SQANTI3 report

Unique Genes: 656 Unique Isoforms: 3925

Gene Classification

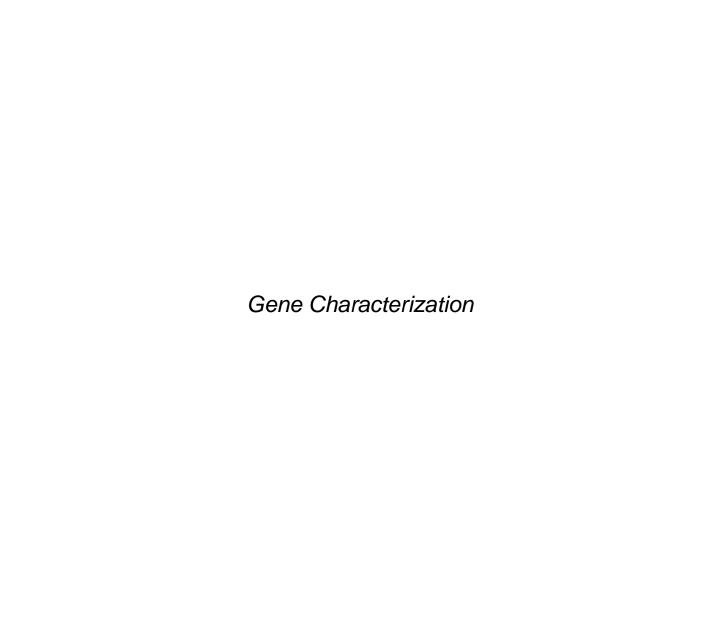
Category	Genes, count	
Annotated Genes	443	
Novel Genes	213	

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

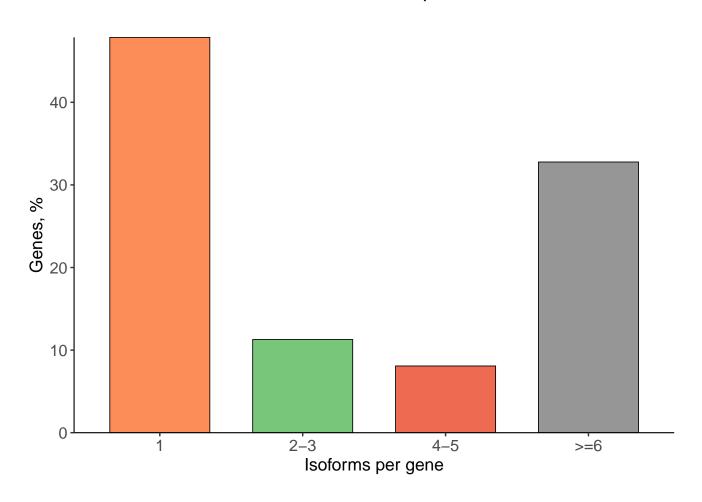
Transcript Classification

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	3374	69.74
Known Non-canonical	4	0.08
Novel canonical	1195	24.70
Novel Non-canonical	265	5.48

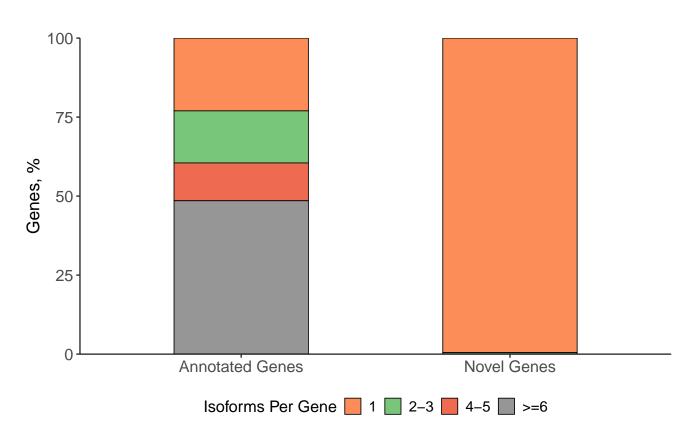


Number of Isoforms per Gene

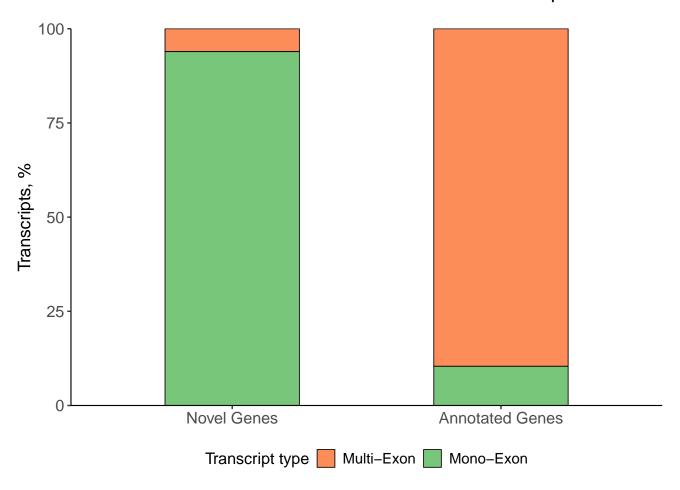


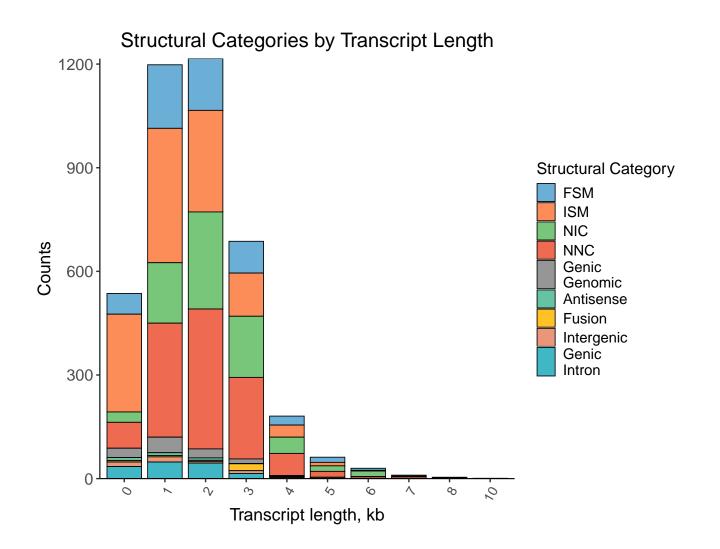
Number of Isoforms per Gene

Known vs Novel Genes

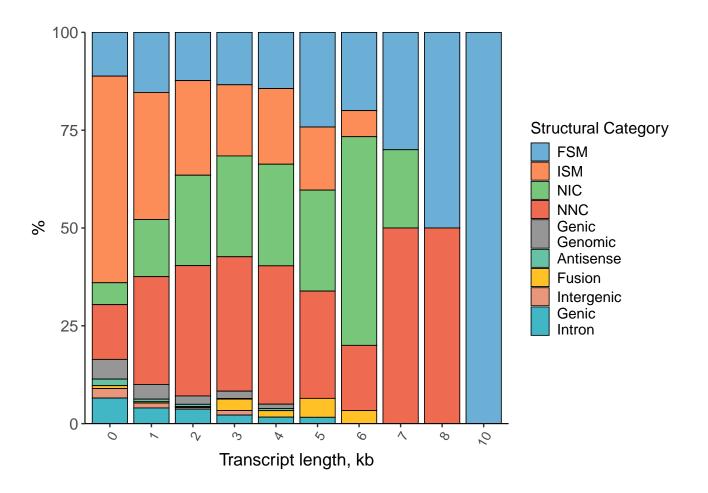


Distribution of Mono- vs Multi-Exon Transcripts

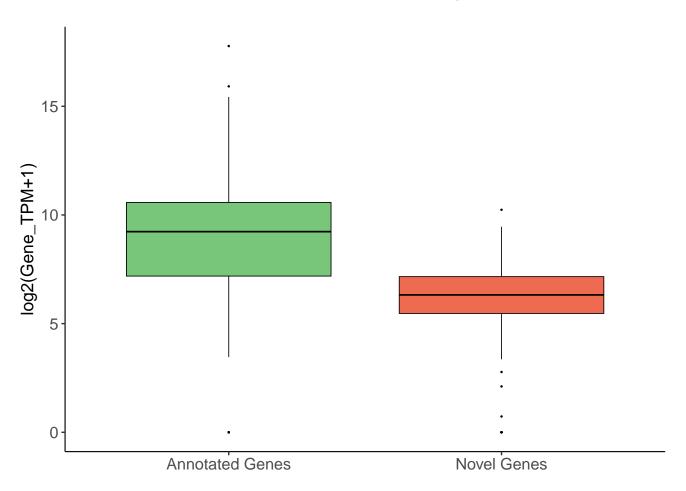




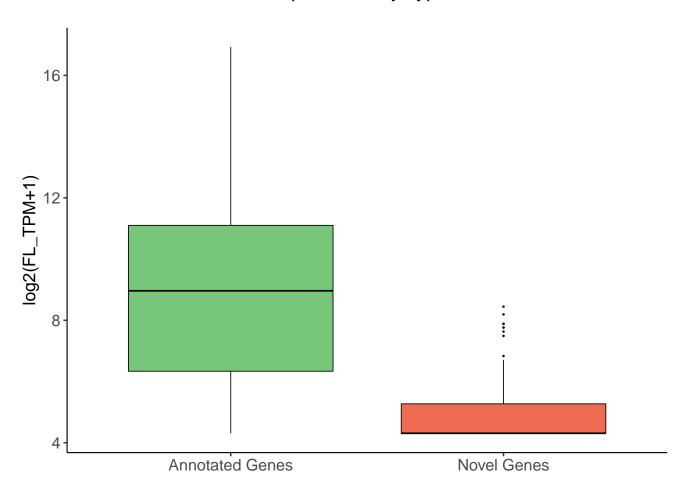
Structural Categories by Transcript Length

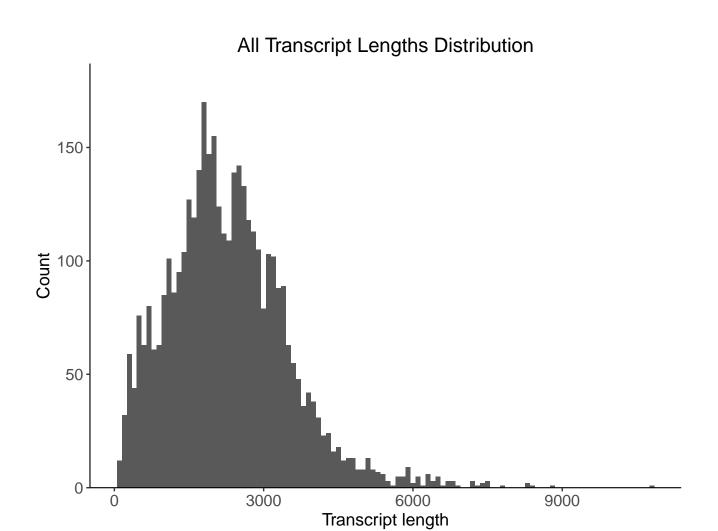


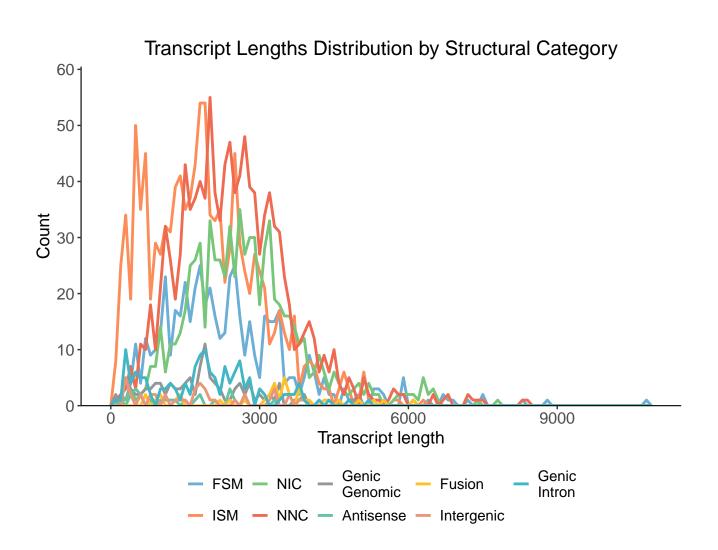
Annotated vs Novel Gene Expression

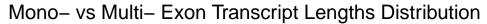


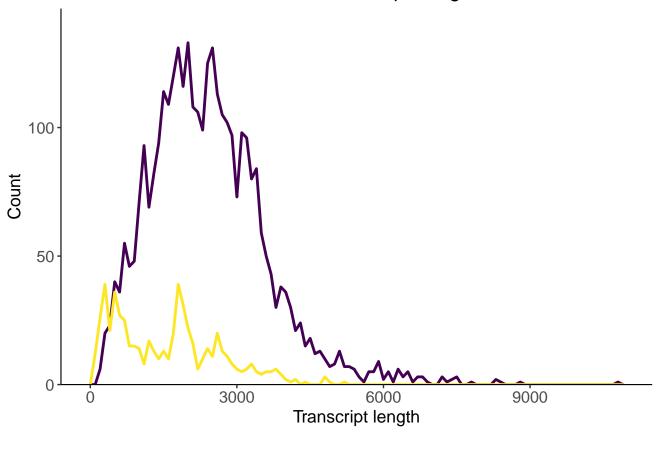
Number of FL reads per Gene by Type of Gene Annotation



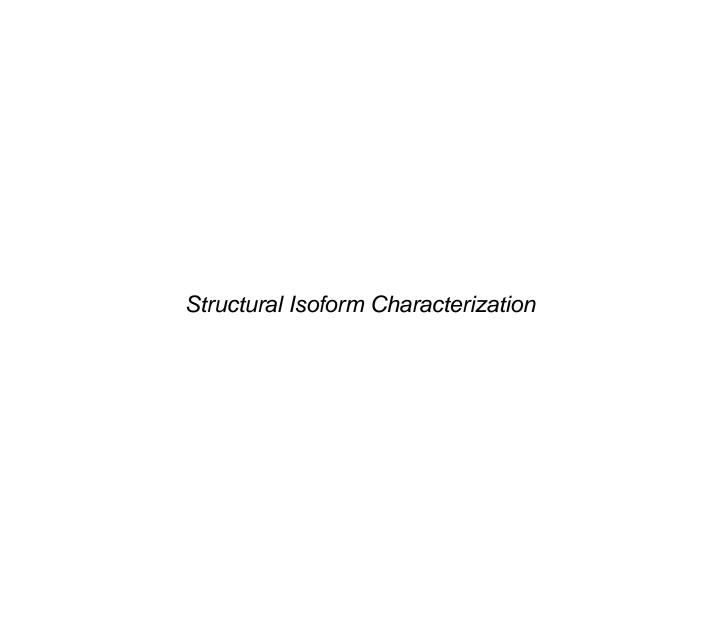




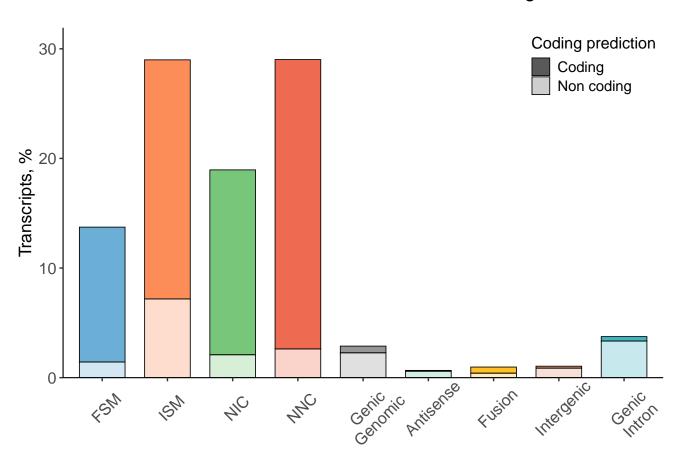




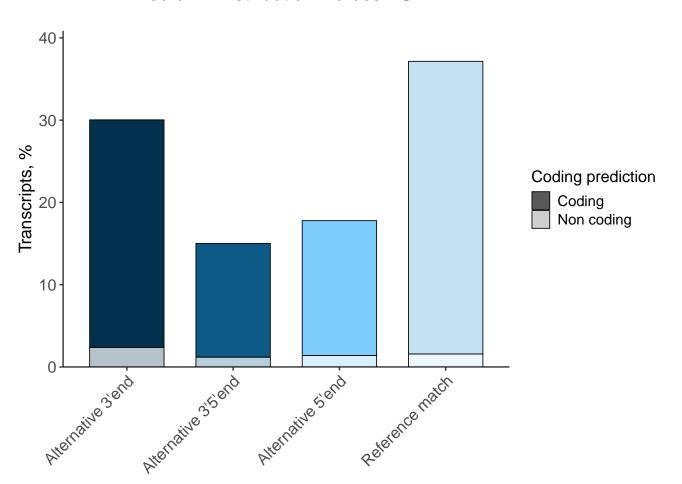
Multi-ExonMono-Exon



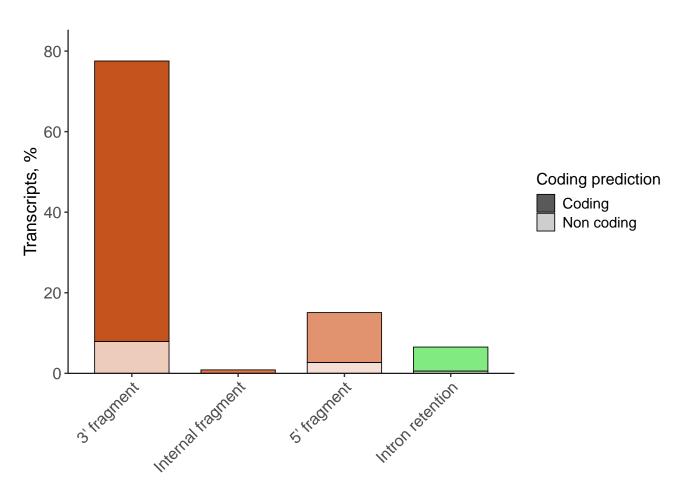
Isoform Distribution Across Structural Categories



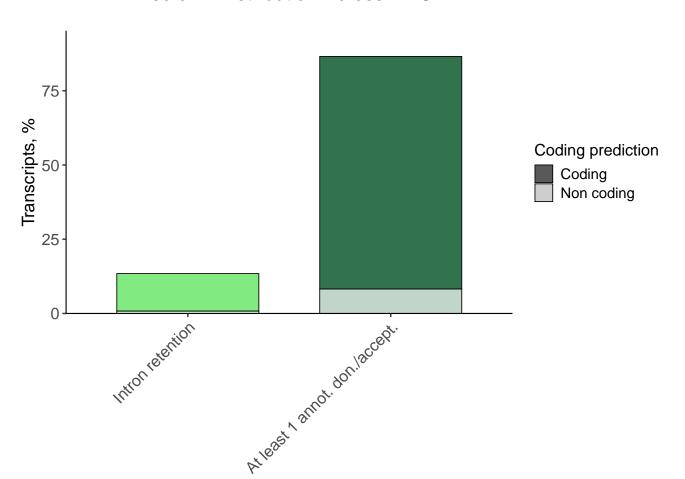
Isoform Distribution Across FSM



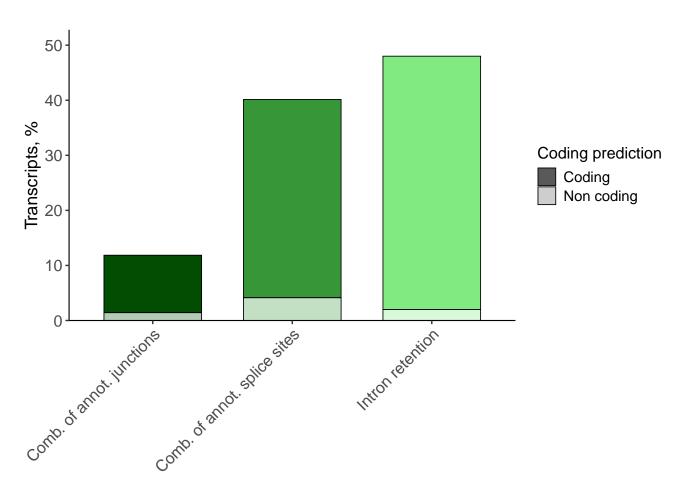
Isoform Distribution Across ISM



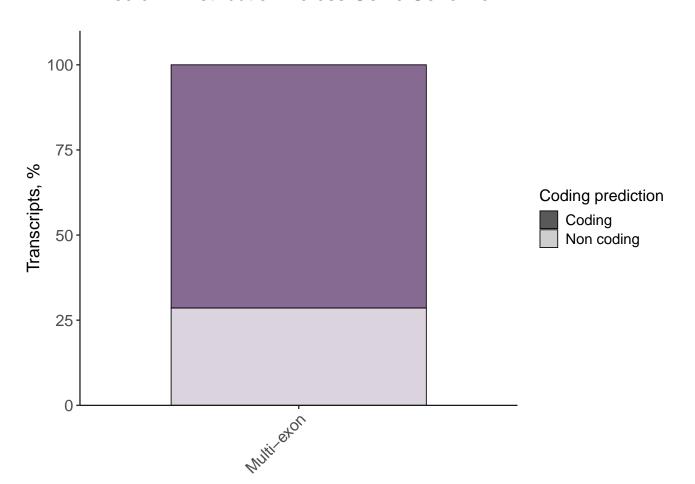
Isoform Distribution Across NNC



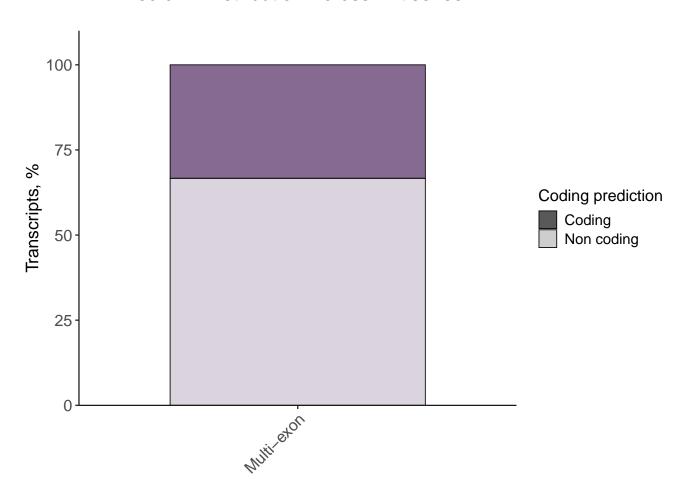
Isoform Distribution Across NIC



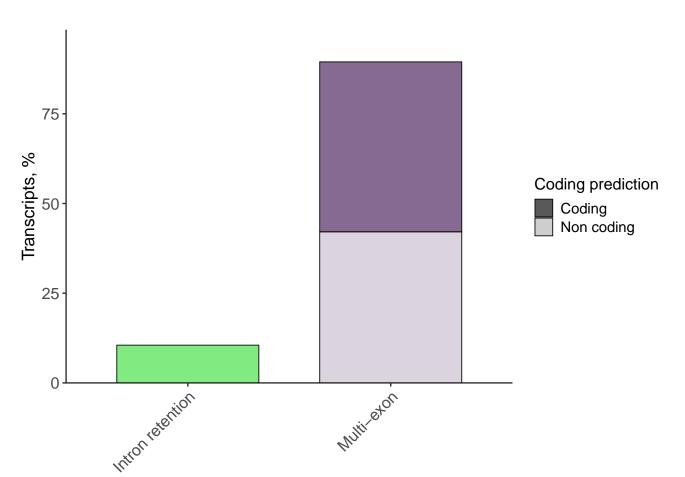
Isoform Distribution Across Genic Genomic



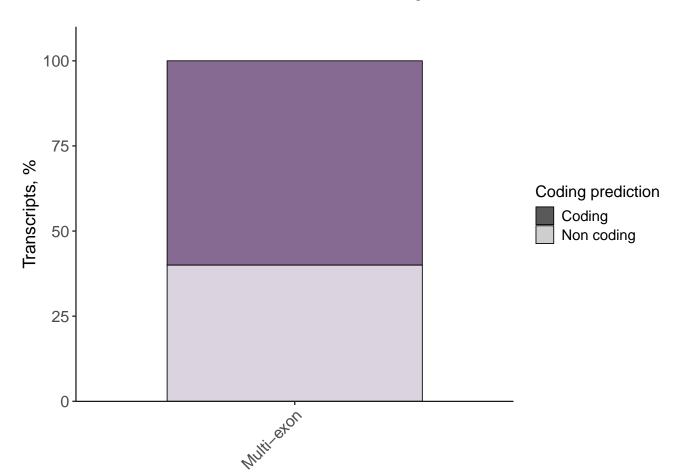
Isoform Distribution Across Antisense



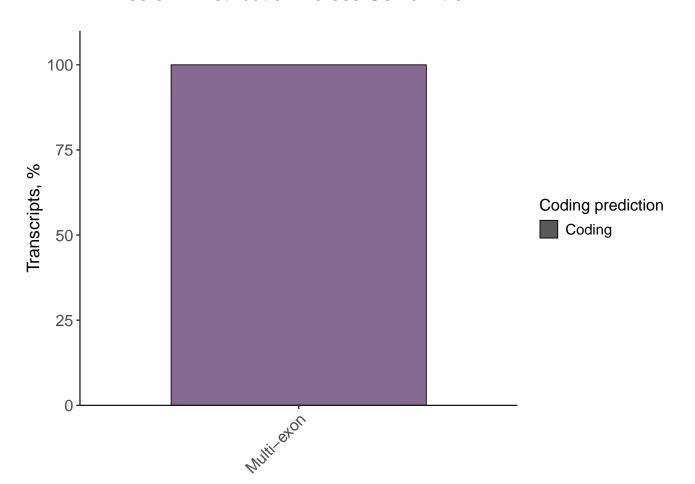
Isoform Distribution Across Fusion



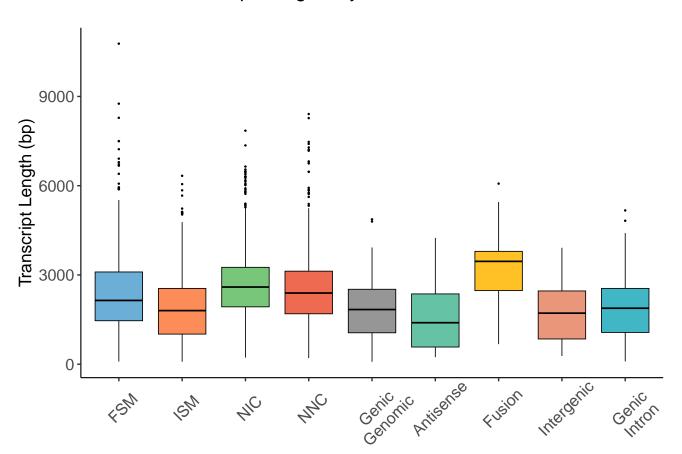
Isoform Distribution Across Intergenic



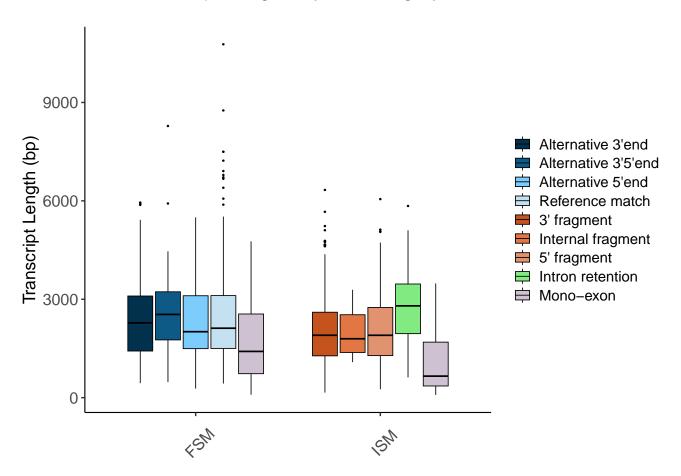
Isoform Distribution Across Genic Intron



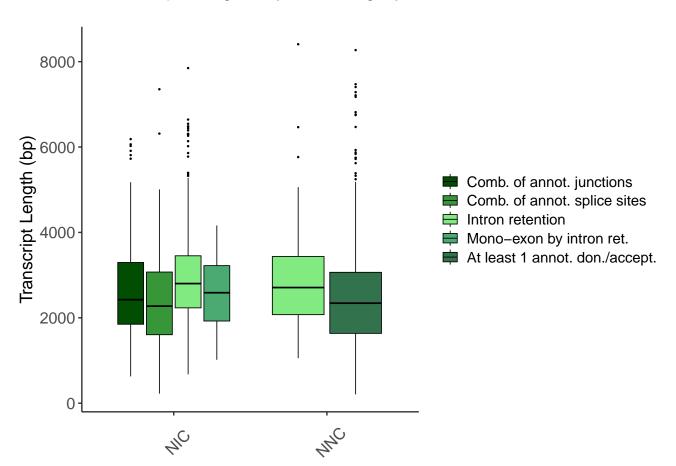
Transcript Lengths by Structural Classification



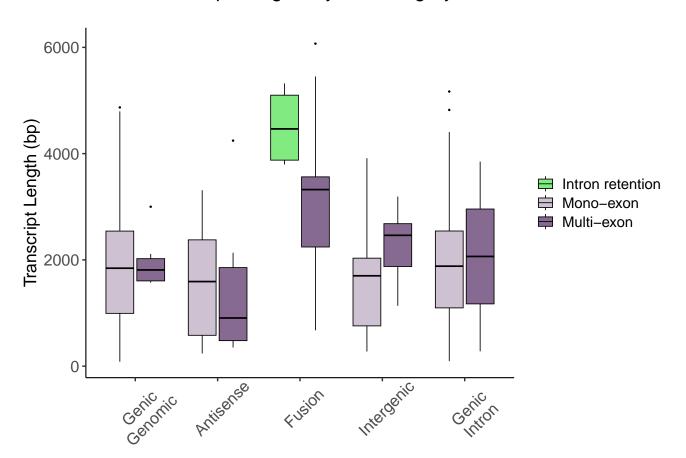
Transcript Lengths by Subcategory



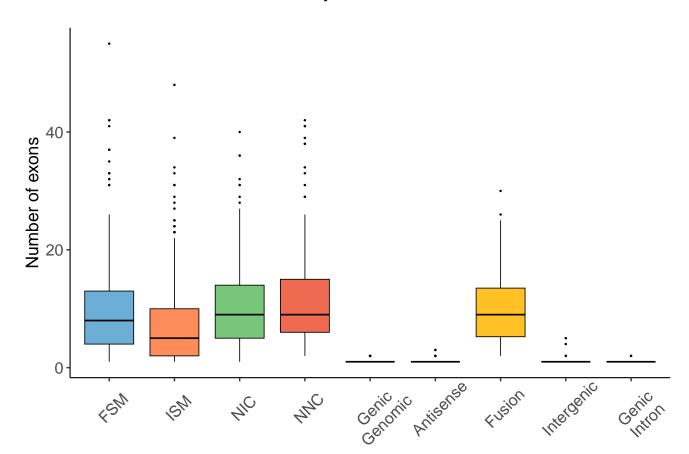
Transcript Lengths by Subcategory



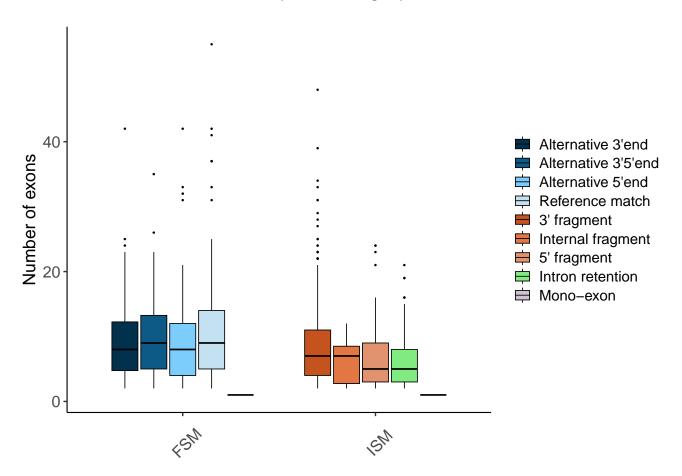
Transcript Lengths by Subcategory



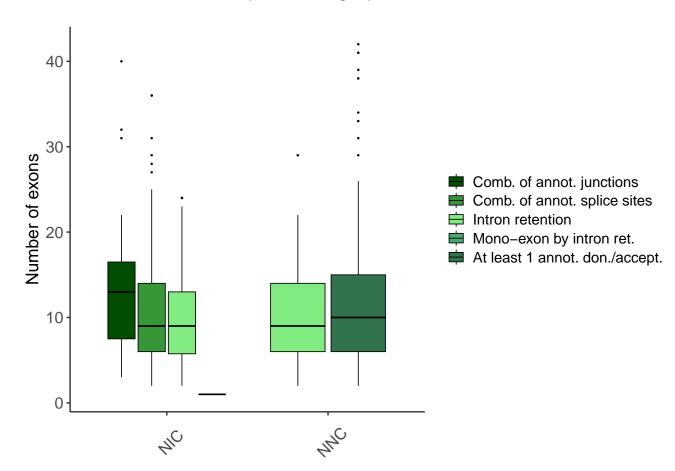
Exon Counts by Structural Classification



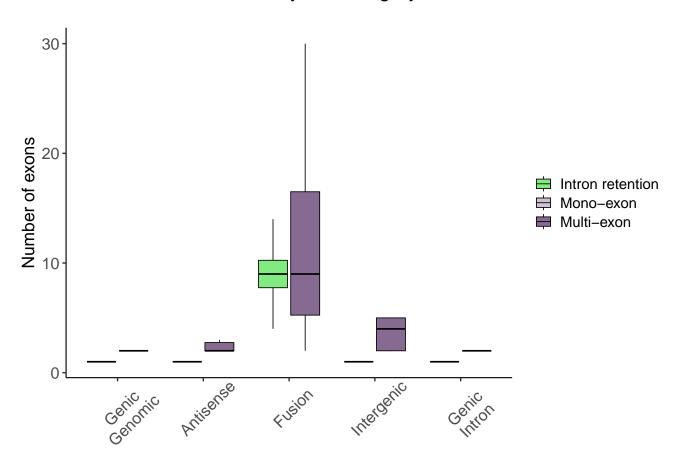
Exon Counts by Subcategory



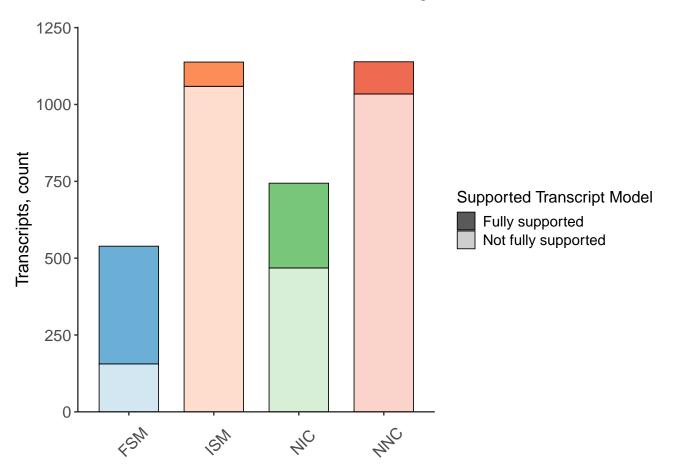
Exon Counts by Subcategory



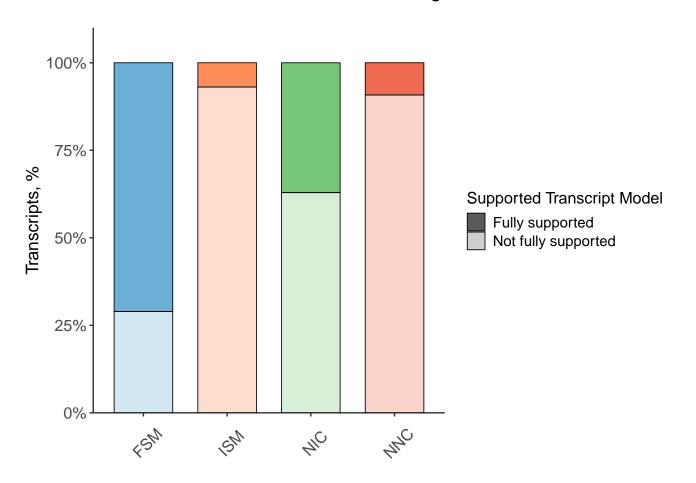
Exon Counts by Subcategory



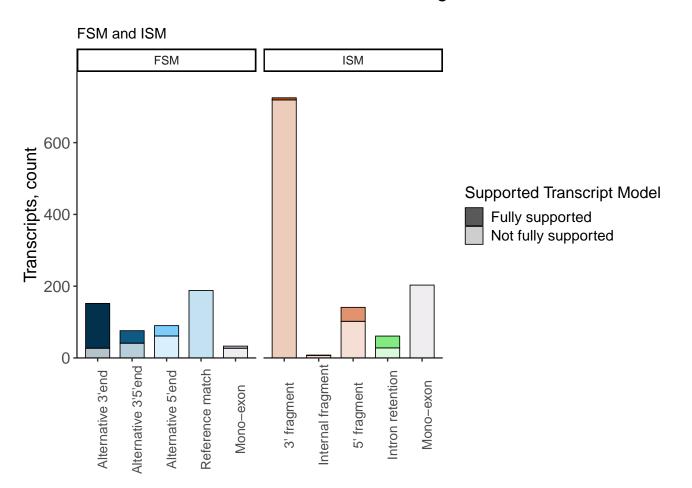
Isoform Distribution Across Structural Categories



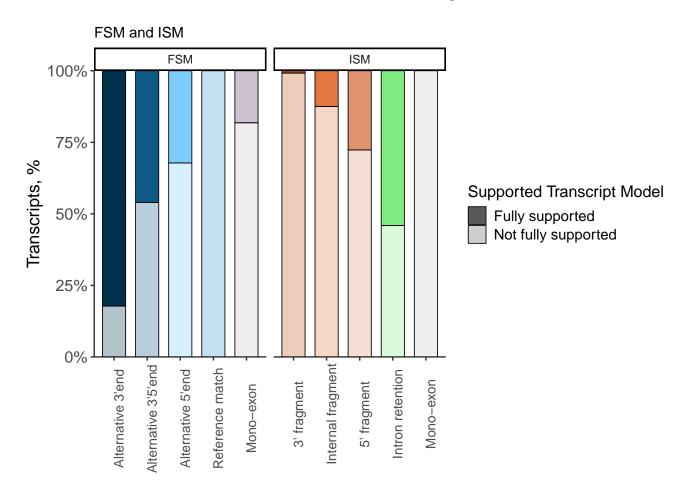
Isoform Distribution Across Structural Categories



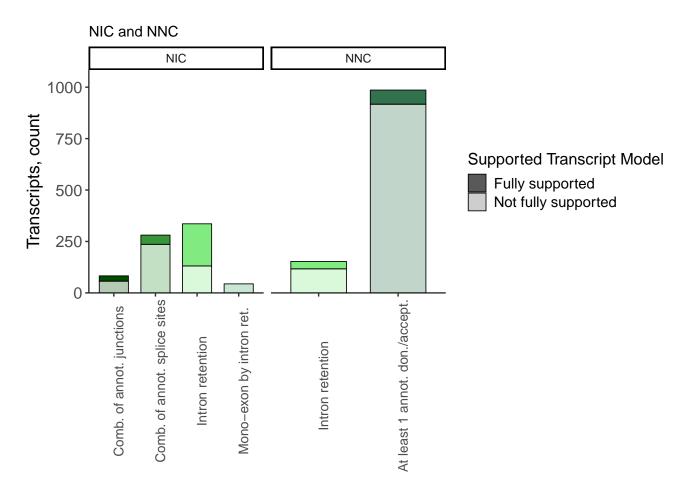
Isoform Distribution Across Structural Subcategories



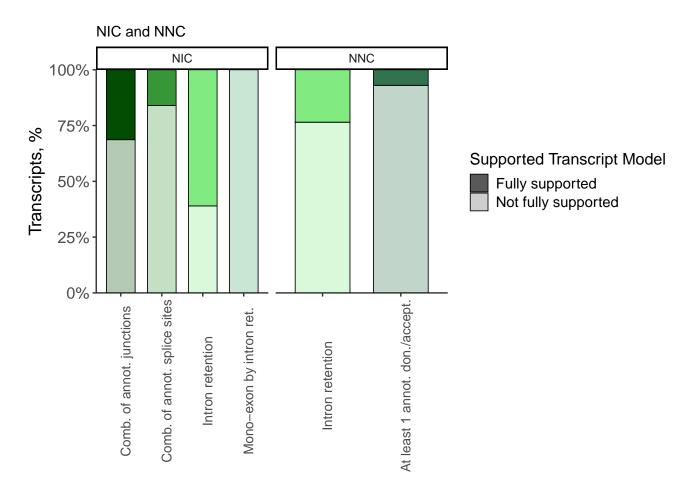
Isoform Distribution Across Structural Subcategories



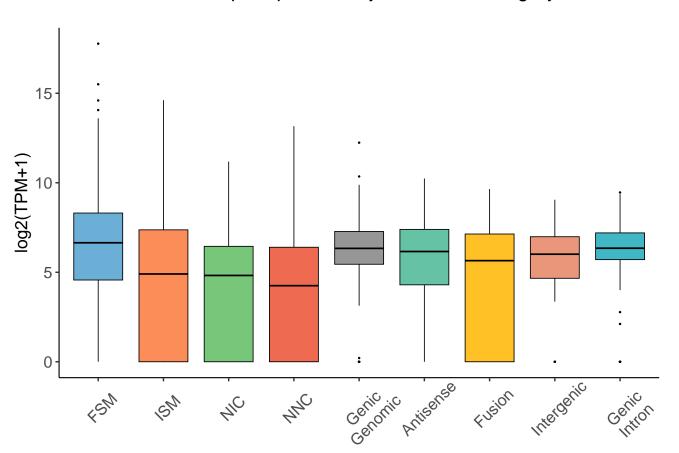
Isoform Distribution Across Structural Subcategories



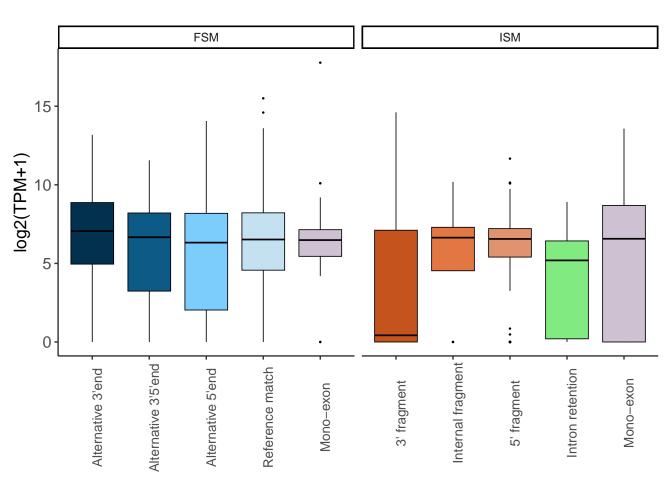
Isoform Distribution Across Structural Subcategories



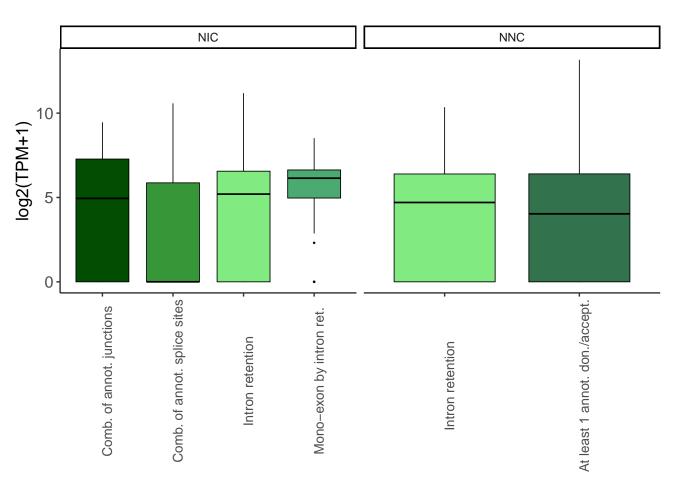
Transcript Expression by Structural Category



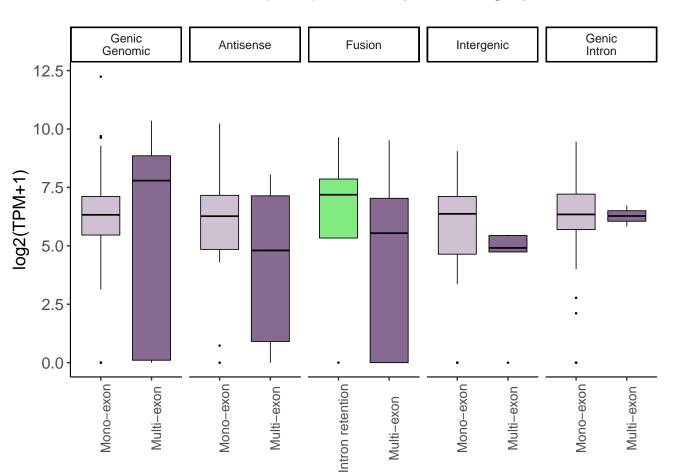
Transcript Expression by Subcategory



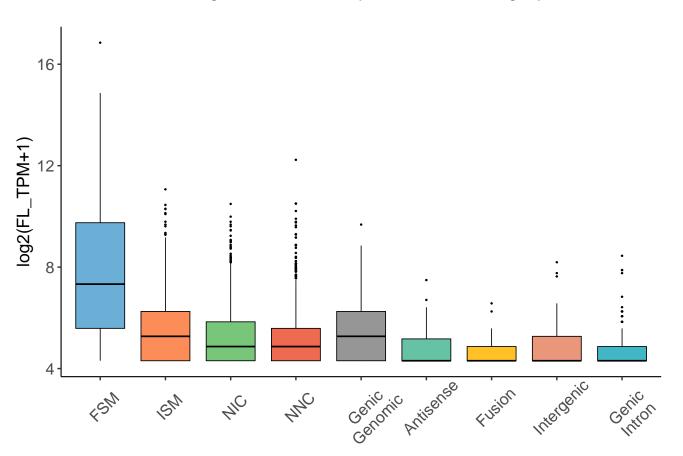
Transcript Expression by Subcategory



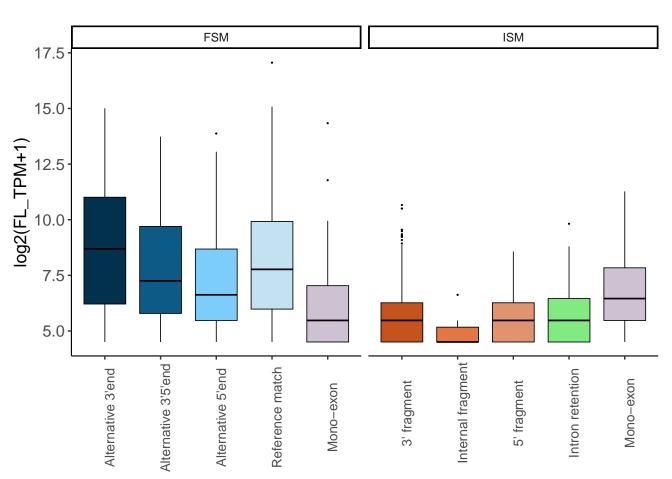
Transcript Expression by Subcategory



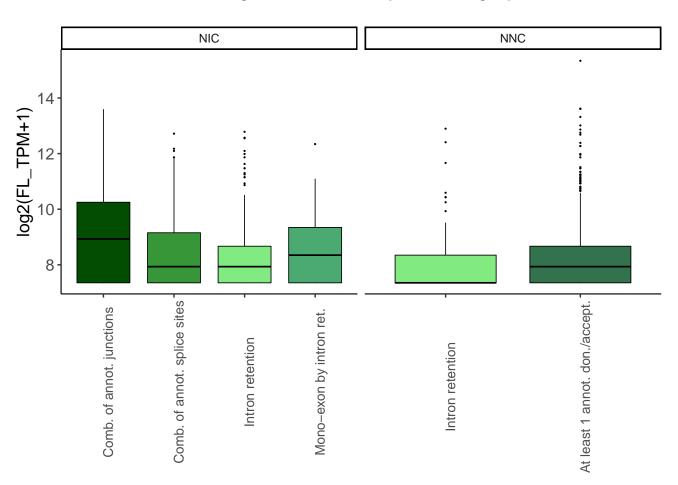
Long Reads Count by Structural Category



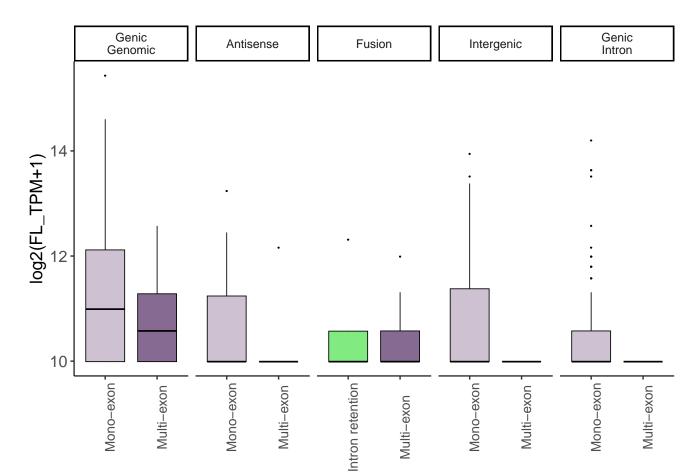
Long Reads Count by Subcategory



Long Reads Count by Subcategory

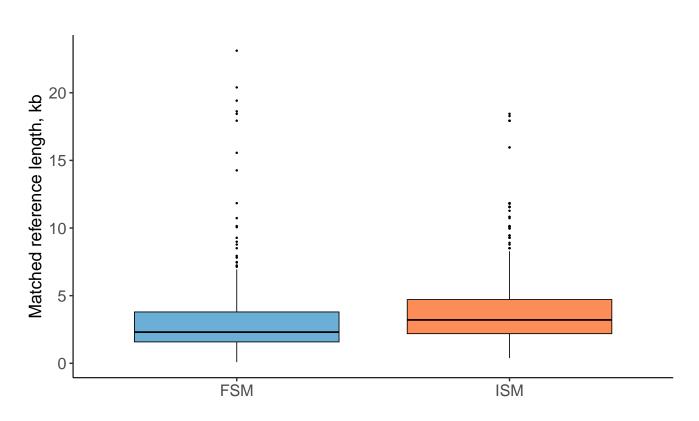


Long Reads Count by Subcategory



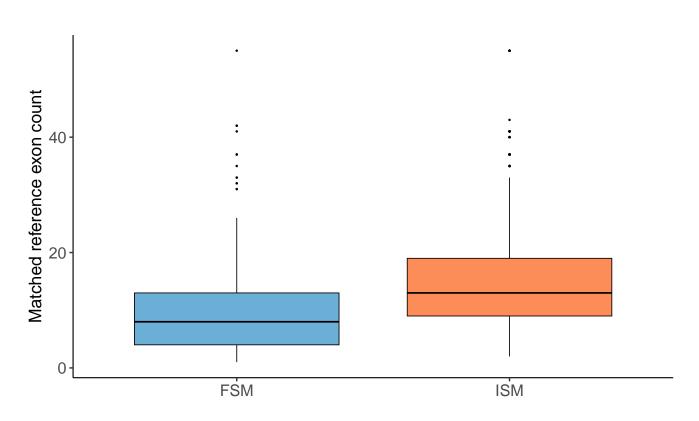
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

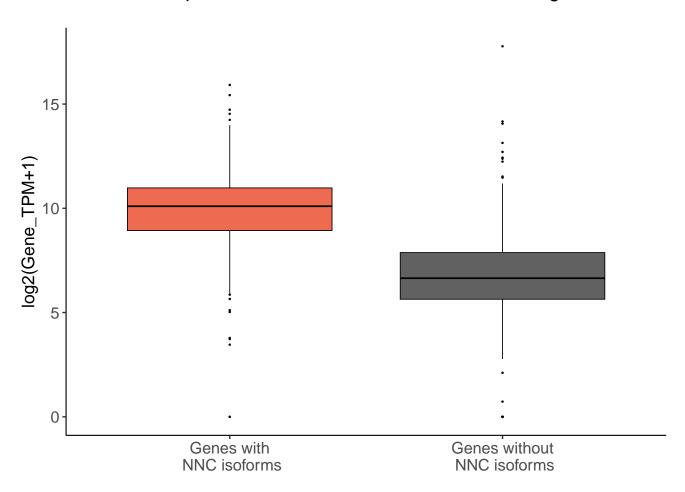


Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

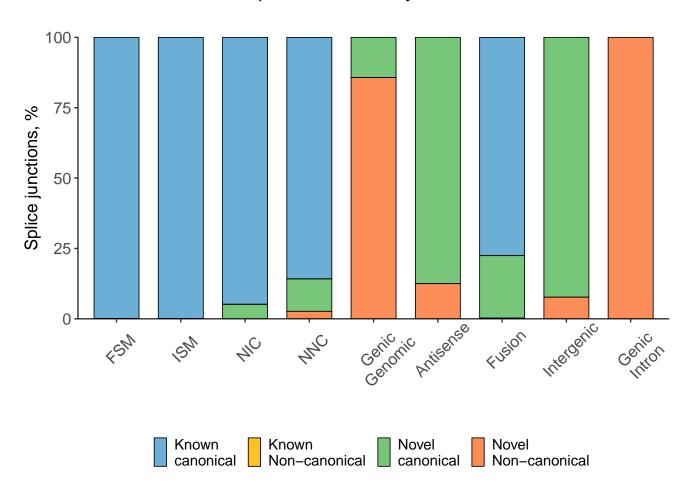


Gene Expression of NNC And Not NNC Containing Genes

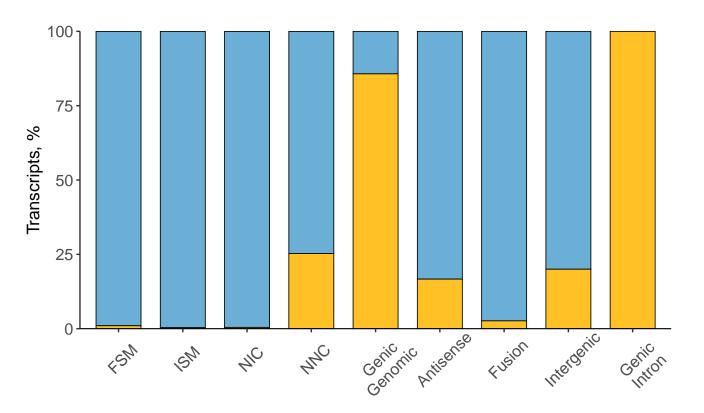




Distribution of Splice Junctions by Structural Classification

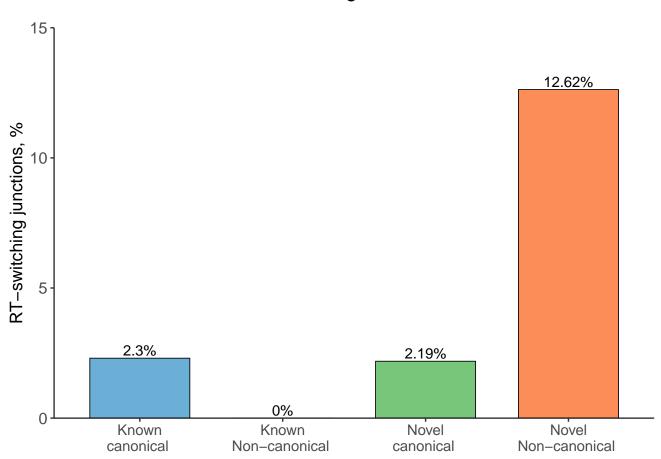


Distribution of Transcripts by Splice Junctions

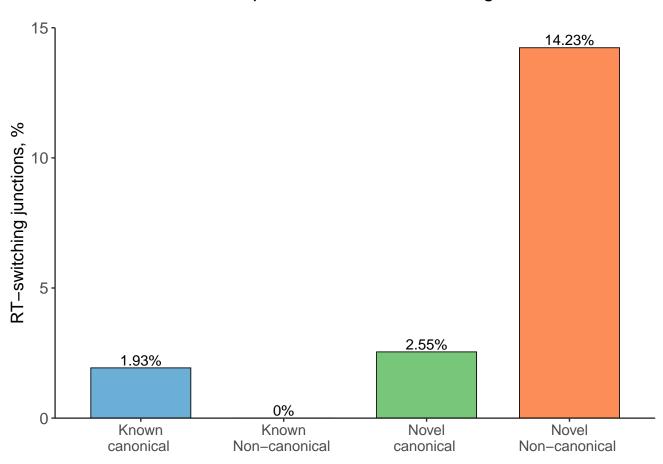


Canonical Non-canonical

RT-Switching All Junctions



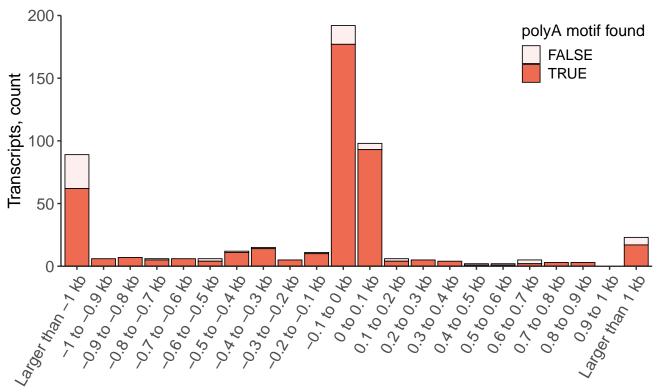
Unique Junctions RT-switching





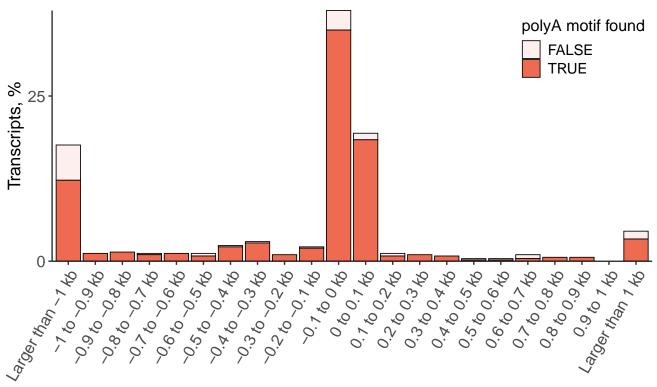
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



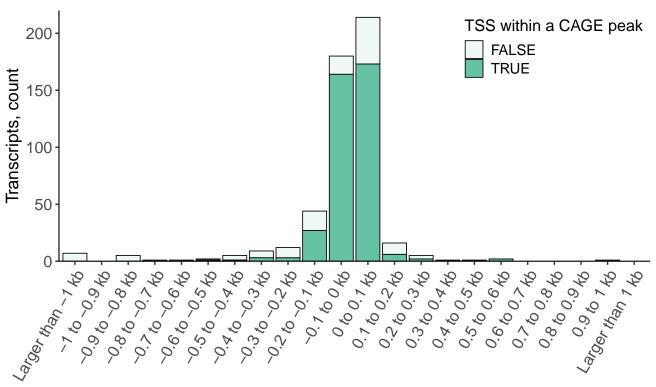
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



Distance to Annotated Transcription Start Site for FSM

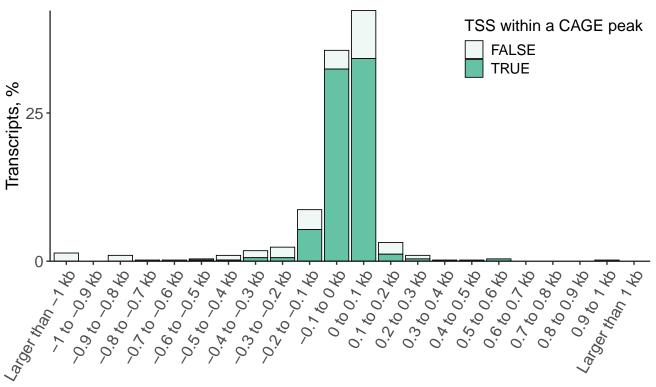
Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site (TSS), bp

Distance to Annotated Transcription Start Site for FSM

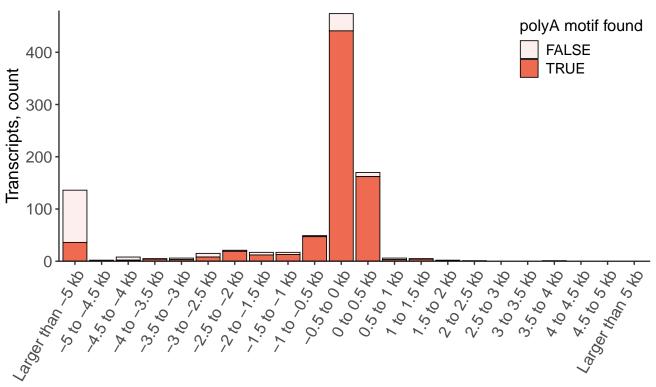
Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site (TSS), bp

Distance to Annotated Transcription Termination Site (TTS)

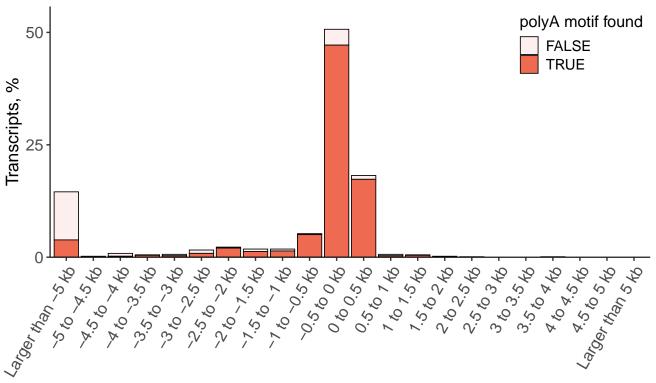
Negative values indicate upstream of annotated TTS



Distance to annotated polyadenylation site, bp

Distance to Annotated Transcription Termination Site (TTS)

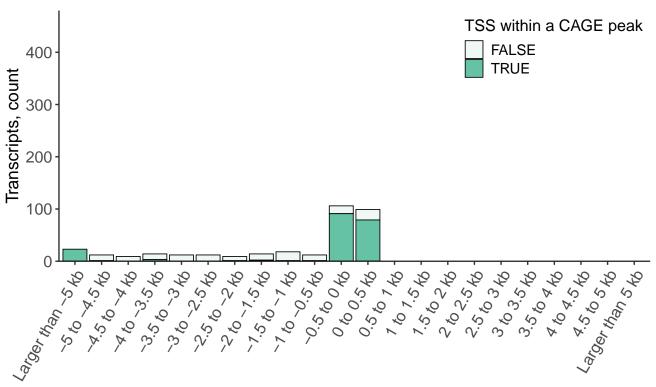
Negative values indicate upstream of annotated TTS



Distance to annotated polyadenylation site, bp

Distance to Annotated Transcription Start Site for ISM

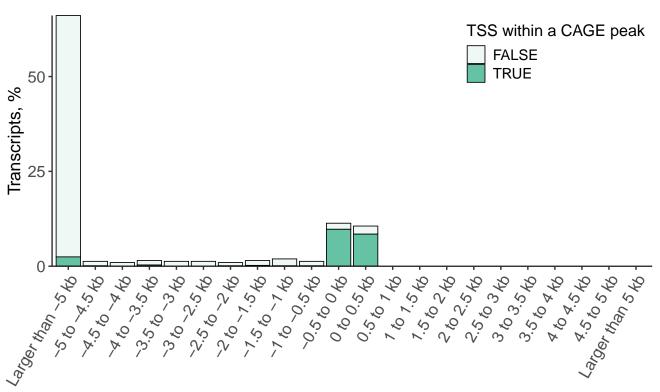
Negative values indicate downstream of annotated TSS



Distance to annotated transcription start site, bp

Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS

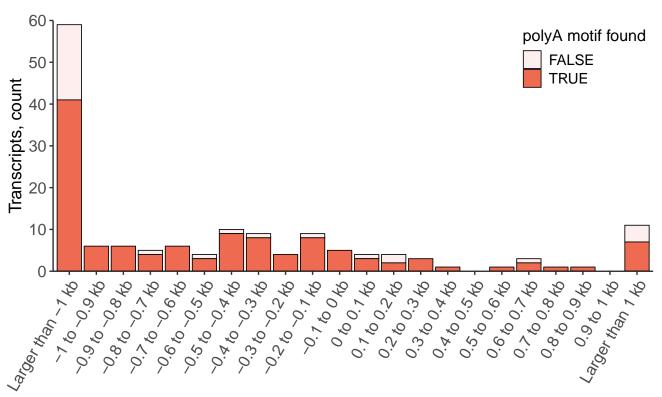


Distance to annotated transcription start site, bp

Comparison With Annotated TSS and TTS by Subcategories

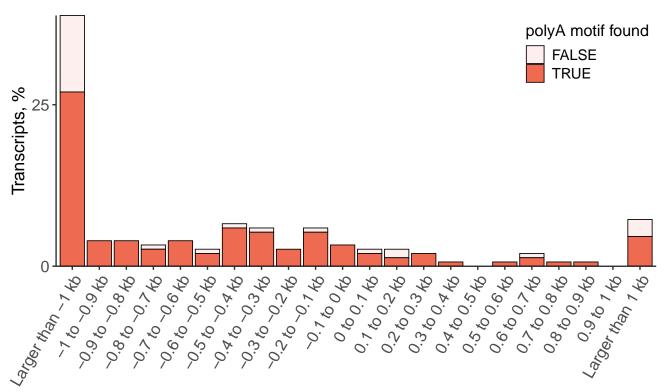
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



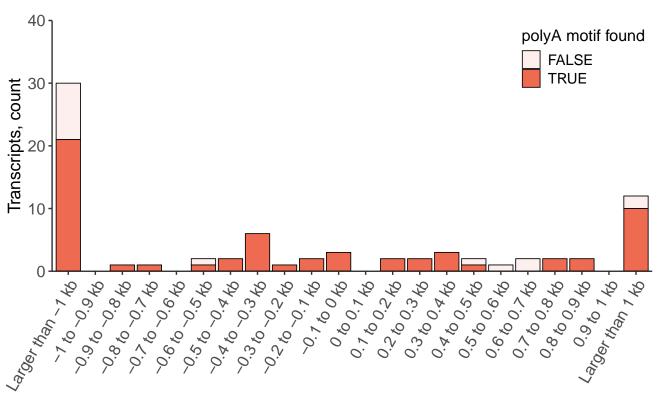
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'End

Negative values indicate upstream of annotated termination site



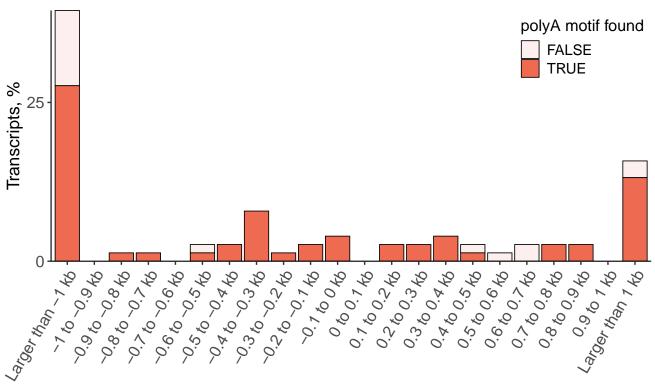
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



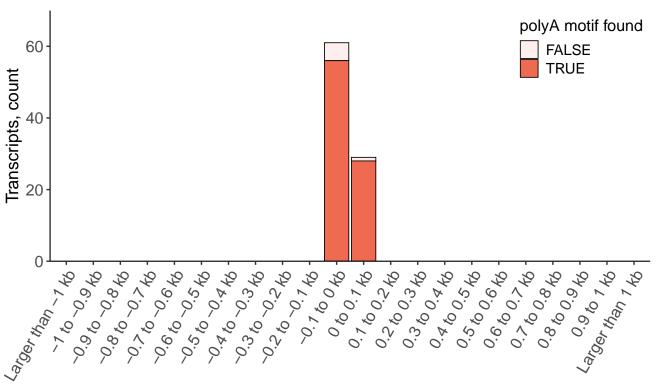
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 3'5'End

Negative values indicate upstream of annotated termination site



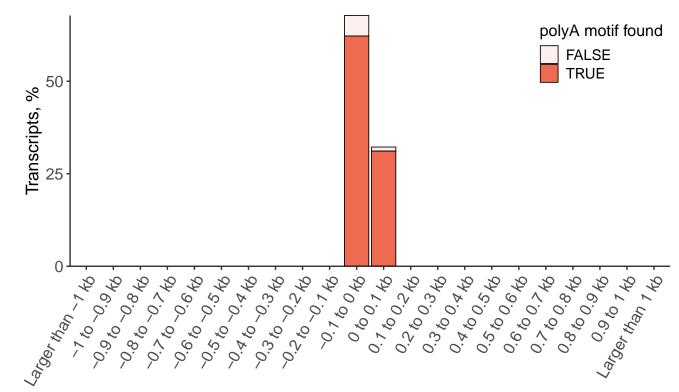
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



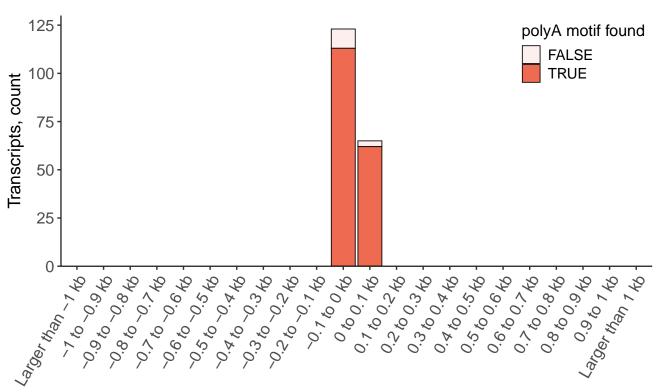
Distance to annotated Transcription Termination Site (TTS) FSM Alternative 5'End

Negative values indicate upstream of annotated termination site



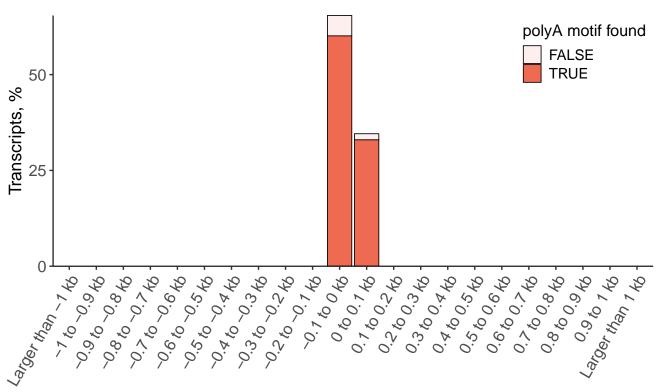
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



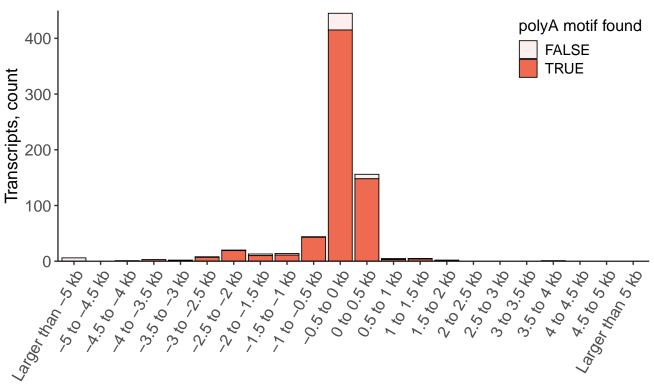
Distance to annotated Transcription Termination Site (TTS) FSM Reference Match

Negative values indicate upstream of annotated termination site



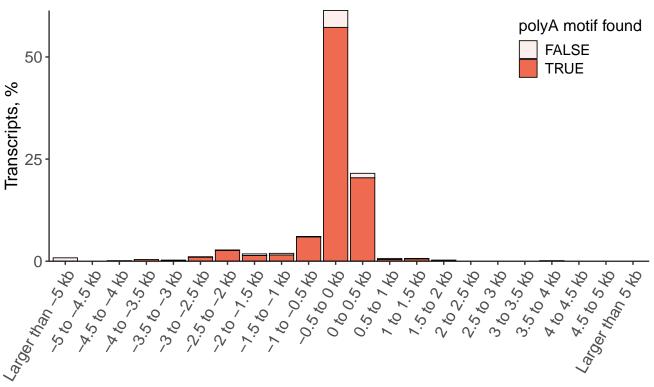
Distance to Annotated Transcription Termination Site for ISM 3' Fragment

Negative values indicate upstream of annotated TTS



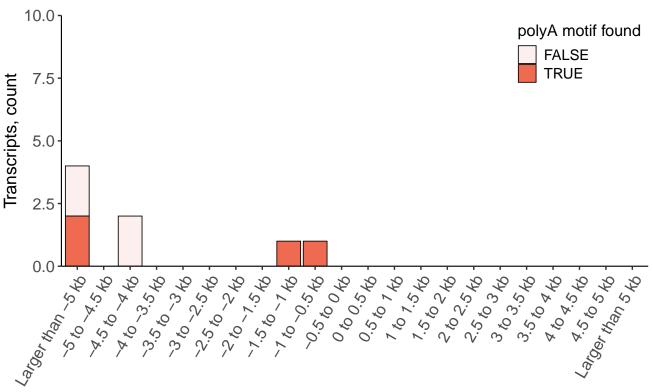
Distance to Annotated Transcription Termination Site for ISM 3' Fragment

Negative values indicate upstream of annotated TTS



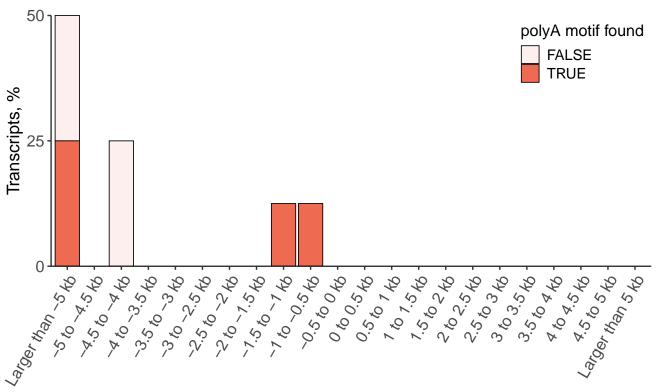
Distance to Annotated Transcription Termination Site for ISM Internal Fragment

Negative values indicate upstream of annotated TTS



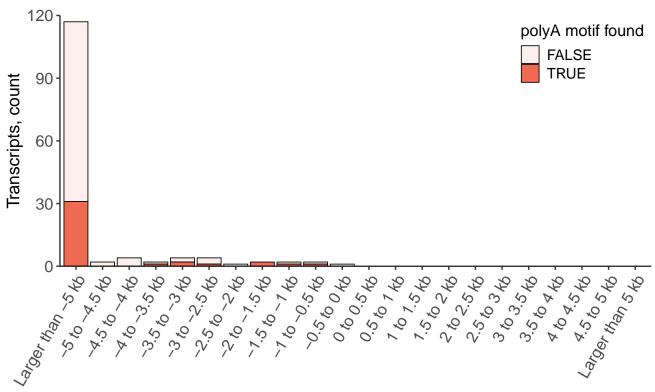
Distance to Annotated Transcription Termination Site for ISM Internal Fragment

Negative values indicate upstream of annotated TTS



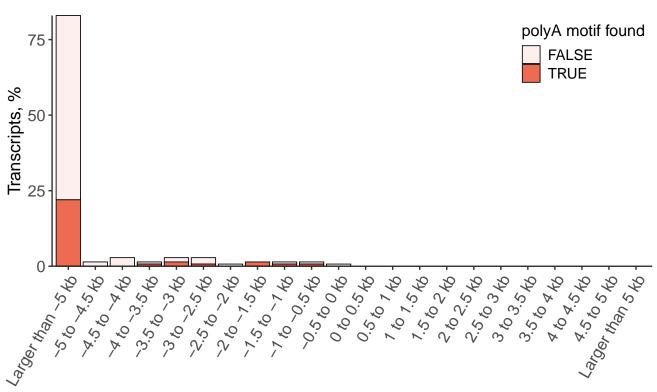
Distance to Annotated Transcription Termination Site for ISM A5' Fragment

Negative values indicate upstream of annotated TTS



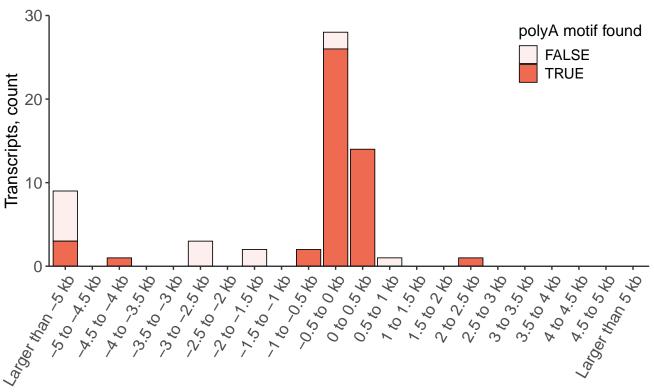
Distance to Annotated Transcription Termination Site for ISM A5' Fragment

Negative values indicate upstream of annotated TTS



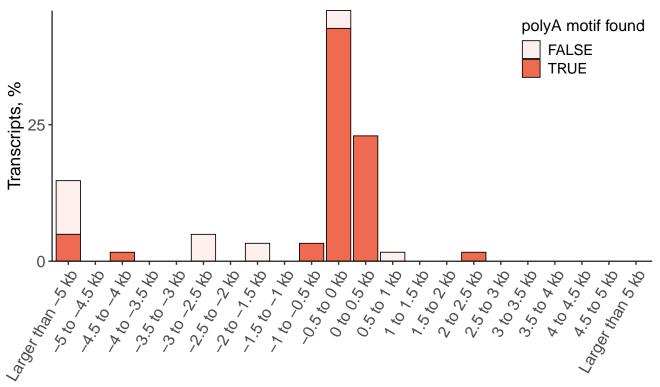
Distance to Annotated Transcription Termination Site for ISM Intron Retention

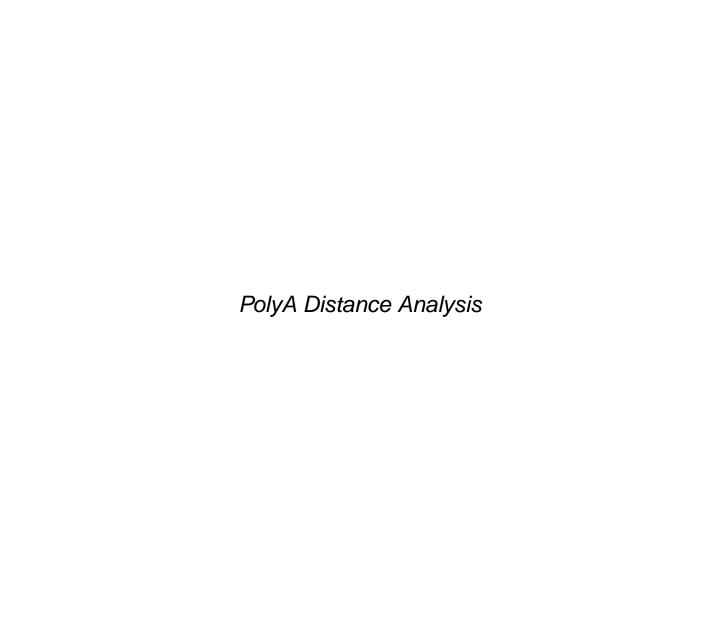
Negative values indicate upstream of annotated TTS

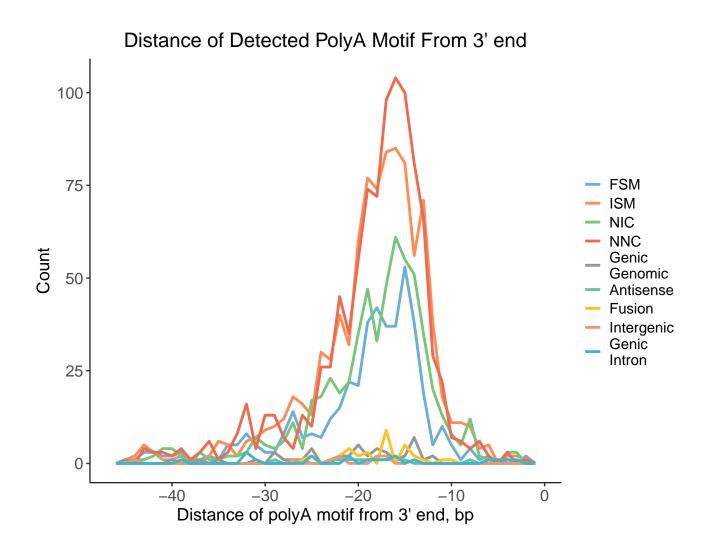


Distance to Annotated Transcription Termination Site for ISM Intron Retention

Negative values indicate upstream of annotated TTS







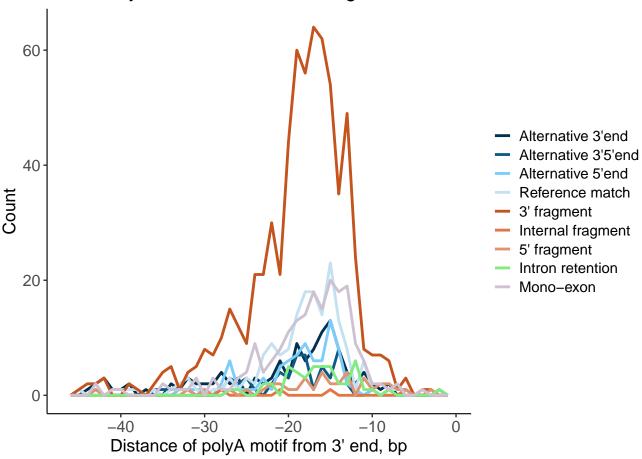
Frequency of PolyA Motifs

Number of polyA Motifs Detected

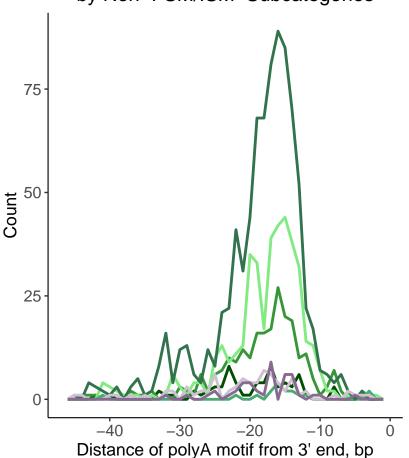
Category	Count	polyA Detected	%
FSM	539	458	85
ISM	1138	942	83
NIC	744	594	80
NNC	1139	981	86
Genic Genomic	113	48	42
Antisense	26	12	46
Fusion	38	34	89
Intergenic	41	10	24
Genic Intron	147	19	13

Motif	Count	%
AATAAA	2014	65.0
ATTAAA	529	17.1
AGTAAA	161	5.2
TATAAA	90	2.9
GATAAA	54	1.7
AAAACA	41	1.3
AATACA	38	1.2
AAAAAG	32	1.0
AATAGA	28	0.9
CATAAA	26	8.0
AAGAAA	24	8.0
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



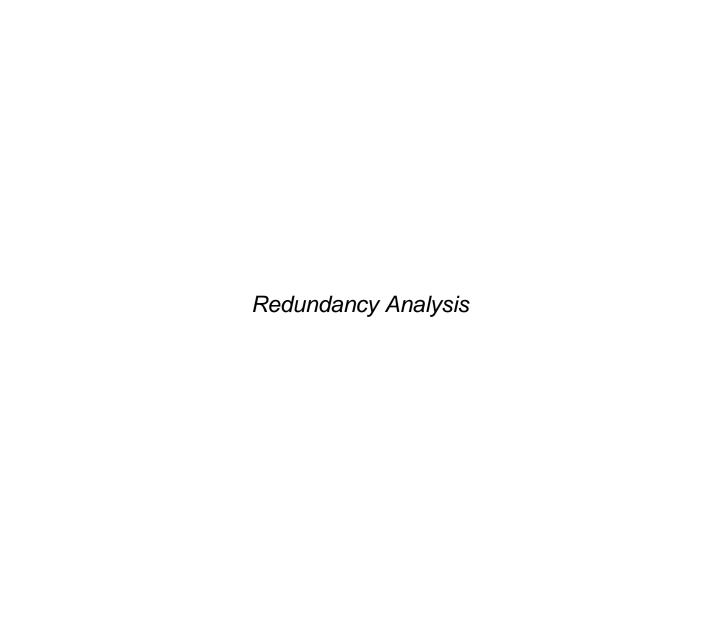
- Comb. of annot. junctions
- Comb. of annot. splice sites
- Intron retention
- Mono-exon by intron ret.
- At least 1 annot. don./accept.
- Mono-exon
- Multi-exon

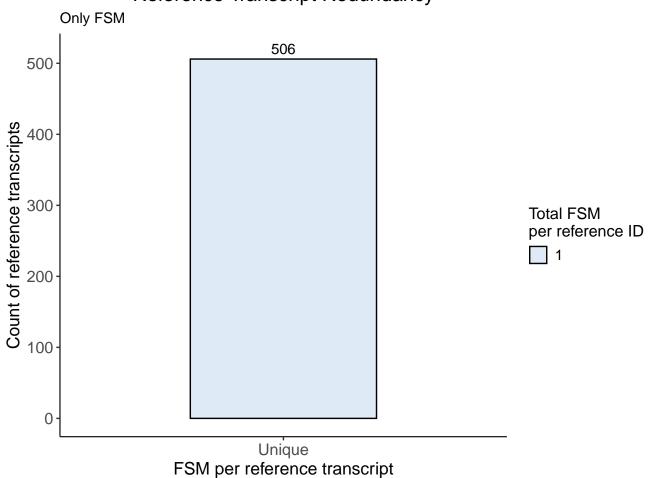
Number of polyA Motifs Detected

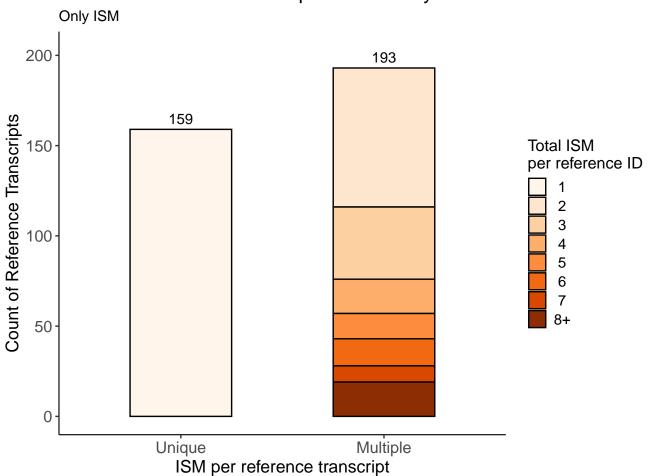
Subcategory	Count	polyA Detected	%
Alternative 3'end	152	121	80
Alternative 3'5'end	76	60	79
Alternative 5'end	90	84	93
Reference match	188	175	93
3' fragment	725	668	92
Internal fragment	8	4	50
5' fragment	141	39	28
Comb. of annot. junctions	83	68	82
Comb. of annot. splice sites	281	235	84
Intron retention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

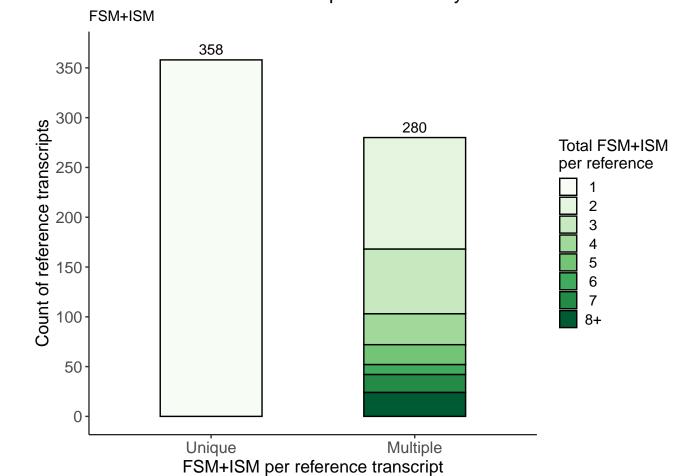
Frequency of PolyA Motifs

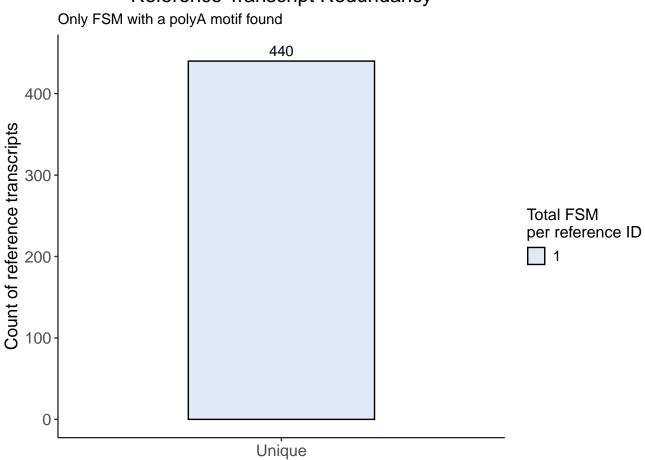
	-	
Motif	Count	%
AATAAA	2014	65.0
ATTAAA	529	17.1
AGTAAA	161	5.2
TATAAA	90	2.9
GATAAA	54	1.7
AAAACA	41	1.3
AATACA	38	1.2
AAAAAG	32	1.0
AATAGA	28	0.9
CATAAA	26	8.0
AAGAAA	24	8.0
AATATA	20	0.6
TTTAAA	16	0.5
AATGAA	13	0.4
ACTAAA	10	0.3
GGGGCT	2	0.1



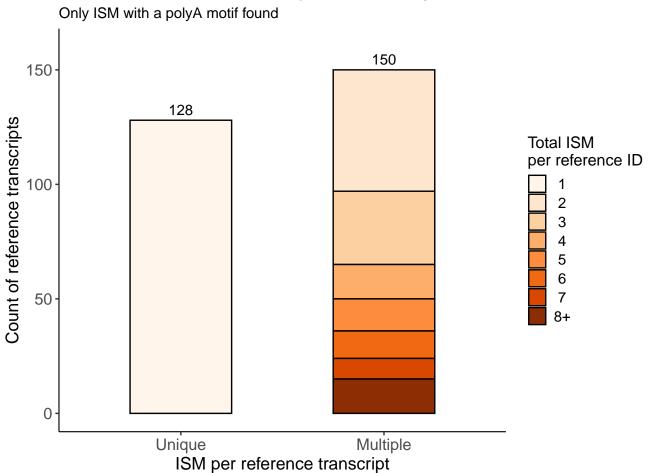


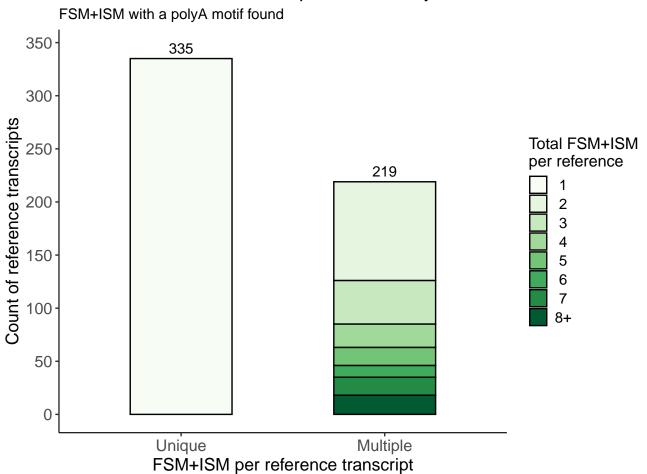






FSM per reference transcript

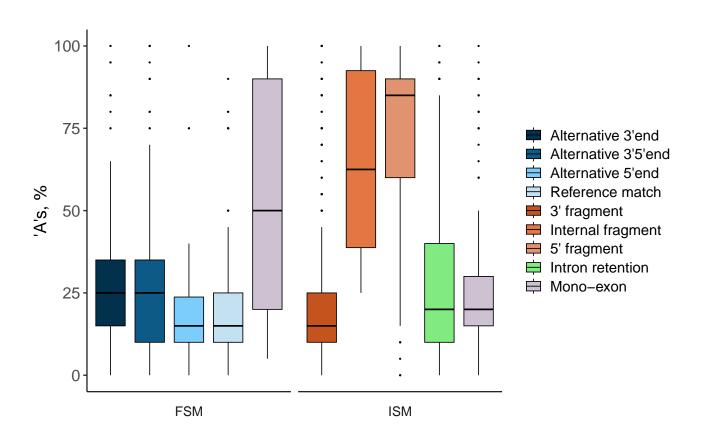






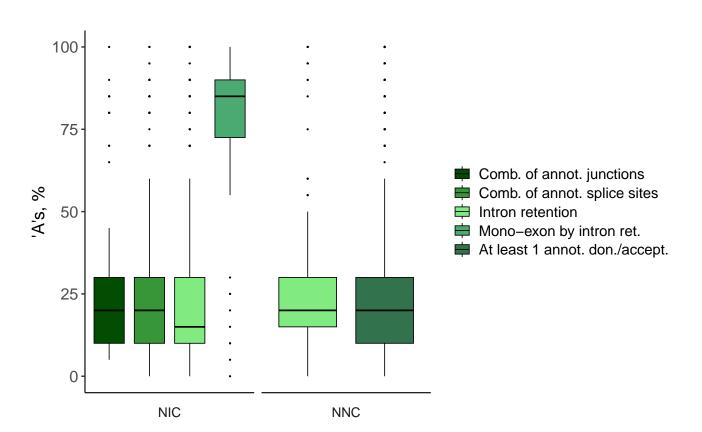
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



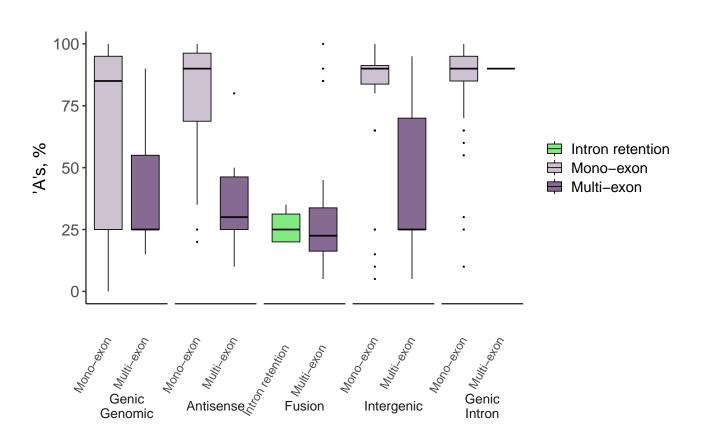
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



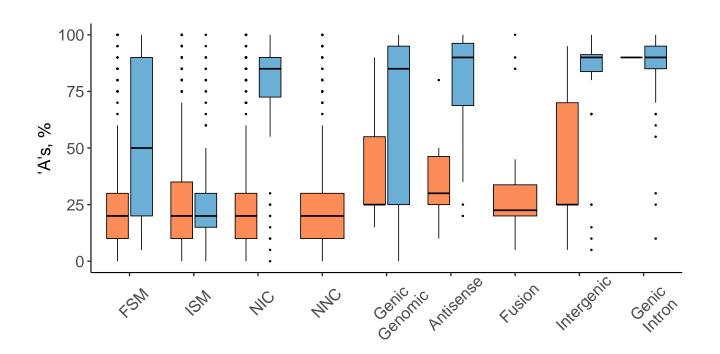
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



Mono- vs Multi-Exon Possible Intra-Priming

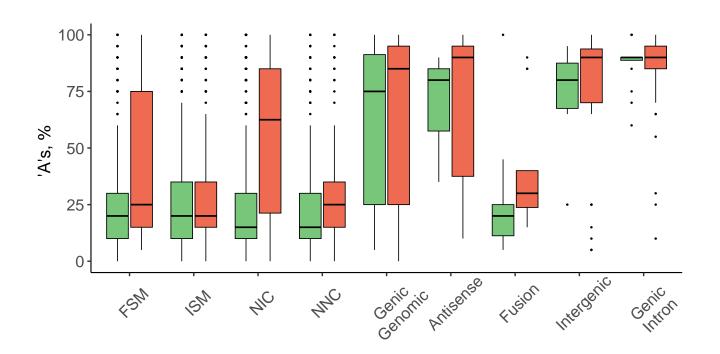
Percent of genomic 'A's in downstream 20 bp



 ➡ Mono-Exon Isoforms
 ➡ Multi-Exon Isoforms

Coding vs Non-Coding Possible Intra-Priming

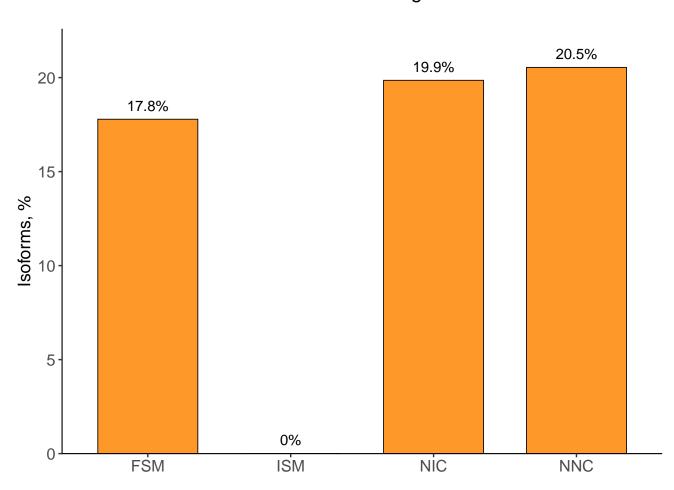
Percent of genomic 'A's in downstream 20 bp



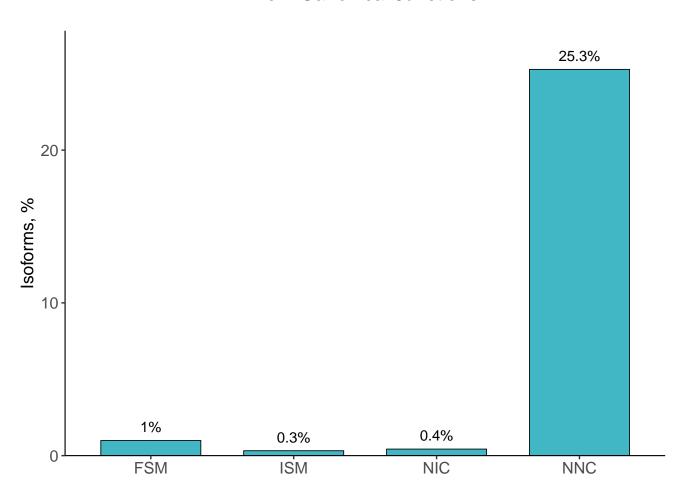
 ➡
 Coding Isoforms
 ➡
 Non–Coding Isoforms



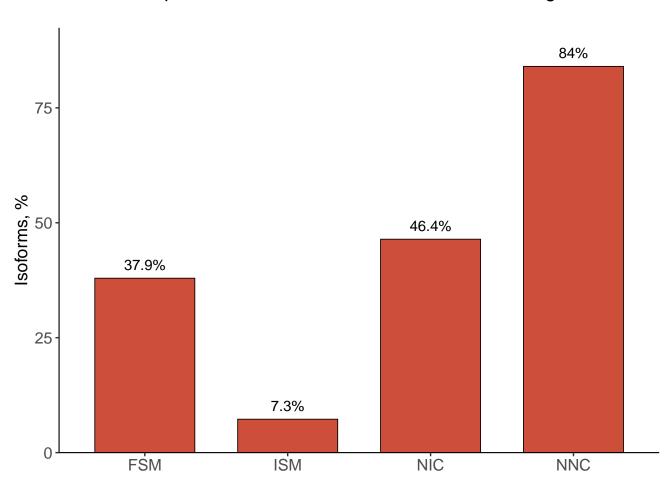
RT-switching



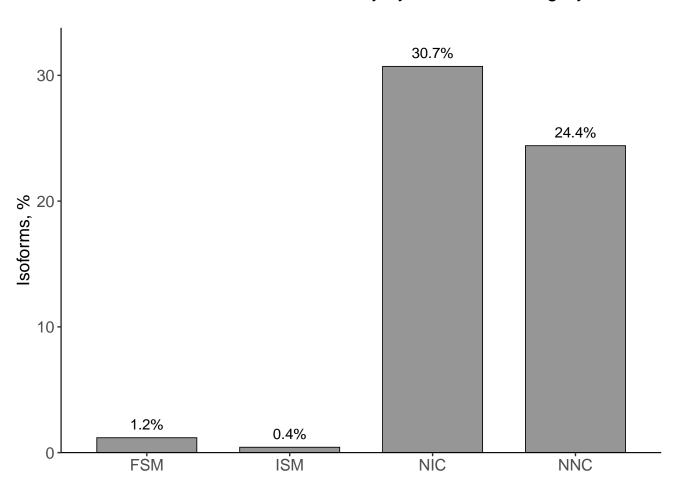
Non-Canonical Junctions



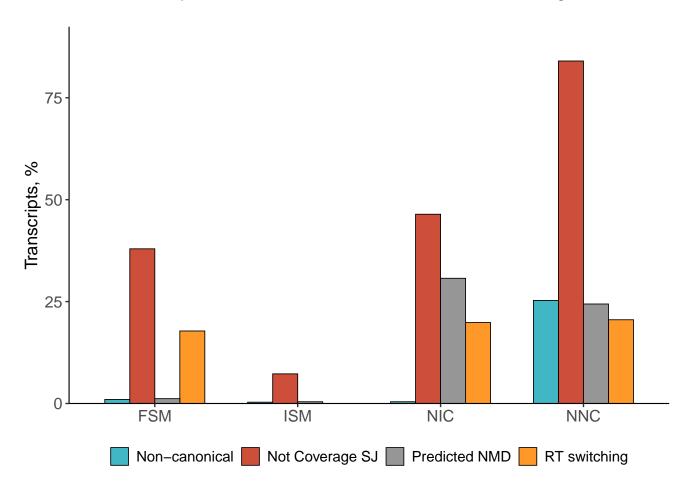
Splice Junctions Without Short Read Coverage



Nonsense-Mediated Decay by Structural Category

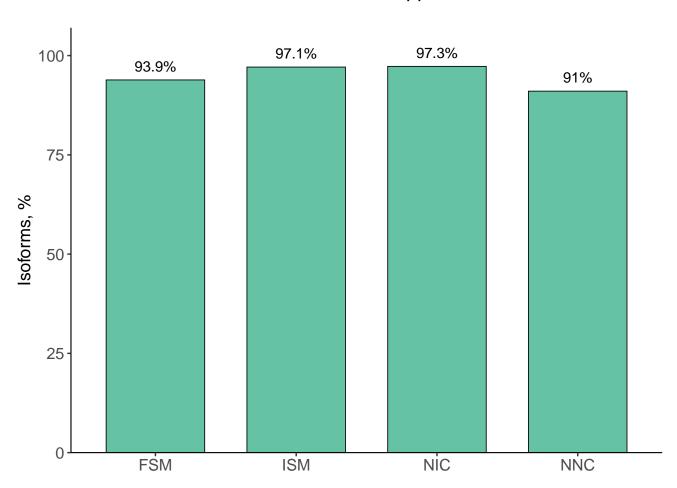


Quality Control Attributes Across Structural Categories

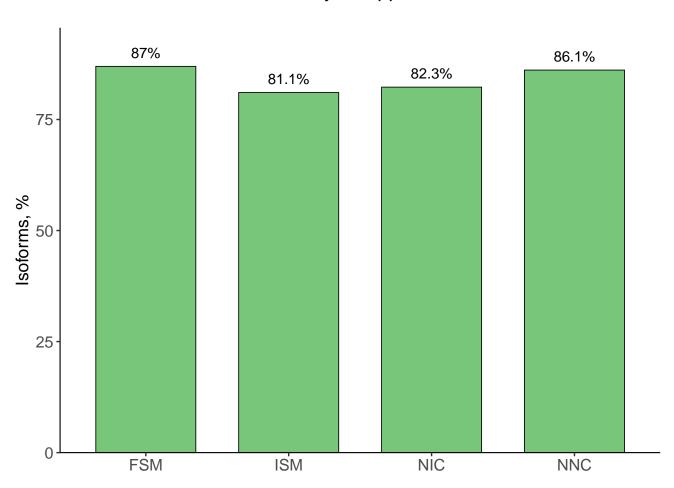




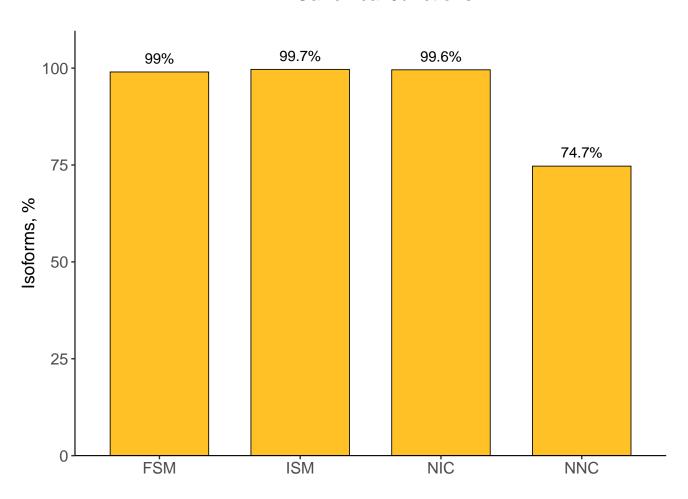
Annotation Support



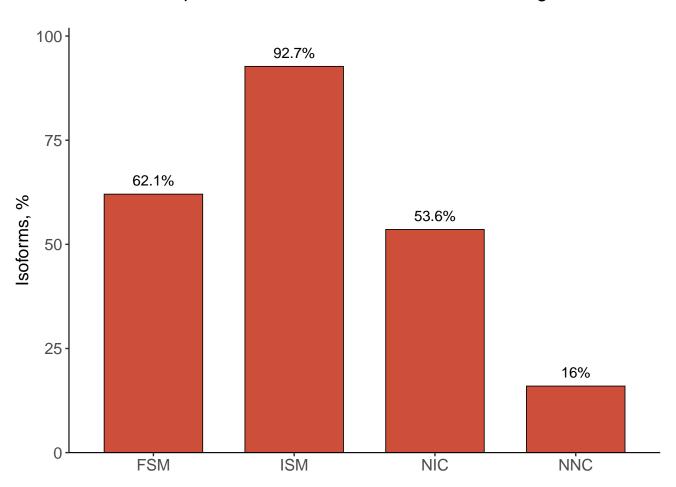
PolyA Support



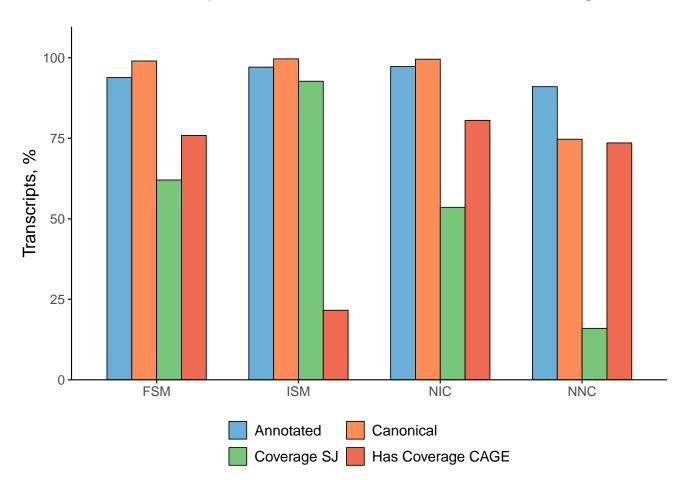
All Canonical Junctions



Splice Junctions With Short Read Coverage



Good Quality Control Attributes Across Structural Categories



TSS Ratio FSM Reference Match vs ISM

