

SQANTI report

Genes: 250

Isoforms: 558

Gene classification

category	# genes
Annotated Genes	231
Novel Genes	19

SJ classification

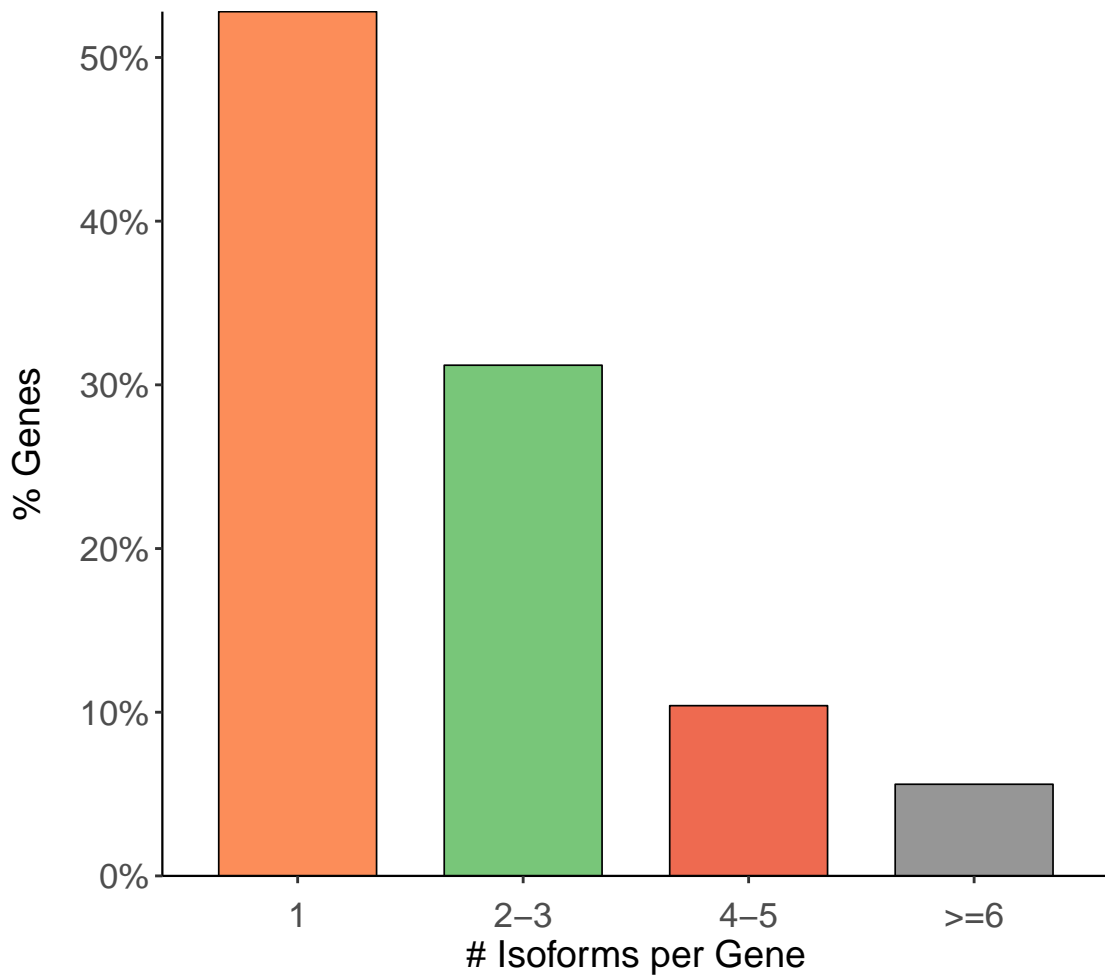
category	# SJ
Known canonical	2199
Known Non-canonical	2
Novel canonical	77
Novel Non-canonical	52

Characterization of transcripts based on splice junctions

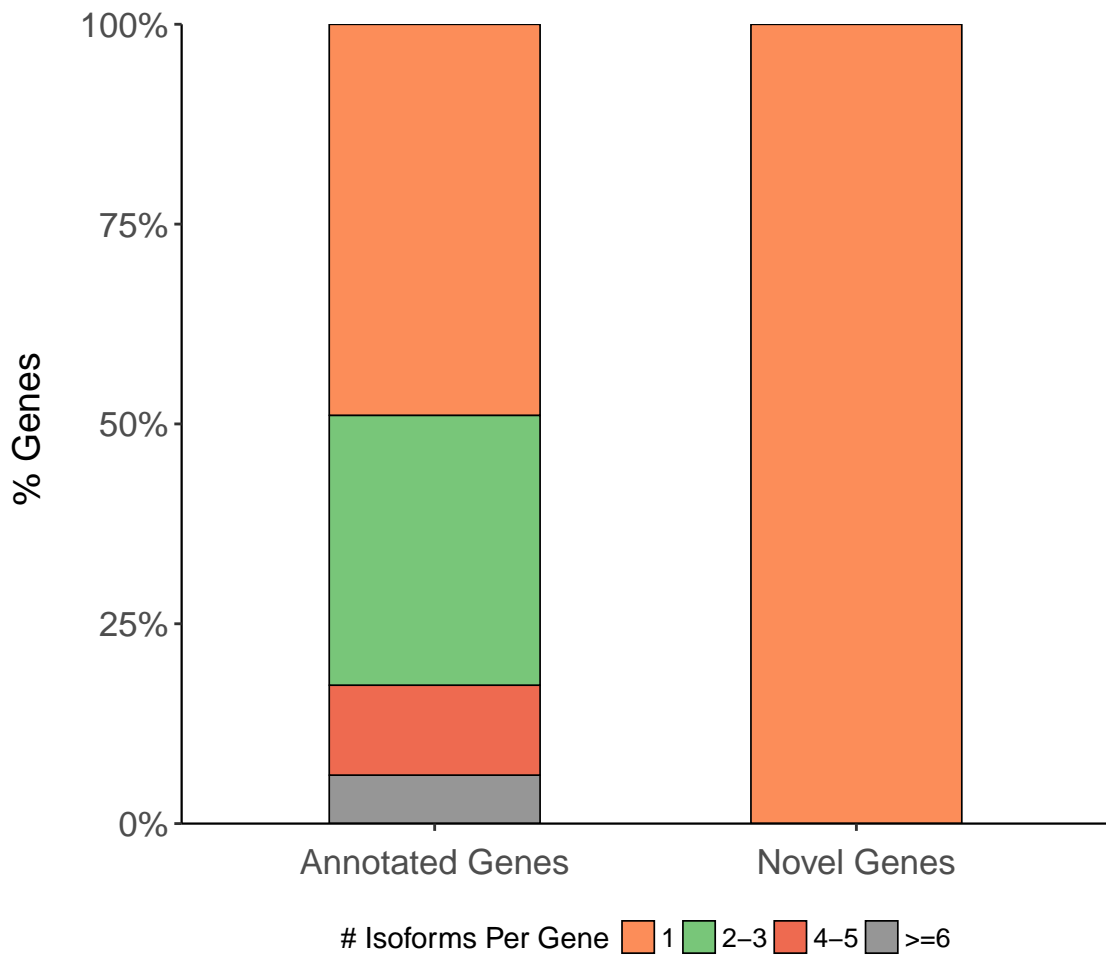
category	# isoforms
FSM	275
NIC	101
NNC	92
ISM	63
Antisense	10
Genic Intron	8
Genic Genomic	7
Fusion	1
Intergenic	1

Gene characterization

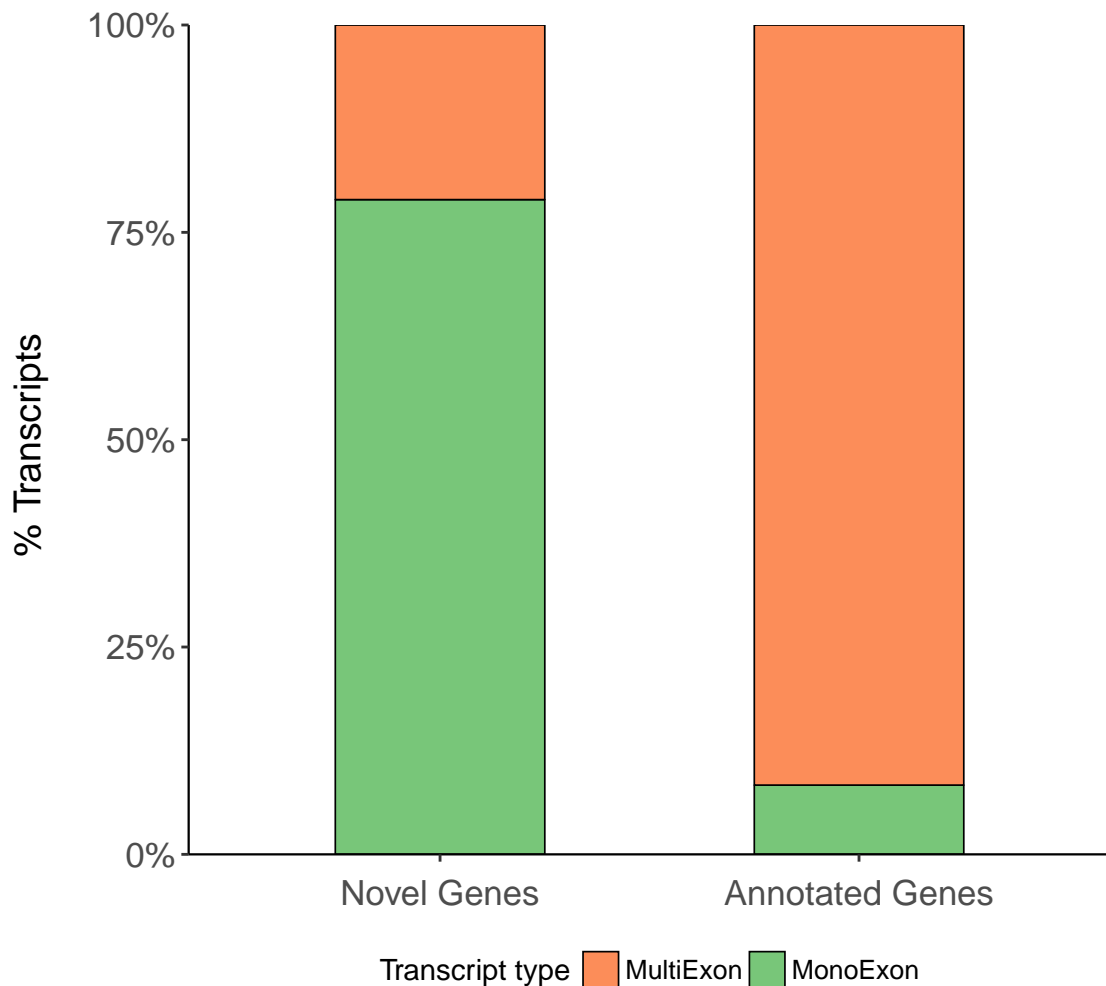
Distribution of isoforms per gene



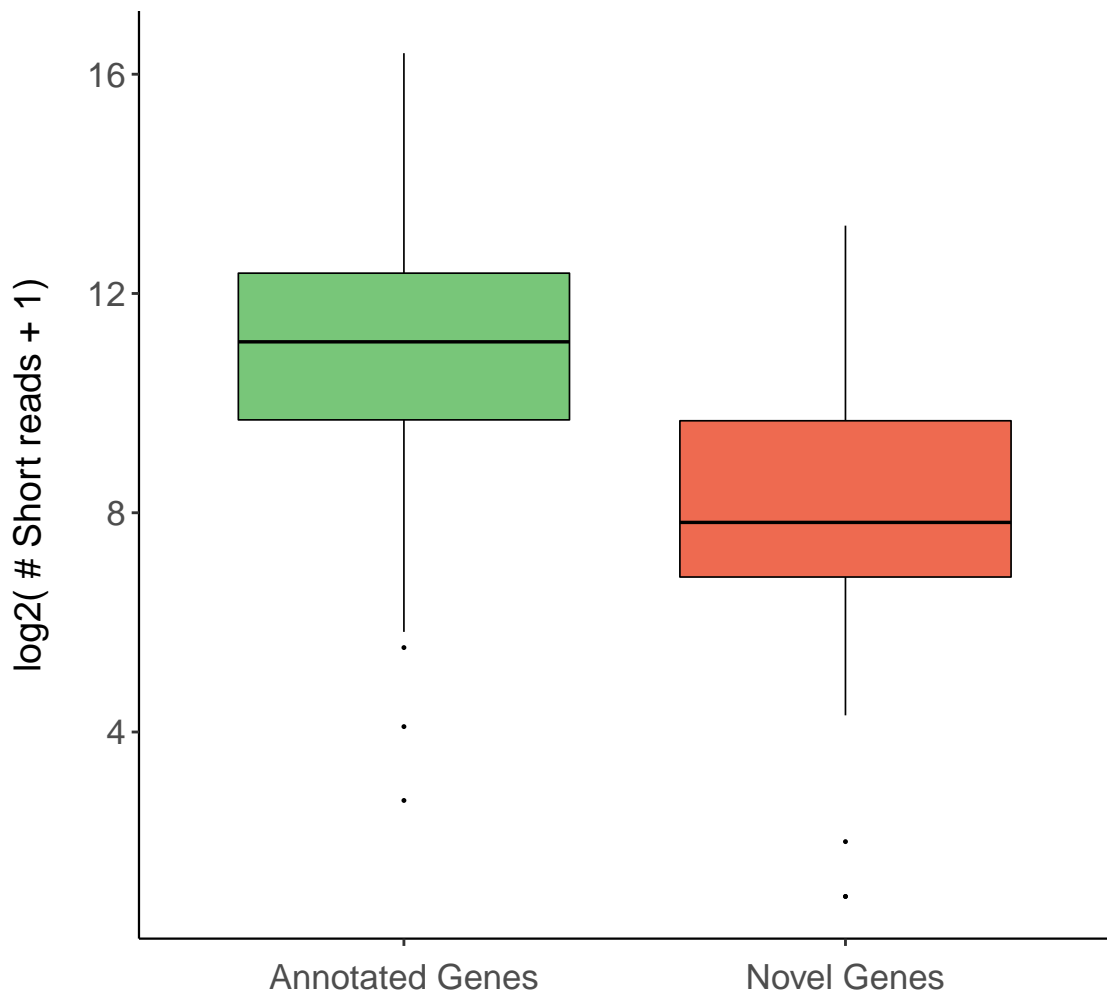
Distribution of number of isoforms



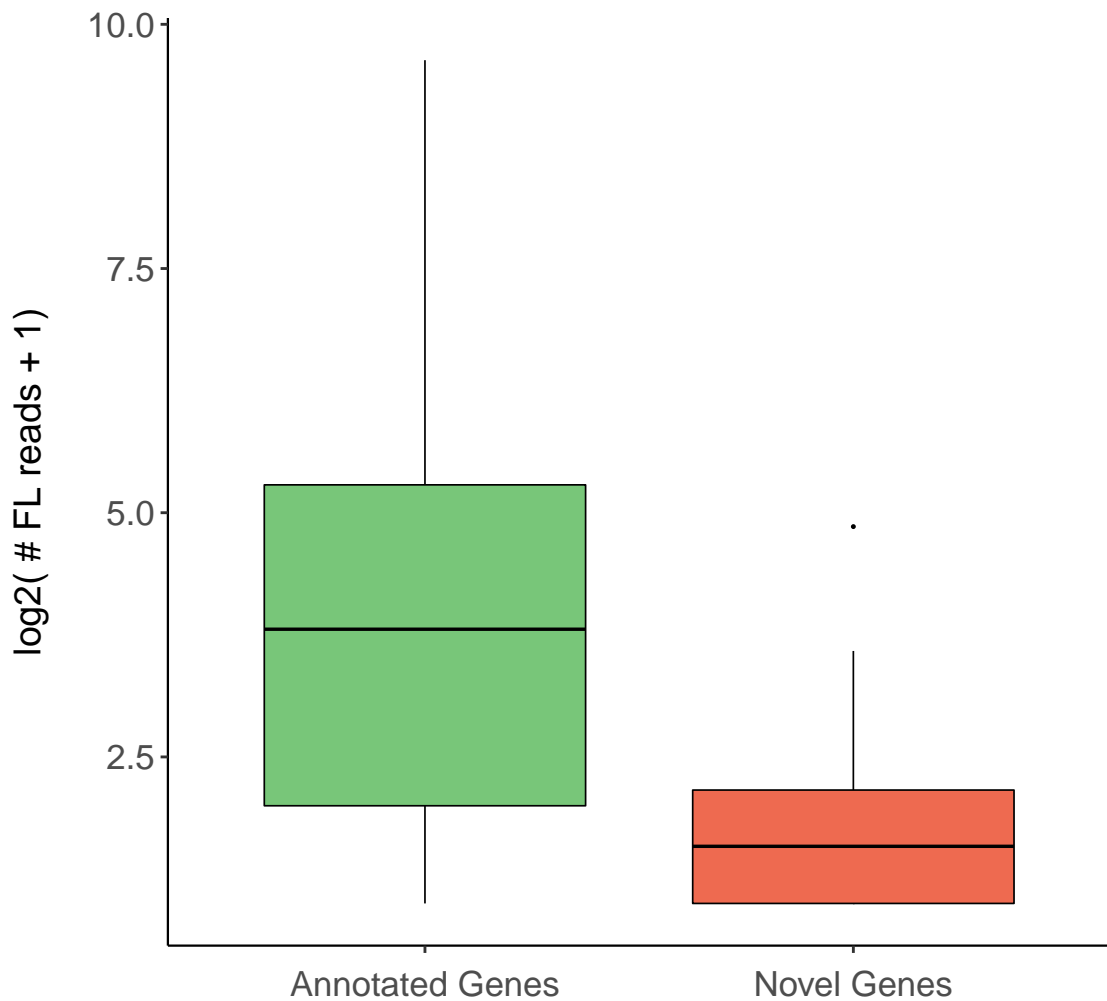
Distribution of mono/multi exon transcripts

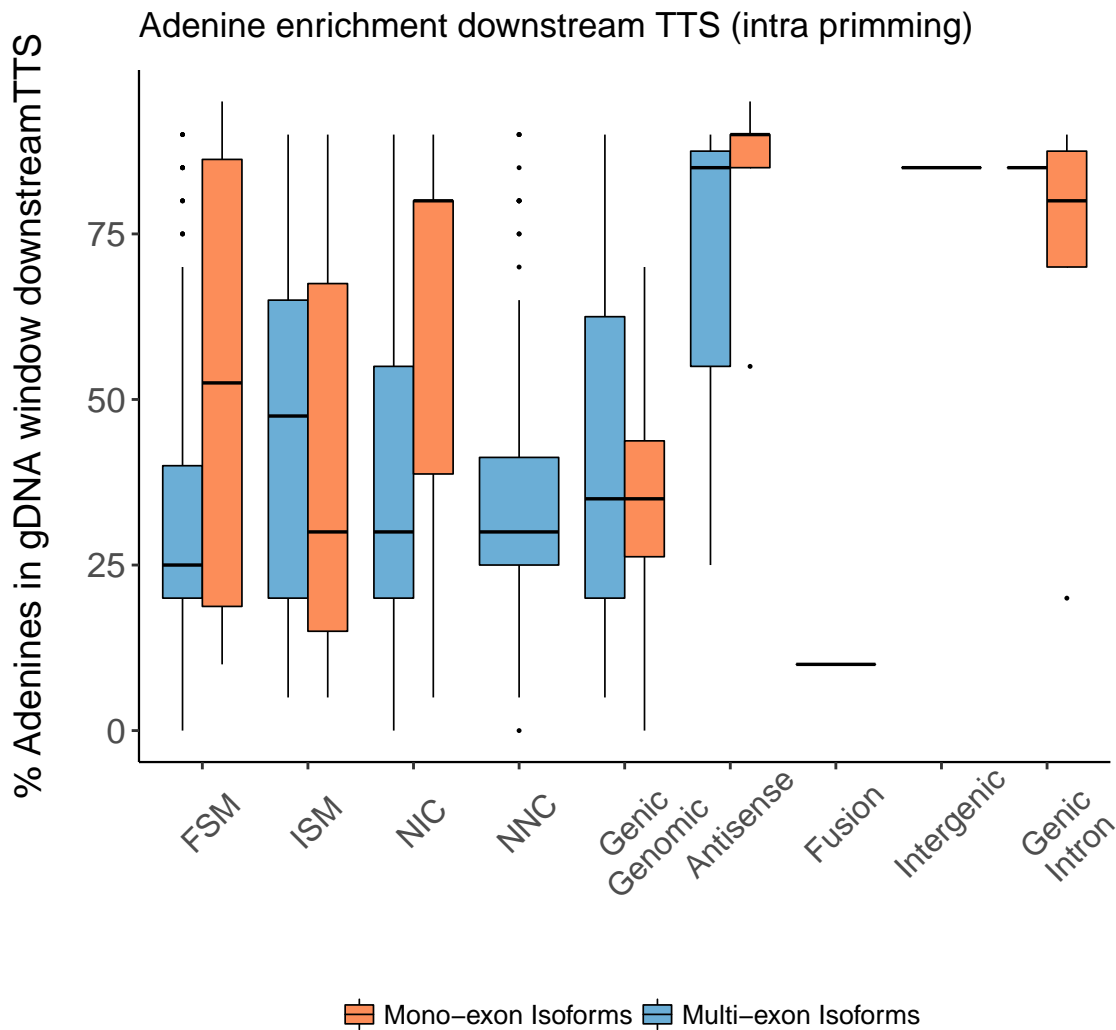


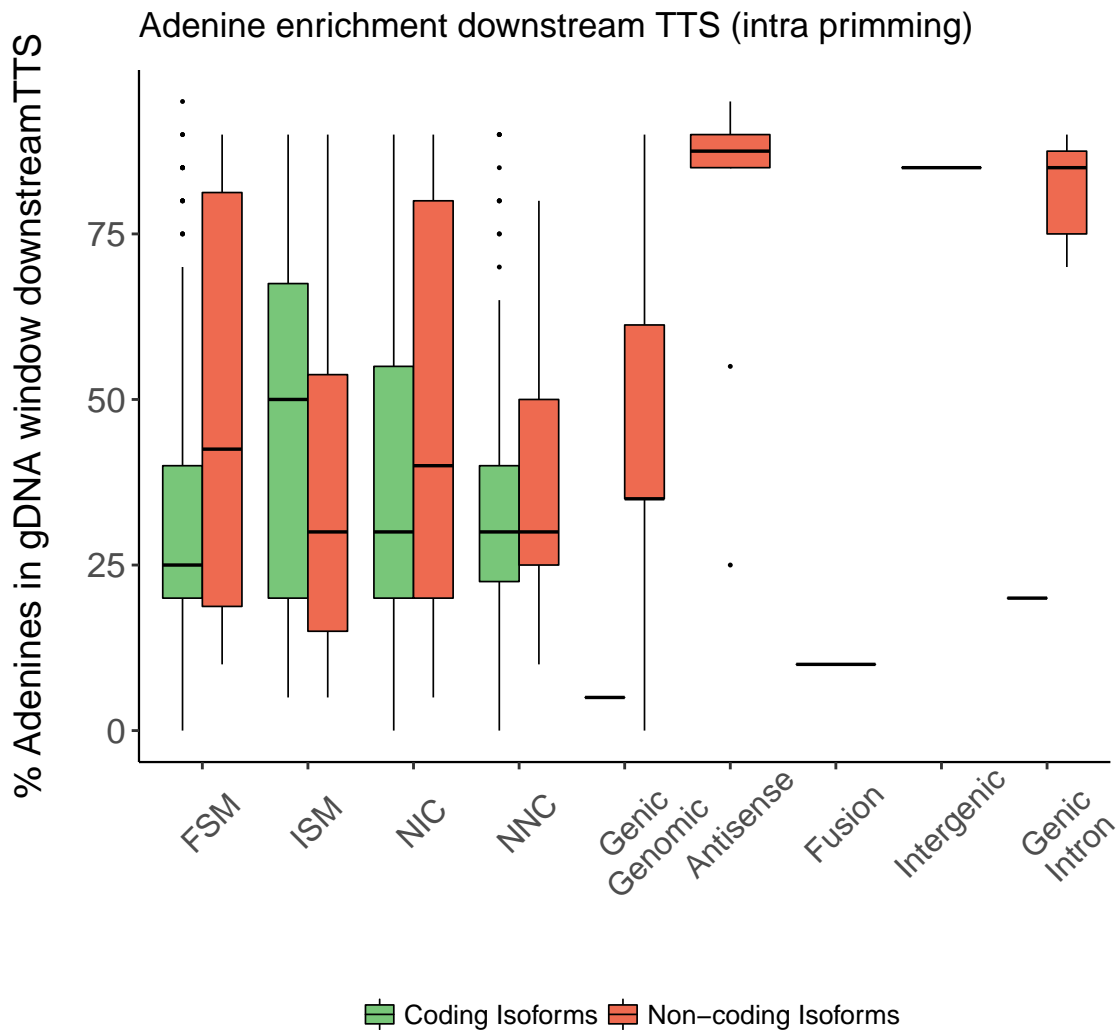
Gene expression by type of gene annotation



Number of FL reads per Gene by type of gene annotation

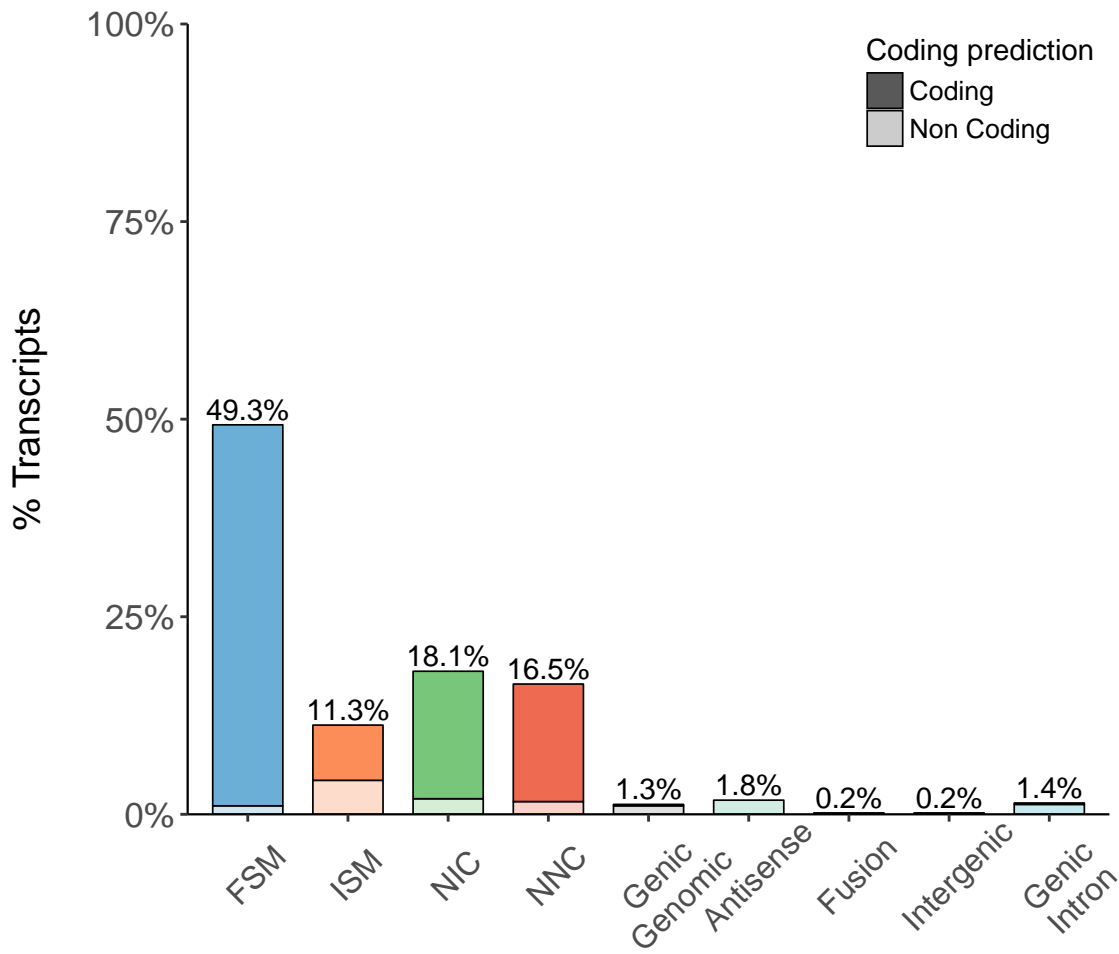




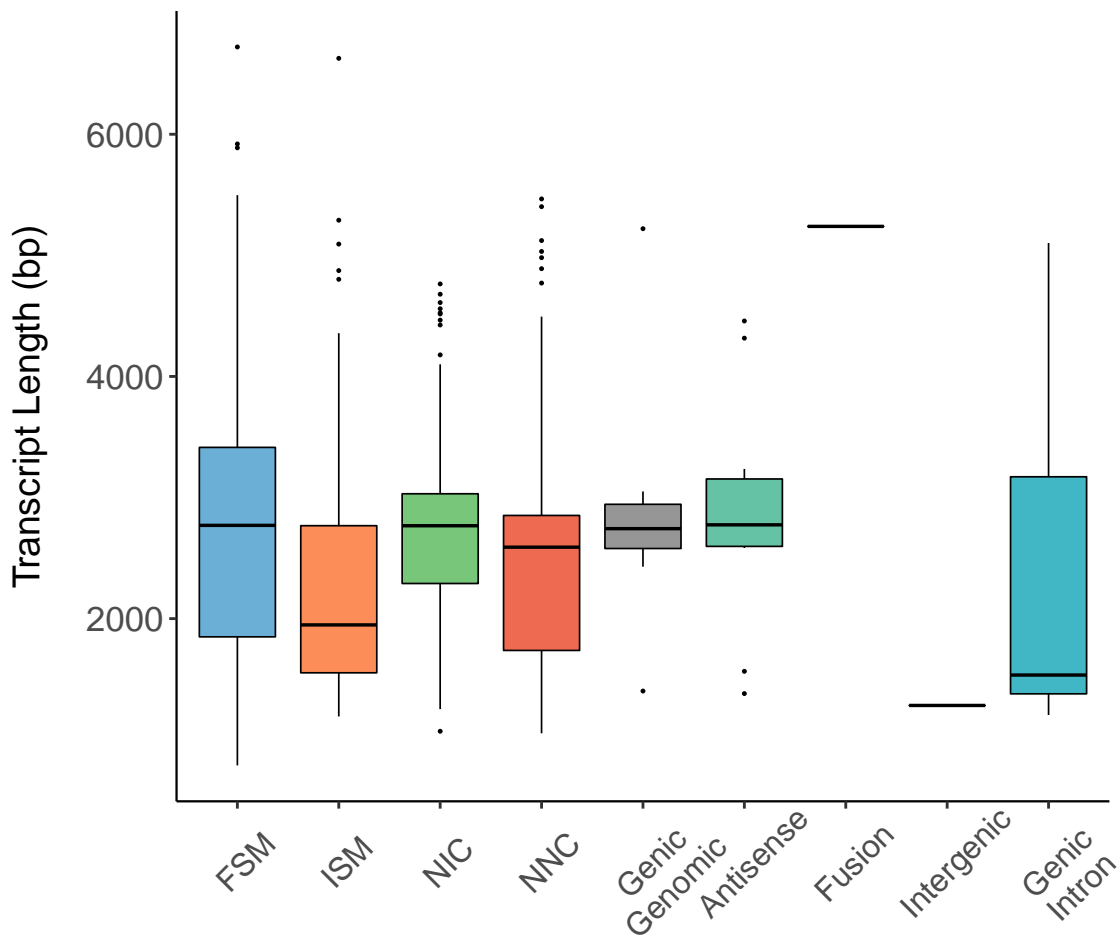


*Structrual Isoform characterization
based on splice junctions*

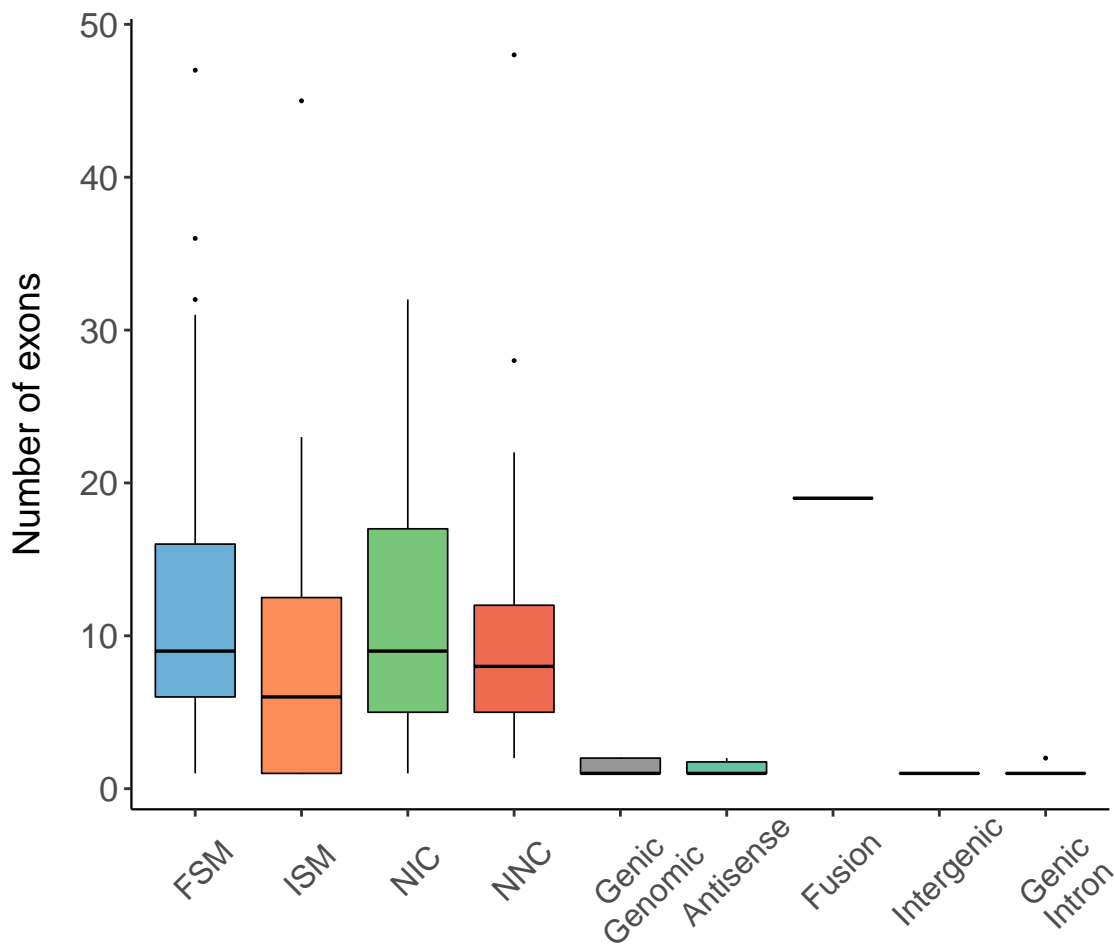
Isoform distribution across structural categories



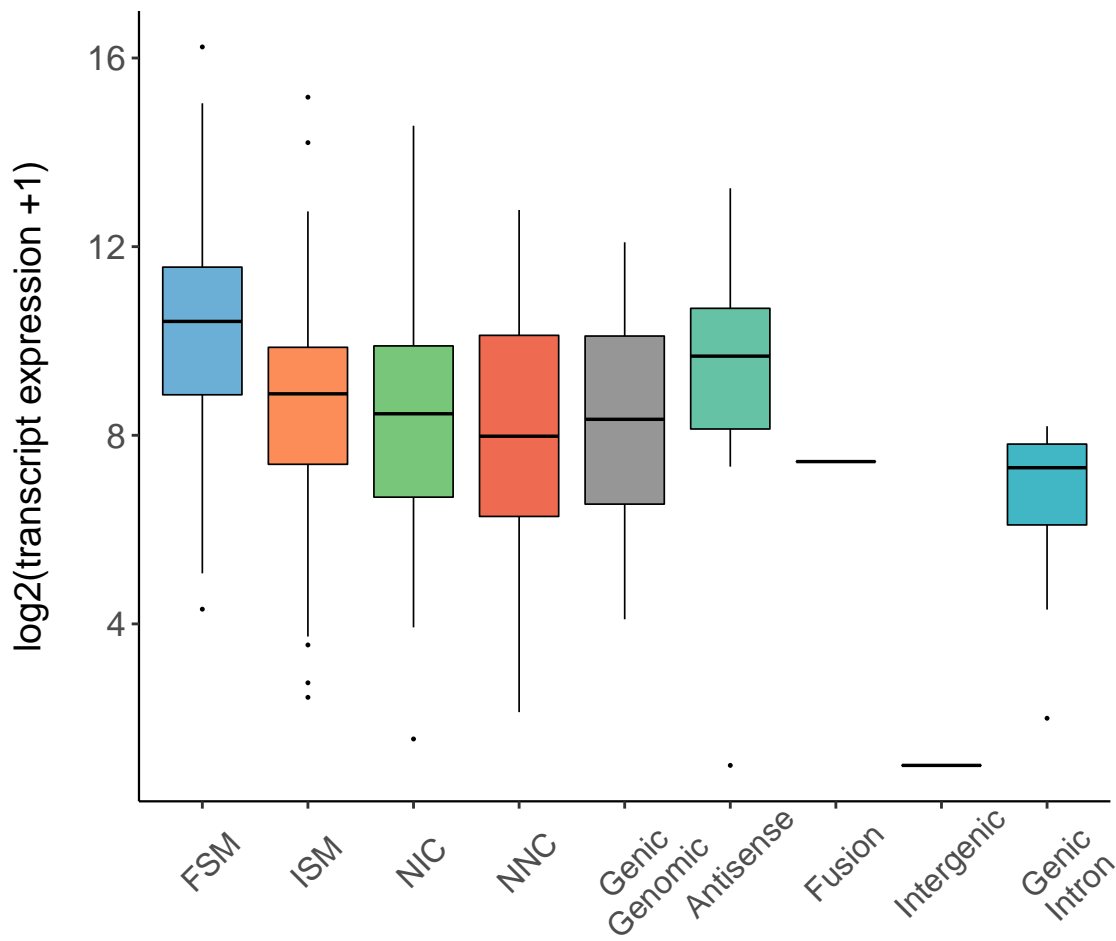
Transcript length distribution by structural classification



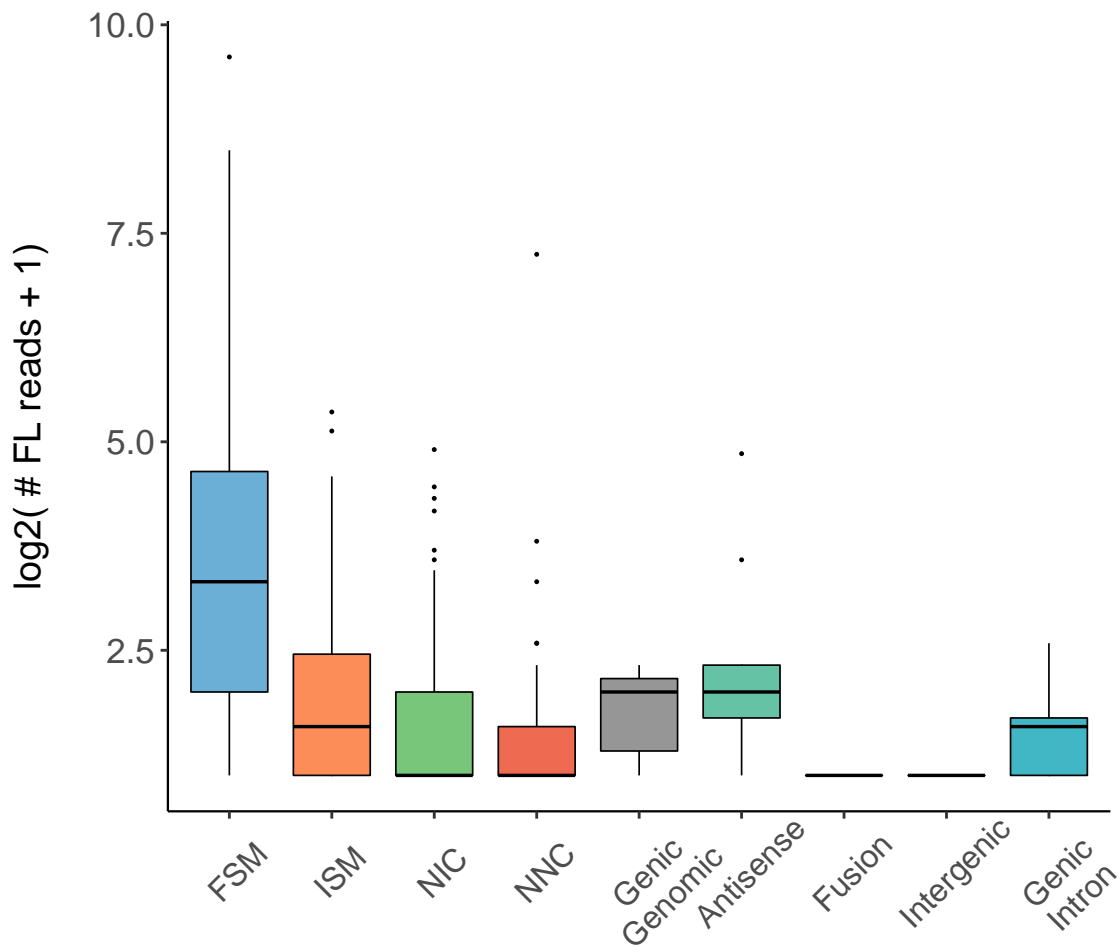
Exon number distribution by structural classification



Transcript expression by structural category

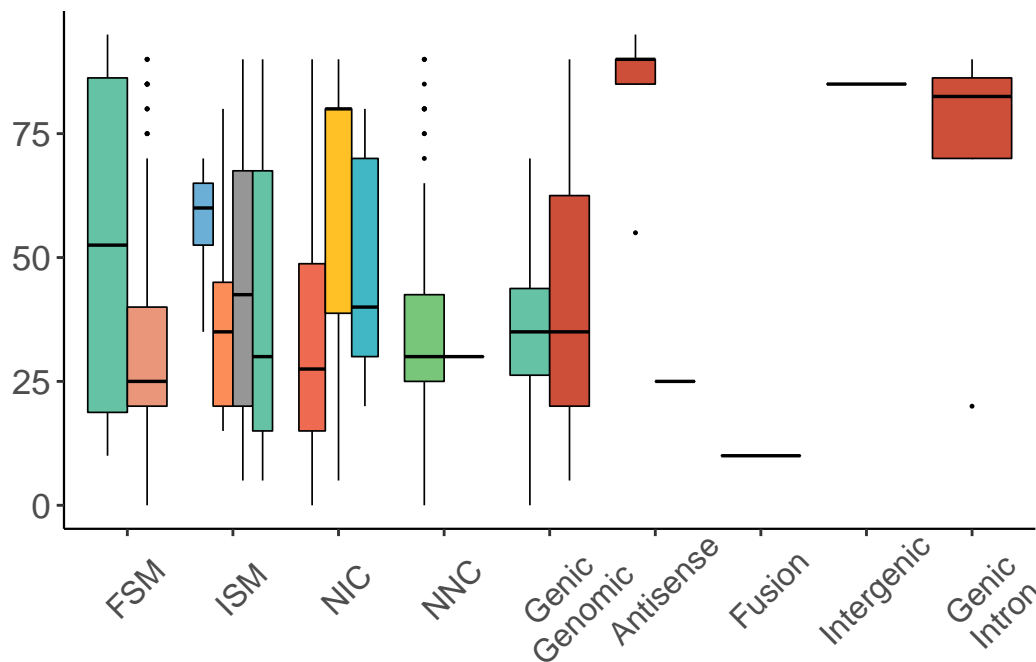


Number of FL reads per transcript by structural category



% Adenines in gDNA window downstream TTS

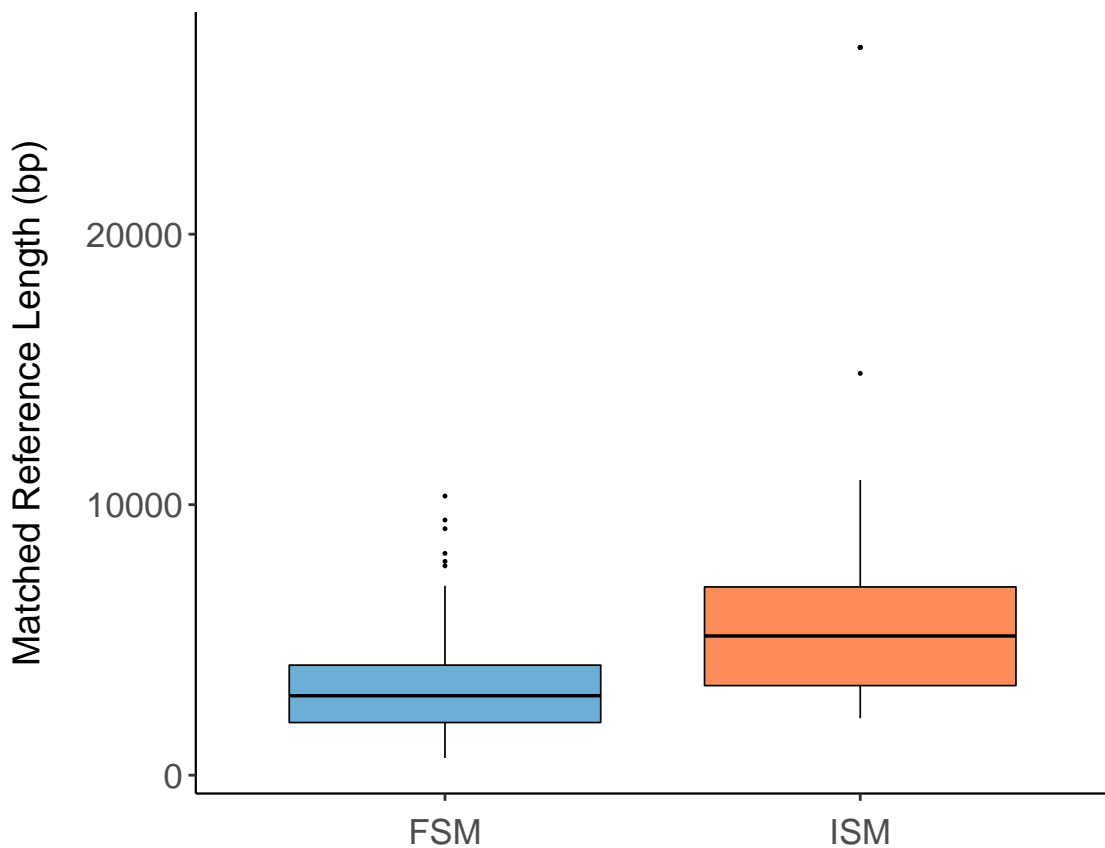
Adenine enrichment downstream TTS (intra primming)



- 3' fragment
- 5' fragment
- Multi-exon
- Not combination of annotated junctions
- Without annotated donors/acceptors
- Internal fragment
- Mono-exon
- Combination of annotated junctions
- Mono-exon by intron retention
- At least one annotated donor/acceptor

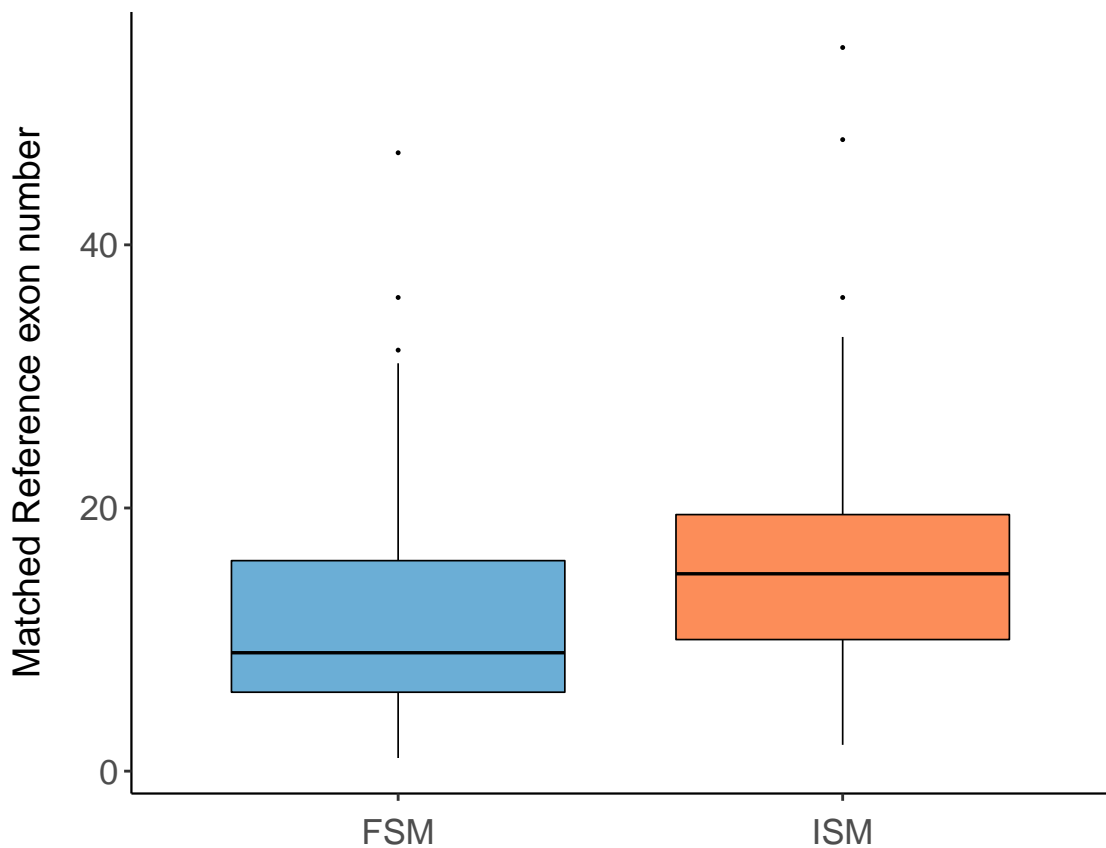
Length distribution of matched reference transcripts

Just applicable to FSM and ISM categories

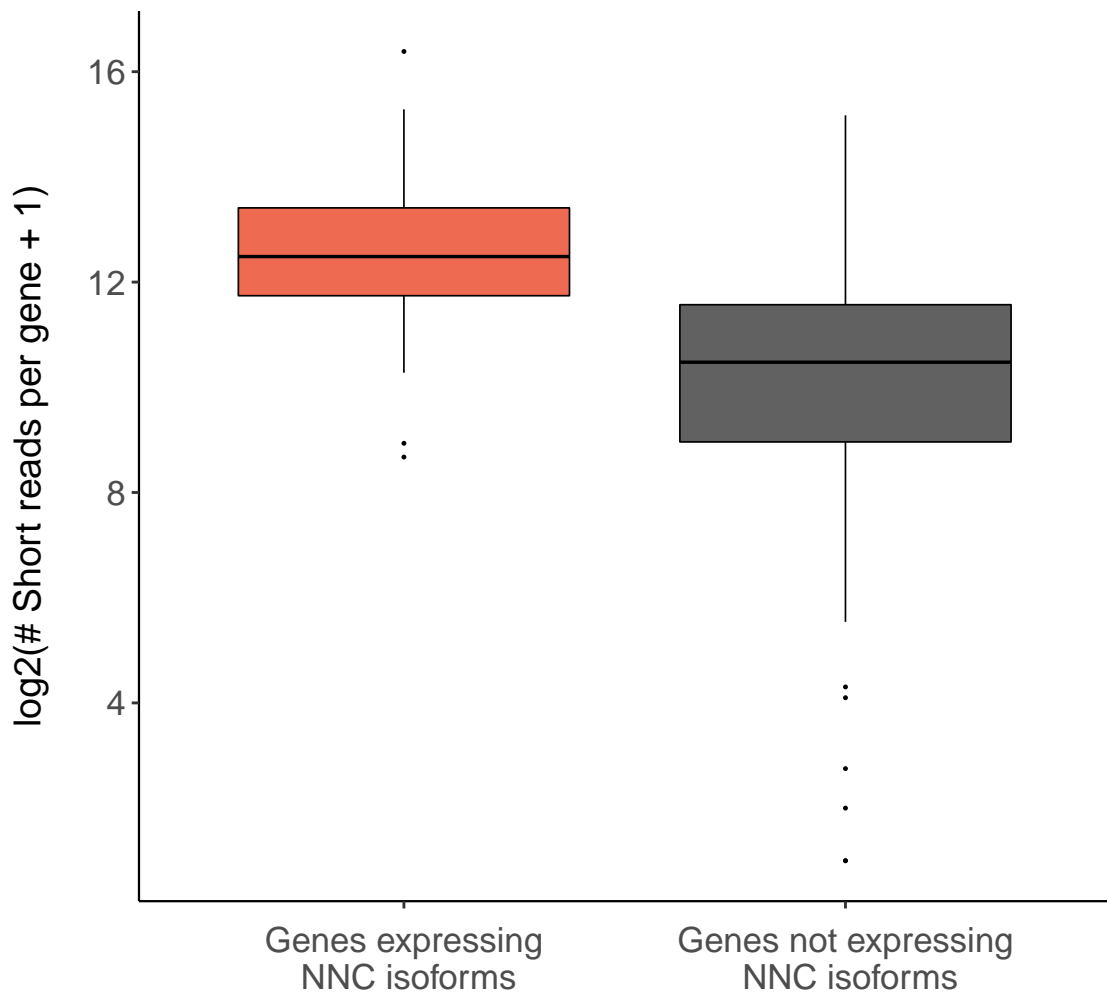


Exon number distribution of matched reference transcripts

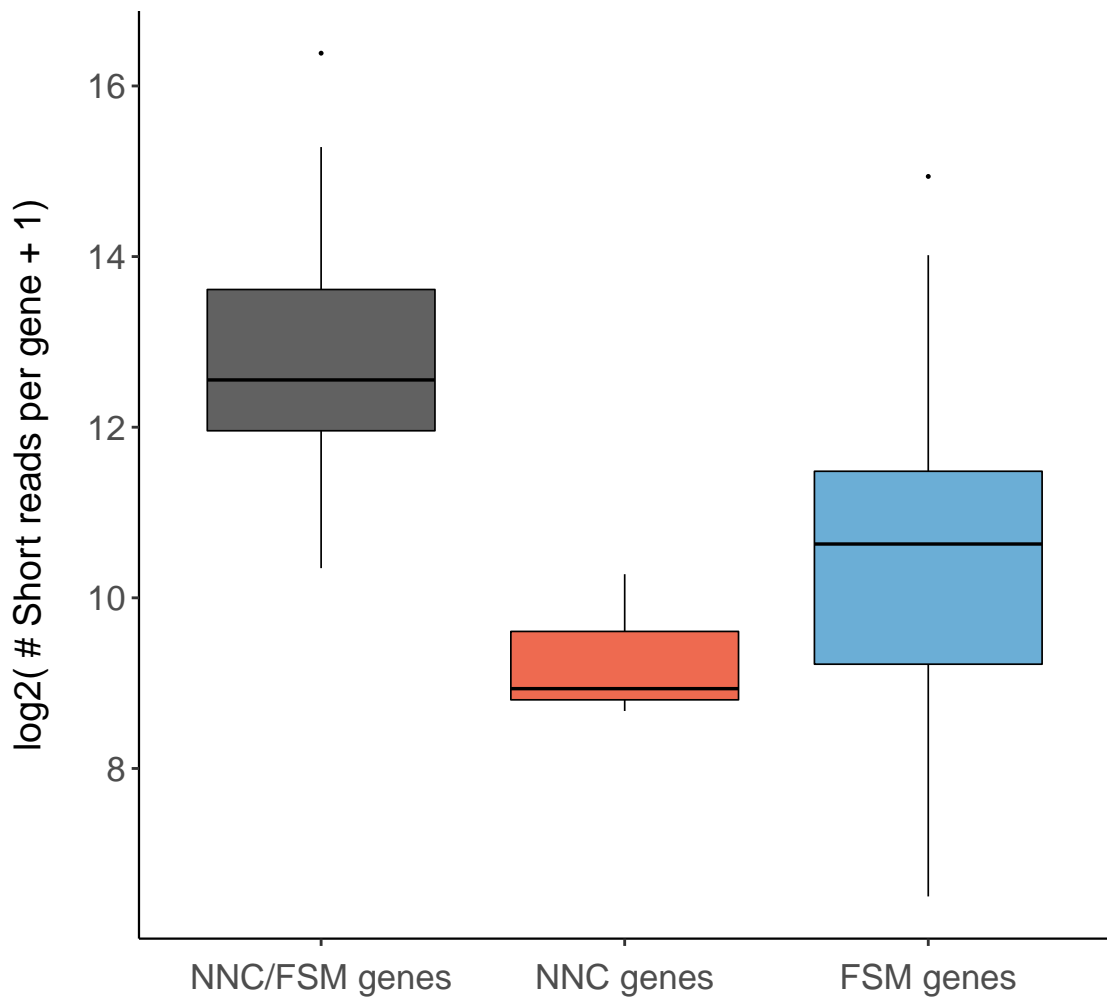
Just applicable to FSM and ISM categories



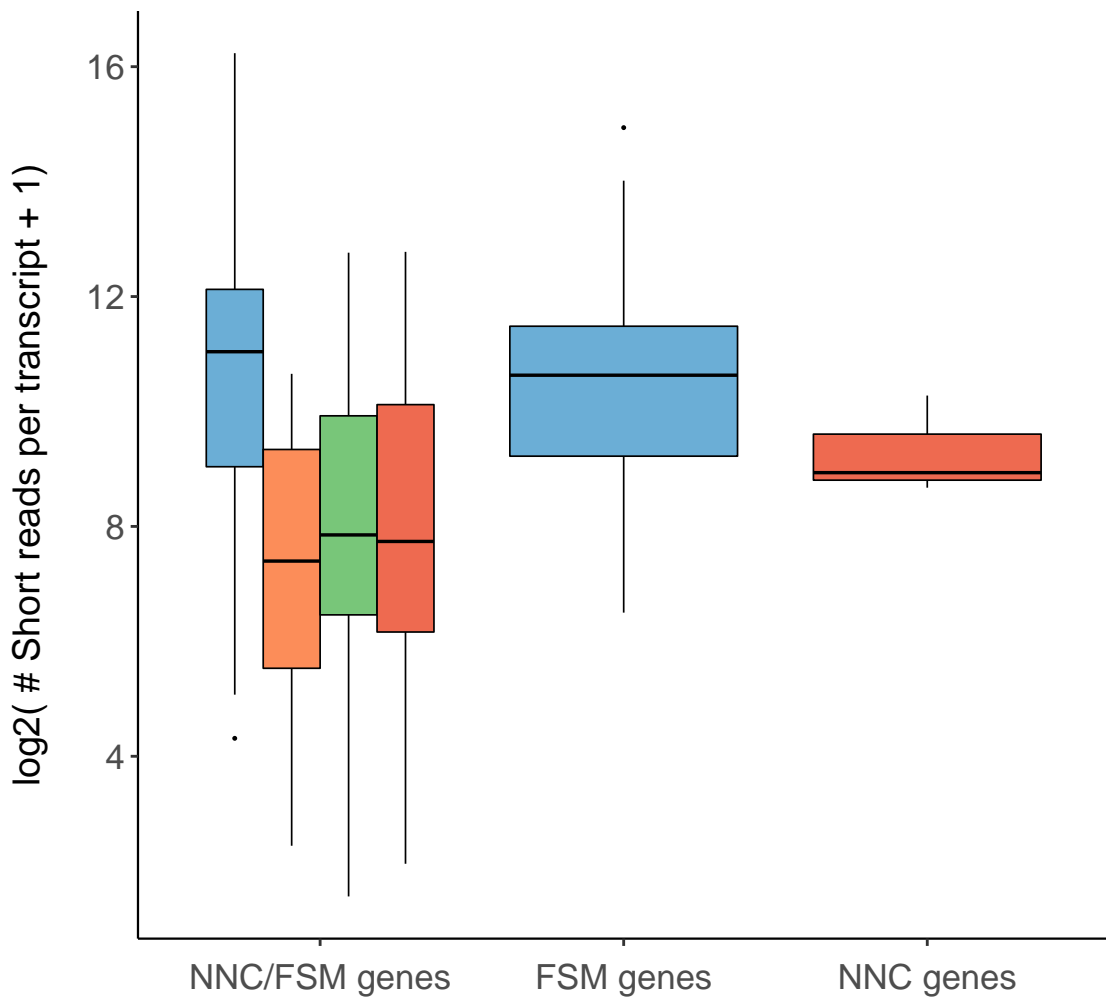
Gene expression levels between NNC and not NNC containing gene



Gene expression level in NNC/FSM containing genes



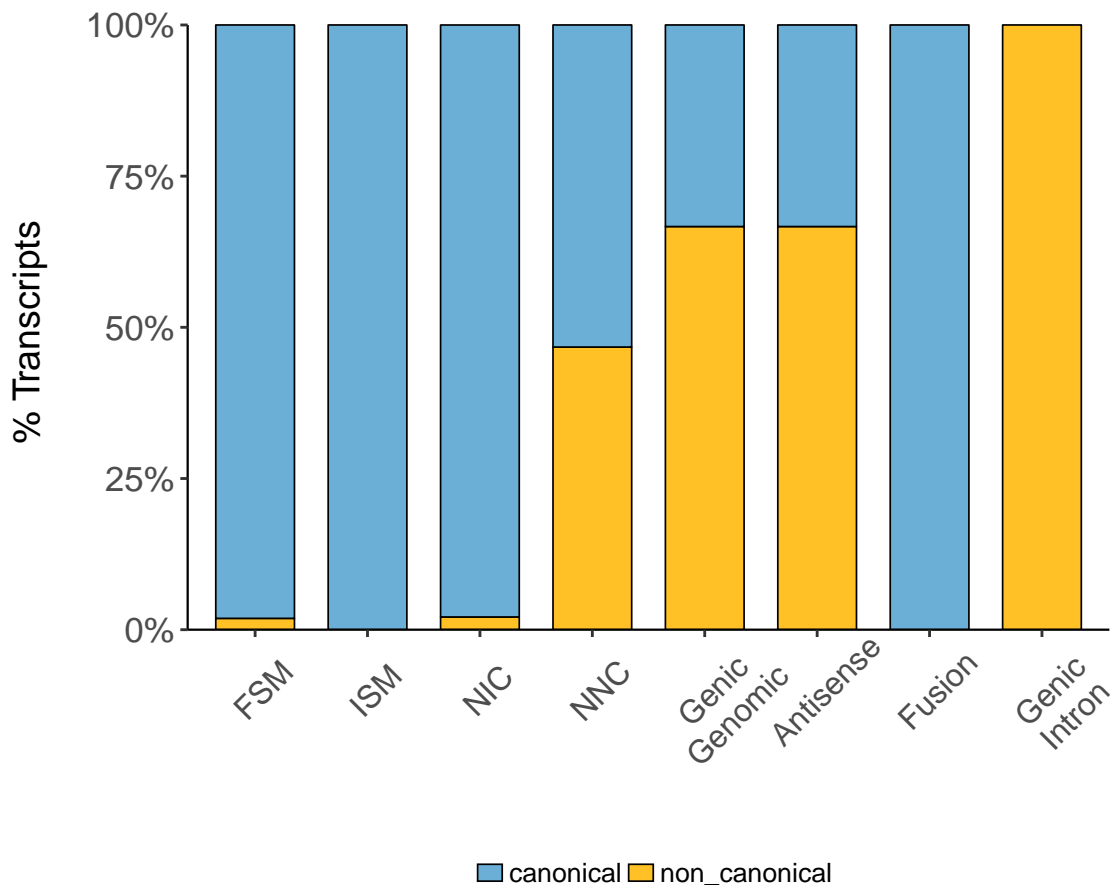
Transcript expression level in NNC/FSM containing genes



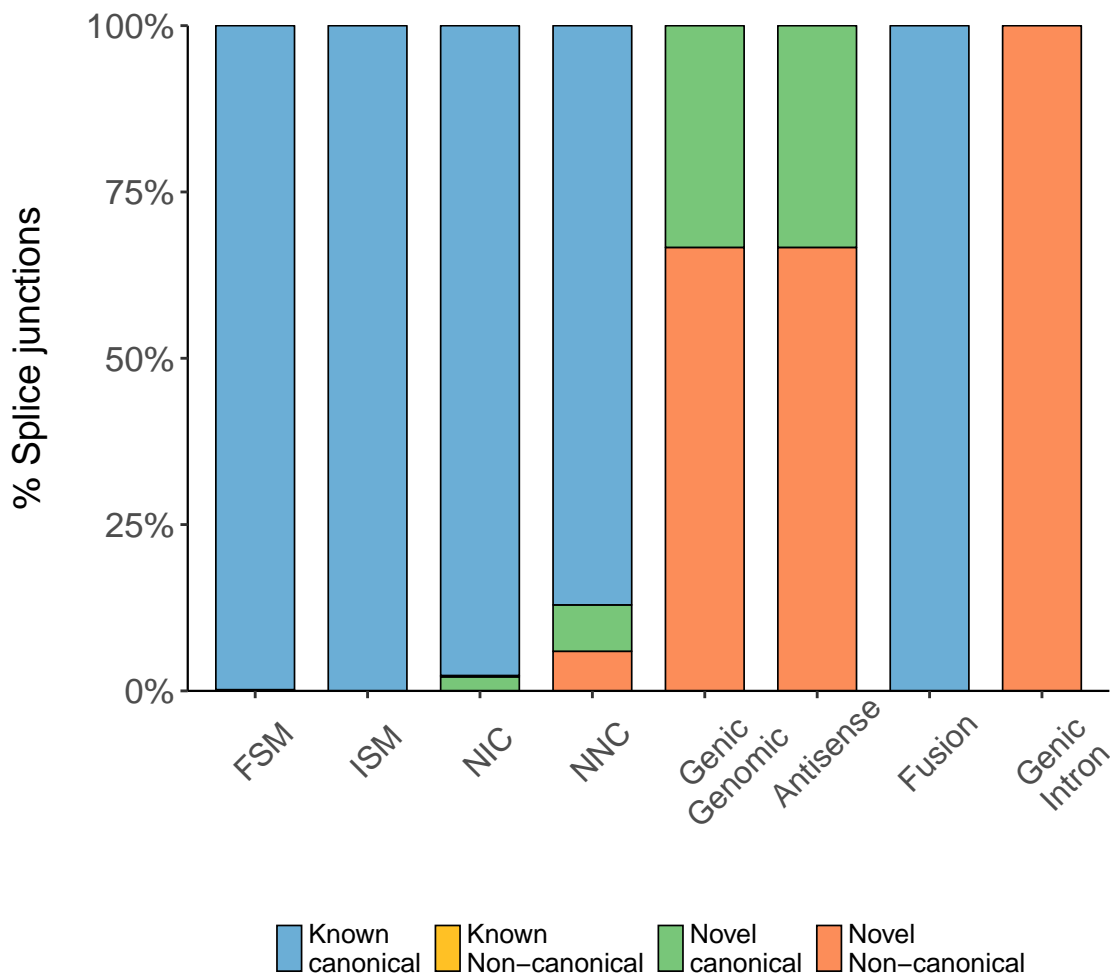
Splice junction characterization

Distribution of transcripts by splice junction category

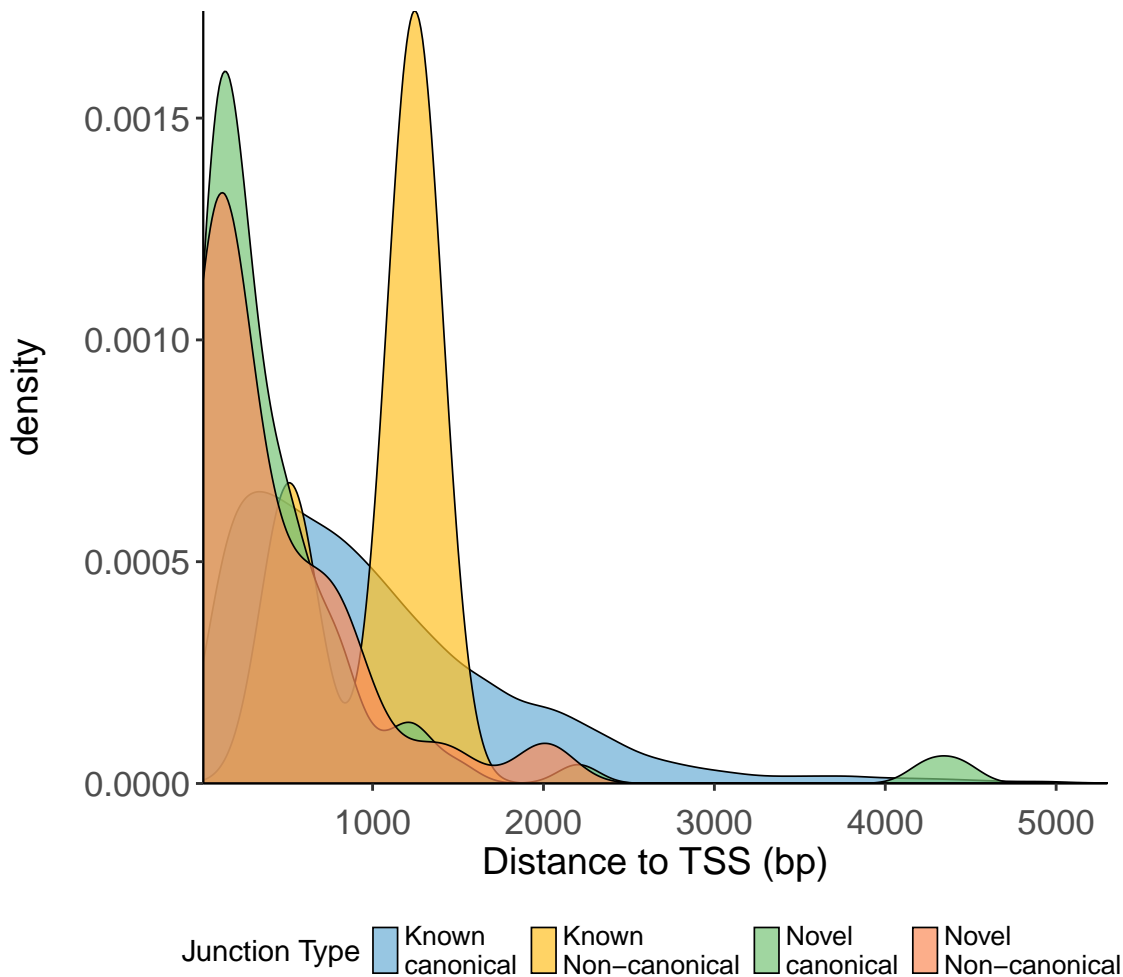
Non canonical transcripts are those with at least one non-canonical junction



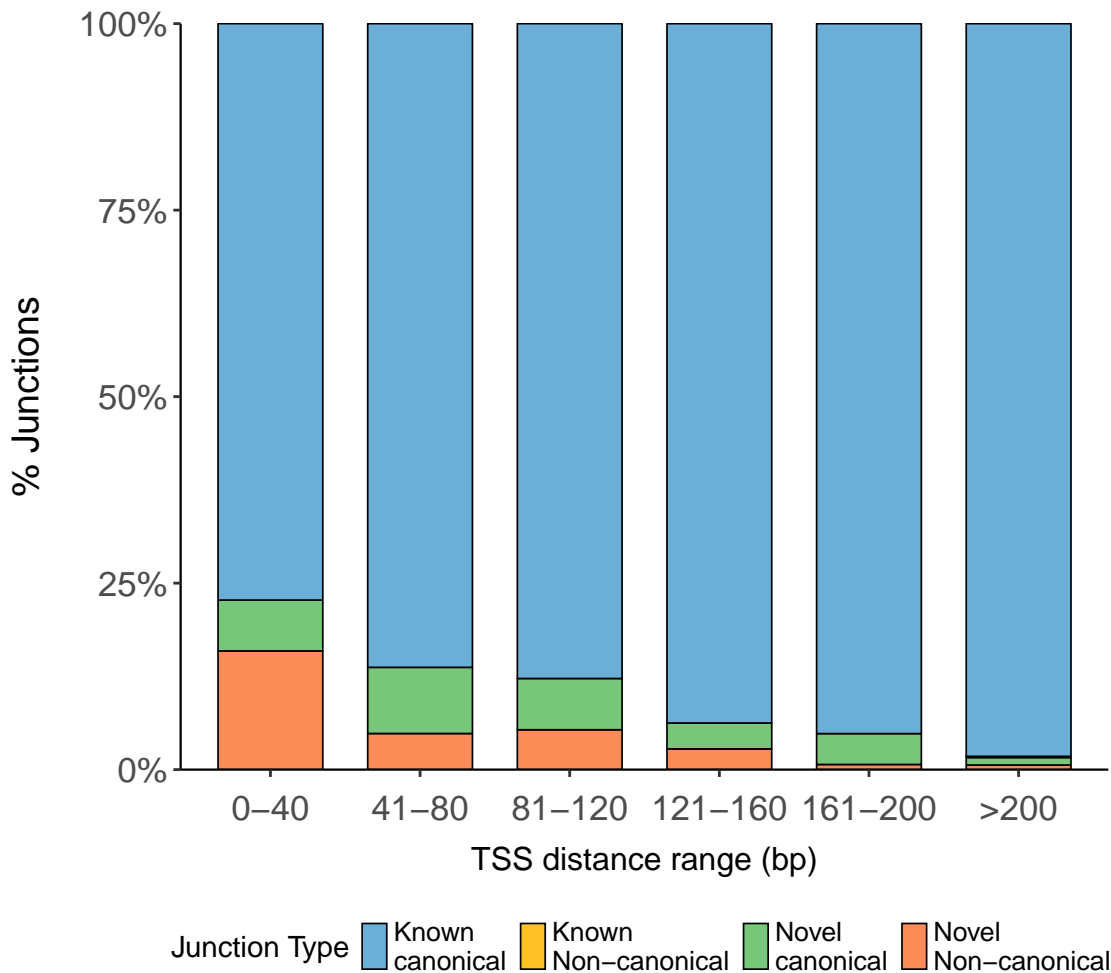
Distribution of SJ type among structural classification



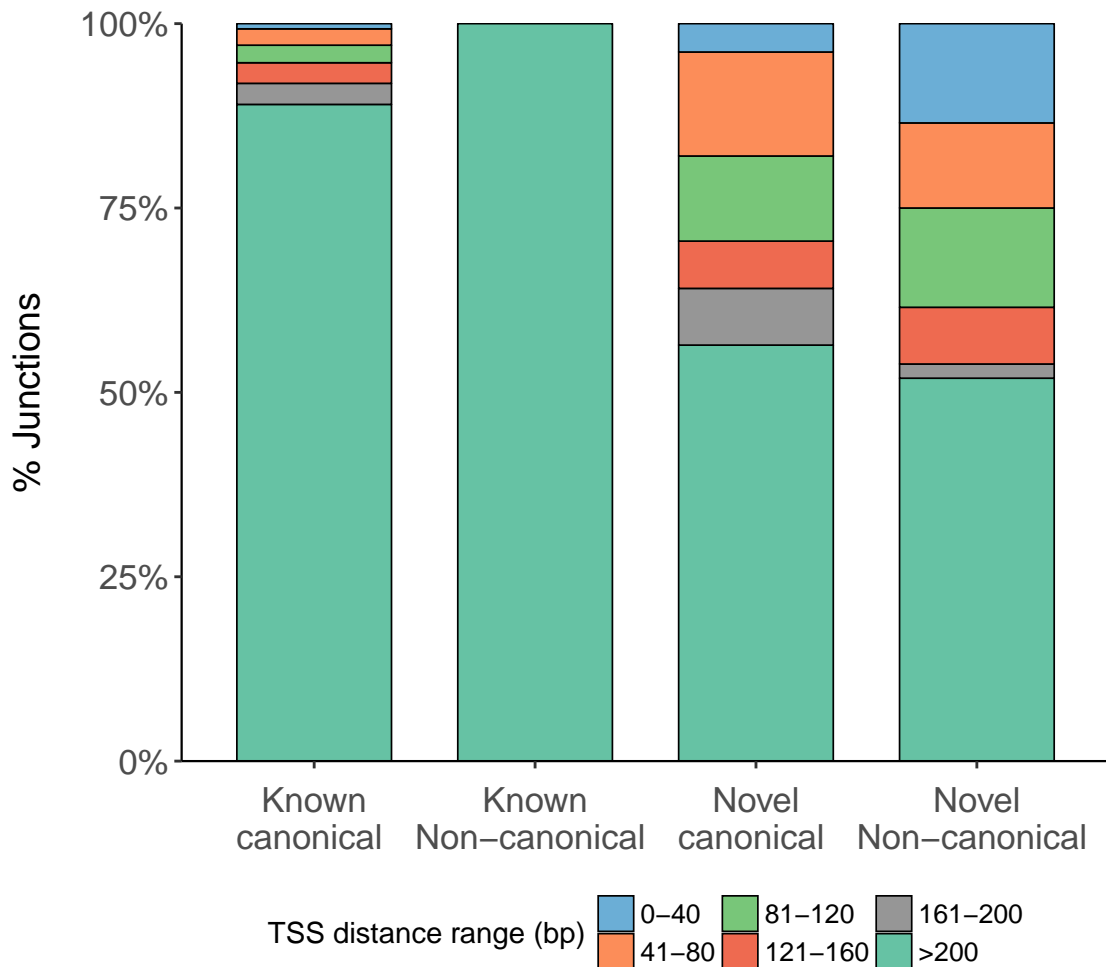
Distribution of splice junctions distance to TSS



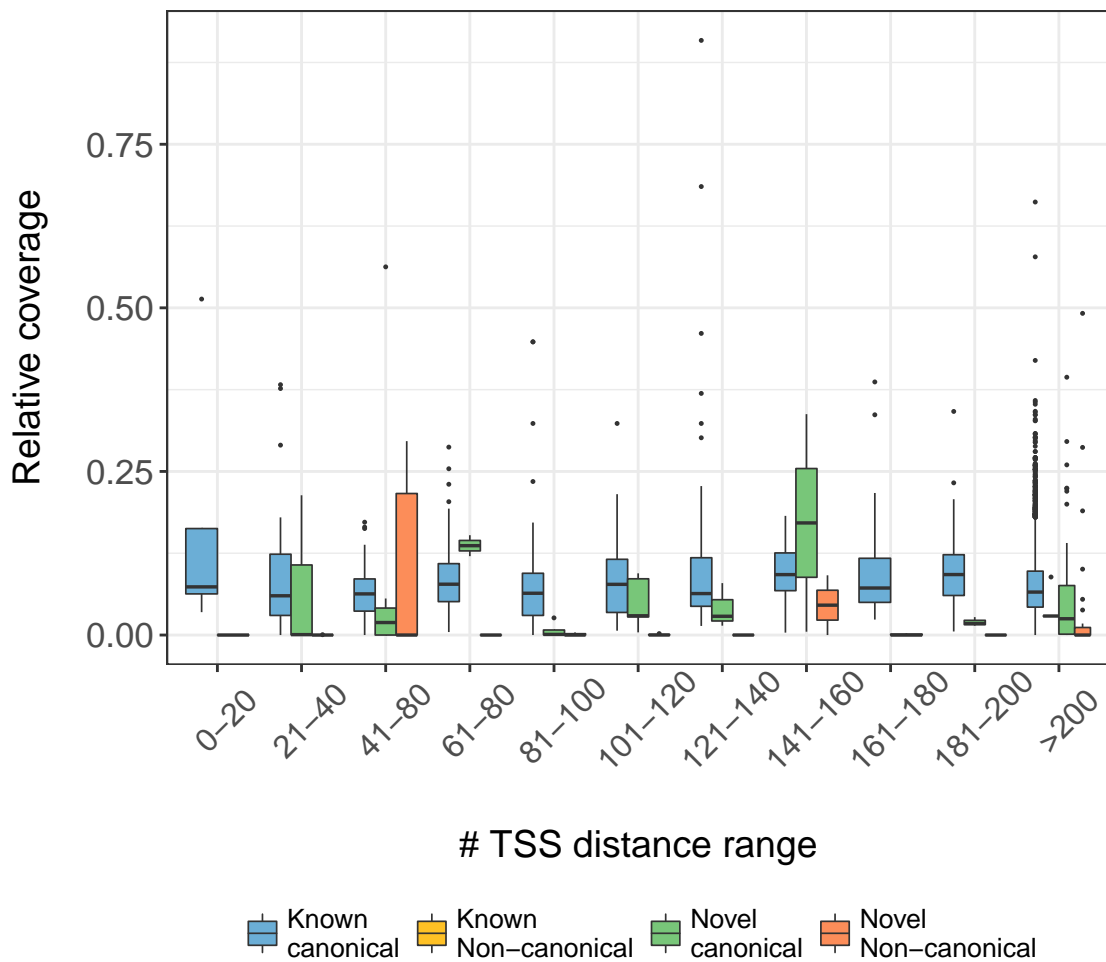
Splice junction distance to TSS across junction type



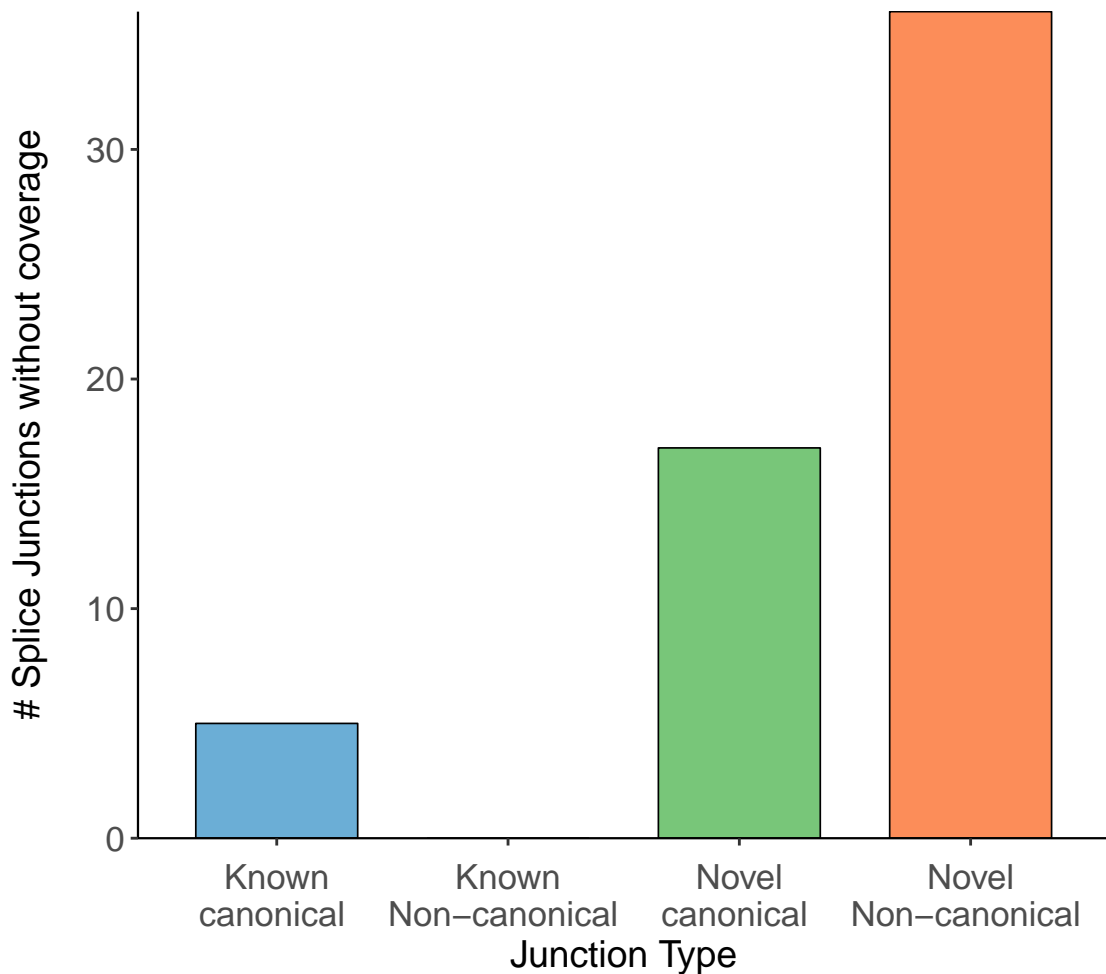
Splice junction distance to TSS across junction type



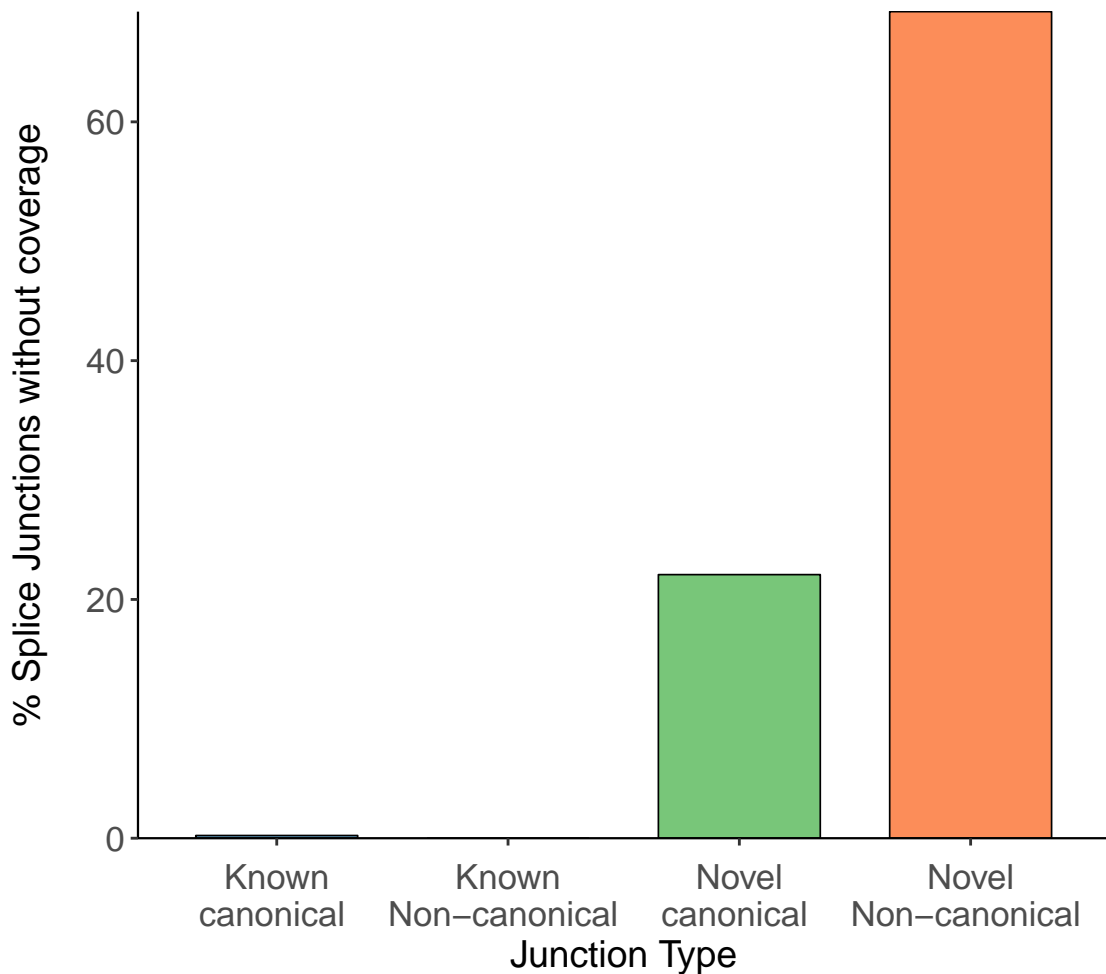
Relative Coverage of junctions



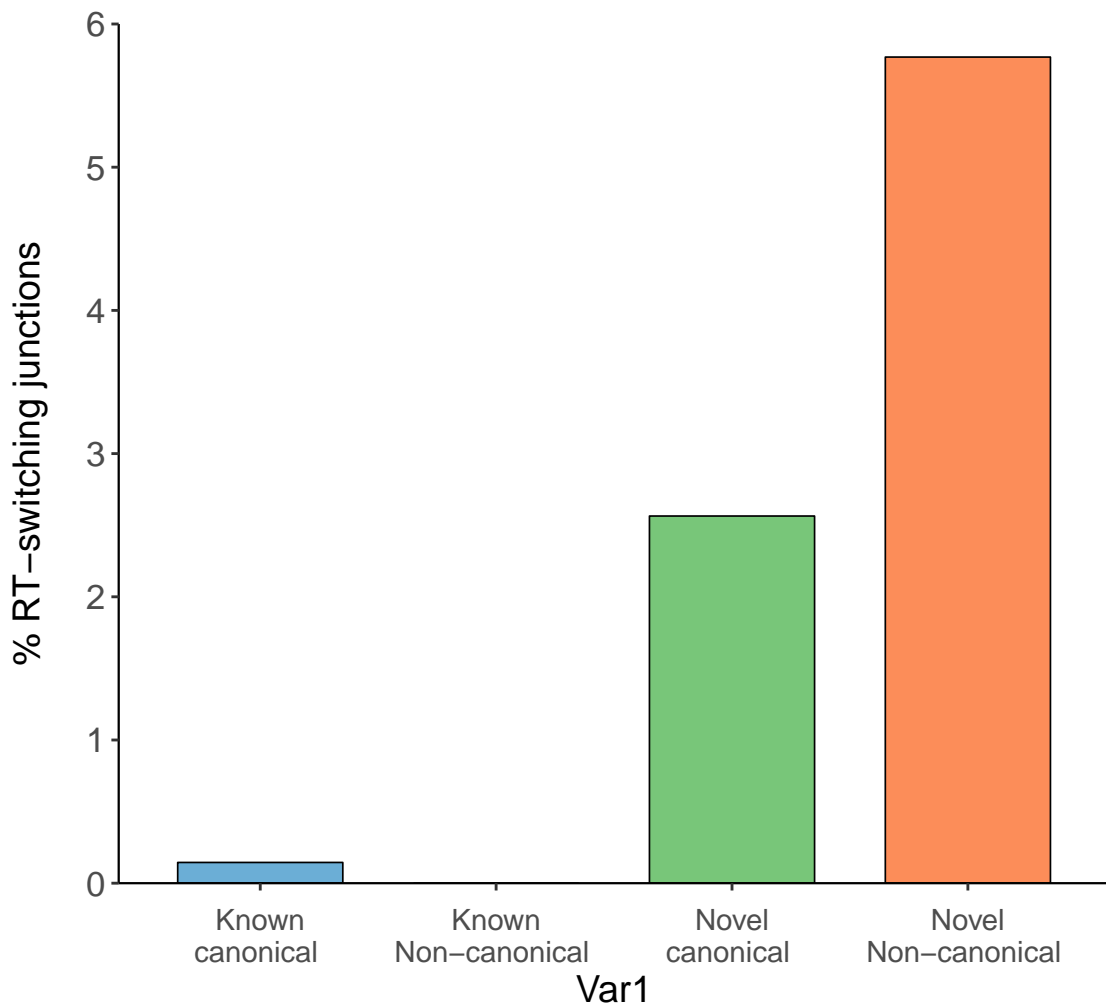
Splice junctions without short-read coverage (unique junctions)



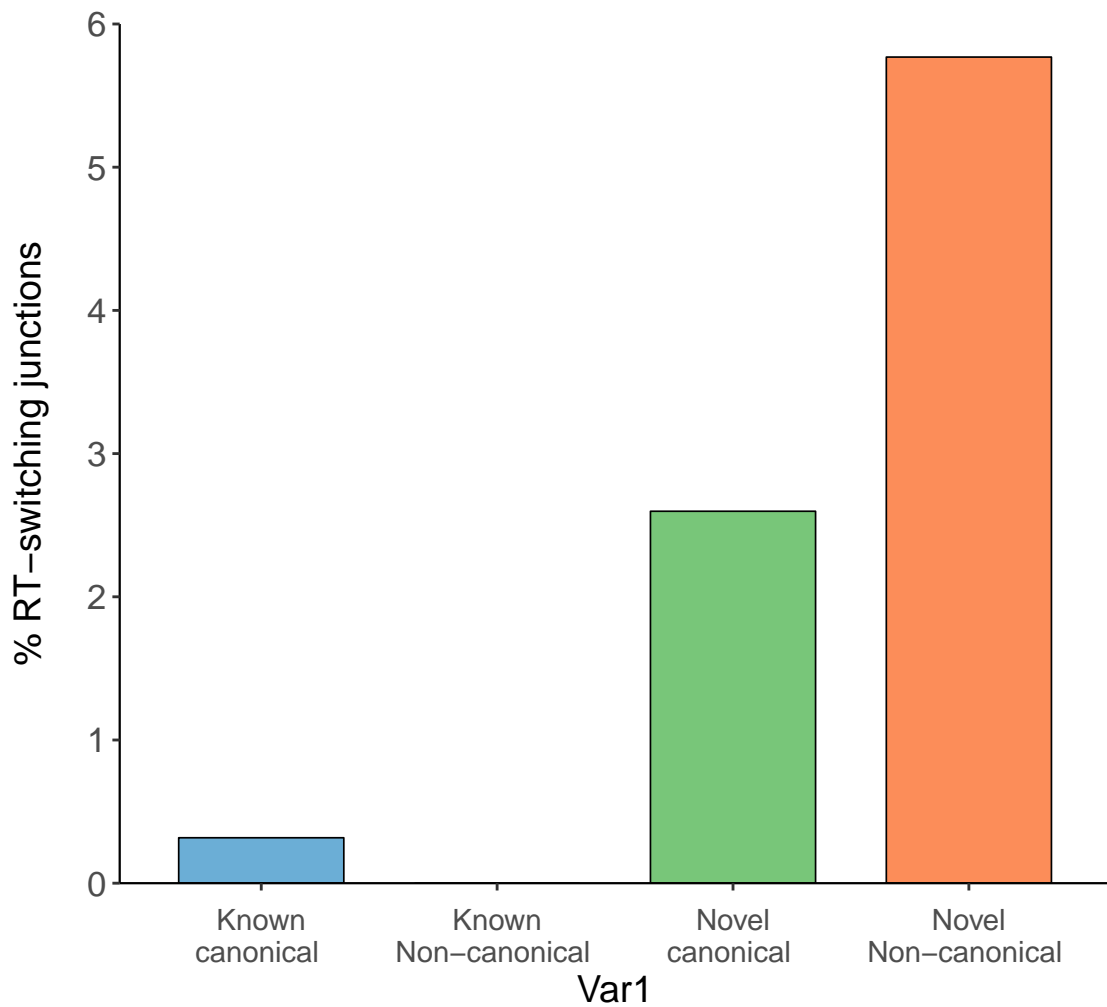
Splice junctions without short-read coverage (unique junctions)



RT-switching by splice junction category



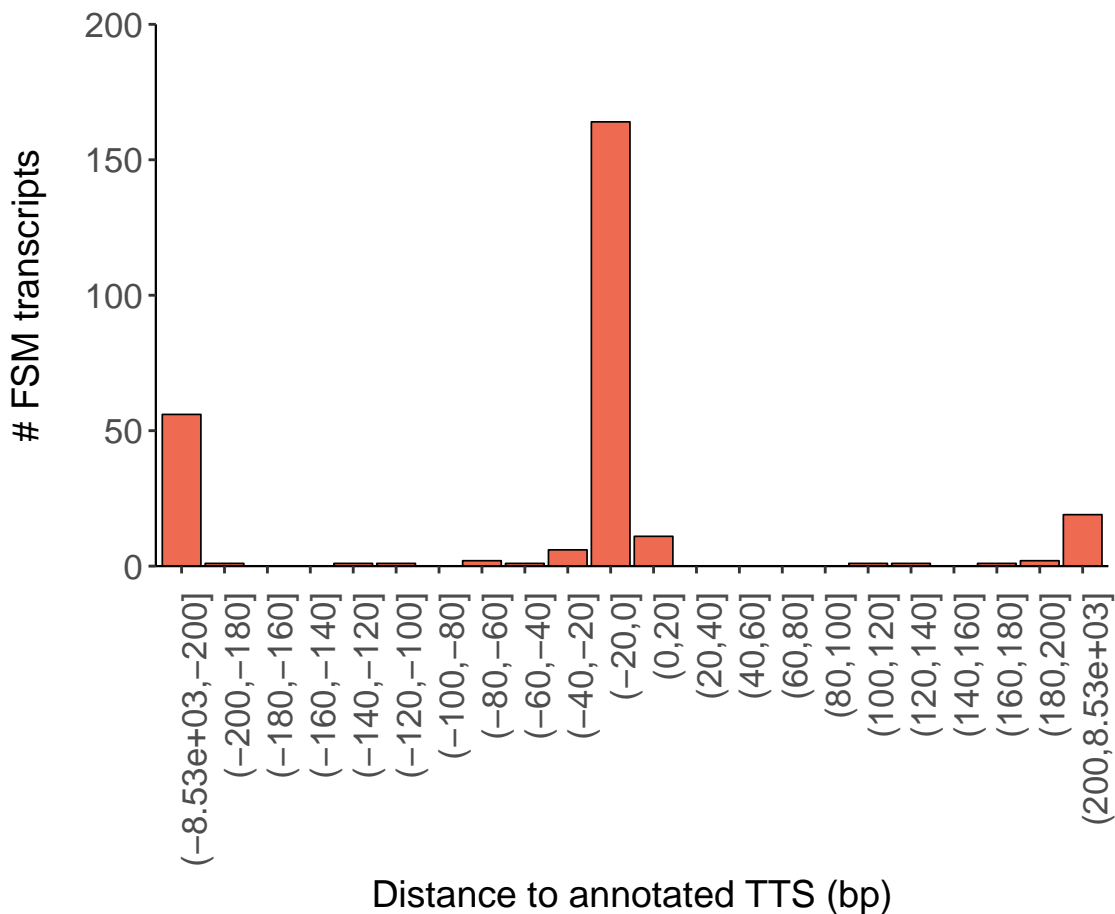
RT-switching by splice junction category (unique junctions)



Full-lengthness characterization of isoforms

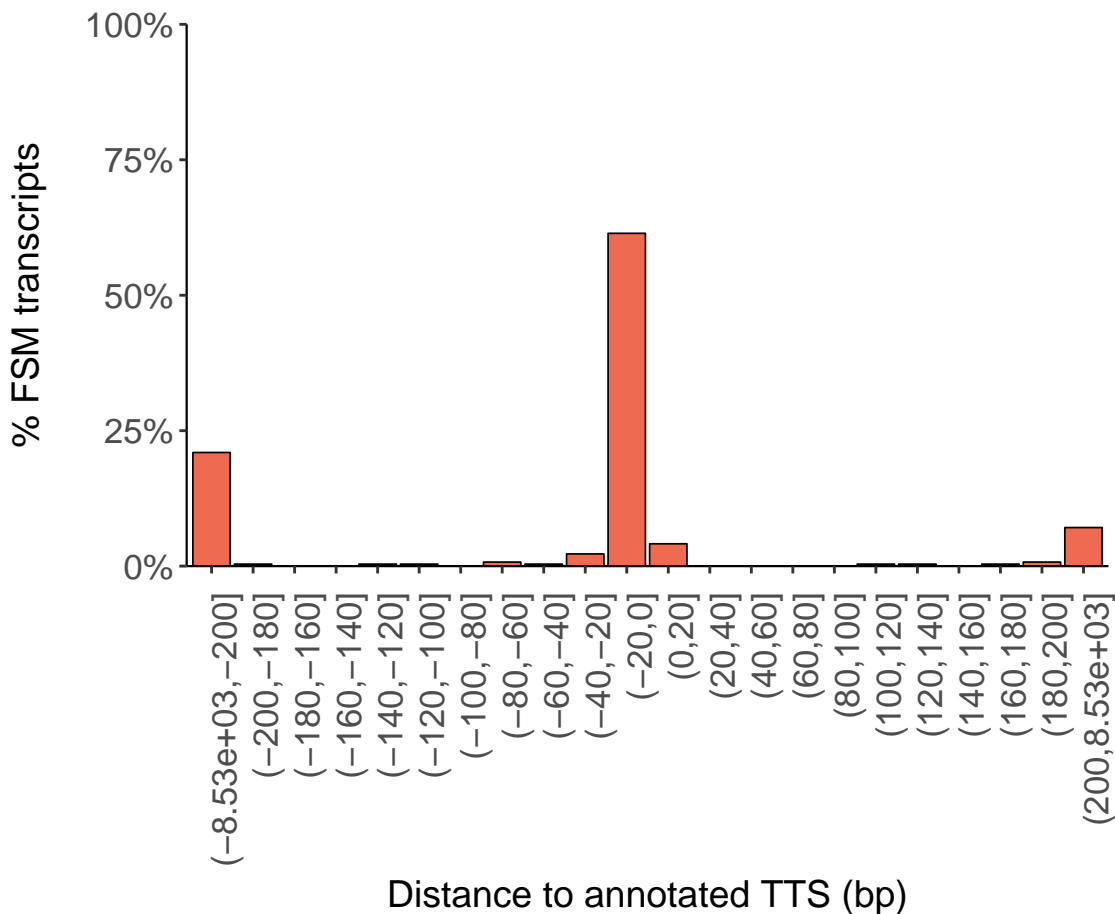
Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is upstream annotated TTS



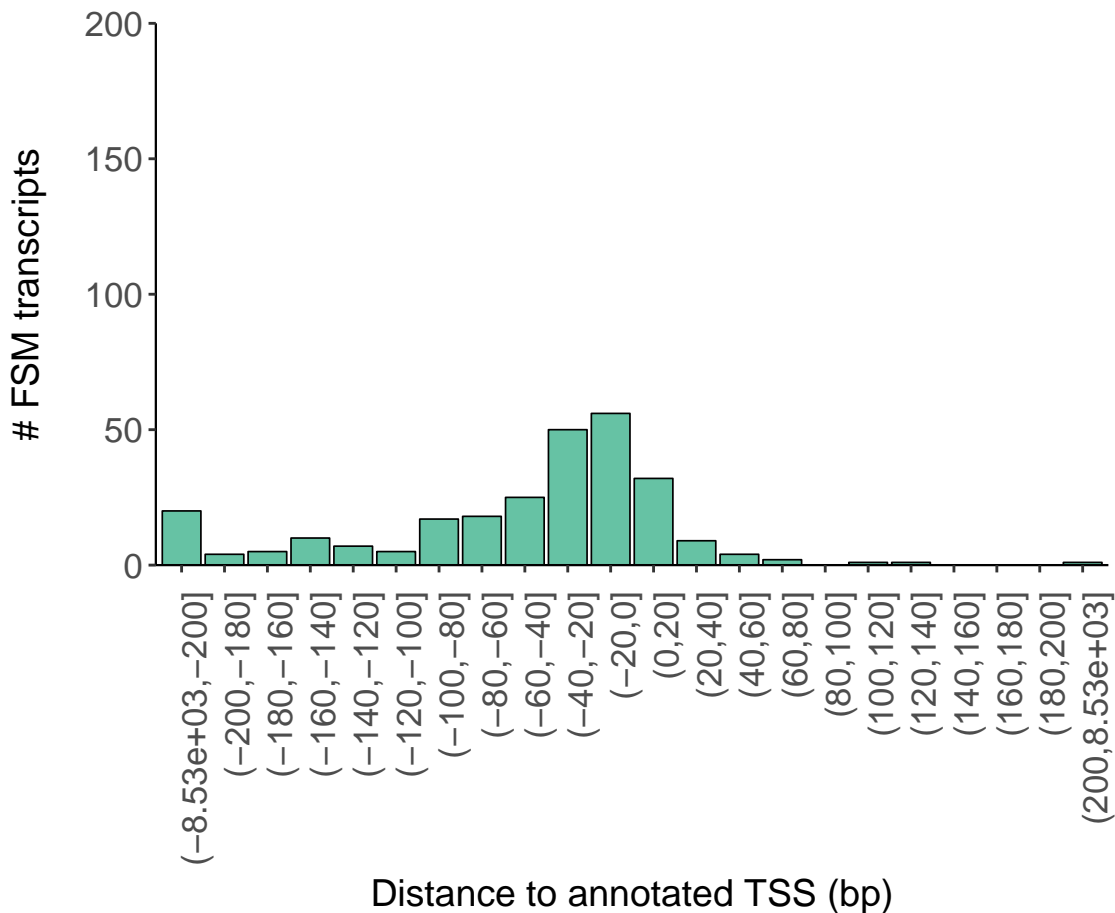
Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is upstream annotated TTS



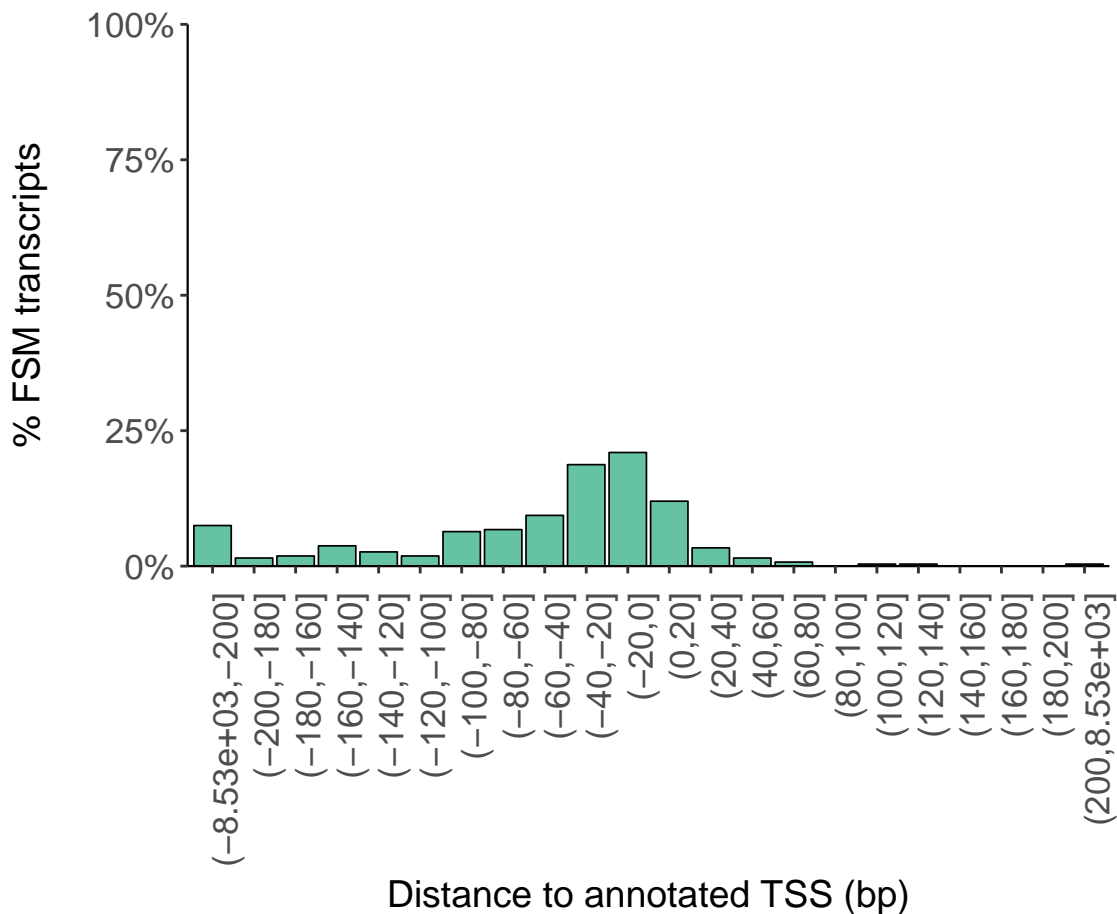
Distance distribution from sequenced to annotated TSS

Negative values indicate that the sequenced TSS is downstream annotated TSS



Distance distribution from sequenced to annotated TSS

Negative values indicate that the sequenced TSS is downstream annotated TSS



Quality control attributes

Quality control attributes across structural categories

