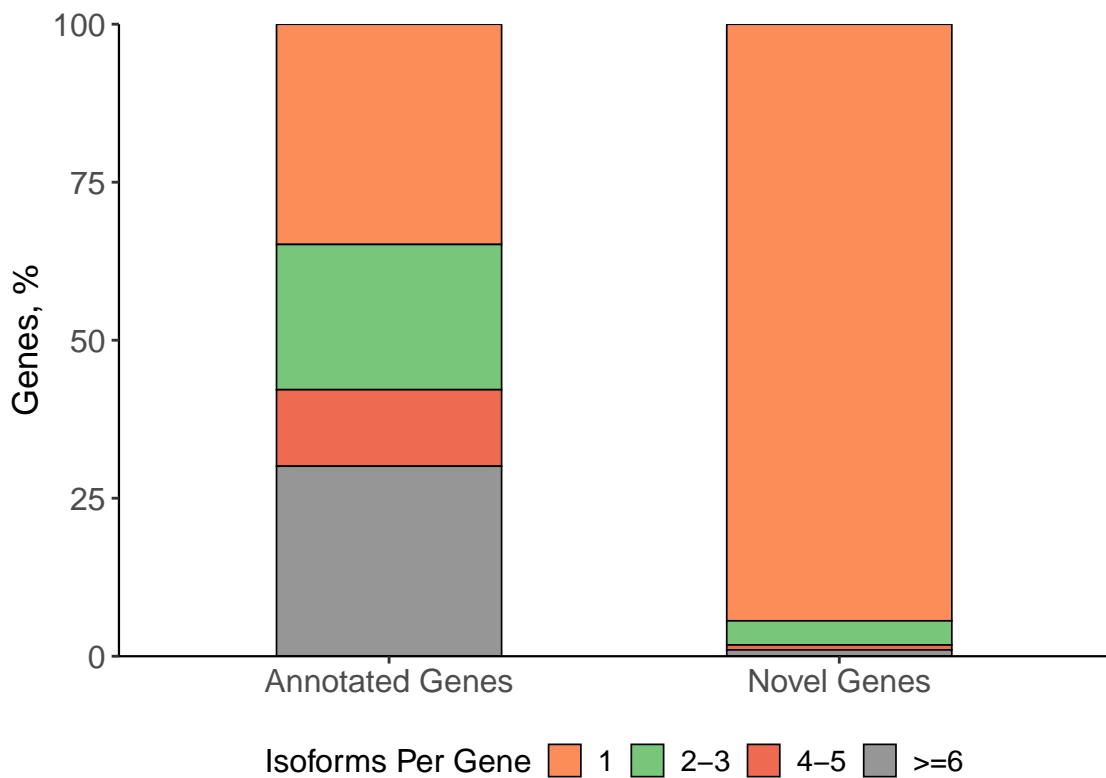
Gene Characterization

Number of Isoforms per Gene

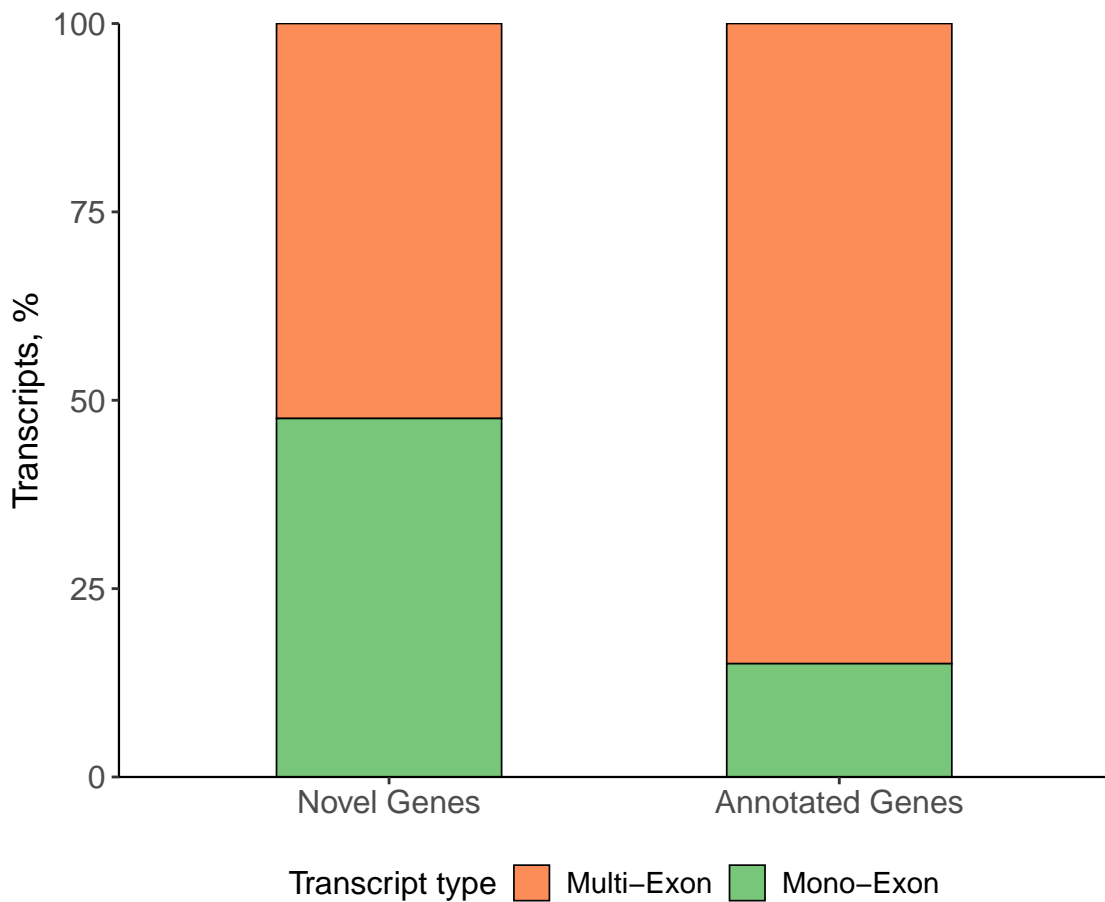


Number of Isoforms per Gene

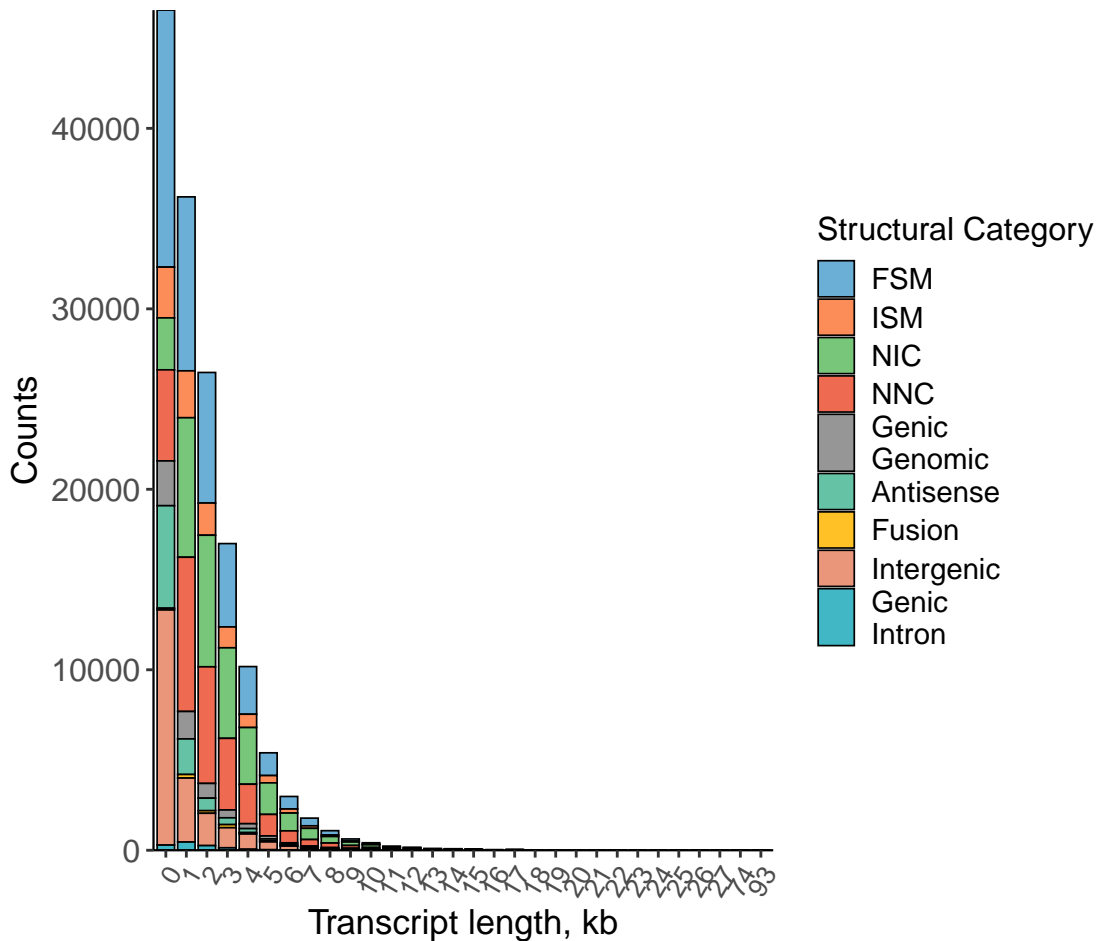
Known vs Novel Genes



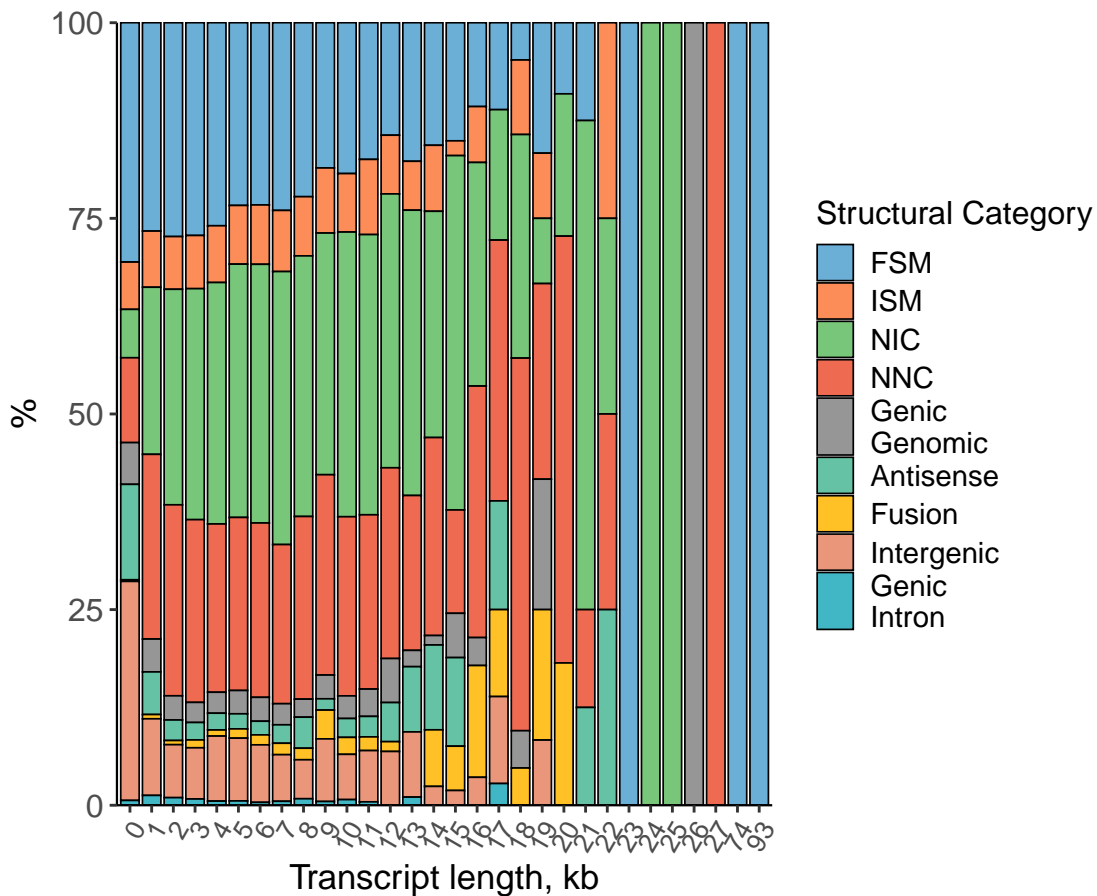
Distribution of Mono- vs Multi-Exon Transcripts



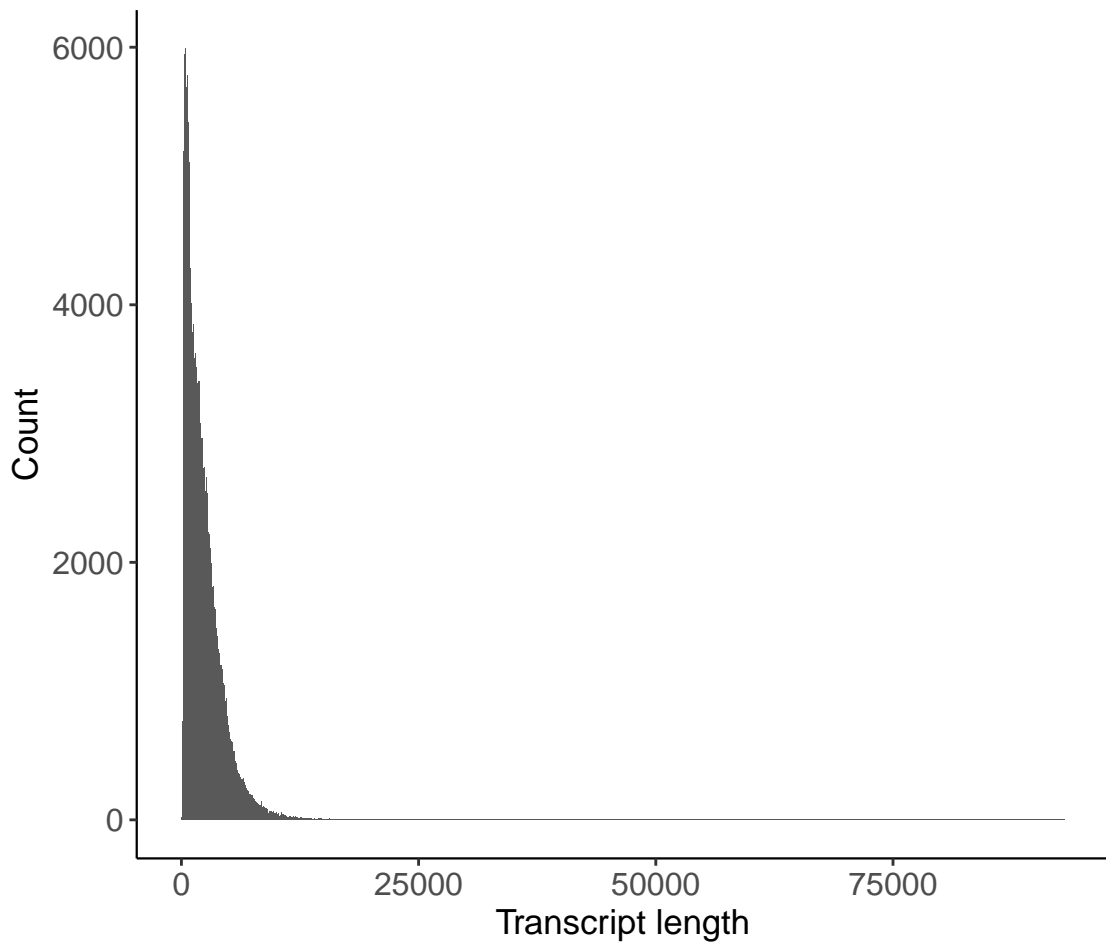
Structural Categories by Transcript Length



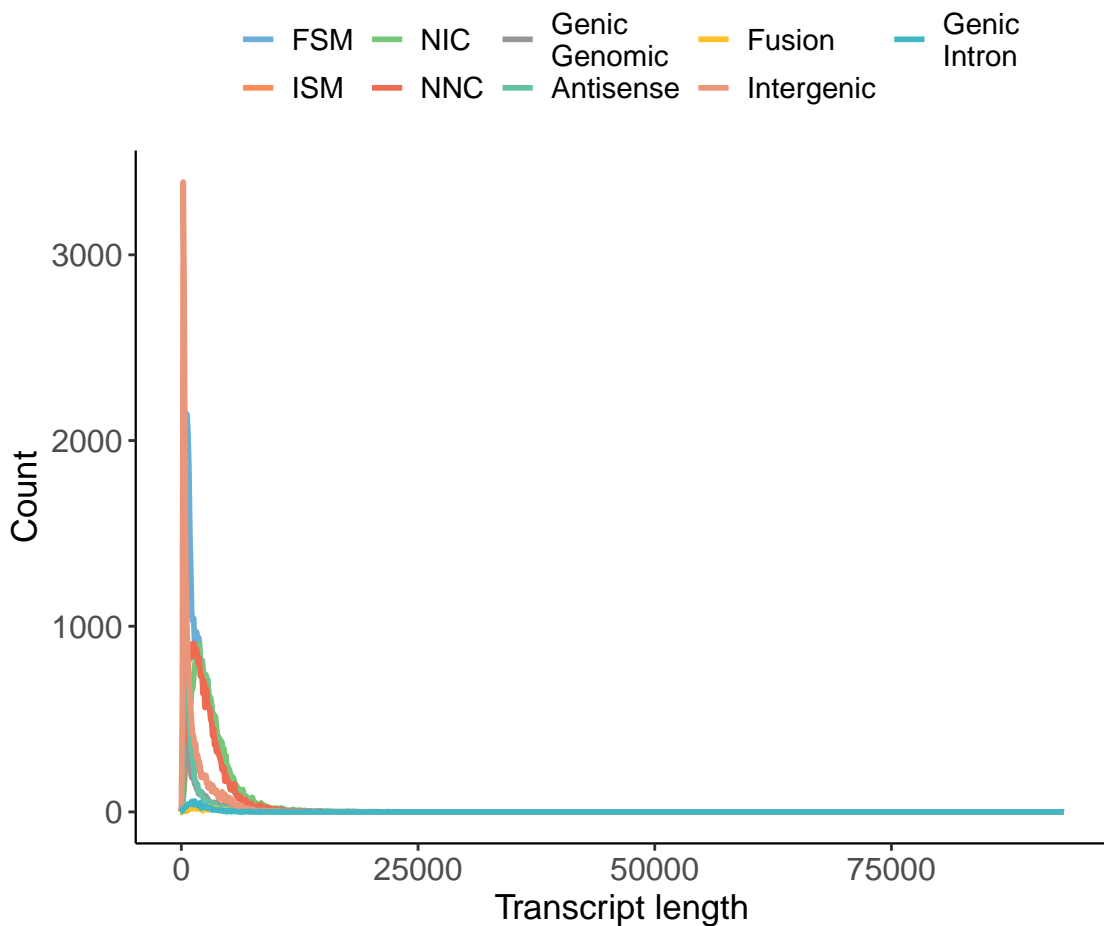
Structural Categories by Transcript Length



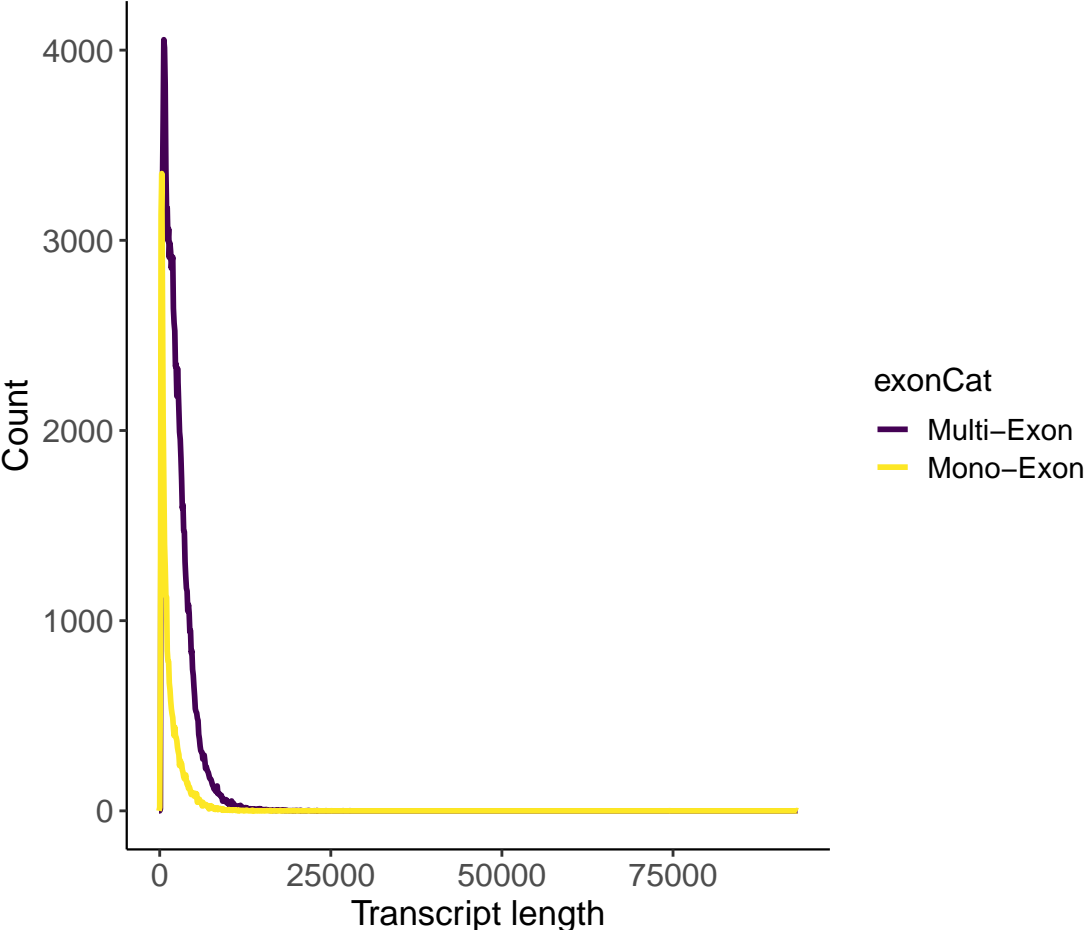
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

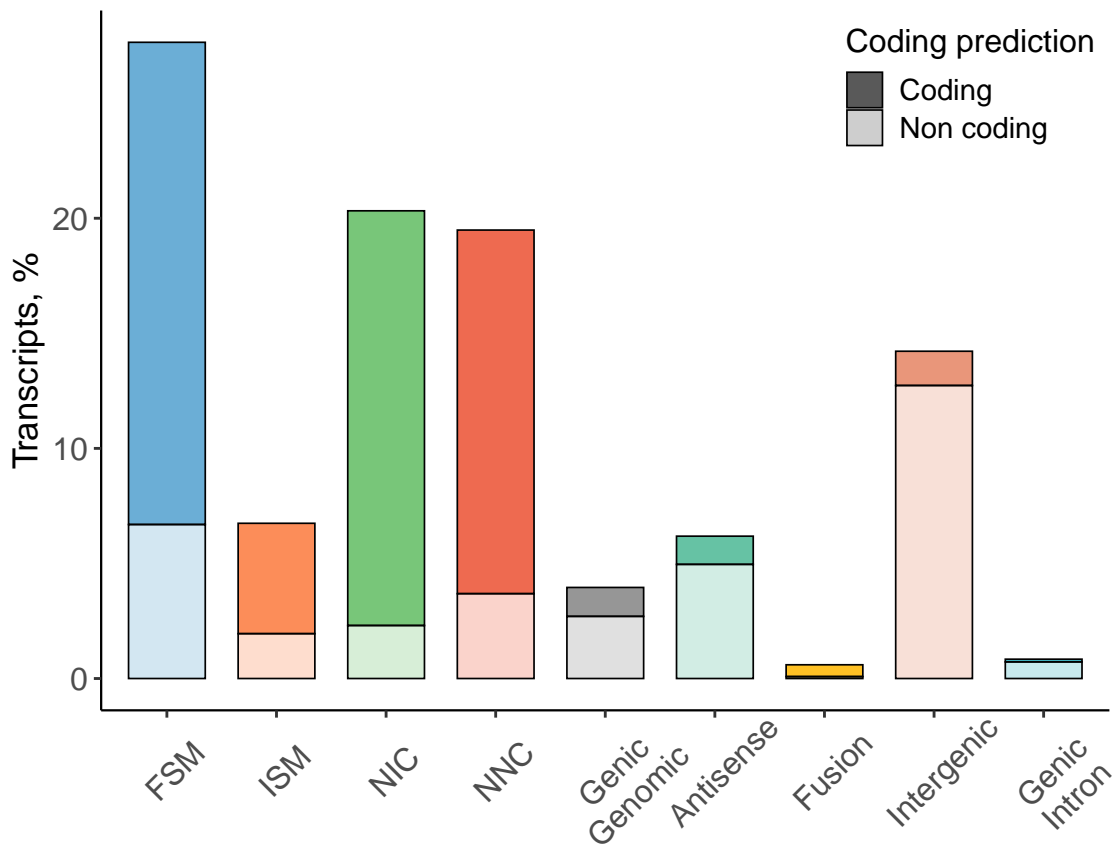


Mono- vs Multi- Exon Transcript Lengths Distribution

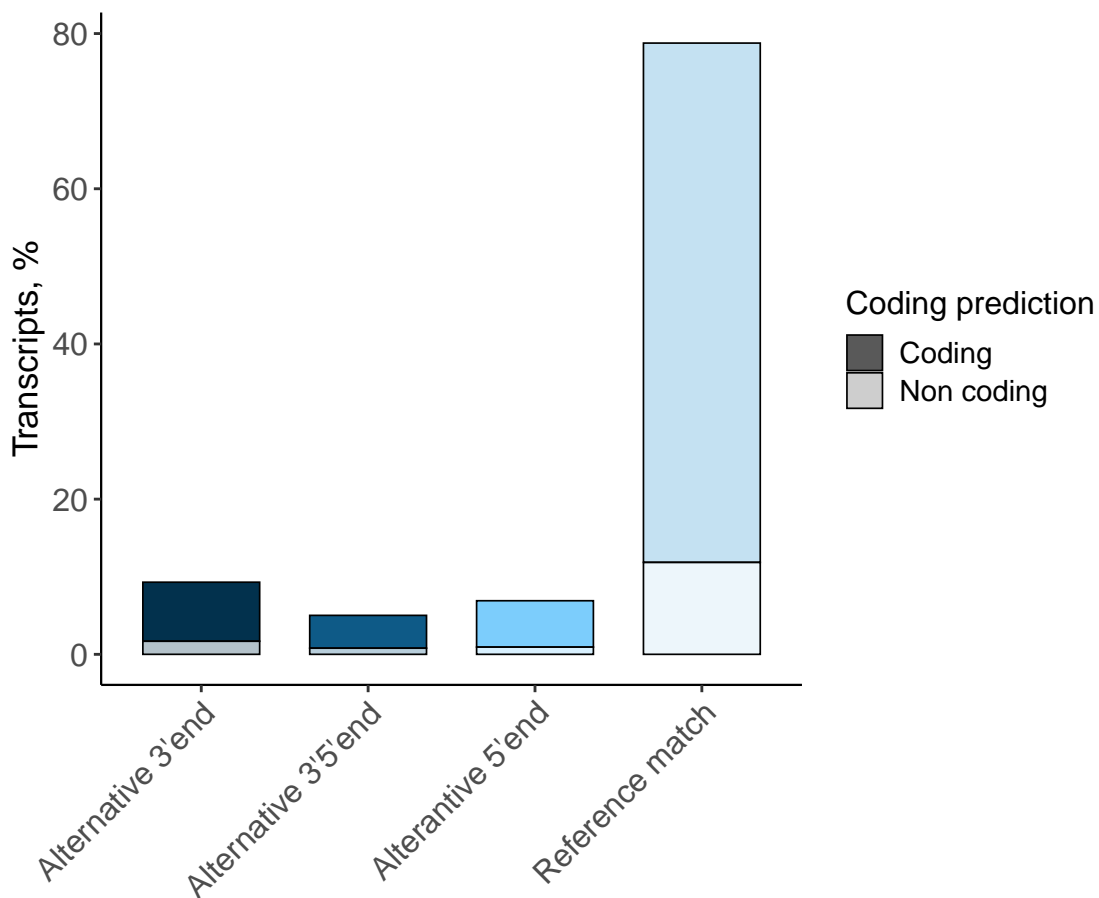


Structural Isoform Characterization

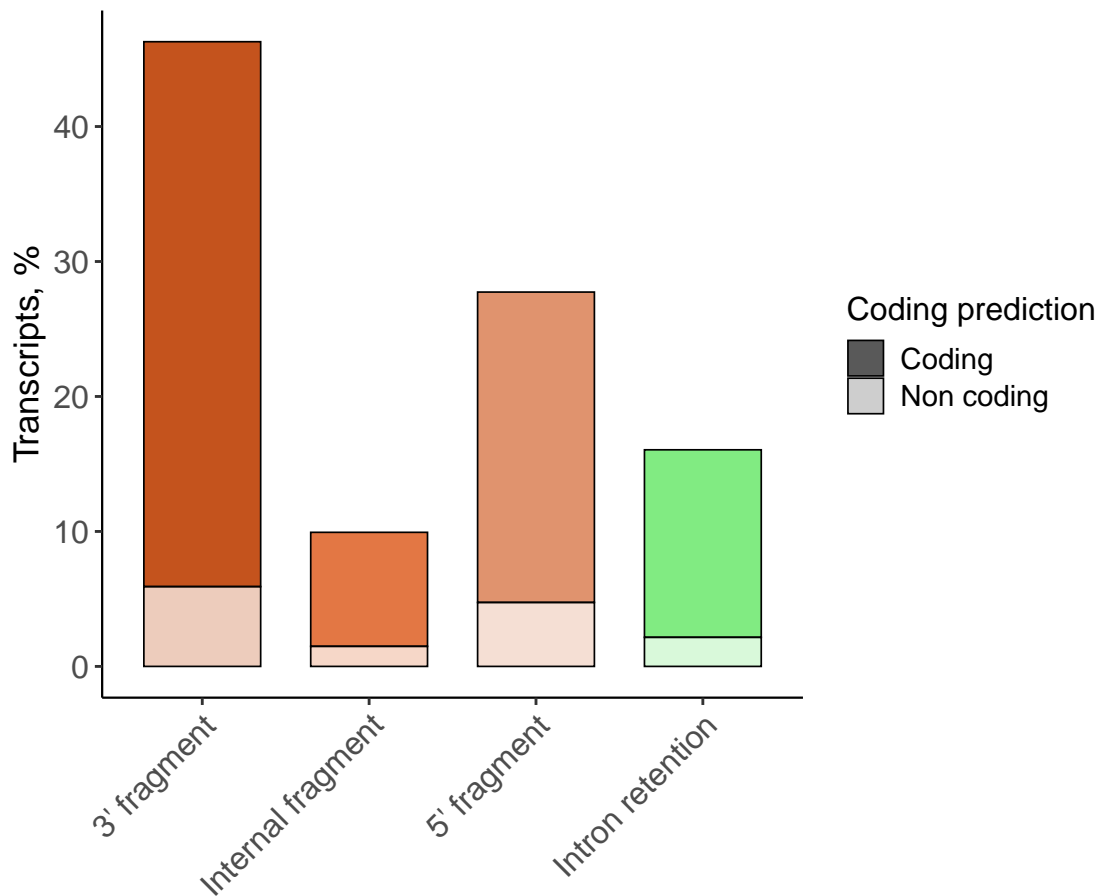
Isoform Distribution Across Structural Categories



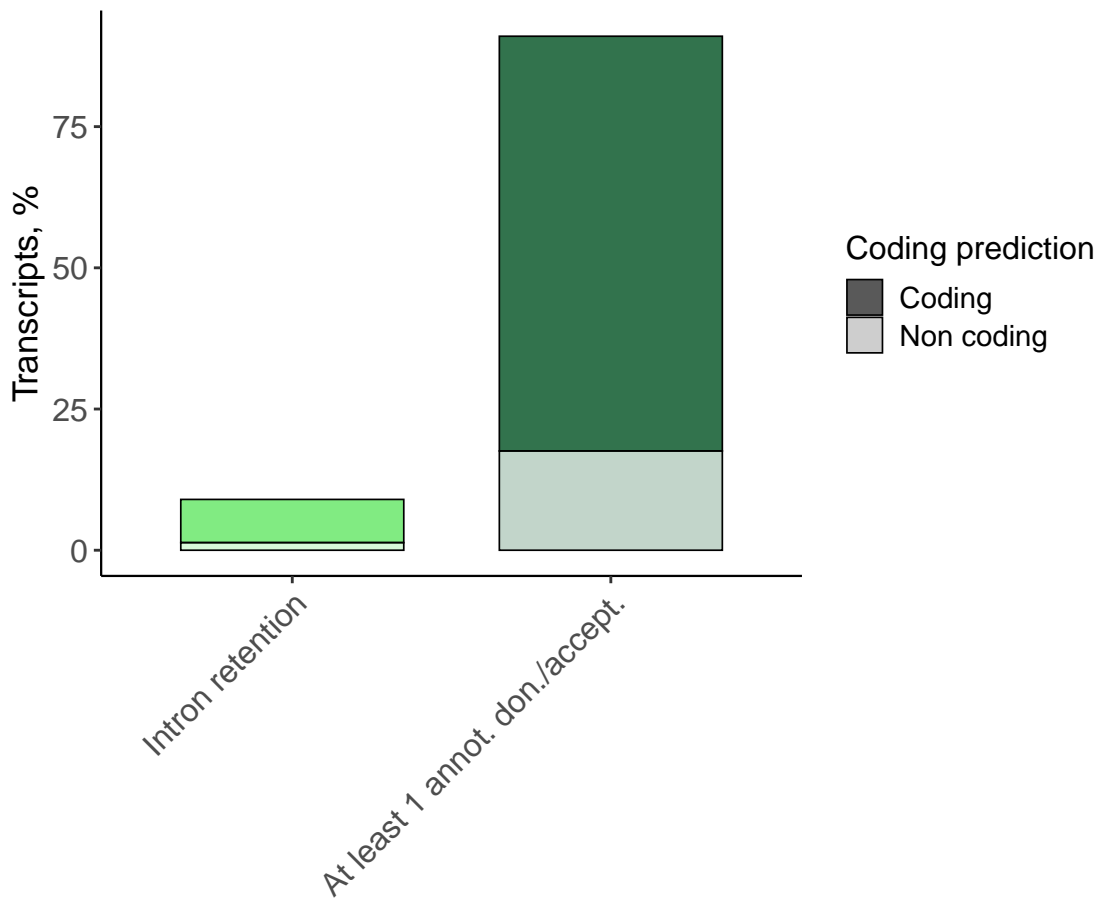
Isoform Distribution Across FSM



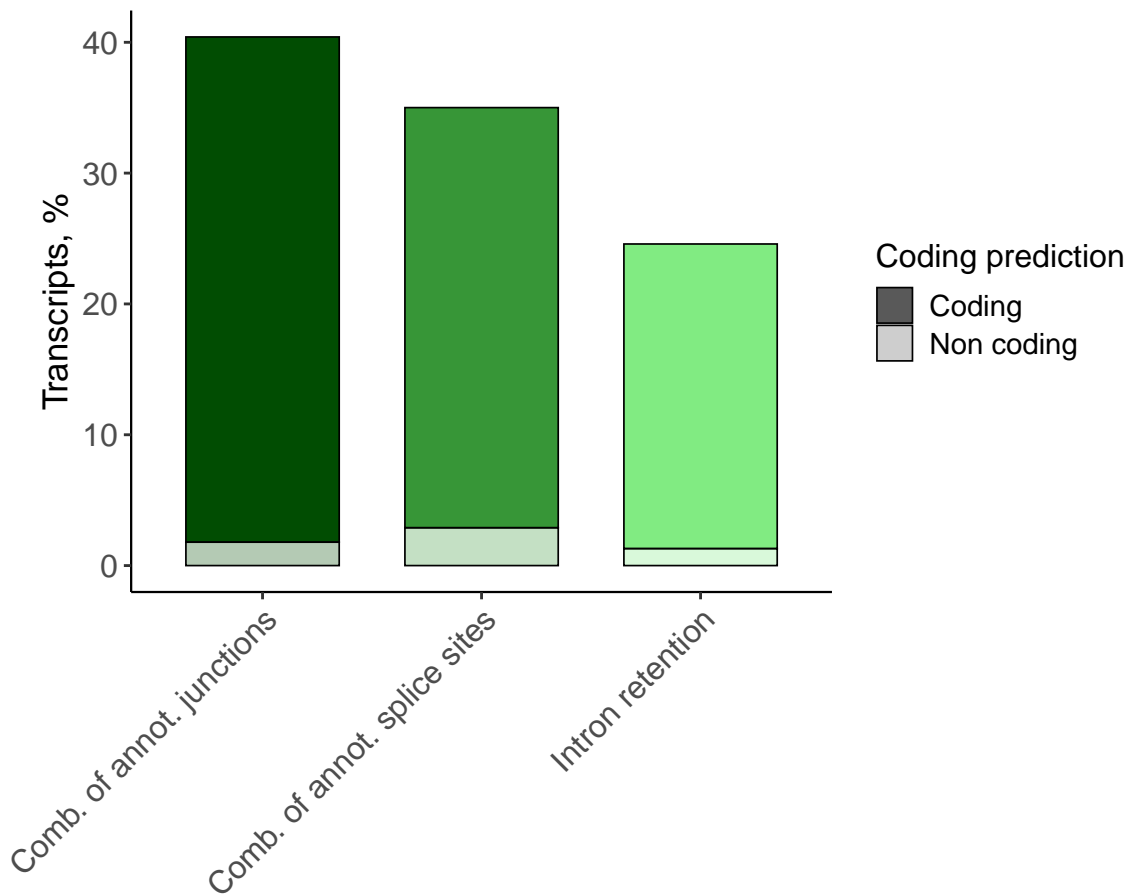
Isoform Distribution Across ISM



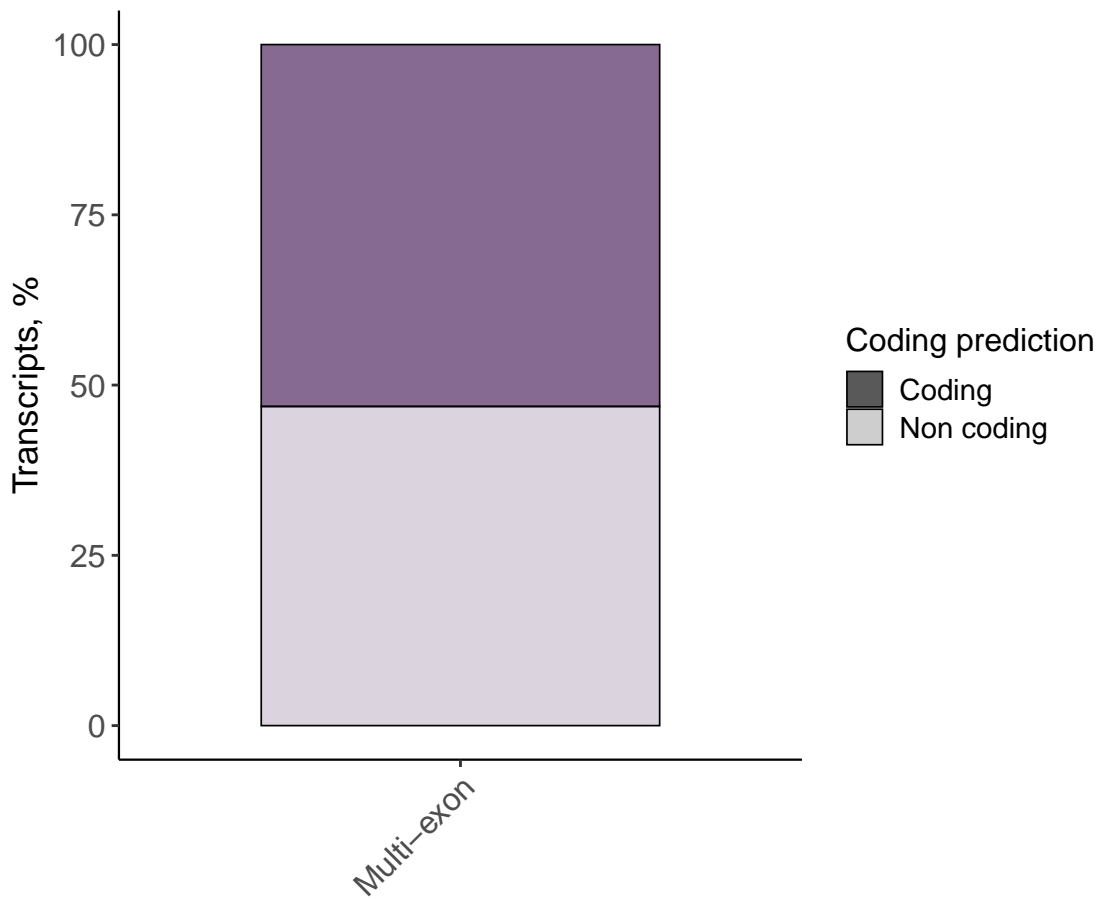
Isoform Distribution Across NNC



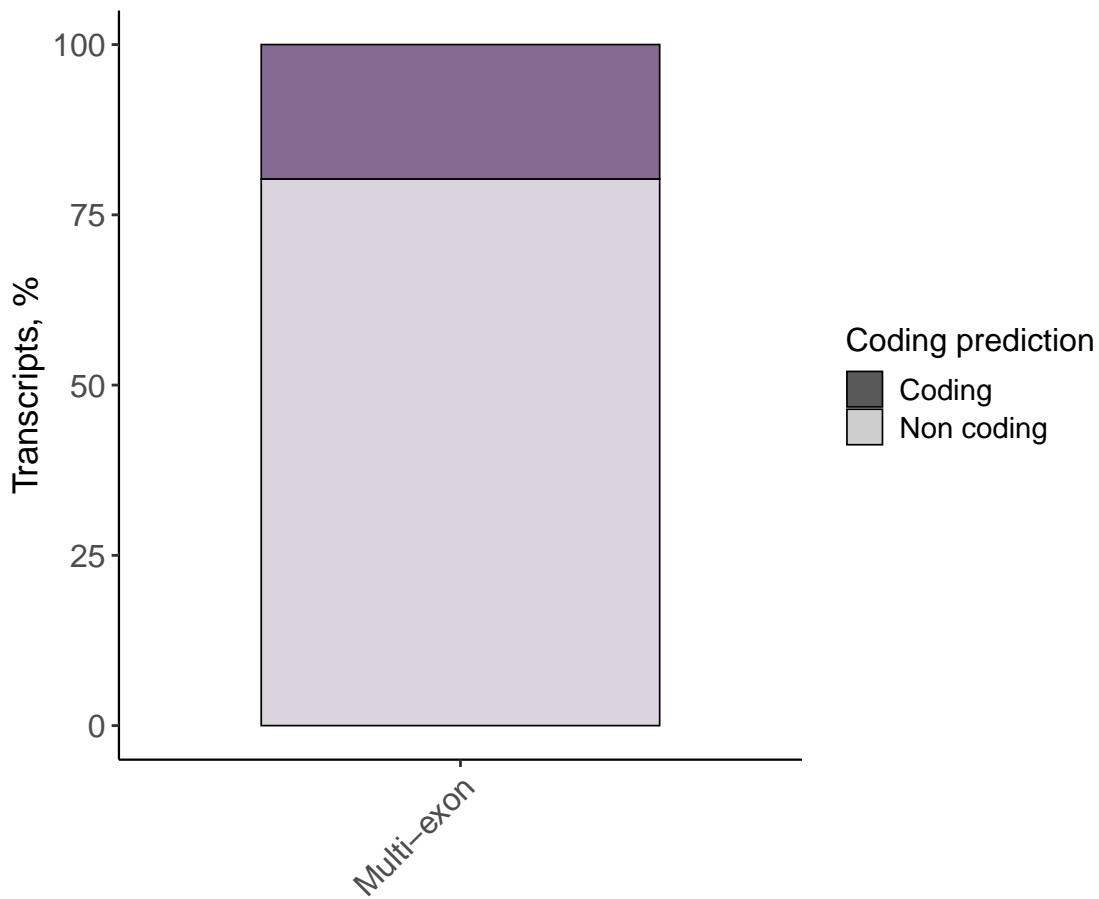
Isoform Distribution Across NIC



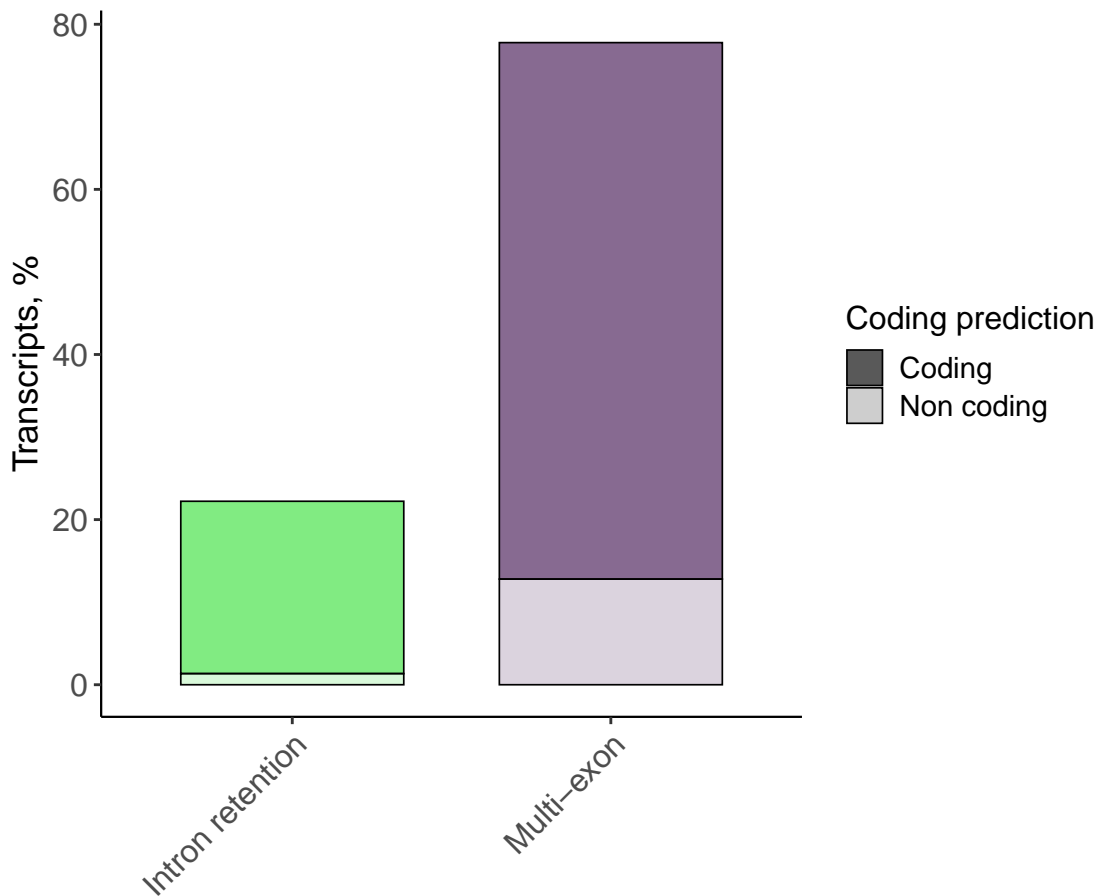
Isoform Distribution Across Genic Genomic



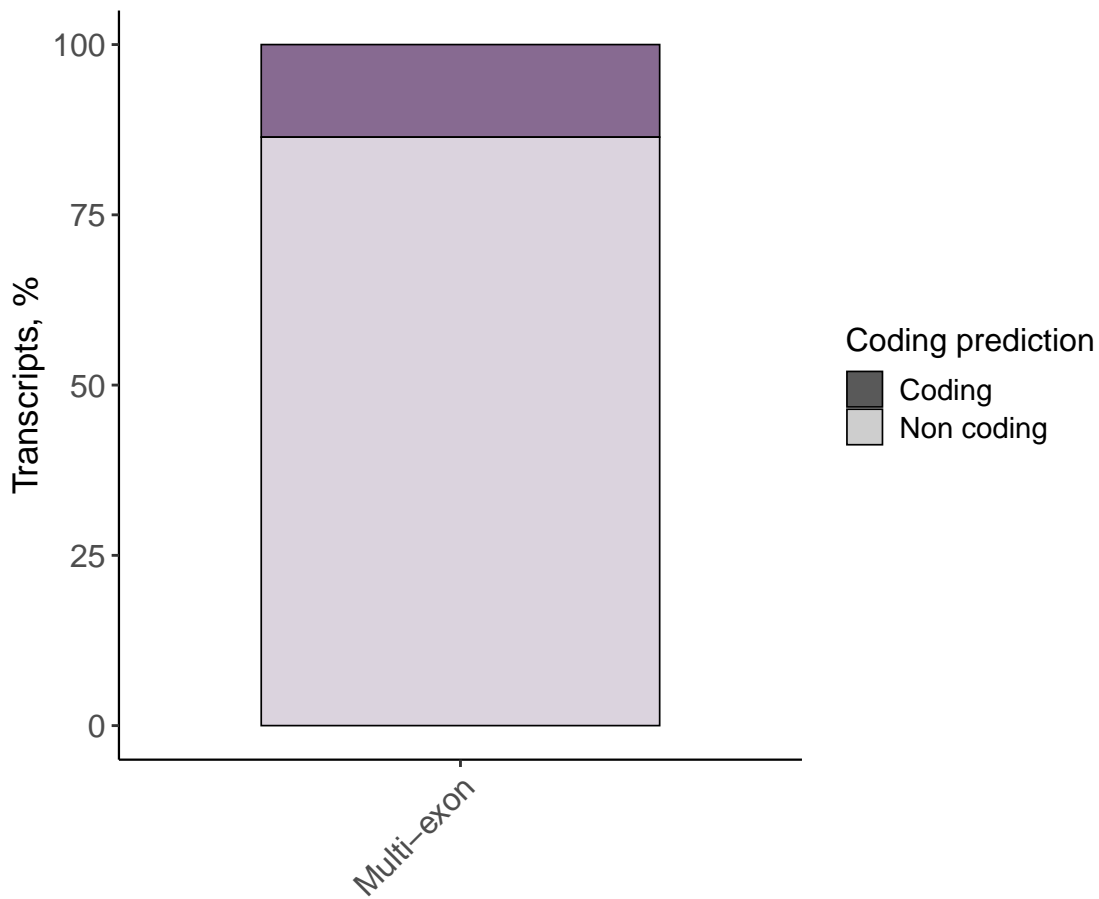
Isoform Distribution Across Antisense



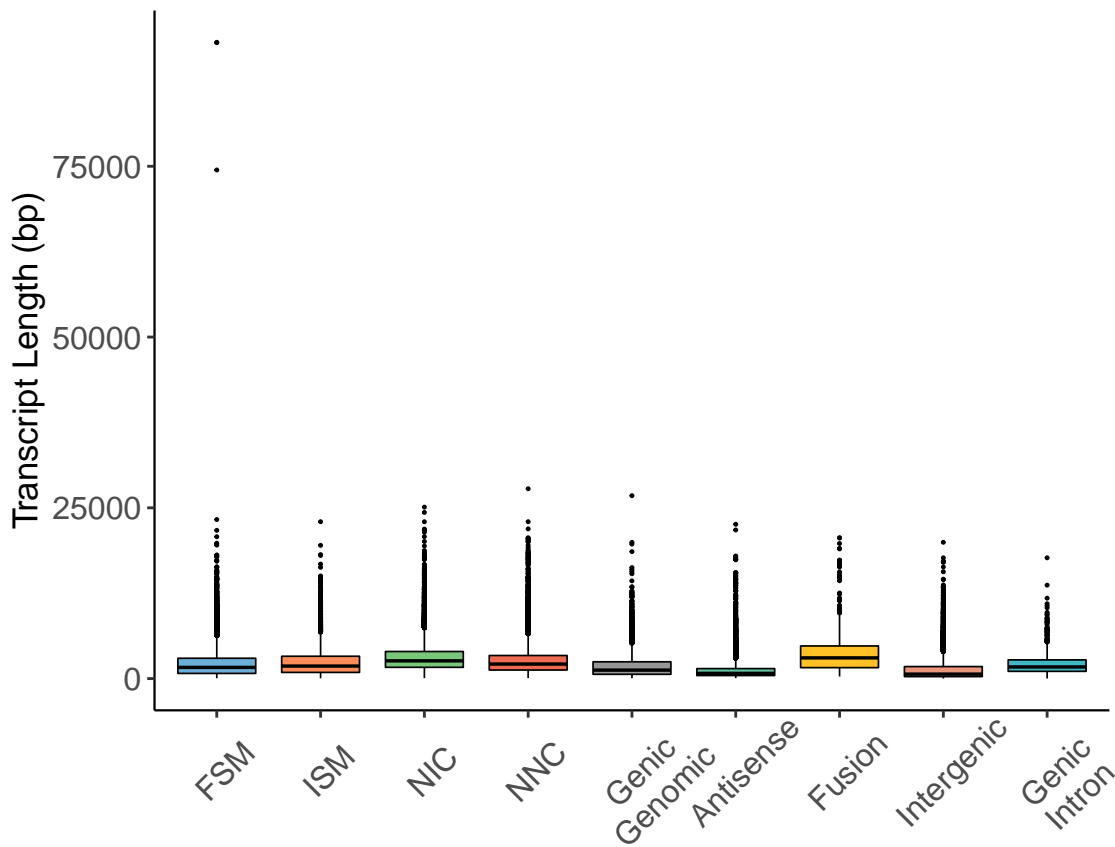
Isoform Distribution Across Fusion



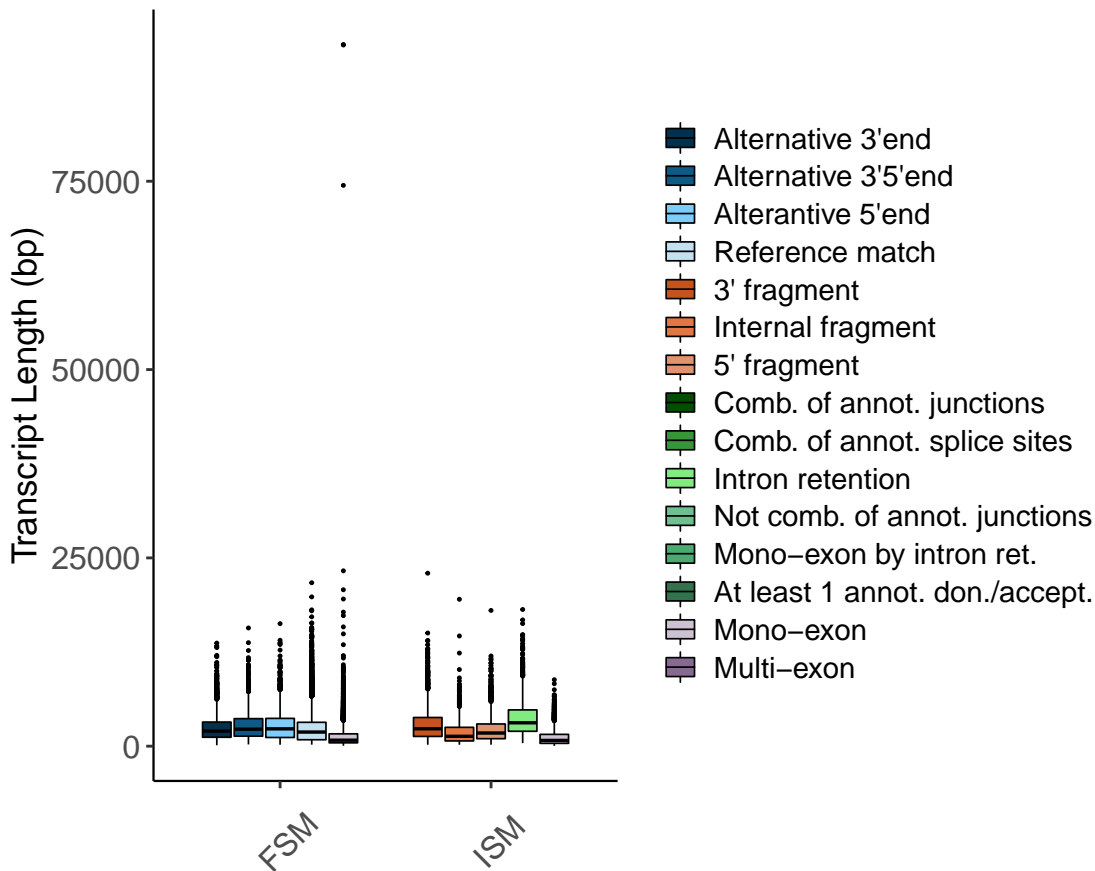
Isoform Distribution Across Intergenic



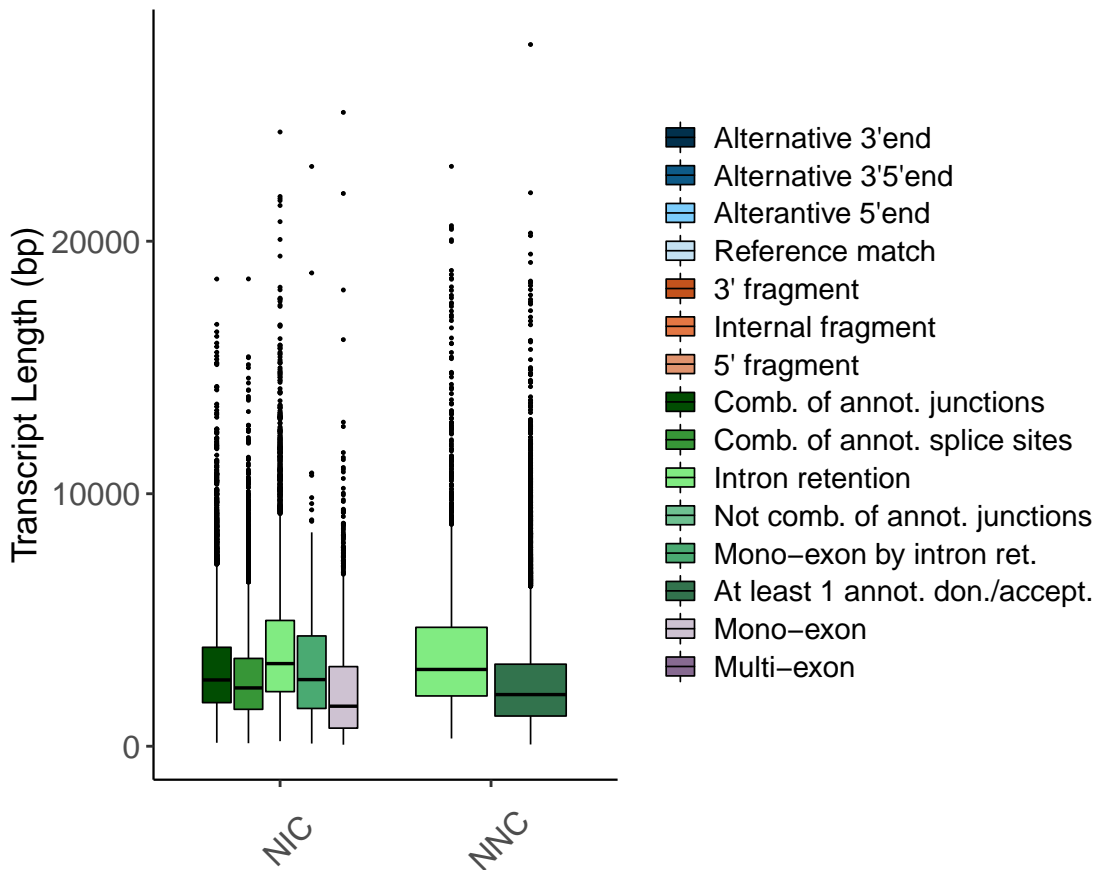
Transcript Lengths by Structural Classification



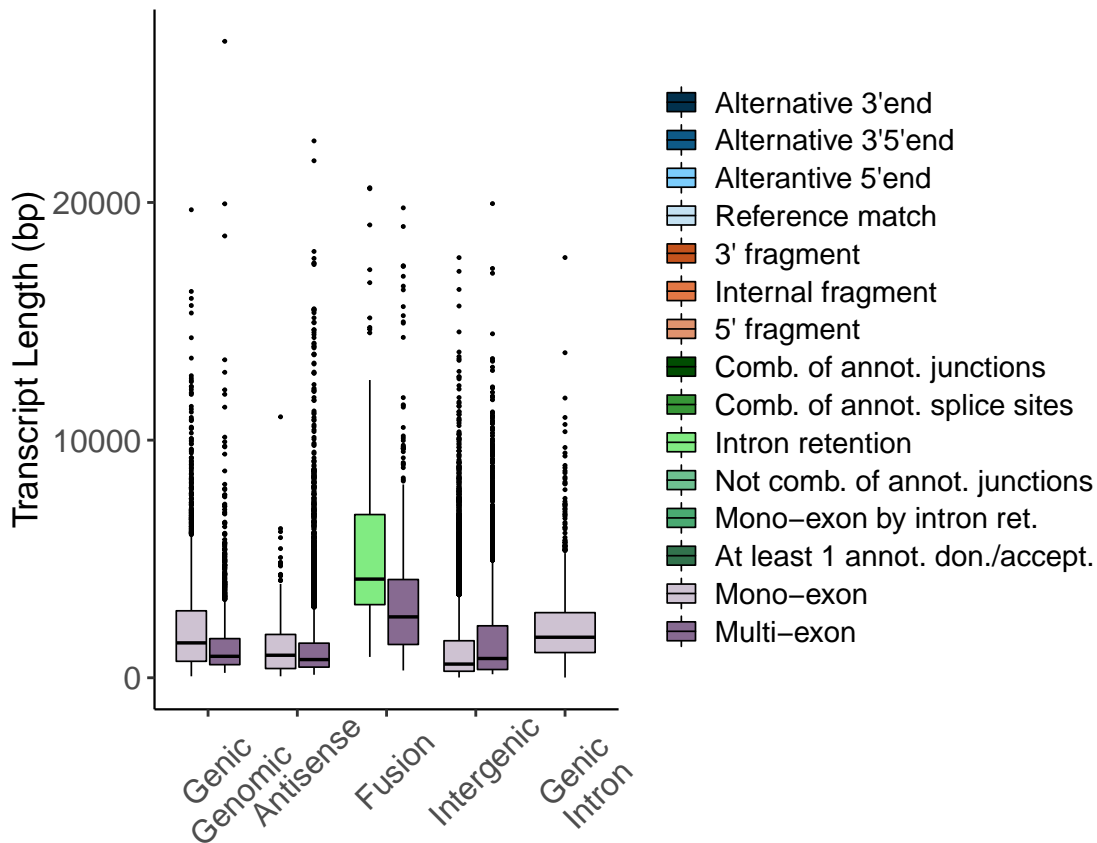
Transcript Lengths by Subcategory



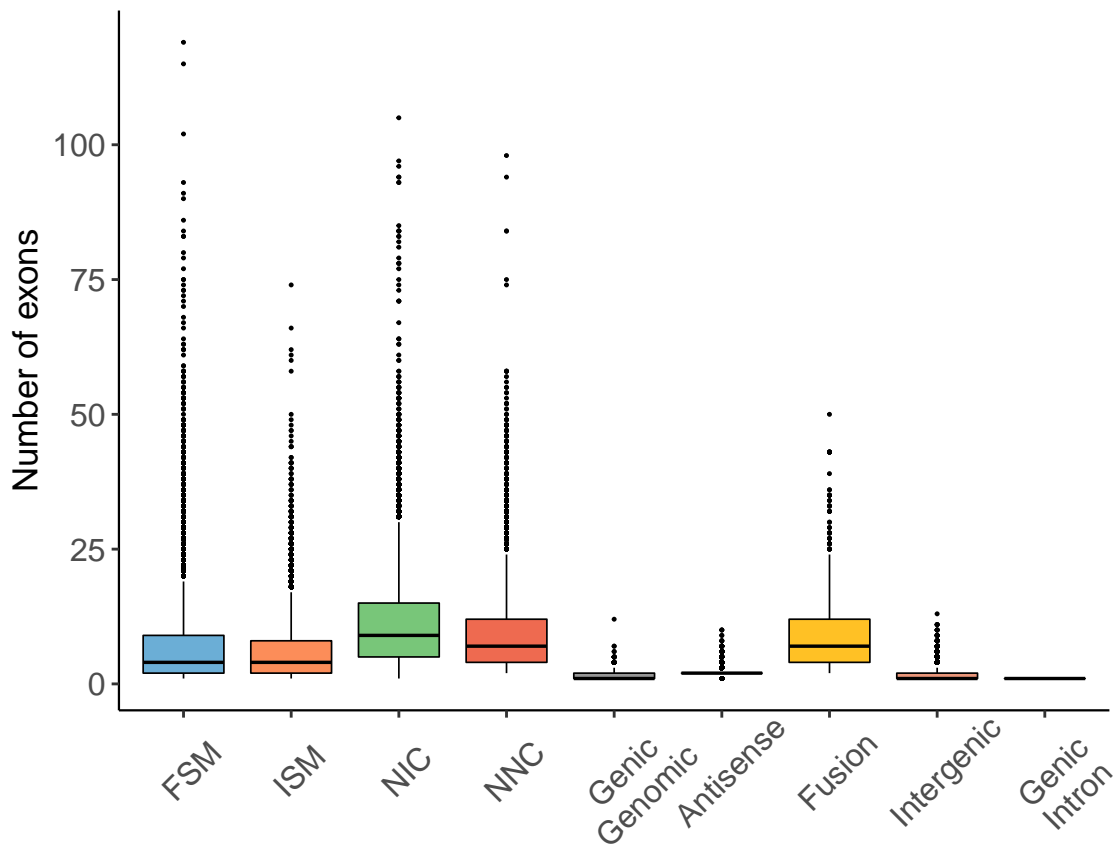
Transcript Lengths by Subcategory



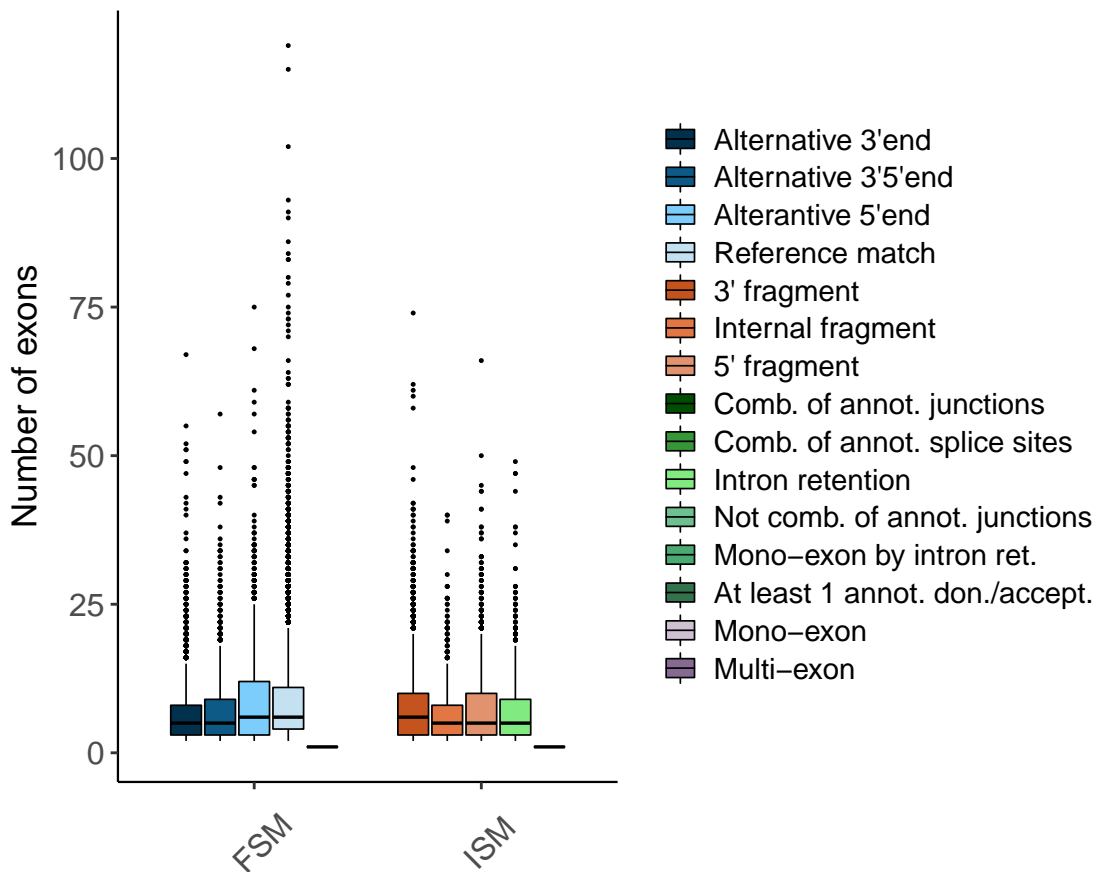
Transcript Lengths by Subcategory



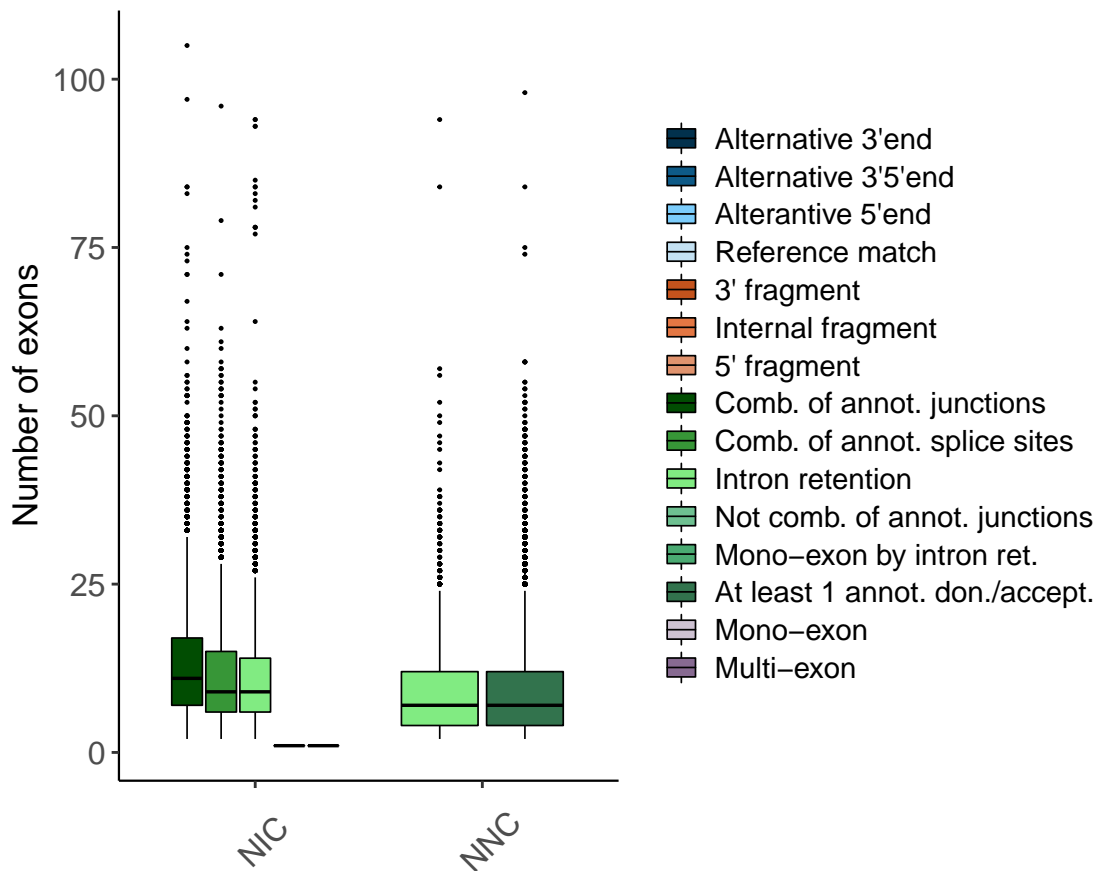
Exon Counts by Structural Classification



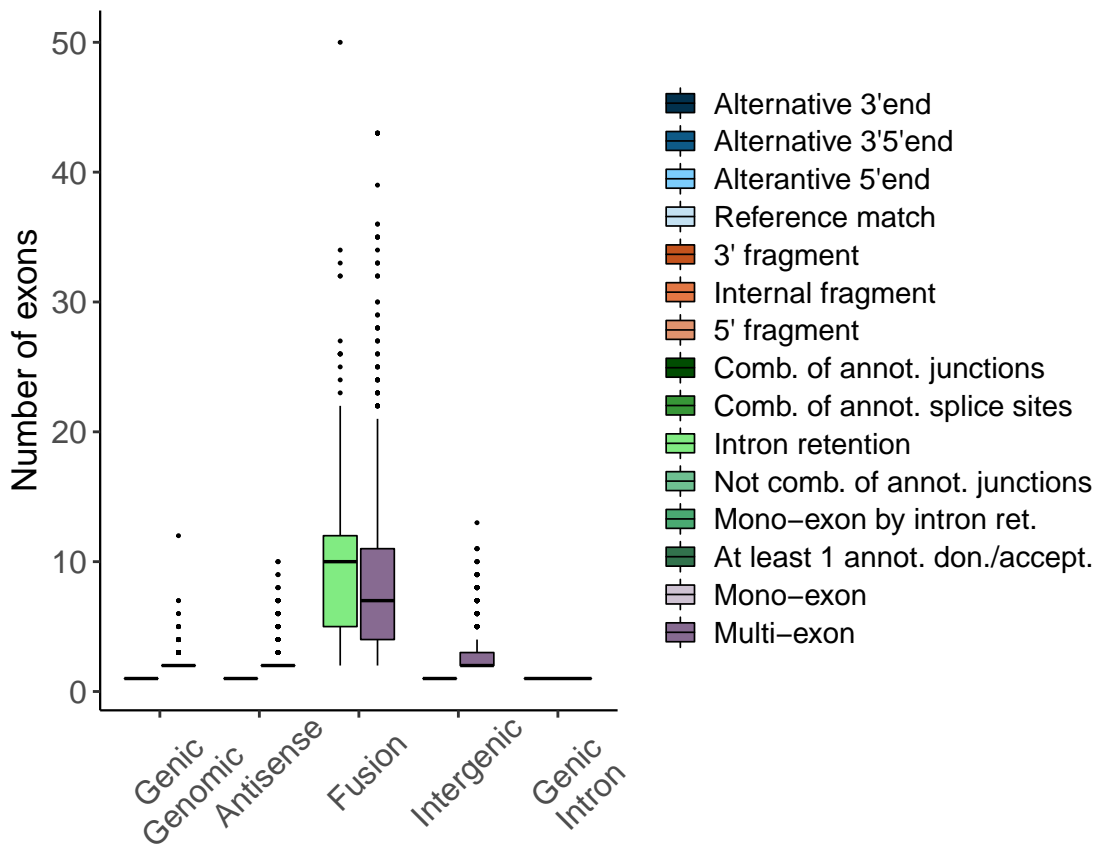
Exon Counts by Subcategory



Exon Counts by Subcategory

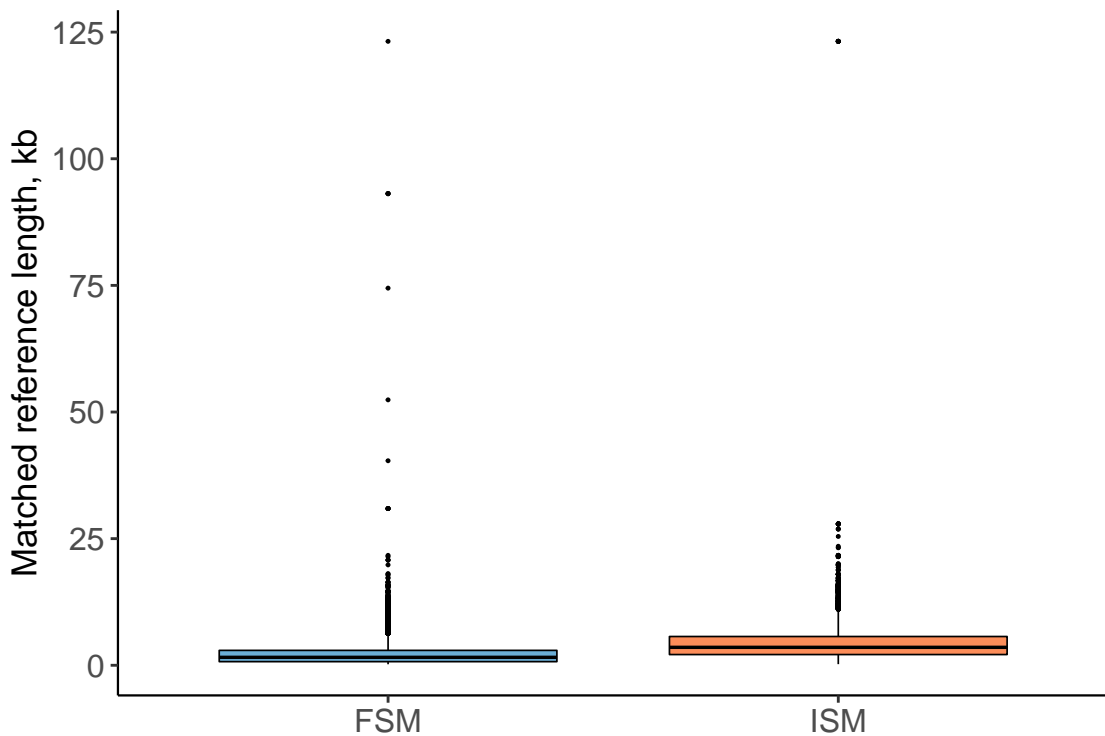


Exon Counts by Subcategory



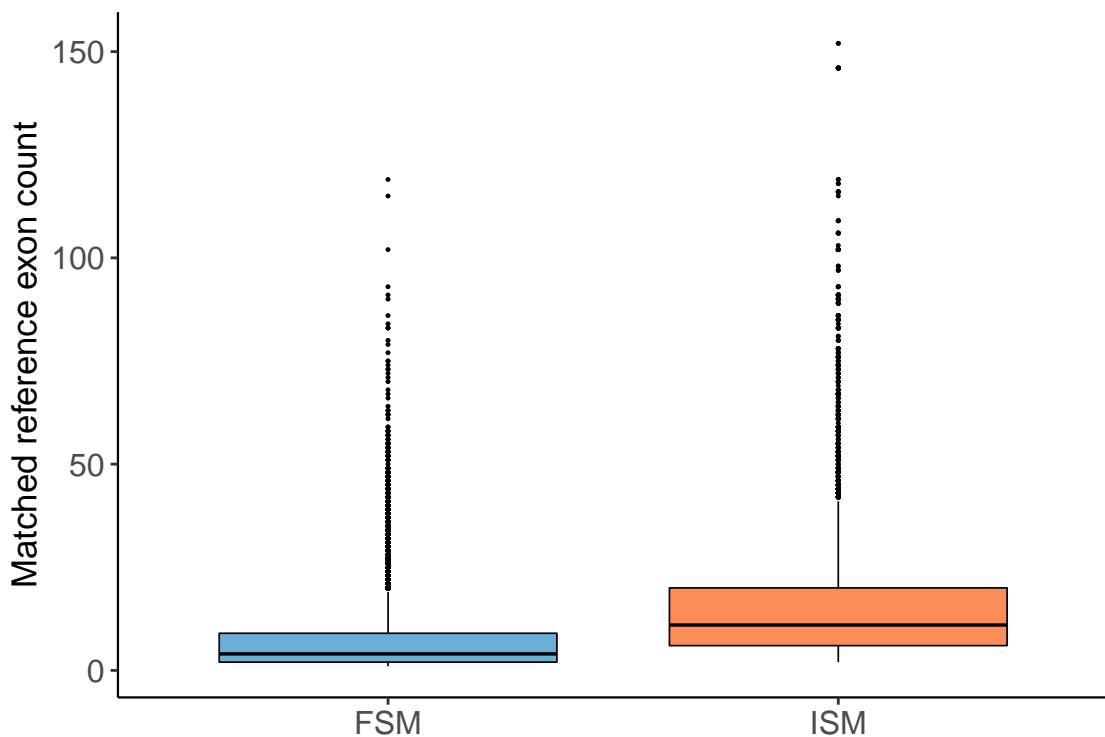
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories



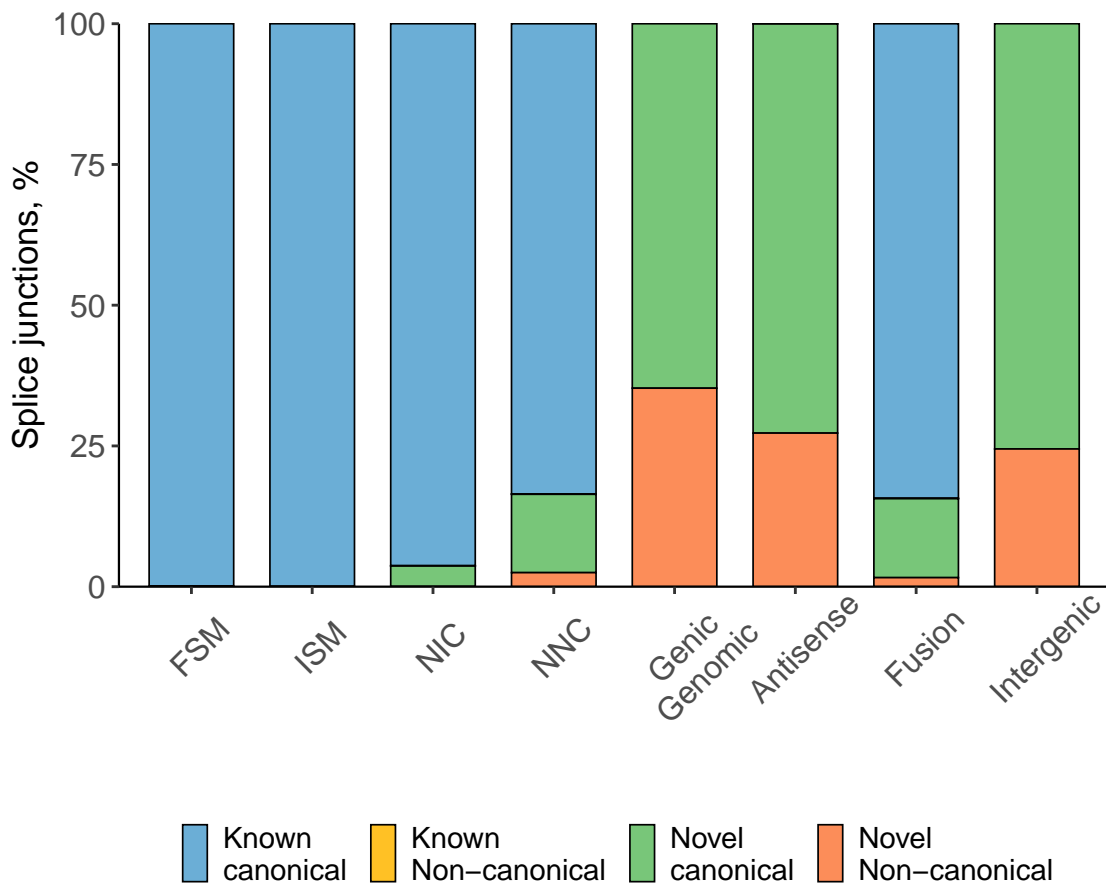
Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

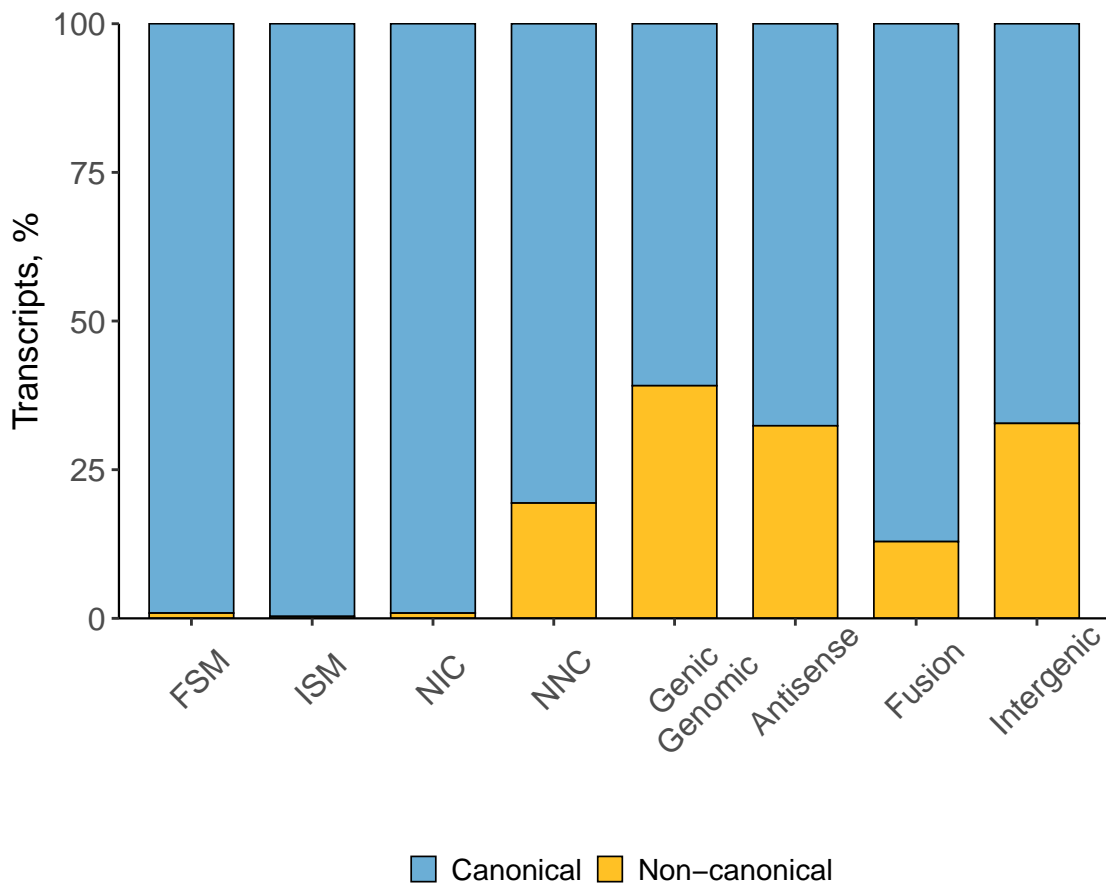


Splice Junction Characterization

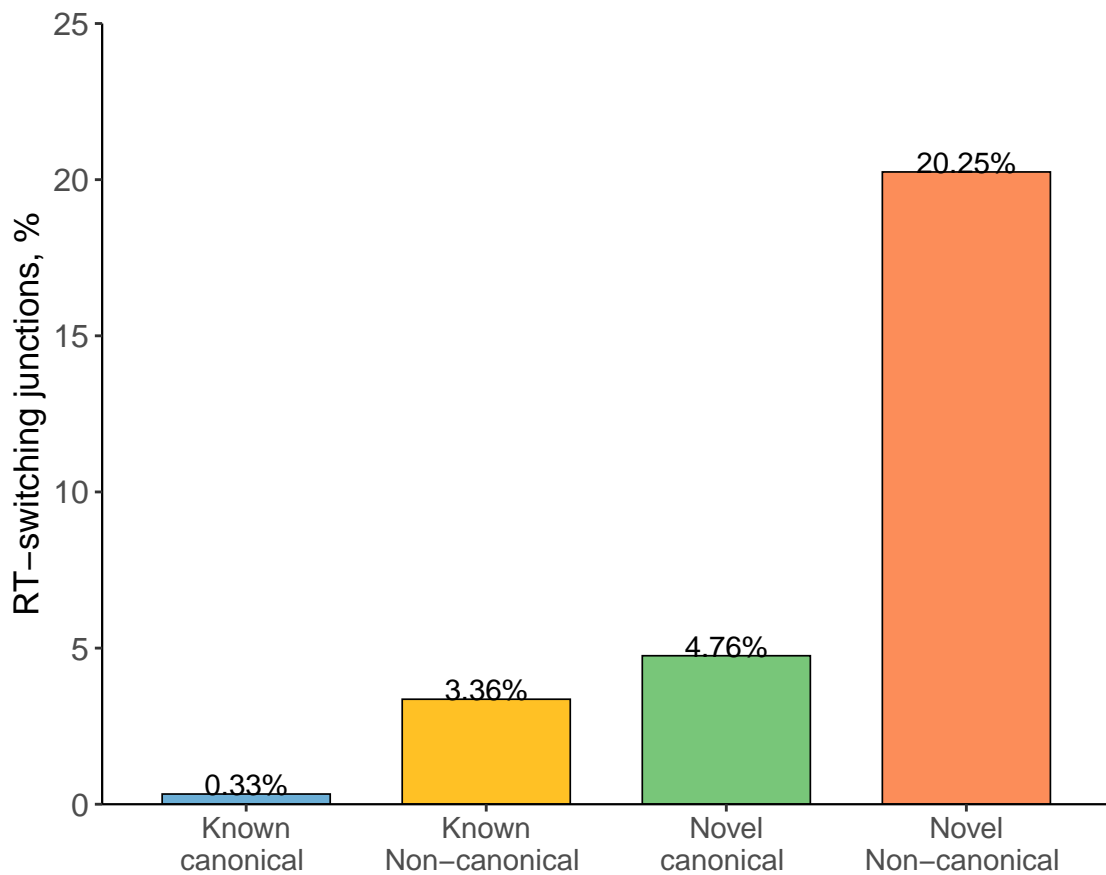
Distribution of Splice Junctions by Structural Classification



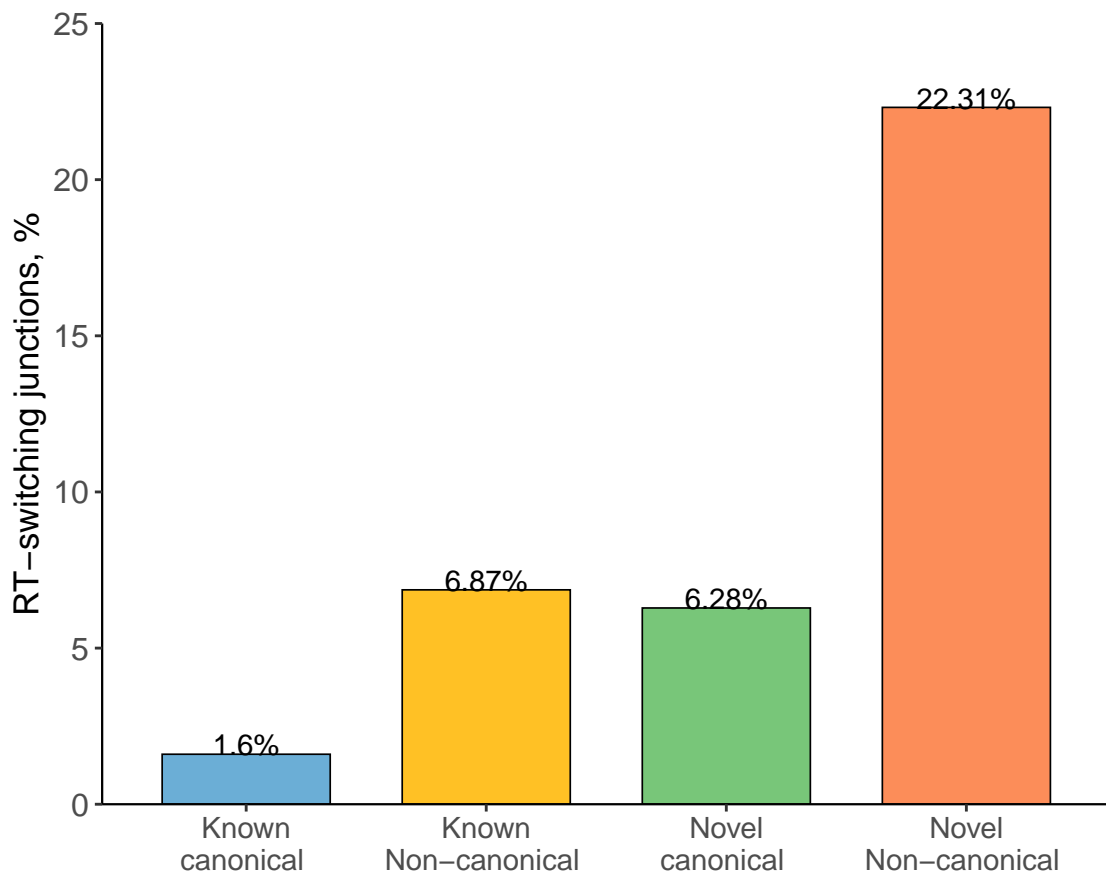
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



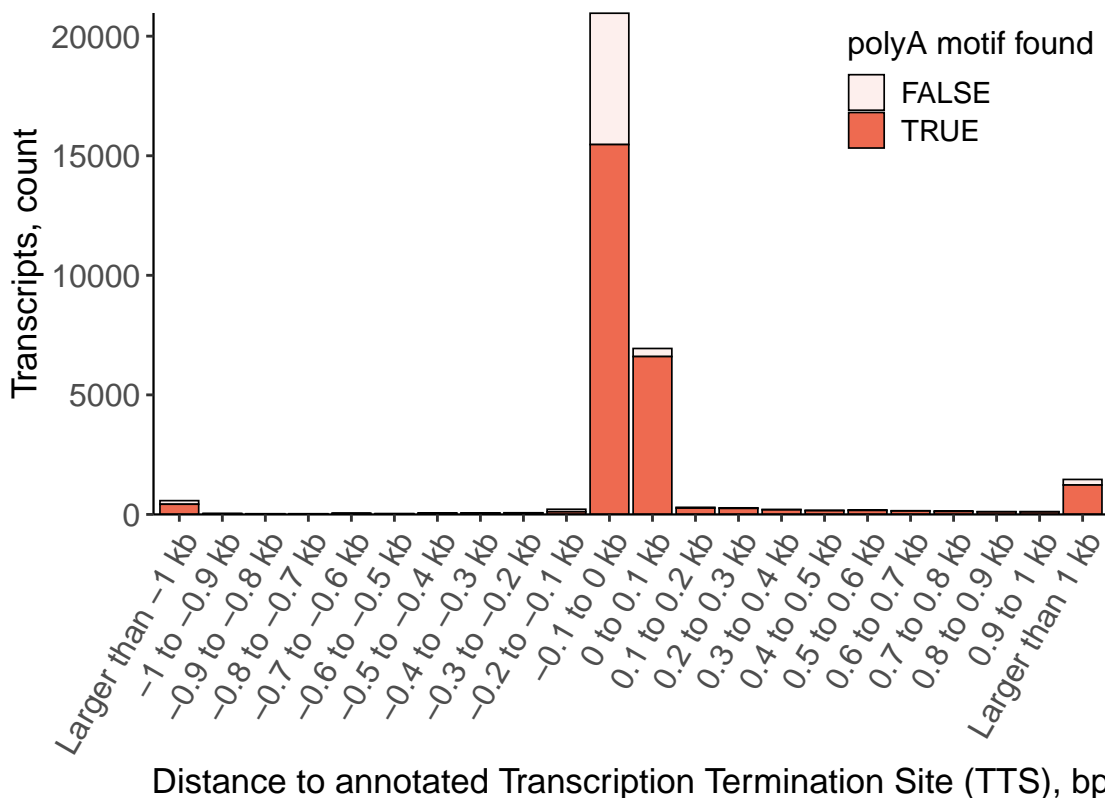
Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

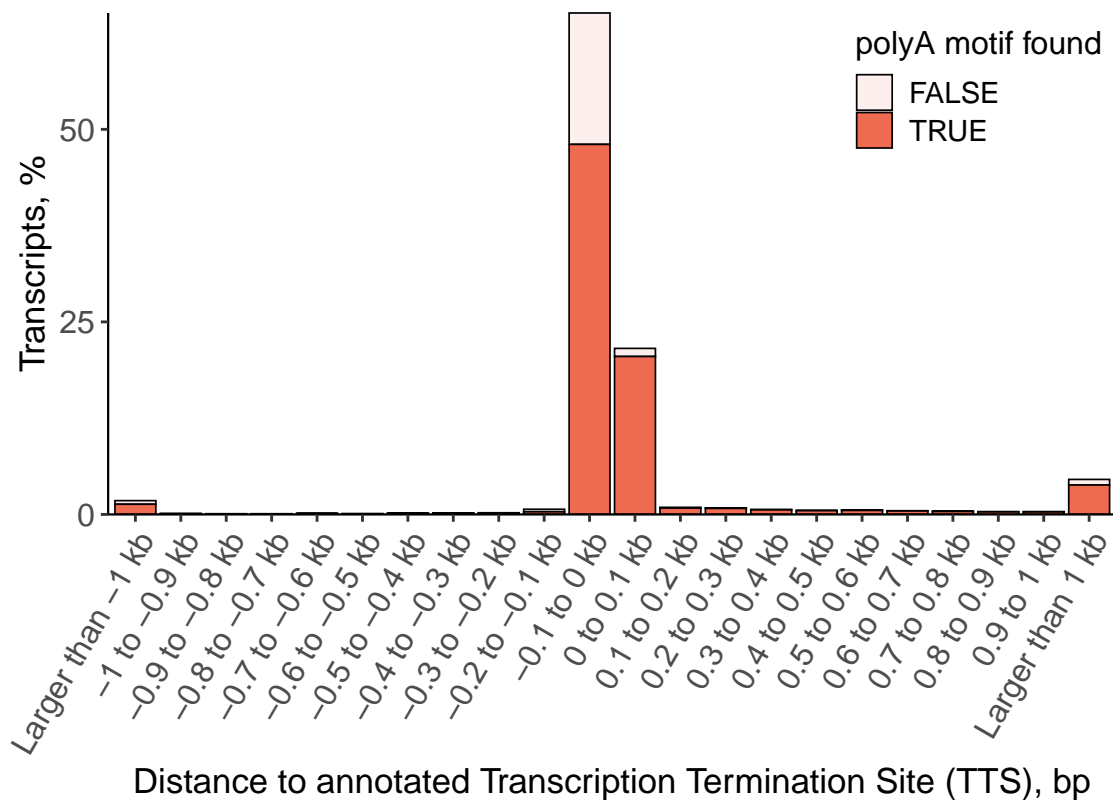
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



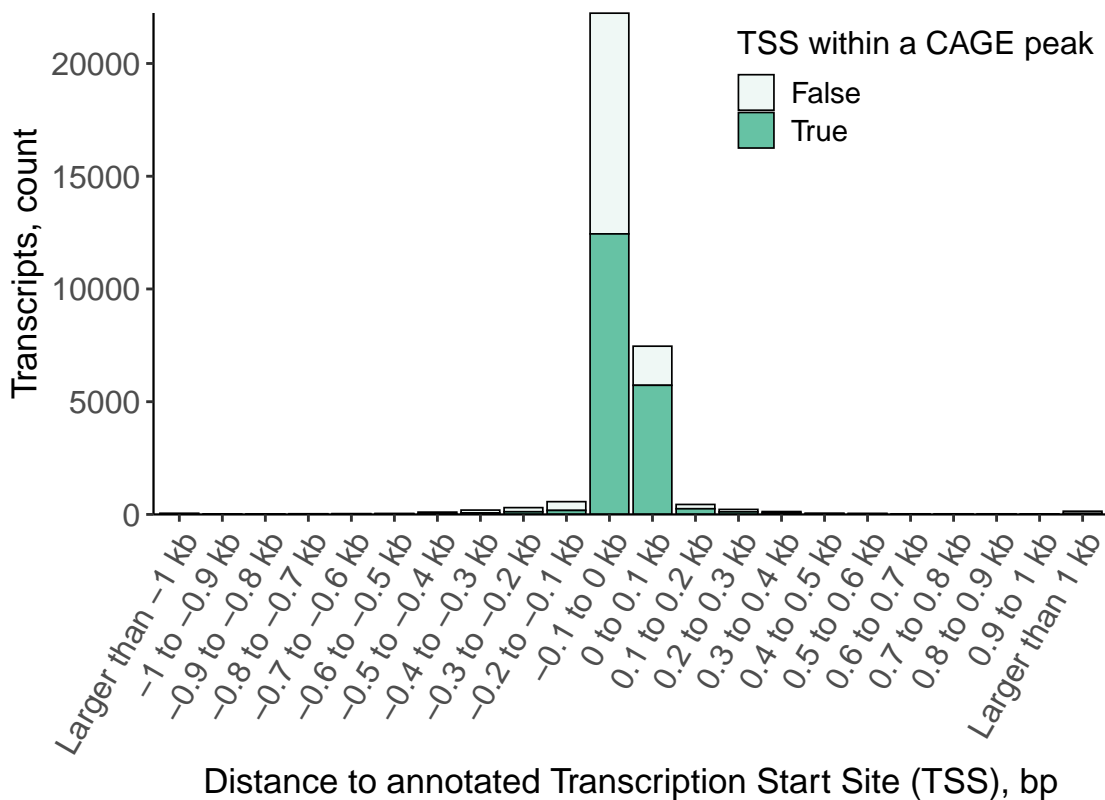
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



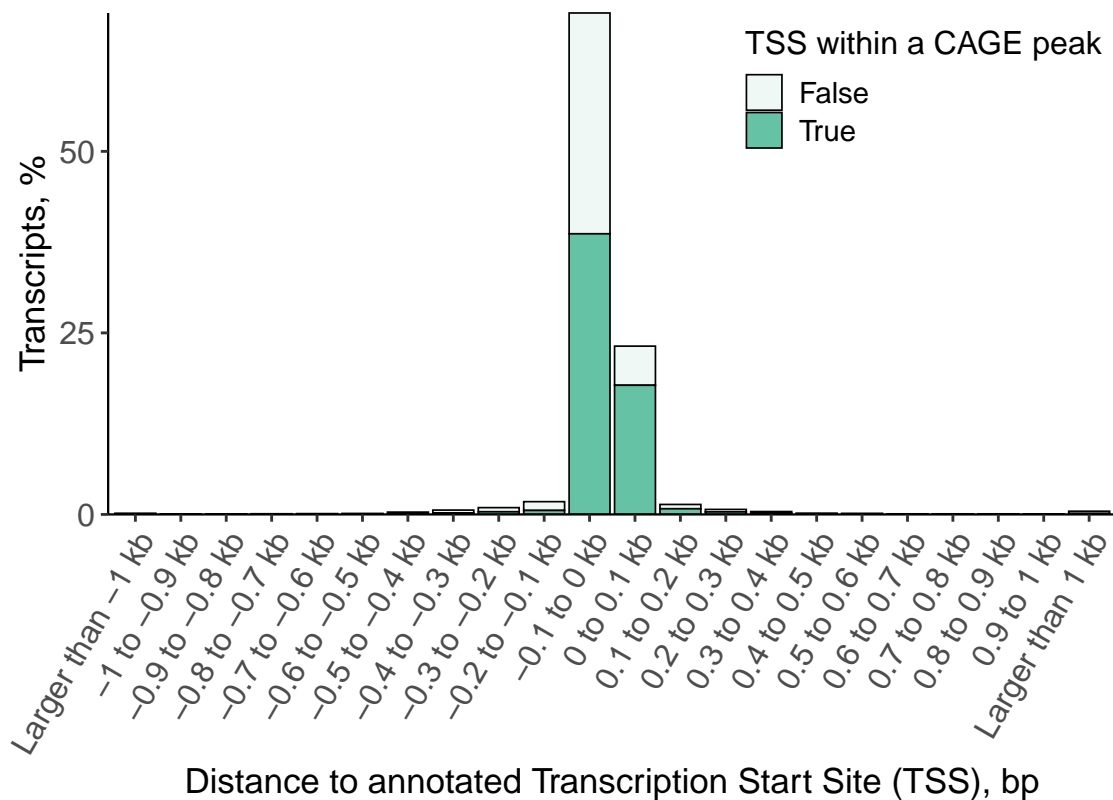
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



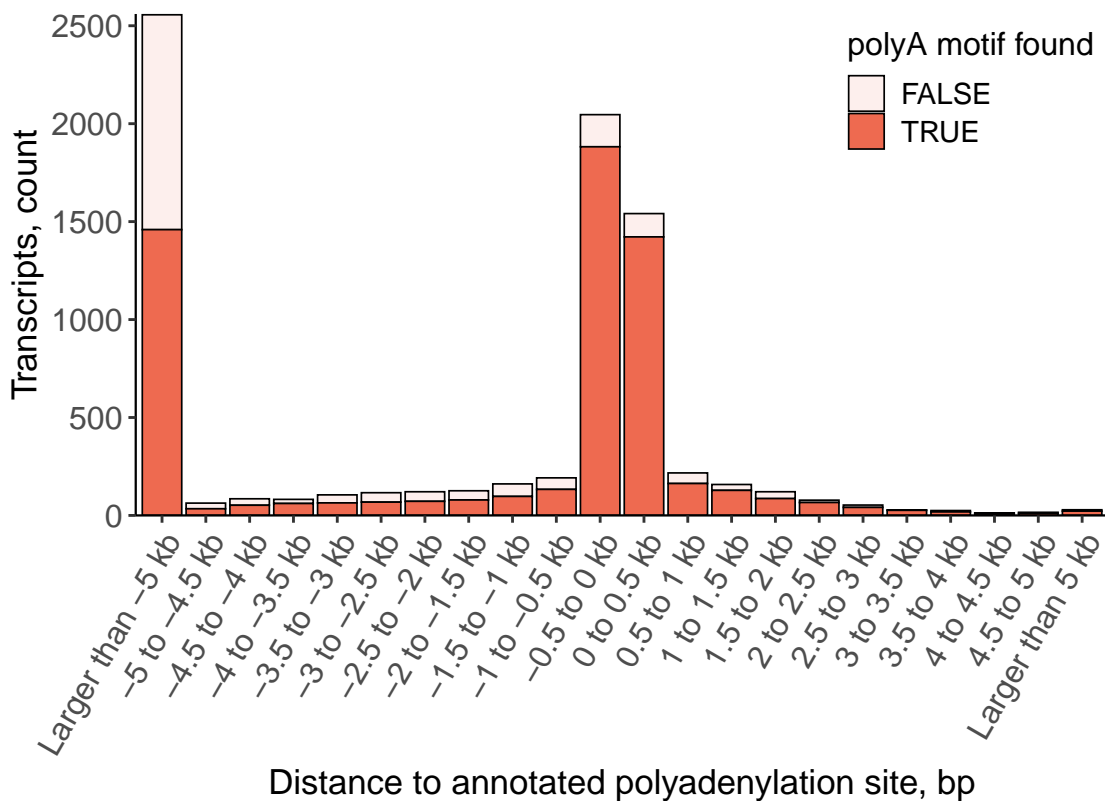
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



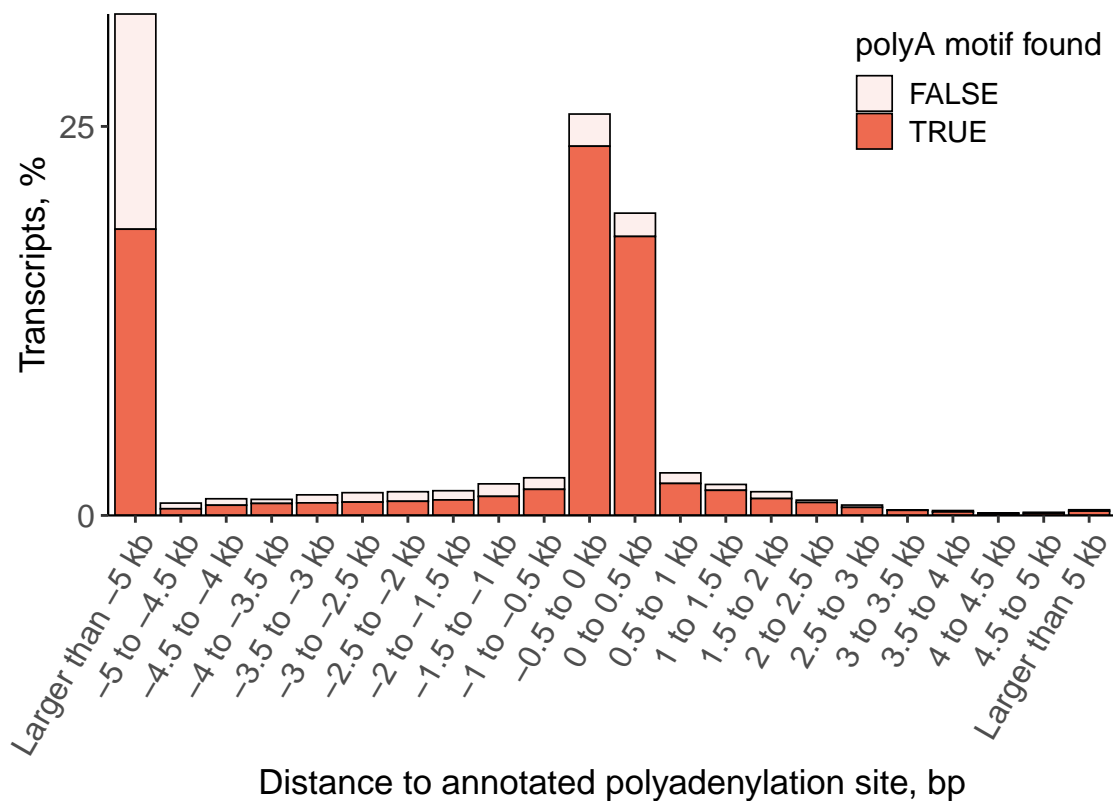
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



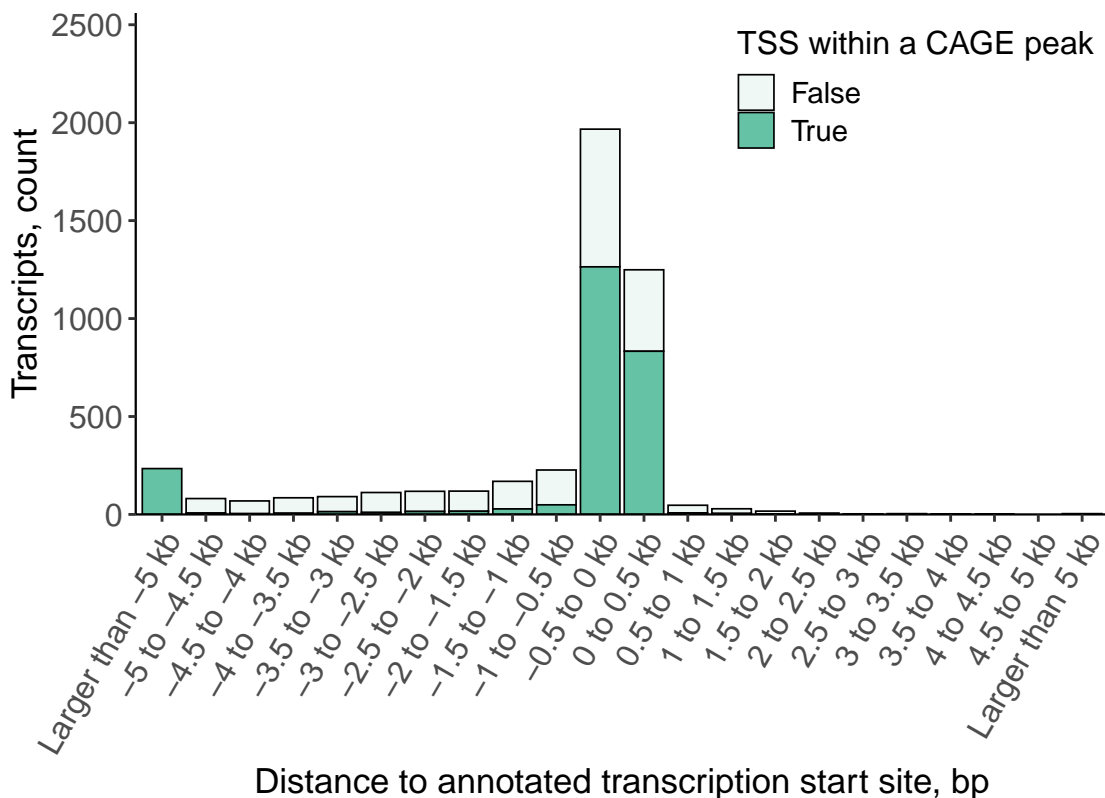
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



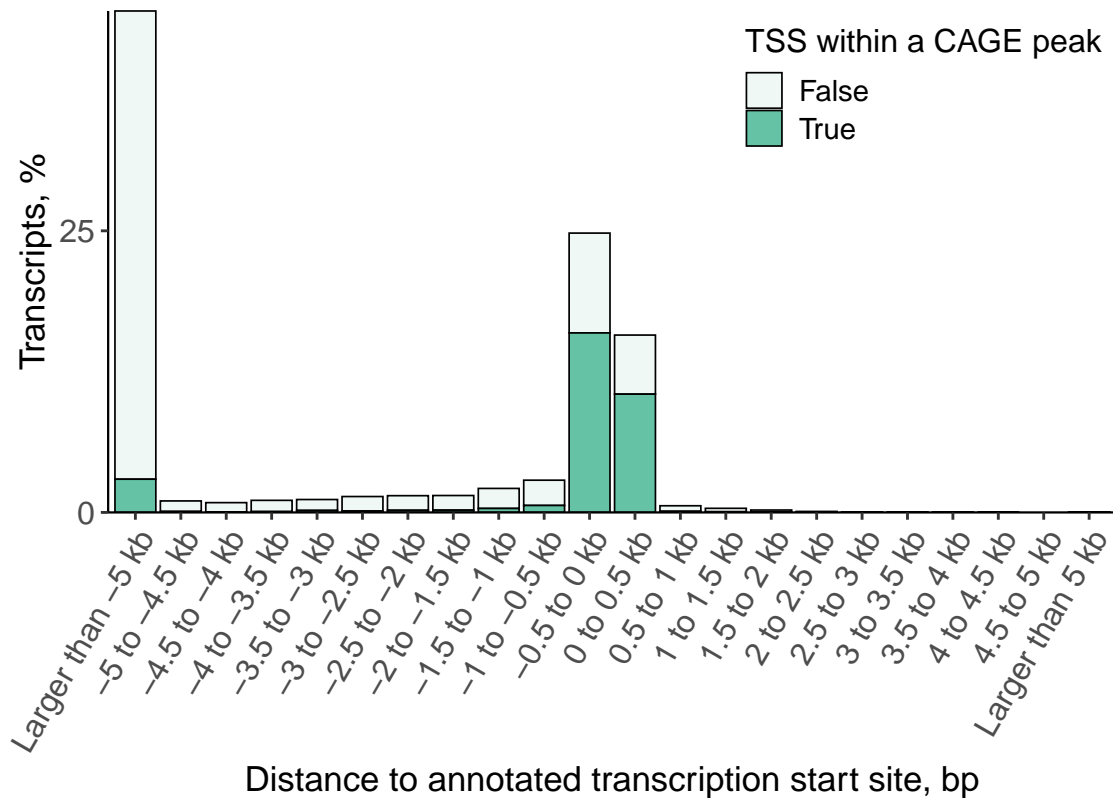
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

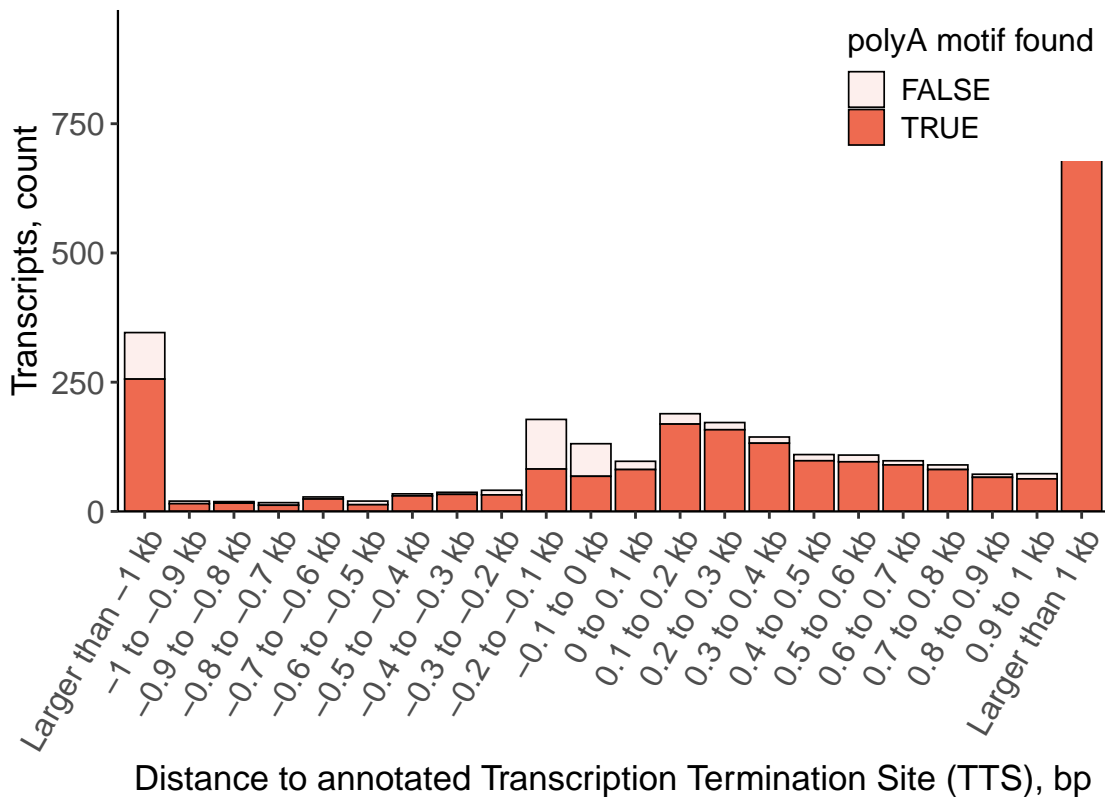
Negative values indicate downstream of annotated TSS



*Comparison With Annotated TSS and TTS
by Subcategories*

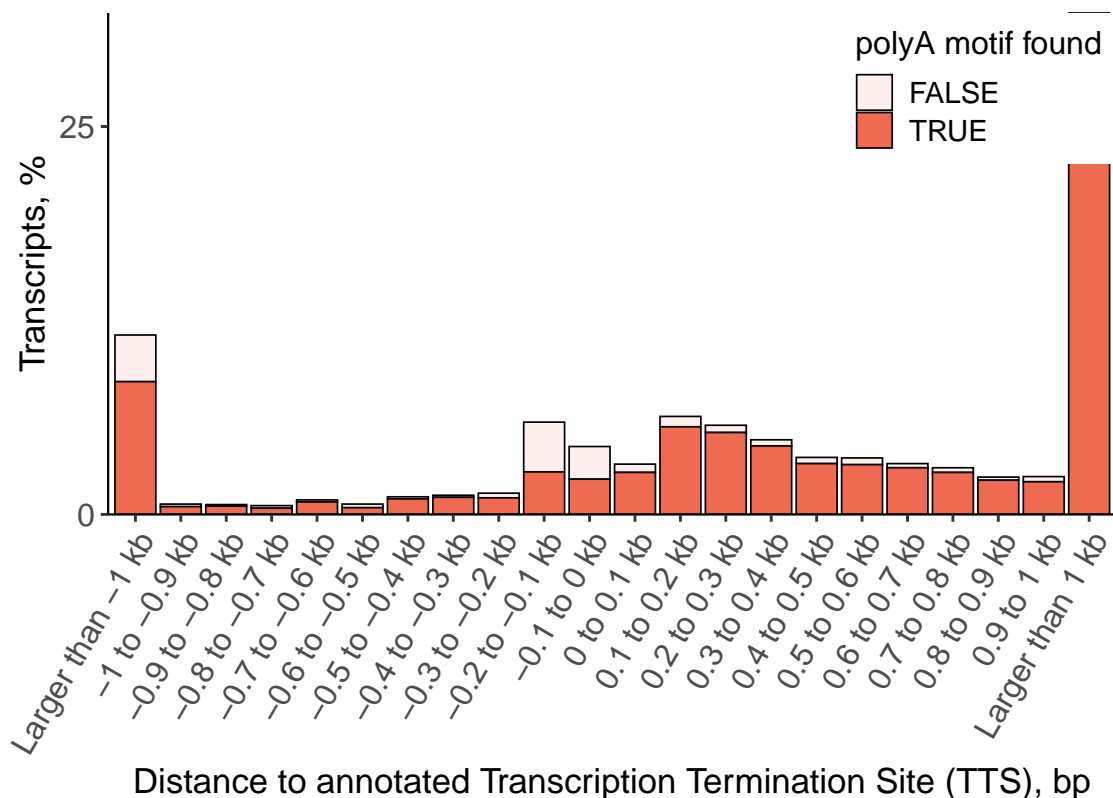
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



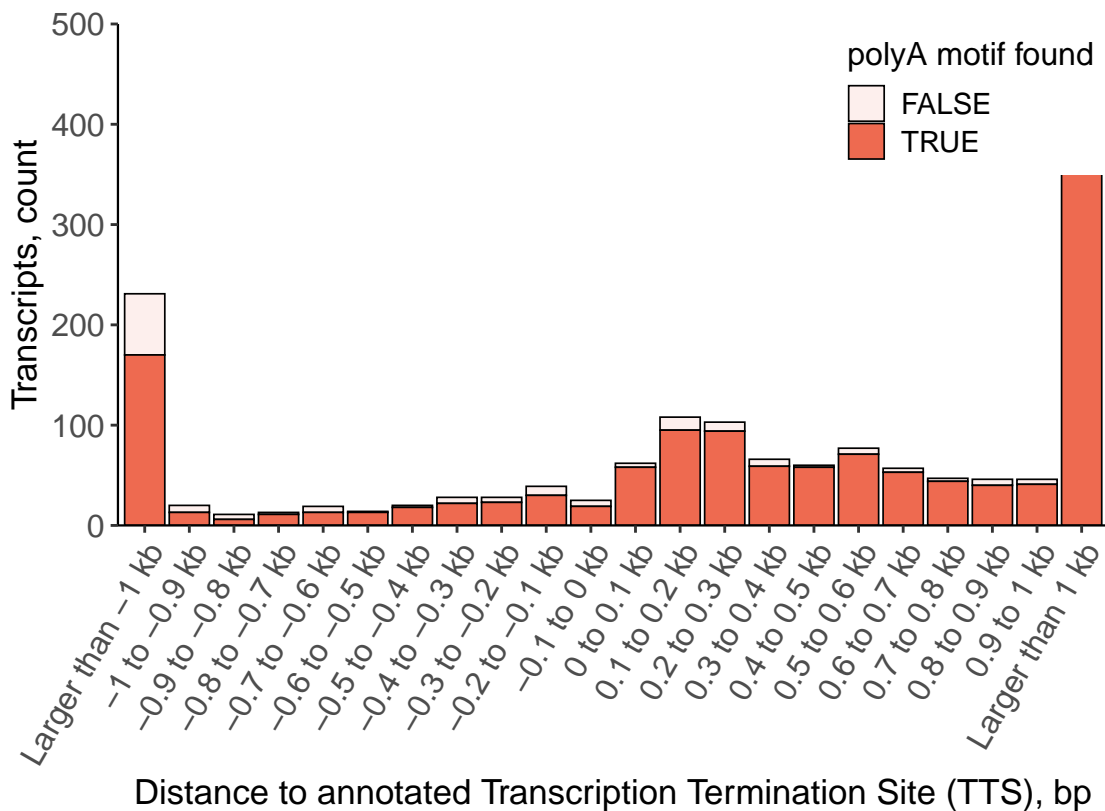
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



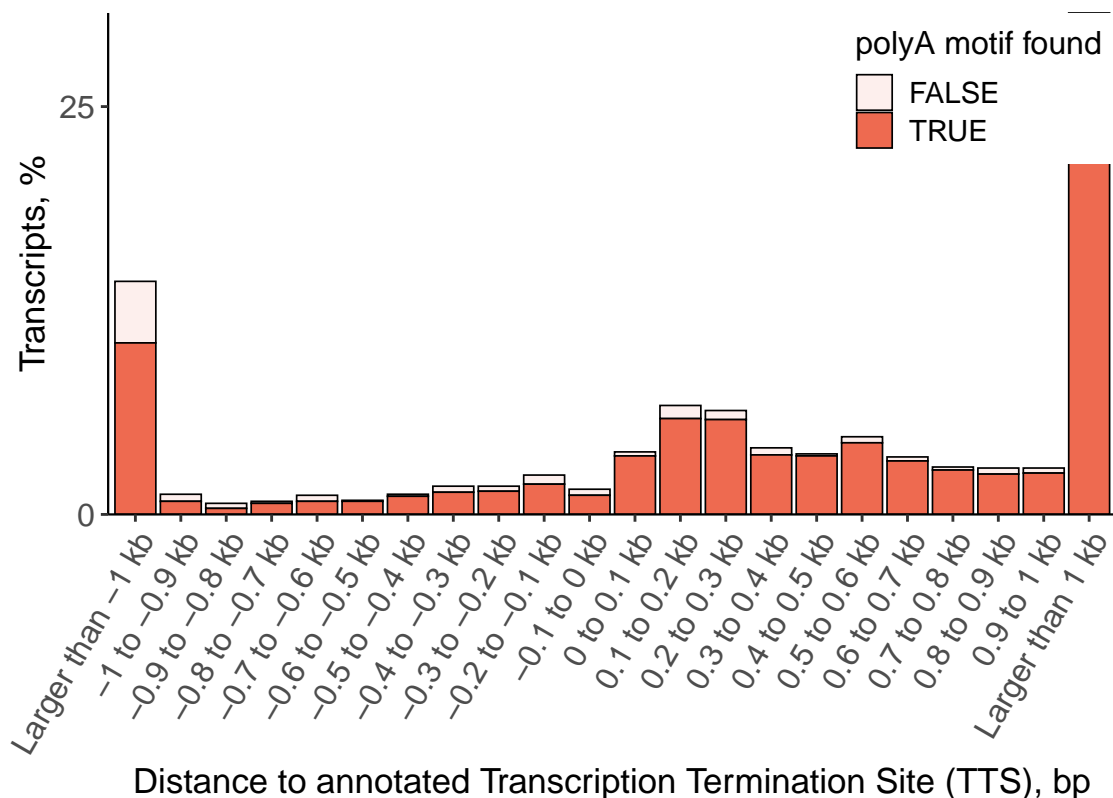
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



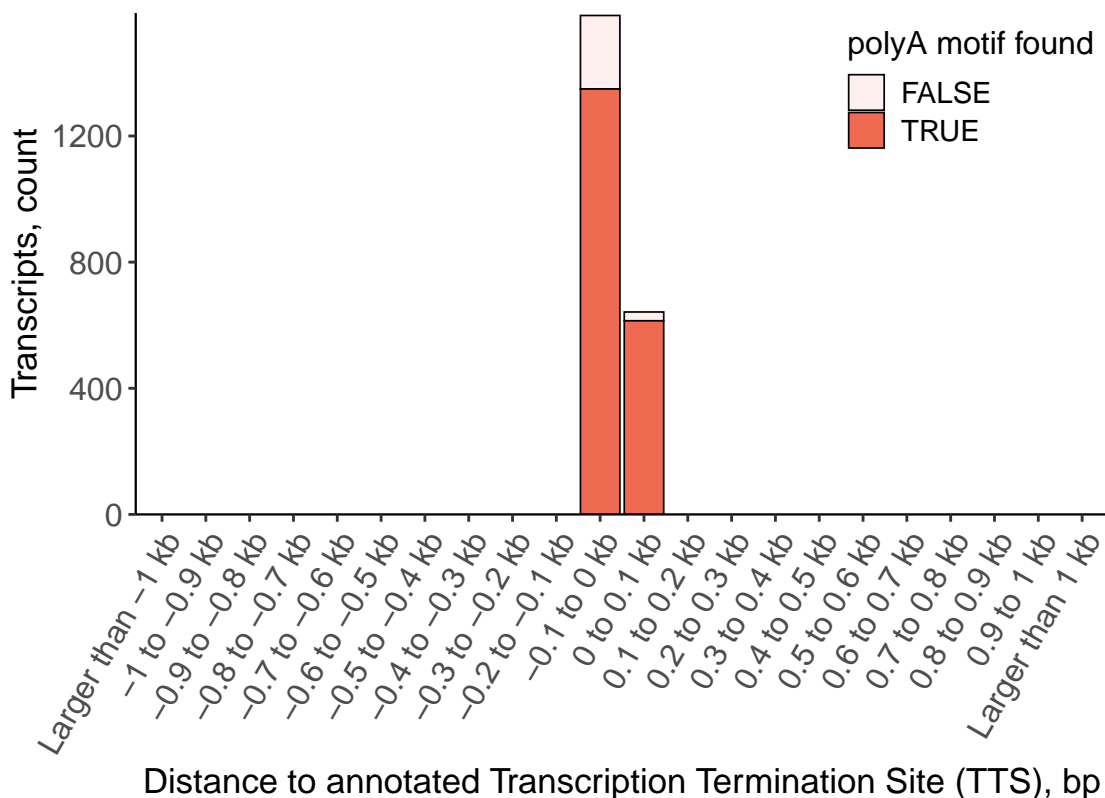
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



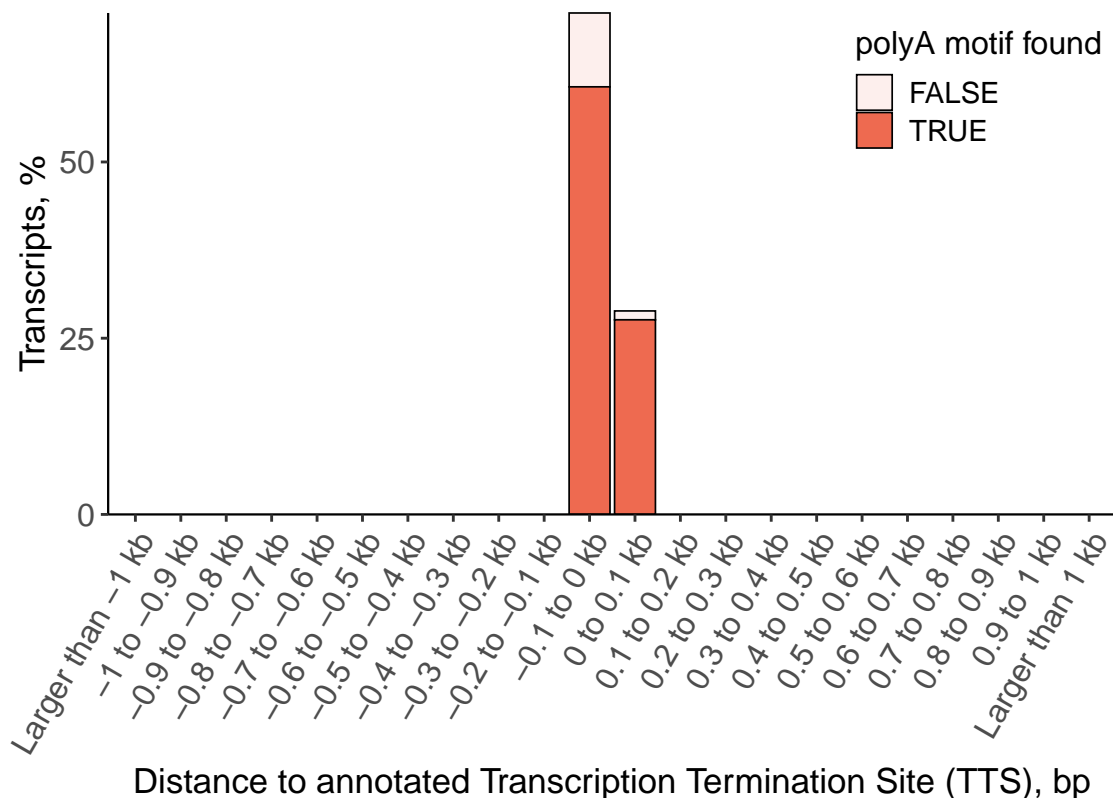
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



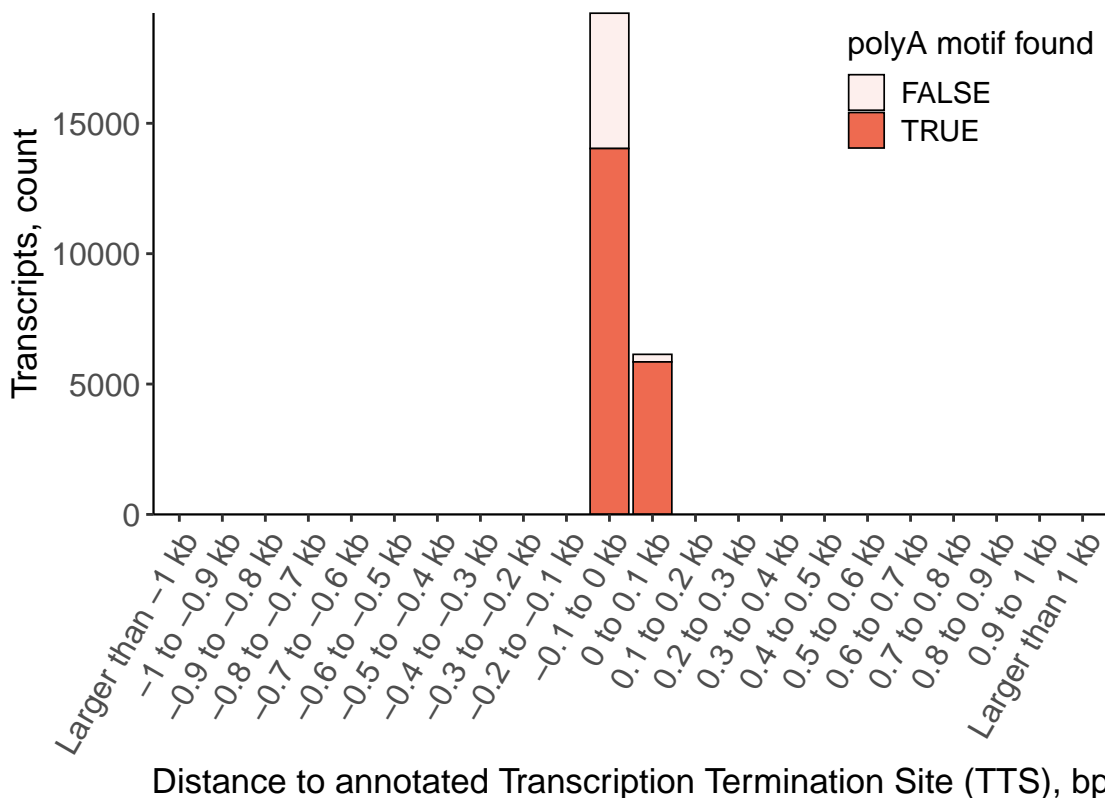
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



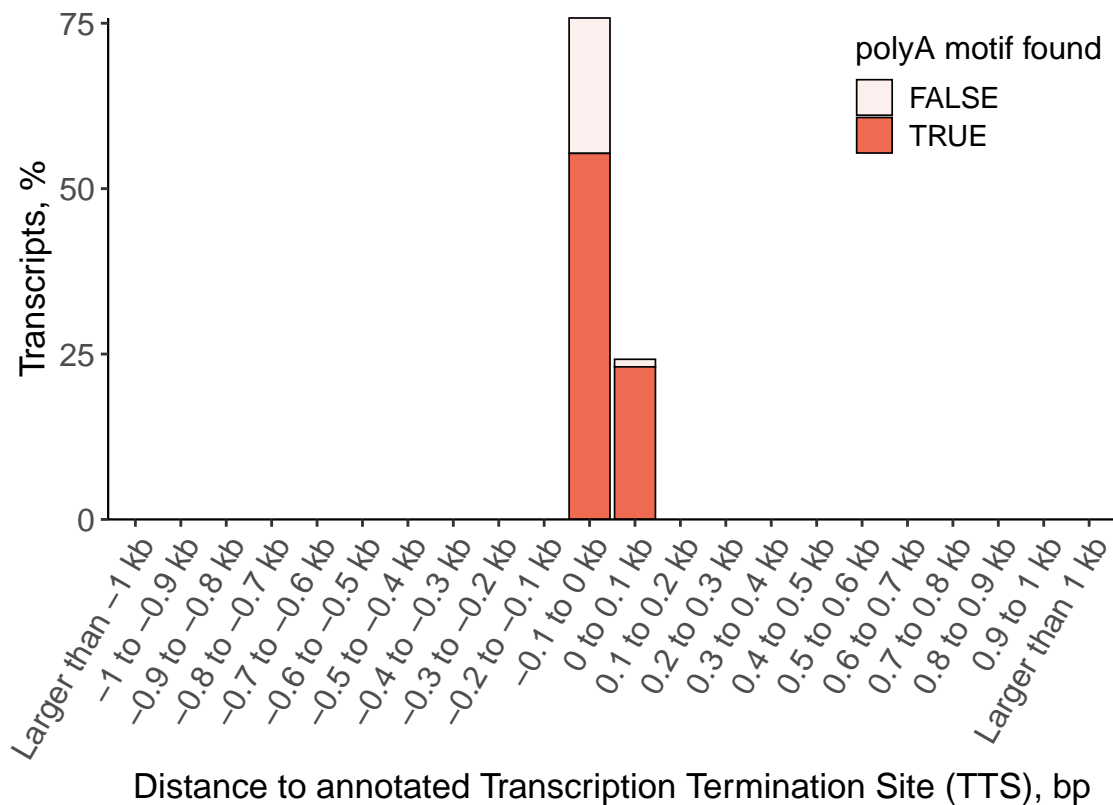
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



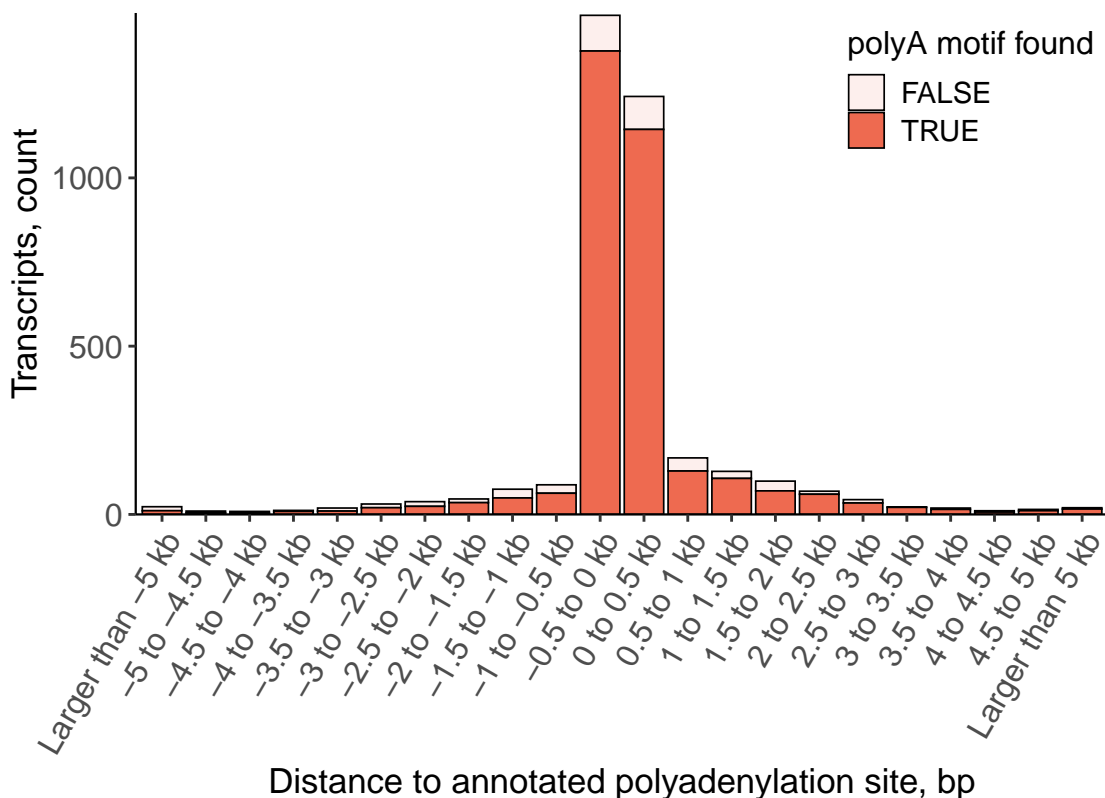
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



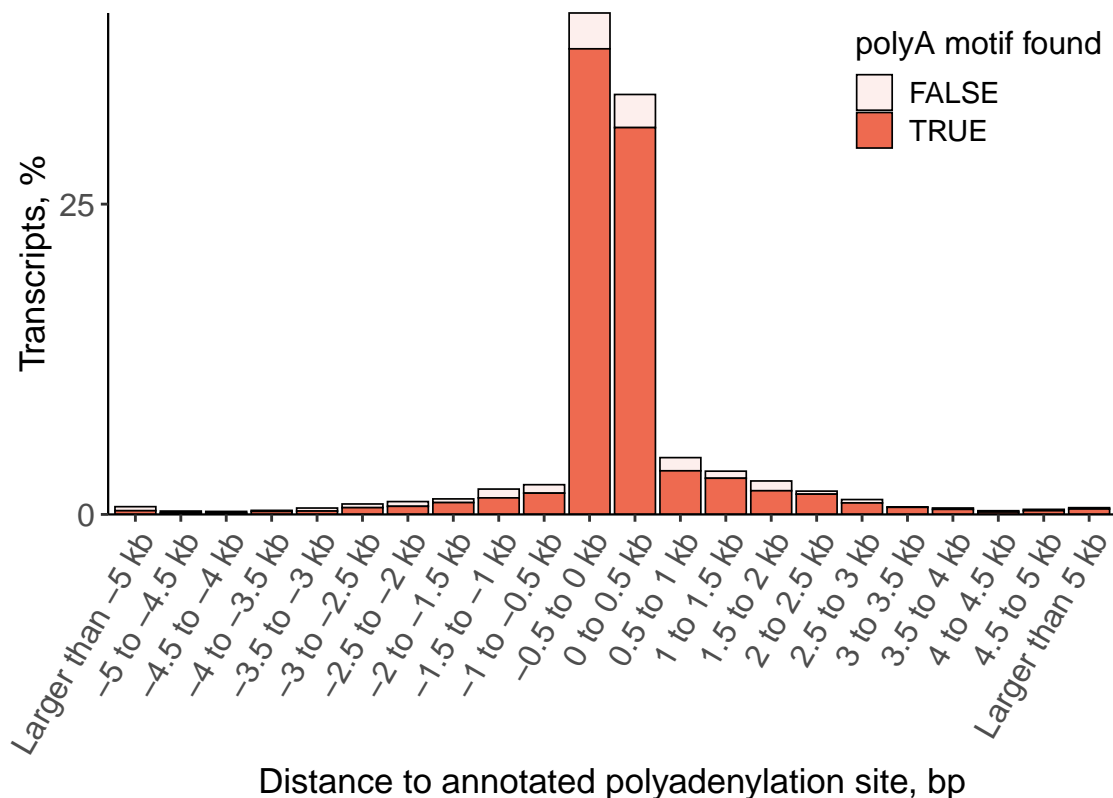
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



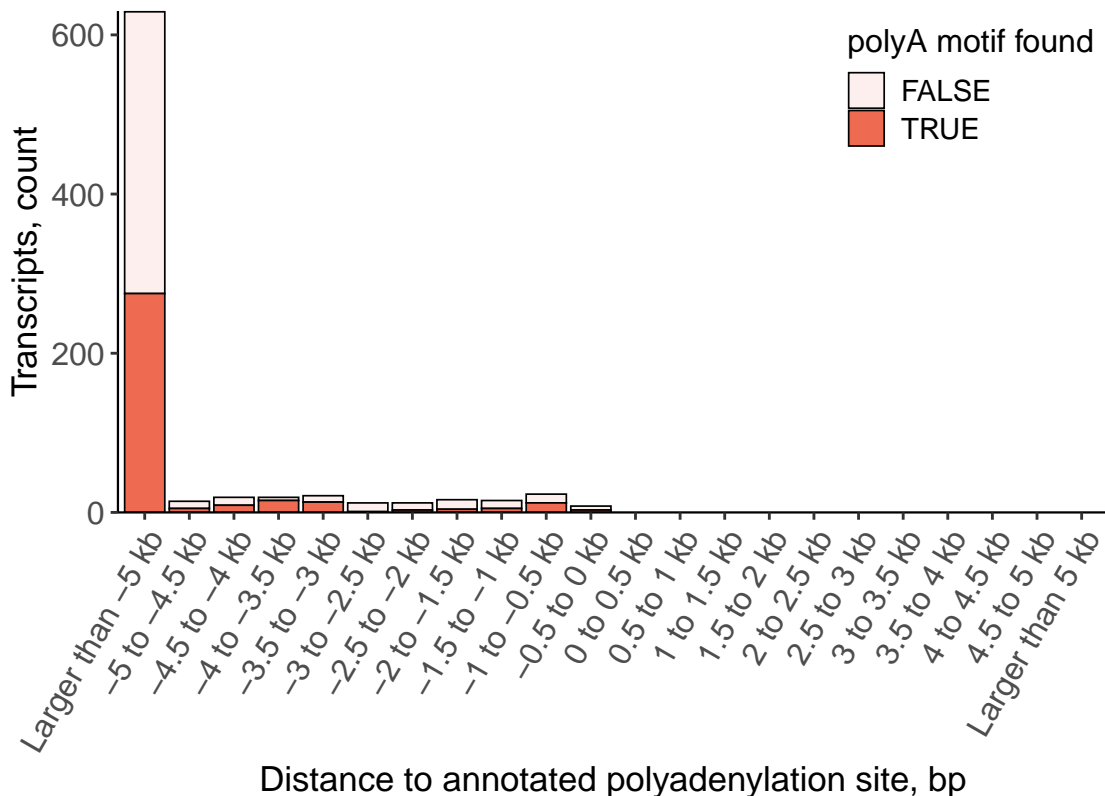
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



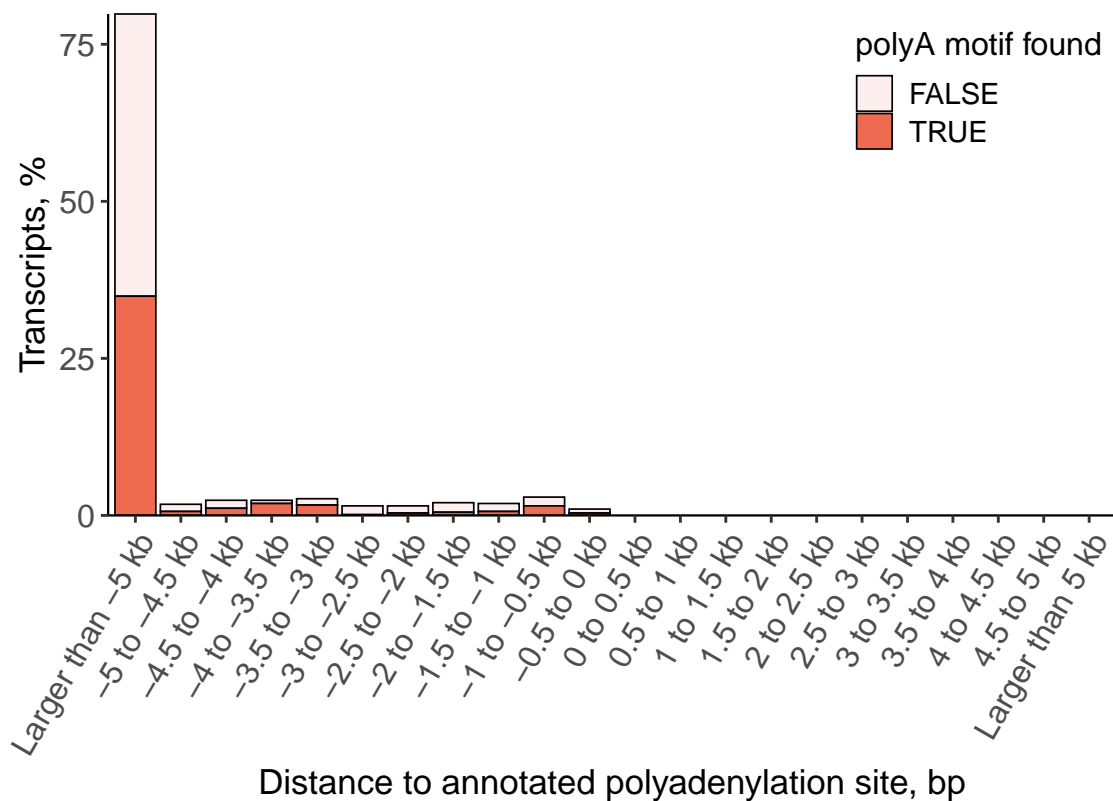
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



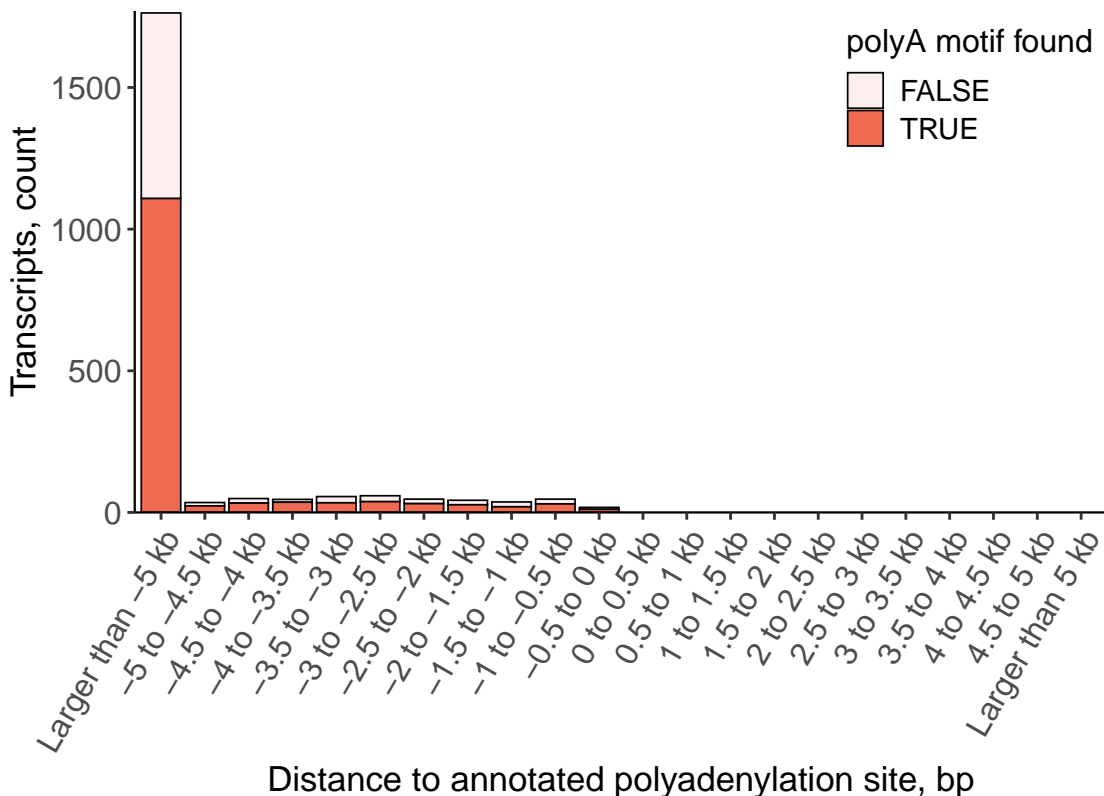
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



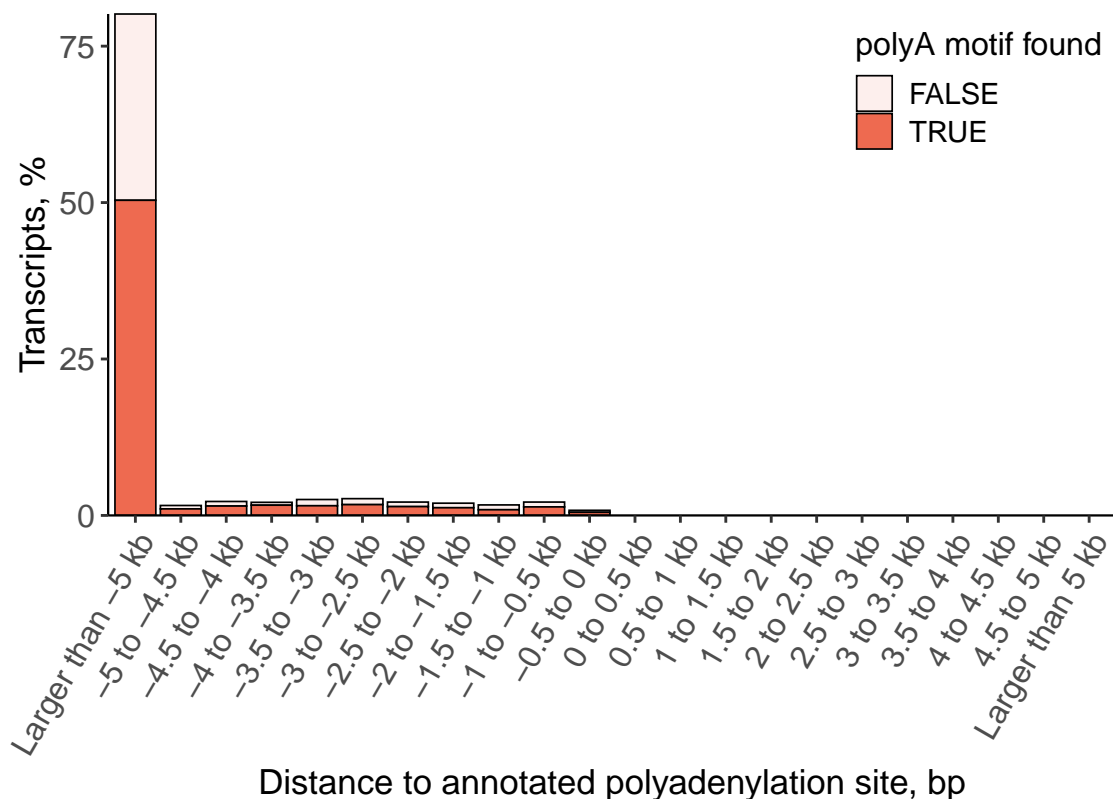
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



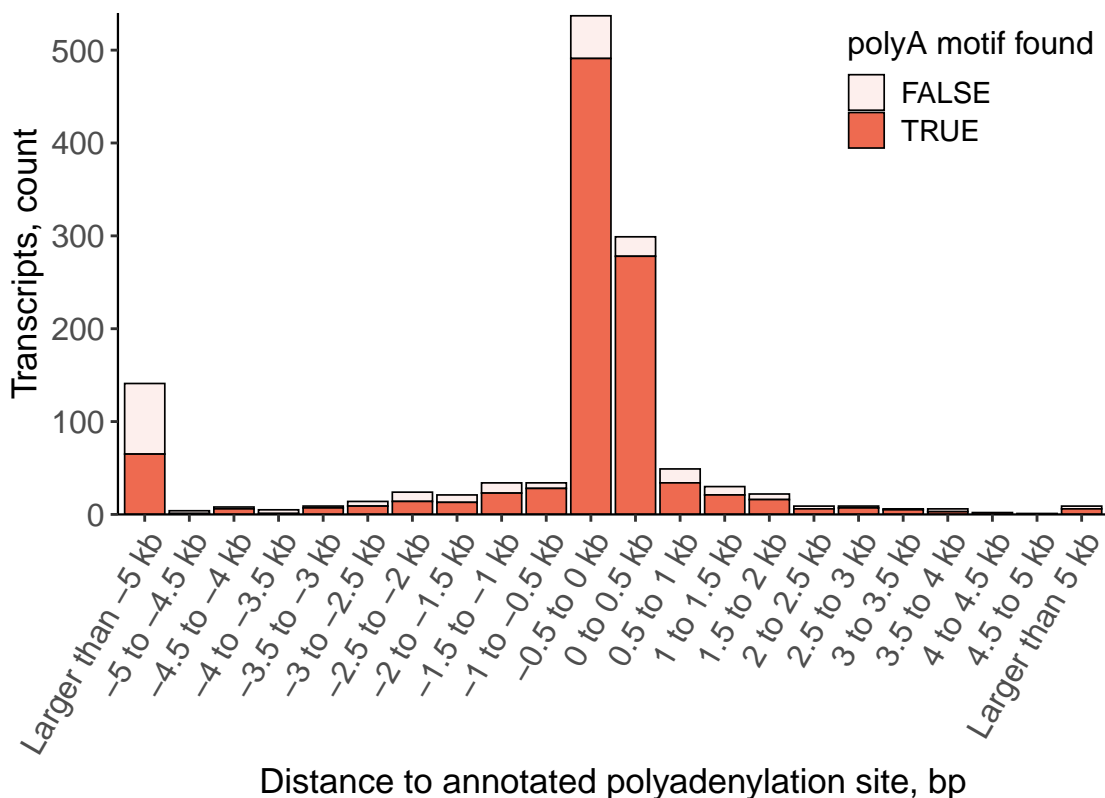
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



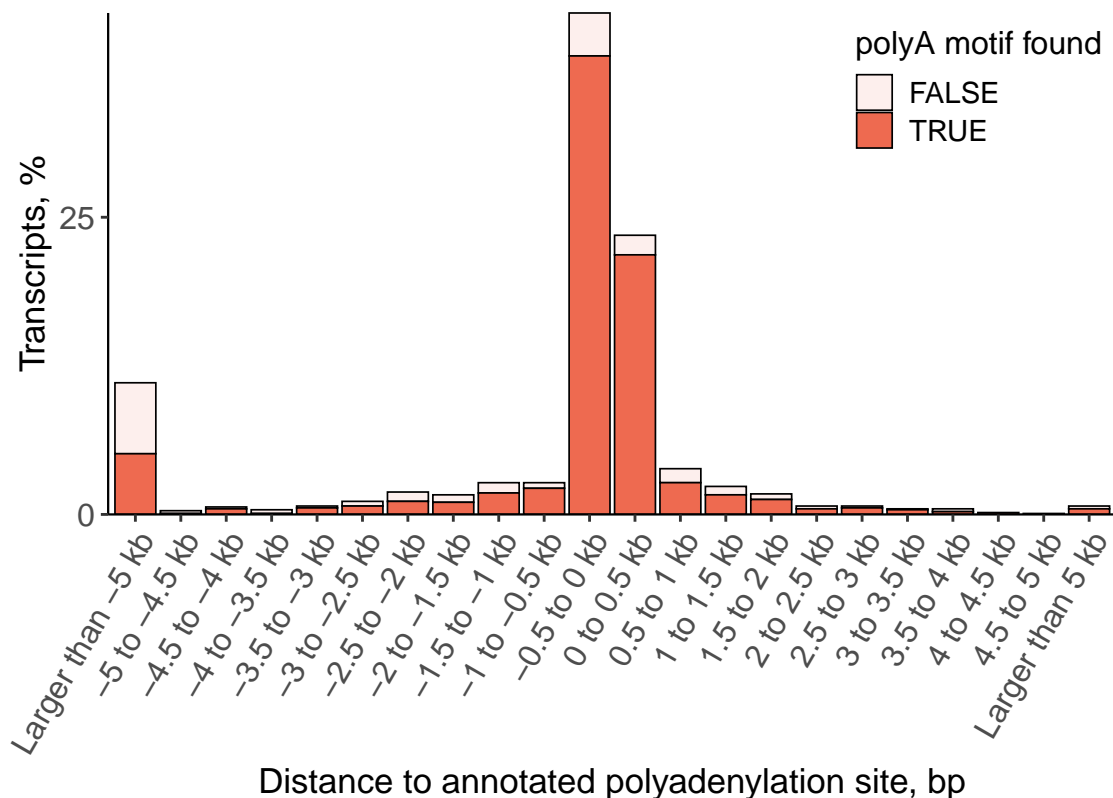
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



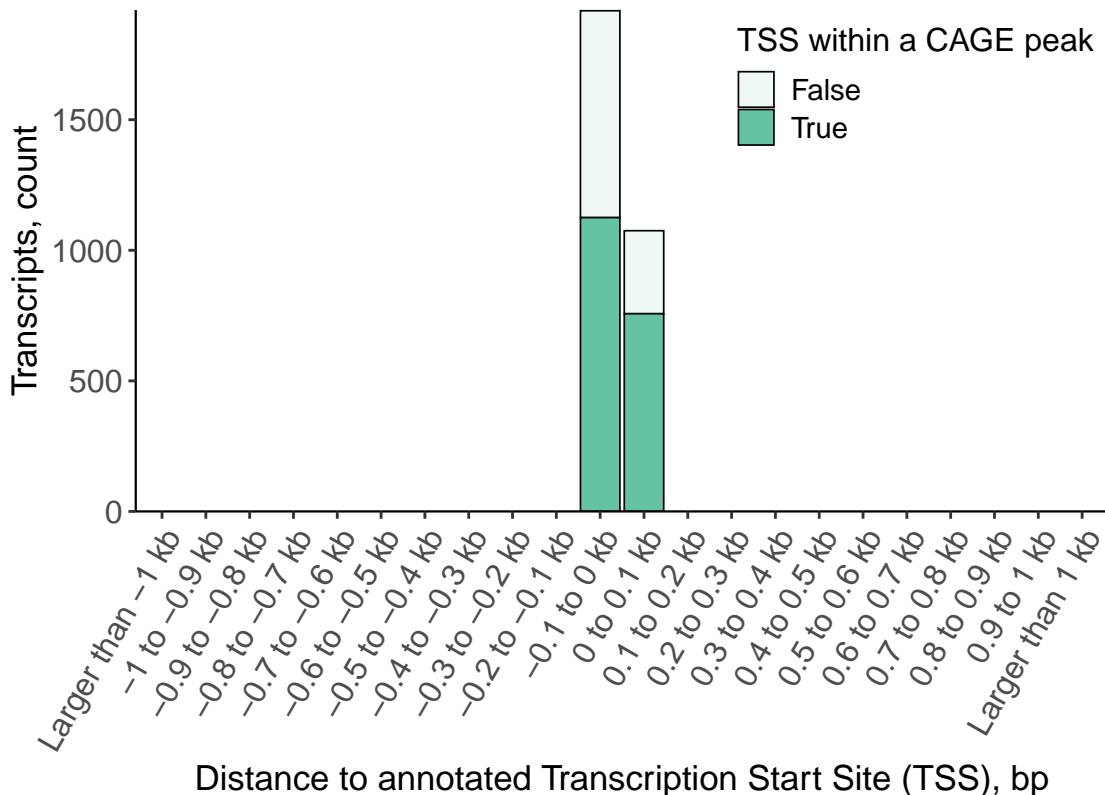
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



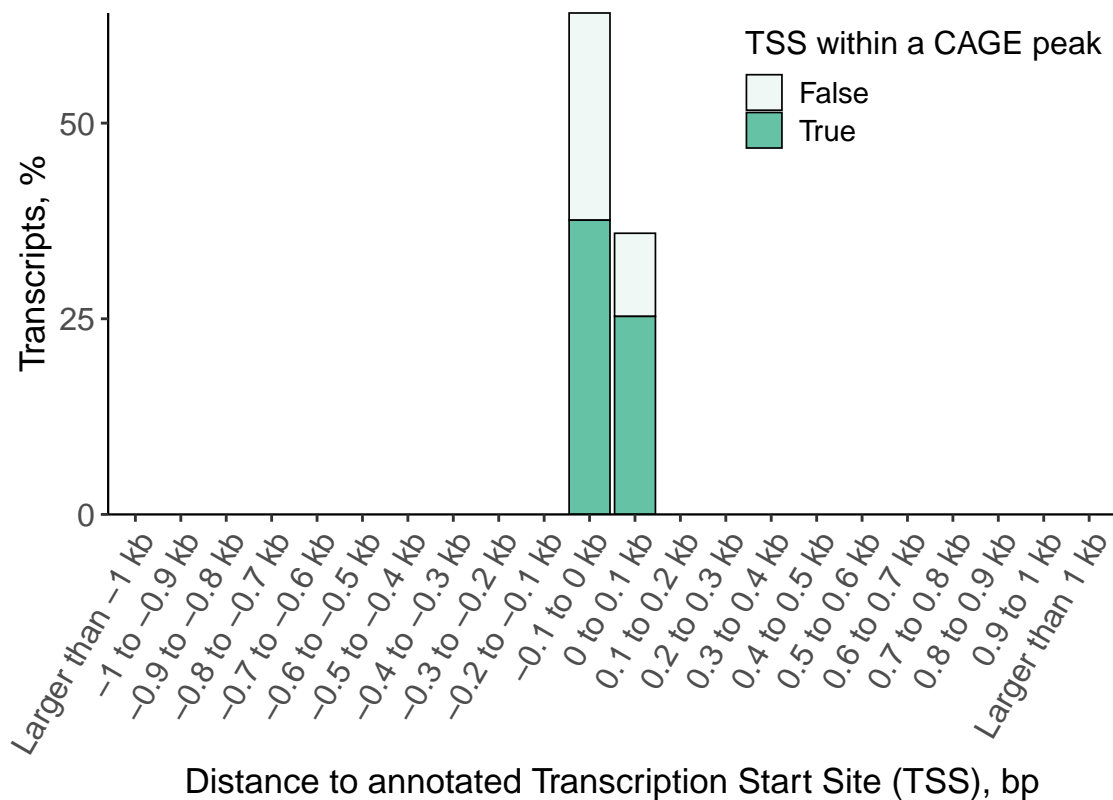
Distance to Annotated Transcription Start Site FSM Alternative 3' End

Negative values indicate downstream of annotated TSS



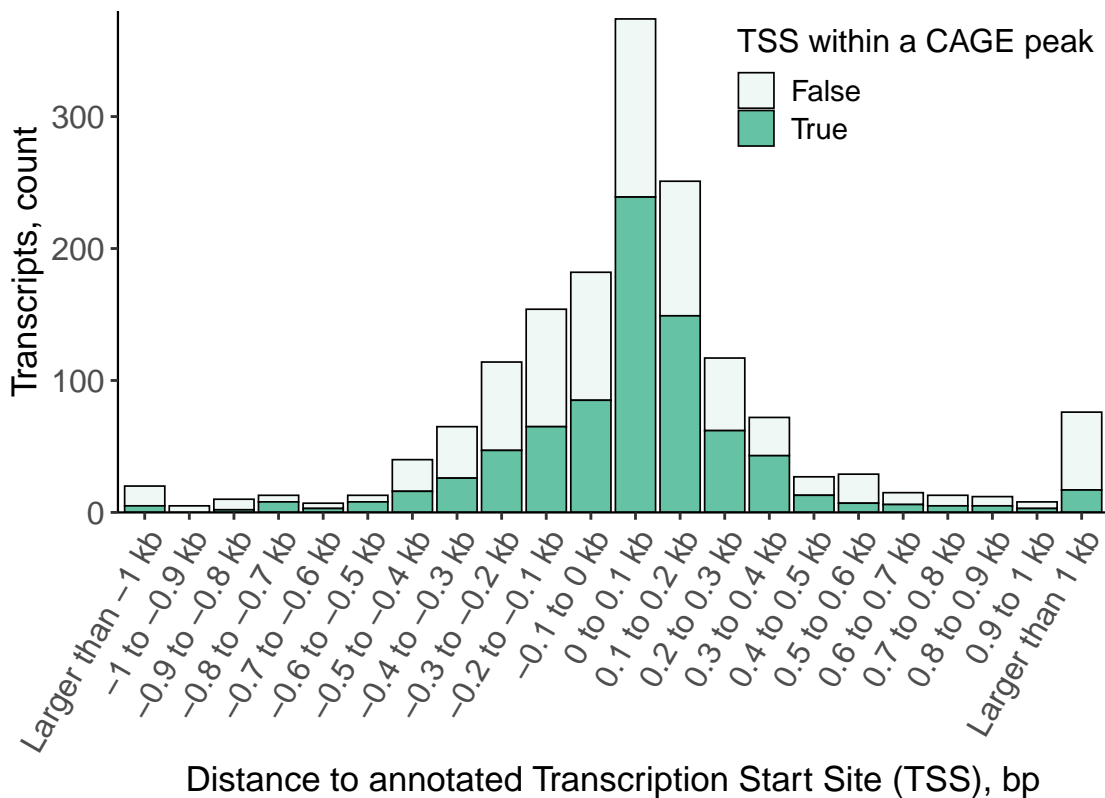
Distance to Annotated Transcription Start Site FSM Alternative 3' End

Negative values indicate downstream of annotated TSS



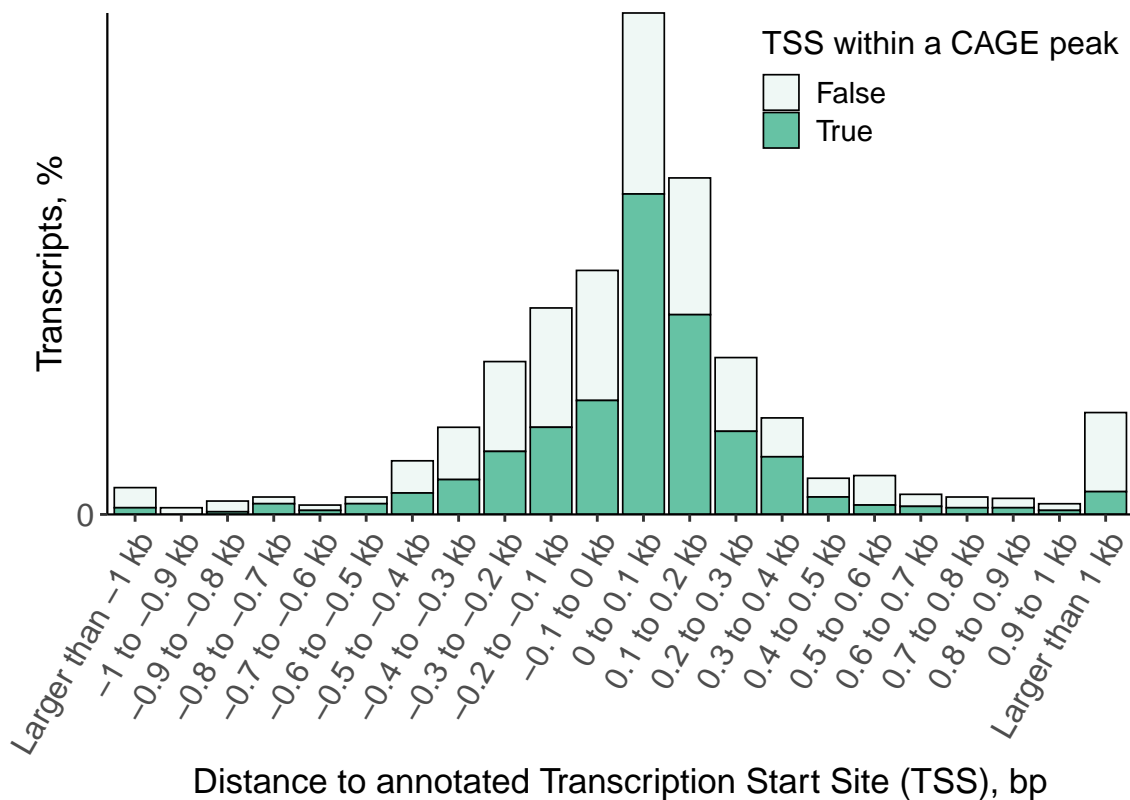
Distance to Annotated Transcription Start Site FSM Alternative 3'5' End

Negative values indicate downstream of annotated TSS



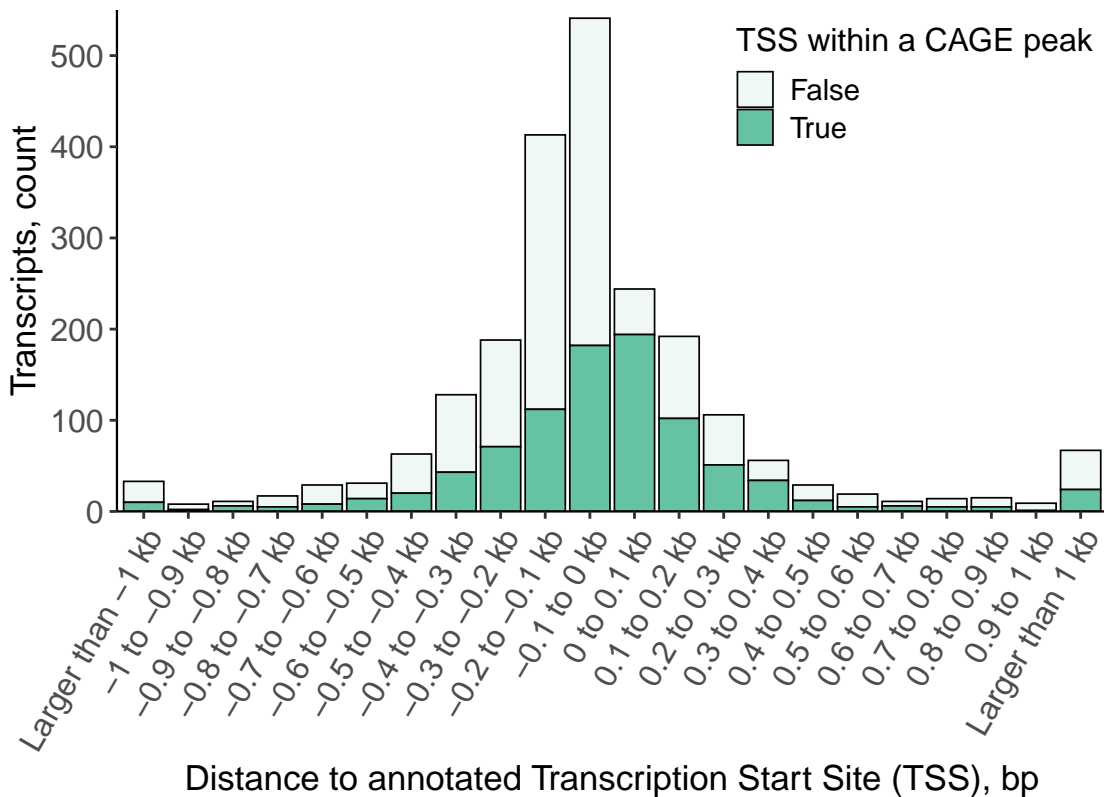
Distance to Annotated Transcription Start Site FSM Alternative 3'5' End

Negative values indicate downstream of annotated TSS



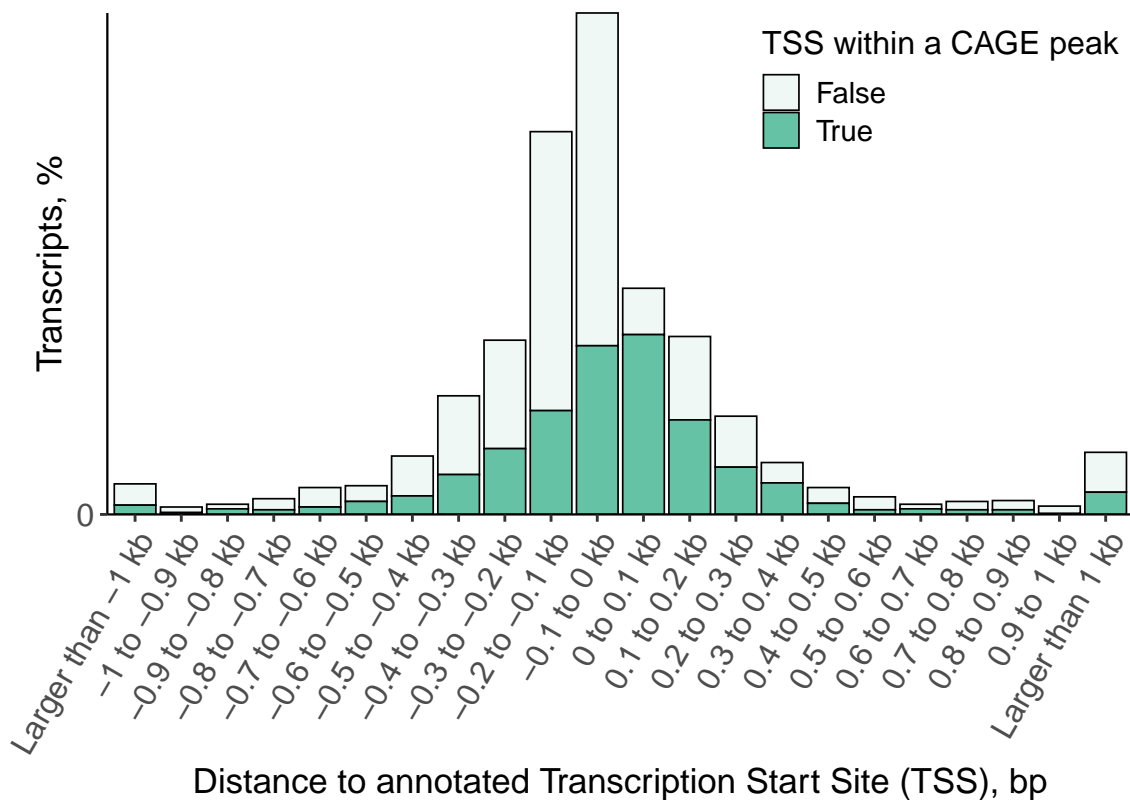
Distance to Annotated Transcription Start Site FSM Alternative 5' End

Negative values indicate downstream of annotated TSS



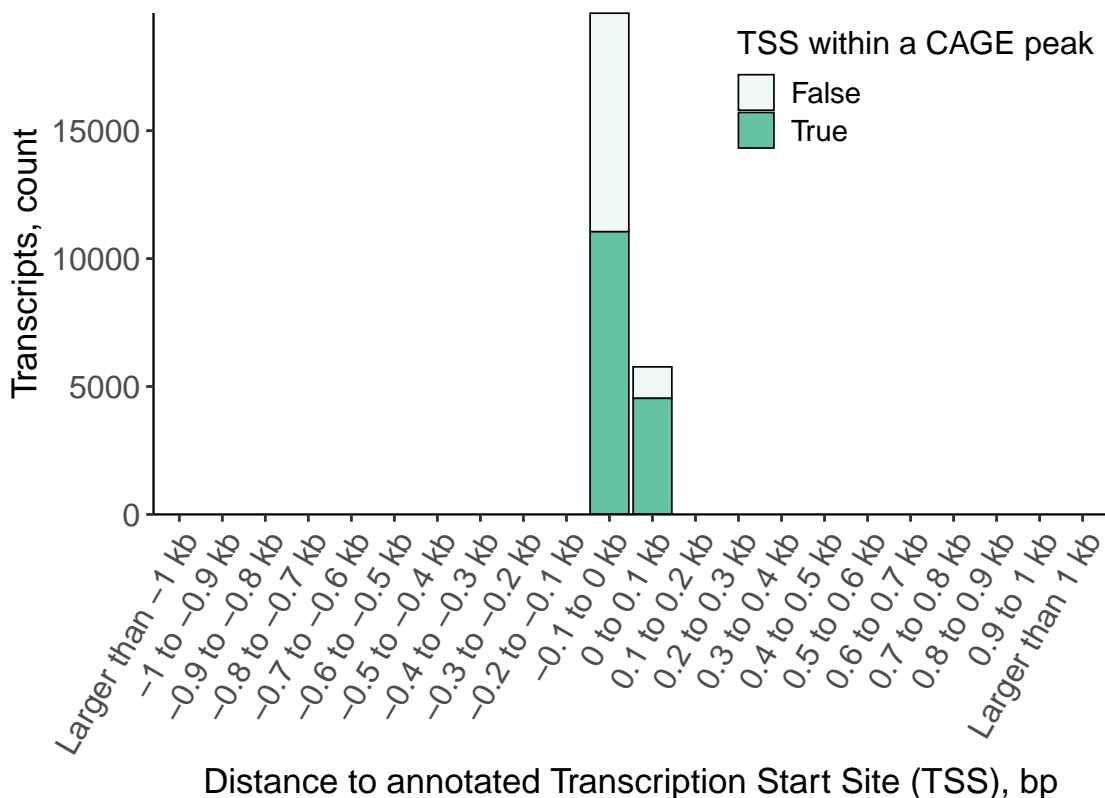
Distance to Annotated Transcription Start Site FSM Alternative 5' End

Negative values indicate downstream of annotated TSS



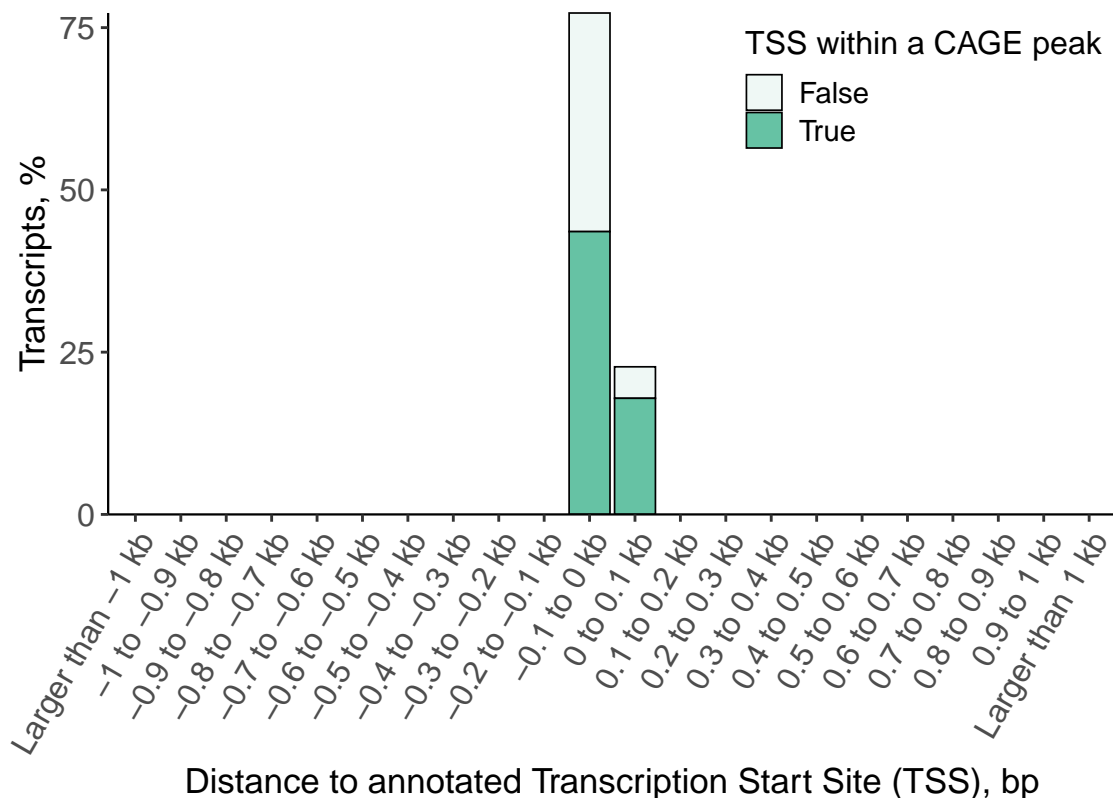
Distance to Annotated Transcription Start Site FSM Reference Match

Negative values indicate downstream of annotated TSS



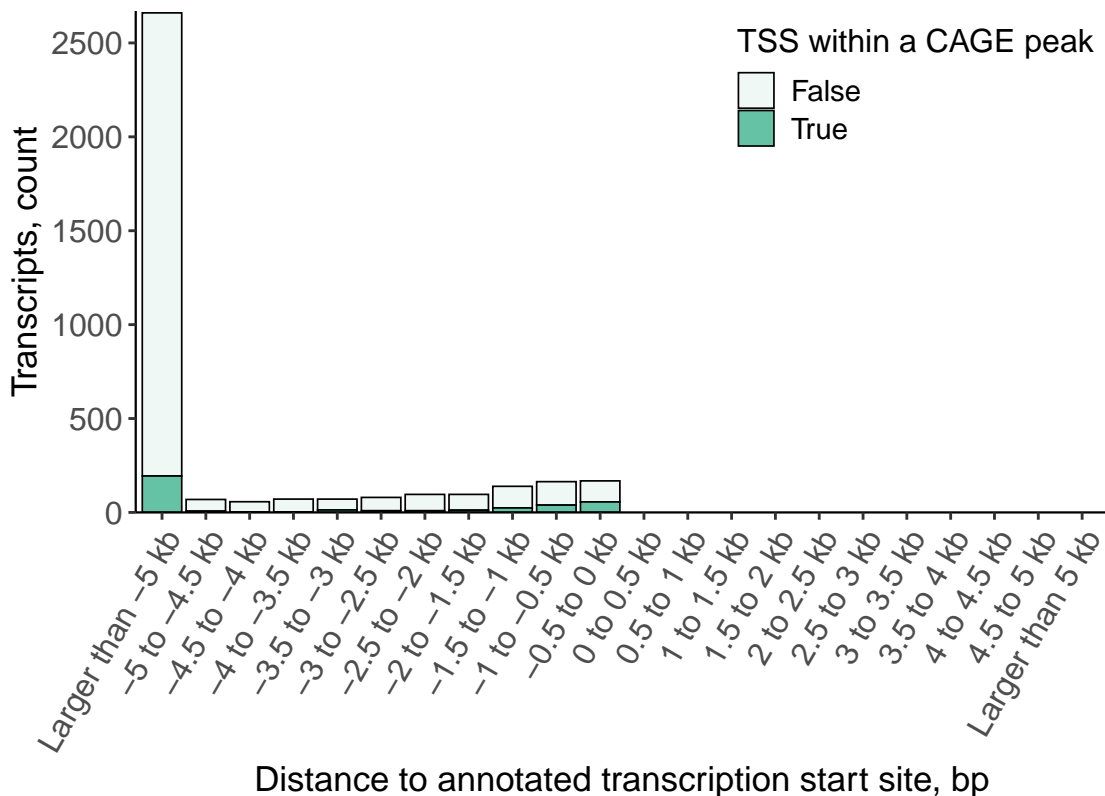
Distance to Annotated Transcription Start Site FSM Reference Match

Negative values indicate downstream of annotated TSS



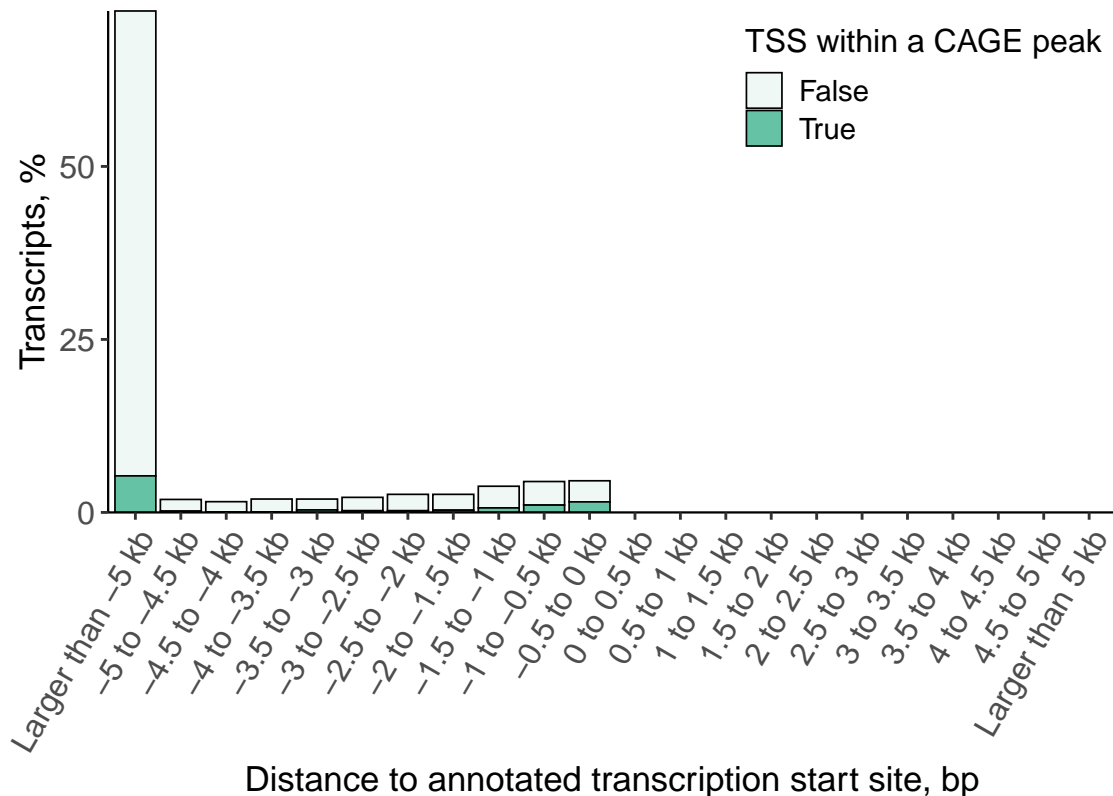
Distance to Annotated Transcription Start Site for ISM 3' Fragment

Negative values indicate downstream of annotated TSS



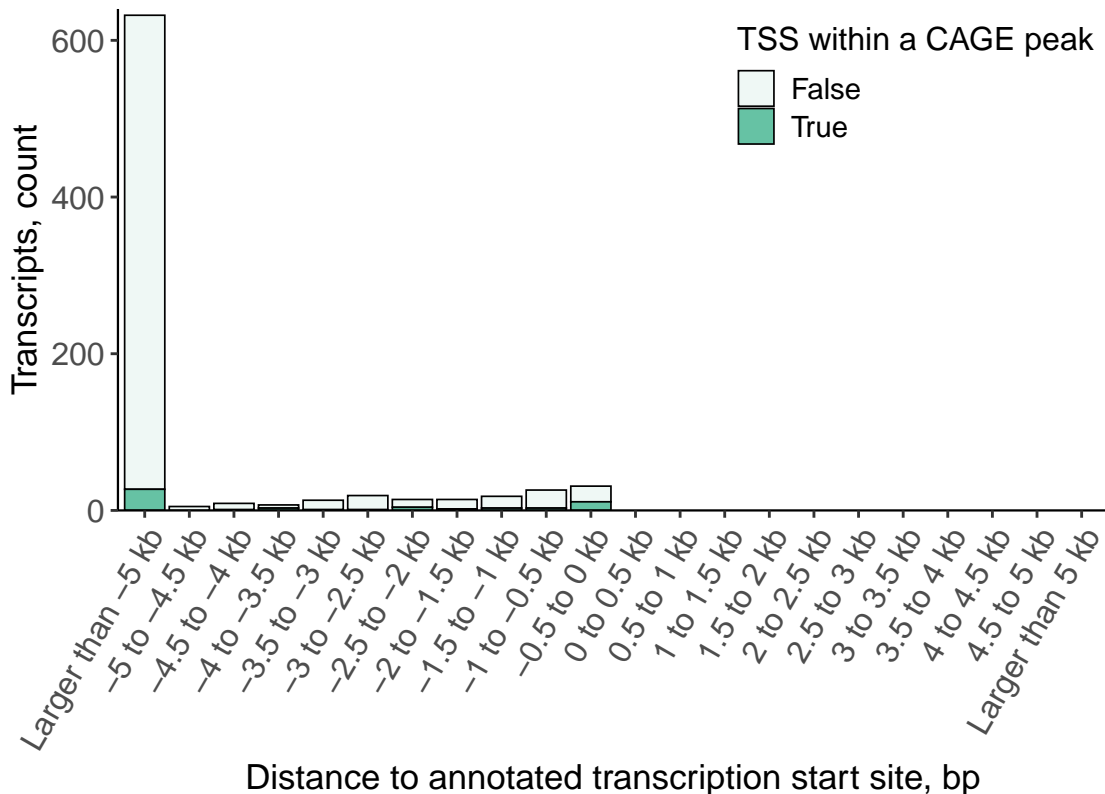
Distance to Annotated Transcription Start Site for ISM 3' Fragment

Negative values indicate downstream of annotated TSS



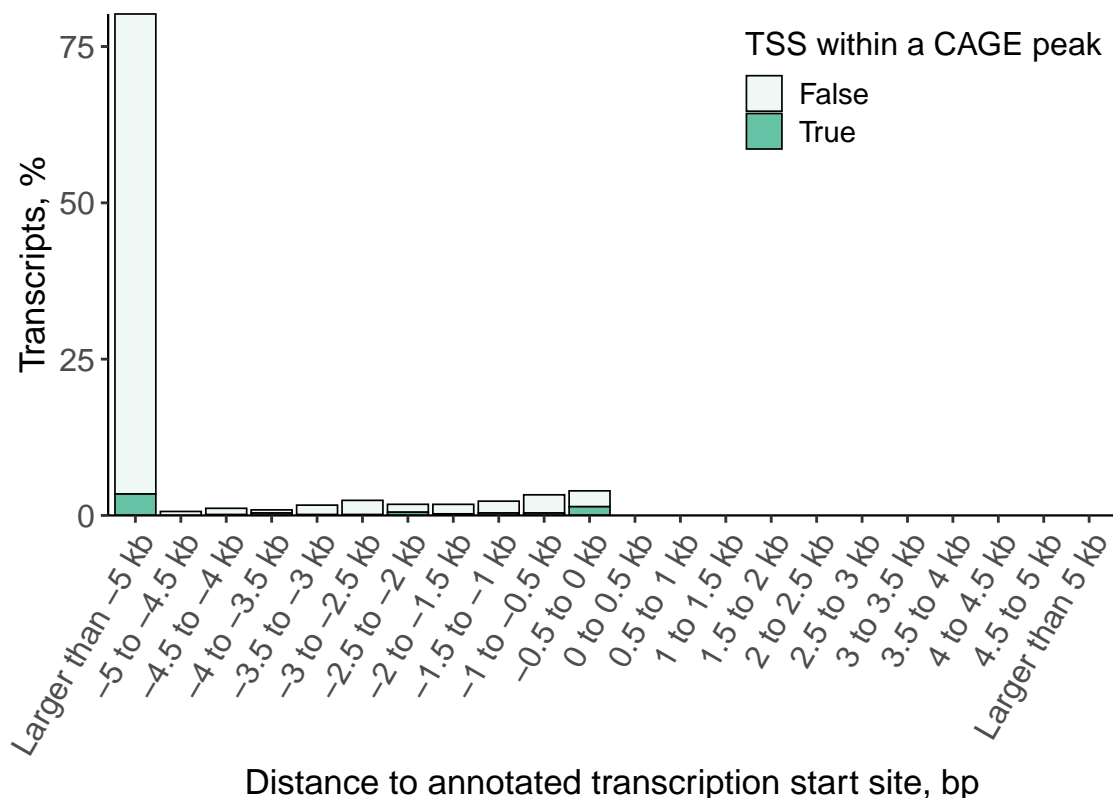
Distance to Annotated Transcription Start Site for ISM Internal Fragment

Negative values indicate downstream of annotated TSS



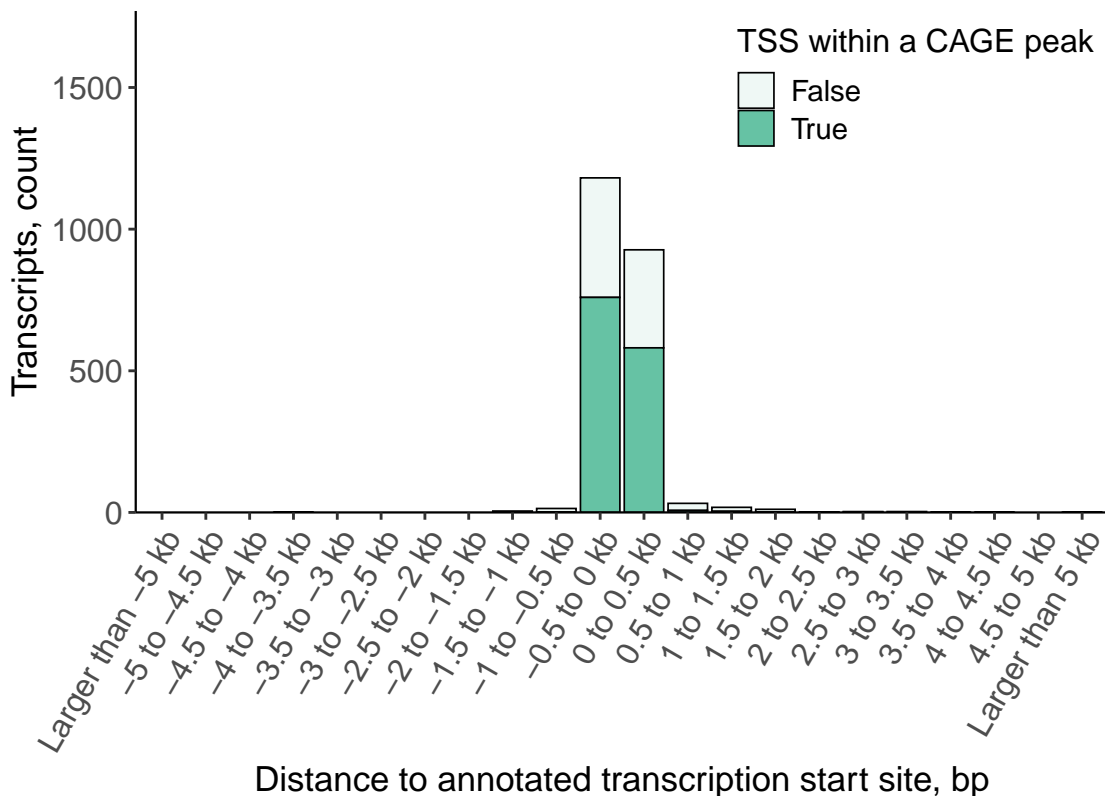
Distance to Annotated Transcription Start Site for ISM Internal Fragment

Negative values indicate downstream of annotated TSS



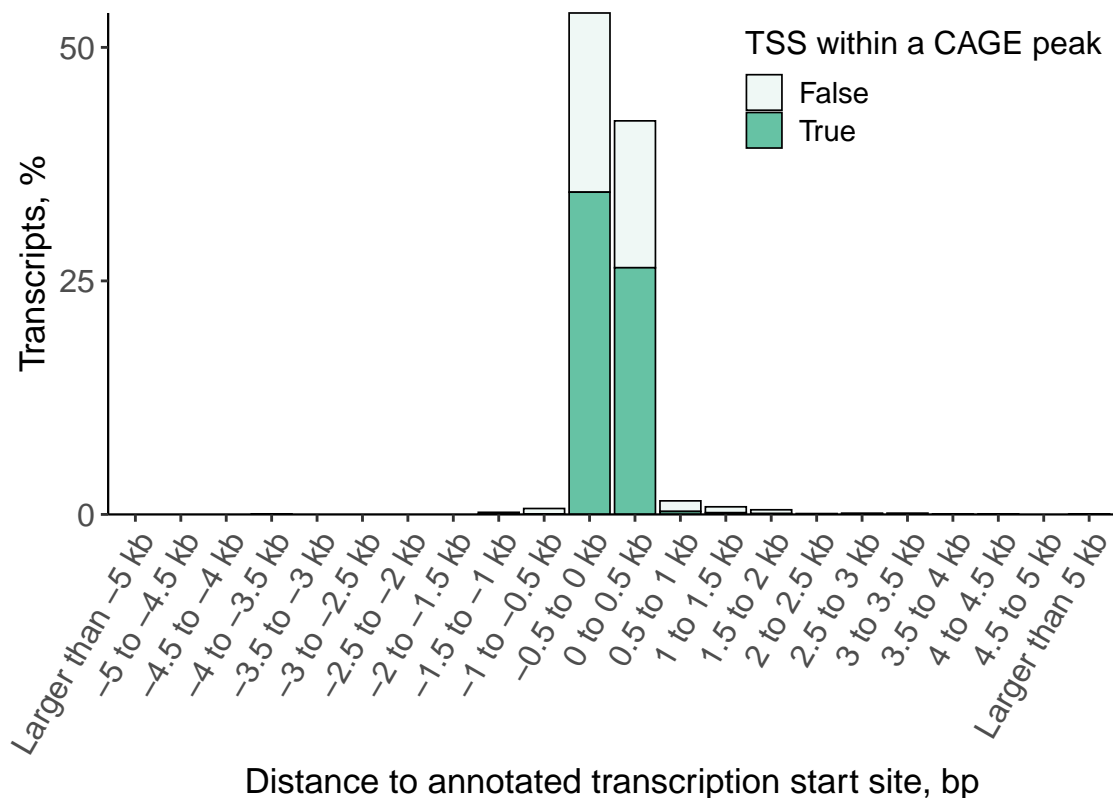
Distance to Annotated Transcription Start Site for ISM A5' Fragment

Negative values indicate downstream of annotated TSS



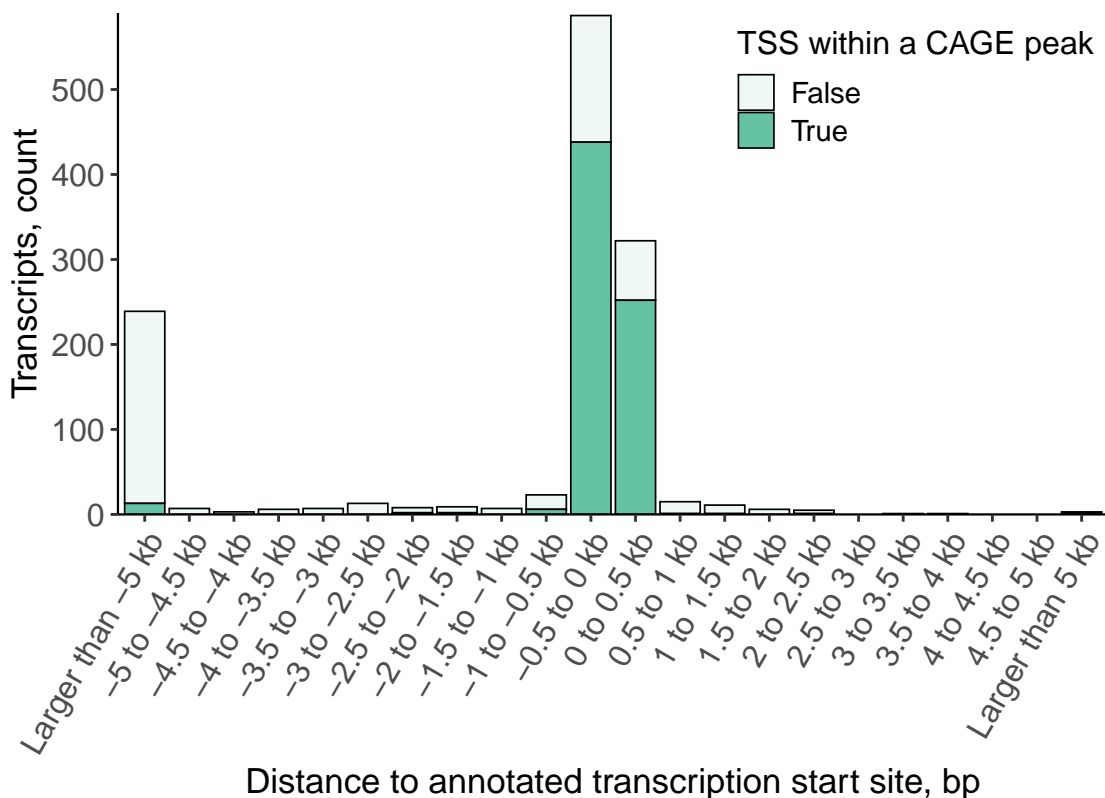
Distance to Annotated Transcription Start Site for ISM A5' Fragment

Negative values indicate downstream of annotated TSS



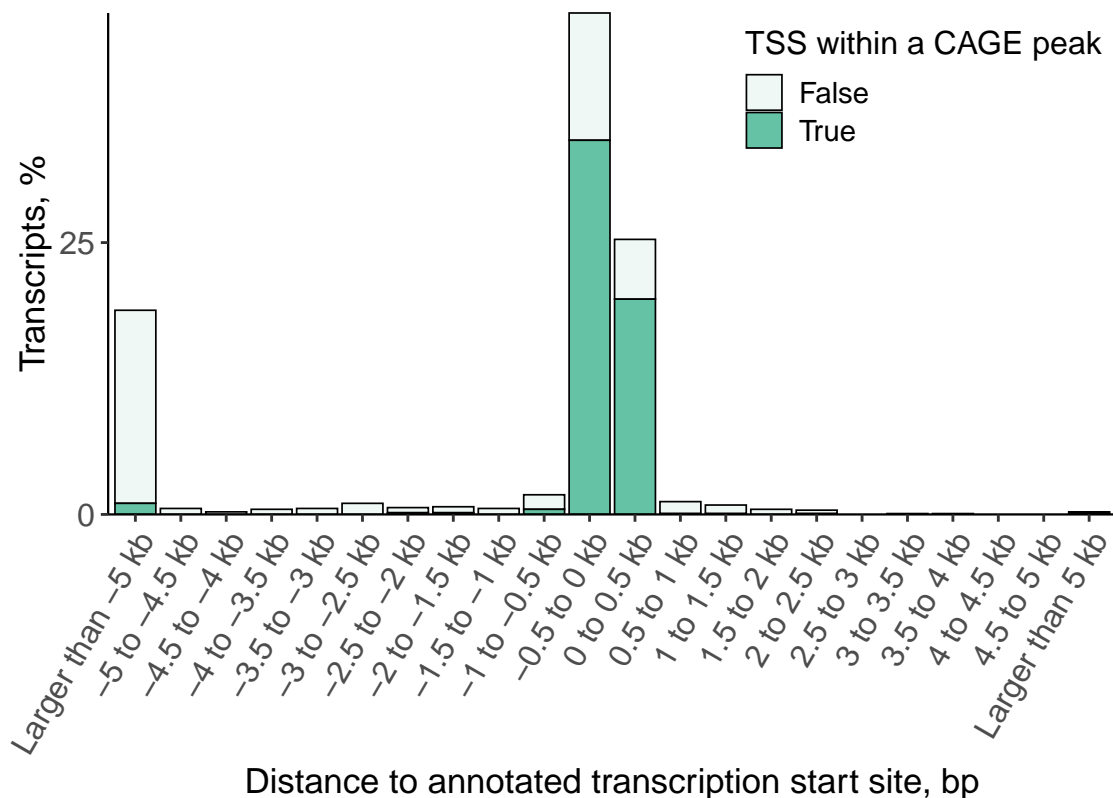
Distance to Annotated Transcription Start Site for ISM Intron Retention

Negative values indicate downstream of annotated TSS



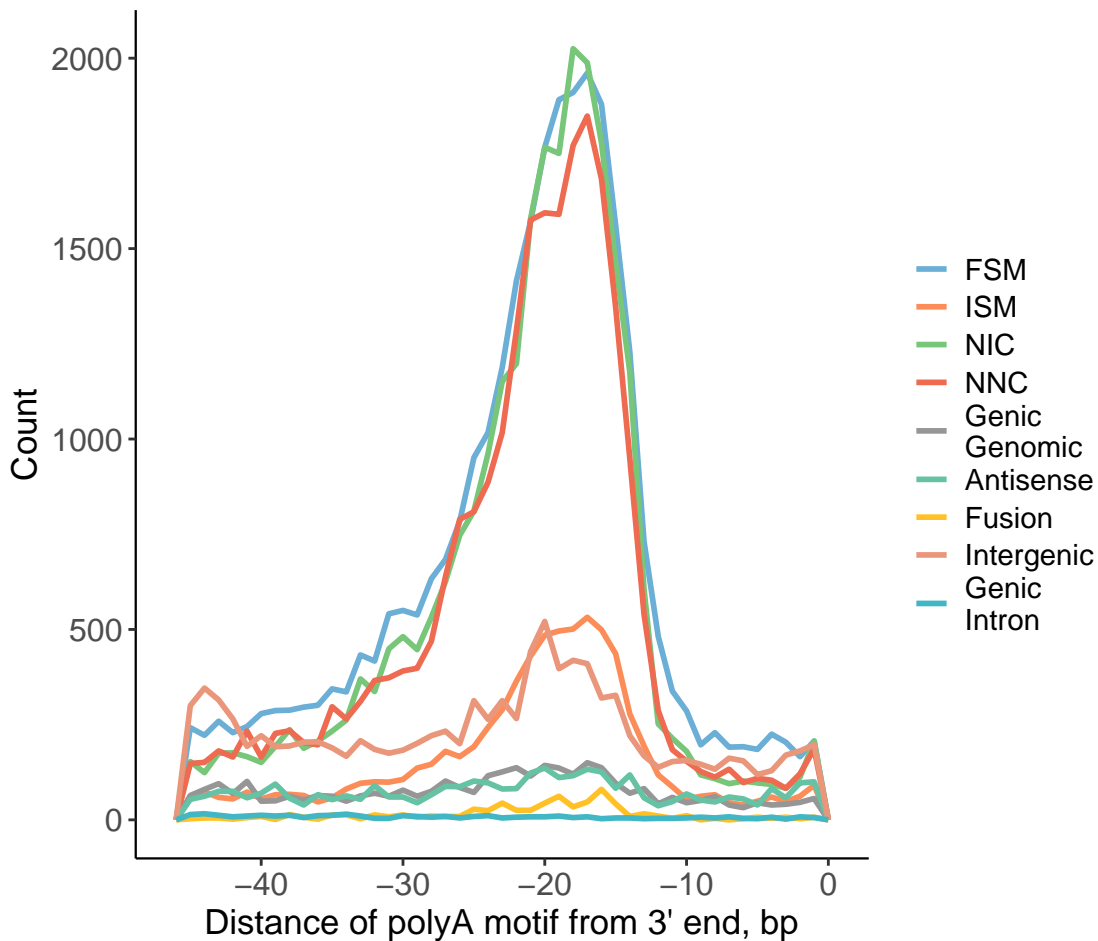
Distance to Annotated Transcription Start Site for ISM Intron Retention

Negative values indicate downstream of annotated TSS



PolyA Distance Analysis

Distance of Detected PolyA Motif From 3' end



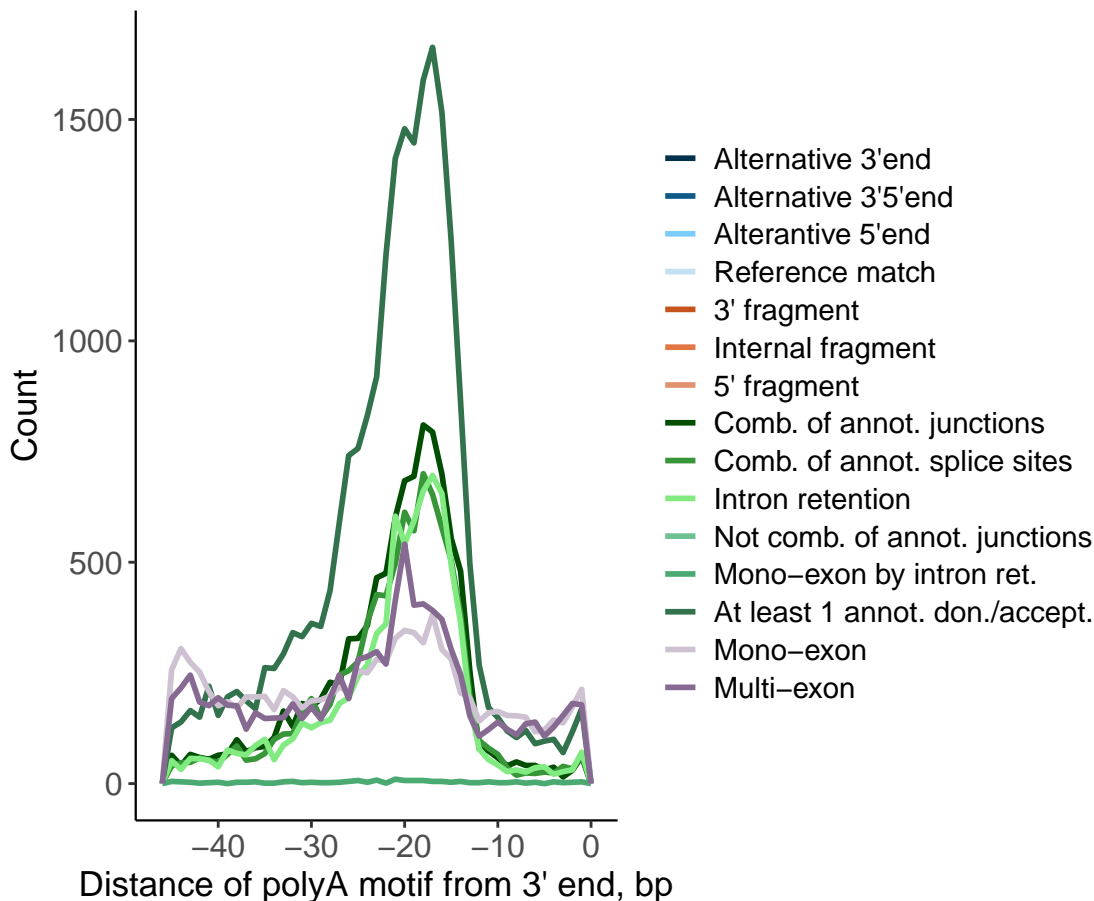
Frequency of PolyA Motifs

Number of polyA Motifs Detected

Category	Count	polyA Detected	%
FSM	41311	29878	72
ISM	10079	7504	74
NIC	30369	26166	86
NNC	29119	24793	85
Genic Genomic	5913	3450	58
Antisense	9243	3425	37
Fusion	891	692	78
Intergenic	21252	10617	50
Genic Intron	1257	348	28

Motif	Count	%
AATAAA	63648	59.6
ATTAAA	15280	14.3
AAAAAG	5489	5.1
TATAAA	3372	3.2
AGTAAA	3138	2.9
AAGAAA	2828	2.6
TTTAAA	2093	2.0
CATAAA	1886	1.8
AATACA	1636	1.5
AAAACA	1627	1.5
AATATA	1417	1.3
GATAAA	1378	1.3
AATGAA	1031	1.0
AATAGA	781	0.7
ACTAAA	757	0.7
GGGGCT	512	0.5

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	2992	2429	81
Alternative 3'5'end	1617	1368	85
Alterantive 5'end	2224	1963	88
Reference match	25361	19881	78
3' fragment	3671	3221	88
Internal fragment	788	345	44
5' fragment	2200	1391	63
Comb. of annot. junctions	11290	10224	91
Comb. of annot. splice sites	9781	8846	90
Intron retention	10958	9354	85
Mono-exon by intron ret.	346	157	45
At least 1 annot. don./accept.	26500	22650	85
Mono-exon	32456	15494	48
Multi-exon	19250	9550	50

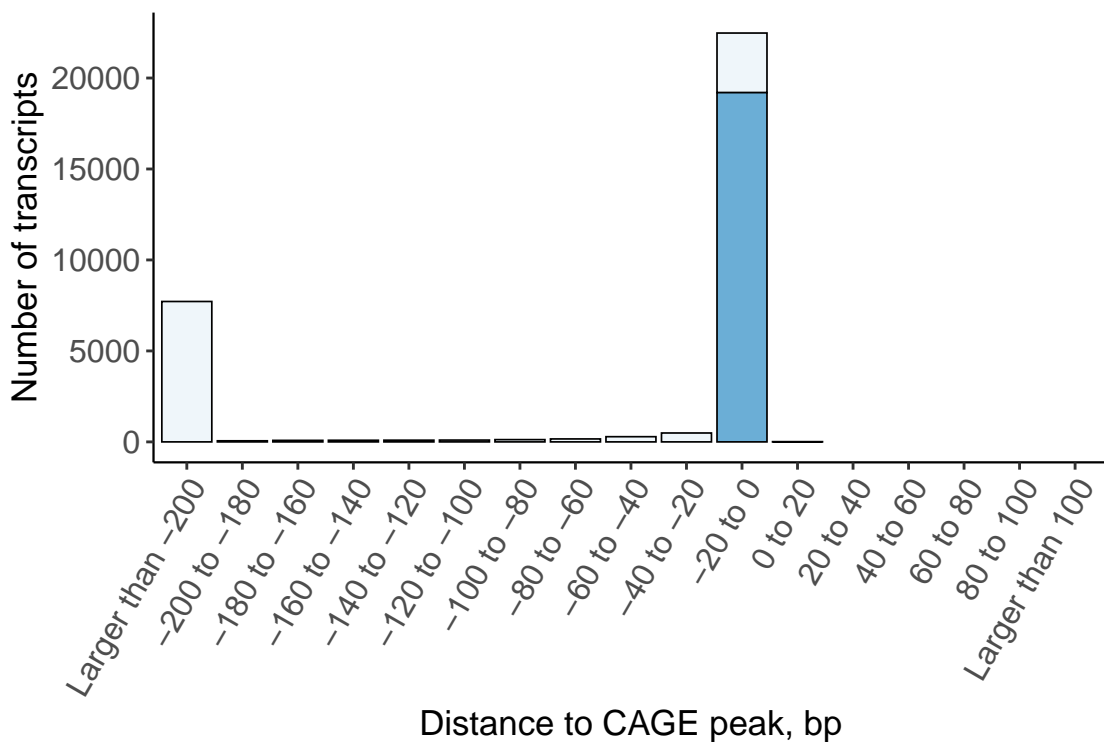
Frequency of PolyA Motifs

Motif	Count	%
AATAAA	63648	59.6
ATTAAA	15280	14.3
AAAAAG	5489	5.1
TATAAA	3372	3.2
AGTAAA	3138	2.9
AAGAAA	2828	2.6
TTTAAA	2093	2.0
CATAAA	1886	1.8
AATACA	1636	1.5
AAAACA	1627	1.5
AATATA	1417	1.3
GATAAA	1378	1.3
AATGAA	1031	1.0
AATAGA	781	0.7
ACTAAA	757	0.7
GGGGCT	512	0.5

CAGE Distances Analysis

Distance to CAGE Peak of Multi-Exonic FSM

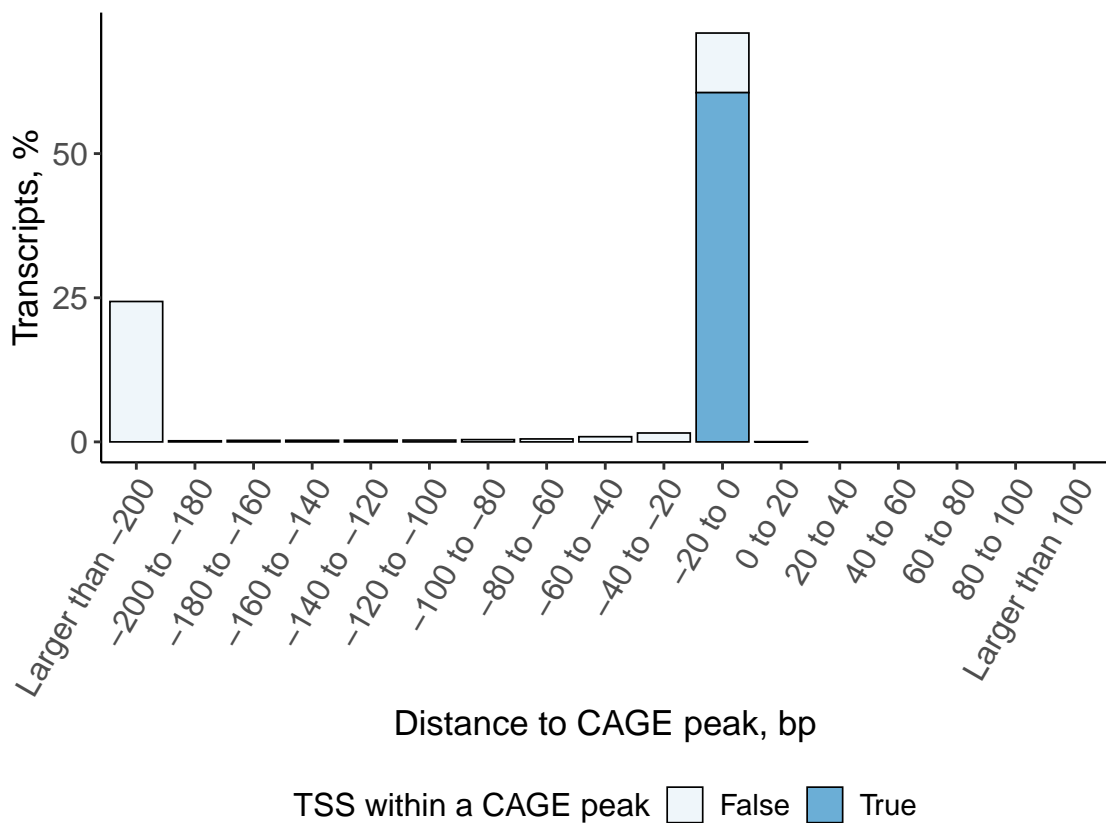
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

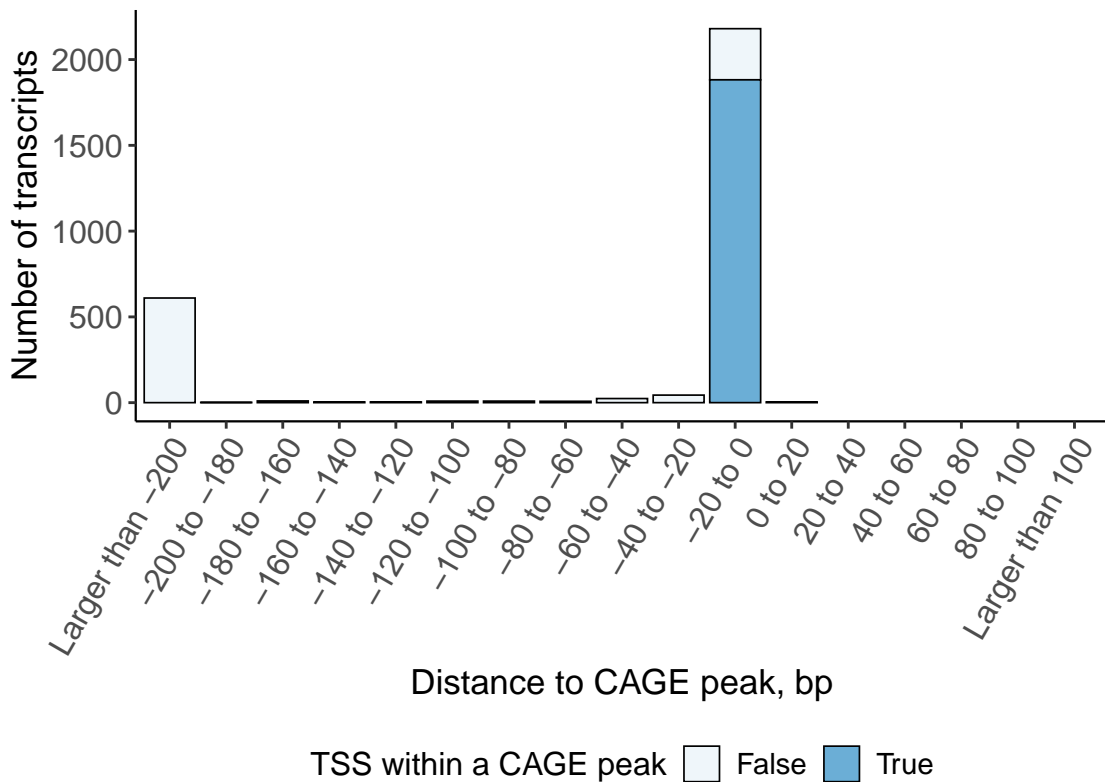
Distance to CAGE Peak of Multi-Exonic FSM

Negative values indicate downstream of annotated CAGE peak



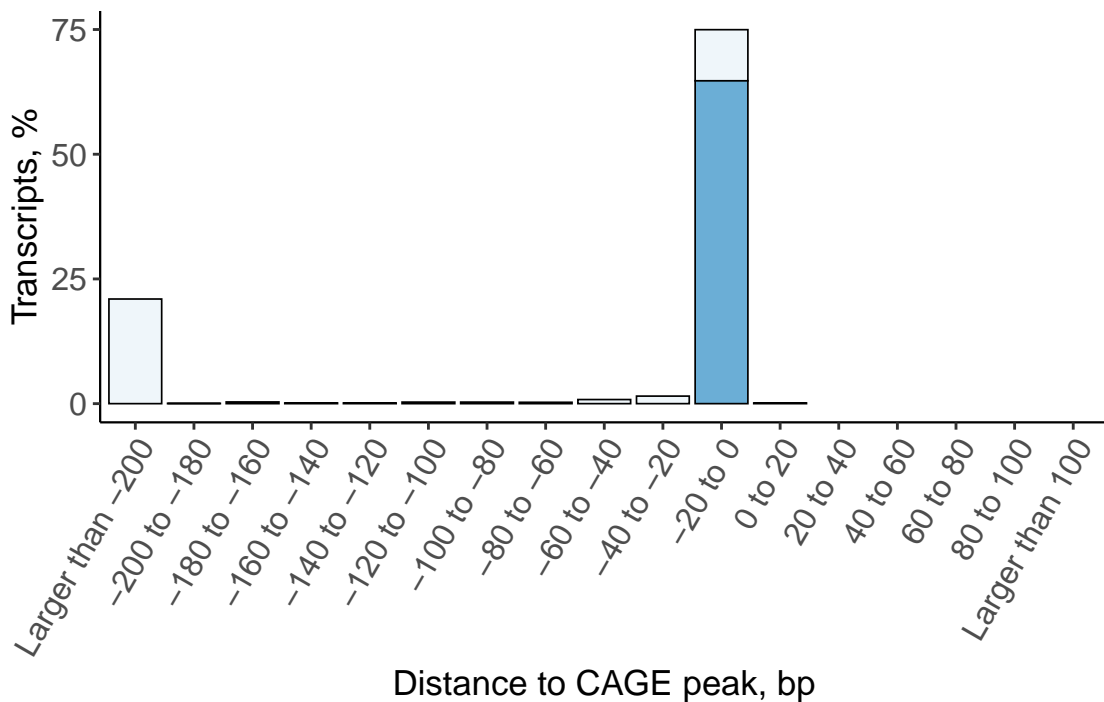
Distance to CAGE Peak of Multi-Exonic FSM Alternative 3' End

Negative values indicate downstream of annotated CAGE peak



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

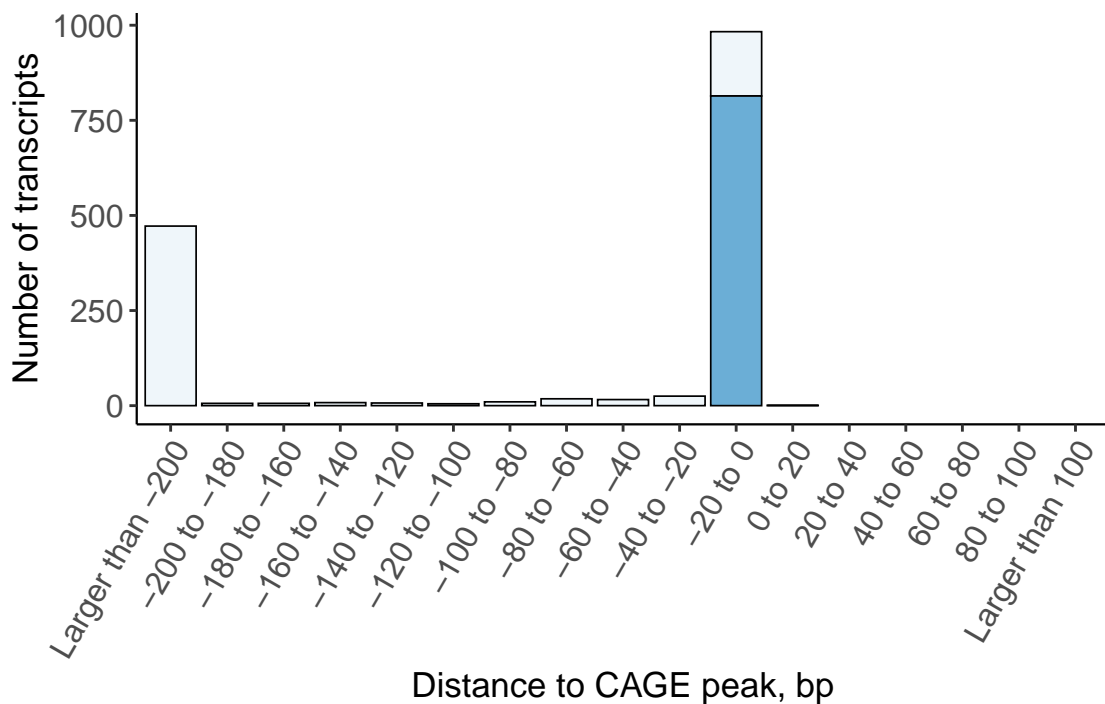
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

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

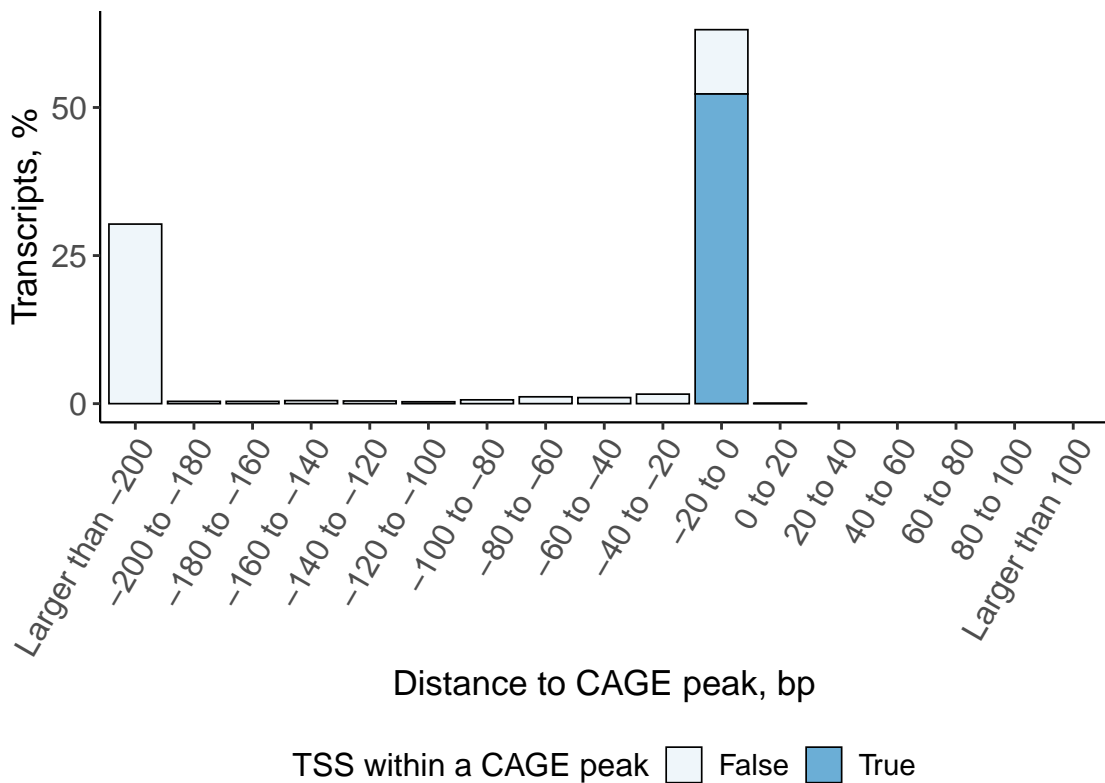
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

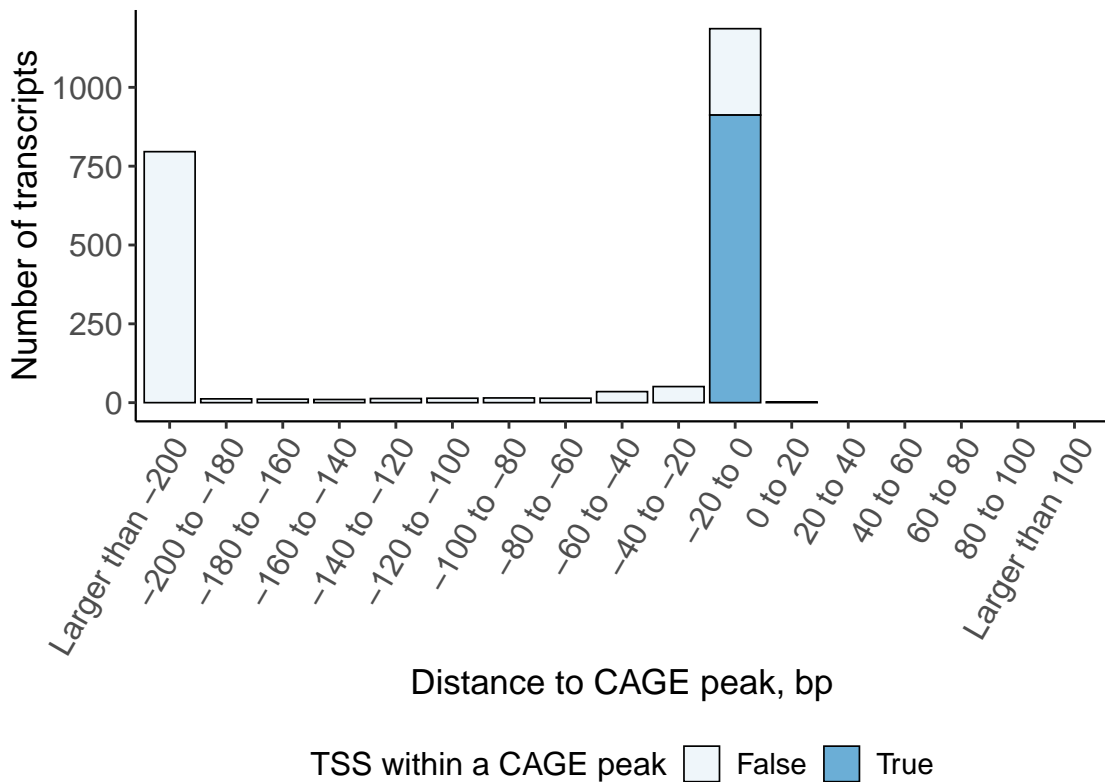
Distance to CAGE Peak of Multi-Exonic FSM Alternative 3'5' End

Negative values indicate downstream of annotated CAGE peak



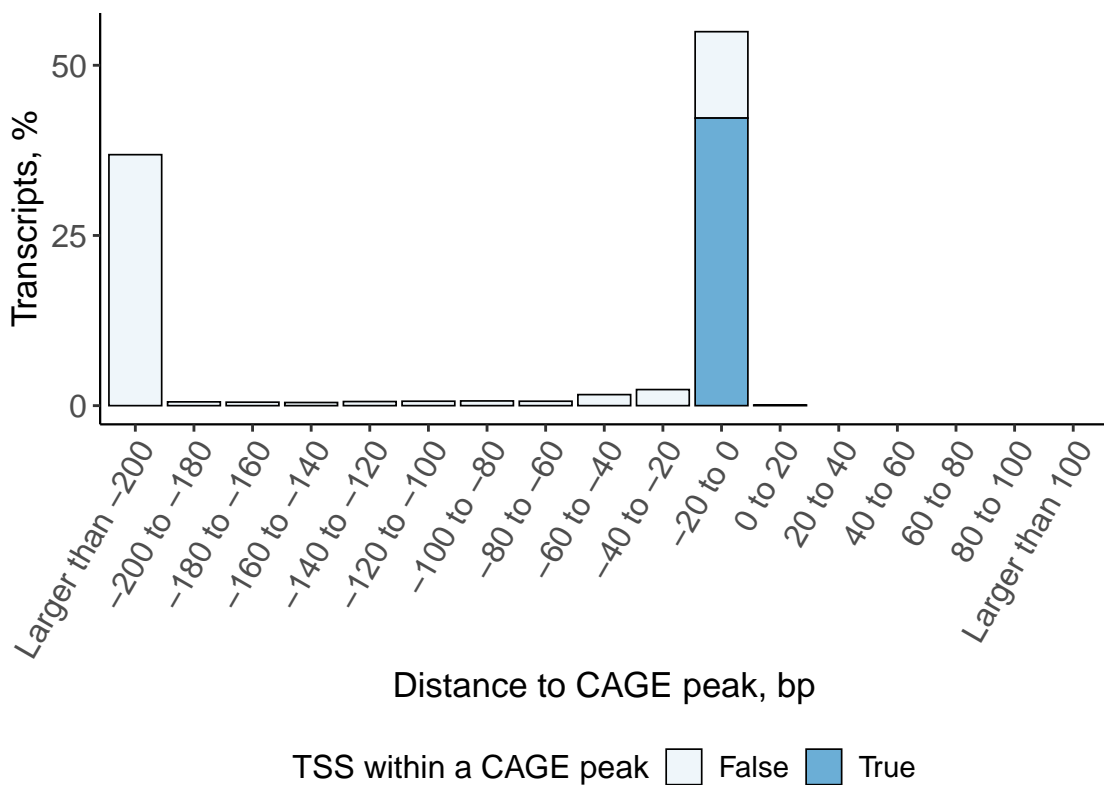
Distance to CAGE Peak of Multi-Exonic FSM Alternative 5' End

Negative values indicate downstream of annotated CAGE peak



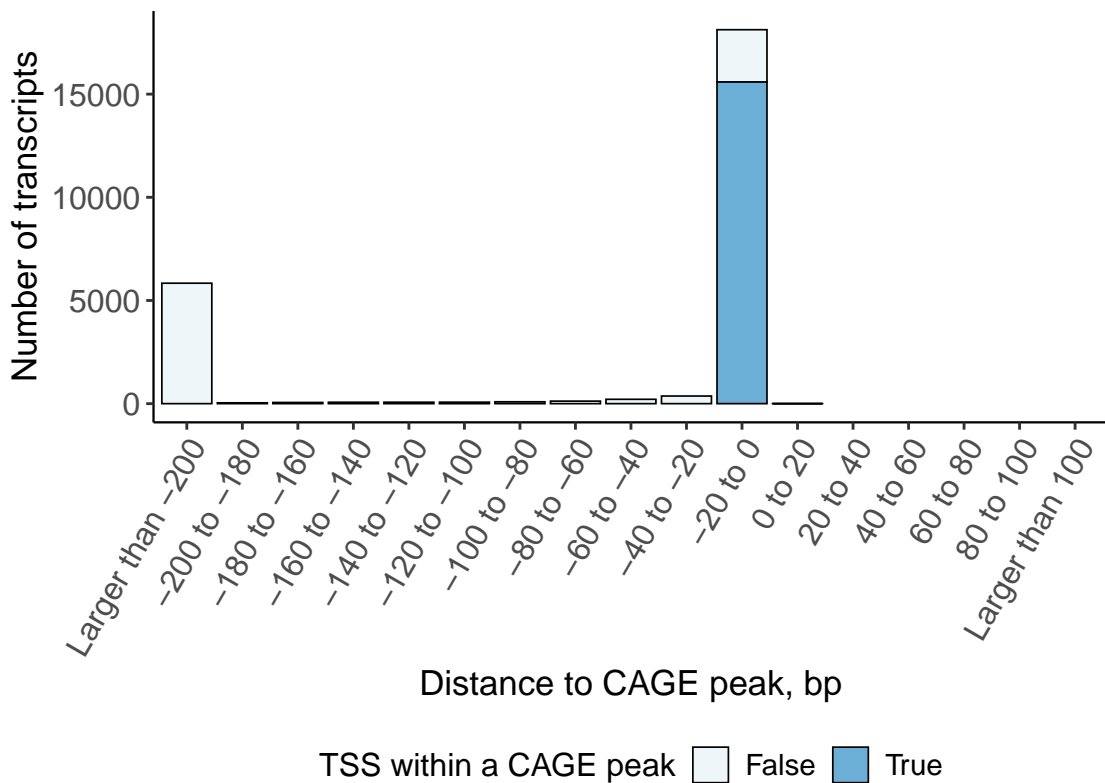
Distance to CAGE Peak of Multi-Exonic FSM Alternative 5' End

Negative values indicate downstream of annotated CAGE peak



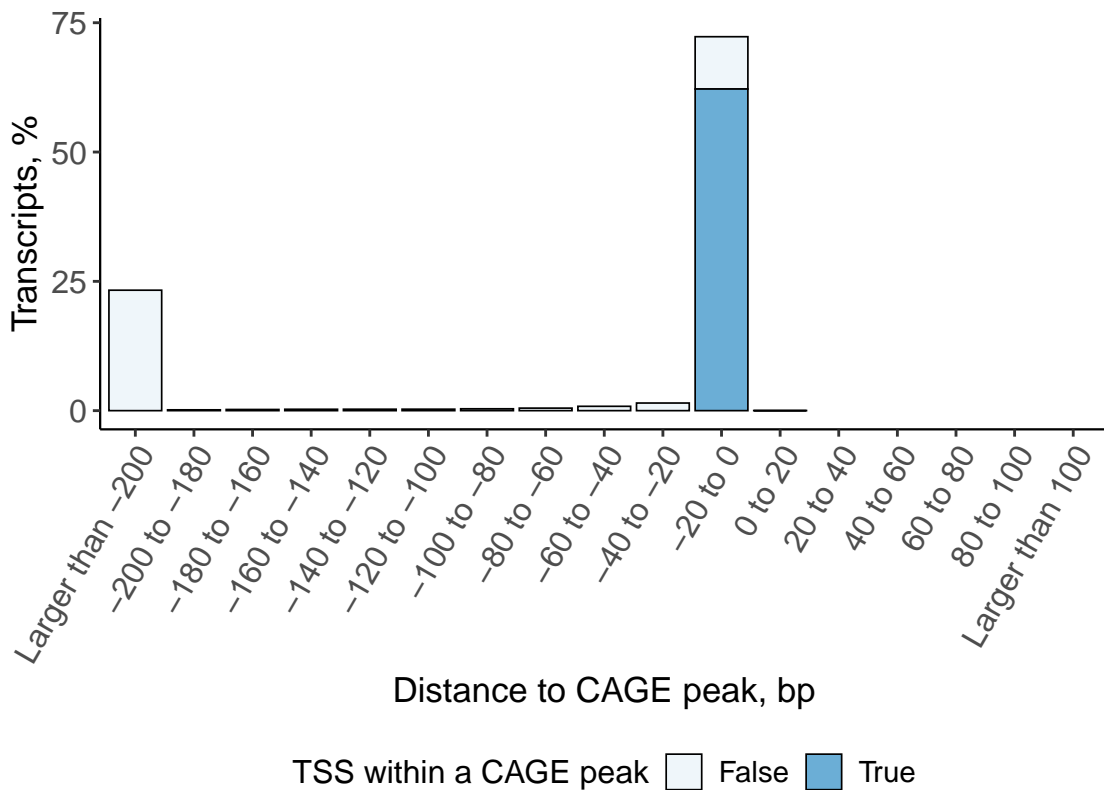
Distance to CAGE Peak of Multi-Exonic FSM Reference Match

Negative values indicate downstream of annotated CAGE peak



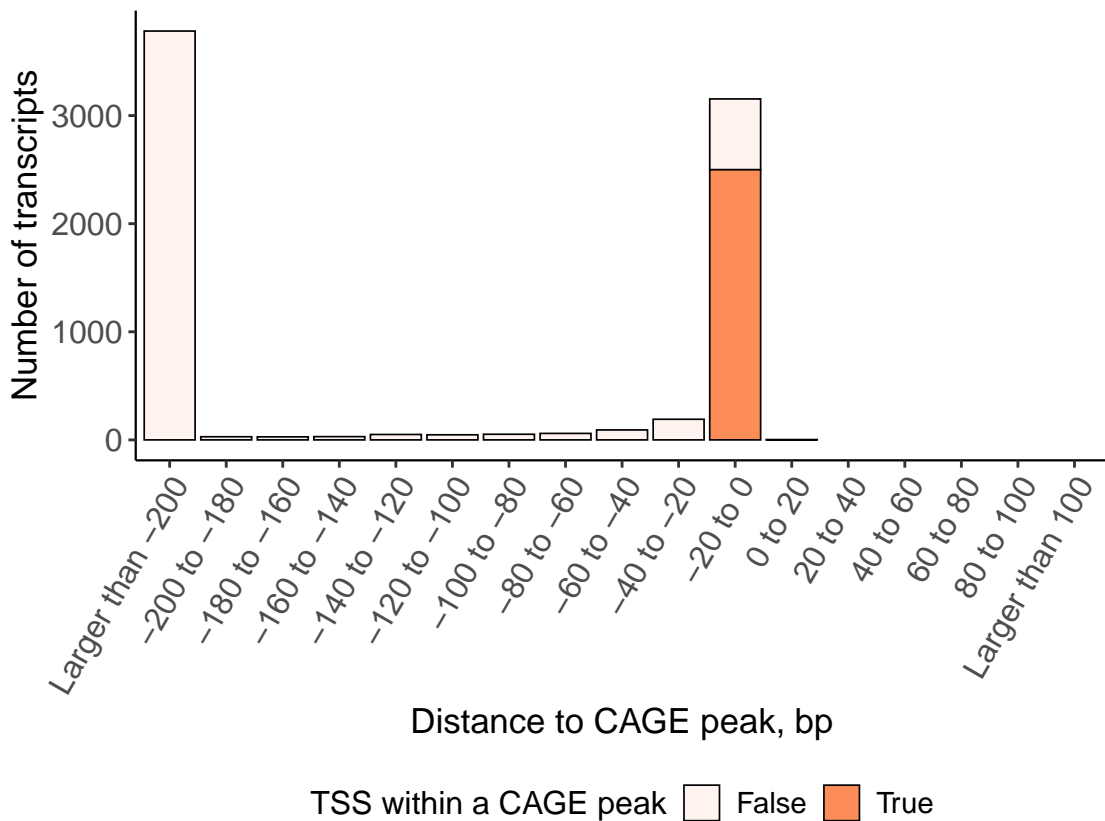
Distance to CAGE Peak of Multi-Exonic FSM Reference Match

Negative values indicate downstream of annotated CAGE peak



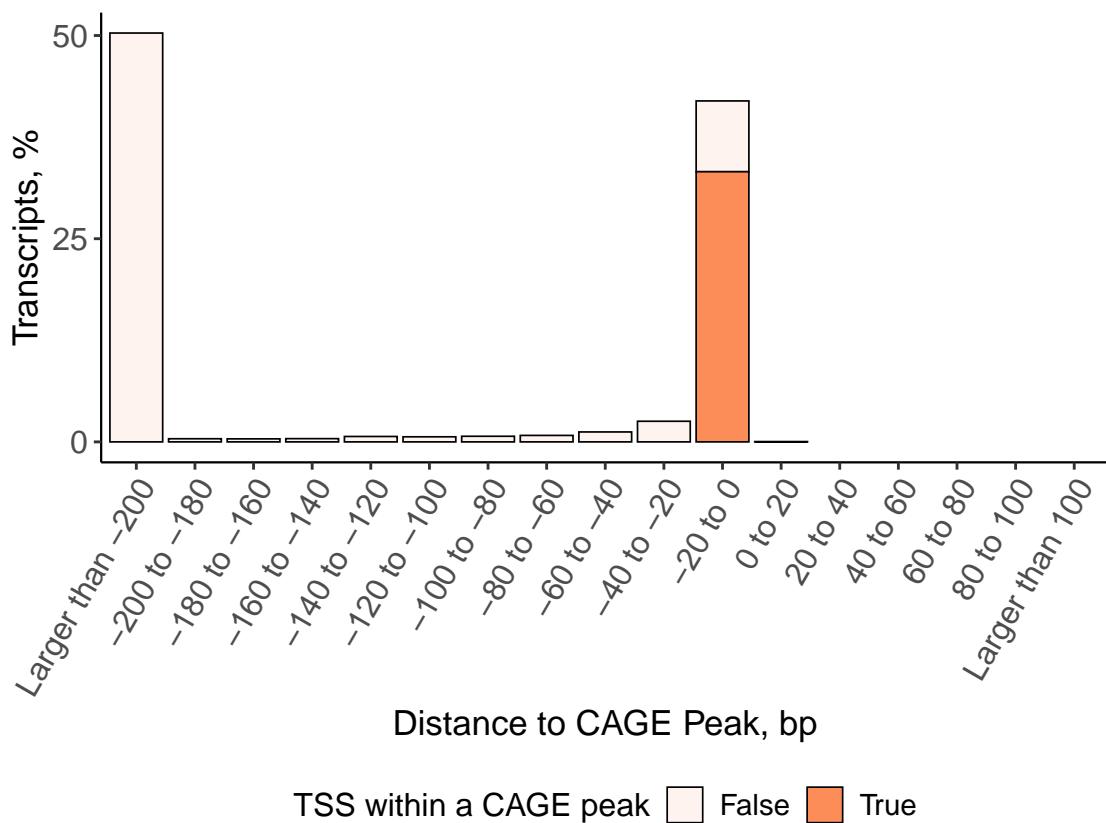
Distance to CAGE Peak of Multi-Exonic ISM

Negative values indicate downstream of annotated CAGE peak



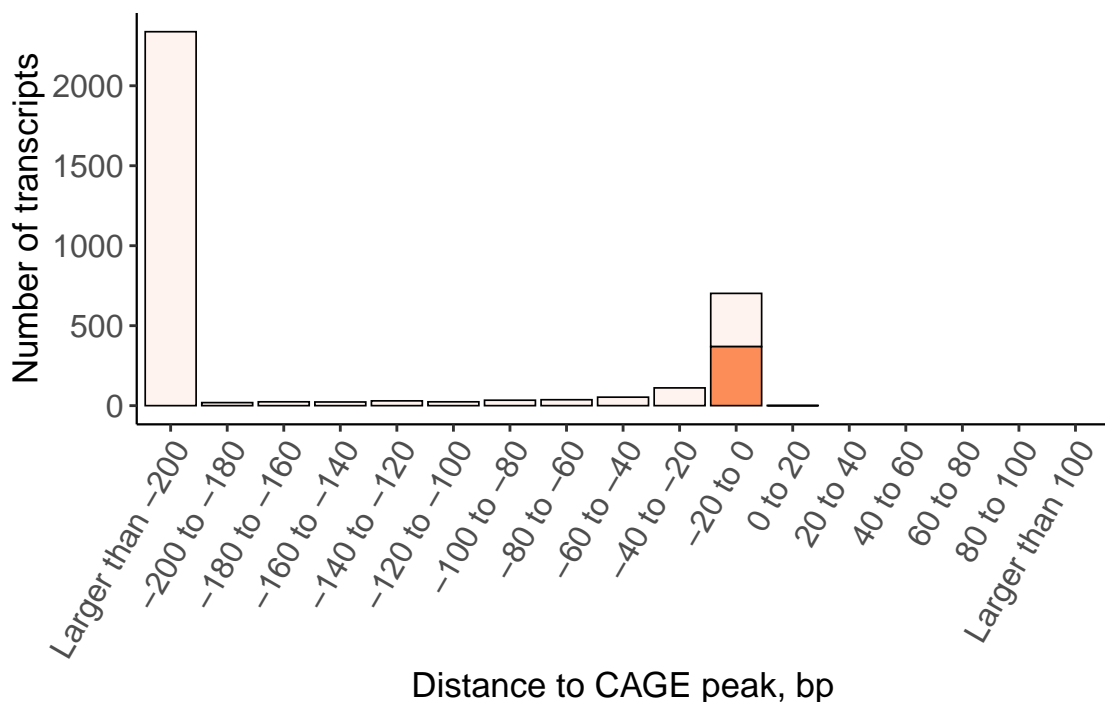
Distance to CAGE Peak of Multi-Exonic ISM

Negative values indicate downstream of annotated CAGE peak



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

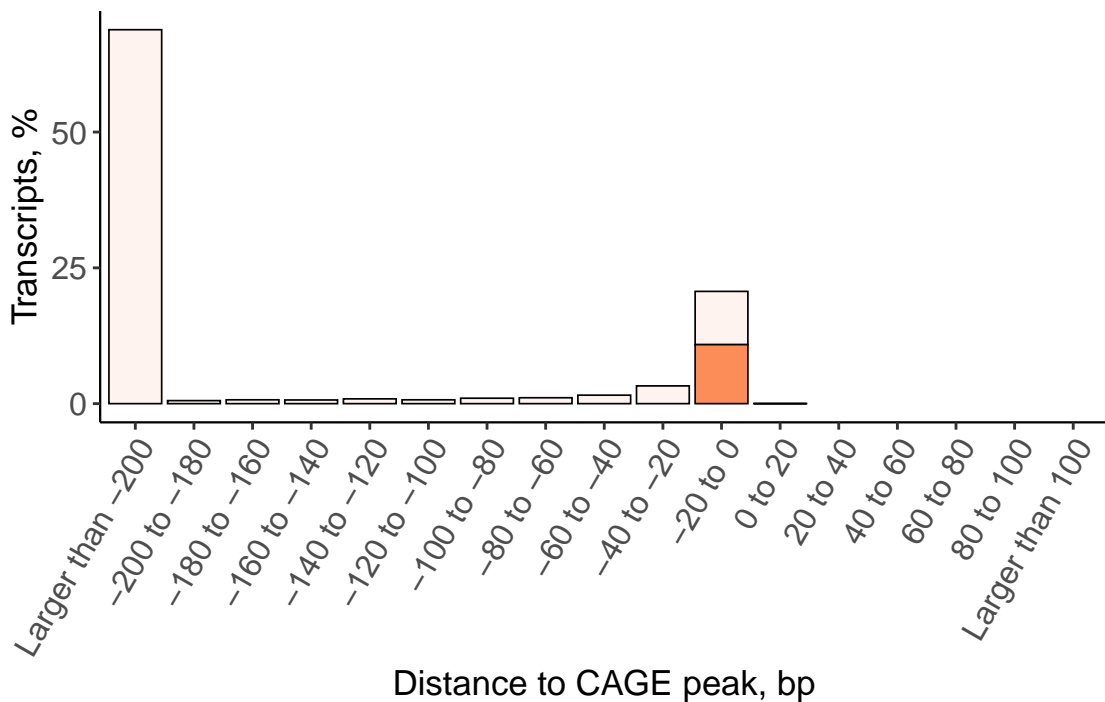
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

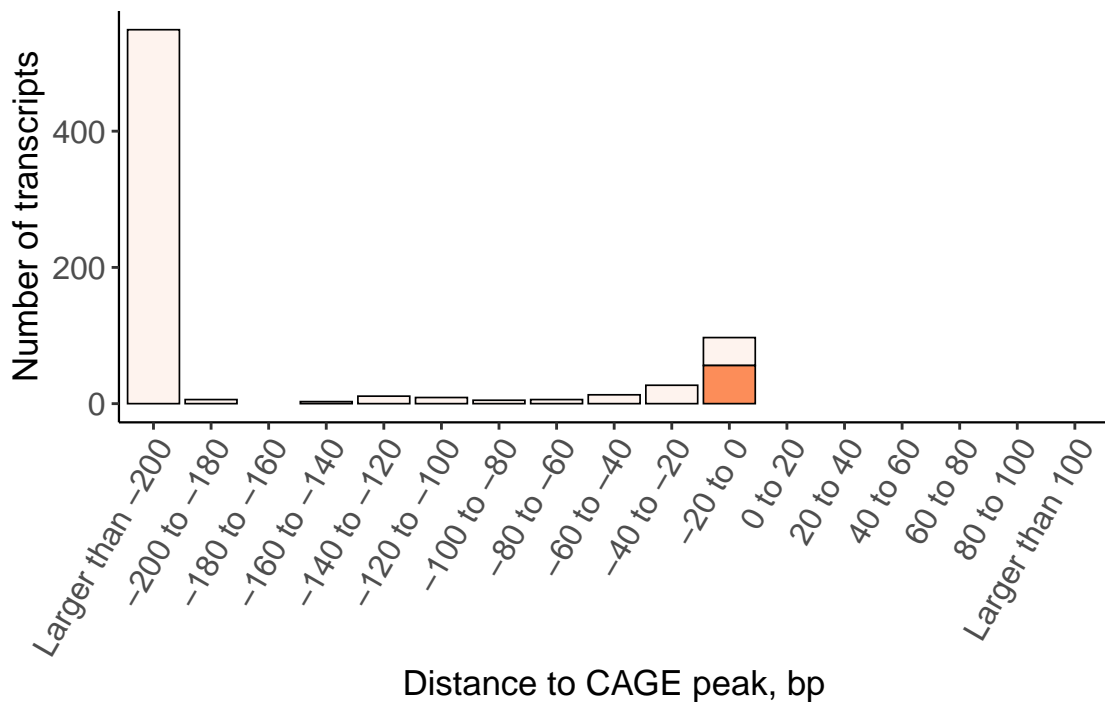
Distance to CAGE Peak of Multi-Exonic ISM 3' Fragment

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic ISM Internal Fragment

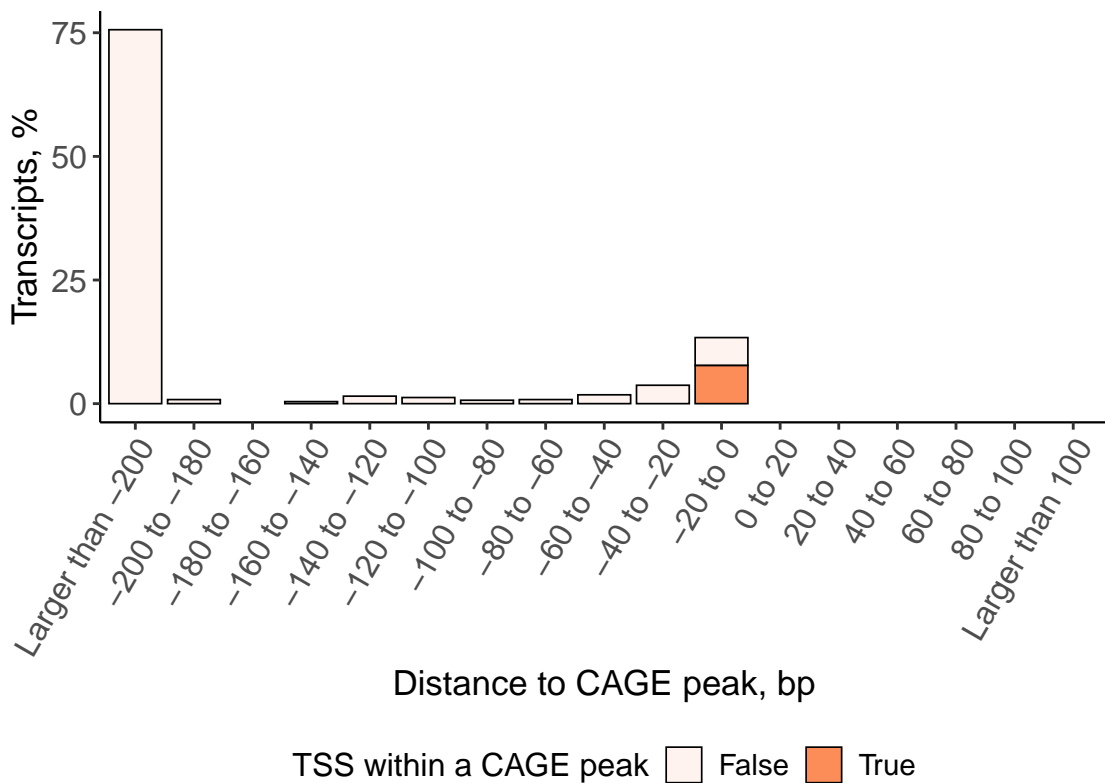
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

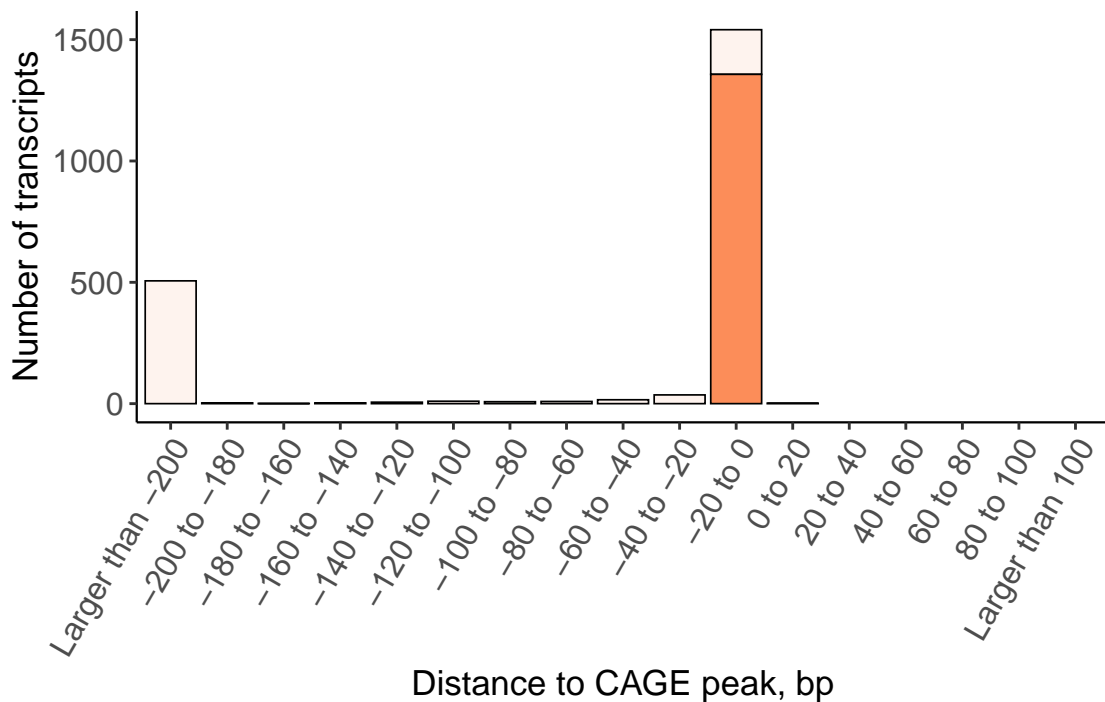
Distance to CAGE Peak of Multi-Exonic ISM Internal Fragment

Negative values indicate downstream of annotated CAGE peak



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

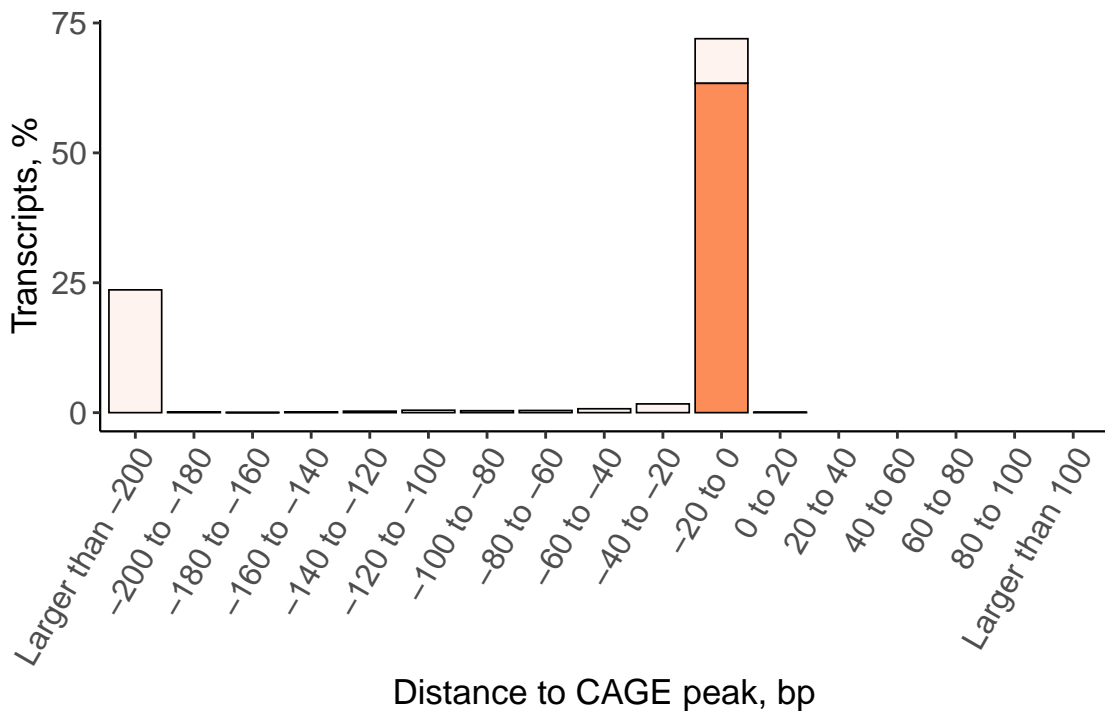
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

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

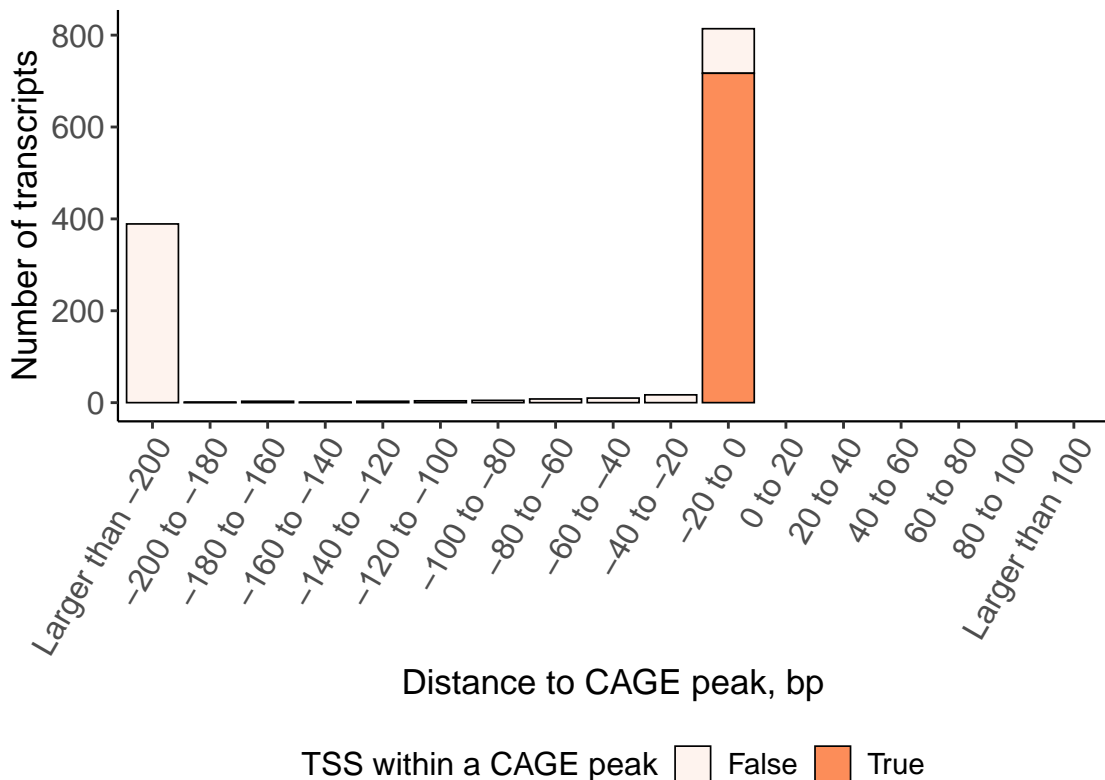
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

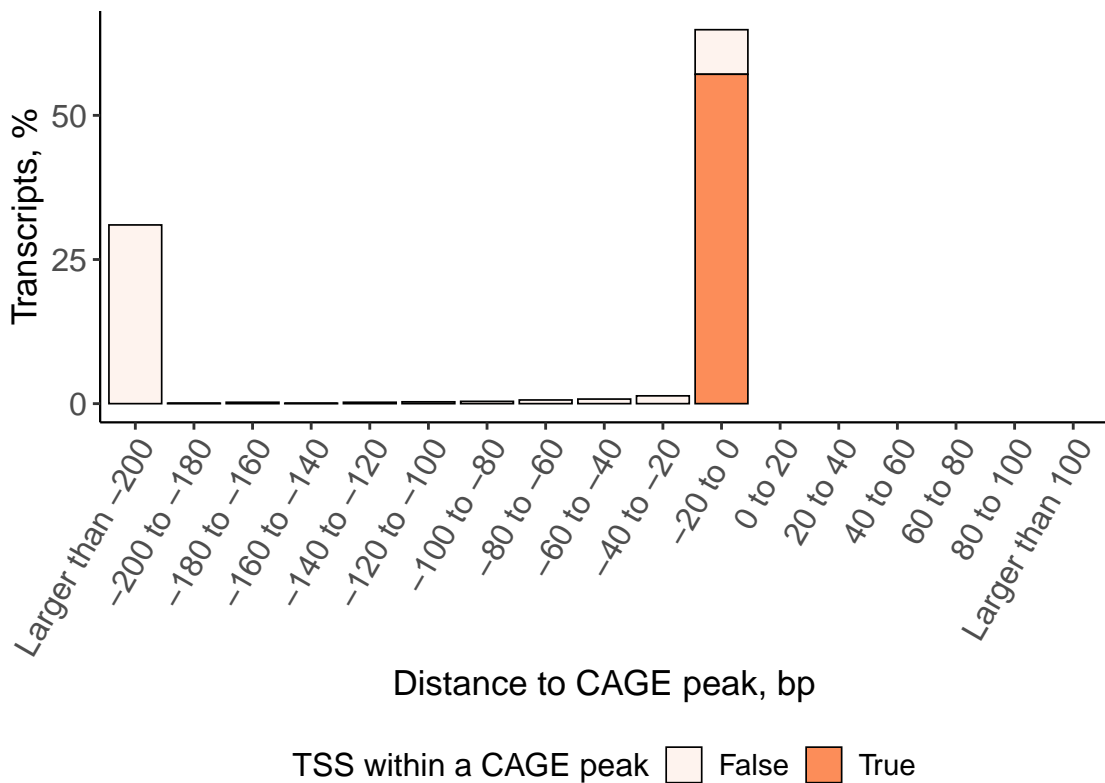
Distance to CAGE Peak of Multi-Exonic ISM Intron Retention

Negative values indicate downstream of annotated CAGE peak



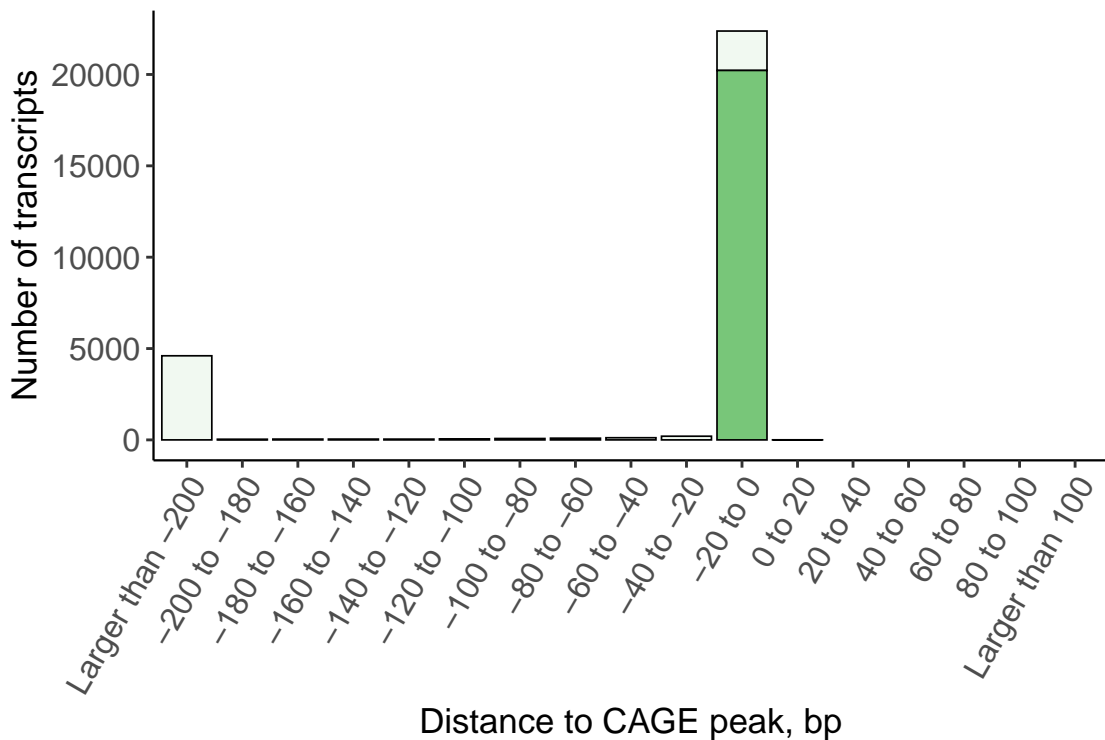
Distance to CAGE Peak of Multi-Exonic ISM Intron Retention

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic NIC

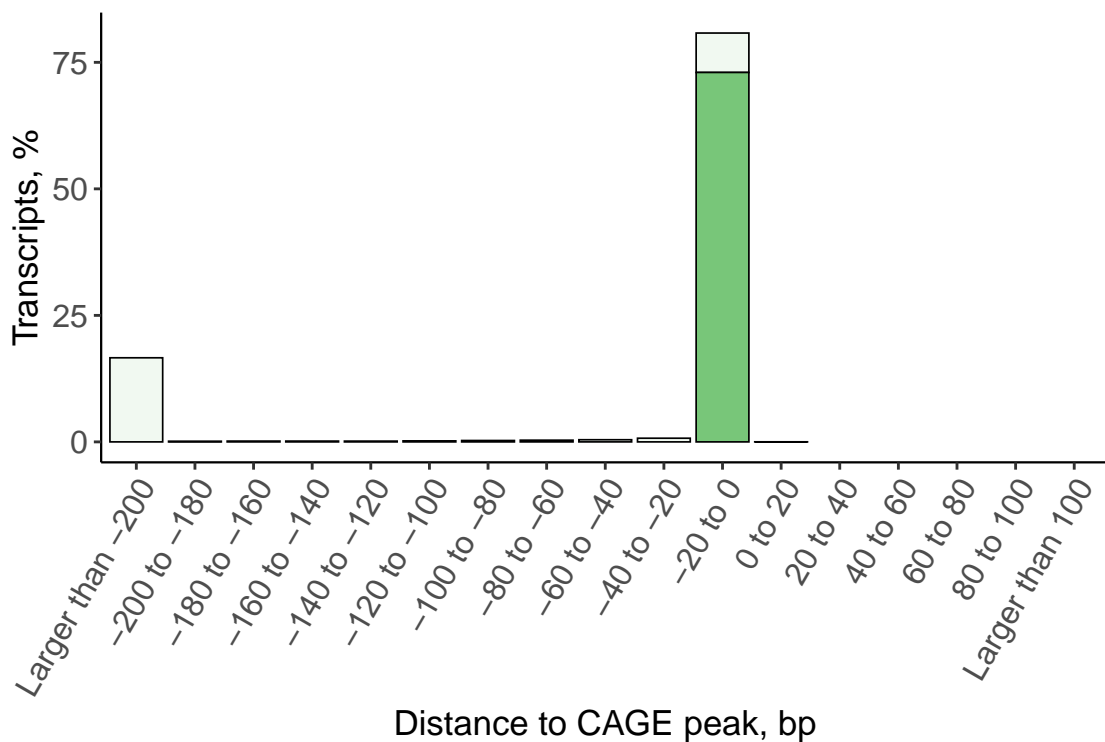
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

Distance to CAGE Peak of Multi-Exonic NIC

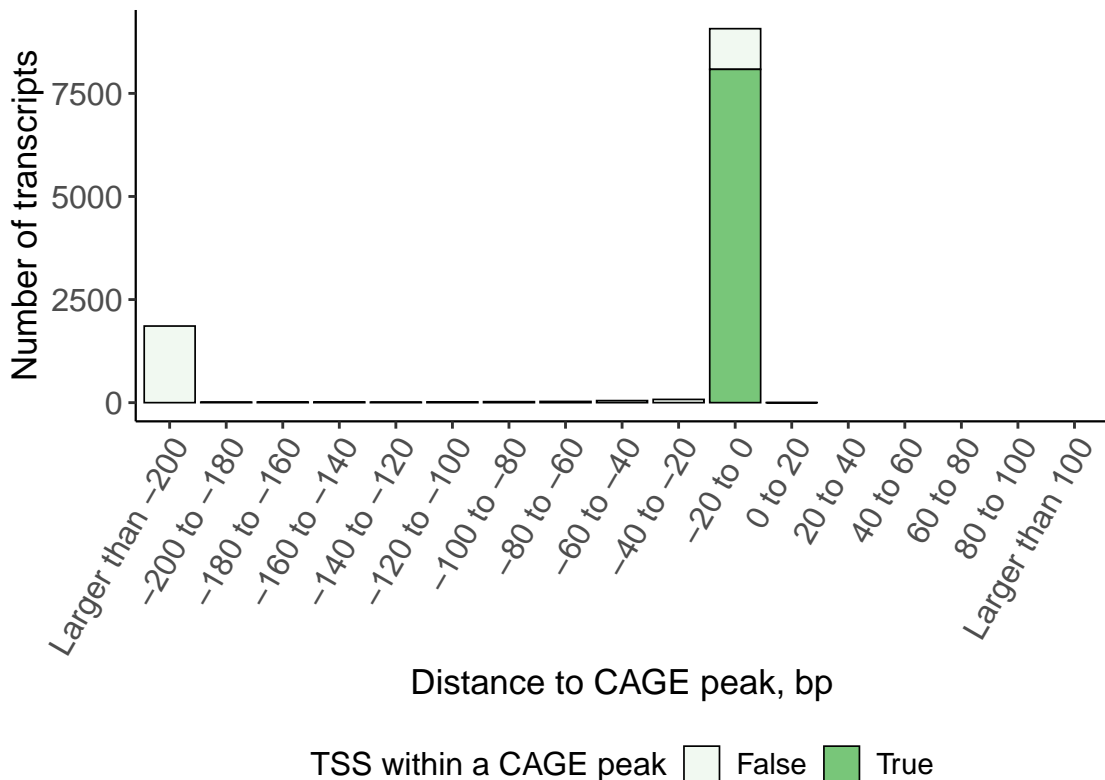
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

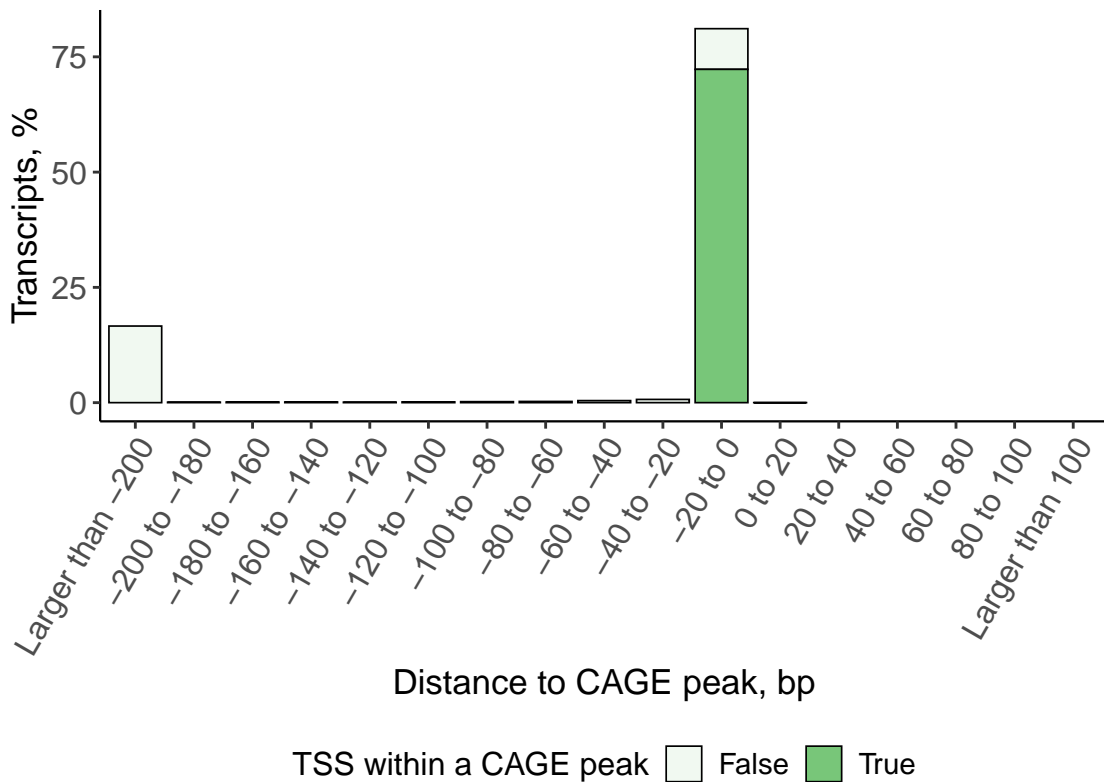
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Junctions

Negative values indicate downstream of annotated CAGE peak



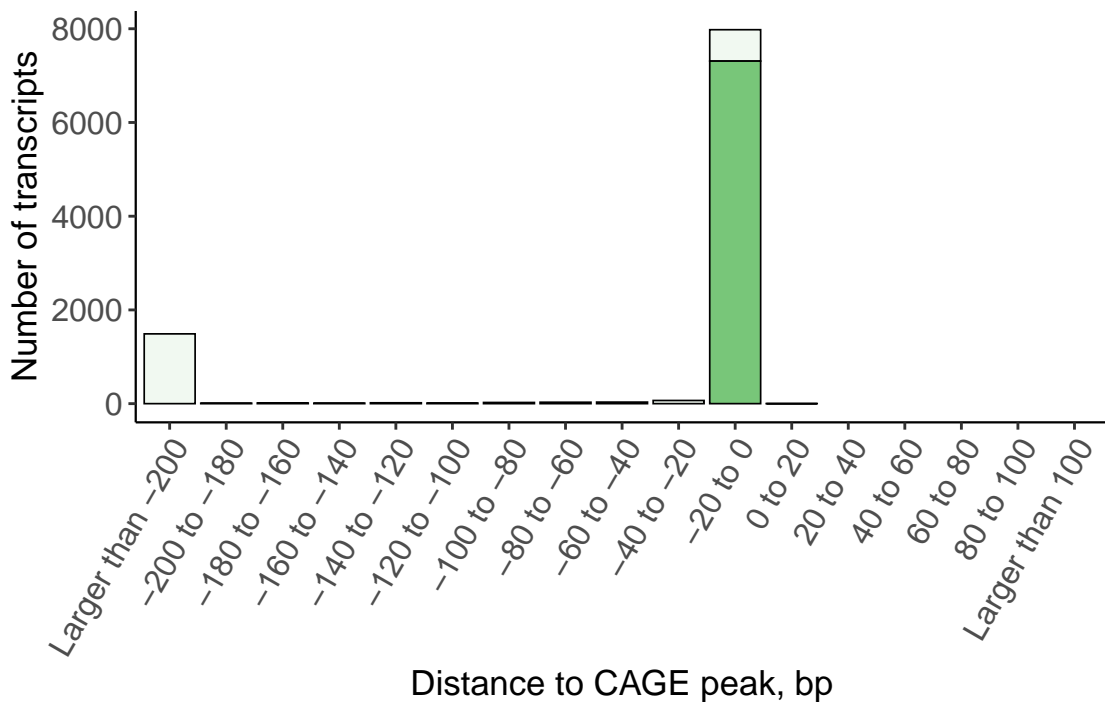
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Junctions

Negative values indicate downstream of annotated CAGE peak



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

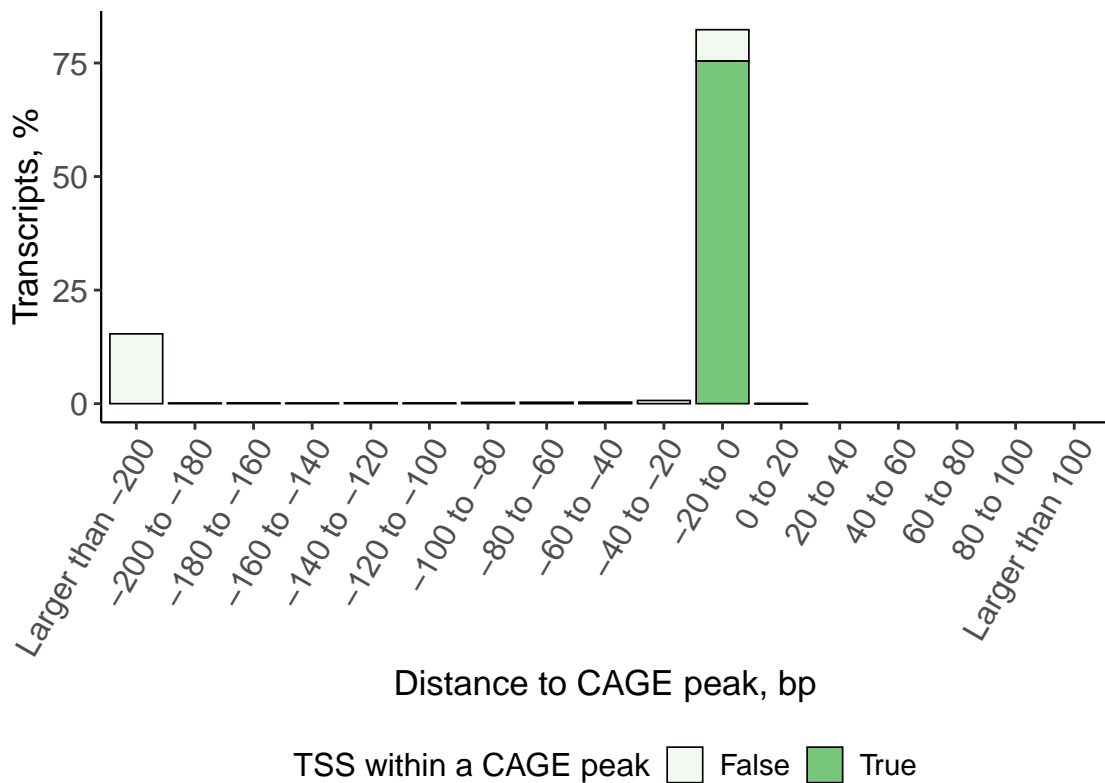
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

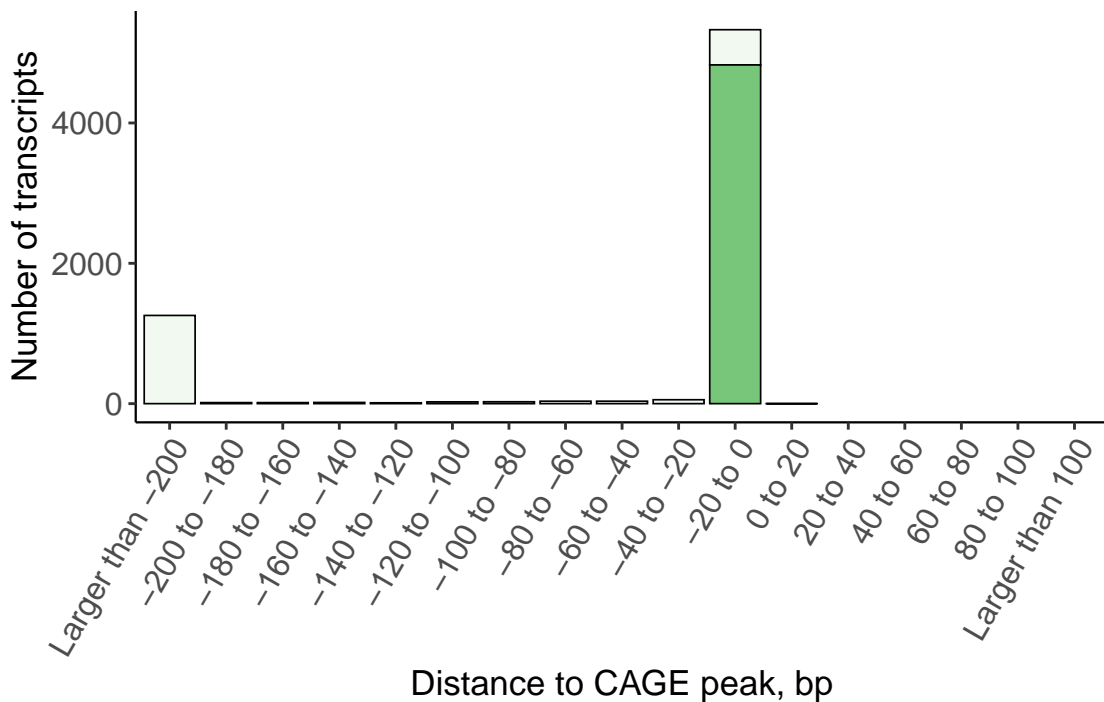
Distance to CAGE Peak of Multi-Exonic NIC Combination of Annotated Splice Sites

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic NIC Intron Retention

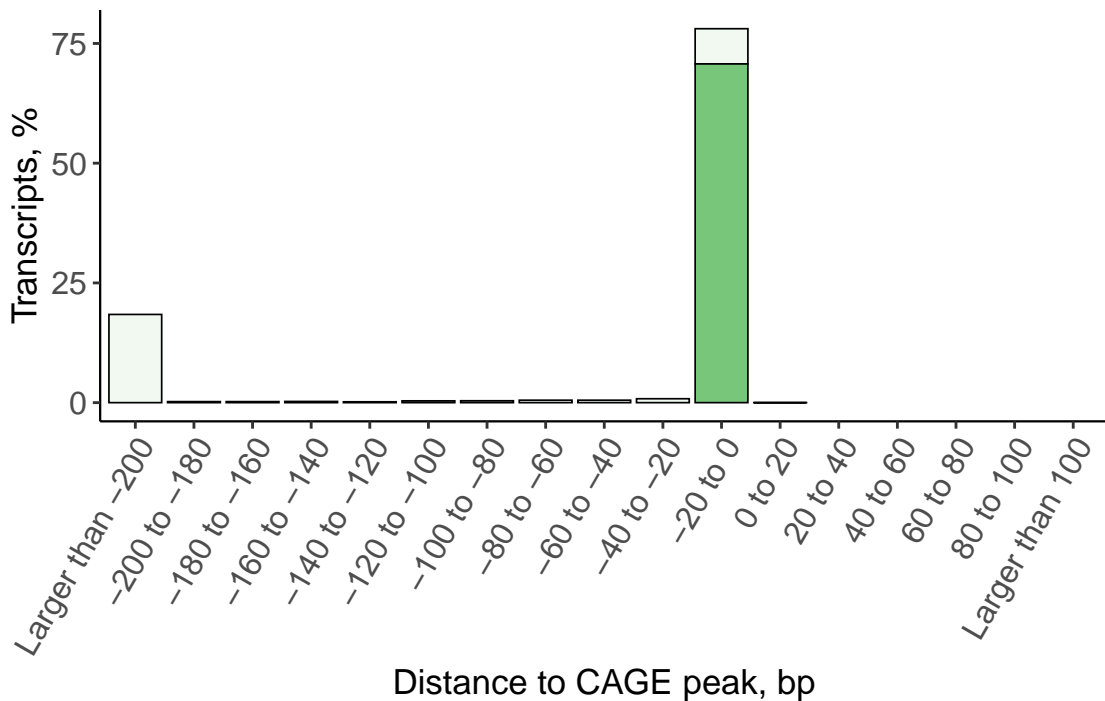
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

Distance to CAGE Peak of Multi-Exonic NIC Intron Retention

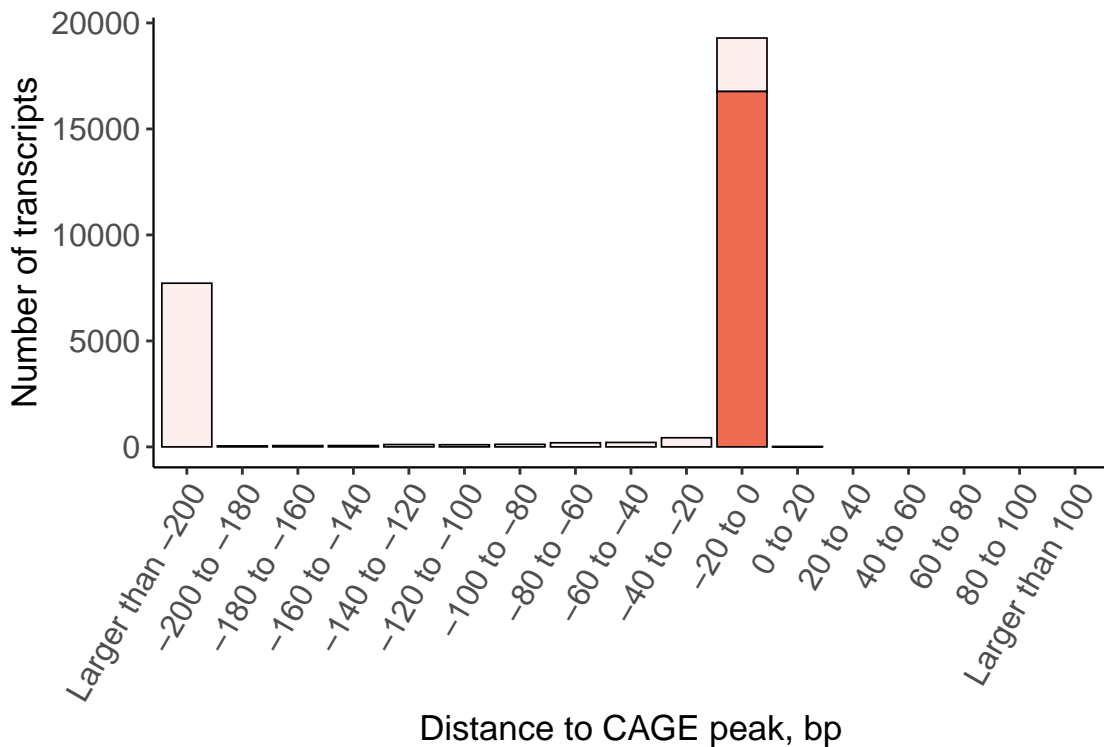
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

Distance to CAGE Peak of Multi-Exonic NNC

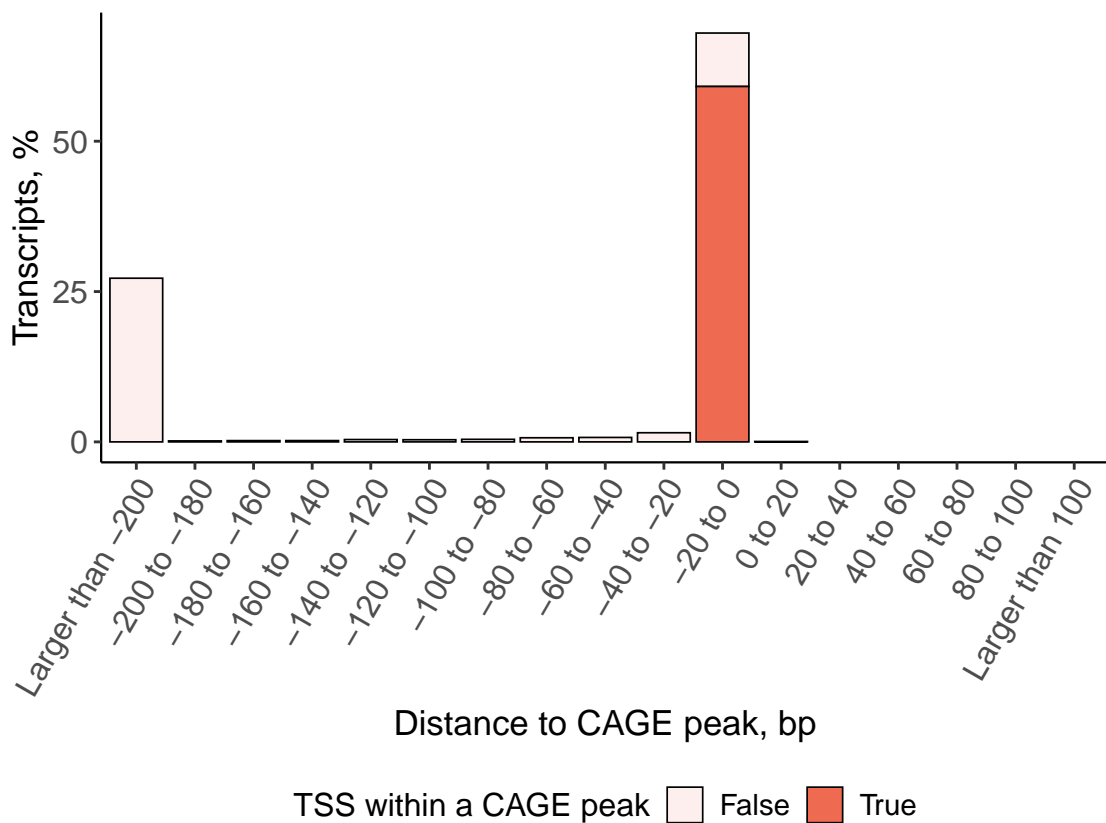
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

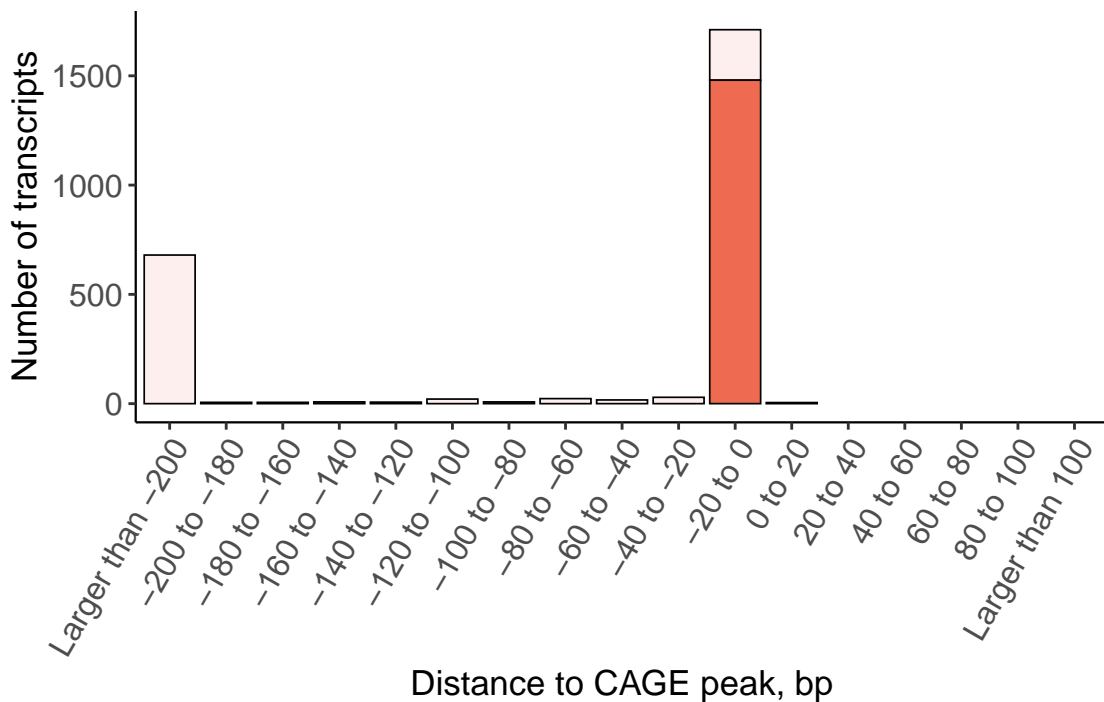
Distance to CAGE Peak of Multi-Exonic NNC

Negative values indicate downstream of annotated CAGE peak



Distance to CAGE Peak of Multi-Exonic NNC Intron Retention

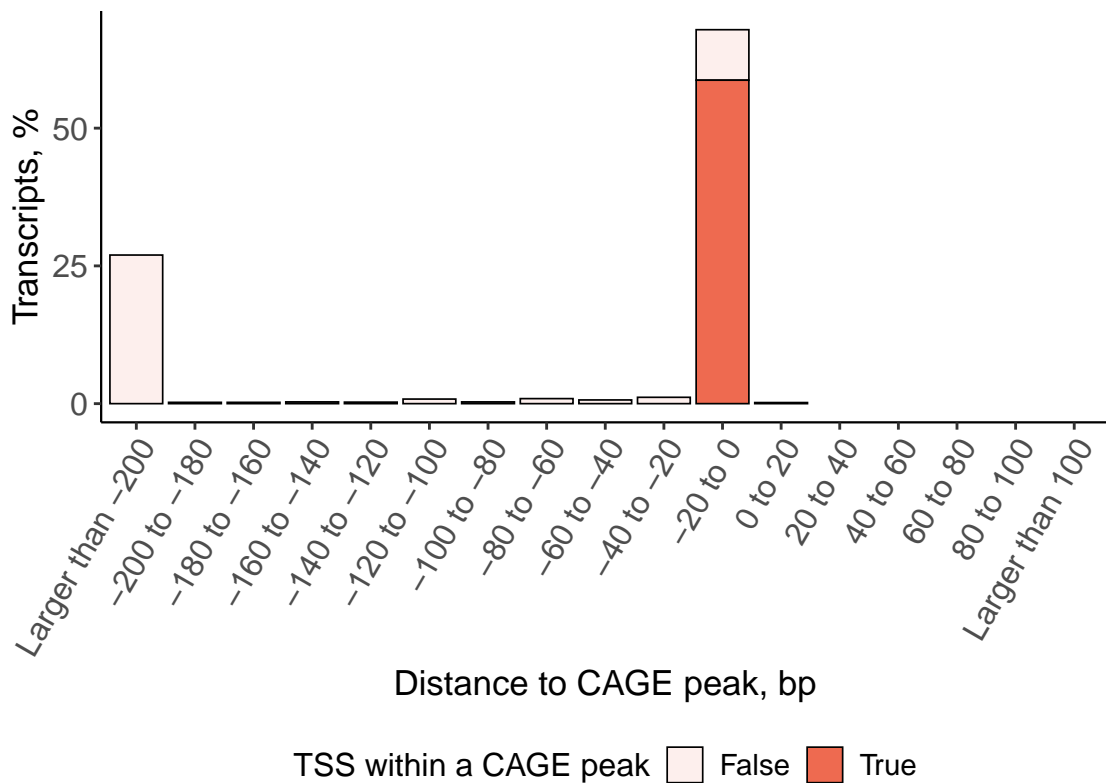
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

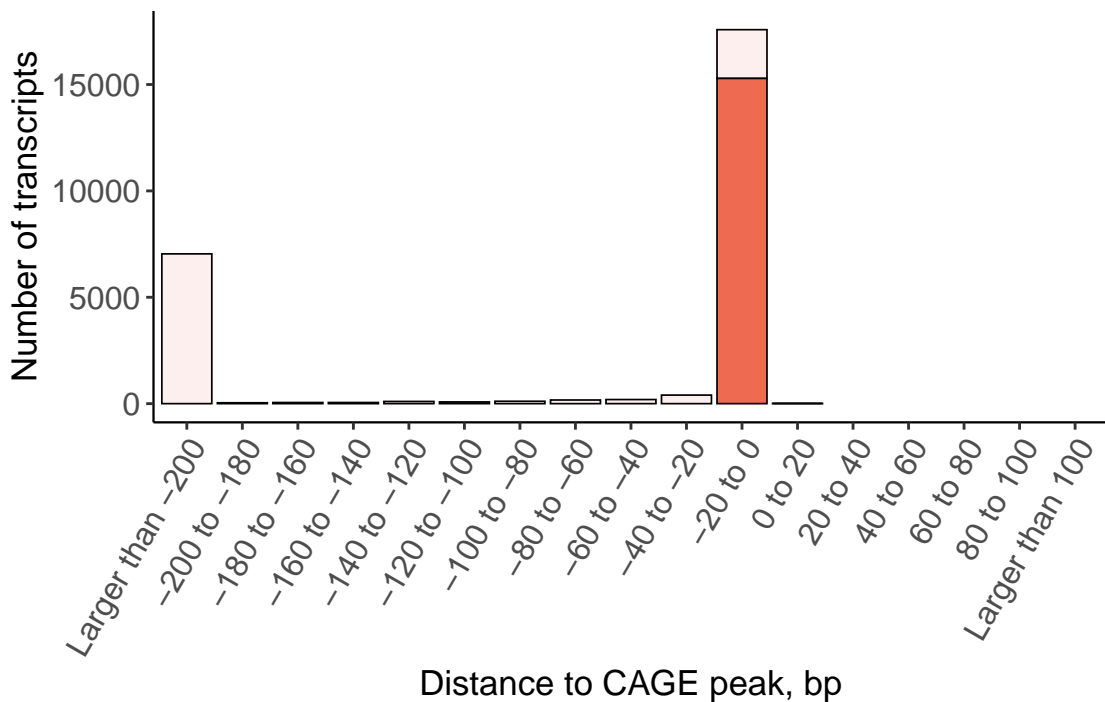
Distance to CAGE Peak of Multi-Exonic NNC Intron Retention

Negative values indicate downstream of annotated CAGE peak



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

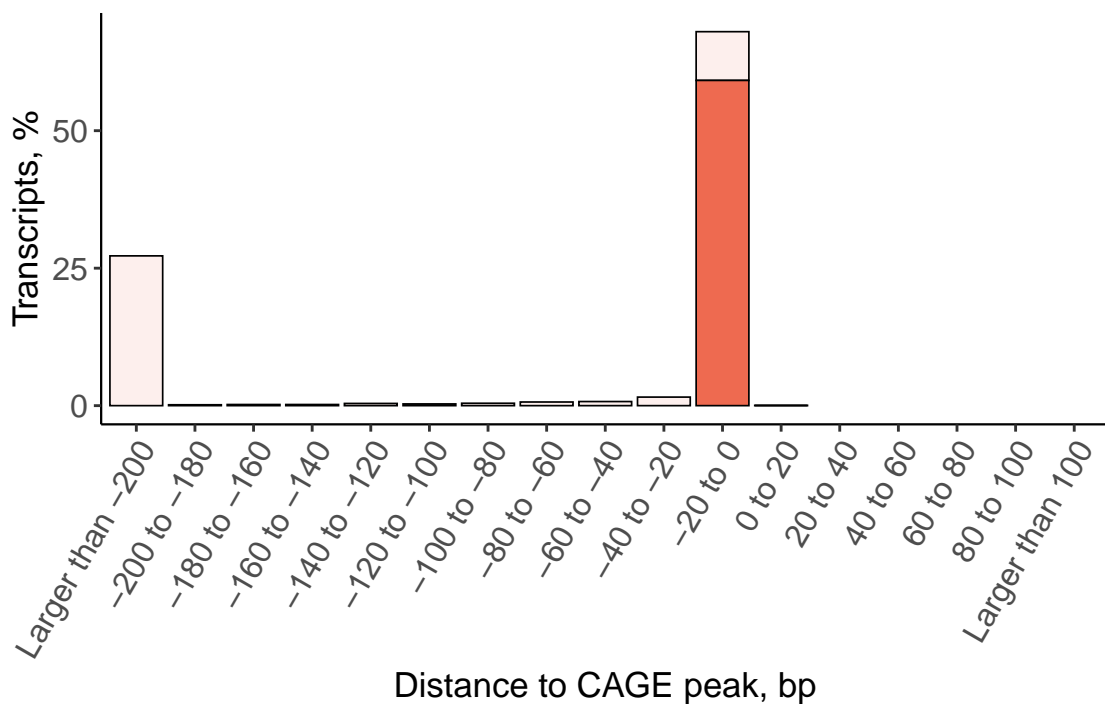
Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

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

Negative values indicate downstream of annotated CAGE peak



TSS within a CAGE peak False True

Number of CAGE Detected

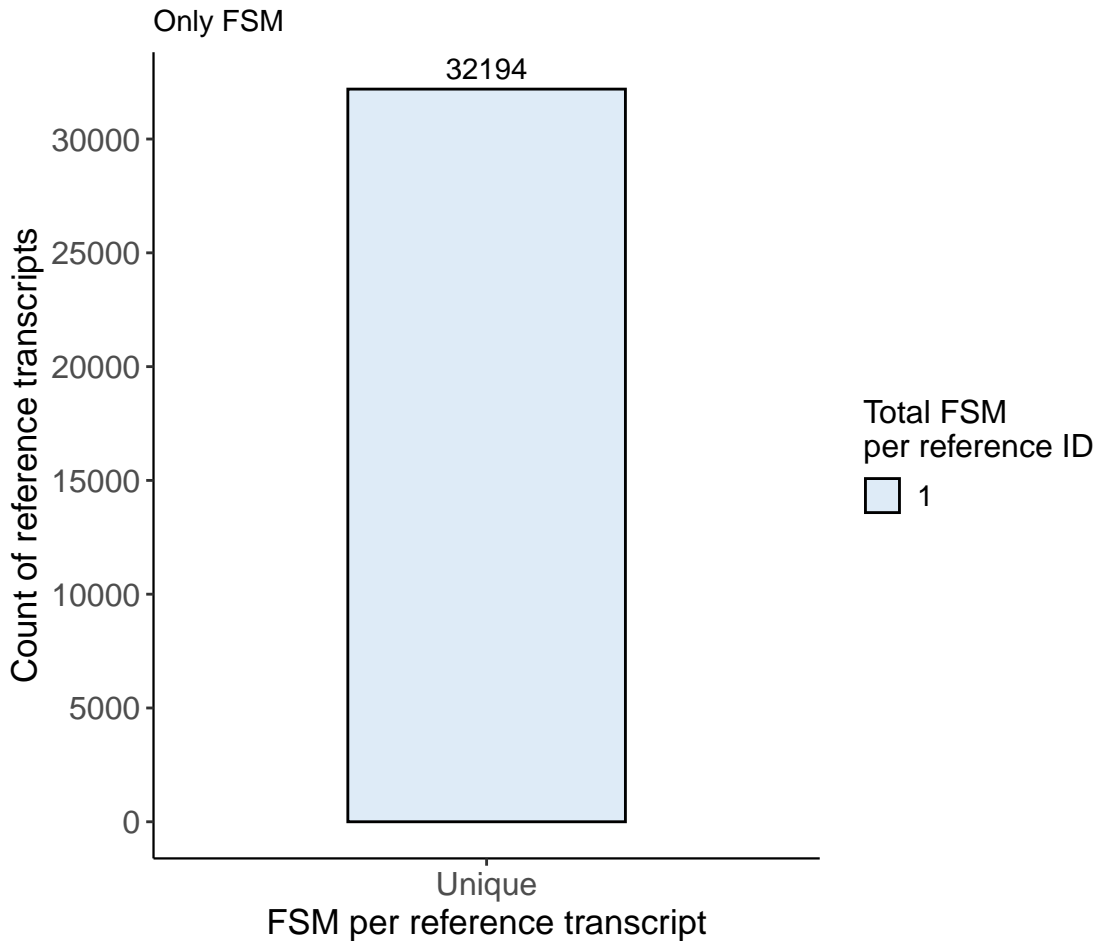
Category	Count	CAGE Detected	%
FSM	41311	20170	49
ISM	10079	2612	26
NIC	30369	20416	67
NNC	29119	16766	58
Genic Genomic	5913	533	9
Antisense	9243	392	4
Fusion	891	441	49
Intergenic	21252	878	4
Genic Intron	1257	85	7

Number of CAGE Detected

Subcategory	Count	CAGE Detected	%
Alternative 3'end	2992	1882	63
Alternative 3'5'end	1617	814	50
Alterantive 5'end	2224	912	41
Reference match	25361	15587	61
3' fragment	3671	369	10
Internal fragment	788	56	7
5' fragment	2200	1357	62
Comb. of annot. junctions	11290	8083	72
Comb. of annot. splice sites	9781	7310	75
Intron retention	10958	7129	65
Mono-exon by intron ret.	346	29	8
At least 1 annot. don./accept.	26500	15286	58
Mono-exon	32456	1847	6
Multi-exon	19250	1632	8

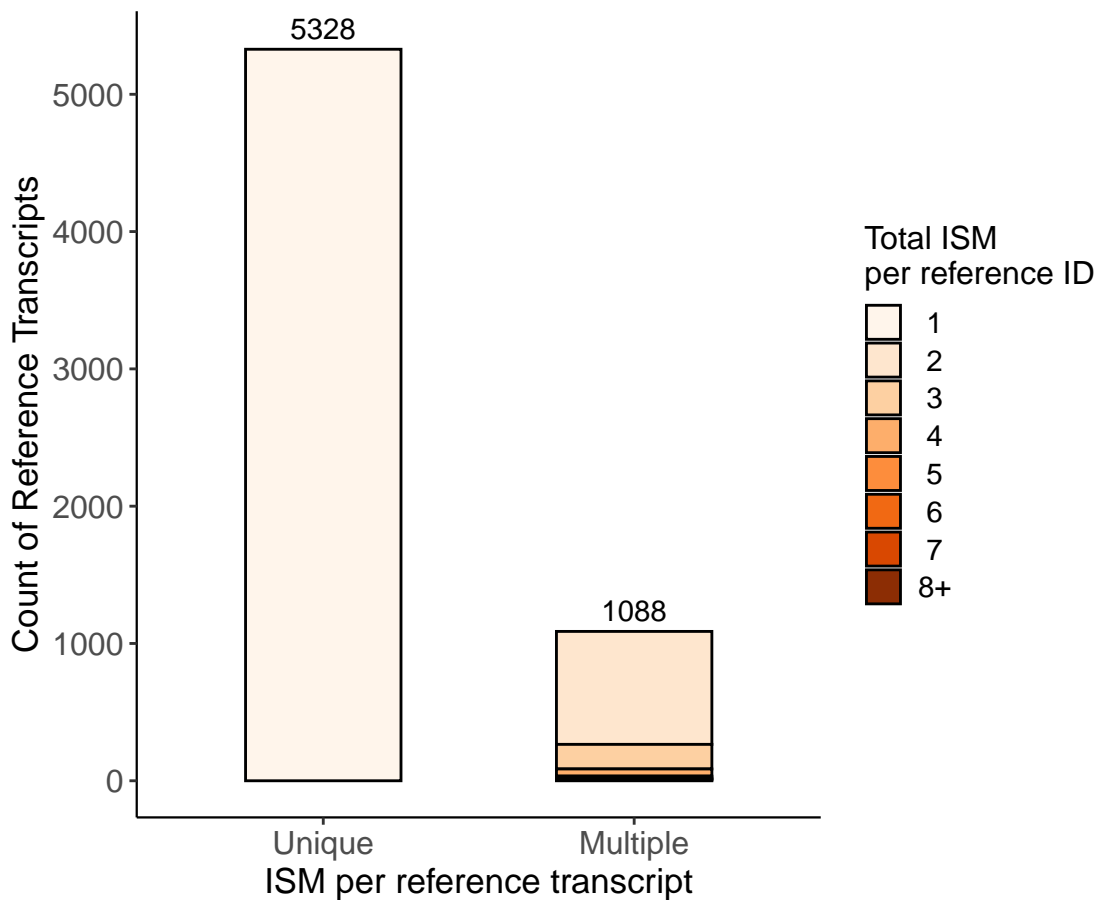
Redundancy Analysis

Reference Transcript Redundancy

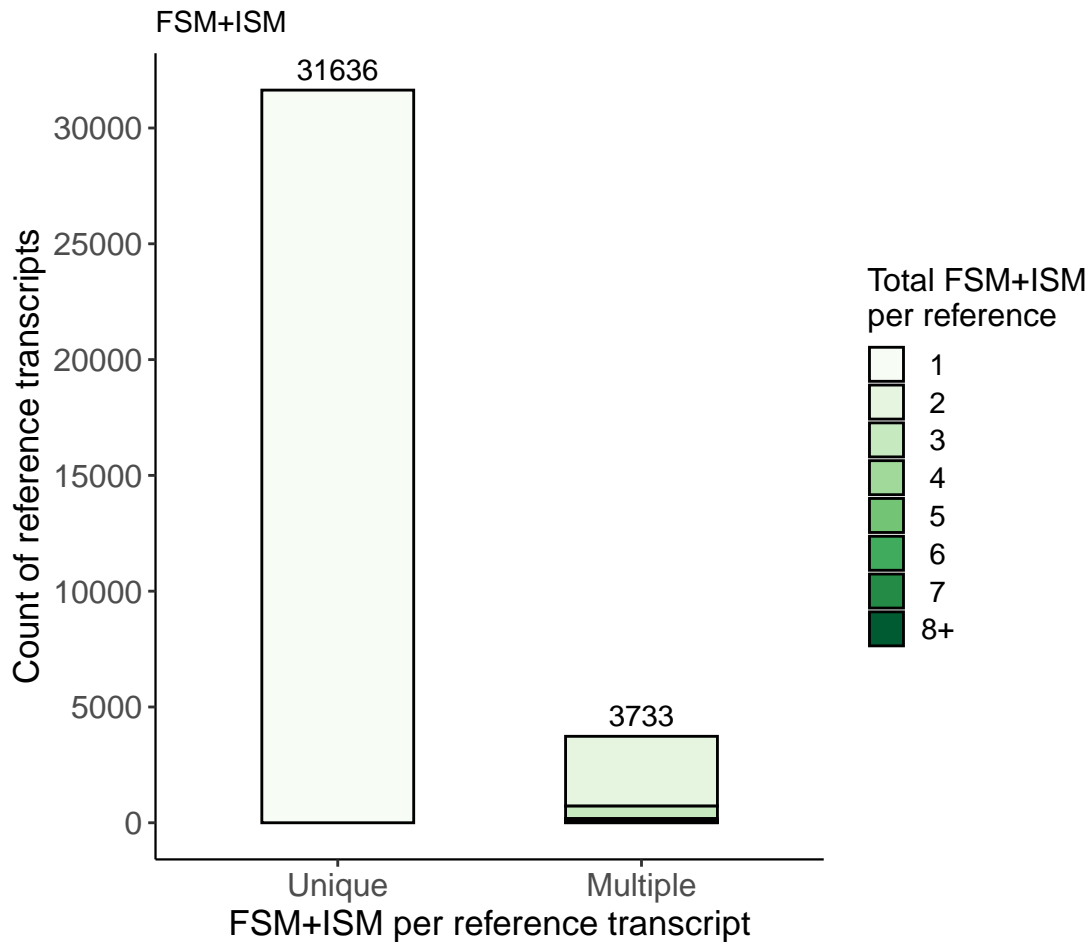


Reference Transcript Redundancy

Only ISM

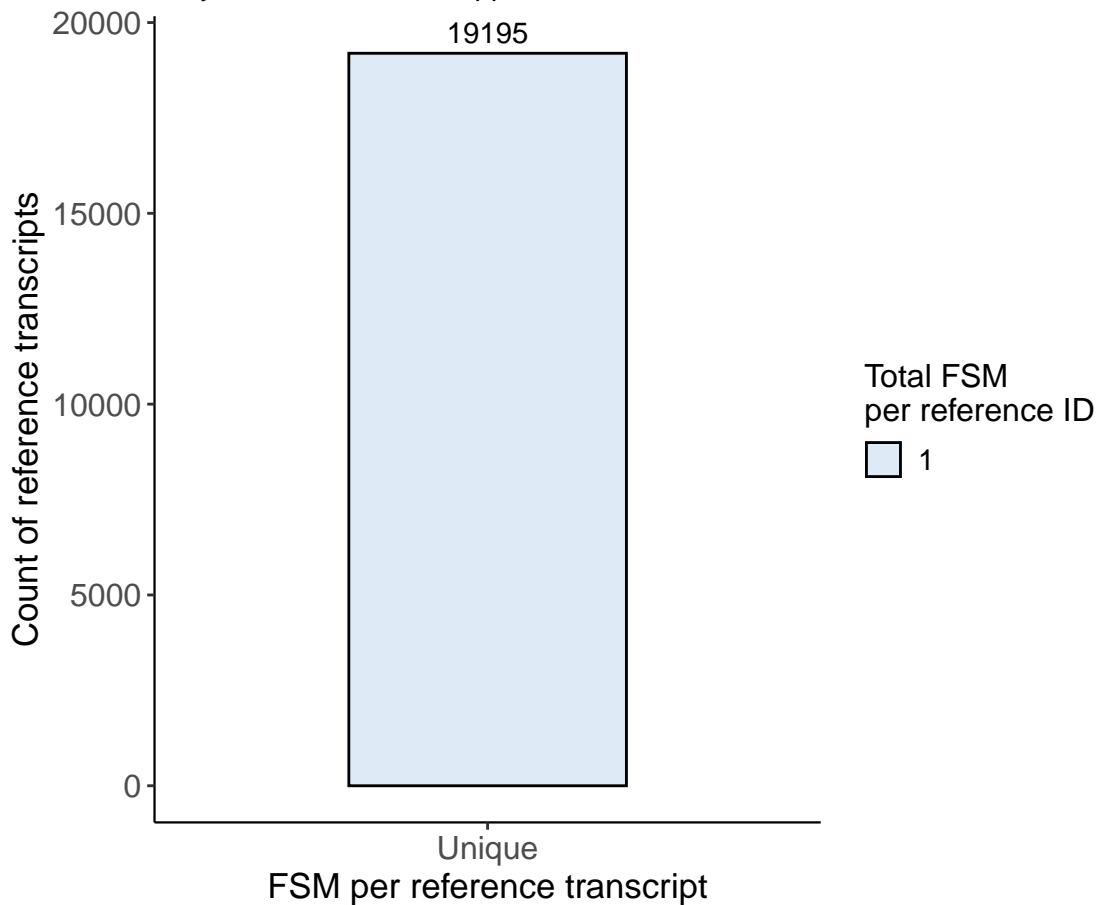


Reference Transcript Redundancy



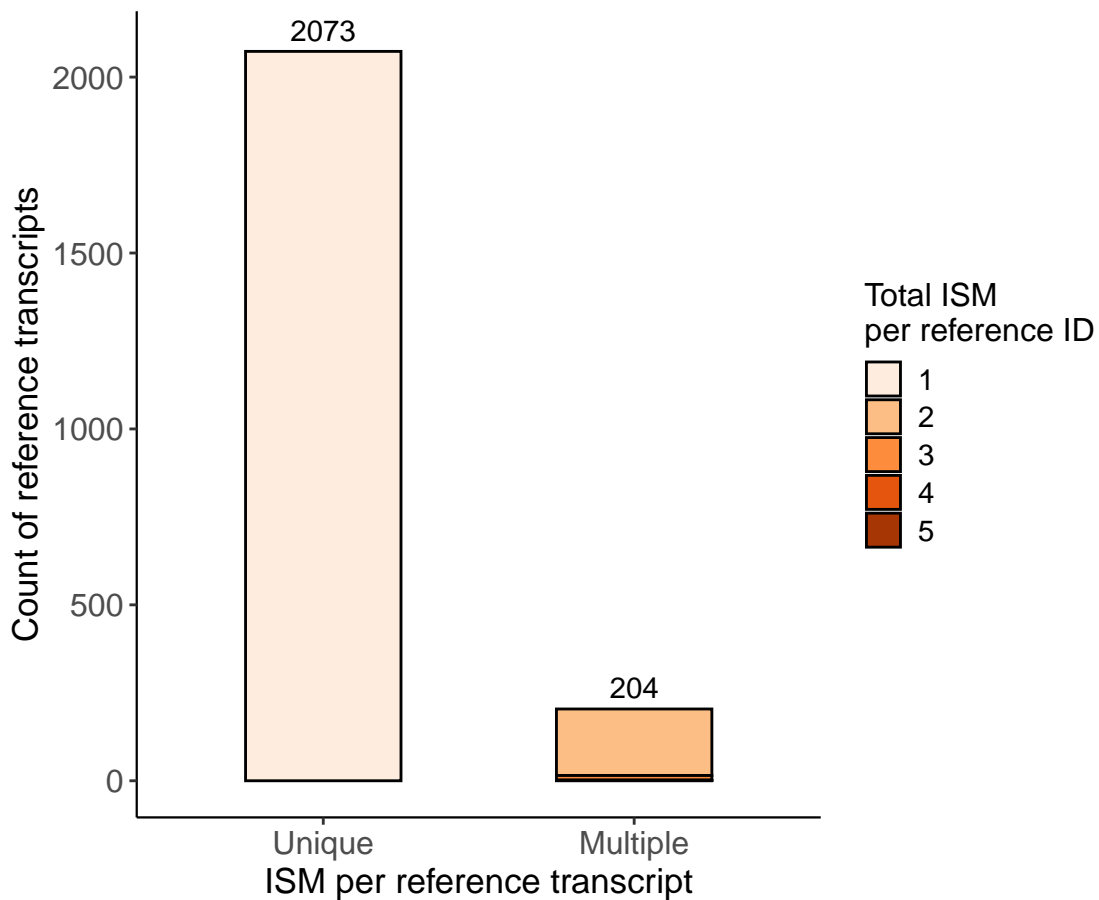
Reference Transcript Redundancy

Only FSM with CAGE support



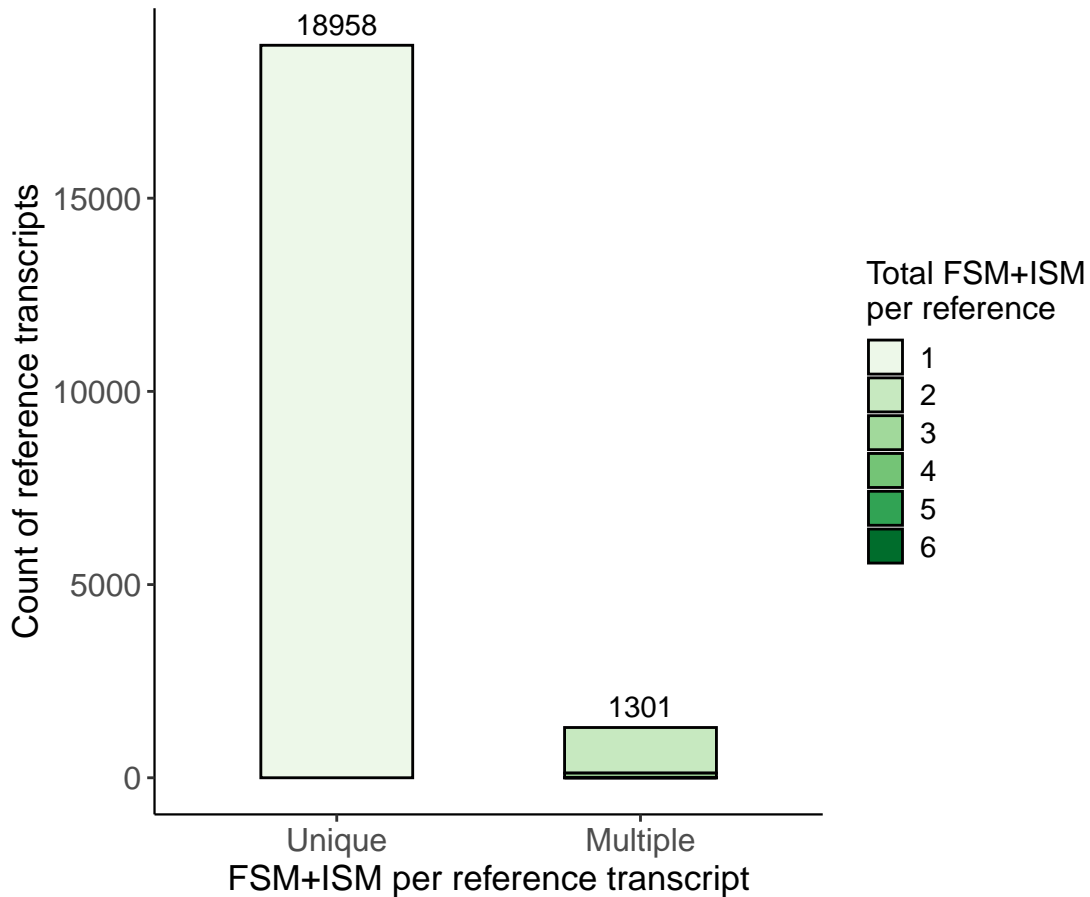
Reference Transcript Redundancy

Only ISM with CAGE support



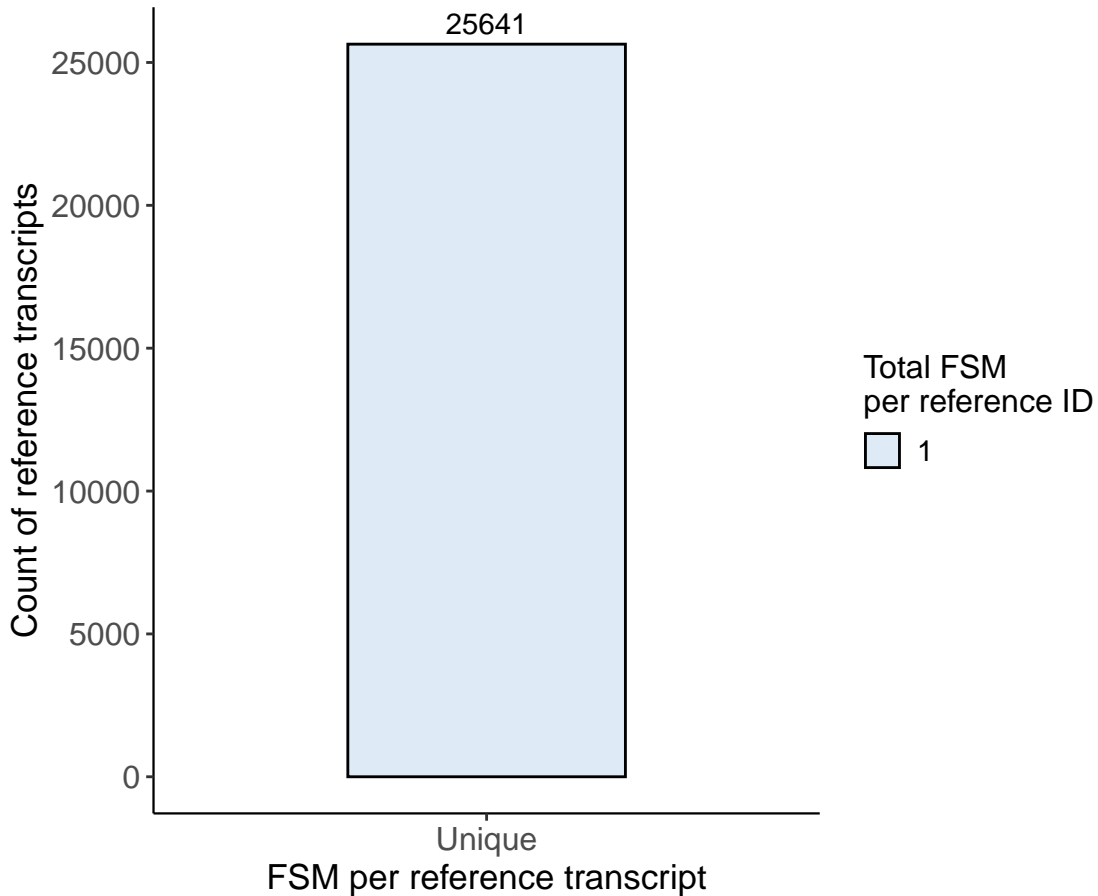
Reference Transcript Redundancy

FSM+ISM with CAGE support



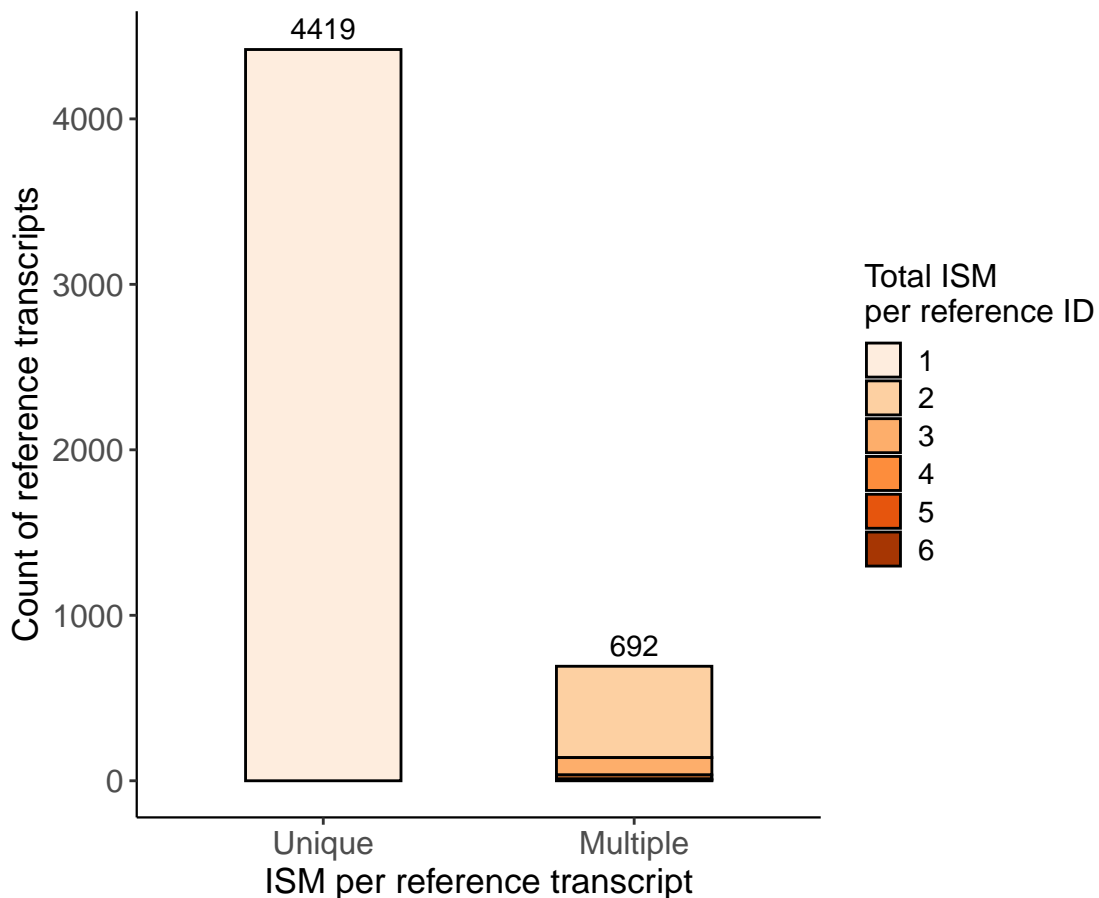
Reference Transcript Redundancy

Only FSM with a polyA motif found



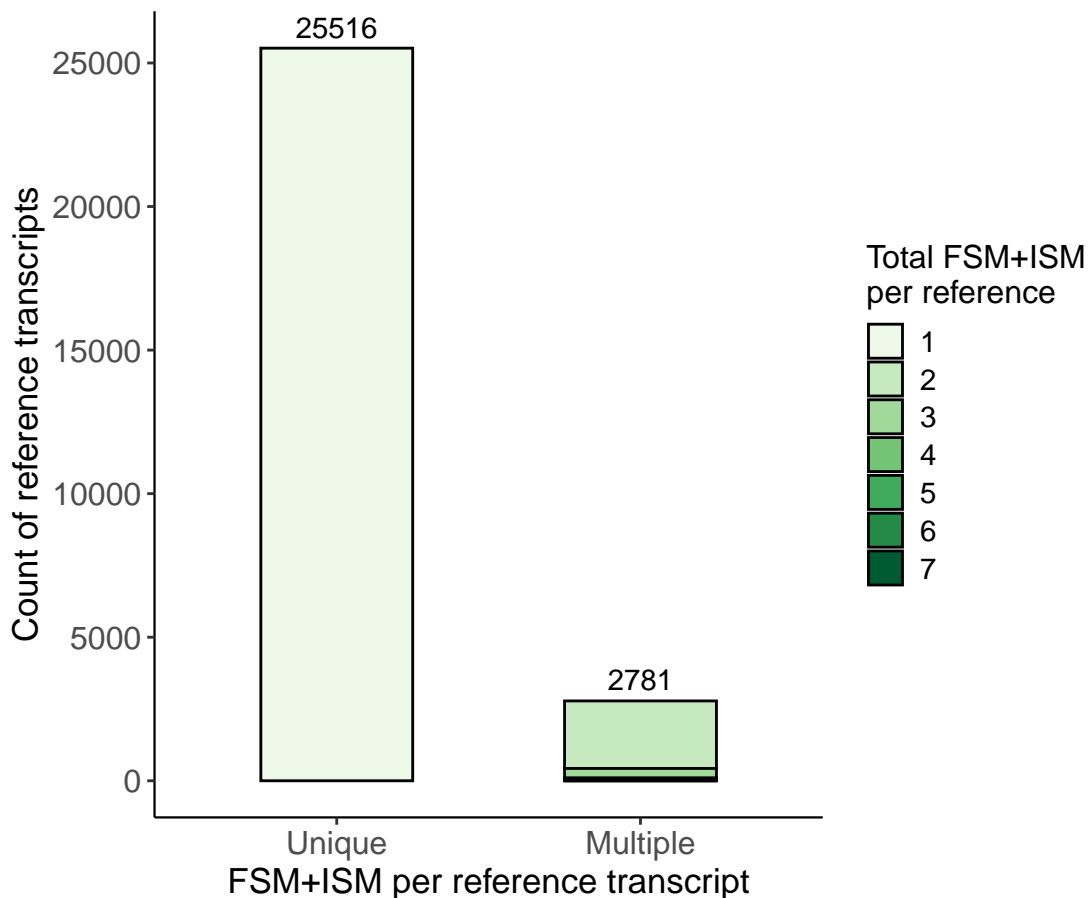
Reference Transcript Redundancy

Only ISM with a polyA motif found



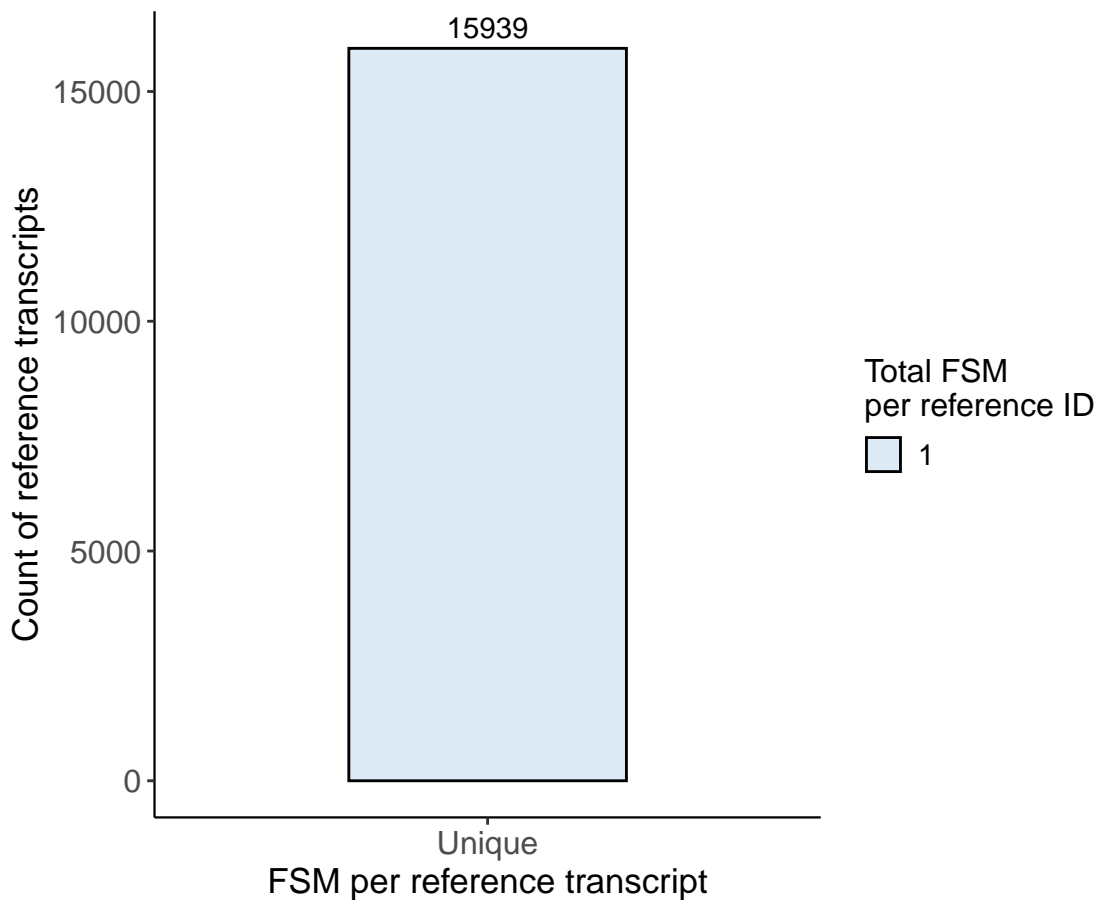
Reference Transcript Redundancy

FSM+ISM with a polyA motif found



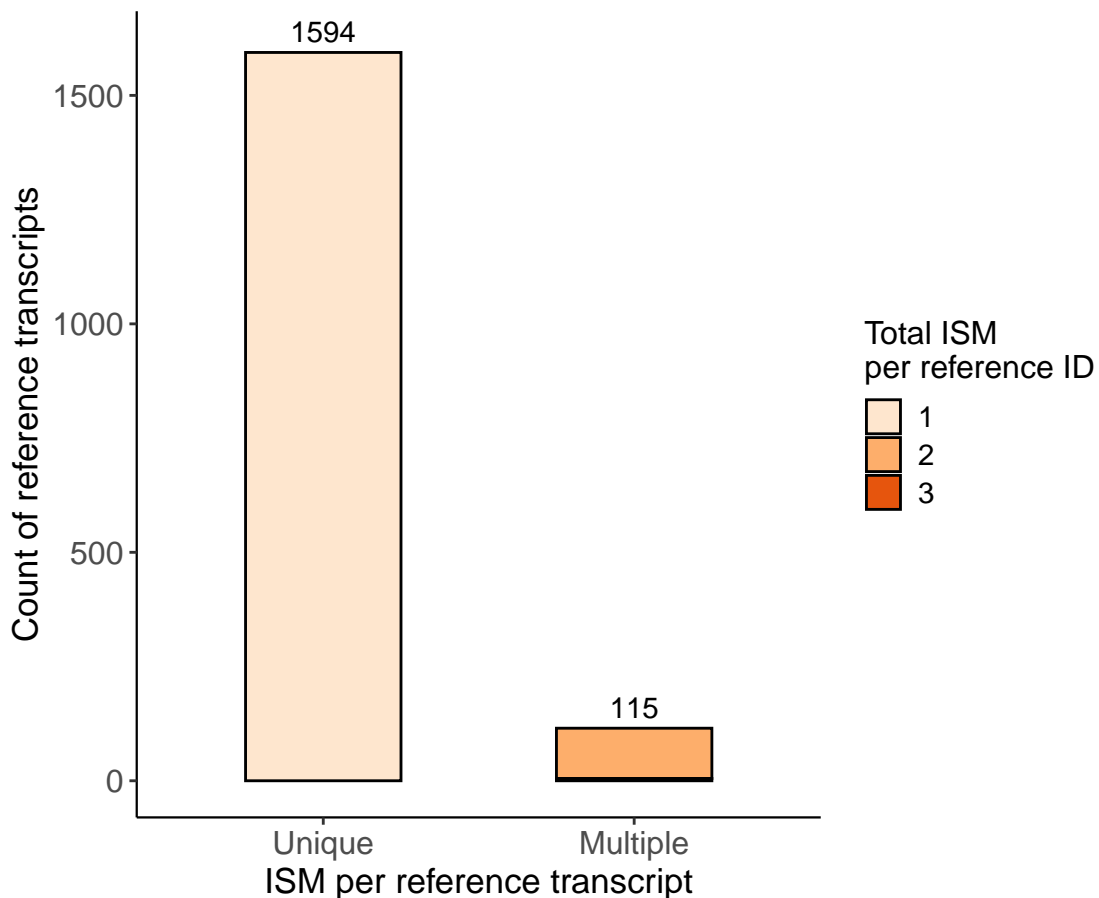
Reference Transcript Redundancy

Only FSM with CAGE support and polyA motif



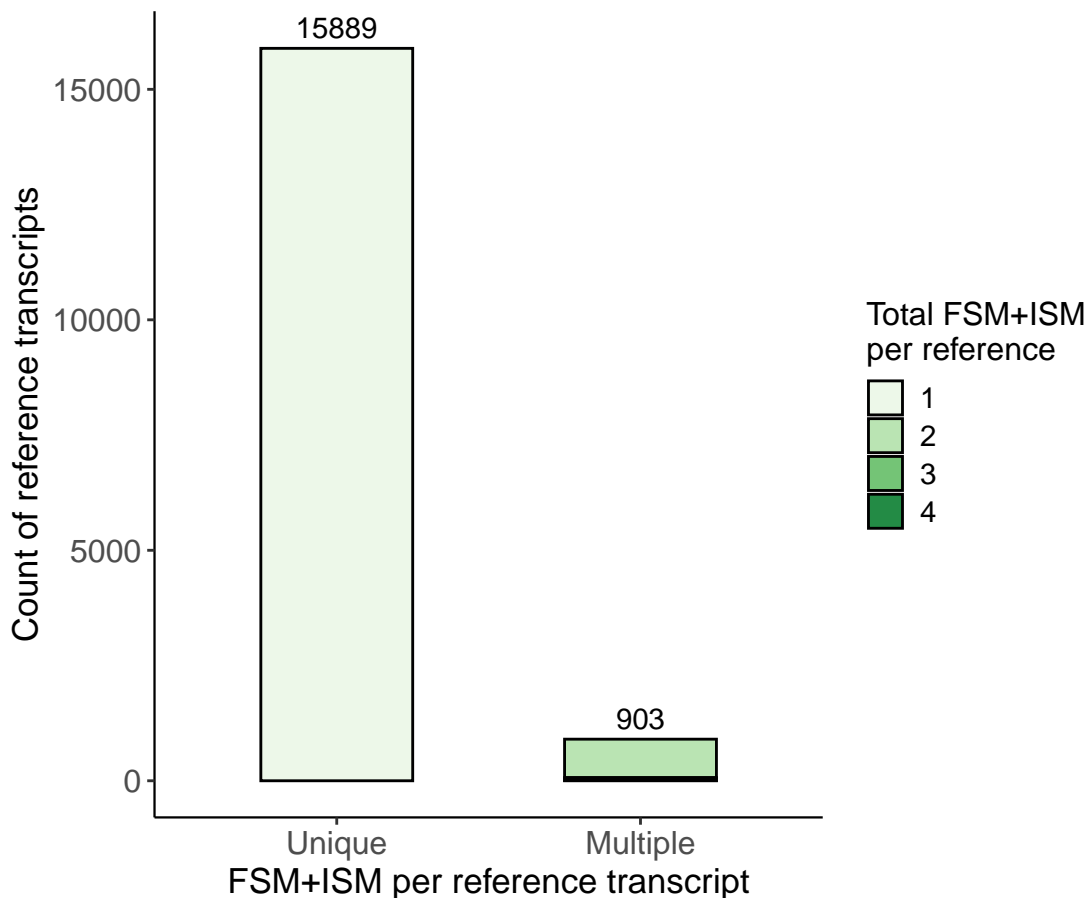
Reference Transcript Redundancy

Only ISM with CAGE support and polyA motif



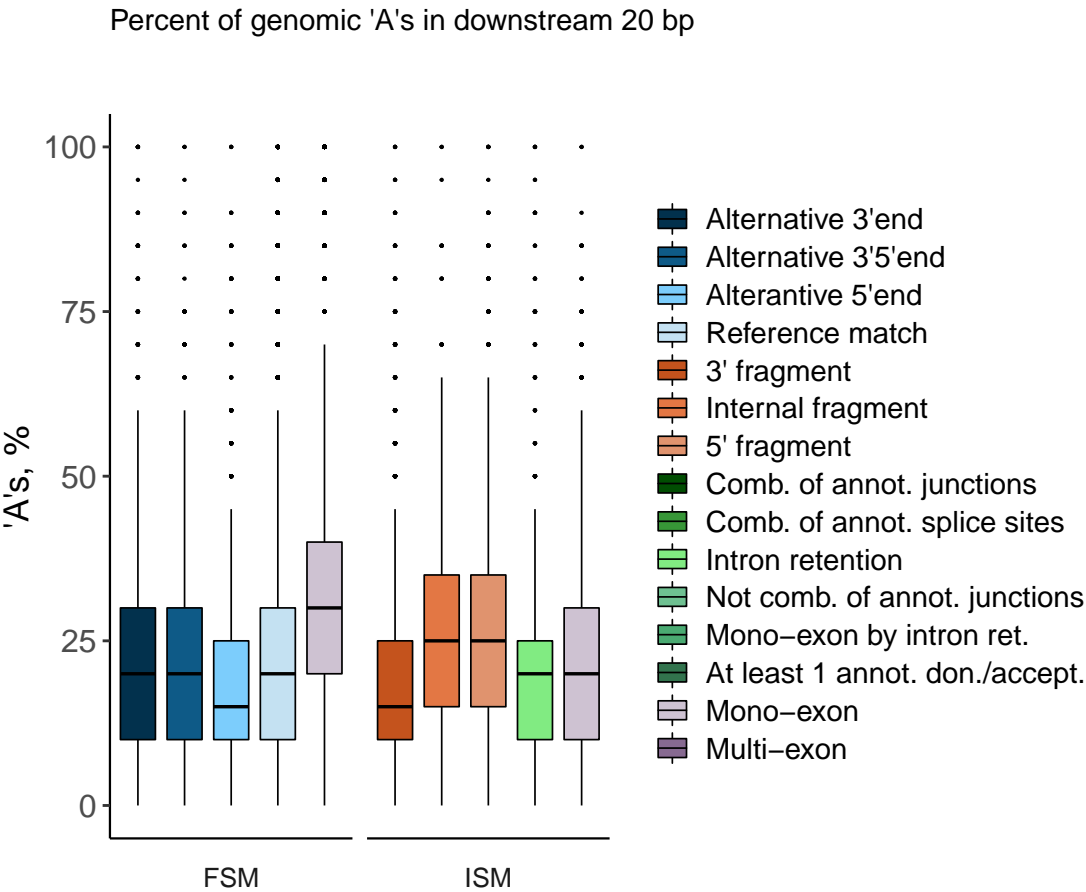
Reference Transcript Redundancy

FSM+ISM with CAGE support and polyA motif

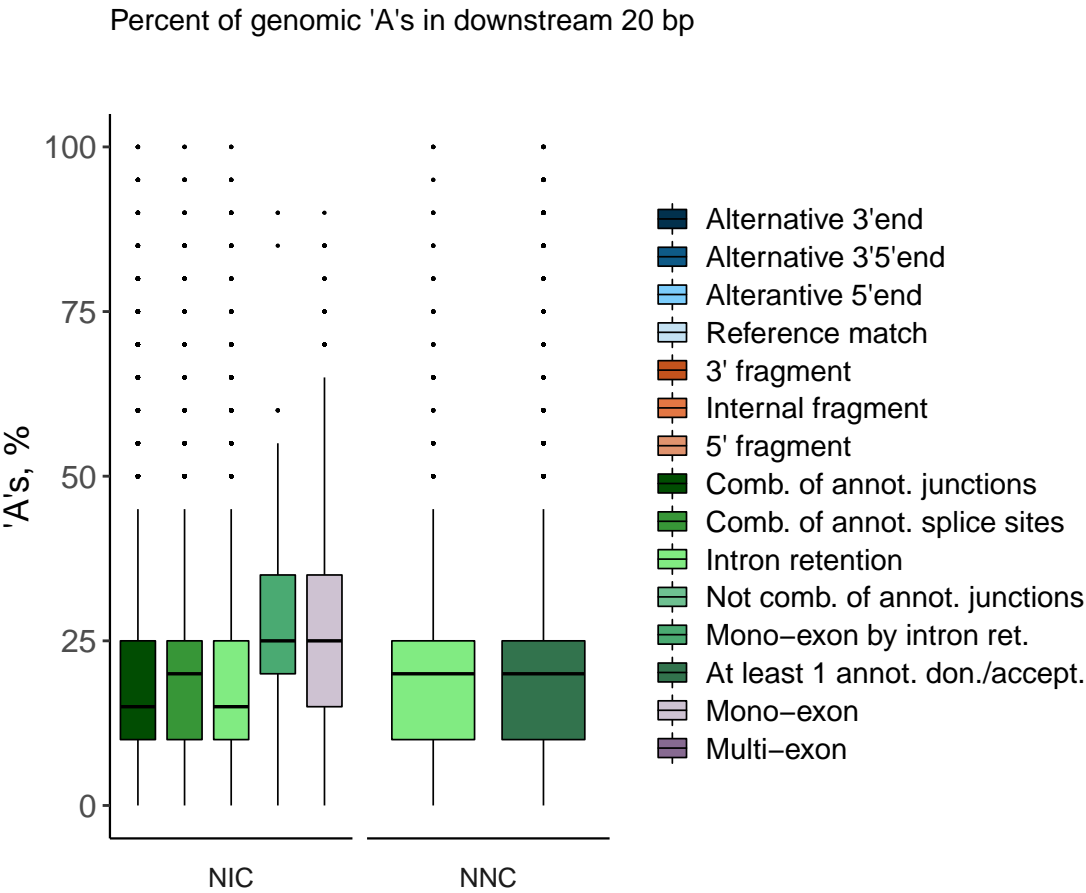


Intra-Priming Quality Check

Possible Intra-Priming by Structural Category

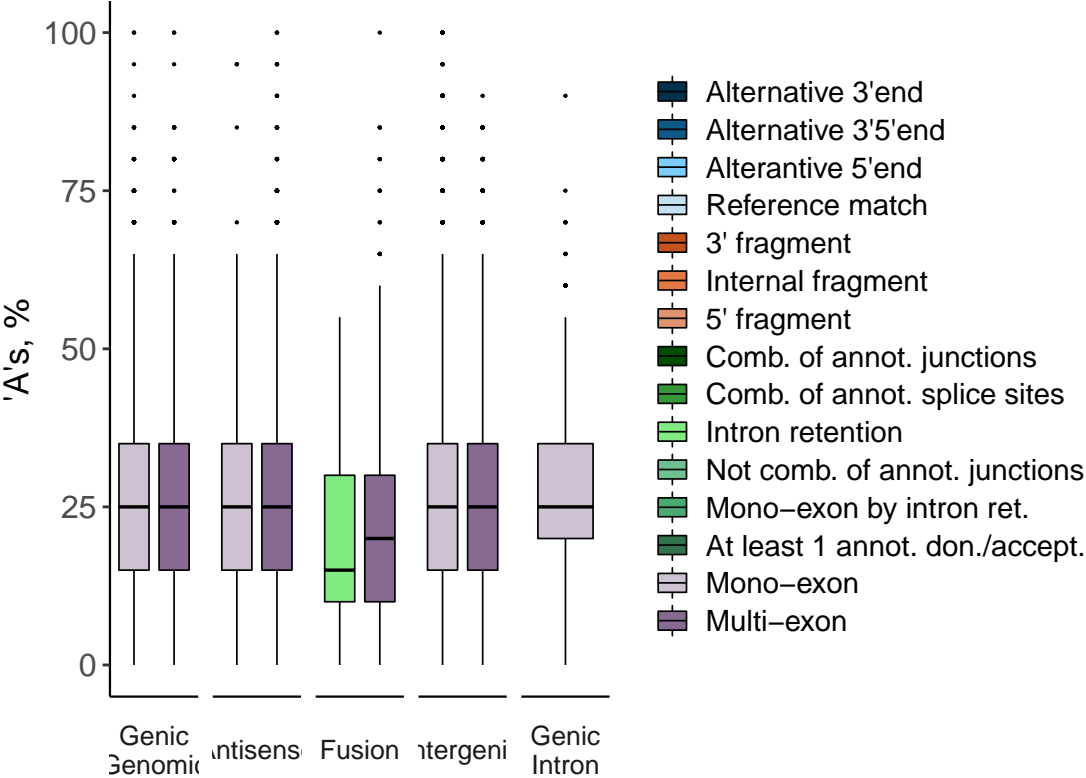


Possible Intra-Priming by Structural Category



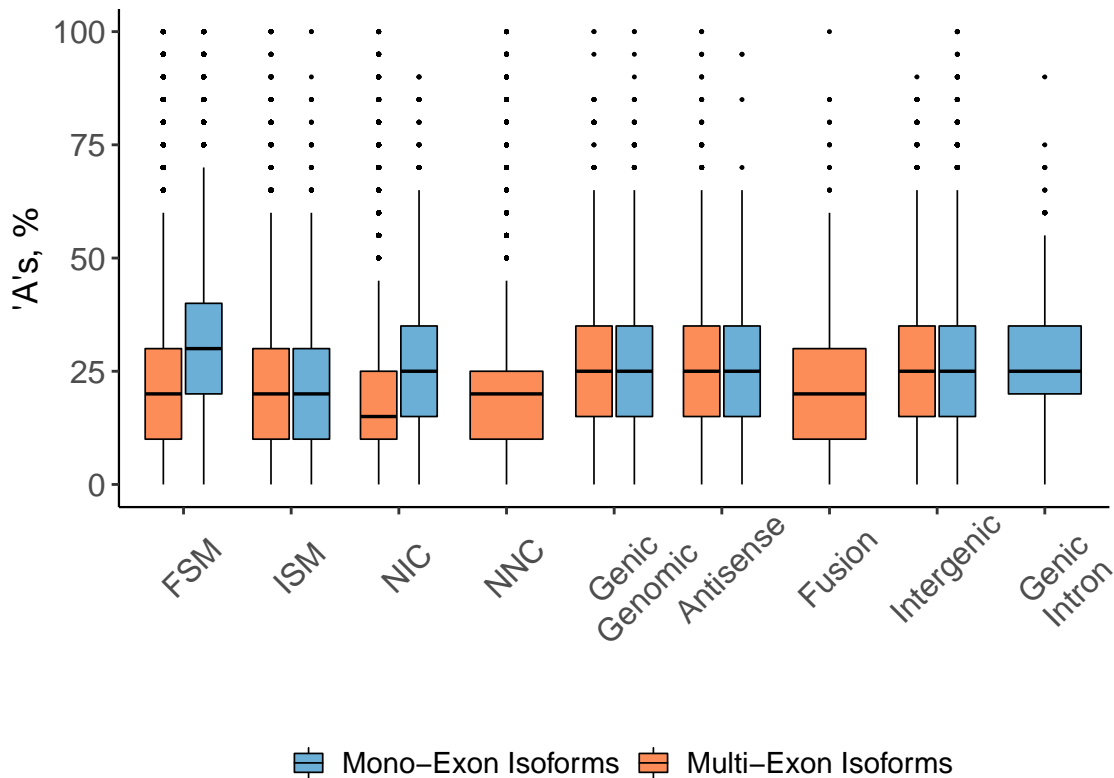
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



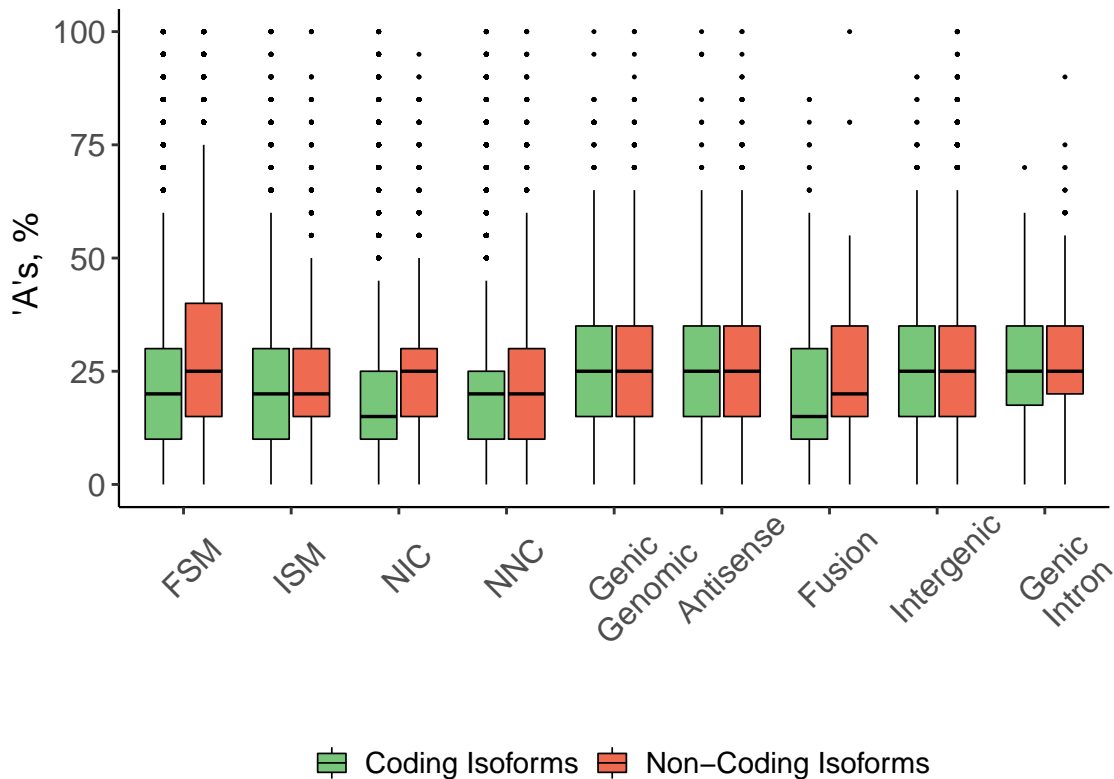
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



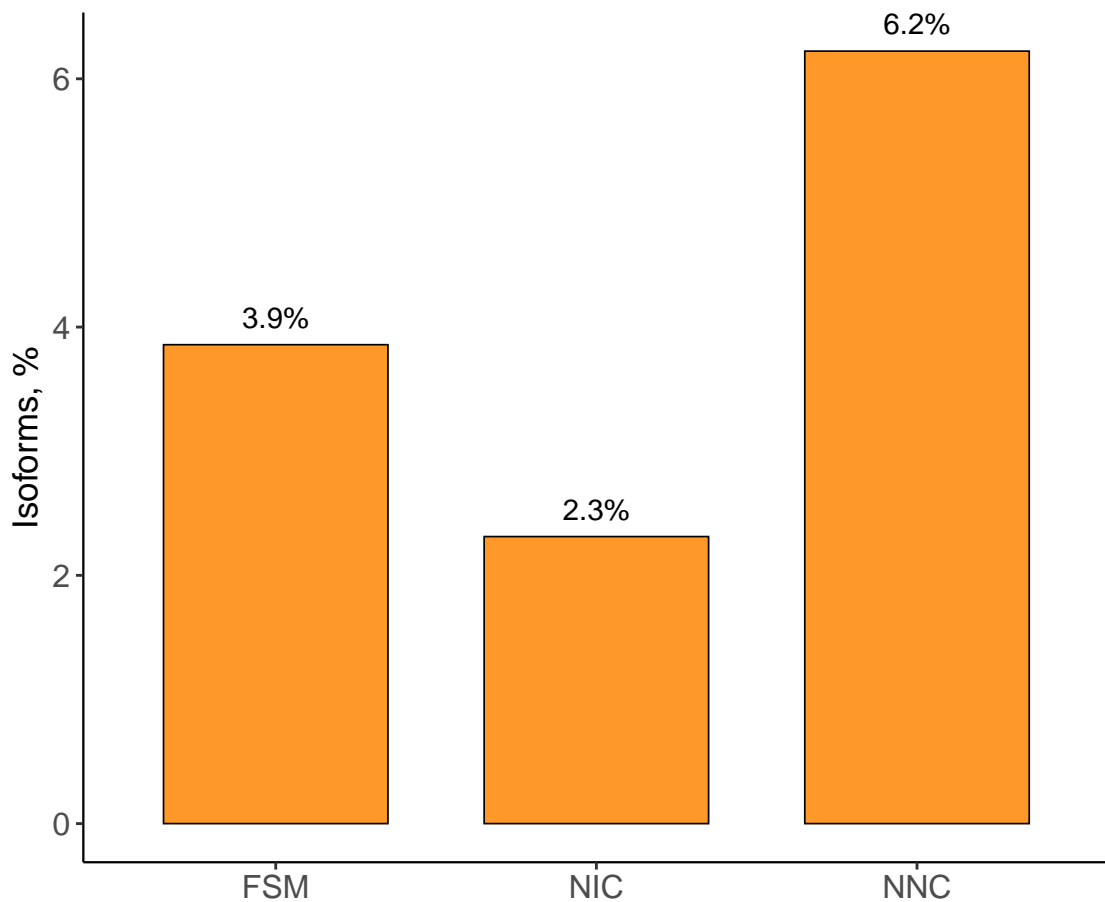
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp

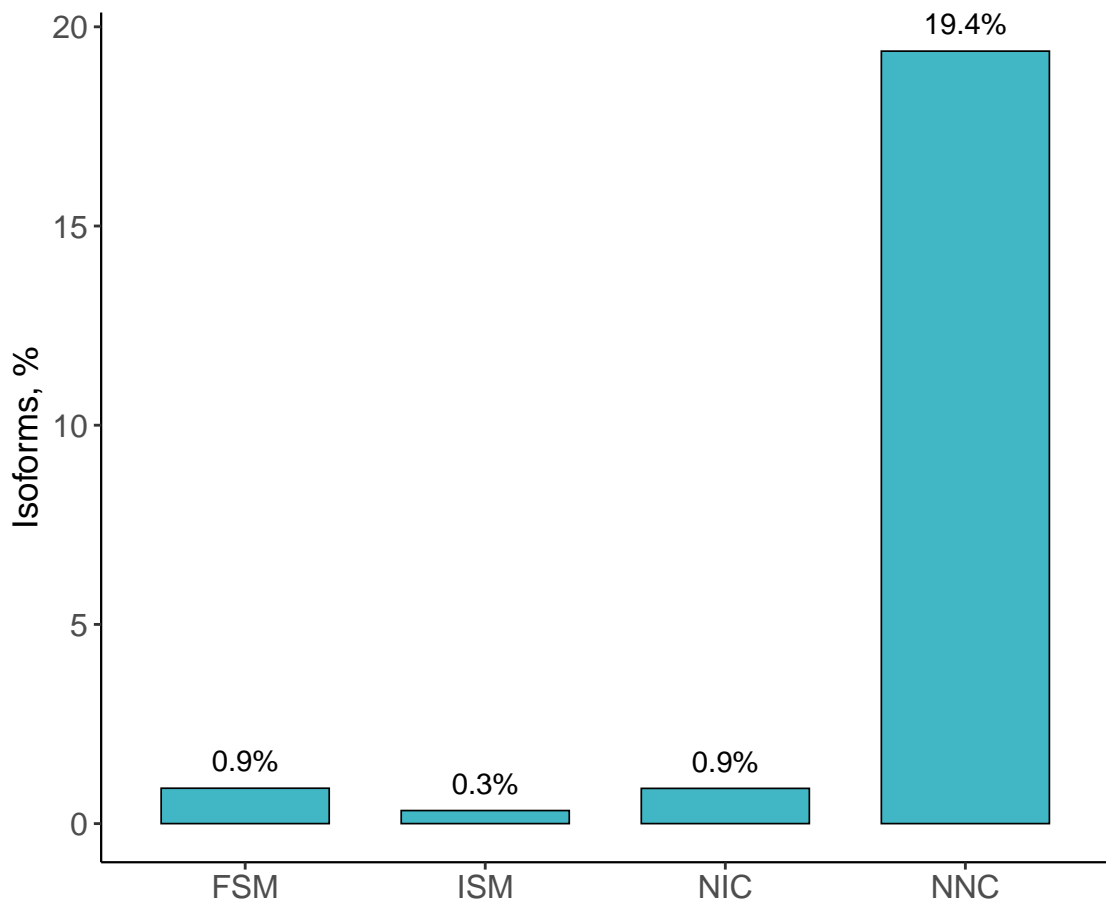


Features of Bad Quality

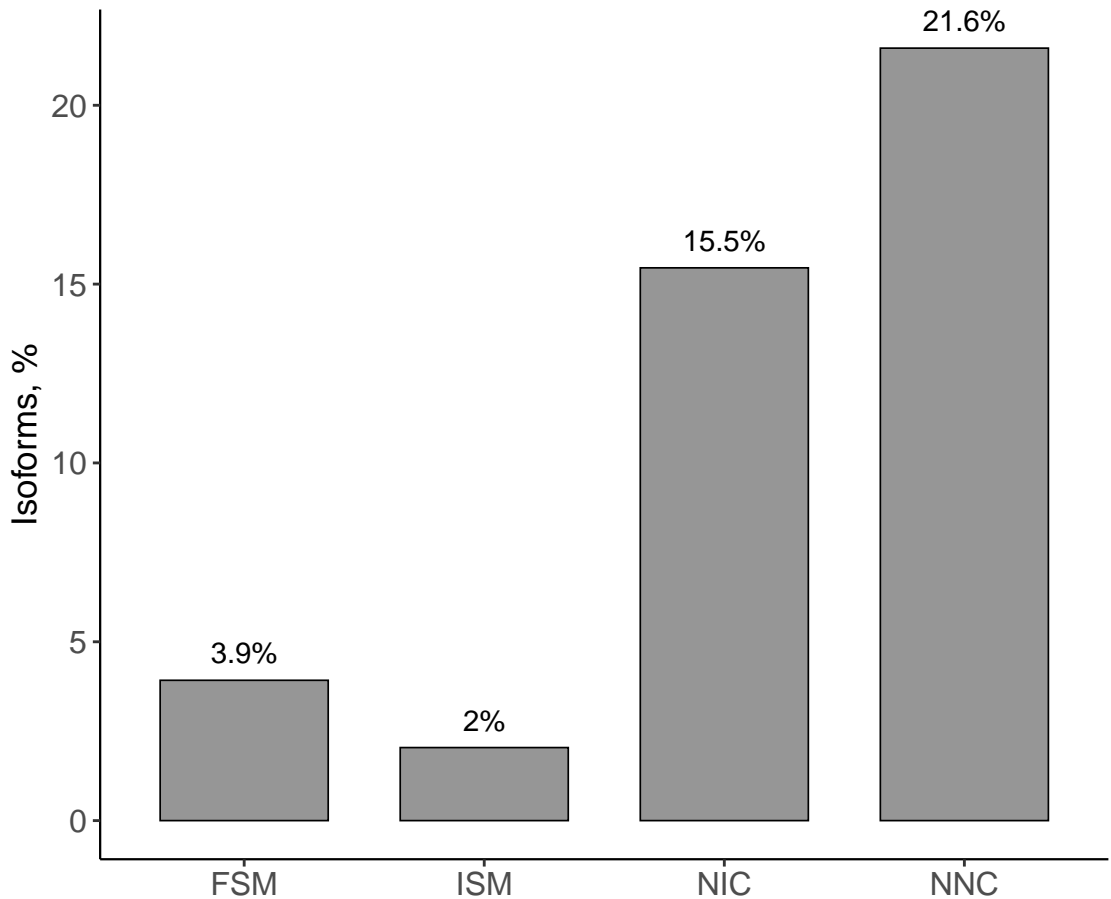
RT-switching



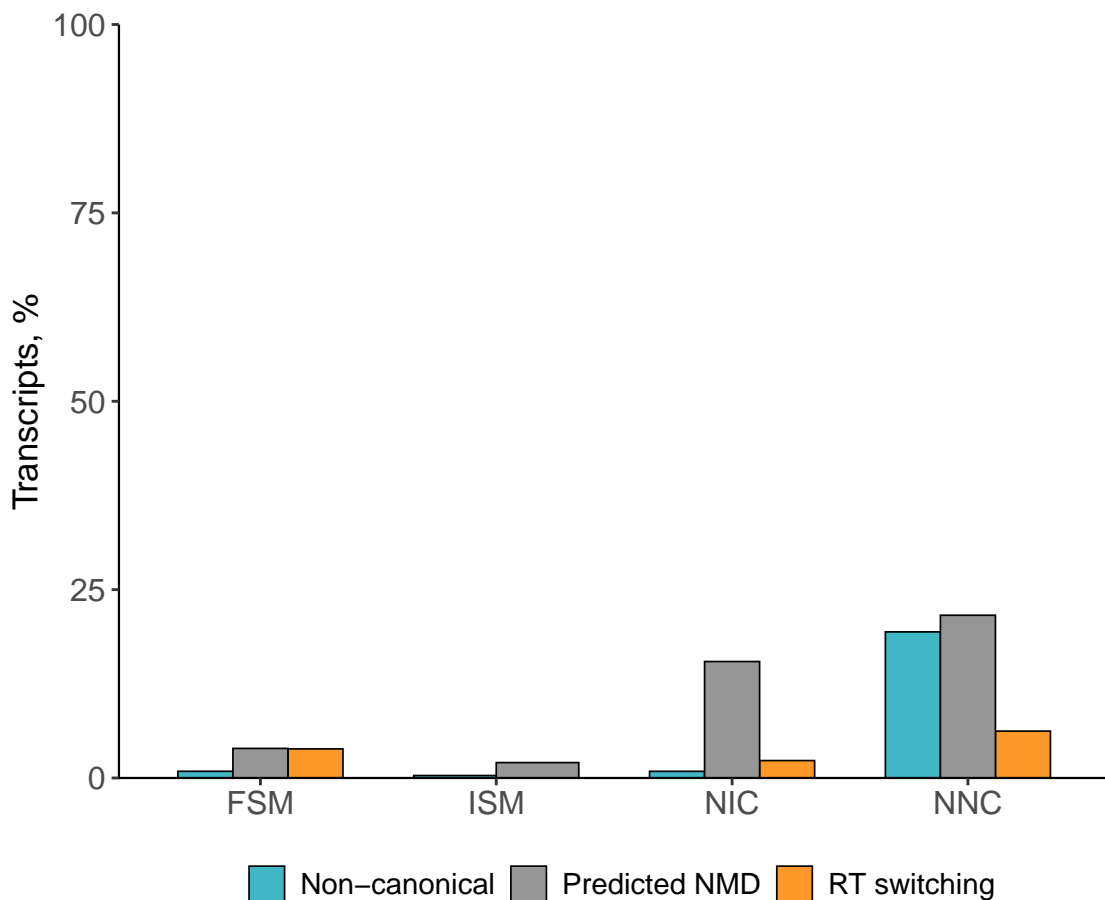
Non-Canonical Junctions



Nonsense-Mediated Decay by Structural Category

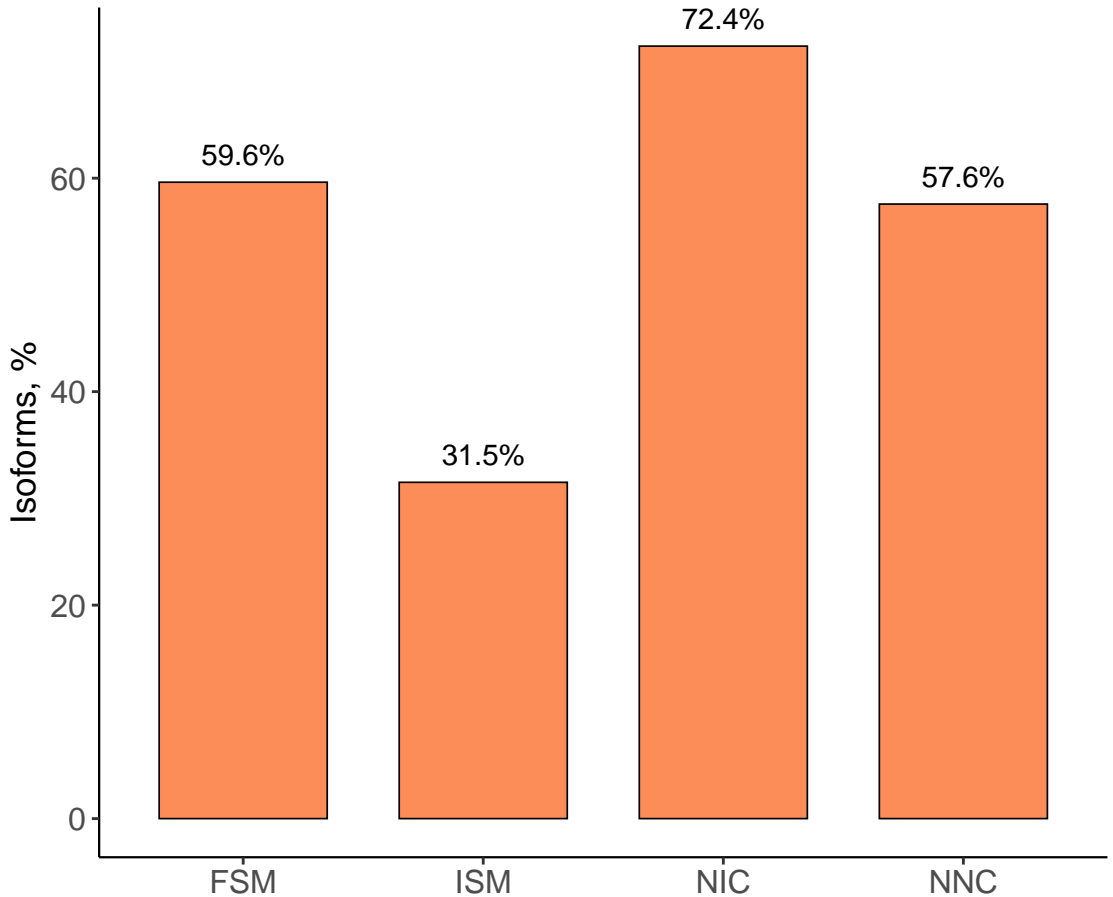


Quality Control Attributes Across Structural Categories

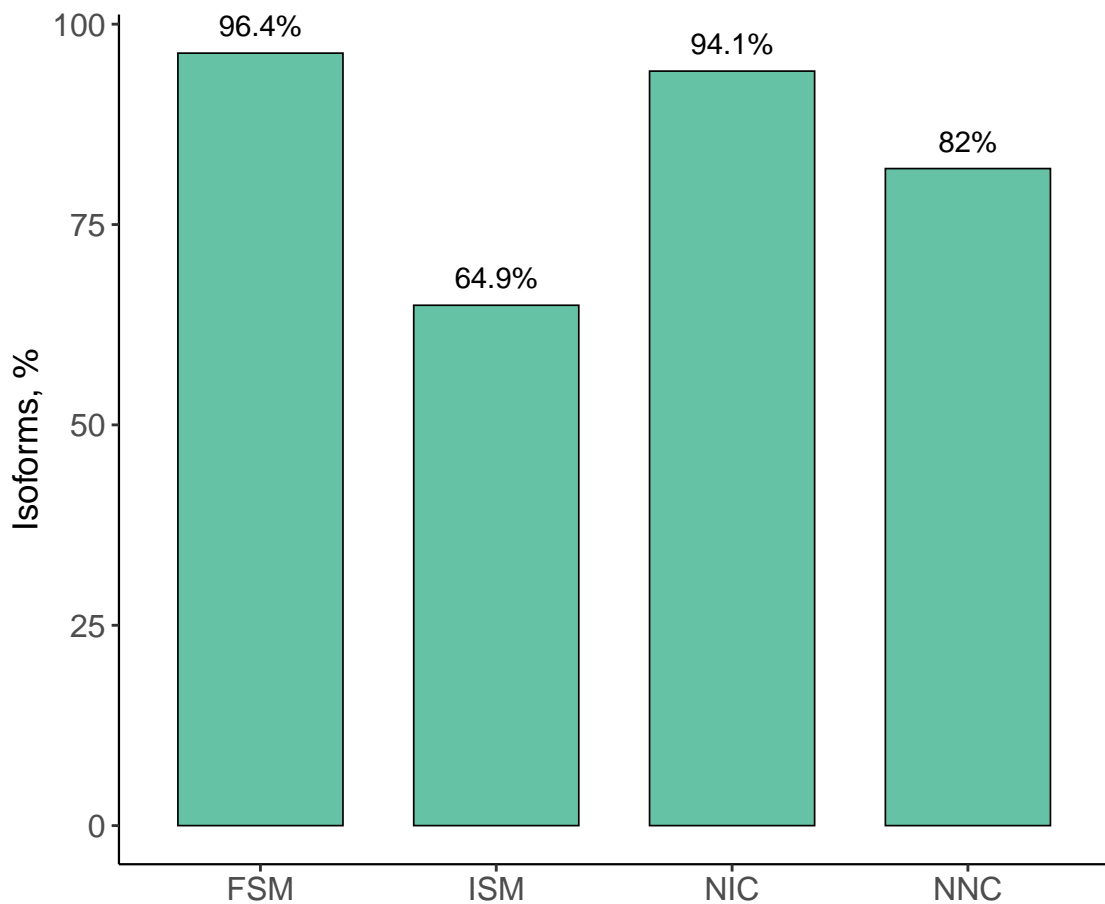


Features of Good Quality

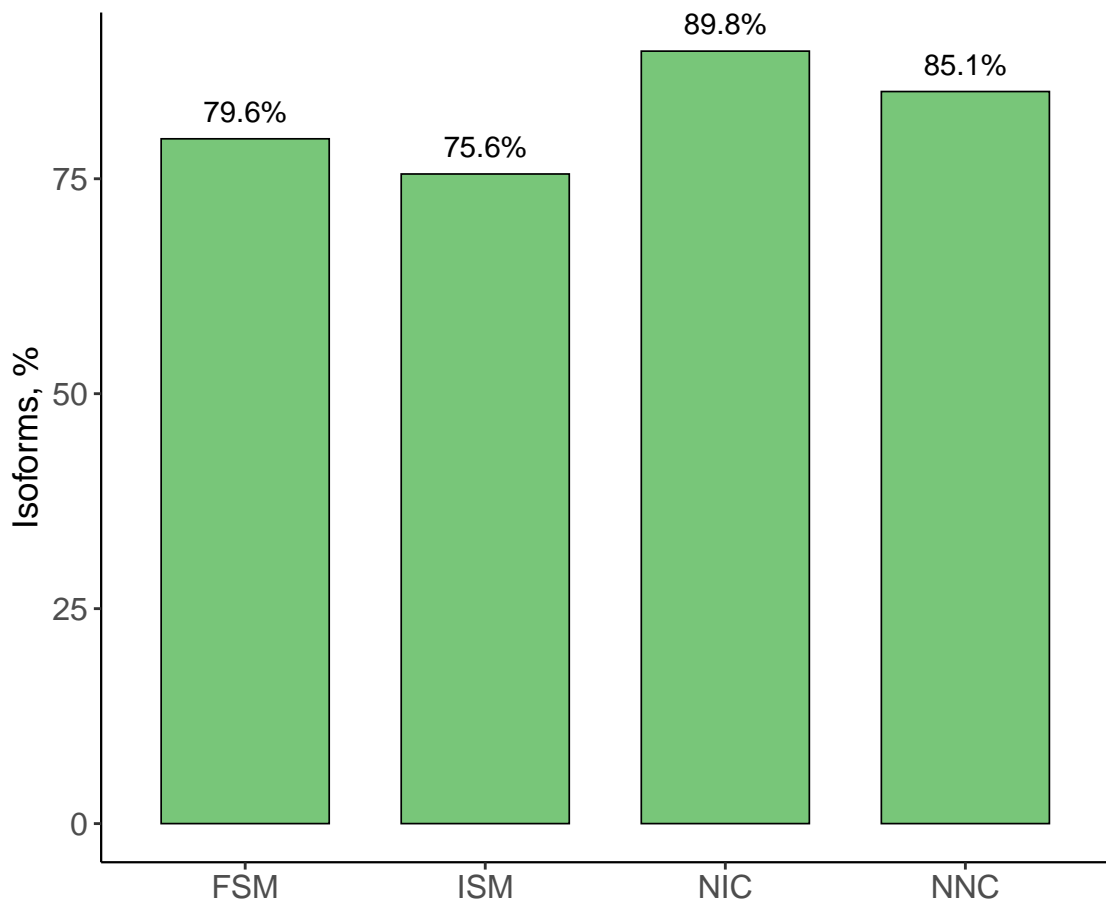
CAGE Support



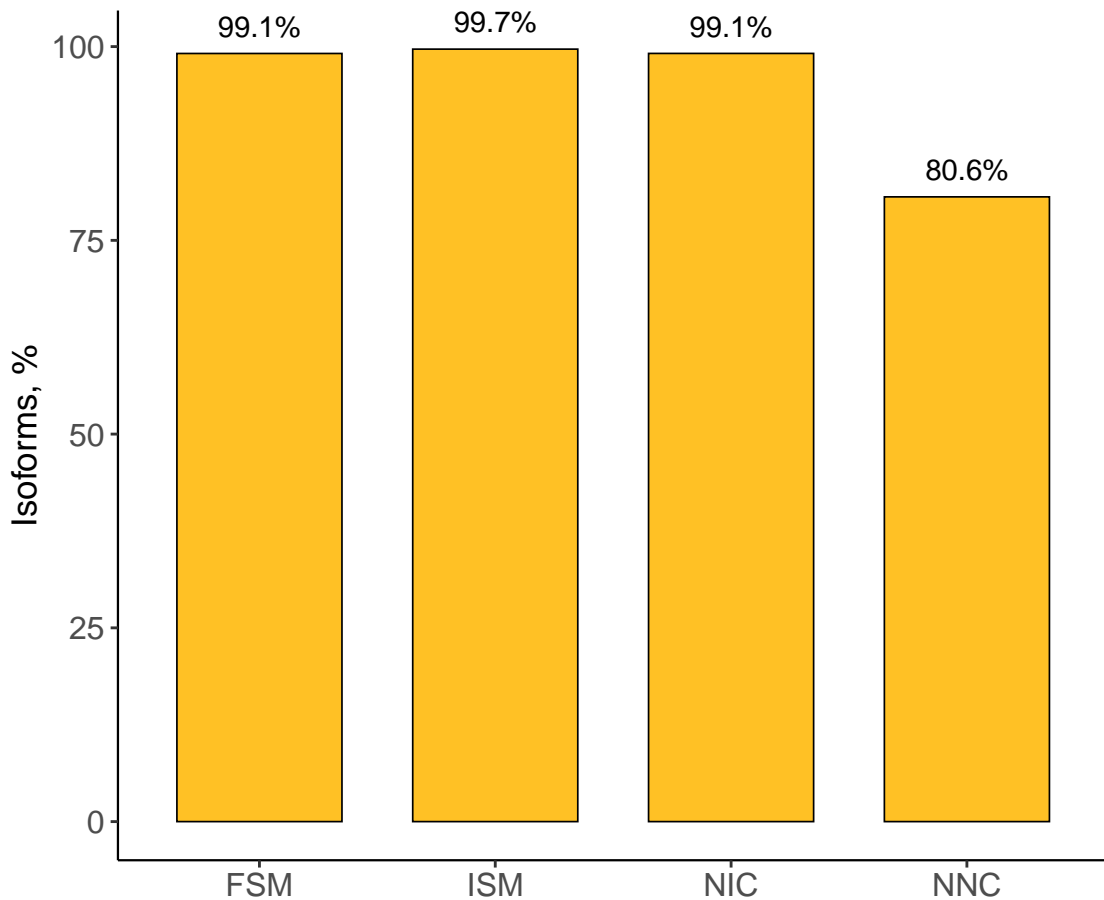
Annotation Support



PolyA Support



All Canonical Junctions



Good Quality Control Attributes Across Structural Categories

