SQANTI3 report

Unique Genes: 21533

Unique Isoforms: 486267

Transcript Classification

Category	Isoforms, count
FSM	126850
ISM	177334
NIC	101120
NNC	75339
Genic Genomic	440
Antisense	1097
Fusion	2298
Intergenic	1737
Genic Intron	0

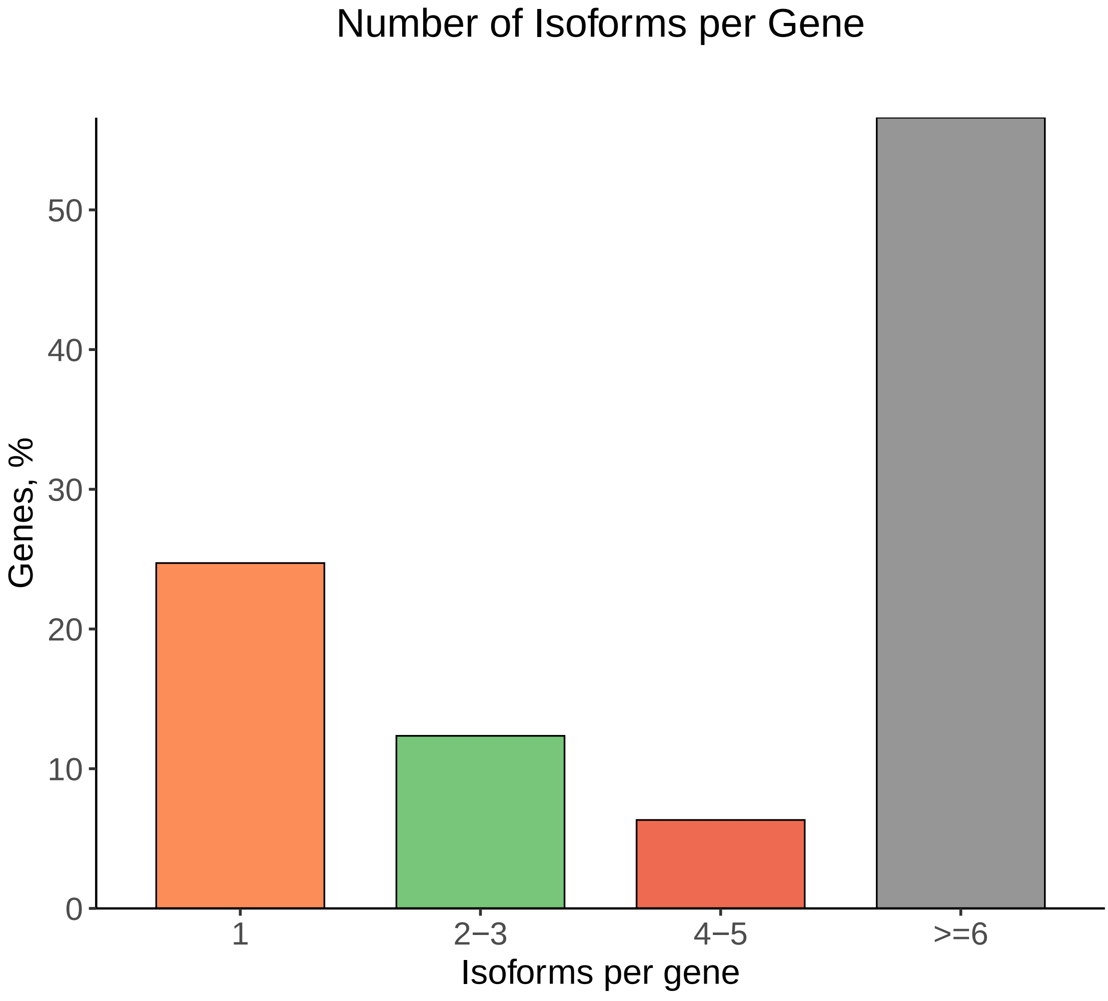
Gene Classification

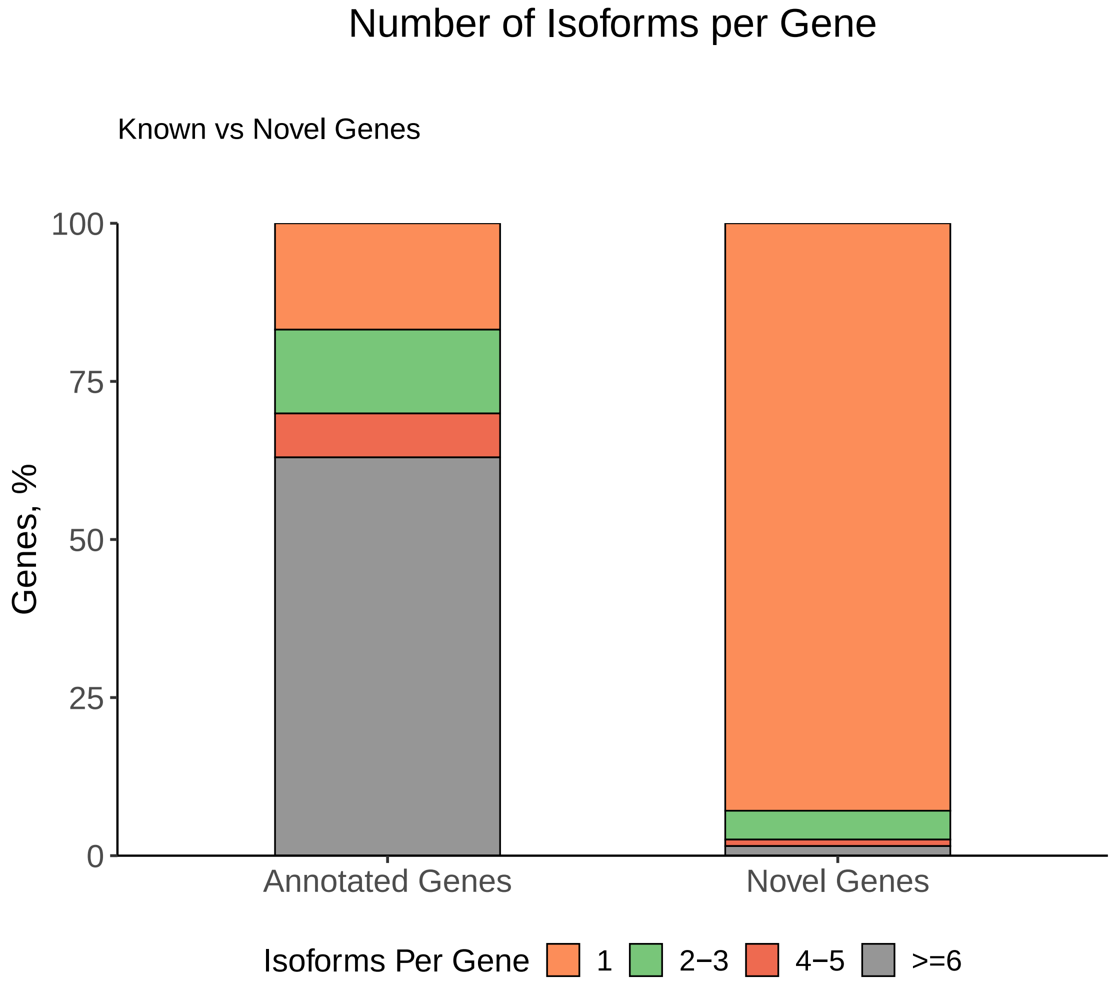
Category	Genes, count
Annotated Genes	19295
Novel Genes	2238

Splice Junction Classification

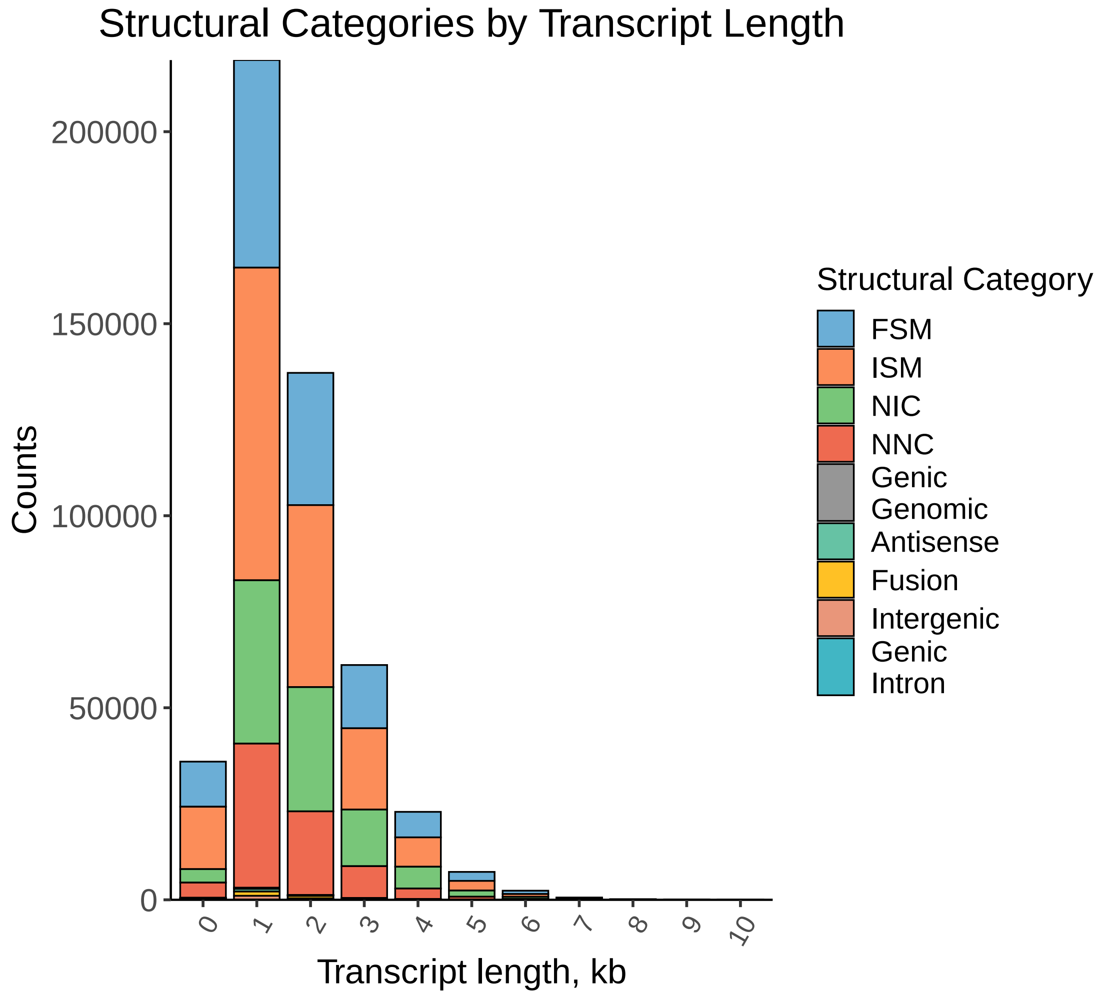
Category	SJs, count	Percent
Known canonical	182885	69.03
Known Non−canonical	81	0.03
Novel canonical	81983	30.94
Novel Non−canonical	0	0.00

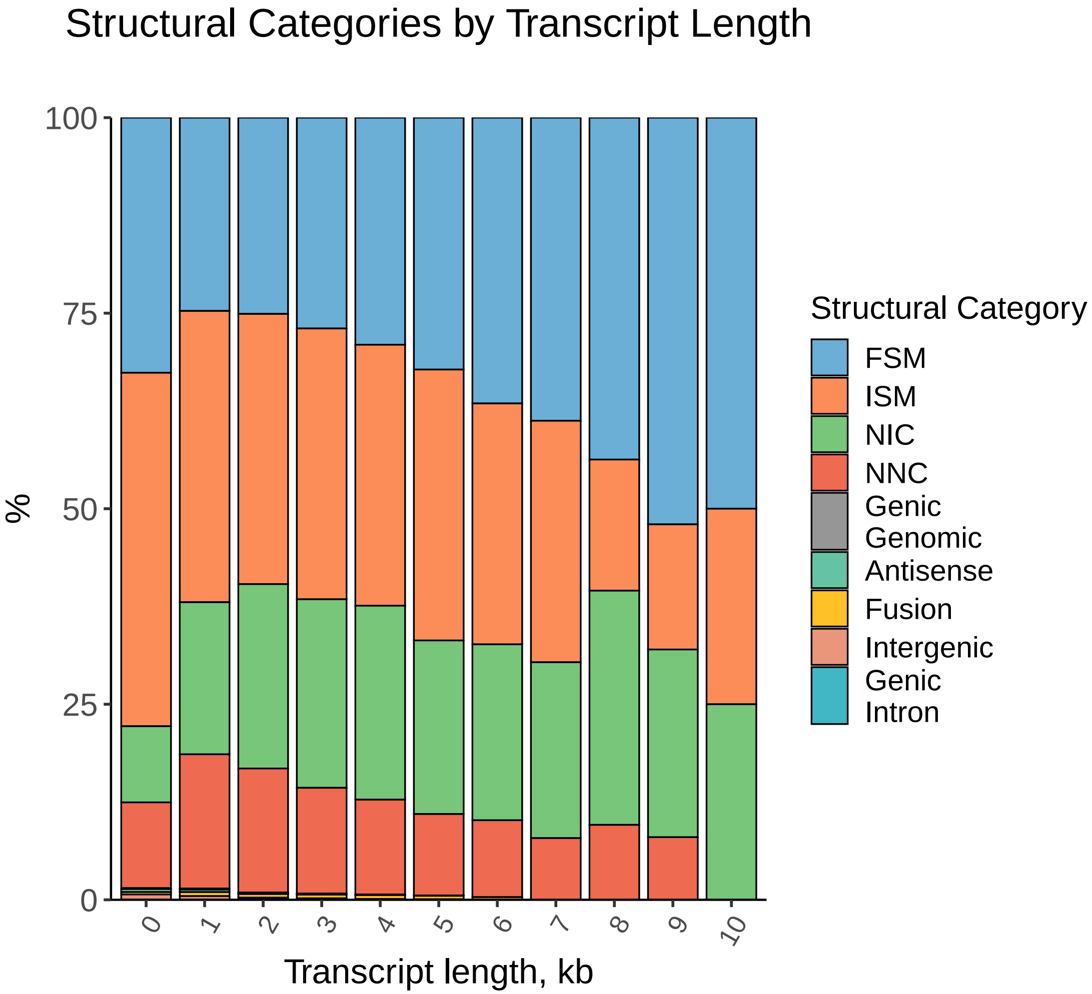
Gene Characterization

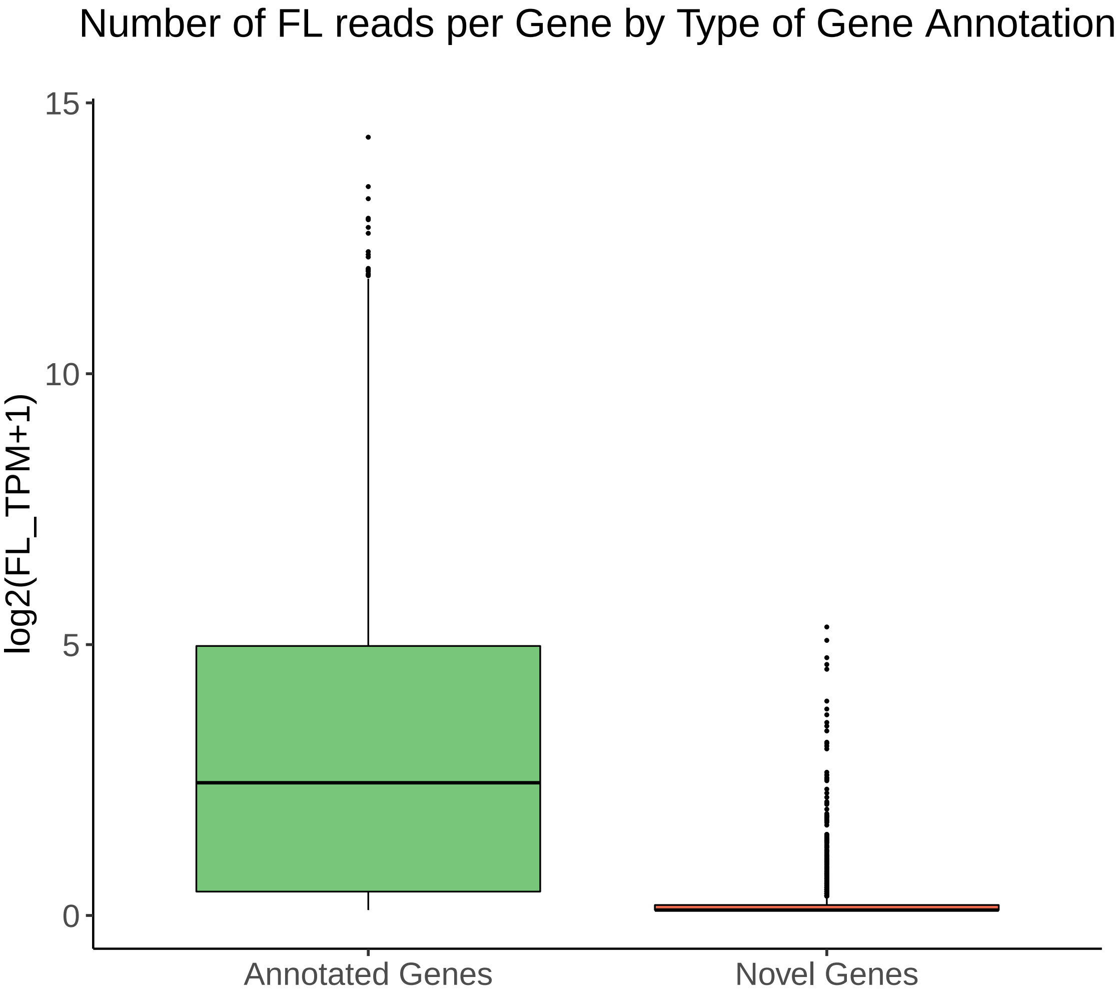

Number of Isoforms per Gene
Genes, %
0
10
20
30
40
50
1
2−3
4−5
>=6
Isoforms per gene

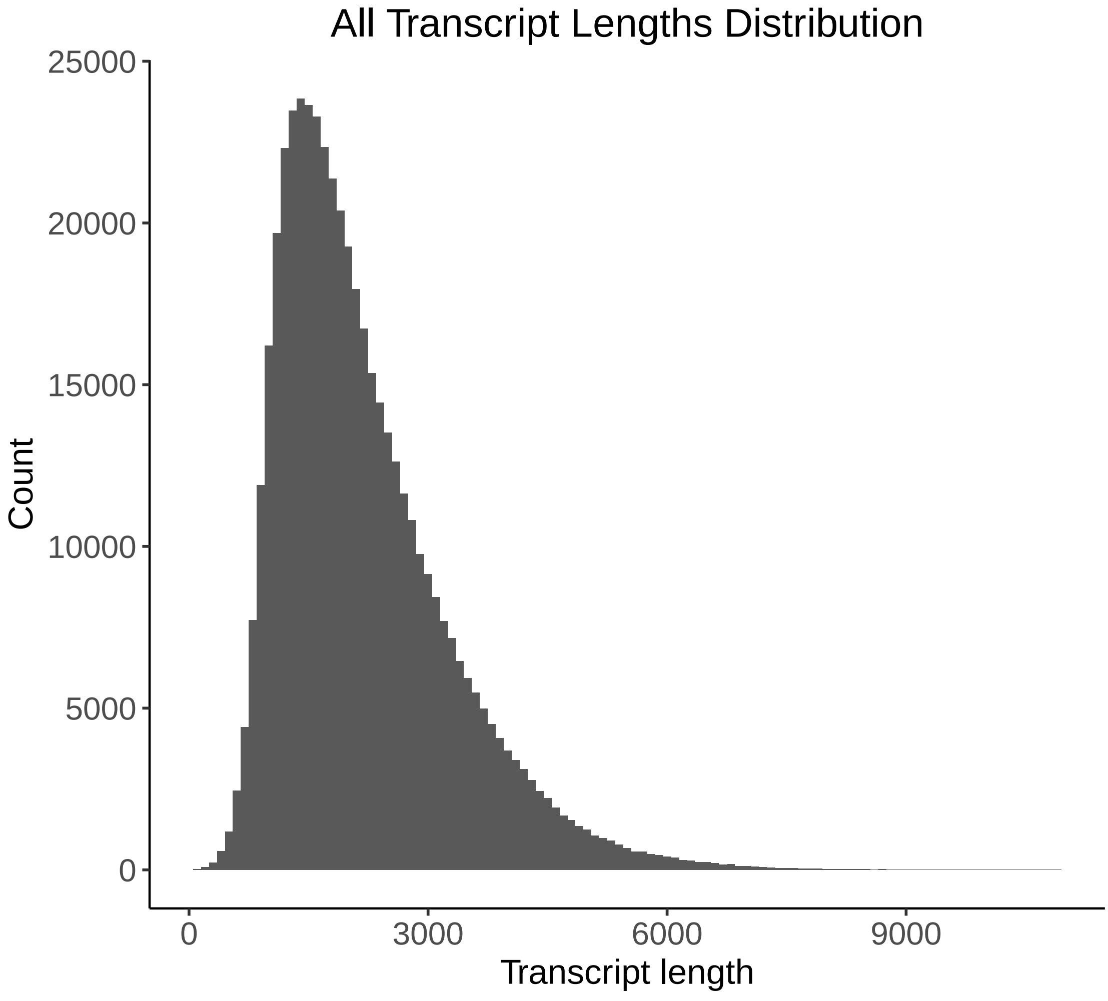

Number of Isoforms per Gene
Known vs Novel Genes
Genes, %
100
75
50
25
0
Annotated Genes
Novel Genes
Isoforms Per Gene
1
2−3
4−5
>=6

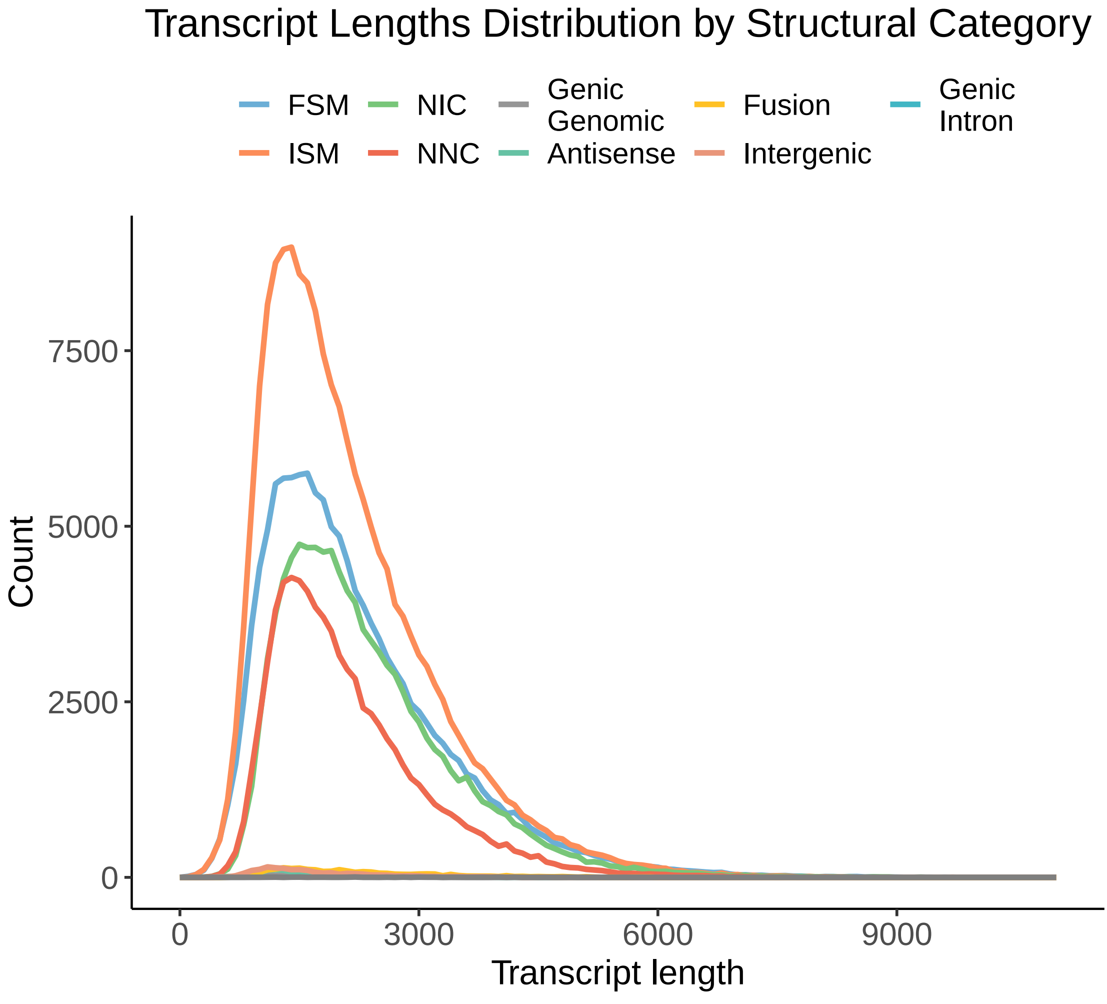

Distribution of Mono− vs Multi−Exon Transcripts
Transcripts, %
100
75
50
25
0
Novel Genes
Annotated Genes
Transcript type
Multi−Exon
Mono−Exon

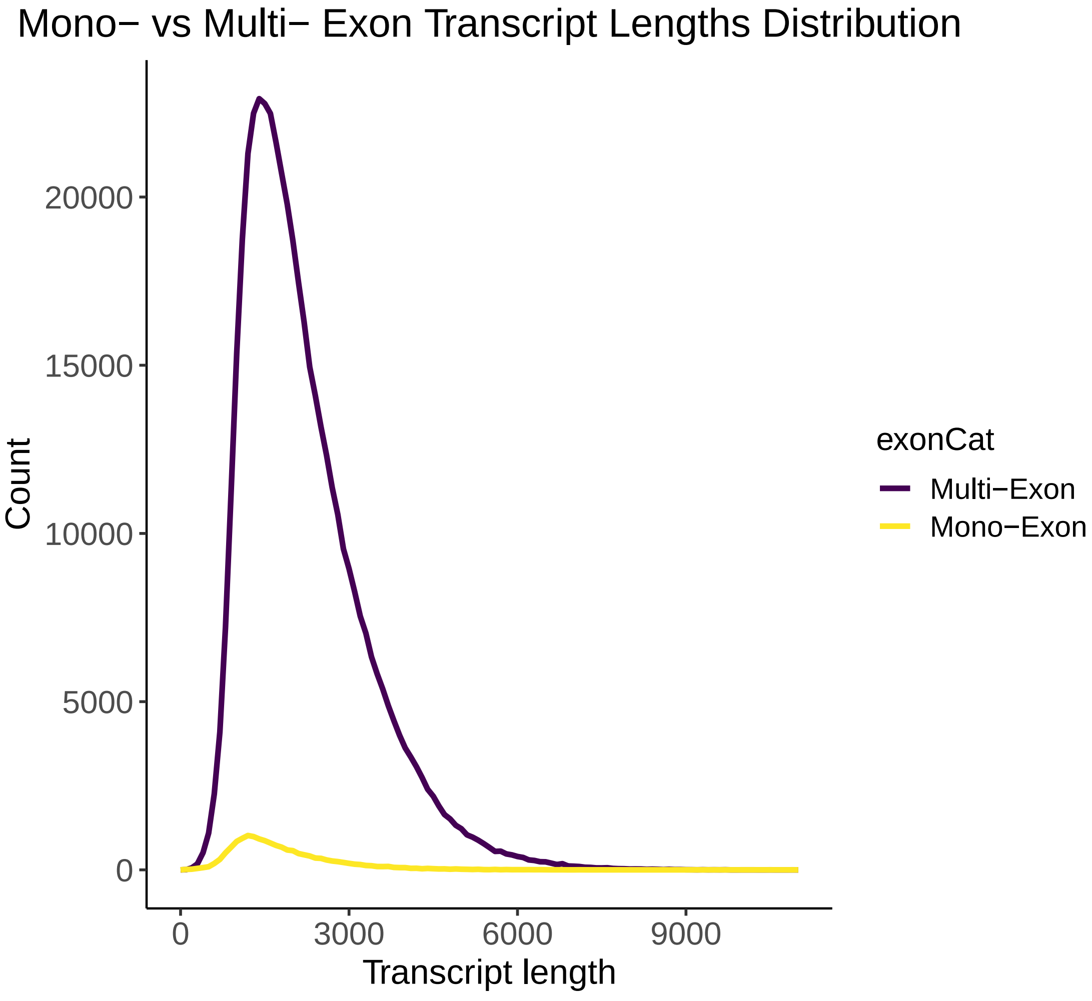

Structural Categories by Transcript Length
Counts
0
50000
100000
150000
200000
0
1
2
3
4
5
6
7
8
9
10
Transcript length, kb
Structural Category
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron

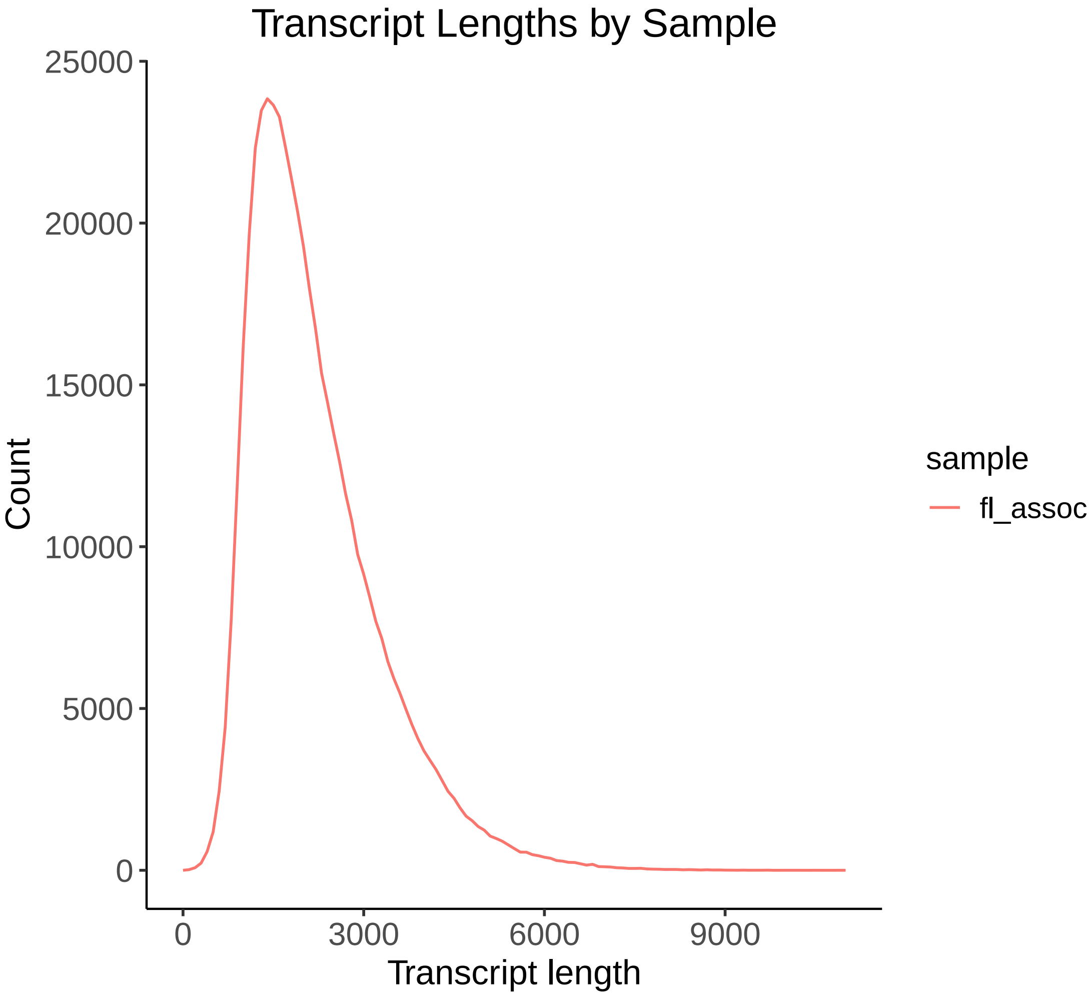

Structural Categories by Transcript Length
%
100
75
50
25
0
0
1
2
3
4
5
6
7
8
9
10
Transcript length, kb
Structural Category
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron

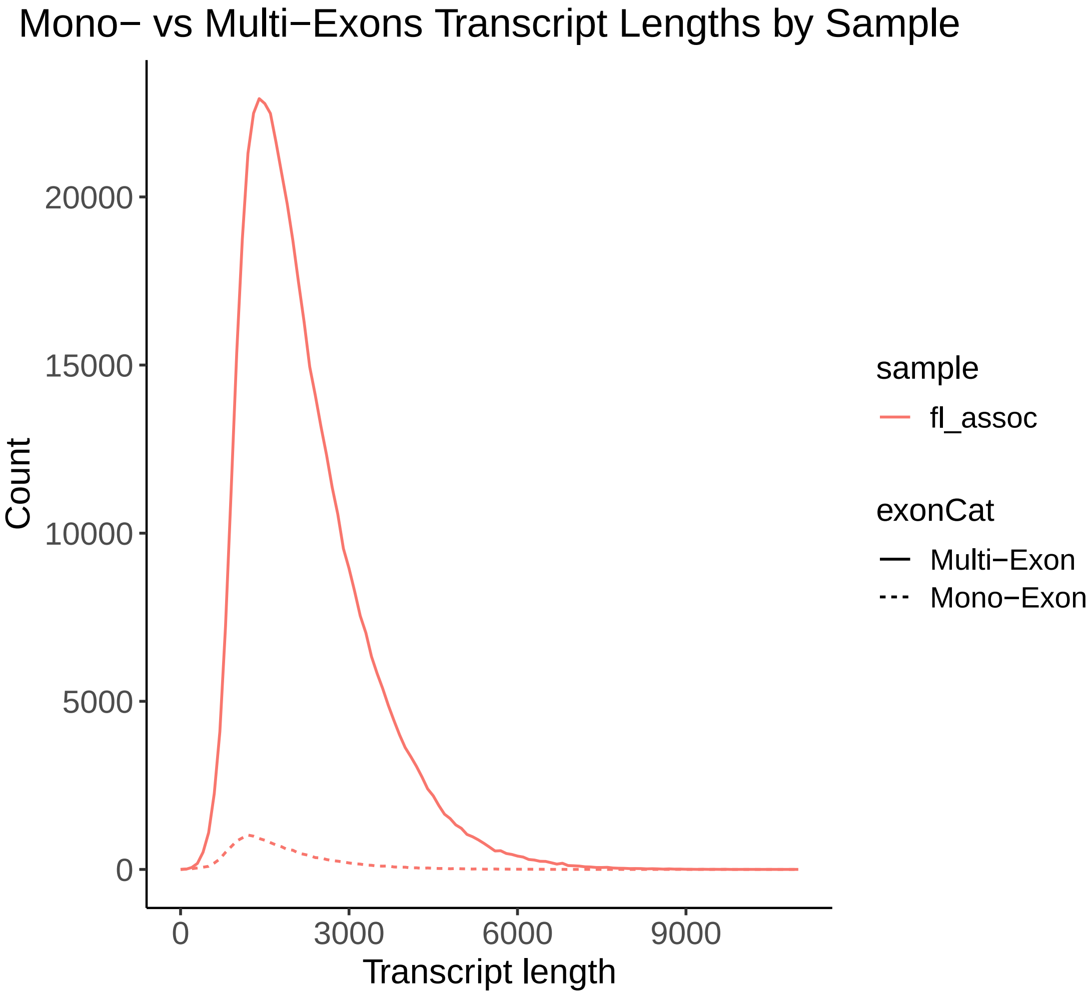

Number of FL reads per Gene by Type of Gene Annotation
log2(FL_TPM+1)
15
10
5
0
Annotated Genes
Novel Genes


All Transcript Lengths Distribution
25000
20000
15000
10000
5000
0
Count
0
3000
6000
9000
Transcript length

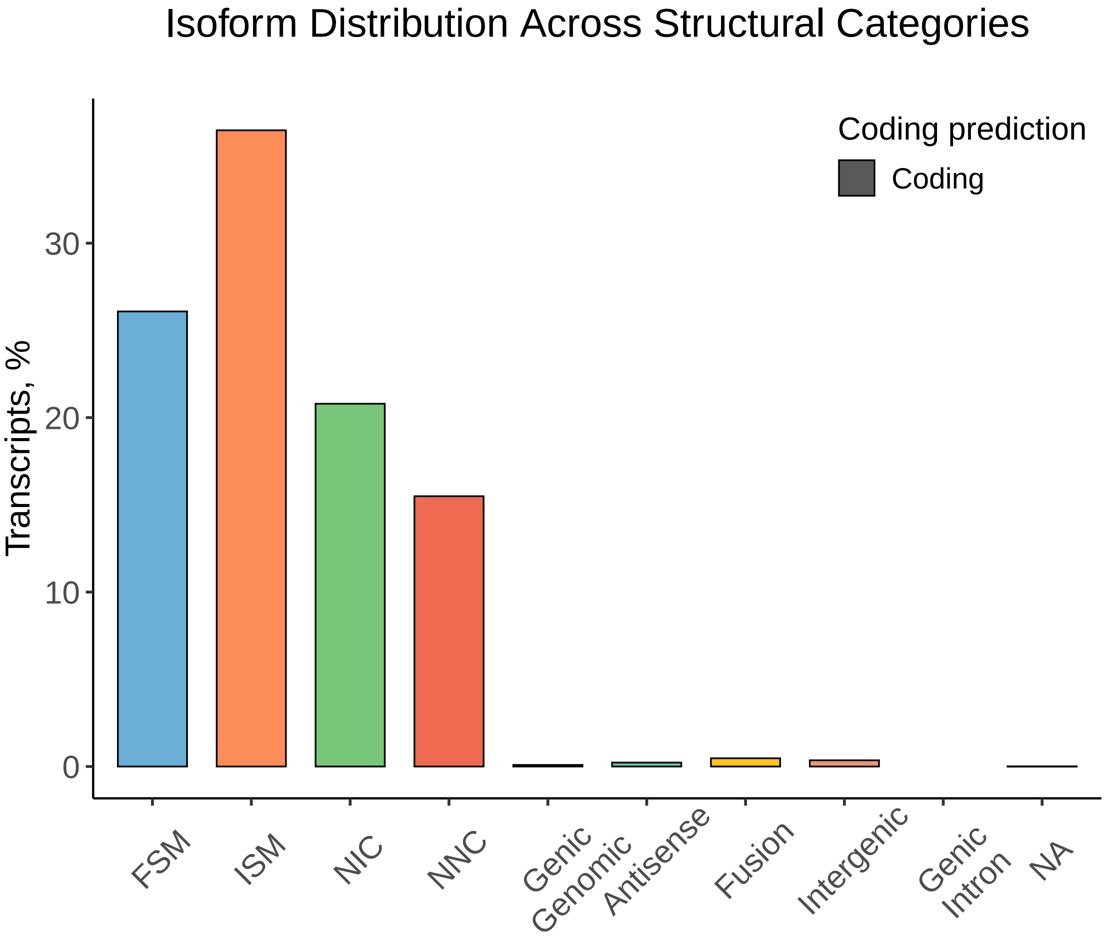

Transcript Lengths Distribution by Structural Category
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron
Count
7500
5000
2500
0
0
3000
6000
9000
Transcript length


Mono− vs Multi− Exon Transcript Lengths Distribution
Count
20000
15000
10000
5000
0
0
3000
6000
9000
Transcript length
exonCat
Multi−Exon
Mono−Exon

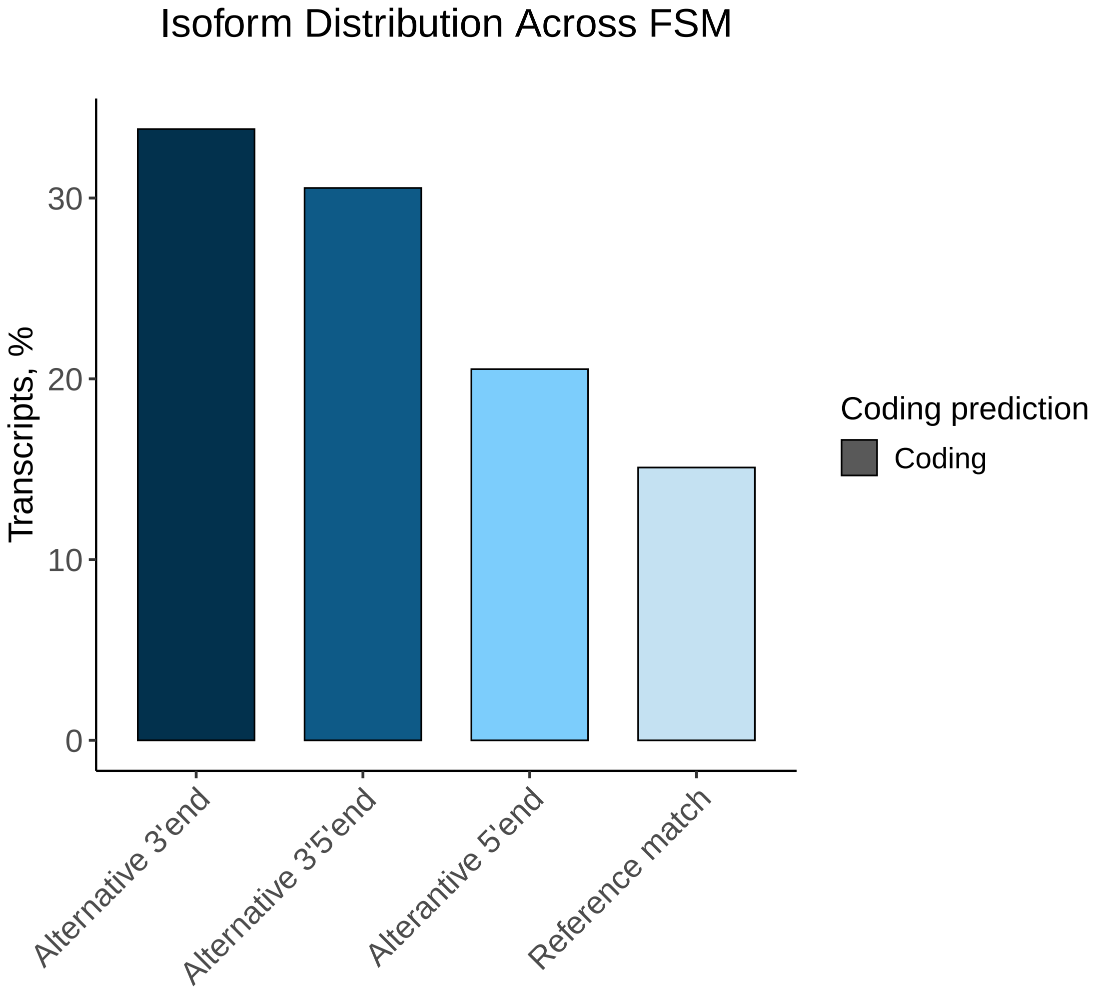

Transcript Lengths by Sample
Count
25000
20000
15000
10000
5000
0
0
3000
6000
9000
Transcript length
sample
fl_assoc

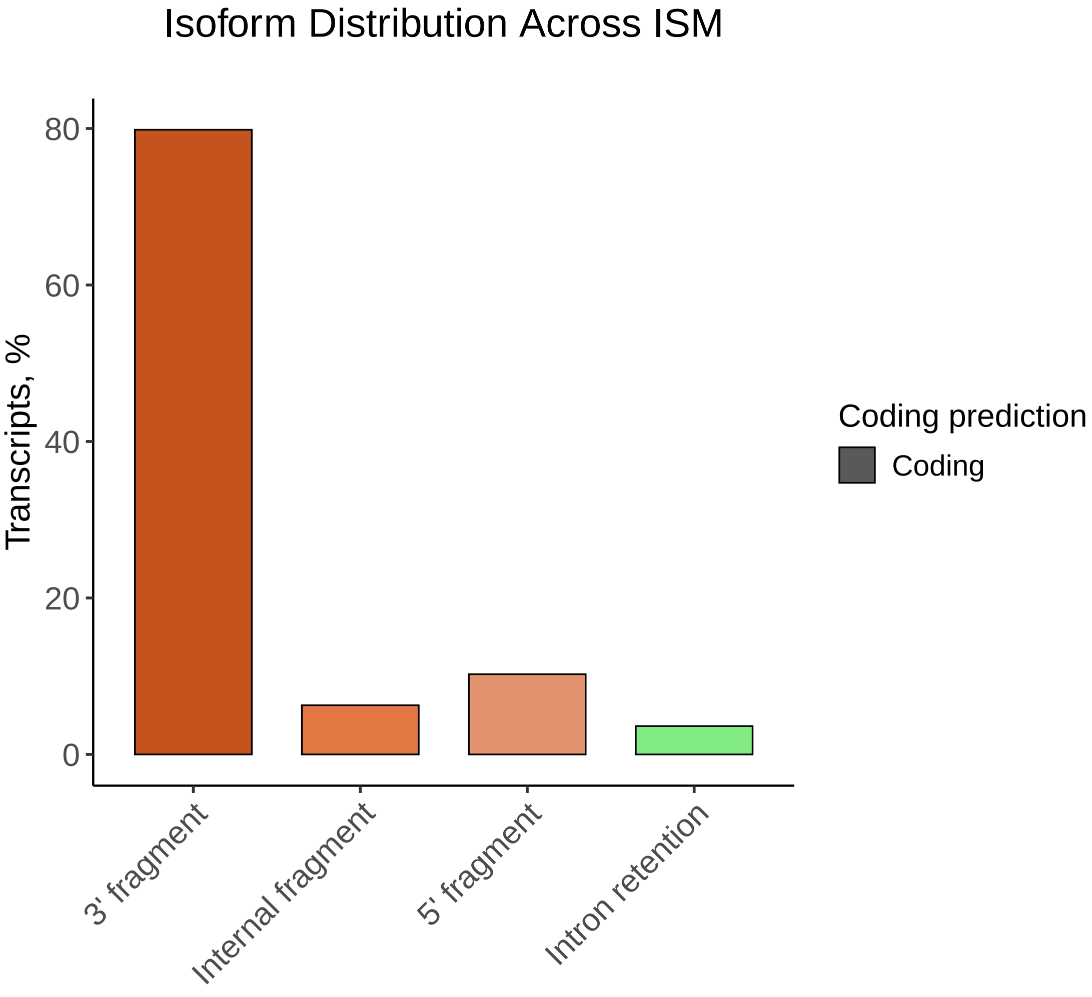

Mono− vs Multi−Exons Transcript Lengths by Sample
Count
20000
15000
10000
5000
0
0
3000
6000
9000
Transcript length
sample
fl_assoc
exonCat
Multi−Exon
Mono−Exon

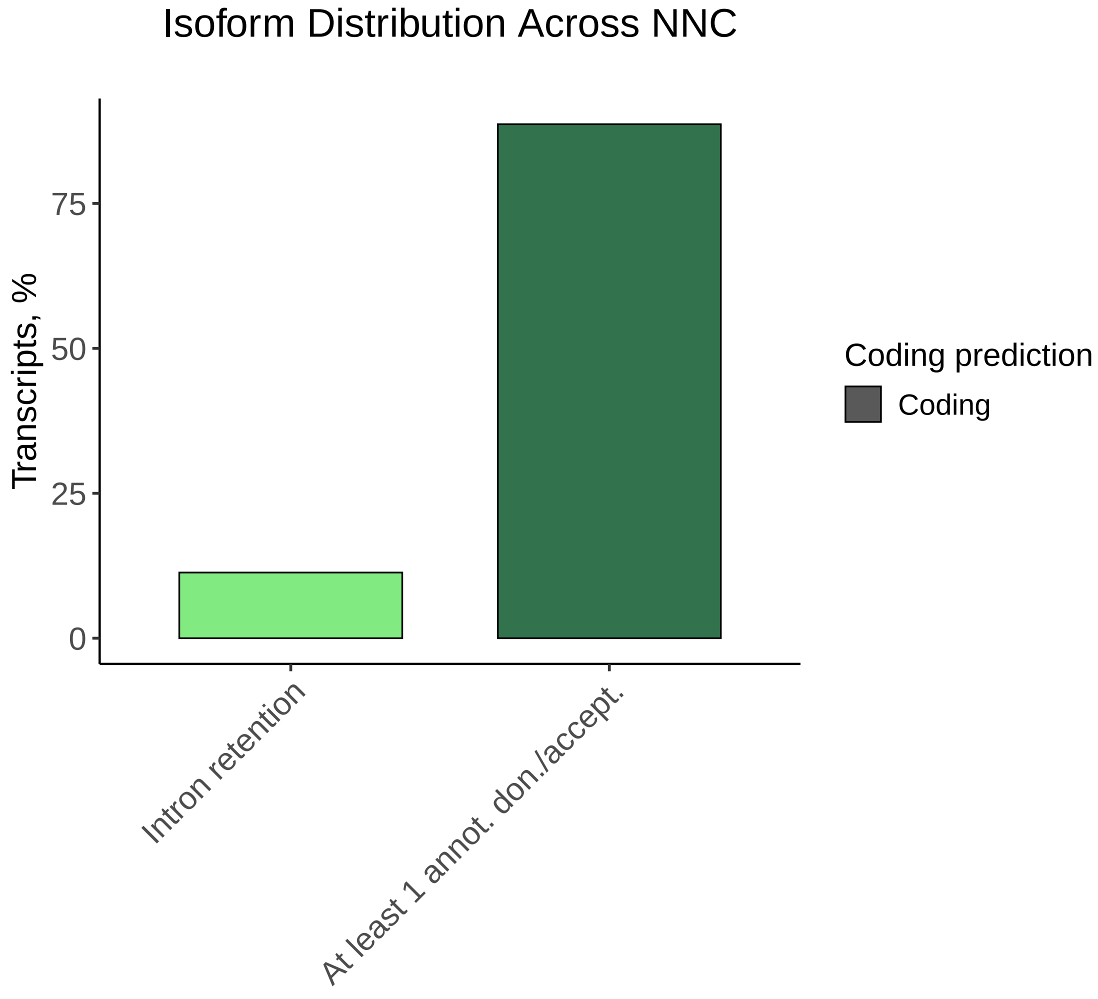
Structural Isoform Characterization



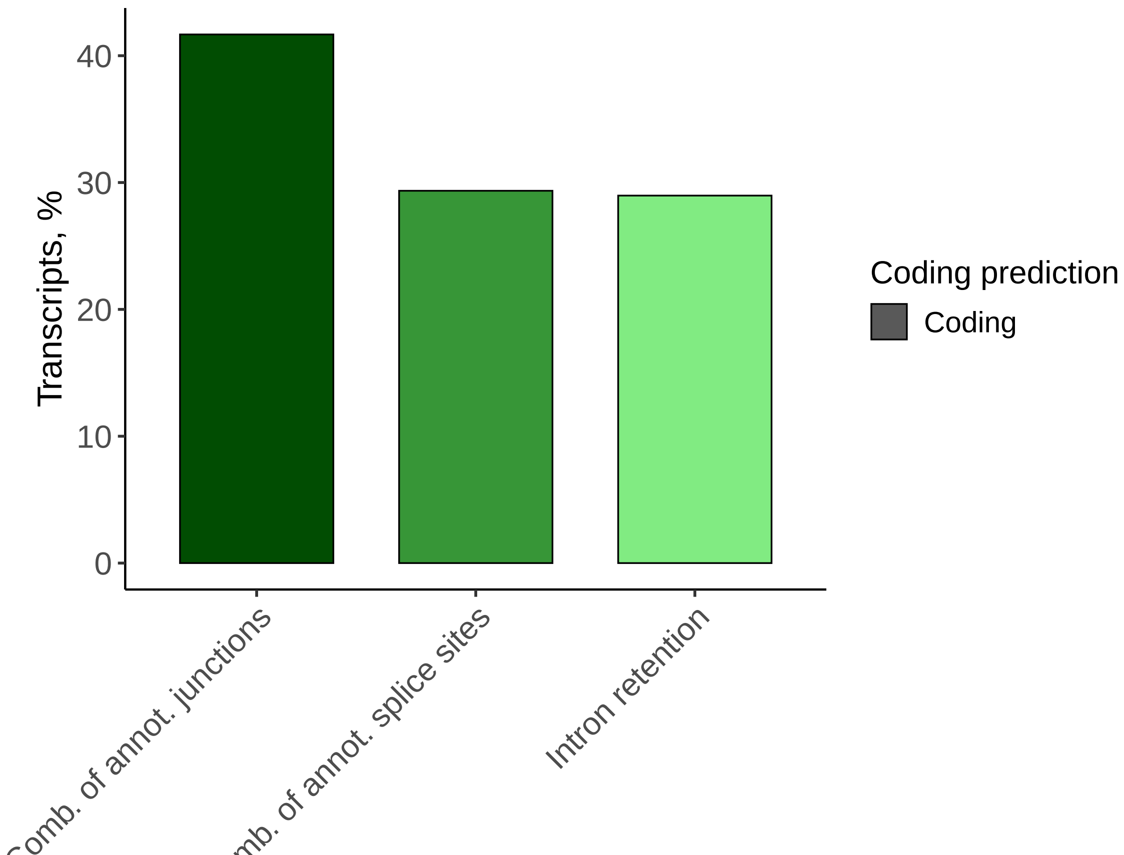
Isoform Distribution Across Structural Categories
Coding prediction
Coding
Transcripts, %
0
10
20
30
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron
NA

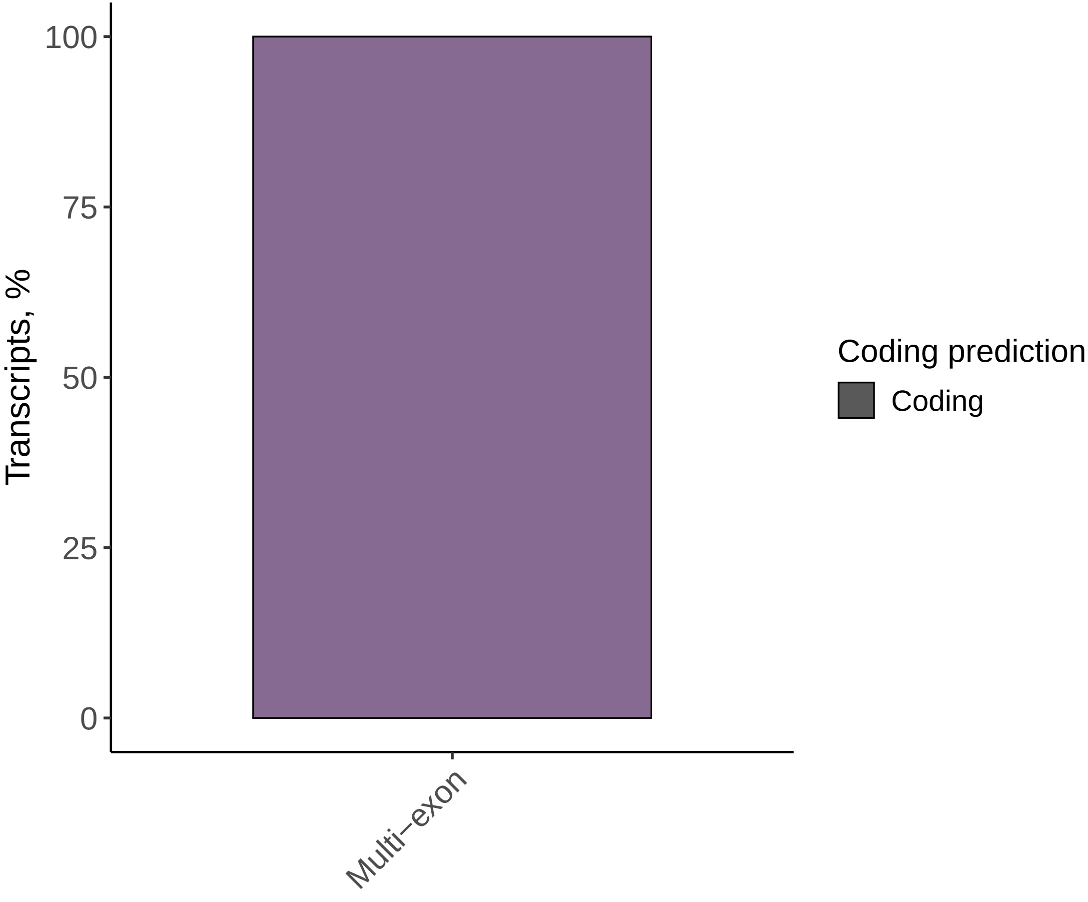

Isoform Distribution Across FSM
Transcripts, %
0
10
20
30
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
Coding prediction
Coding


Isoform Distribution Across ISM
Transcripts, %
80
60
40
20
0
3' fragment
Internal fragment
5' fragment
Intron retention
Coding prediction
Coding

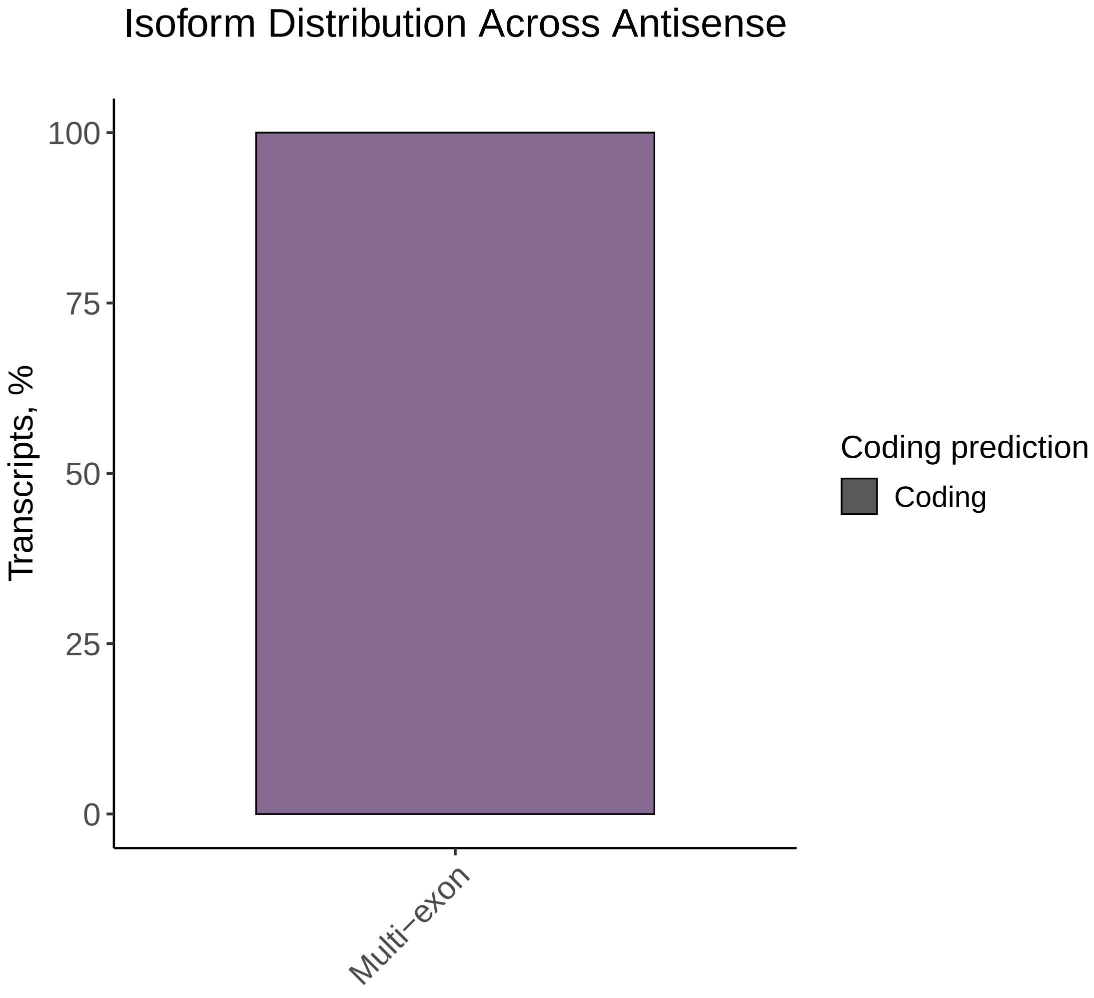

Isoform Distribution Across NNC
Transcripts, %
0
25
50
75
Intron retention
At least 1 annot. don./accept.
Coding prediction
Coding

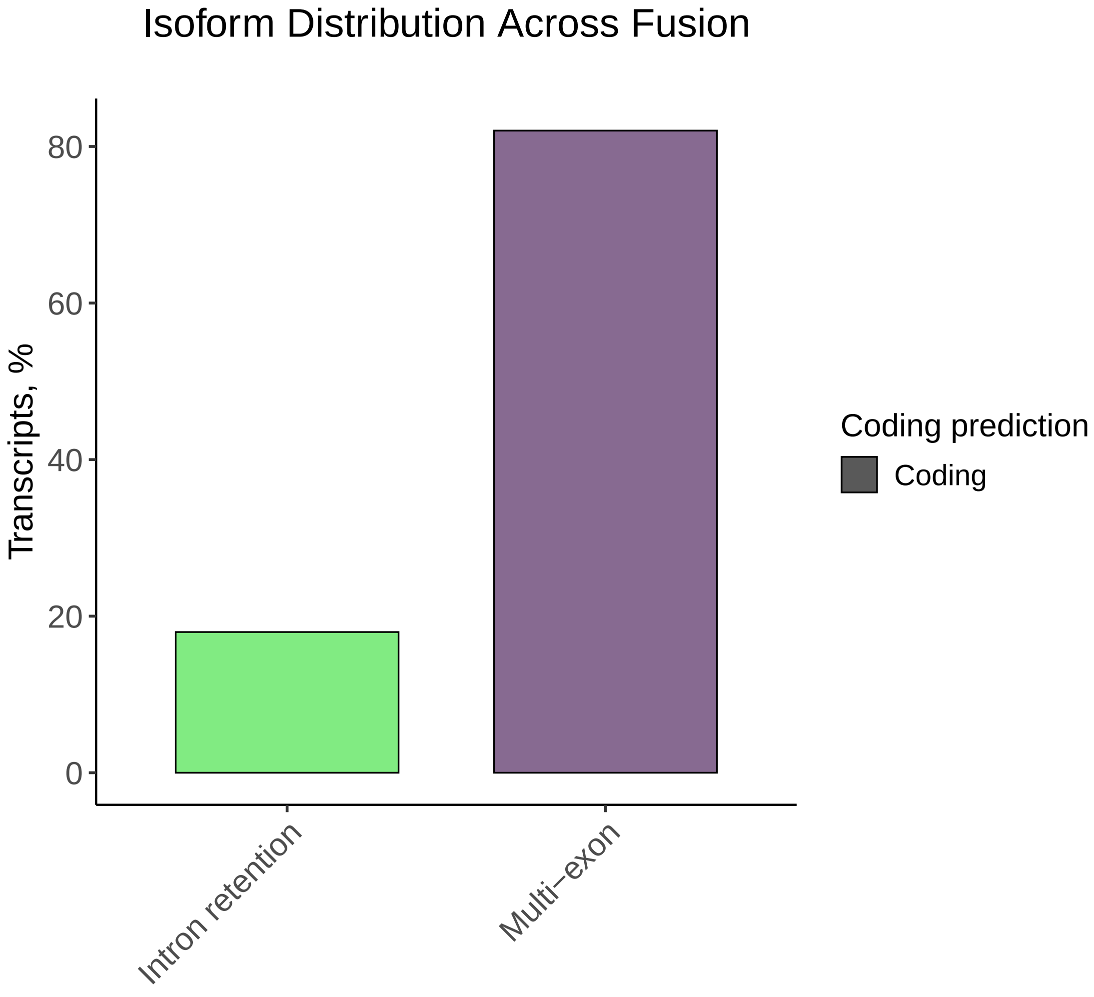
Isoform Distribution Across NIC

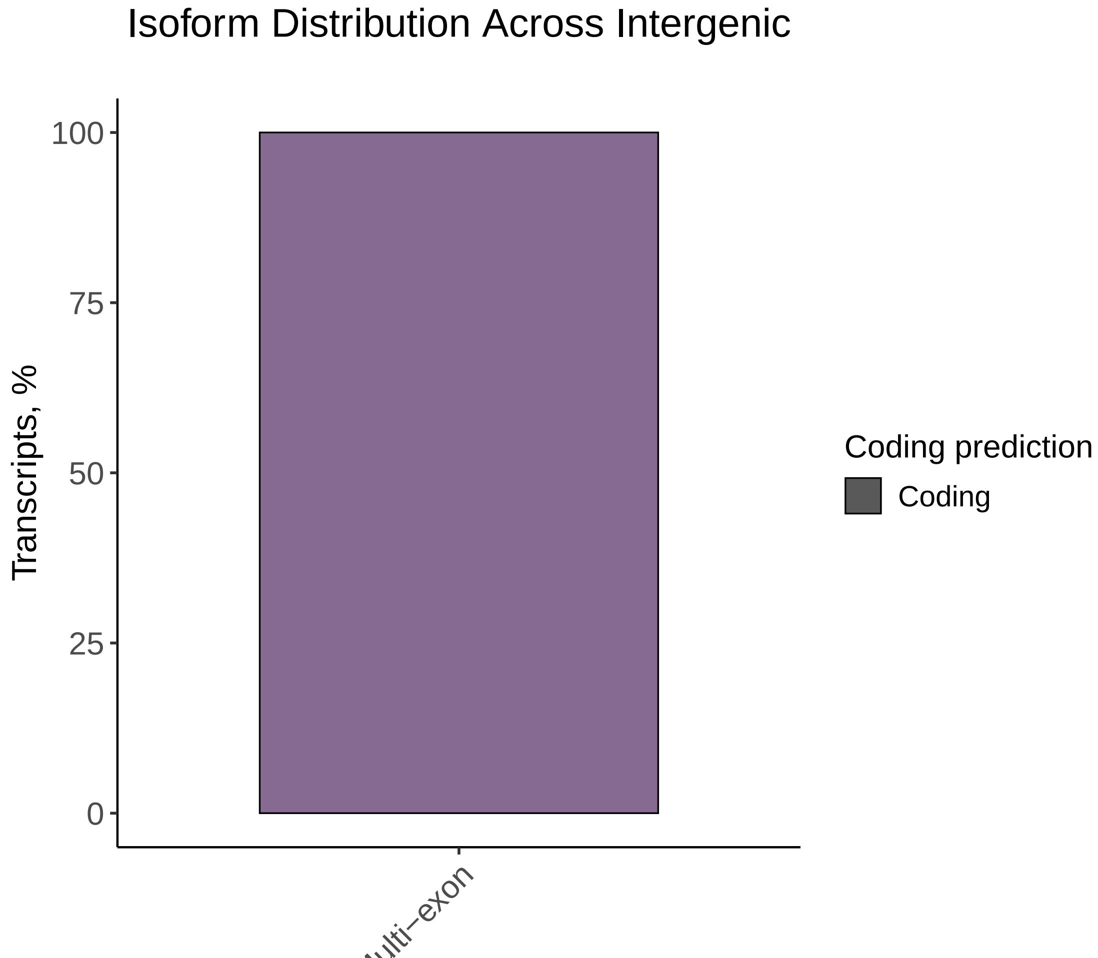


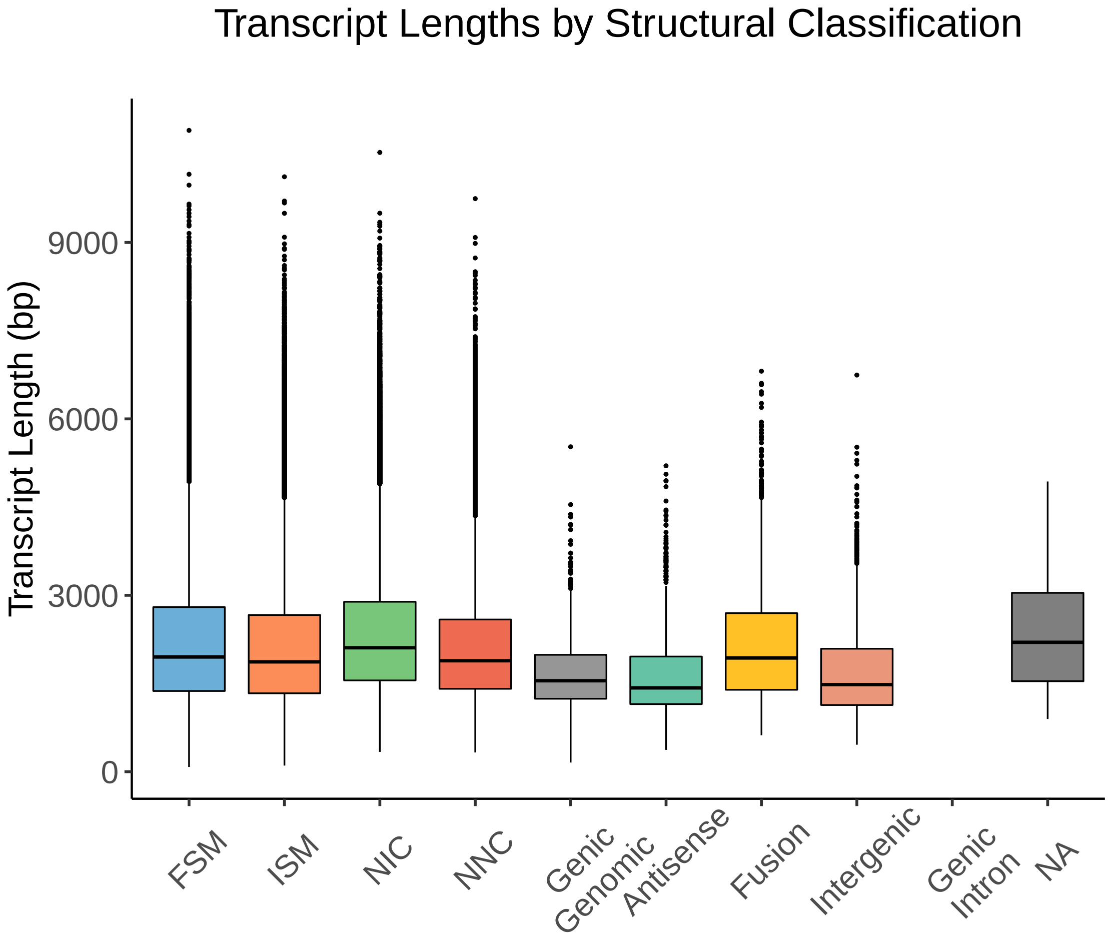


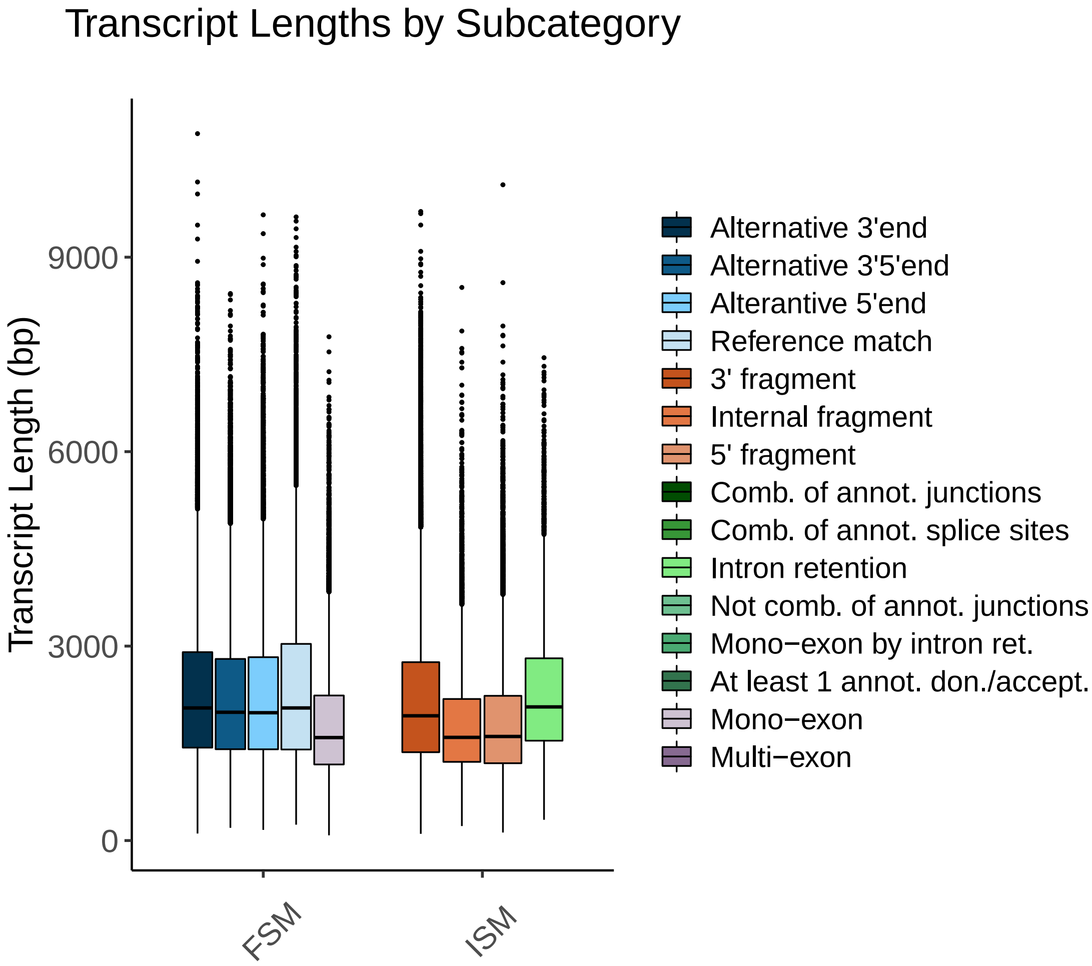
Isoform Distribution Across Genic Genomic

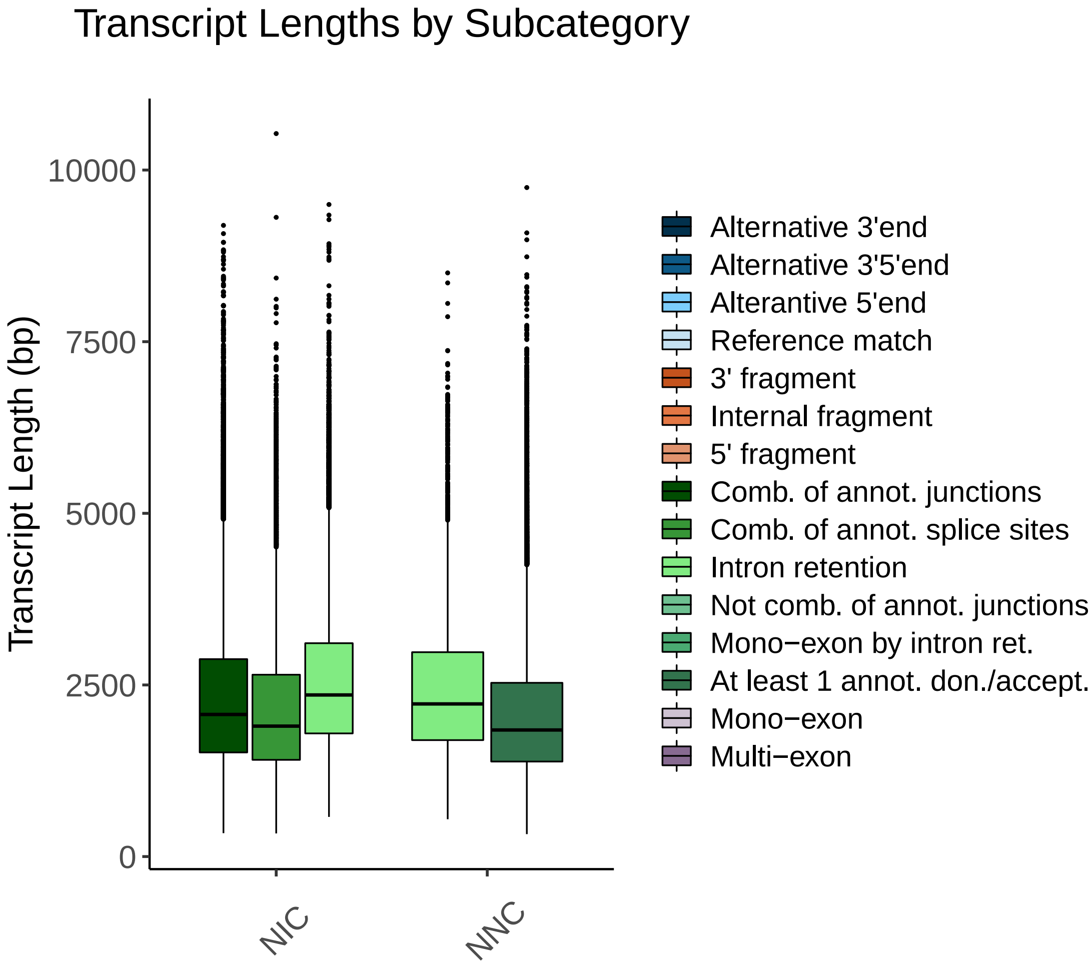

Isoform Distribution Across Antisense
Transcripts, %
100
75
50
25
0
Multi–exon
Coding prediction
Coding

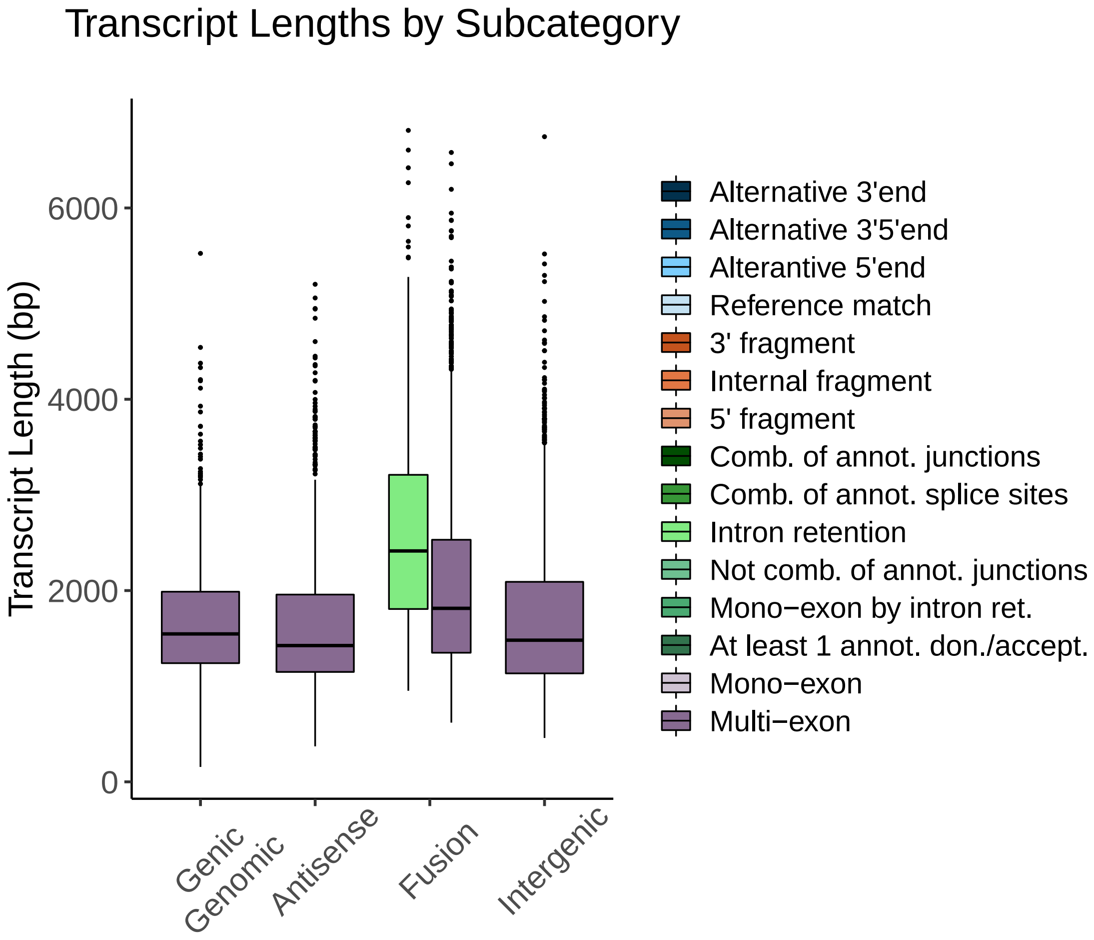

Isoform Distribution Across Fusion
Transcripts, %
0
20
40
60
80
Intron retention
Multi−exon
Coding prediction
Coding

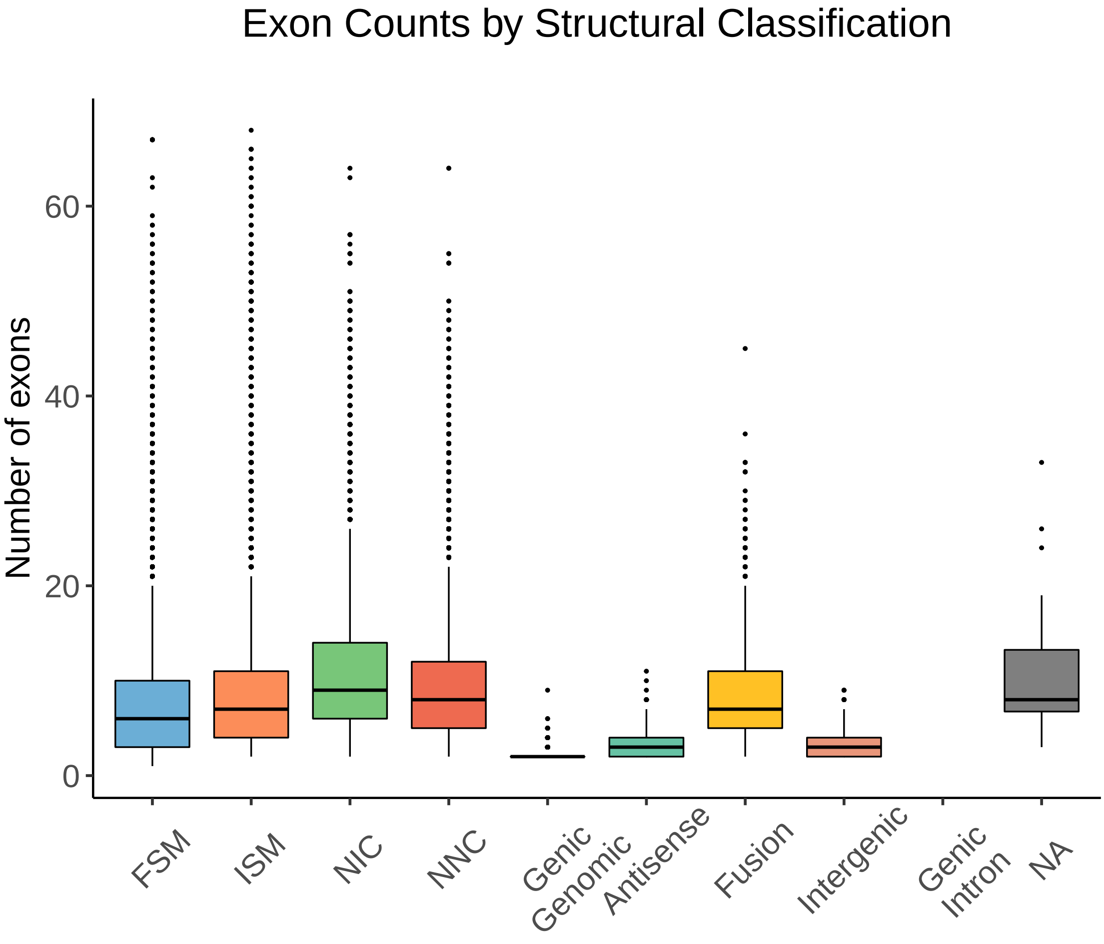

Isoform Distribution Across Intergenic
Transcripts, %
100
75
50
25
0
Multi−exon
Coding prediction
Coding

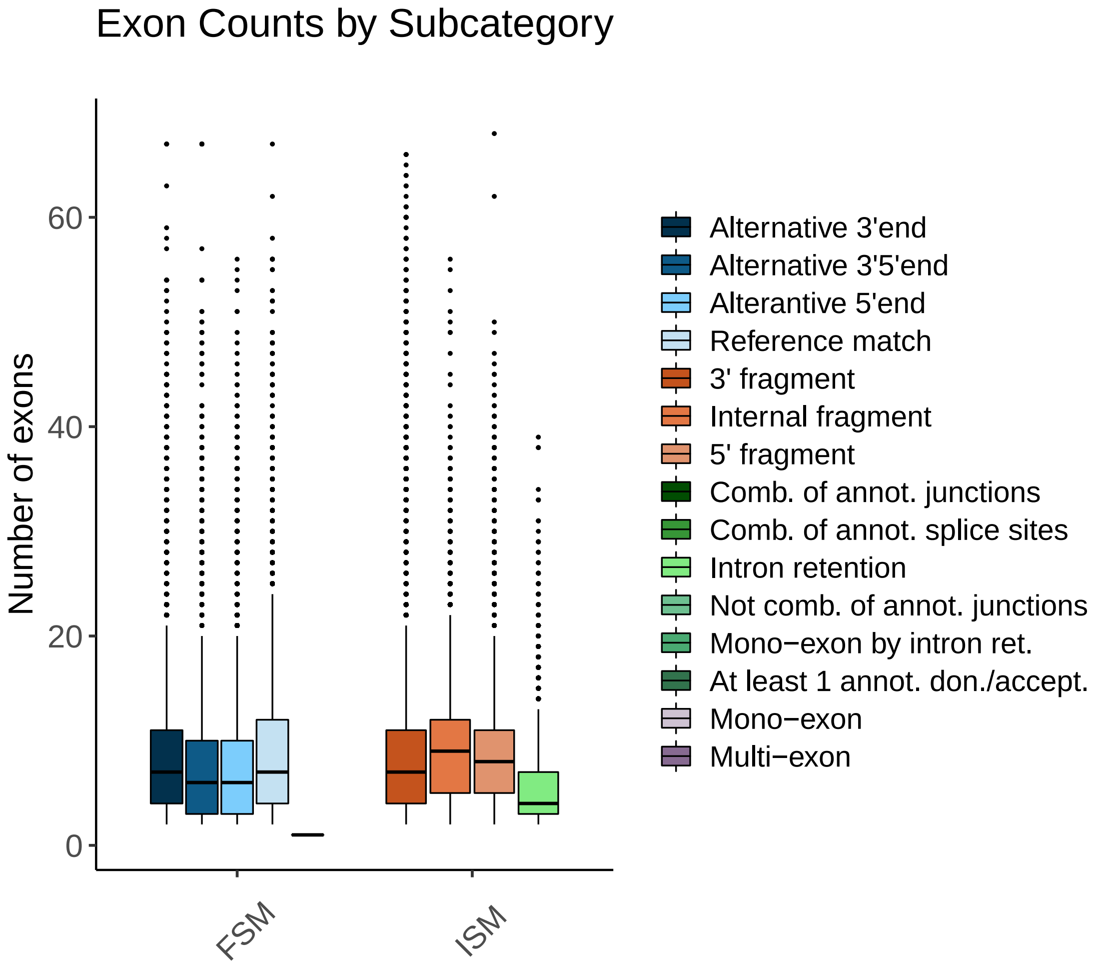

Transcript Lengths by Structural Classification
Transcript Length (bp)
0
3000
6000
9000
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron
NA

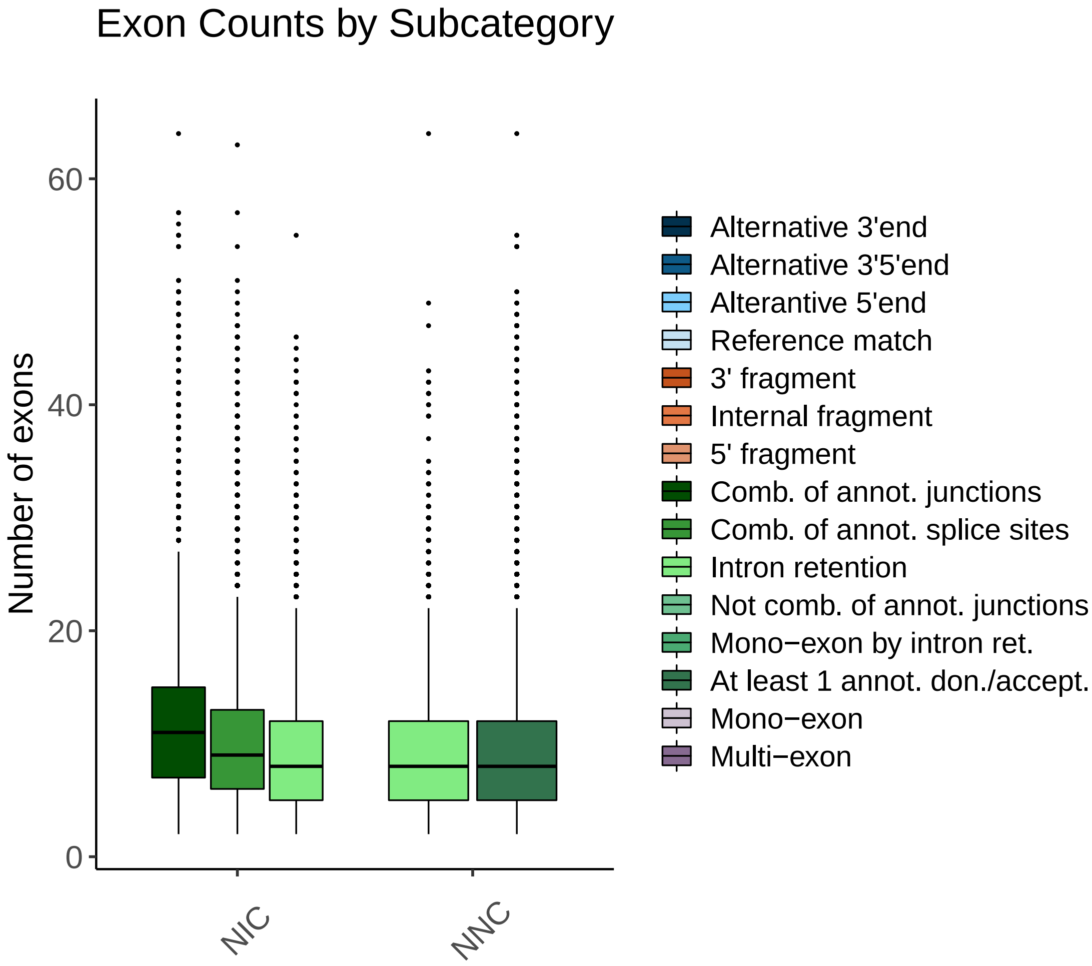

Transcript Lengths by Subcategory
Transcript Length (bp)
9000
6000
3000
0
FSM
ISM
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon

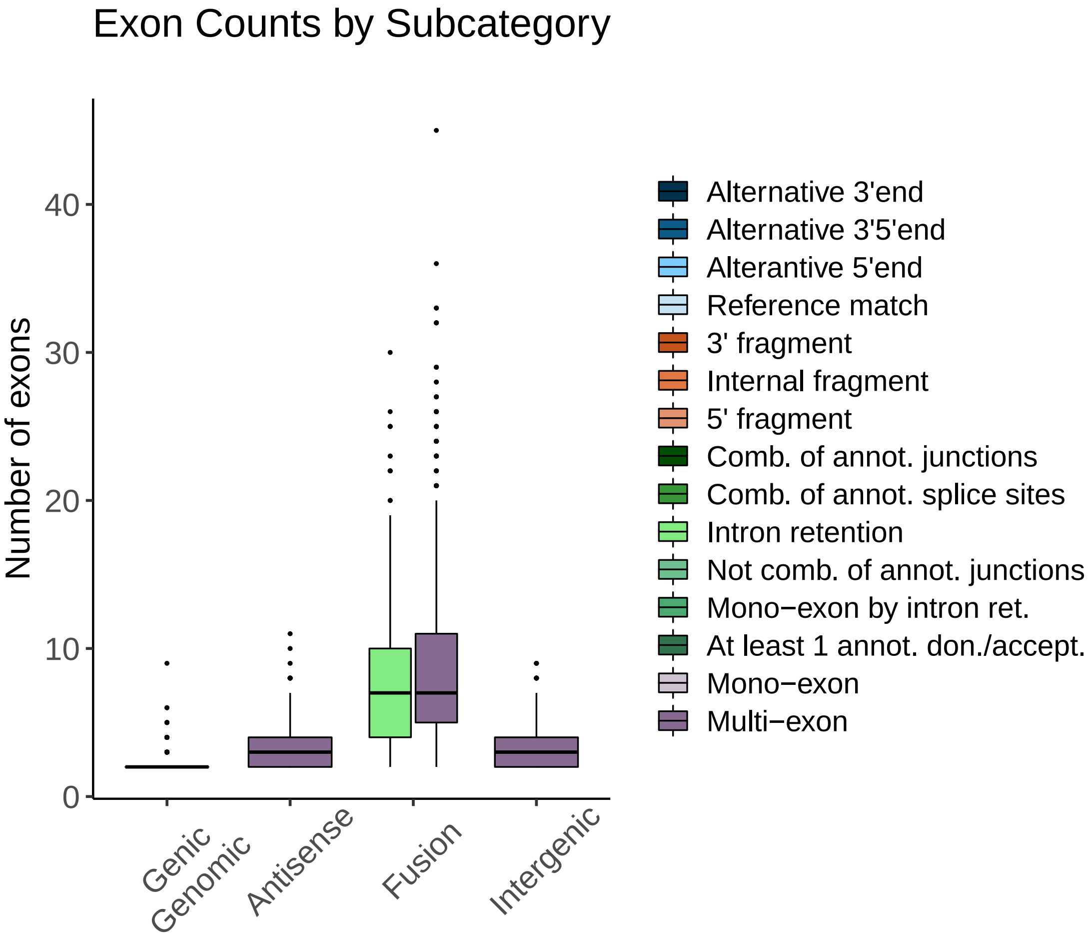

Transcript Lengths by Subcategory
Transcript Length (bp)
10000
7500
5000
2500
0
NIC
NNC
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon

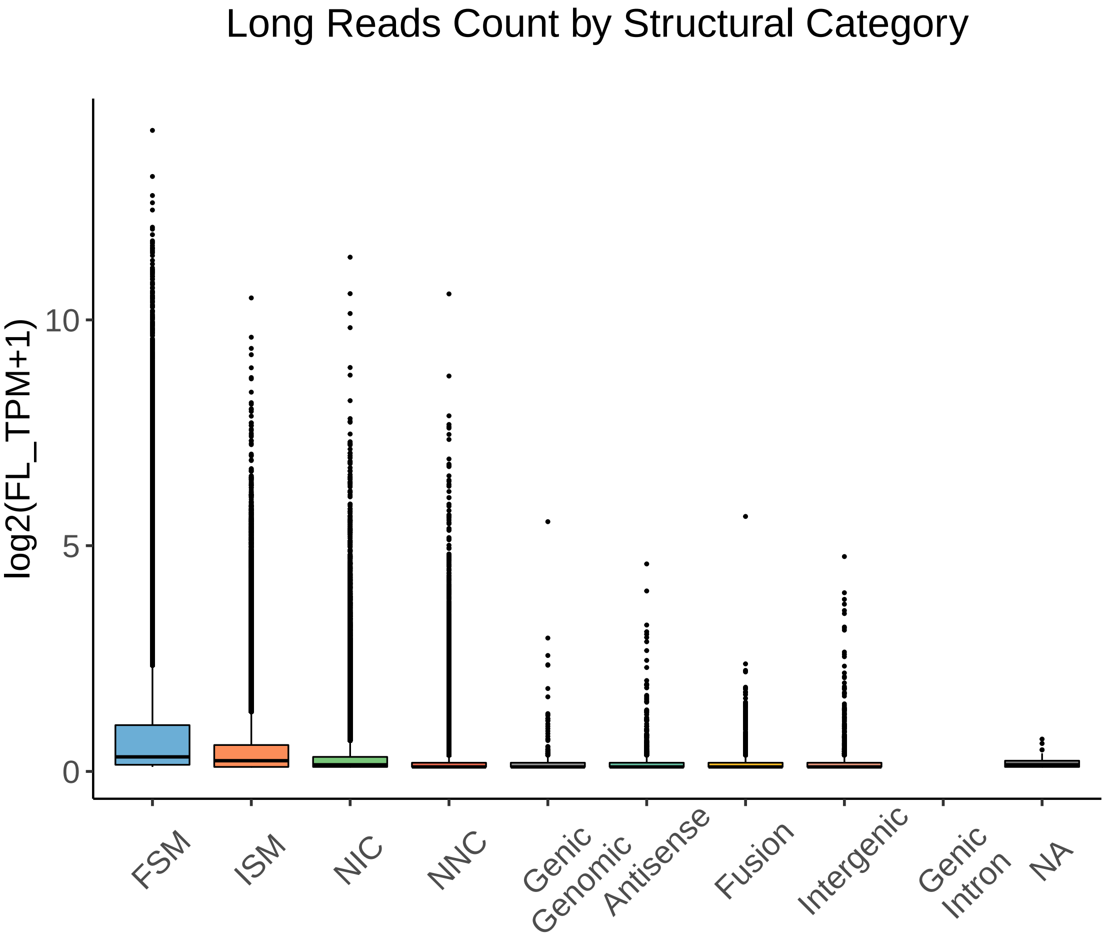

Transcript Lengths by Subcategory
Transcript Length (bp)
0
2000
4000
6000
Genic Genomic
Antisense
Fusion
Intergenic
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon


Exon Counts by Structural Classification
Number of exons
0
20
40
60
FSM
ISM
NIC
NNC
Genic
Genomic
Antisense
Fusion
Intergenic
Genic
Intron
NA


Exon Counts by Subcategory
Number of exons
0
20
40
60
FSM
ISM
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon

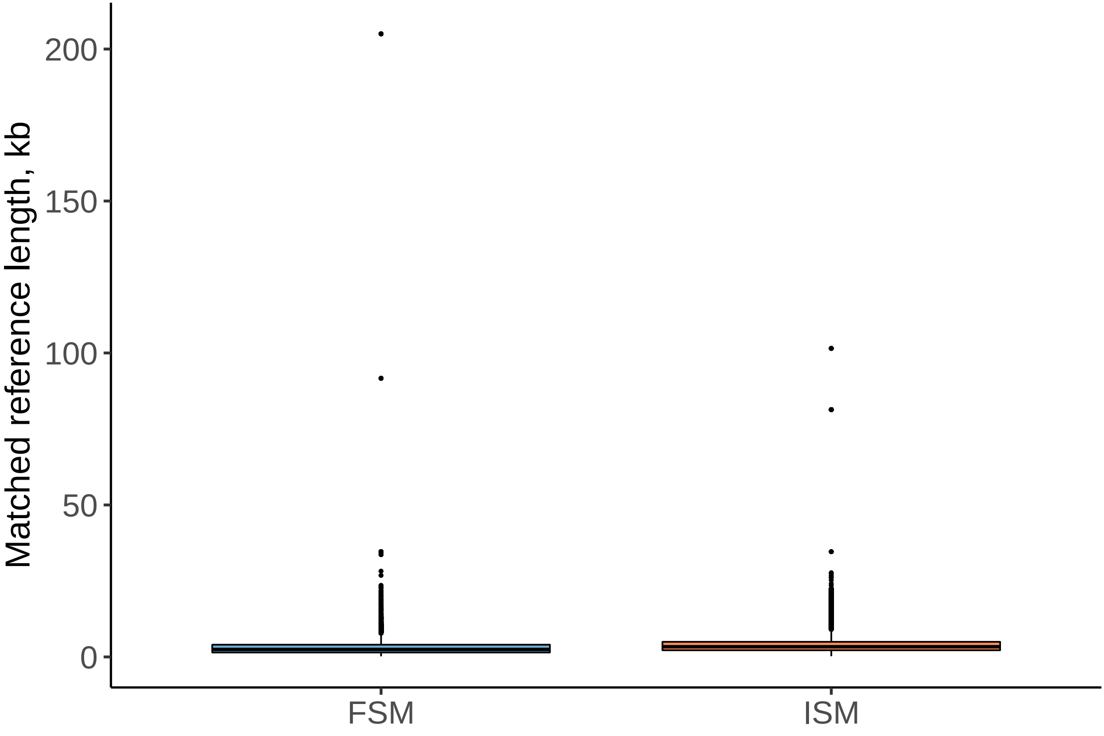

Exon Counts by Subcategory
Number of exons
0
20
40
60
NIC
NNC
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon

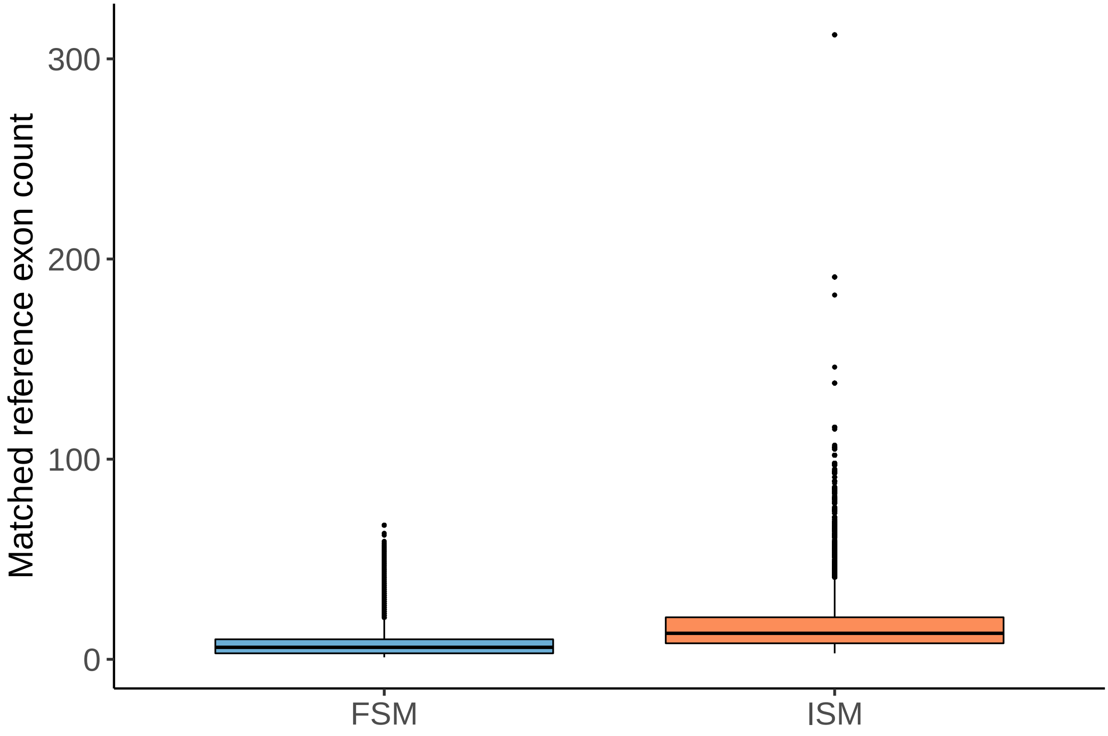

Exon Counts by Subcategory
Number of exons
0
10
20
30
40
Genic
Genomic
Antisense
Fusion
Intergenic
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon


Long Reads Count by Structural Category
log2(FL_TPM+1)
10
5
0
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron
NA

Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

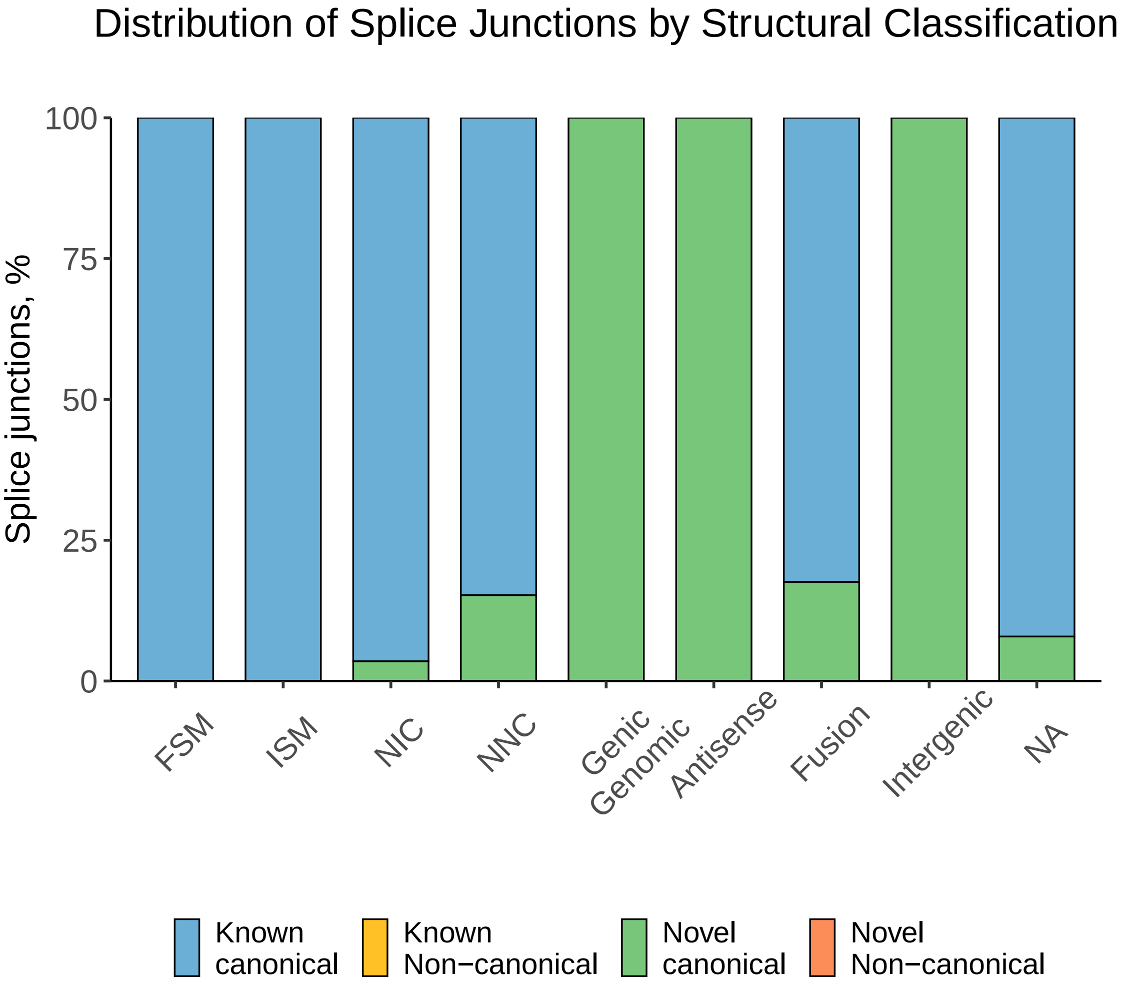


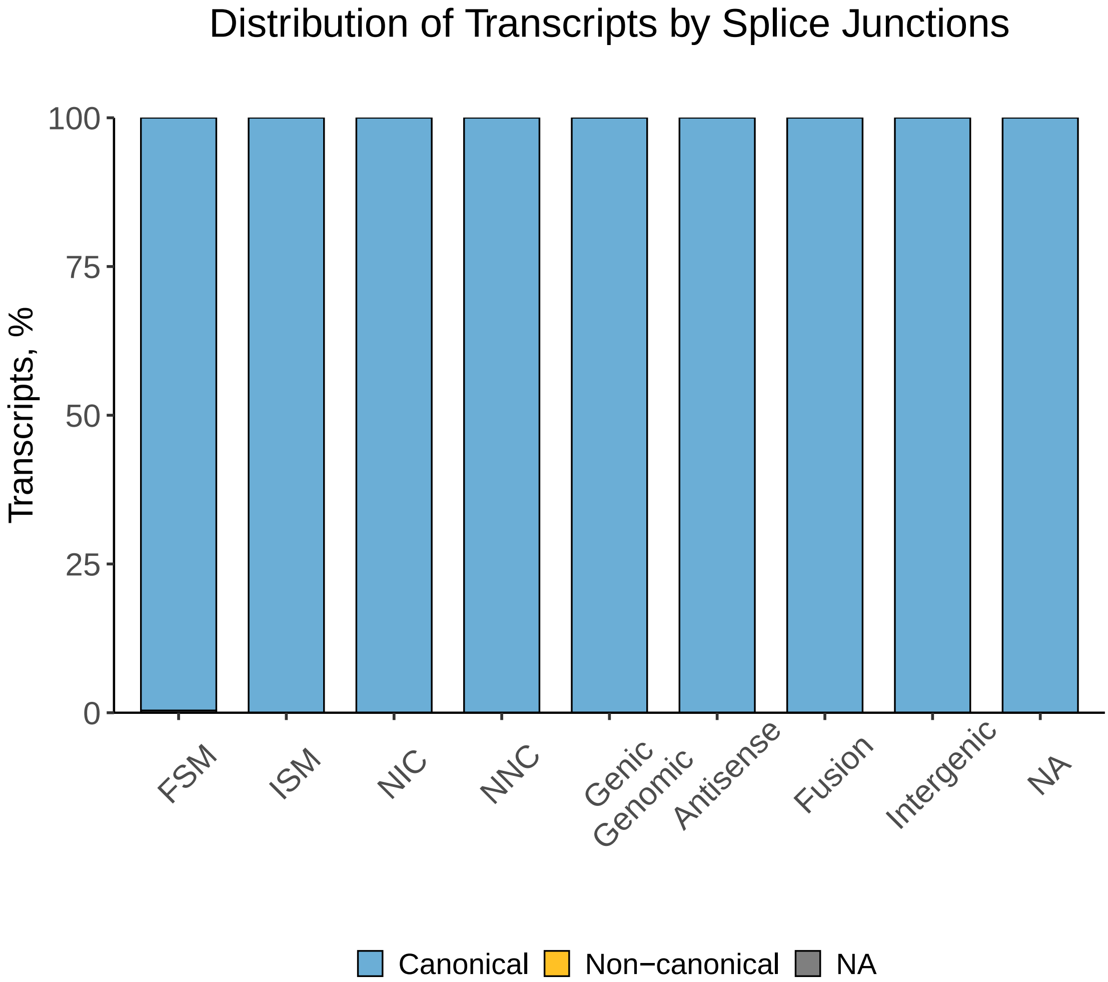


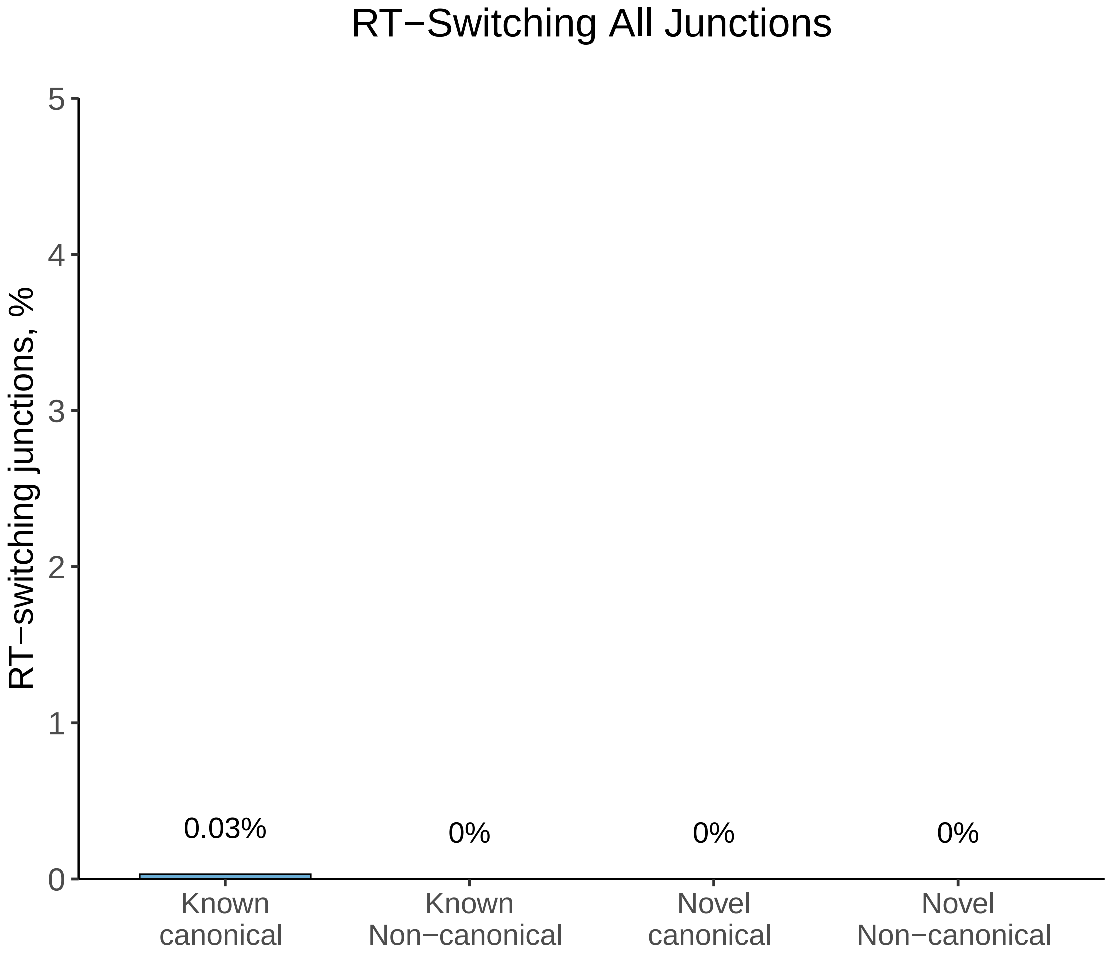
Exon Count Distribution of Matched Reference Transcripts

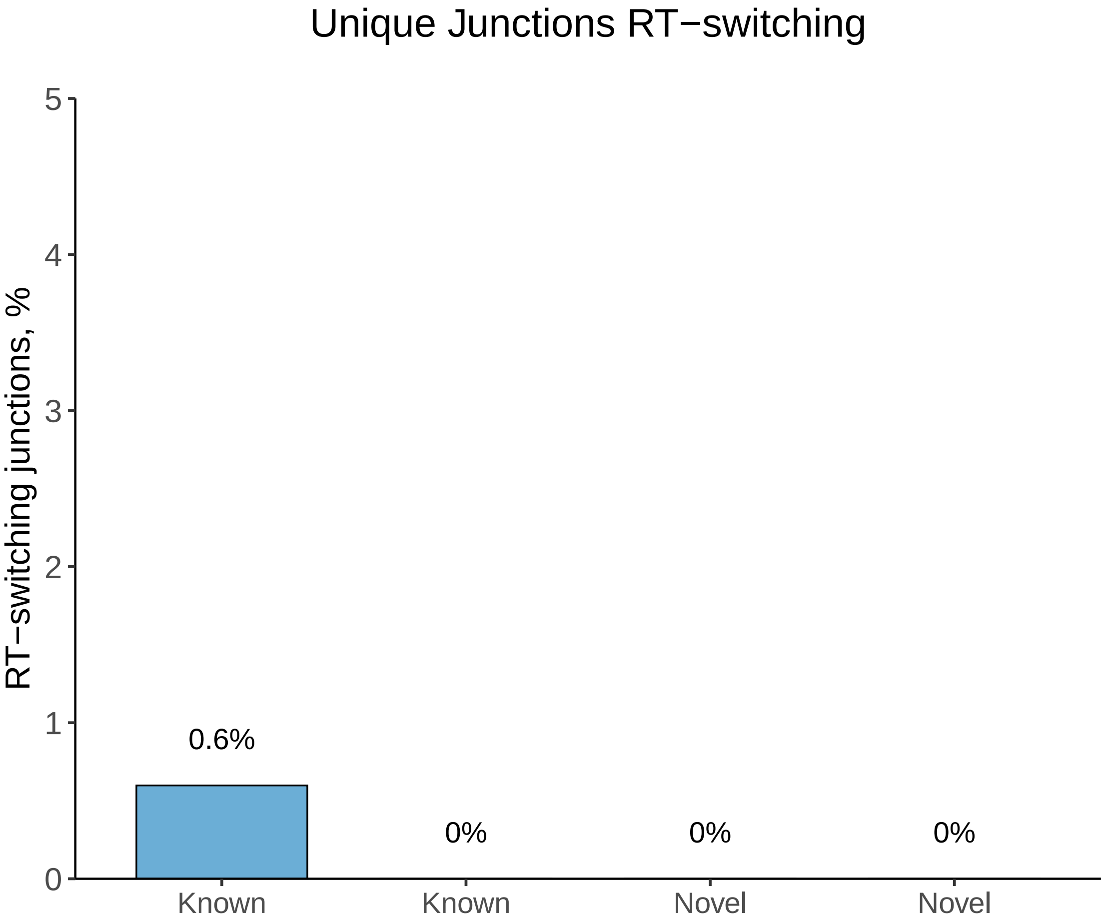
Applicable Only to FSM and ISM Categories

Splice Junction Characterization

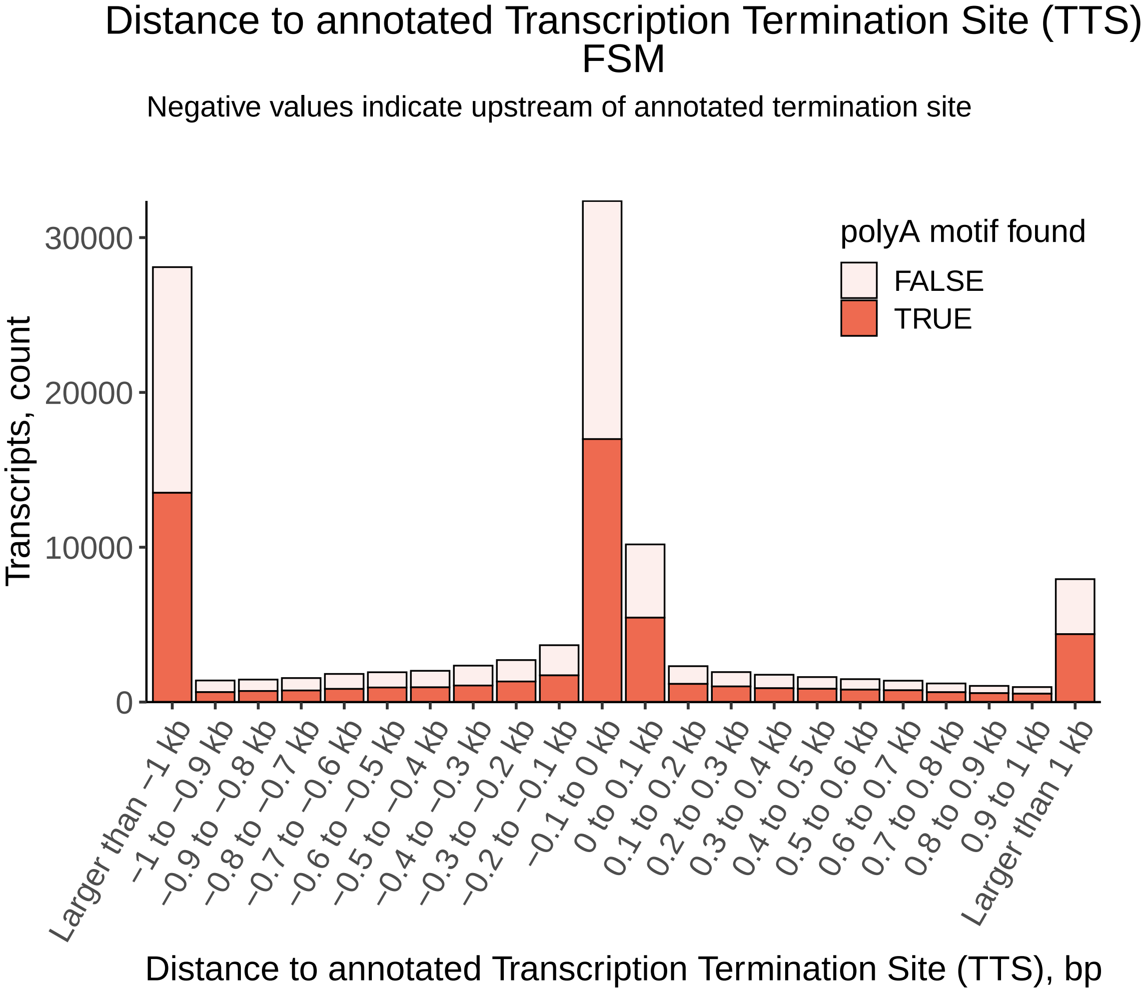

Distribution of Splice Junctions by Structural Classification
Splice junctions, %
100
75
50
25
0
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
NA
Known canonical
Known Non−canonical
Novel canonical
Novel Non−canonical

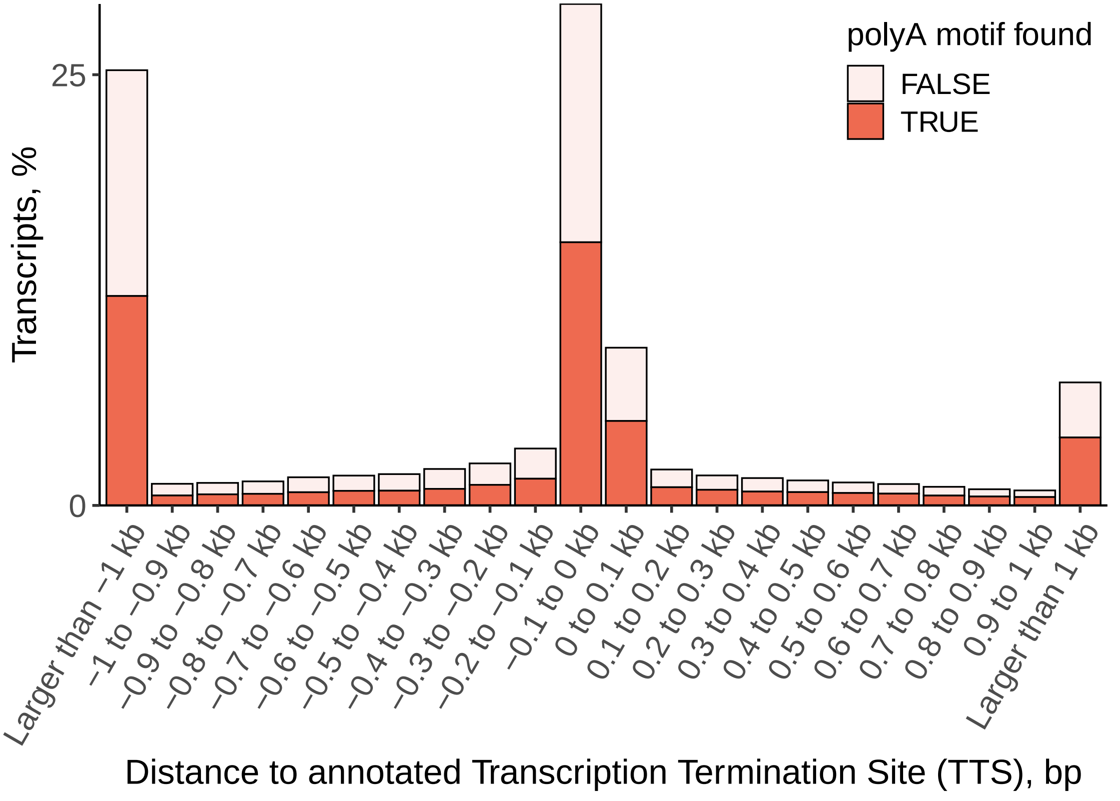

Distribution of Transcripts by Splice Junctions
Transcripts, %
100
75
50
25
0
FSM
ISM
NIC
NNC
Genic
Genomic
Antisense
Fusion
Intergenic
NA
Canonical
Non−canonical
NA


RT−Switching All Junctions
RT−switching junctions, %
5
4
3
2
1
0
0.03%
0%
0%
0%
Known canonical
Known Non−canonical
Novel canonical
Novel Non−canonical


Unique Junctions RT−switching
RT−switching junctions, %
5
4
3
2
1
0
0.6%
0%
0%
0%
Known canonical
Known Non−canonical
Novel canonical
Novel Non−canonical

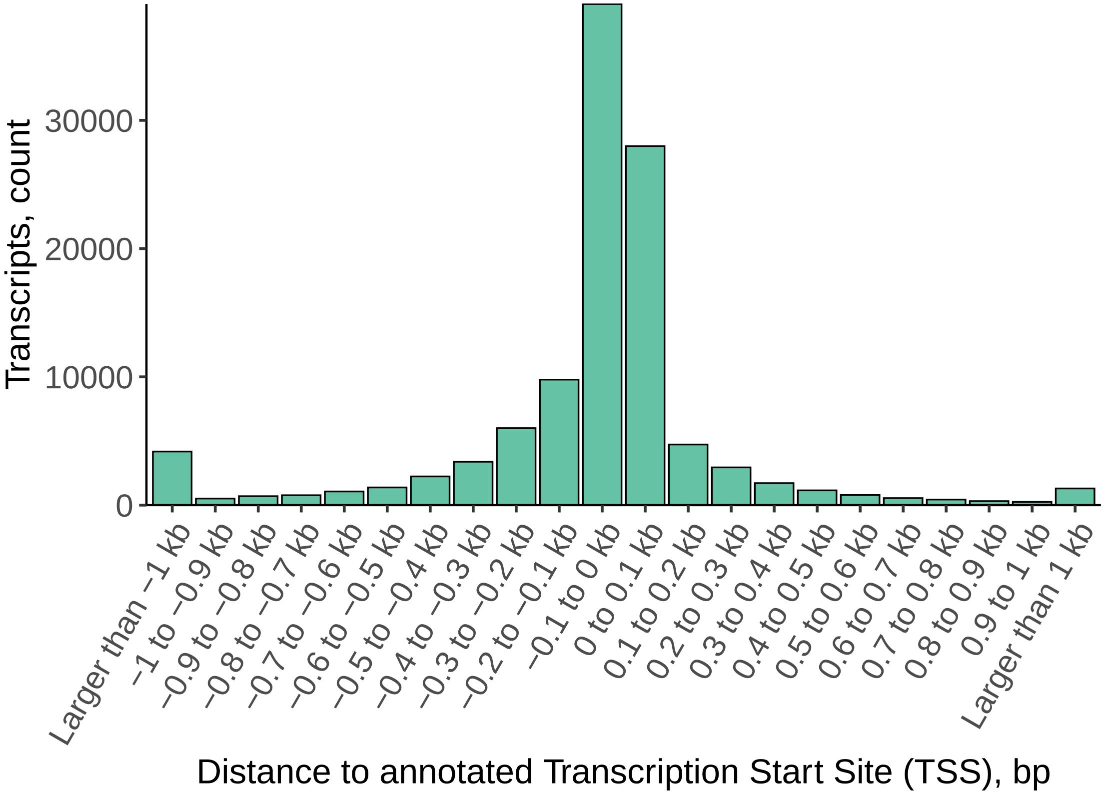
Comparison With Annotated TSS and TTS


Distance to annotated Transcription Termination Site (TTS)
FSM
Negative values indicate upstream of annotated termination site
Transcripts, count
0
10000
20000
30000
polyA motif found
FALSE
TRUE
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp



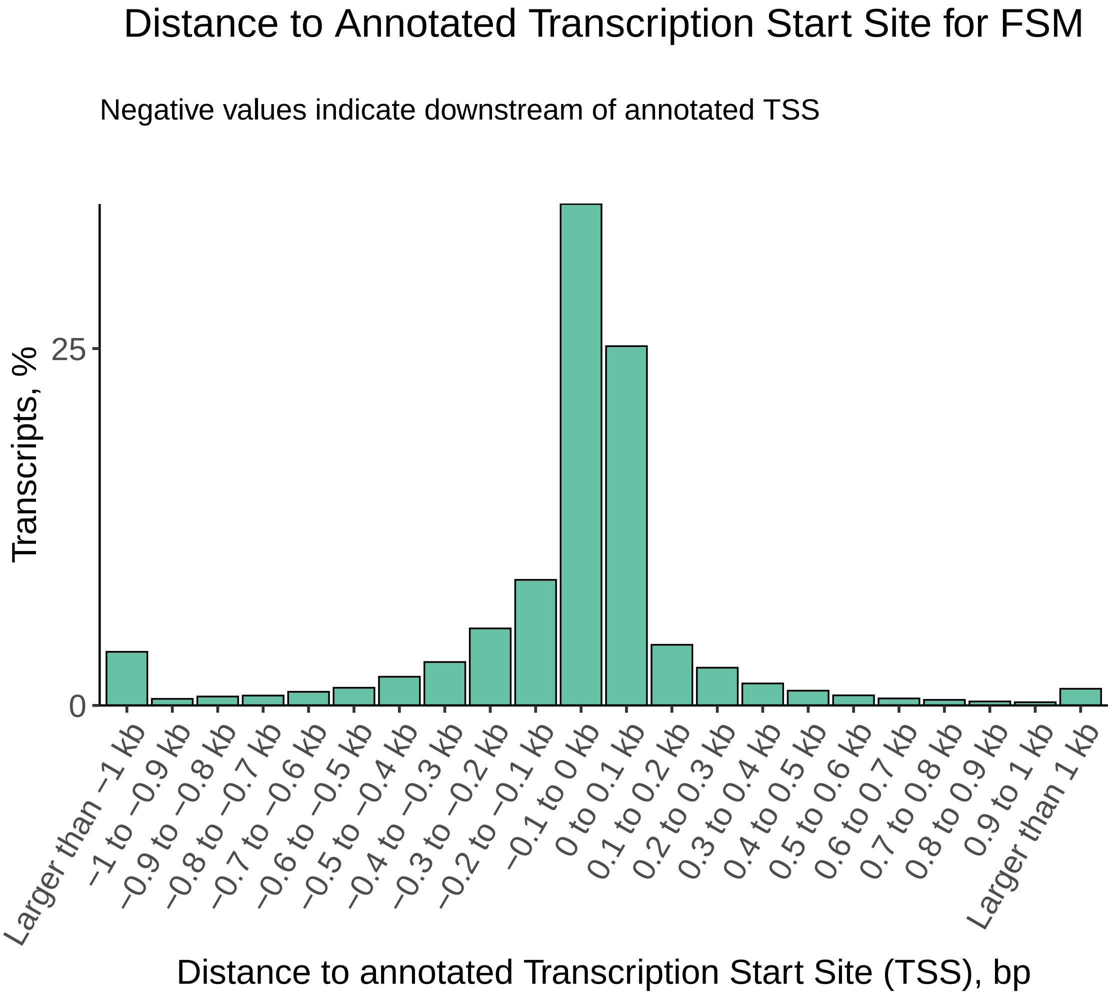
Distance to annotated Transcription Termination Site (TTS)
FSM

Negative values indicate upstream of annotated termination site



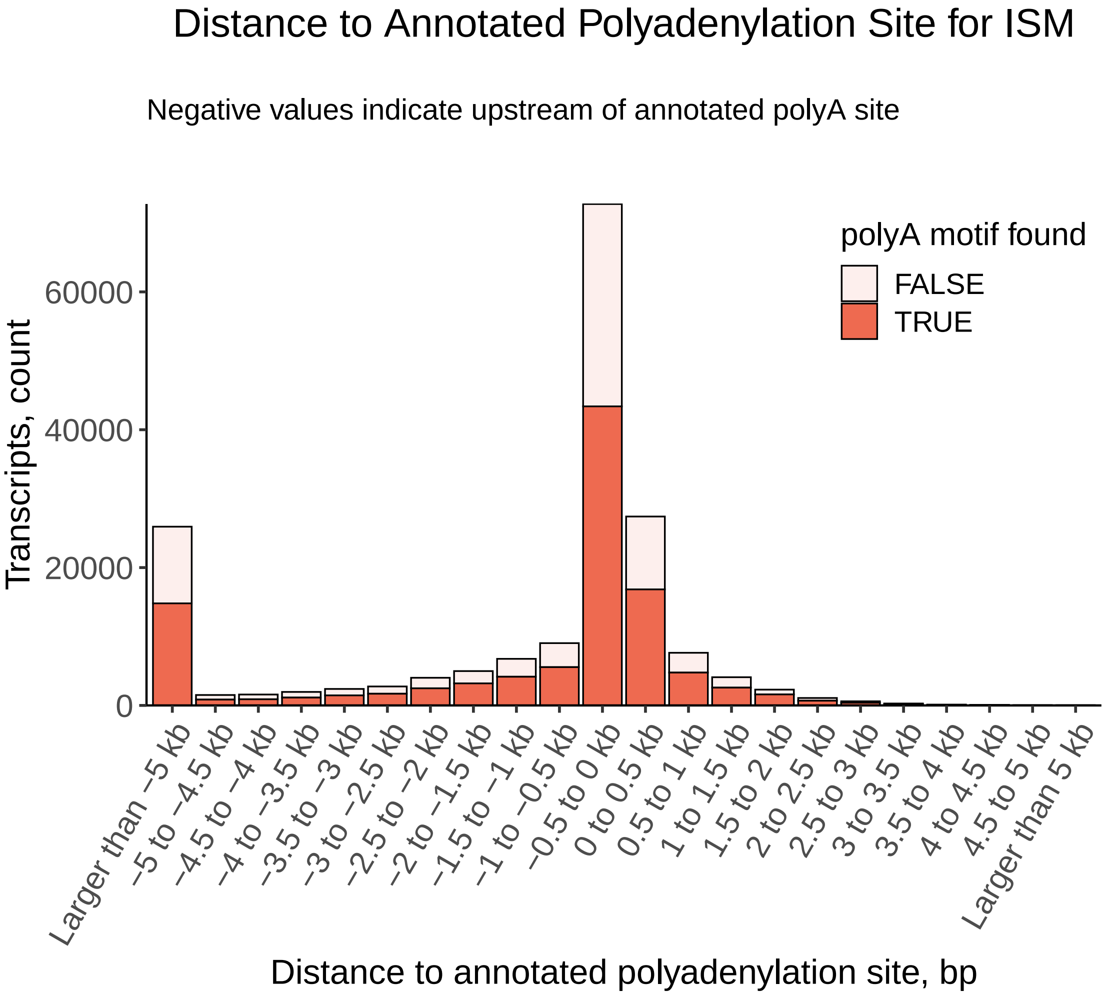
Distance to Annotated Transcription Start Site for FSM

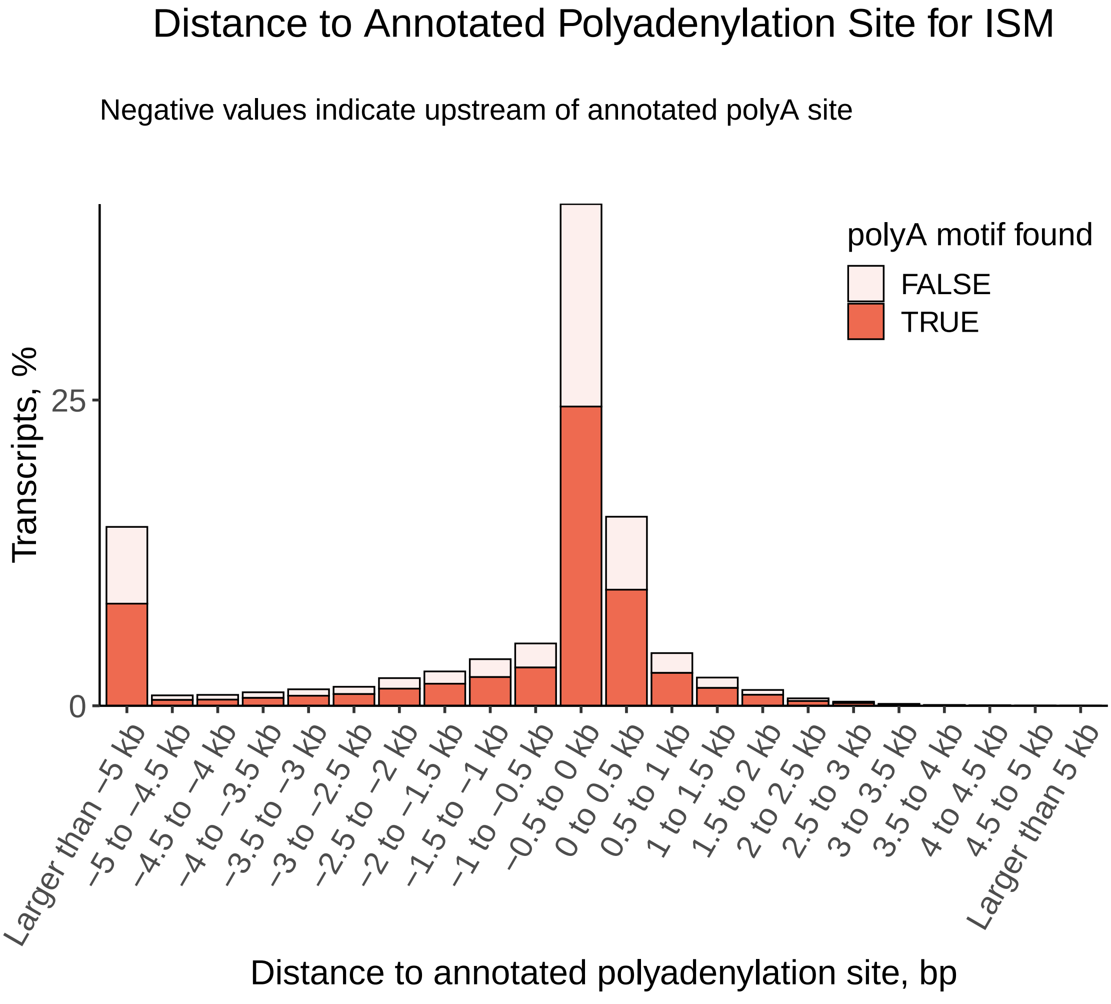
Negative values indicate downstream of annotated TSS



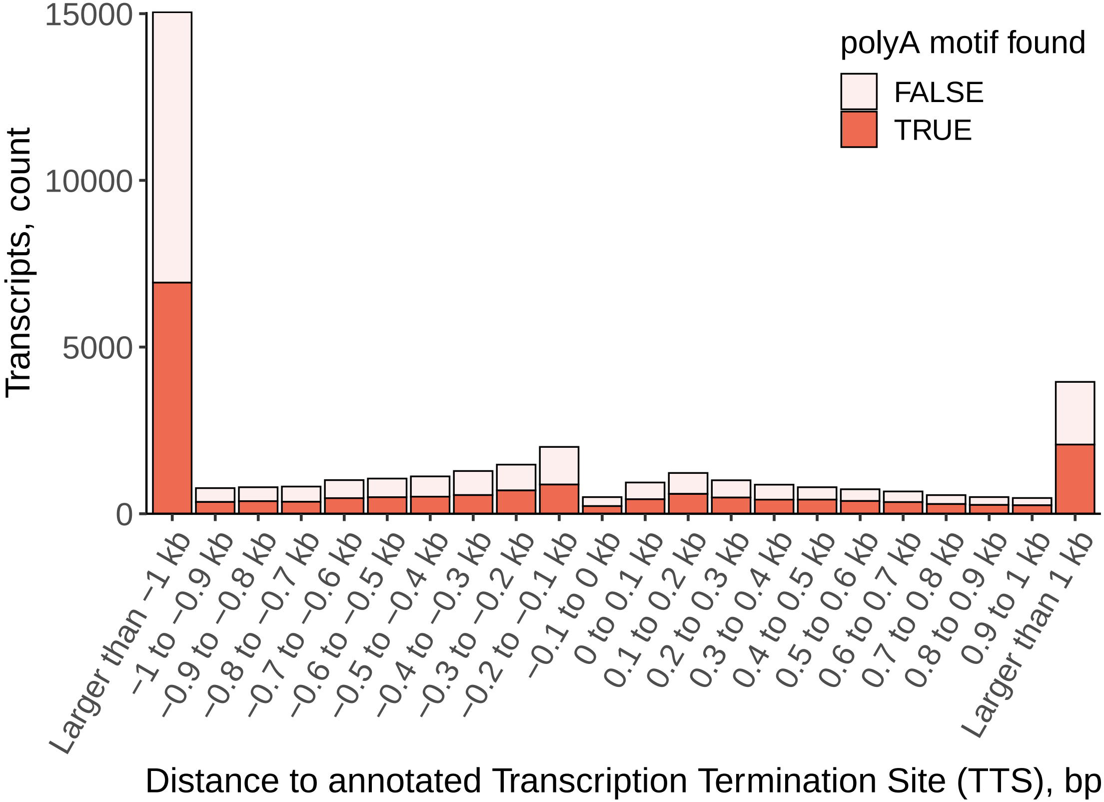
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS


Distance to Annotated Polyadenylation Site for ISM
Negative values indicate upstream of annotated polyA site
polyA motif found
FALSE
TRUE
Transcripts, count
60000
40000
20000
0
Larger than −5 kb
−5 to −4.5 kb
−4.5 to −4 kb
−4 to −3.5 kb
−3.5 to −3 kb
−3 to −2.5 kb
−2.5 to −2 kb
−2 to −1.5 kb
−1.5 to −1 kb
−1 to −0.5 kb
−0.5 to 0 kb
0 to 0.5 kb
0.5 to 1 kb
1 to 1.5 kb
1.5 to 2 kb
2 to 2.5 kb
2.5 to 3 kb
3 to 3.5 kb
3.5 to 4 kb
4 to 4.5 kb
4.5 to 5 kb
Larger than 5 kb
Distance to annotated polyadenylation site, bp

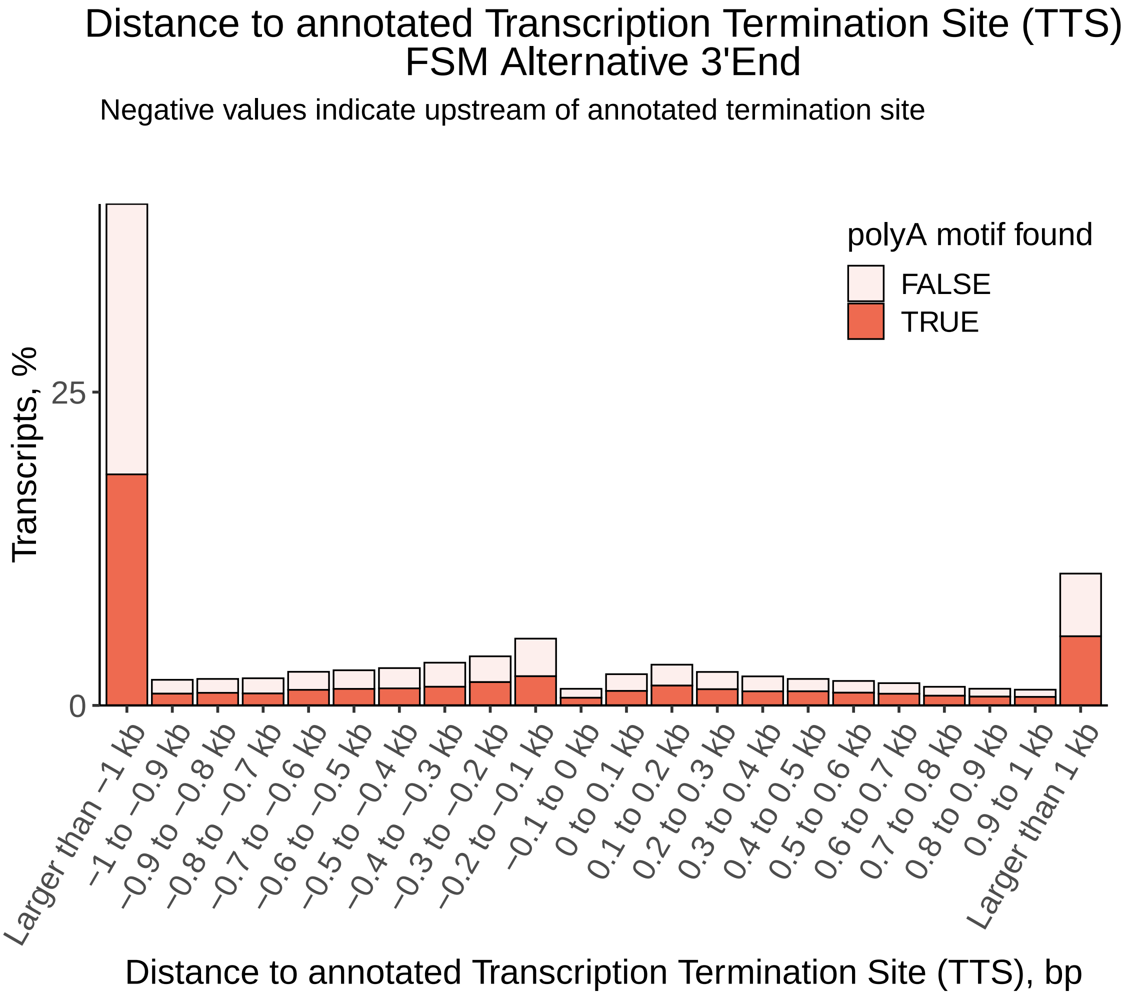

Distance to Annotated Polyadenylation Site for ISM
Negative values indicate upstream of annotated polyA site
Transcripts, %
25
0
polyA motif found
FALSE
TRUE
Larger than −5 kb
−5 to −4.5 kb
−4.5 to −4 kb
−4 to −3.5 kb
−3.5 to −3 kb
−3 to −2.5 kb
−2.5 to −2 kb
−2 to −1.5 kb
−1.5 to −1 kb
−1 to −0.5 kb
−0.5 to 0 kb
0 to 0.5 kb
0.5 to 1 kb
1 to 1.5 kb
1.5 to 2 kb
2 to 2.5 kb
2.5 to 3 kb
3 to 3.5 kb
3.5 to 4 kb
4 to 4.5 kb
4.5 to 5 kb
Larger than 5 kb
Distance to annotated polyadenylation site, bp

Comparison With Annotated TSS and TTS by Subcategories



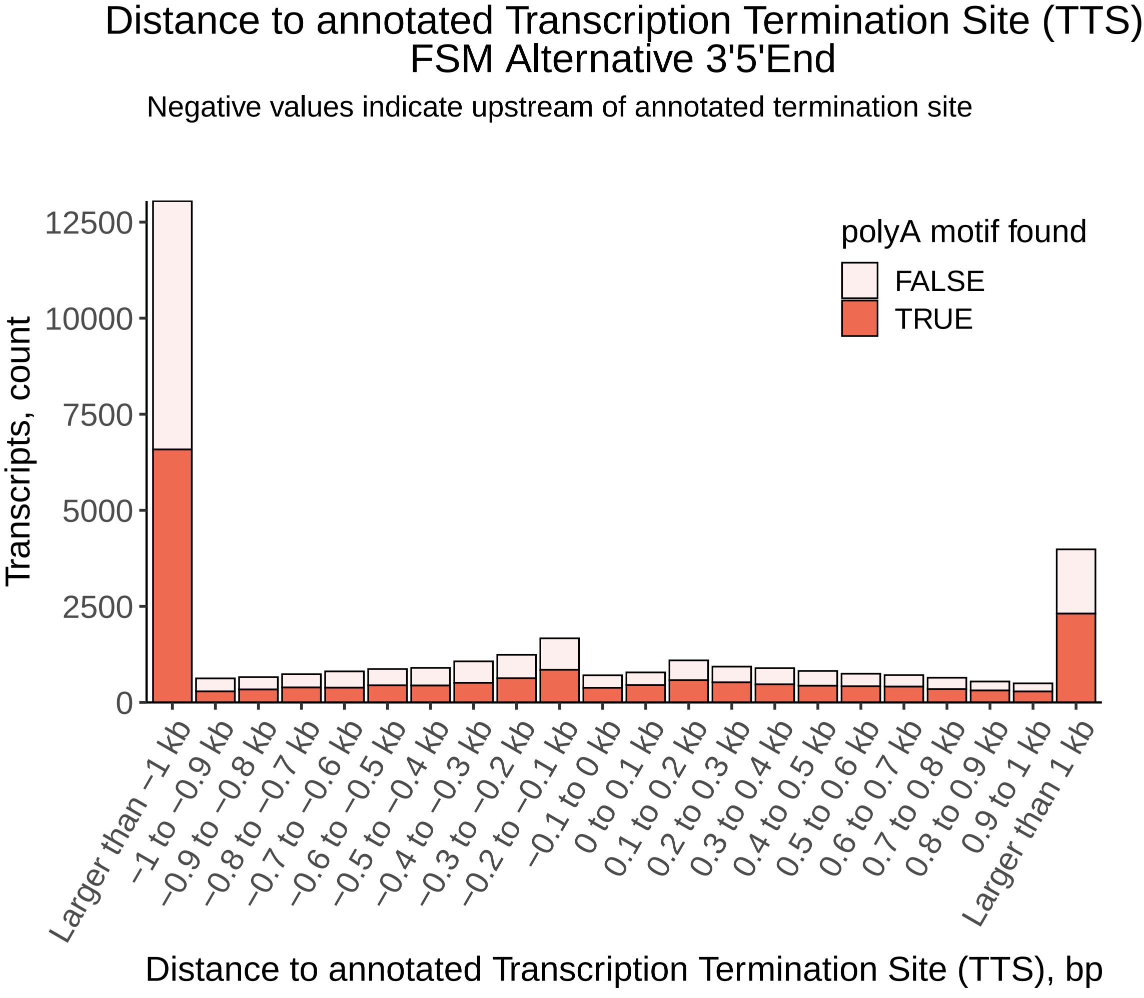
Distance to annotated Transcription Termination Site (TTS)
FSM Alternative 3'End

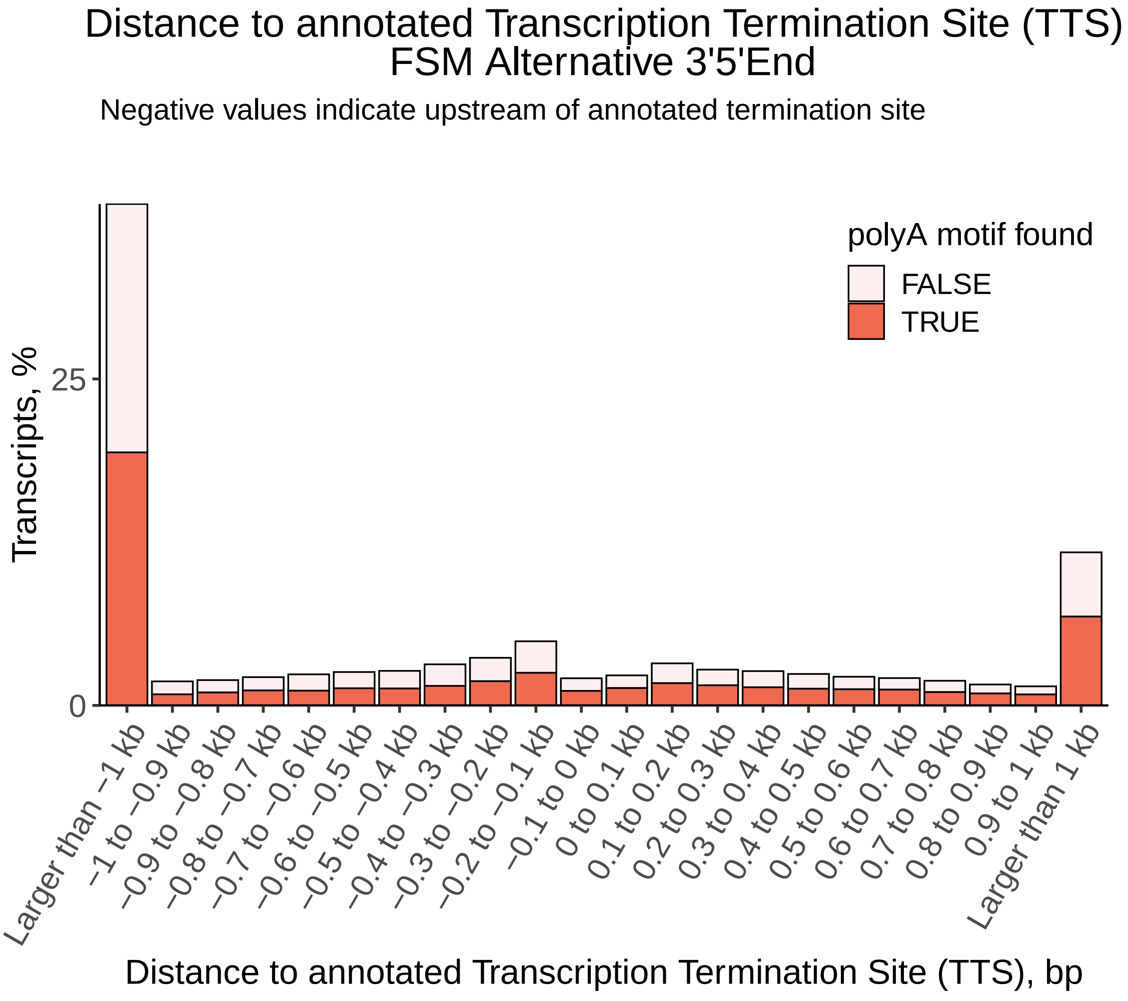
Negative values indicate upstream of annotated termination site

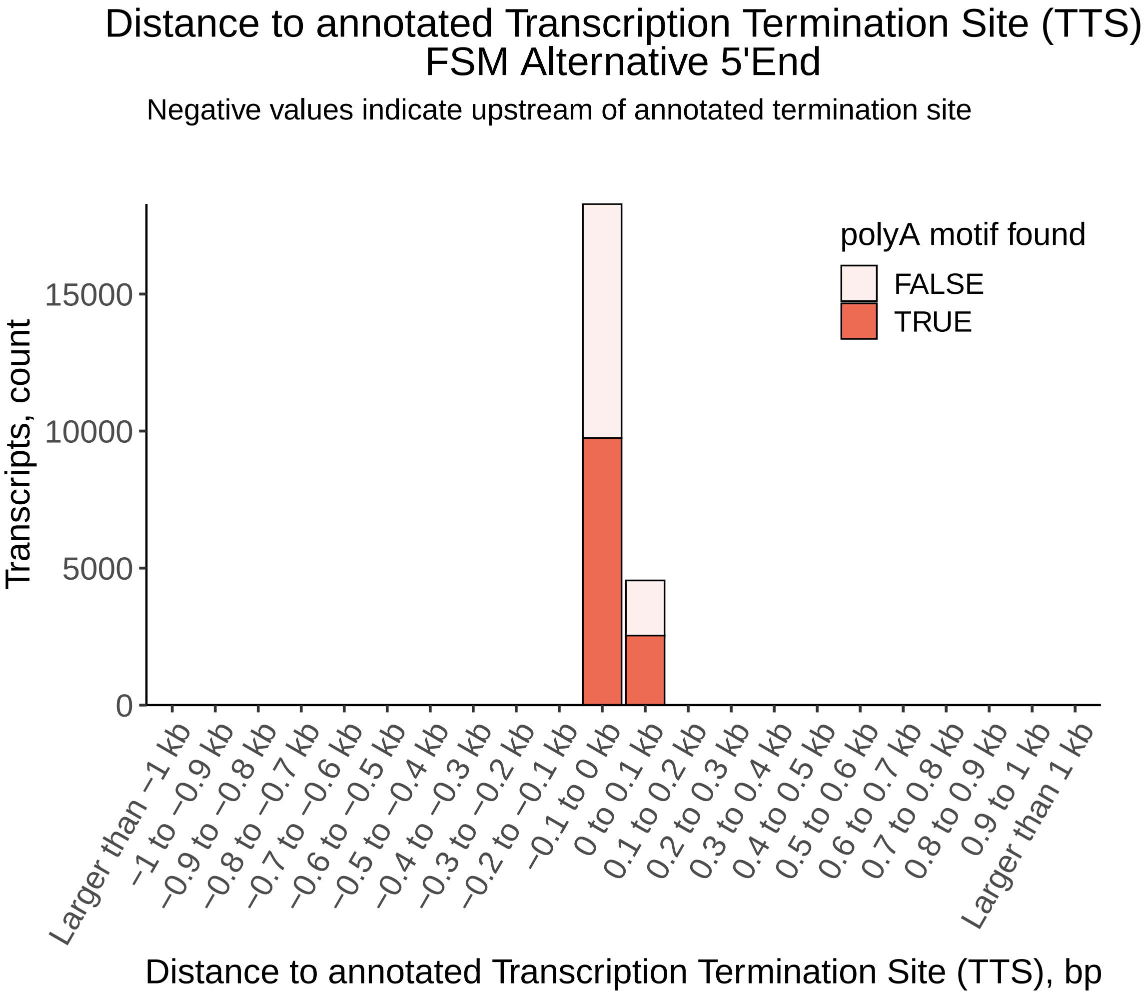


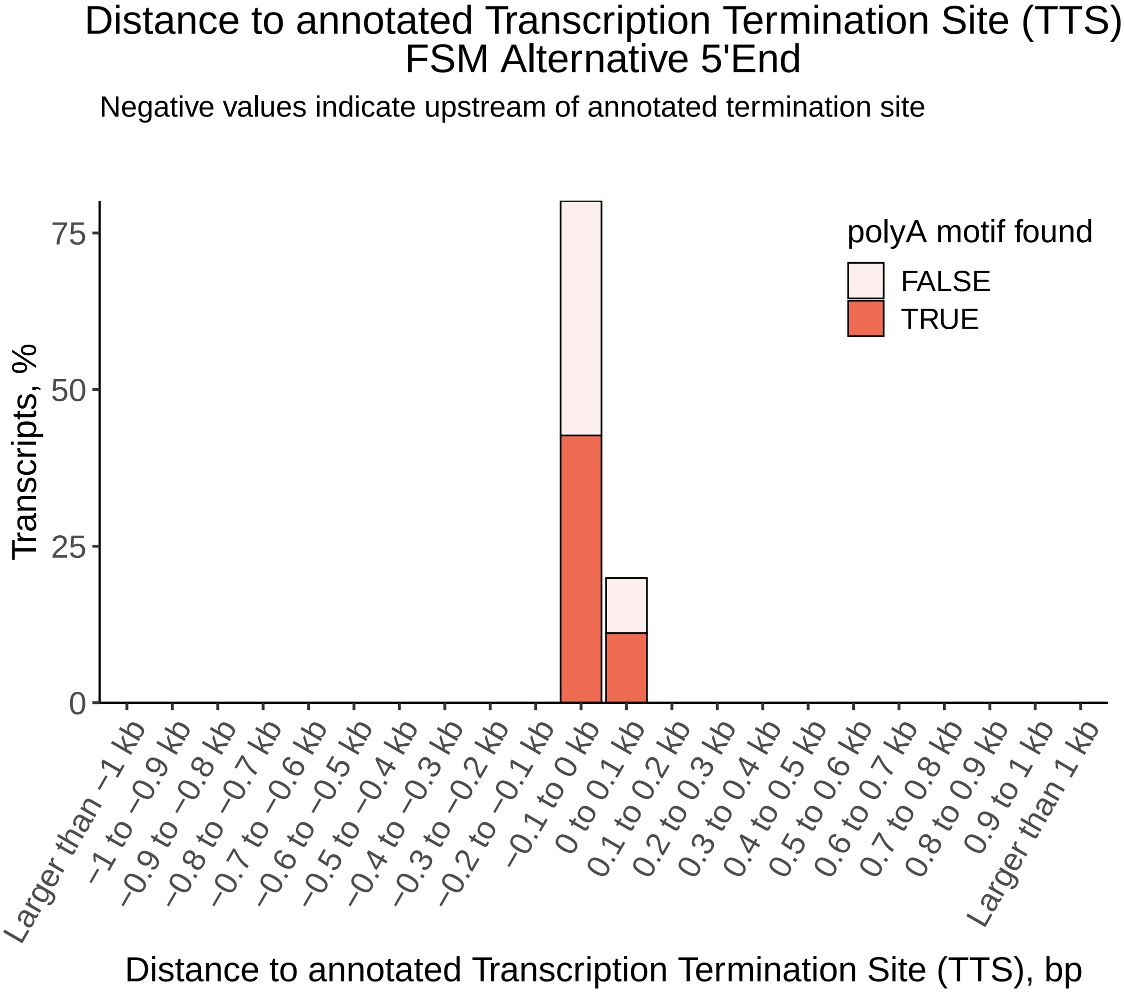
Distance to annotated Transcription Termination Site (TTS)
FSM Alternative 3'End

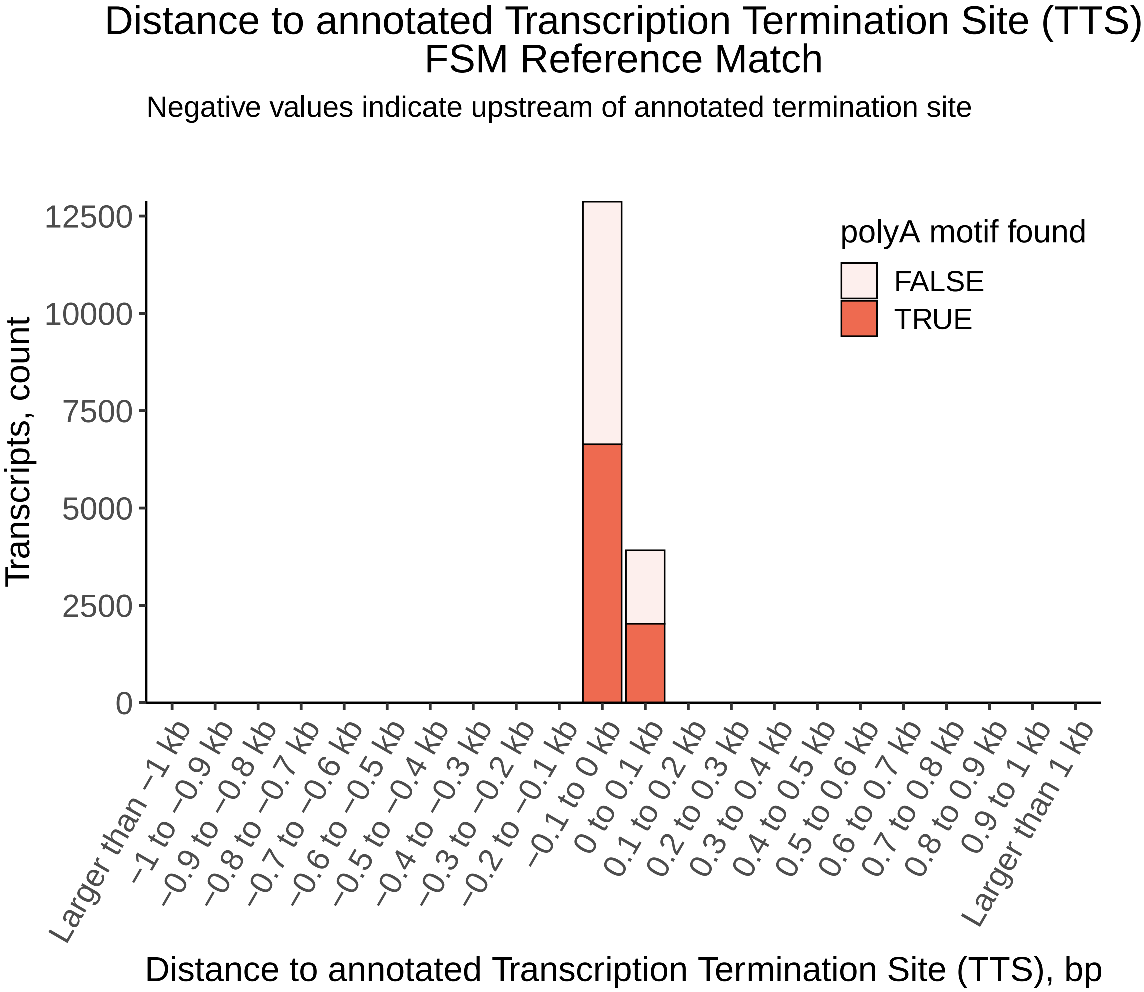
Negative values indicate upstream of annotated termination site

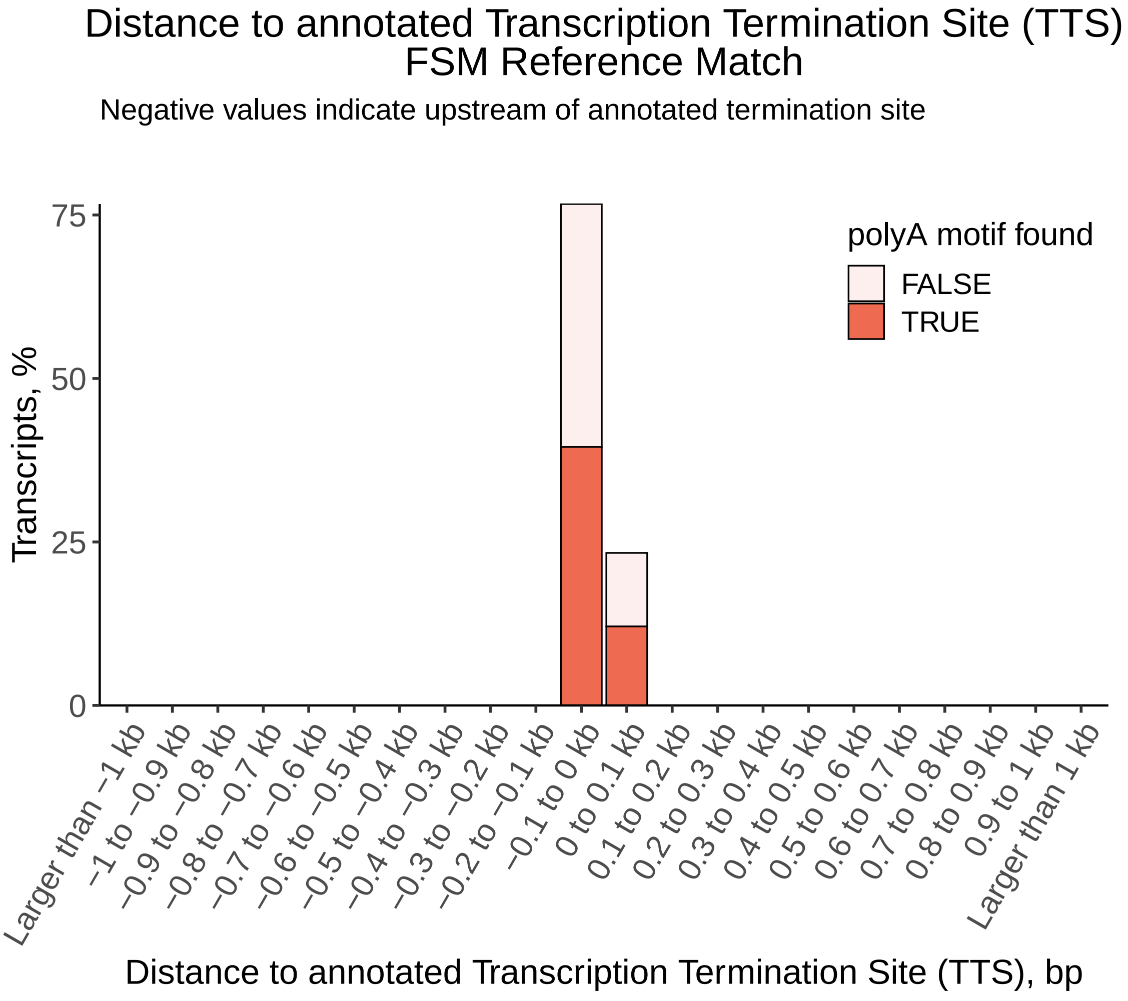

Distance to annotated Transcription Termination Site (TTS)
FSM Alternative 3'5'End
Negative values indicate upstream of annotated termination site
polyA motif found
FALSE
TRUE
Transcripts, count
0
2500
5000
7500
10000
12500
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp

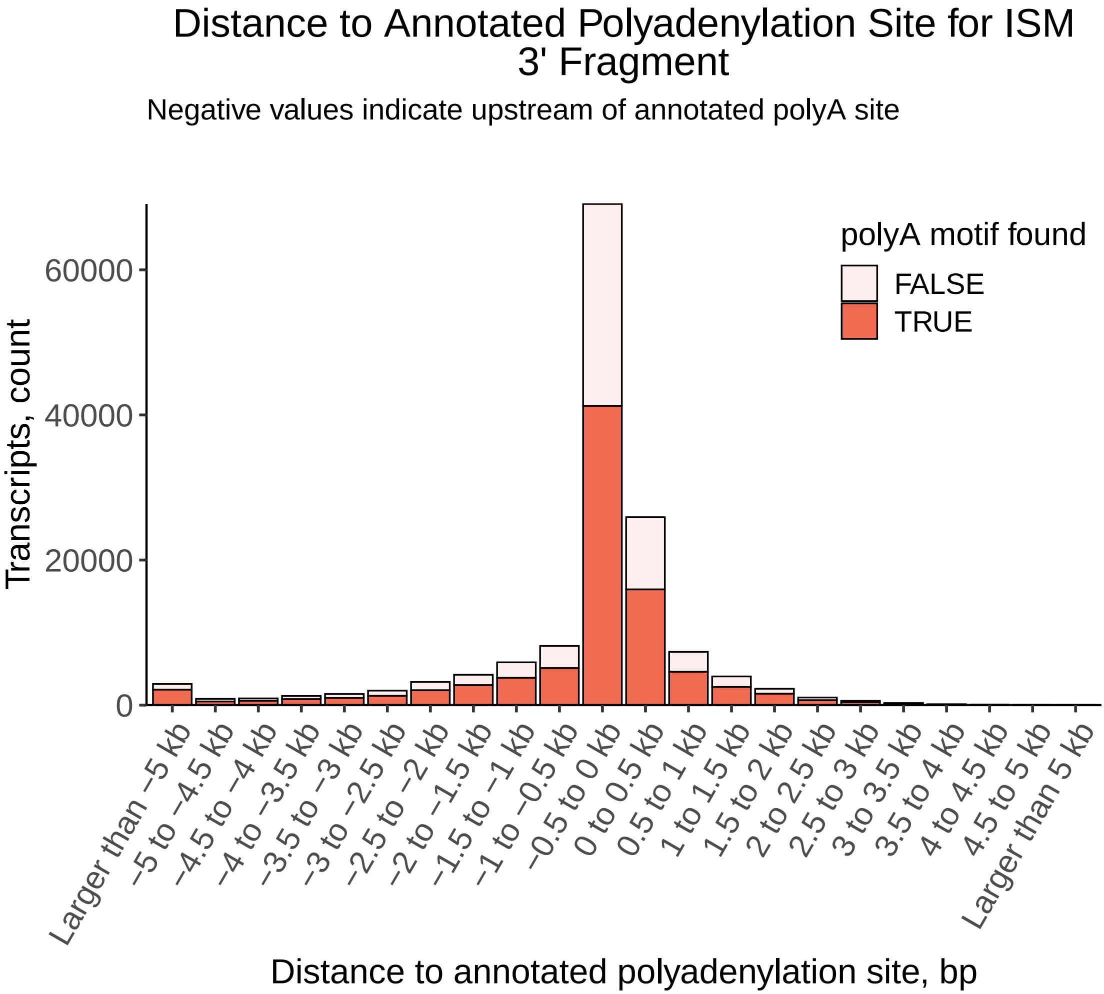

Distance to annotated Transcription Termination Site (TTS)
FSM Alternative 3'5'End
Negative values indicate upstream of annotated termination site
polyA motif found
FALSE
TRUE
Transcripts, %
25
0
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp


Distance to annotated Transcription Termination Site (TTS)
FSM Alternative 5'End
Negative values indicate upstream of annotated termination site
Transcripts, count
15000
10000
5000
0
polyA motif found
FALSE
TRUE
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp


Distance to annotated Transcription Termination Site (TTS)
FSM Alternative 5'End
Negative values indicate upstream of annotated termination site
Transcripts, %
0
25
50
75
polyA motif found
FALSE
TRUE
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp

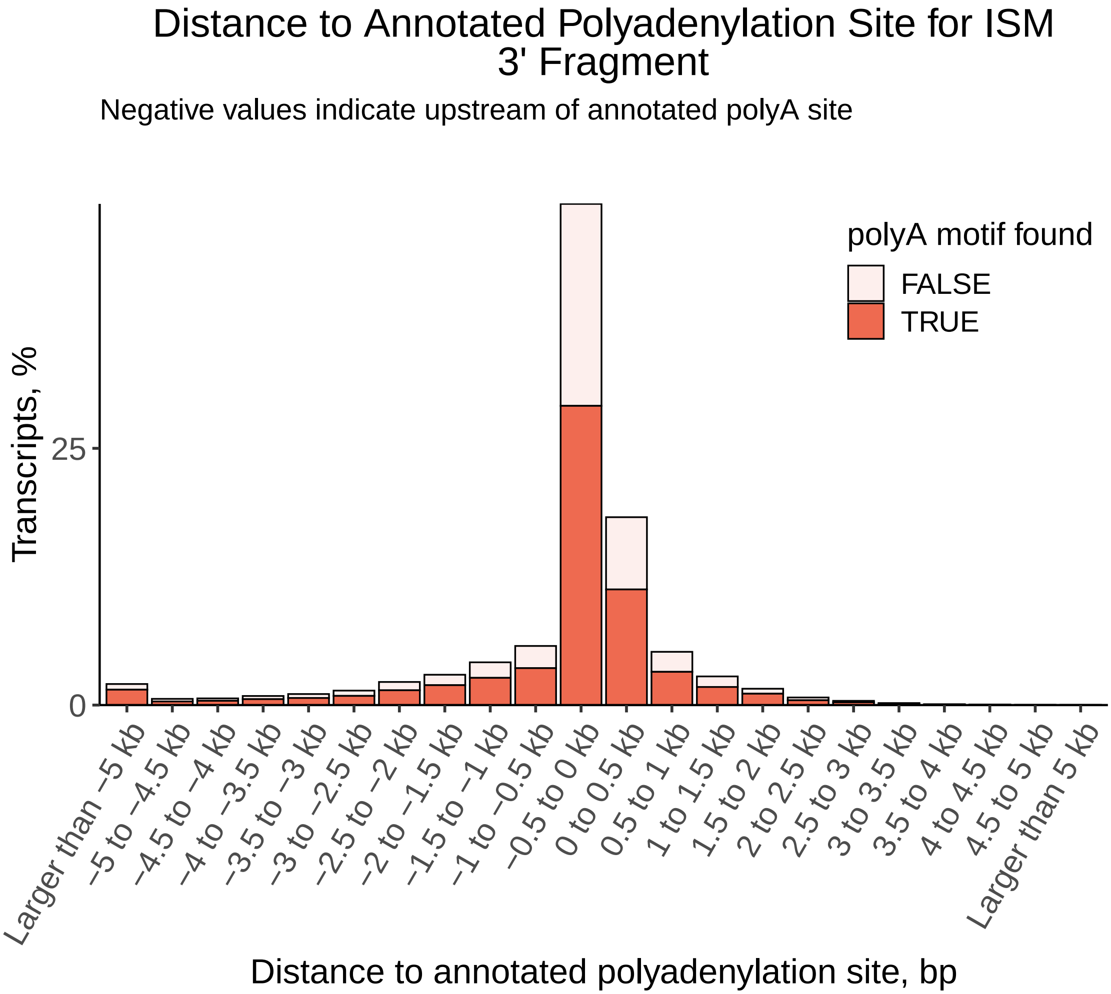

Distance to annotated Transcription Termination Site (TTS)
FSM Reference Match
Negative values indicate upstream of annotated termination site
Transcripts, count
0
2500
5000
7500
10000
12500
polyA motif found
FALSE
TRUE
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp

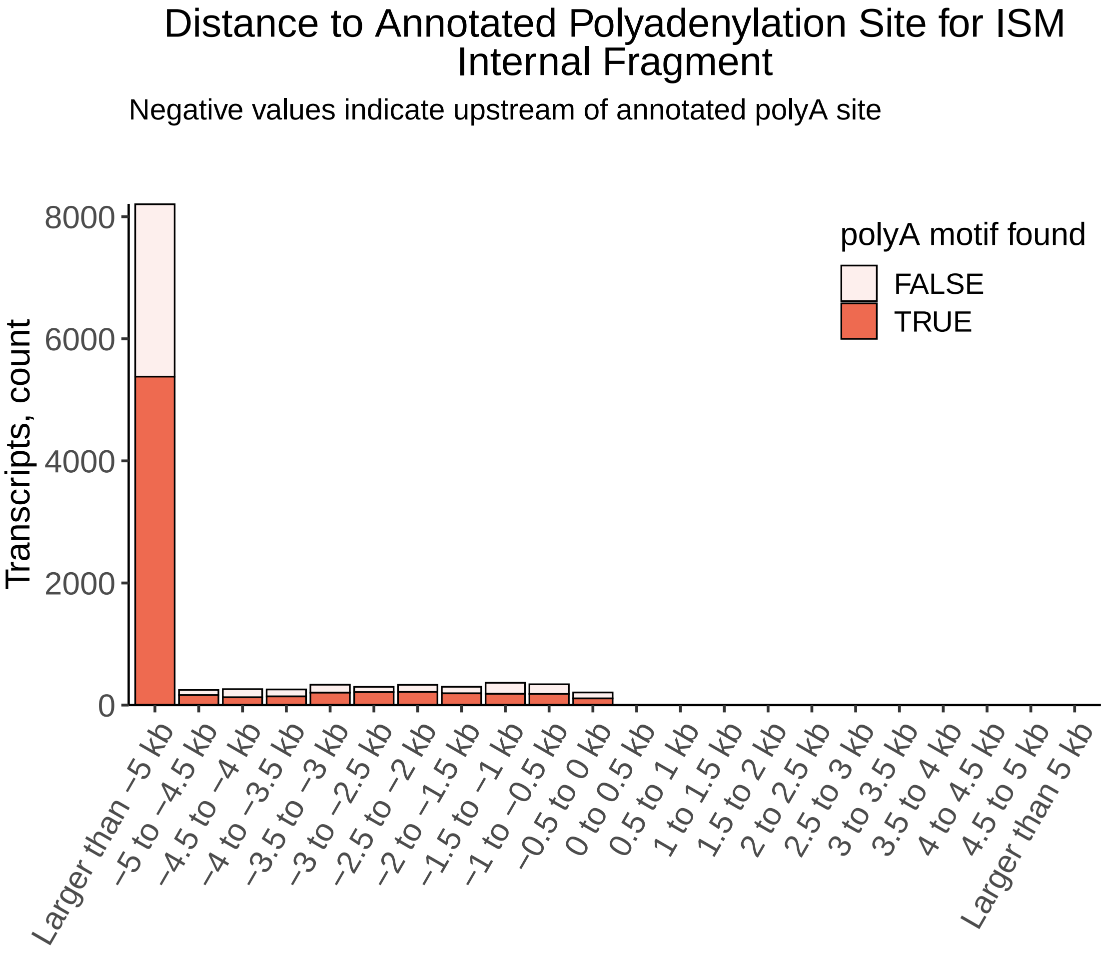

Distance to annotated Transcription Termination Site (TTS)
FSM Reference Match
Negative values indicate upstream of annotated termination site
Transcripts, %
75
50
25
0
polyA motif found
FALSE
TRUE
Larger than −1 kb
−1 to −0.9 kb
−0.9 to −0.8 kb
−0.8 to −0.7 kb
−0.7 to −0.6 kb
−0.6 to −0.5 kb
−0.5 to −0.4 kb
−0.4 to −0.3 kb
−0.3 to −0.2 kb
−0.2 to −0.1 kb
−0.1 to 0 kb
0 to 0.1 kb
0.1 to 0.2 kb
0.2 to 0.3 kb
0.3 to 0.4 kb
0.4 to 0.5 kb
0.5 to 0.6 kb
0.6 to 0.7 kb
0.7 to 0.8 kb
0.8 to 0.9 kb
0.9 to 1 kb
Larger than 1 kb
Distance to annotated Transcription Termination Site (TTS), bp

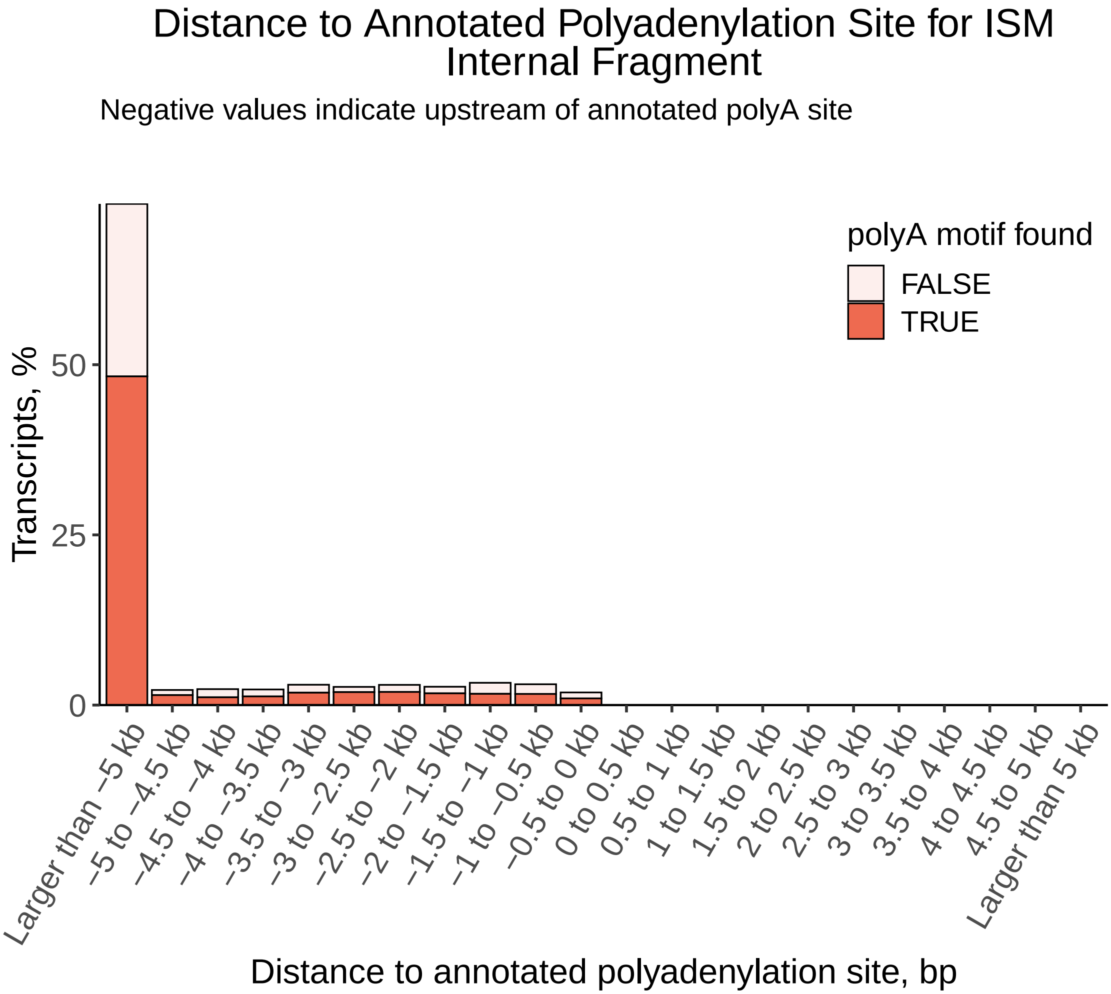


Distance to Annotated Polyadenylation Site for ISM 3' Fragment

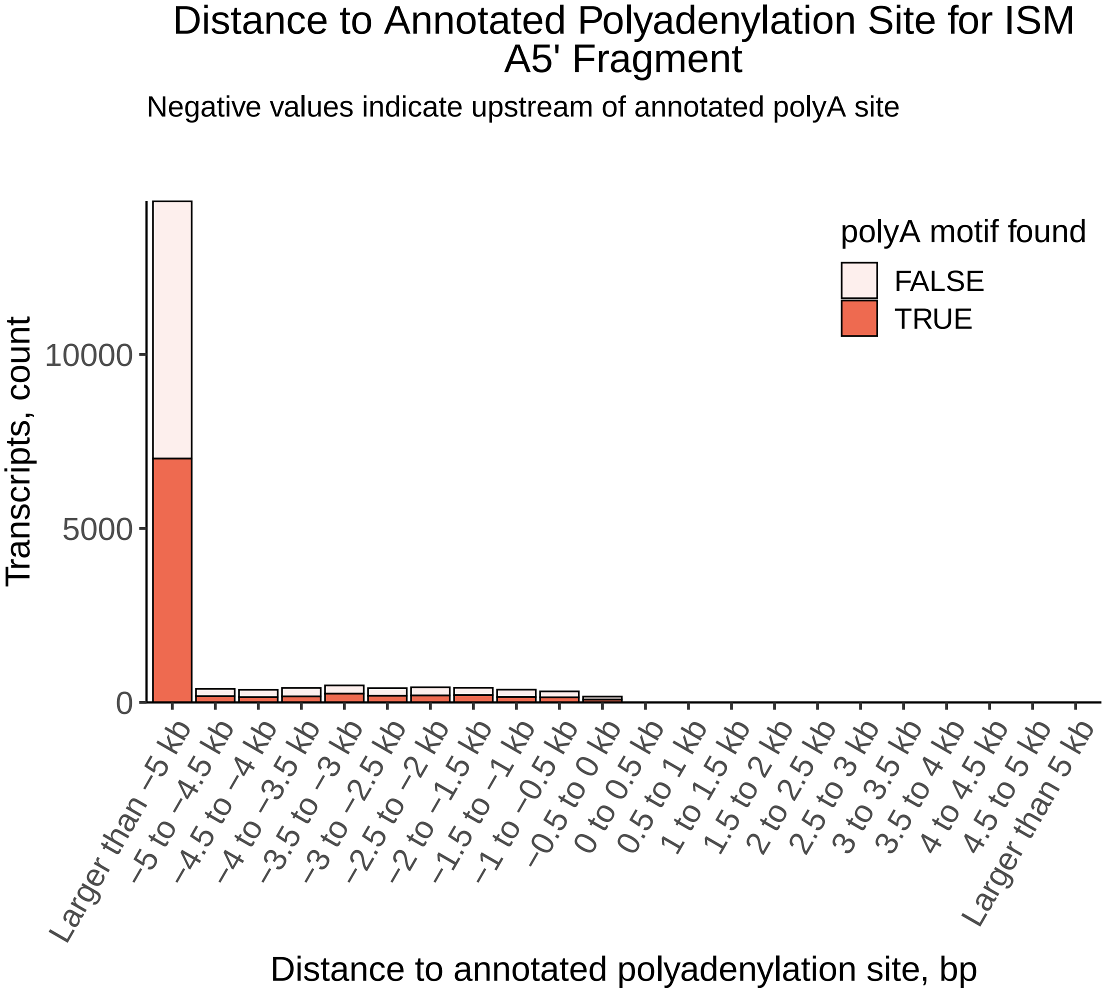
Negative values indicate upstream of annotated polyA site

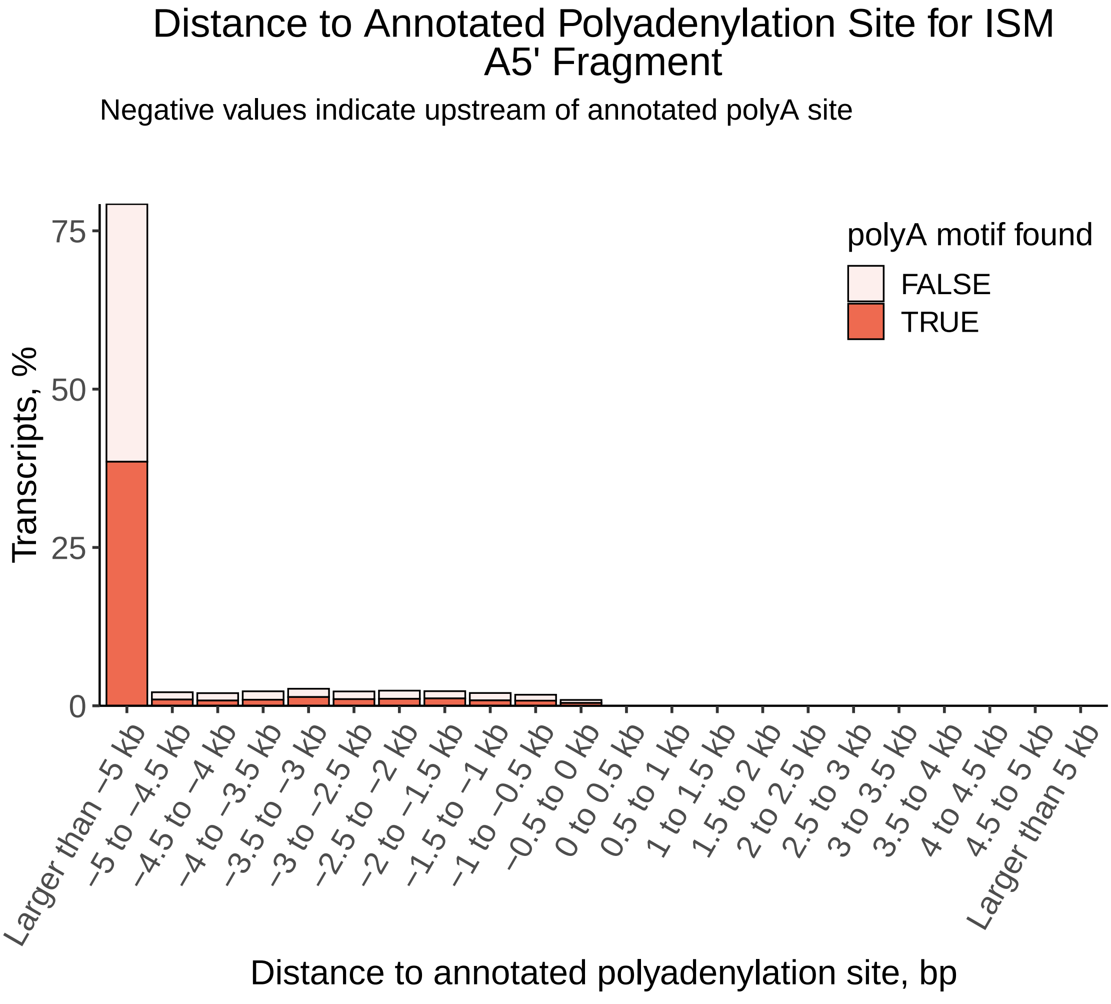

Distance to Annotated Polyadenylation Site for ISM 3' Fragment
Negative values indicate upstream of annotated polyA site
polyA motif found
FALSE
TRUE
Transcripts, %
25
0
Larger than −5 kb
−5 to −4.5 kb
−4.5 to −4 kb
−4 to −3.5 kb
−3.5 to −3 kb
−3 to −2.5 kb
−2.5 to −2 kb
−2 to −1.5 kb
−1.5 to −1 kb
−1 to −0.5 kb
−0.5 to 0 kb
0 to 0.5 kb
0.5 to 1 kb
1 to 1.5 kb
1.5 to 2 kb
2 to 2.5 kb
2.5 to 3 kb
3 to 3.5 kb
3.5 to 4 kb
4 to 4.5 kb
4.5 to 5 kb
Larger than 5 kb
Distance to annotated polyadenylation site, bp

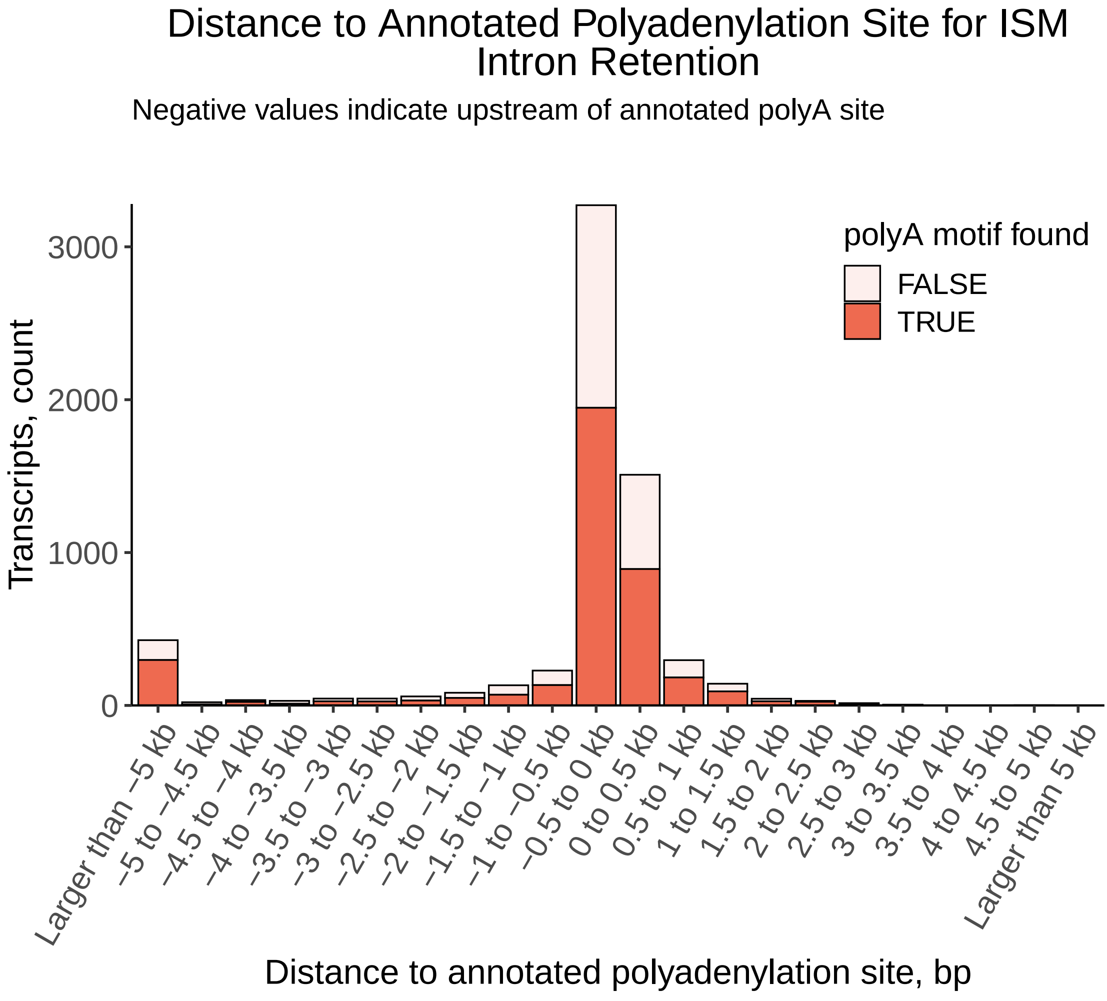

Distance to Annotated Polyadenylation Site for ISM Internal Fragment
Negative values indicate upstream of annotated polyA site
Transcripts, count
0
2000
4000
6000
8000
polyA motif found
FALSE
TRUE
Larger than −5 kb
−5 to −4.5 kb
−4.5 to −4 kb
−4 to −3.5 kb
−3.5 to −3 kb
−3 to −2.5 kb
−2.5 to −2 kb
−2 to −1.5 kb
−1.5 to −1 kb
−1 to −0.5 kb
−0.5 to 0 kb
0 to 0.5 kb
0.5 to 1 kb
1 to 1.5 kb
1.5 to 2 kb
2 to 2.5 kb
2.5 to 3 kb
3 to 3.5 kb
3.5 to 4 kb
4 to 4.5 kb
4.5 to 5 kb
Larger than 5 kb
Distance to annotated polyadenylation site, bp


Distance to Annotated Polyadenylation Site for ISM Internal Fragment

Negative values indicate upstream of annotated polyA site

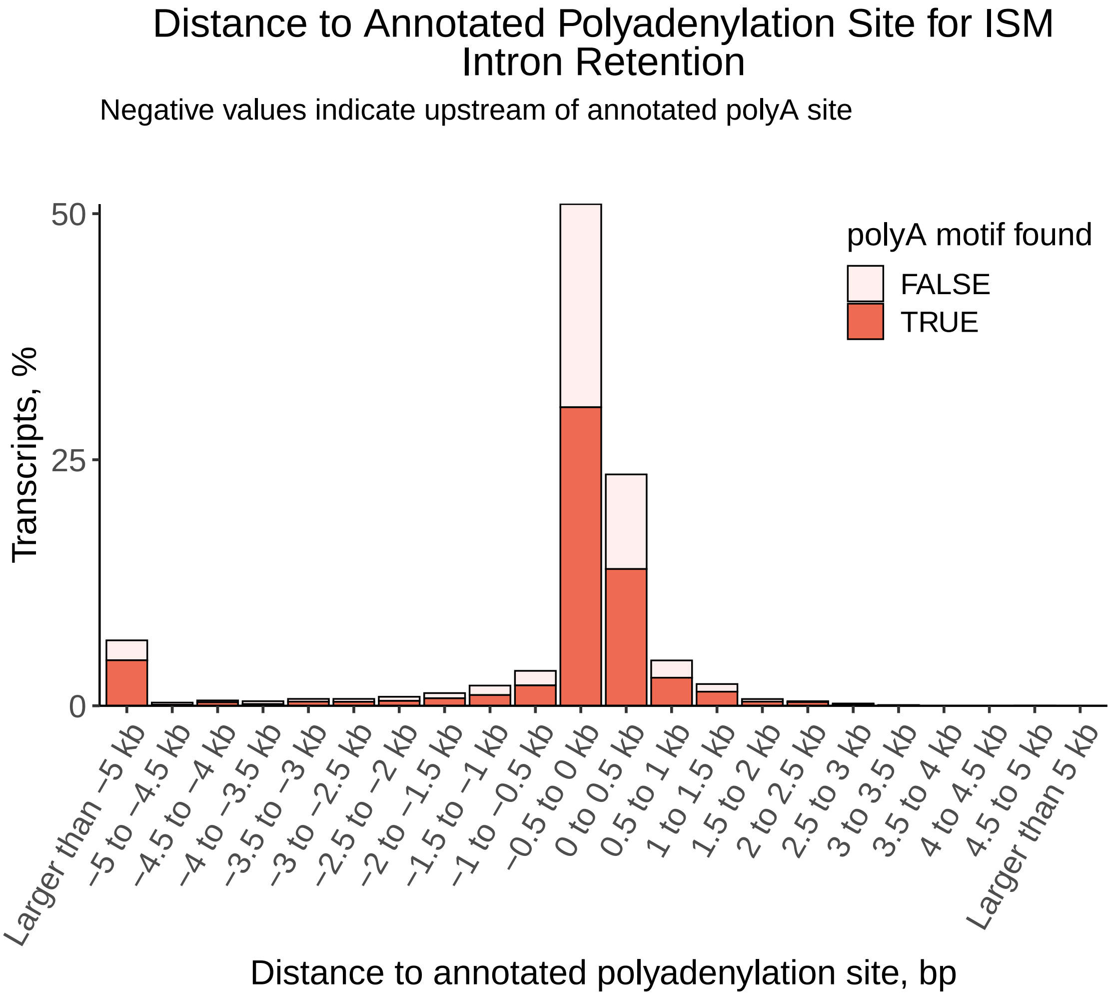

Distance to Annotated Polyadenylation Site for ISM A5' Fragment
Negative values indicate upstream of annotated polyA site
polyA motif found
FALSE
TRUE
Transcripts, count
0
5000
10000
Larger than −5 kb
−5 to −4.5 kb
−4.5 to −4 kb
−4 to −3.5 kb
−3.5 to −3 kb
−3 to −2.5 kb
−2.5 to −2 kb
−2 to −1.5 kb
−1.5 to −1 kb
−1 to −0.5 kb
−0.5 to 0 kb
0 to 0.5 kb
0.5 to 1 kb
1 to 1.5 kb
1.5 to 2 kb
2 to 2.5 kb
2.5 to 3 kb
3 to 3.5 kb
3.5 to 4 kb
4 to 4.5 kb
4.5 to 5 kb
Larger than 5 kb
Distance to annotated polyadenylation site, bp


Distance to Annotated Polyadenylation Site for ISM A5' Fragment
Negative values indicate upstream of annotated polyA site
polyA motif found
FALSE
TRUE
Transcripts, %
75
50
25
0
Larger than −5 kb
−5 to −4.5 kb
−4.5 to −4 kb
−4 to −3.5 kb
−3.5 to −3 kb
−3 to −2.5 kb
−2.5 to −2 kb
−2 to −1.5 kb
−1.5 to −1 kb
−1 to −0.5 kb
−0.5 to 0 kb
0 to 0.5 kb
0.5 to 1 kb
1 to 1.5 kb
1.5 to 2 kb
2 to 2.5 kb
2.5 to 3 kb
3 to 3.5 kb
3.5 to 4 kb
4 to 4.5 kb
4.5 to 5 kb
Larger than 5 kb
Distance to annotated polyadenylation site, bp



Distance to Annotated Polyadenylation Site for ISM Intron Retention

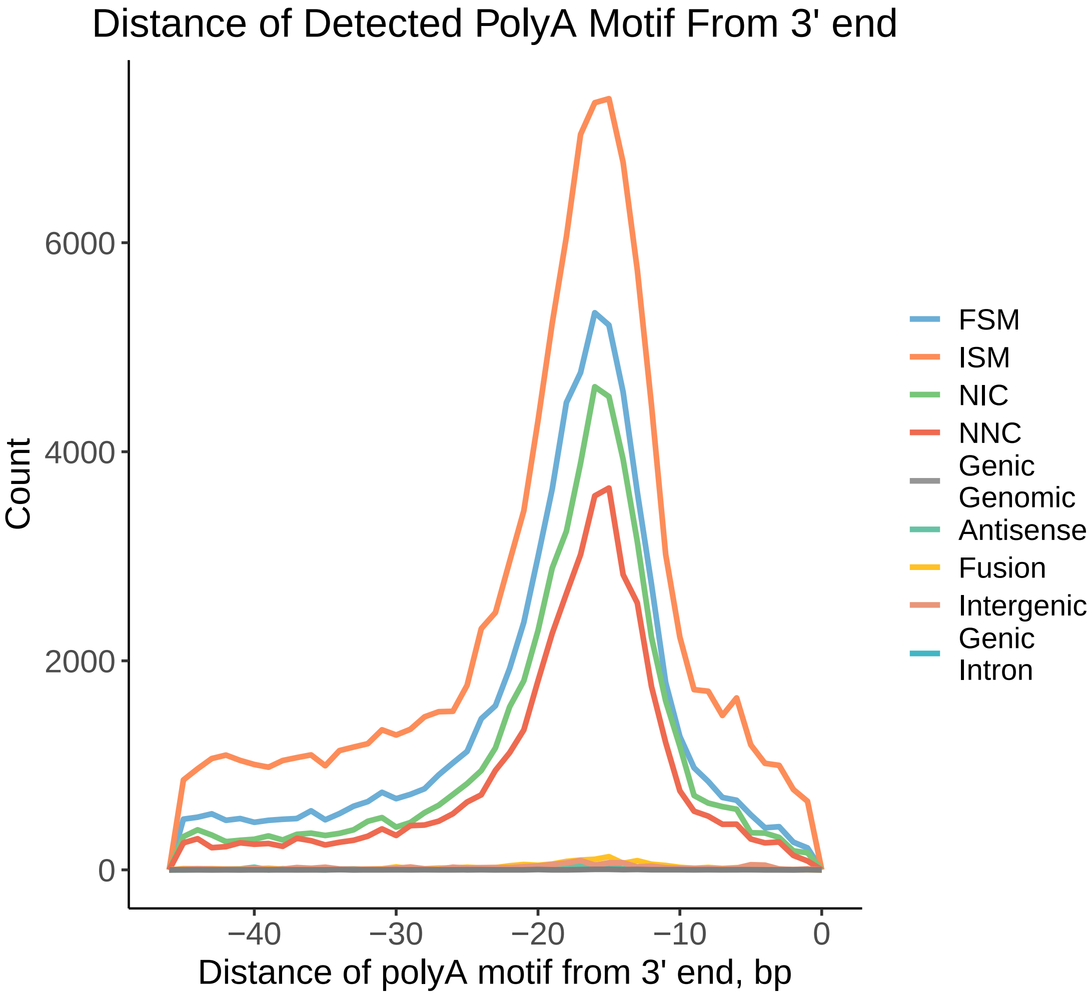
Negative values indicate upstream of annotated polyA site



Distance to Annotated Polyadenylation Site for ISM Intron Retention

Negative values indicate upstream of annotated polyA site

PolyA Distance Analysis

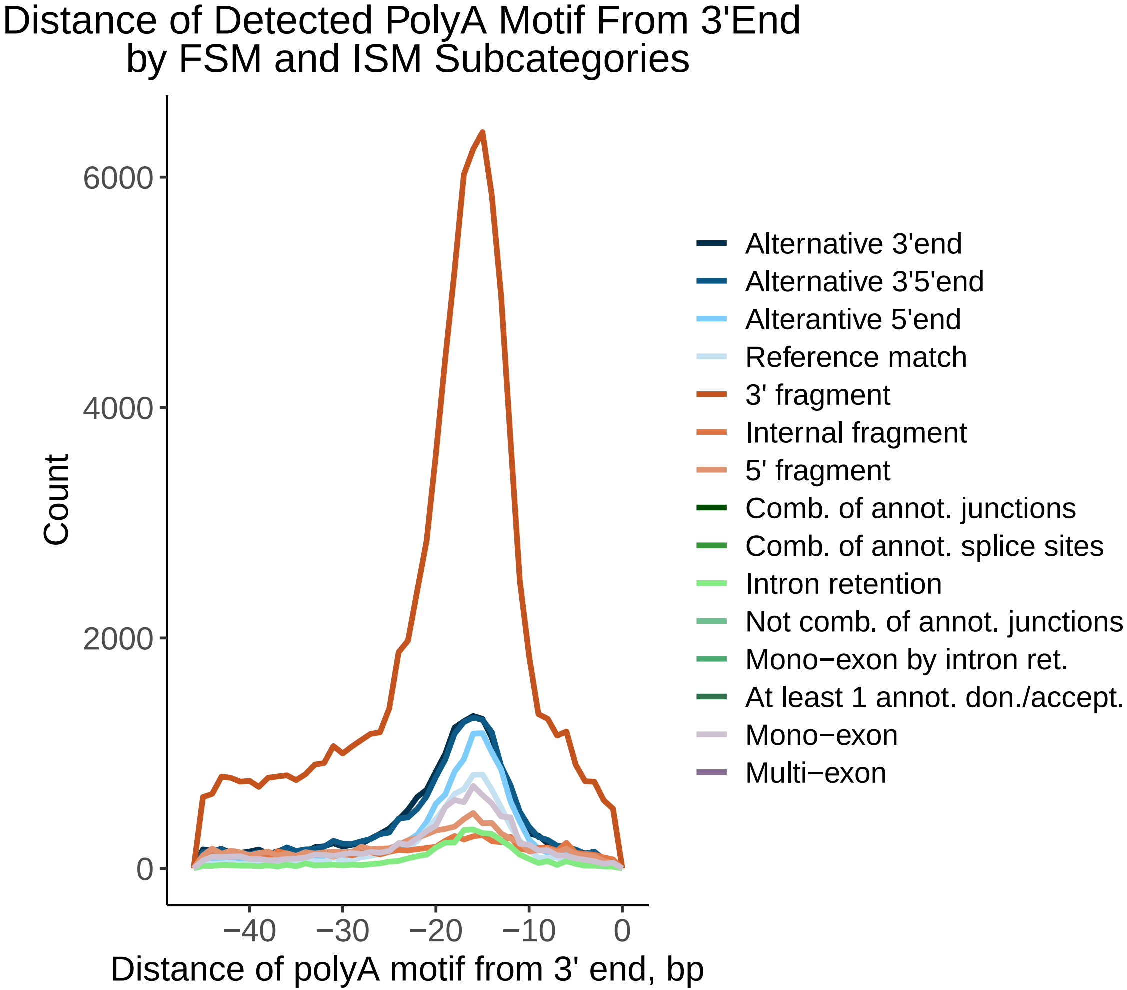

Distance of Detected PolyA Motif From 3' end
Count
6000
4000
2000
0
−40
−30
−20
−10
0
Distance of polyA motif from 3' end, bp
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron

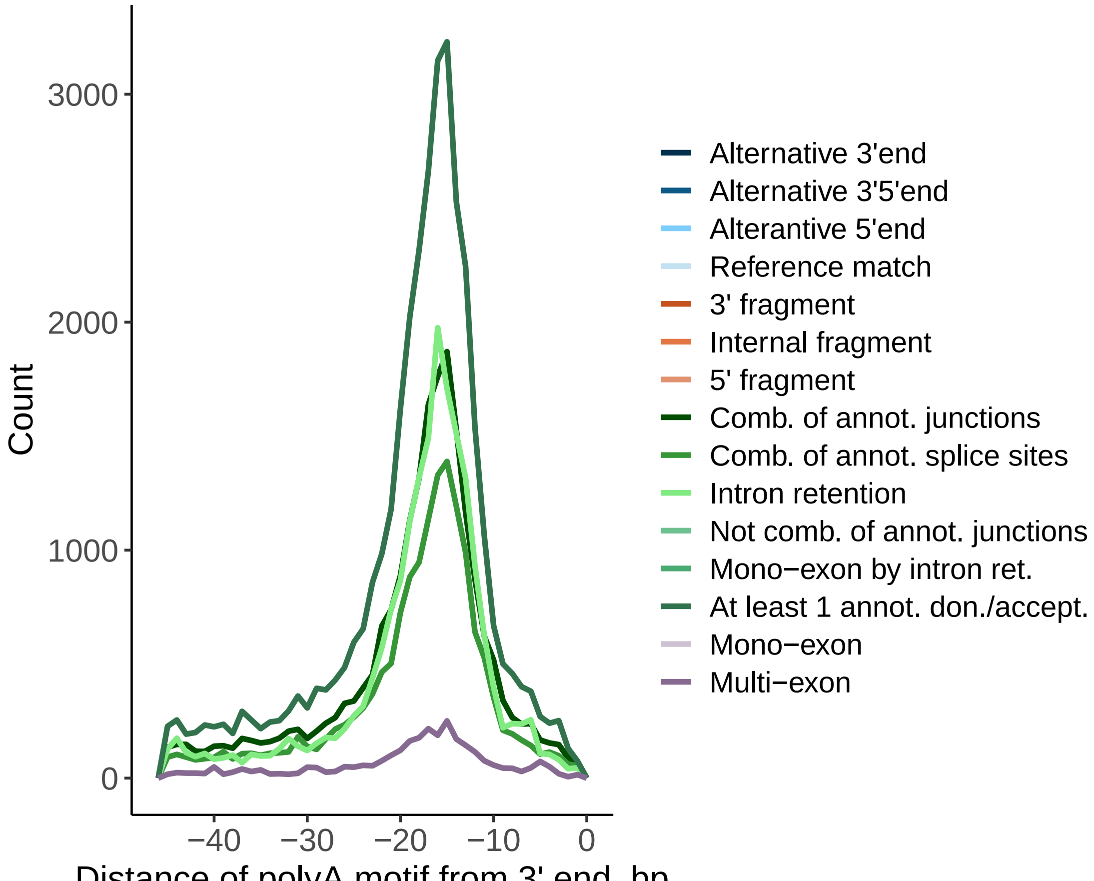
Number of polyA Motifs Detected

Category	Count	polyA Detected	%
FSM	126850	65925	52
ISM	177334	106885	60
NIC	101120	51709	51
NNC	75339	40070	53
Genic Genomic	440	235	53
Antisense	1097	610	56
Fusion	2298	1240	54
Intergenic	1737	1037	60
NA	52	34	65

Frequency of PolyA Motifs

Motif	Count	%
AATAAA	133270	49.8
ATTAAA	39125	14.6
TATAAA	11200	4.2
AGTAAA	9881	3.7
AAAAAG	9625	3.6
AAGAAA	9385	3.5
GGGGCT	8093	3.0
TTTAAA	7244	2.7
AATATA	6011	2.2
CATAAA	5835	2.2
AATACA	5827	2.2
GATAAA	5785	2.2
AAAACA	5428	2.0
AATGAA	5021	1.9
AATAGA	3104	1.2
ACTAAA	2911	1.1


Distance of Detected PolyA Motif From 3'End
by FSM and ISM Subcategories
Count
6000
4000
2000
0
−40
−30
−20
−10
0
Distance of polyA motif from 3' end, bp
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon



Distance of Detected PolyA Motif From 3'End
by Non−FSM/ISM Subcategories

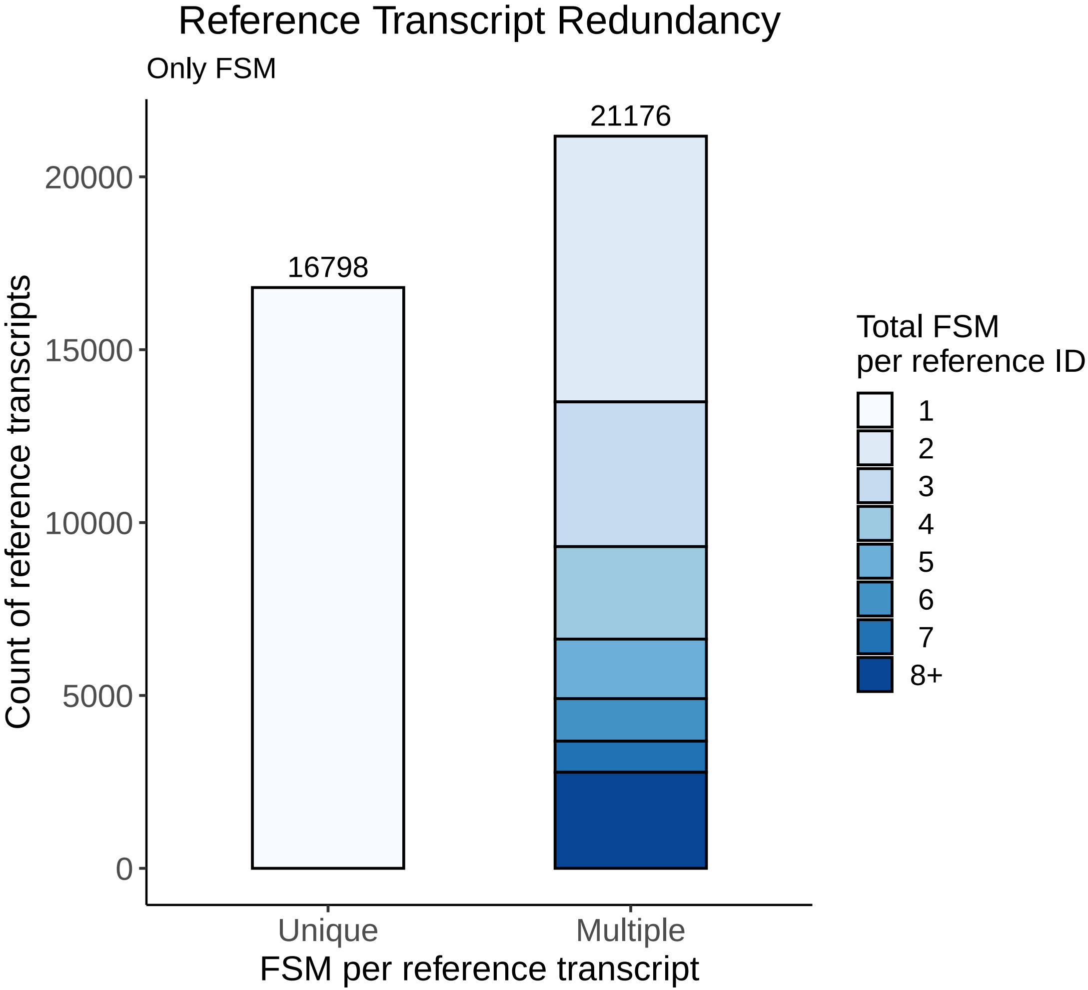
Number of polyA Motifs Detected

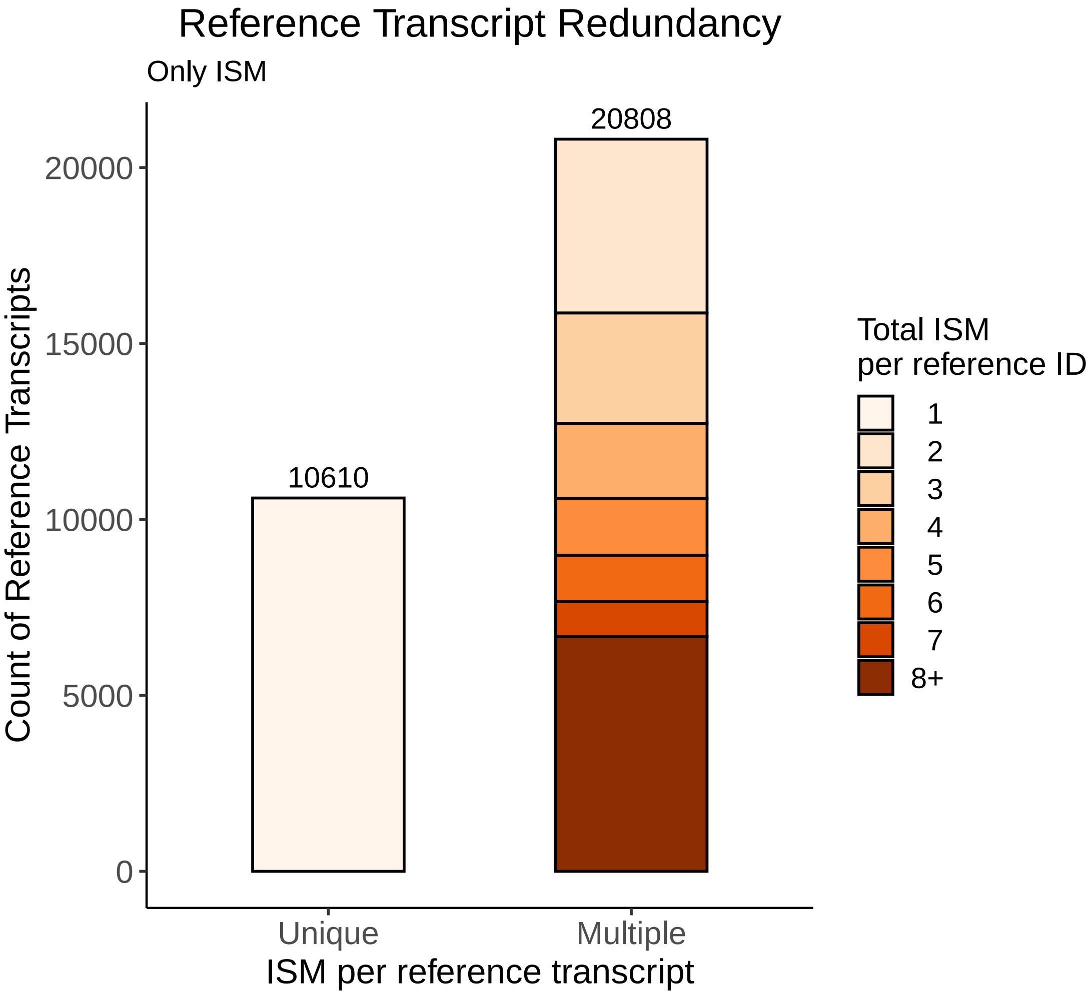
Subcategory	Count	polyA Detected	%
Alternative 3'end	37604	17844	47
Alternative 3'5'end	33979	17784	52
Alterantive 5'end	22835	12281	54
Reference match	16784	8662	52
3' fragment	141591	87175	62
Internal fragment	11143	7109	64
5' fragment	18181	8747	48
Comb. of annot. junctions	42142	21157	50
Comb. of annot. splice sites	29681	15634	53
Intron retention	44671	23342	52
At least 1 annot. don./accept.	66803	35713	53
Mono−exon	15648	9354	60
Multi−exon	5159	2915	57
NA	46	28	61

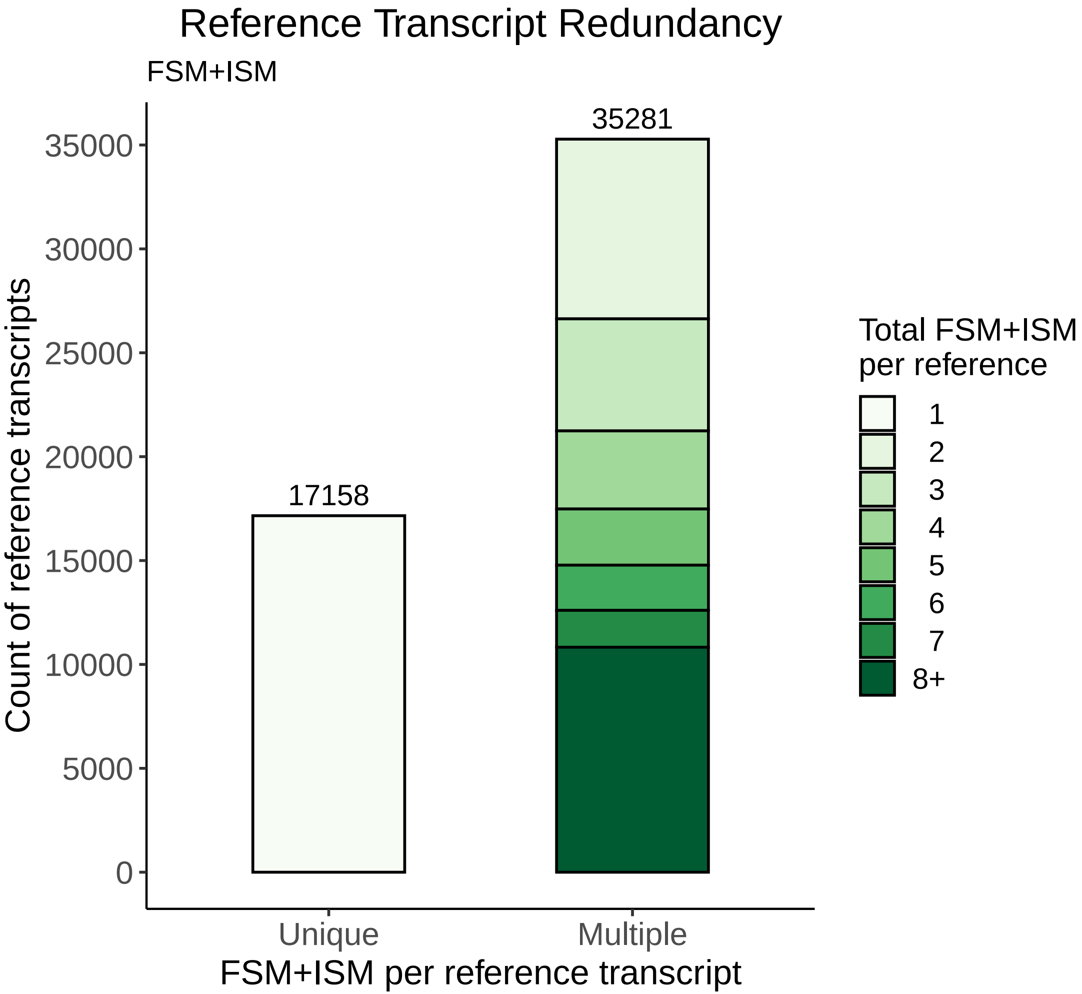
Frequency of PolyA Motifs

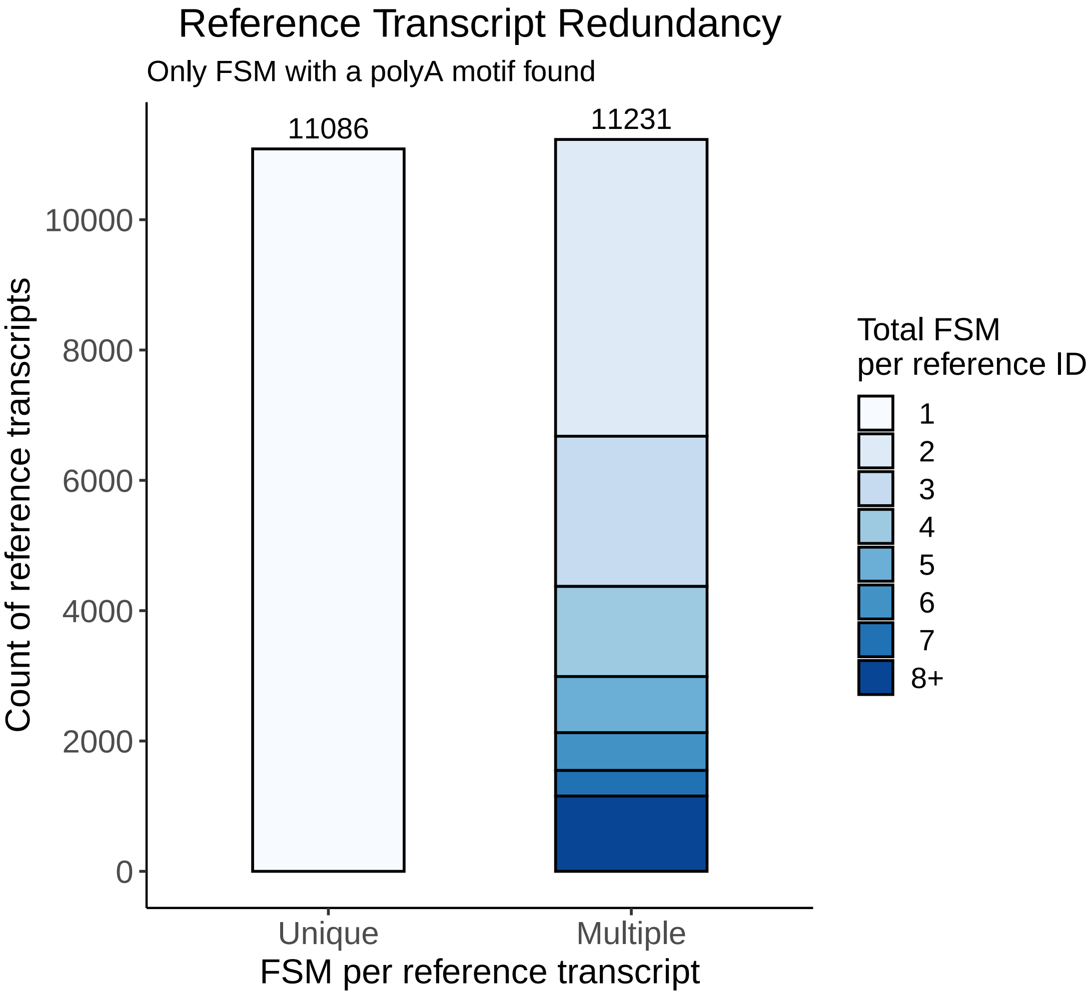
Motif	Count	%
AATAAA	133270	49.8
ATTAAA	39125	14.6
TATAAA	11200	4.2
AGTAAA	9881	3.7
AAAAAG	9625	3.6
AAGAAA	9385	3.5
GGGGCT	8093	3.0
TTTAAA	7244	2.7
AATATA	6011	2.2
CATAAA	5835	2.2
AATACA	5827	2.2
GATAAA	5785	2.2
AAAACA	5428	2.0
AATGAA	5021	1.9
AATAGA	3104	1.2
ACTAAA	2911	1.1

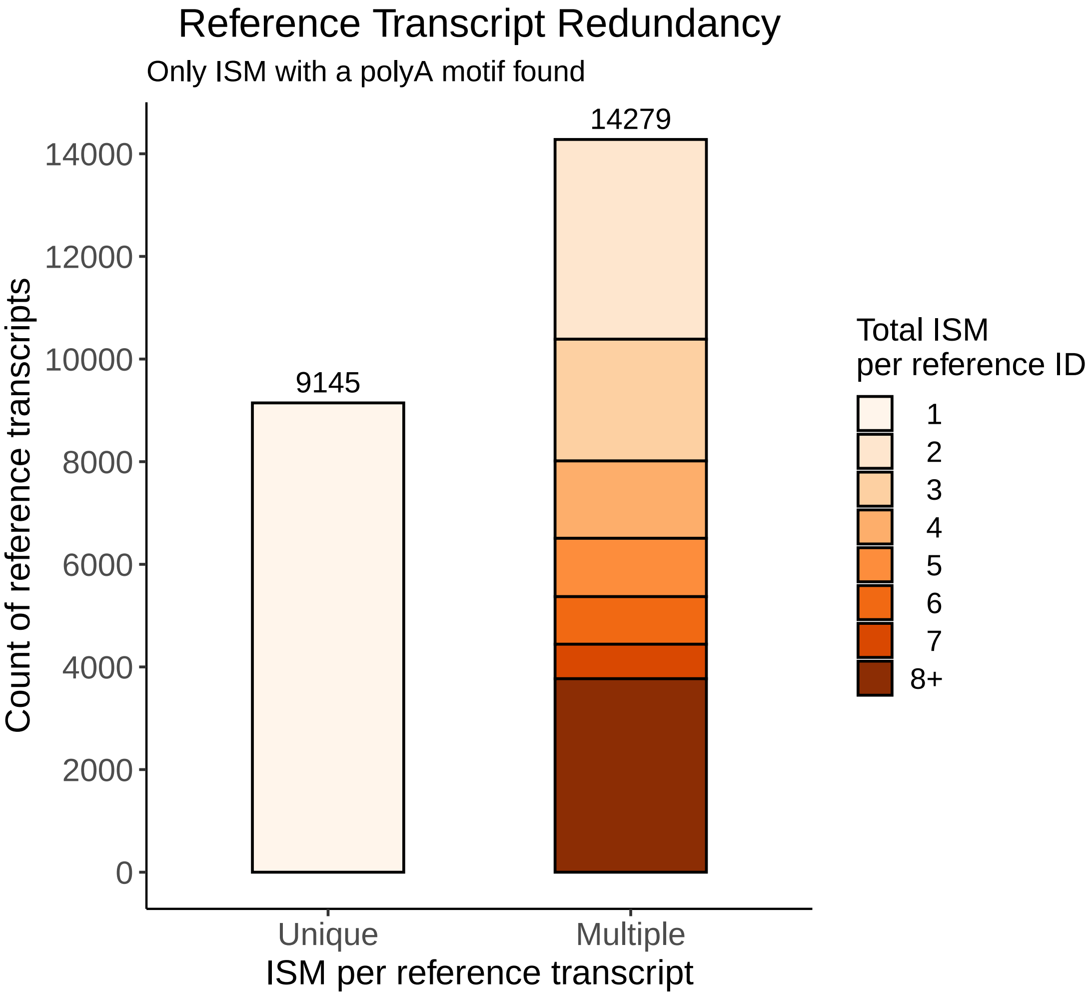
Redundancy Analysis

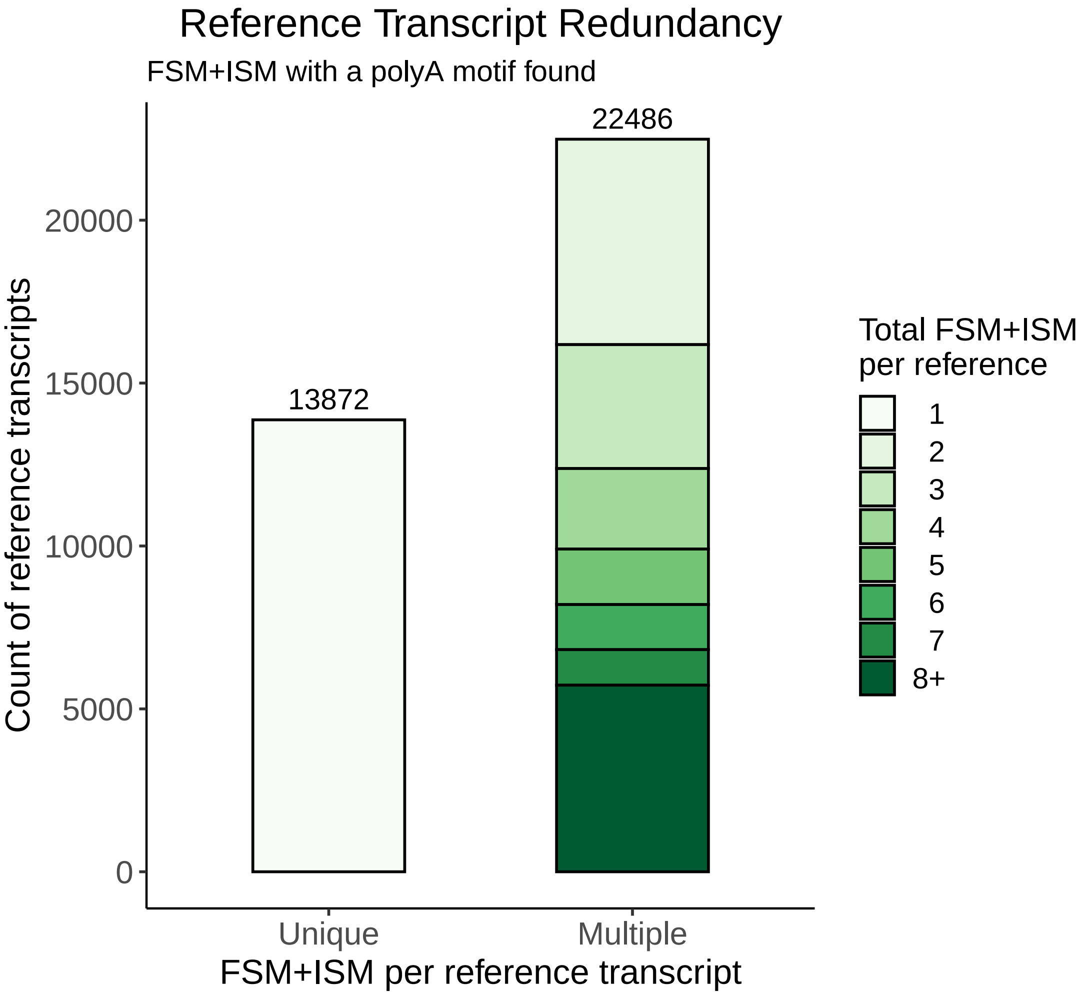

Reference Transcript Redundancy
Only FSM
16798
21176
Count of reference transcripts
20000
15000
10000
5000
0
Unique
Multiple
FSM per reference transcript
Total FSM
per reference ID
1
2
3
4
5
6
7
8+


Reference Transcript Redundancy
Only ISM
Count of Reference Transcripts
20000
15000
10000
5000
0
10610
20808
Unique
Multiple
ISM per reference transcript
Total ISM
per reference ID
1
2
3
4
5
6
7
8+

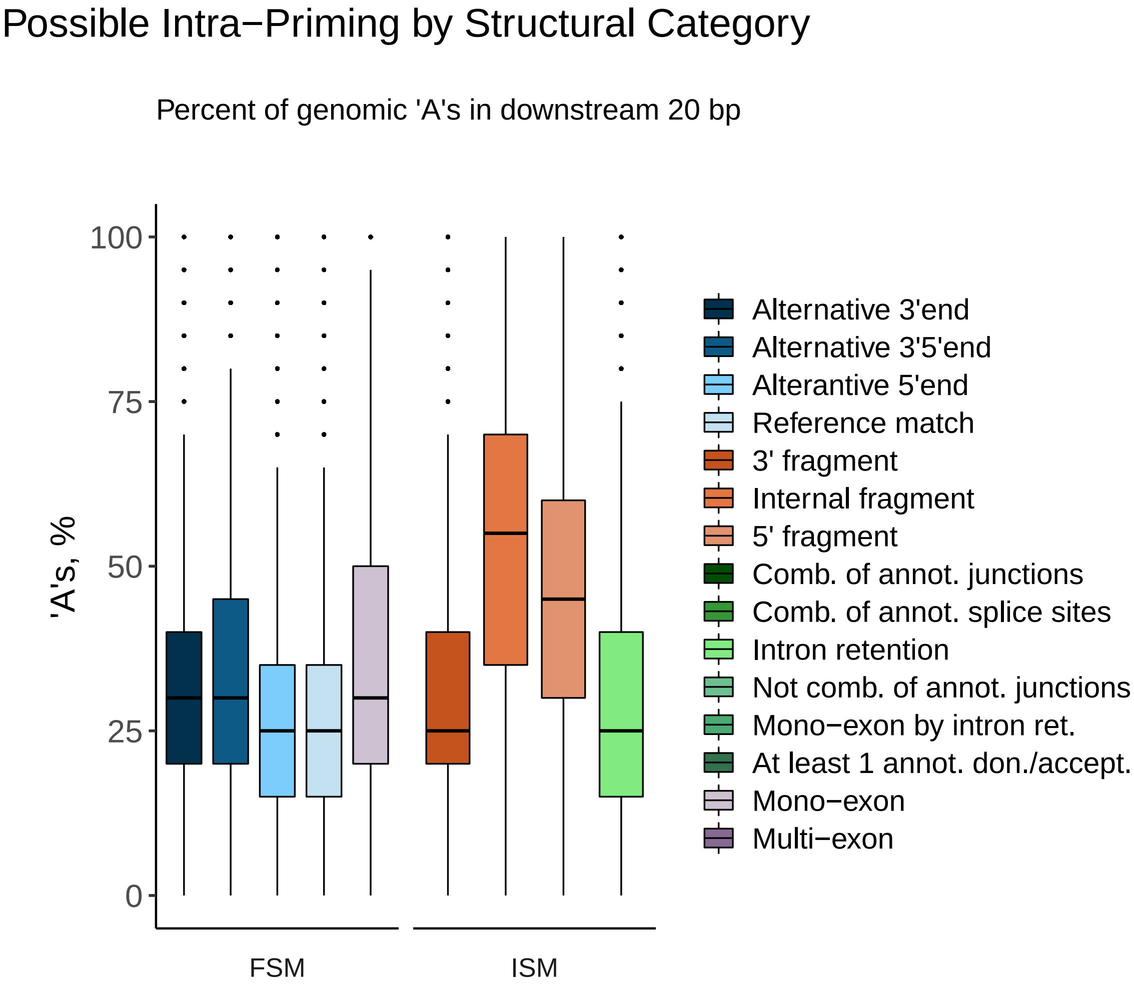

Reference Transcript Redundancy
FSM+ISM
35281
17158
35000
30000
25000
20000
15000
10000
5000
0
Count of reference transcripts
Unique
Multiple
FSM+ISM per reference transcript
Total FSM+ISM per reference
1
2
3
4
5
6
7
8+

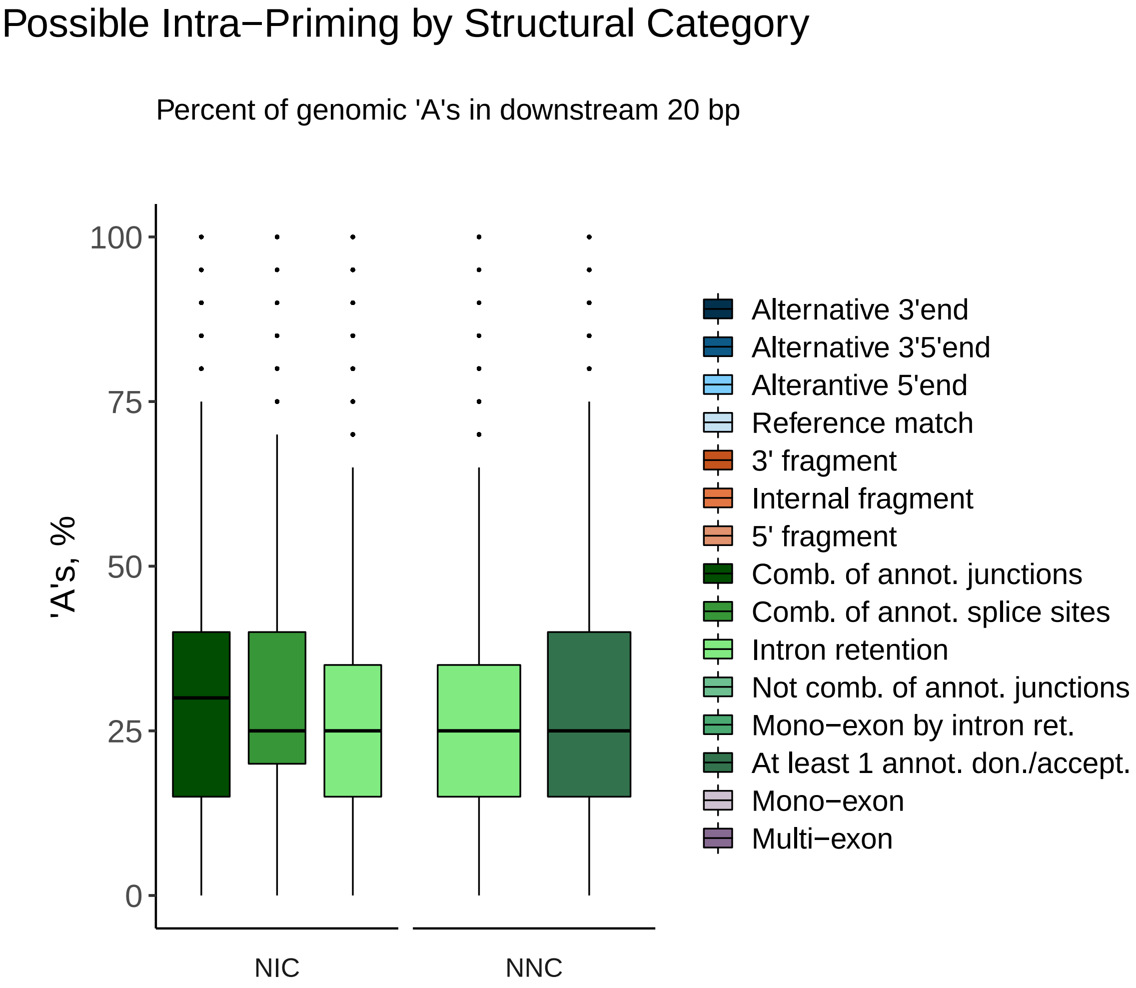

Reference Transcript Redundancy
Only FSM with a polyA motif found
11086
11231
10000
8000
6000
4000
2000
0
Count of reference transcripts
Unique
Multiple
FSM per reference transcript
Total FSM
per reference ID
1
2
3
4
5
6
7
8+

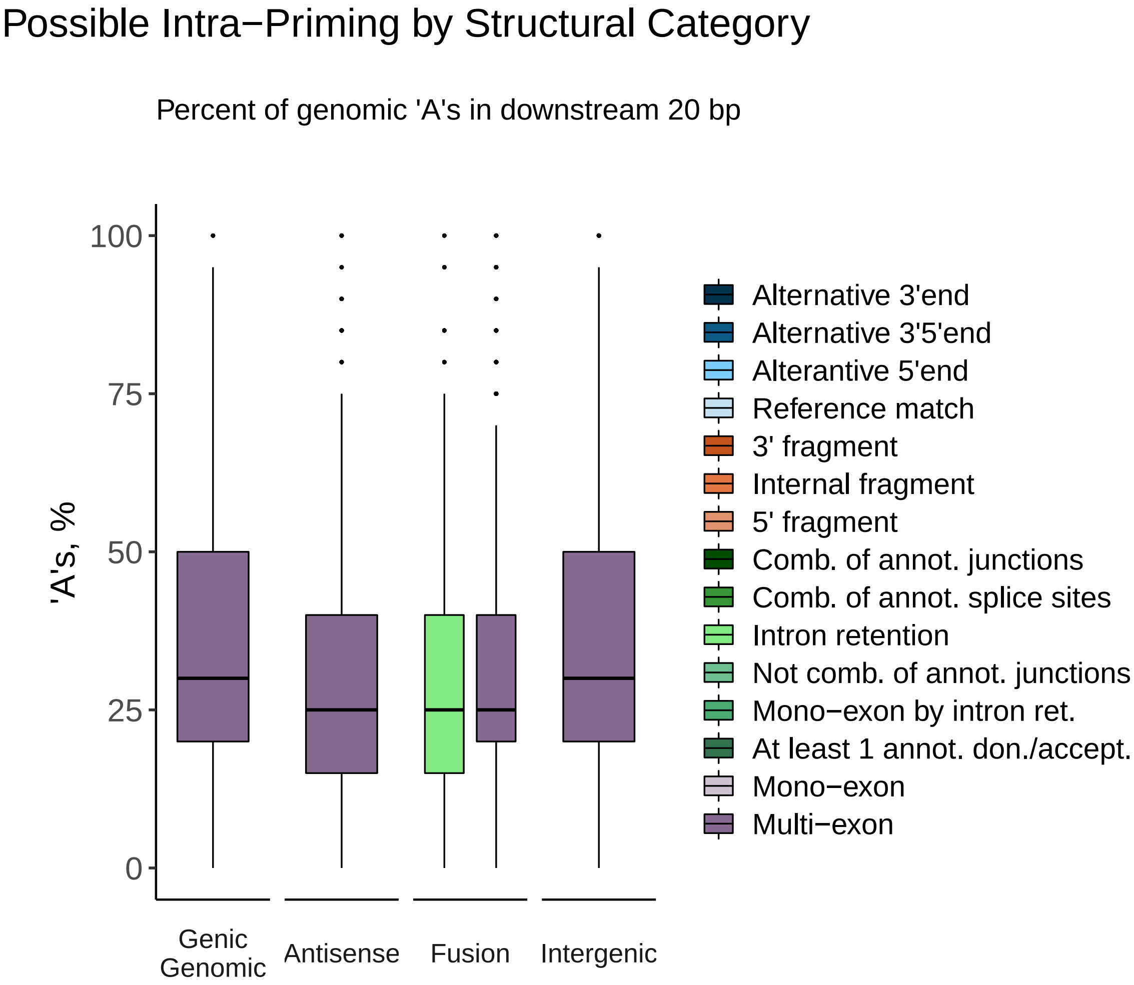

Reference Transcript Redundancy
Only ISM with a polyA motif found
Count of reference transcripts
14000
12000
10000
8000
6000
4000
2000
0
9145
14279
Unique
Multiple
ISM per reference transcript
Total ISM
per reference ID
1
2
3
4
5
6
7
8+

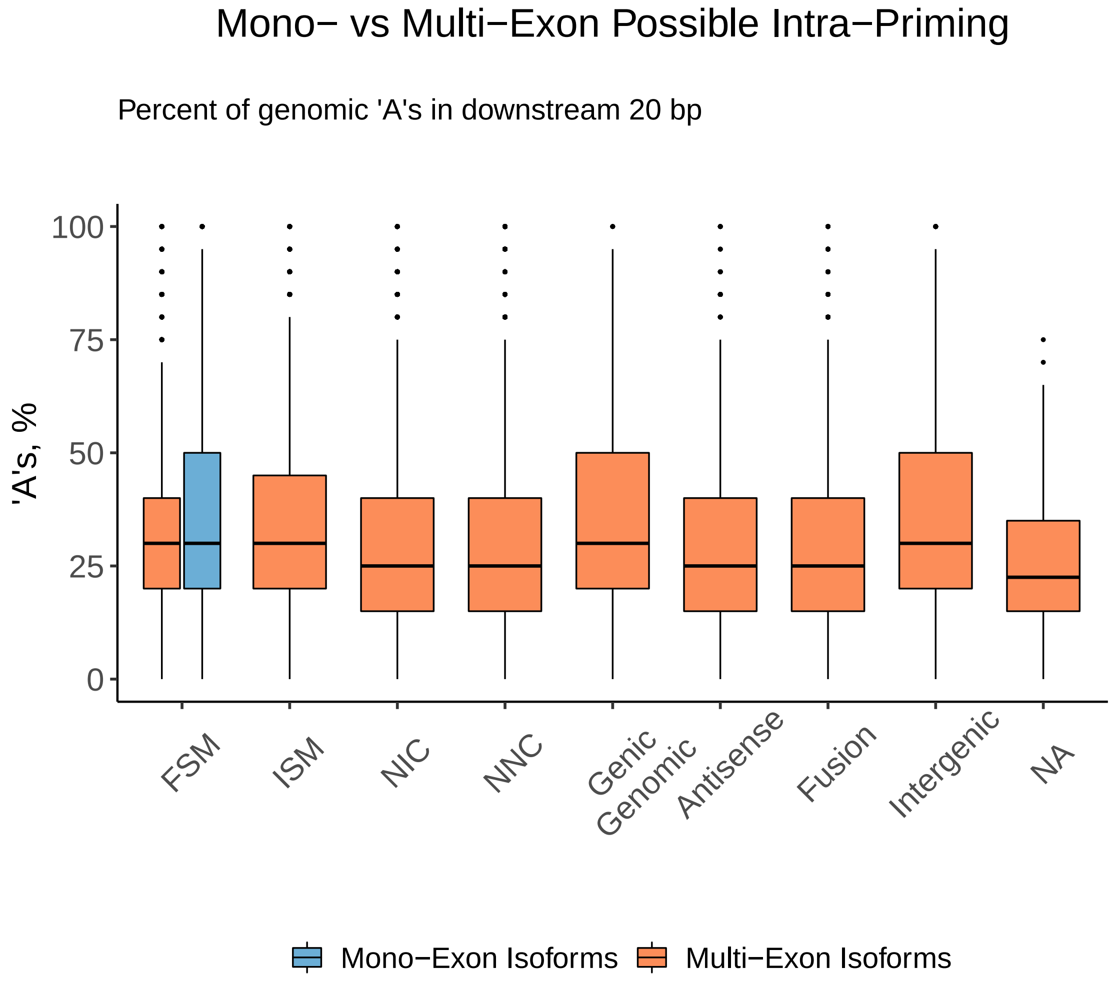

Reference Transcript Redundancy
FSM+ISM with a polyA motif found
Count of reference transcripts
20000
15000
10000
5000
0
13872
22486
Unique
Multiple
FSM+ISM per reference transcript
Total FSM+ISM per reference
1
2
3
4
5
6
7
8+

Intra−Priming Quality Check

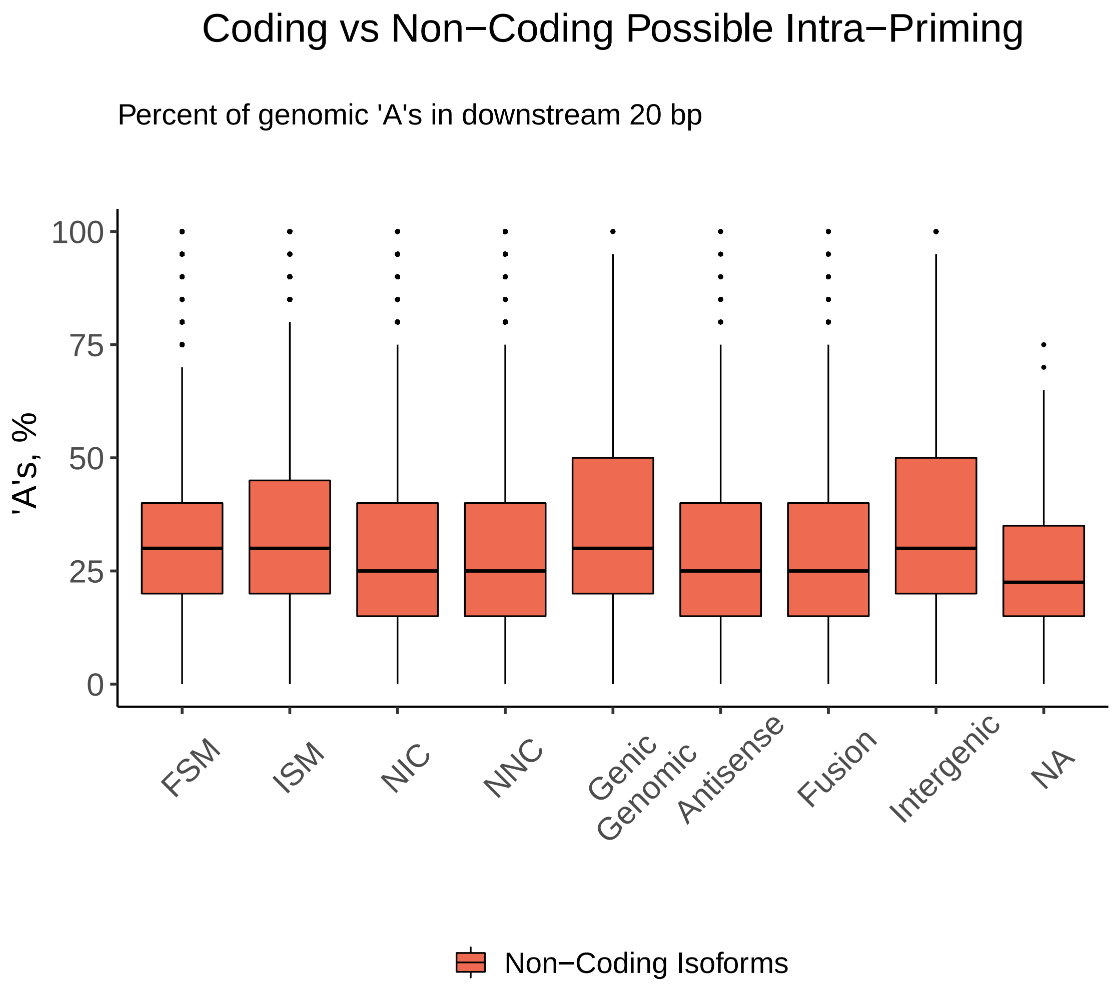

Possible Intra−Priming by Structural Category
Percent of genomic 'A's in downstream 20 bp
'A's, %
100
75
50
25
0
FSM
ISM
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon


Possible Intra−Priming by Structural Category
Percent of genomic 'A's in downstream 20 bp
'A's, %
100
75
50
25
0
NIC
NNC
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon

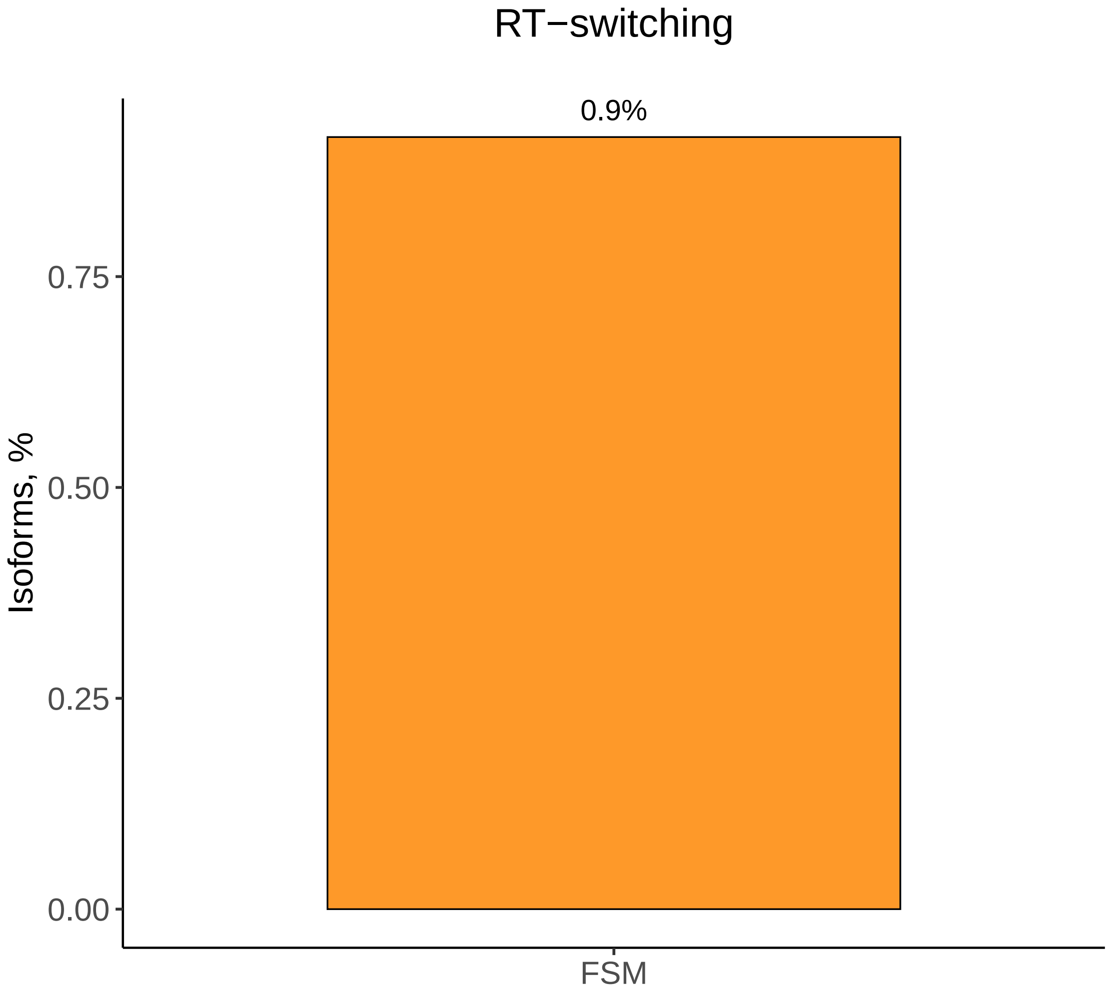

Possible Intra−Priming by Structural Category
Percent of genomic 'A's in downstream 20 bp
'A's, %
100
75
50
25
0
Genic Genomic
Antisense
Fusion
Intergenic
Alternative 3'end
Alternative 3'5'end
Alterantive 5'end
Reference match
3' fragment
Internal fragment
5' fragment
Comb. of annot. junctions
Comb. of annot. splice sites
Intron retention
Not comb. of annot. junctions
Mono−exon by intron ret.
At least 1 annot. don./accept.
Mono−exon
Multi−exon

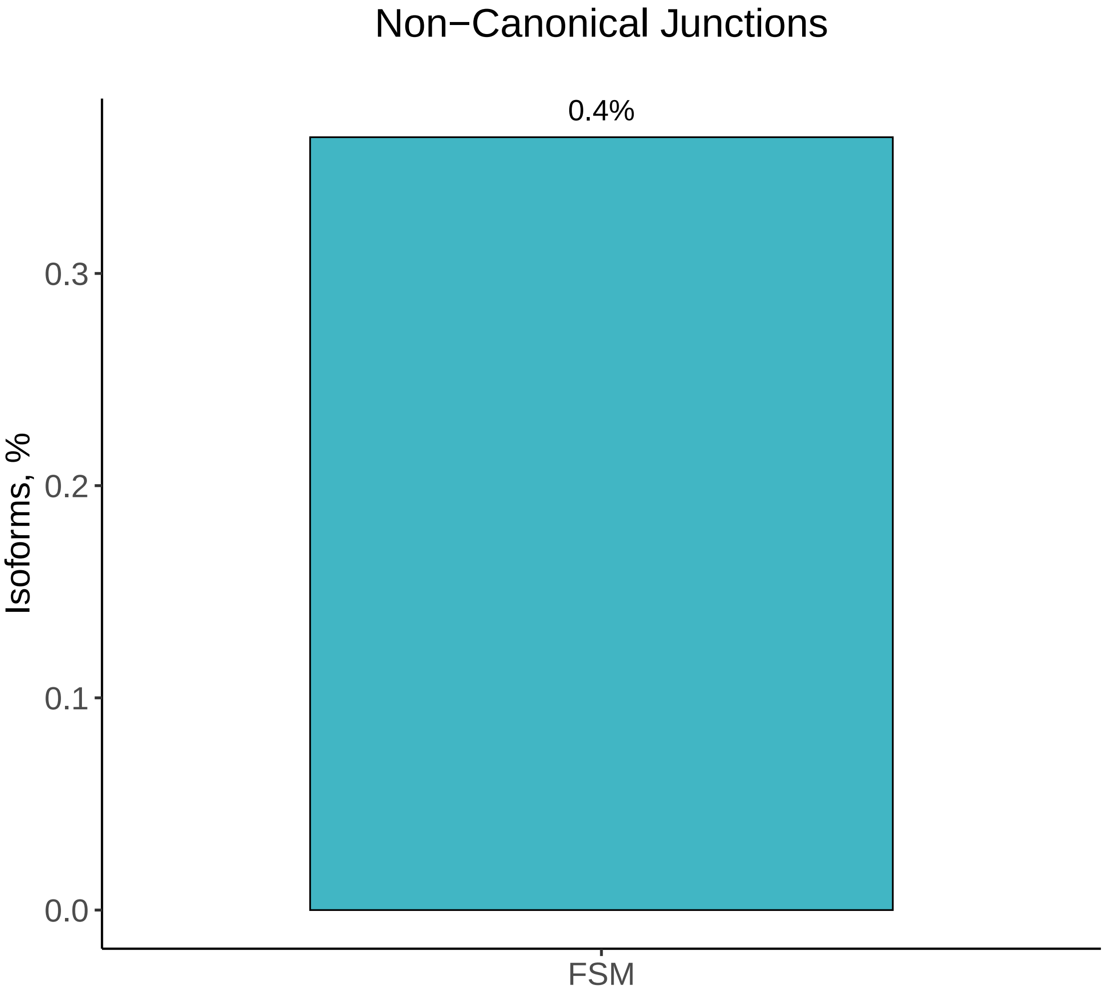

Mono− vs Multi−Exon Possible Intra−Priming

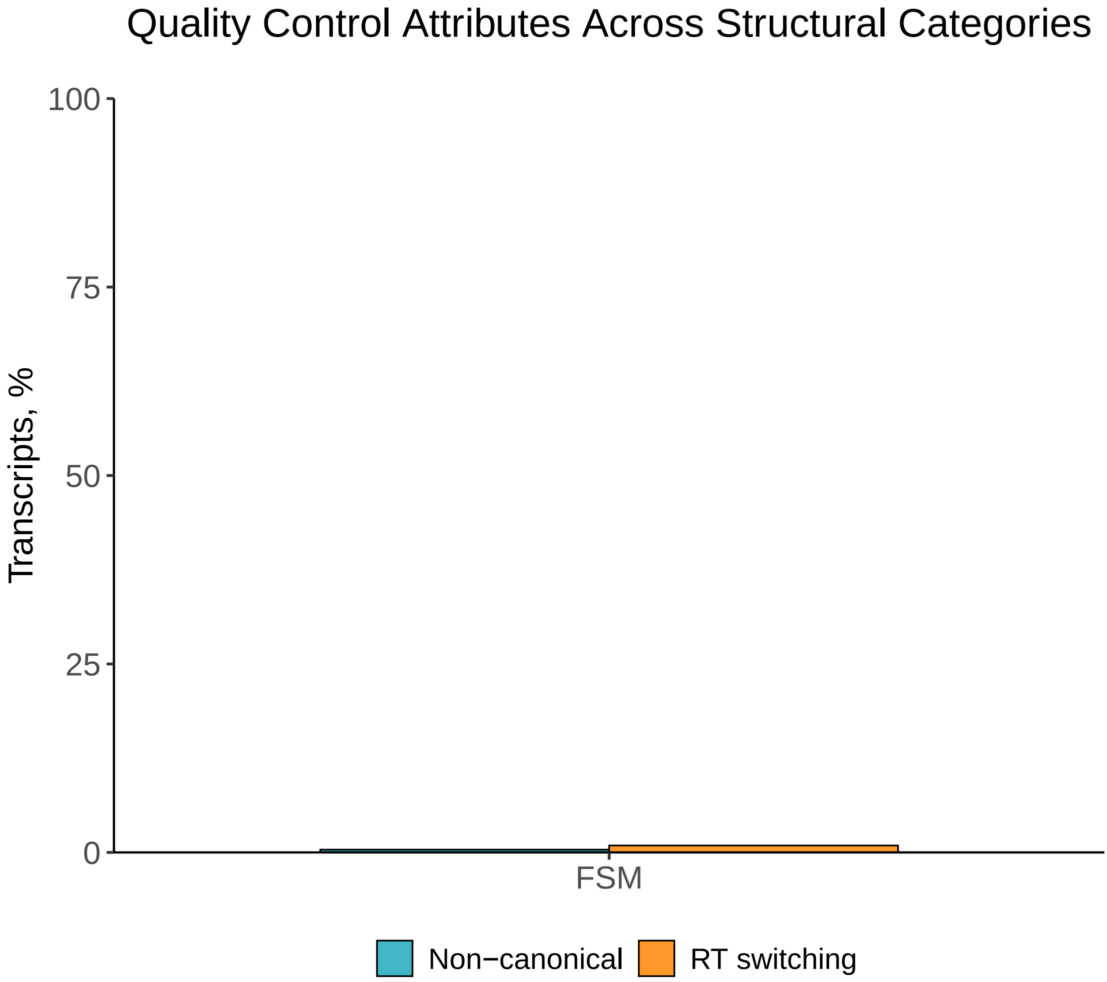
Percent of genomic 'A's in downstream 20 bp


Coding vs Non−Coding Possible Intra−Priming
Percent of genomic 'A's in downstream 20 bp
'A's, %
100
75
50
25
0
FSM
ISM
NIC
NNC
Genic
Genomic
Antisense
Fusion
Intergenic
NA
Non−Coding Isoforms

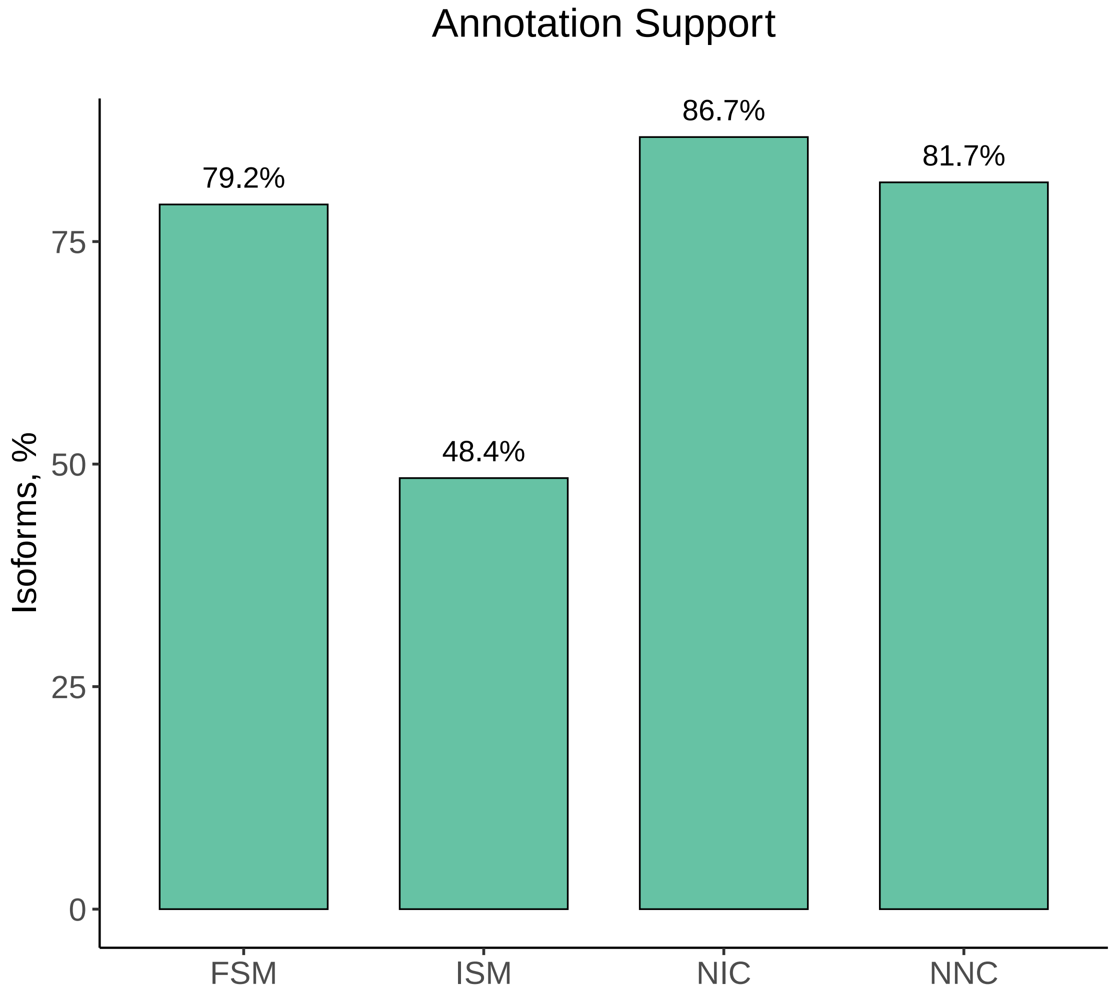
Features of Bad Quality

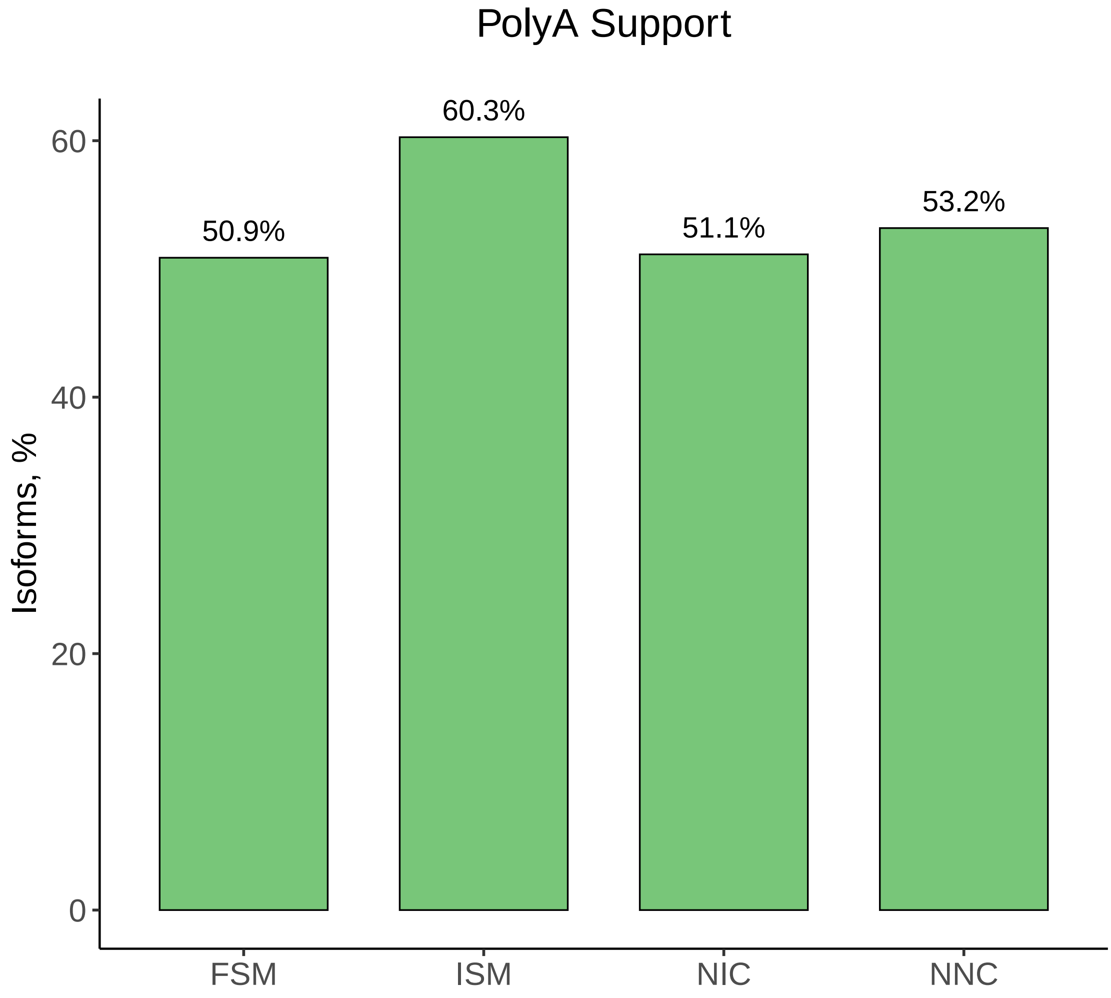

RT−switching
0.9%
Isoforms, %
0.75
0.50
0.25
0.00
FSM

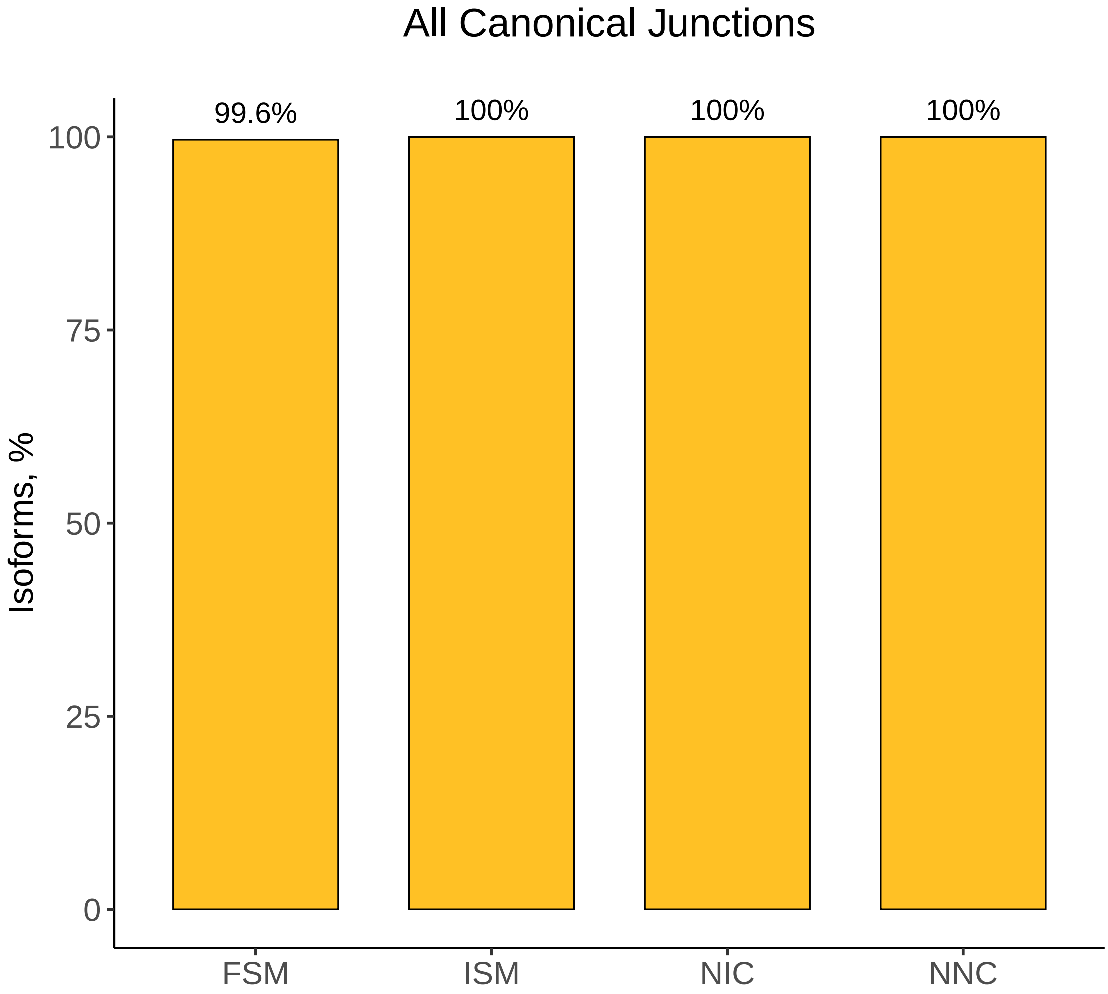

Non−Canonical Junctions
0.4%
0.3
0.2
0.1
0.0
Isoforms, %
FSM

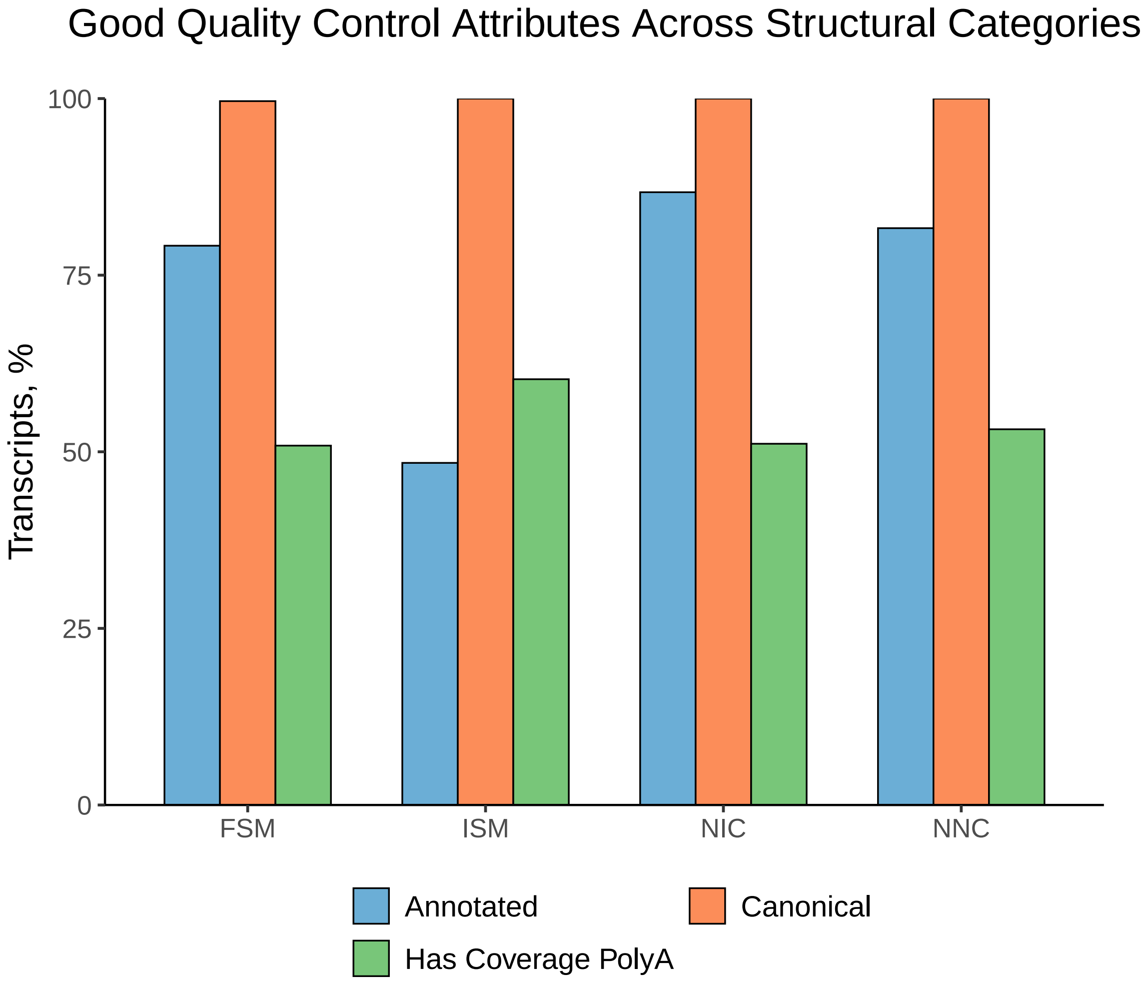

Quality Control Attributes Across Structural Categories
Transcripts, %
100
75
50
25
0
FSM
Non−canonical
RT switching

Features of Good Quality


Annotation Support
Isoforms, %
0
25
50
75
FSM
ISM
NIC
NNC
79.2%
48.4%
86.7%
81.7%


PolyA Support
Isoforms, %
60
40
20
0
50.9%
60.3%
51.1%
53.2%
FSM
ISM
NIC
NNC


All Canonical Junctions
Isoforms, %
0
25
50
75
100
99.6%
100%
100%
100%
FSM
ISM
NIC
NNC


Good Quality Control Attributes Across Structural Categories
Transcripts, %
100
75
50
25
0
FSM
ISM
NIC
NNC
Annotated
Canonical
Has Coverage PolyA