SQANTI report

 # Genes: 7694
 # Isoforms: 16104

Gene classification

category	# genes
Annotated Genes	7183
Novel Genes	511

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

SJ classification

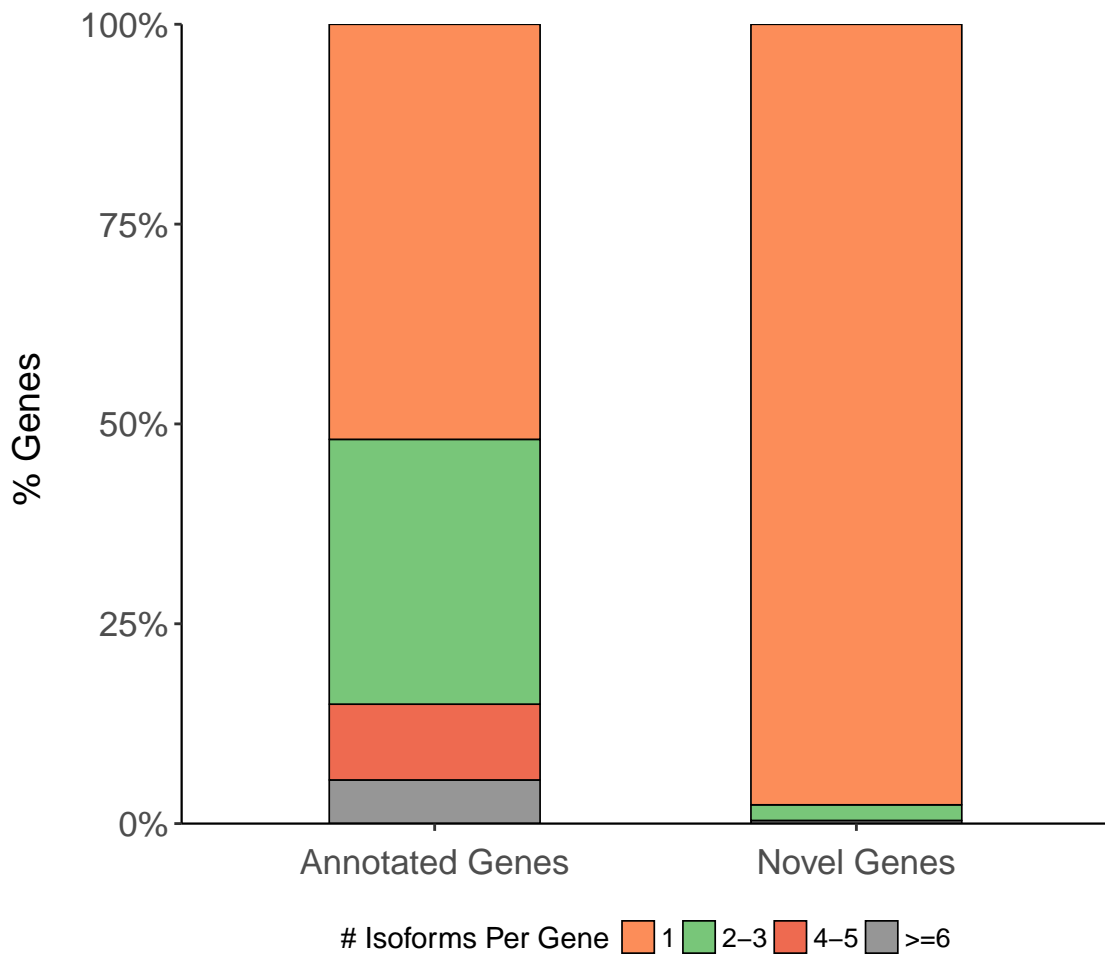| category	# SJ
Known canonical	67680
Known Non−canonical	78
Novel canonical	2489
Novel Non−canonical	1140

Gene characterization
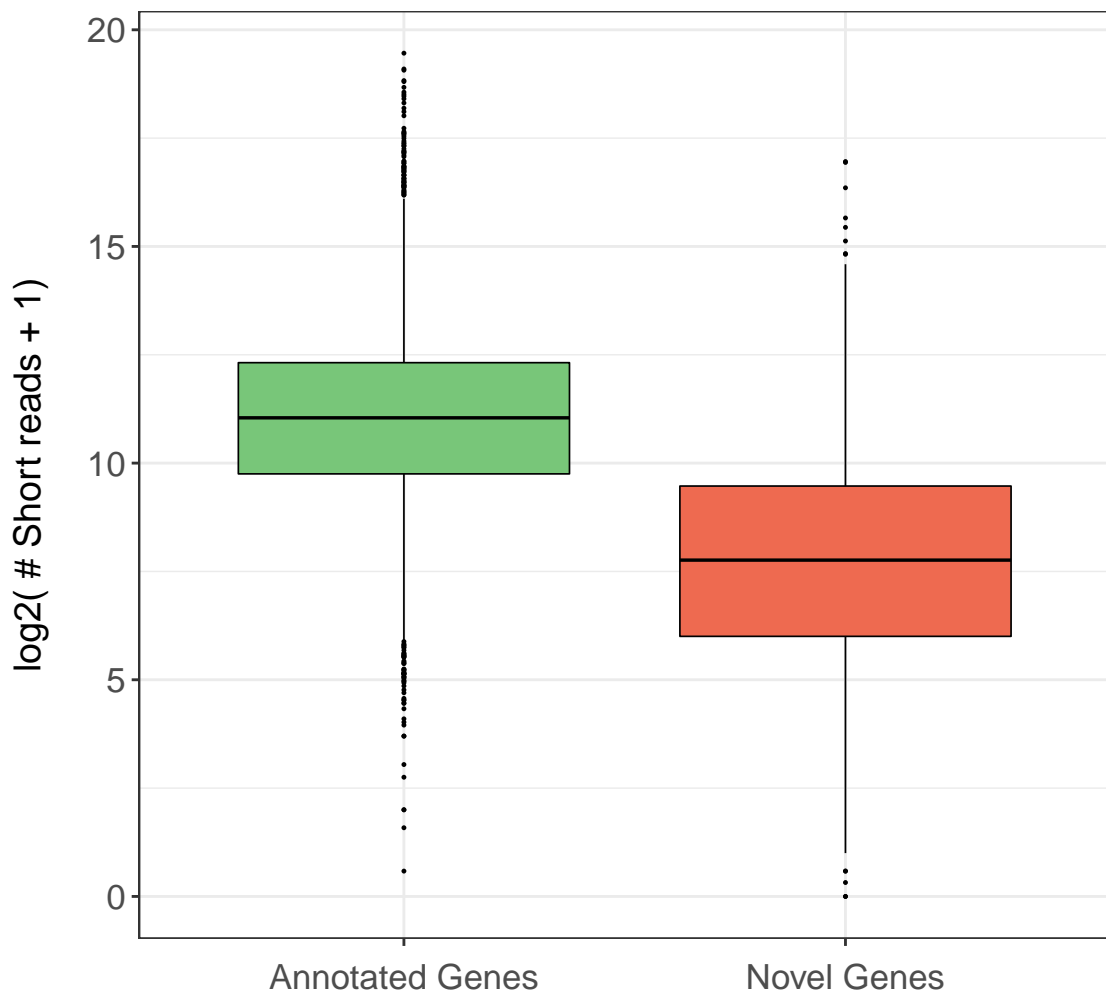
Distribution of isoforms per gene
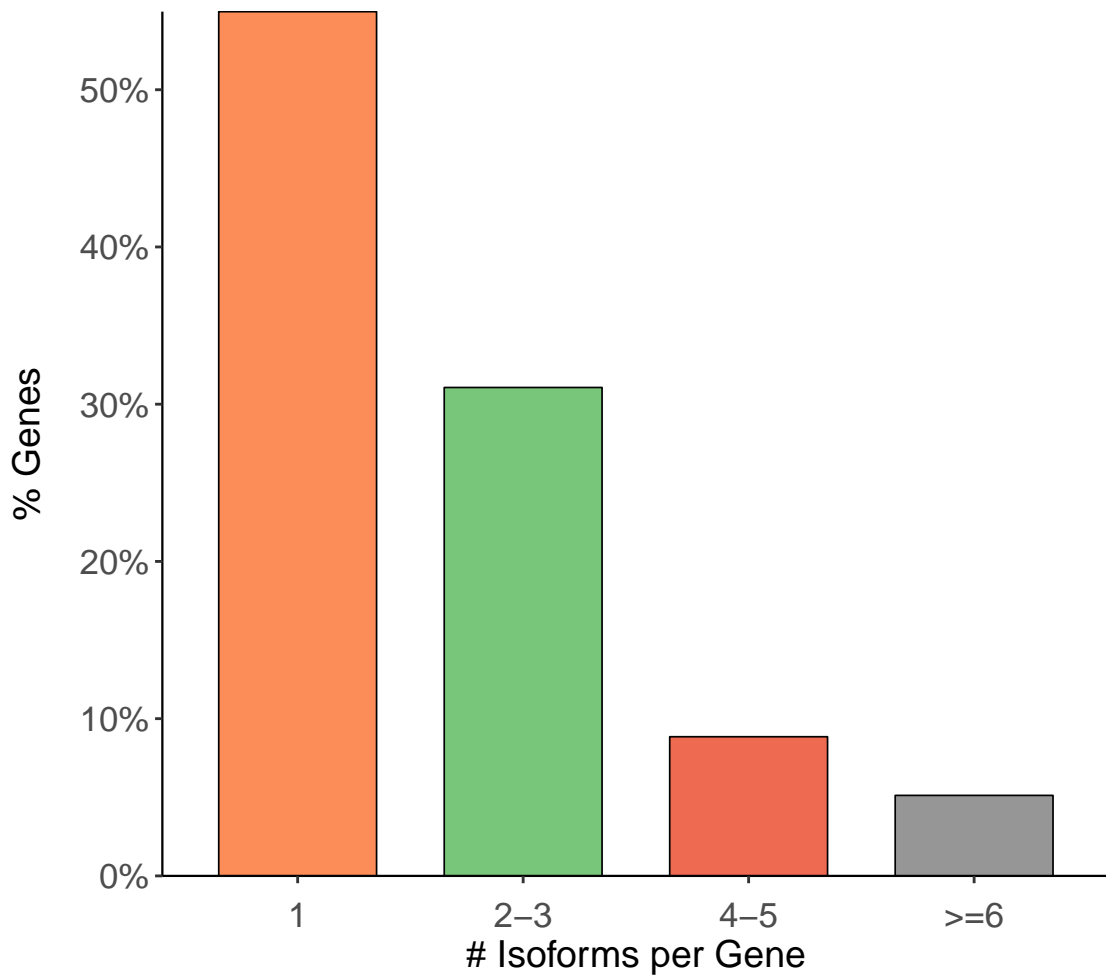
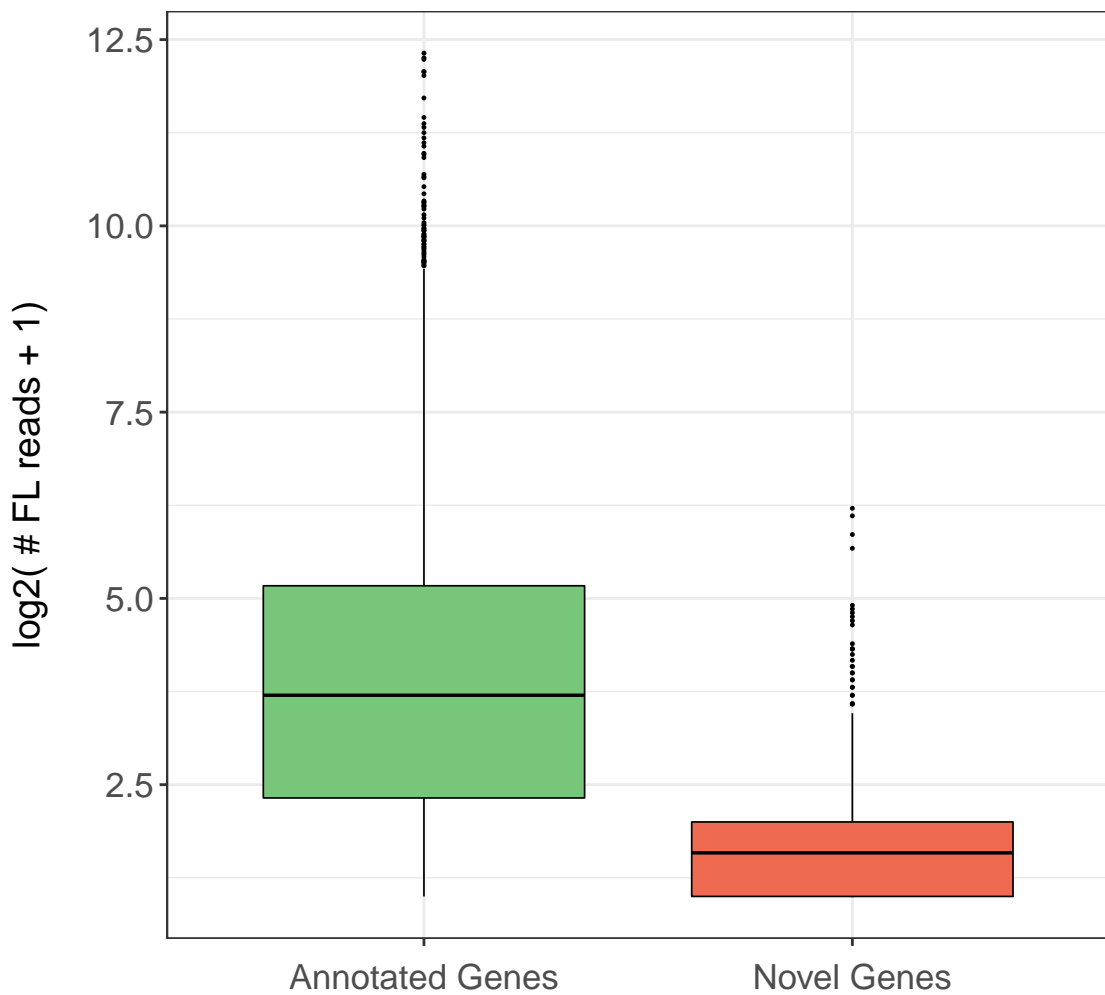Distribution of mono/multi exon transcripts
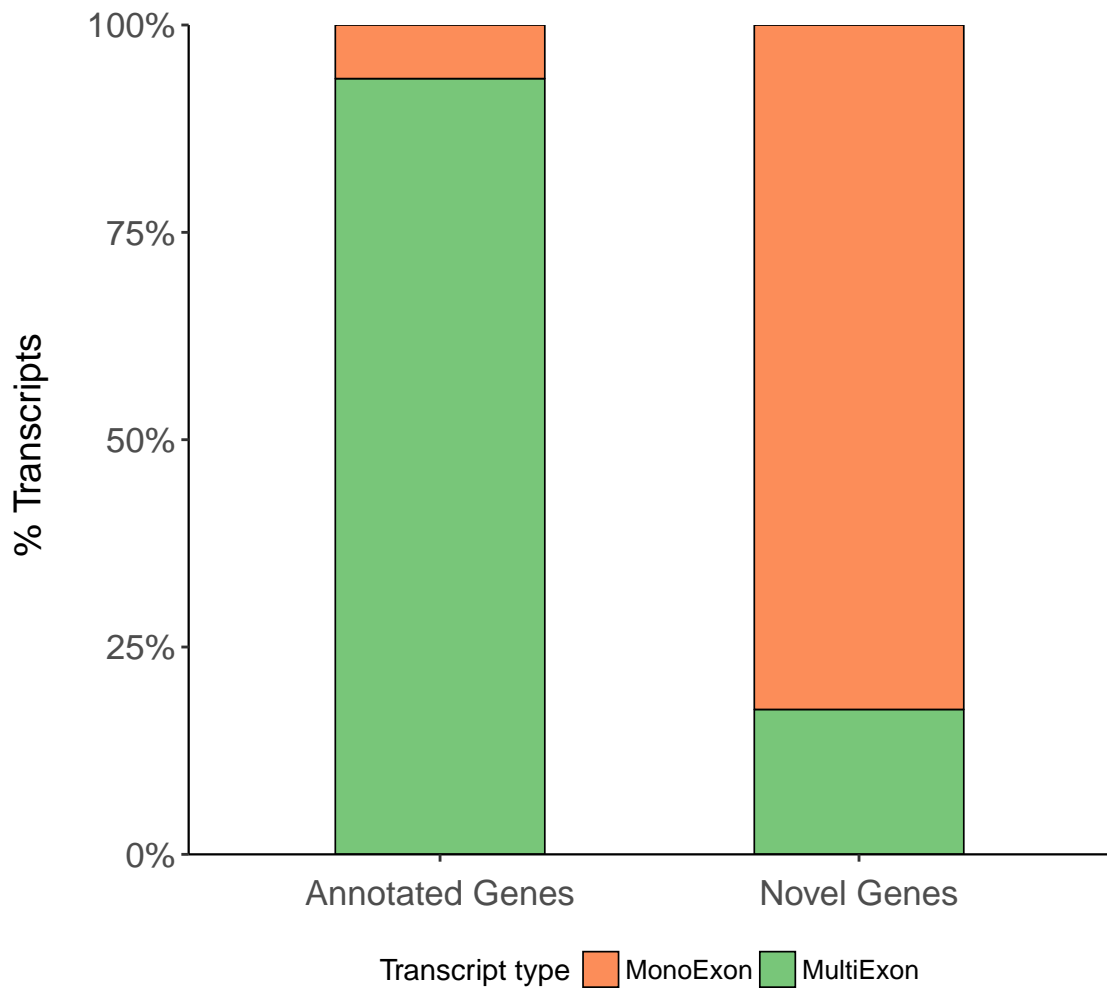
Distribution of number of isoforms
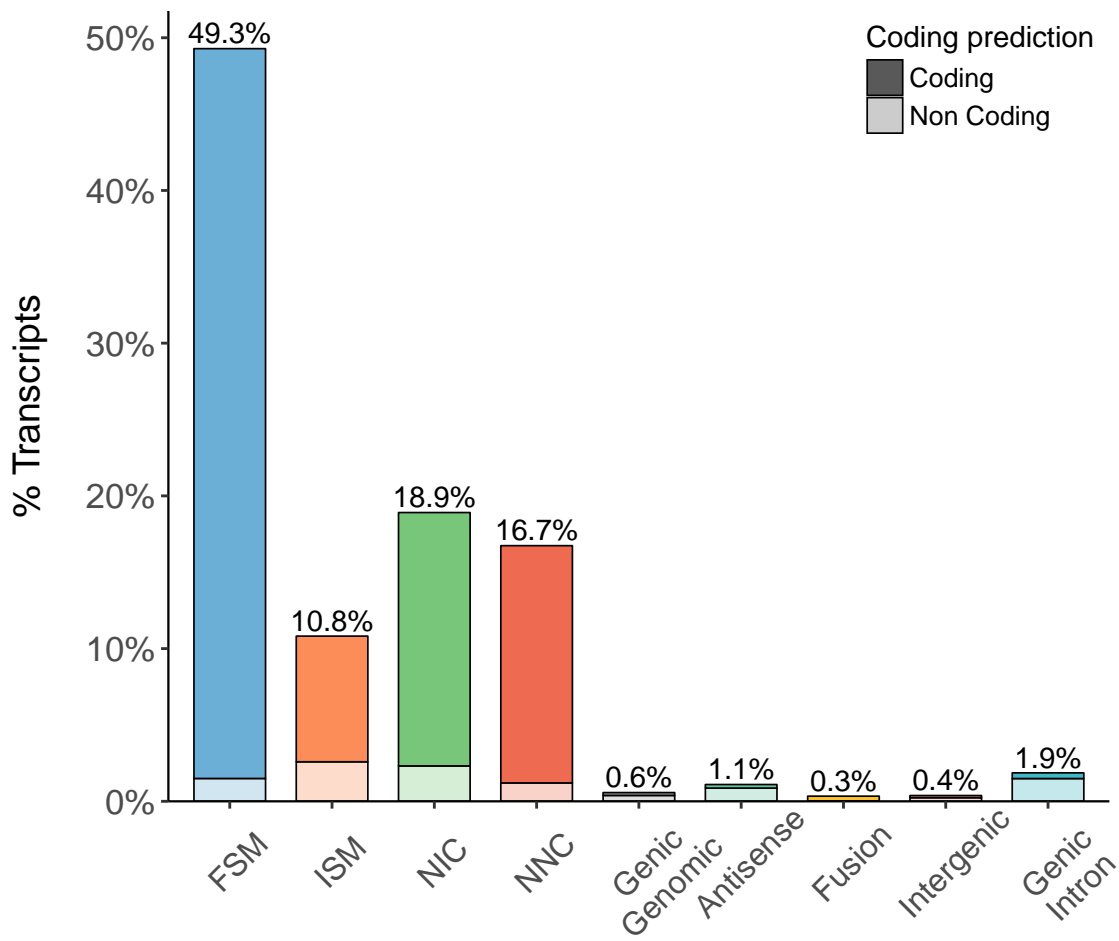
Gene expression by type of gene annotation

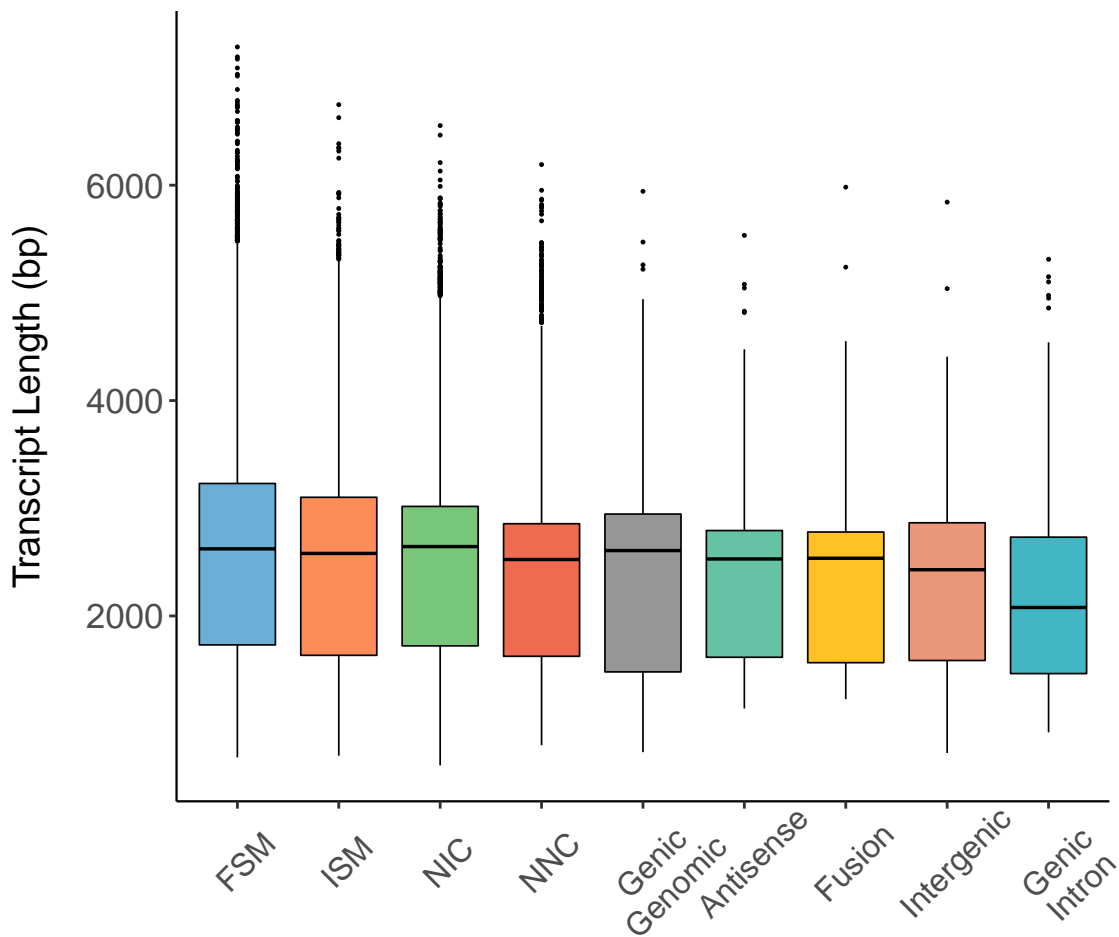Number of FL reads per Gene by type of gene annotation

*Structrual Isoform characterization
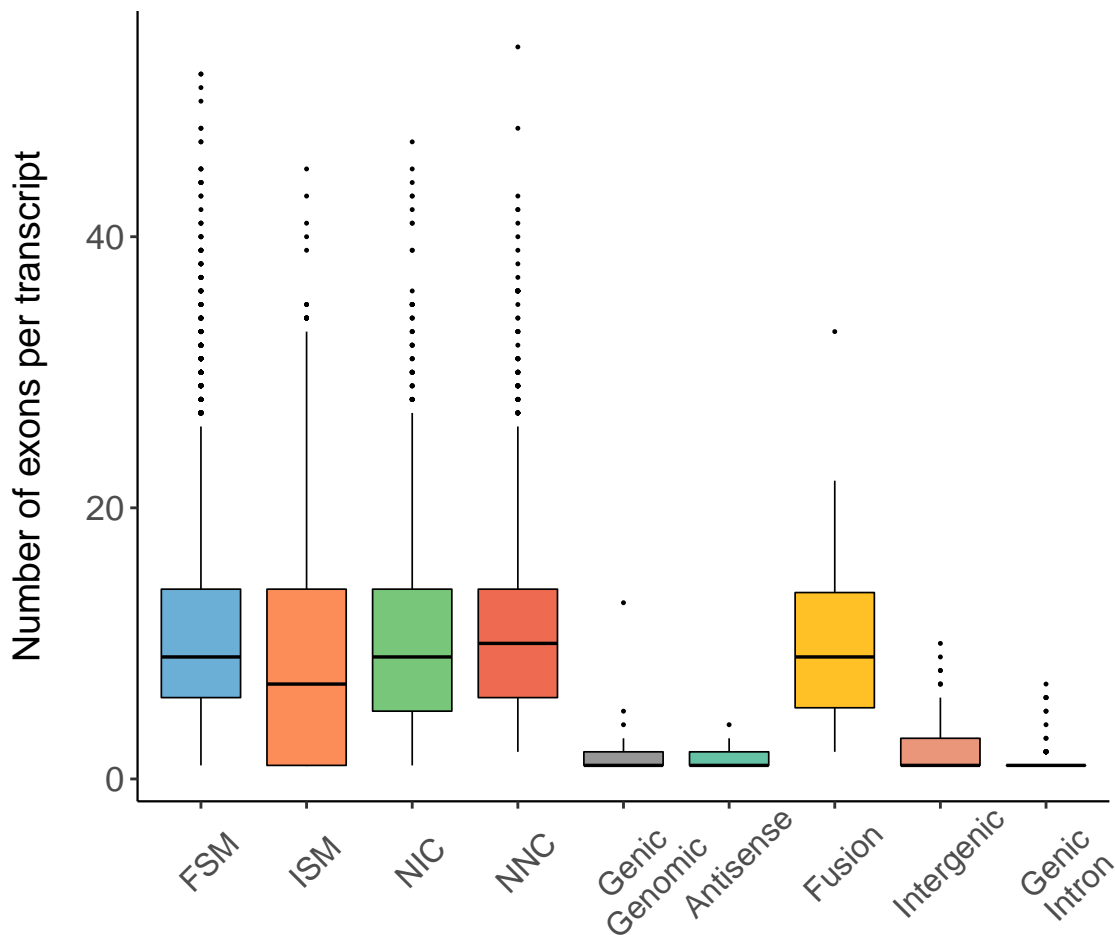based on splice junctions*

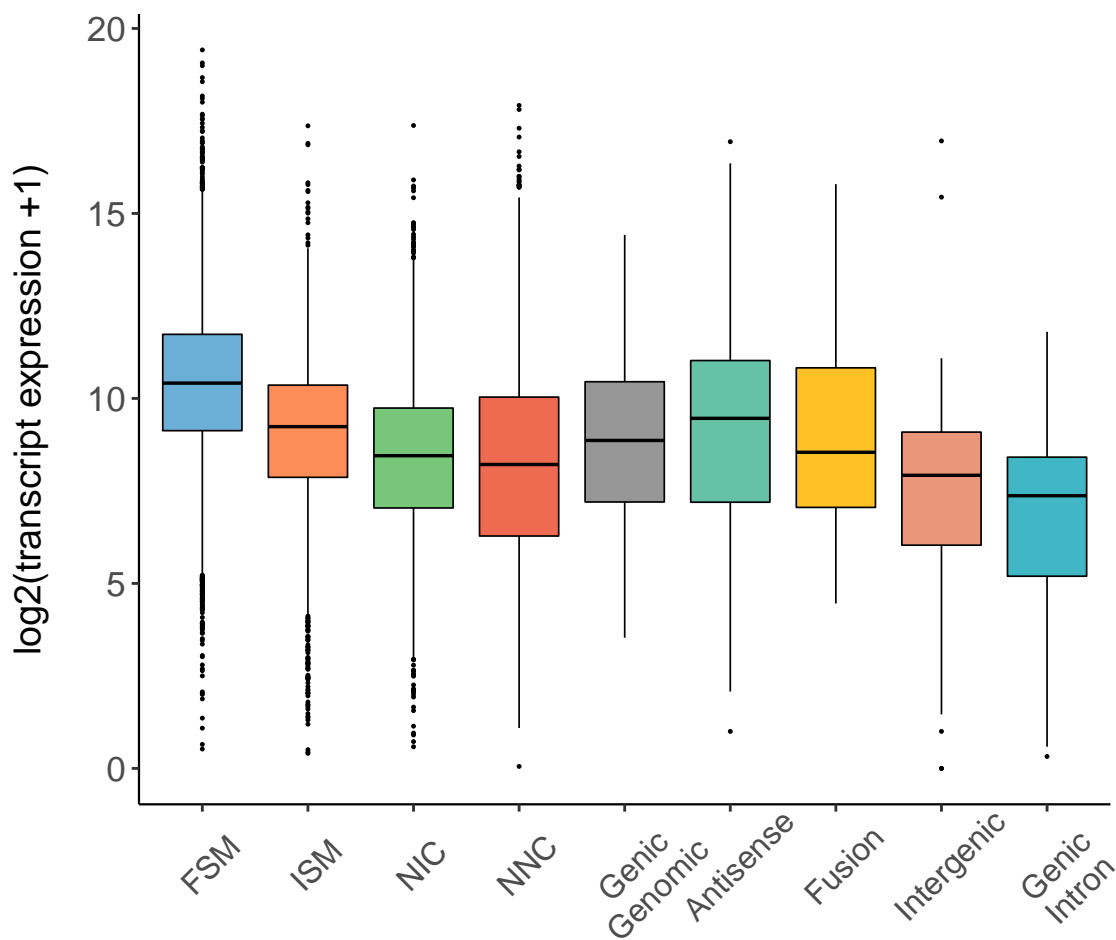Isoform distribution across structural categories

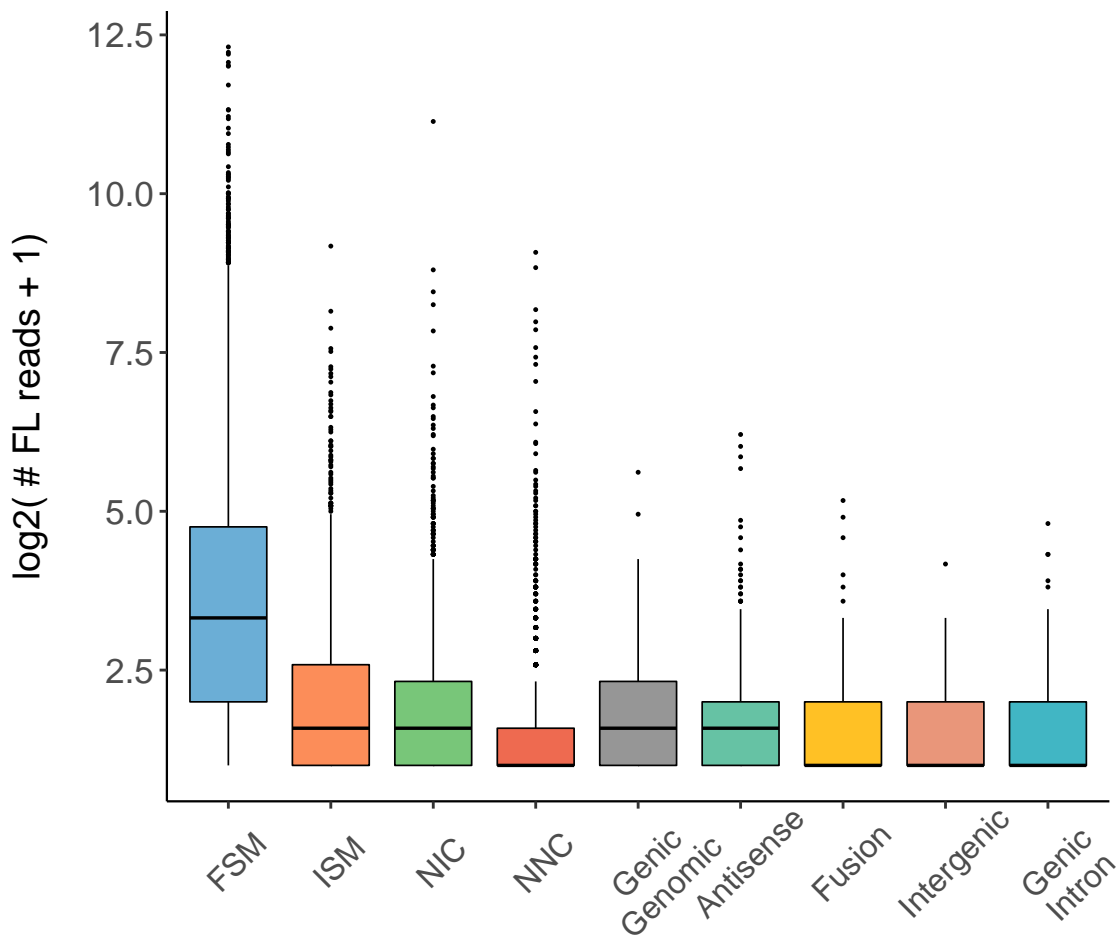Transcript length distribution by structural classification

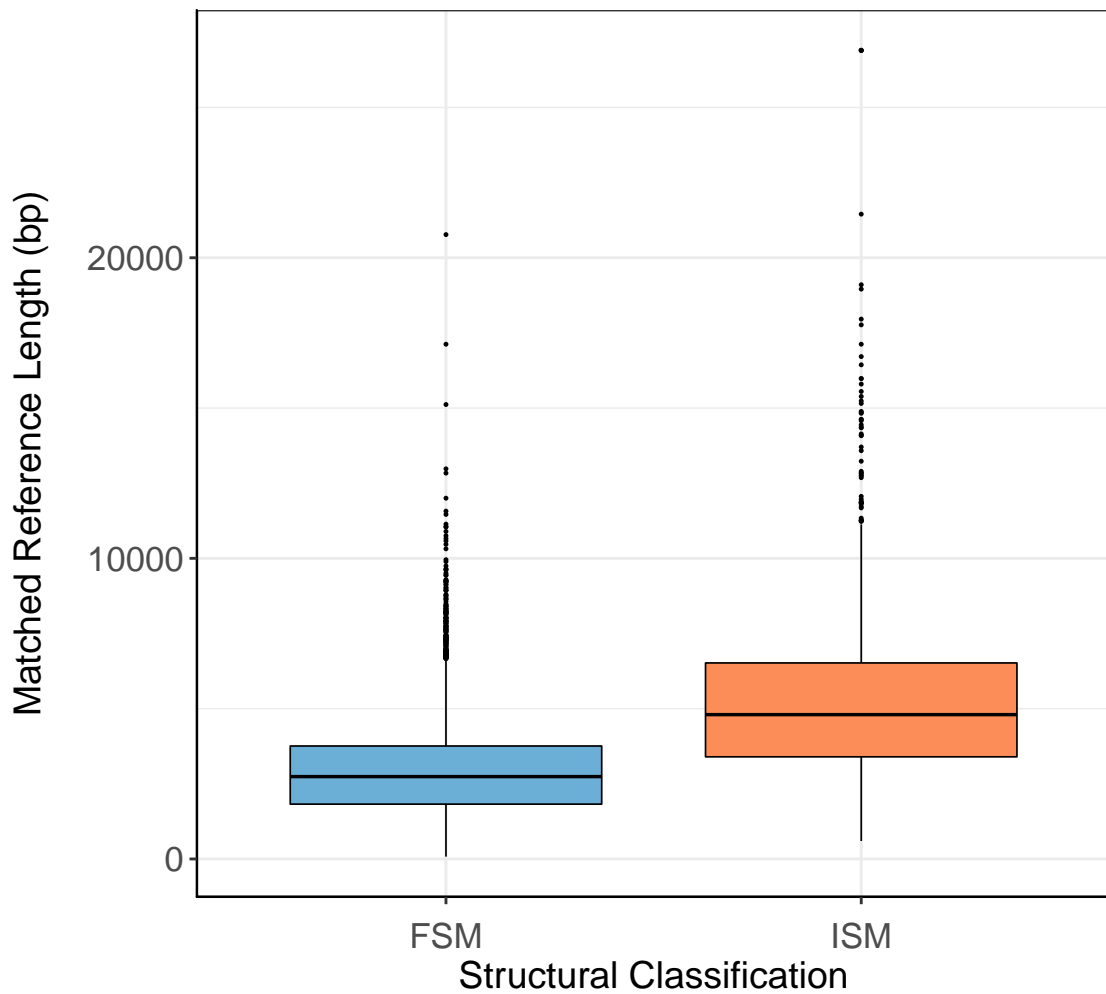Exon number distribution by structural classification
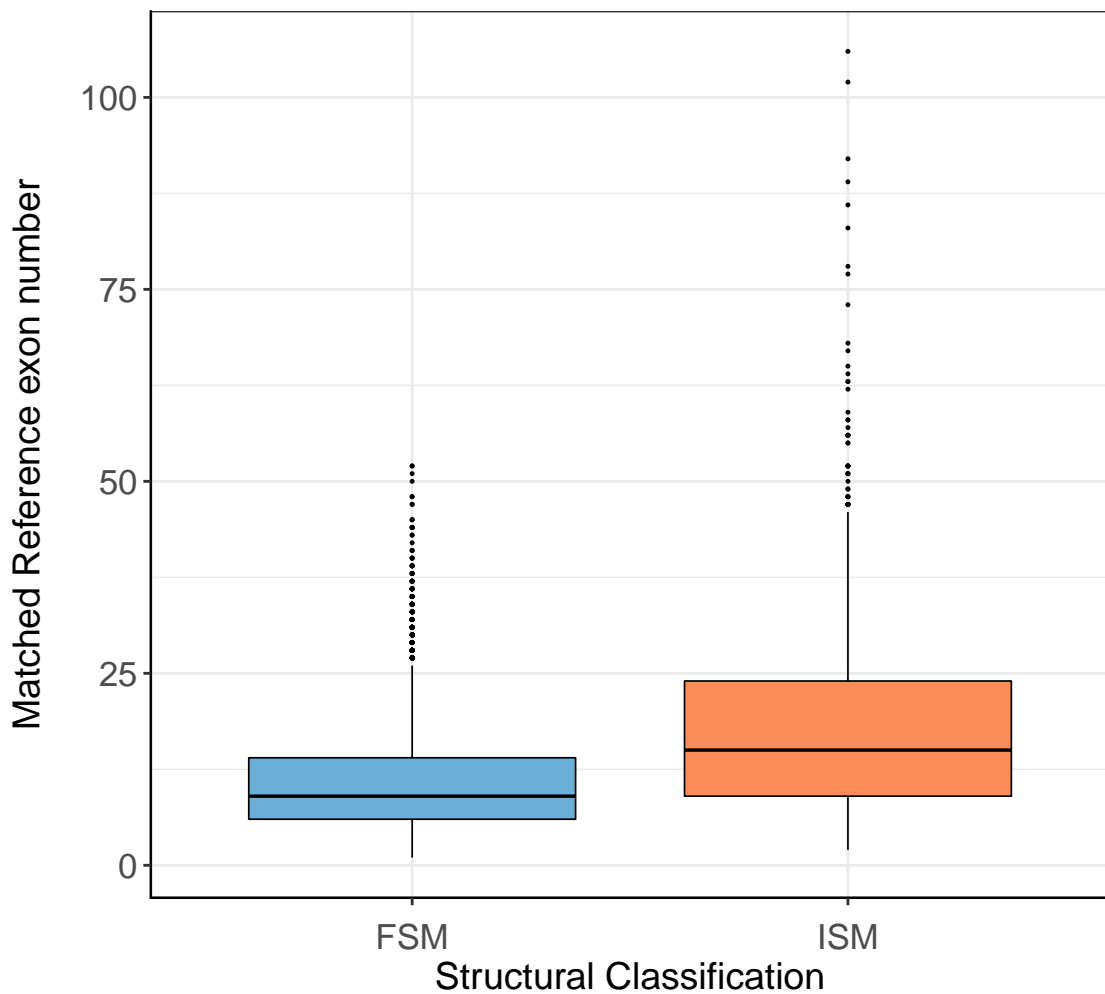
Transcript expression by structural category

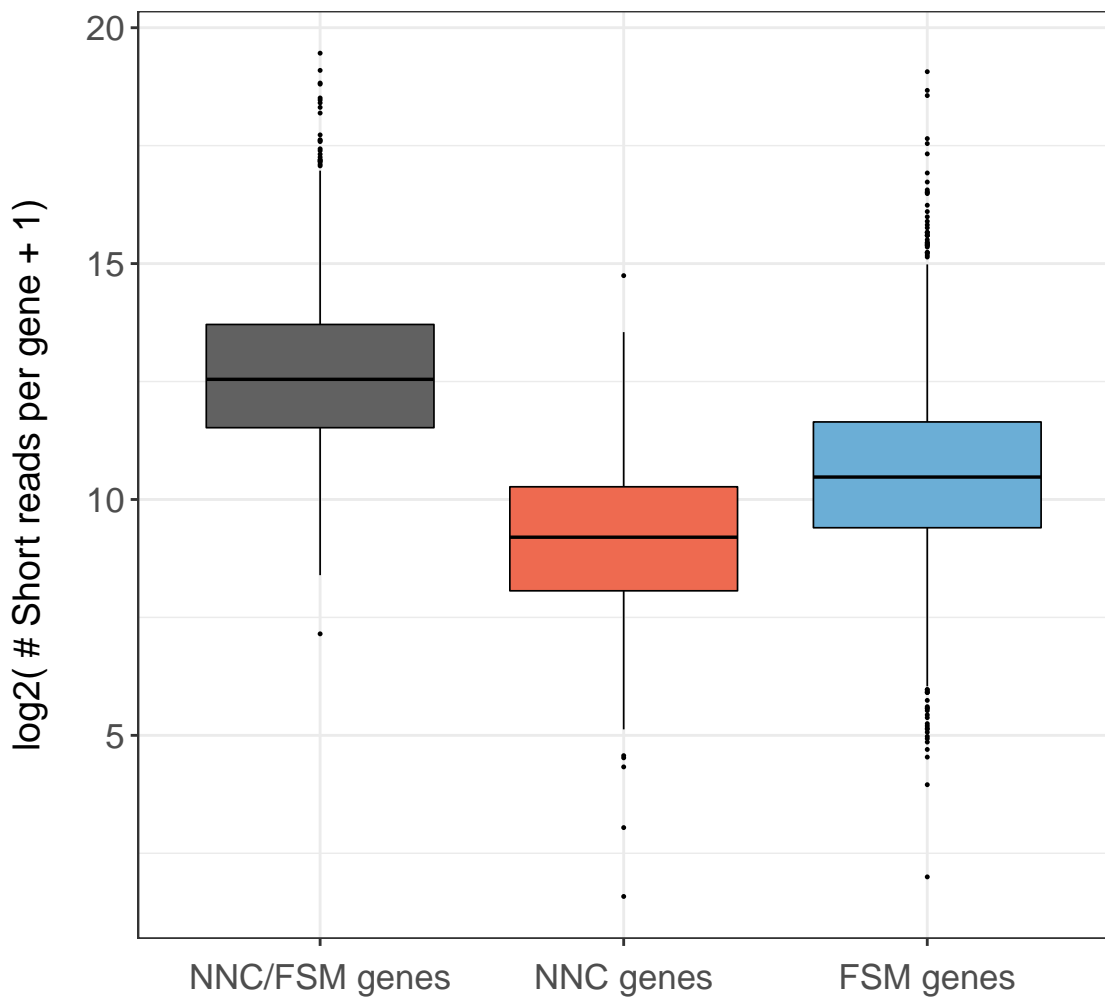Number of FL reads per transcript by structural category

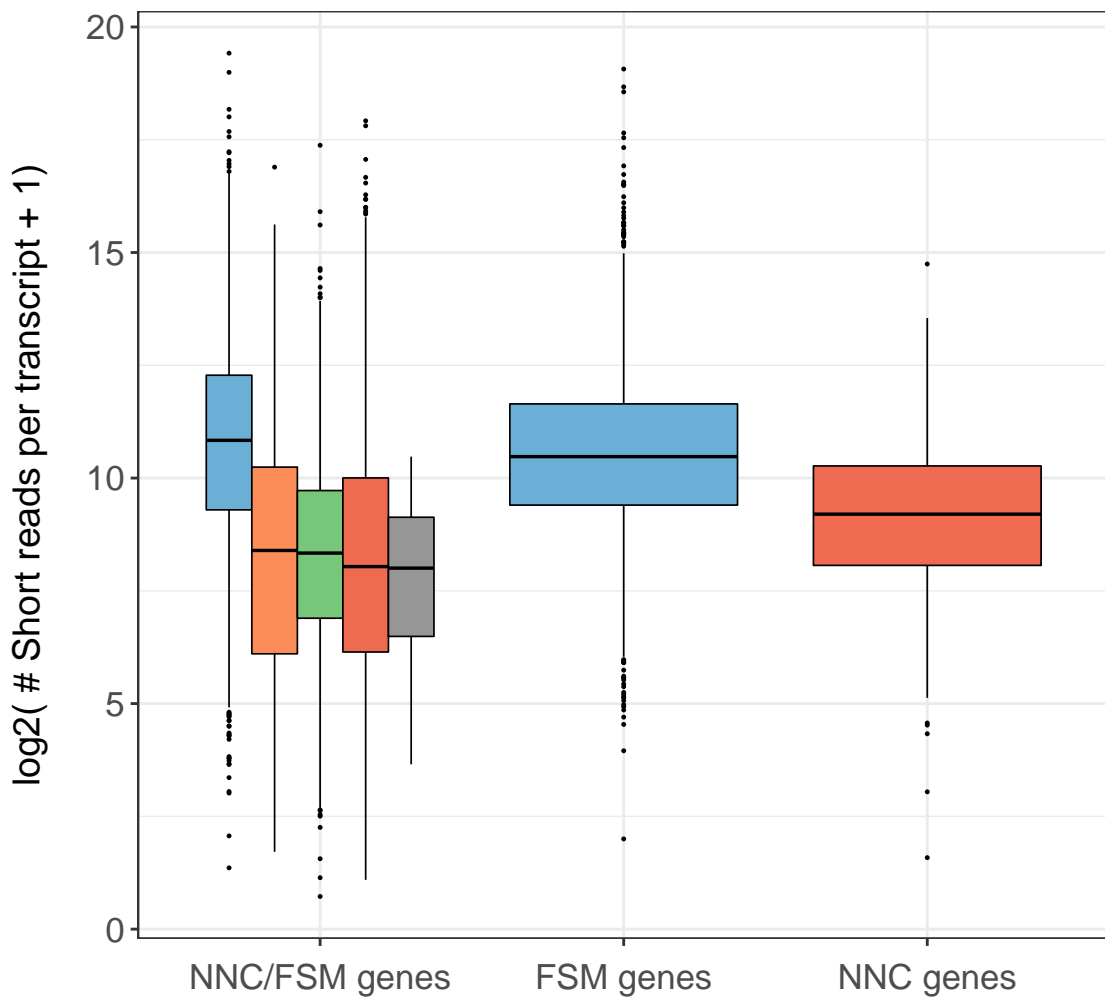Length distribution of matched reference transcripts

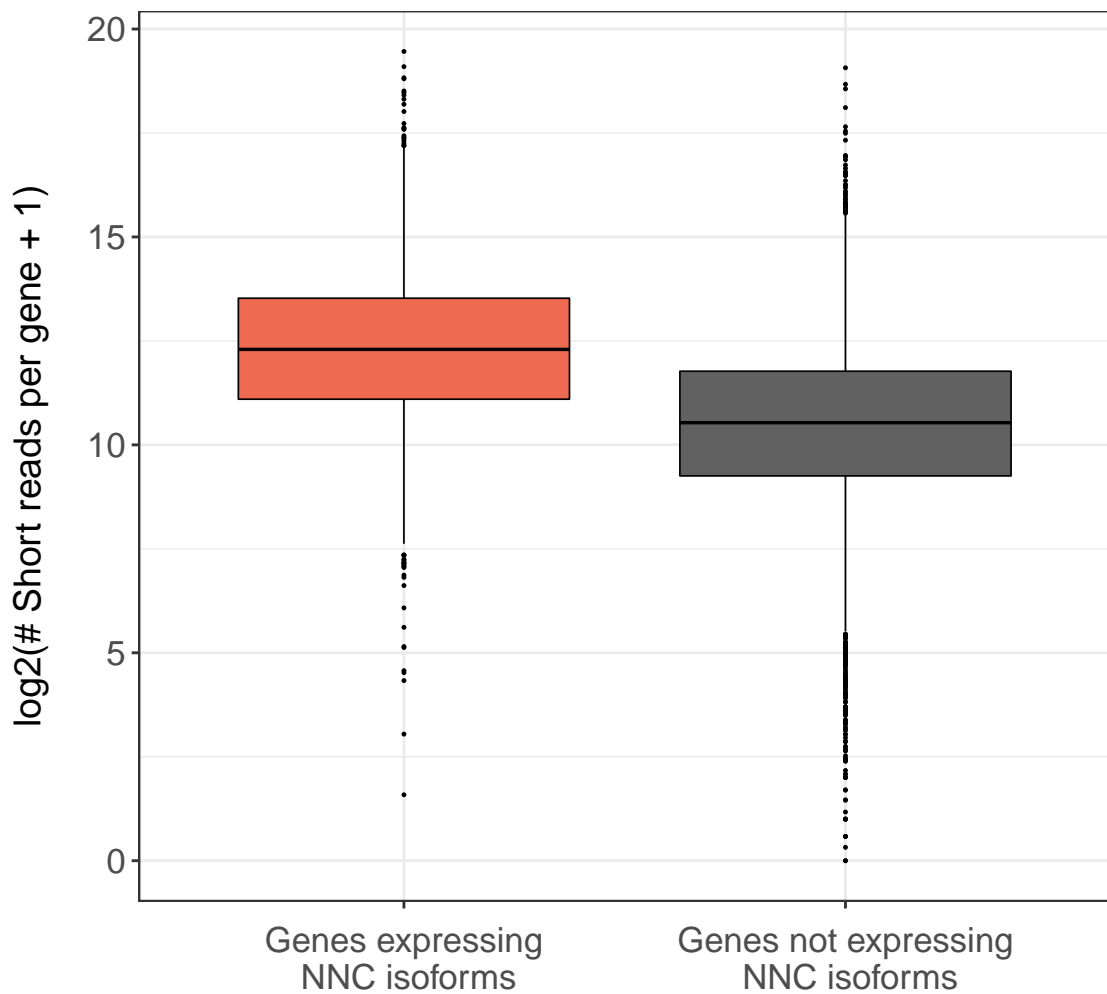Exon Number distribution of matched reference transcripts

Gene Expression level in NNC/FSM containing genes

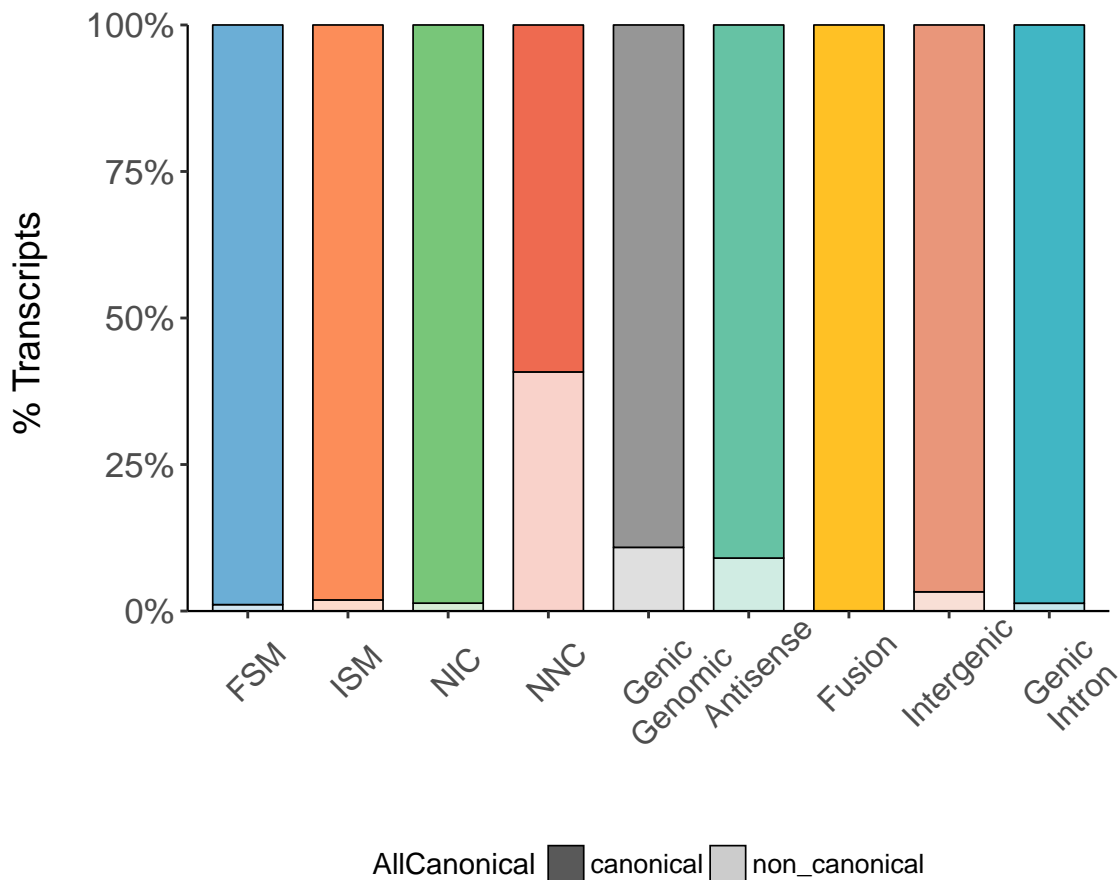Transcript Expression level in NNC/FSM containing genes

Gene expression levels between NNC and not NNC containing gene
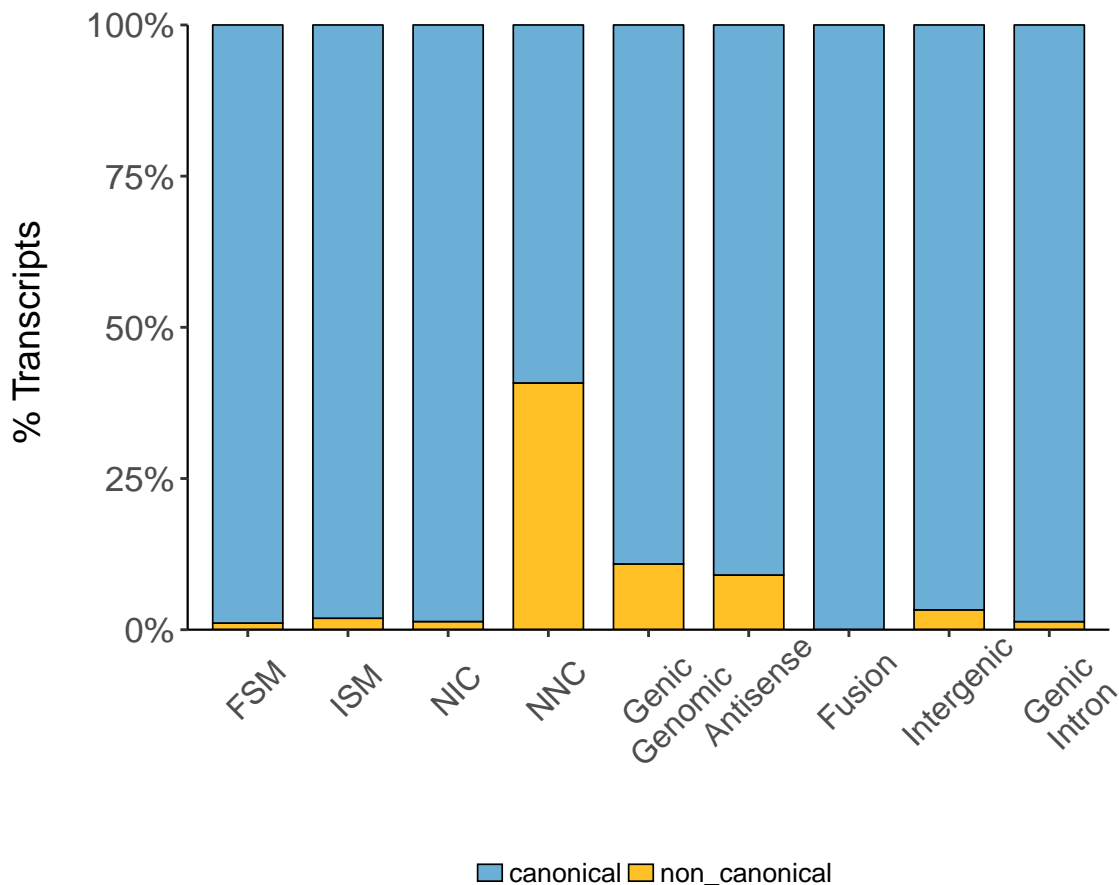
Splice junction characterization

Distribution of transcripts by splice junction category

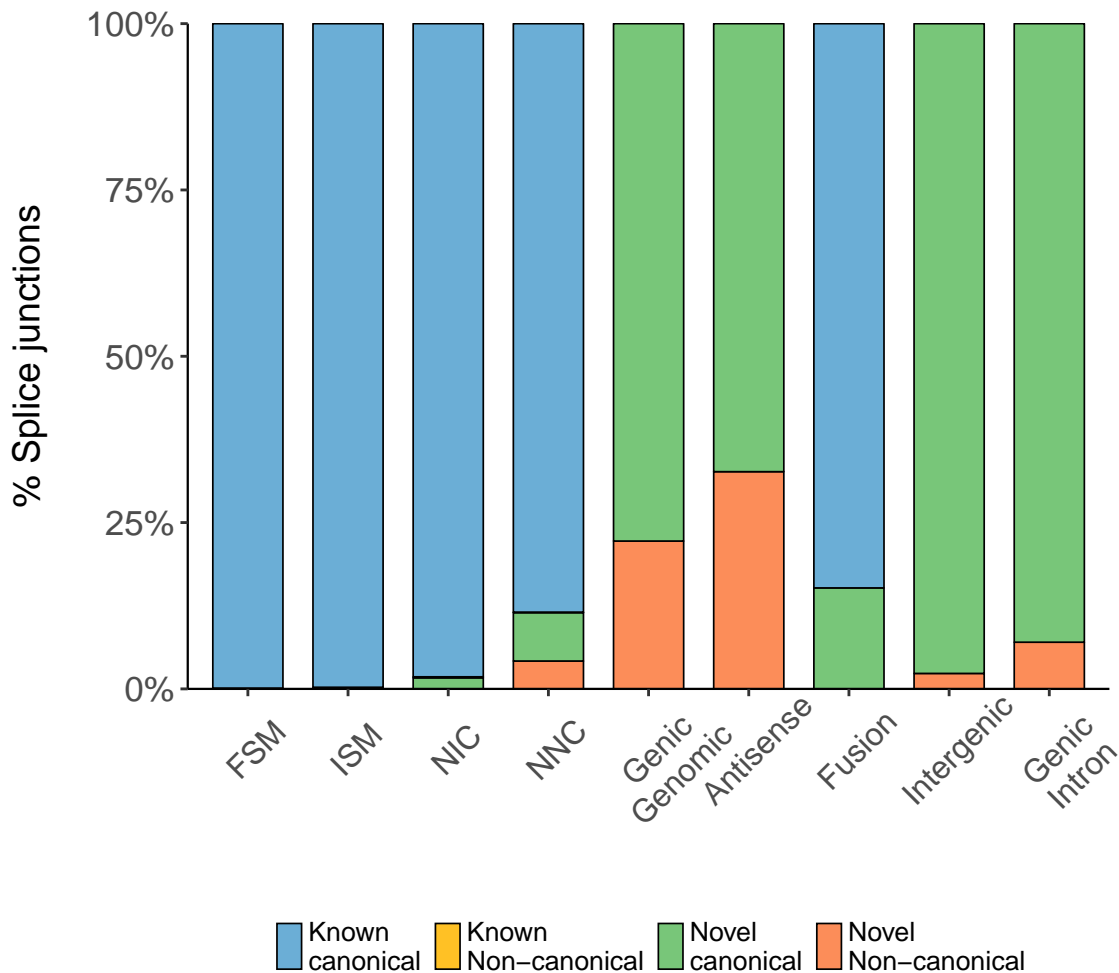Non canonical transcripts are those with at least one non−canonical junction

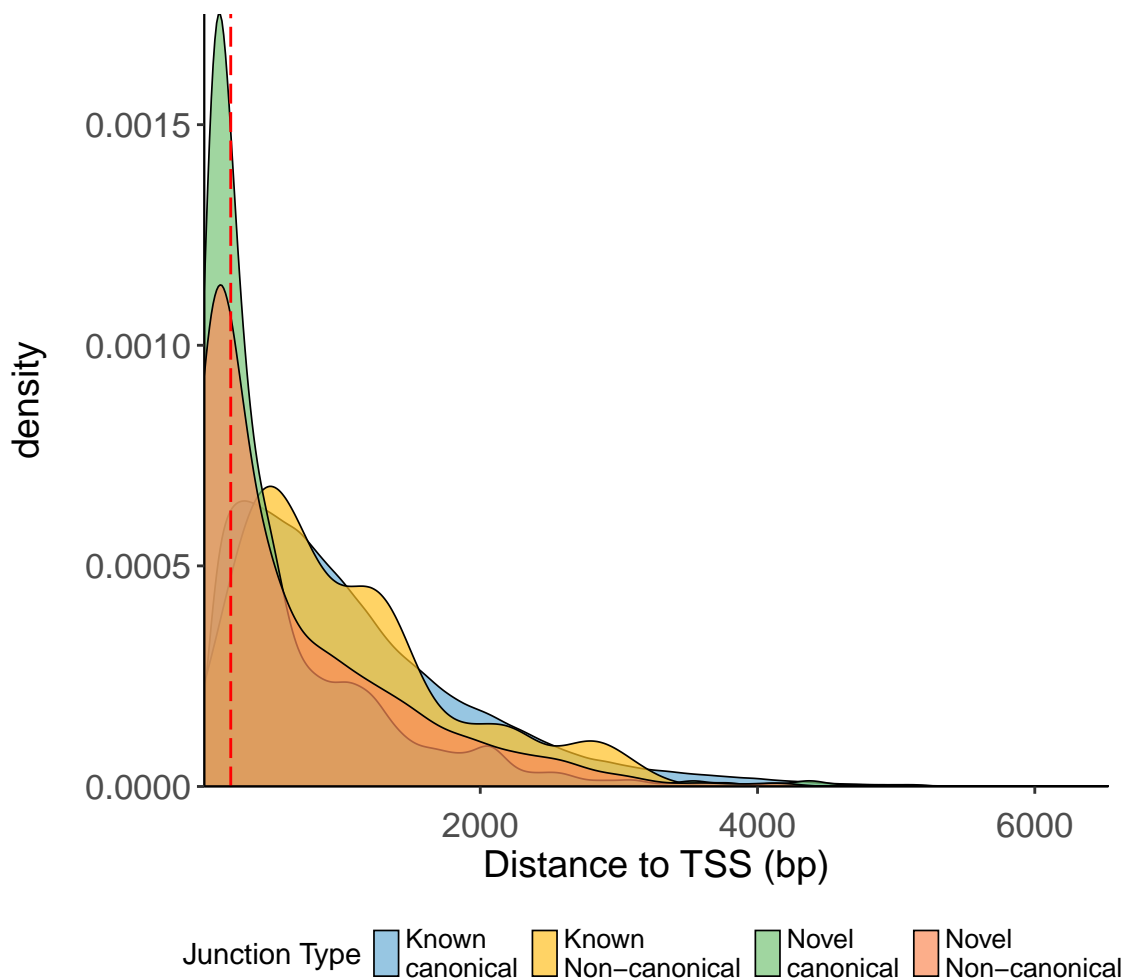Distribution of transcripts by splice junction category

Non canonical transcripts are those with at least one non−canonical junction
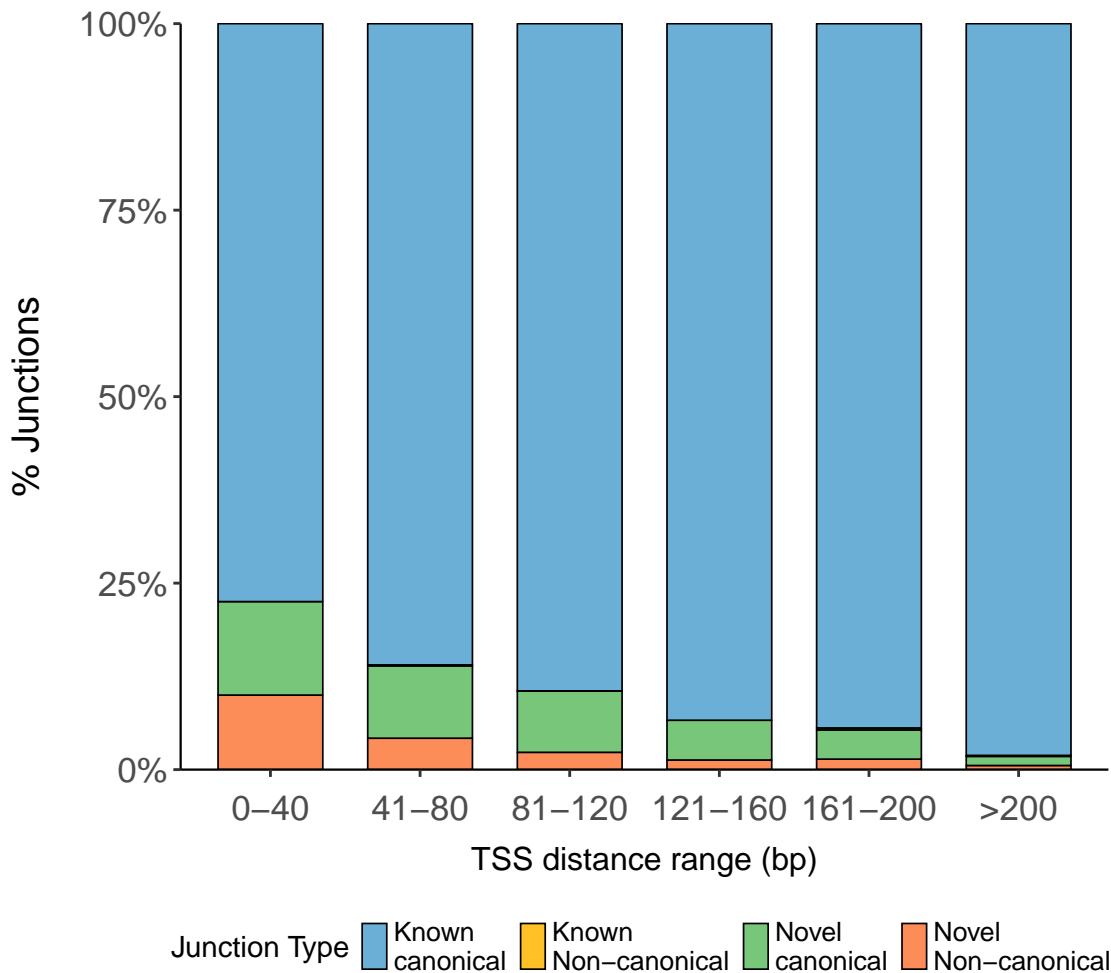
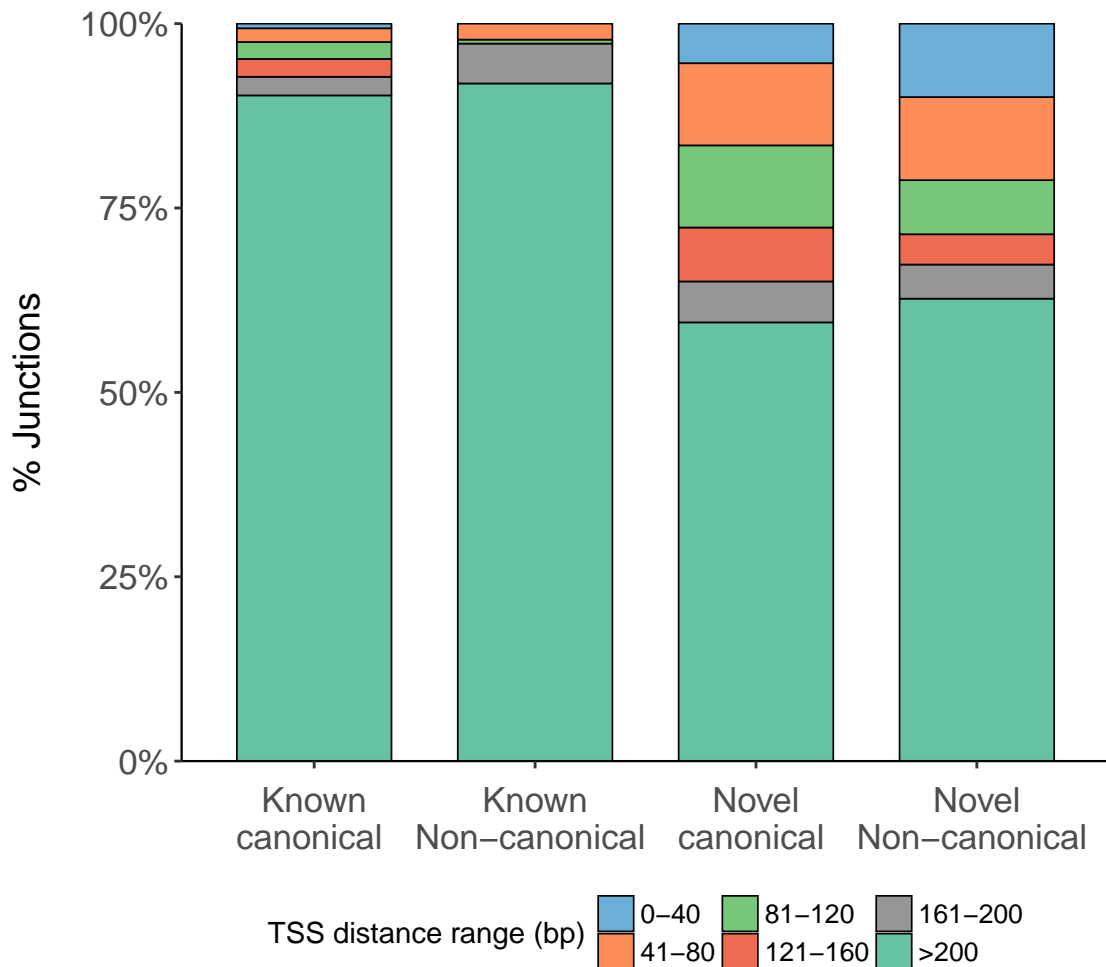Distribution of SJ type among structural classification

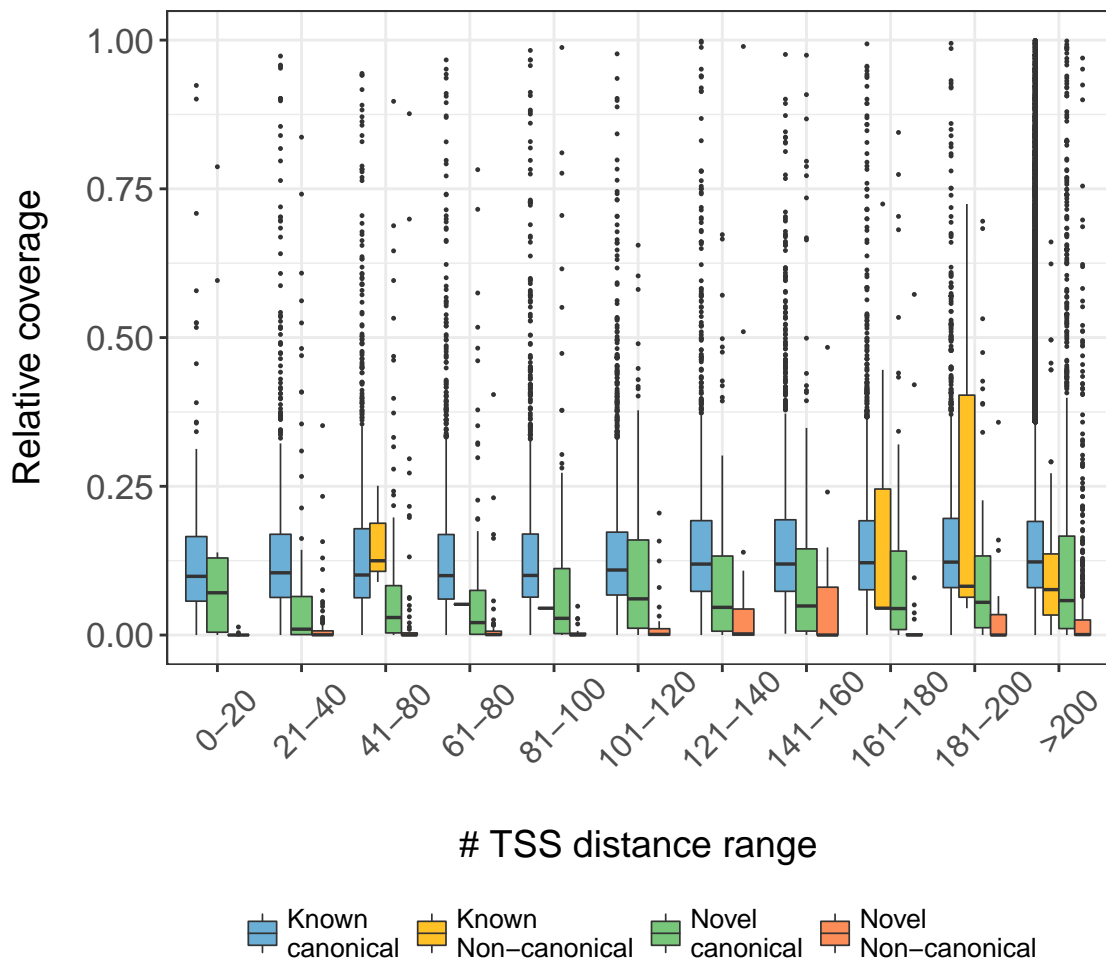Distribution of splice junctions distance to TSS

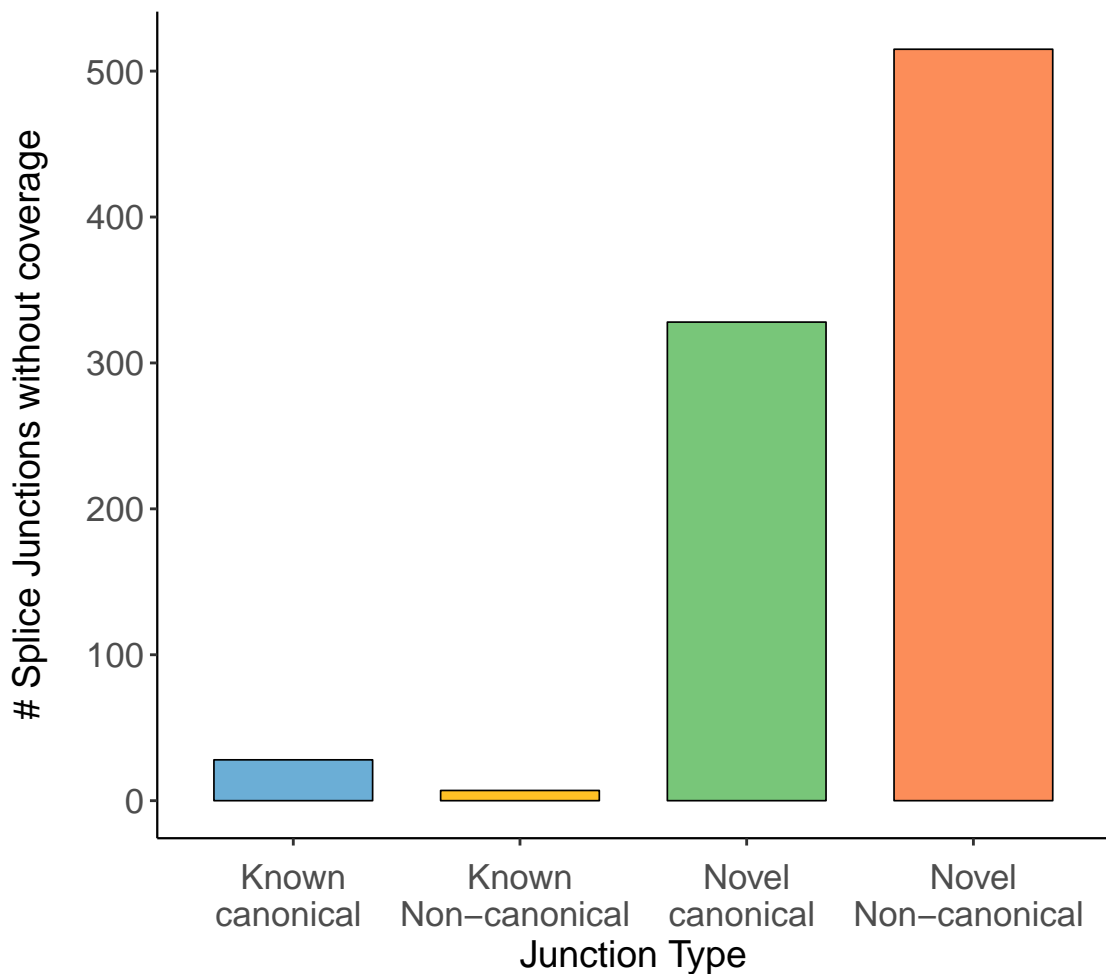Splice junction distance to TSS across junction type

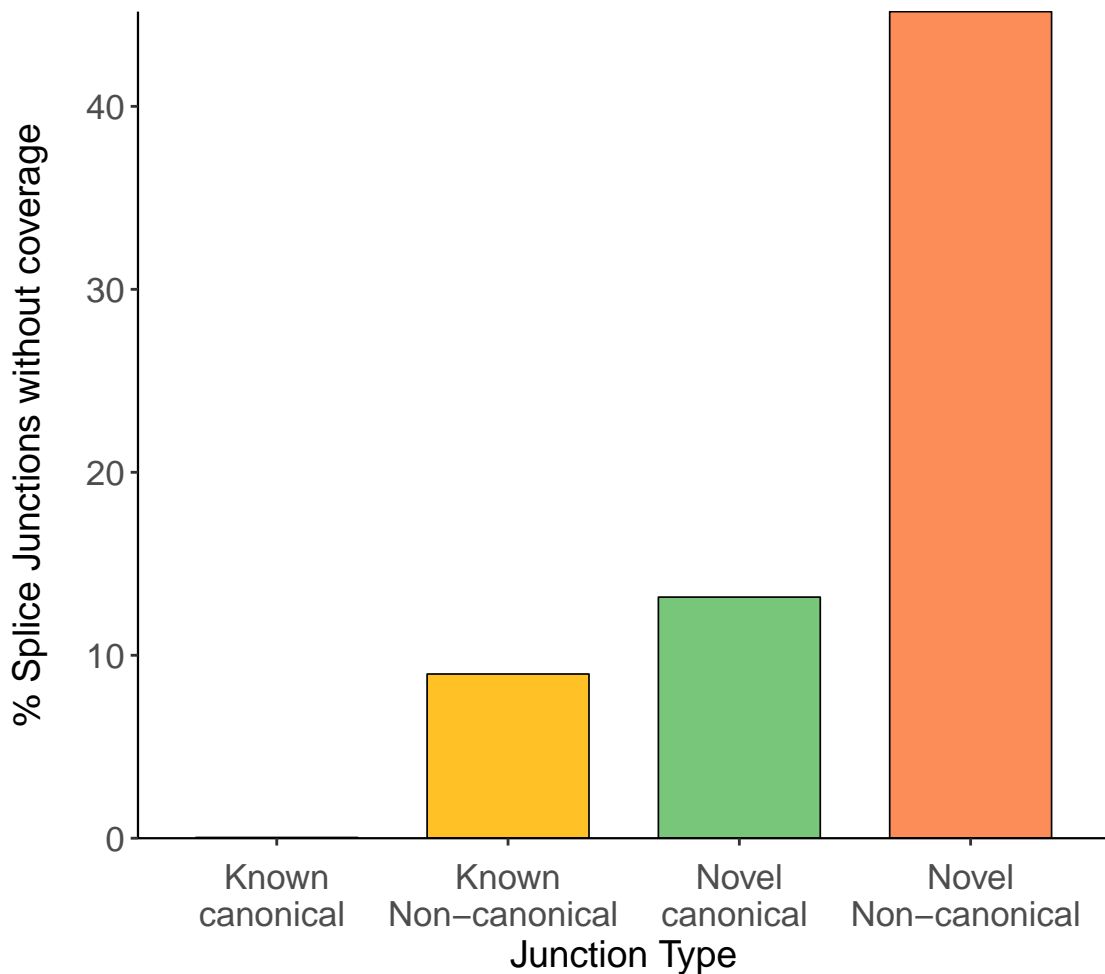Splice junction distance to TSS across junction type
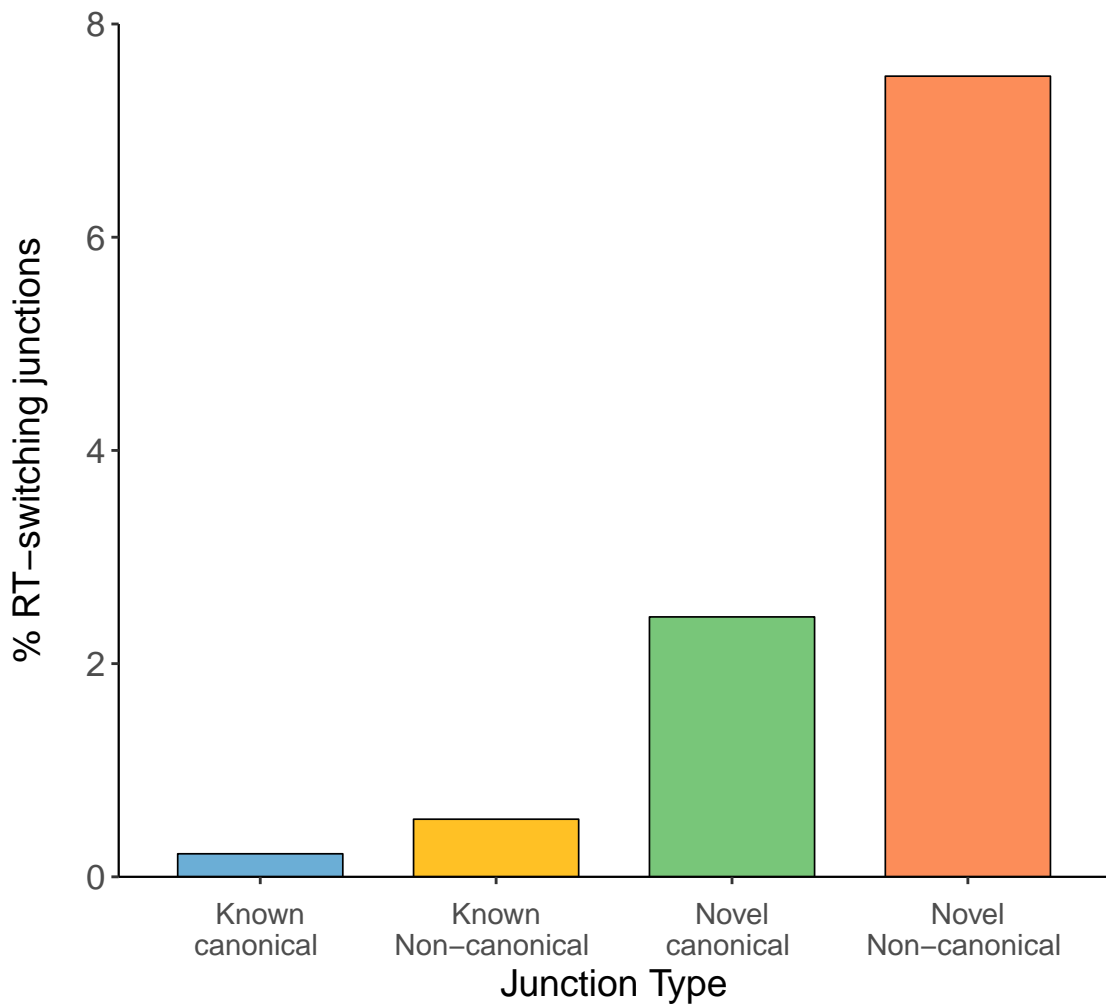
Relative Coverage of junctions

Splice junctions without short−read coverage (unique junctions)
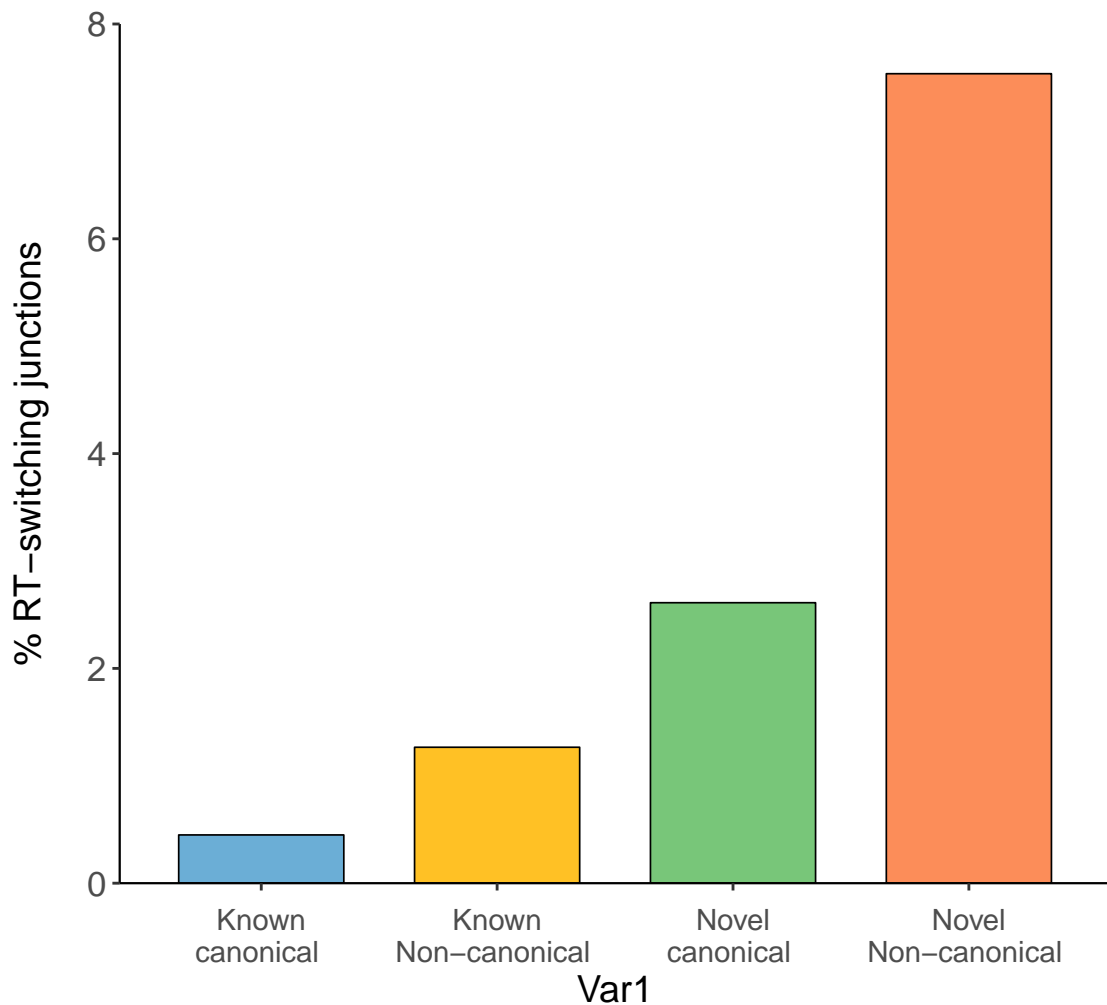
Splice junctions without short−read coverage (unique junctions)
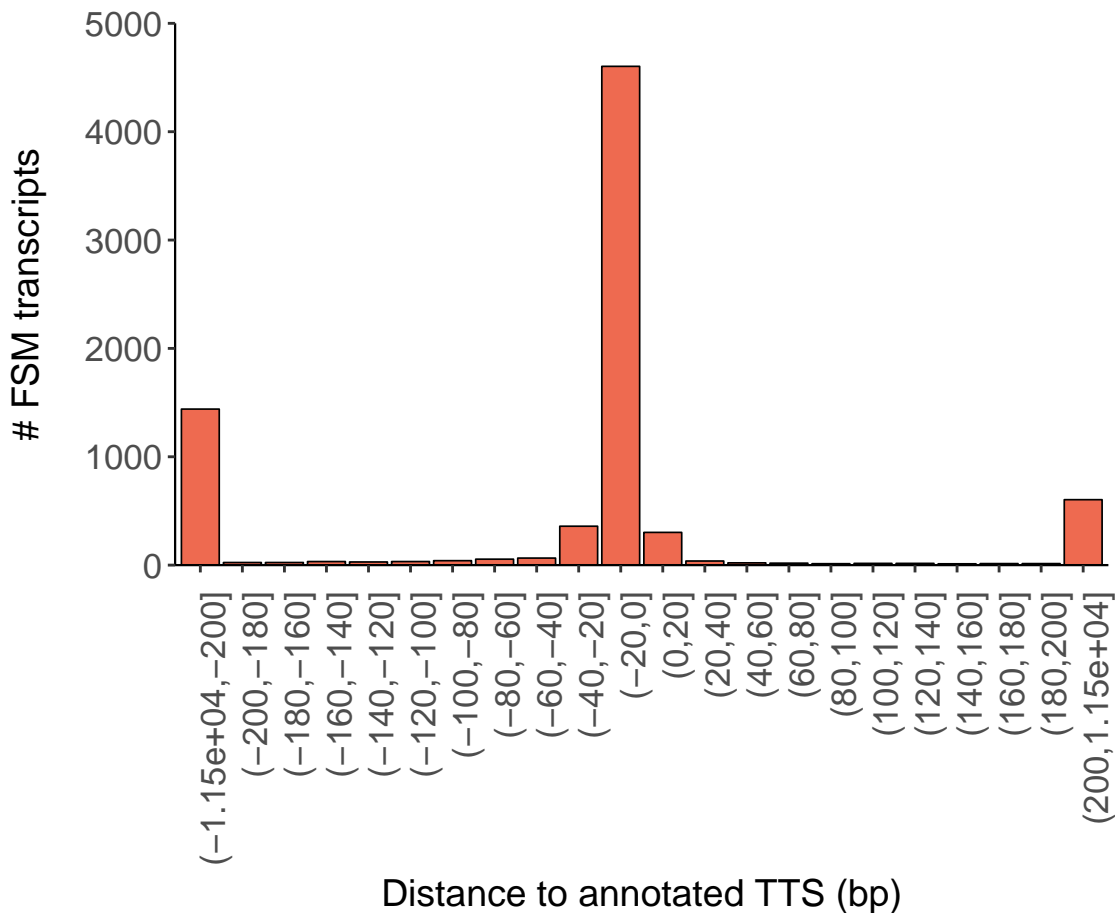
RT−switching by splice junction category

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
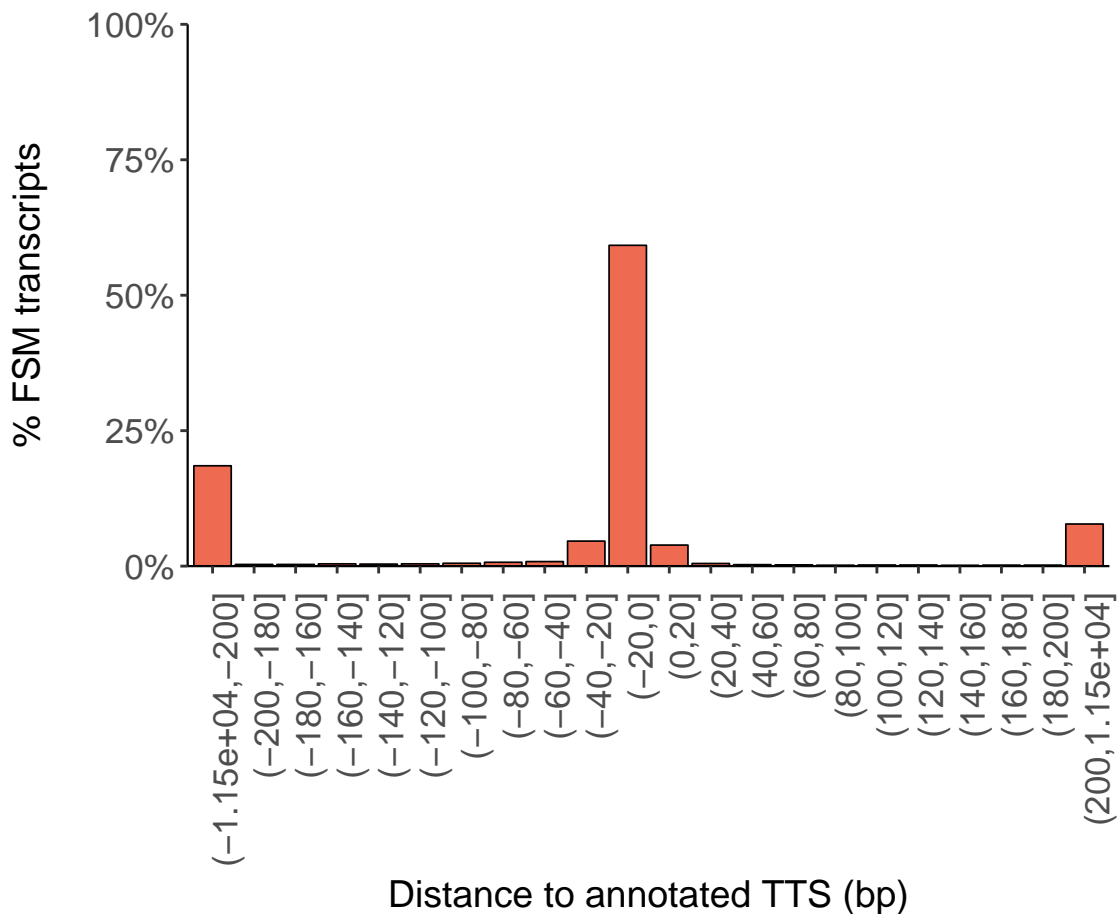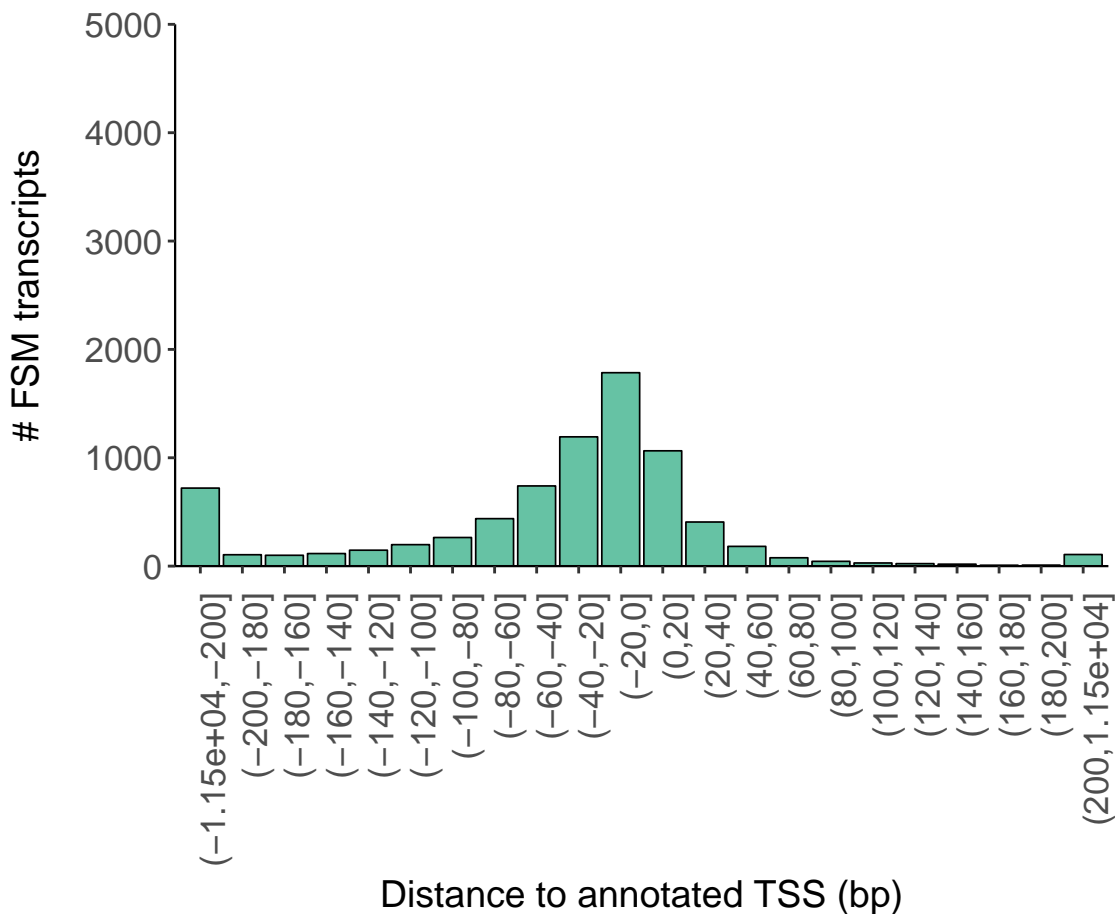
Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is downstream annotated TTS
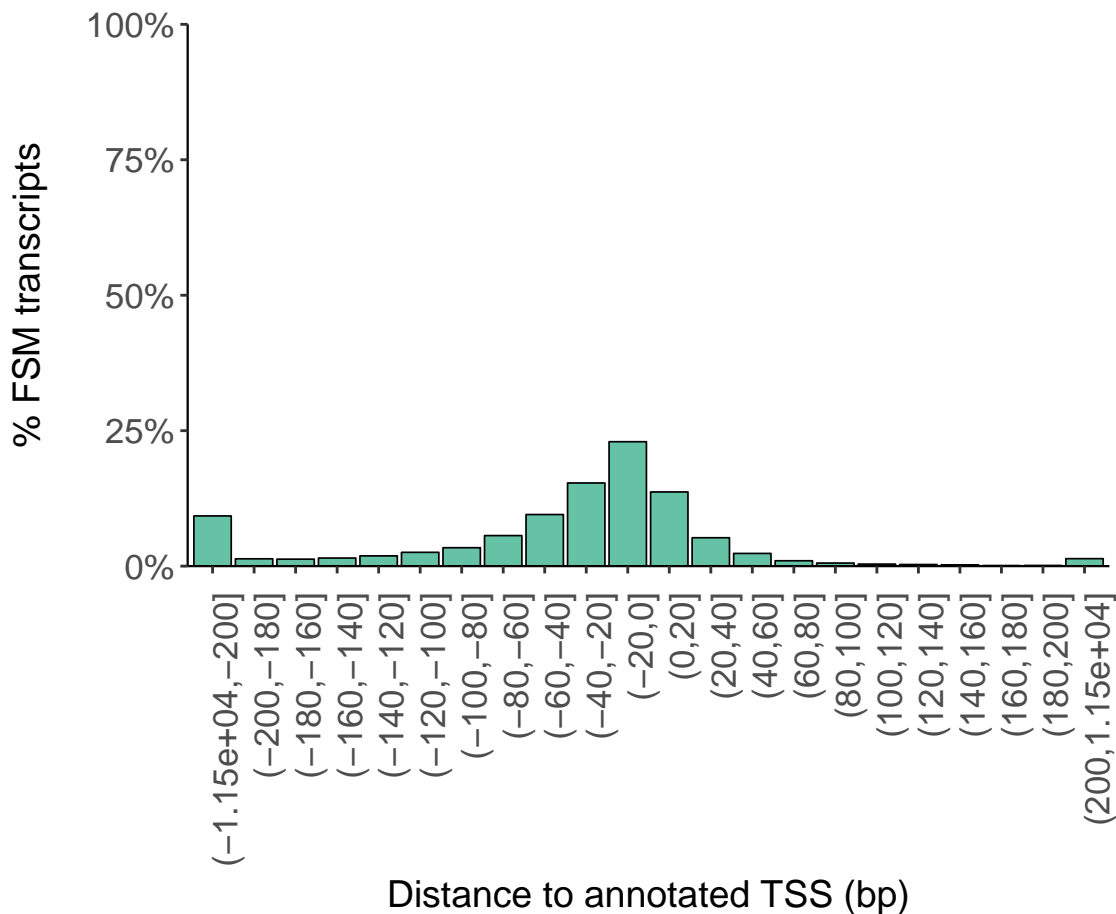
Distance distribution from sequenced to annotated TSS

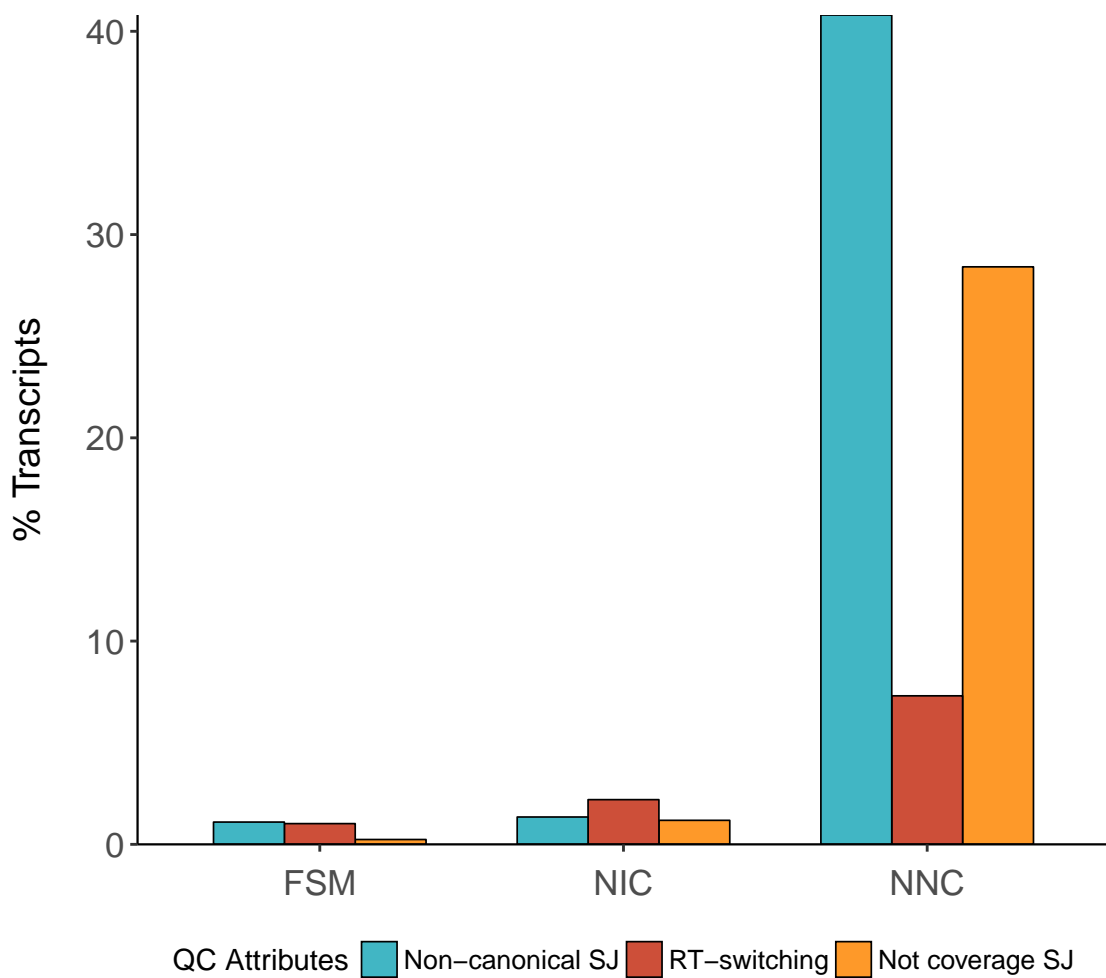Negative values indicate that the sequenced TSS is upstream annotated TSS

Distance distribution from sequenced to annotated TSS

Negative values indicate that the sequenced TSS is upsteam 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