

*SQANTI report*

*# Genes: 250*

*# Isoforms: 558*

### *Gene classification*

category	# genes
Annotated Genes	231
Novel Genes	19

### *SJ classification*

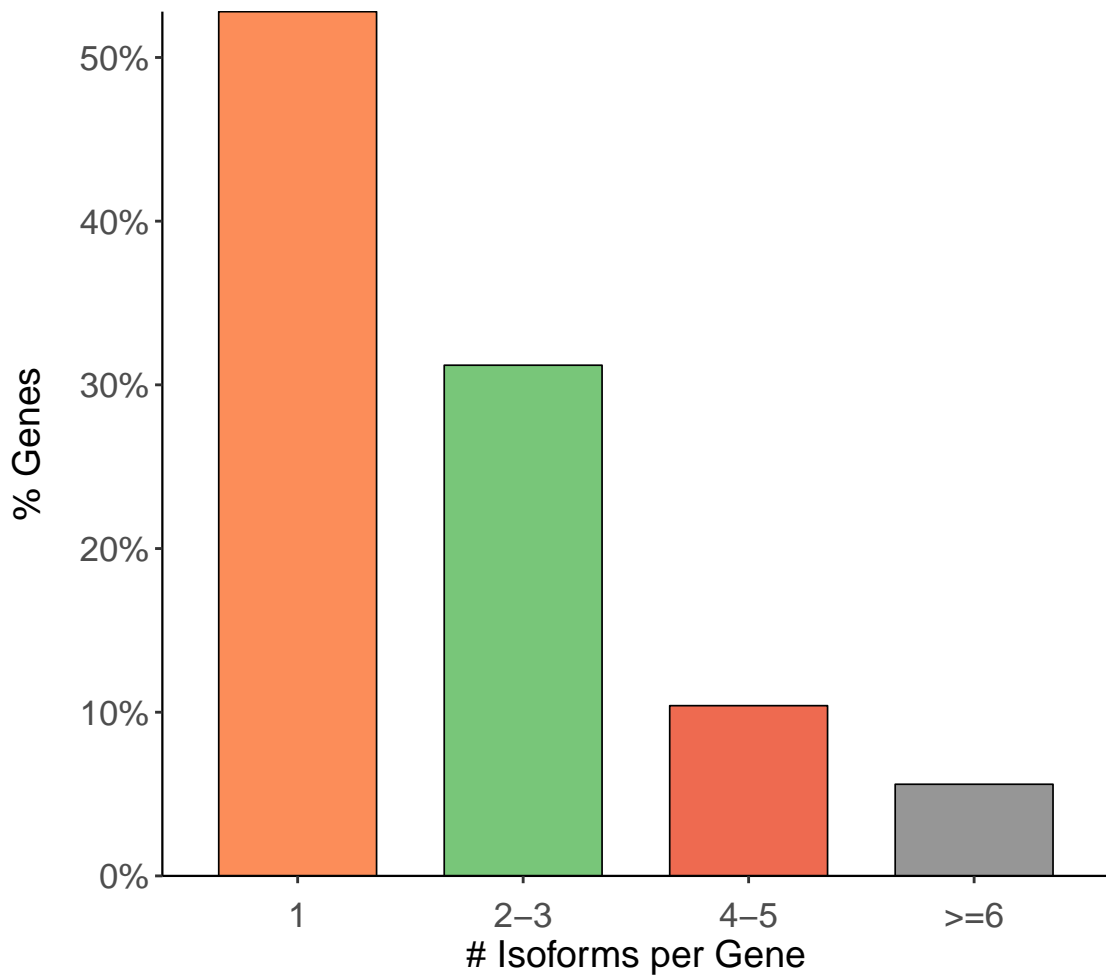
category	# SJ
Known canonical	2195
Known Non-canonical	2
Novel canonical	76
Novel Non-canonical	48

### *Characterization of transcripts based on splice junctions*

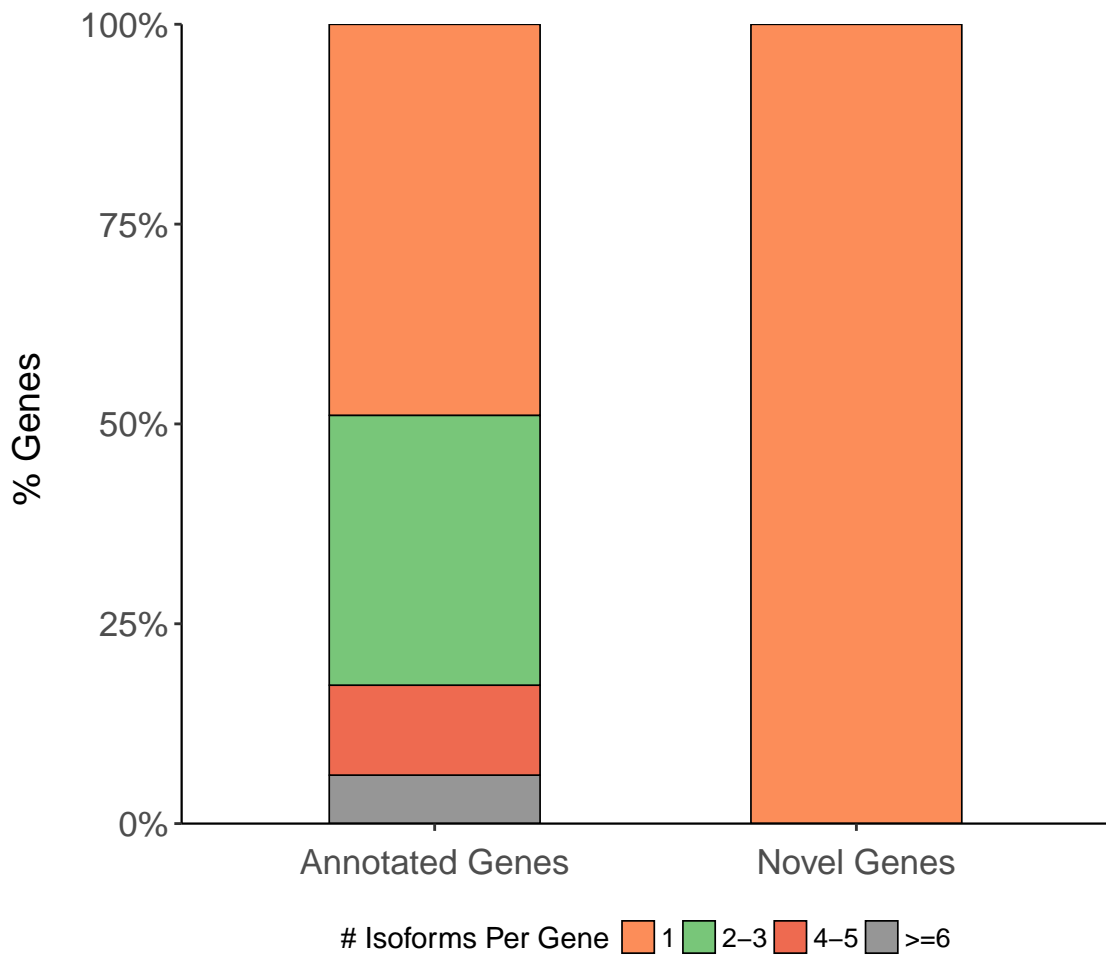
category	# isoforms
FSM	276
NIC	102
NNC	92
ISM	61
Antisense	10
Genic Intron	8
Genic Genomic	7
Fusion	1
Intergenic	1

*Gene characterization*

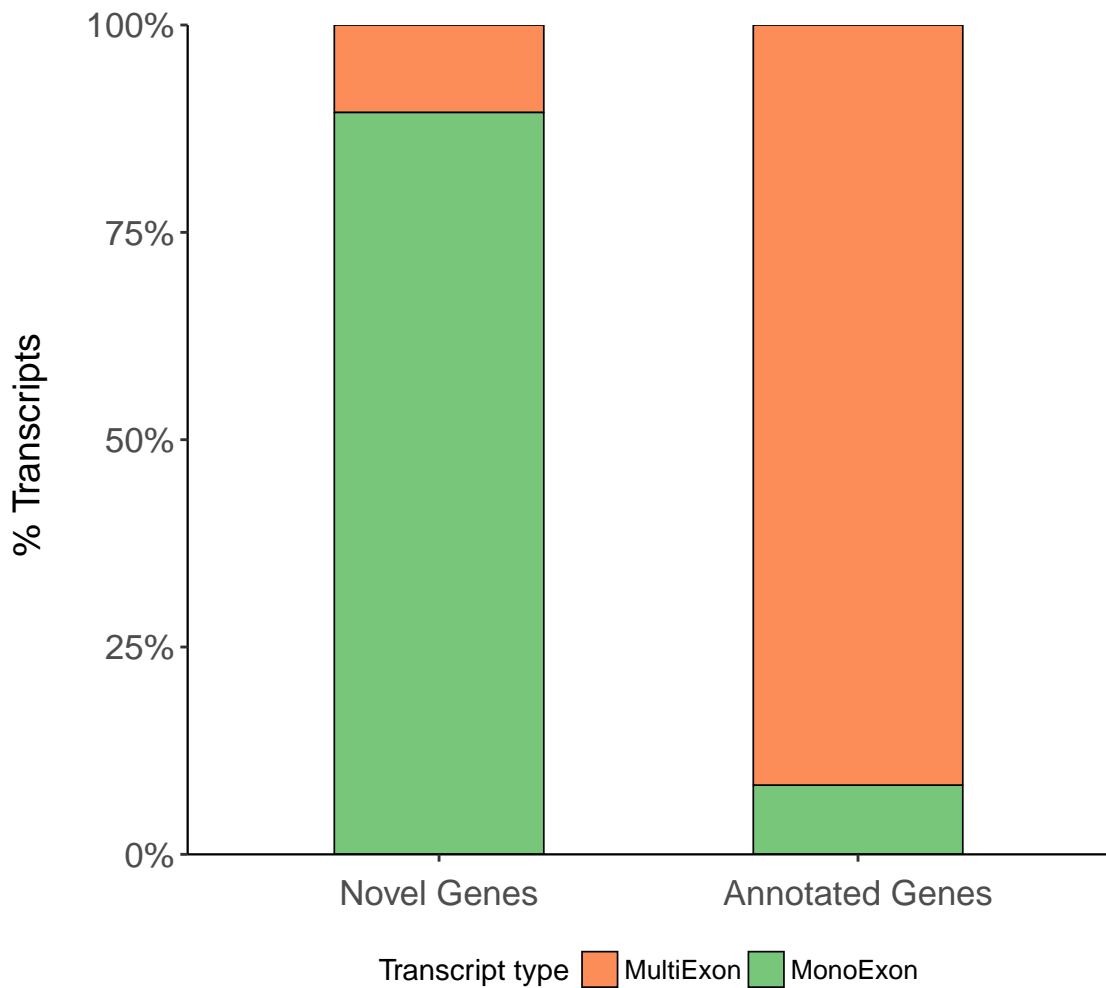
Distribution of isoforms per gene



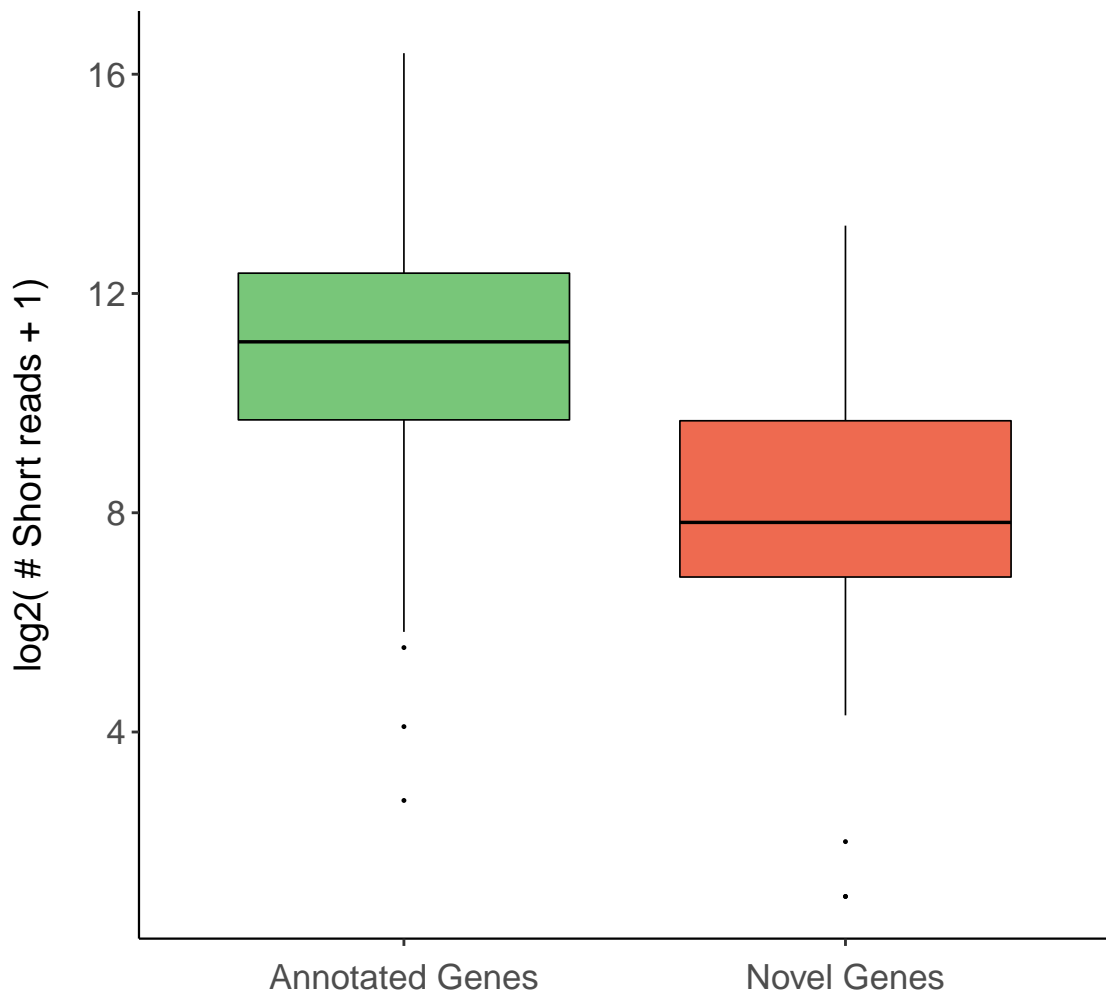
Distribution of number of isoforms



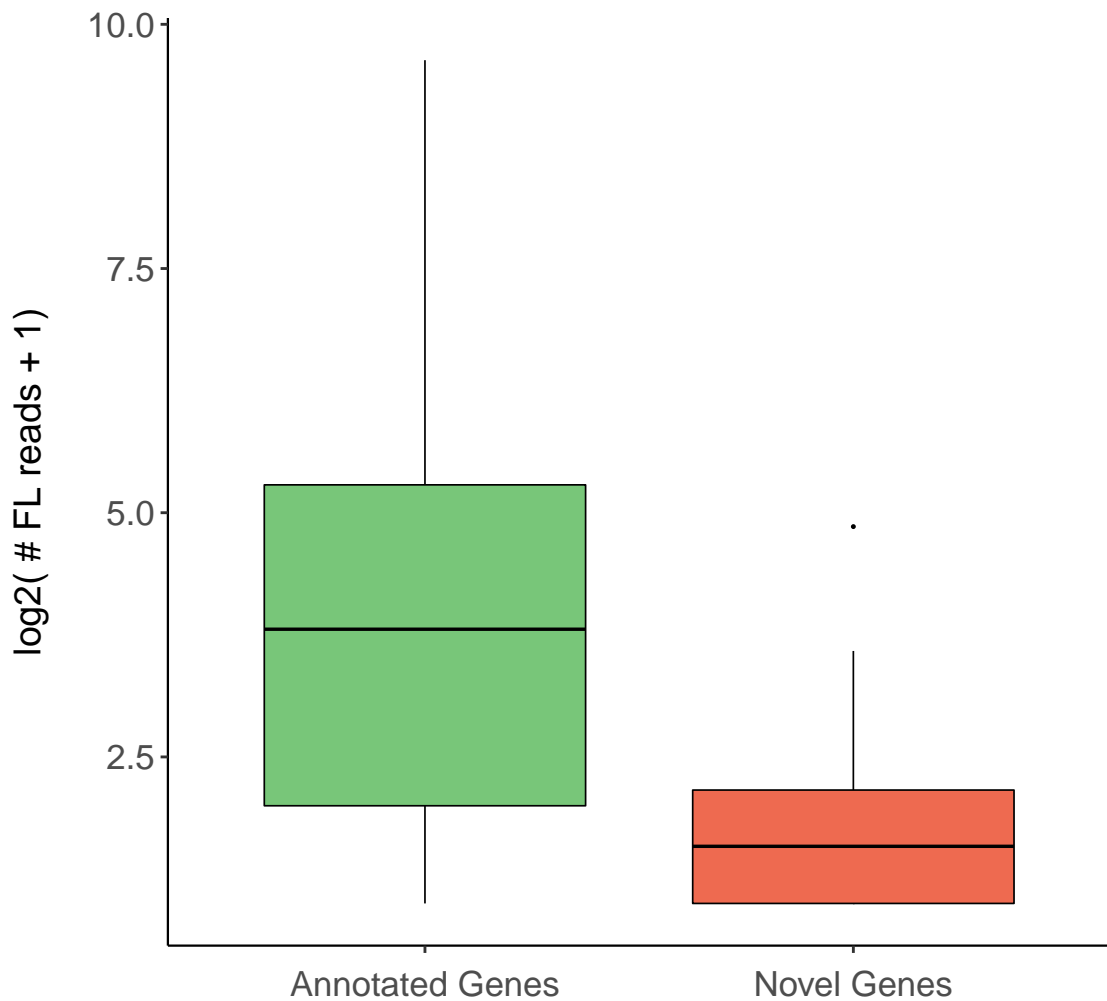
Distribution of mono/multi exon transcripts



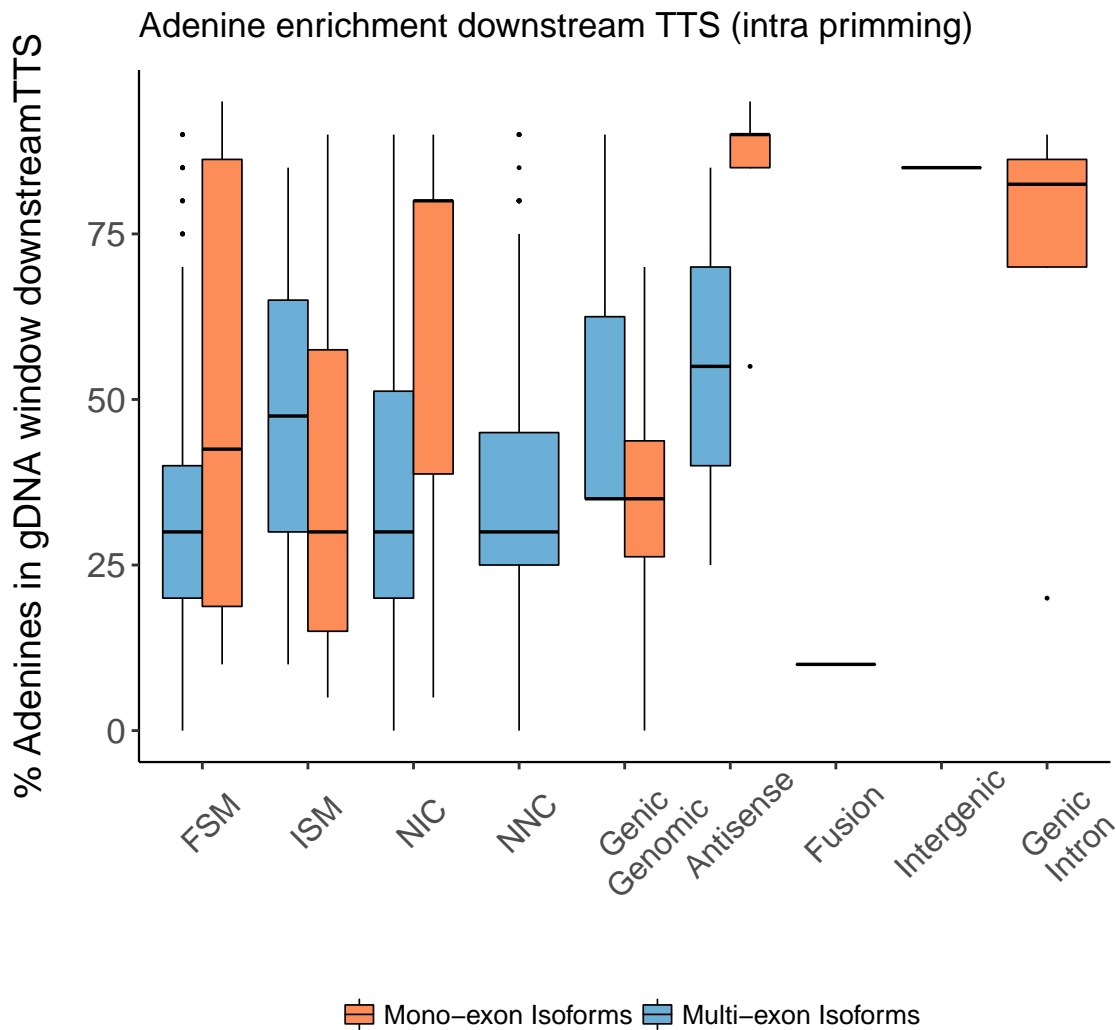
Gene expression by type of gene annotation

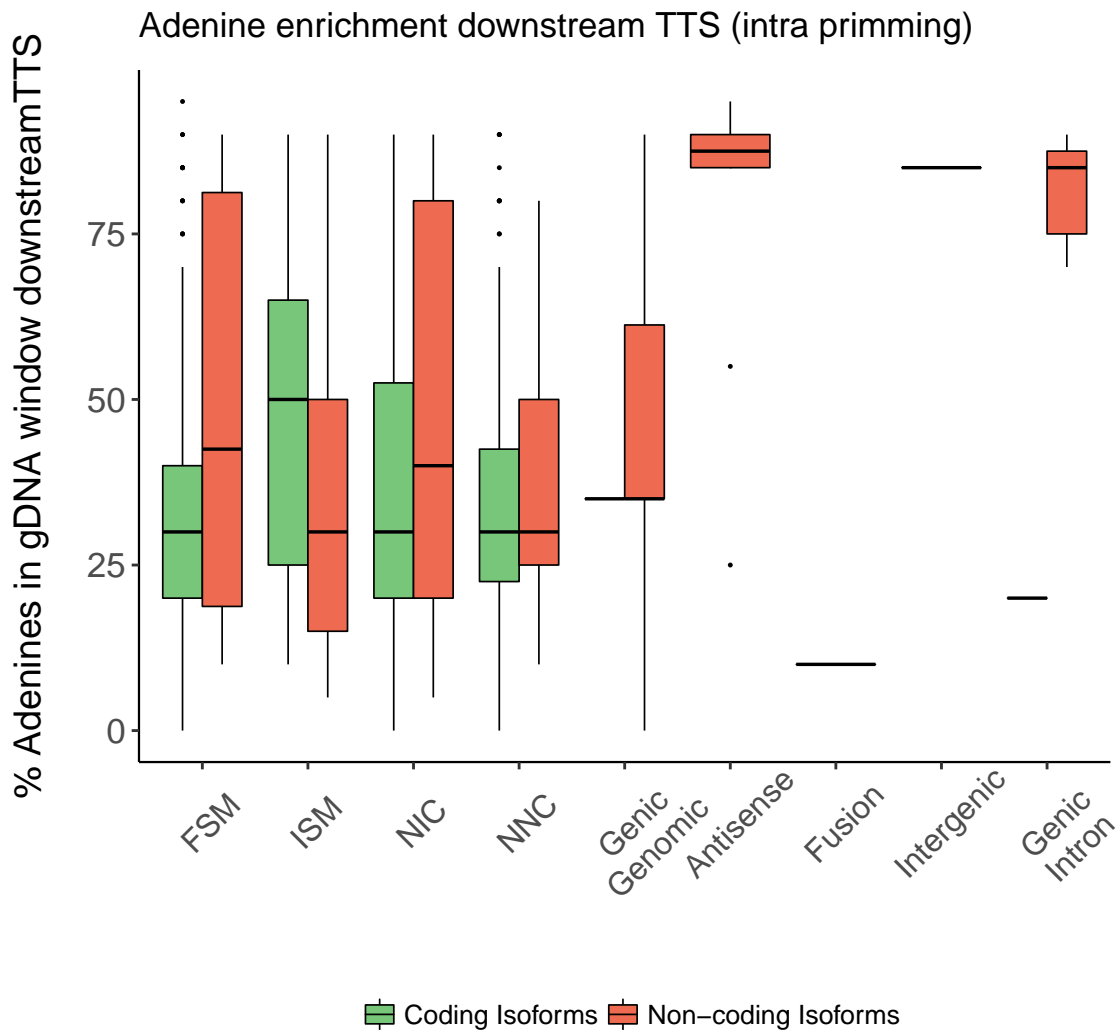


Number of FL reads per Gene by type of gene annotation



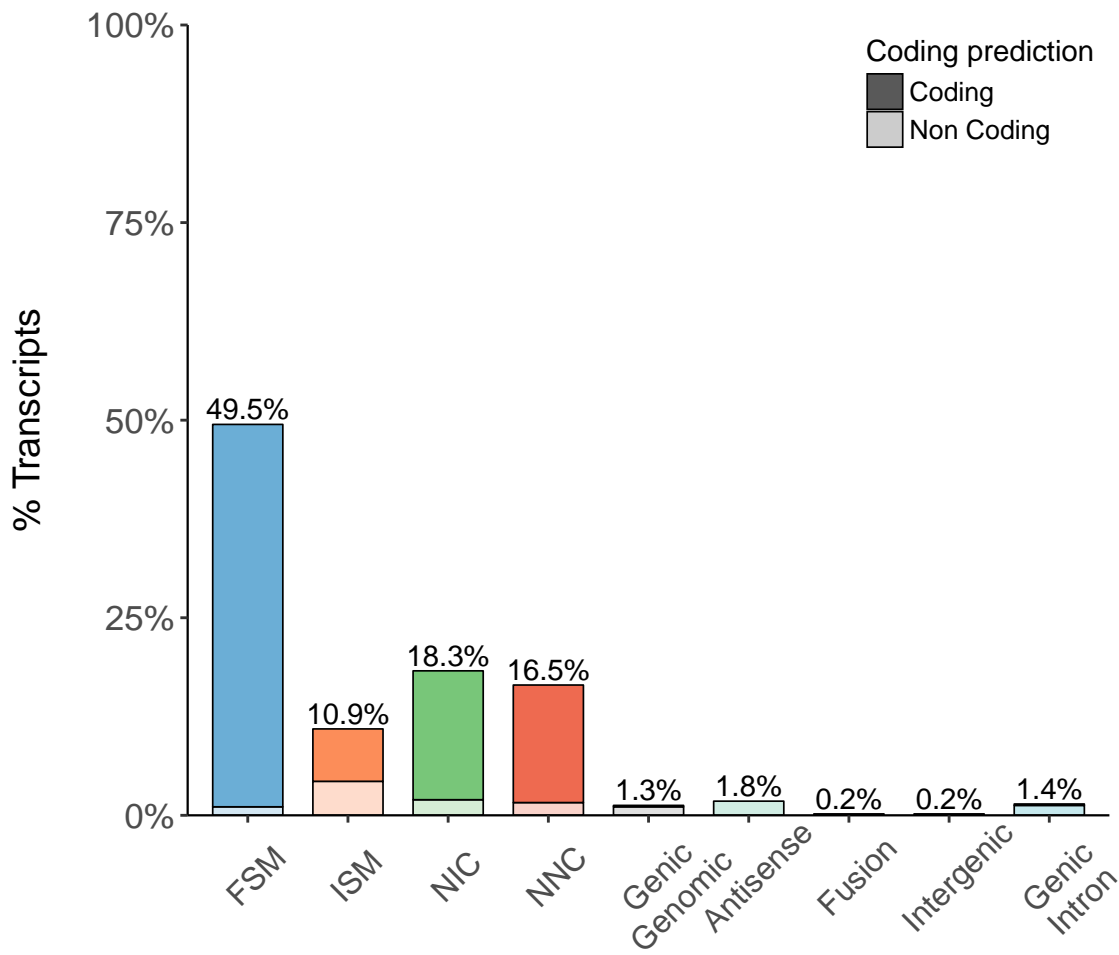




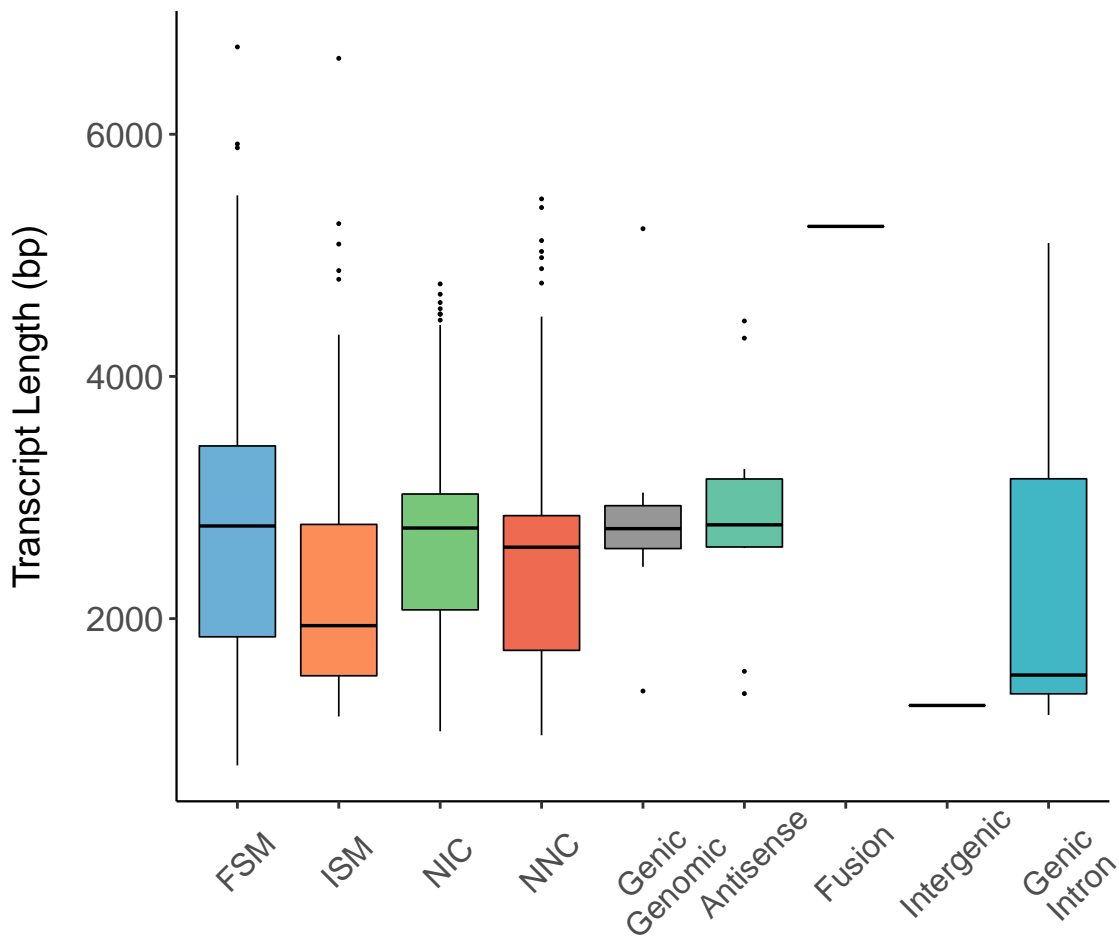


*Structrual Isoform characterization  
based on splice junctions*

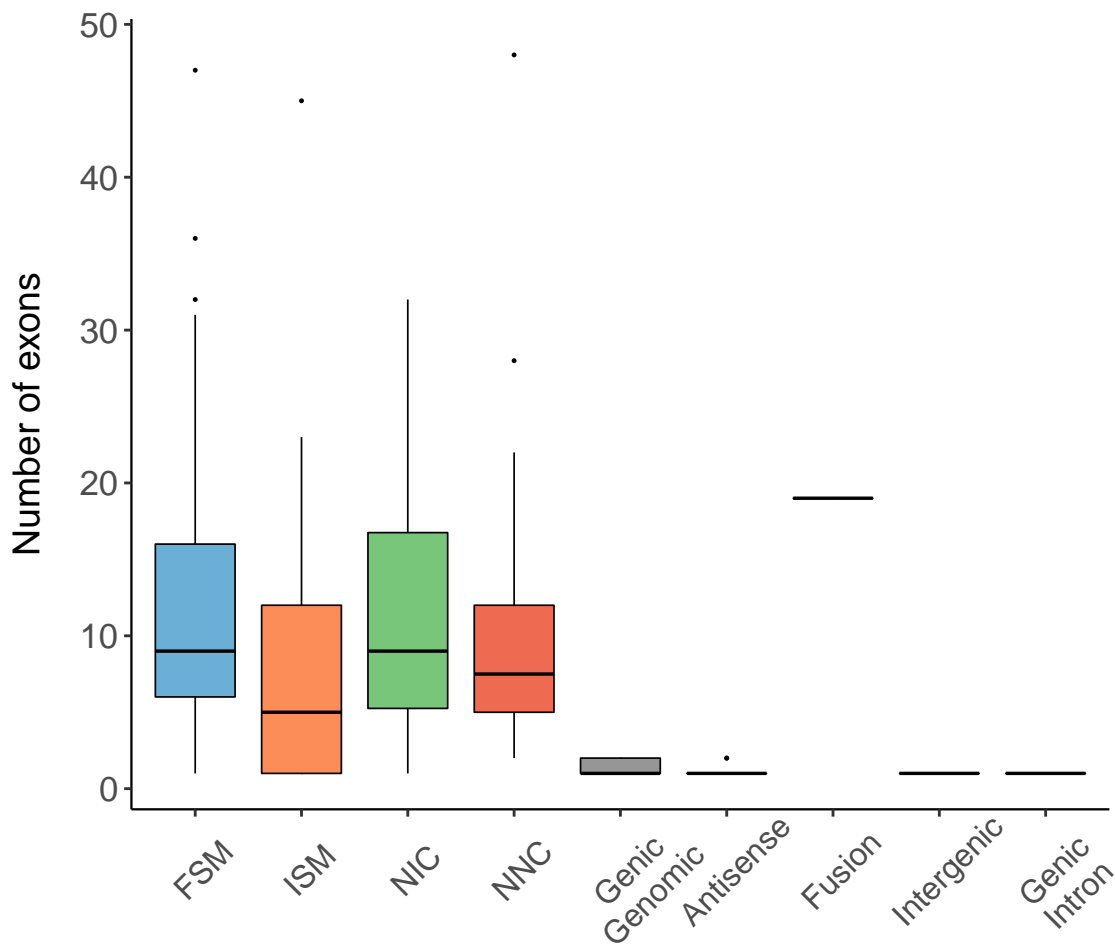
Isoform distribution across structural categories



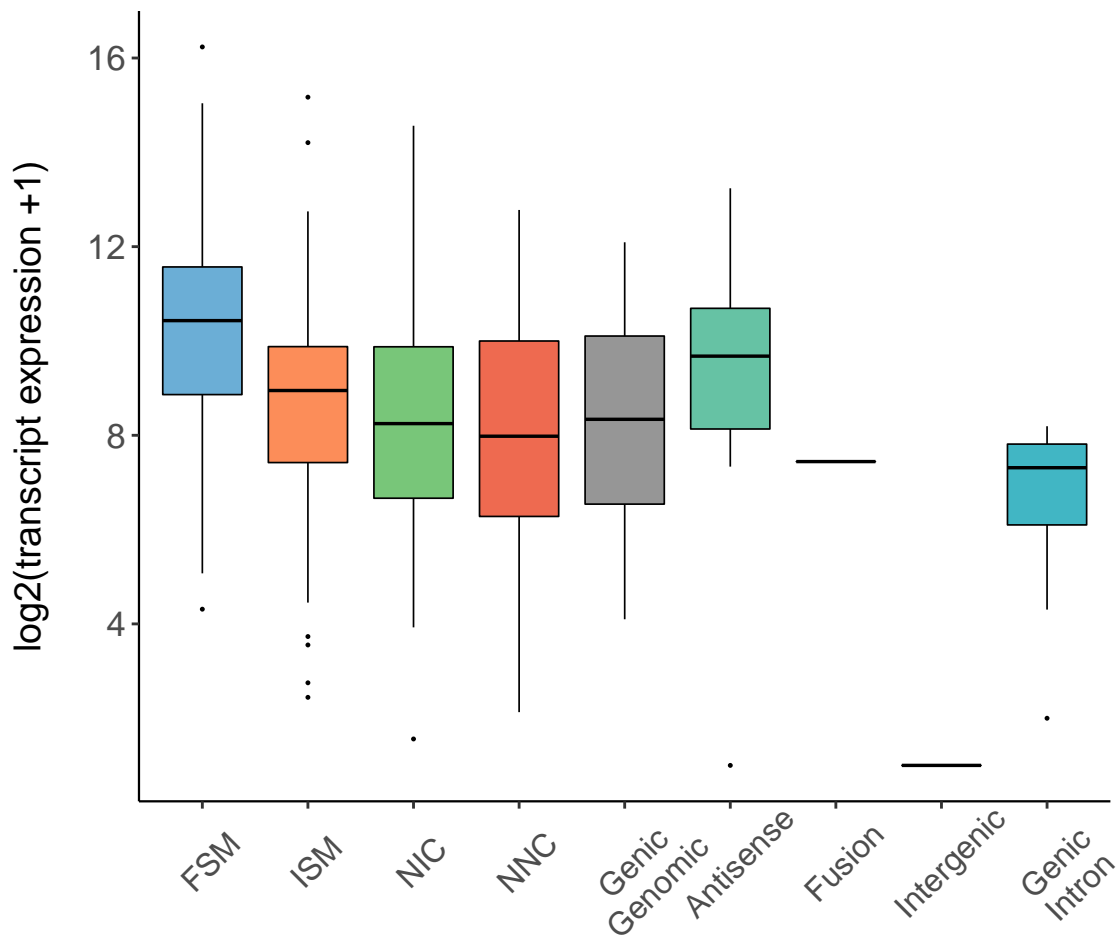
Transcript length distribution by structural classification



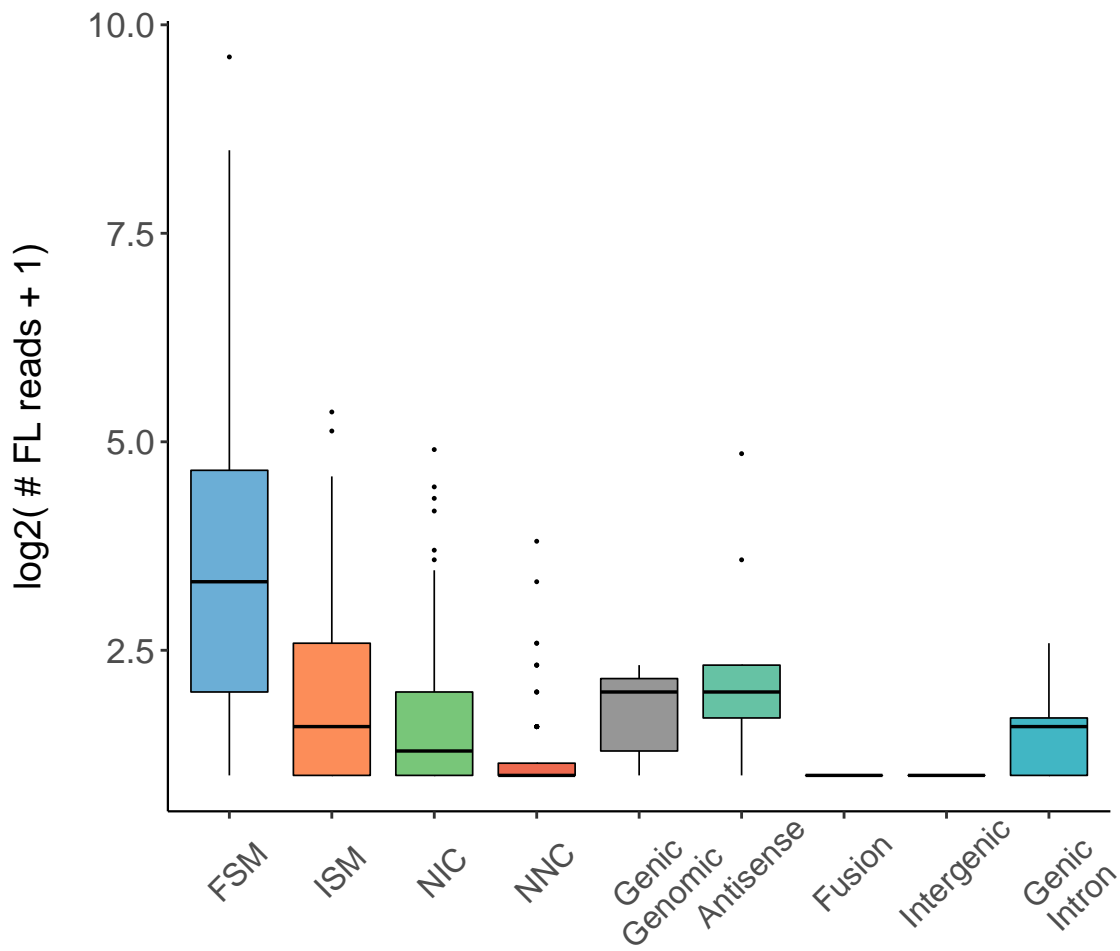
Exon number distribution by structural classification



Transcript expression by structural category



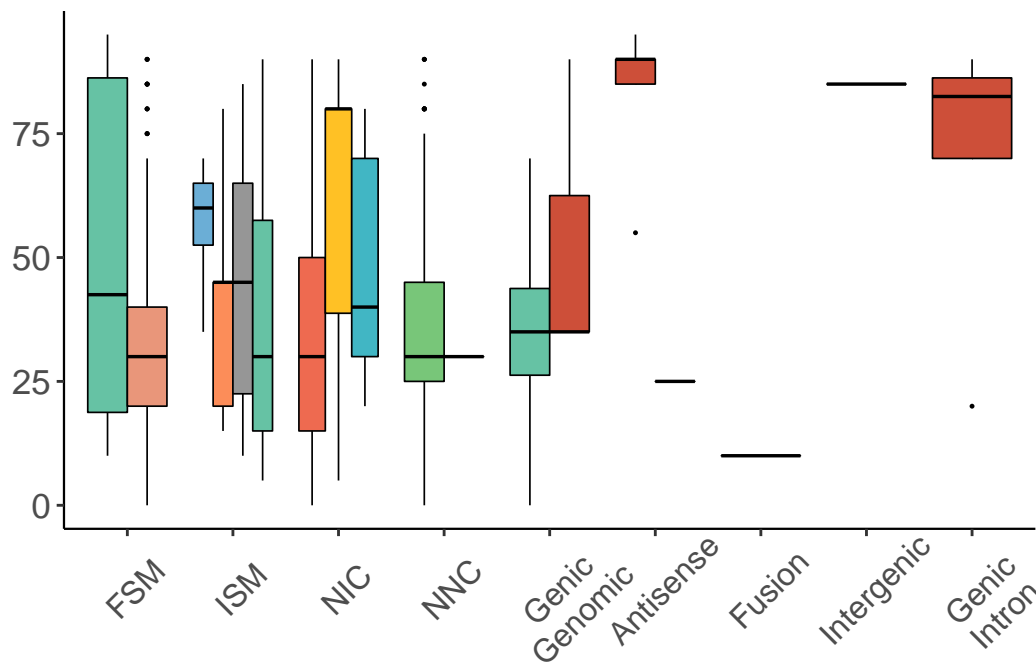
Number of FL reads per transcript by structural category





% 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

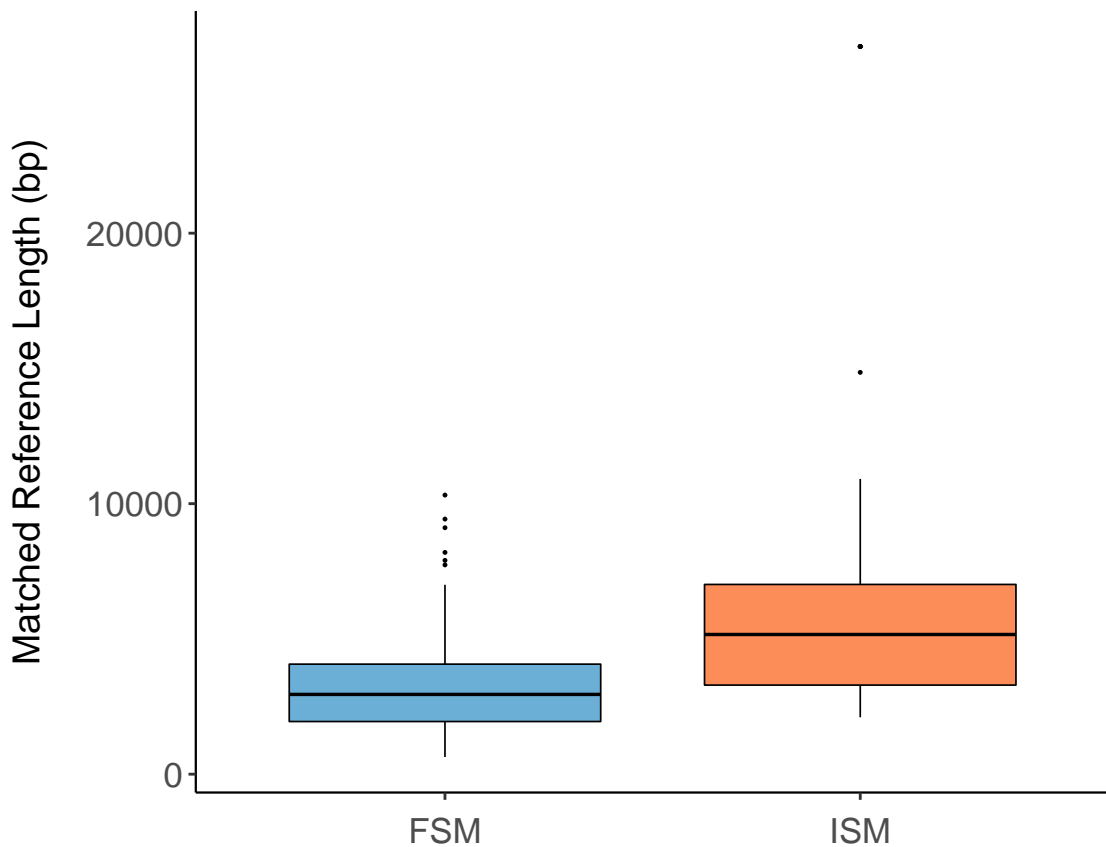
Combination of annotated junctions

Mono-exon by intron retention

At least one annotated donor/acceptor

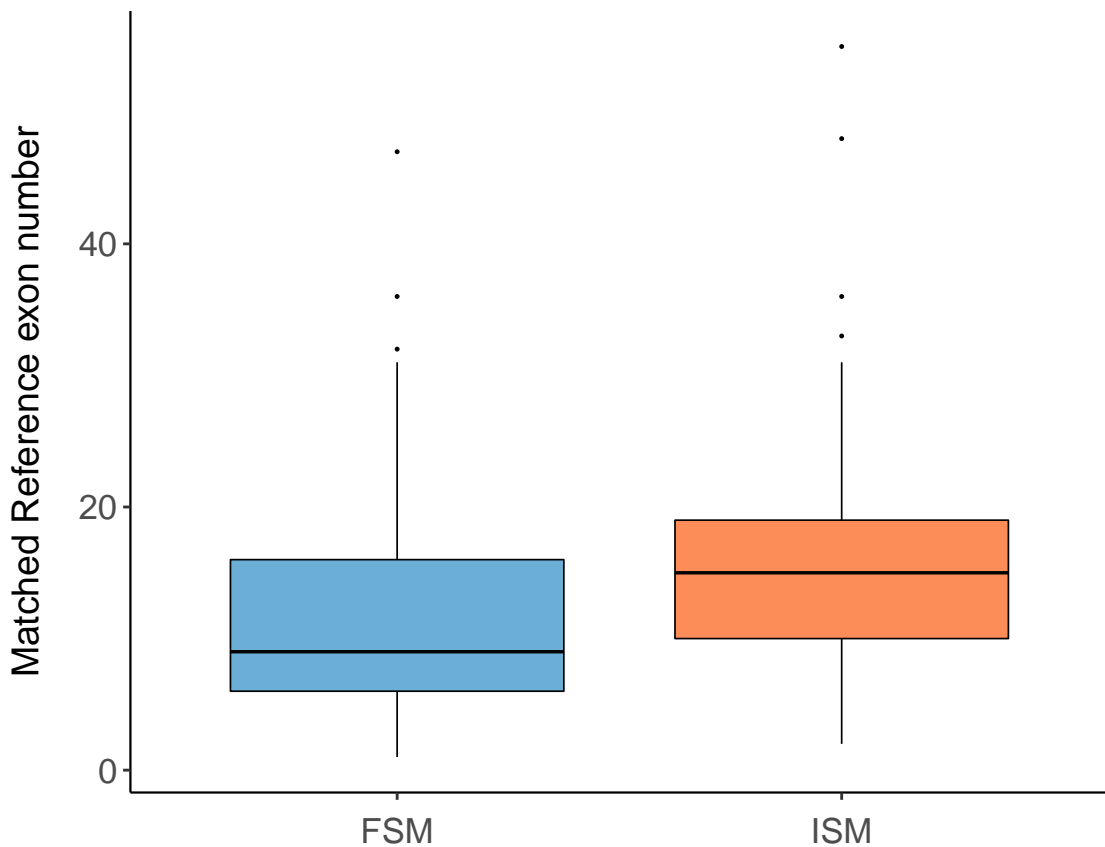
## Length distribution of matched reference transcripts

Just applicable to FSM and ISM categories

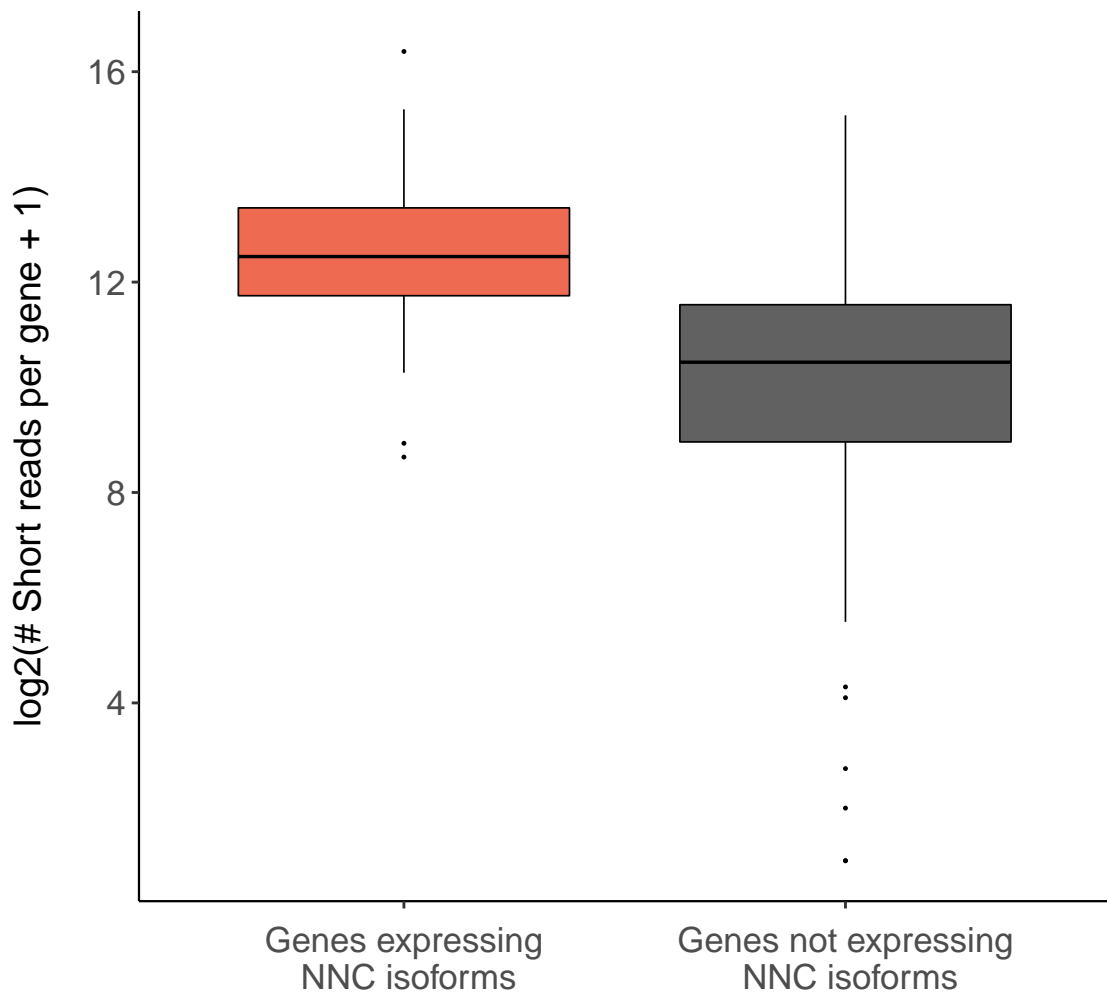


## Exon number distribution of matched reference transcripts

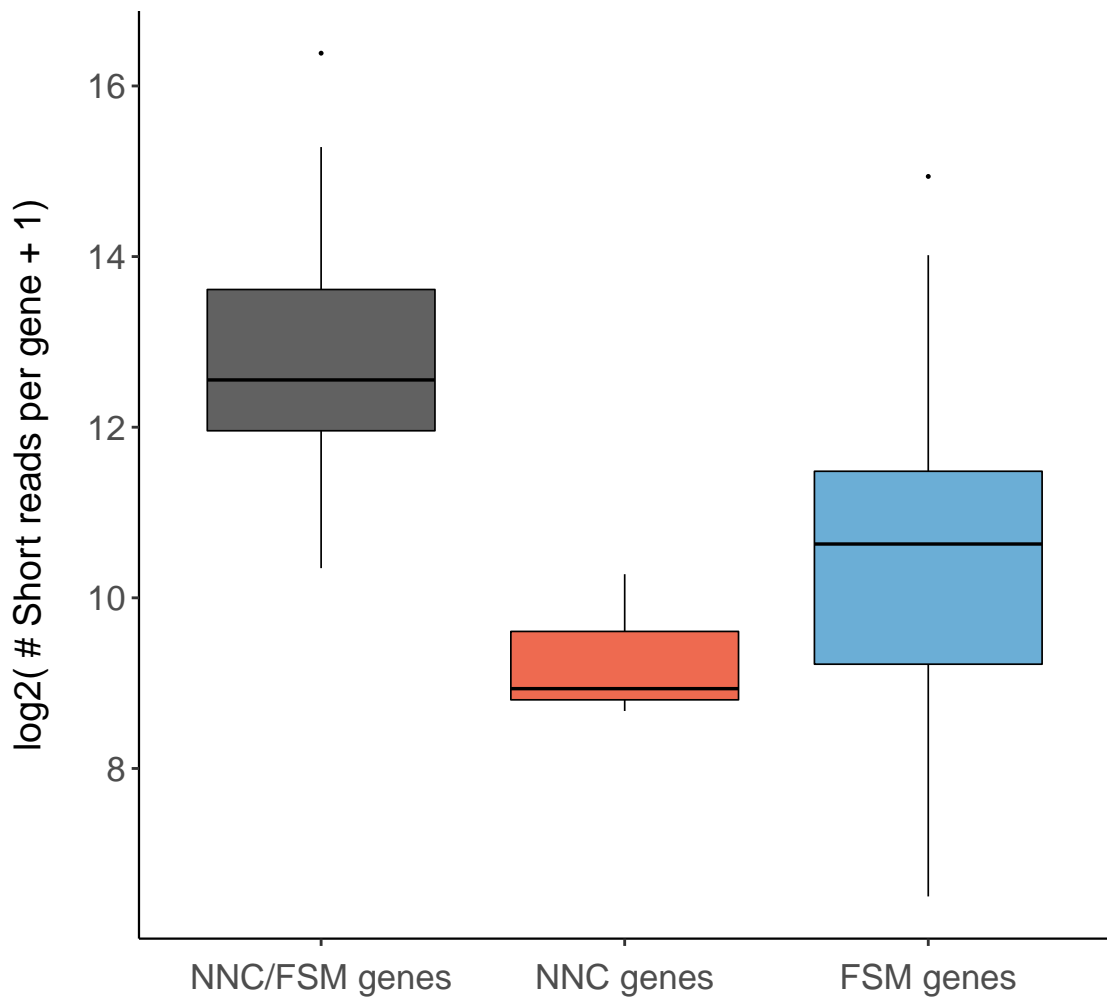
Just applicable to FSM and ISM categories



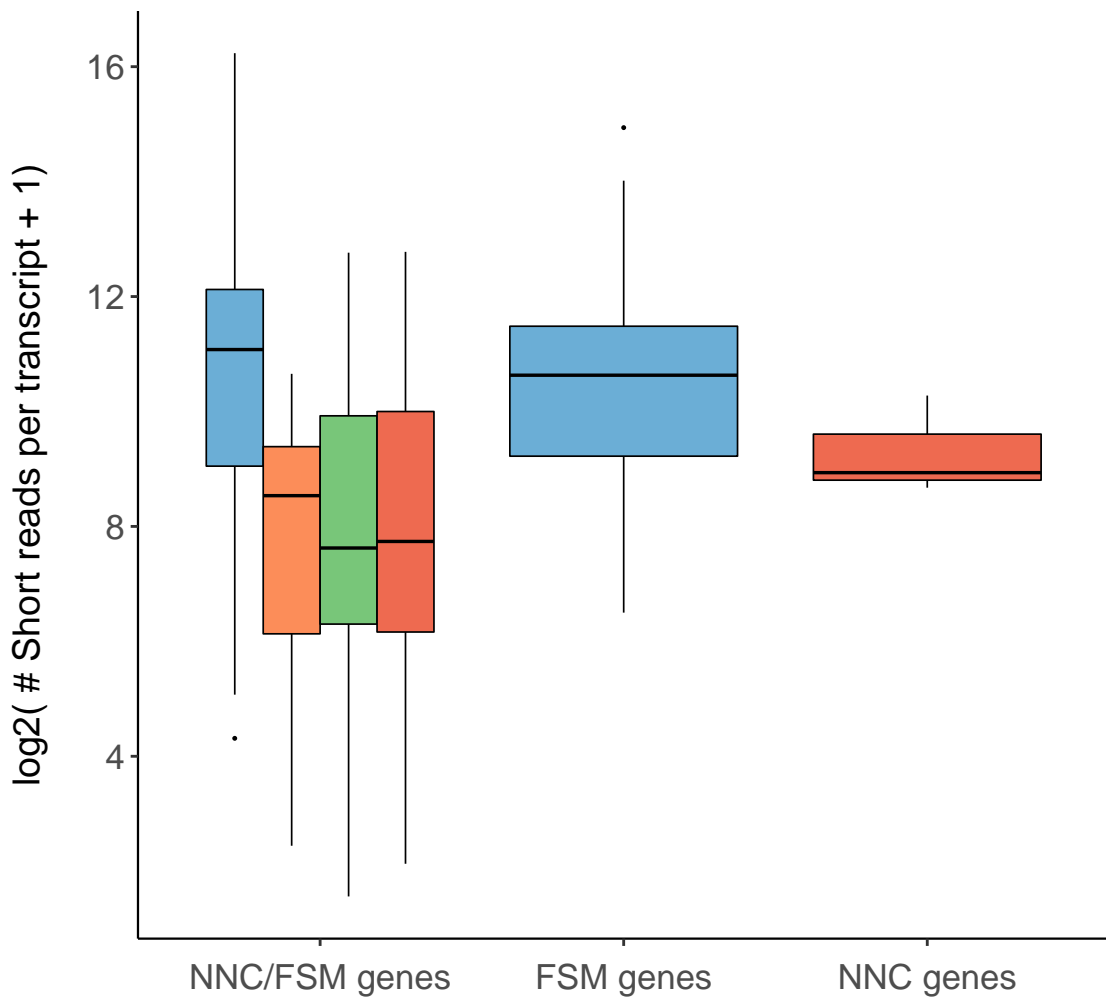
Gene expression levels between NNC and not NNC containing gene



Gene expression level in NNC/FSM containing genes



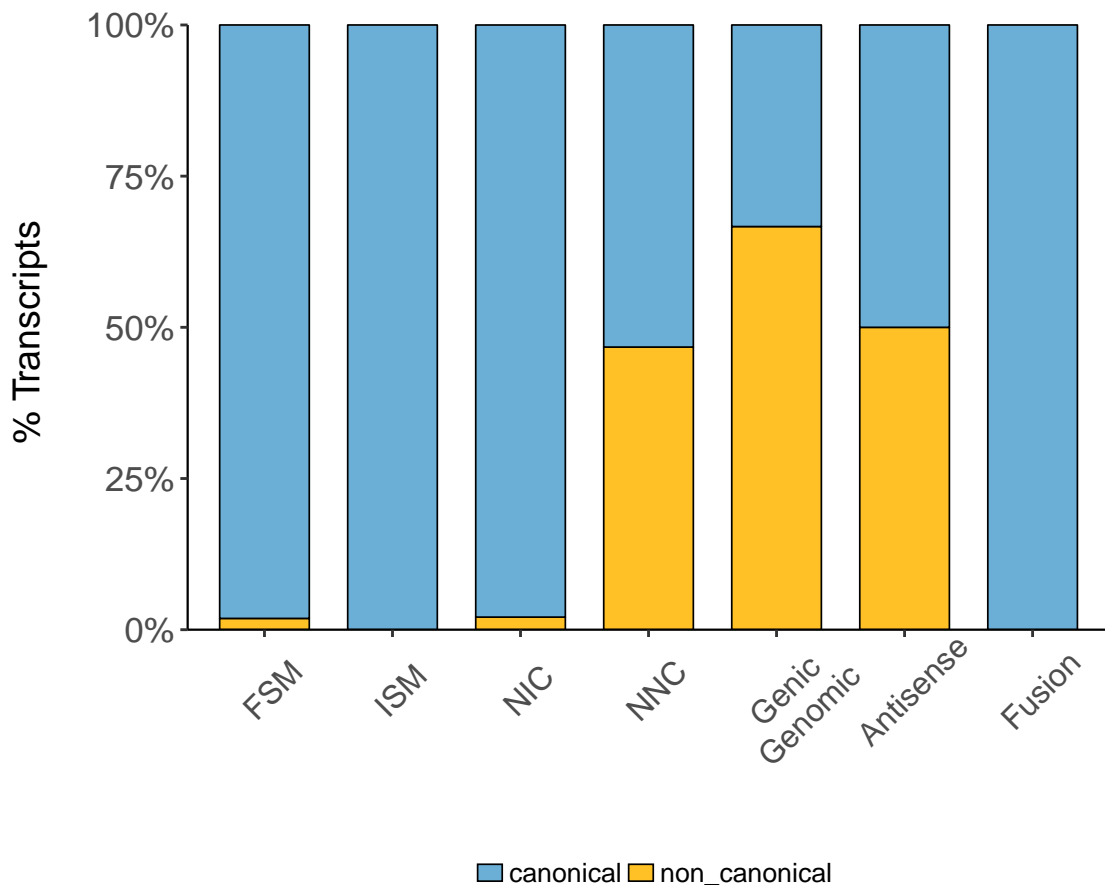
Transcript expression level in NNC/FSM containing genes



*Splice junction characterization*

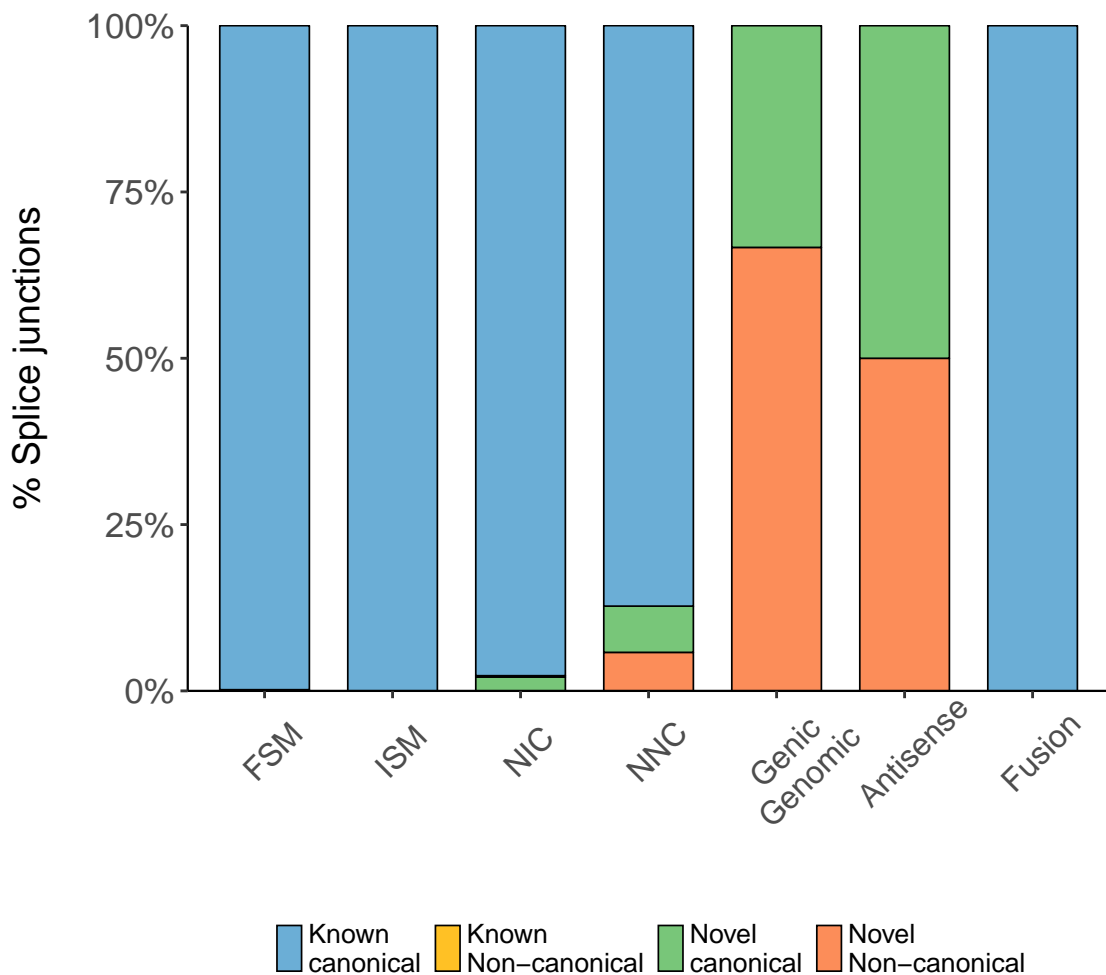
## Distribution of transcripts by splice junction category

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

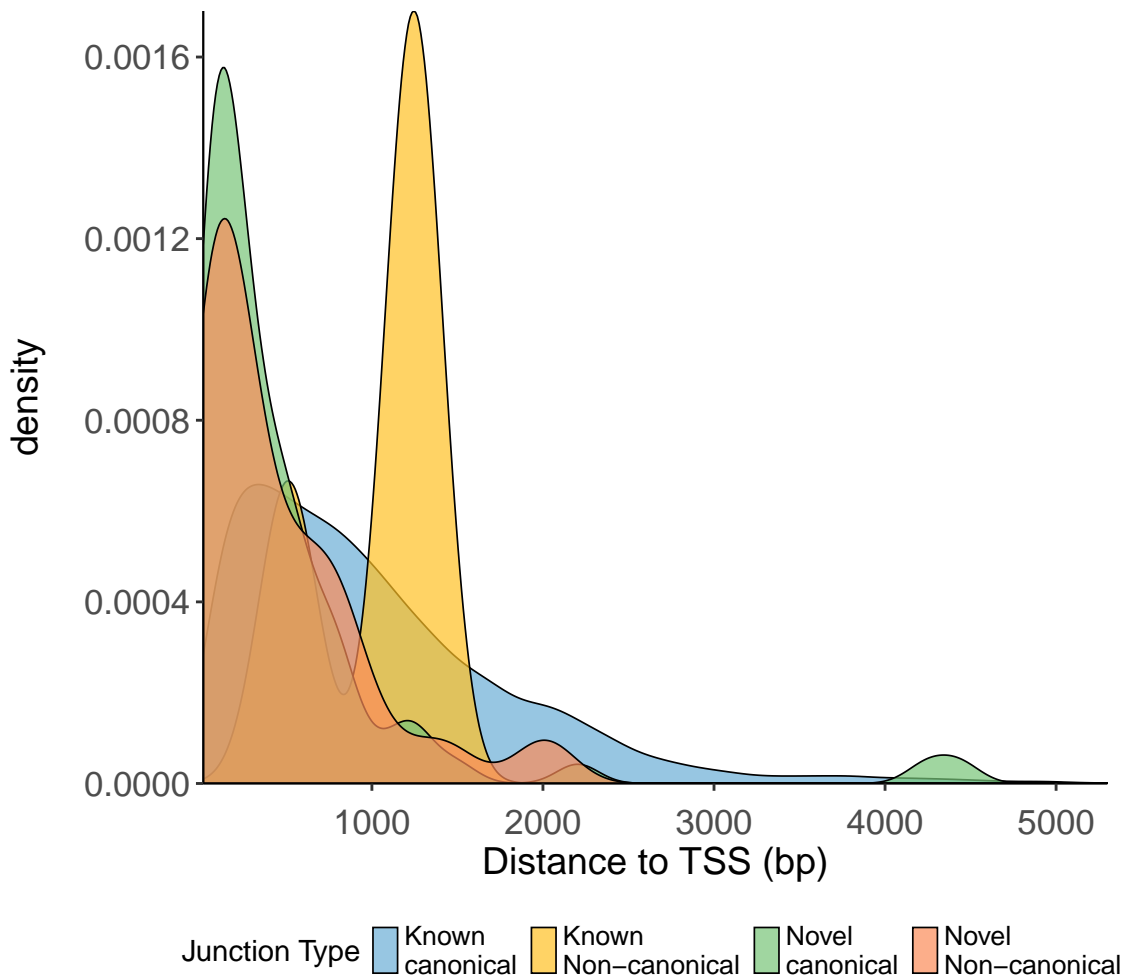




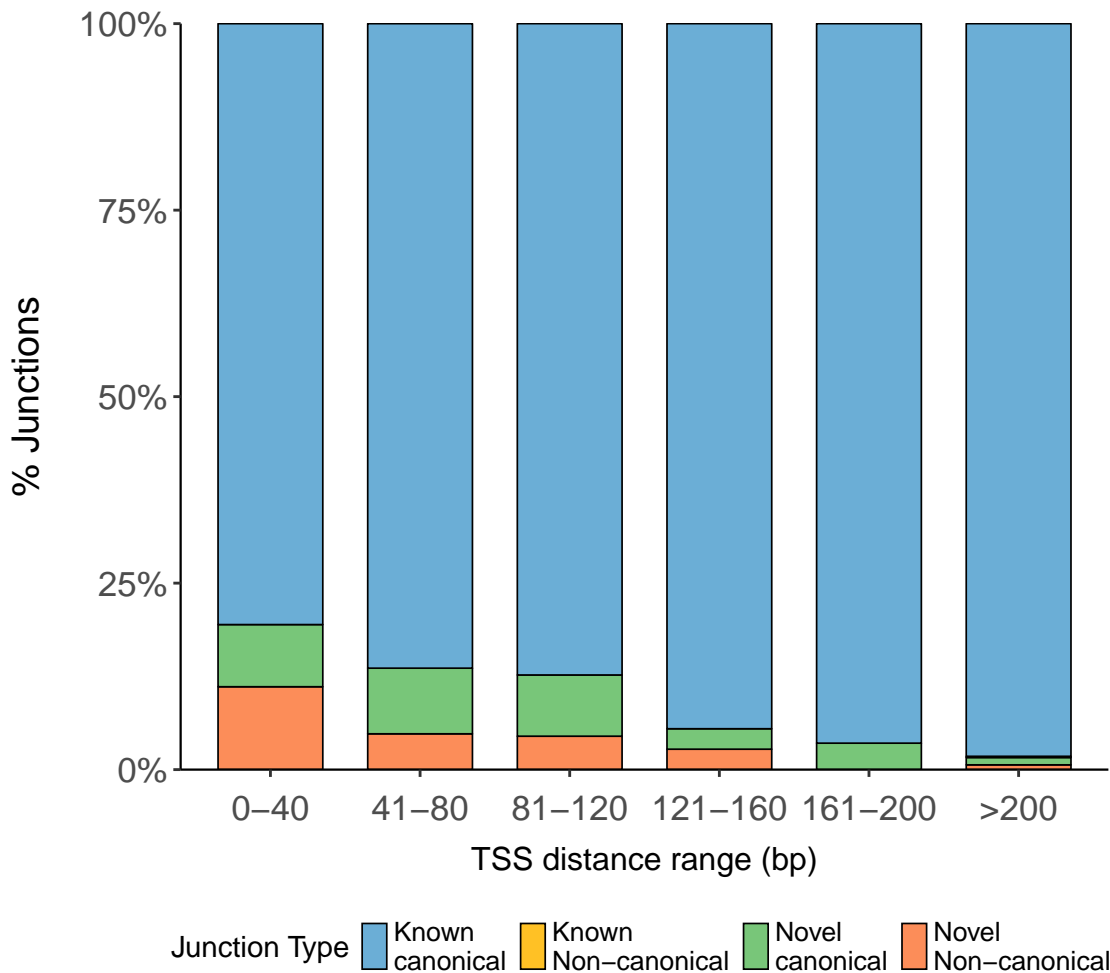
Distribution of SJ type among structural classification



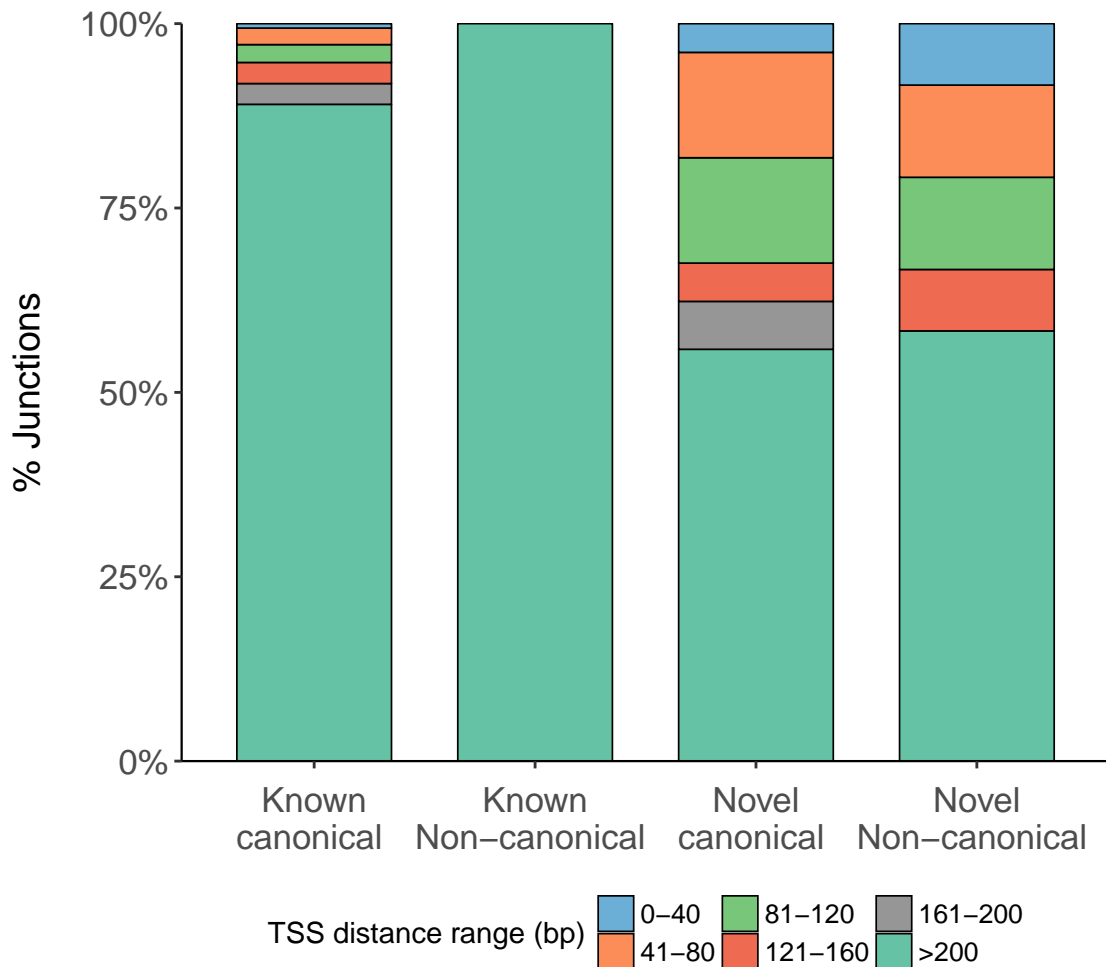
Distribution of splice junctions distance to TSS



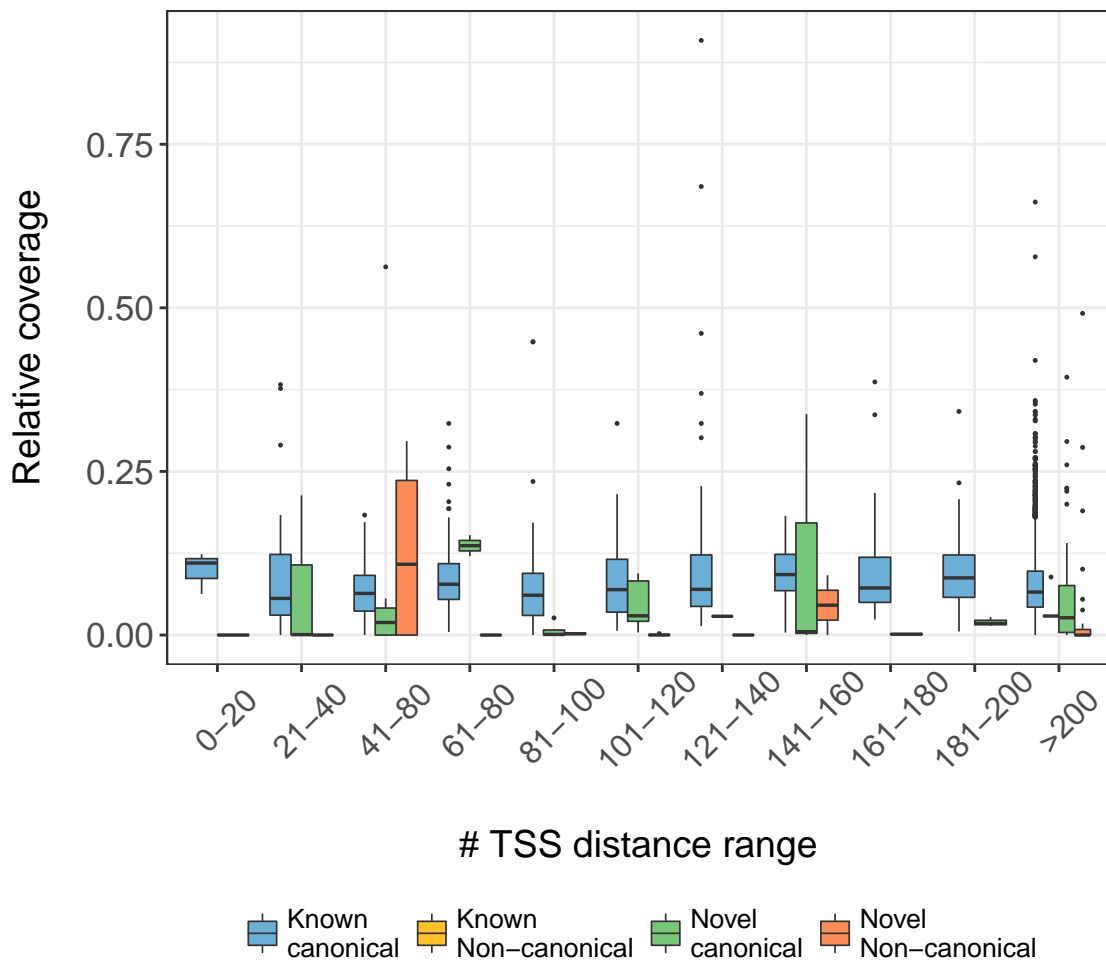
Splice junction distance to TSS across junction type



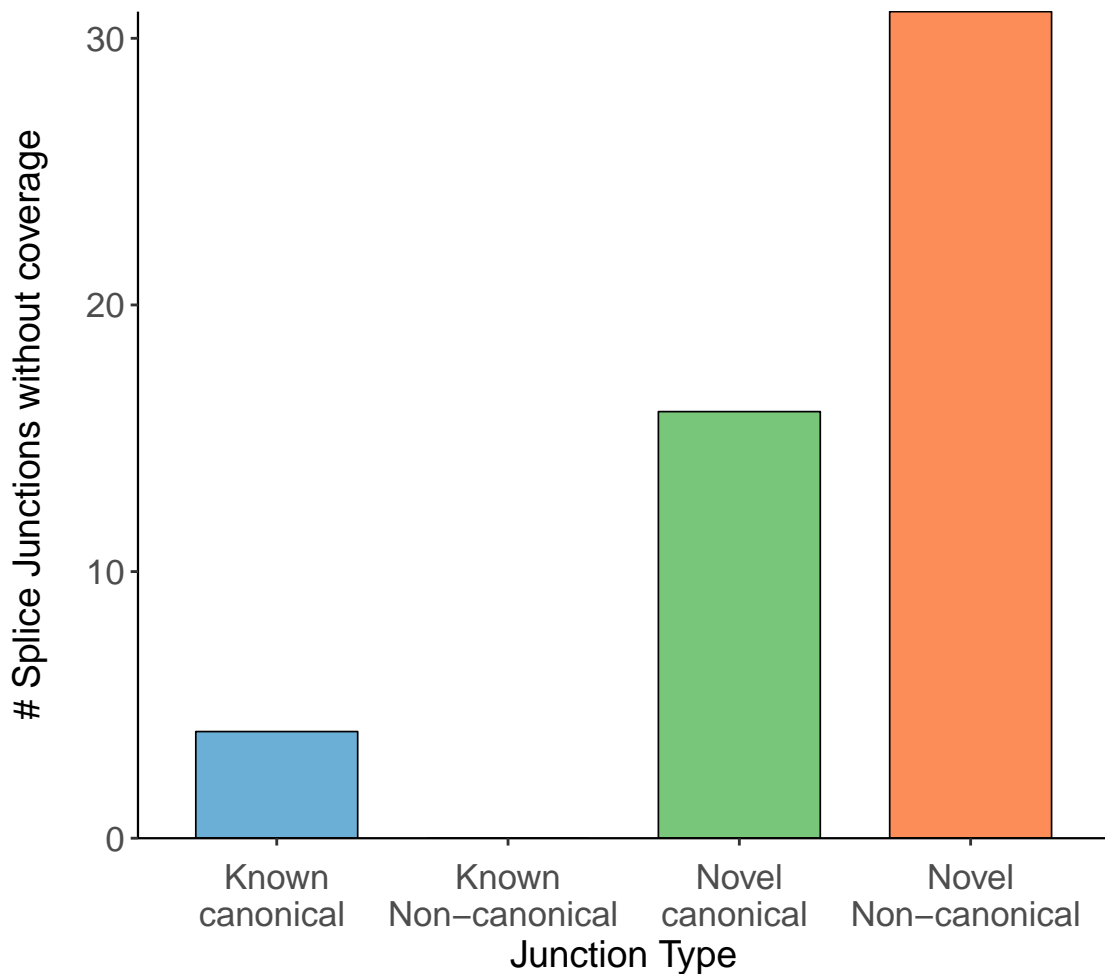
Splice junction distance to TSS across junction type



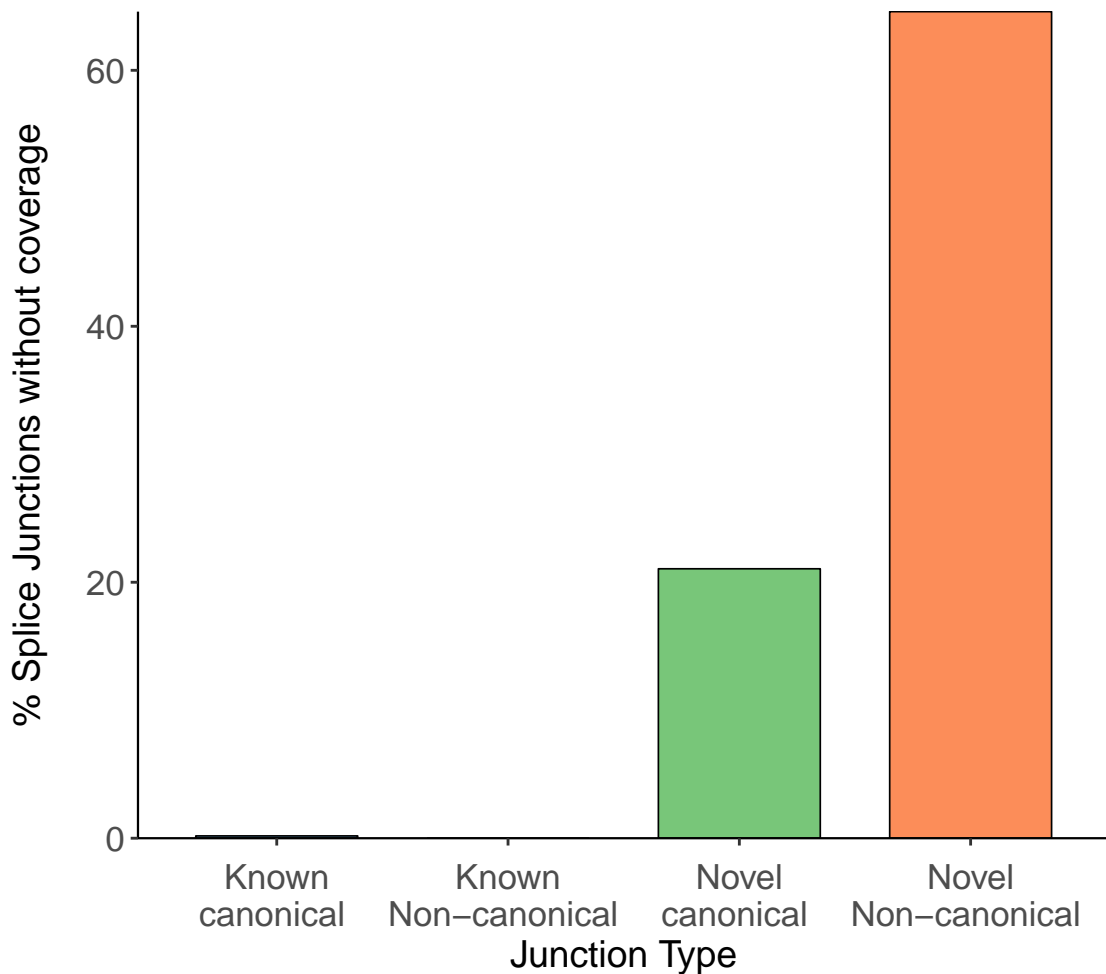
## Relative Coverage of junctions



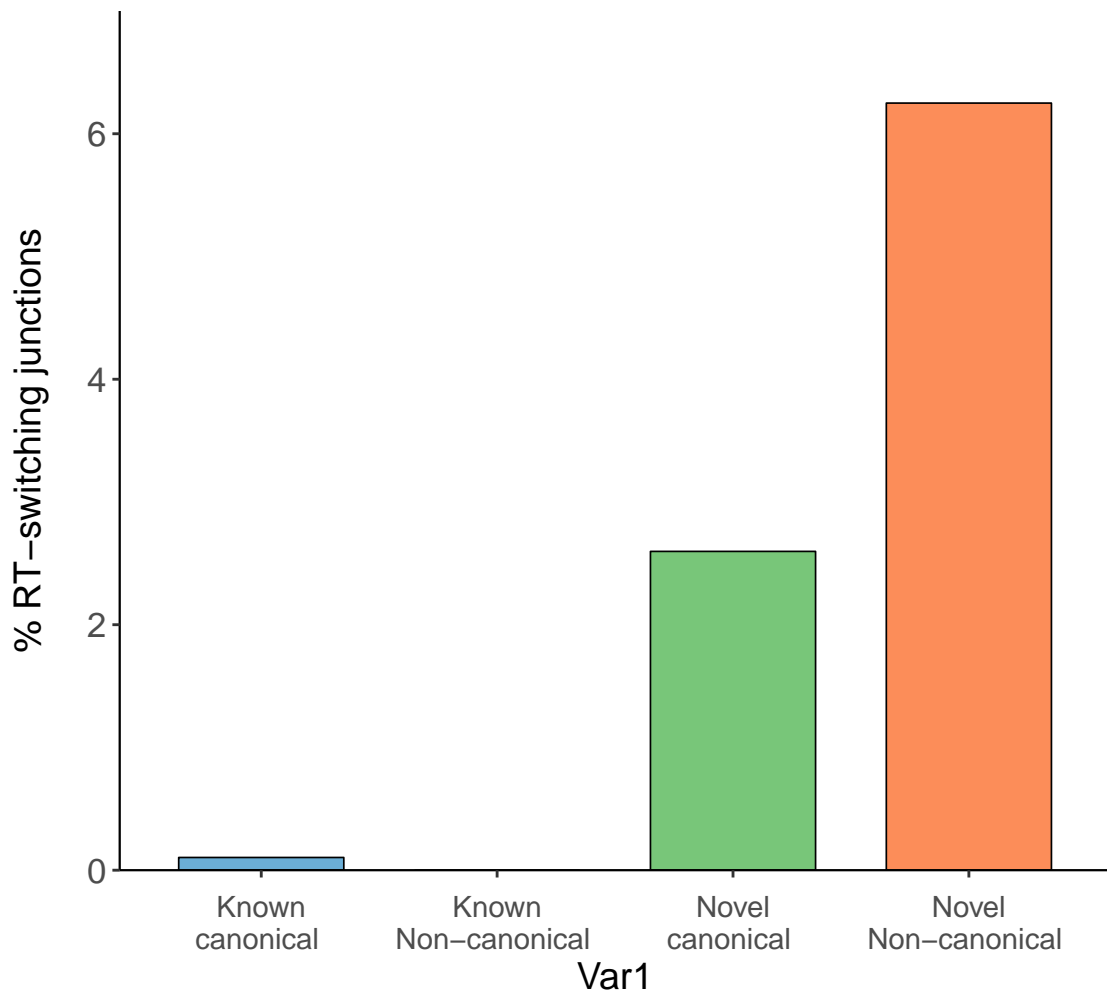
Splice junctions without short-read coverage (unique junctions)



Splice junctions without short-read coverage (unique junctions)

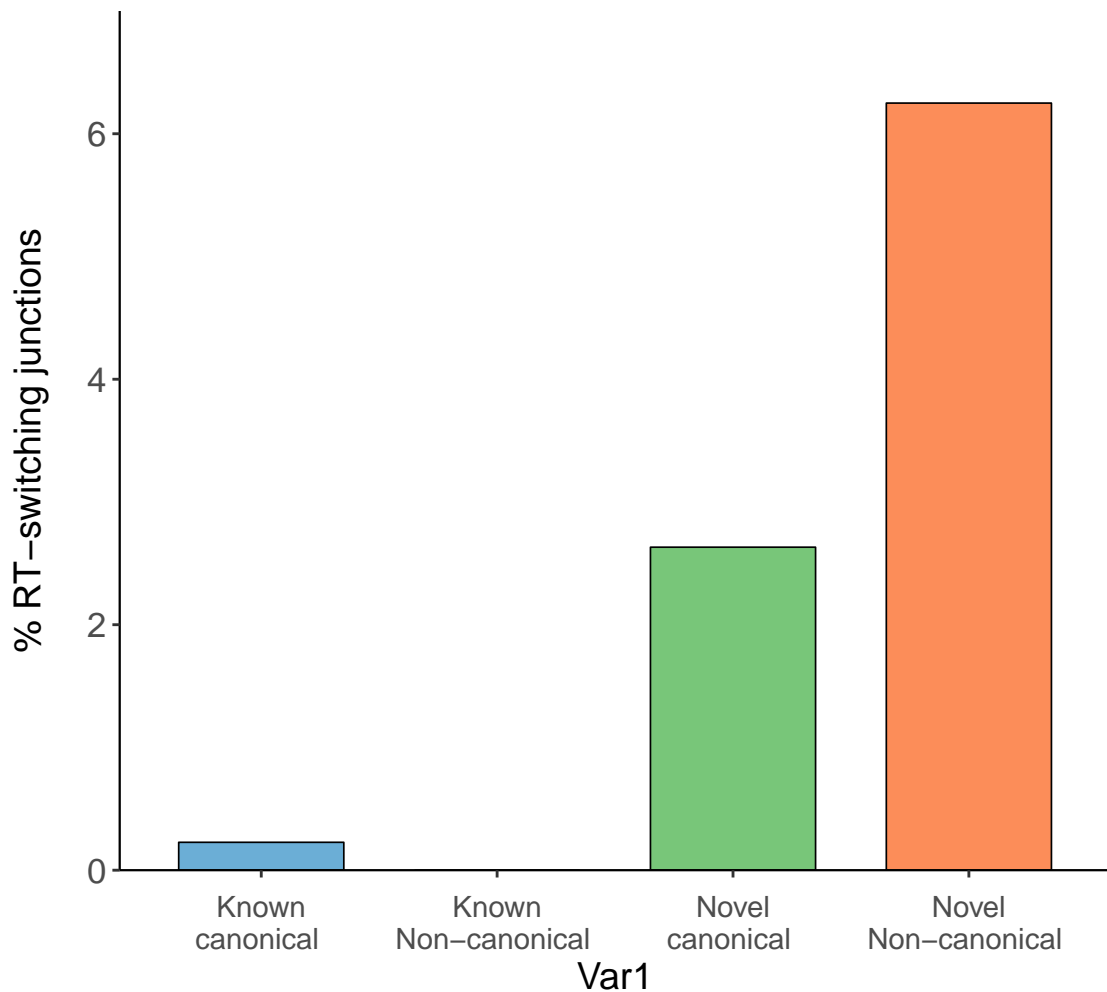


RT-switching by splice junction category





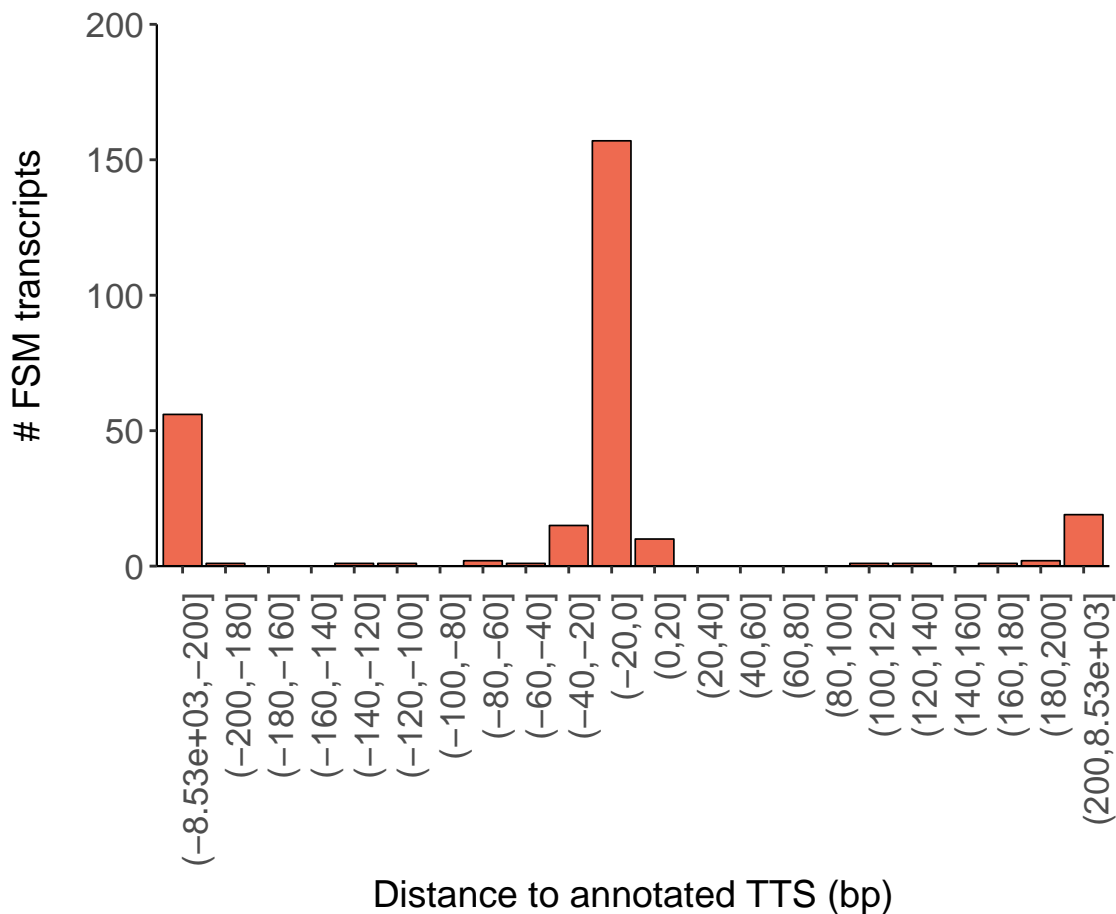
RT-switching by splice junction category (unique junctions)



*Full-lengthness characterization of isoforms*

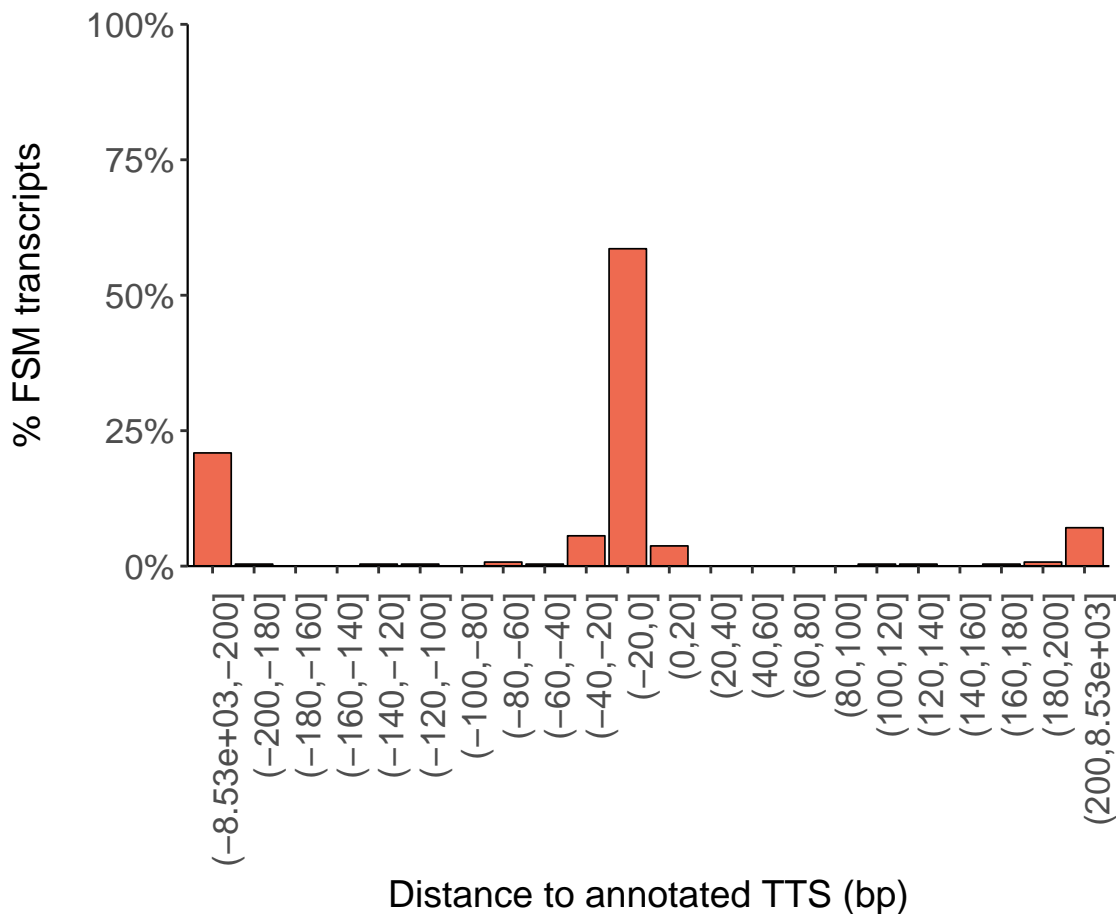
## Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is upstream annotated TTS



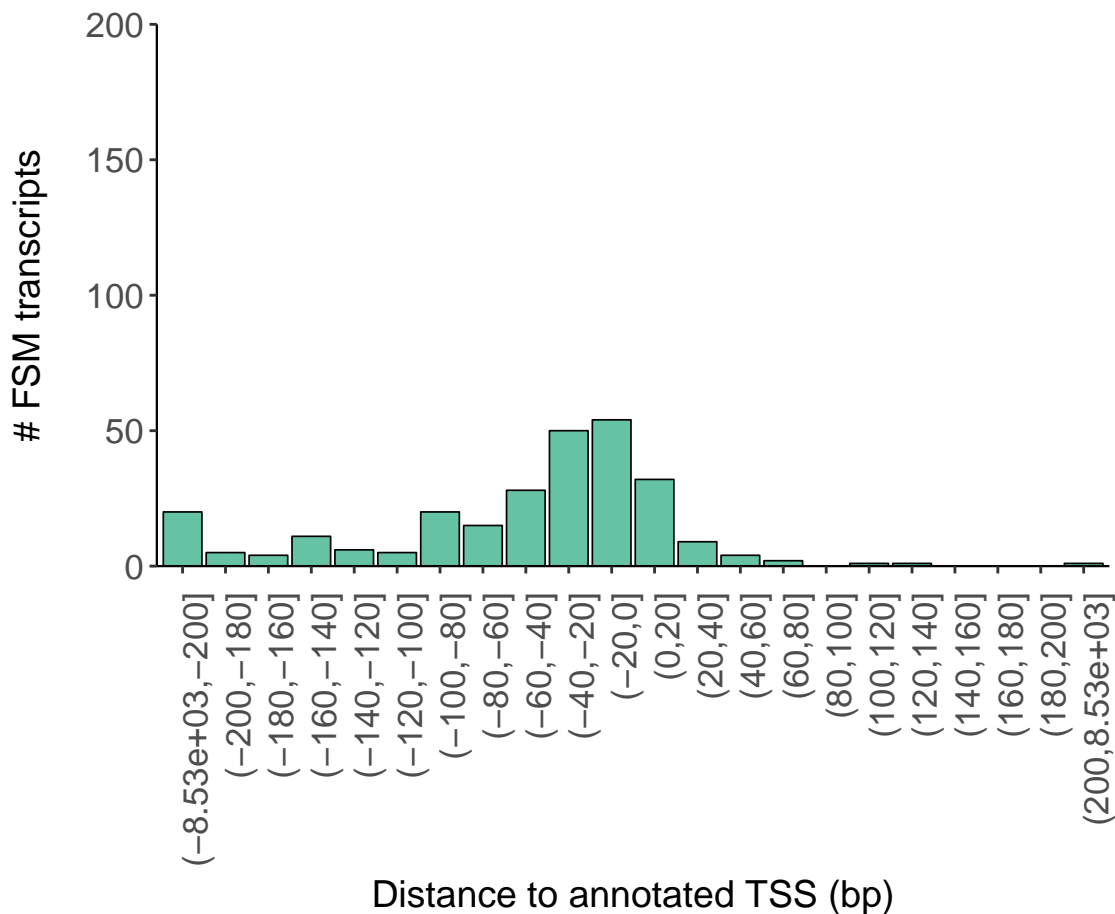
## Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is upstream annotated TTS



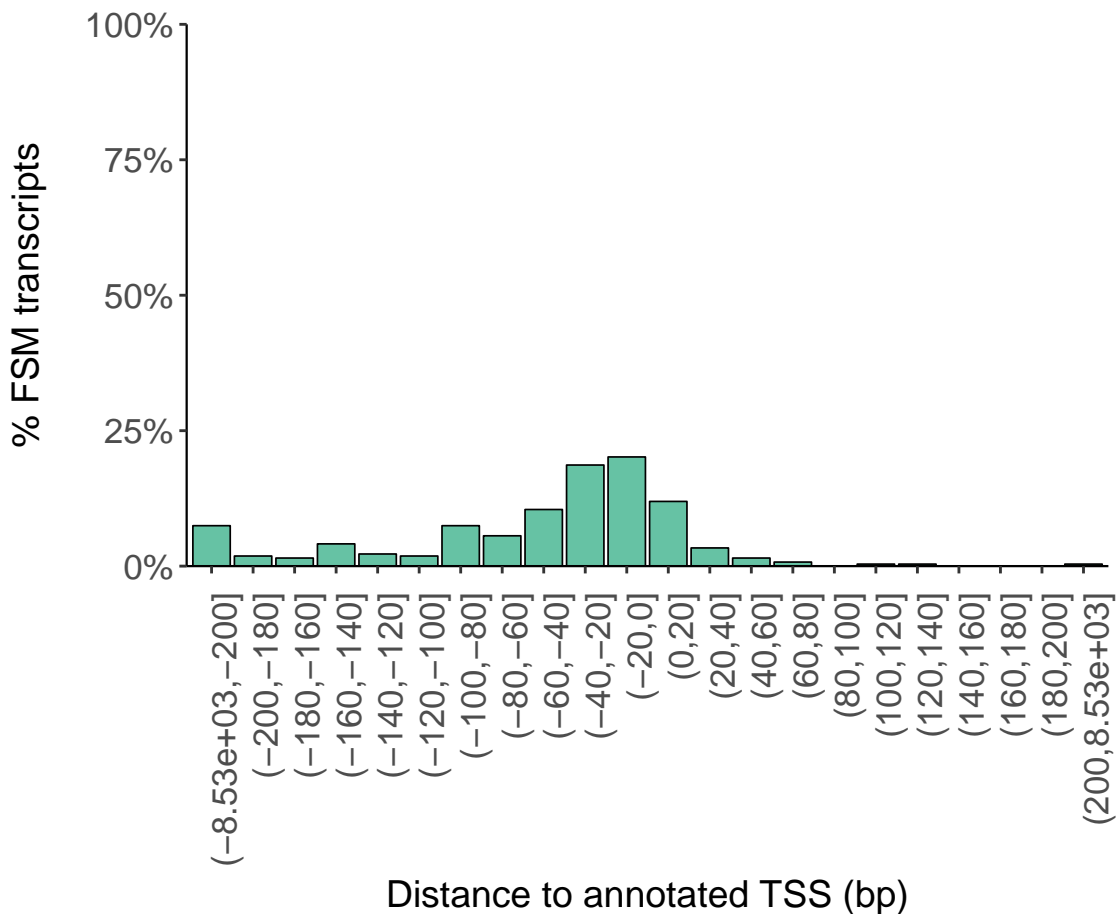
## Distance distribution from sequenced to annotated TSS

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

