

*SQANTI report*

*# Genes: 7694*

*# Isoforms: 16104*

*Gene classification*

category	# genes
Annotated Genes	7183
Novel Genes	511

*SJ classification*

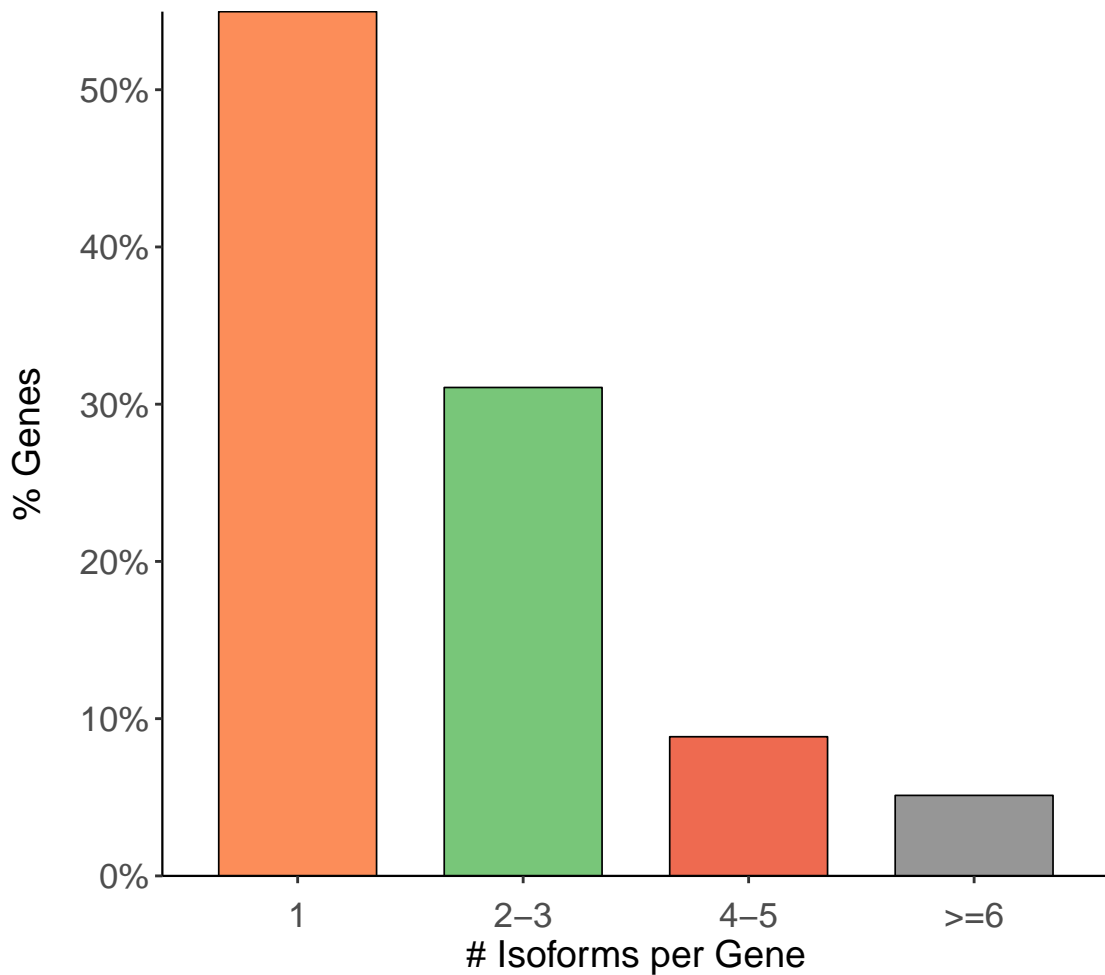
category	# SJ
Known canonical	67680
Known Non-canonical	78
Novel canonical	2489
Novel Non-canonical	1140

*Characterization of transcripts  
based on splice junctions*

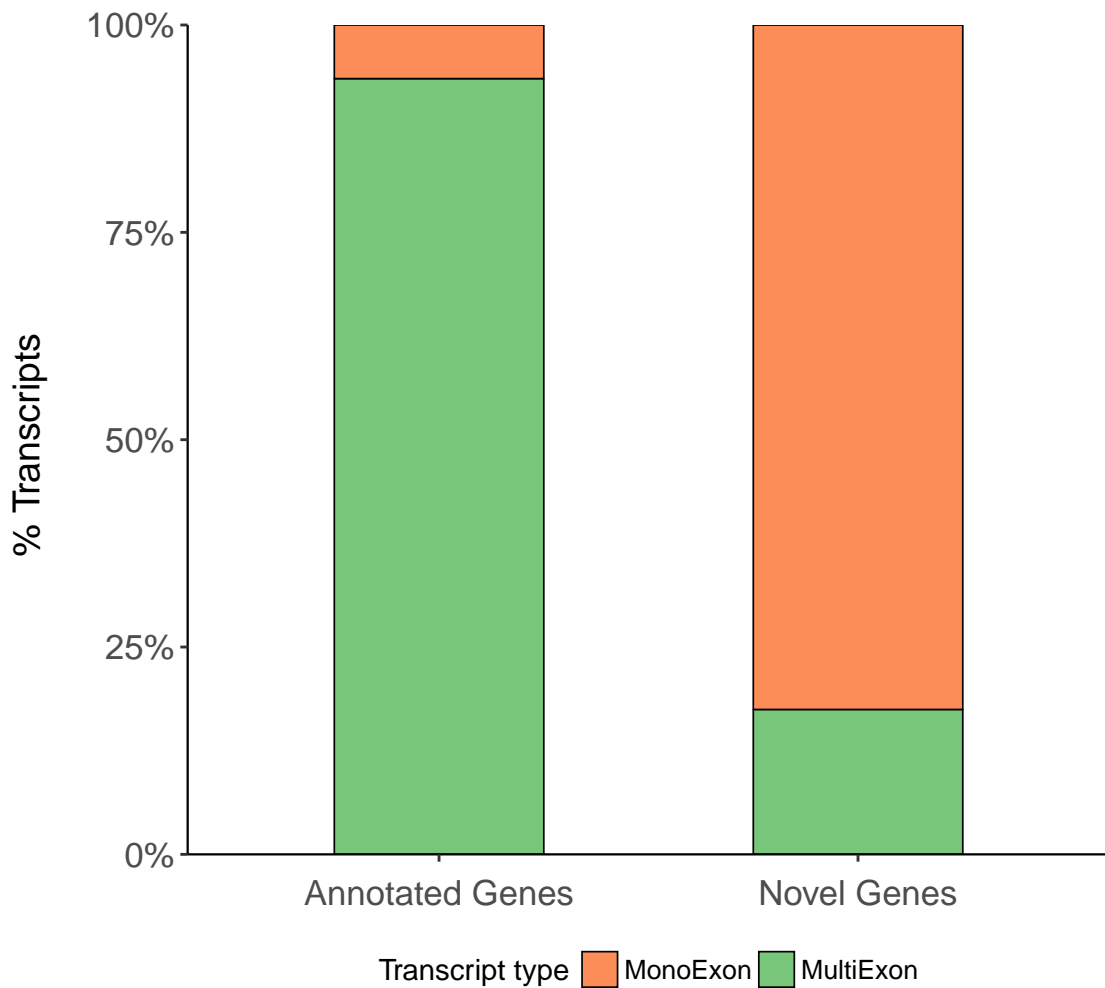
category	# isoforms
FSM	7937
NIC	3045
NNC	2696
ISM	1742
Genic Intron	300
Antisense	177
Genic Genomic	92
Intergenic	61
Fusion	54

*Gene characterization*

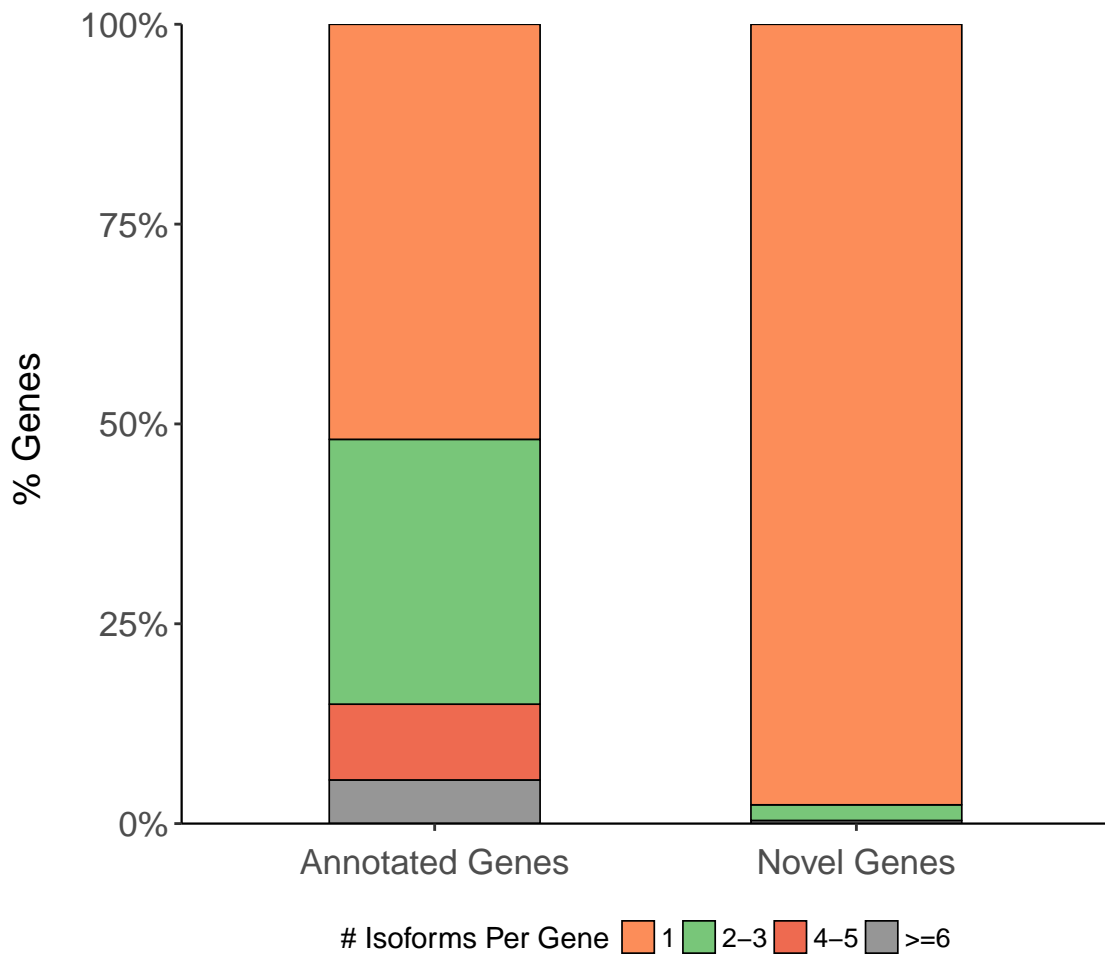
Distribution of isoforms per gene



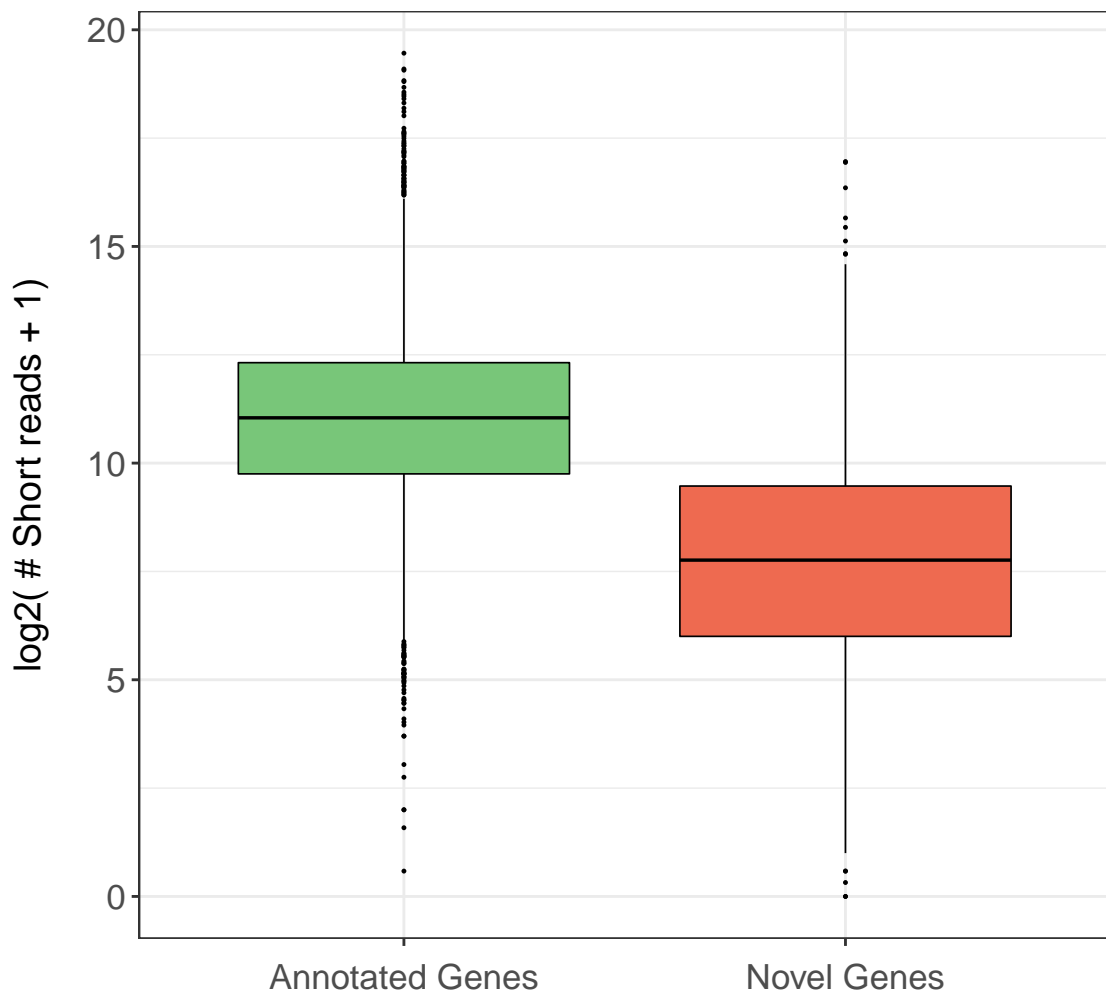
Distribution of mono/multi exon transcripts



Distribution of number of isoforms



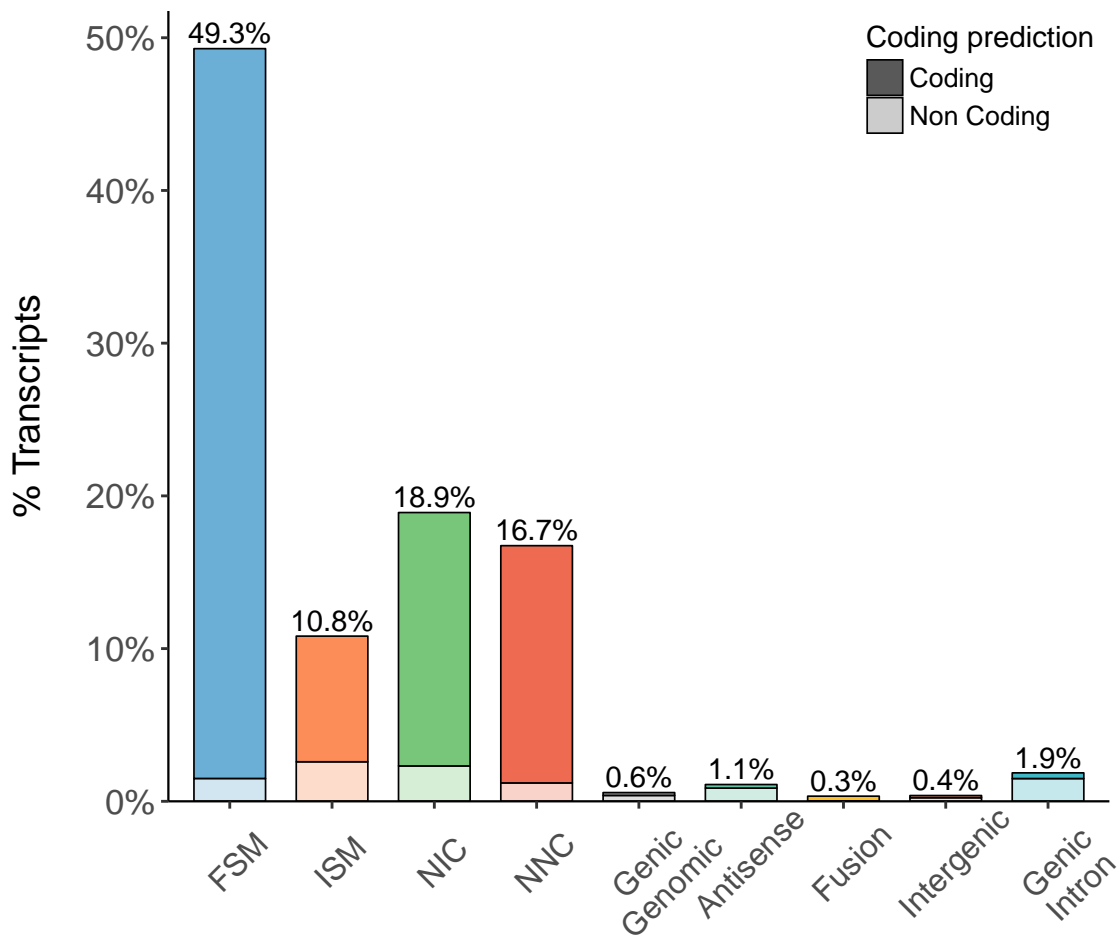
Gene expression by type of gene annotation



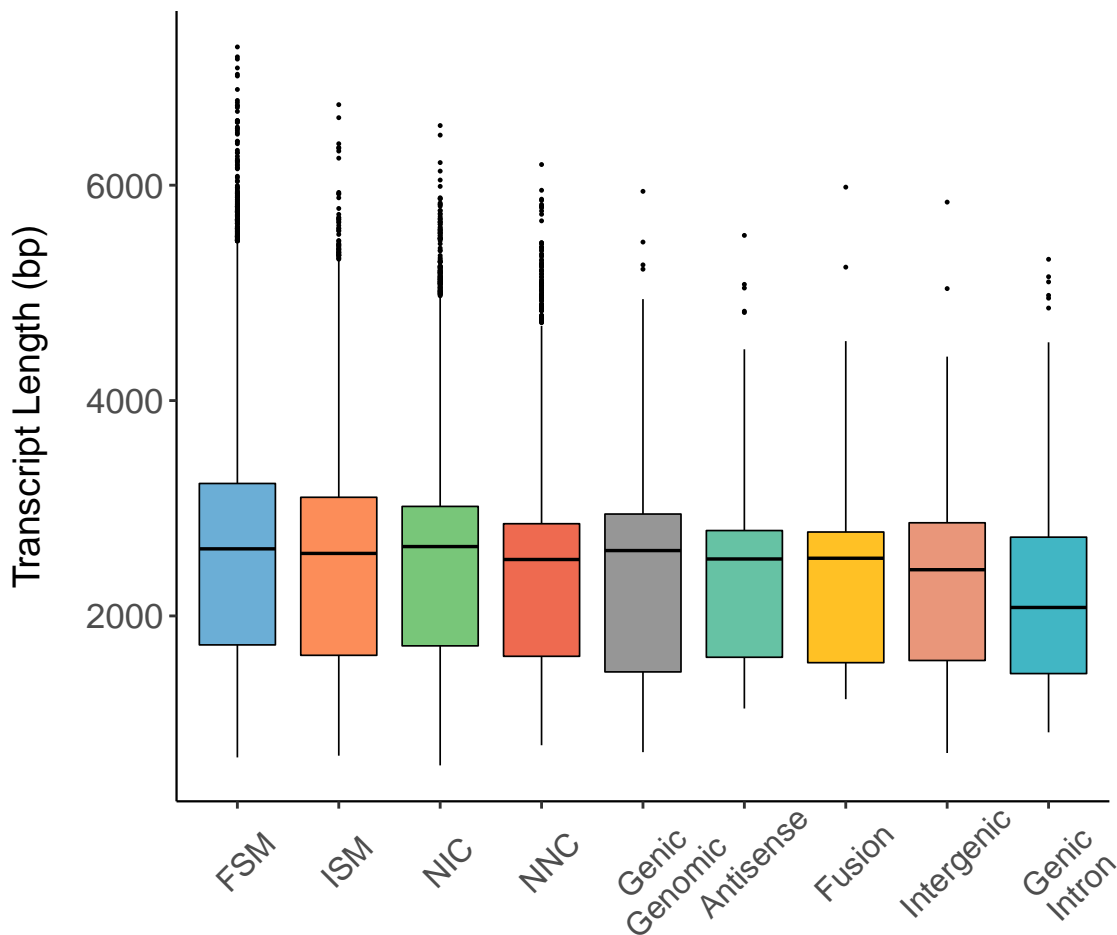
*Structrual Isoform characterization  
based on splice junctions*



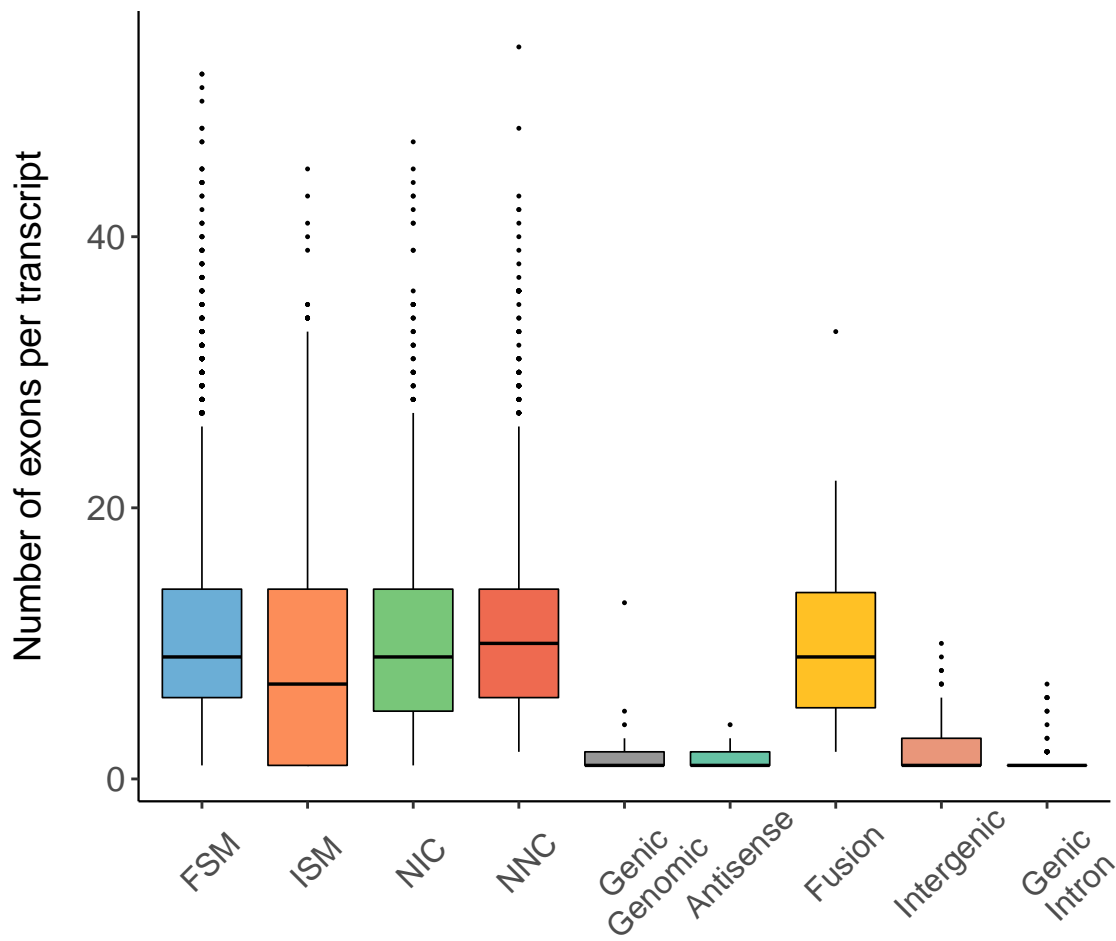
Isoform distribution across structural categories



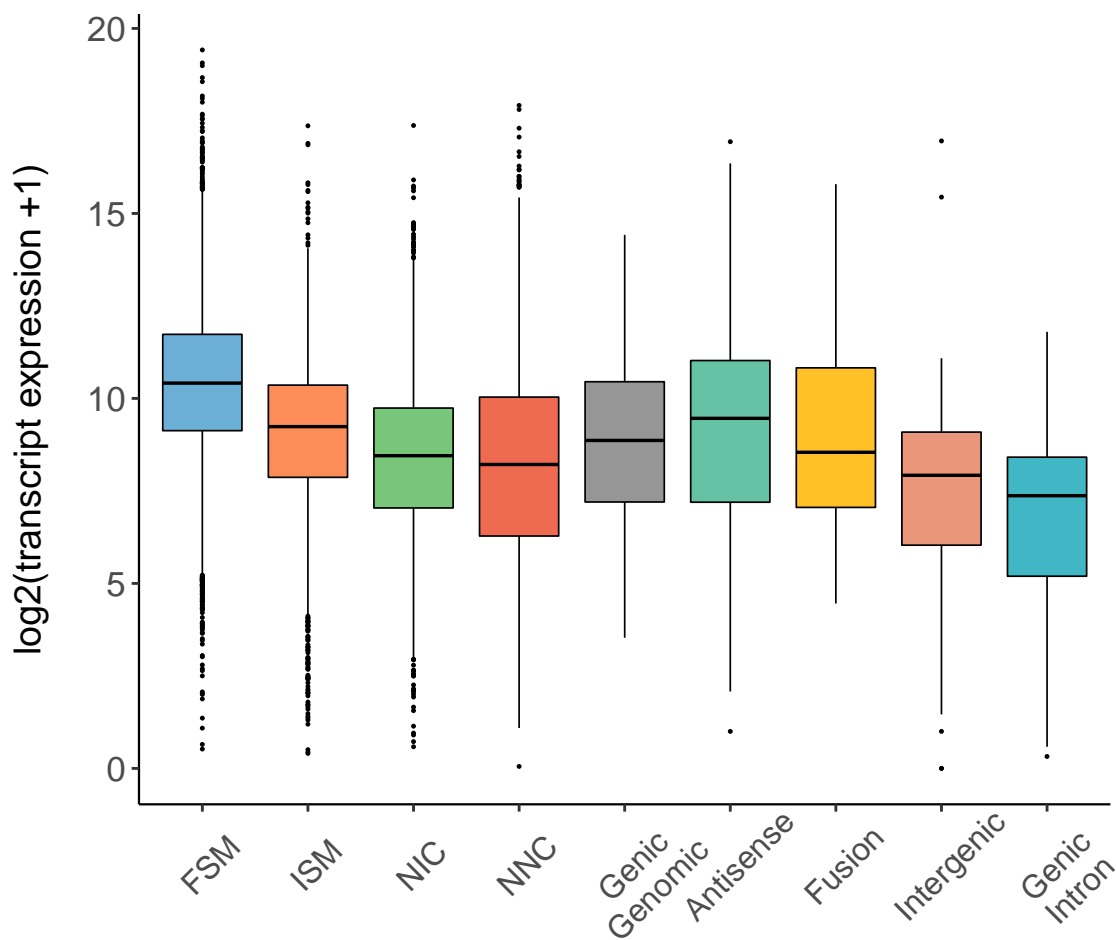
Transcript length distribution by structural classification



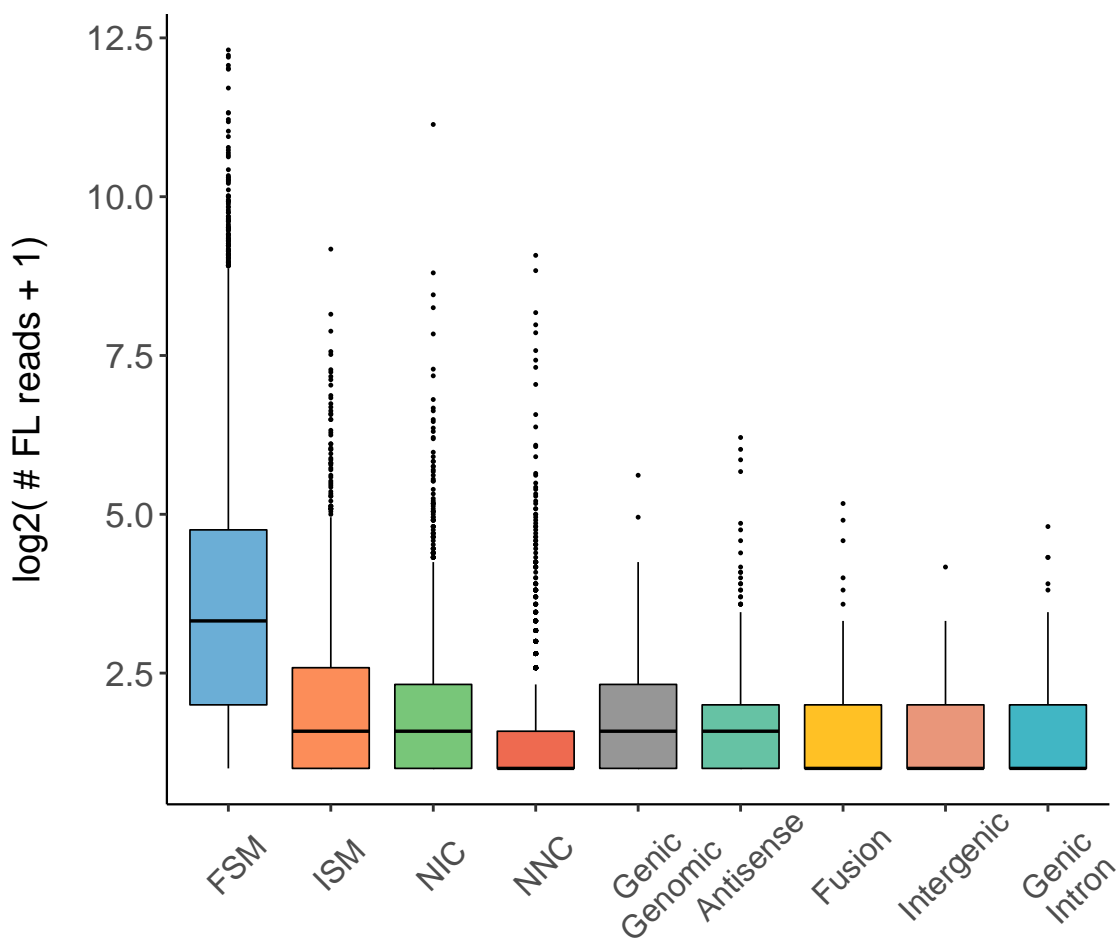
Exon number distribution by structural classification



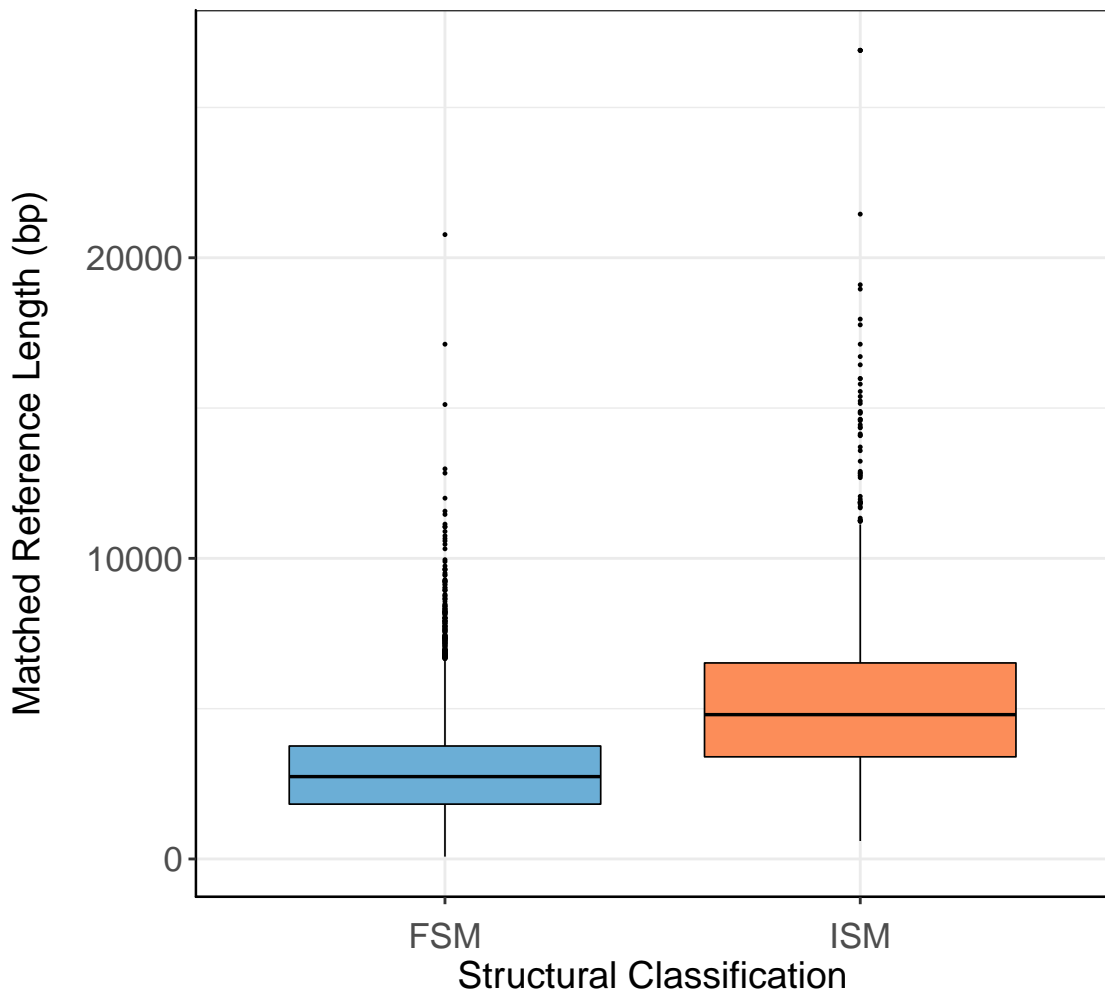
Transcript expression by structural category



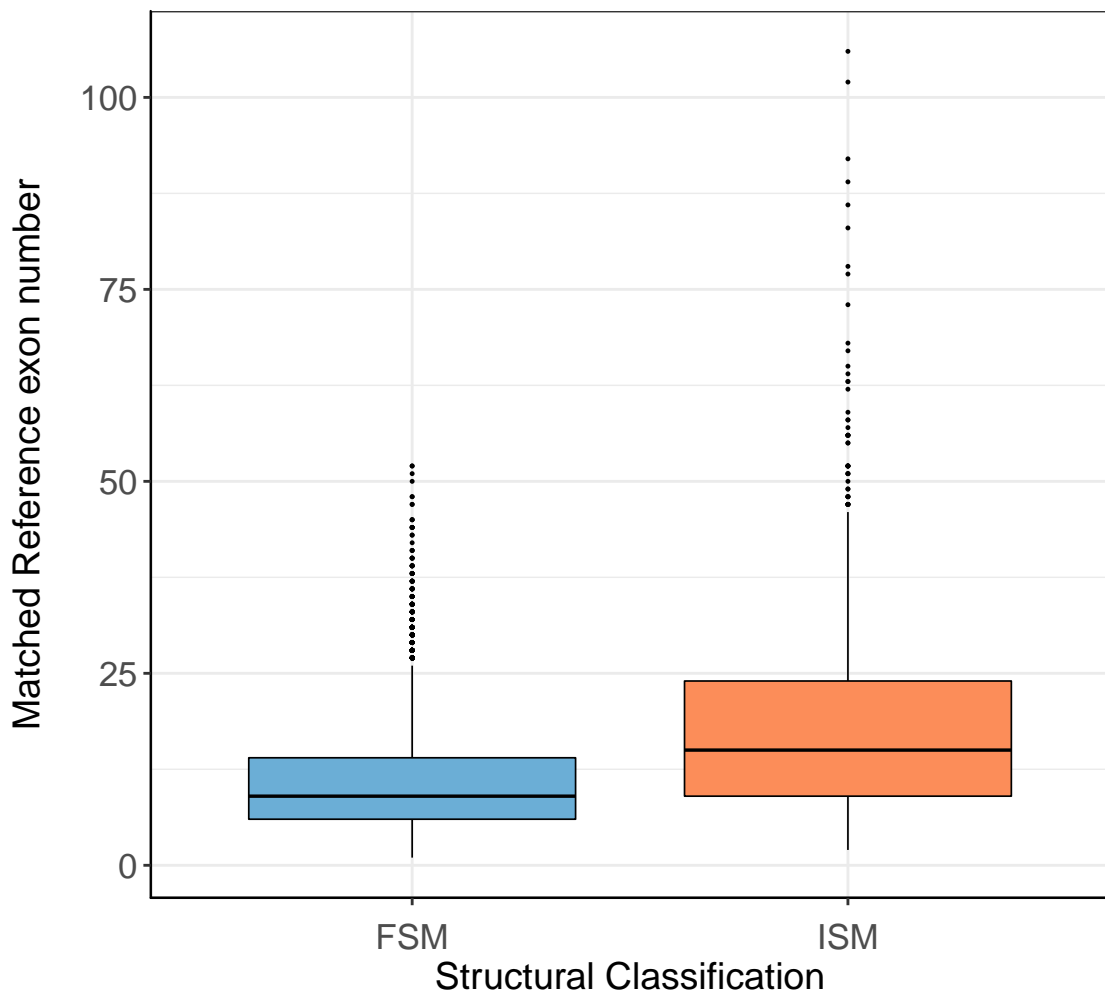
Number of FL reads per transcript by structural category



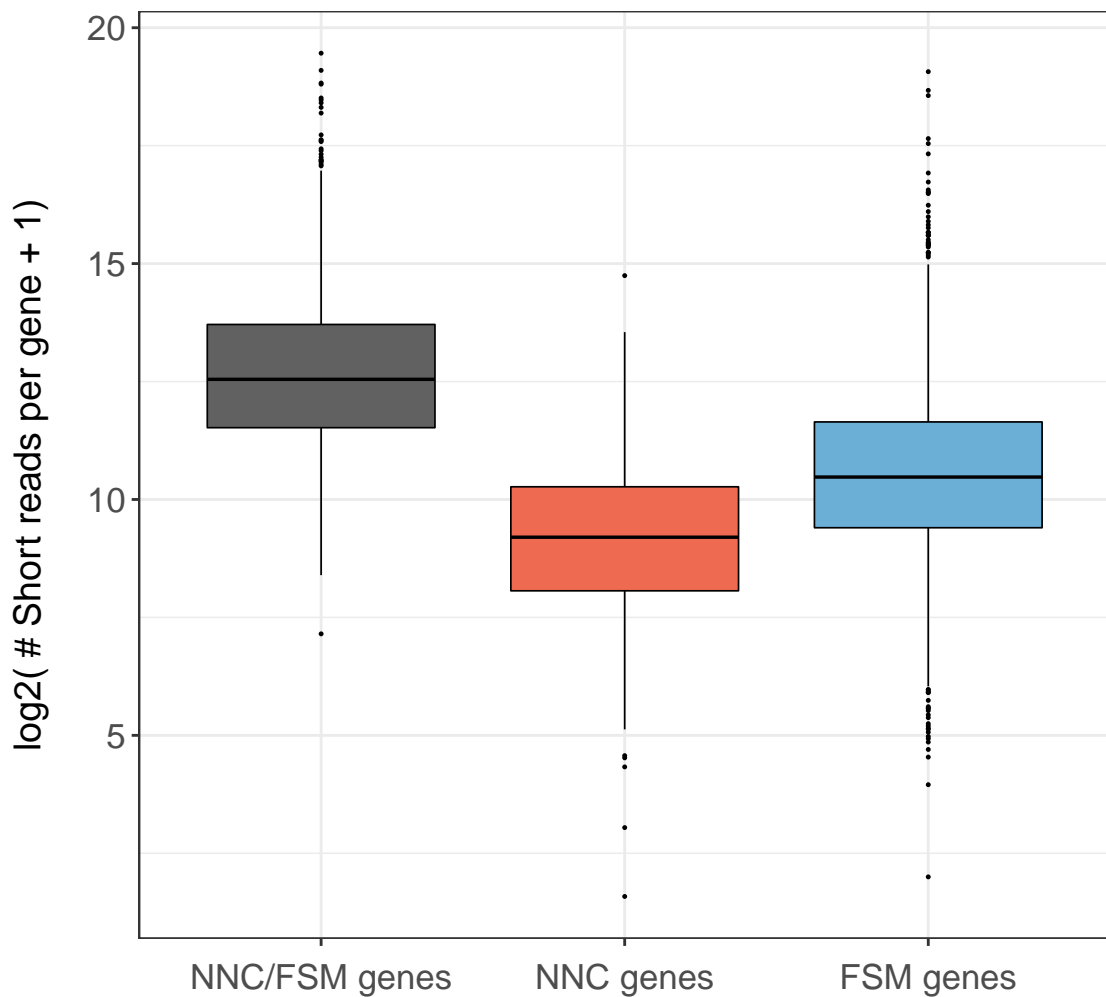
Length distribution of matched reference transcripts



Exon Number distribution of matched reference transcripts

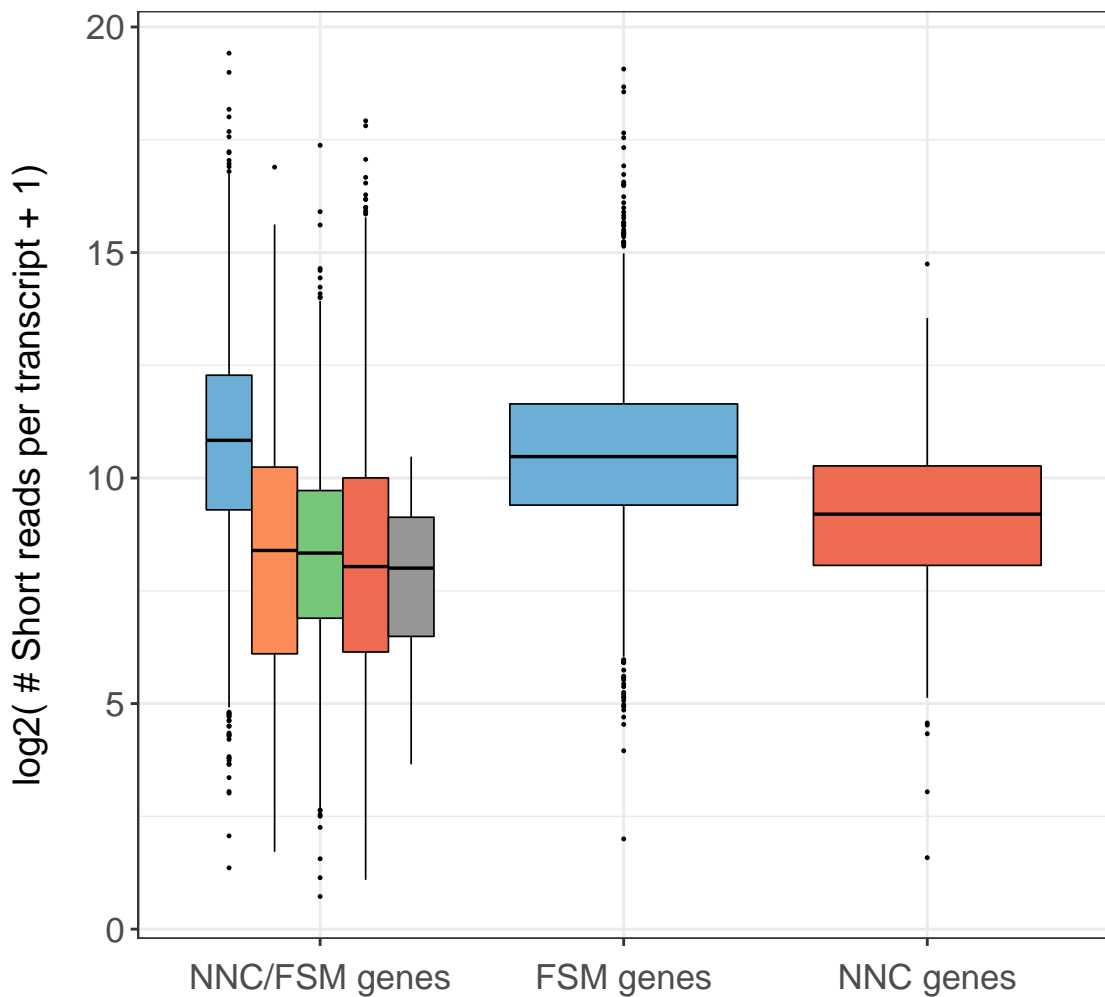


Gene Expression level in NNC/FSM containing genes

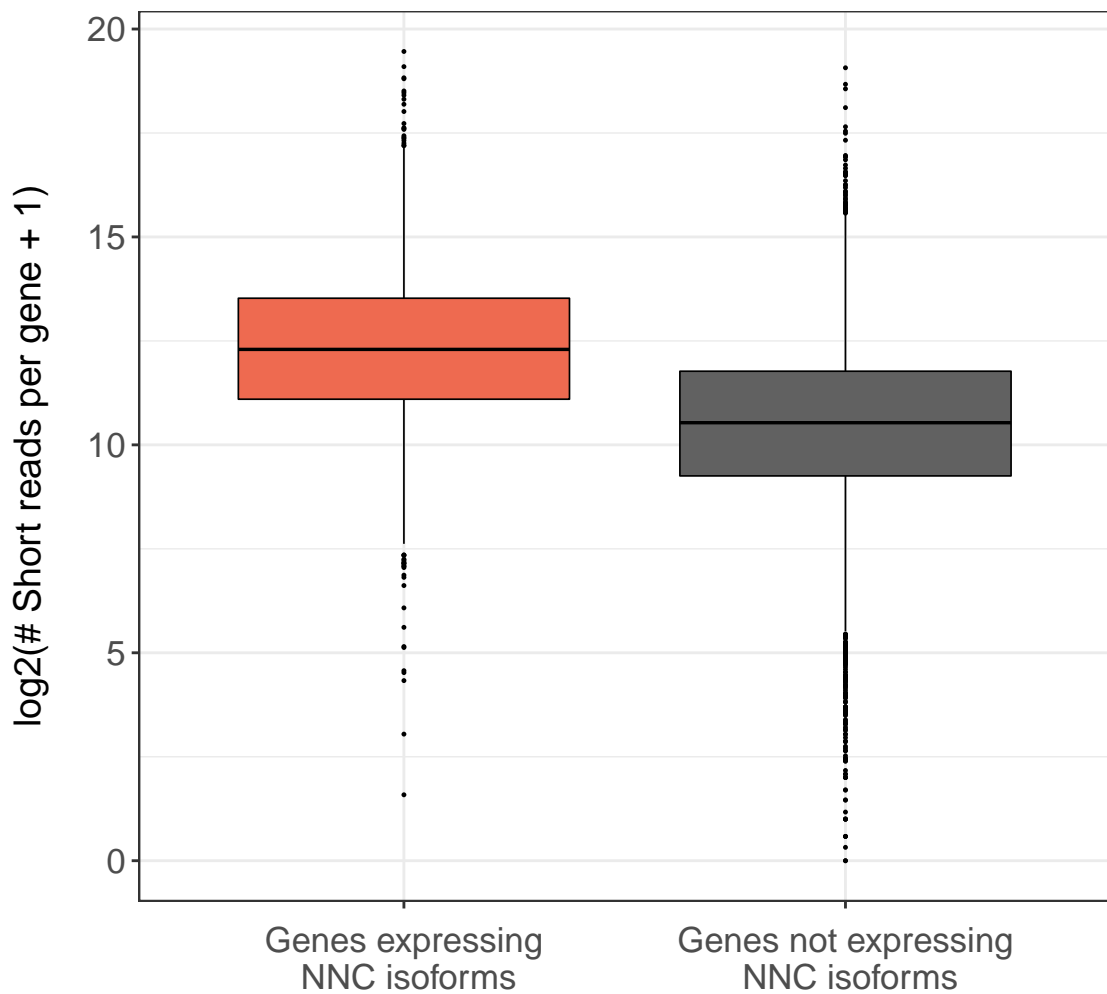




Transcript Expression level in NNC/FSM containing genes



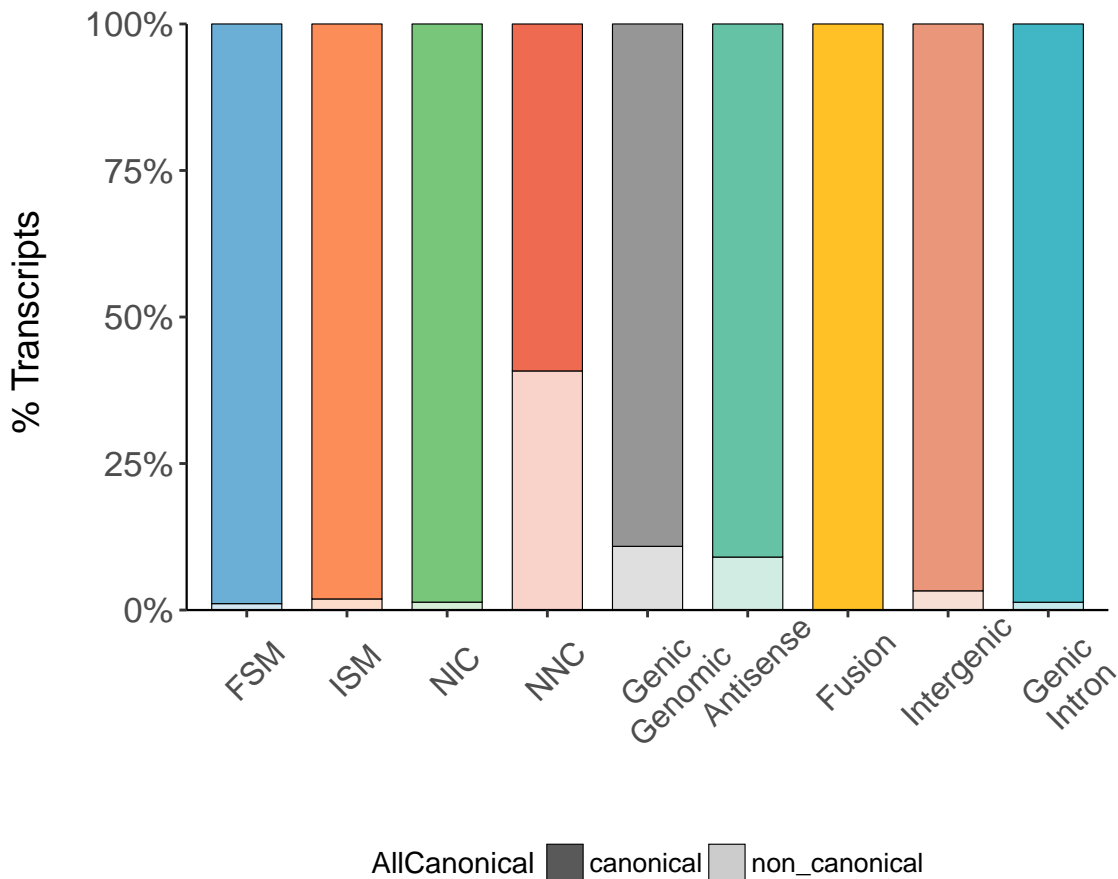
Gene expression levels between NNC and not NNC containing gene



*Splice junction characterization*

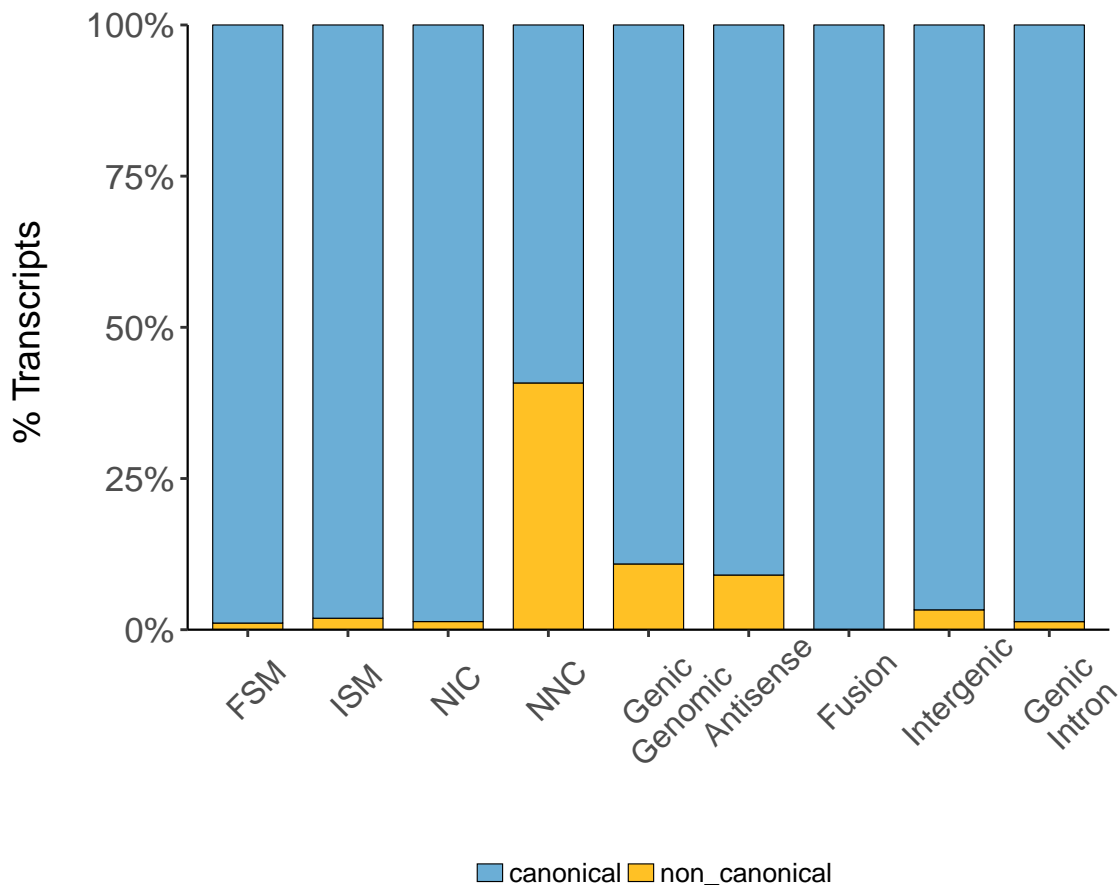
## Distribution of transcripts by splice junction category

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

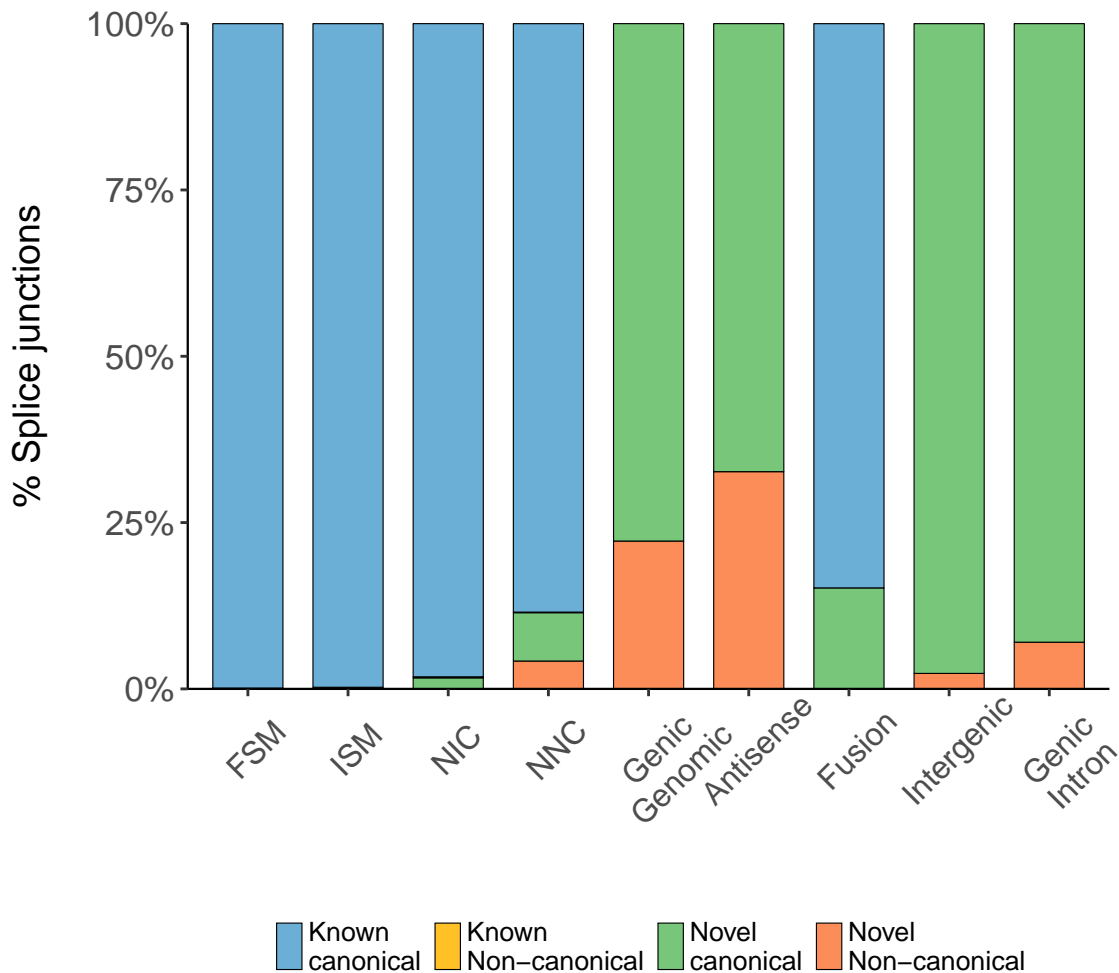


## Distribution of transcripts by splice junction category

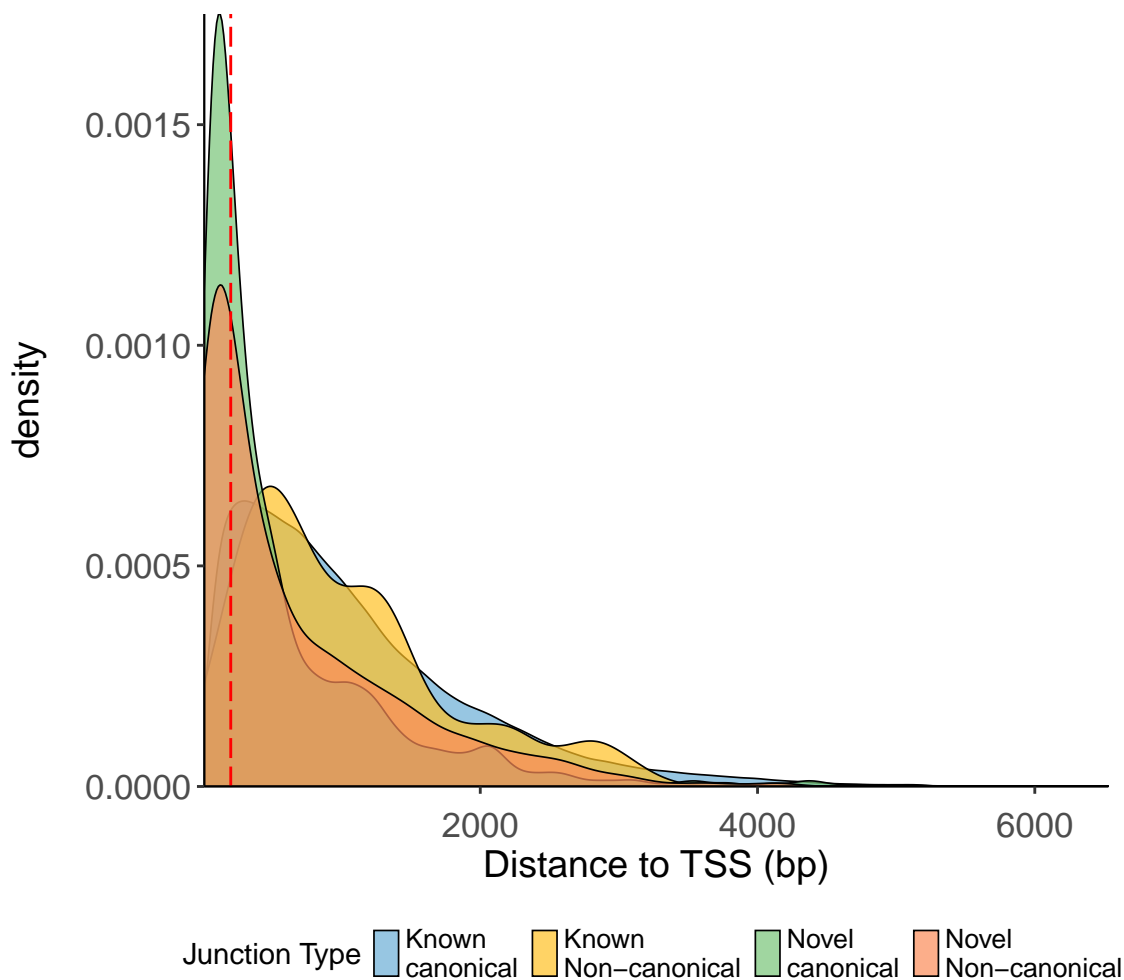
Non canonical transcripts are those with at least one non-canonical junction



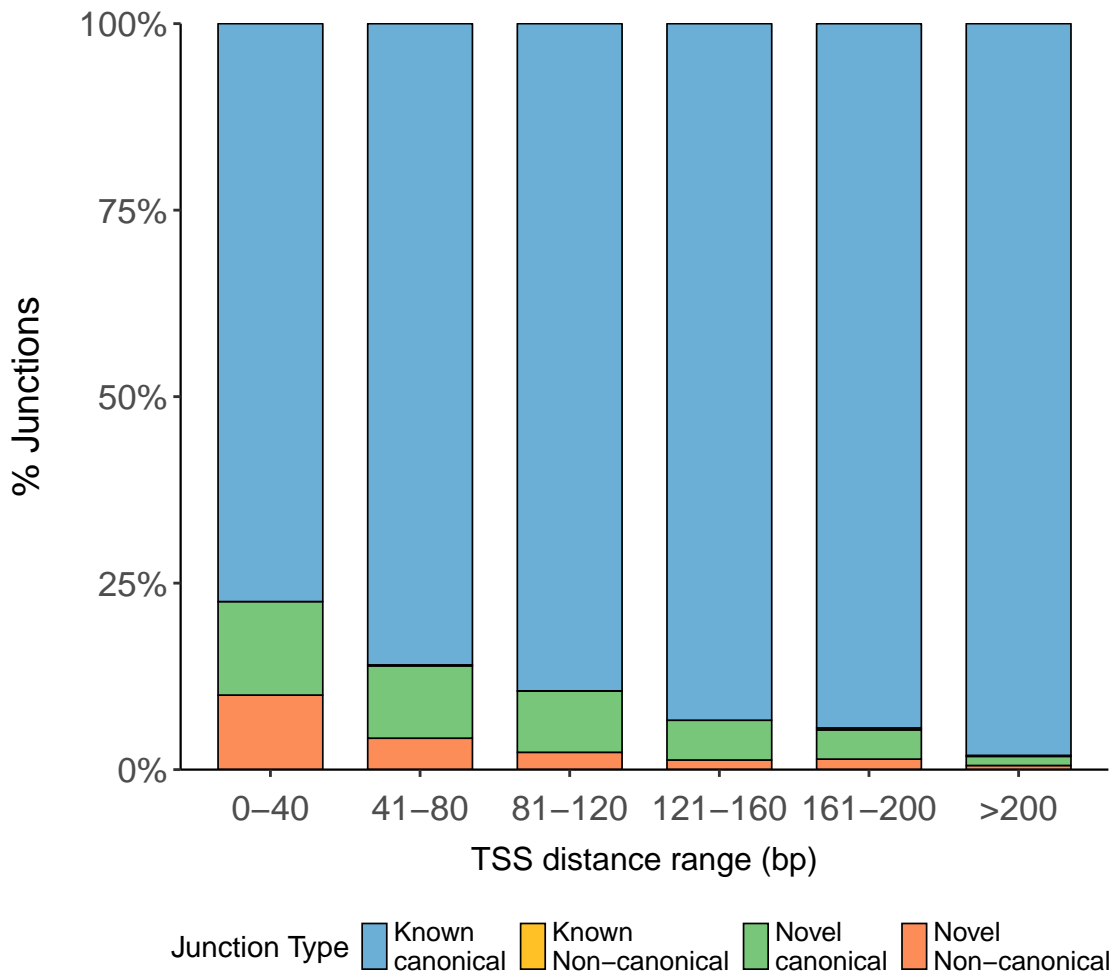
Distribution of SJ type among structural classification



Distribution of splice junctions distance to TSS

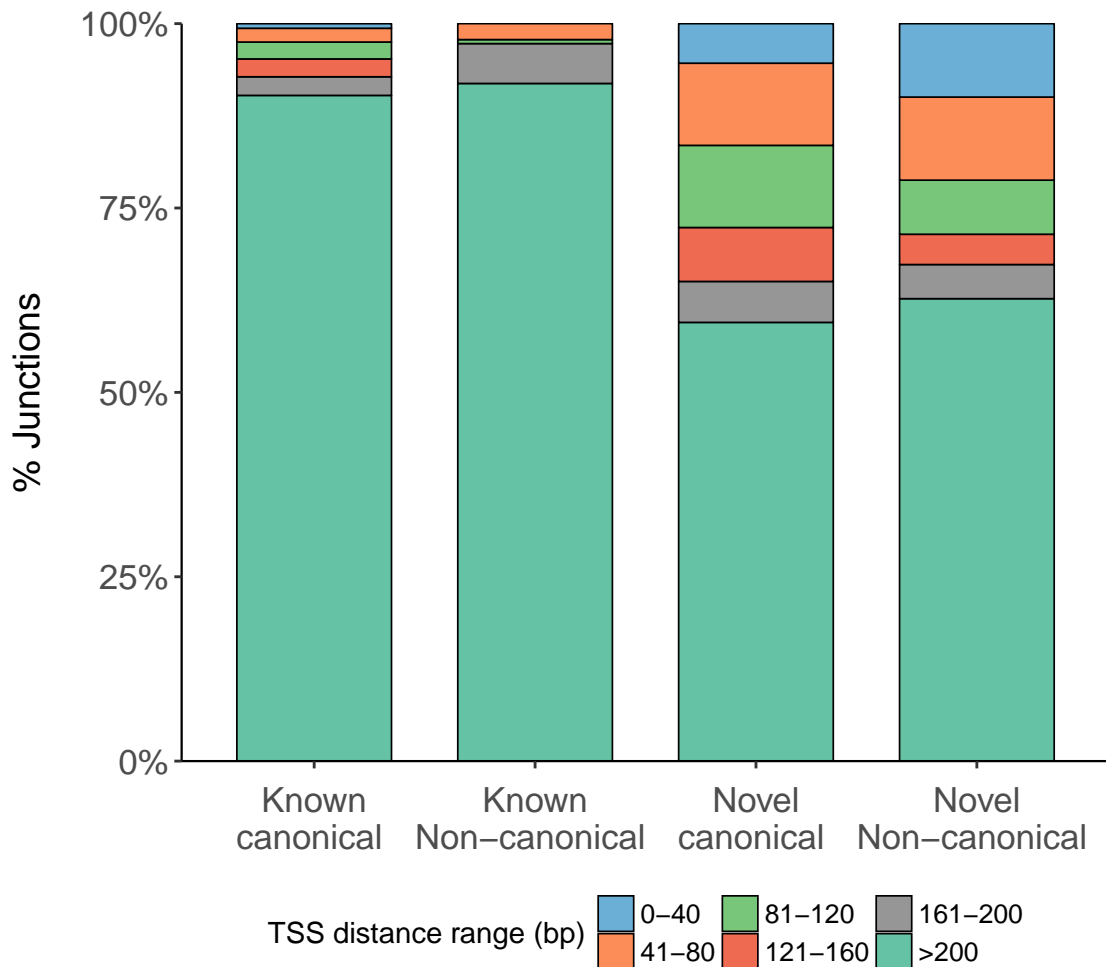


Splice junction distance to TSS across junction type

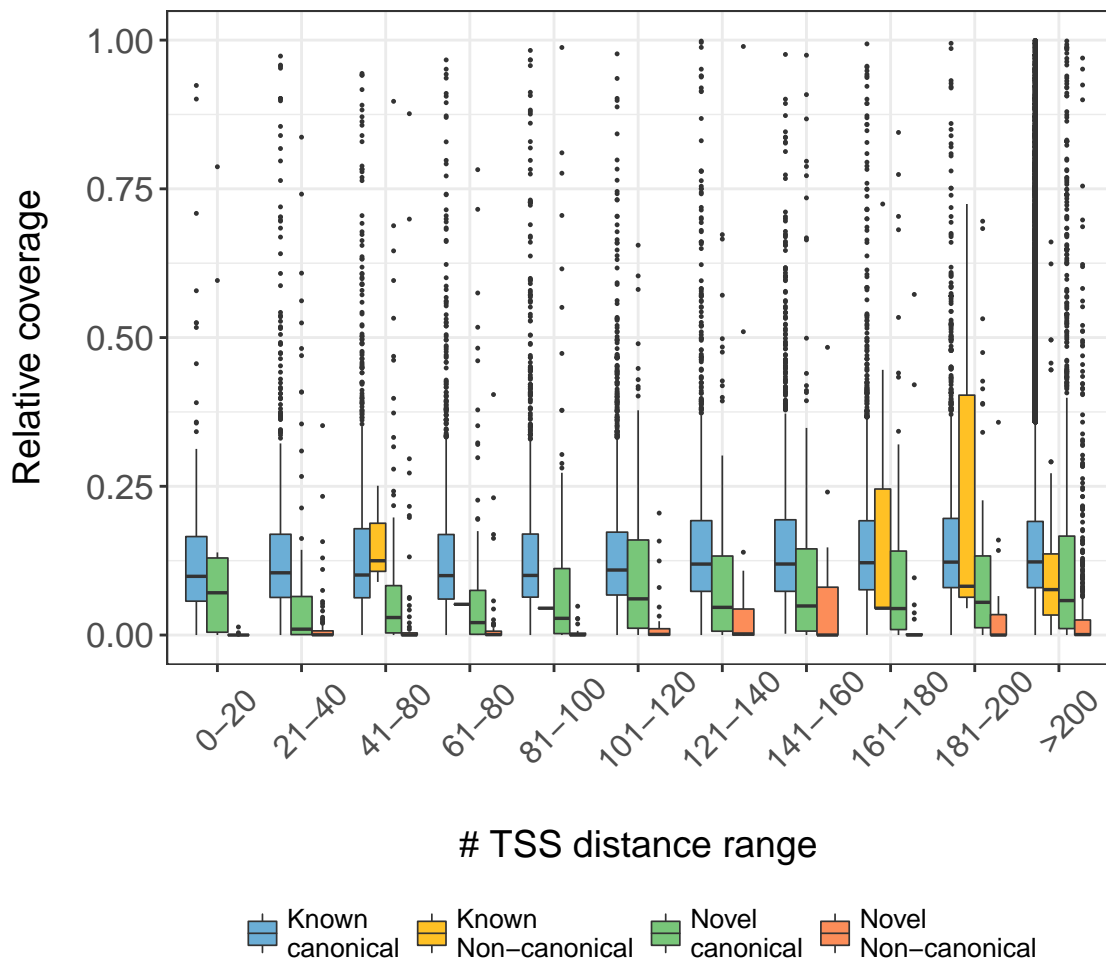




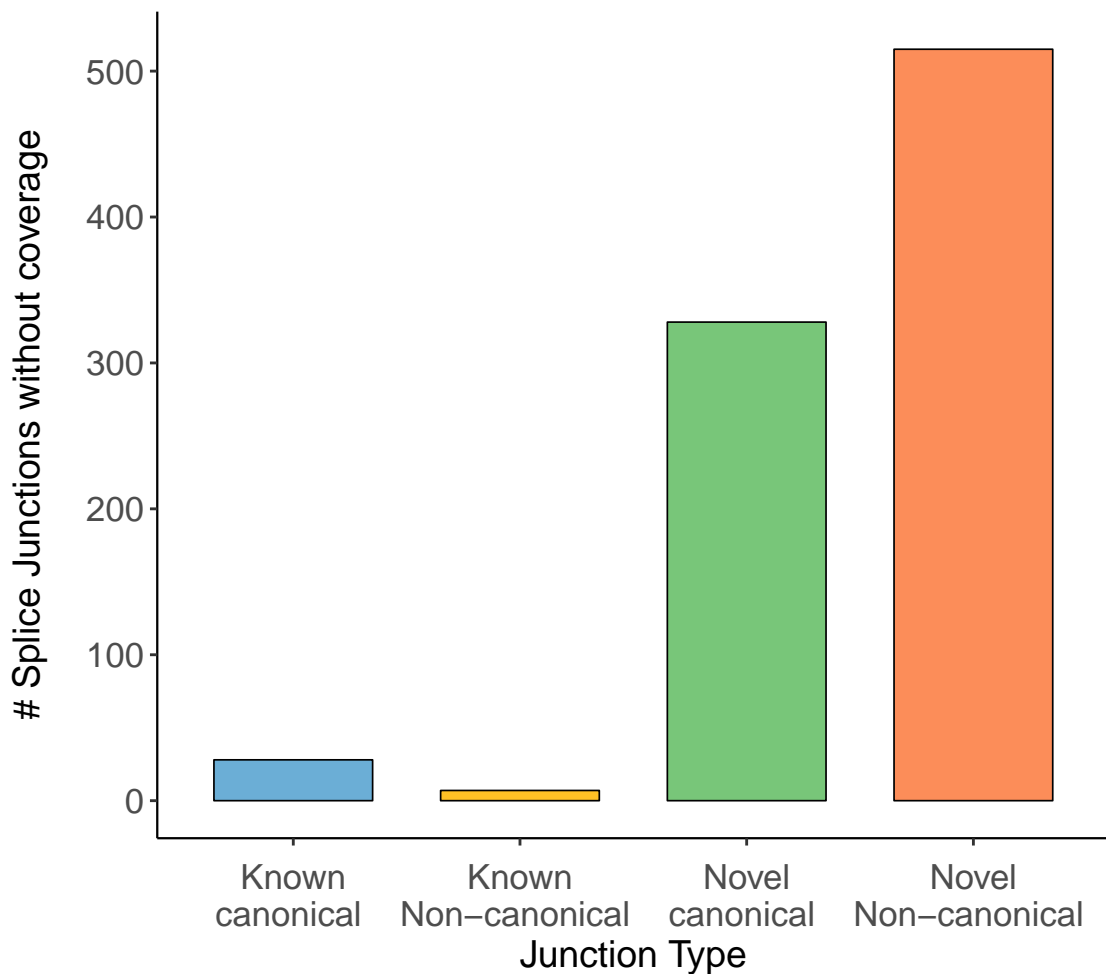
Splice junction distance to TSS across junction type



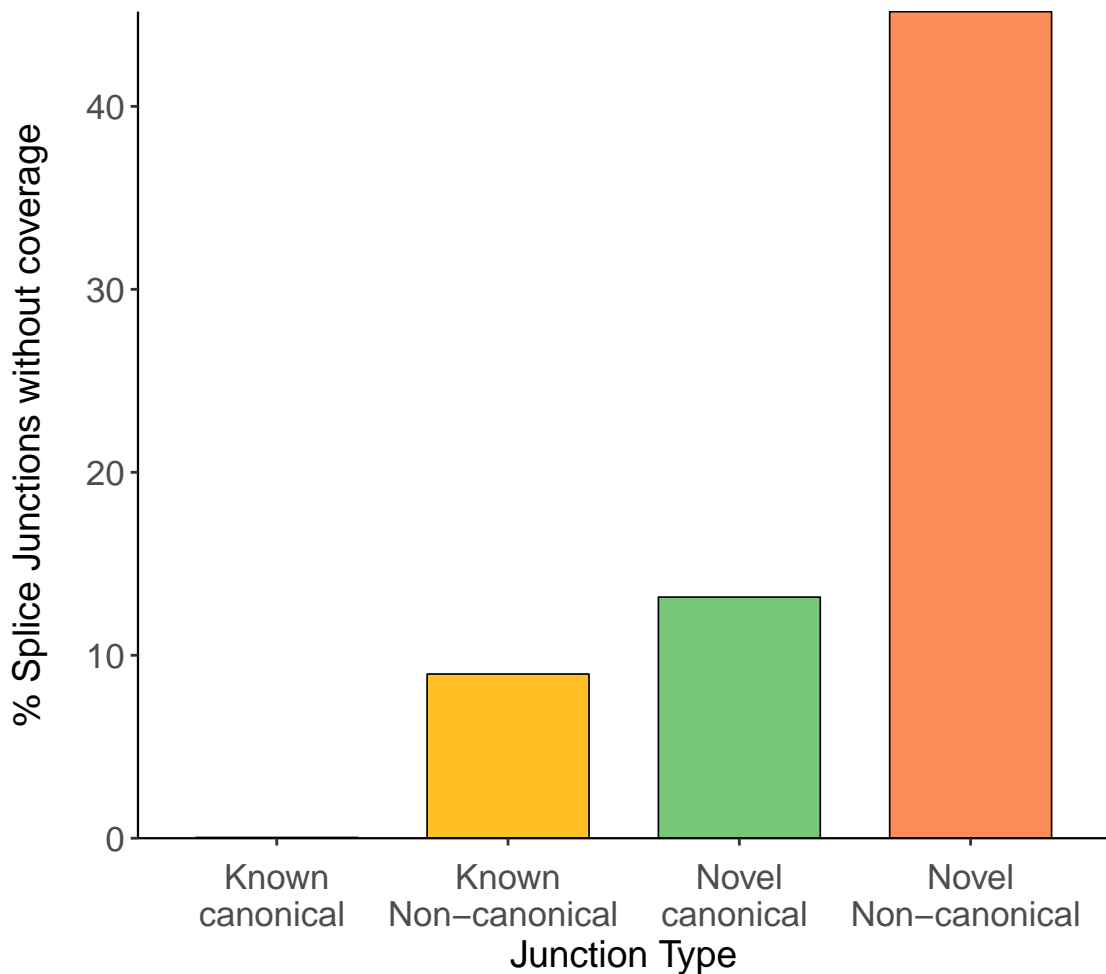
## Relative Coverage of junctions



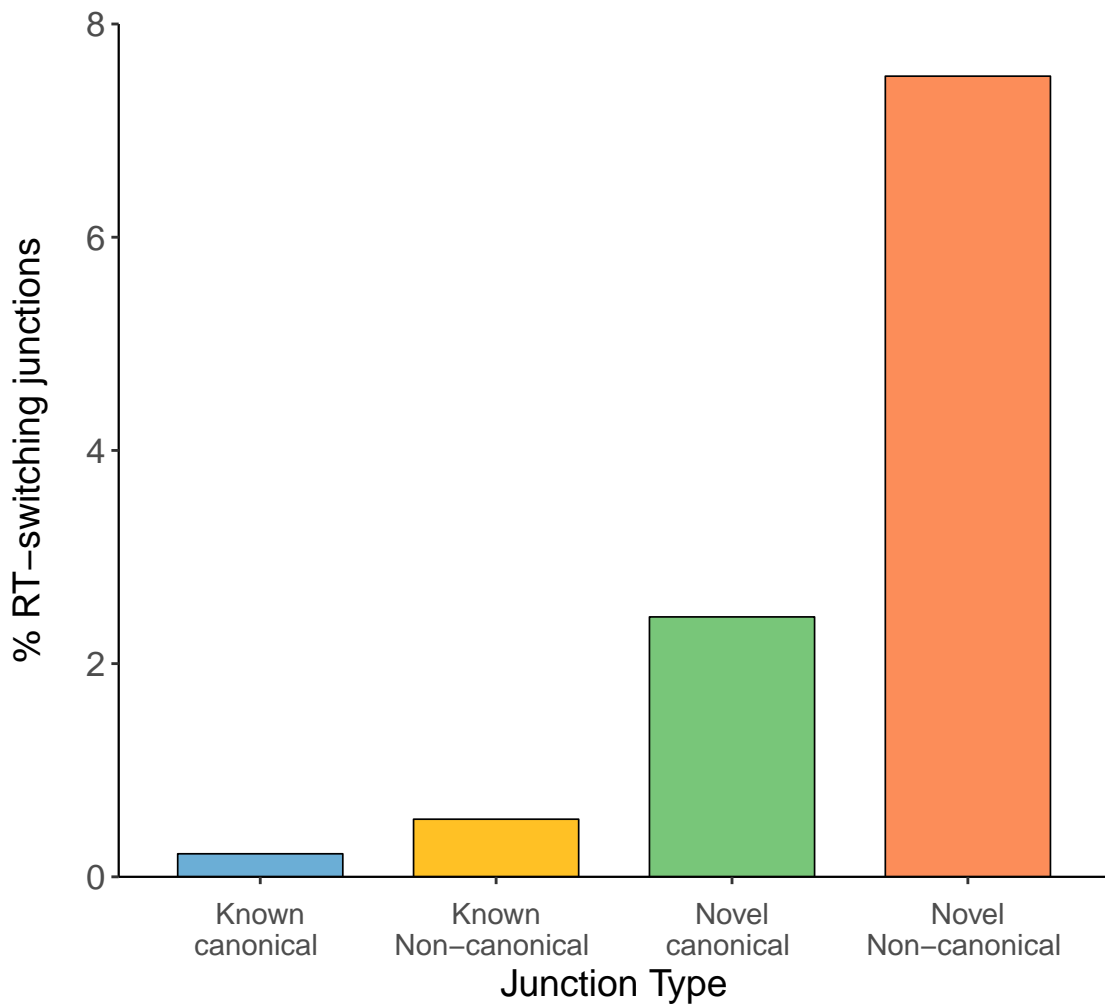
Splice junctions without short-read coverage (unique junctions)



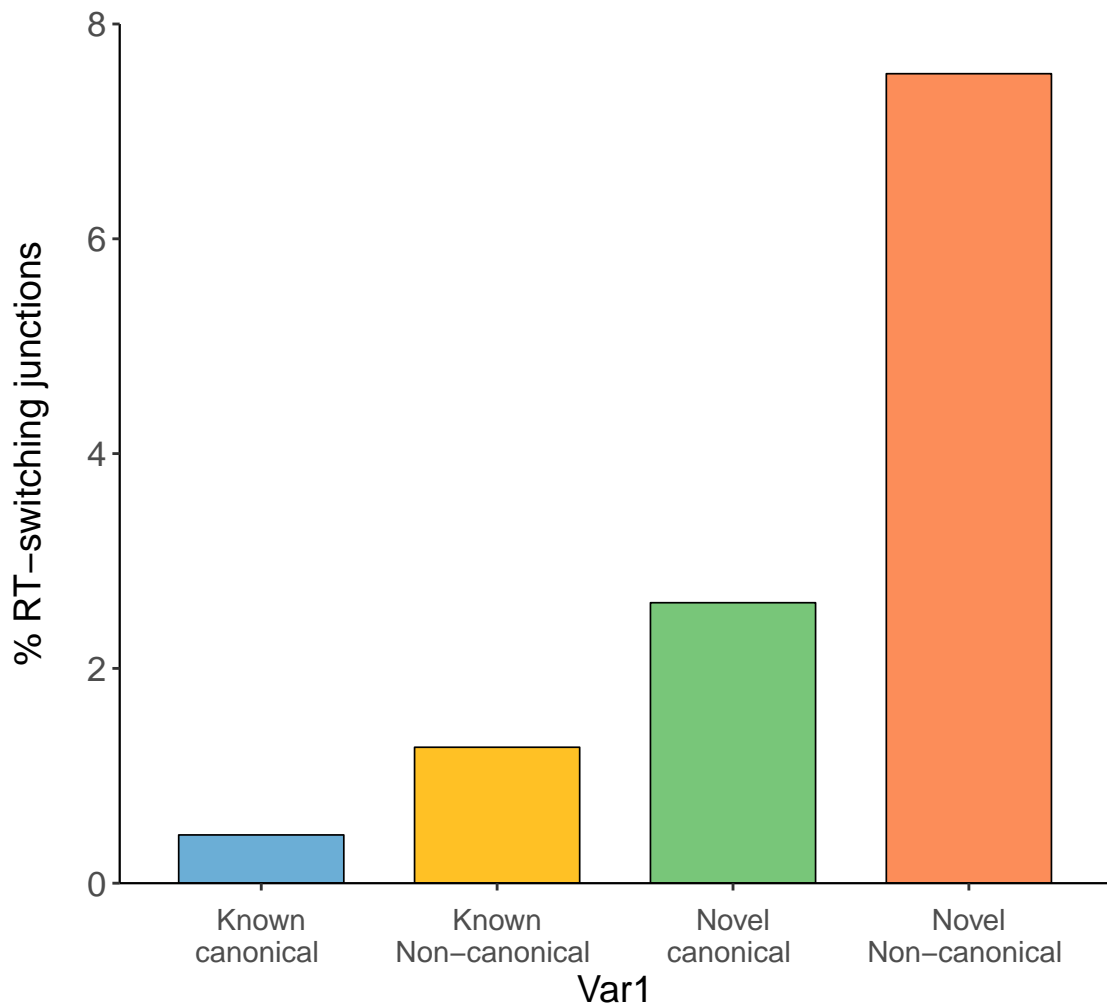
# Splice junctions without short-read coverage (unique junctions)



RT-switching by splice junction category



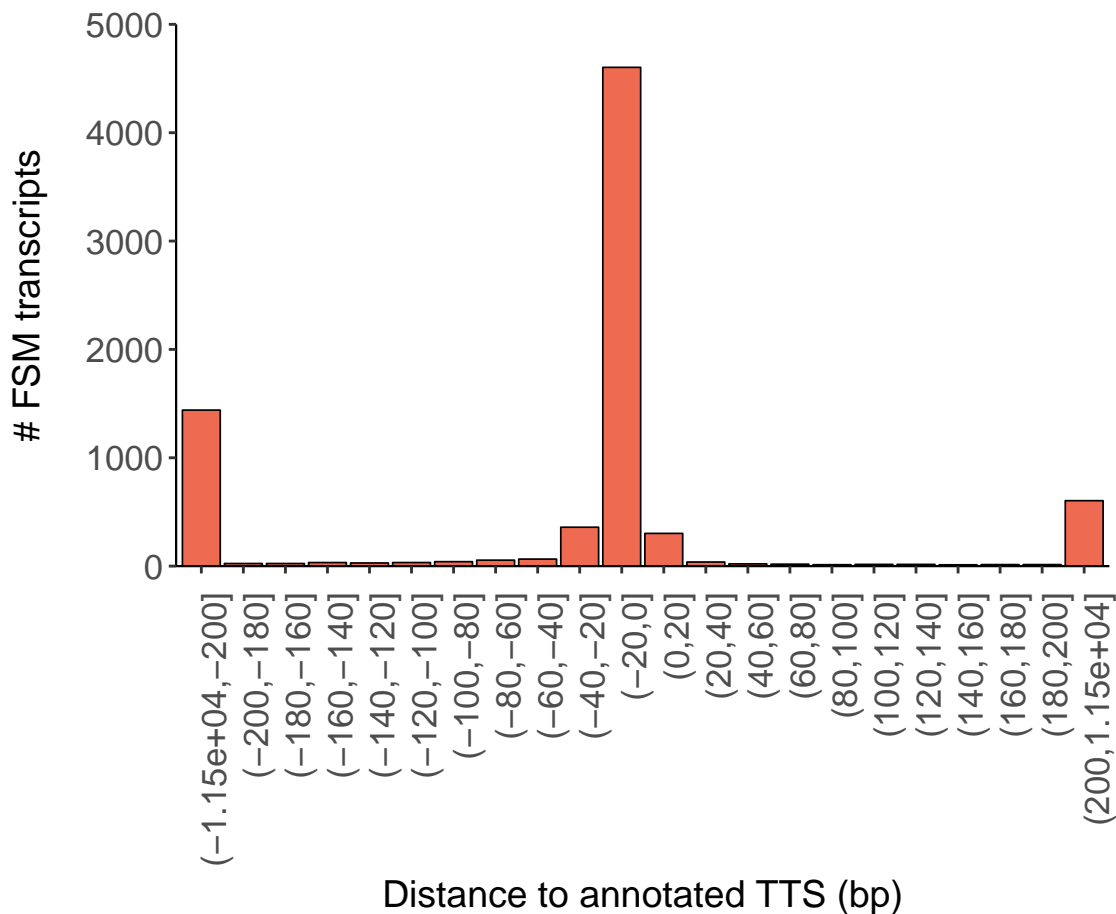
RT-switching by splice junction category (unique junctions)



*Full-lengthness characterization of isoforms*

# Distance distribution from sequenced to annotated TTS

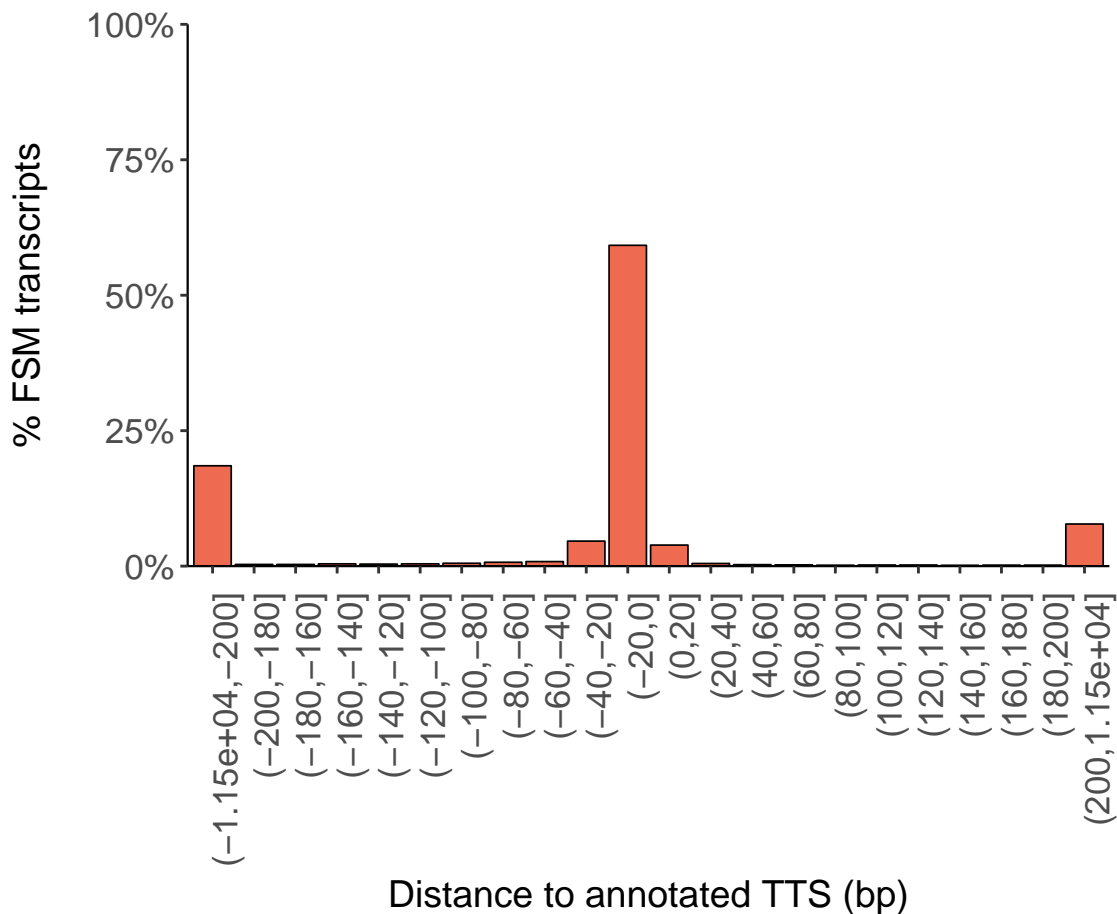
Negative values indicate that the sequenced TTS is downstream annotated TTS





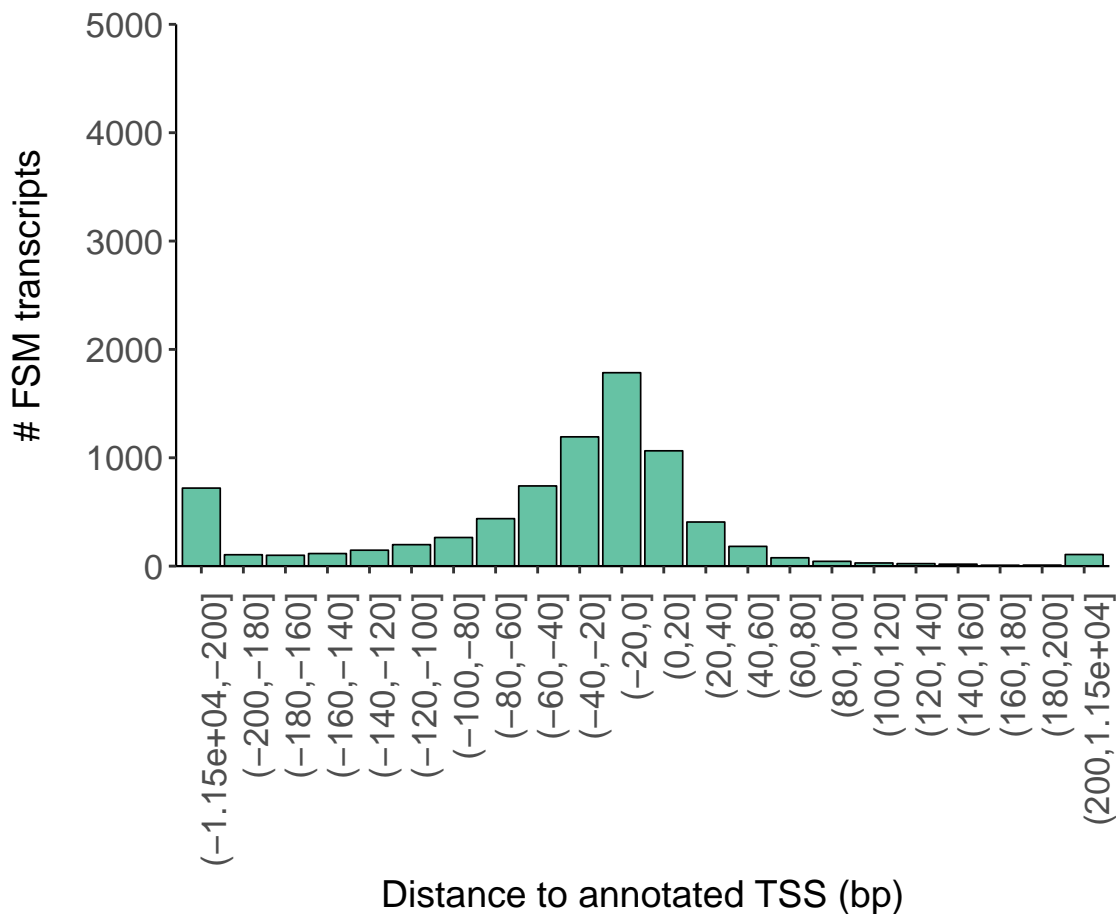
## Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is downstream annotated TTS



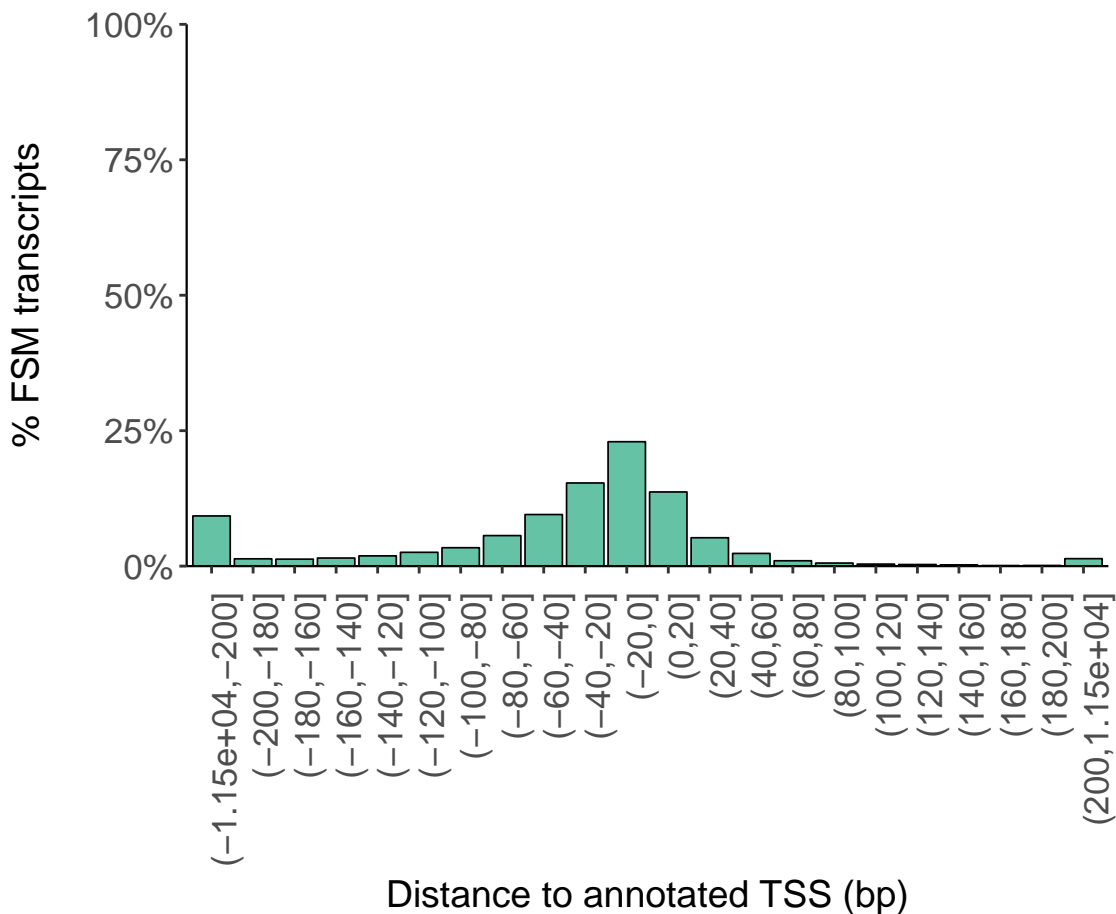
## Distance distribution from sequenced to annotated TSS

Negative values indicate that the sequenced TSS is upstream annotated TSS



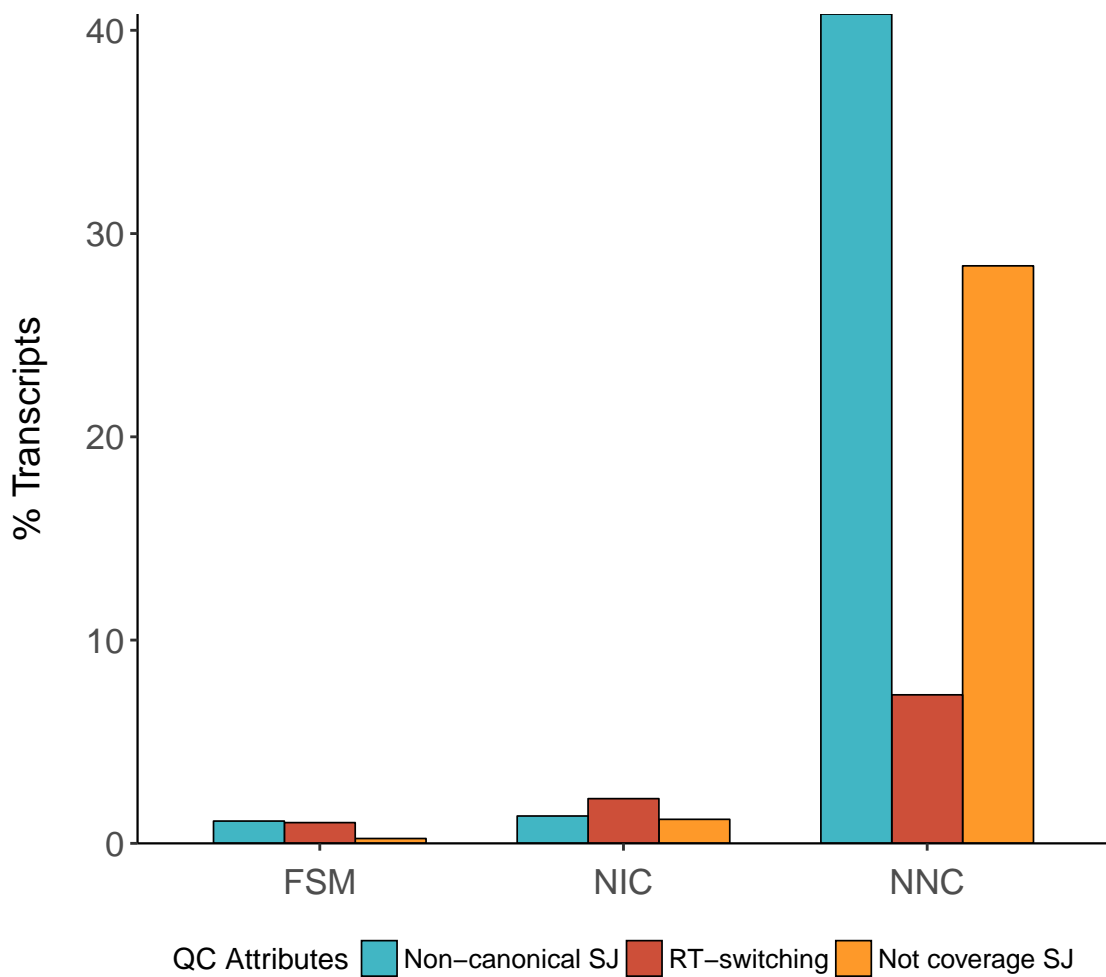
## Distance distribution from sequenced to annotated TSS

Negative values indicate that the sequenced TSS is upstream annotated TSS



*Quality control attributes*

Quality control attributes across structural categories



## Quality control attributes across structural categories

Categories are divided into NNC/FSM containing genes

