

SQANTI3 report

Unique Genes: 30229
Unique Isoforms: 228379

Transcript Classification

Category	Isoforms, count
FSM	56795
ISM	67804
NIC	48878
NNC	35743
Genic Genomic	3407
Antisense	4234
Fusion	1149
Intergenic	10368
Genic Intron	1

Gene Classification

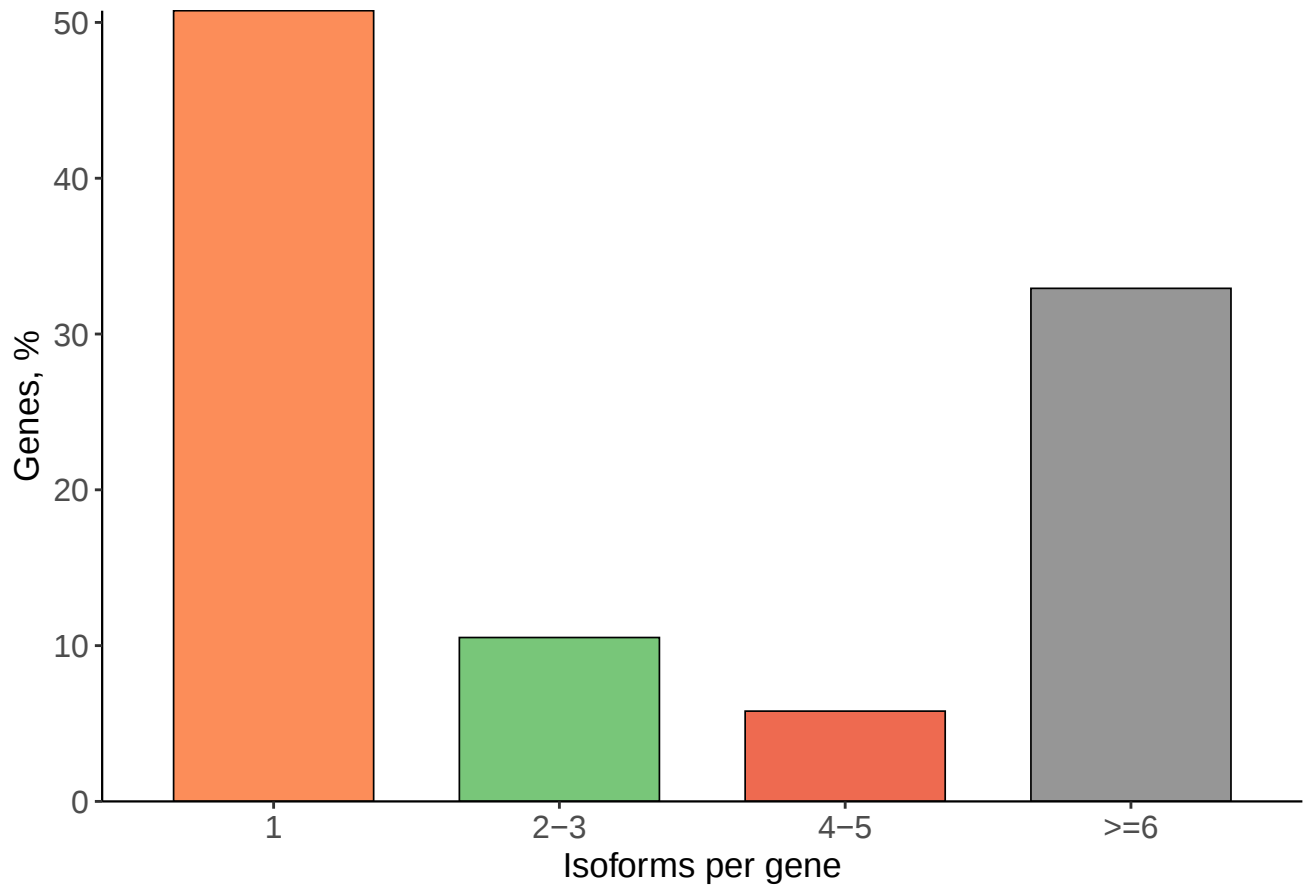
Category	Genes, count
Annotated Genes	17467
Novel Genes	12762

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	168094	78.19
Known Non-canonical	611	0.28
Novel canonical	38969	18.13
Novel Non-canonical	7307	3.40

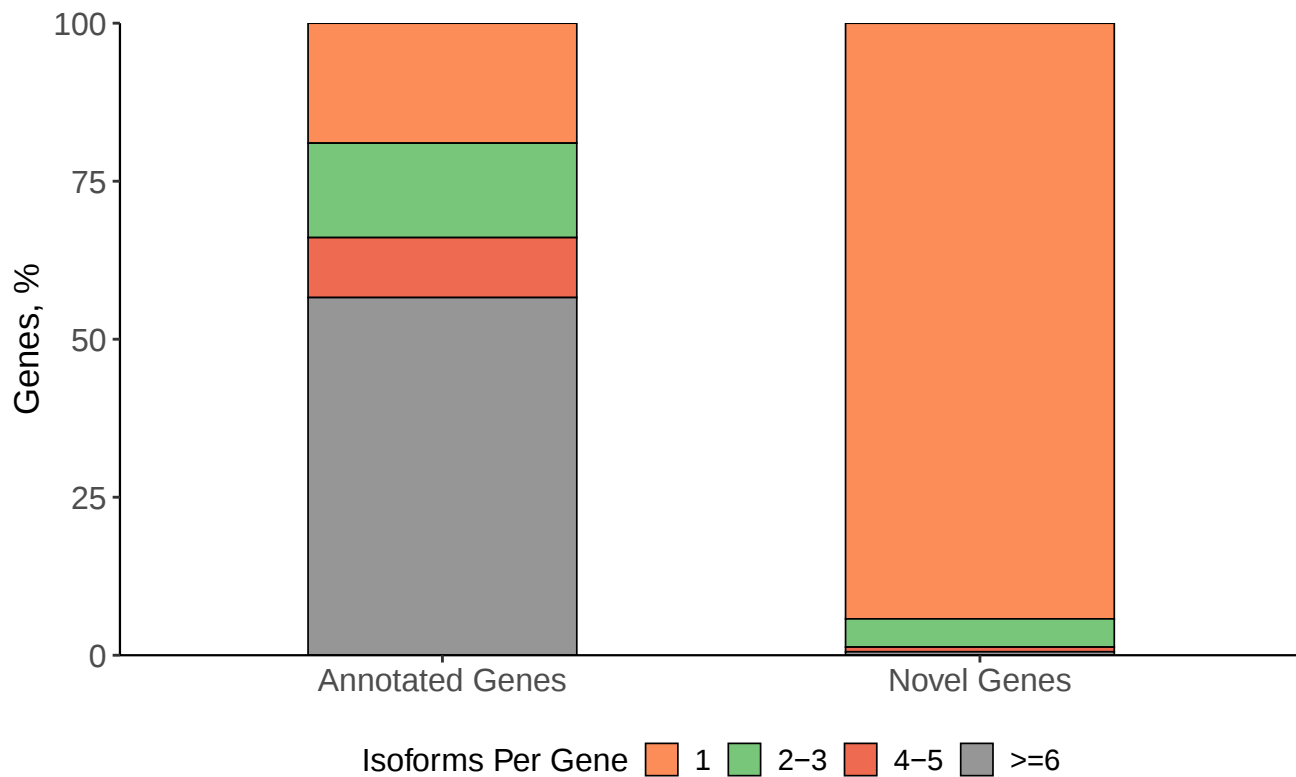
Gene Characterization

Number of Isoforms per Gene

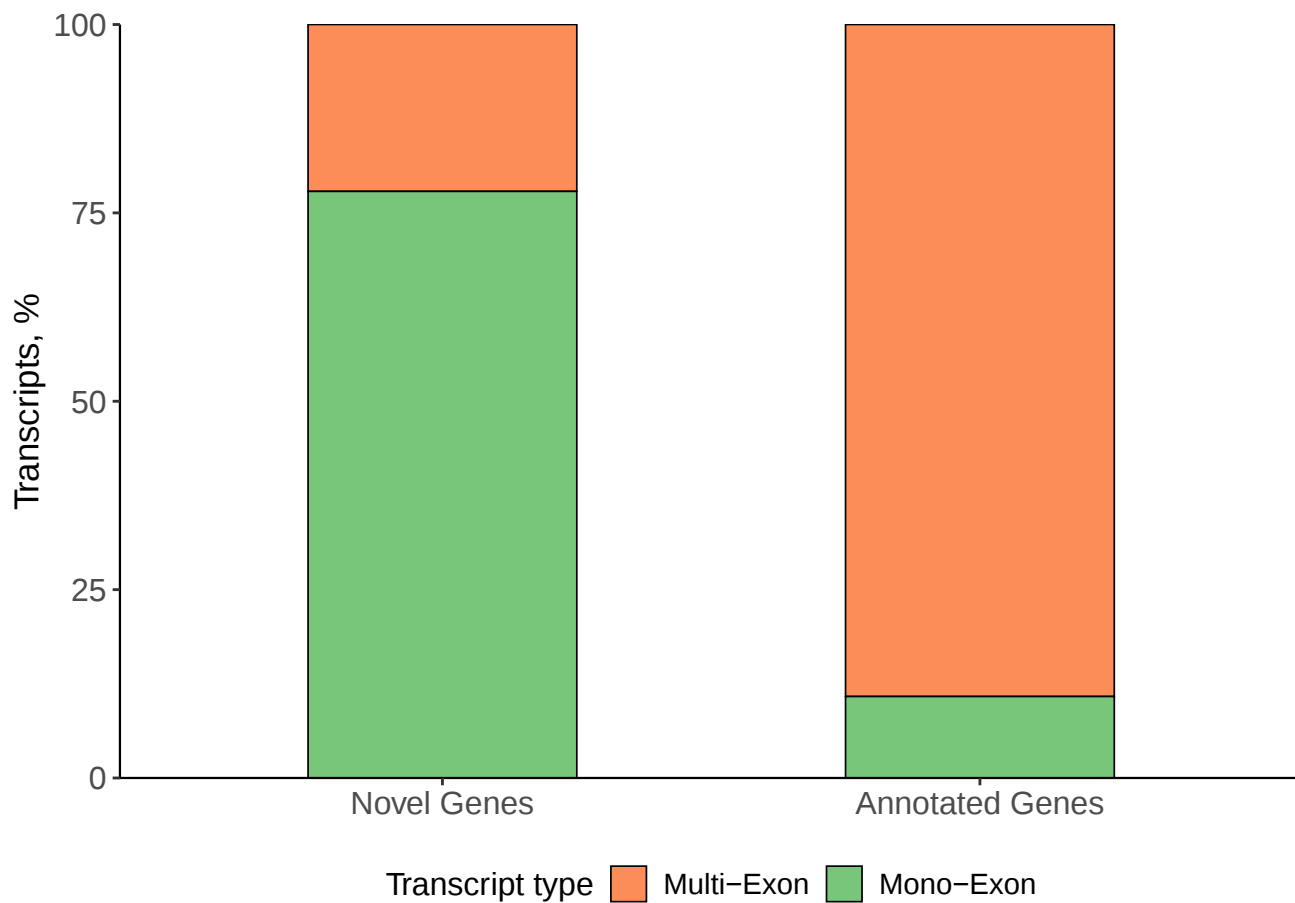


Number of Isoforms per Gene

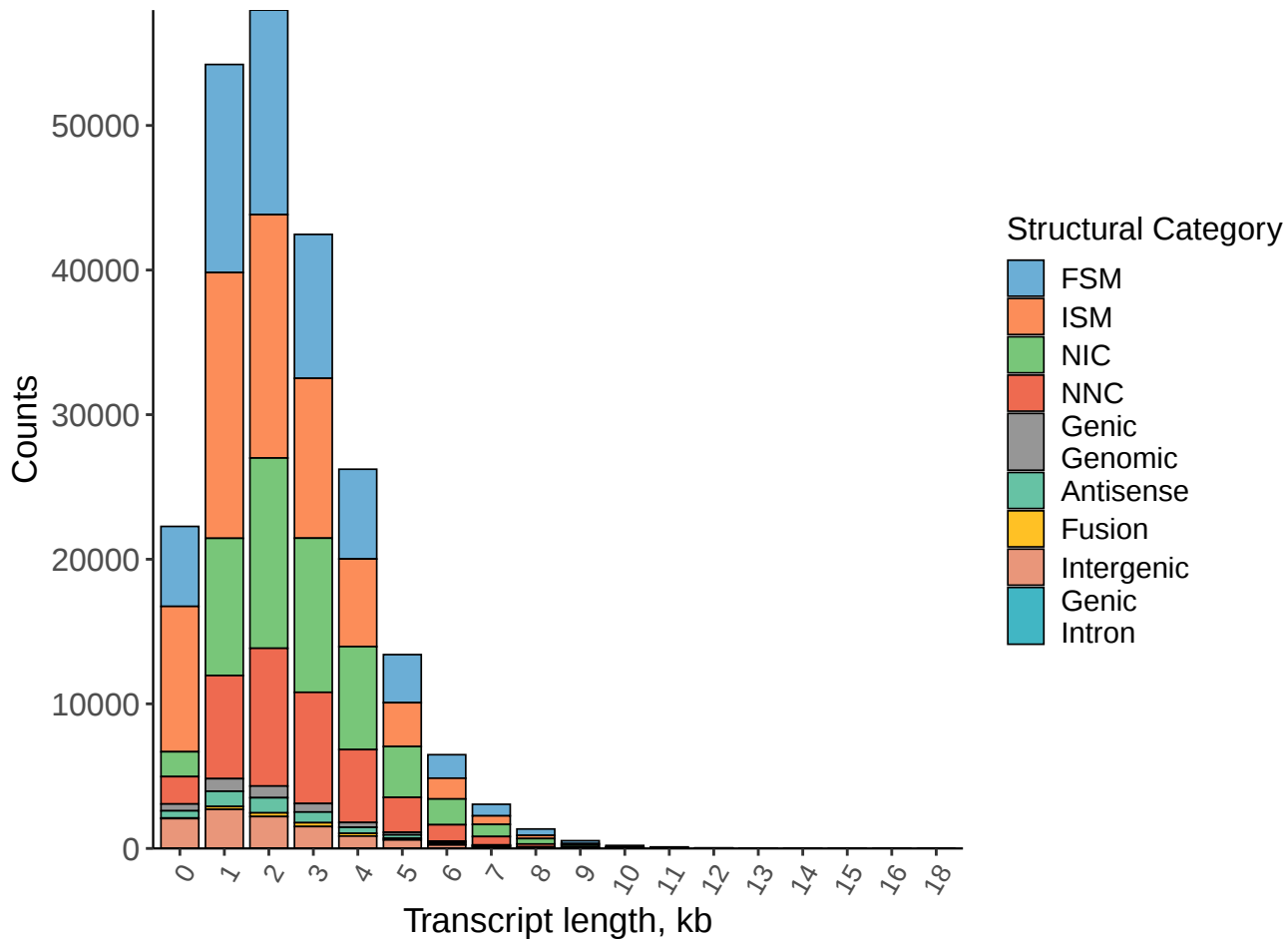
Known vs Novel Genes



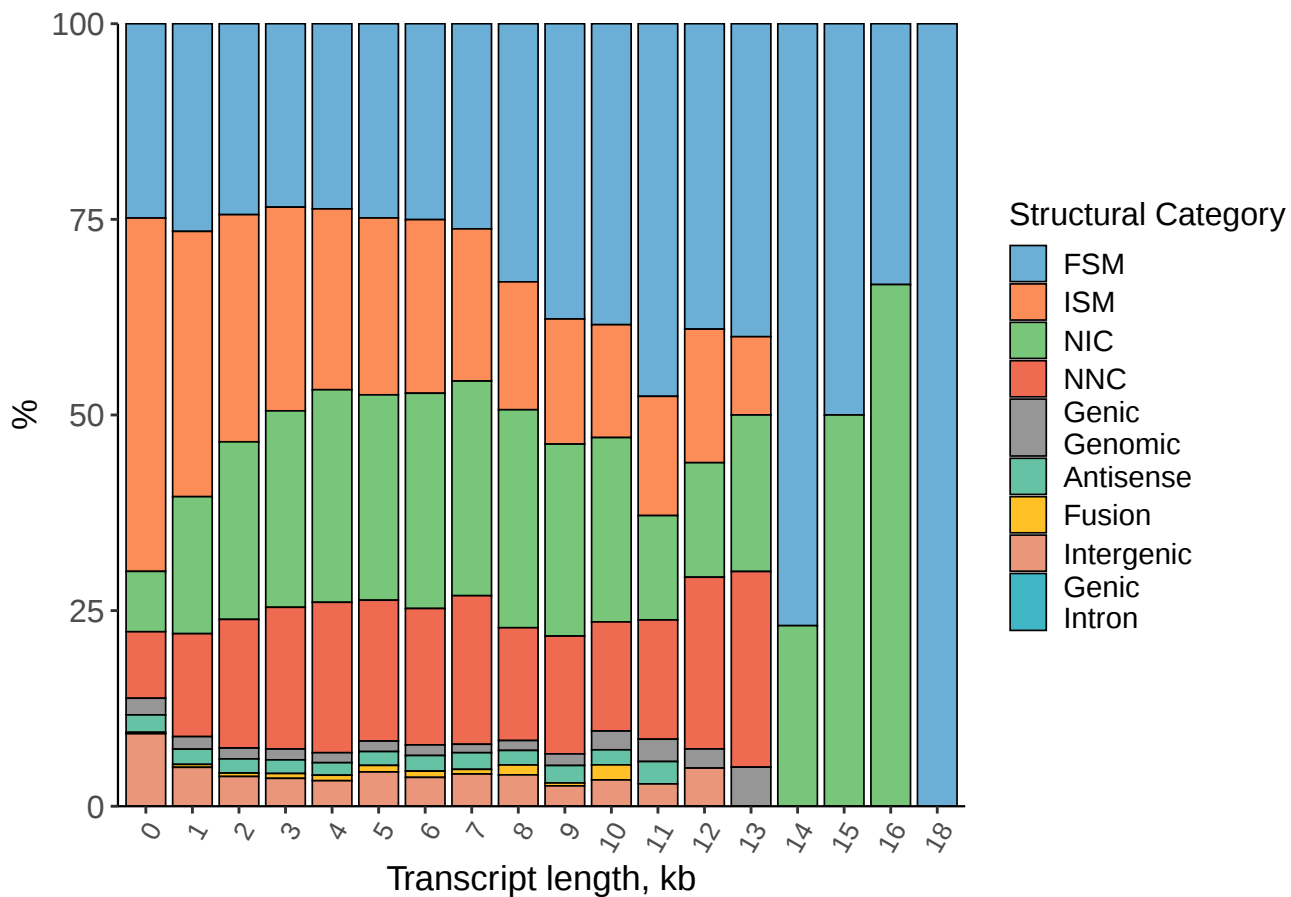
Distribution of Mono- vs Multi-Exon Transcripts



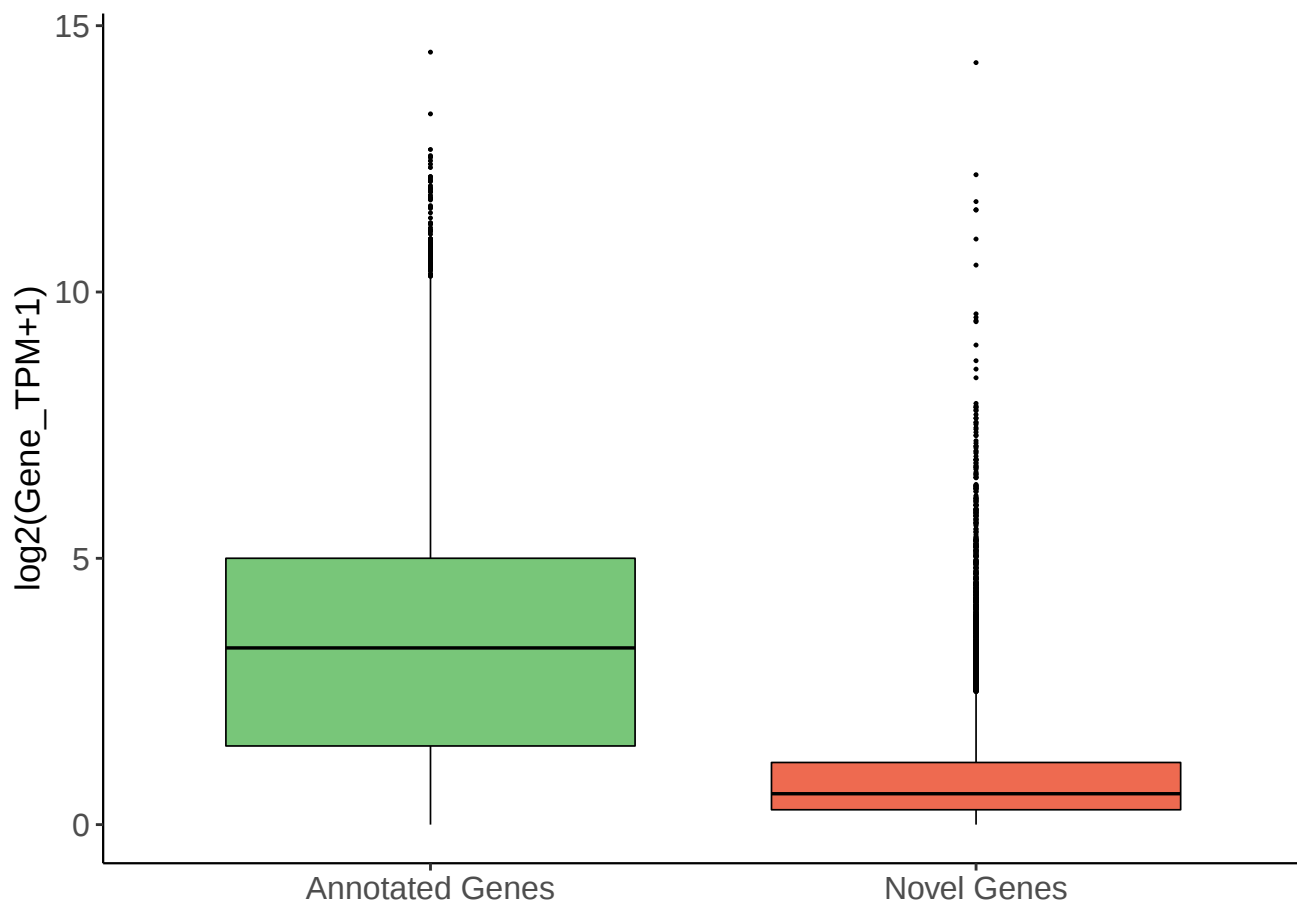
Structural Categories by Transcript Length



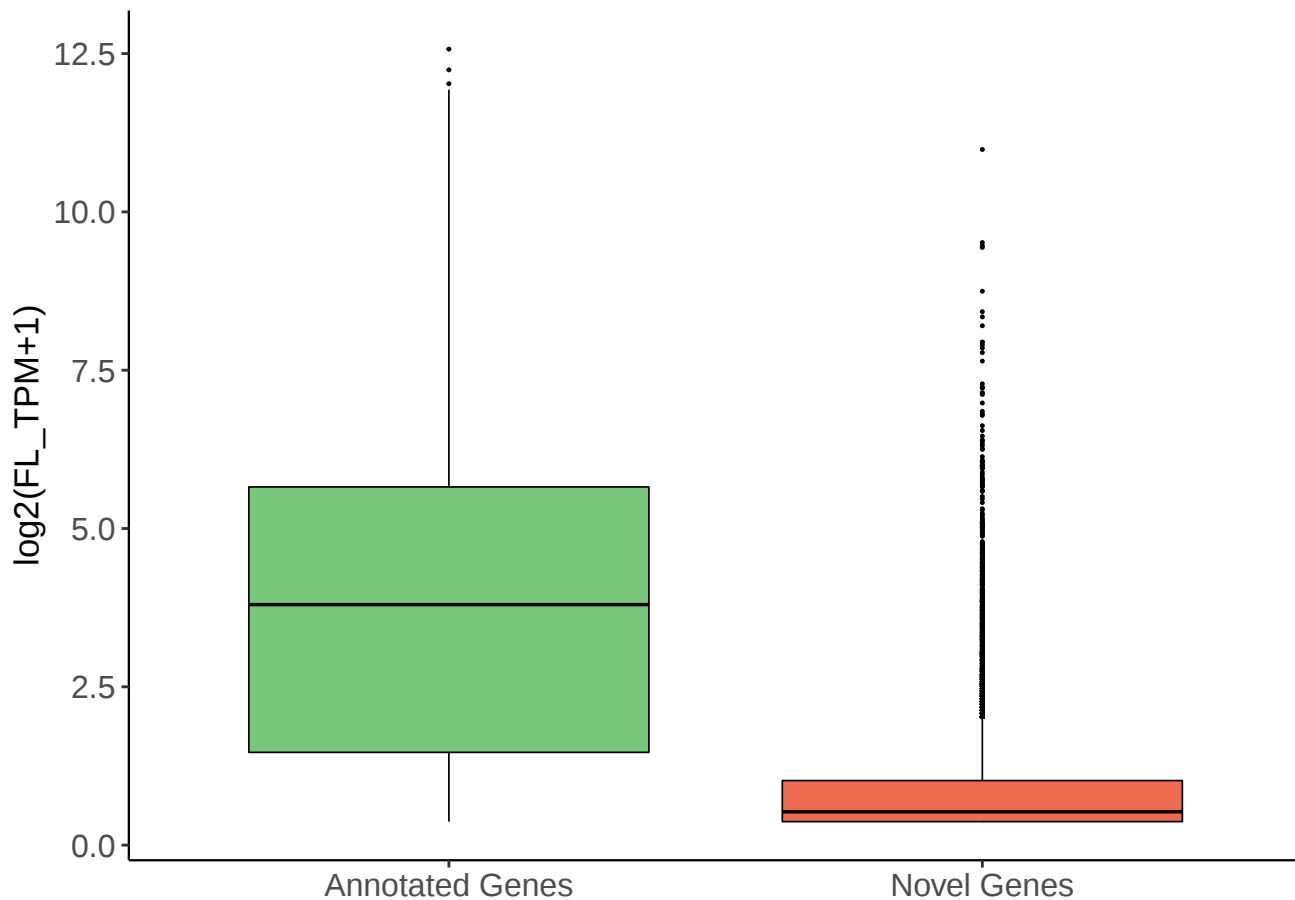
Structural Categories by Transcript Length



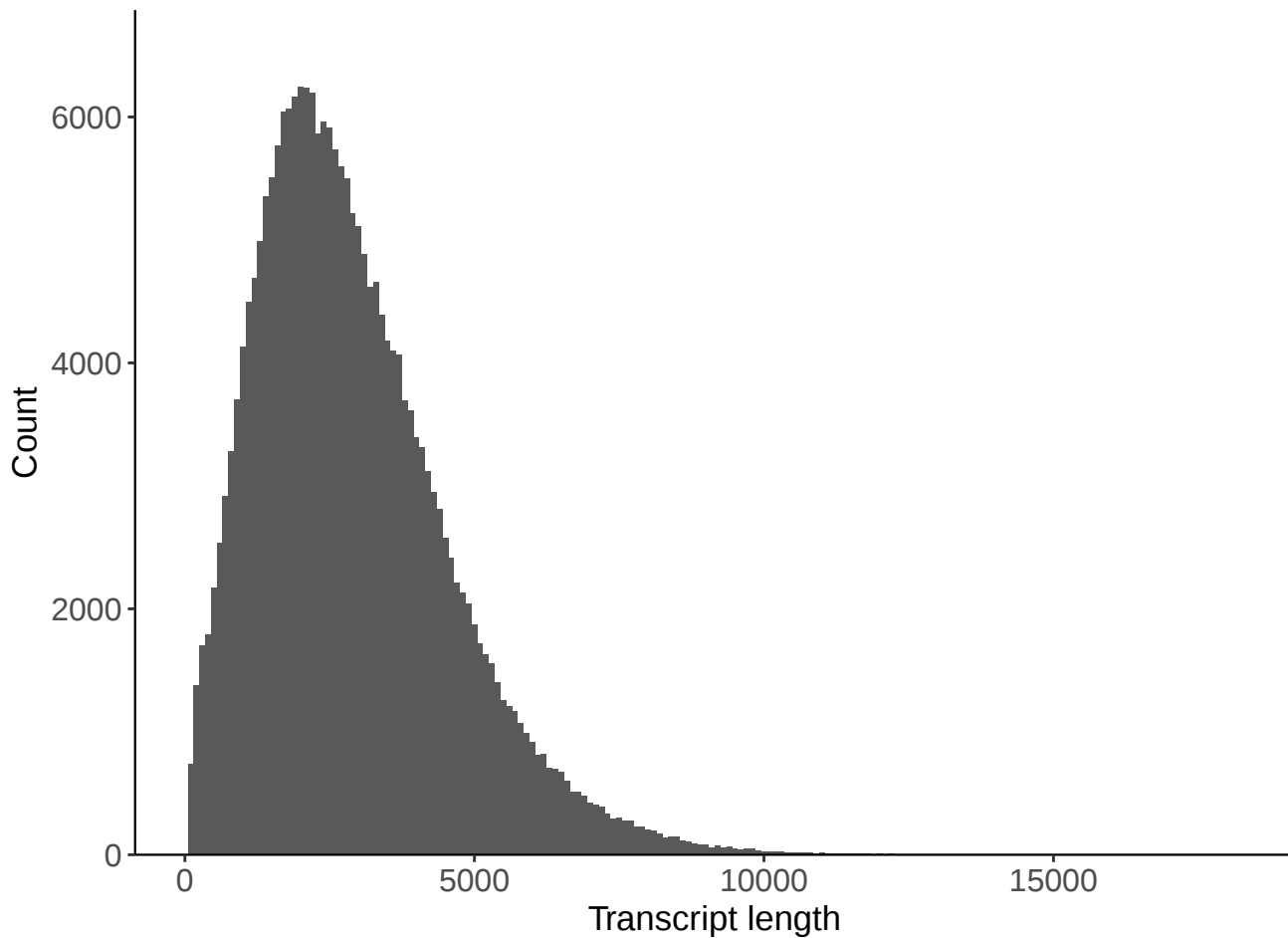
Annotated vs Novel Gene Expression



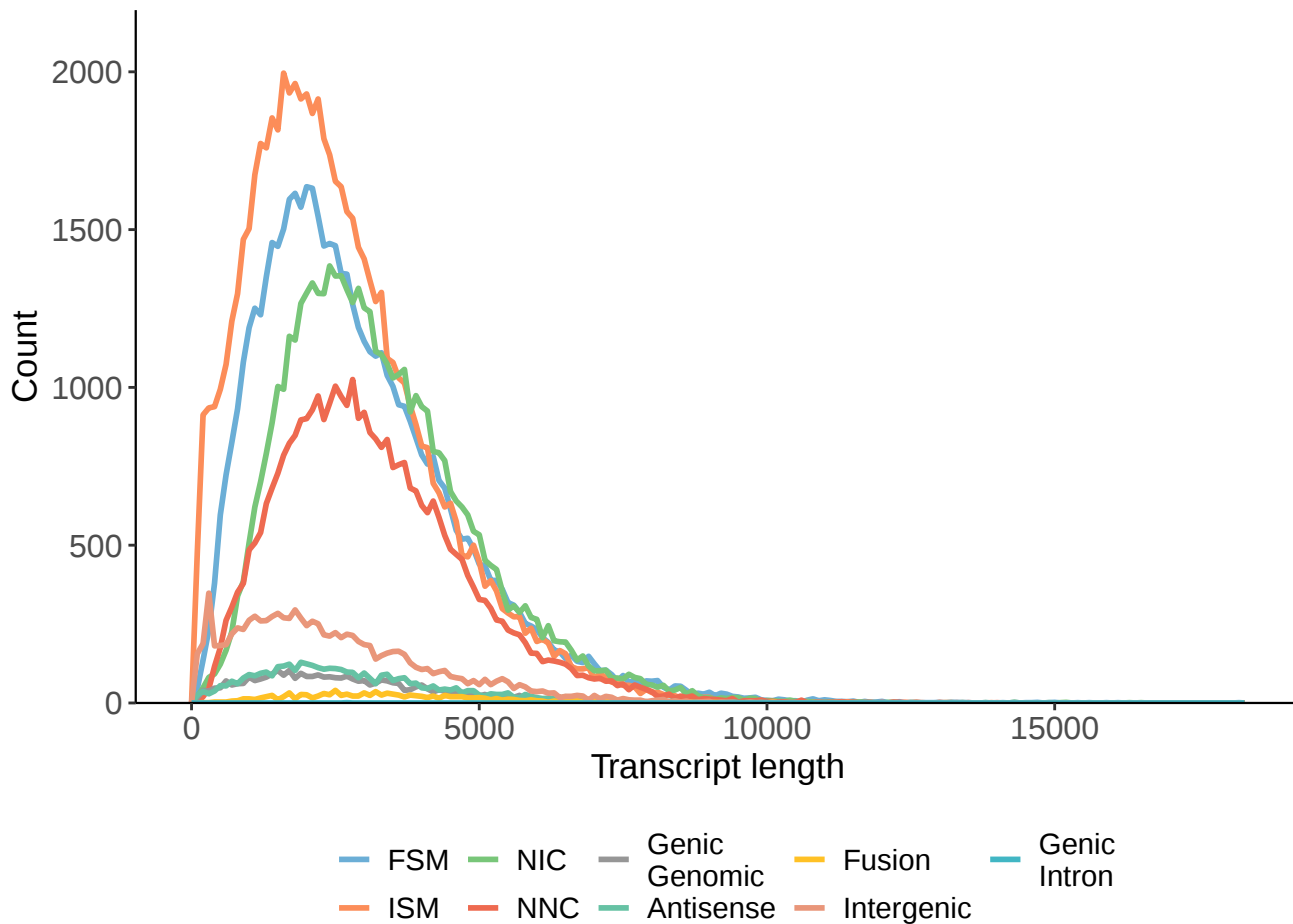
Number of FL reads per Gene by Type of Gene Annotation



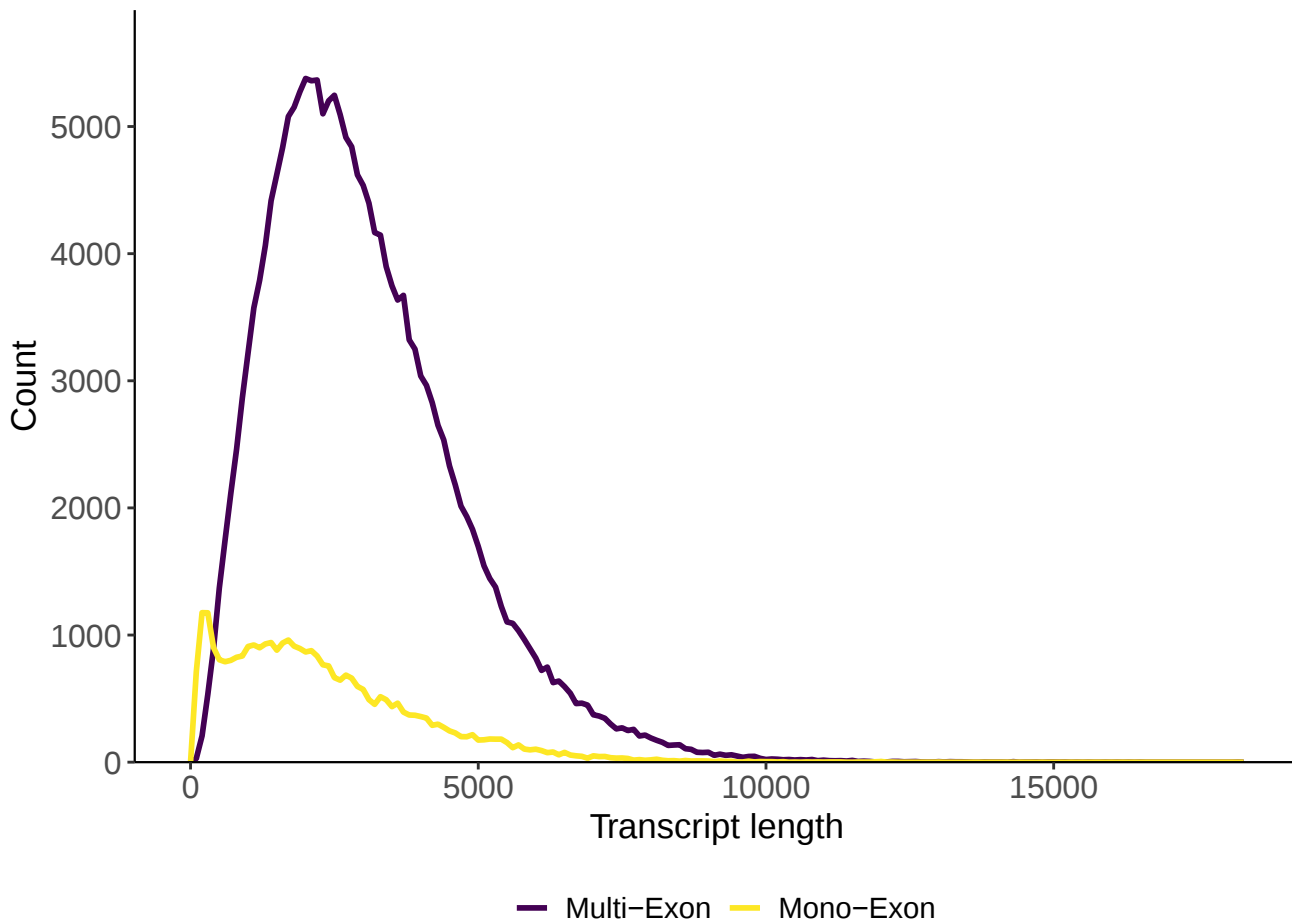
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

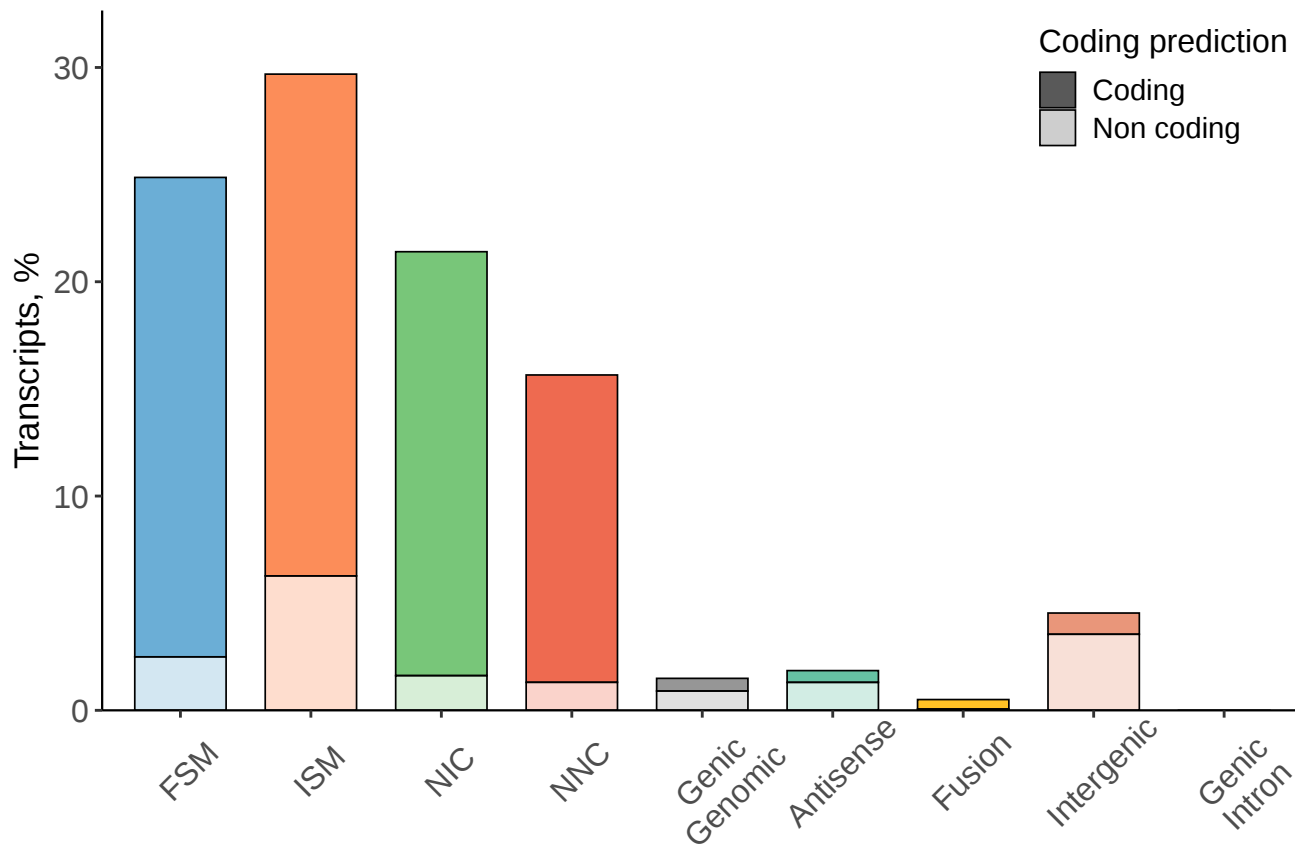


Mono- vs Multi- Exon Transcript Lengths Distribution

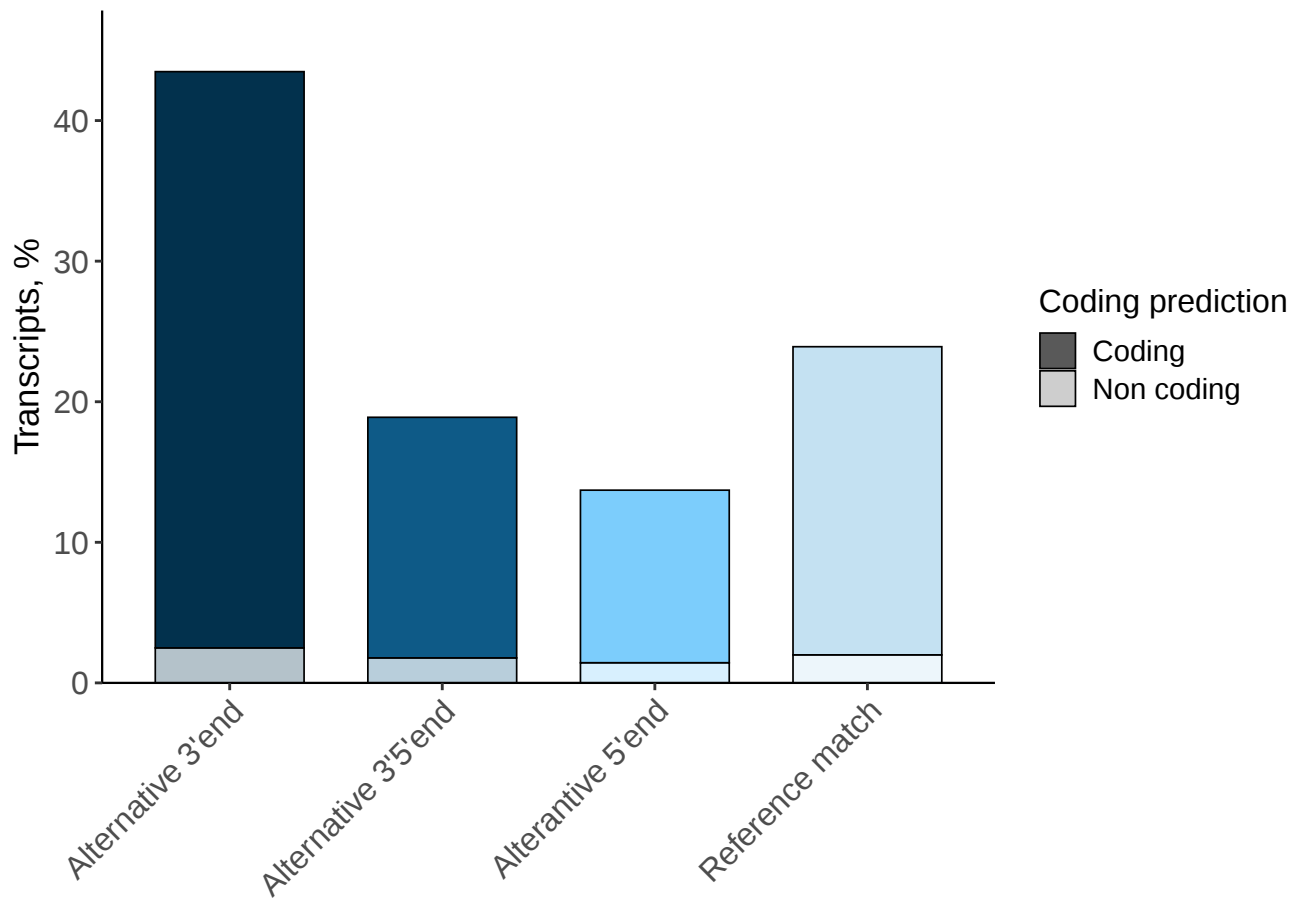


Structural Isoform Characterization

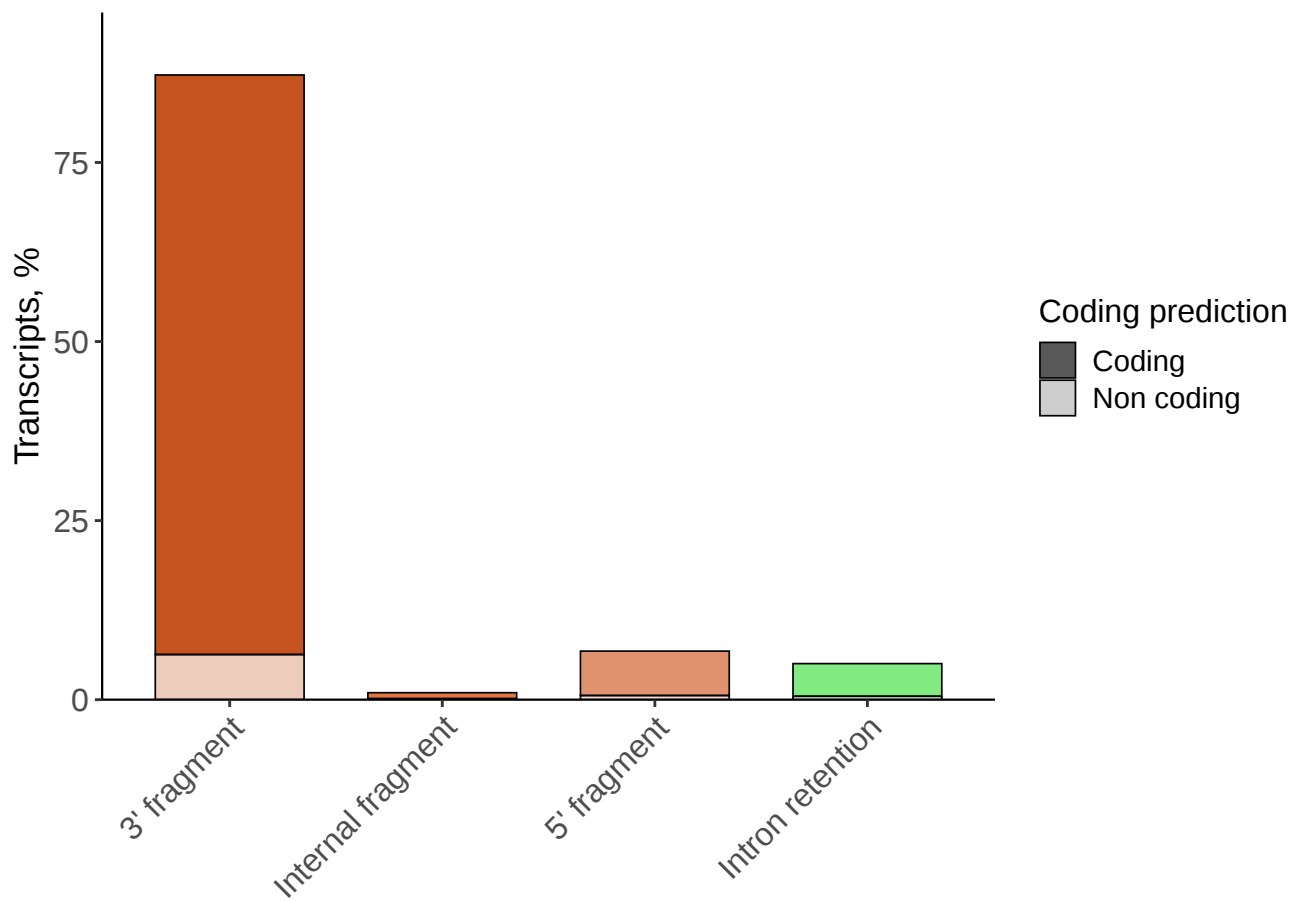
Isoform Distribution Across Structural Categories



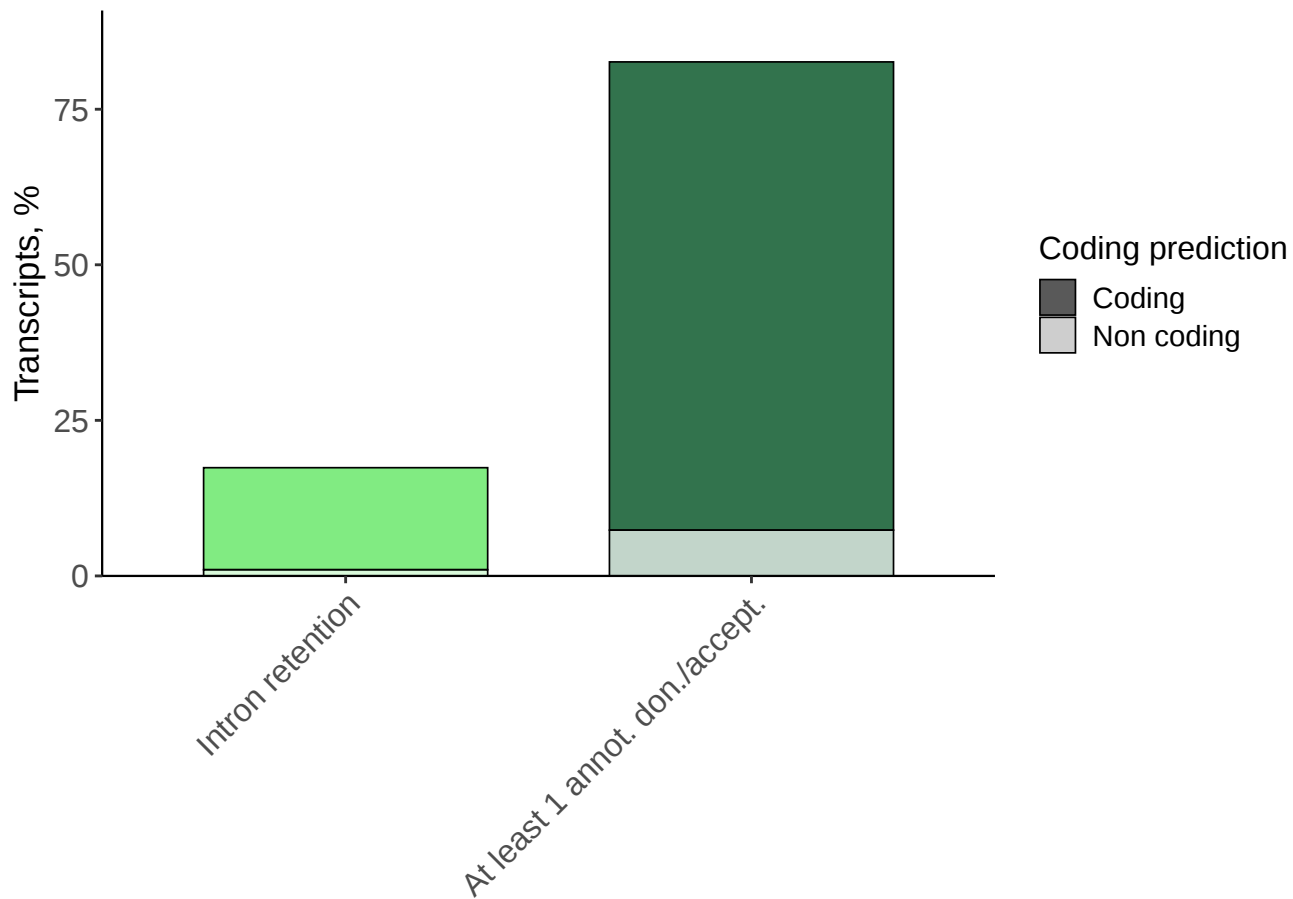
Isoform Distribution Across FSM



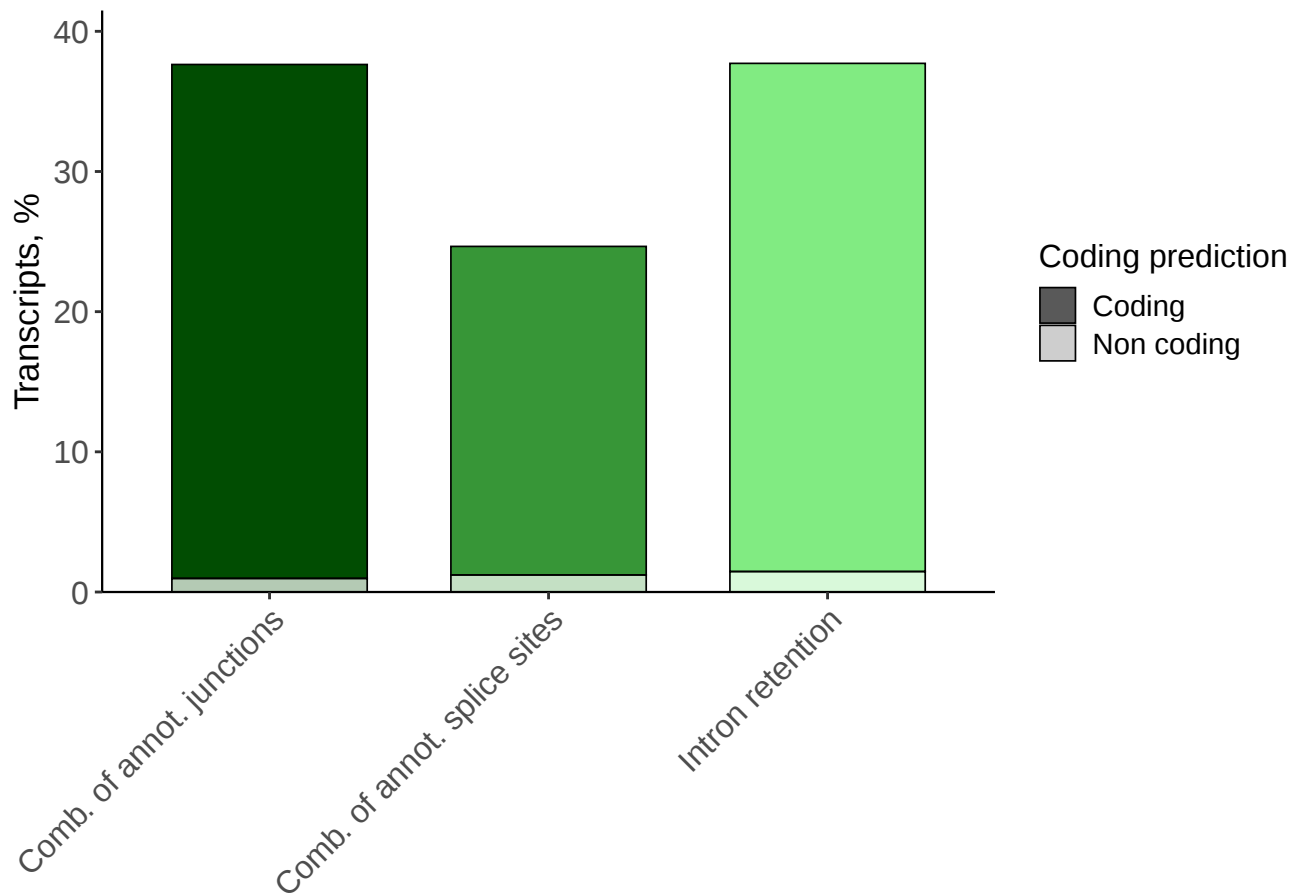
Isoform Distribution Across ISM



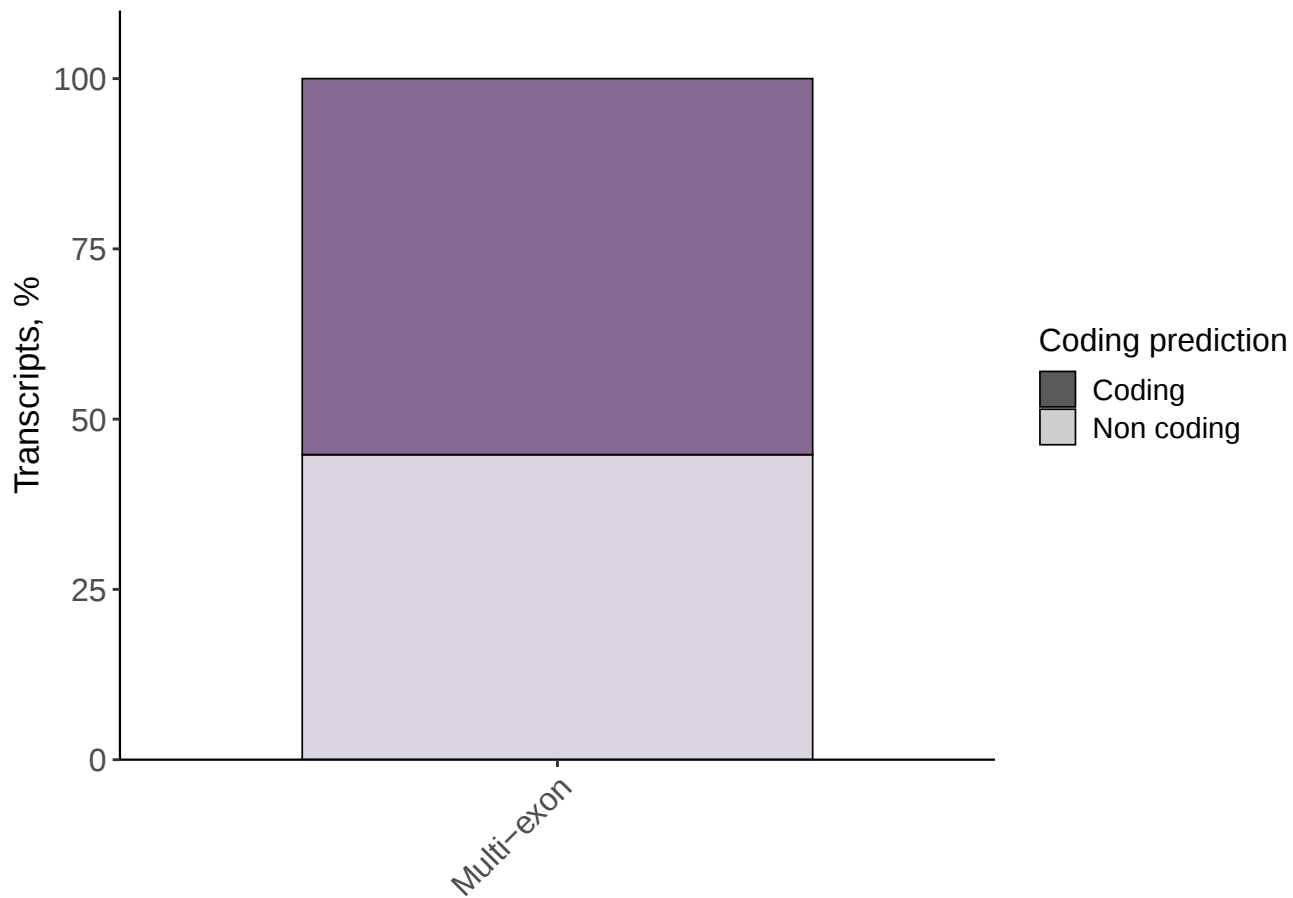
Isoform Distribution Across NNC



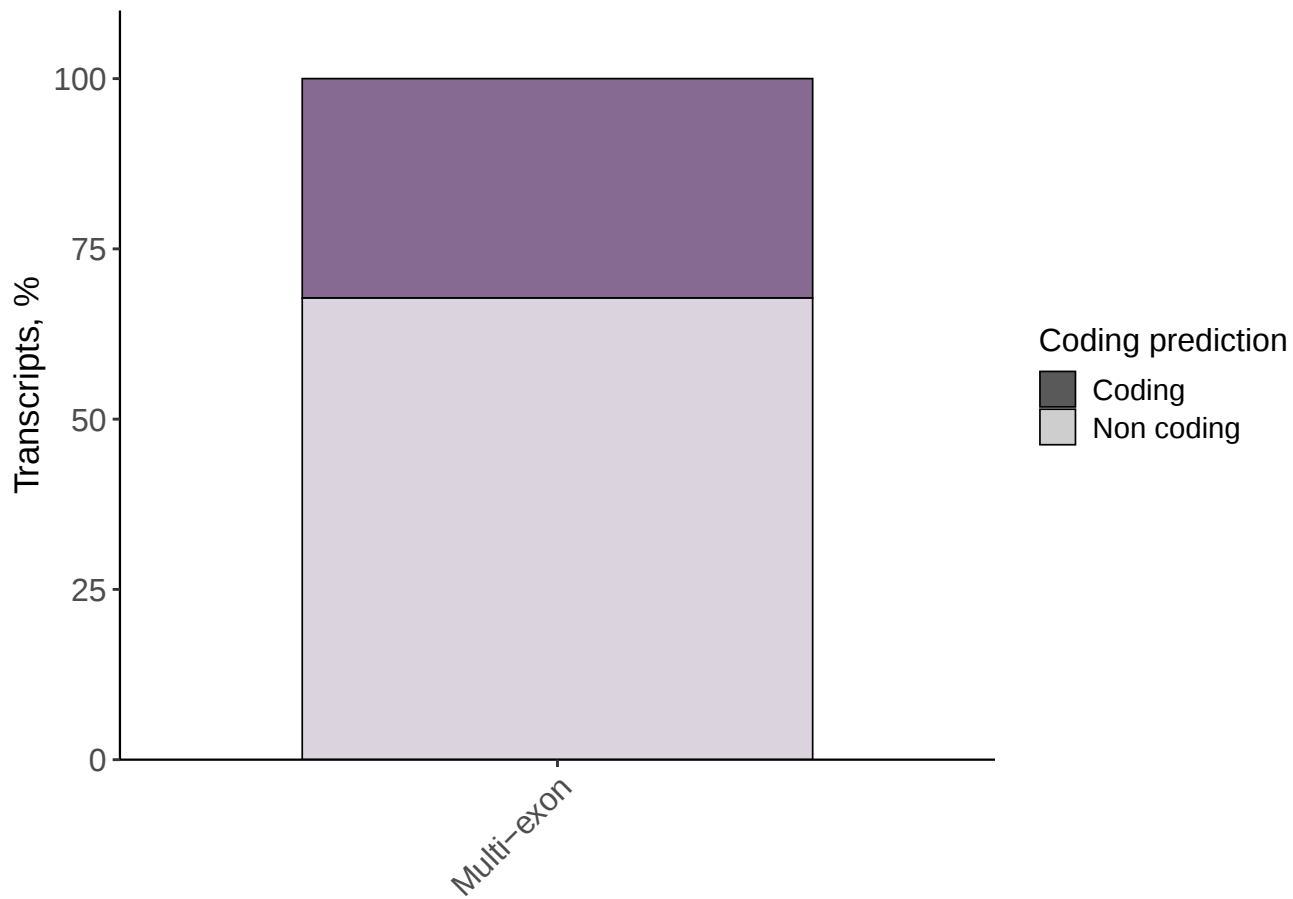
Isoform Distribution Across NIC



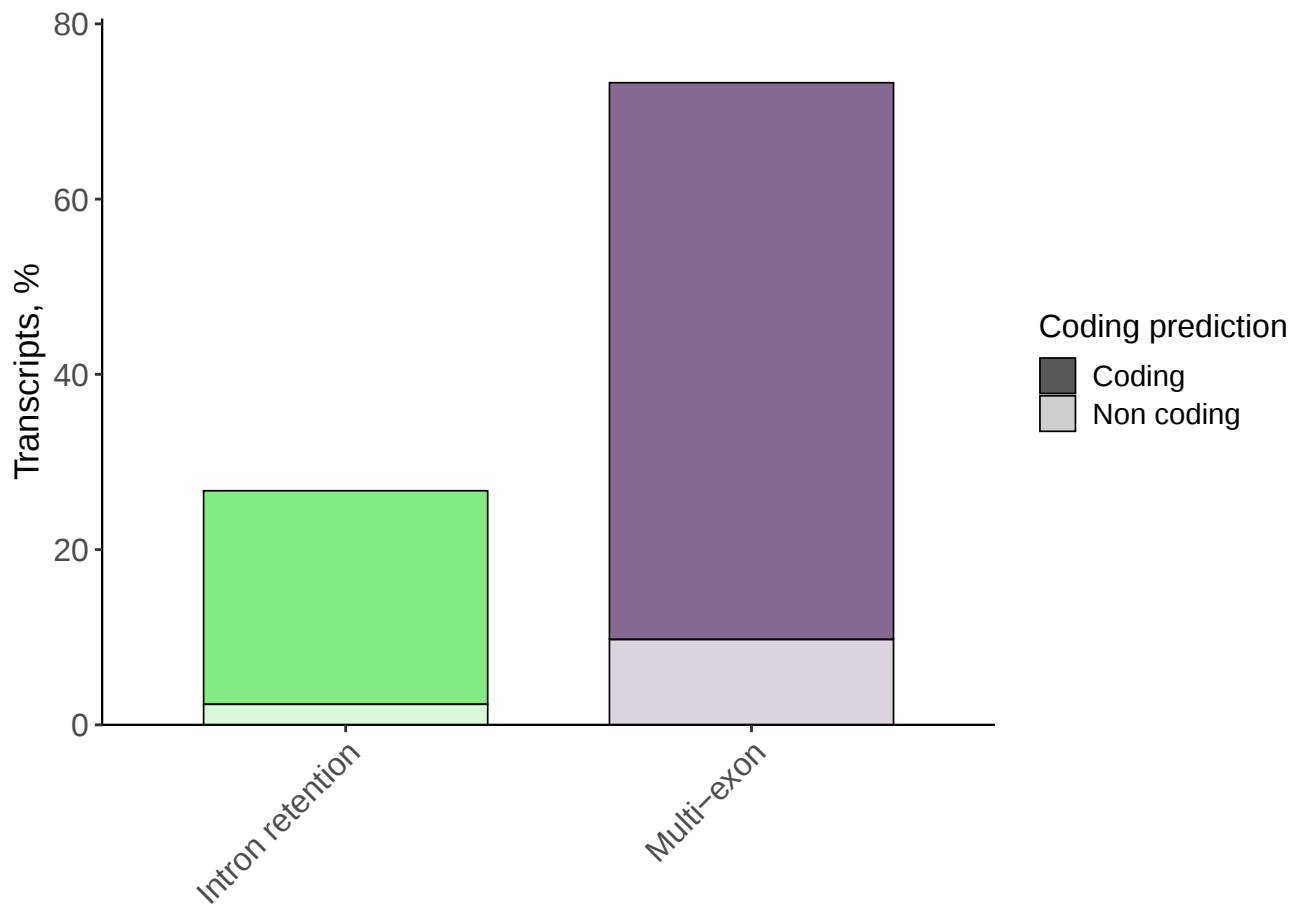
Isoform Distribution Across Genic Genomic



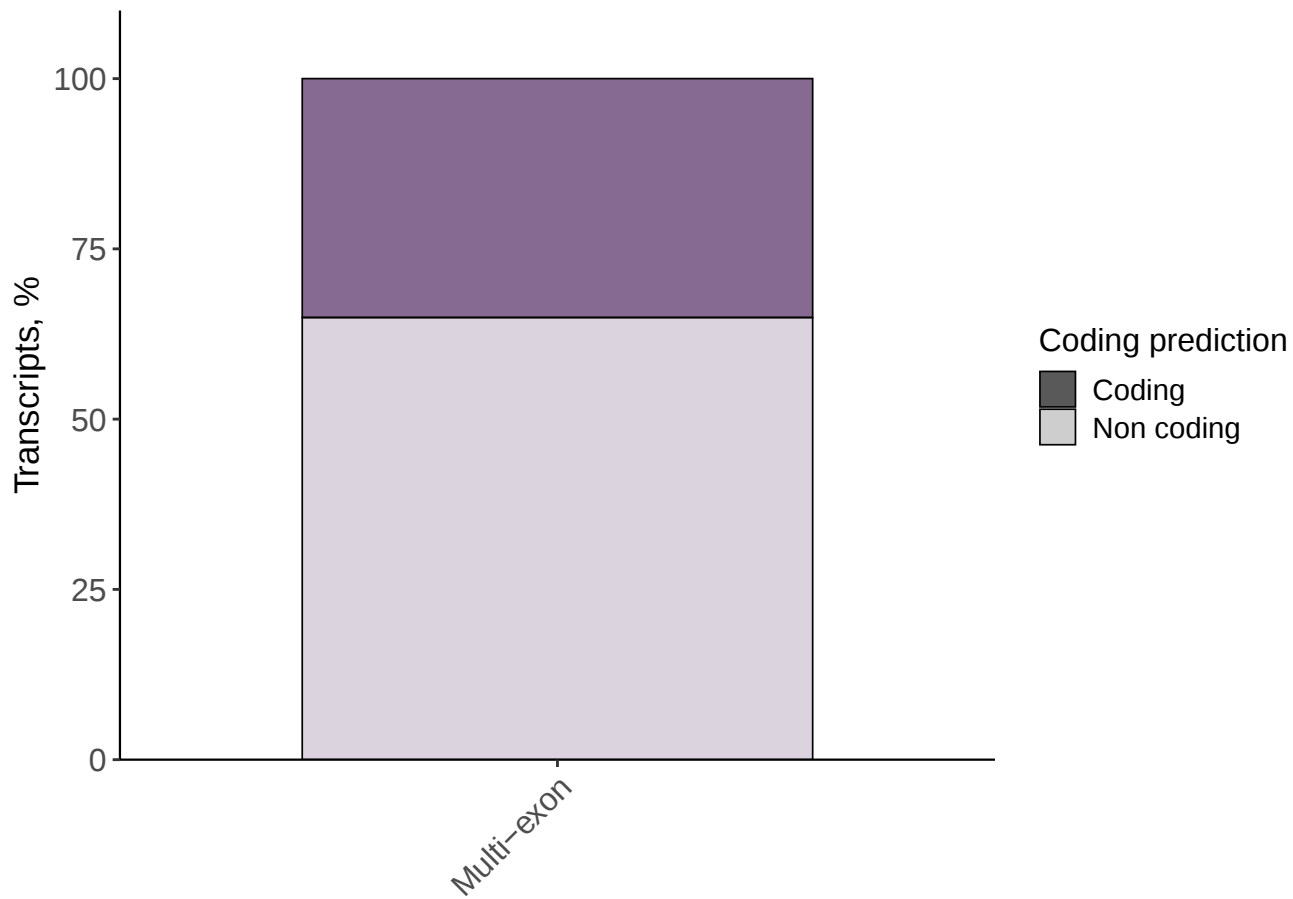
Isoform Distribution Across Antisense



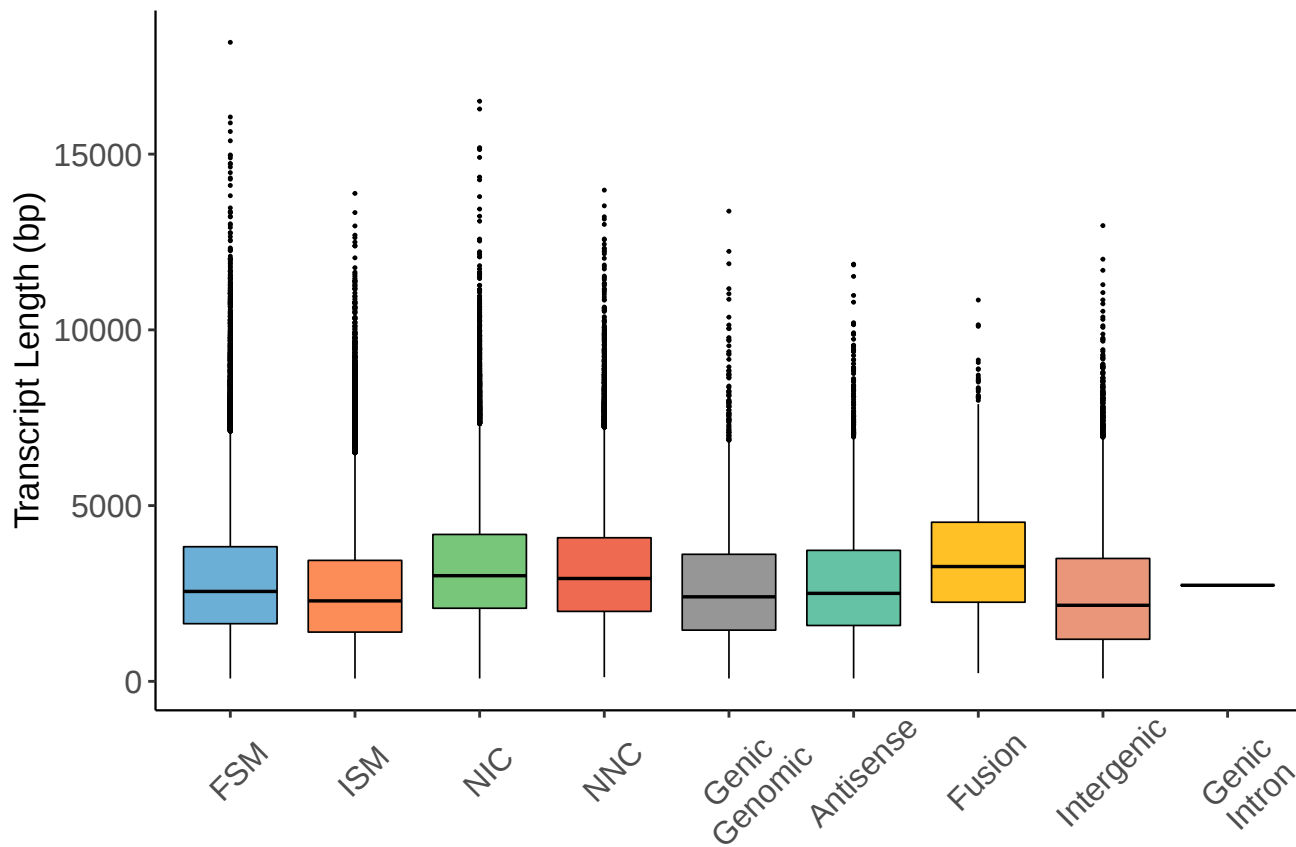
Isoform Distribution Across Fusion



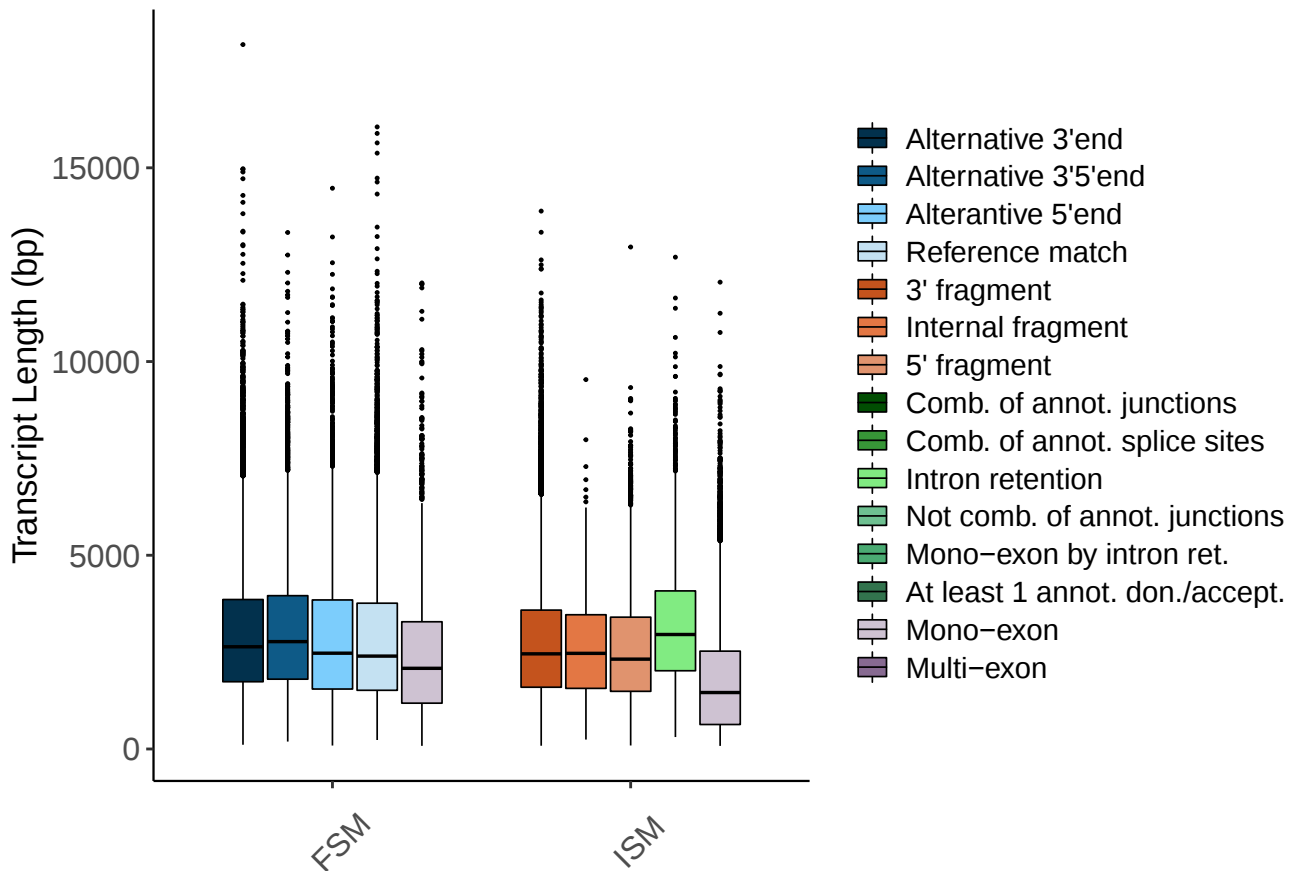
Isoform Distribution Across Intergenic



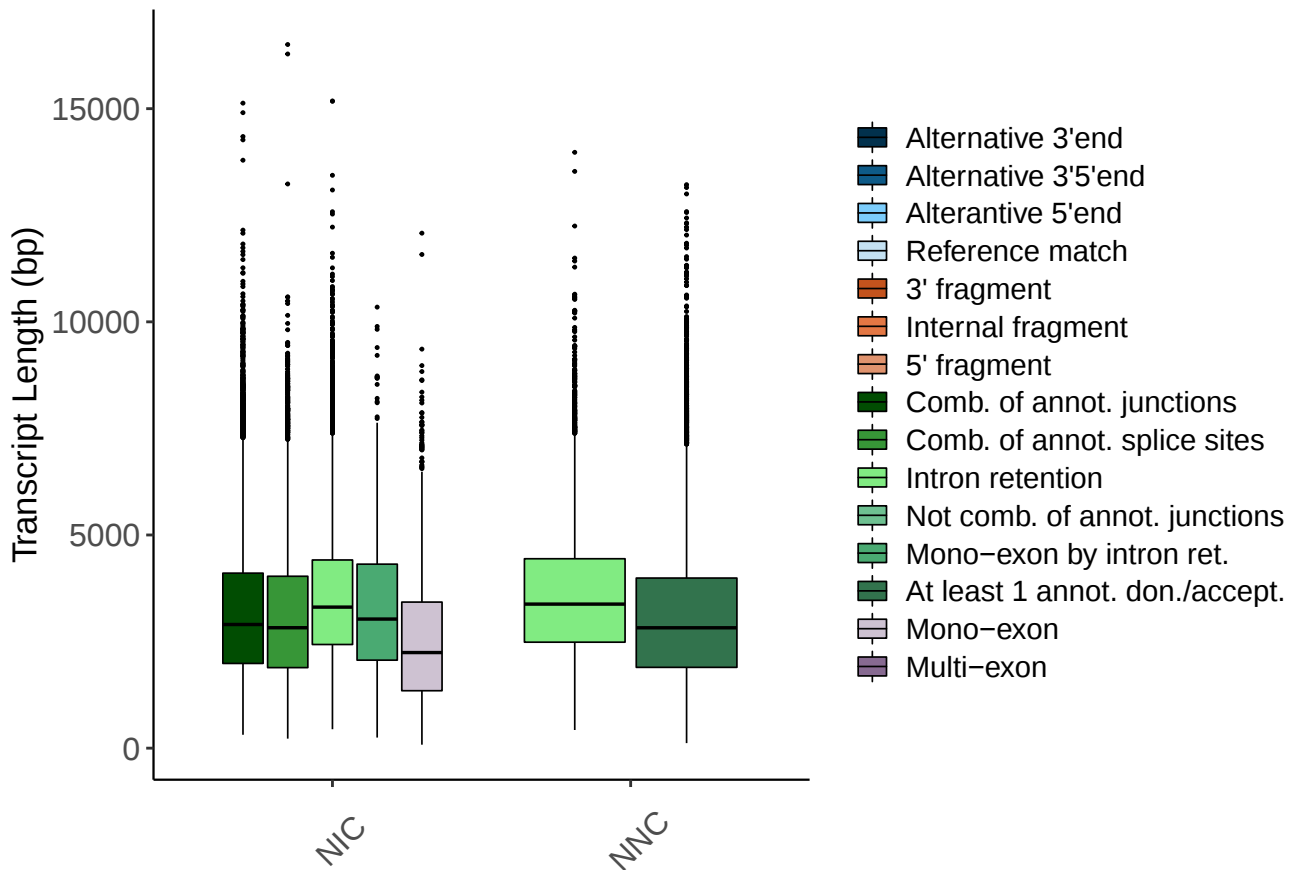
Transcript Lengths by Structural Classification



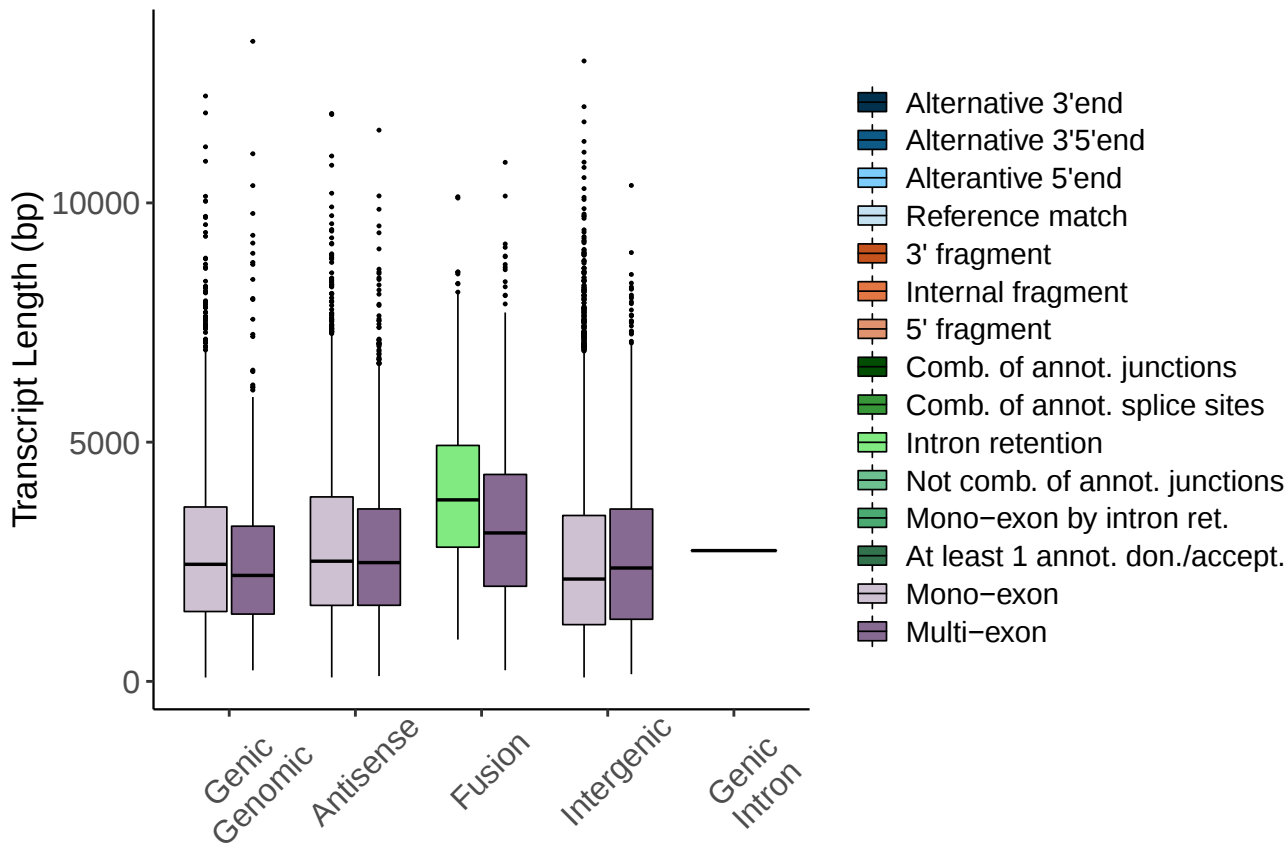
Transcript Lengths by Subcategory



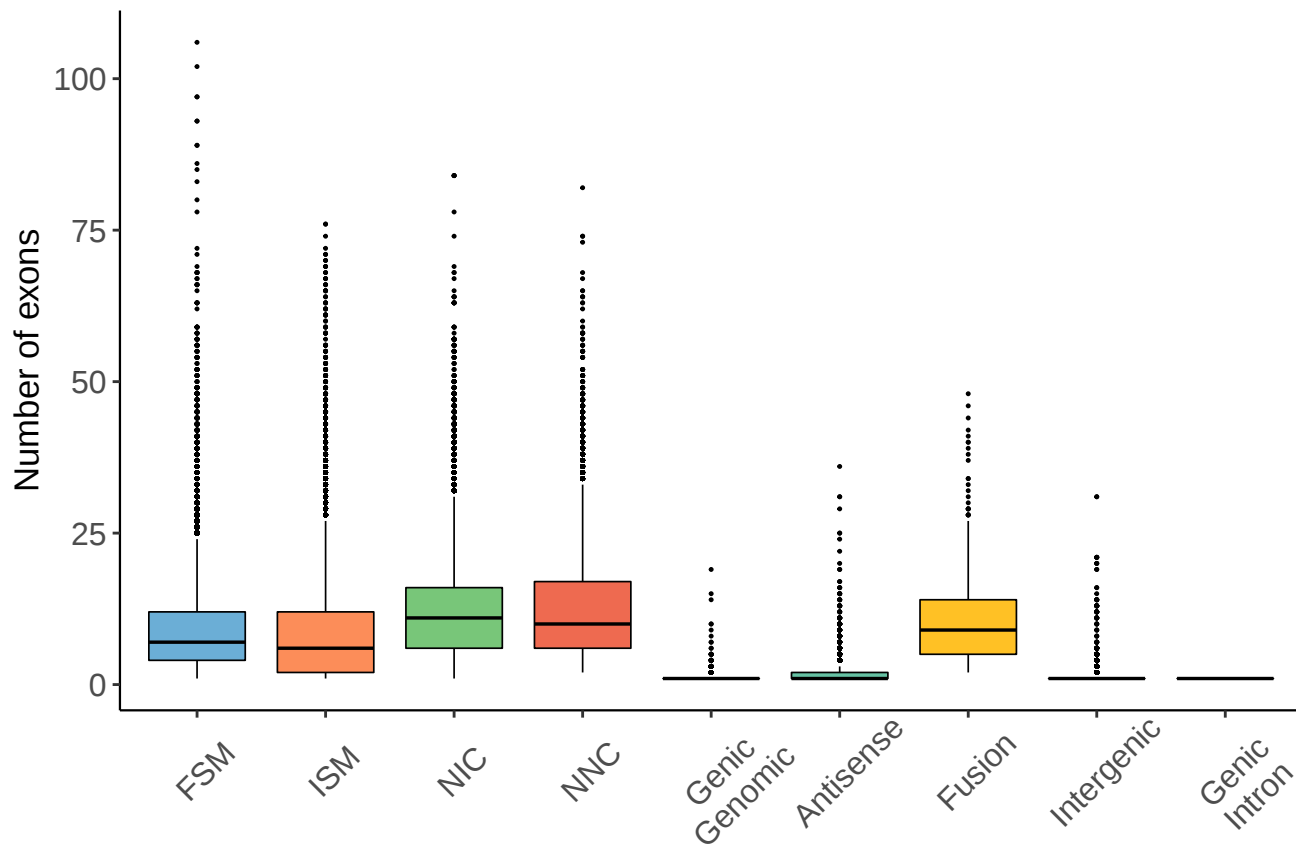
Transcript Lengths by Subcategory



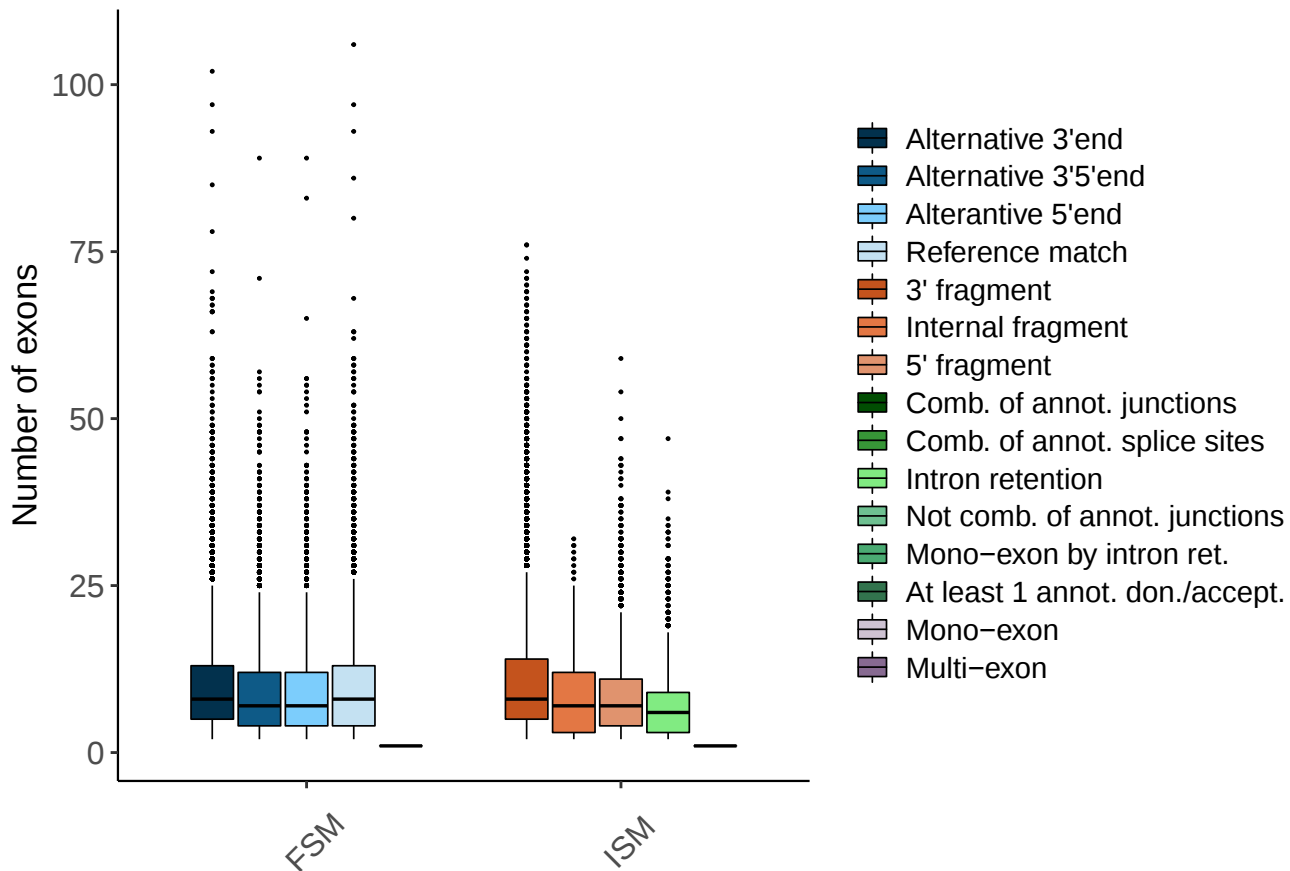
Transcript Lengths by Subcategory



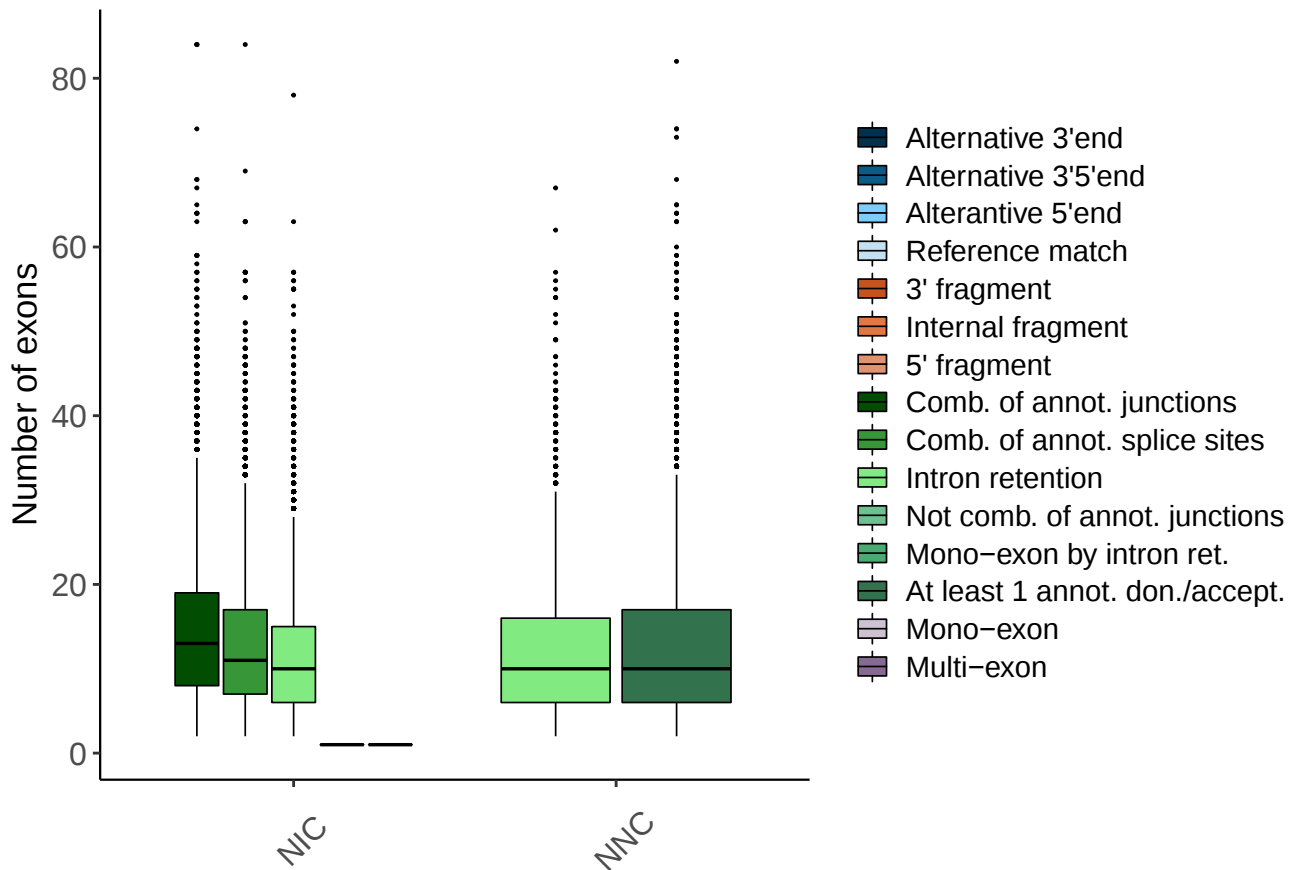
Exon Counts by Structural Classification



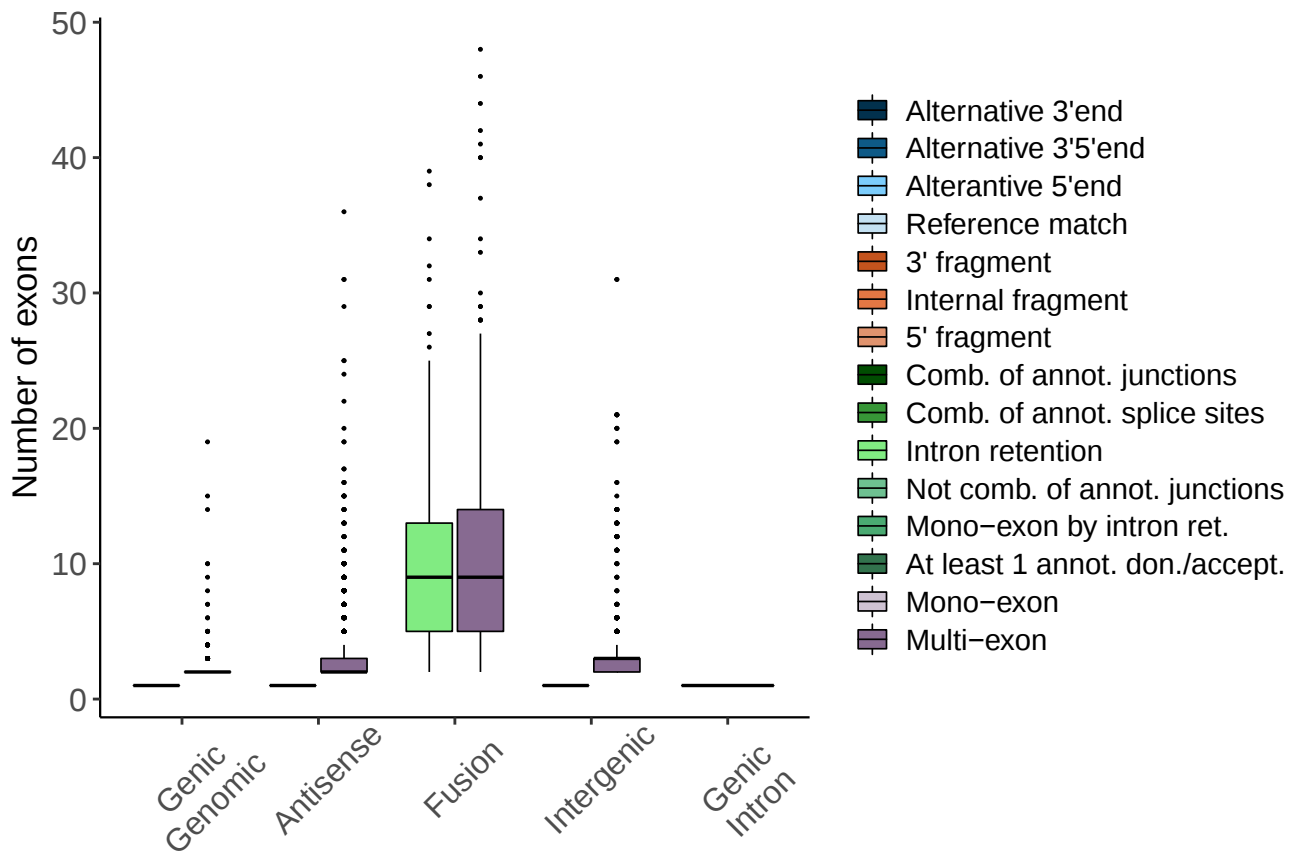
Exon Counts by Subcategory



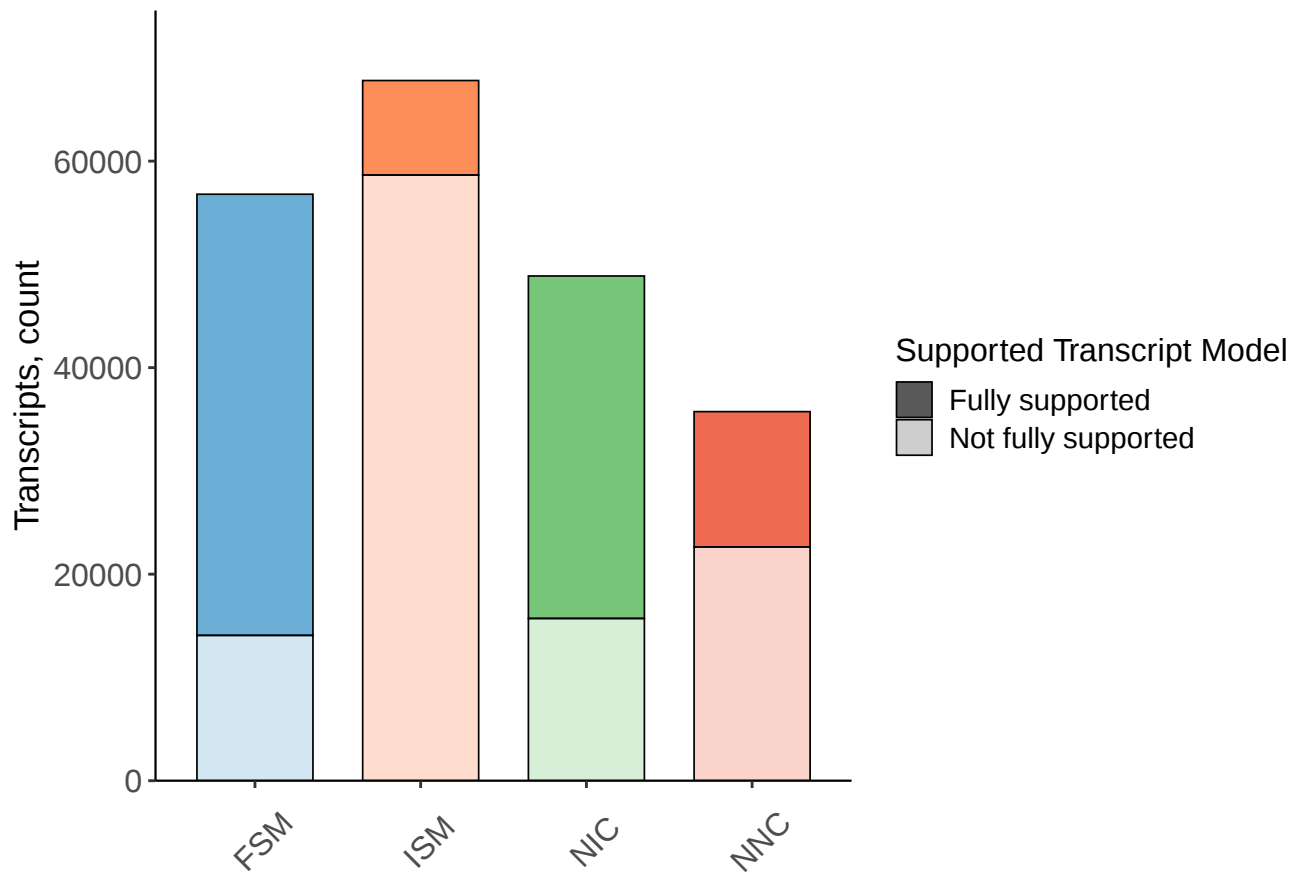
Exon Counts by Subcategory



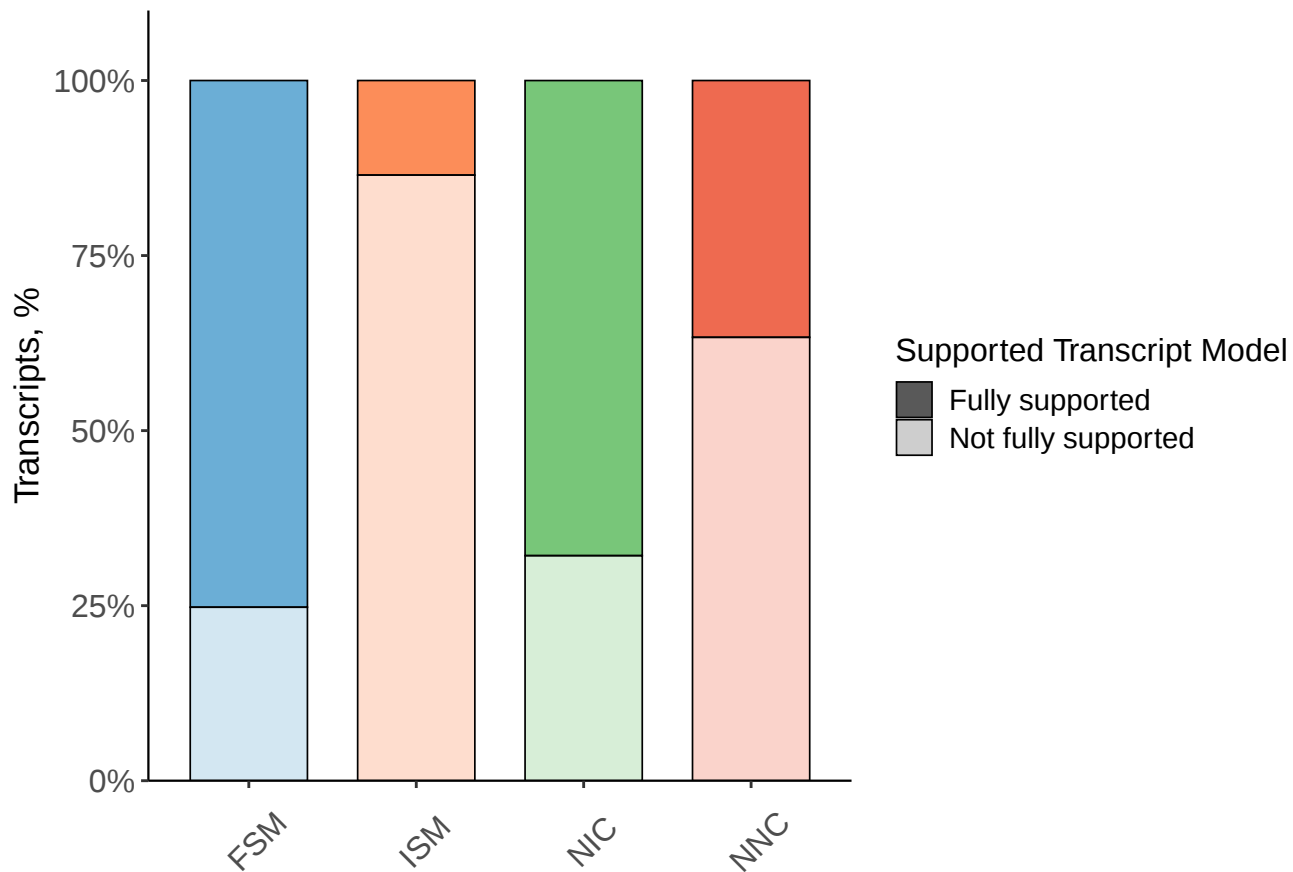
Exon Counts by Subcategory



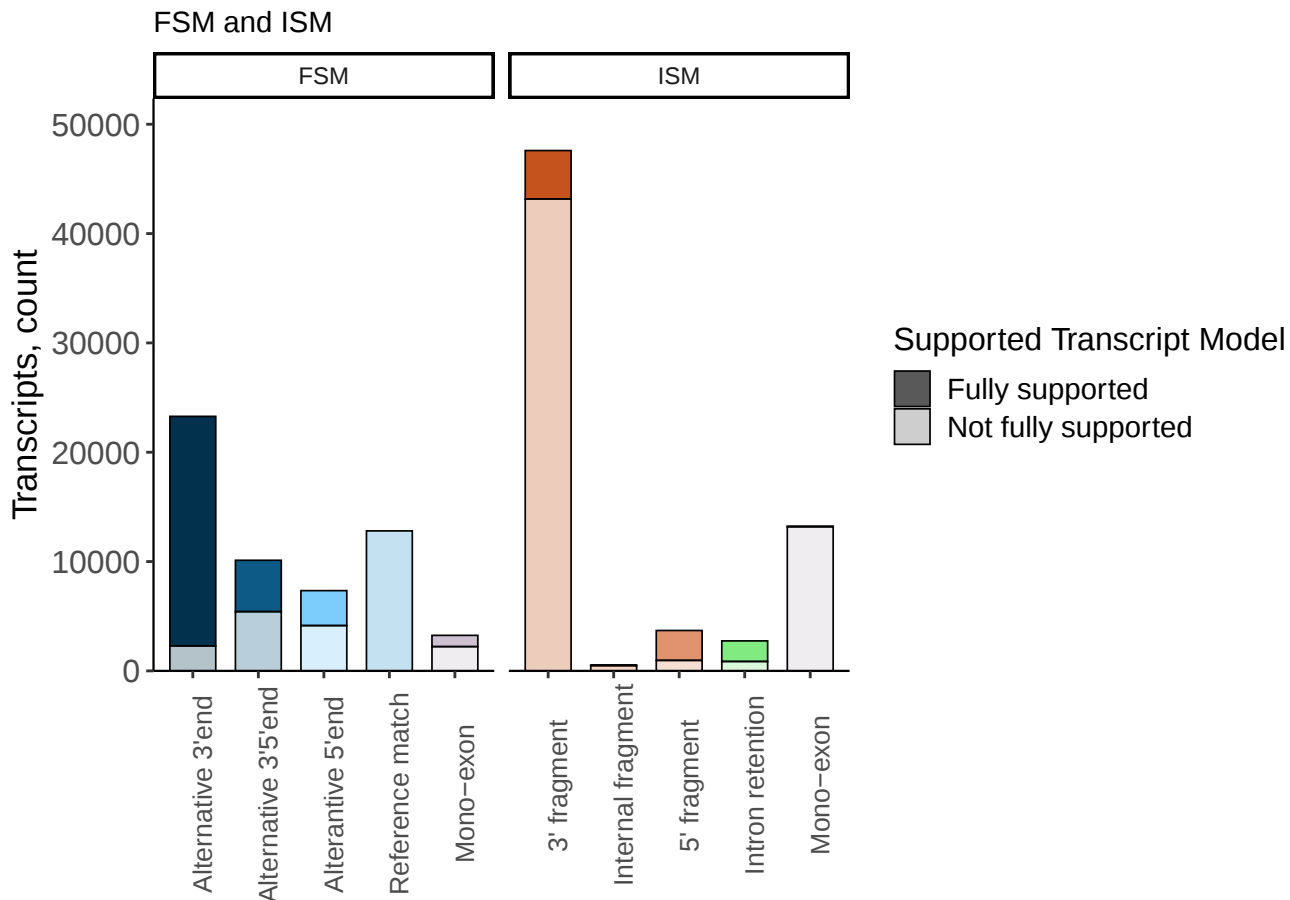
Isoform Distribution Across Structural Categories



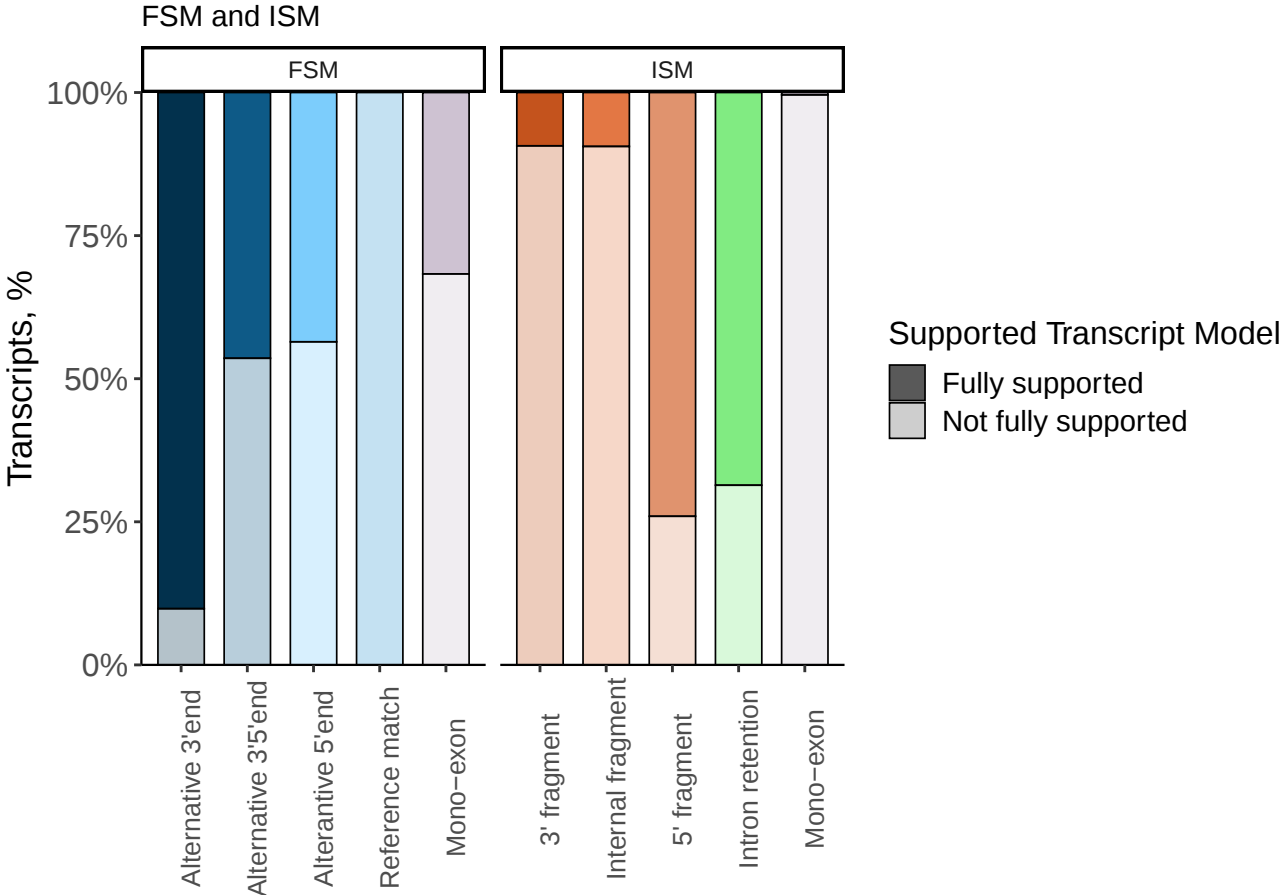
Isoform Distribution Across Structural Categories



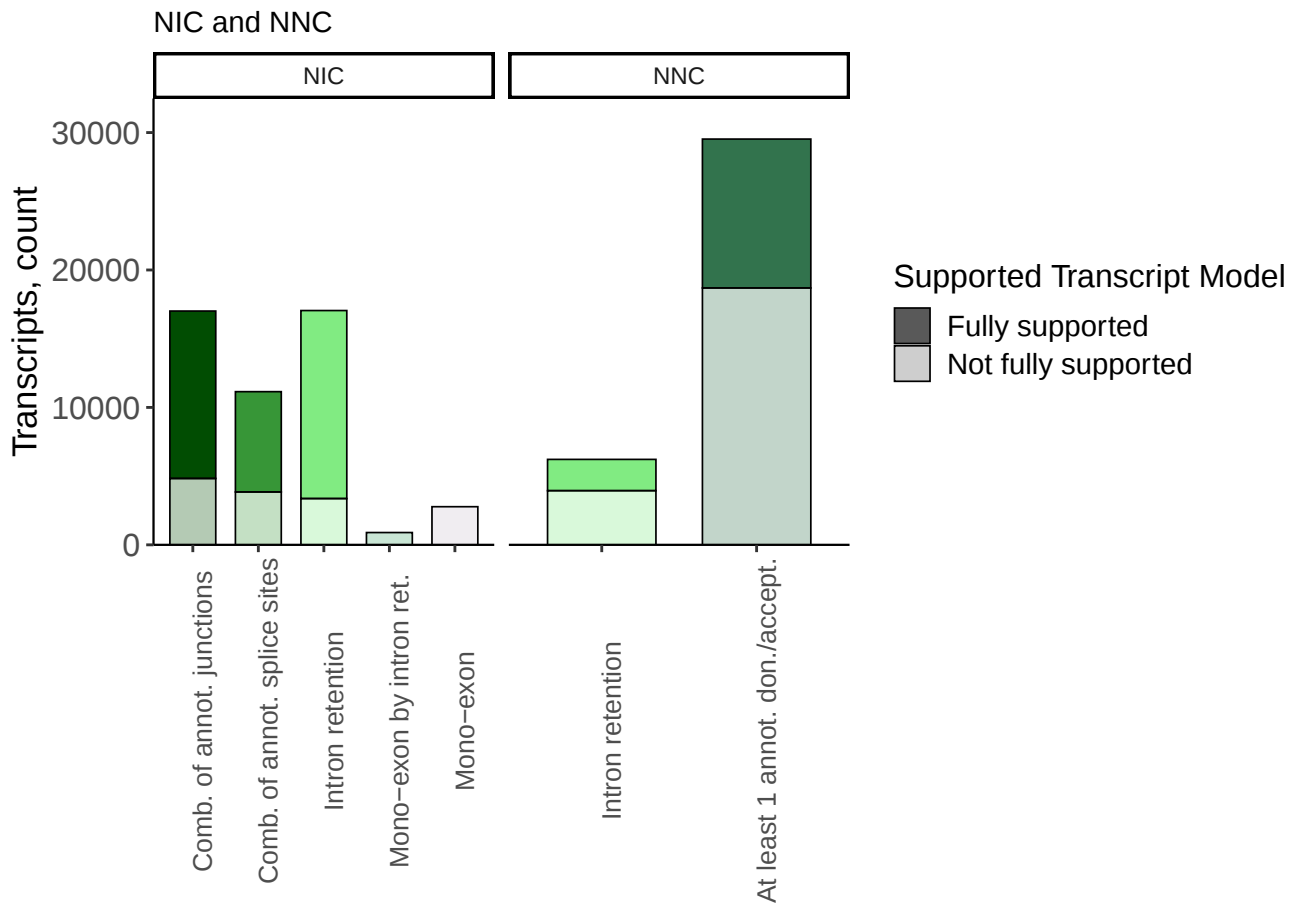
Isoform Distribution Across Structural Subcategories



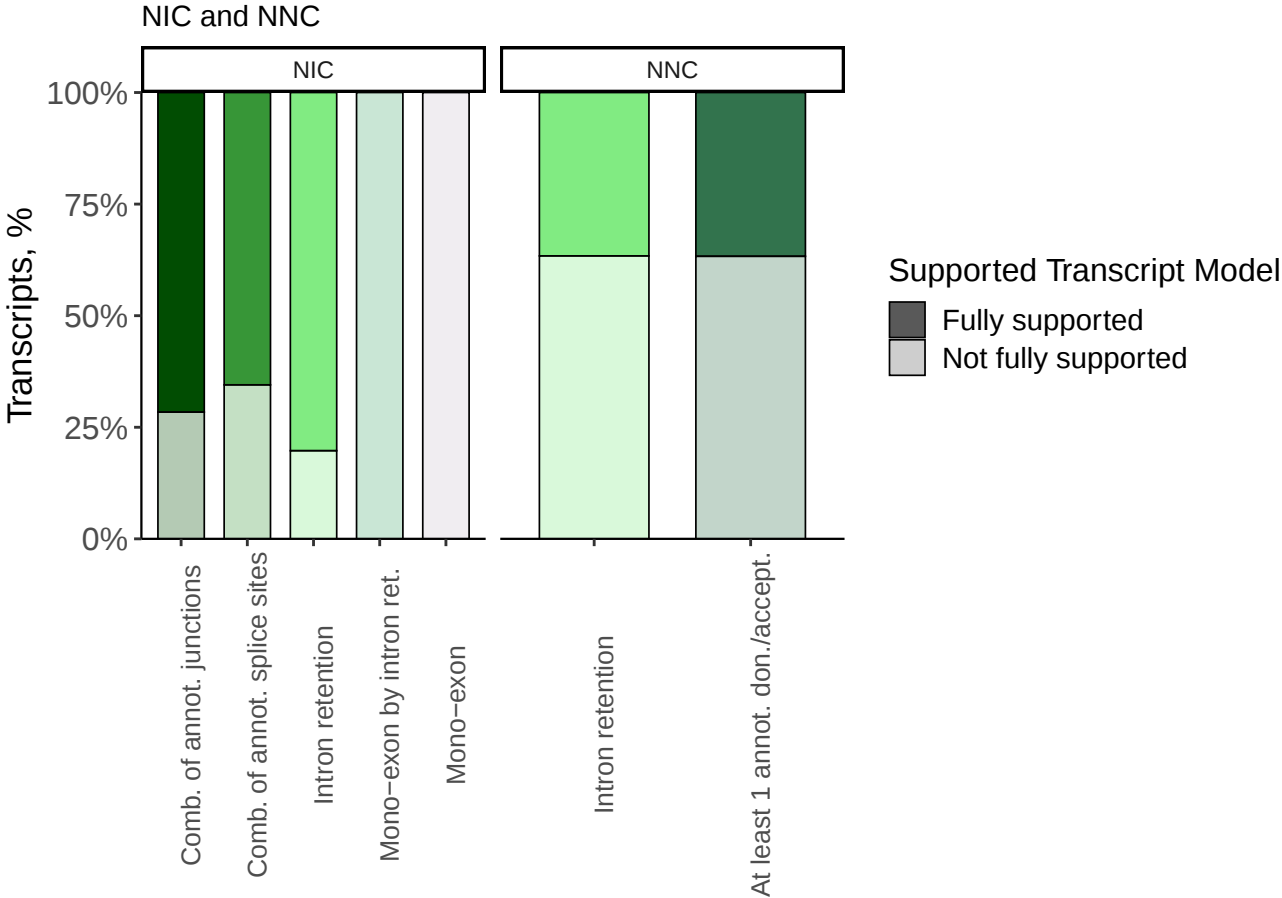
Isoform Distribution Across Structural Subcategories



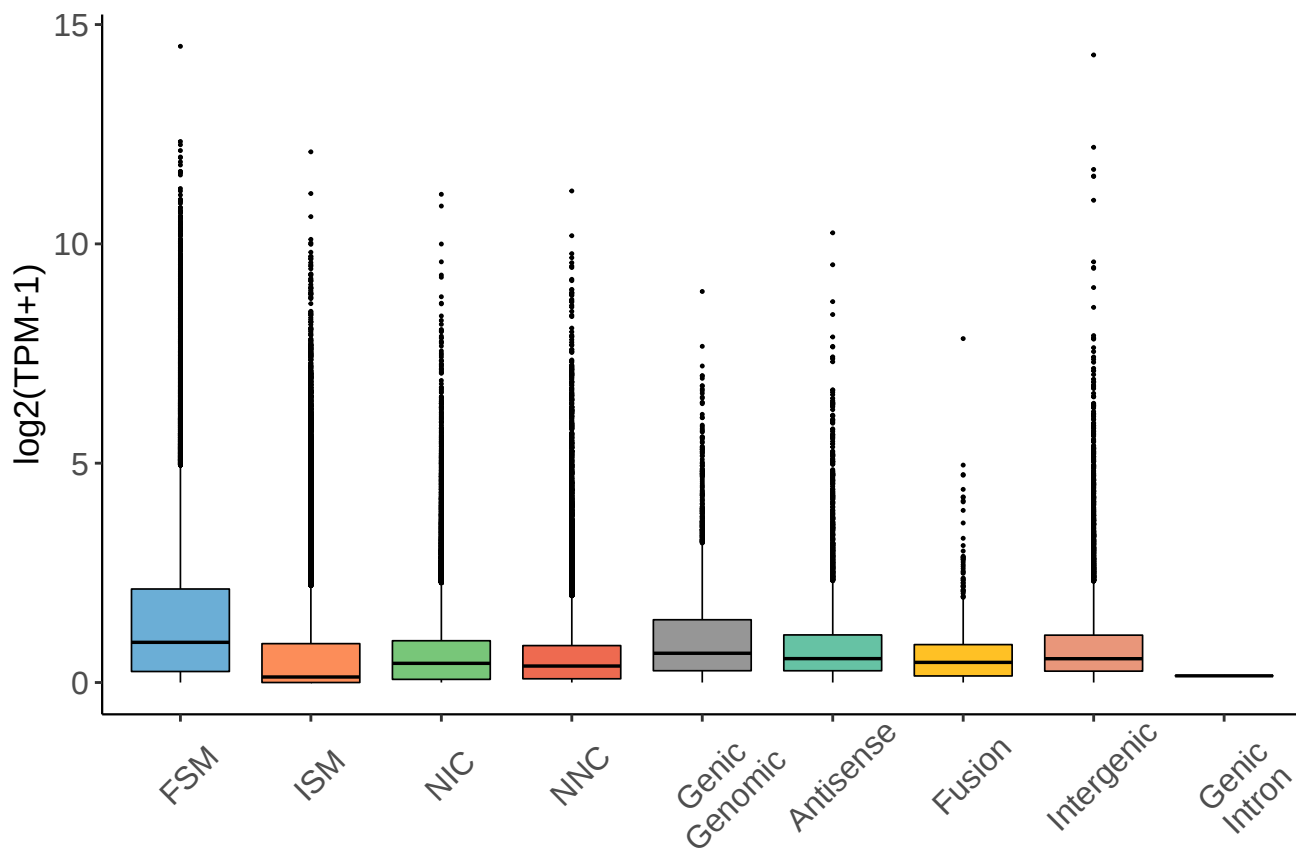
Isoform Distribution Across Structural Subcategories



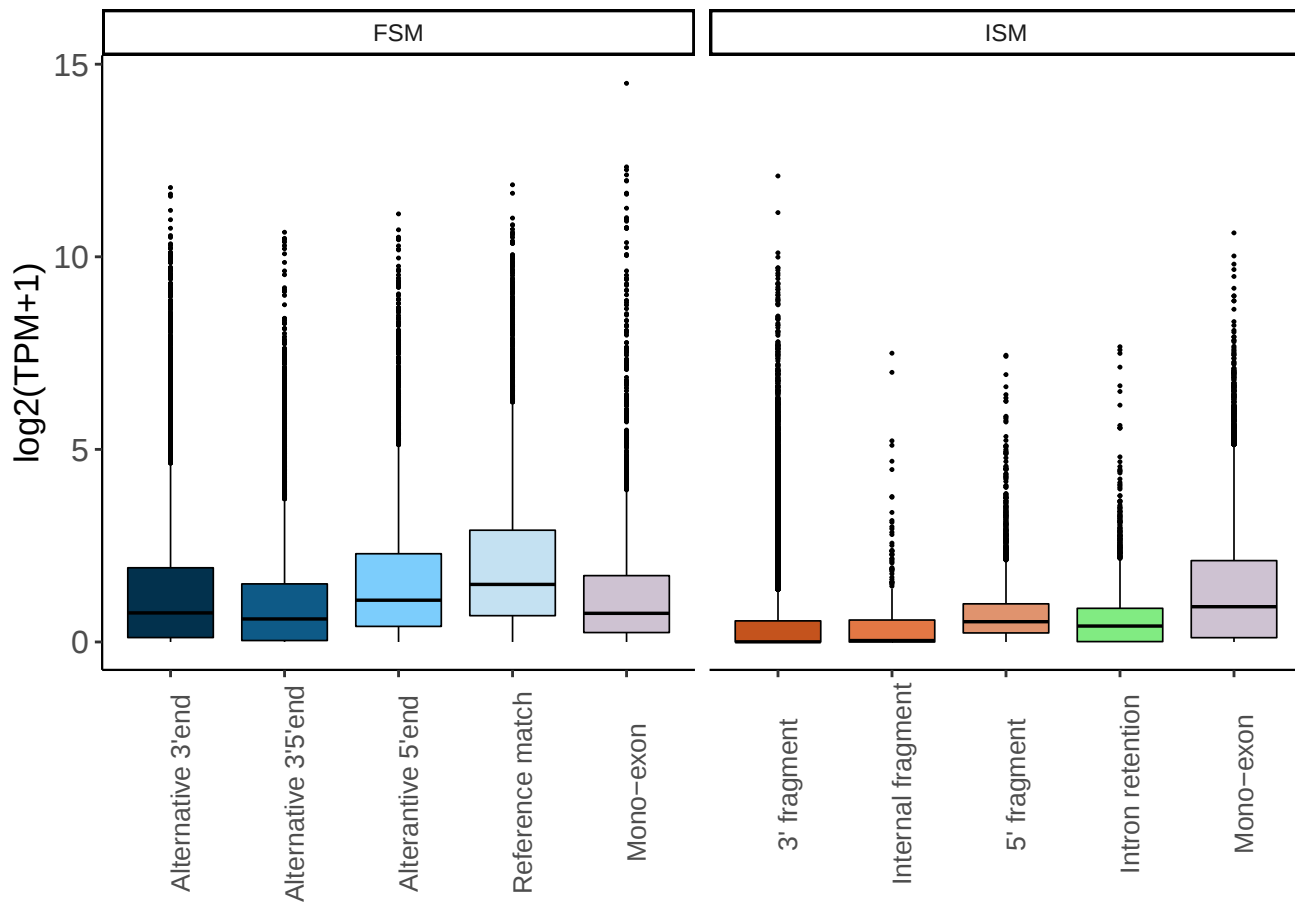
Isoform Distribution Across Structural Subcategories



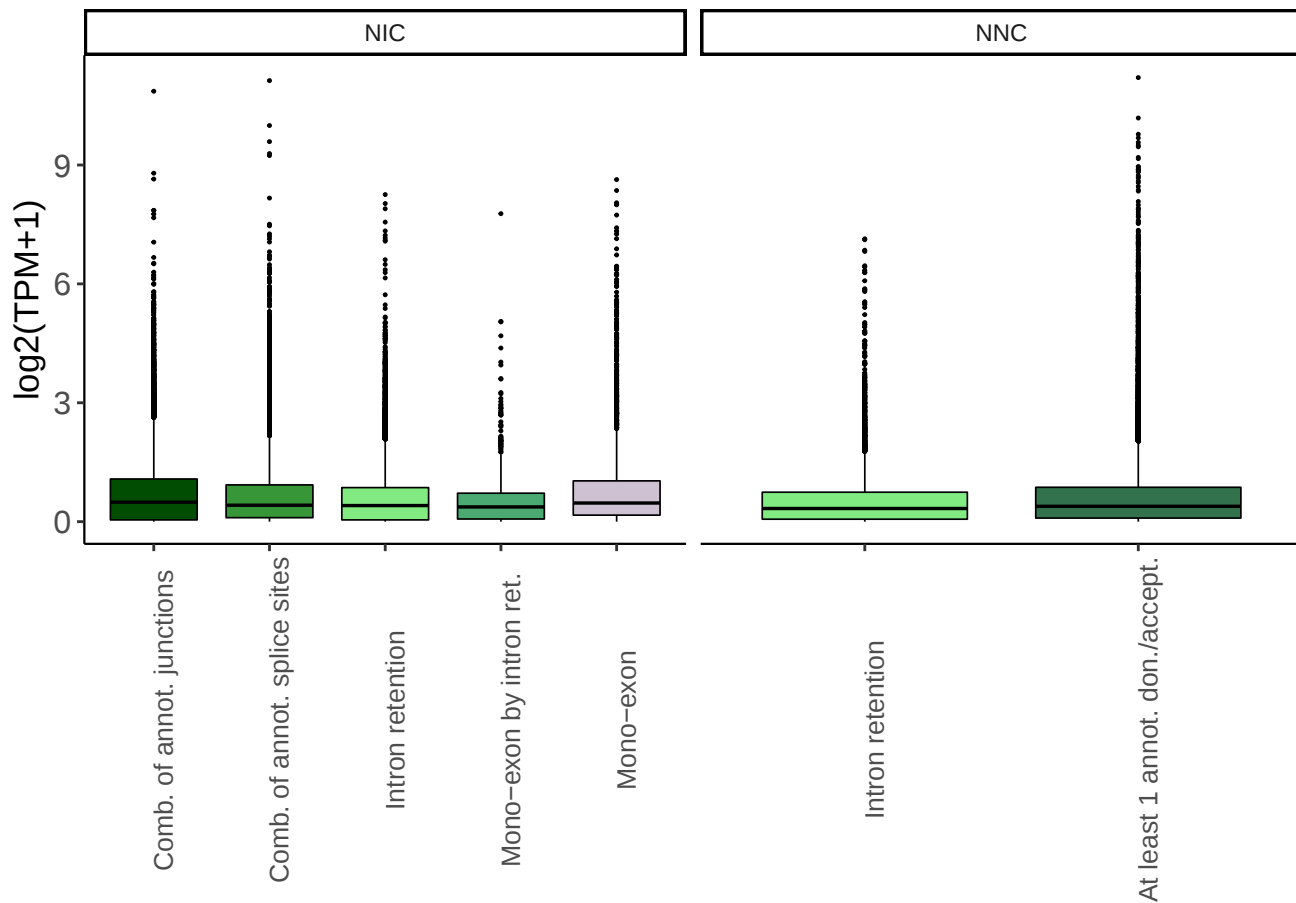
Transcript Expression by Structural Category



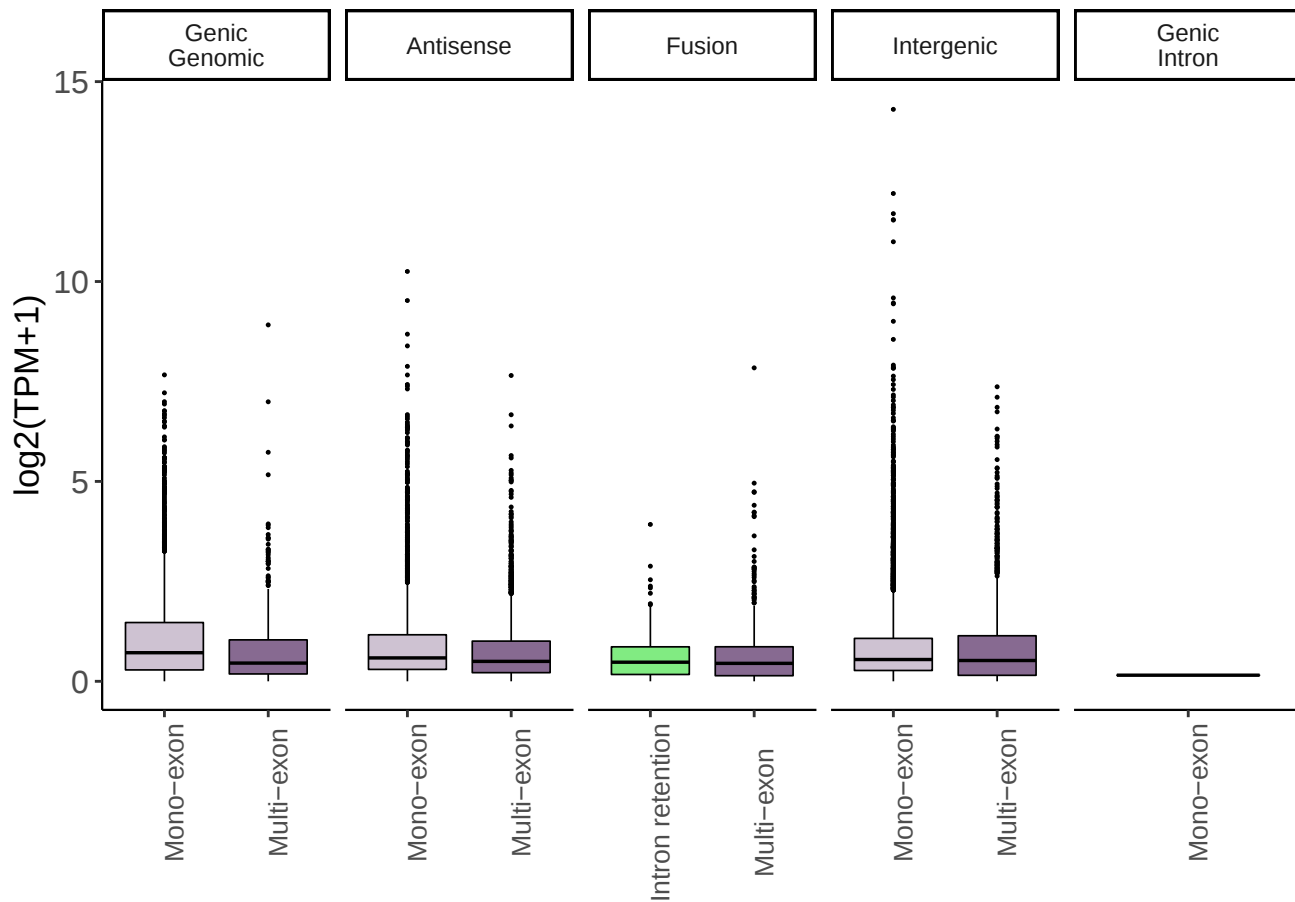
Transcript Expression by Subcategory



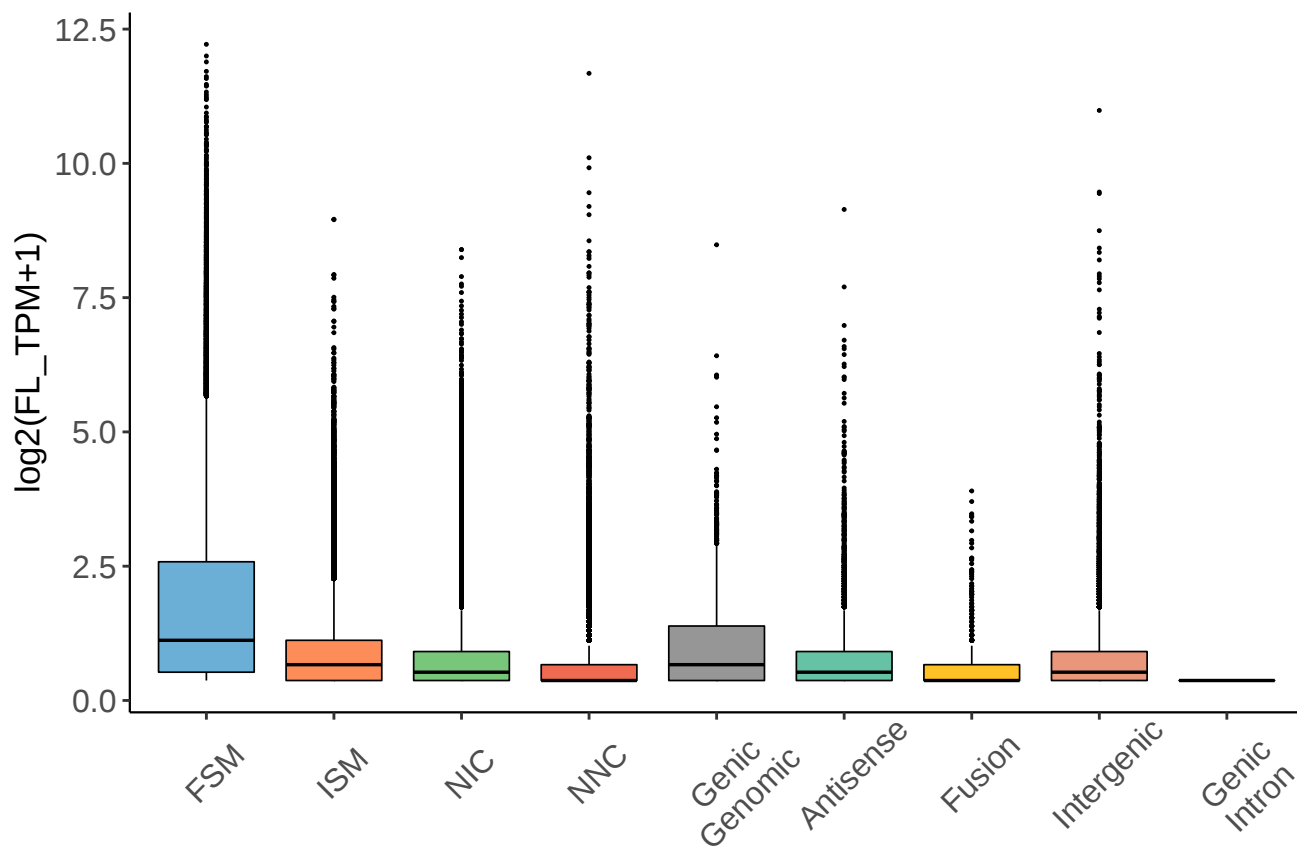
Transcript Expression by Subcategory



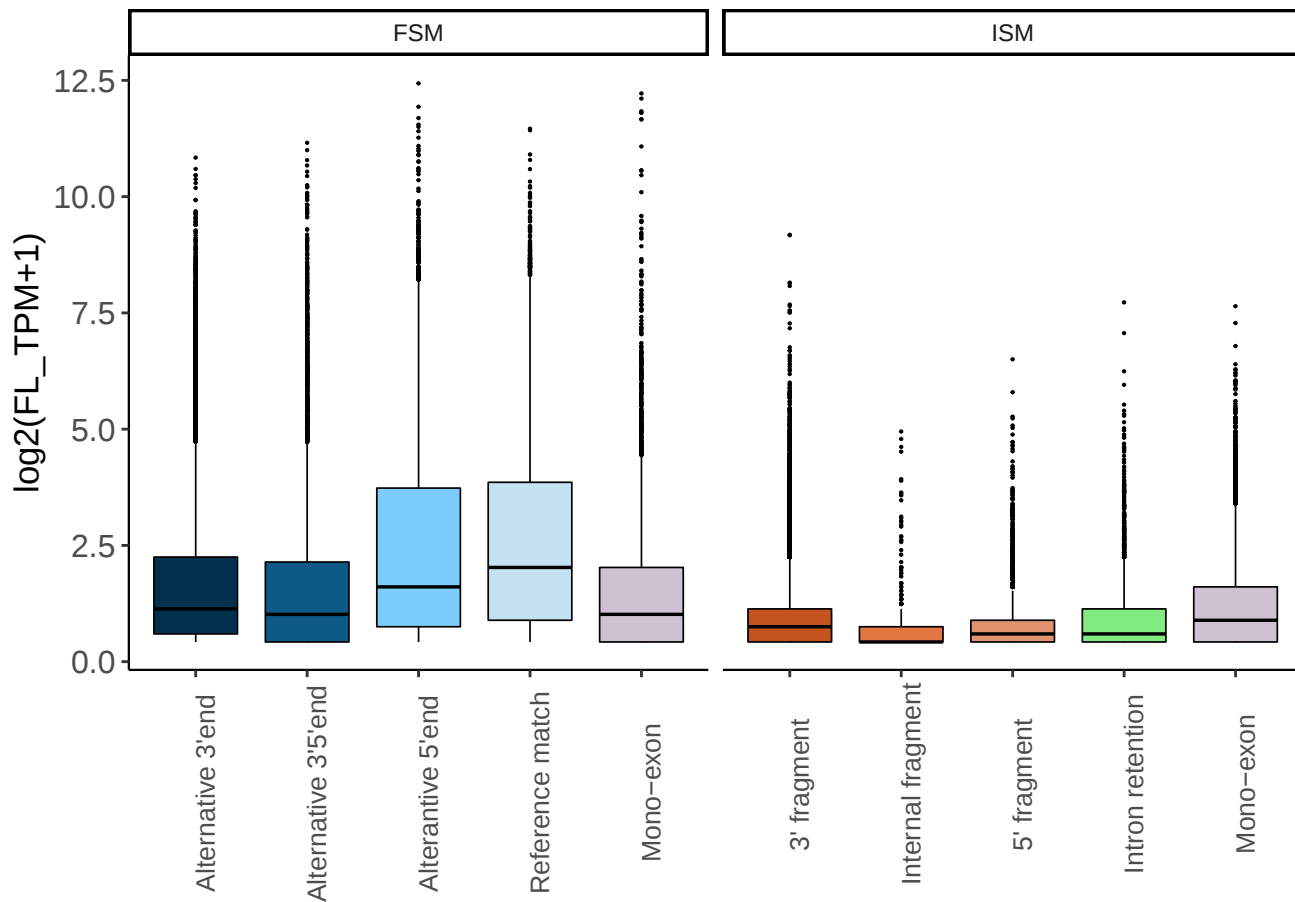
Transcript Expression by Subcategory



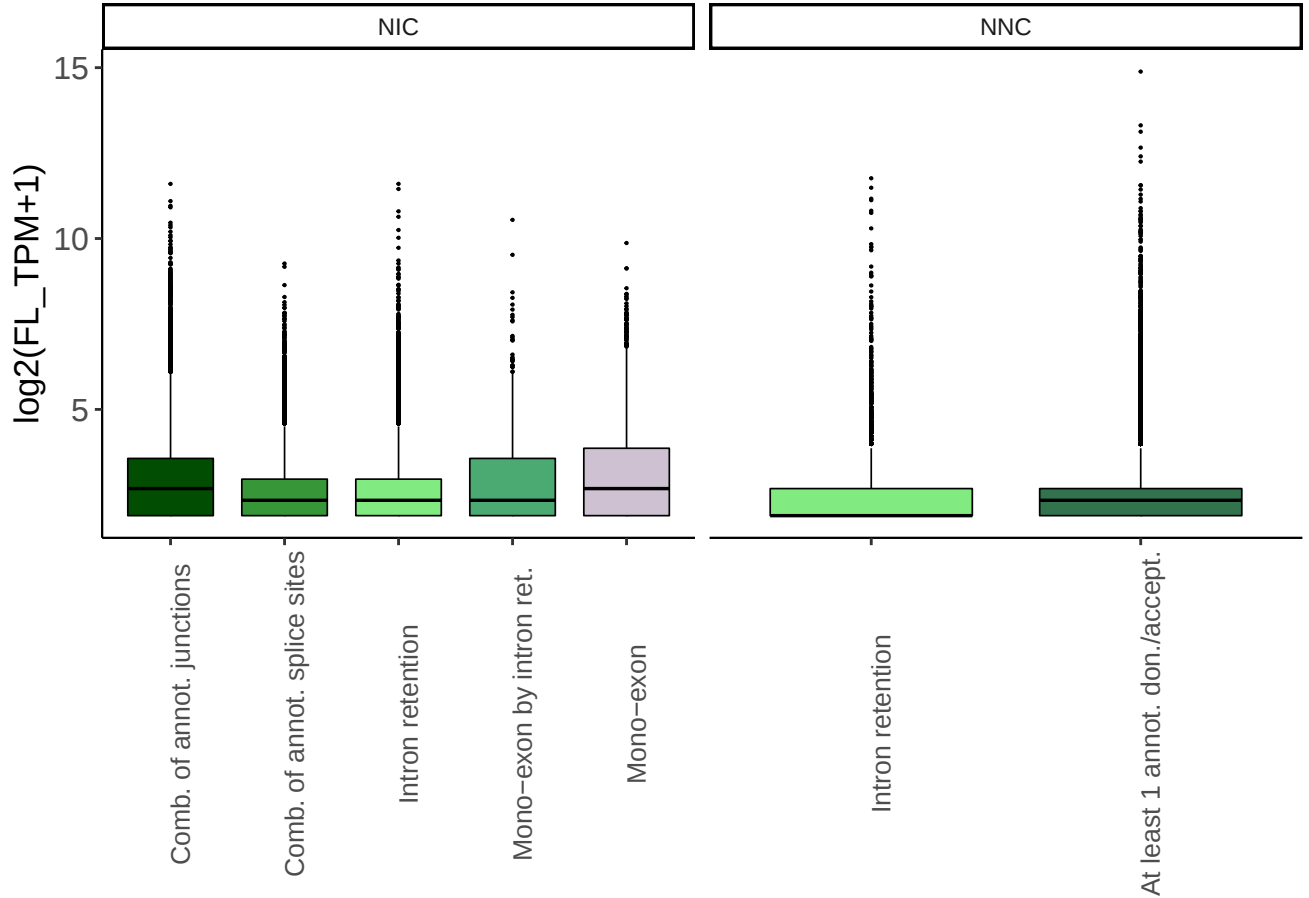
Long Reads Count by Structural Category



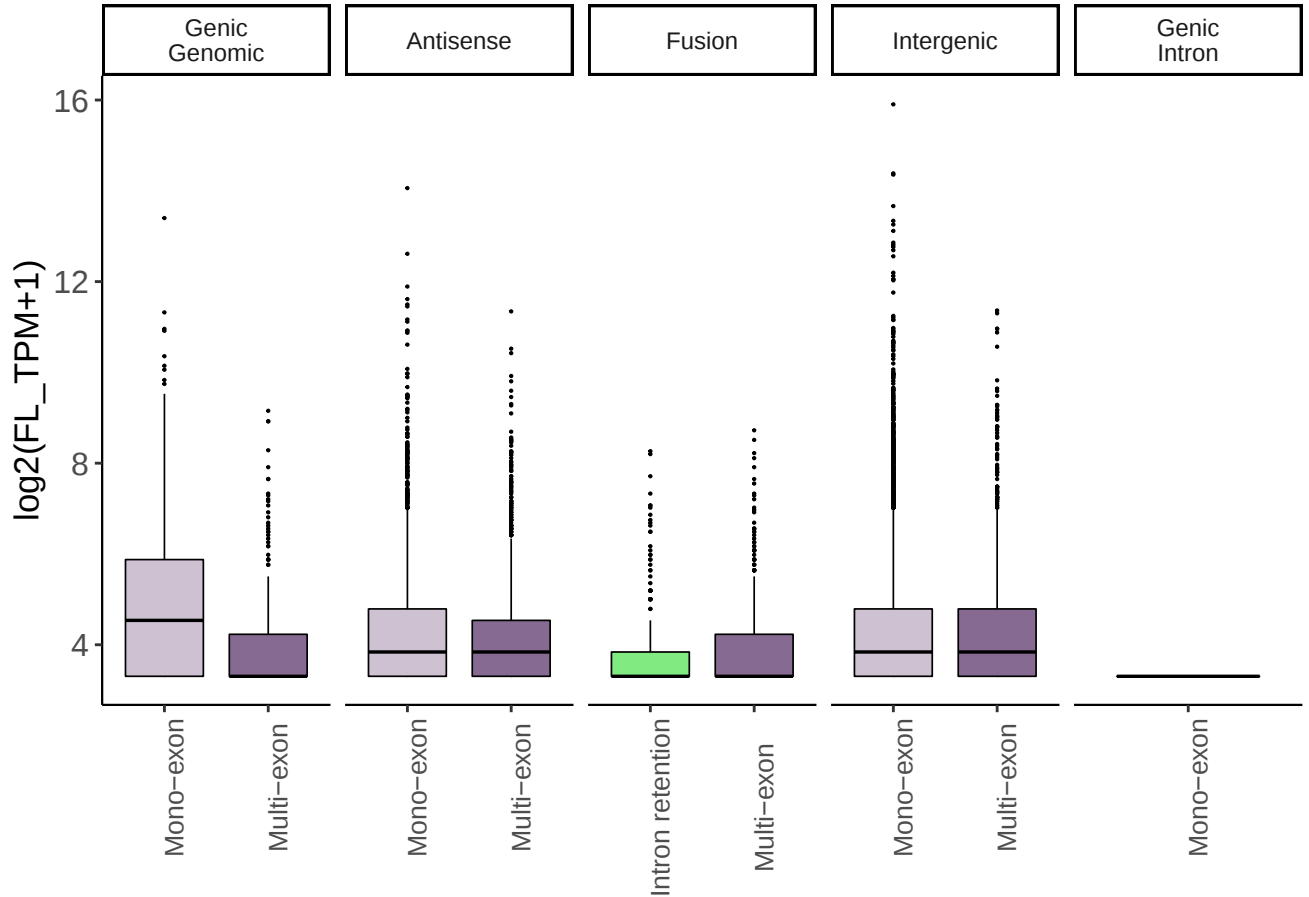
Long Reads Count by Subcategory



Long Reads Count by Subcategory

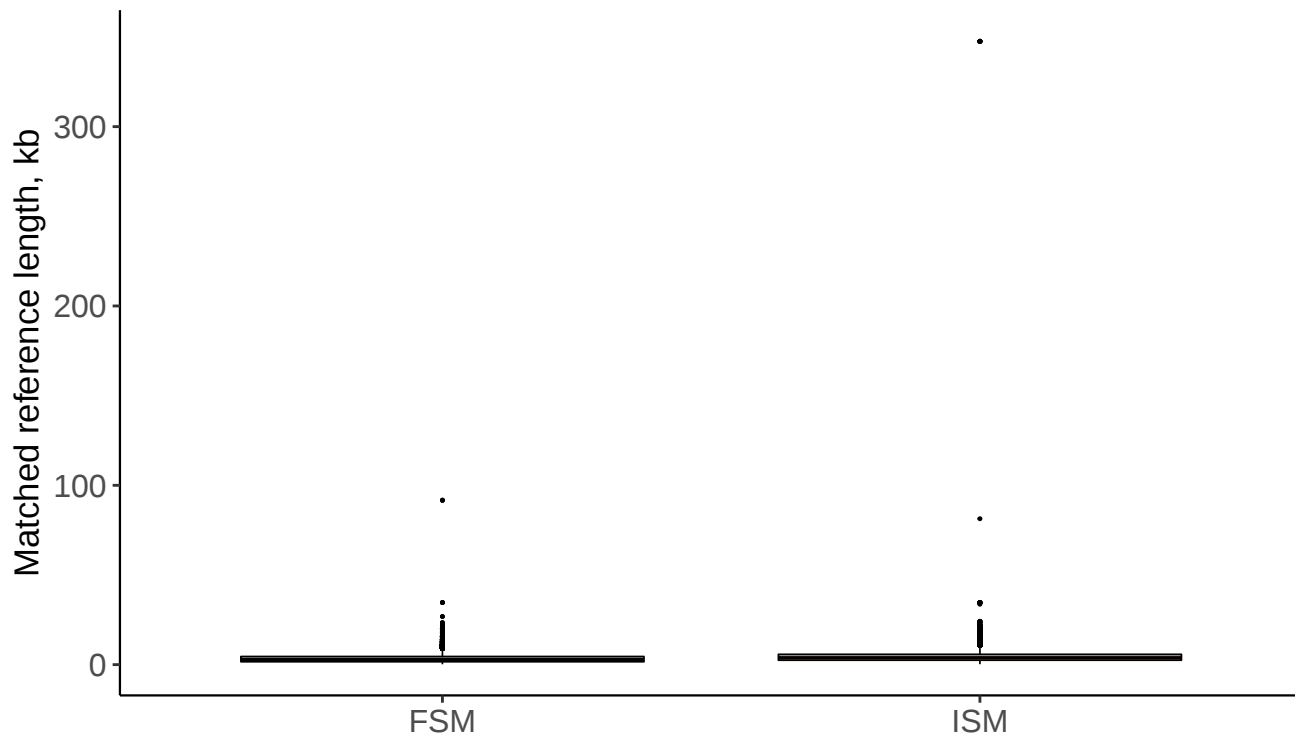


Long Reads Count by Subcategory



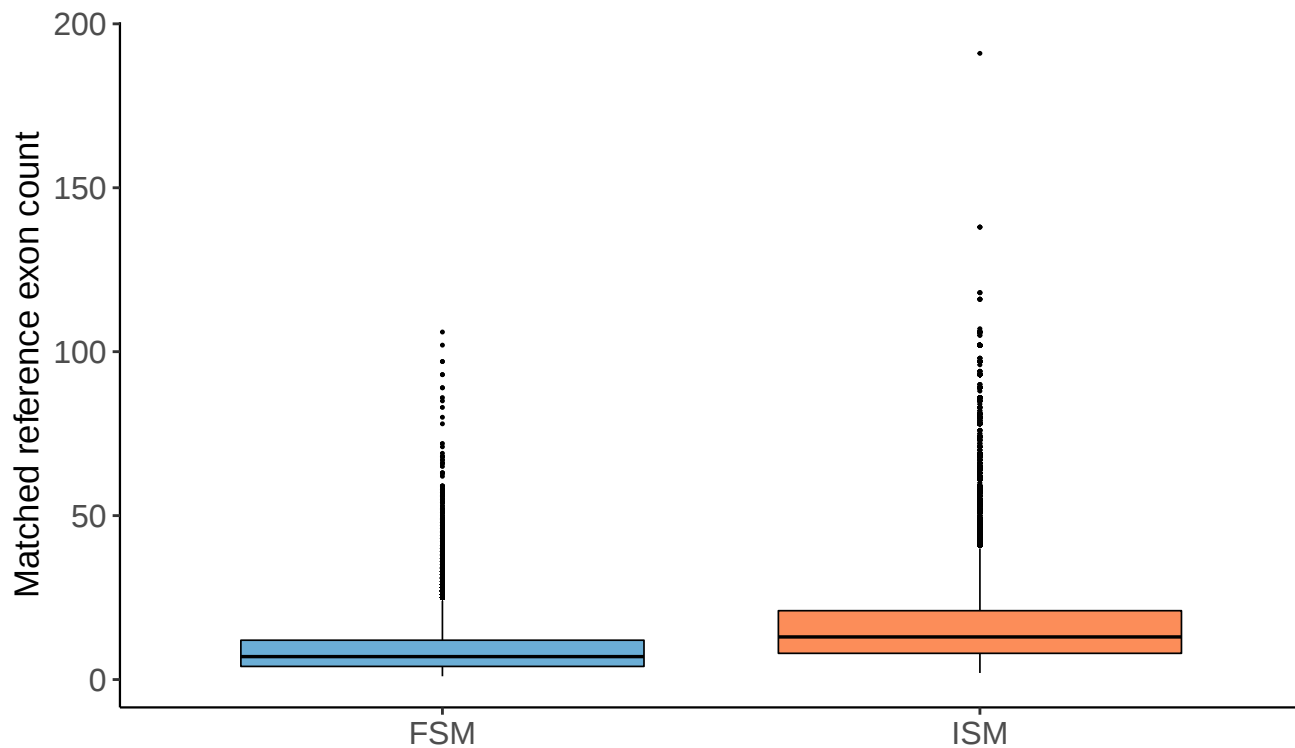
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

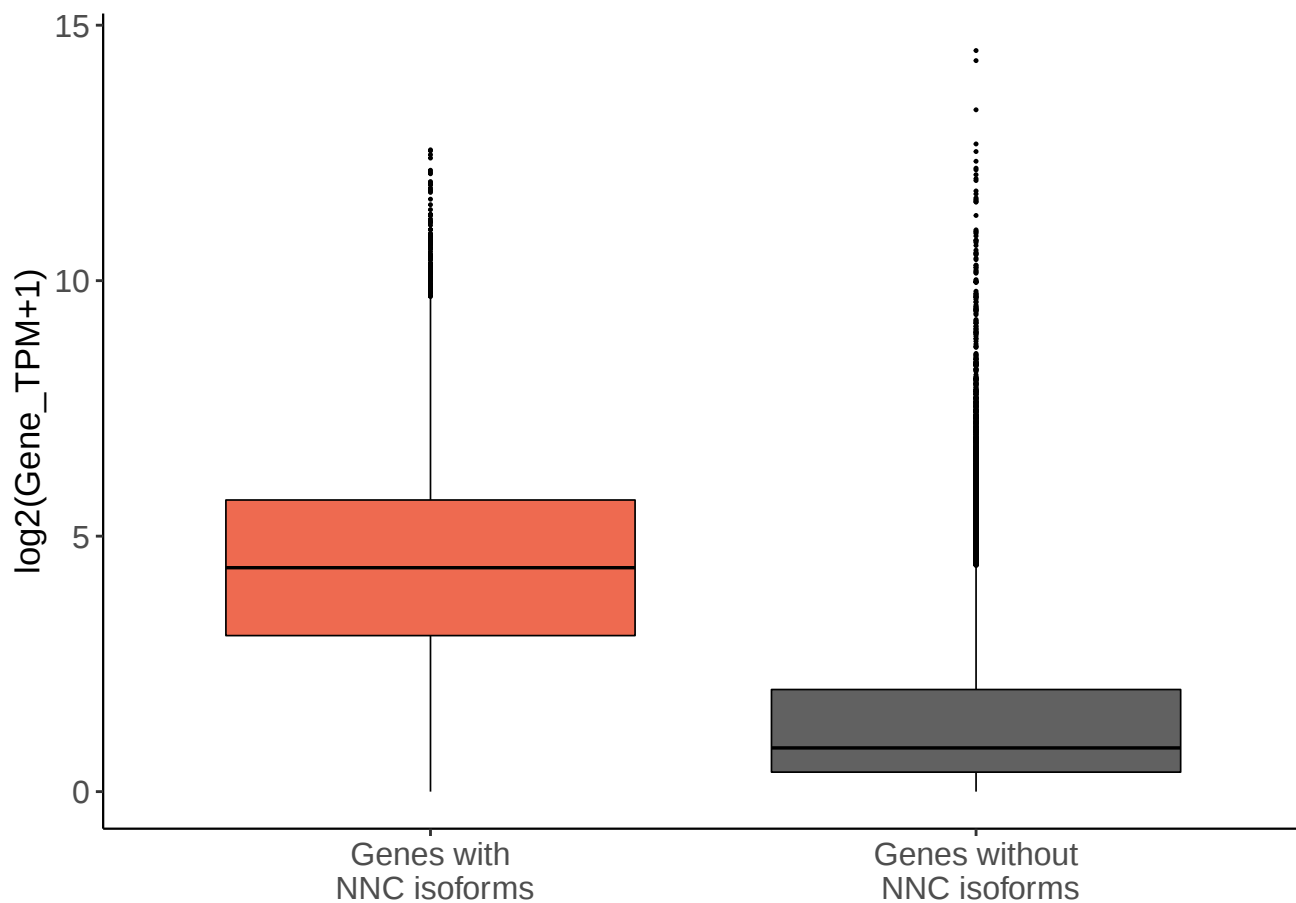


Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

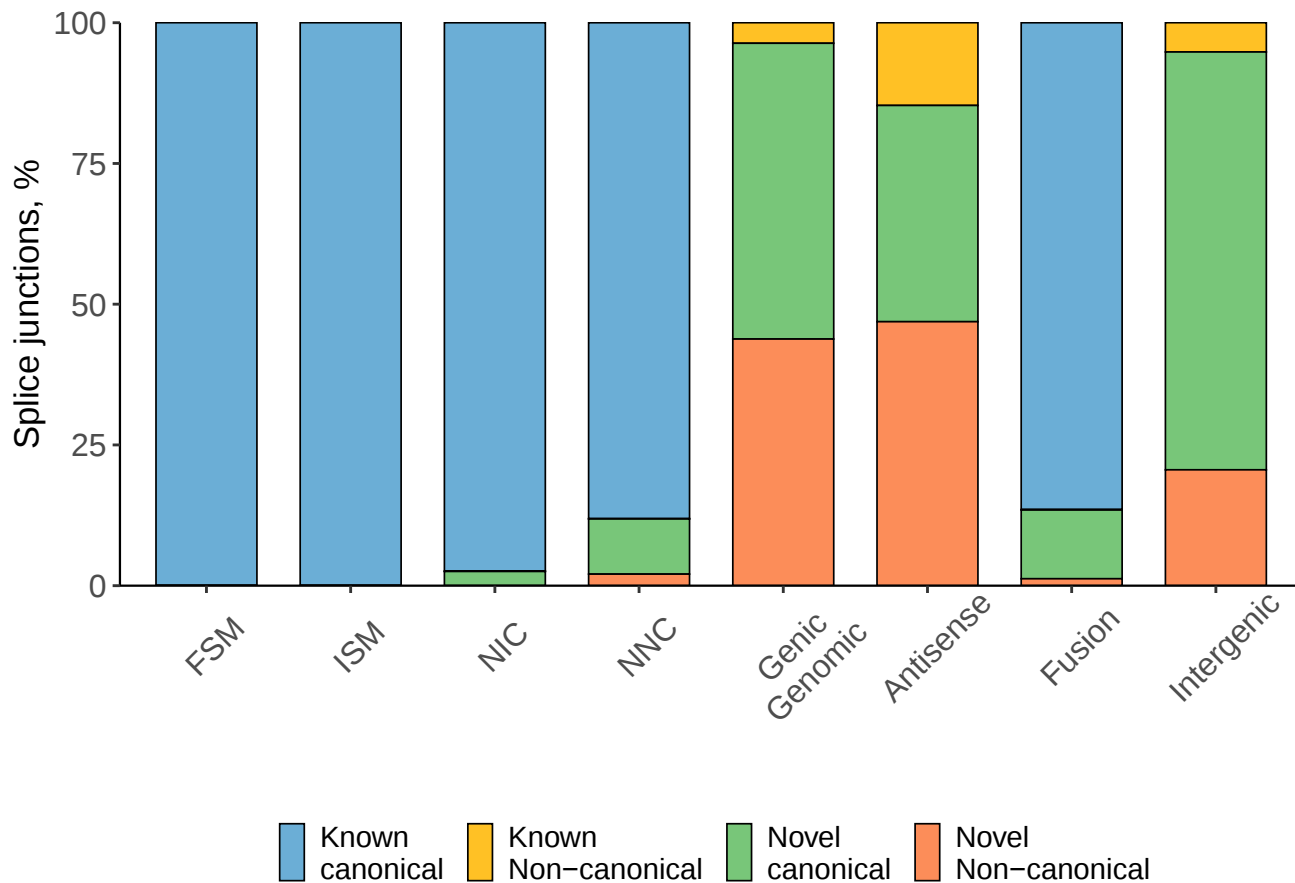


Gene Expression of NNC And Not NNC Containing Genes

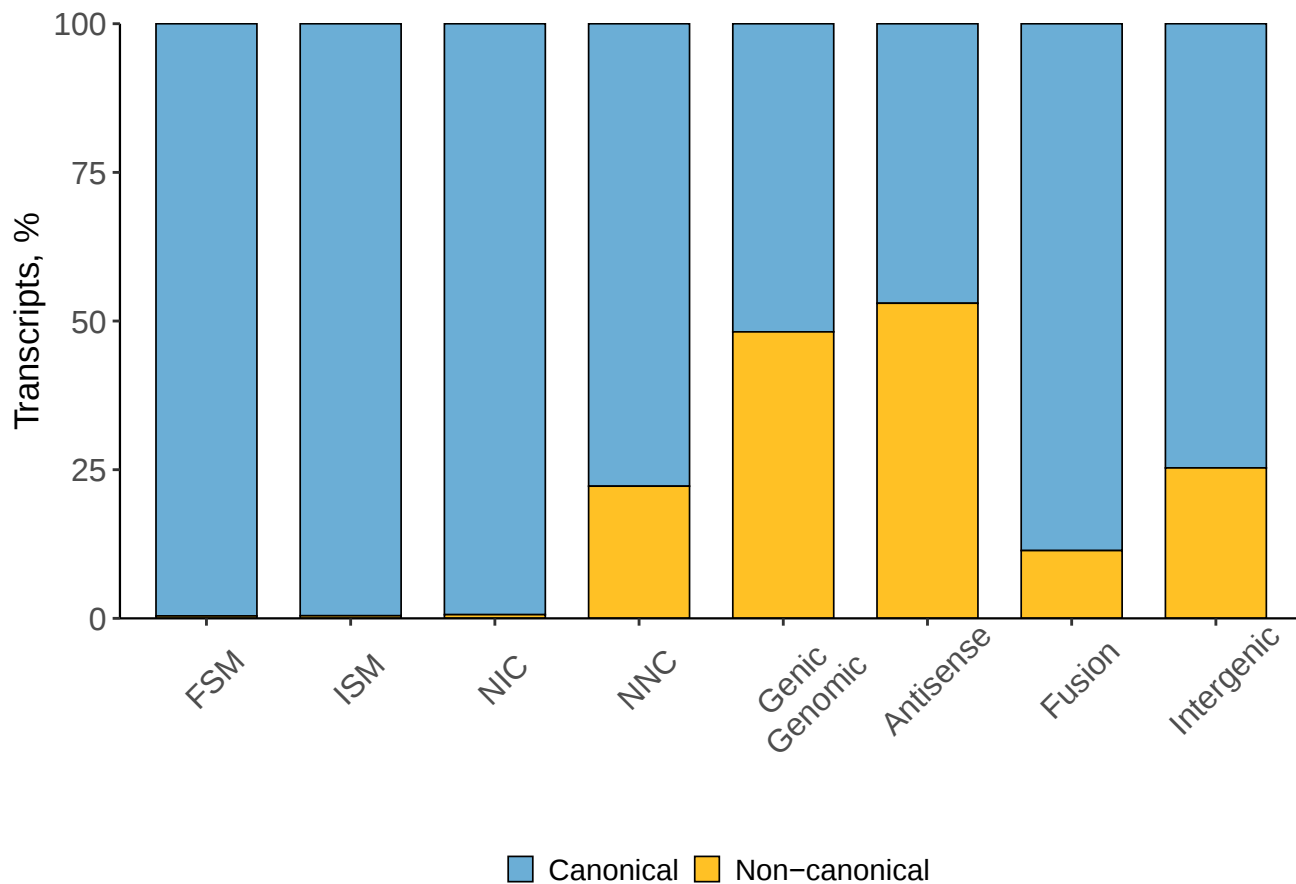


Splice Junction Characterization

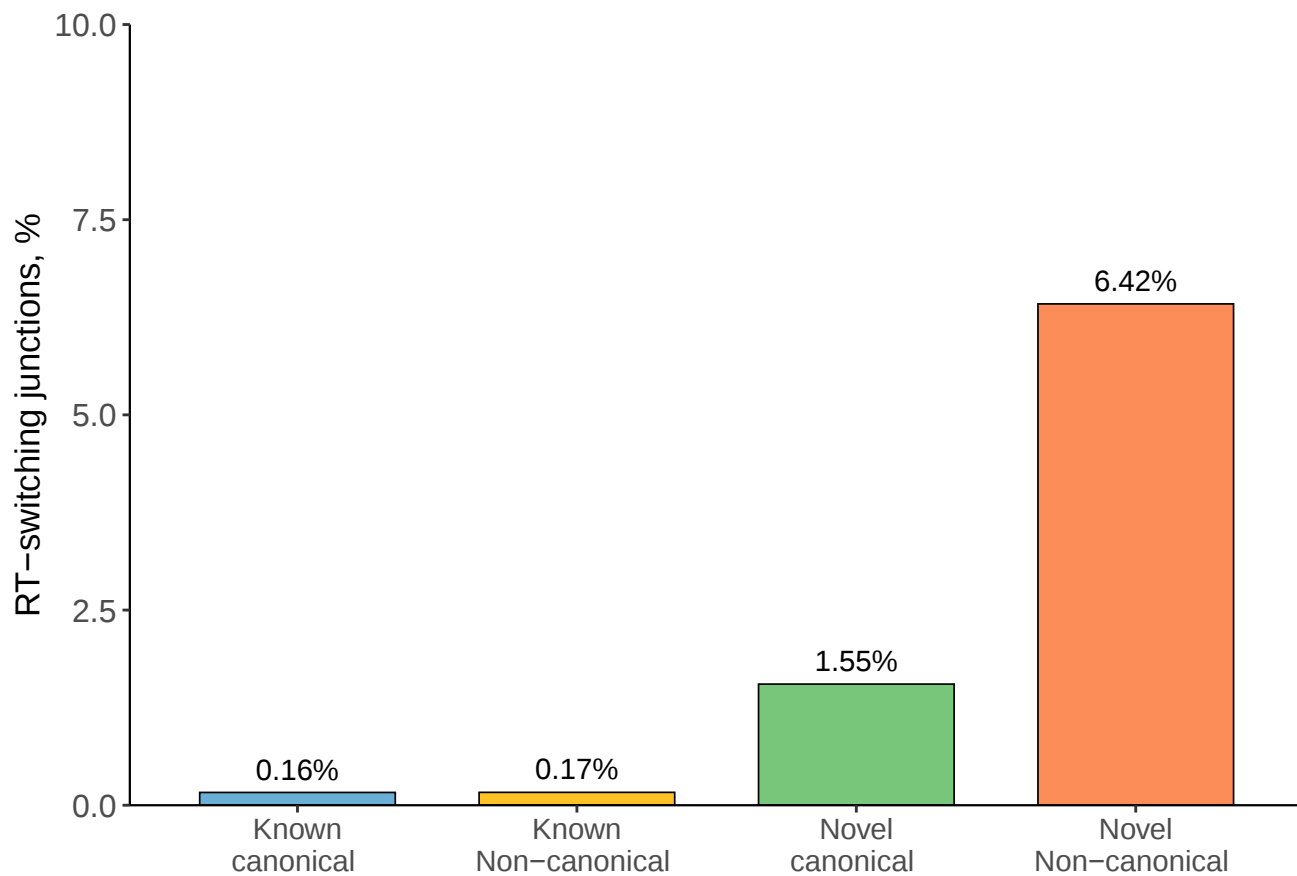
Distribution of Splice Junctions by Structural Classification



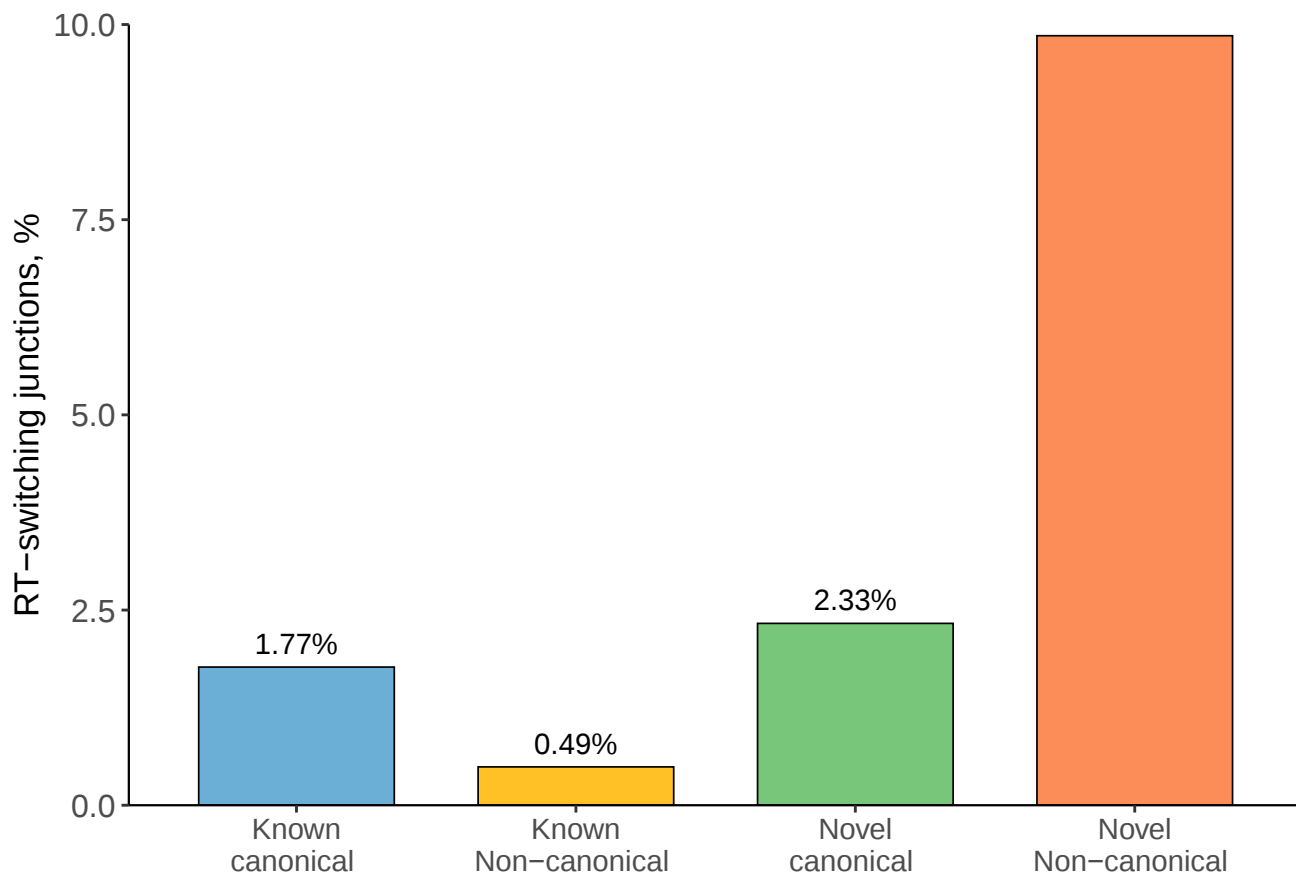
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



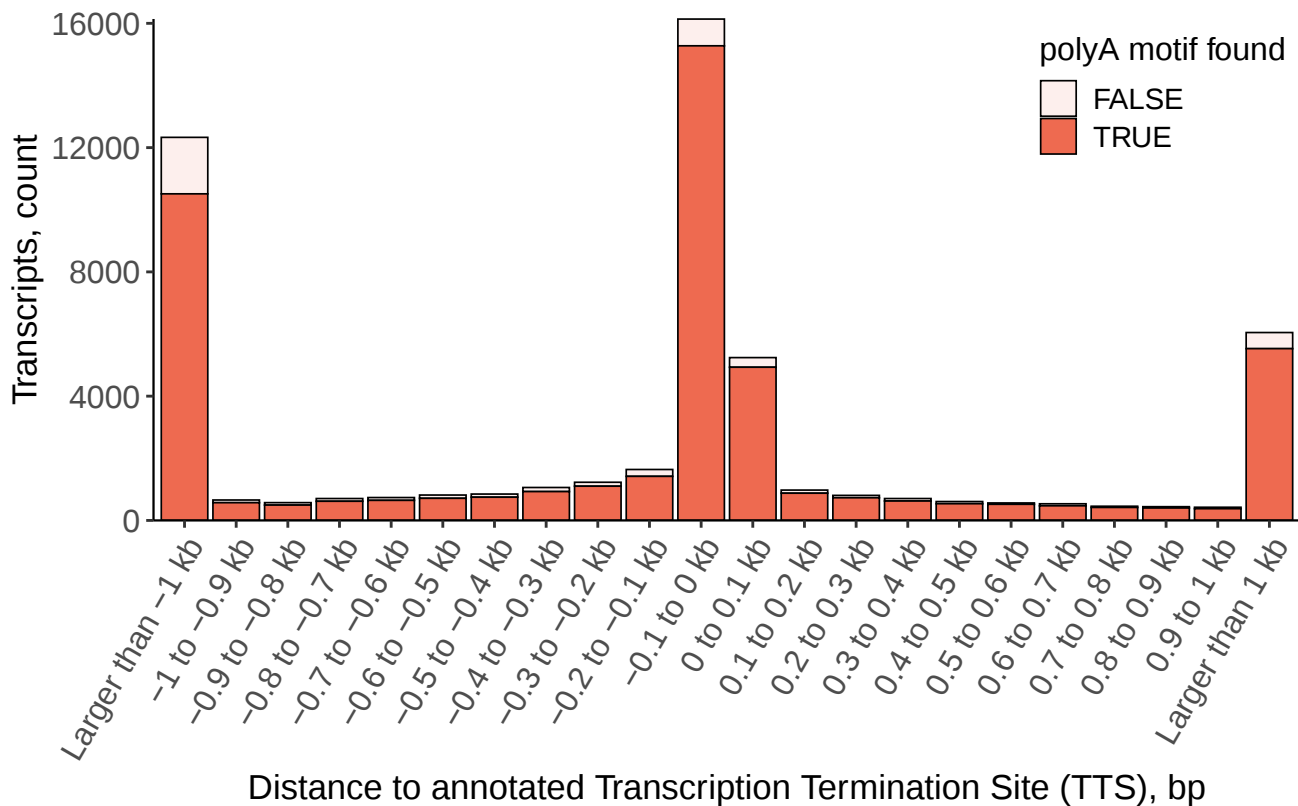
Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

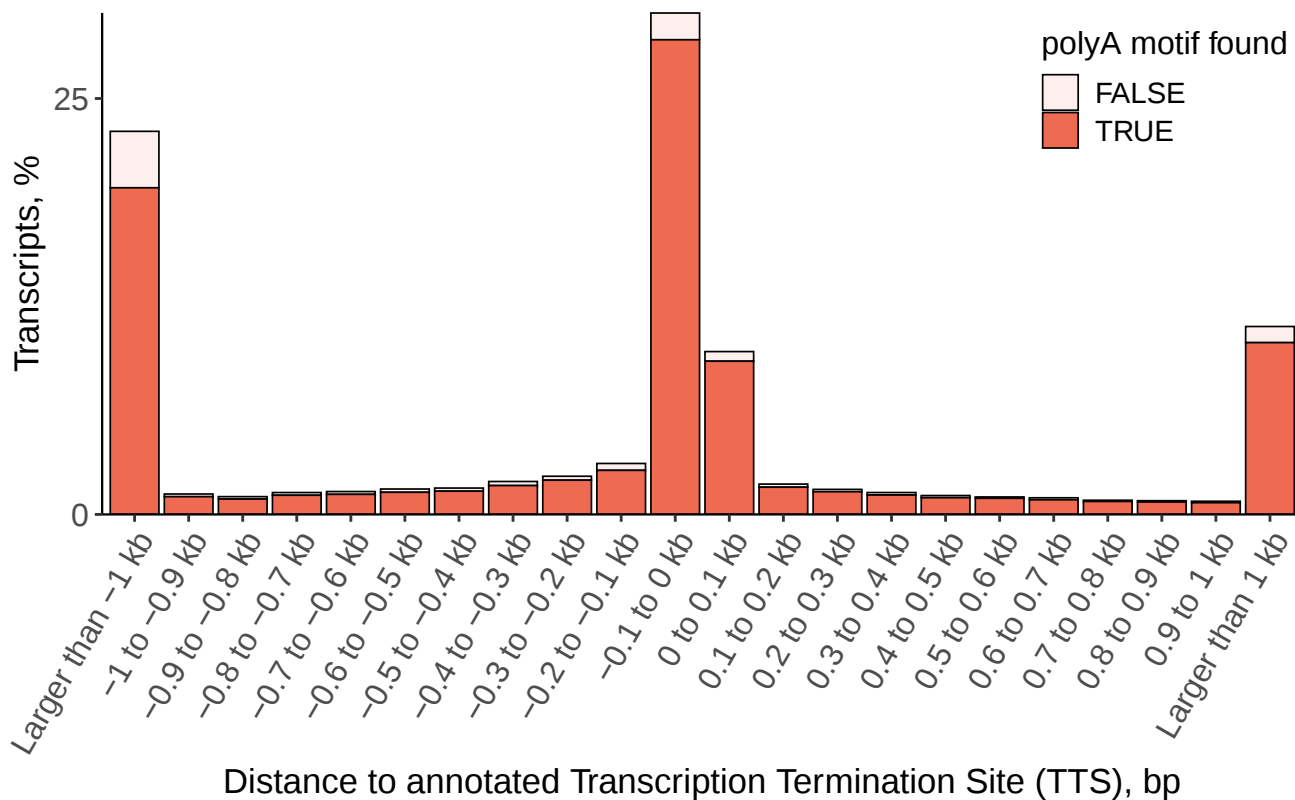
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



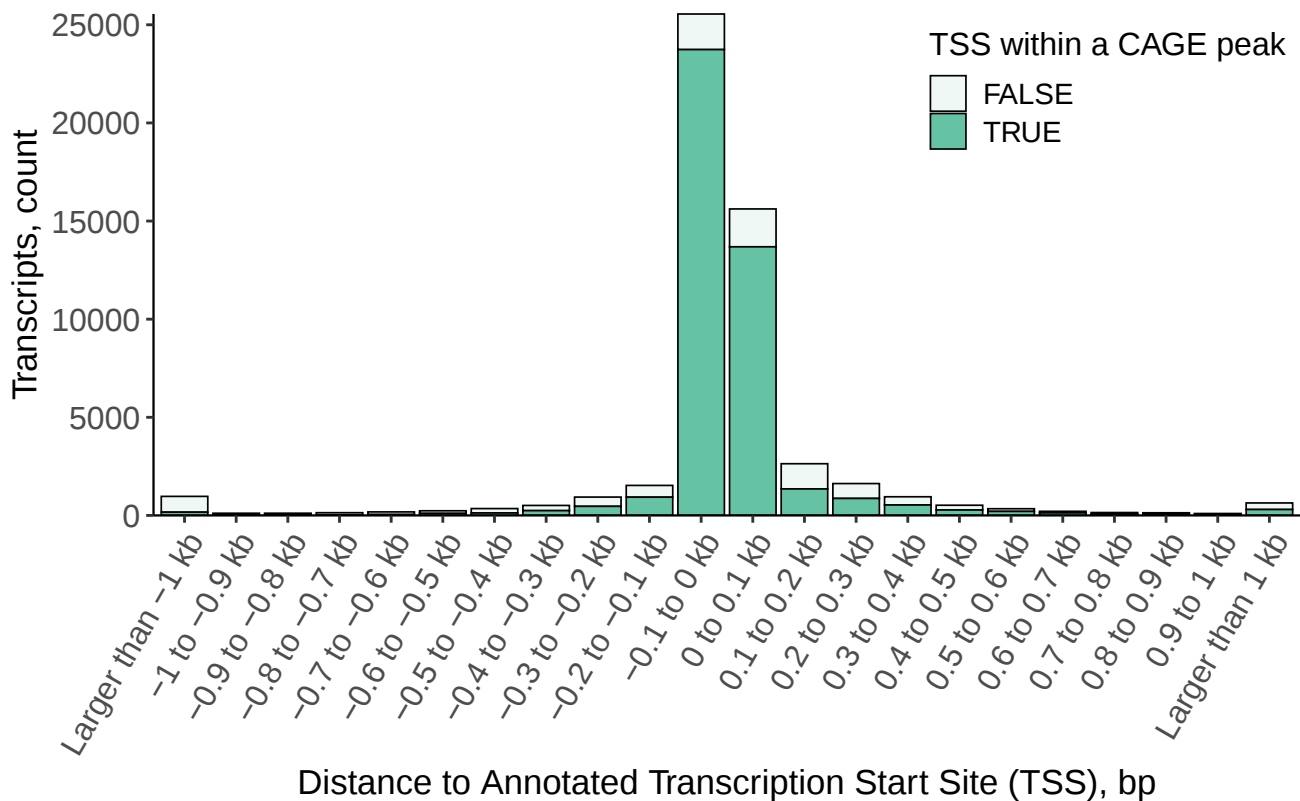
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



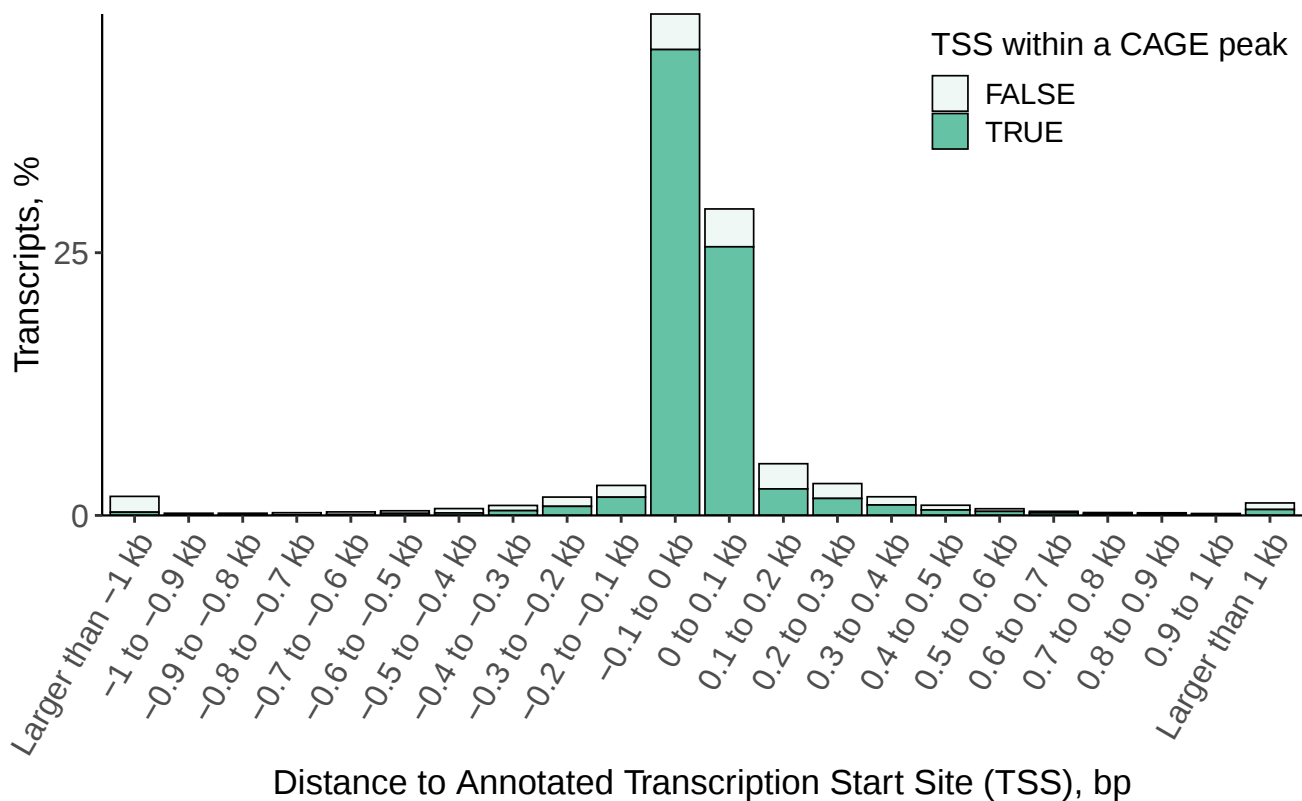
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



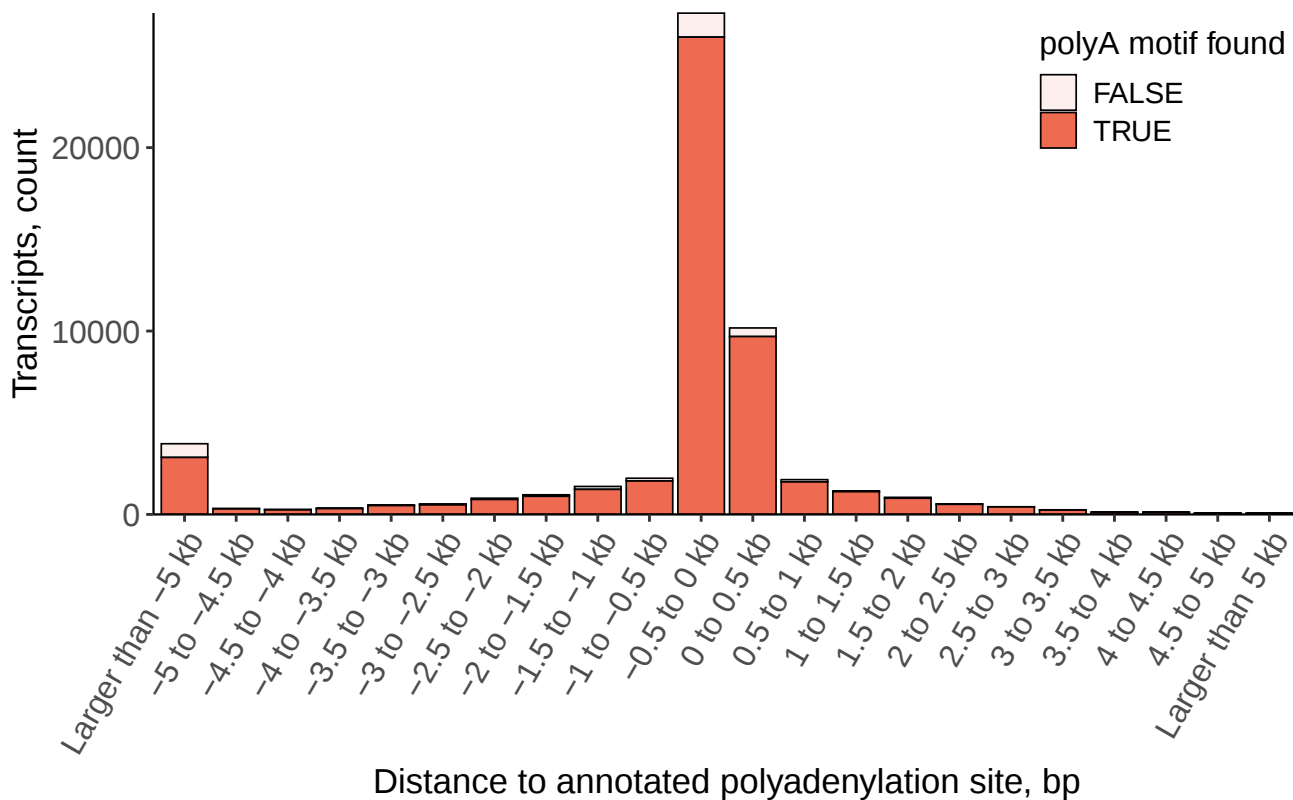
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



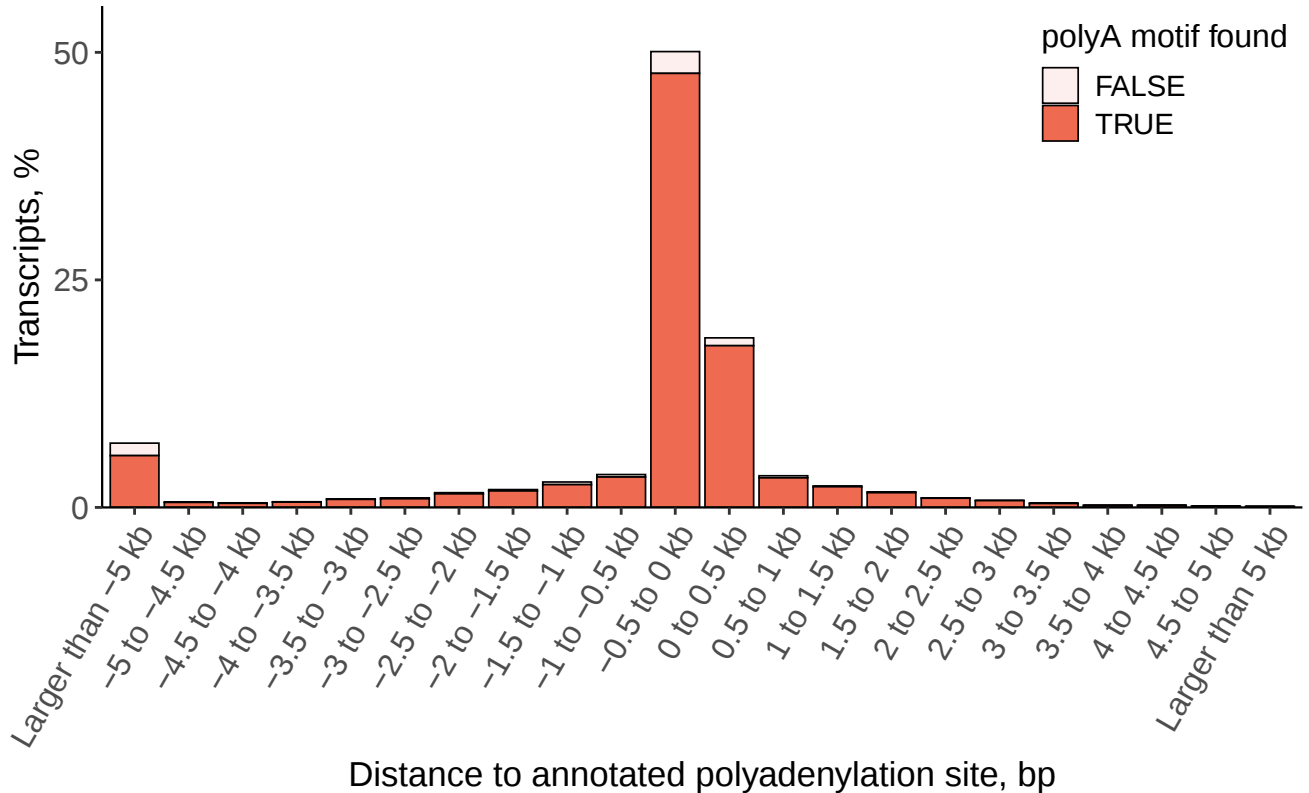
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



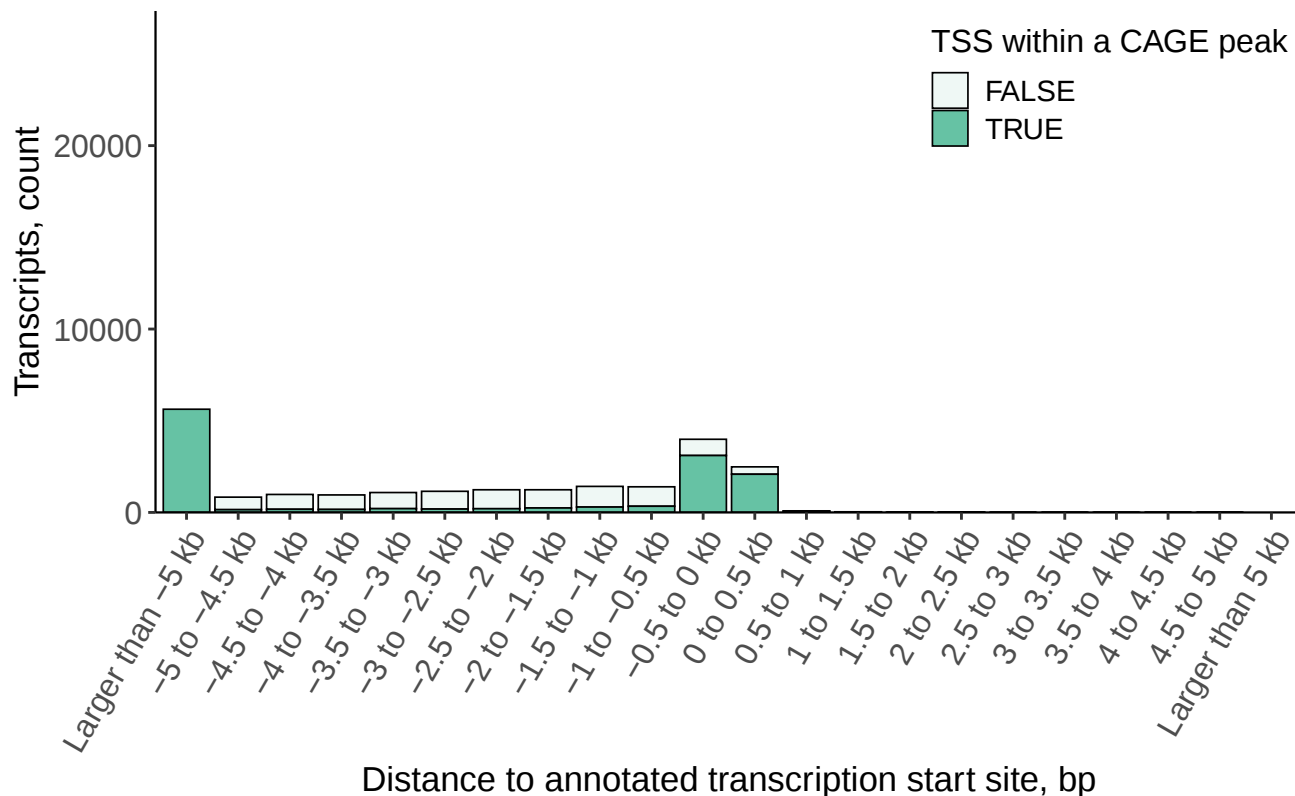
Distance to Annotated Polyadenylation Site for ISM

Negative values indicate upstream of annotated polyA site



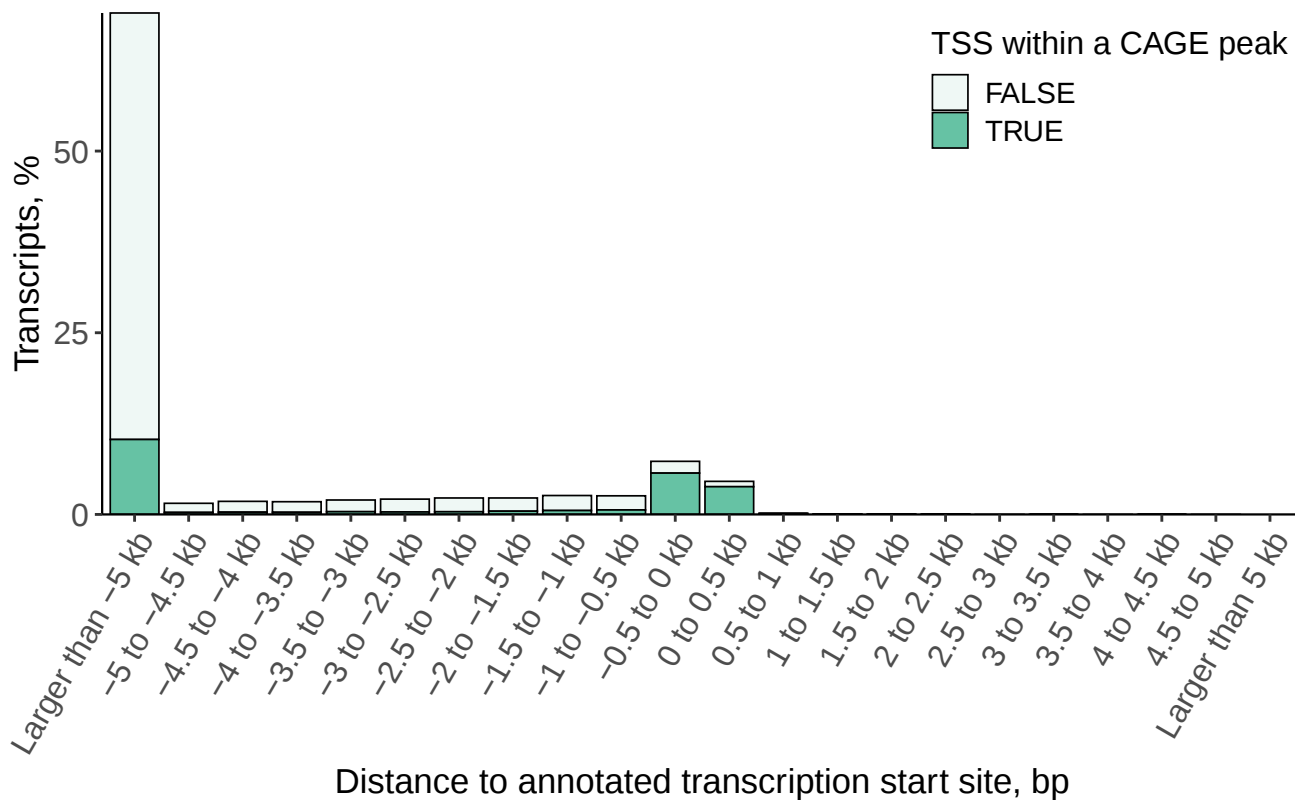
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

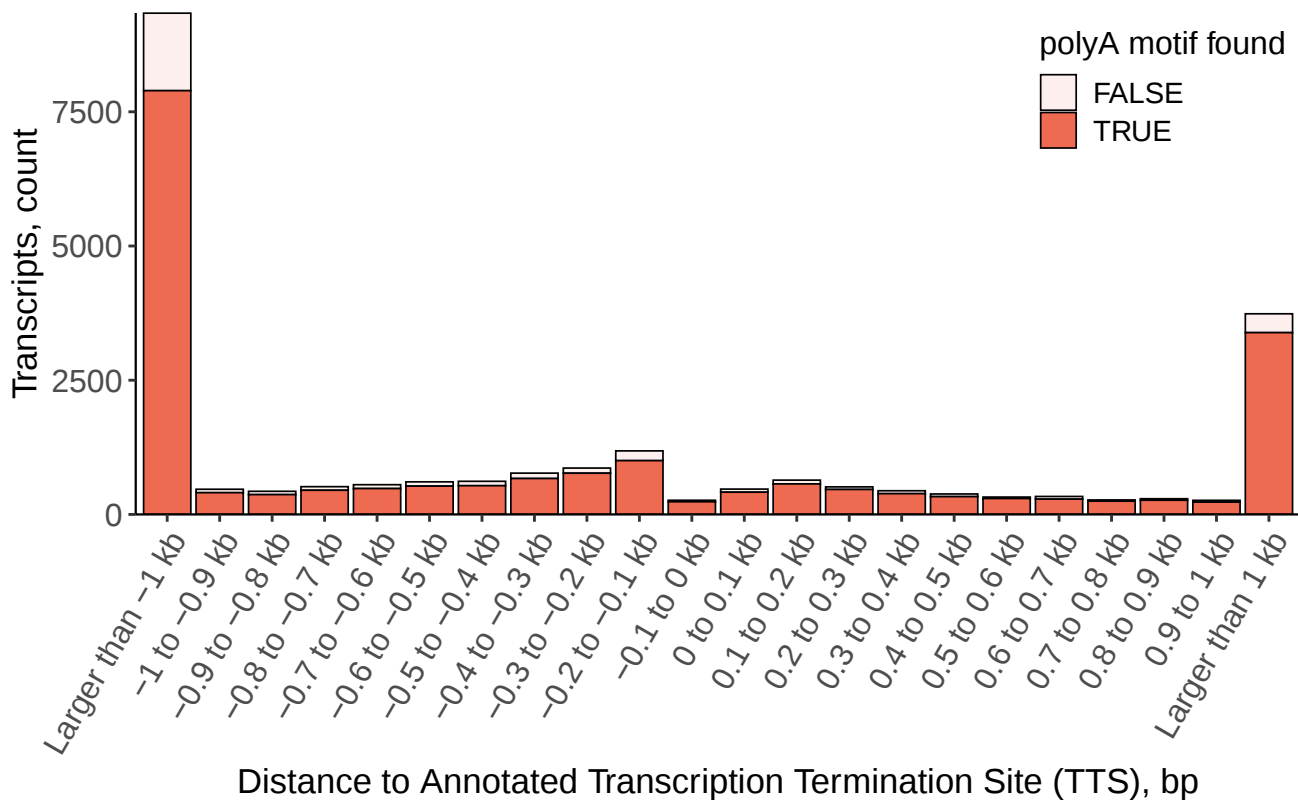
Negative values indicate downstream of annotated TSS



*Comparison With Annotated TSS and TTS
by Subcategories*

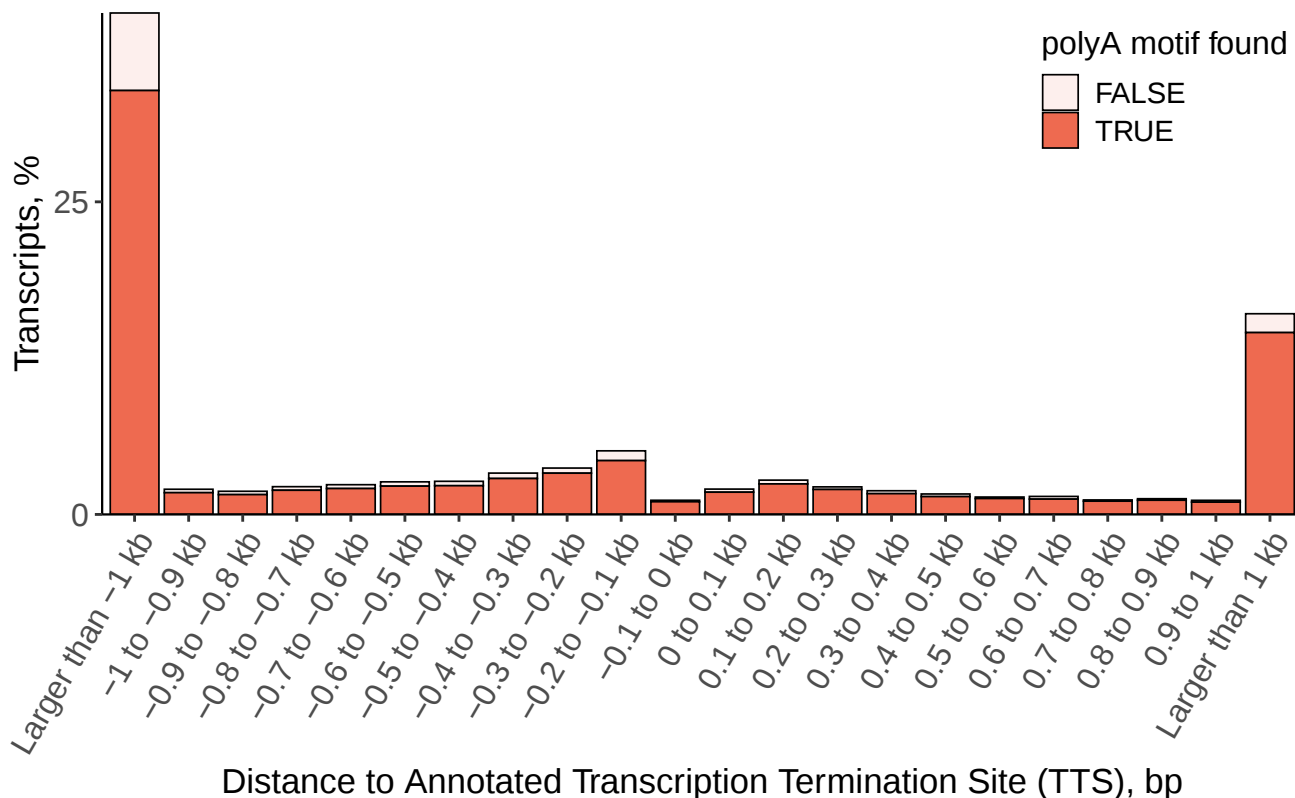
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



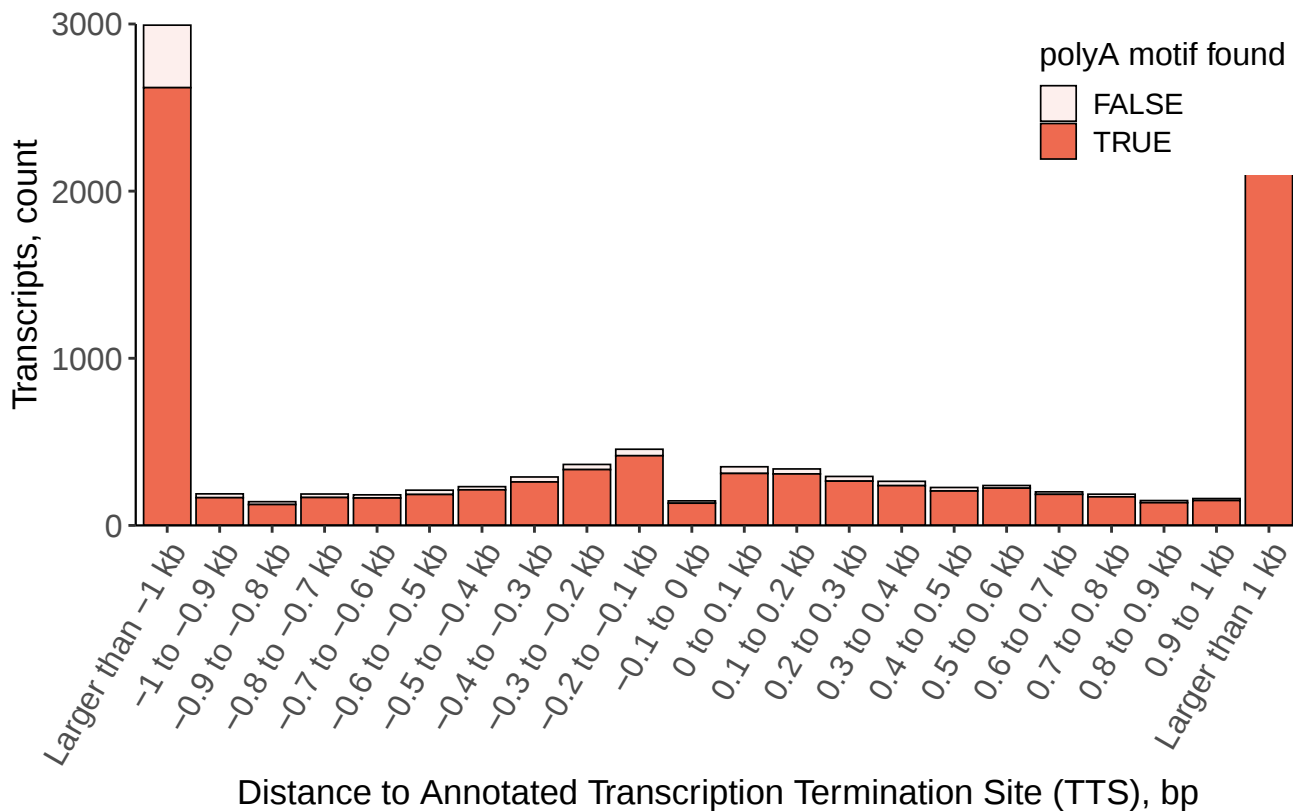
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



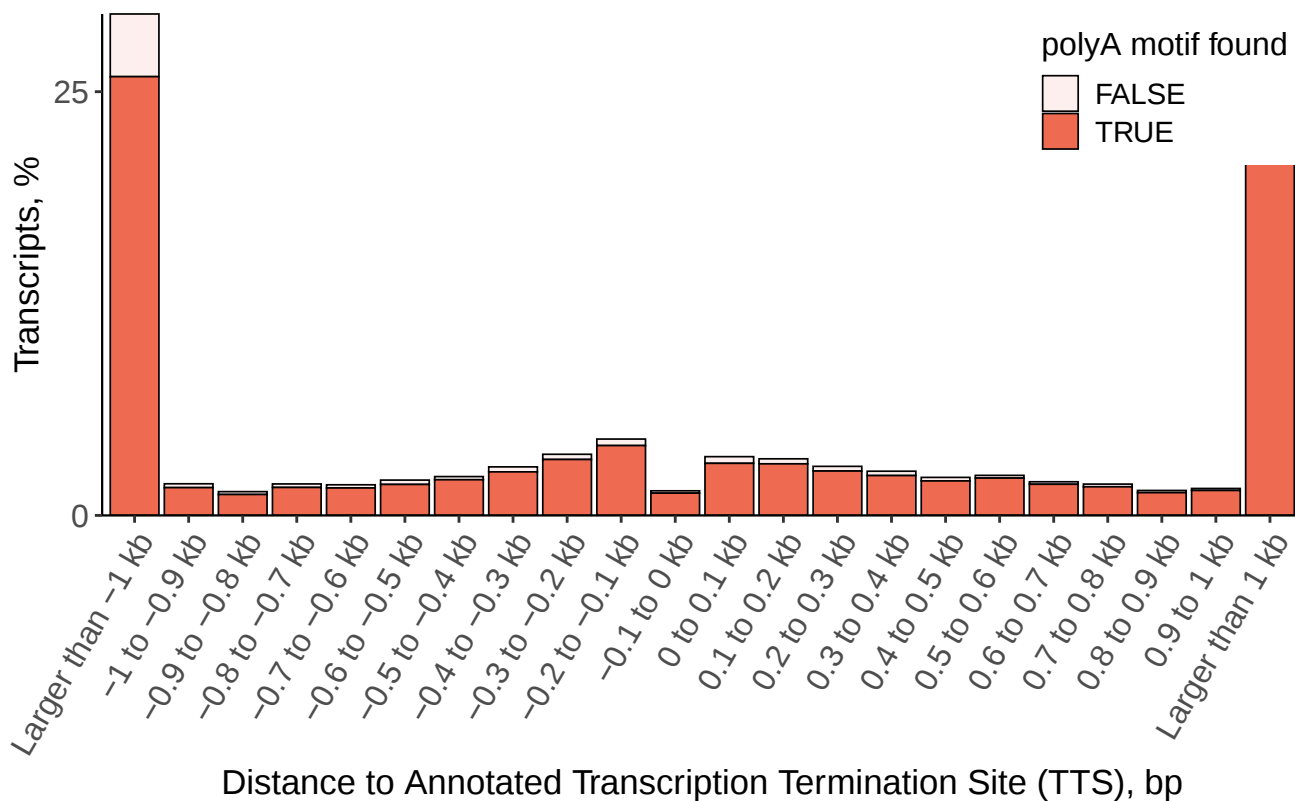
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



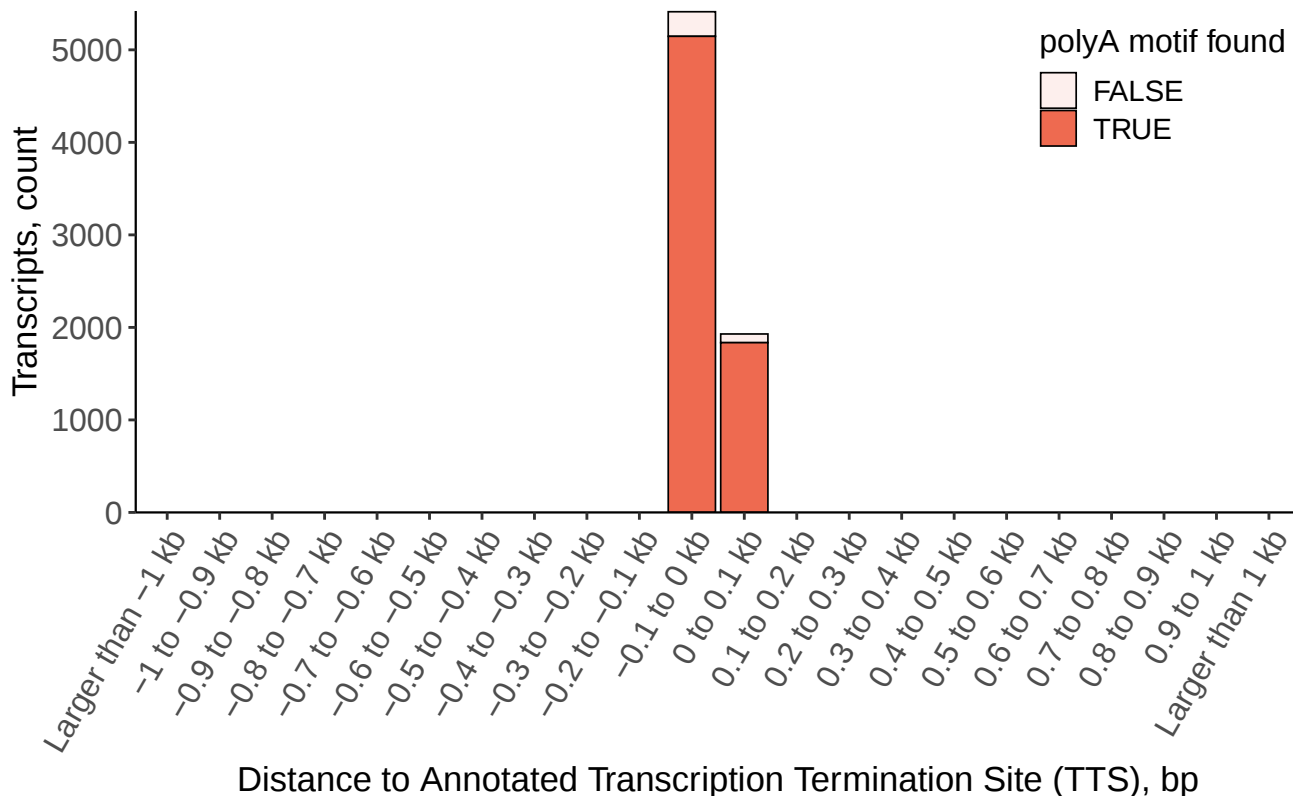
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



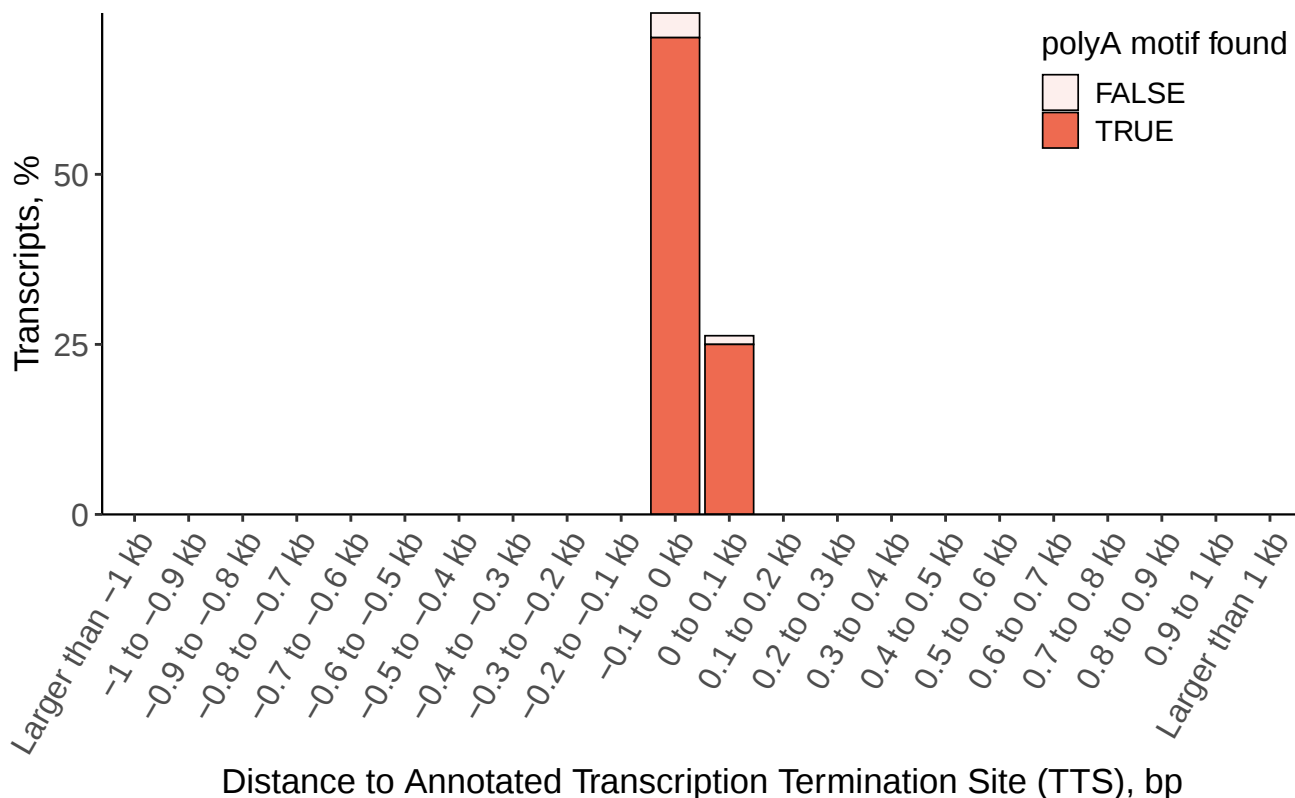
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



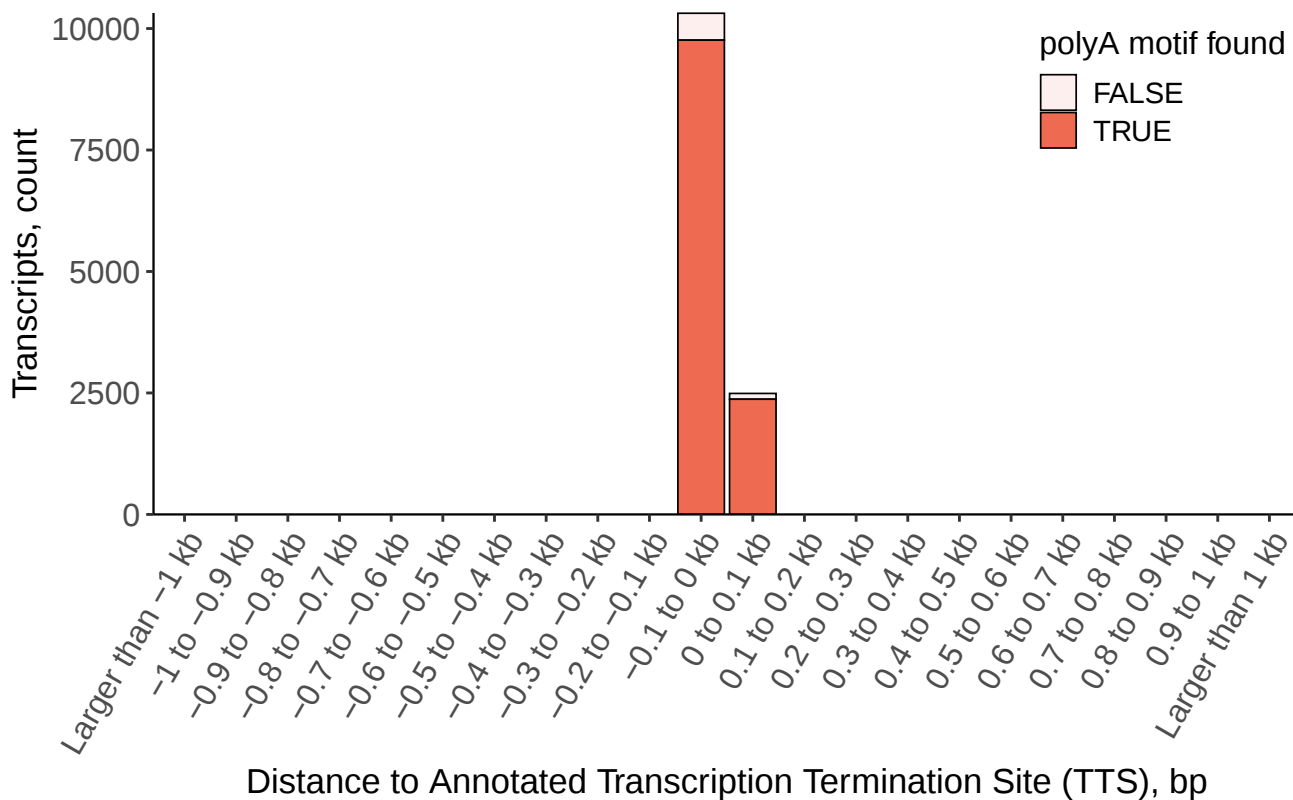
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



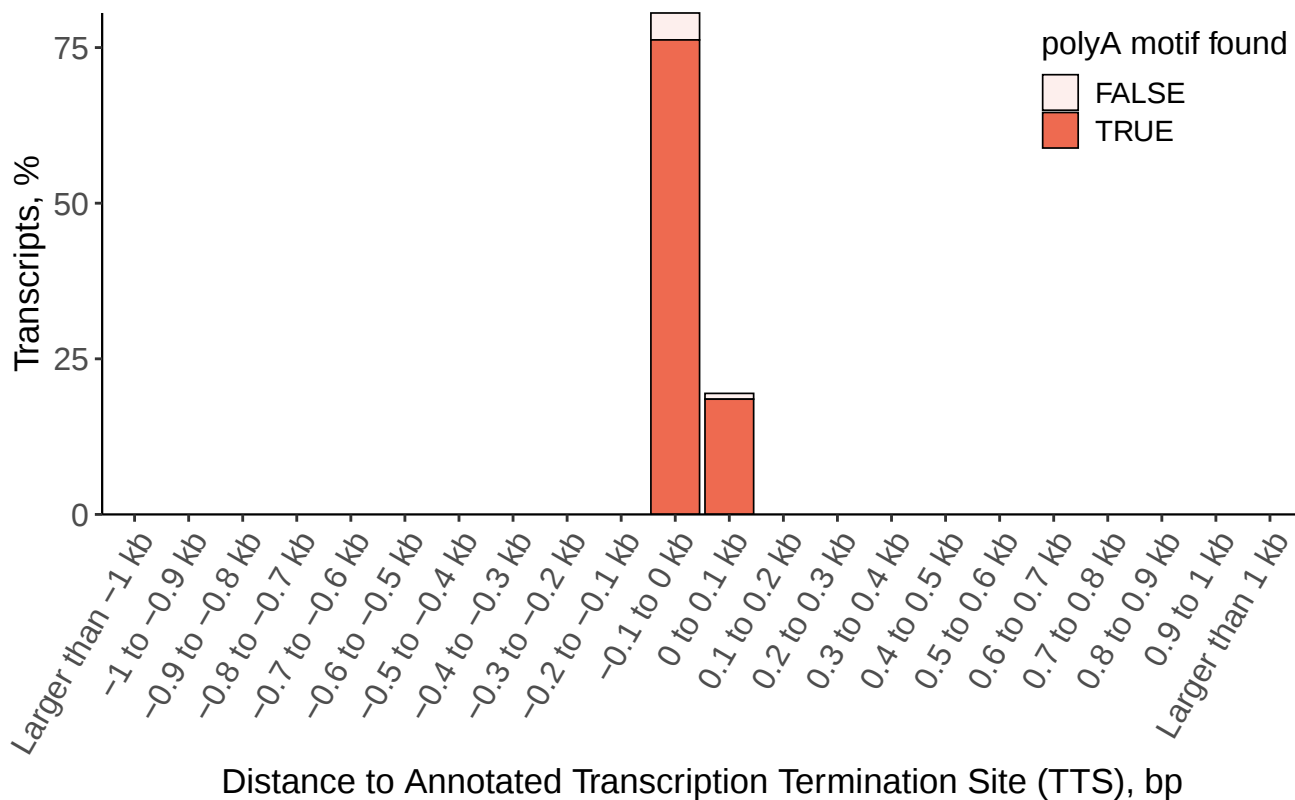
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



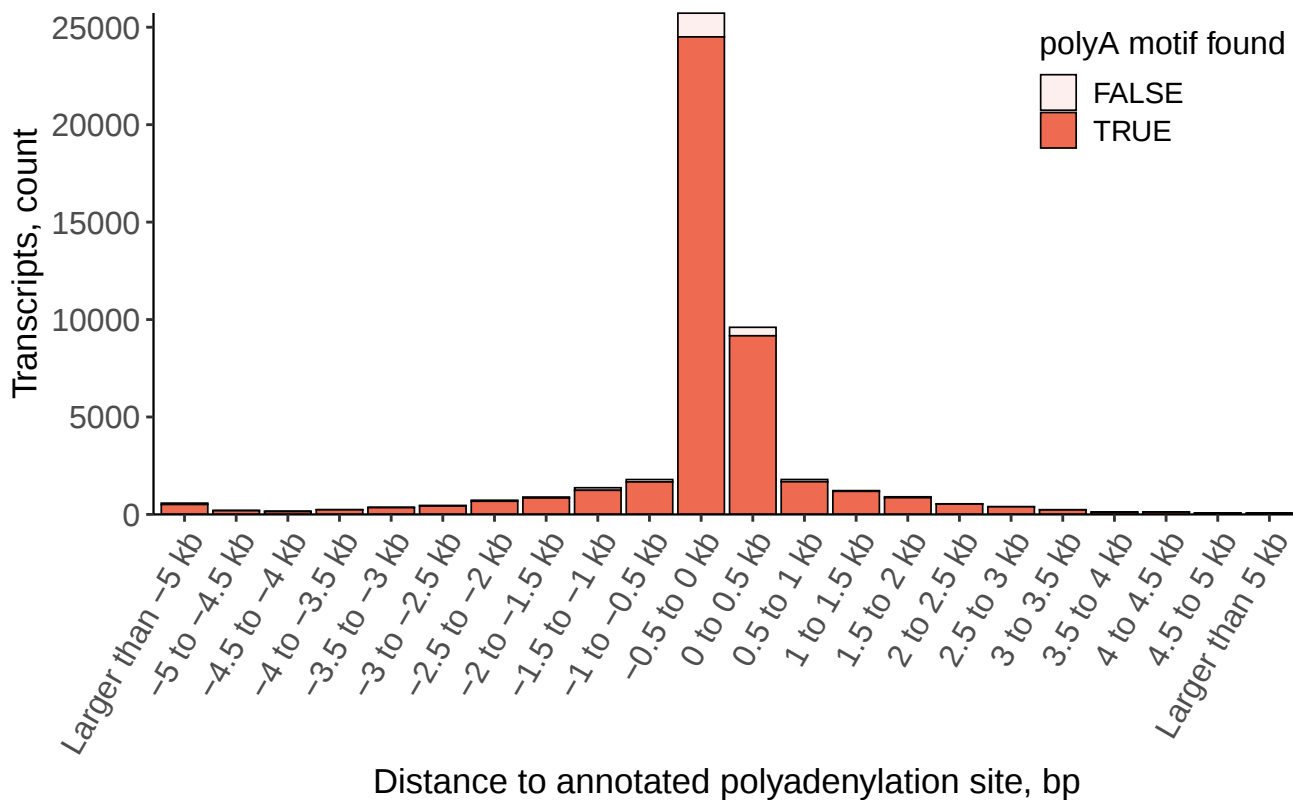
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



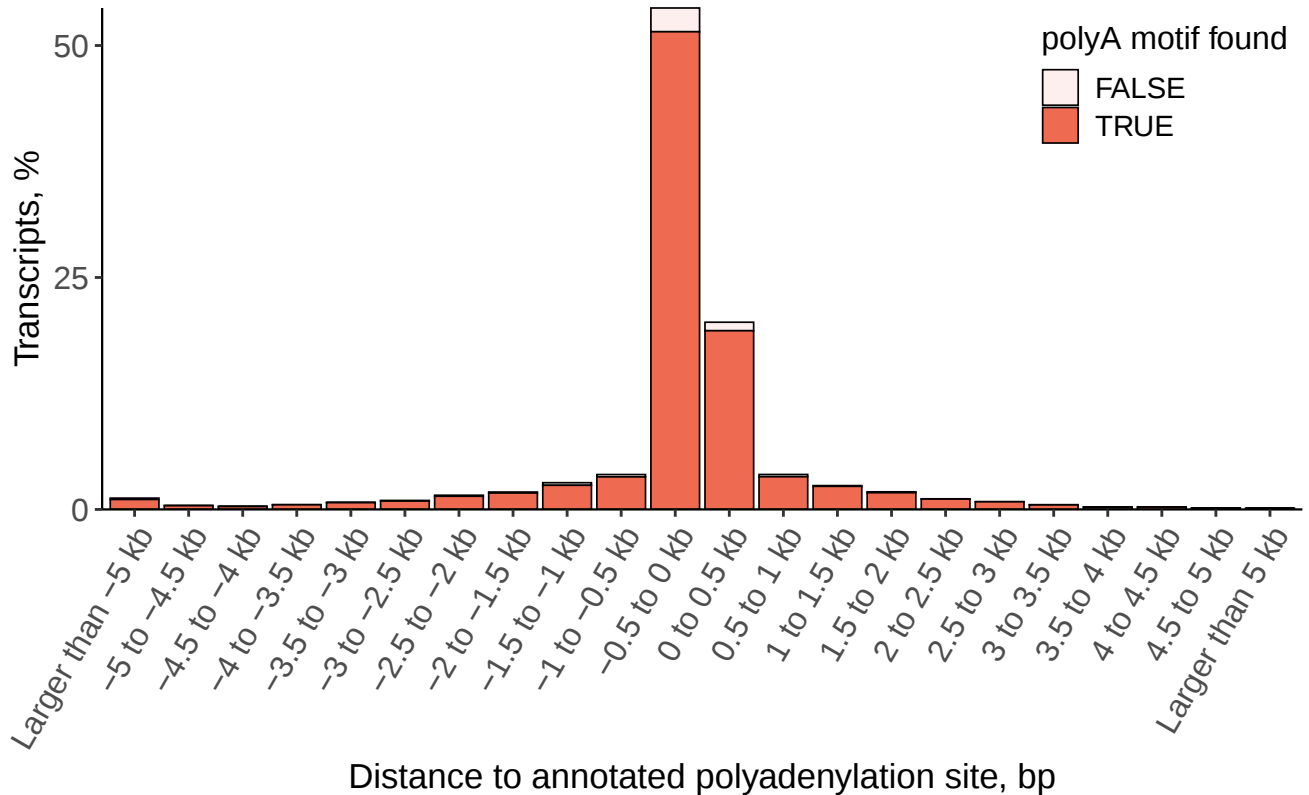
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



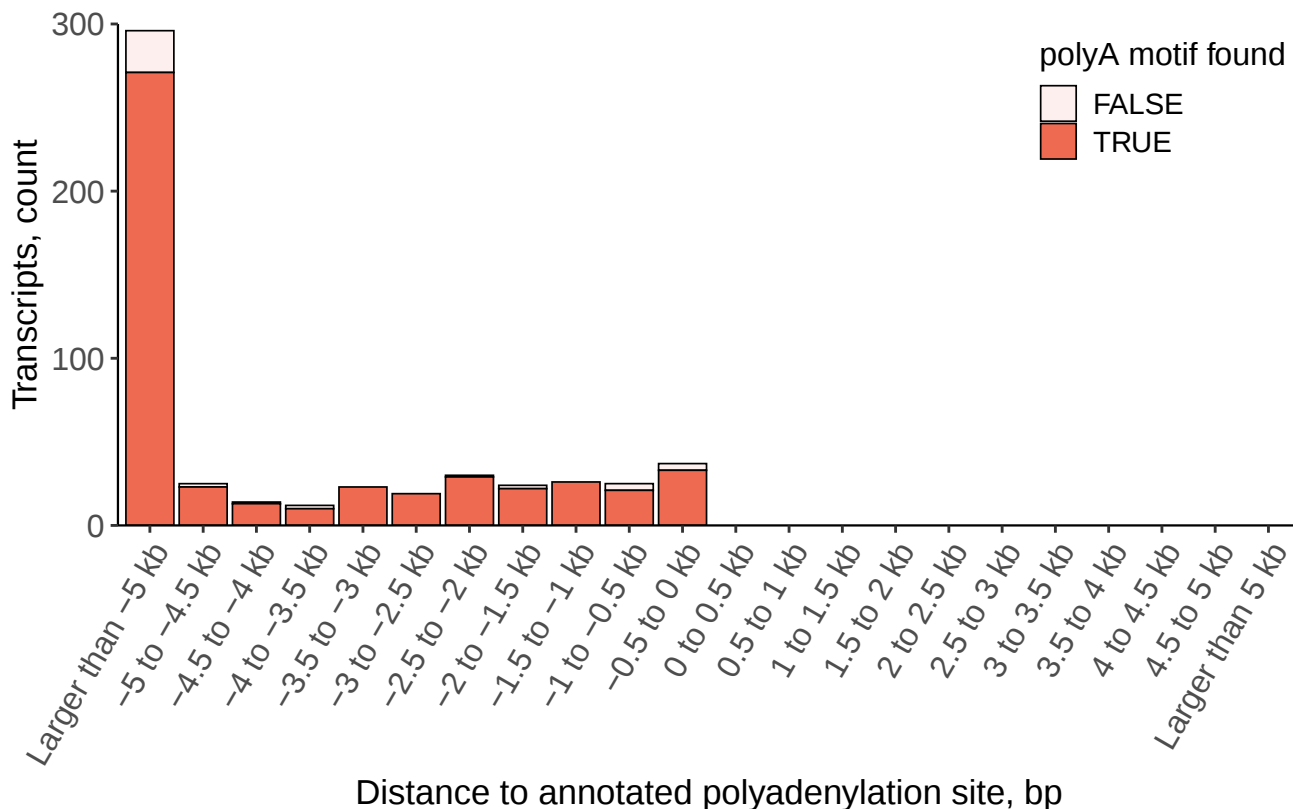
Distance to Annotated Polyadenylation Site for ISM 3' Fragment

Negative values indicate upstream of annotated polyA site



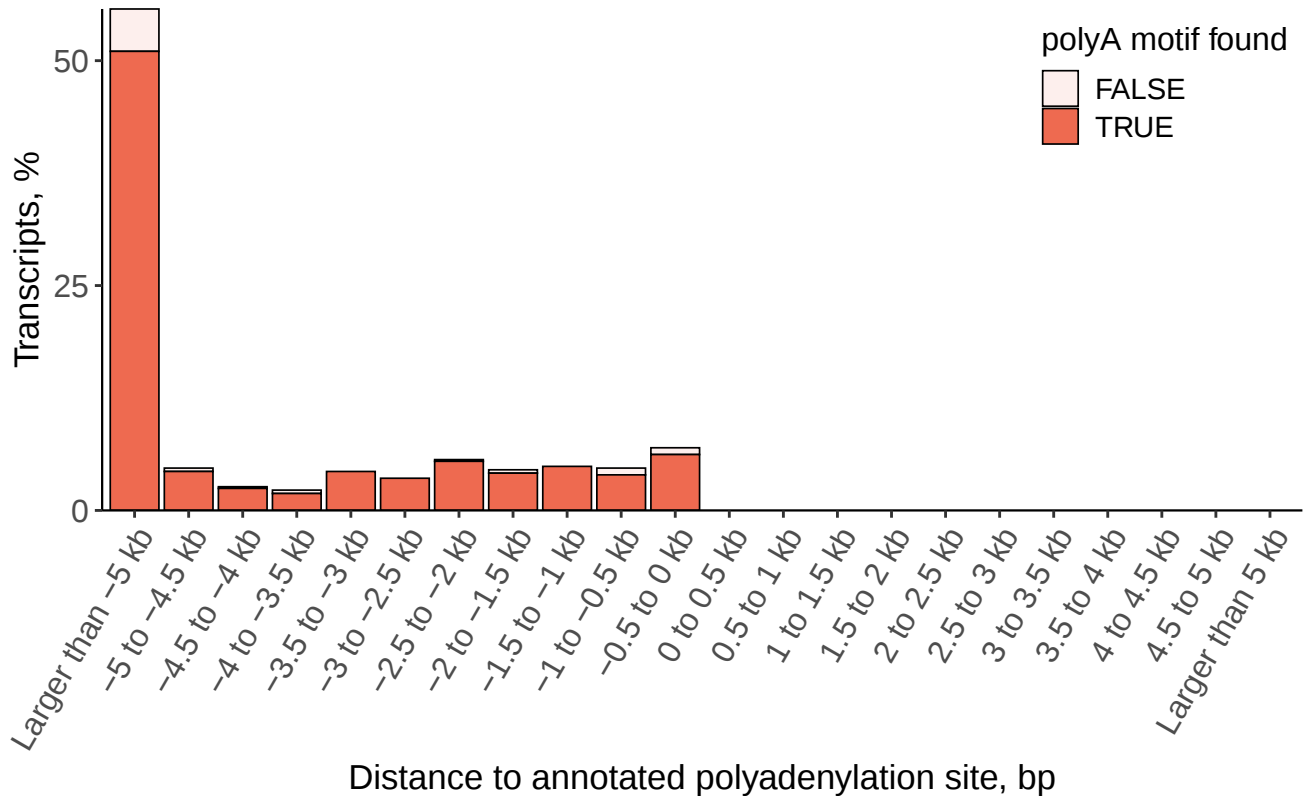
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



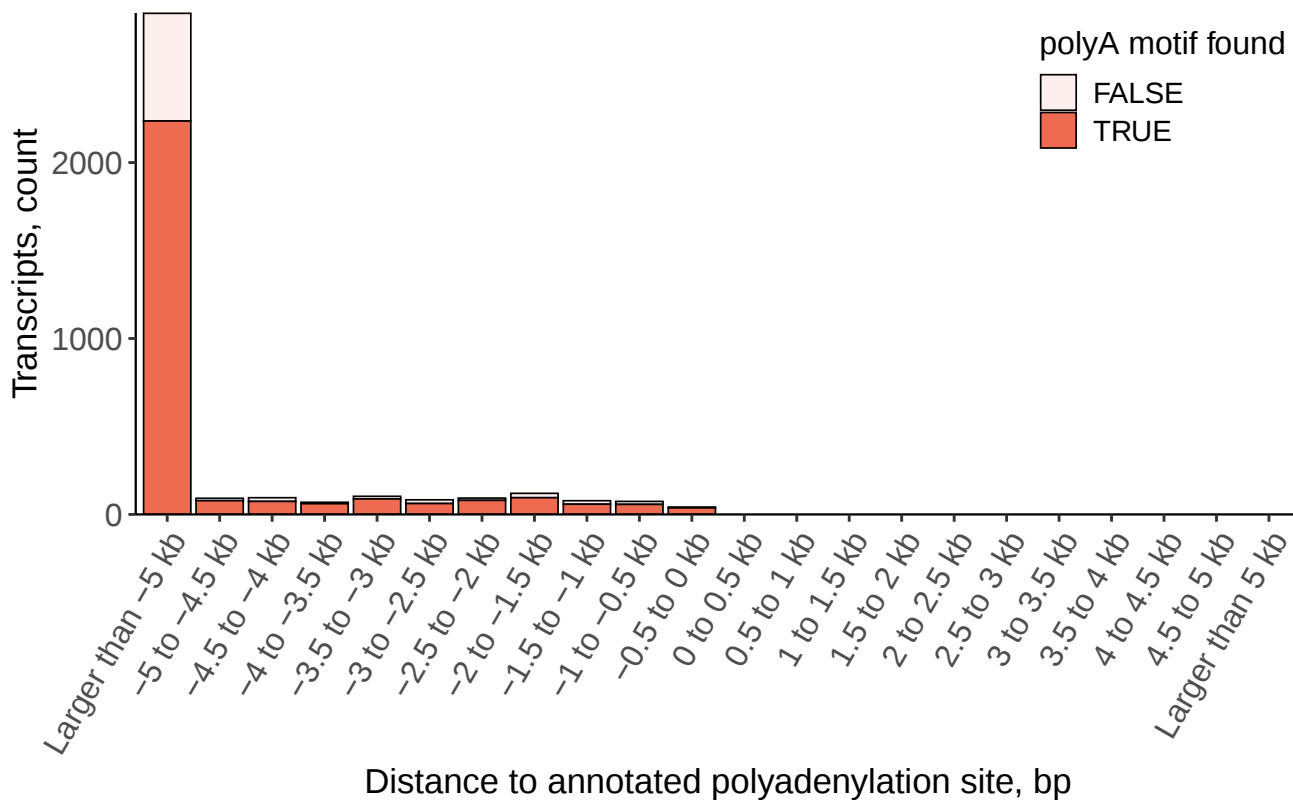
Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site



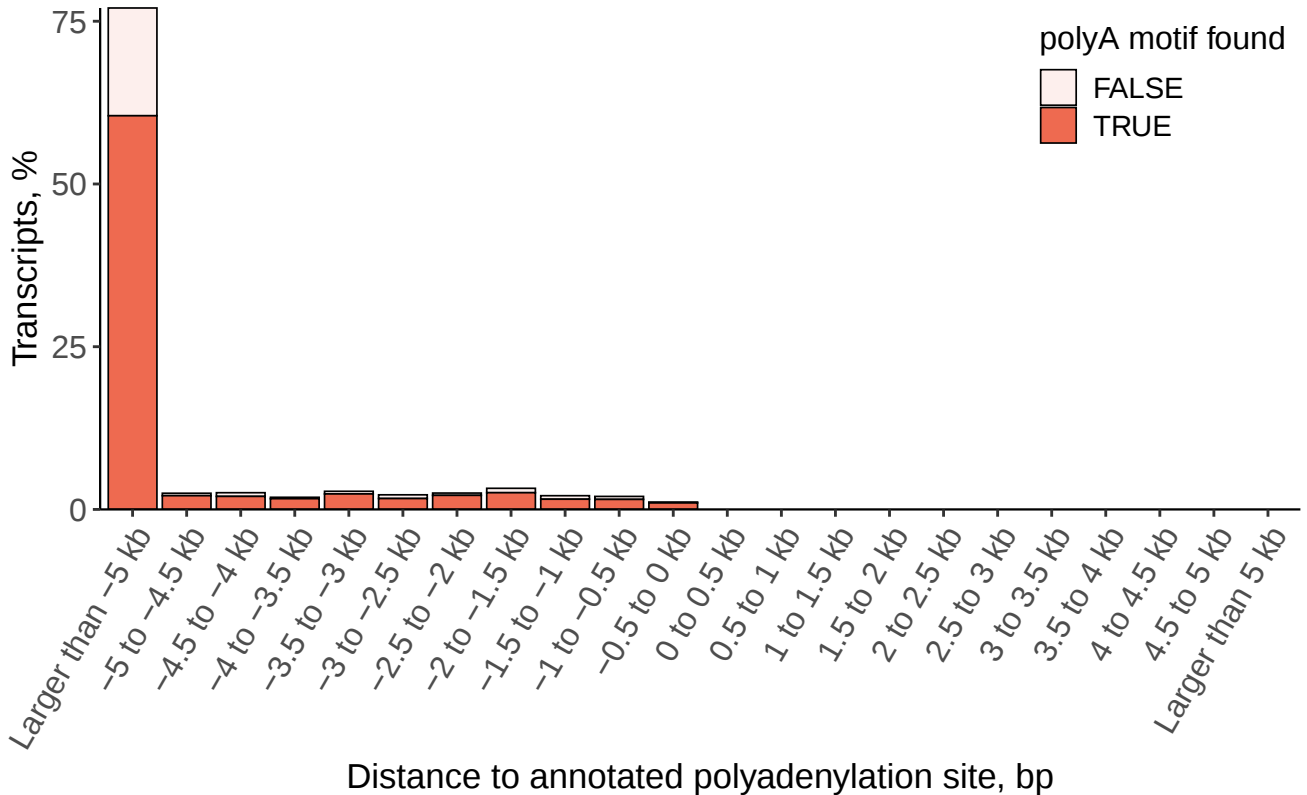
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



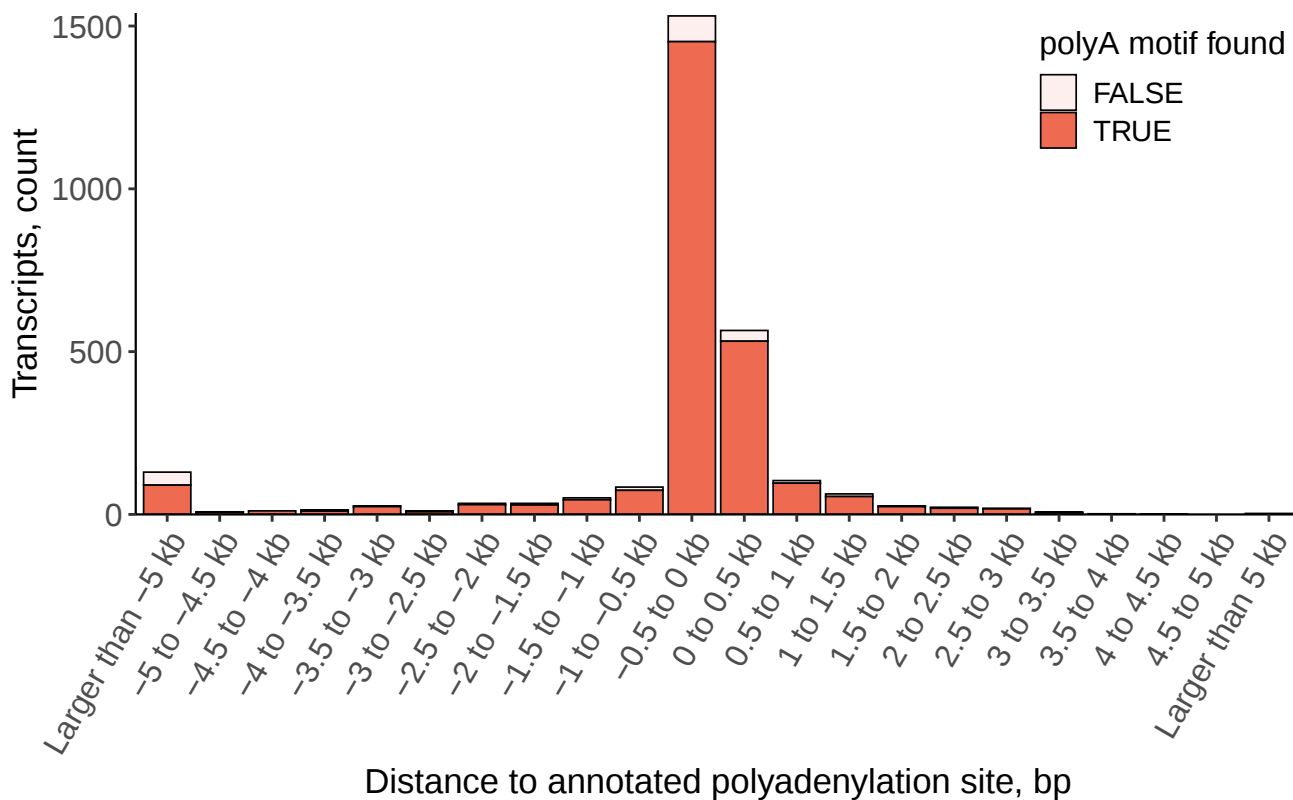
Distance to Annotated Polyadenylation Site for ISM A5' Fragment

Negative values indicate upstream of annotated polyA site



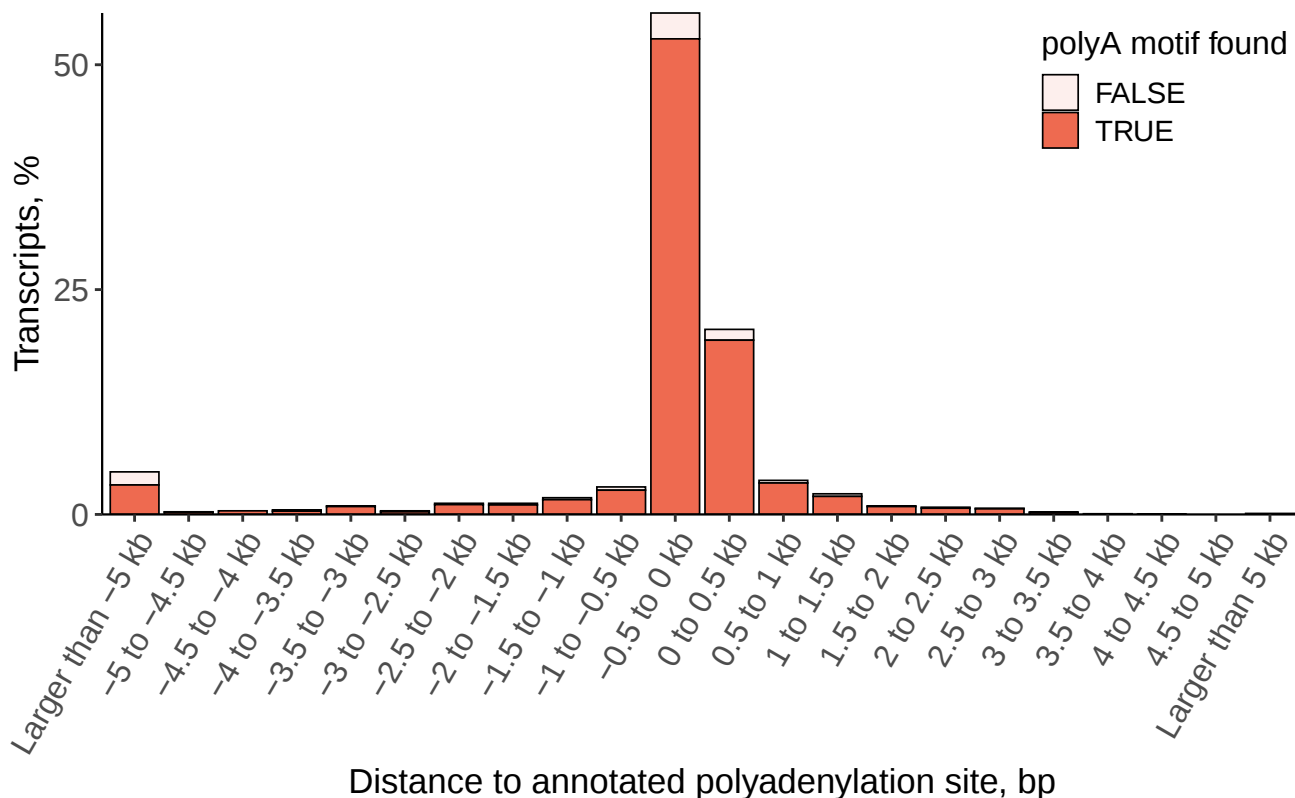
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



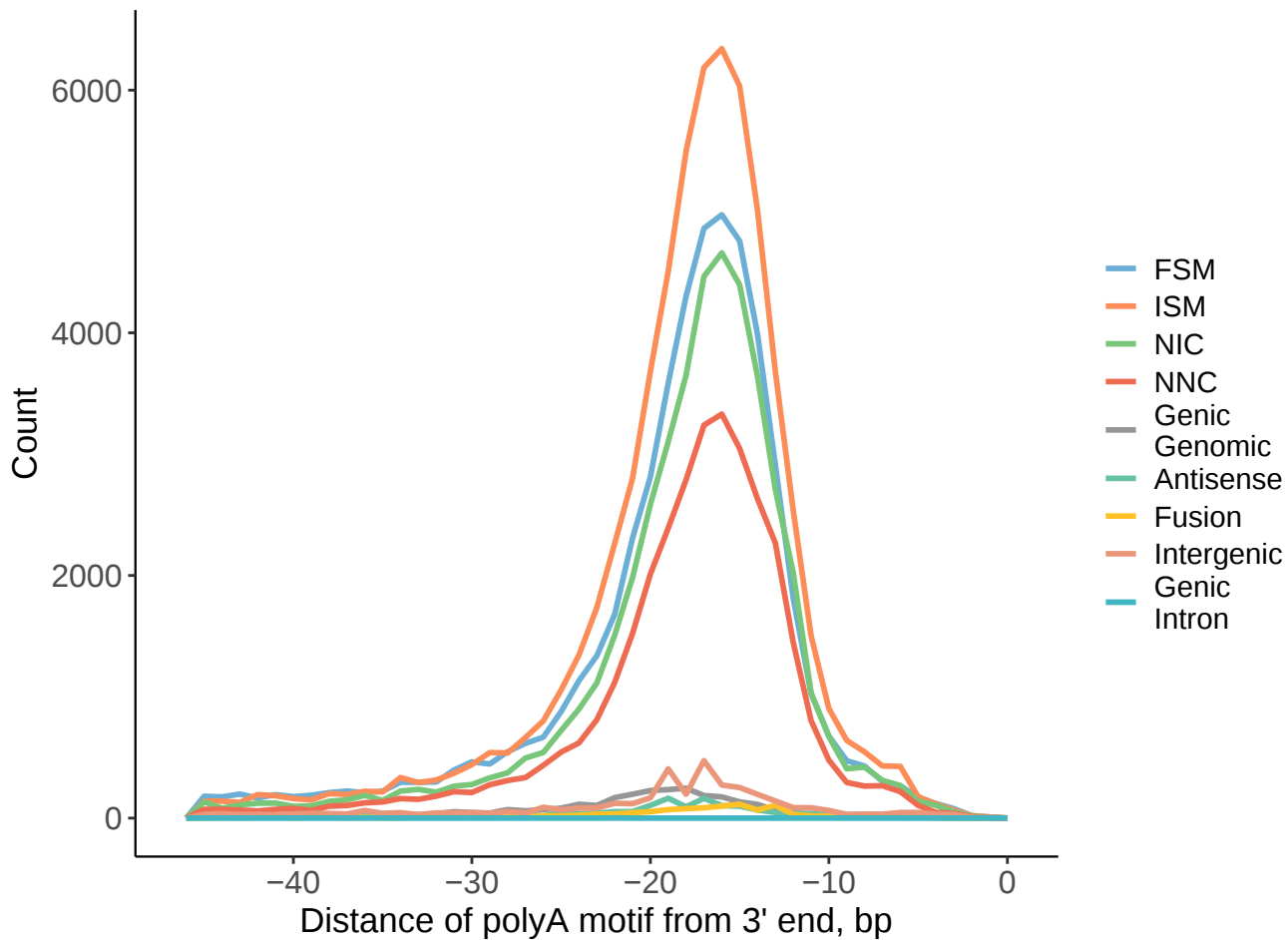
Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site



PolyA Distance Analysis

Distance of Detected PolyA Motif From 3' end



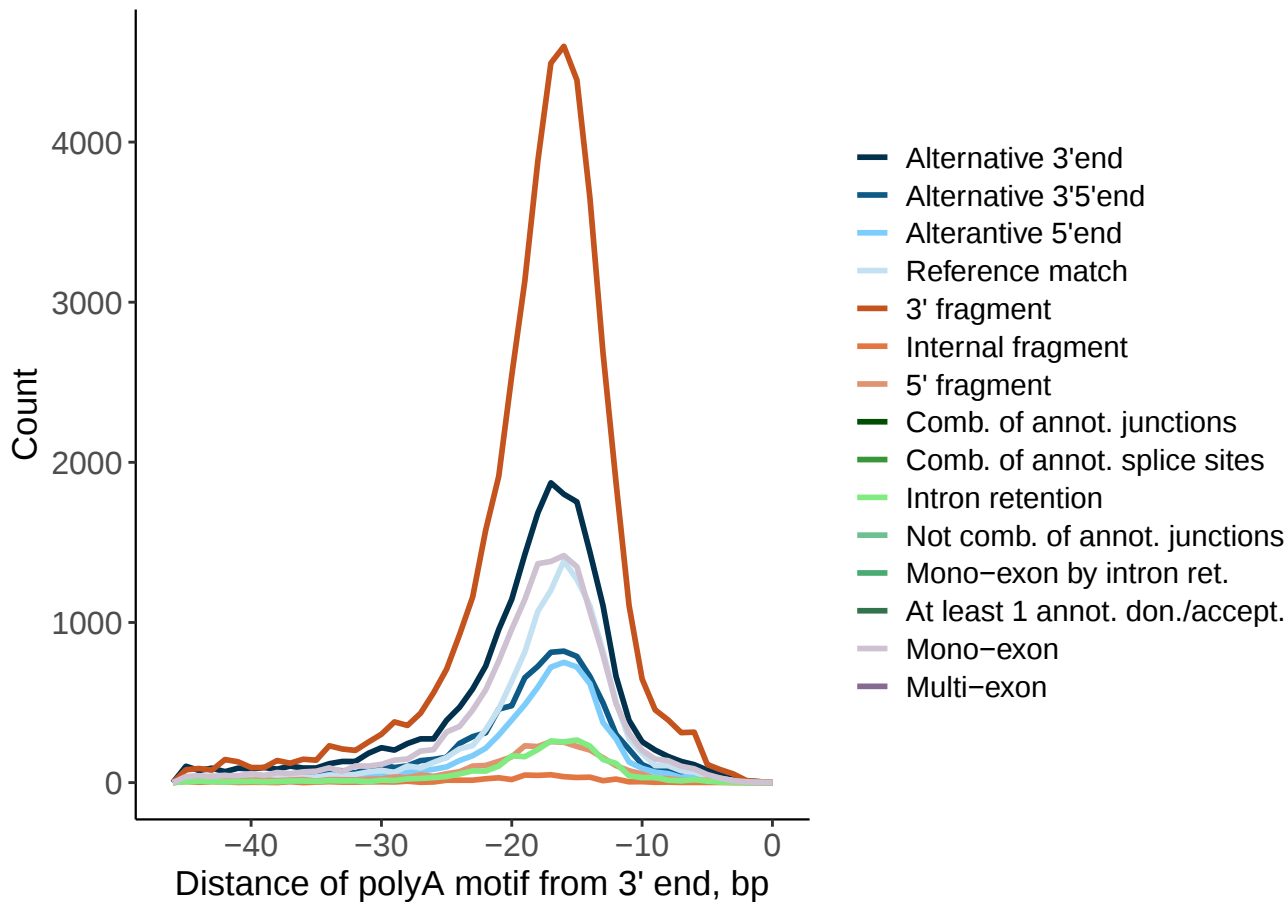
Frequency of PolyA Motifs

Number of polyA Motifs Detected

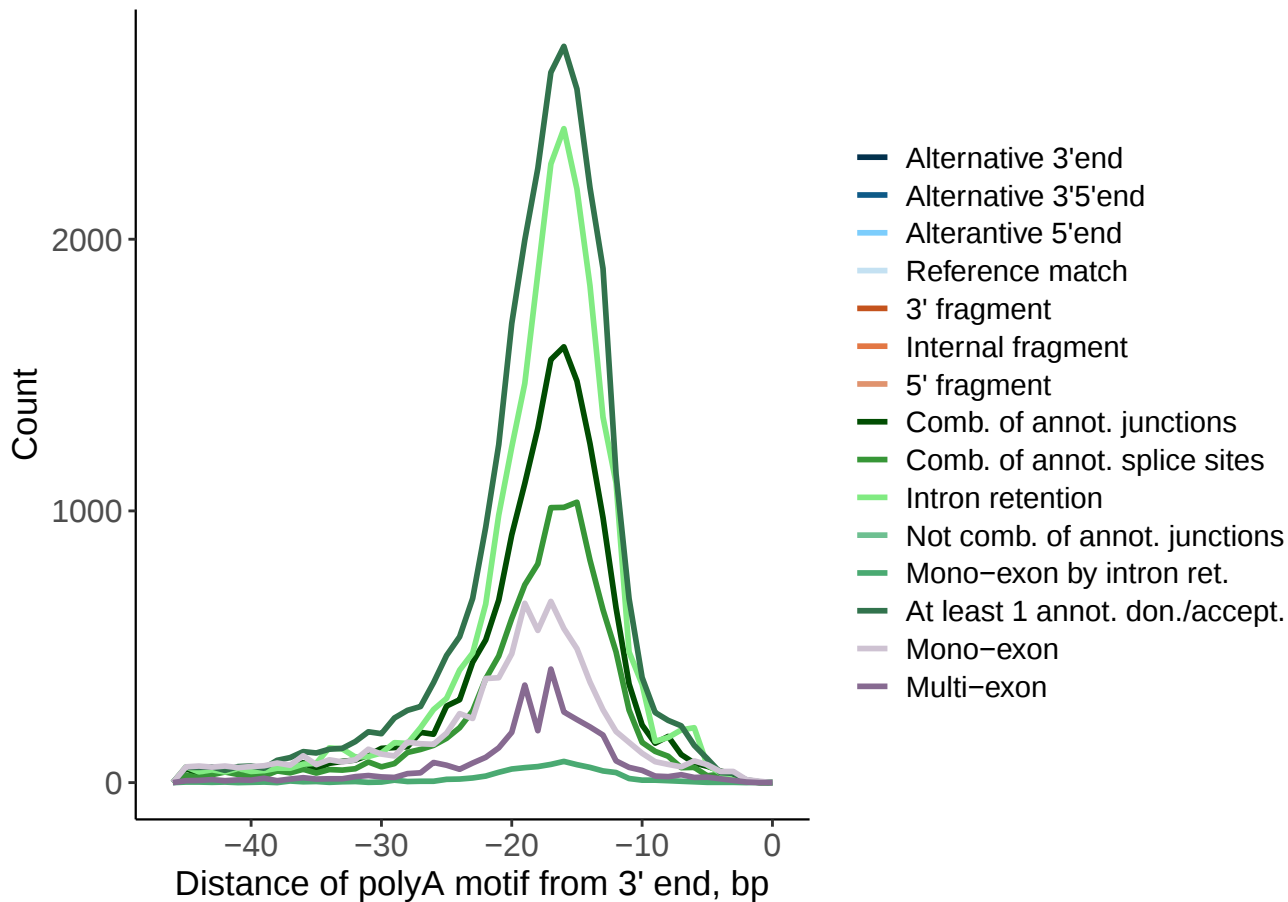
Category	Count	polyA Detected	%
FSM	56795	51082	90
ISM	67804	63746	94
NIC	48878	45224	93
NNC	35743	33525	94
Genic Genomic	3407	2828	83
Antisense	4234	1576	37
Fusion	1149	1059	92
Intergenic	10368	3912	38
Genic Intron	1	1	100

Motif	Count	%
AATAAA	137097	67.6
ATTAAA	34451	17.0
AGTAAA	6161	3.0
TATAAA	6035	3.0
AATATA	2889	1.4
AATACA	2839	1.4
CATAAA	2693	1.3
GATAAA	2196	1.1
TTTAAA	1787	0.9
AAGAAA	1479	0.7
AAAAAG	1352	0.7
AATGAA	1172	0.6
AATAGA	1012	0.5
ACTAAA	913	0.4
AAAACA	704	0.3
GGGGCT	173	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

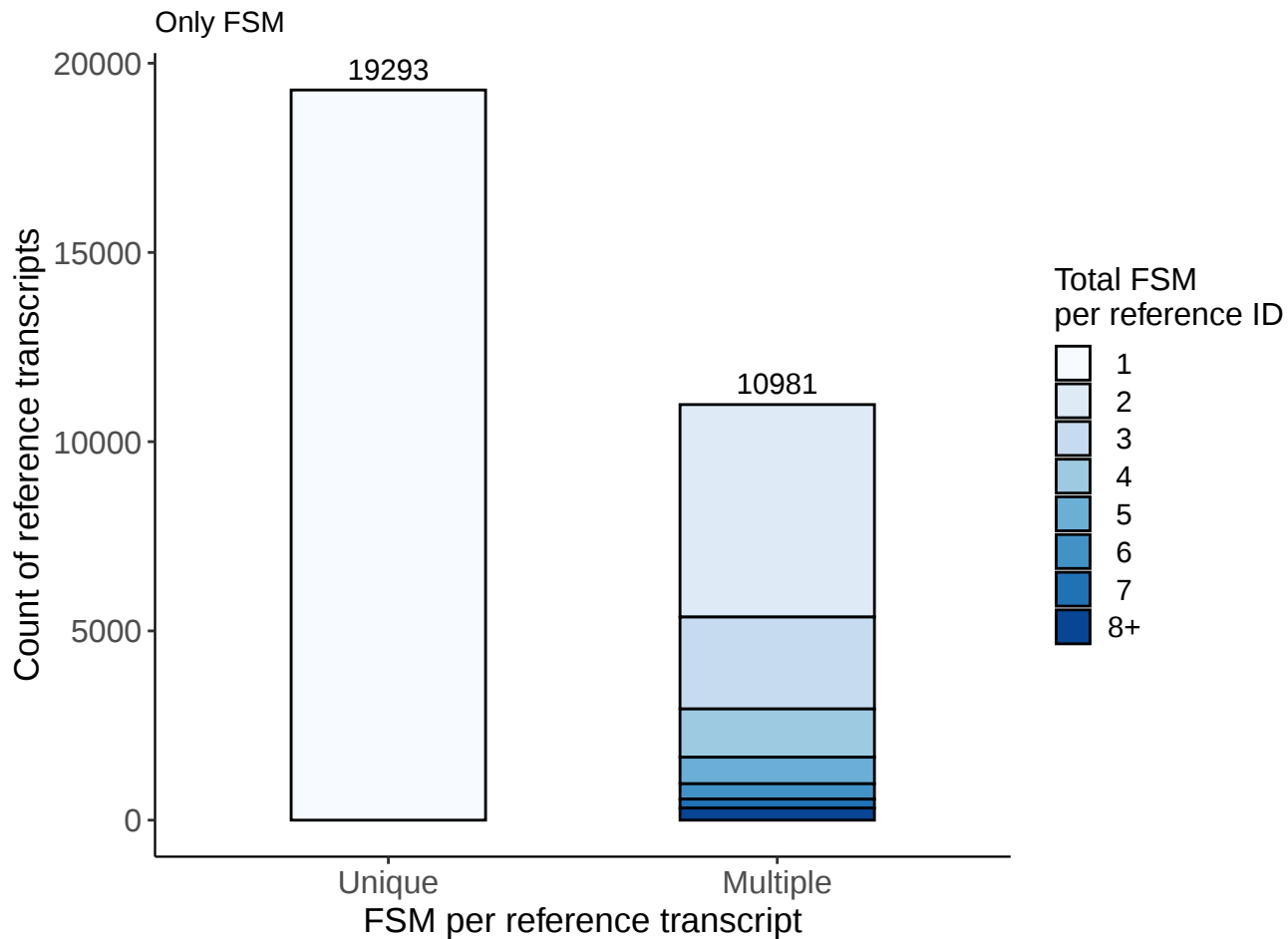
Subcategory	Count	polyA Detected	%
Alternative 3'end	23282	20209	87
Alternative 3'5'end	10117	9119	90
Alterantive 5'end	7341	6981	95
Reference match	12805	12132	95
3' fragment	47594	45191	95
Internal fragment	531	490	92
5' fragment	3697	2926	79
Comb. of annot. junctions	17013	15875	93
Comb. of annot. splice sites	11146	10488	94
Intron retention	26321	24655	94
Mono-exon by intron ret.	895	724	81
At least 1 annot. don./accept.	29525	27683	94
Mono-exon	33596	23352	70
Multi-exon	4516	3128	69

Frequency of PolyA Motifs

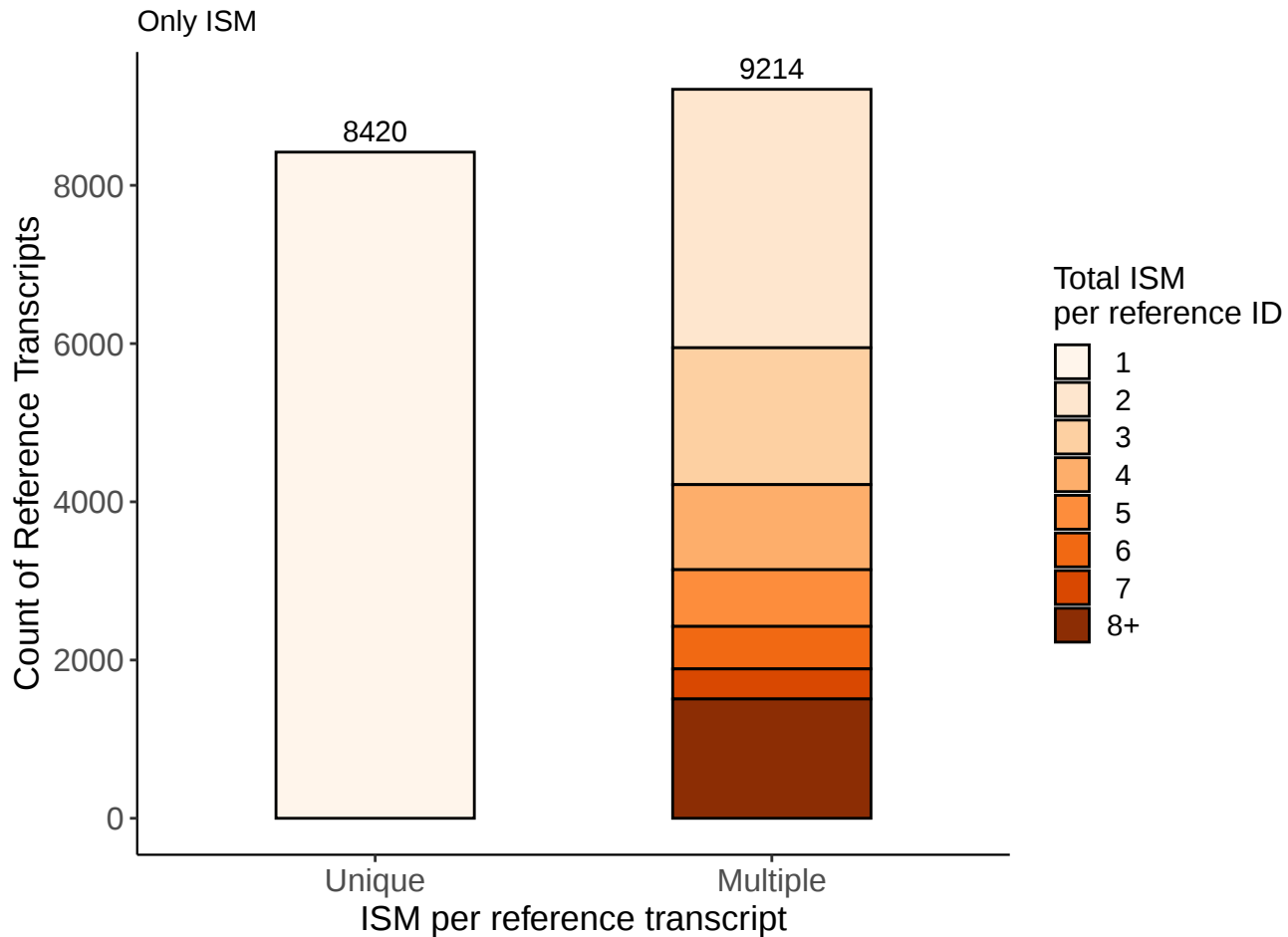
Motif	Count	%
AATAAA	137097	67.6
ATTAAA	34451	17.0
AGTAAA	6161	3.0
TATAAA	6035	3.0
AATATA	2889	1.4
AATACA	2839	1.4
CATAAA	2693	1.3
GATAAA	2196	1.1
TTTAAA	1787	0.9
AAGAAA	1479	0.7
AAAAAG	1352	0.7
AATGAA	1172	0.6
AATAGA	1012	0.5
ACTAAA	913	0.4
AAAACA	704	0.3
GGGGCT	173	0.1

Redundancy Analysis

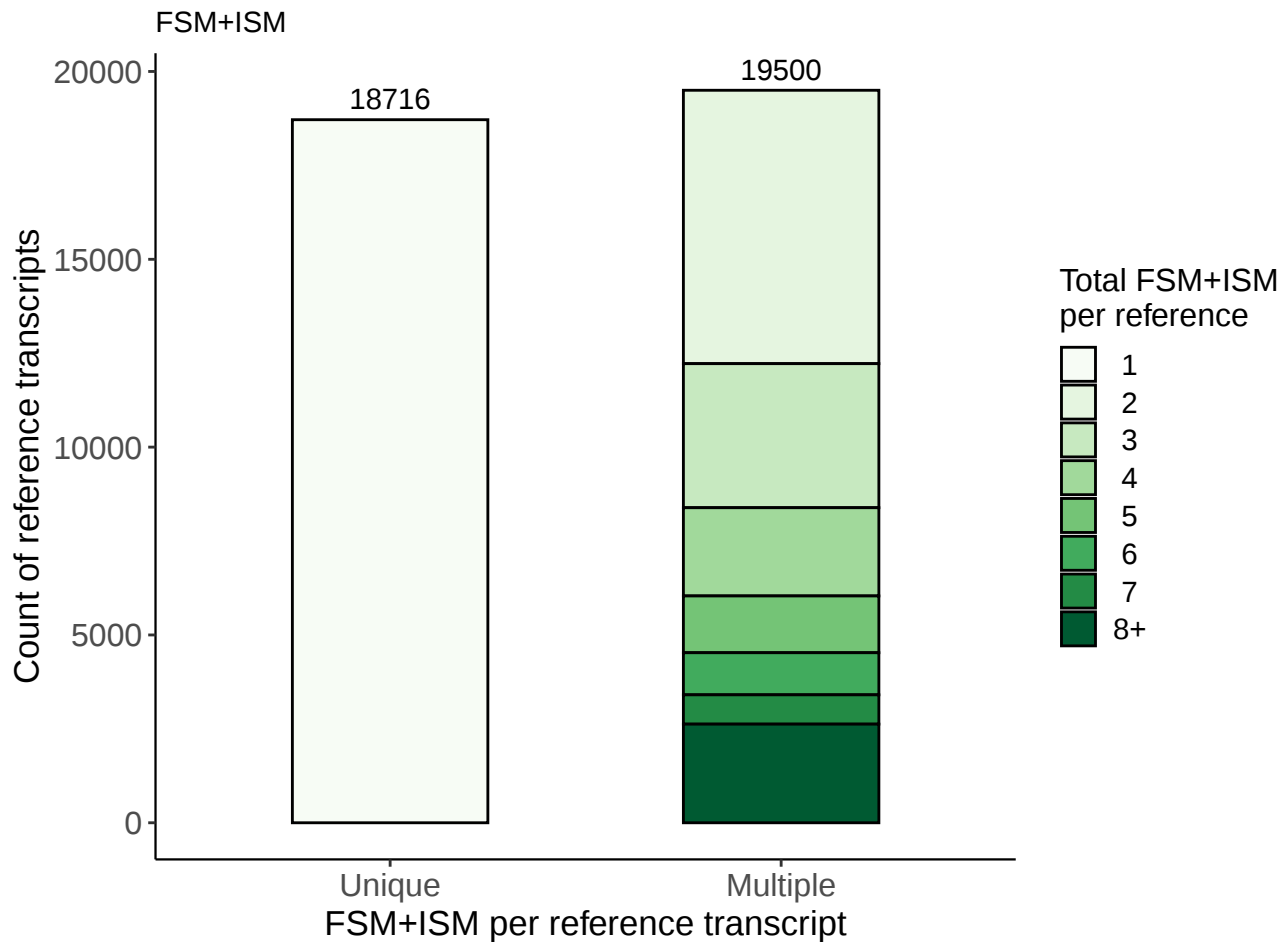
Reference Transcript Redundancy



Reference Transcript Redundancy

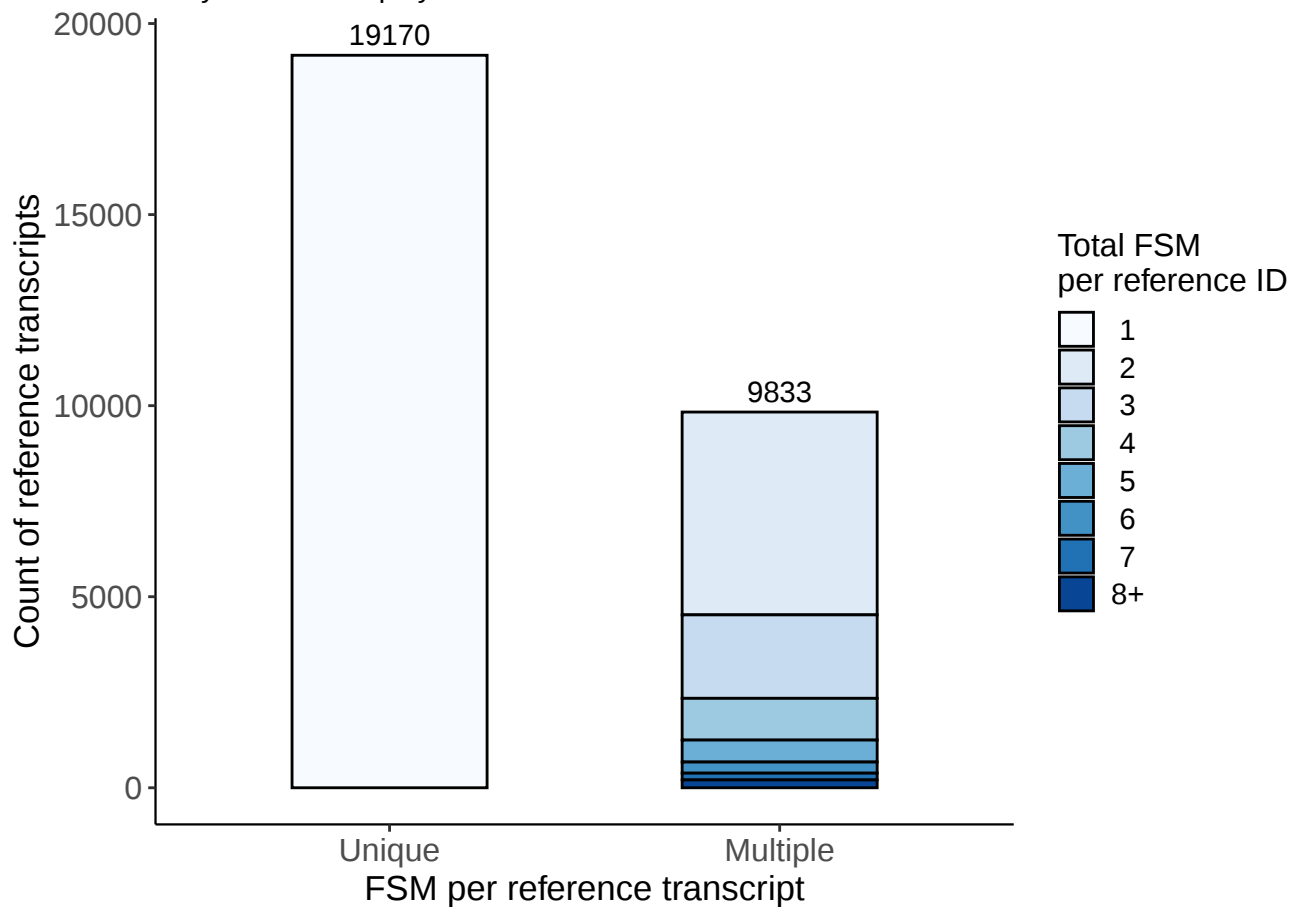


Reference Transcript Redundancy



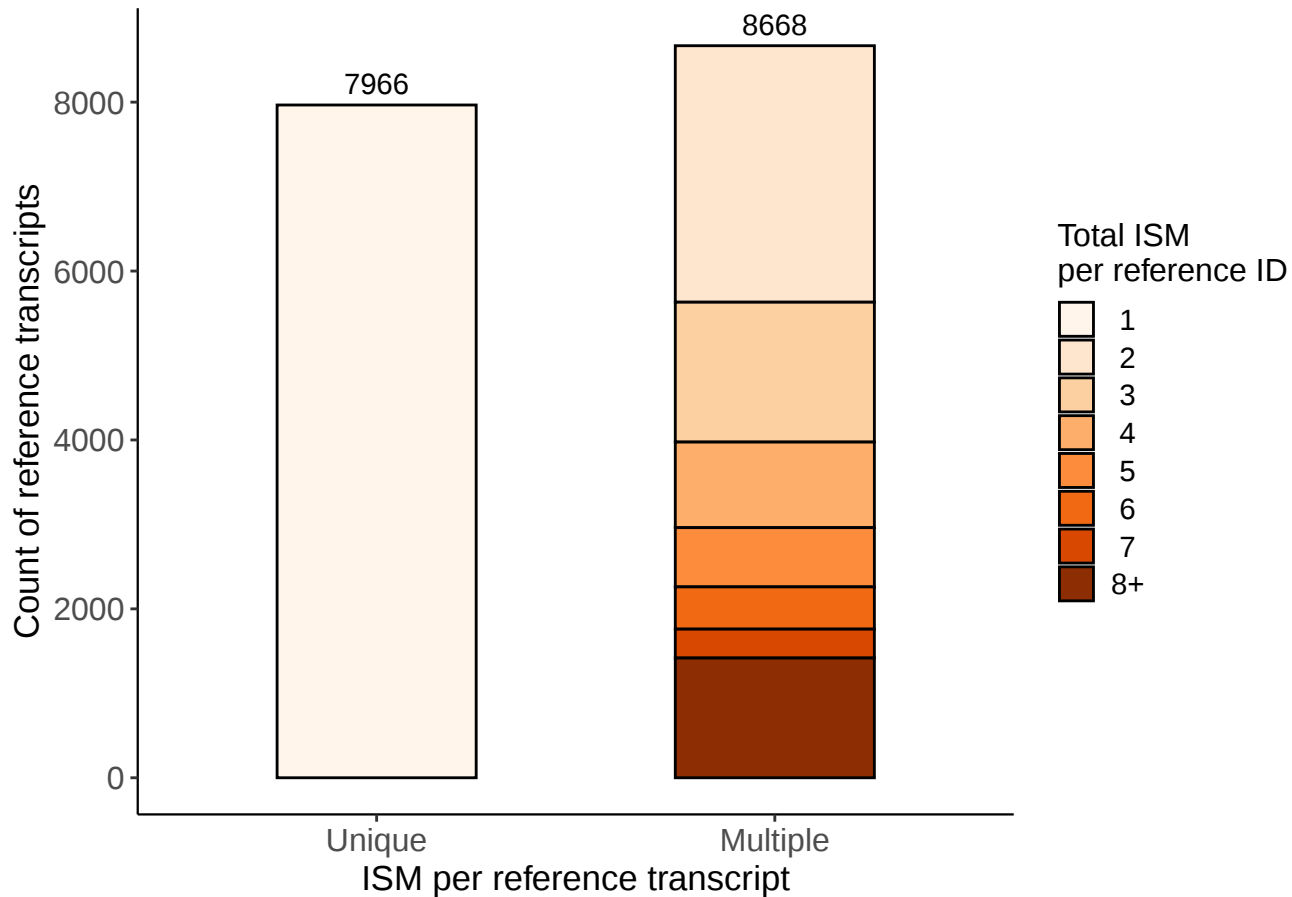
Reference Transcript Redundancy

Only FSM with a polyA motif found



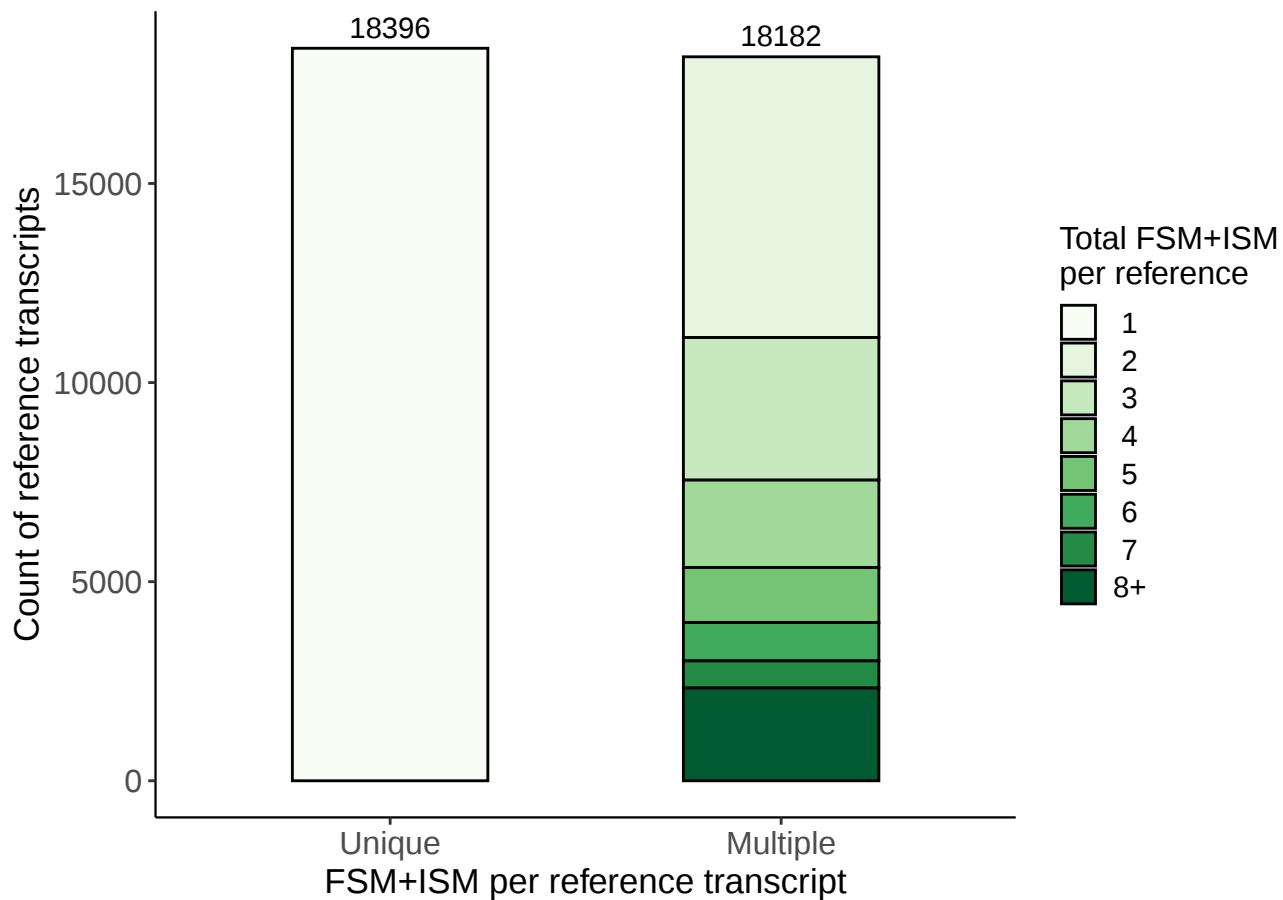
Reference Transcript Redundancy

Only ISM with a polyA motif found



Reference Transcript Redundancy

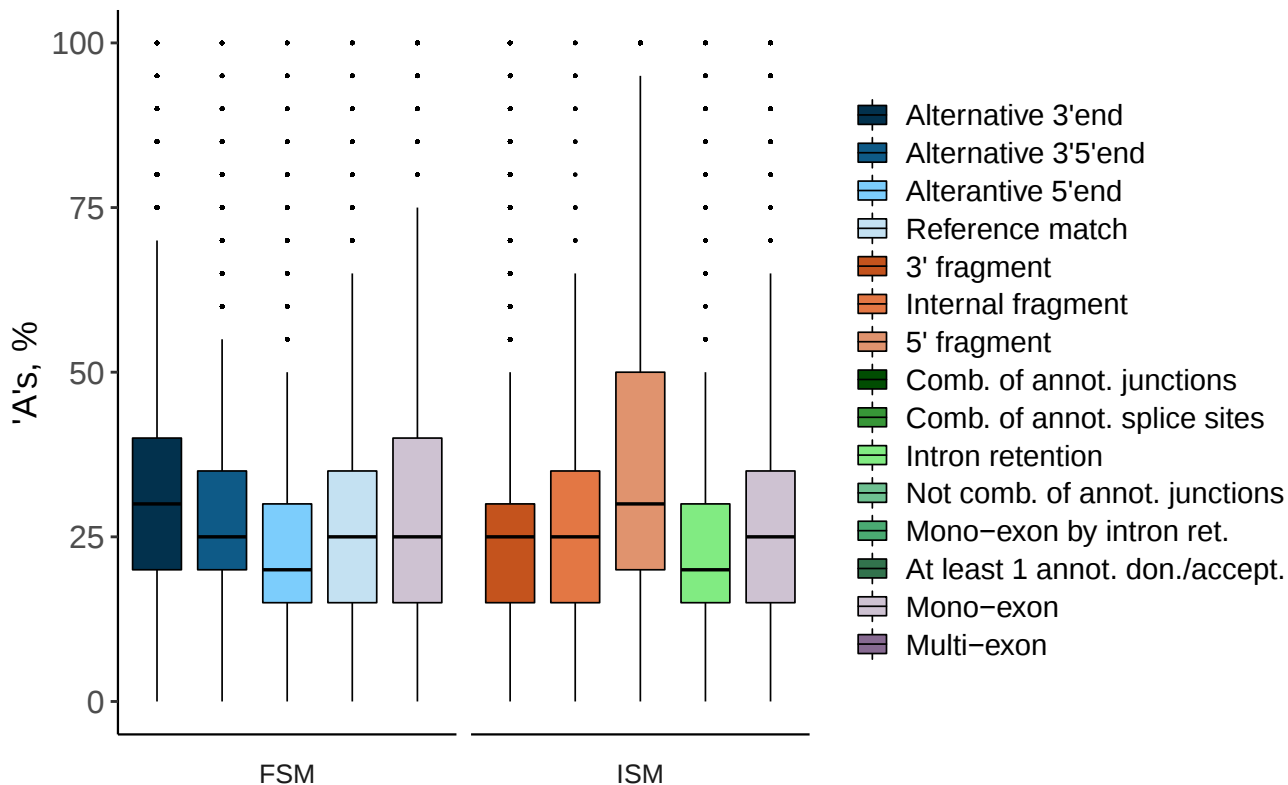
FSM+ISM with a polyA motif found



Intra-Priming Quality Check

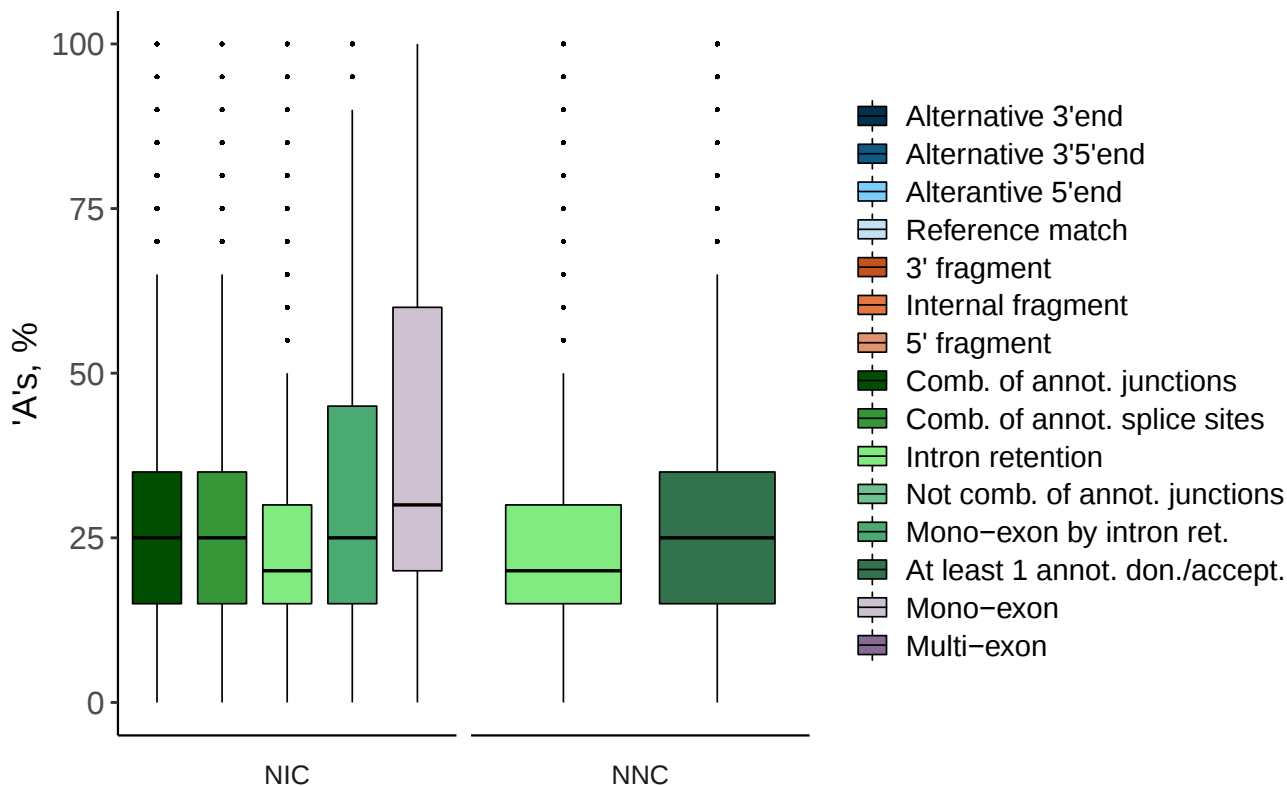
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



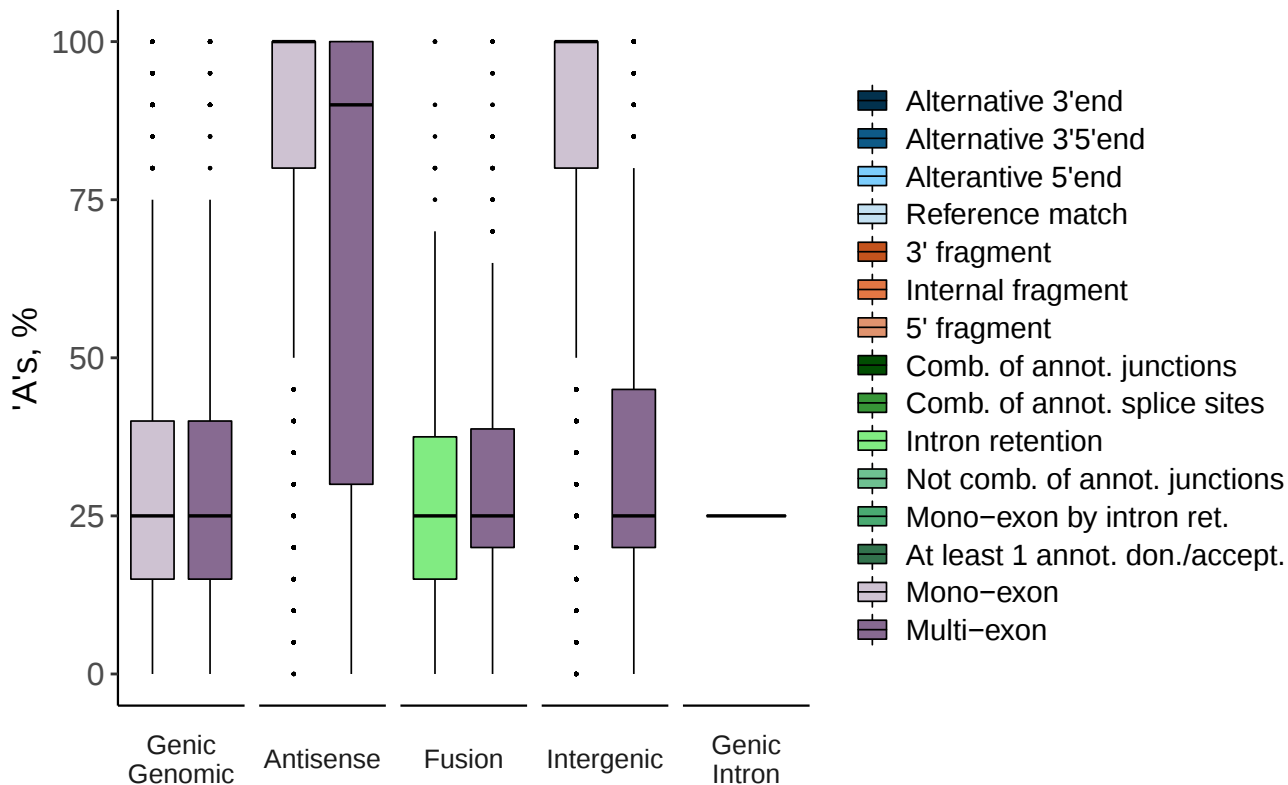
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



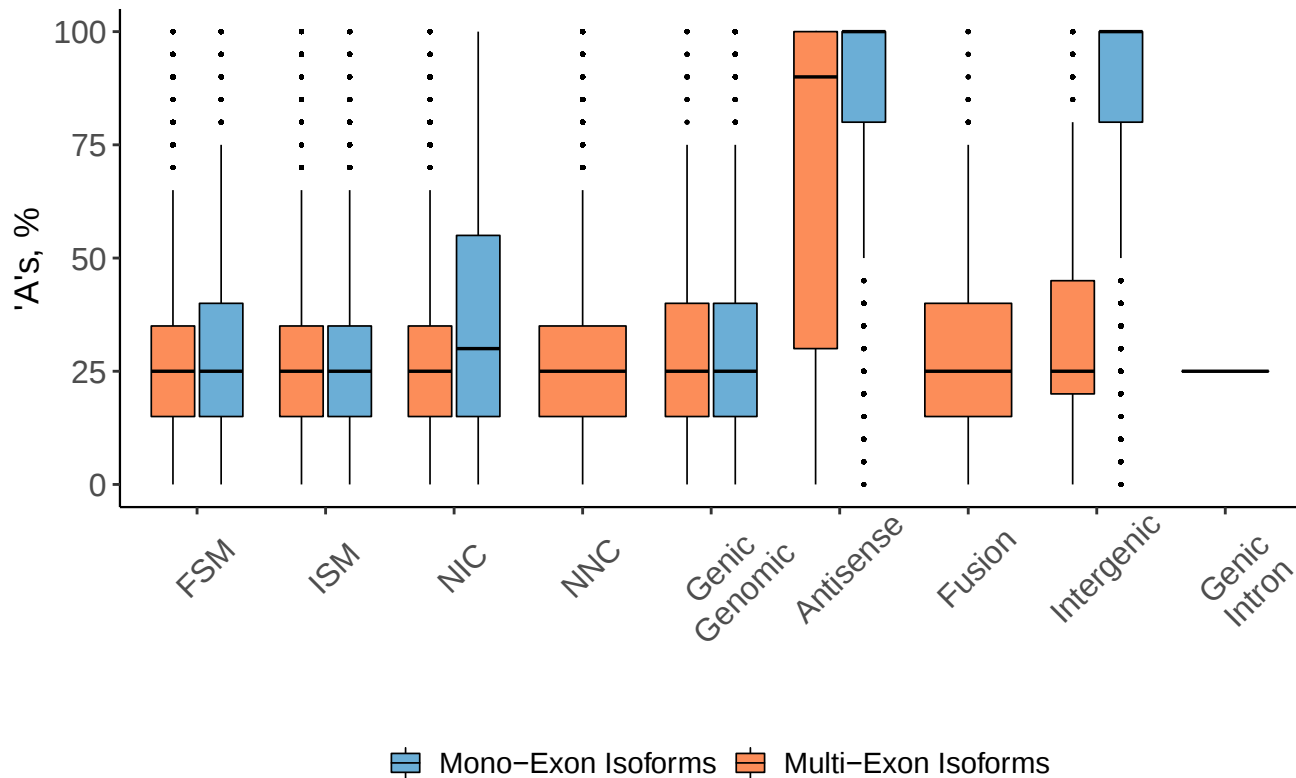
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



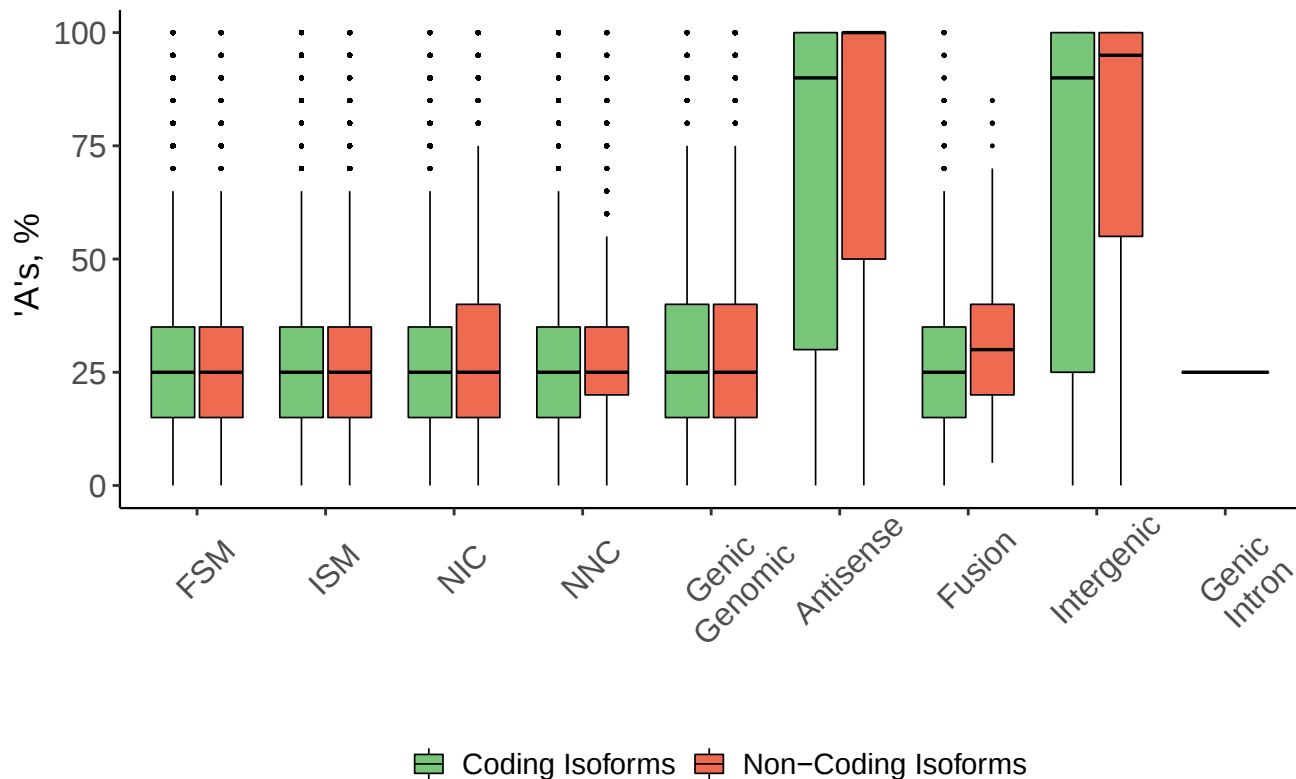
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



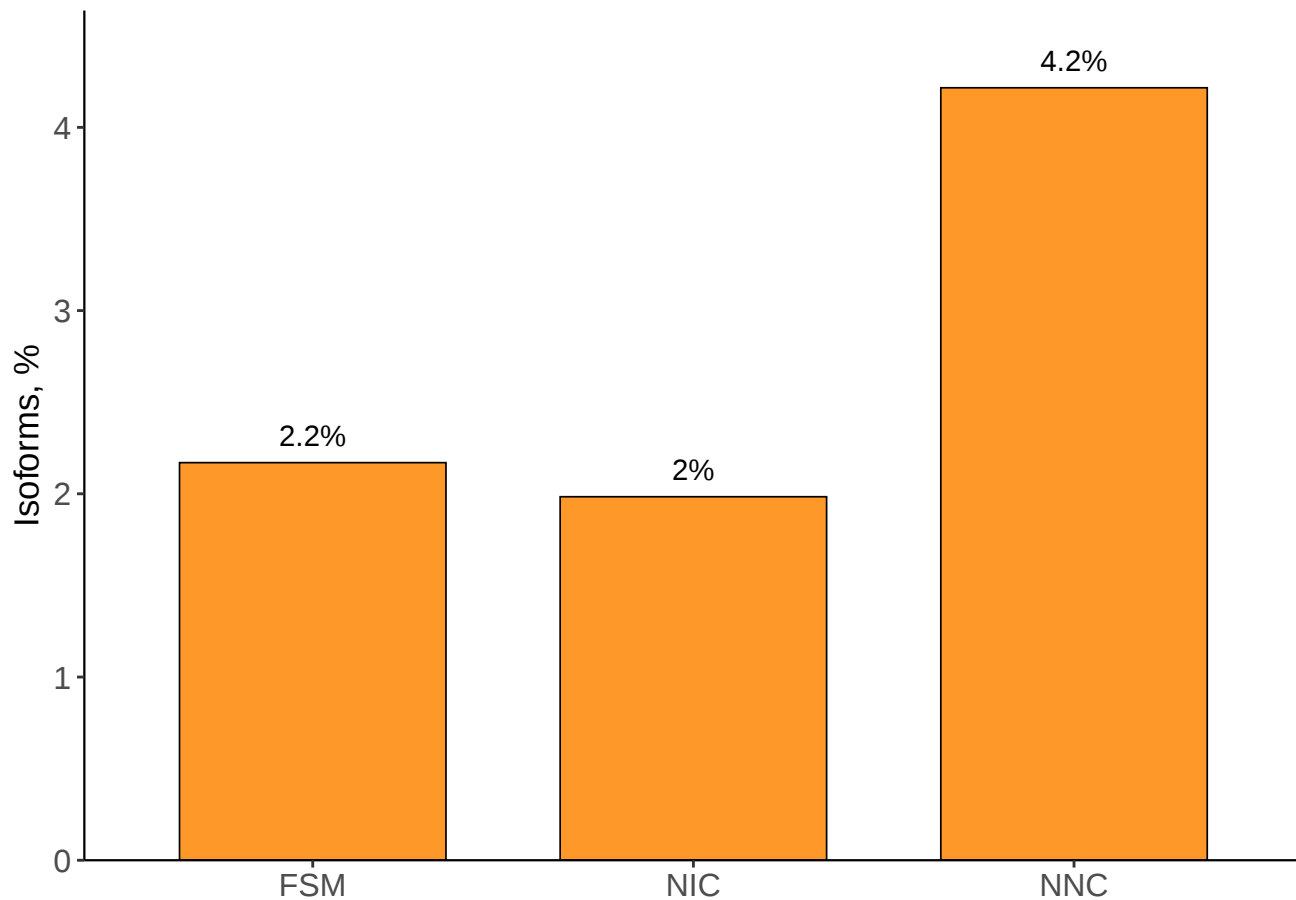
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp

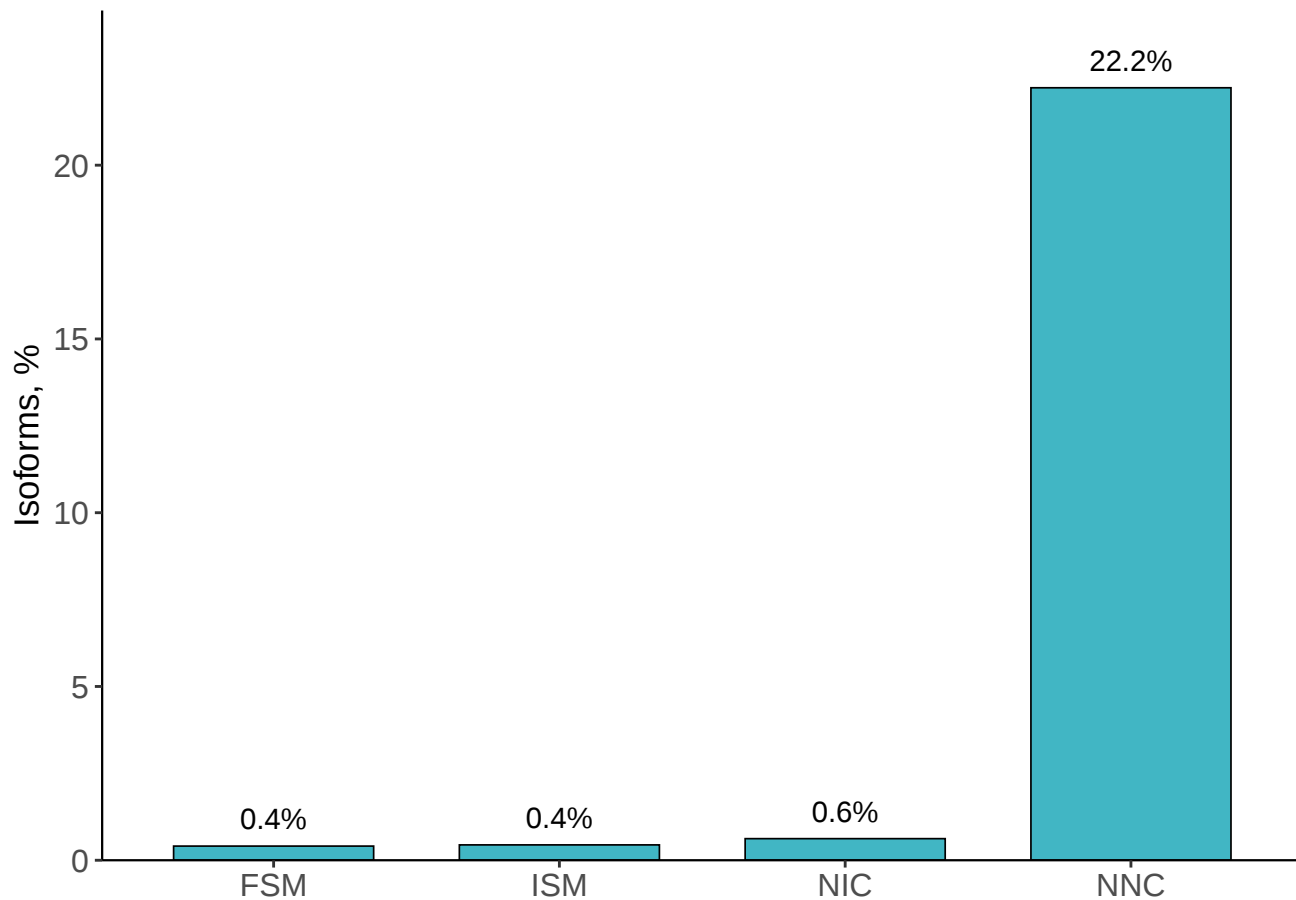


Features of Bad Quality

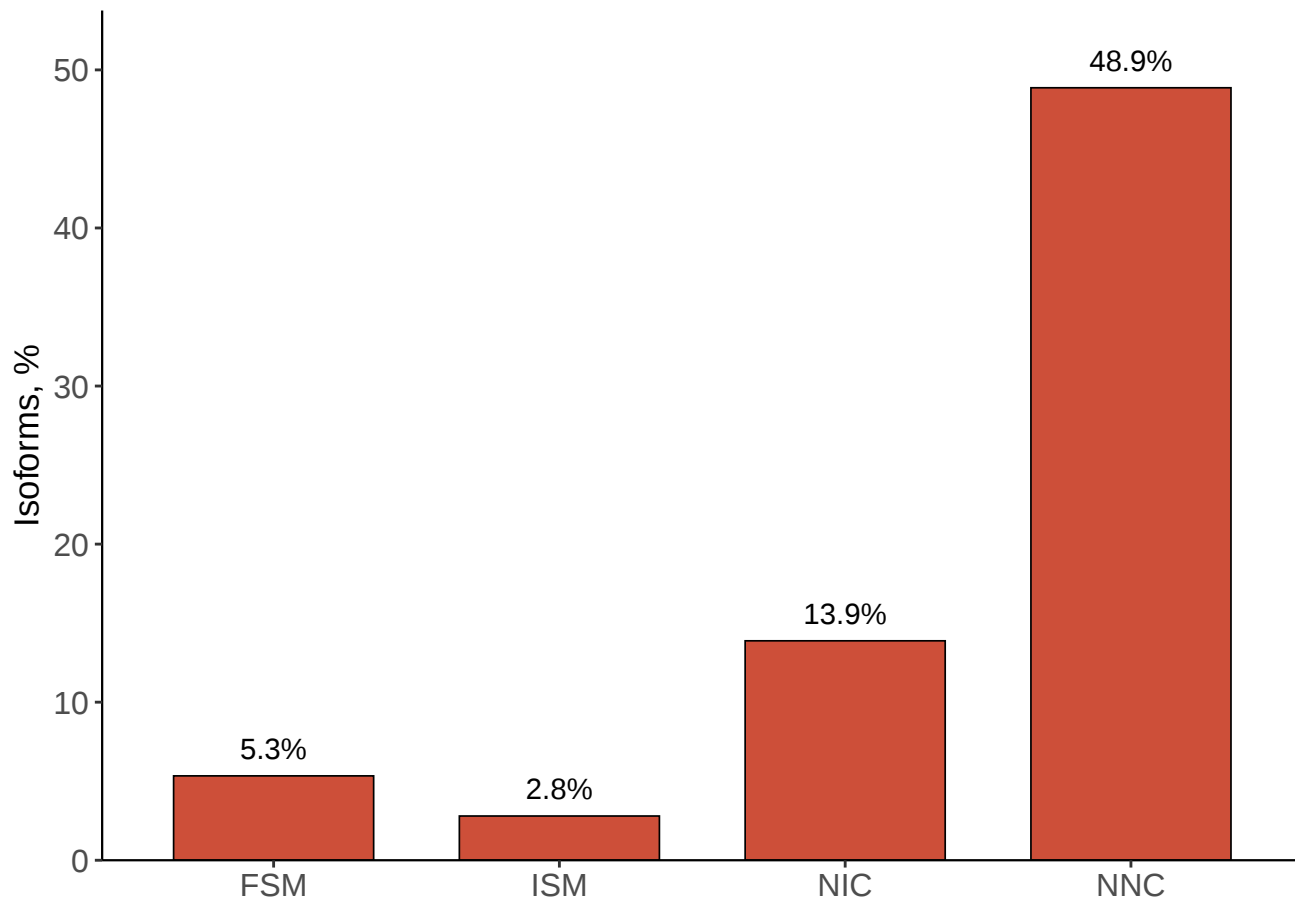
RT-switching



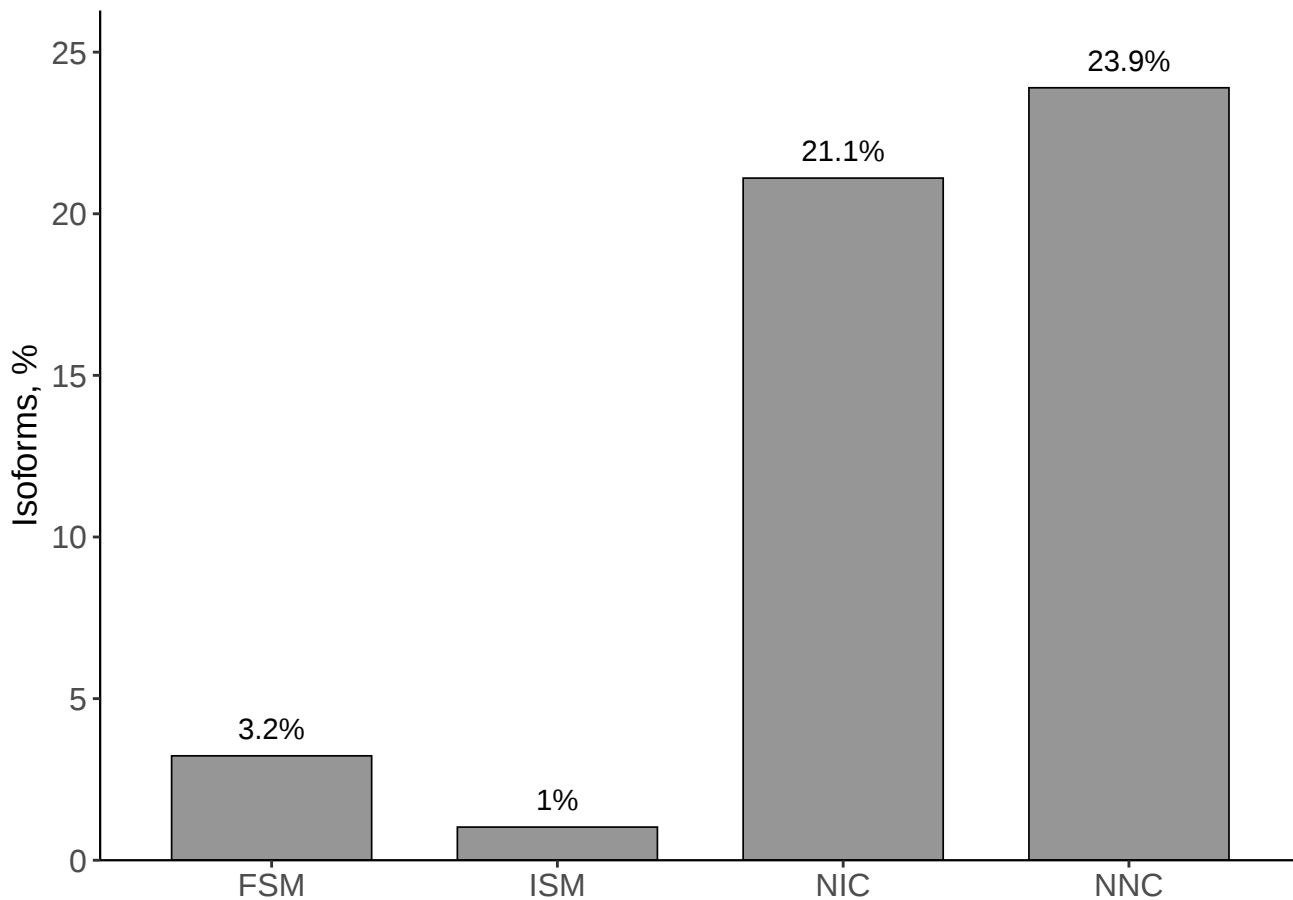
Non-Canonical Junctions



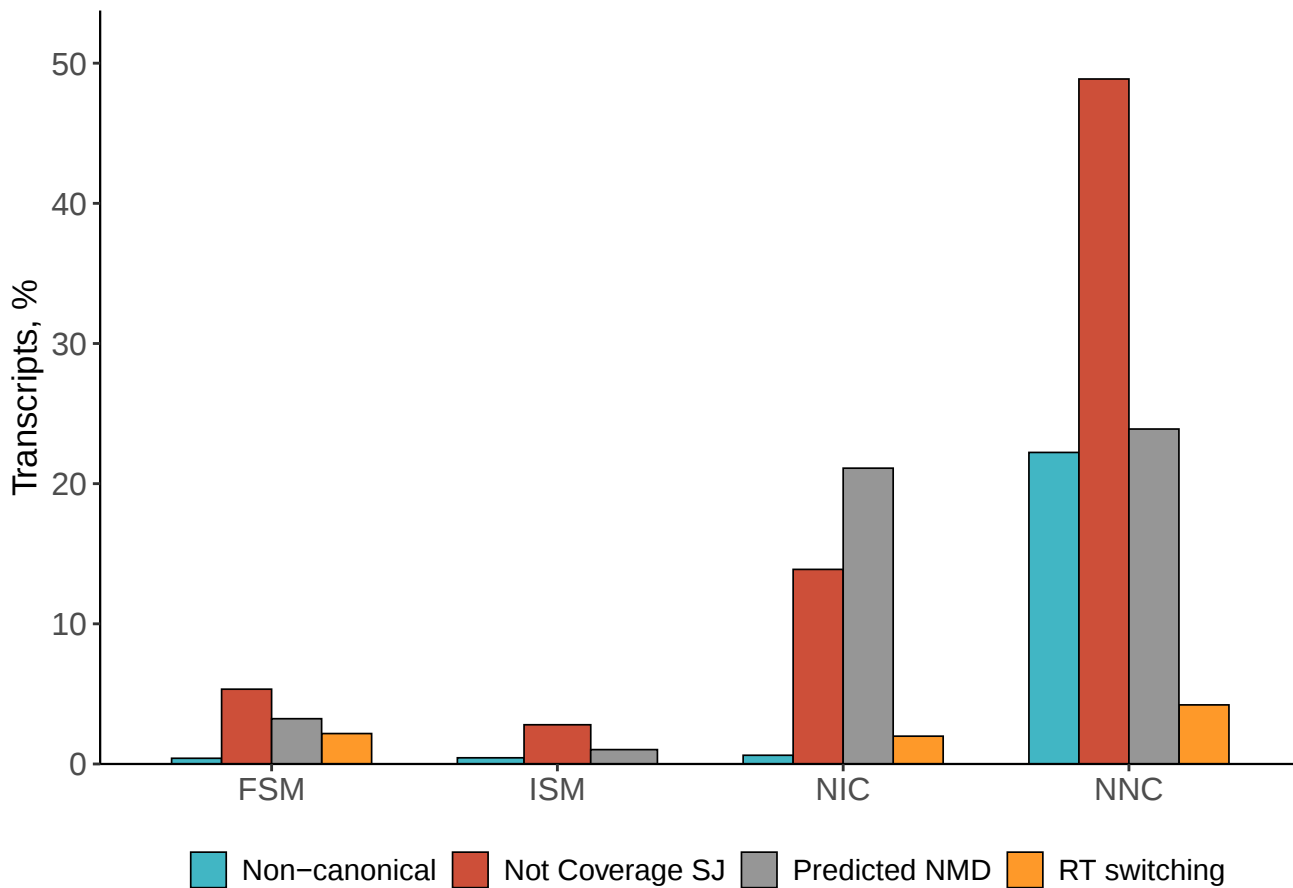
Splice Junctions Without Short Read Coverage



Nonsense-Mediated Decay by Structural Category

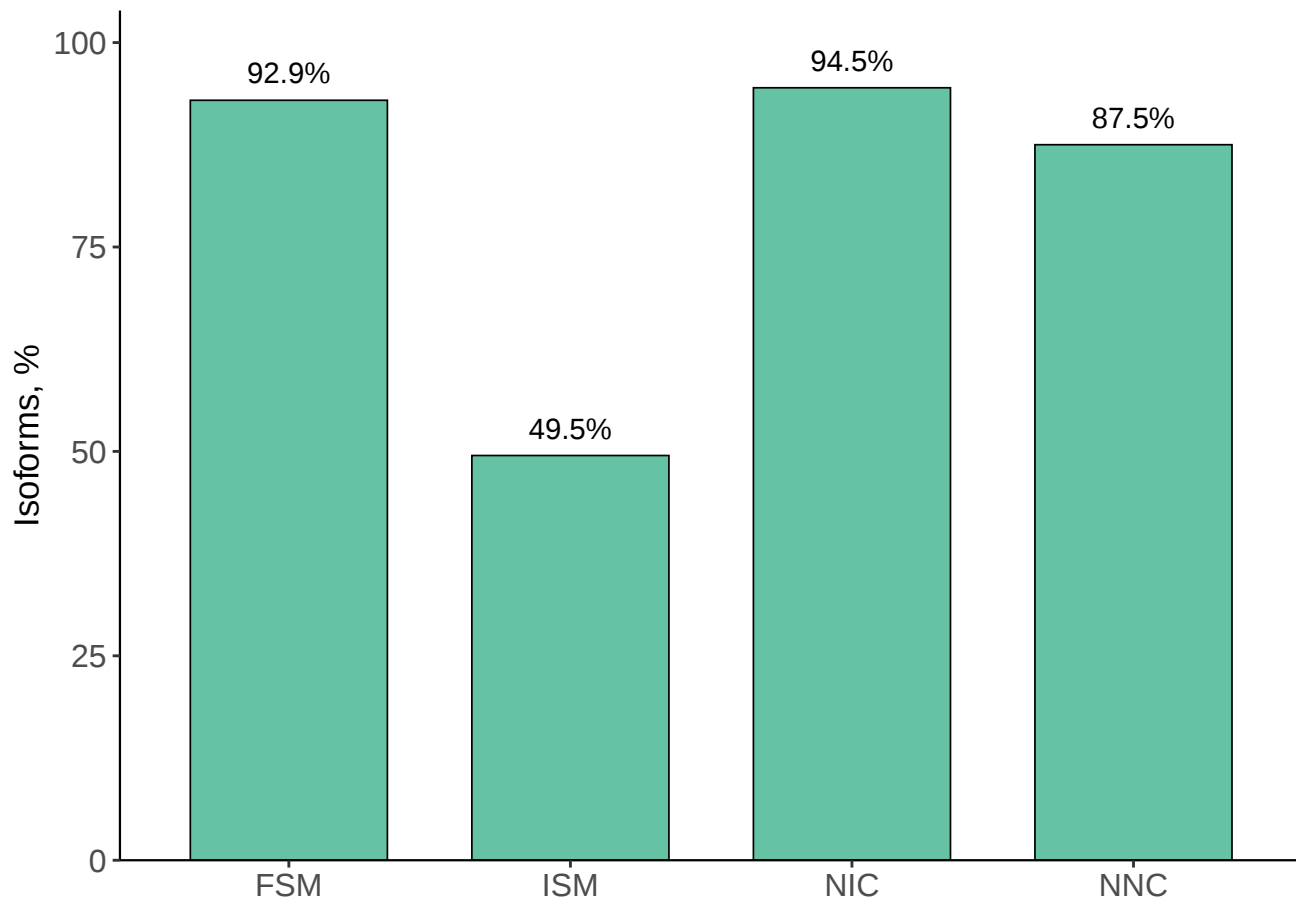


Quality Control Attributes Across Structural Categories

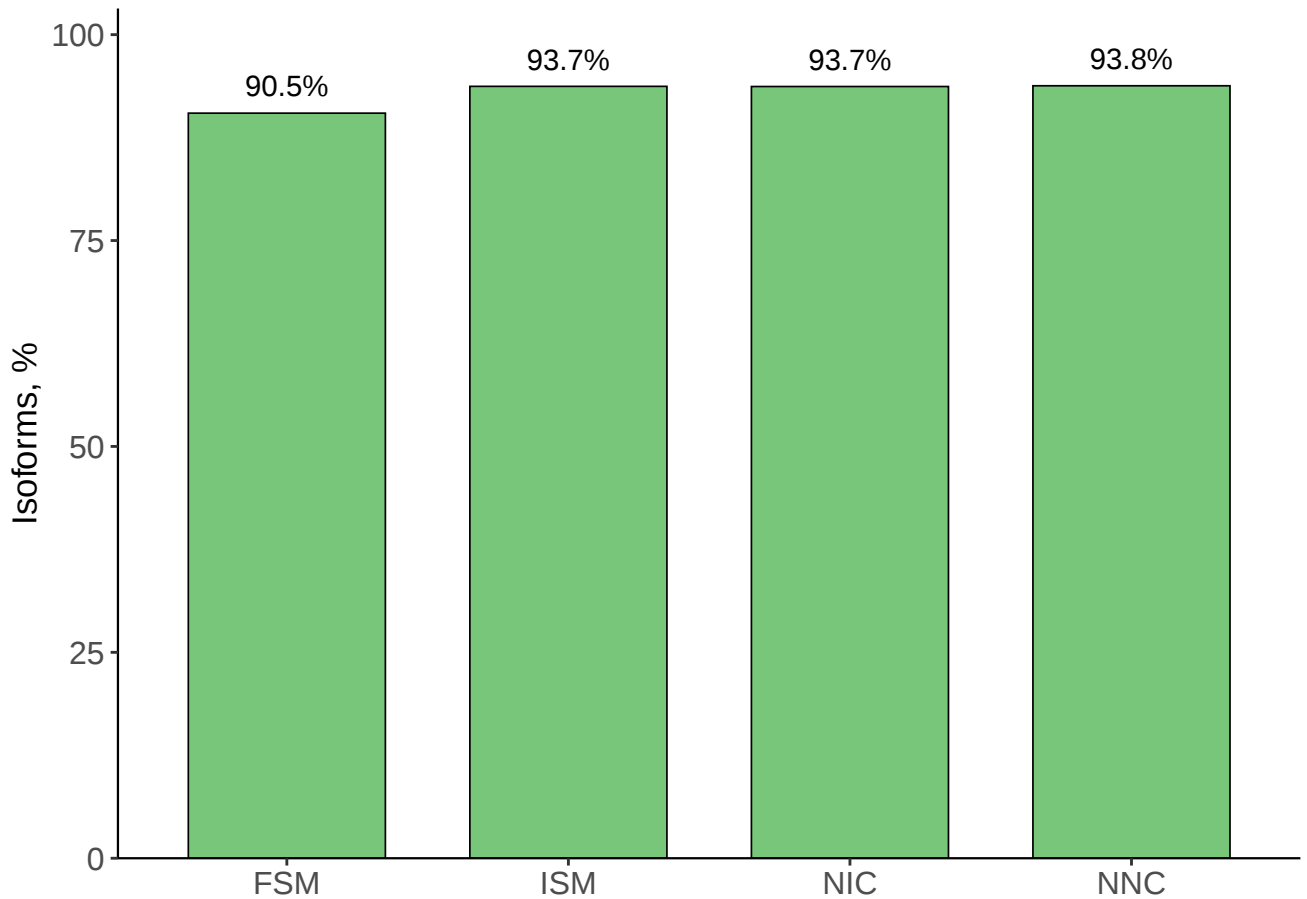


Features of Good Quality

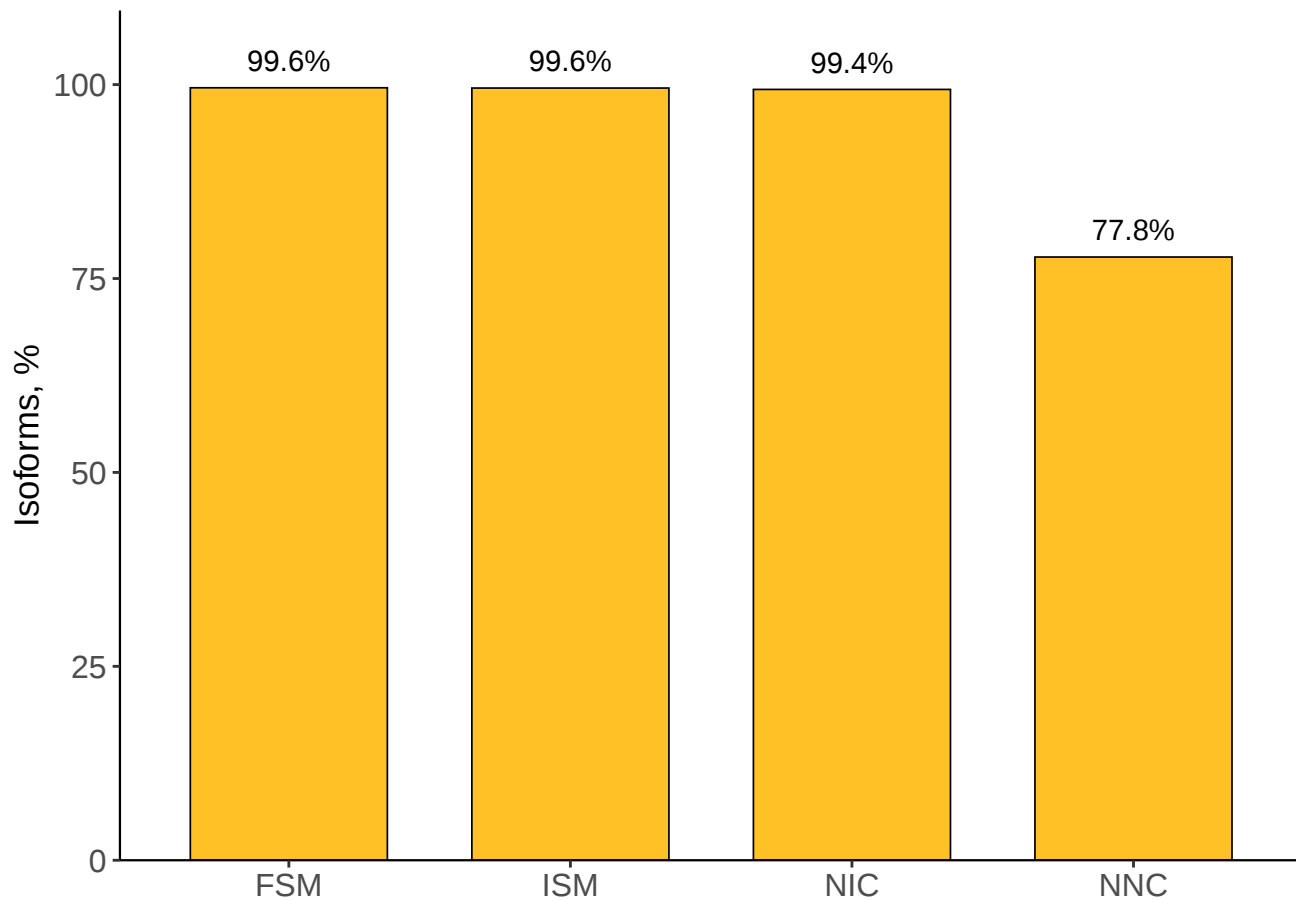
Annotation Support



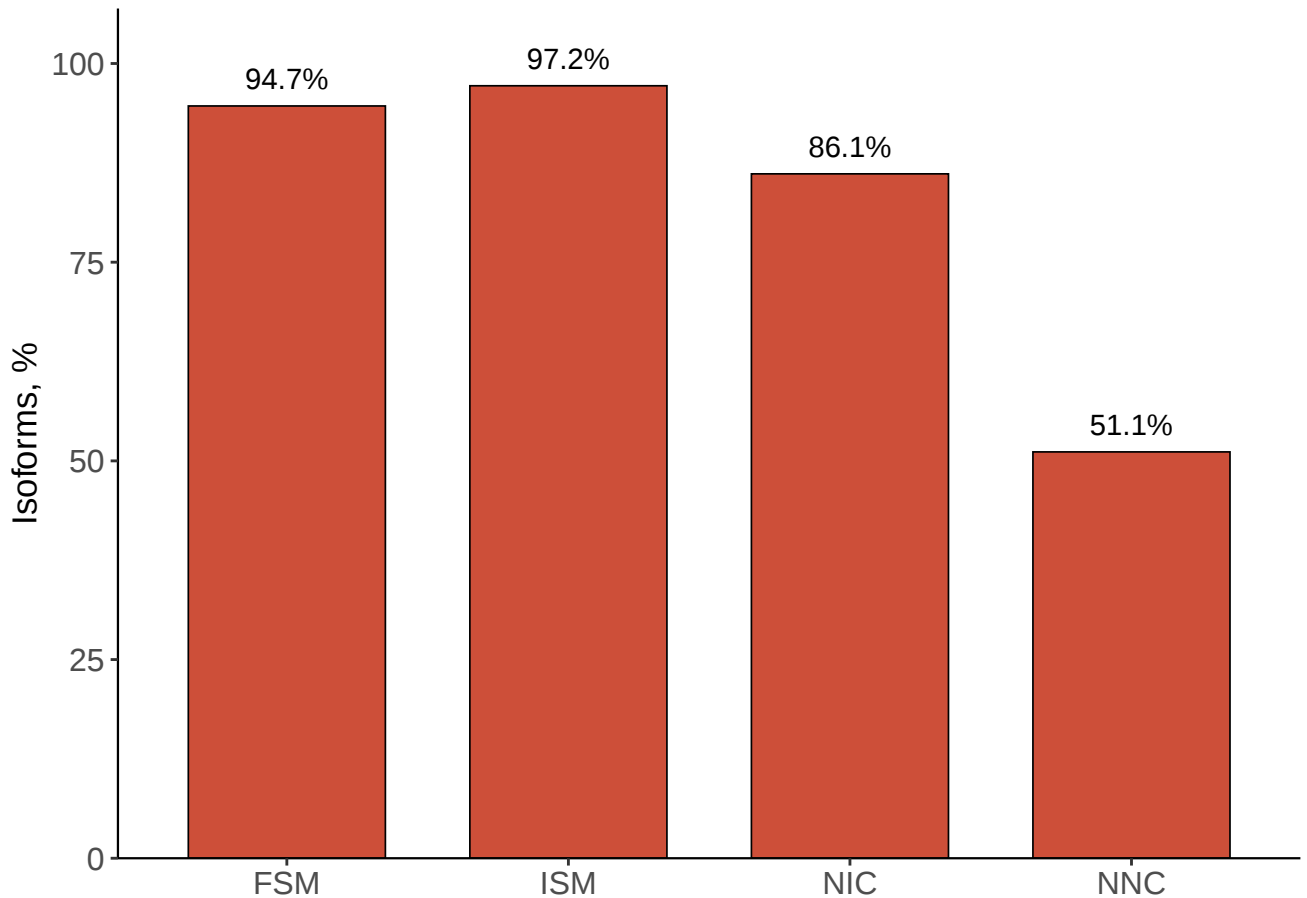
PolyA Support



All Canonical Junctions



Splice Junctions With Short Read Coverage



Good Quality Control Attributes Across Structural Categories

