

SQANTI report

Genes: 3280

Isoforms: 8746

Gene classification

category	# genes
Annotated Genes	2184
Novel Genes	1096

SJ classification

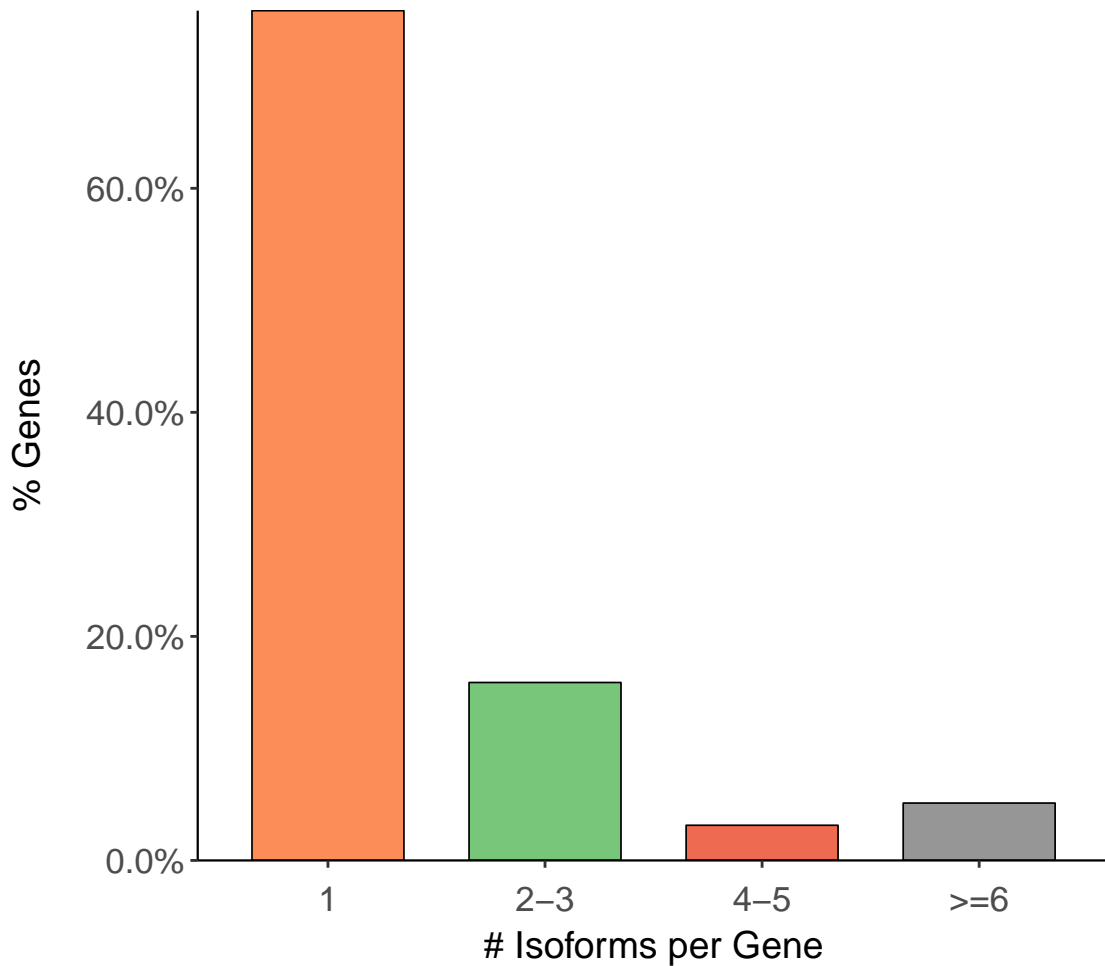
category	# SJ
Known canonical	10006
Known Non-canonical	3
Novel canonical	421
Novel Non-canonical	694

*Characterization of transcripts
based on splice junctions*

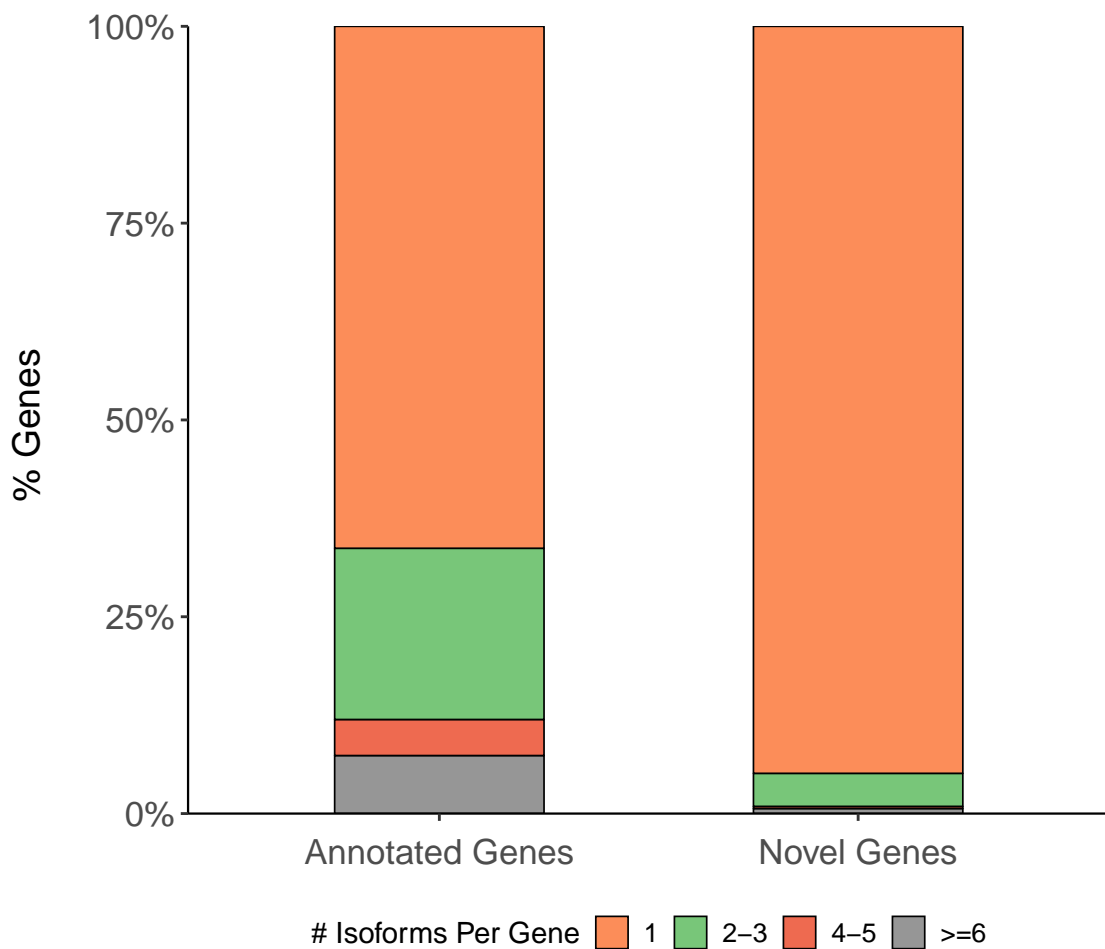
category	# isoforms
FSM	4469
ISM	1752
Genic Intron	899
NNC	686
NIC	495
Antisense	273
Genic Genomic	78
Intergenic	65
Fusion	29

Gene characterization

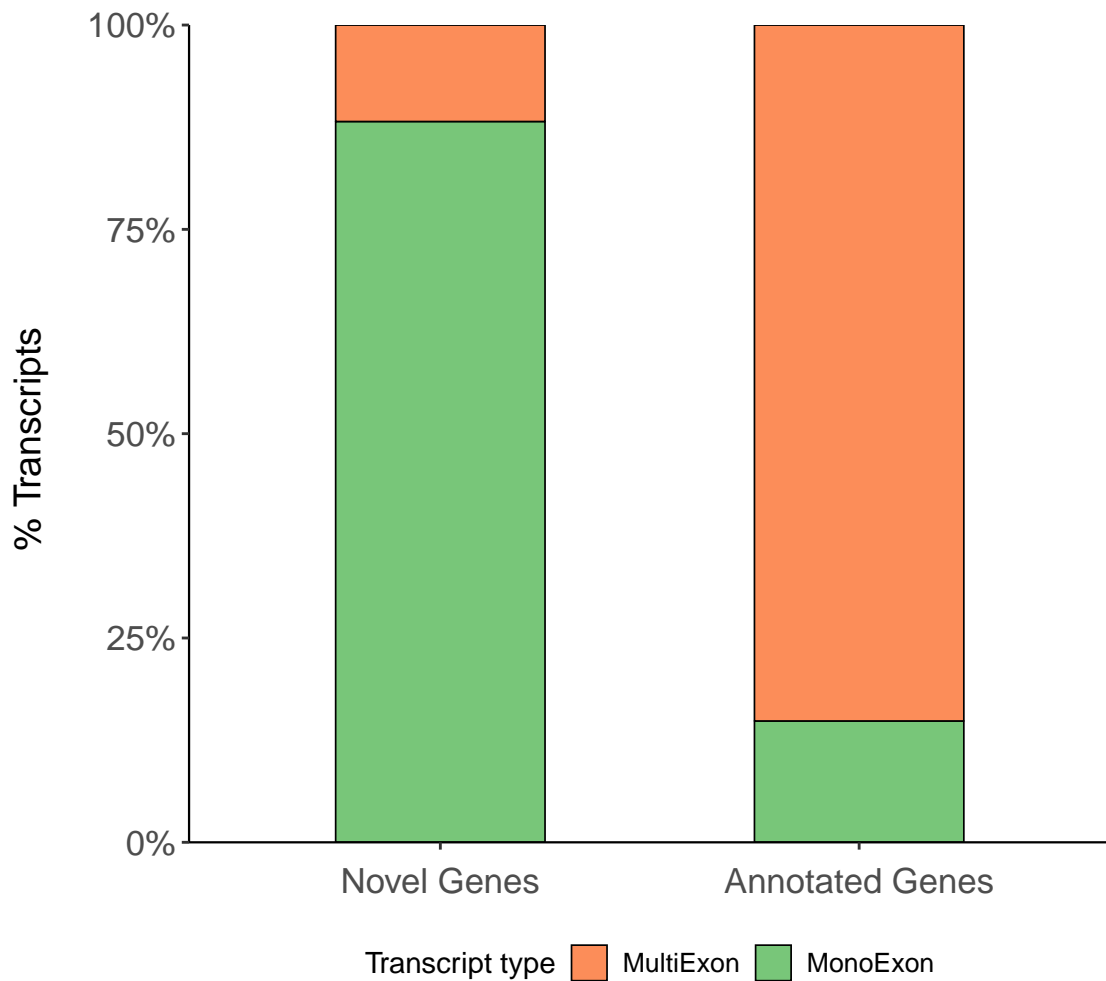
Distribution of isoforms per gene



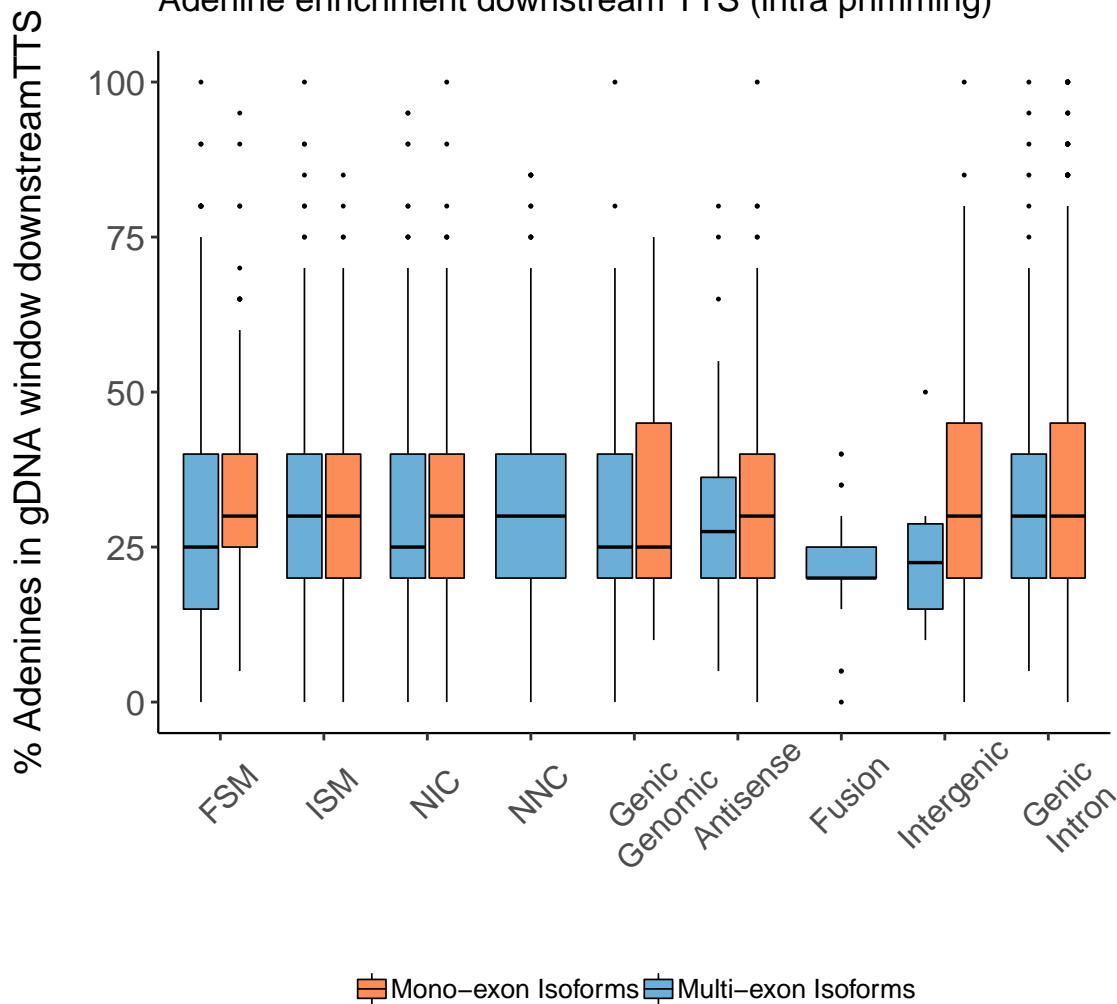
Distribution of number of isoforms



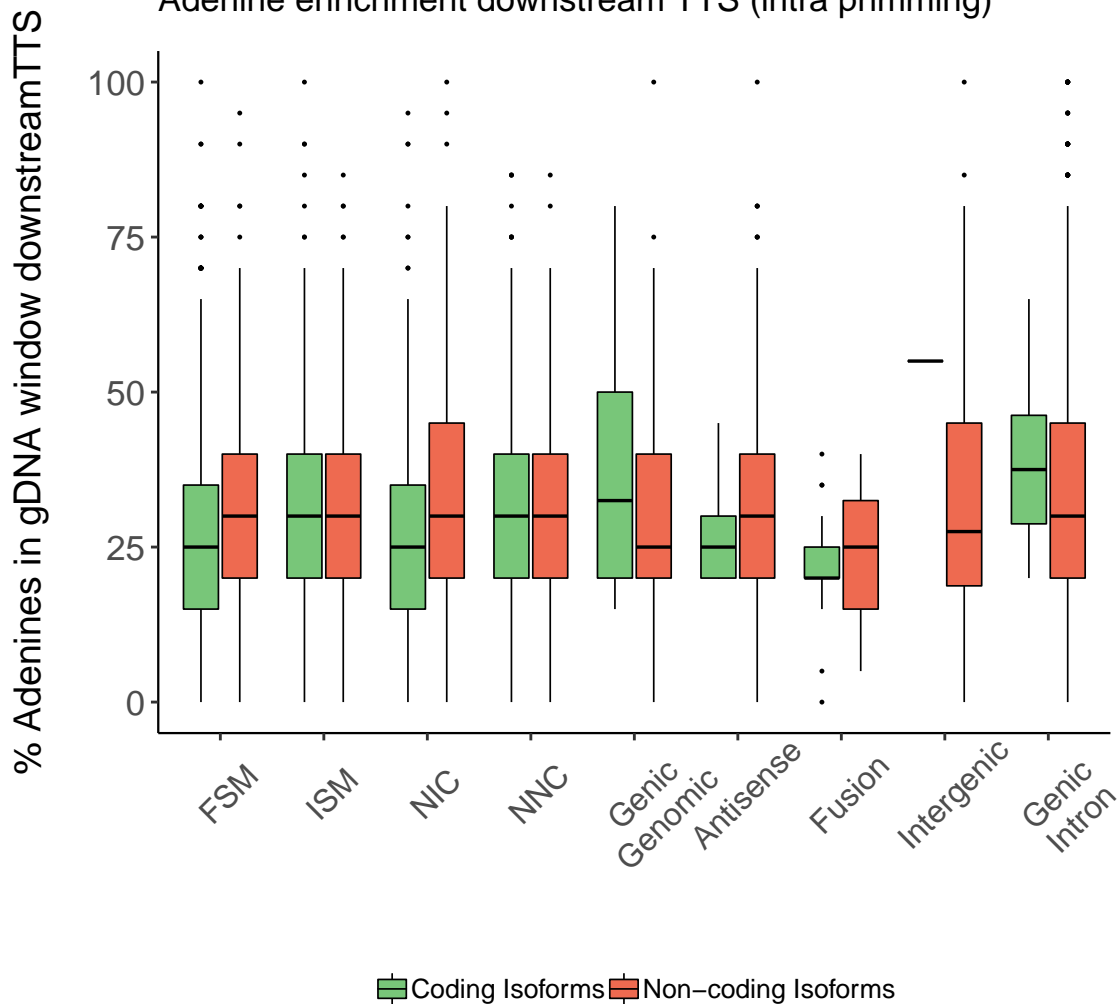
Distribution of mono/multi exon transcripts



Adenine enrichment downstream TTS (intra primming)

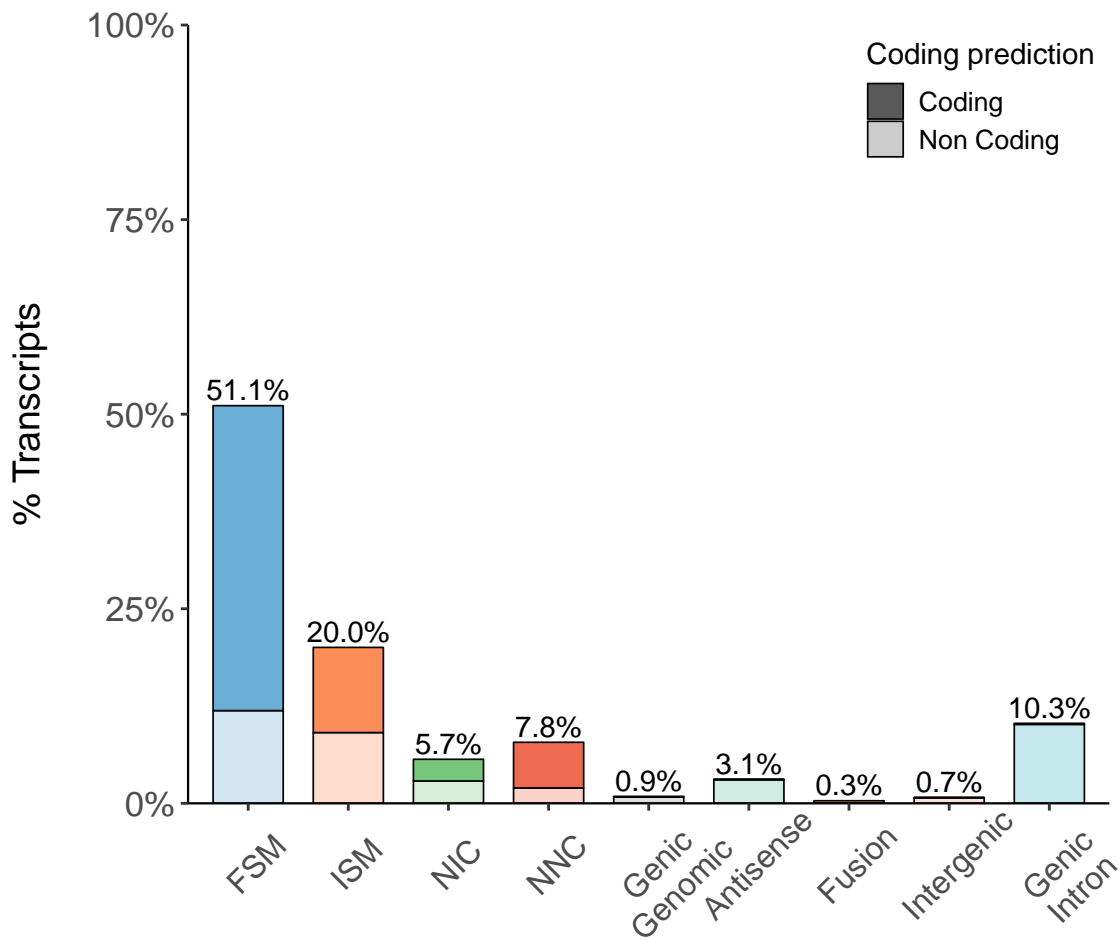


Adenine enrichment downstream TTS (intra primming)

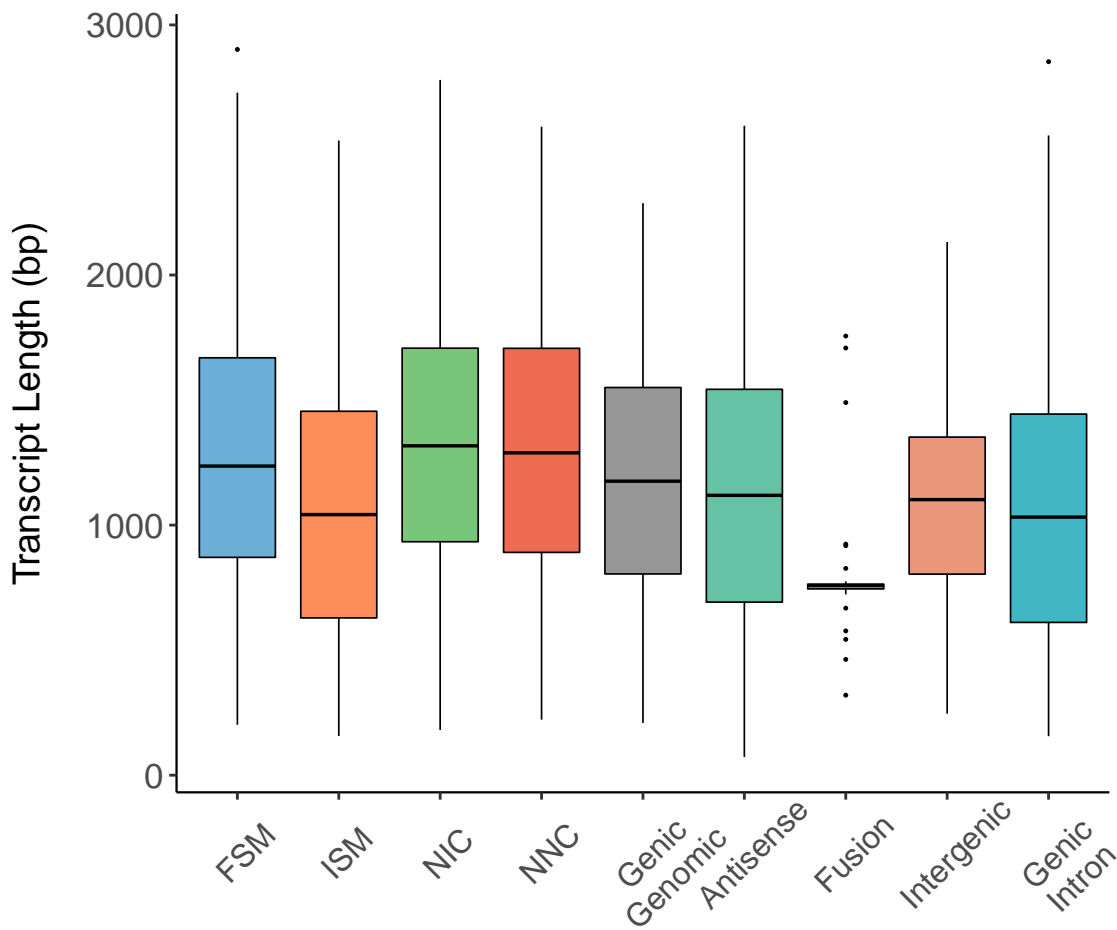


*Structrual Isoform characterization
based on splice junctions*

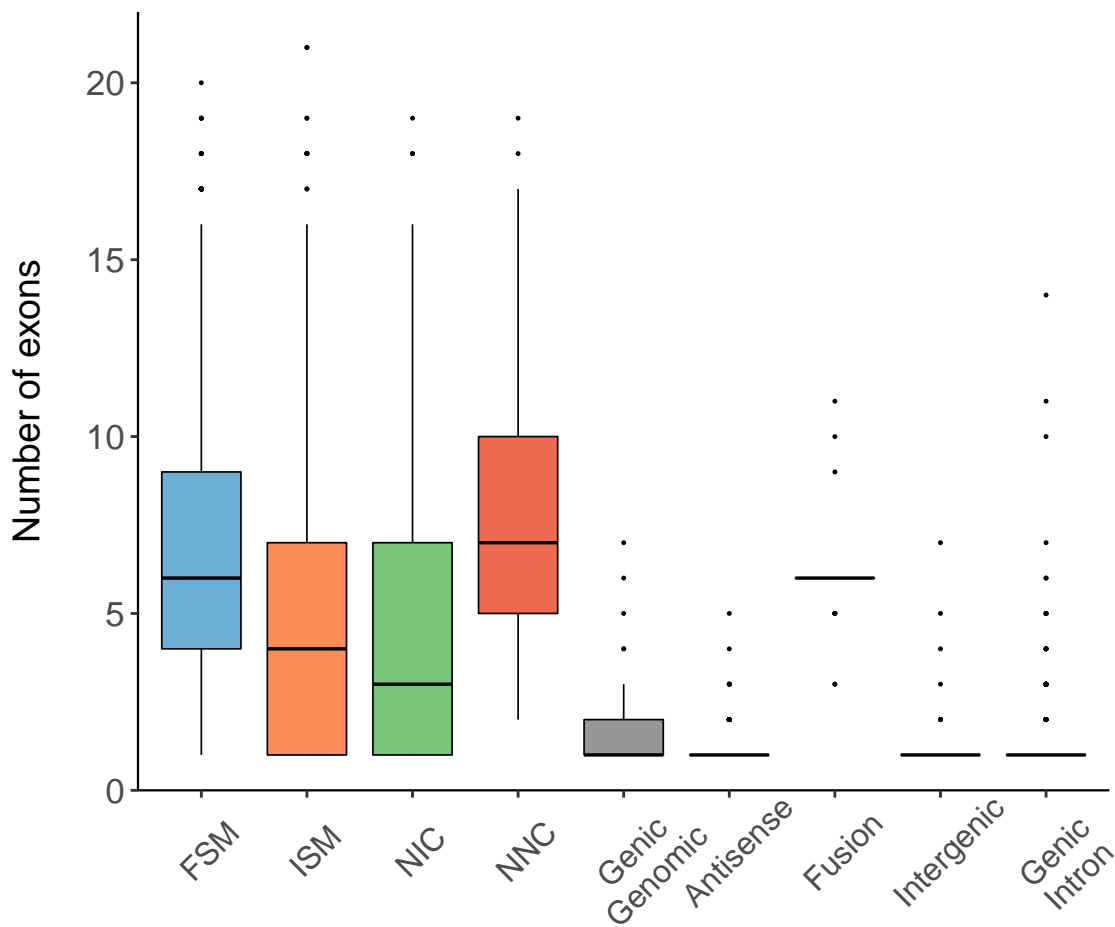
Isoform distribution across structural categories



Transcript length distribution by structural classification

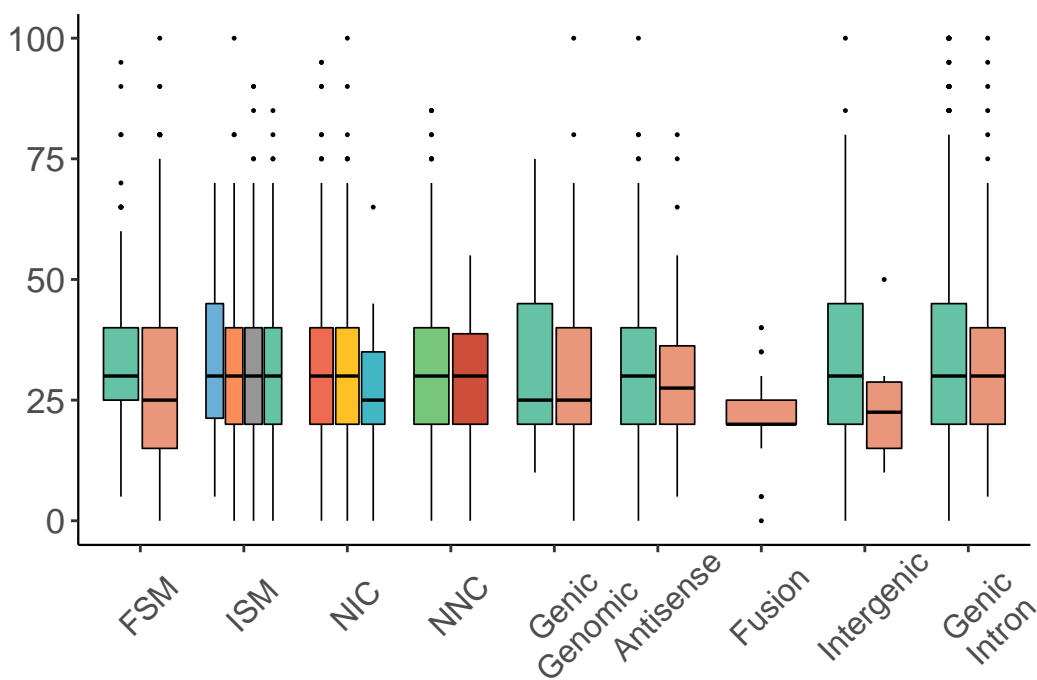


Exon number distribution by structural classification



% Adenines in gDNA window downstream TTS

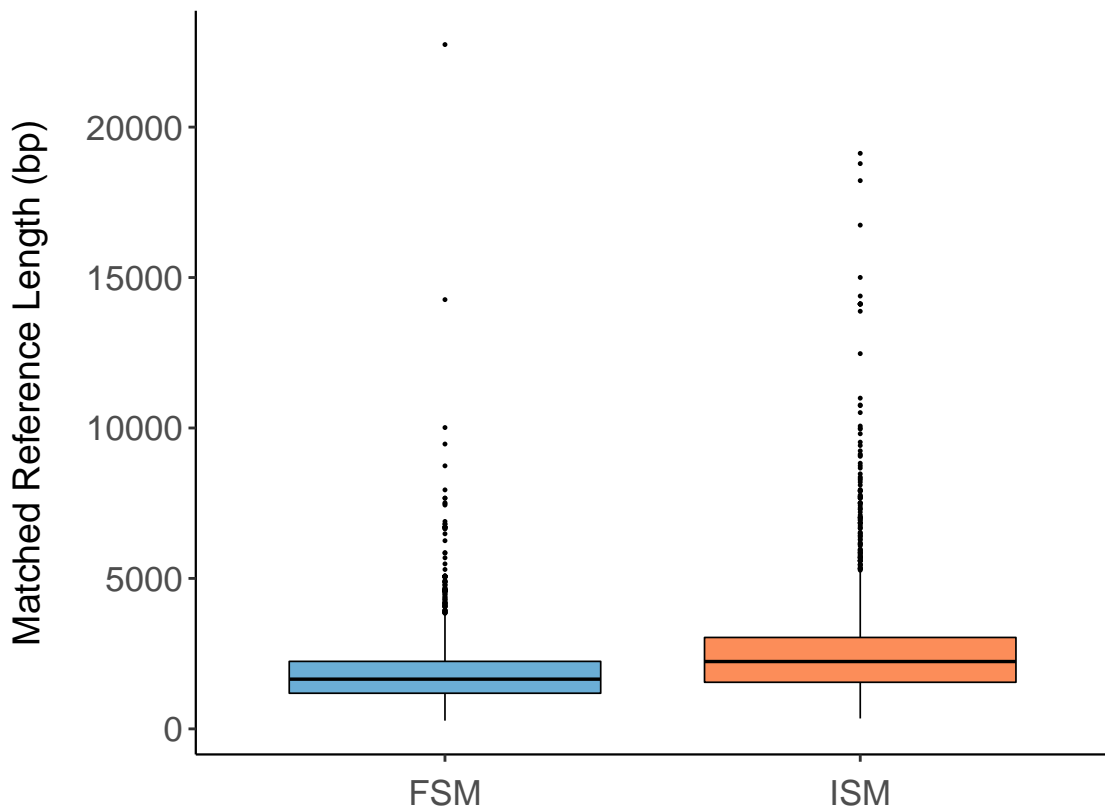
Adenine enrichment downstream TTS (intra primming)



- 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

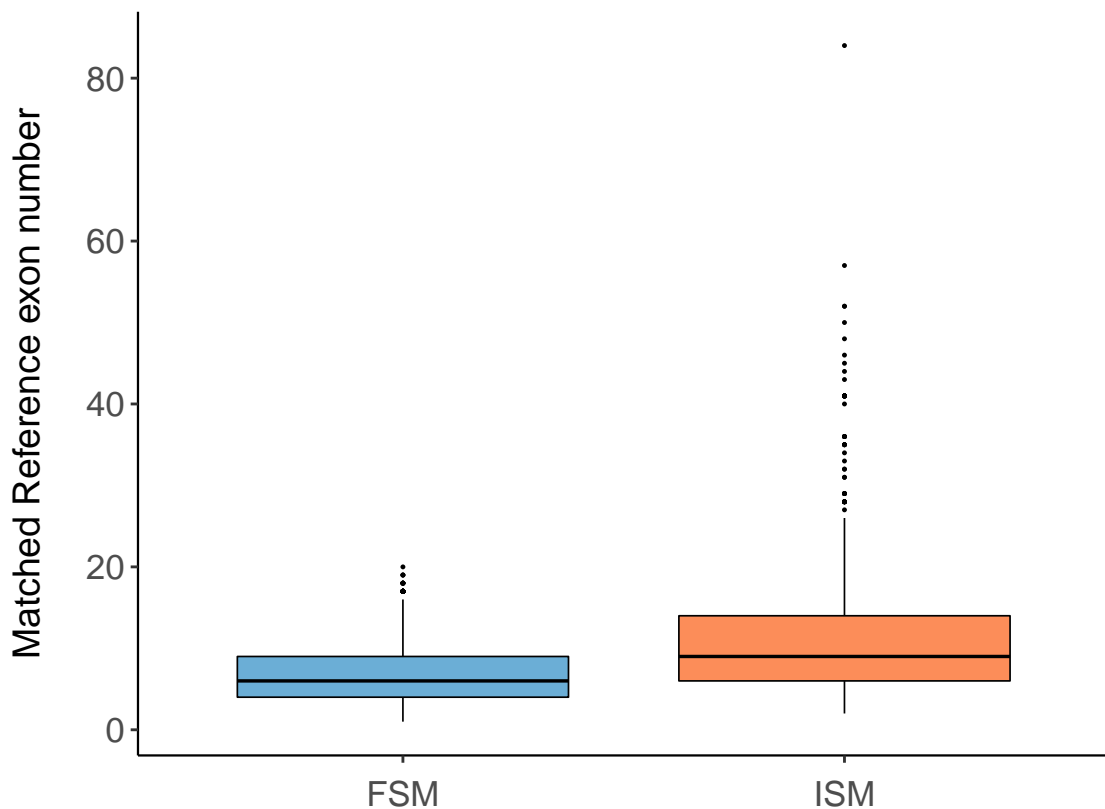
Length distribution of matched reference transcripts

Just applicable to FSM and ISM categories



Exon number distribution of matched reference transcripts

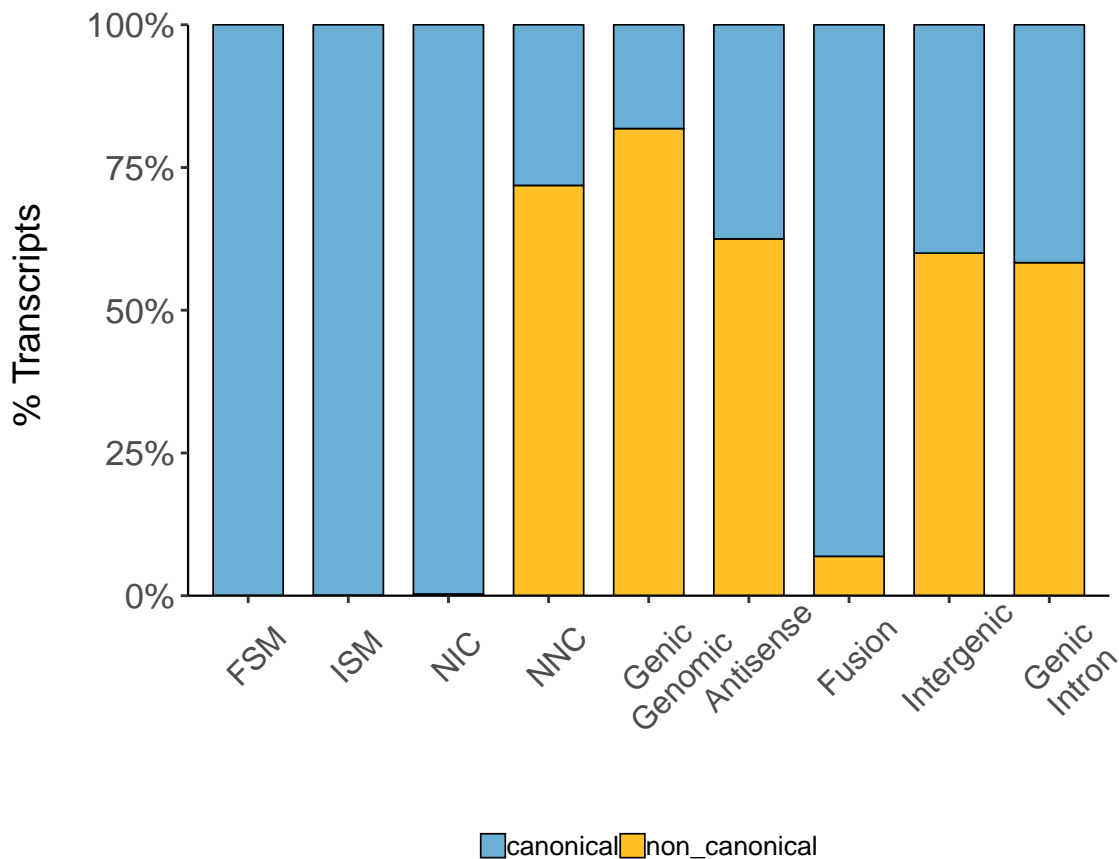
Just applicable to FSM and ISM categories



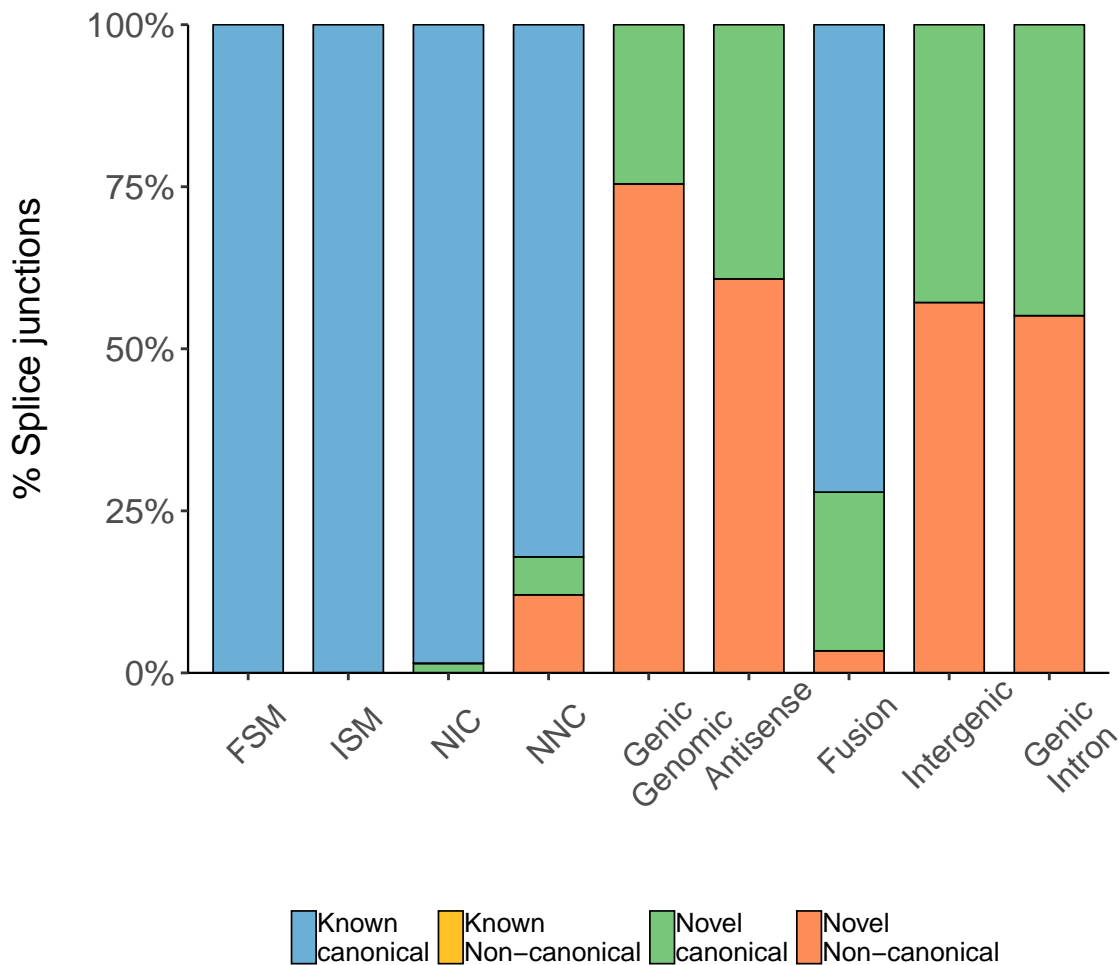
Splice junction characterization

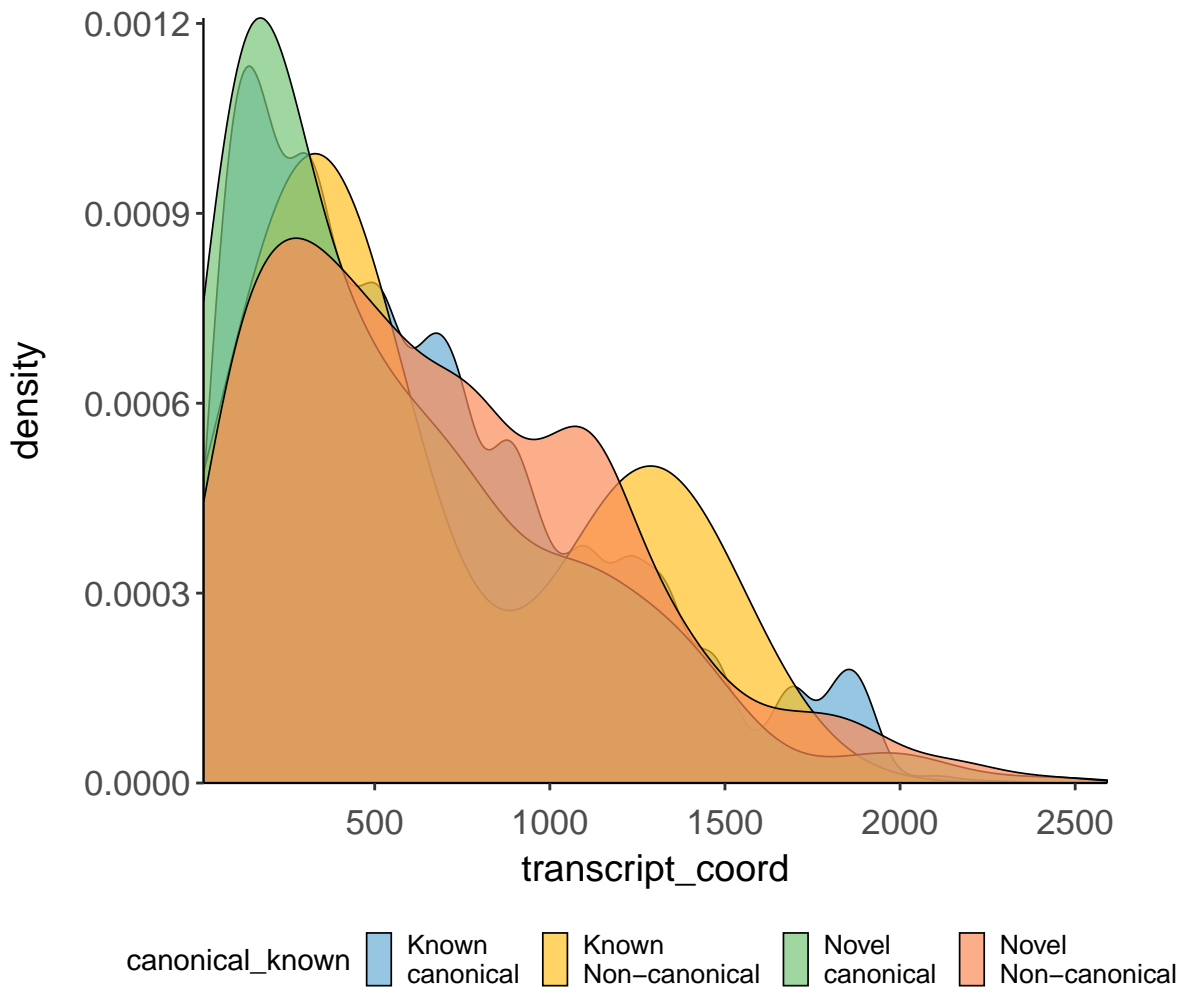
Distribution of transcripts by splice junction category

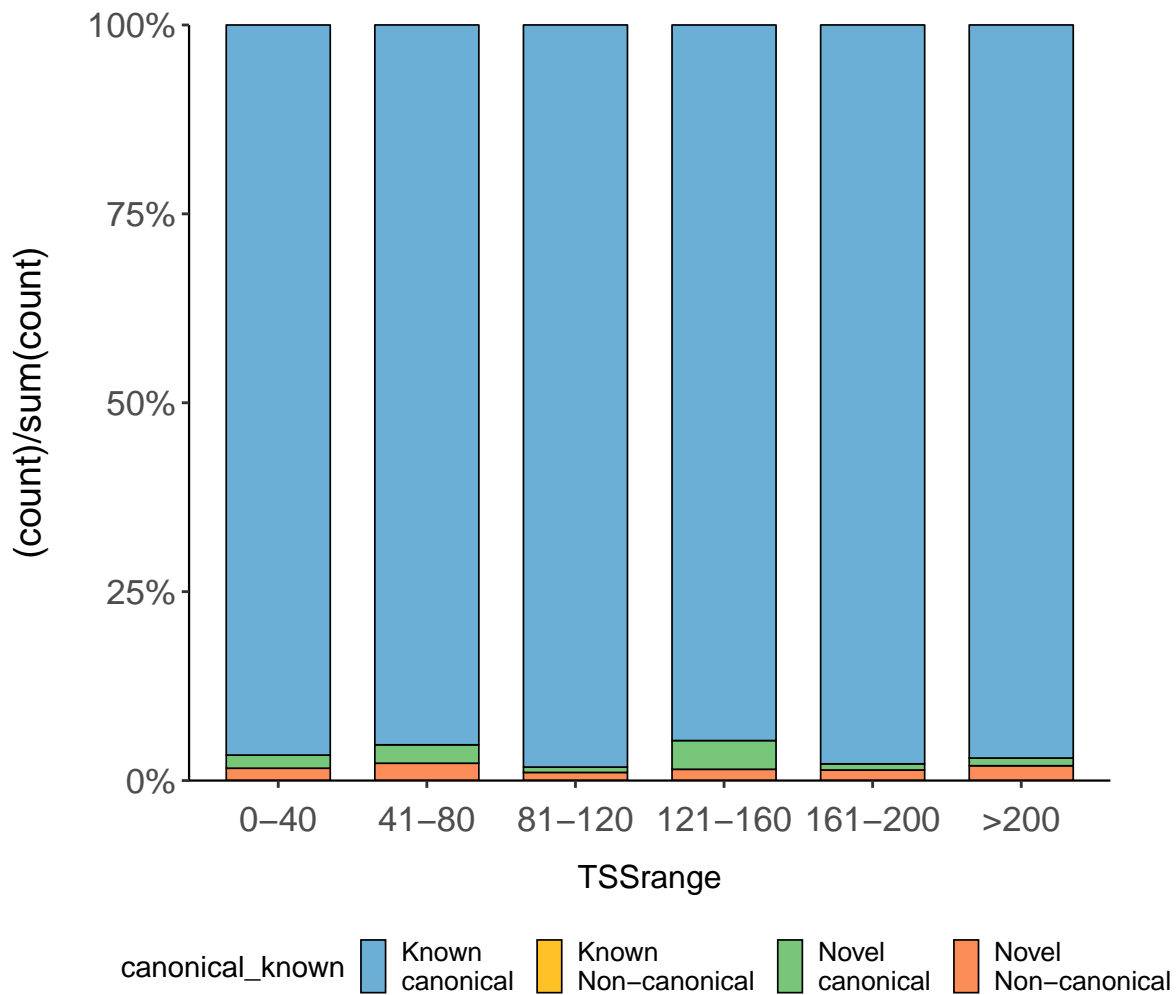
Non canonical transcripts are those with at least one non-canonical junction



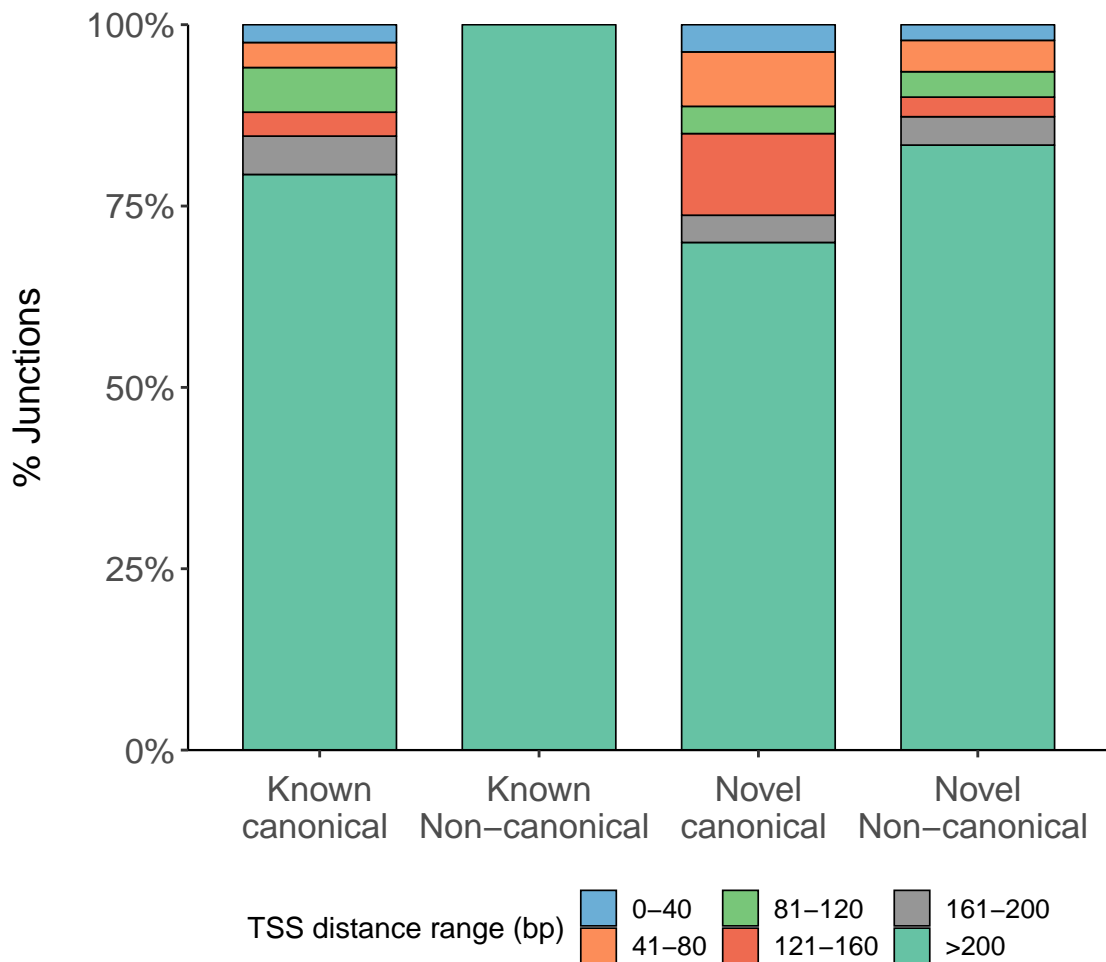
Distribution of SJ type among structural classification



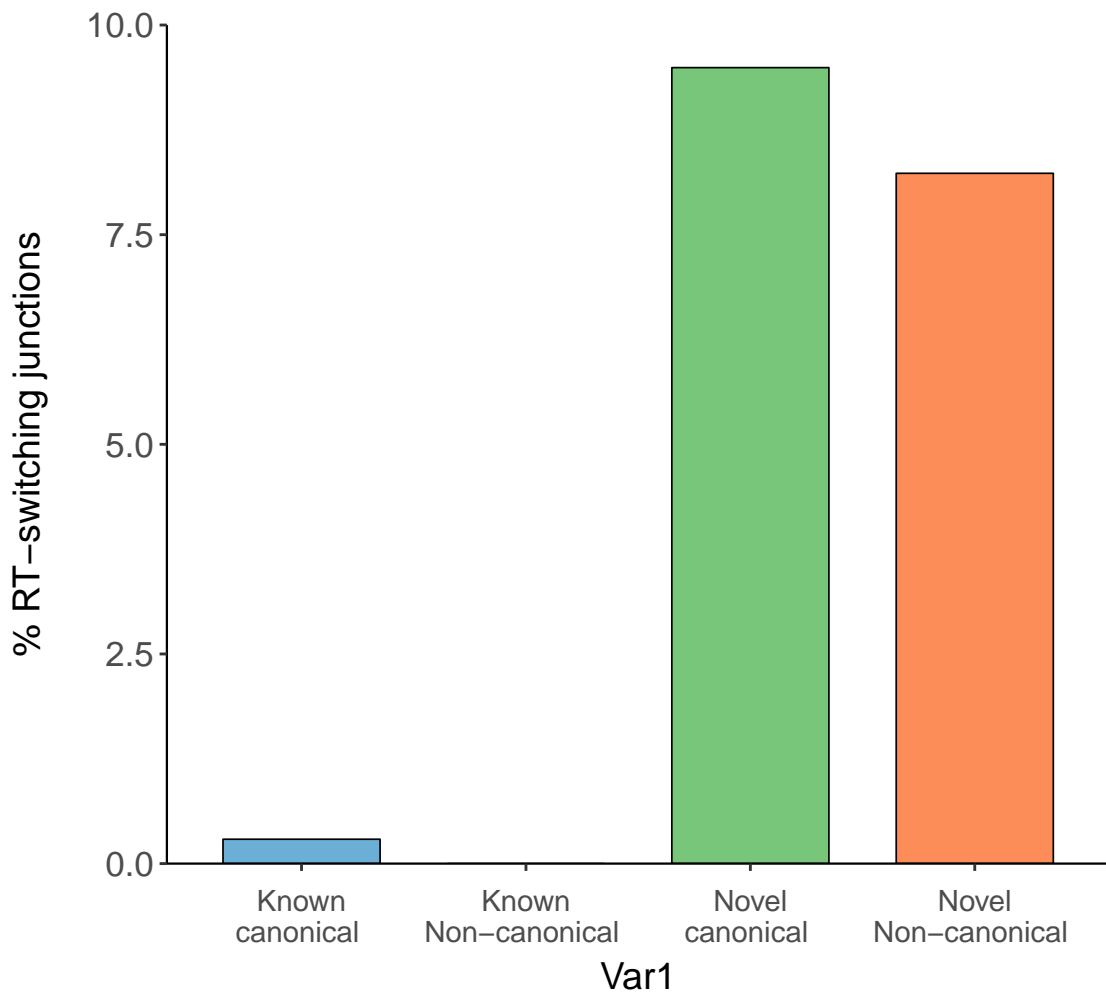




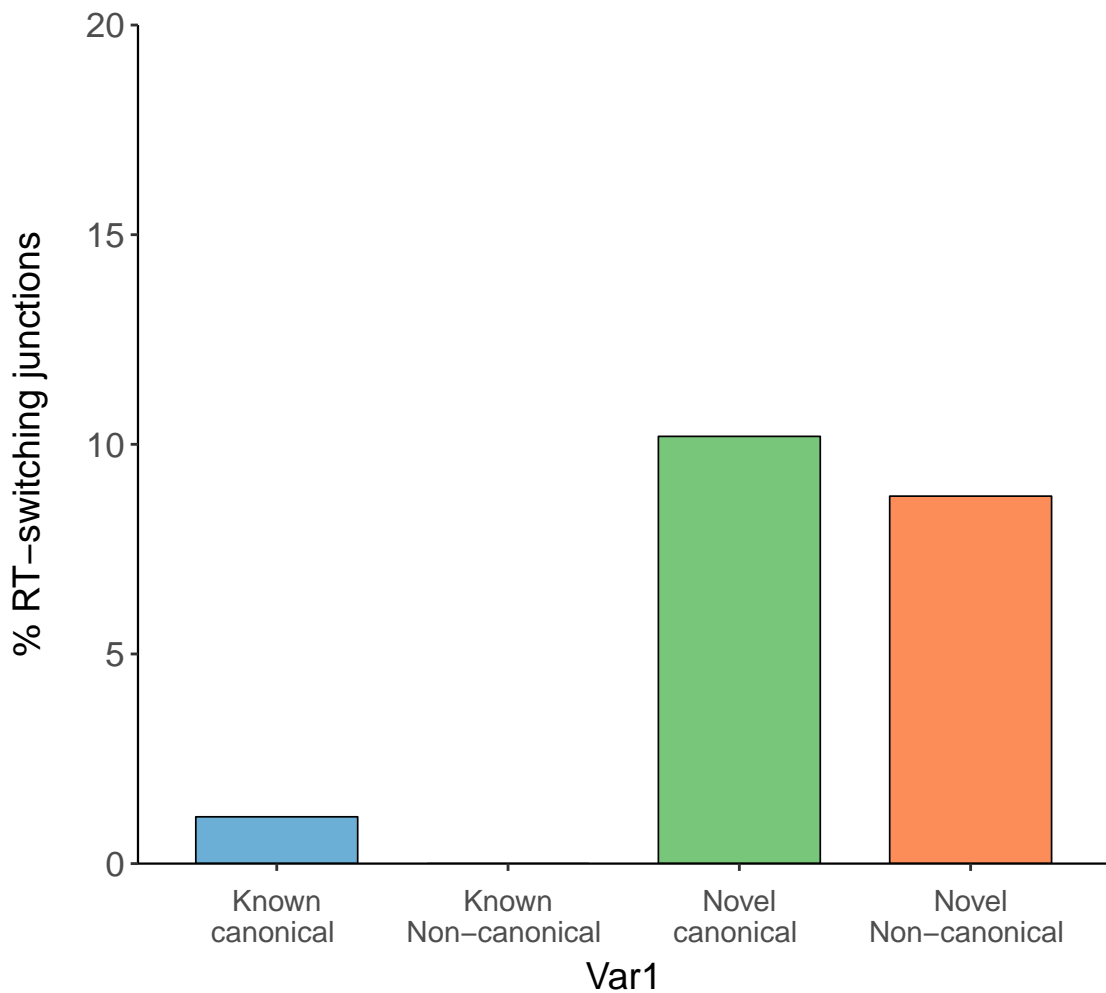
Splice junction distance to TSS across junction type



RT-switching by splice junction category



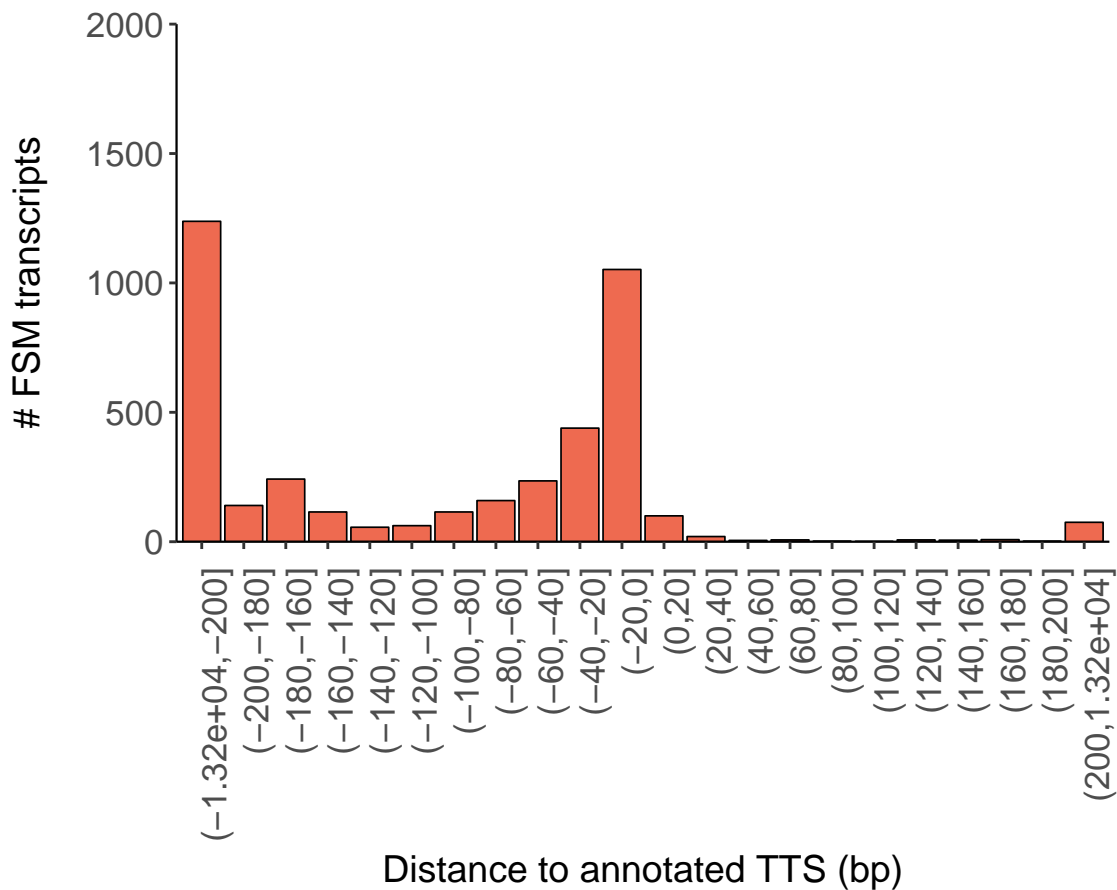
RT-switching by splice junction category (unique junctions)



Full-lengthness characterization of isoforms

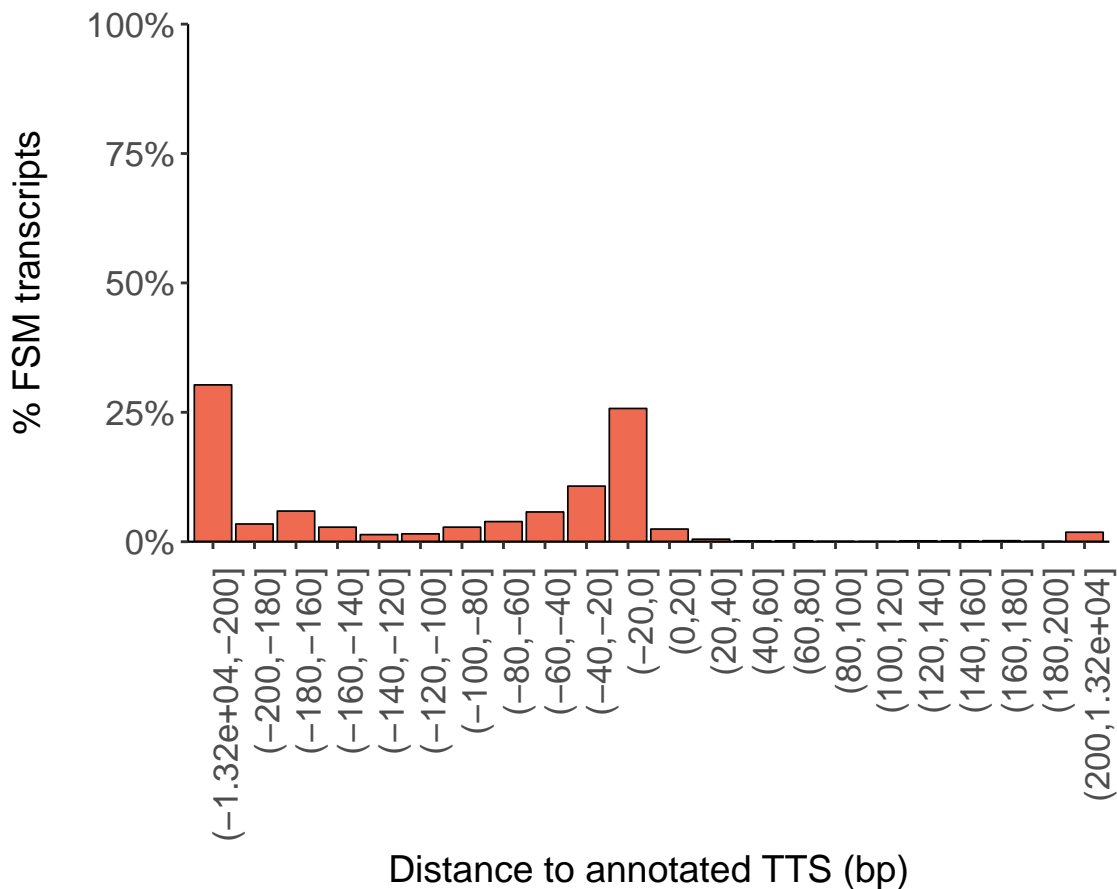
Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is upstream annotated TTS



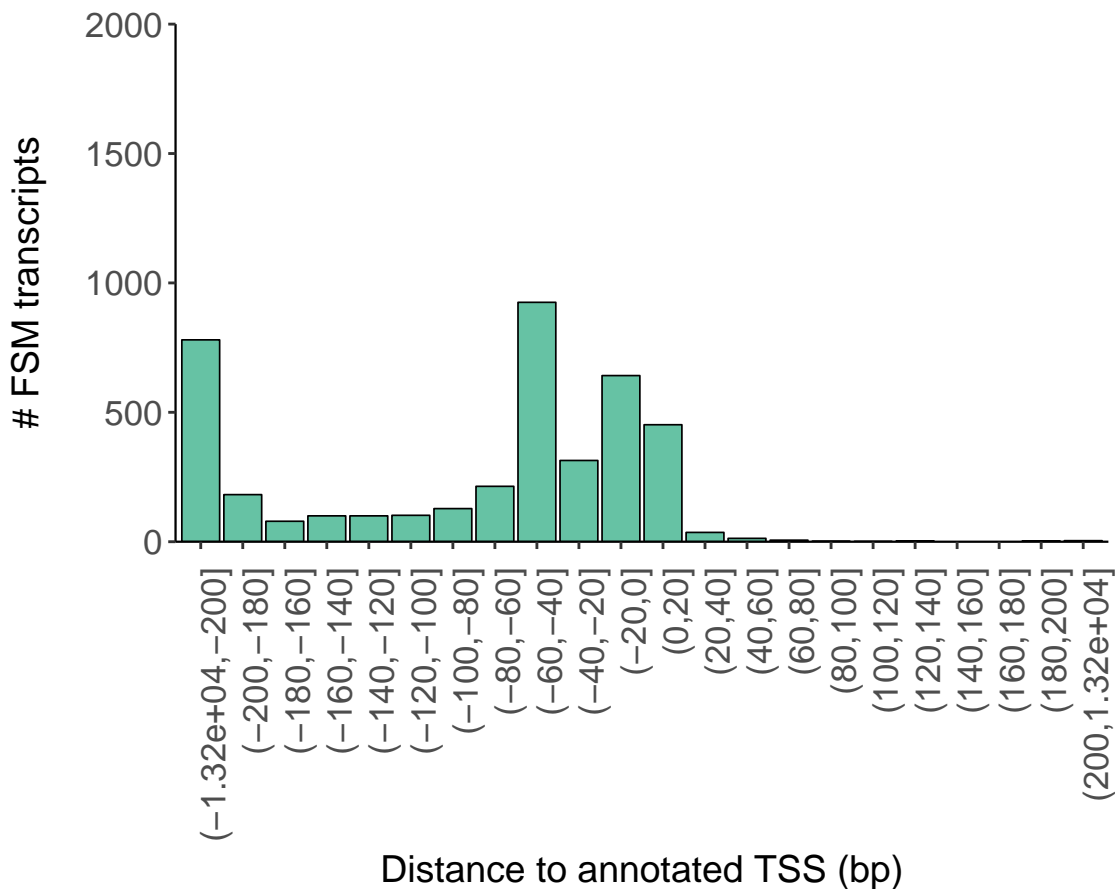
Distance distribution from sequenced to annotated TTS

Negative values indicate that the sequenced TTS is upstream annotated TTS



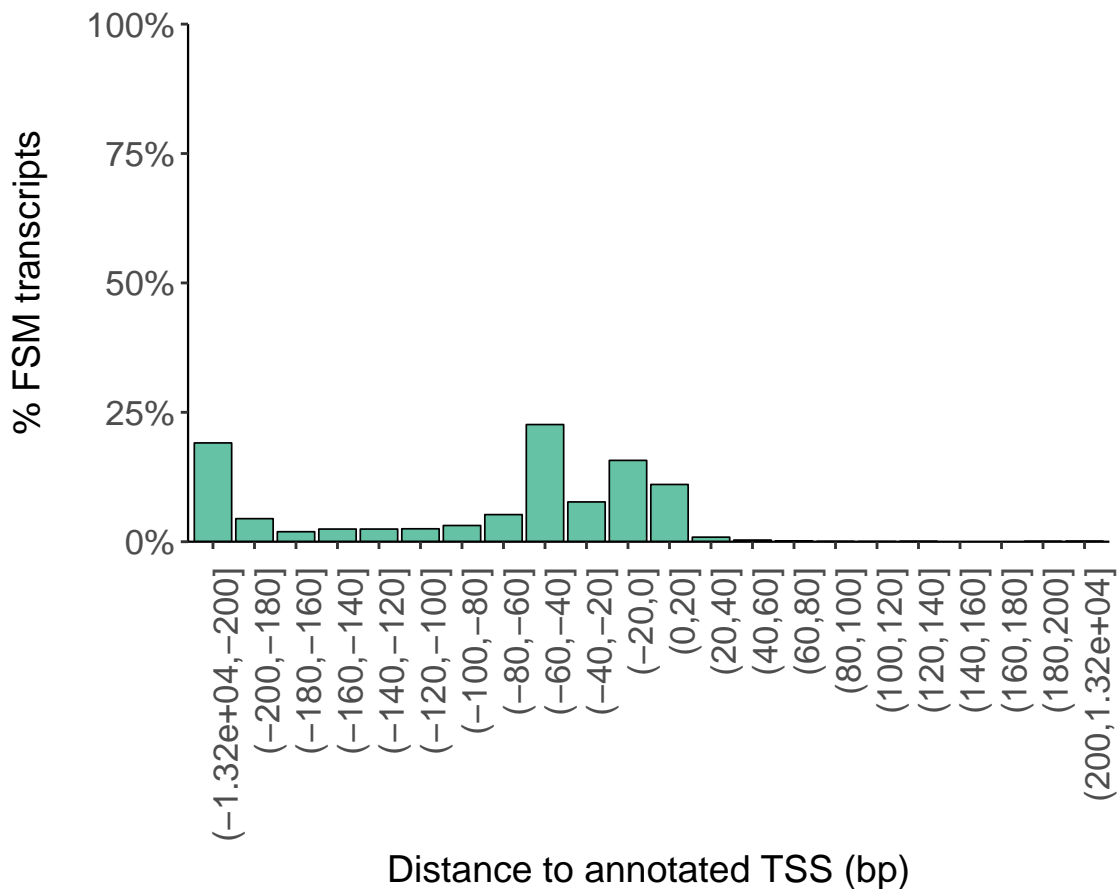
Distance distribution from sequenced to annotated TSS

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 T



Quality control attributes

Quality control attributes across structural categories

