SQANTI2 report

Unique Genes: 14301

Unique Isoforms: 46327

Gene classification

Category	# Genes
Annotated Genes	14300
Novel Genes	1

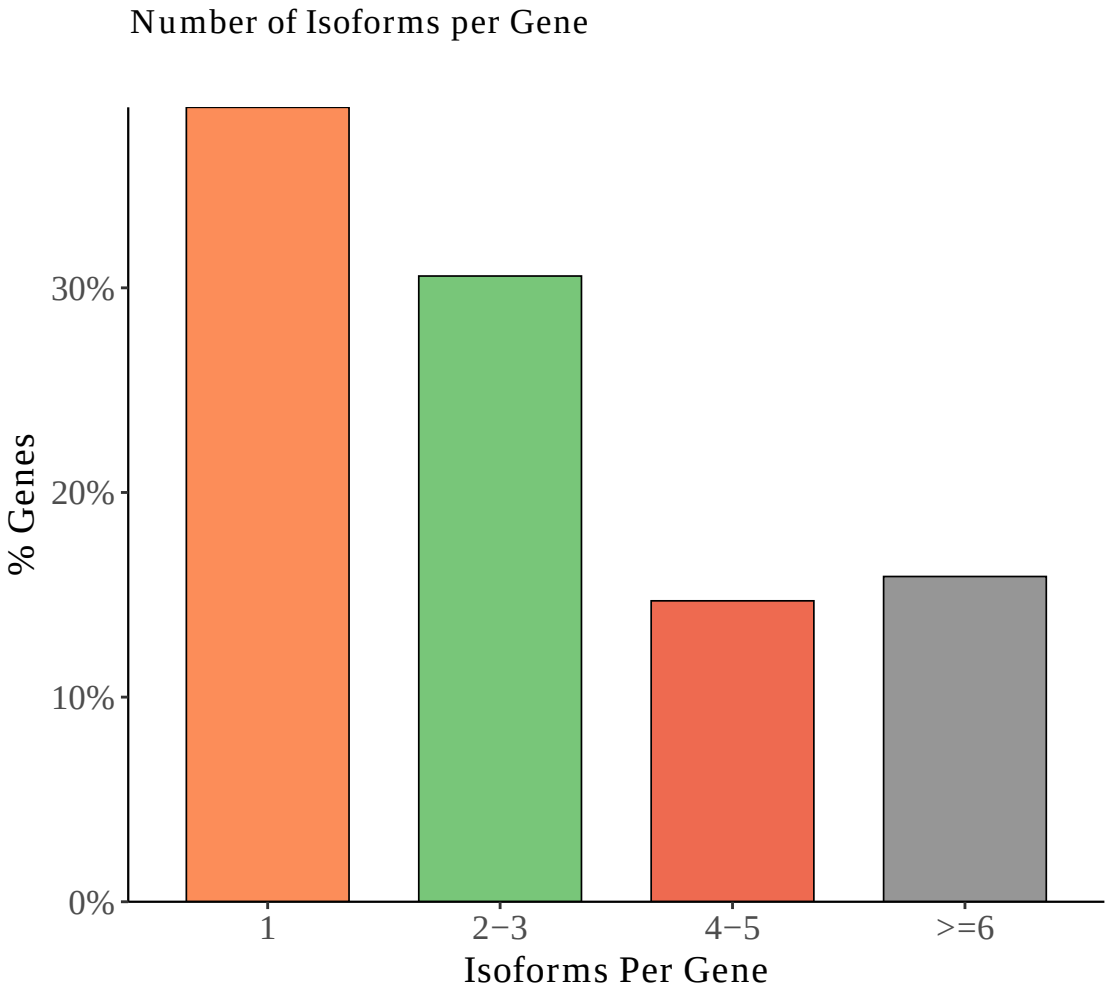
Splice Junction Classification

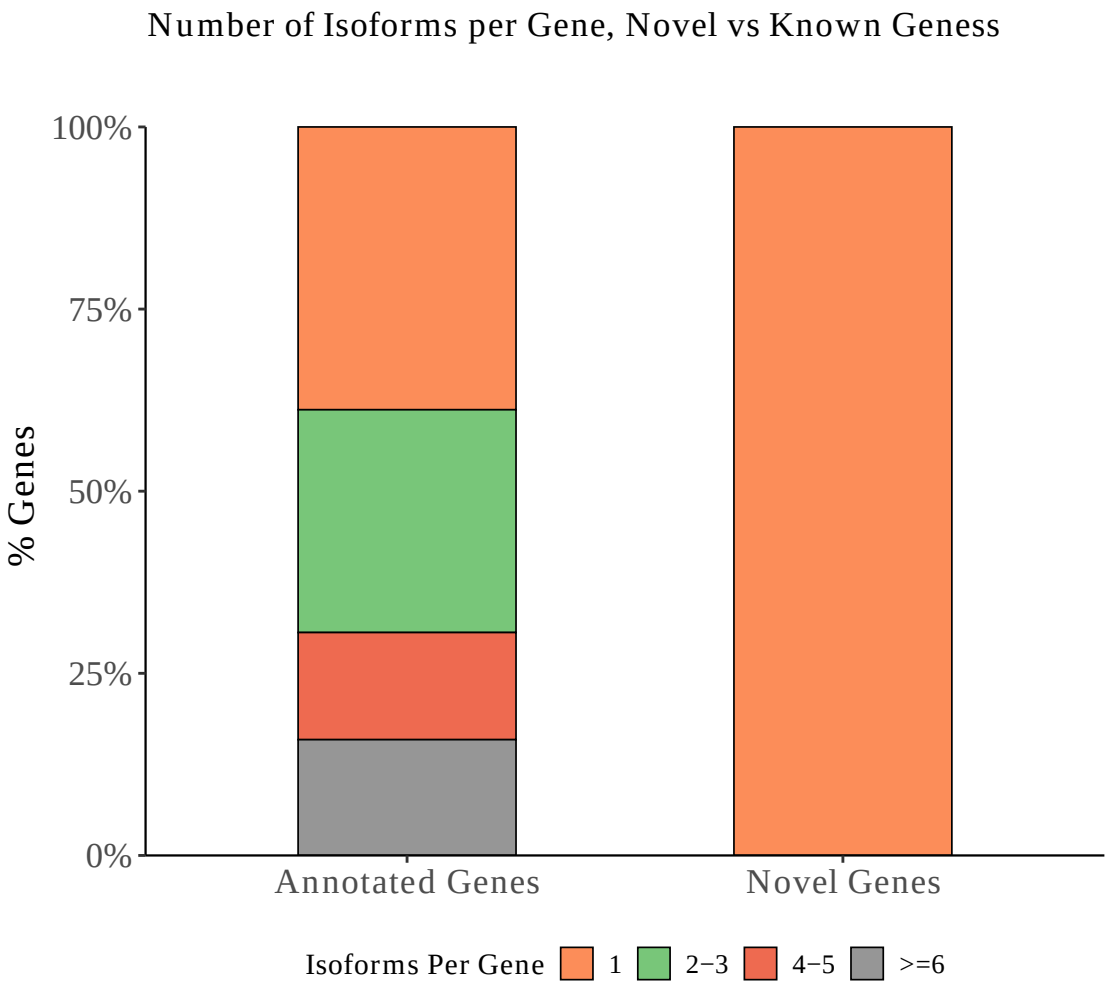
Category	# SJs	Percent
Known canonical	135209	95.57
Known Non−canonical	74	0.05
Novel canonical	6192	4.38
Novel Non−canonical	0	0.00

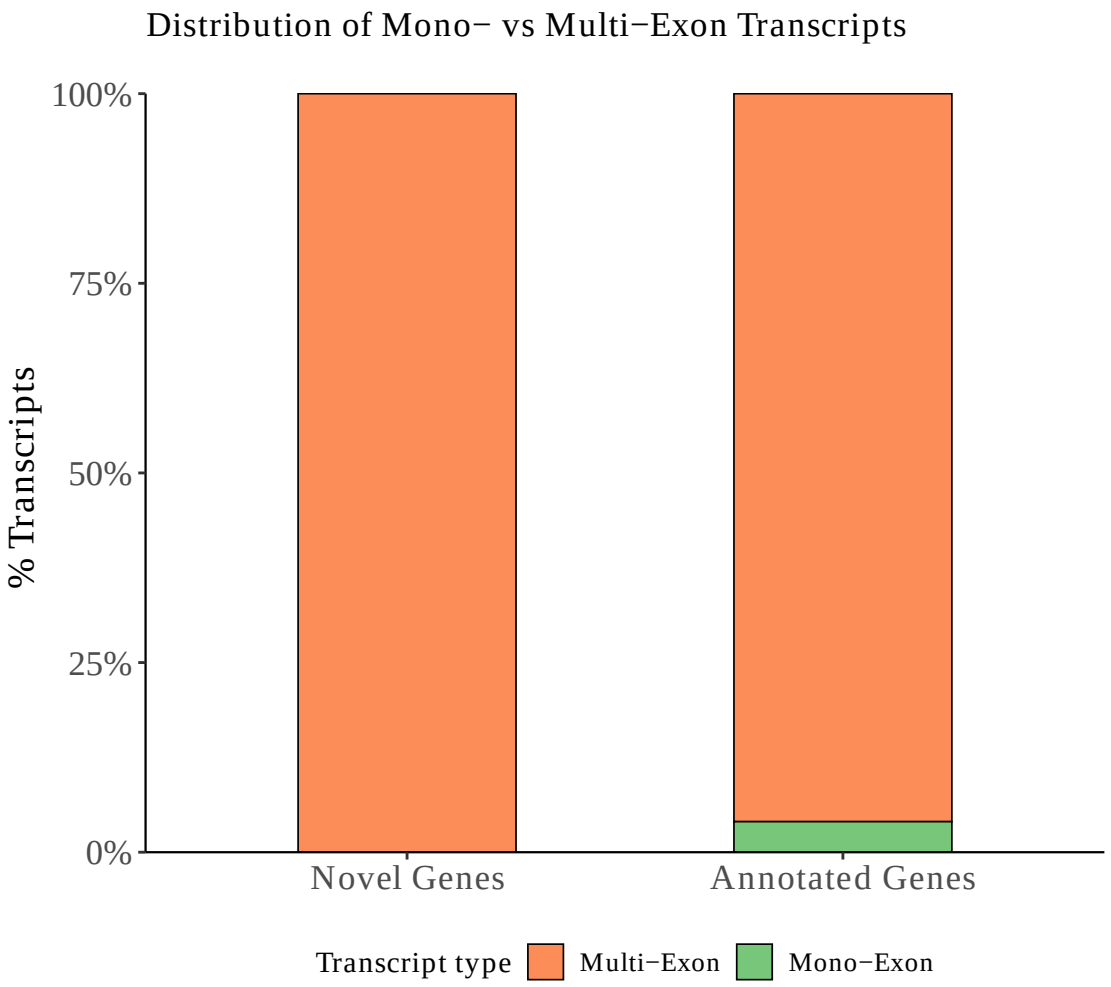
Characterization of transcripts based on splice junctions

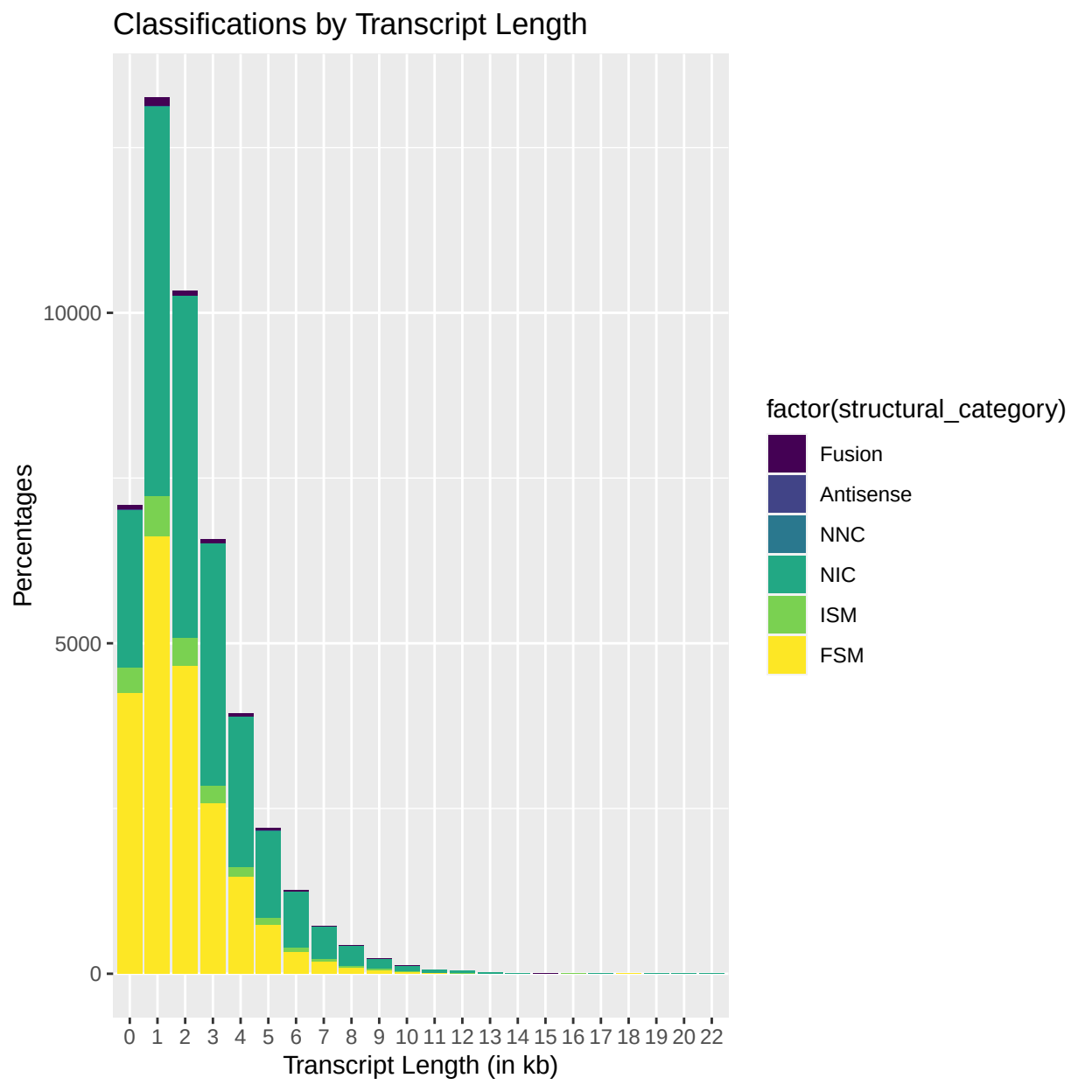
Category	# Isoforms	# Genes
FSM	21043	12412
ISM	2139	1865
NIC	22680	7357
NNC	24	19
Antisense	1	1
Fusion	440	317

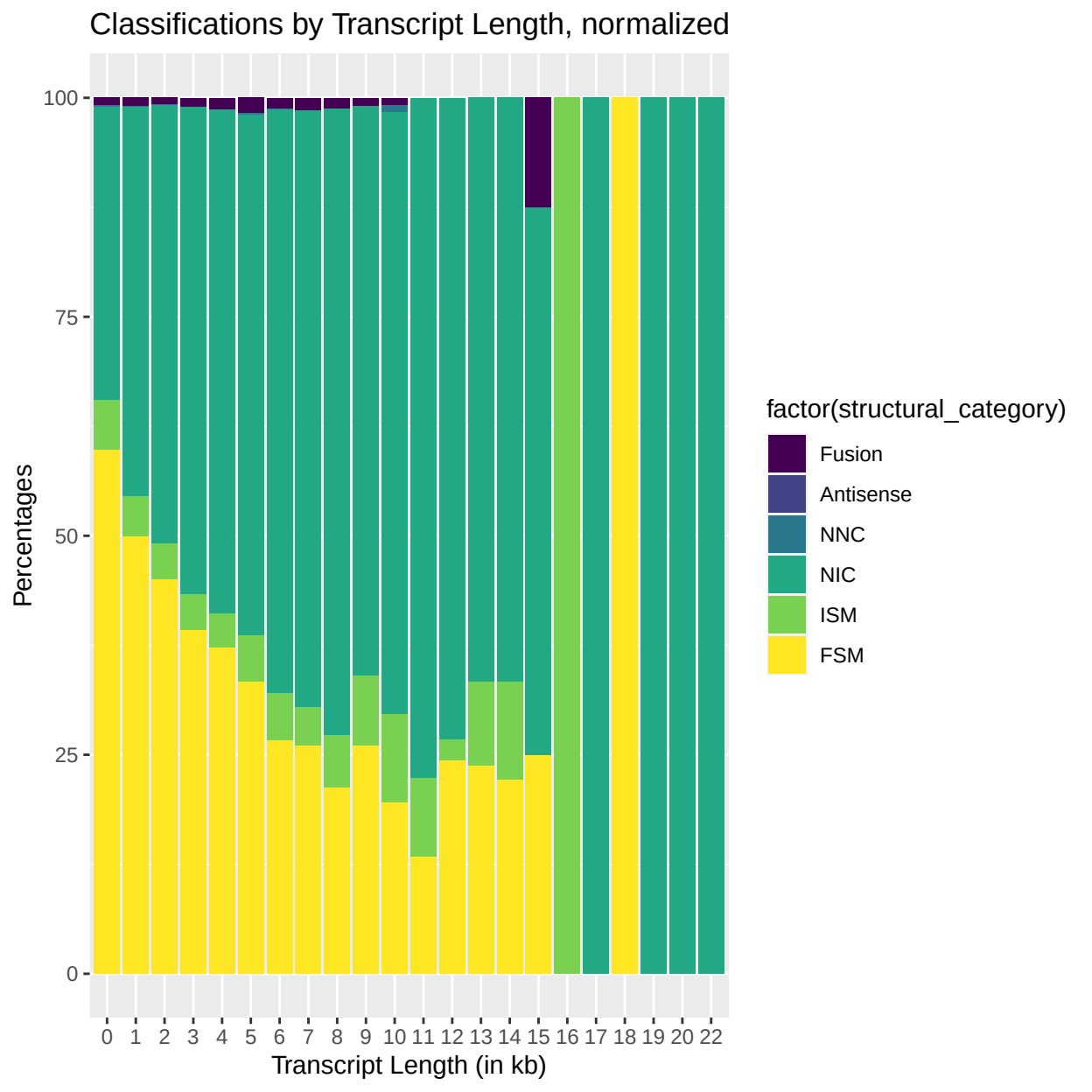
Gene Characterization

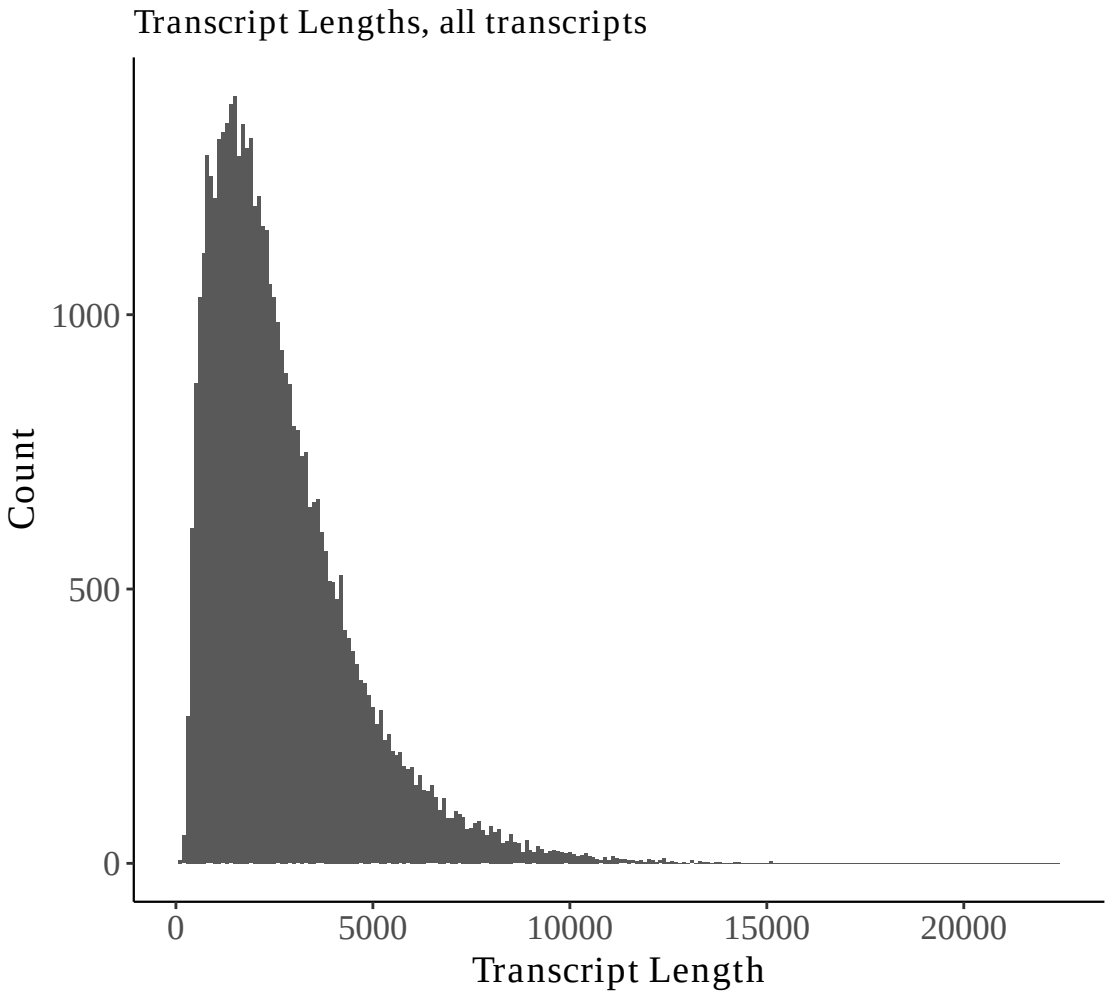

Number of Isoforms per Gene
% Genes
30%
20%
10%
0%
1
2−3
4−5
>=6
Isoforms Per Gene

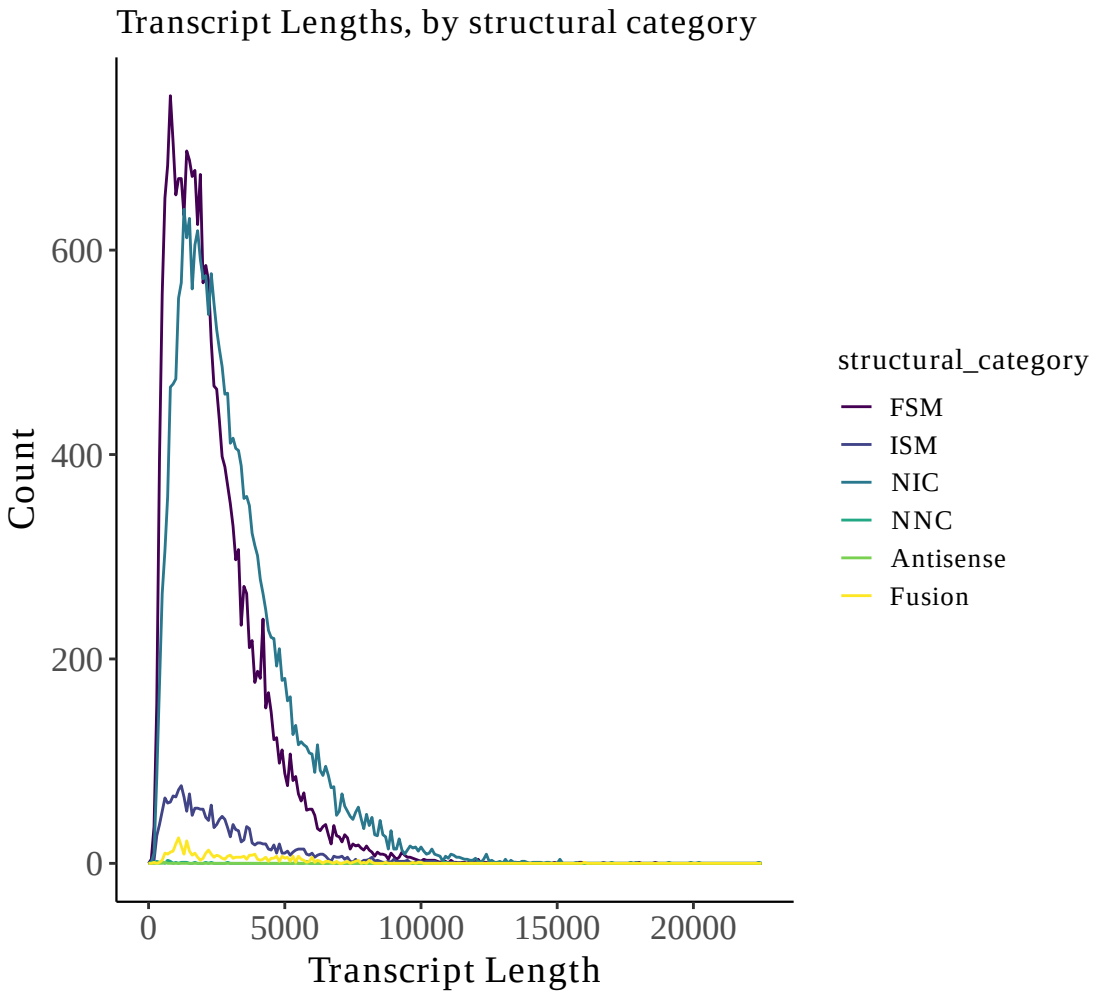

Number of Isoforms per Gene, Novel vs Known Geness
100%
75%
50%
25%
0%
% Genes
Annotated Genes
Novel Genes
Isoforms Per Gene
1
2−3
4−5
>=6

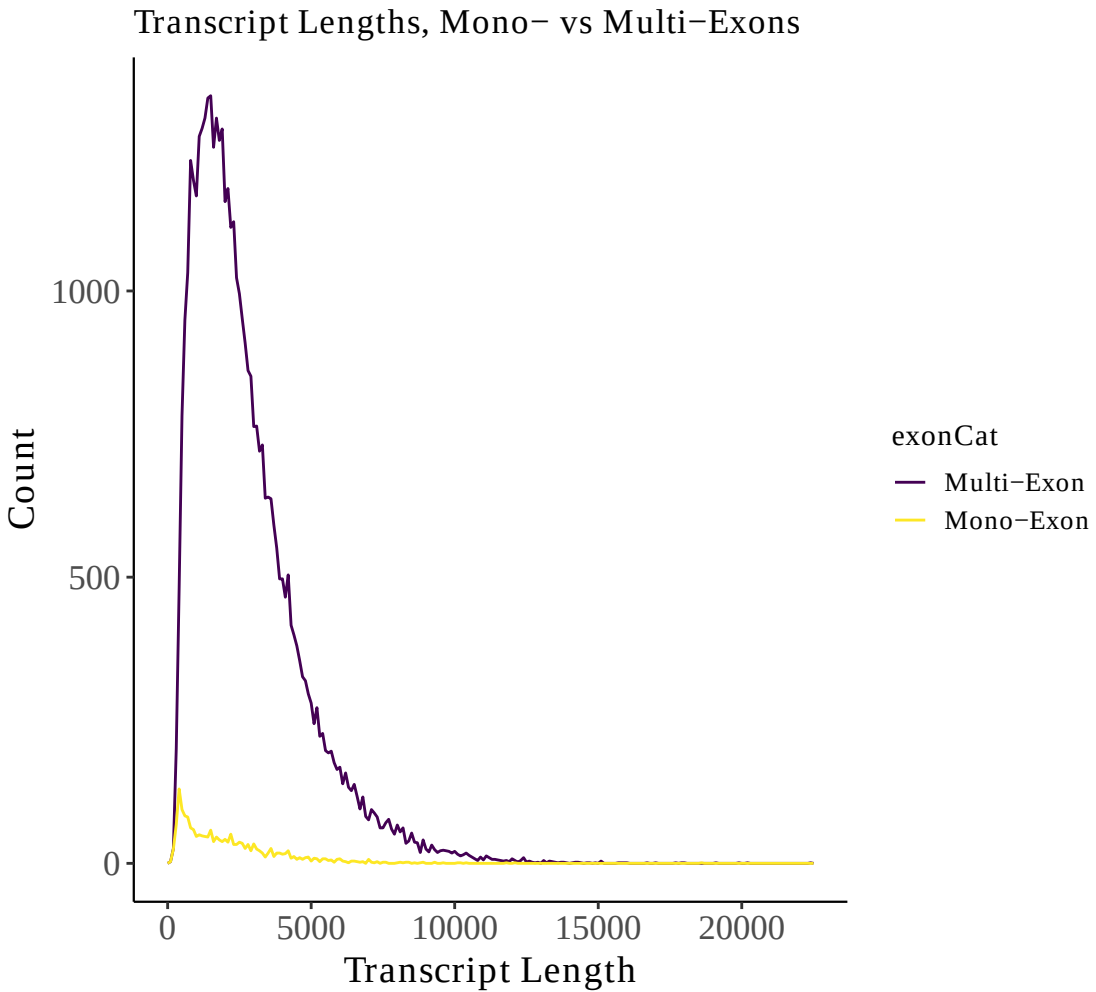

Distribution of Mono− vs Multi−Exon Transcripts
100%
75%
50%
25%
0%
% Transcripts
Novel Genes
Annotated Genes
Transcript type
Multi−Exon
Mono−Exon


Classifications by Transcript Length
Percentages
10000
5000
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 22
Transcript Length (in kb)
factor(structural_category)
Fusion
Antisense
NNC
NIC
ISM
FSM

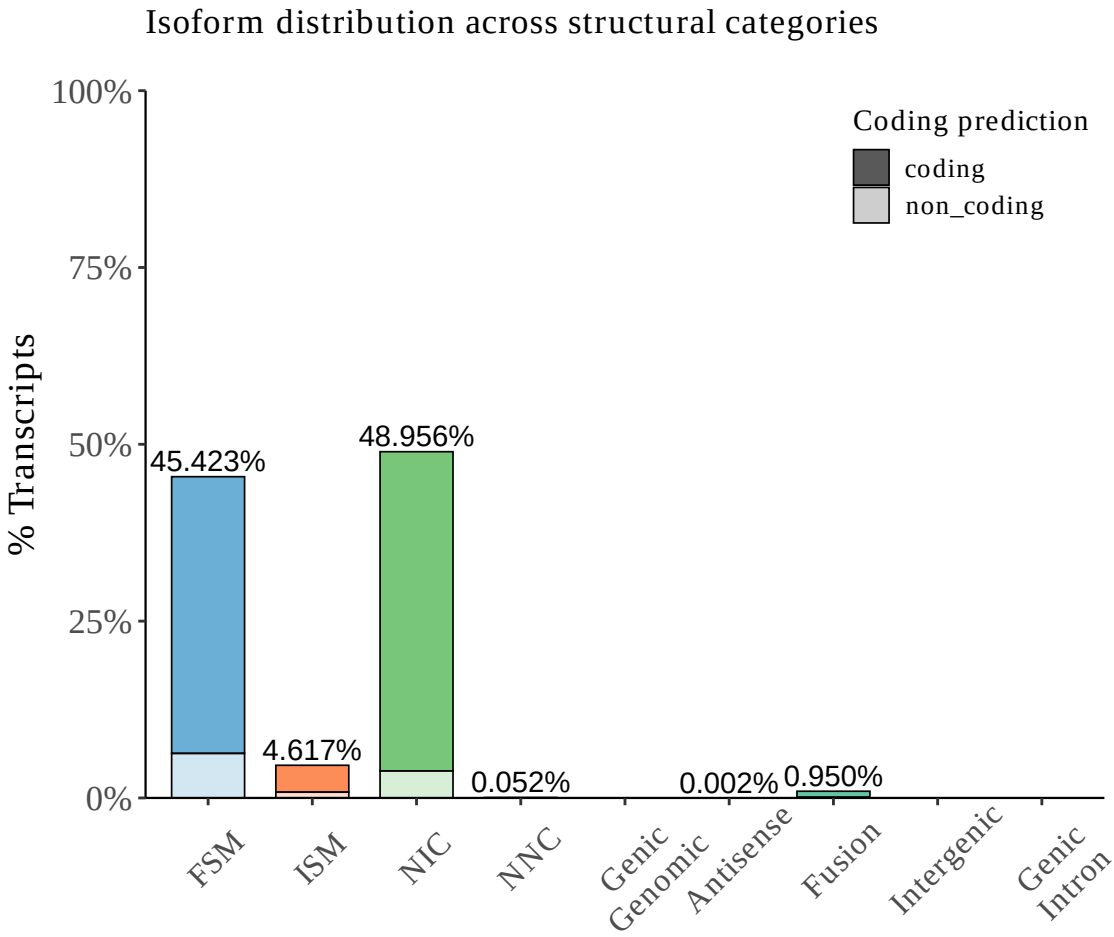

Classifications by Transcript Length, normalized
Percentages
100
75
50
25
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 22
Transcript Length (in kb)
factor(structural_category)
Fusion
Antisense
NNC
NIC
ISM
FSM

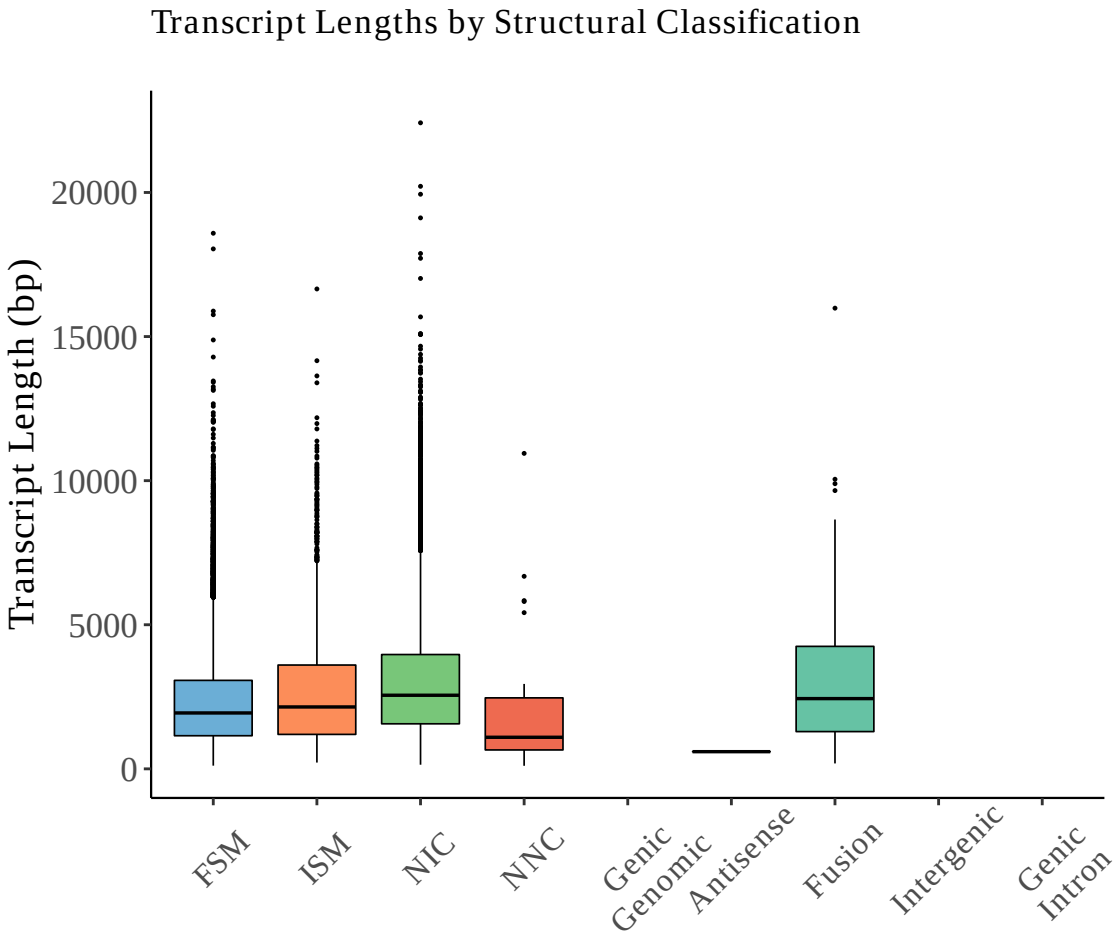

Transcript Lengths, all transcripts
Count
1000
500
0
0
5000
10000
15000
20000
Transcript Length

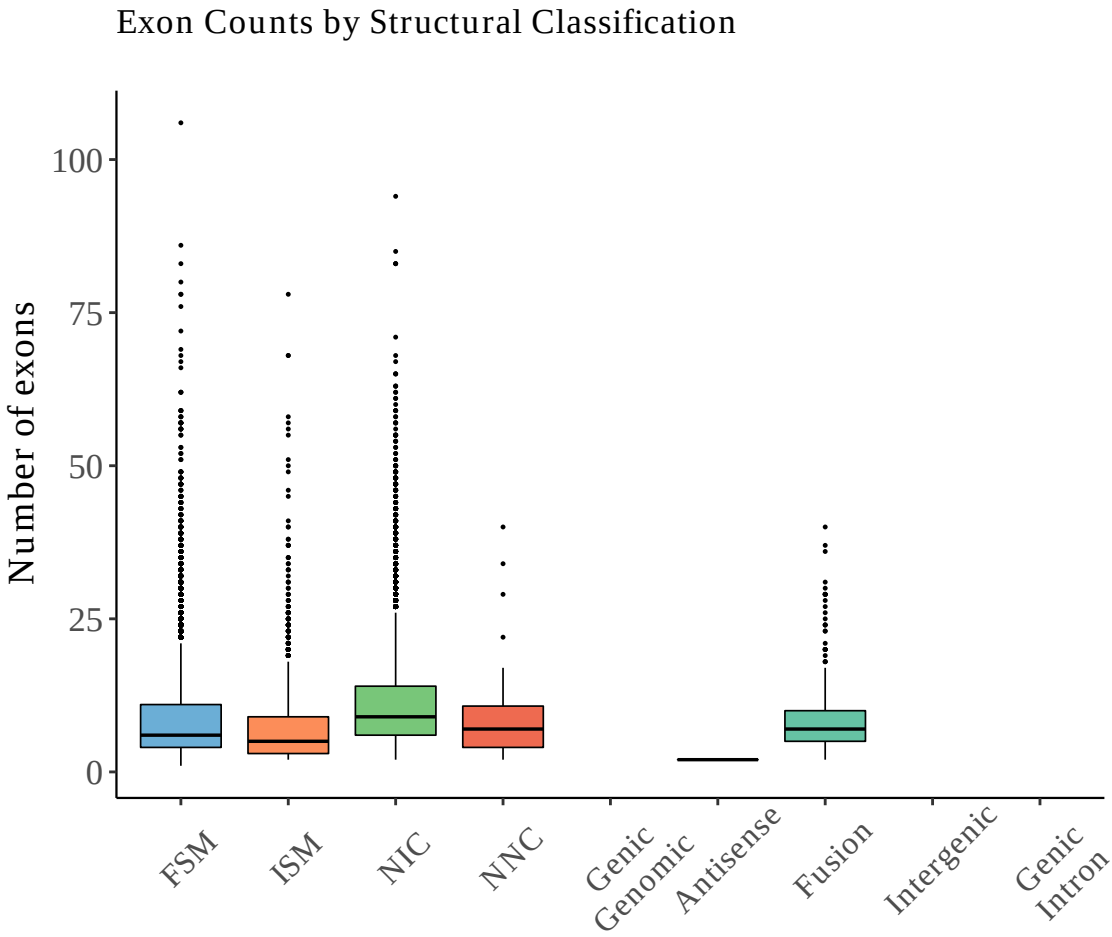

Transcript Lengths, by structural category
Count
600
400
200
0
0
5000
10000
15000
20000
Transcript Length
structural_category
FSM
ISM
NIC
NNC
Antisense
Fusion


Transcript Lengths, Mono− vs Multi−Exons
Count
1000
500
0
0
5000
10000
15000
20000
Transcript Length
exonCat
Multi−Exon
Mono−Exon

Structural Isoform Characterization by Splice Junctions

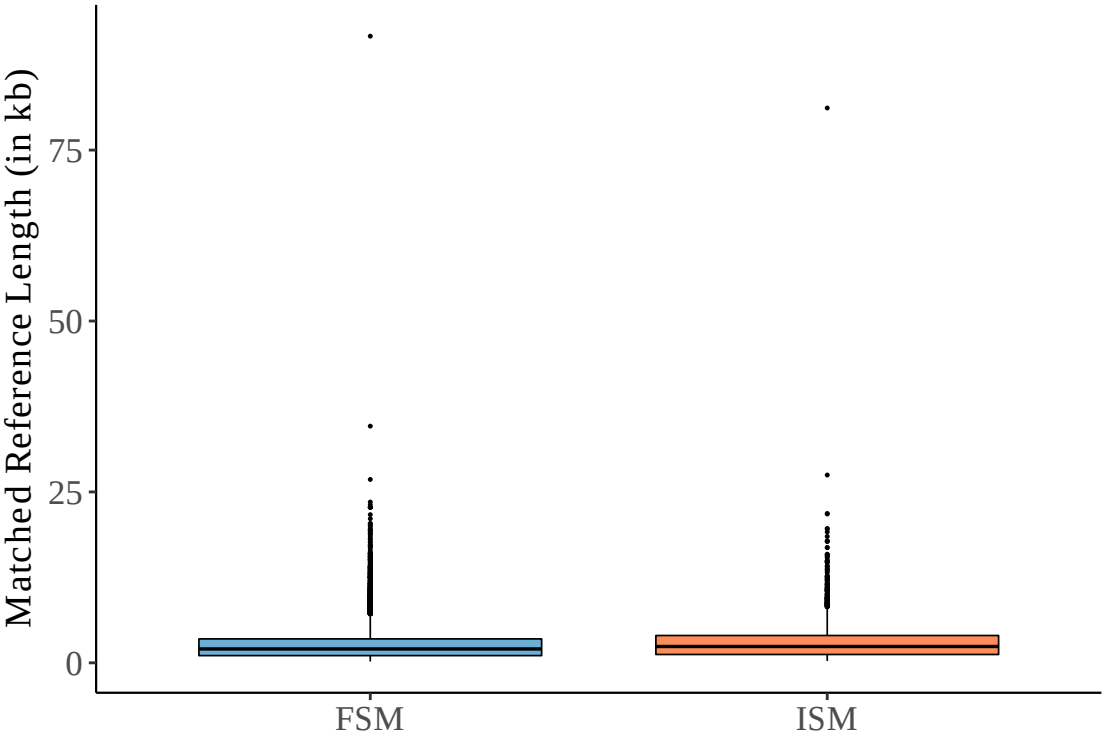

Isoform distribution across structural categories
100%
75%
50%
25%
0%
% Transcripts
Coding prediction
coding
non_coding
45.423%
4.617%
48.956%
0.052%
0.002%
0.950%
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron

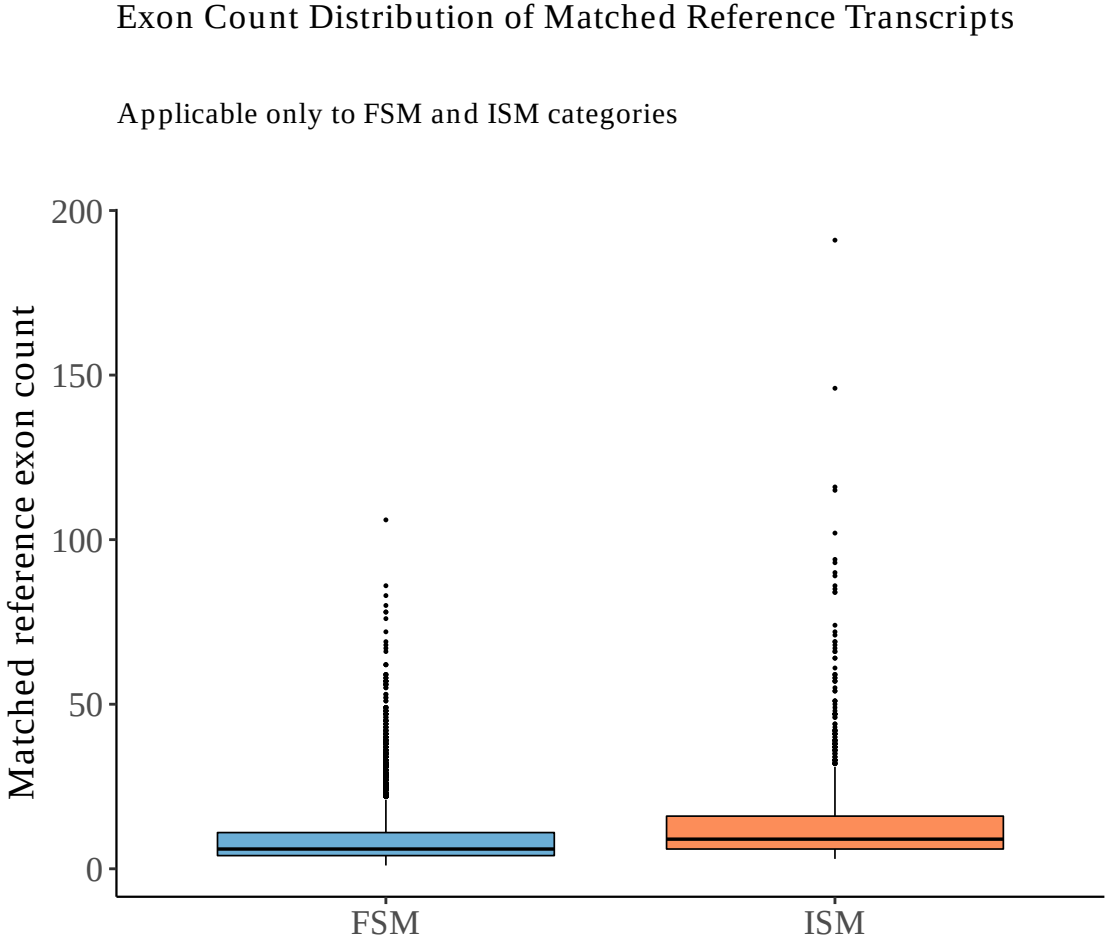

Transcript Lengths by Structural Classification
Transcript Length (bp)
20000
15000
10000
5000
0
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron


Exon Counts by Structural Classification
Number of exons
100
75
50
25
0
FSM
ISM
NIC
NNC
Genic Genomic
Antisense
Fusion
Intergenic
Genic Intron

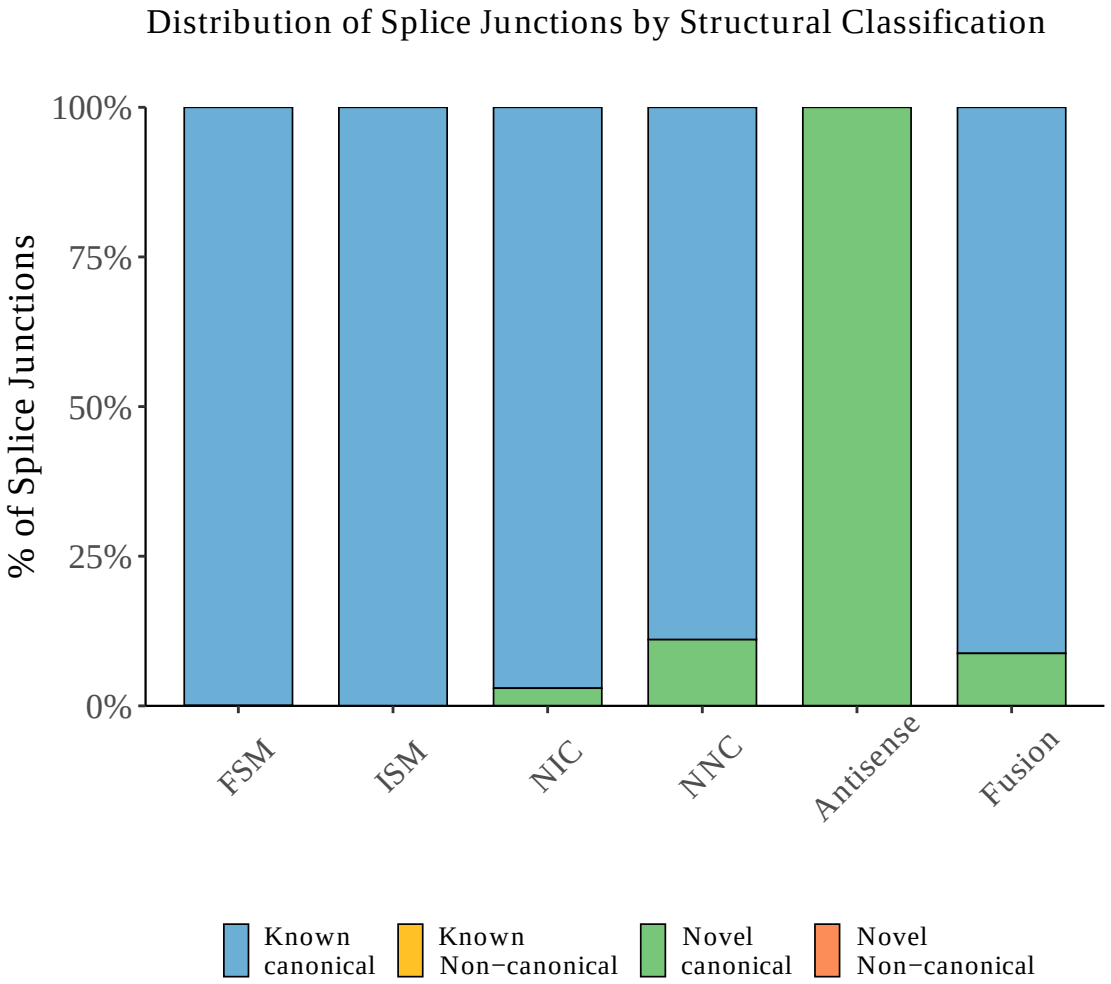
Length Distribution of Matched Reference Transcripts

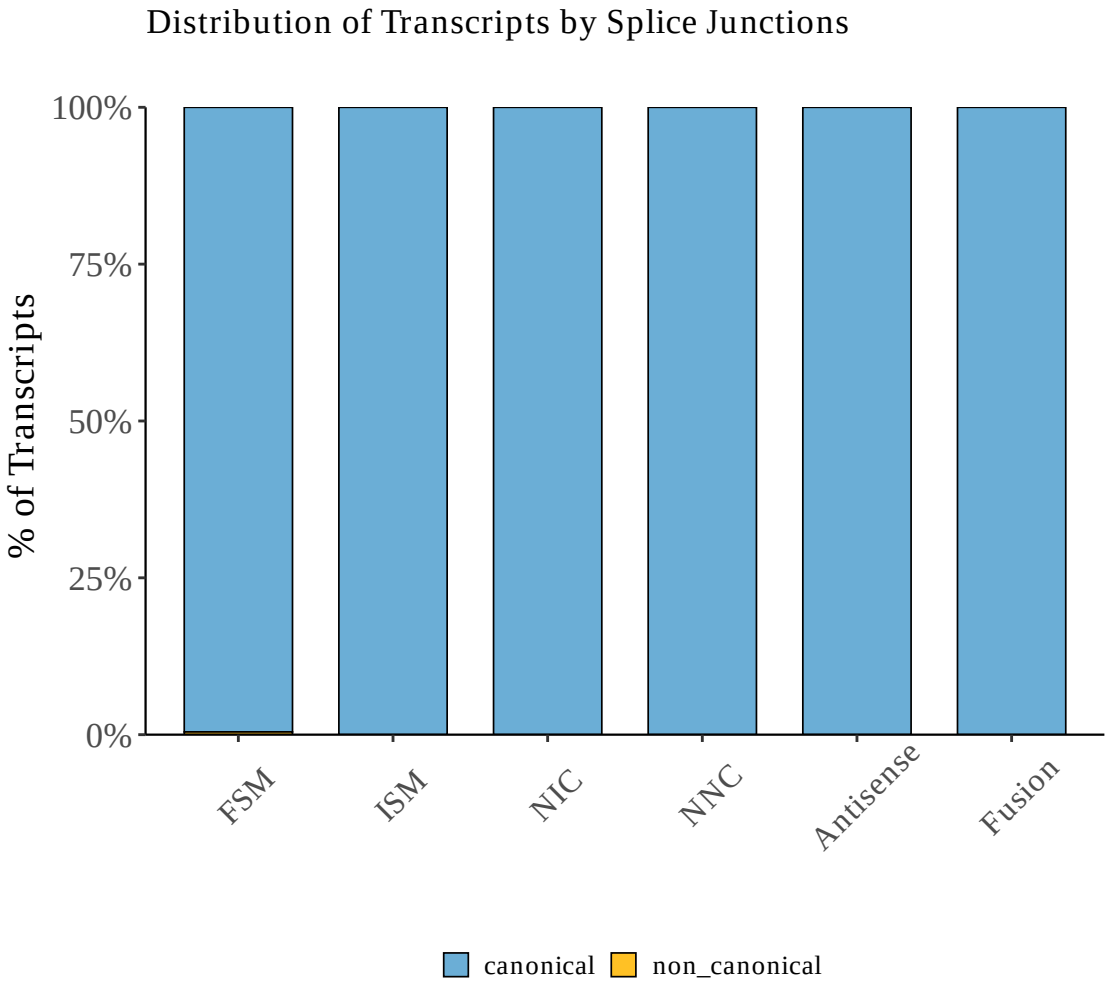
Applicable only to FSM and ISM categories

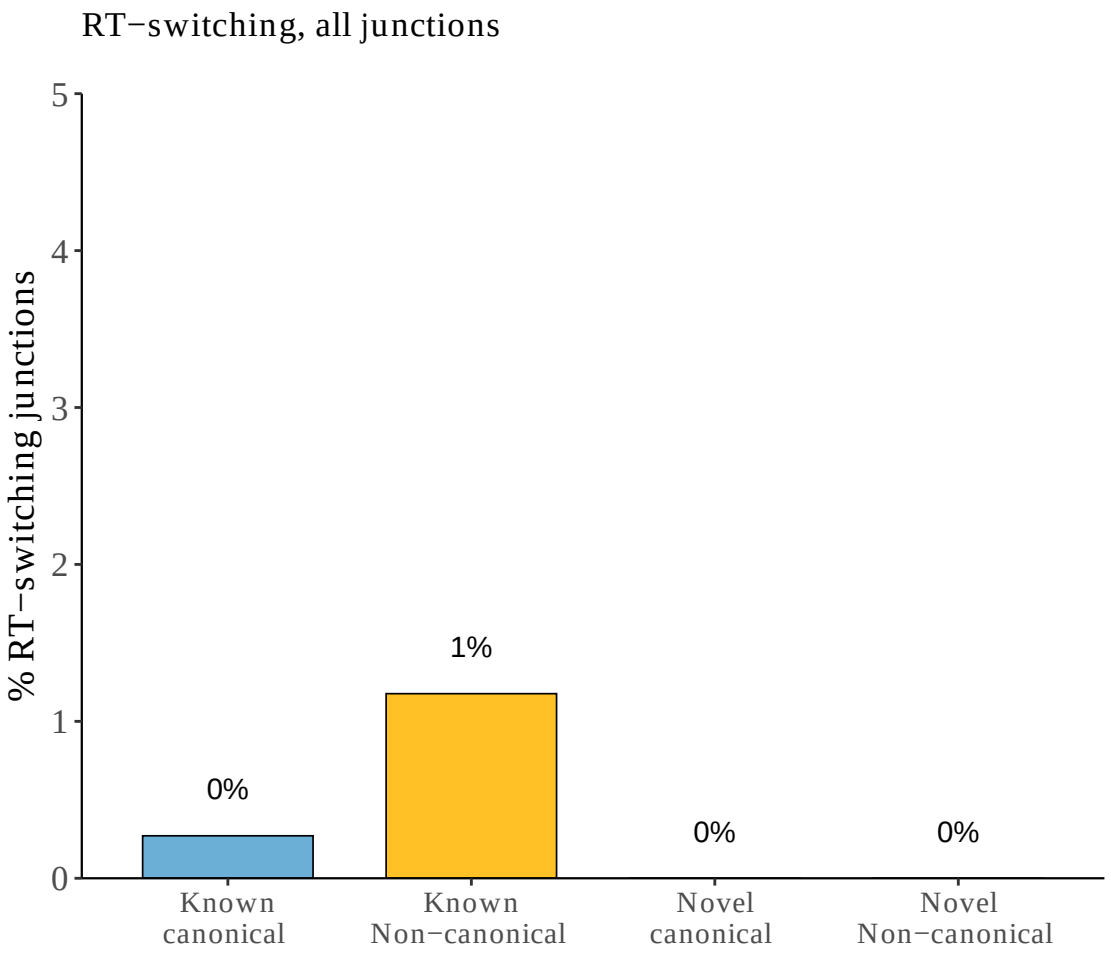


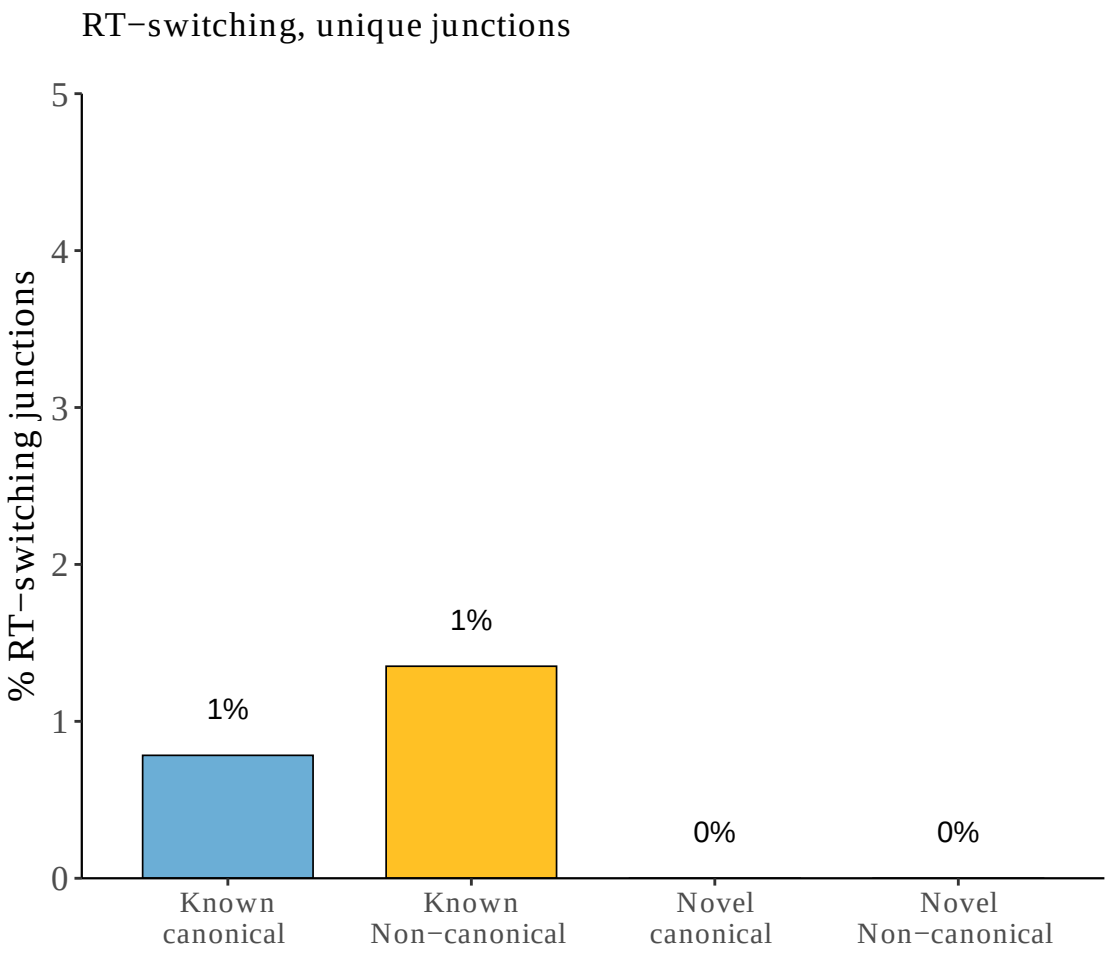

Exon Count Distribution of Matched Reference Transcripts
Applicable only to FSM and ISM categories
Matched reference exon count
200
150
100
50
0
FSM
ISM

Splice Junction Characterization

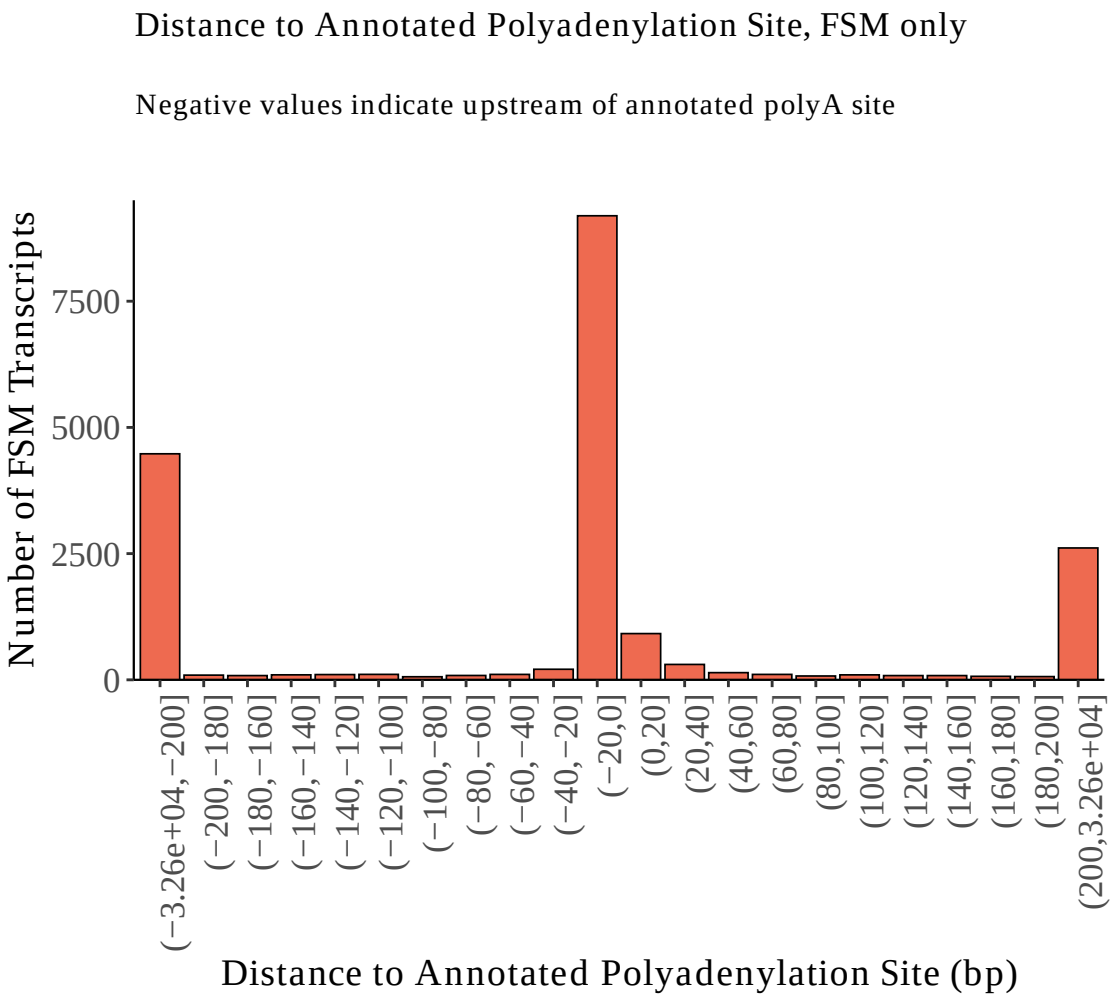

Distribution of Splice Junctions by Structural Classification
% of Splice Junctions
100%
75%
50%
25%
0%
FSM
ISM
NIC
NNC
Antisense
Fusion
Known canonical
Known Non−canonical
Novel canonical
Novel Non−canonical


Distribution of Transcripts by Splice Junctions
% of Transcripts
100%
75%
50%
25%
0%
FSM
ISM
NIC
NNC
Antisense
Fusion
canonical
non_canonical


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

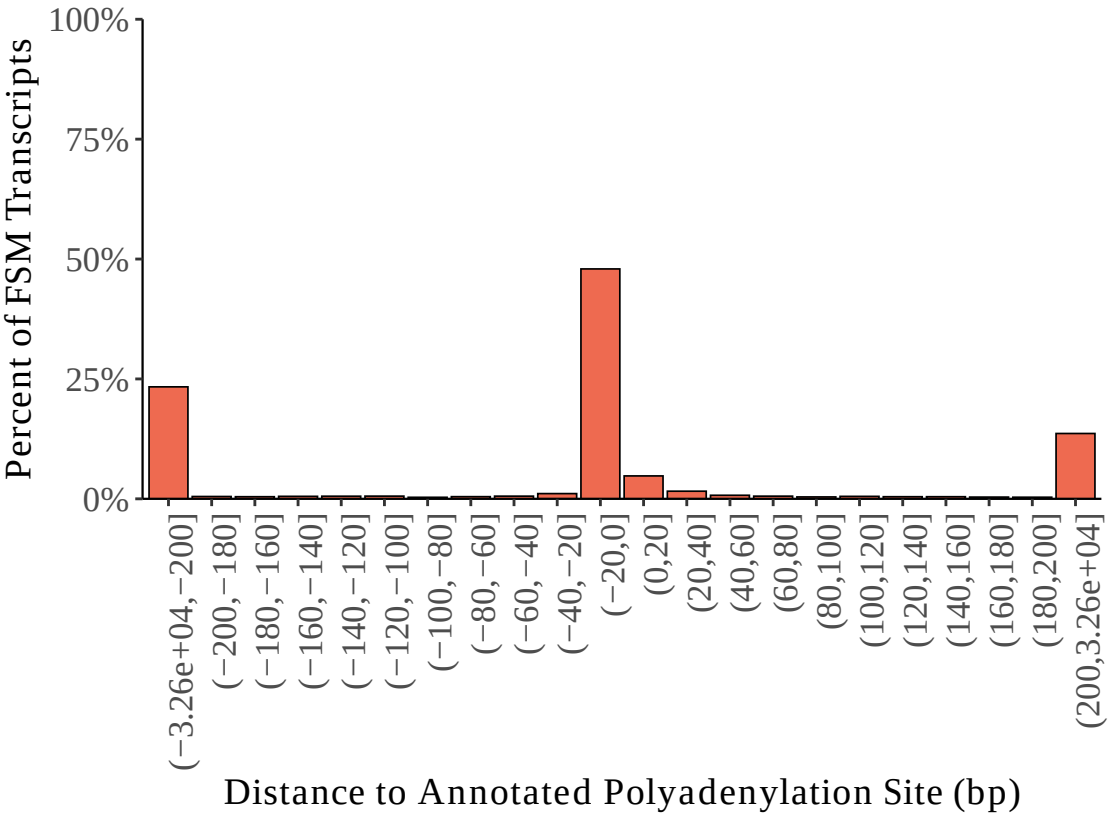

RT−switching, unique junctions
% RT−switching junctions
5
4
3
2
1
0
1%
1%
0%
0%
Known canonical
Known Non−canonical
Novel canonical
Novel Non−canonical

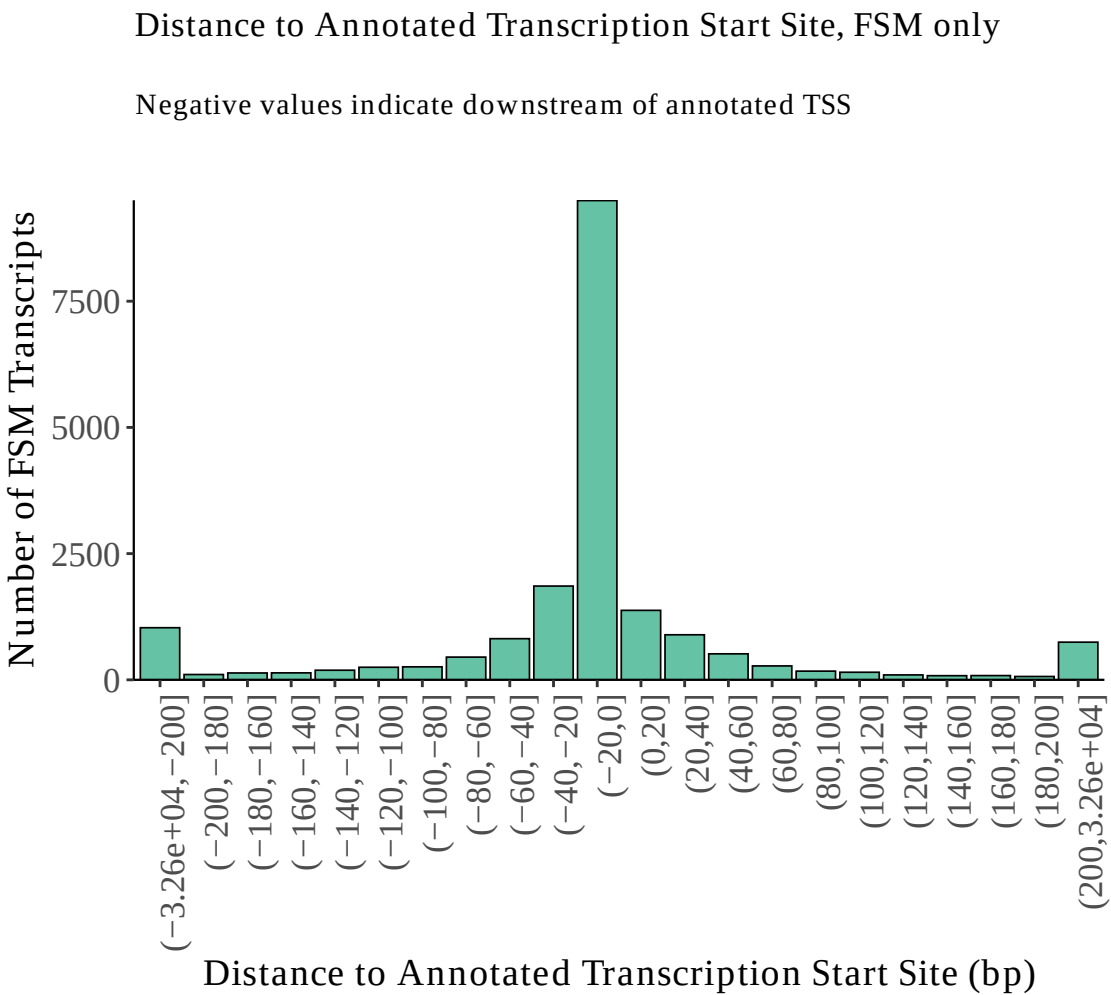
Comparison with Annotated TSS and PolyA Sites

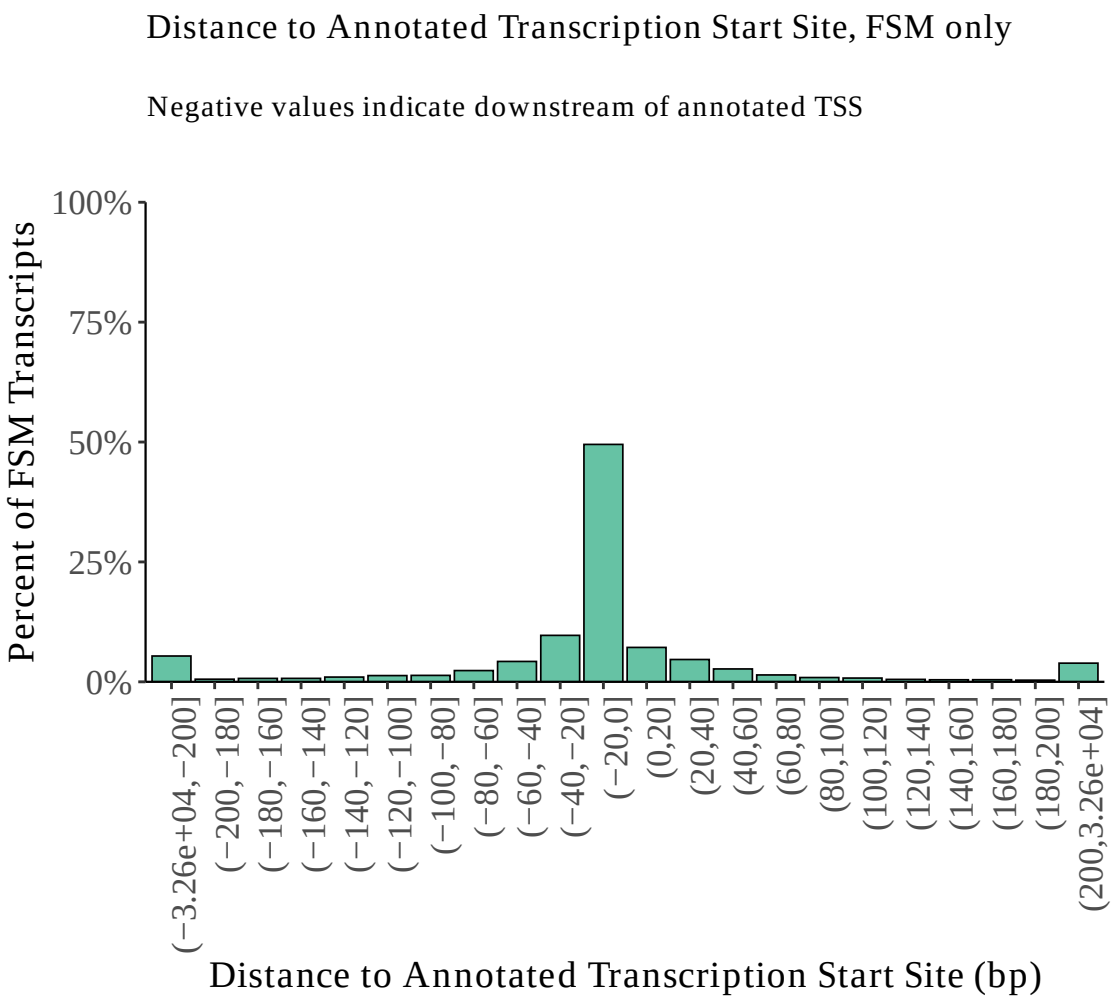

Distance to Annotated Polyadenylation Site, FSM only
Negative values indicate upstream of annotated polyA site
Number of FSM Transcripts
0
2500
5000
7500
(−3.26e+04,−200]
(−200,−180]
(−180,−160]
(−160,−140]
(−140,−120]
(−120,−100]
(−100,−80]
(−80,−60]
(−60,−40]
(−40,−20]
(−20,0]
(0,20]
(20,40]
(40,60]
(60,80]
(80,100]
(100,120]
(120,140]
(140,160]
(160,180]
(180,200]
(200,3.26e+04]
Distance to Annotated Polyadenylation Site (bp)

Distance to Annotated Polyadenylation Site, FSM only

Negative values indicate upstream of annotated polyA site

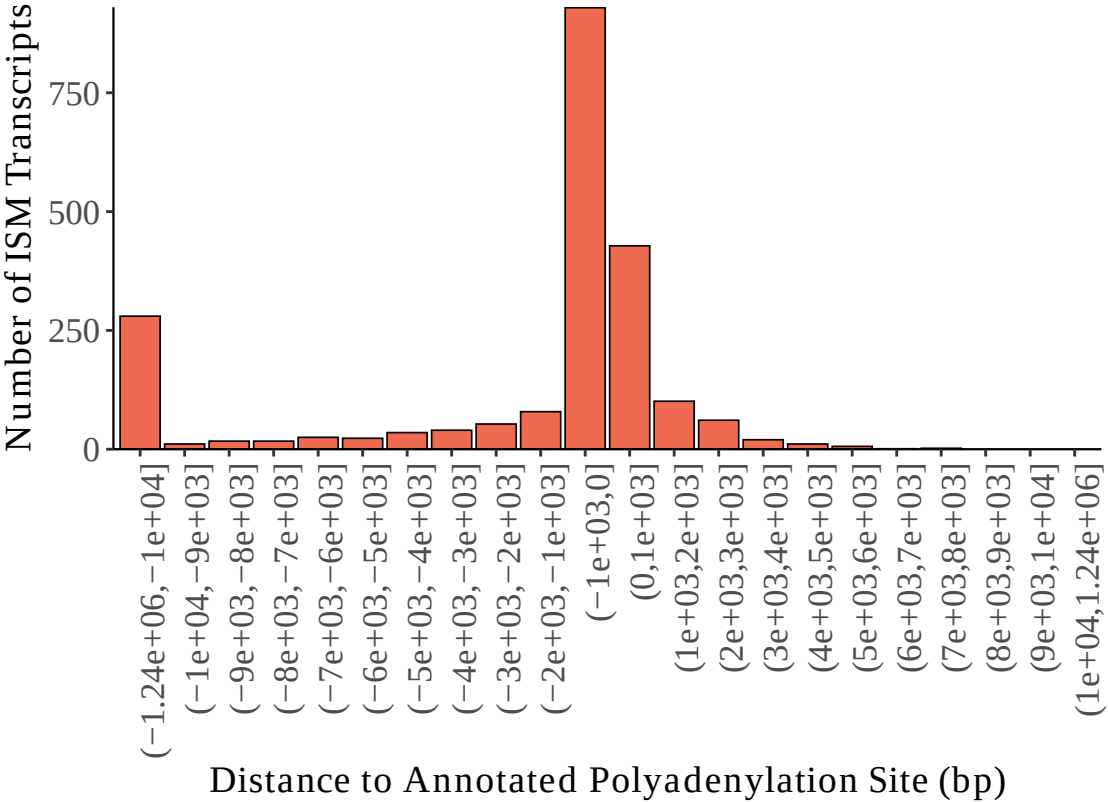



Distance to Annotated Transcription Start Site, FSM only
Negative values indicate downstream of annotated TSS
Number of FSM Transcripts
0
2500
5000
7500
(−3.26e+04,−200]
(−200,−180]
(−180,−160]
(−160,−140]
(−140,−120]
(−120,−100]
(−100,−80]
(−80,−60]
(−60,−40]
(−40,−20]
(−20,0]
(0,20]
(20,40]
(40,60]
(60,80]
(80,100]
(100,120]
(120,140]
(140,160]
(160,180]
(180,200]
(200,3.26e+04]
Distance to Annotated Transcription Start Site (bp)


Distance to Annotated Transcription Start Site, FSM only
Negative values indicate downstream of annotated TSS
Percent of FSM Transcripts
100%
75%
50%
25%
0%
(−3.26e+04,−200]
(−200,−180]
(−180,−160]
(−160,−140]
(−140,−120]
(−120,−100]
(−100,−80]
(−80,−60]
(−60,−40]
(−40,−20]
(−20,0]
(0,20]
(20,40]
(40,60]
(60,80]
(80,100]
(100,120]
(120,140]
(140,160]
(160,180]
(180,200]
(200,3.26e+04]
Distance to Annotated Transcription Start Site (bp)

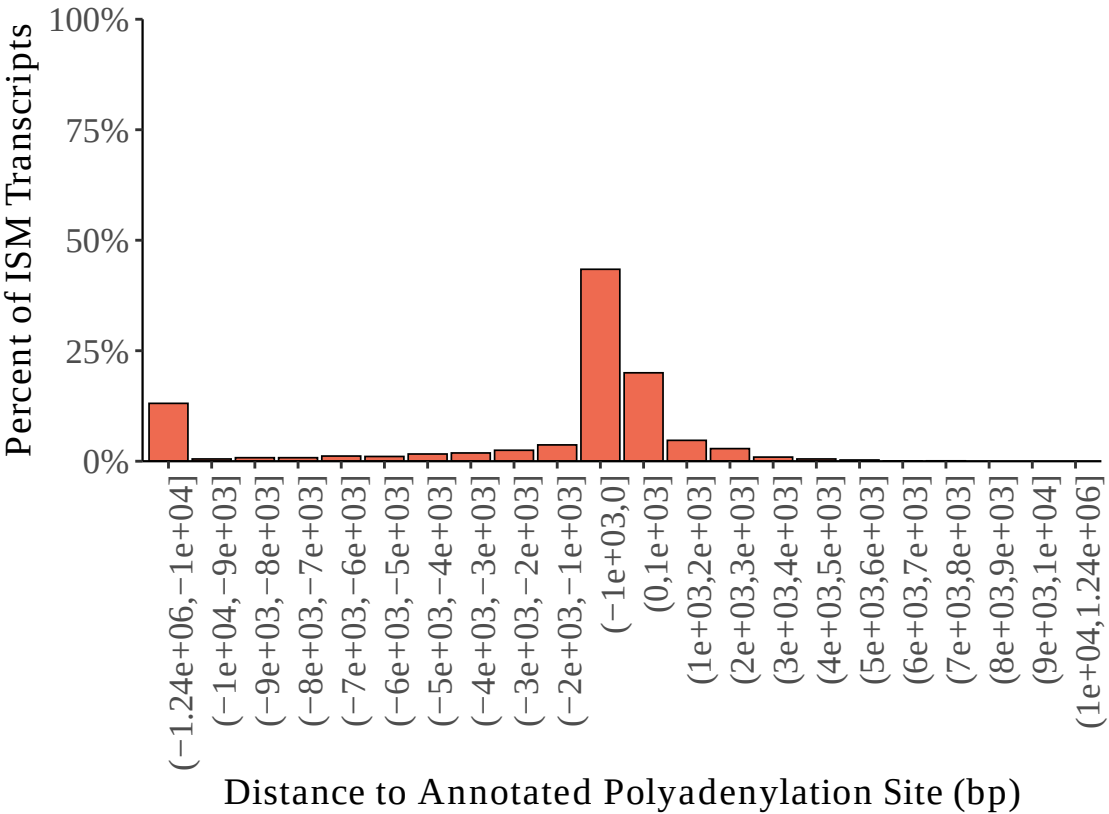
Distance to Annotated Polyadenylation Site, ISM only

Negative values indicate upstream of annotated polyA site



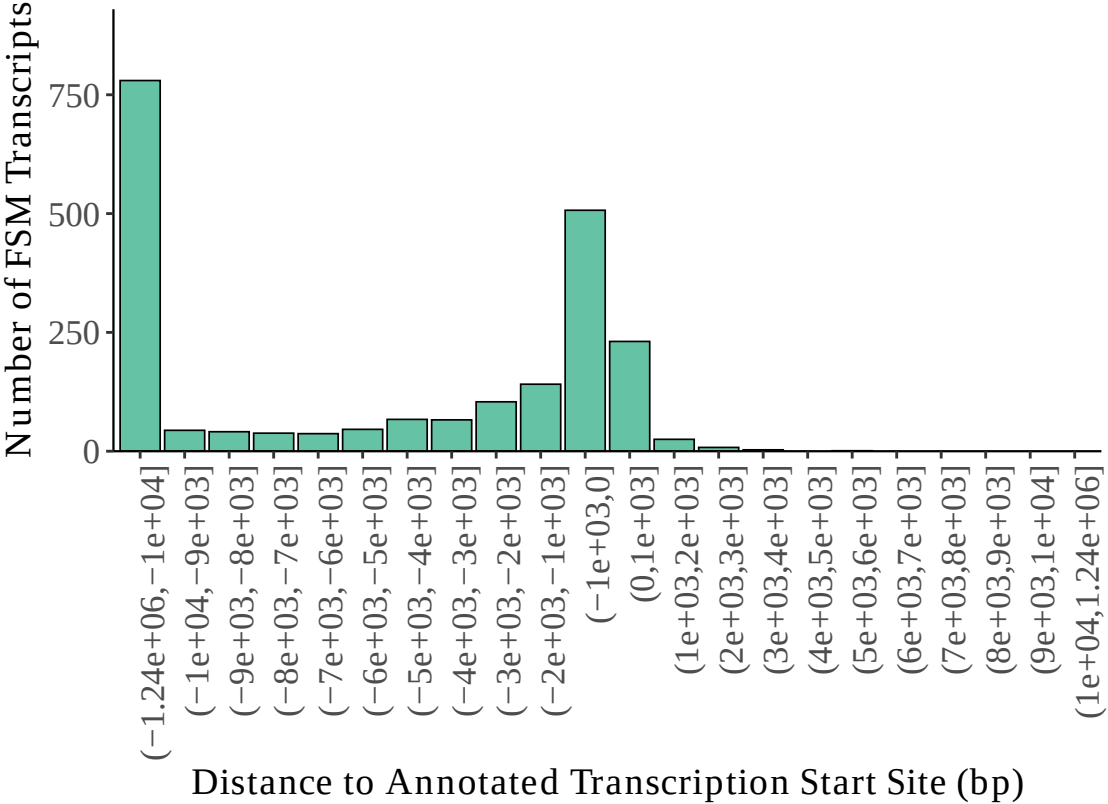
Distance to Annotated Polyadenylation Site, ISM only

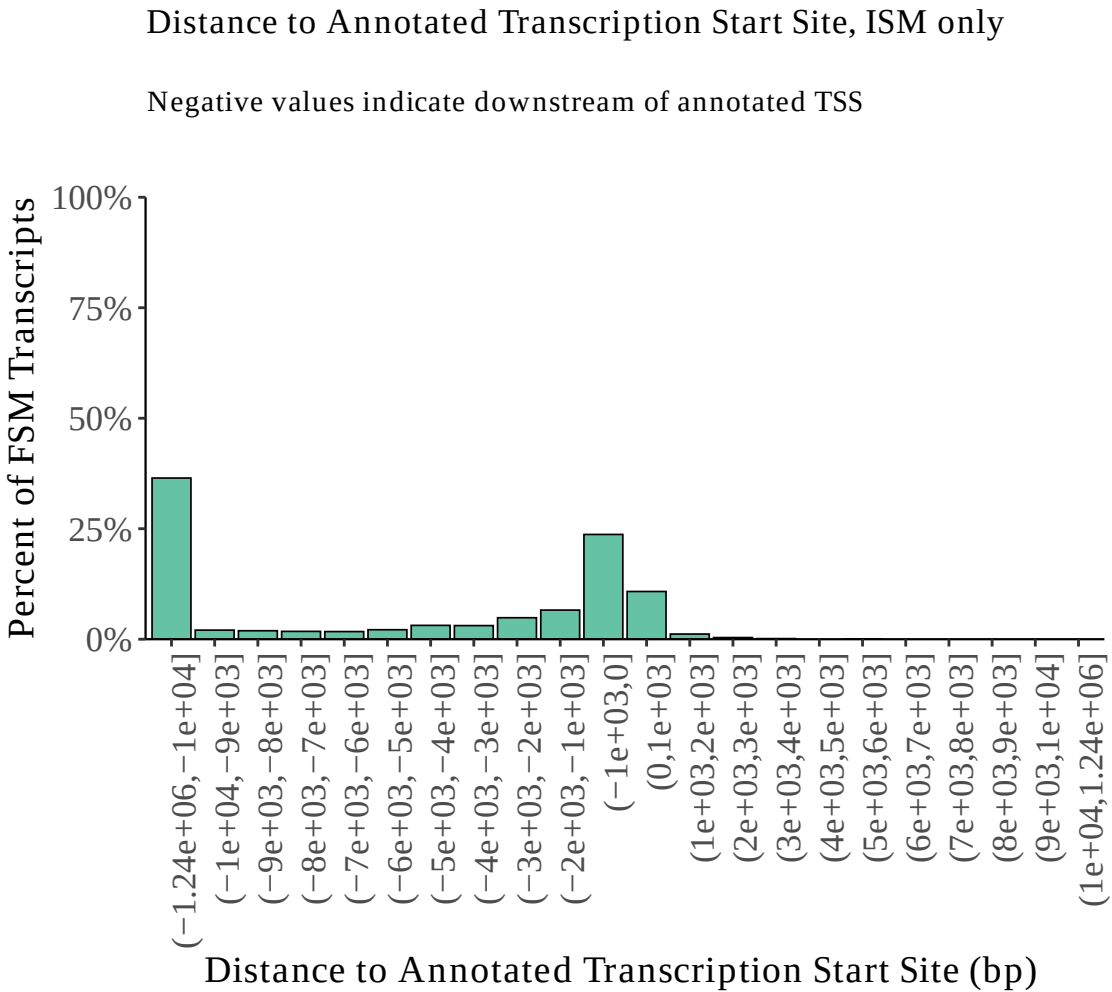
Negative values indicate upstream of annotated polyA site



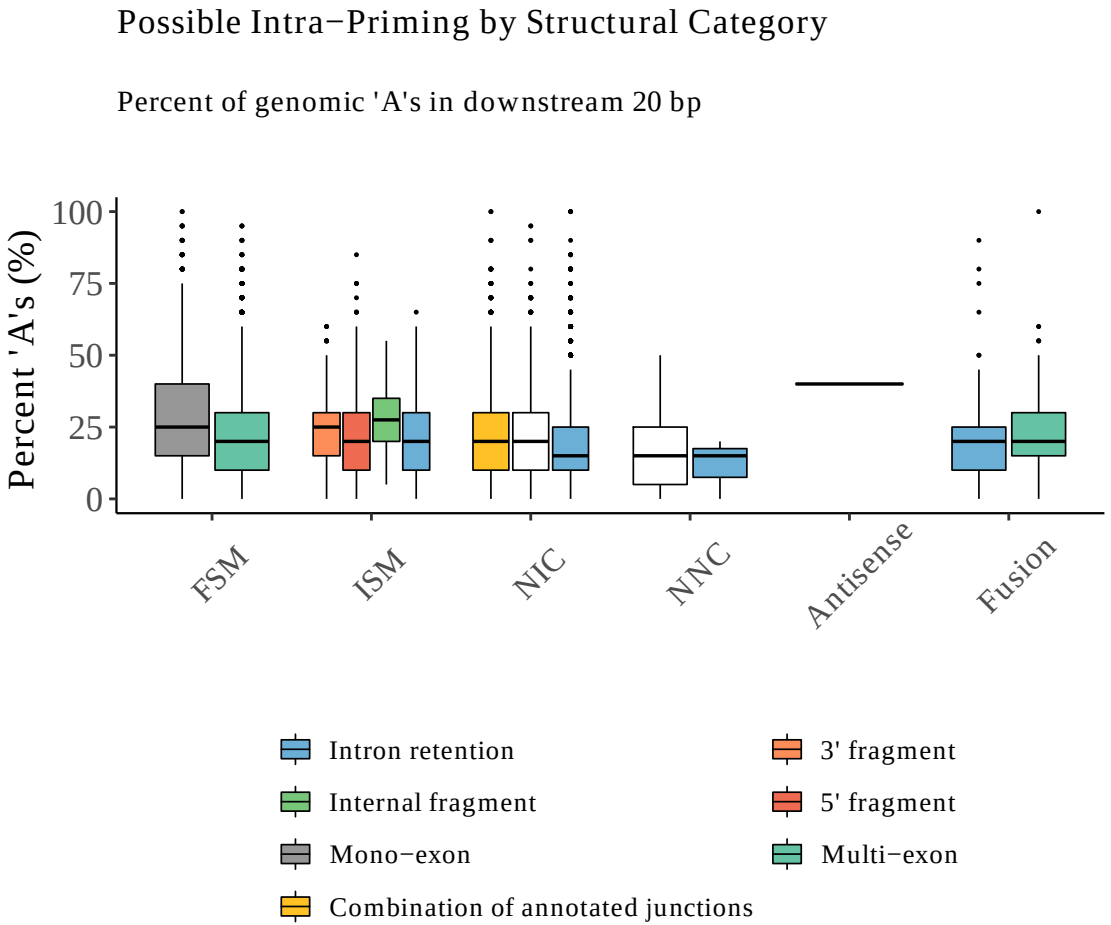
Distance to Annotated Transcription Start Site, ISM only

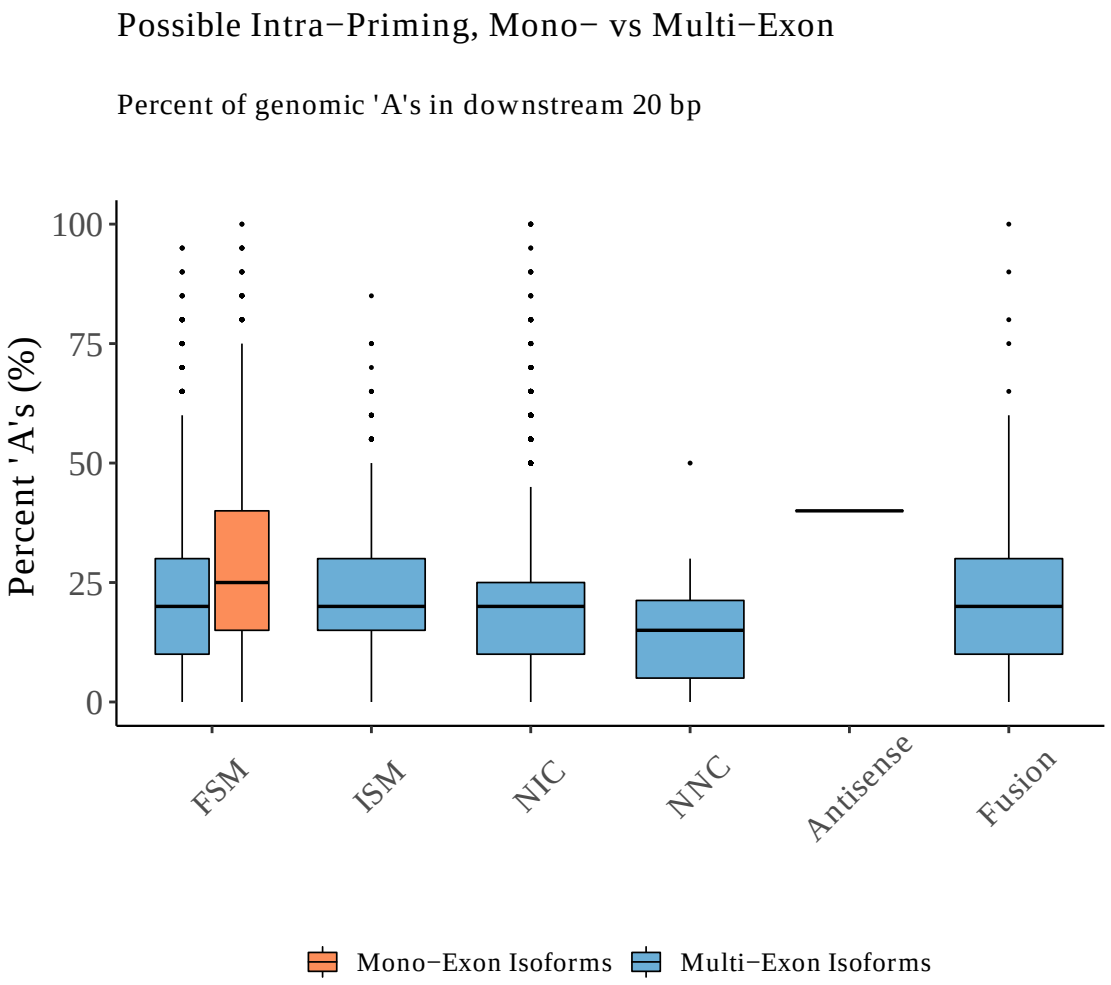
Negative values indicate downstream of annotated TSS

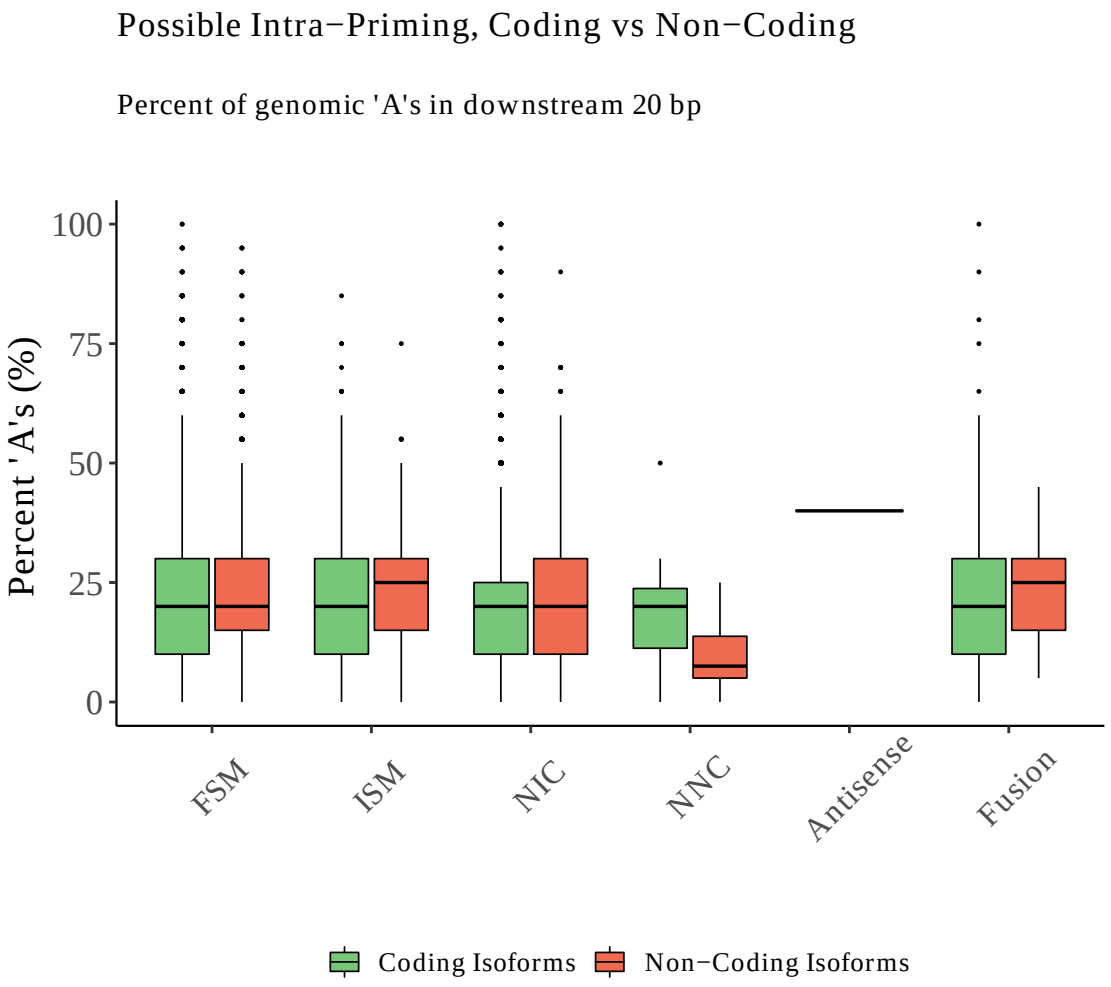



Distance to Annotated Transcription Start Site, ISM only
Negative values indicate downstream of annotated TSS
Percent of FSM Transcripts
100%
75%
50%
25%
0%
(−1.24e+06,−1e+04]
(−1e+04,−9e+03]
(−9e+03,−8e+03]
(−8e+03,−7e+03]
(−7e+03,−6e+03]
(−6e+03,−5e+03]
(−5e+03,−4e+03]
(−4e+03,−3e+03]
(−3e+03,−2e+03]
(−2e+03,−1e+03]
(−1e+03,0]
(0,1e+03]
(1e+03,2e+03]
(2e+03,3e+03]
(3e+03,4e+03]
(4e+03,5e+03]
(5e+03,6e+03]
(6e+03,7e+03]
(7e+03,8e+03]
(8e+03,9e+03]
(9e+03,1e+04]
(1e+04,1.24e+06]
Distance to Annotated Transcription Start Site (bp)

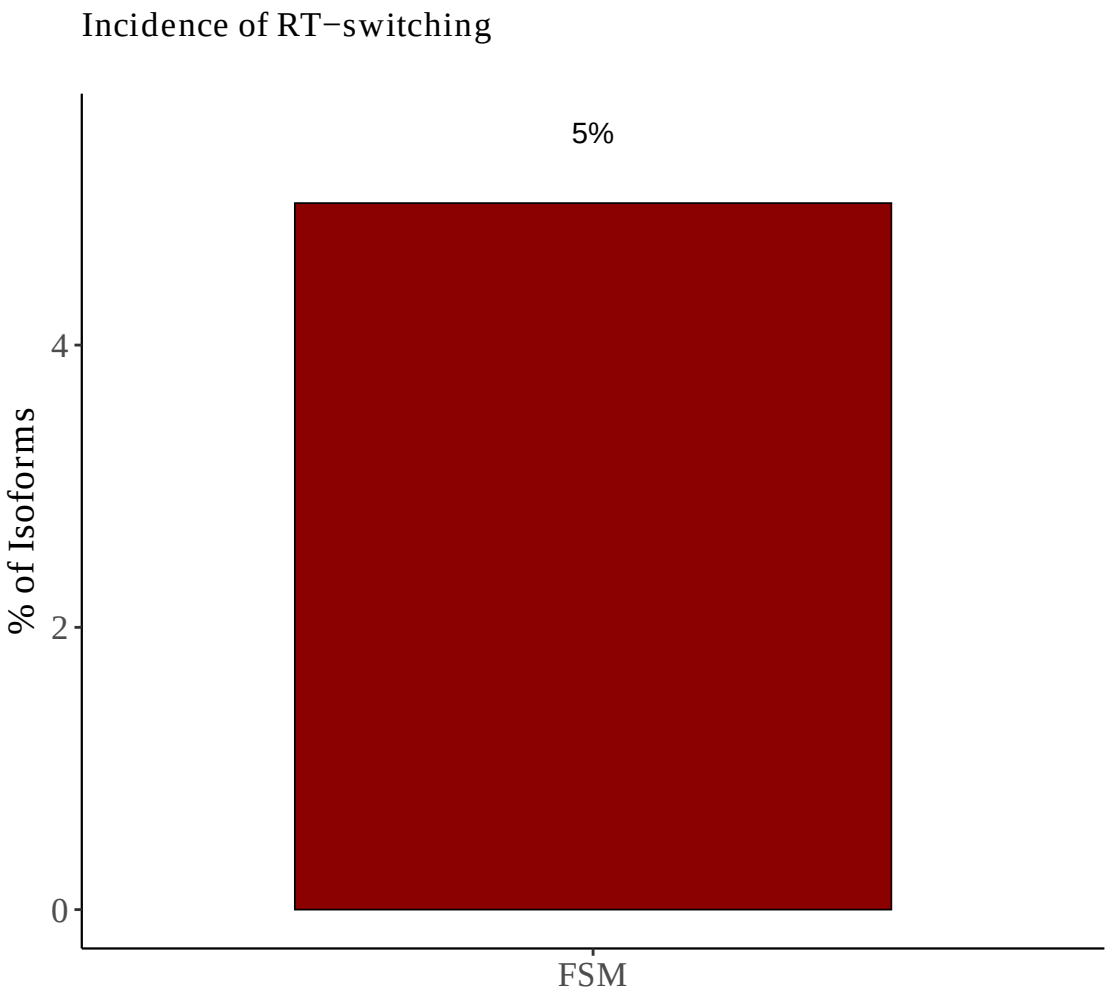
Intra−Priming Quality Check

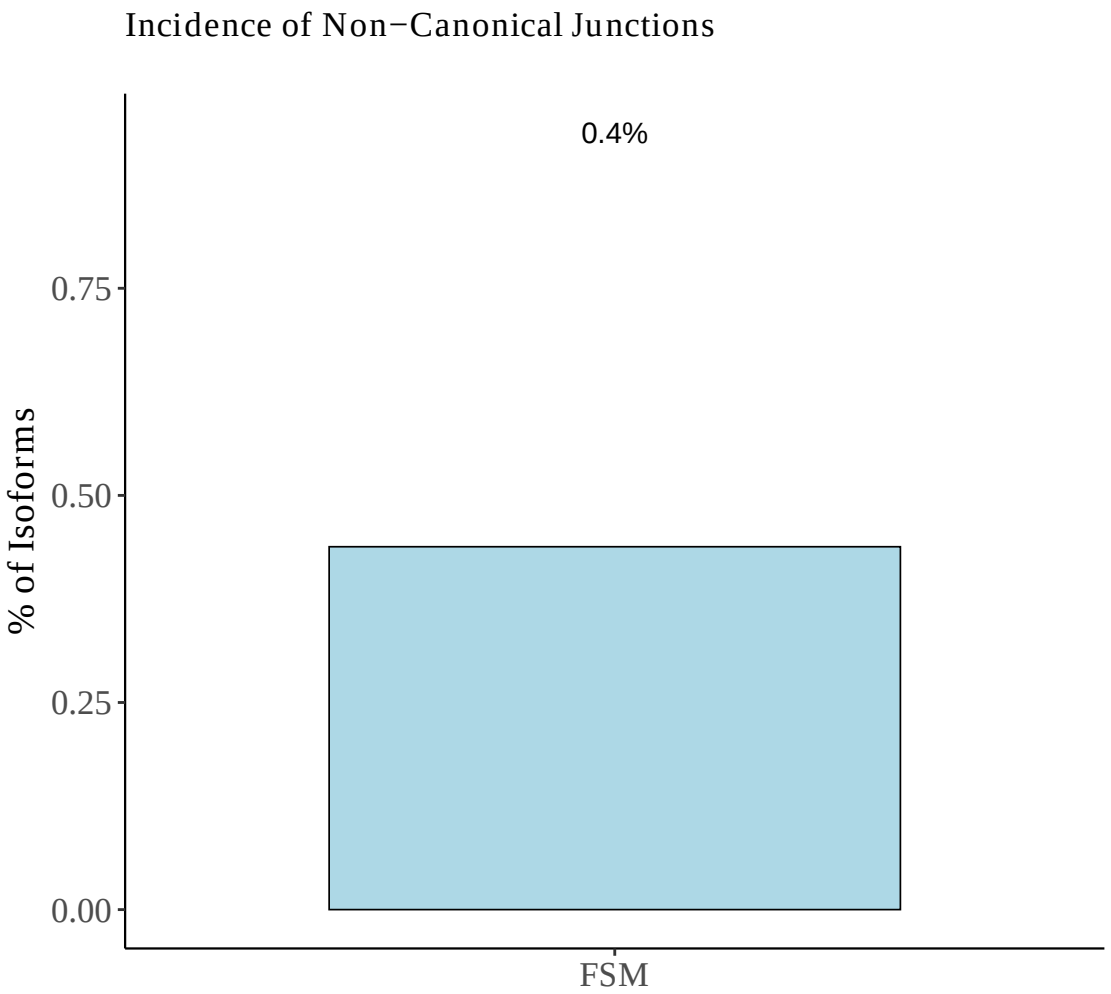

Possible Intra−Priming by Structural Category
Percent of genomic 'A's in downstream 20 bp
Percent 'A's (%)
100
75
50
25
0
FSM
ISM
NIC
NNC
Antisense
Fusion
Intron retention
Internal fragment
Mono−exon
Combination of annotated junctions
3' fragment
5' fragment
Multi−exon


Possible Intra−Priming, Mono− vs Multi−Exon
Percent of genomic 'A's in downstream 20 bp
Percent 'A's (%)
100
75
50
25
0
FSM
ISM
NIC
NNC
Antisense
Fusion
Mono−Exon Isoforms
Multi−Exon Isoforms


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

Quality Controls


Incidence of RT−switching
5%
% of Isoforms
4
2
0
FSM


Incidence of Non−Canonical Junctions
0.4%
0.75
0.50
0.25
0.00
% of Isoforms
FSM