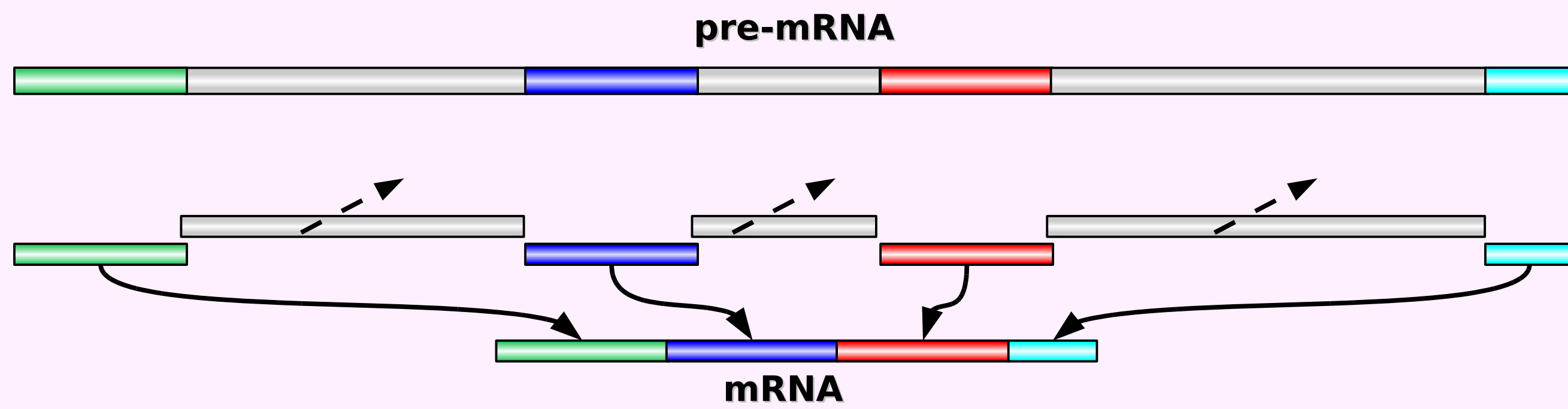
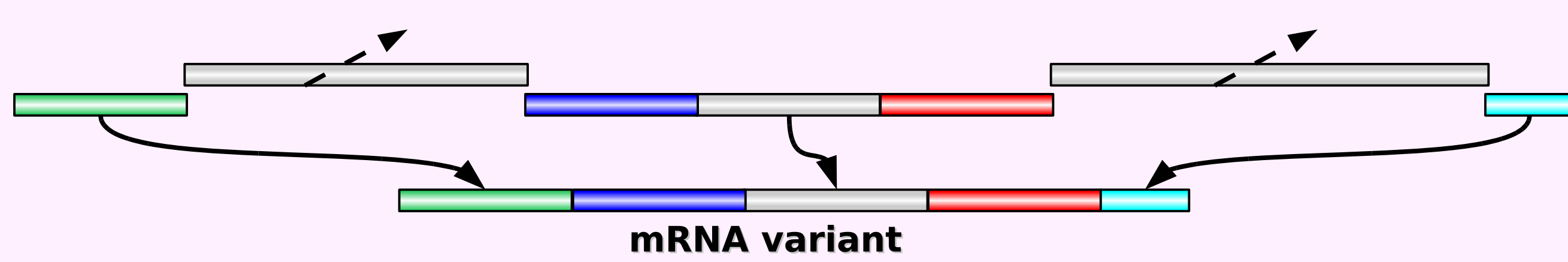


Alternative Splicing

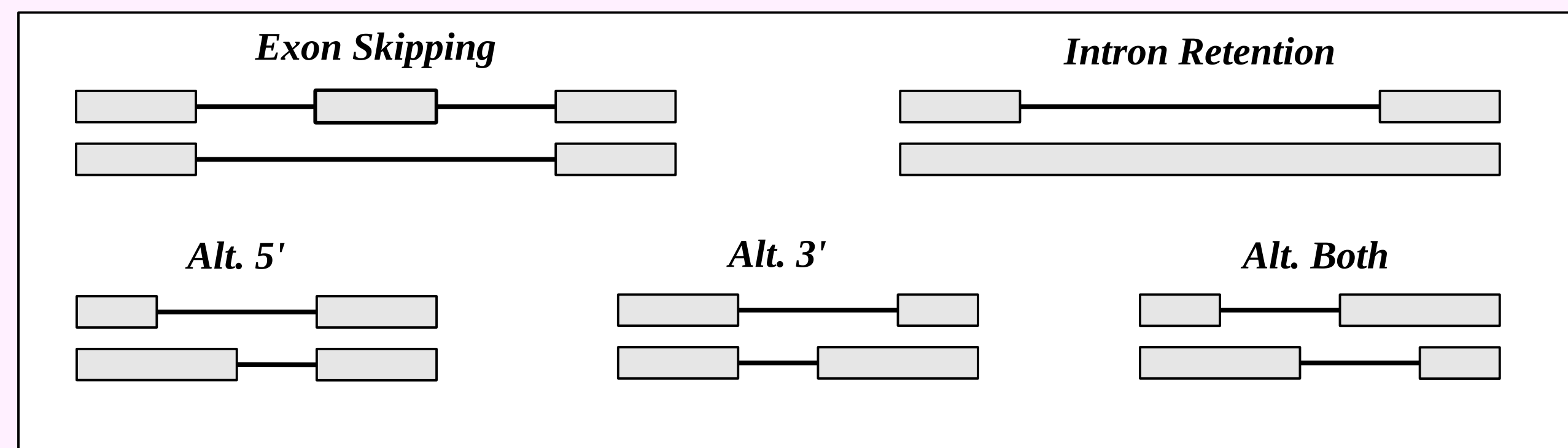
Non-protein-coding introns are excised from **precursor mRNA** at splice sites while exons are joined to form **mRNA**.



An **alternatively spliced** gene can use different splice sites to produce multiple mRNA variants:



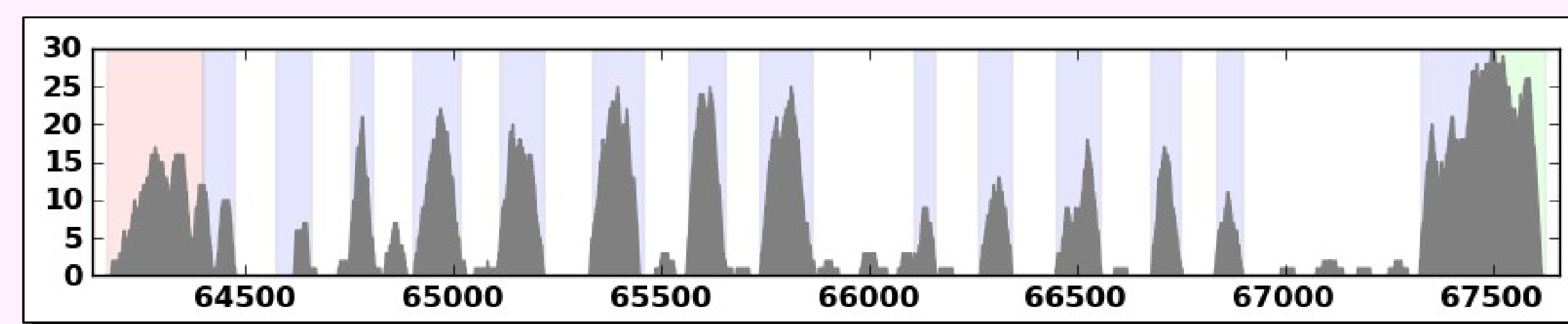
Splice variants fall into several categories:



Relevant Data

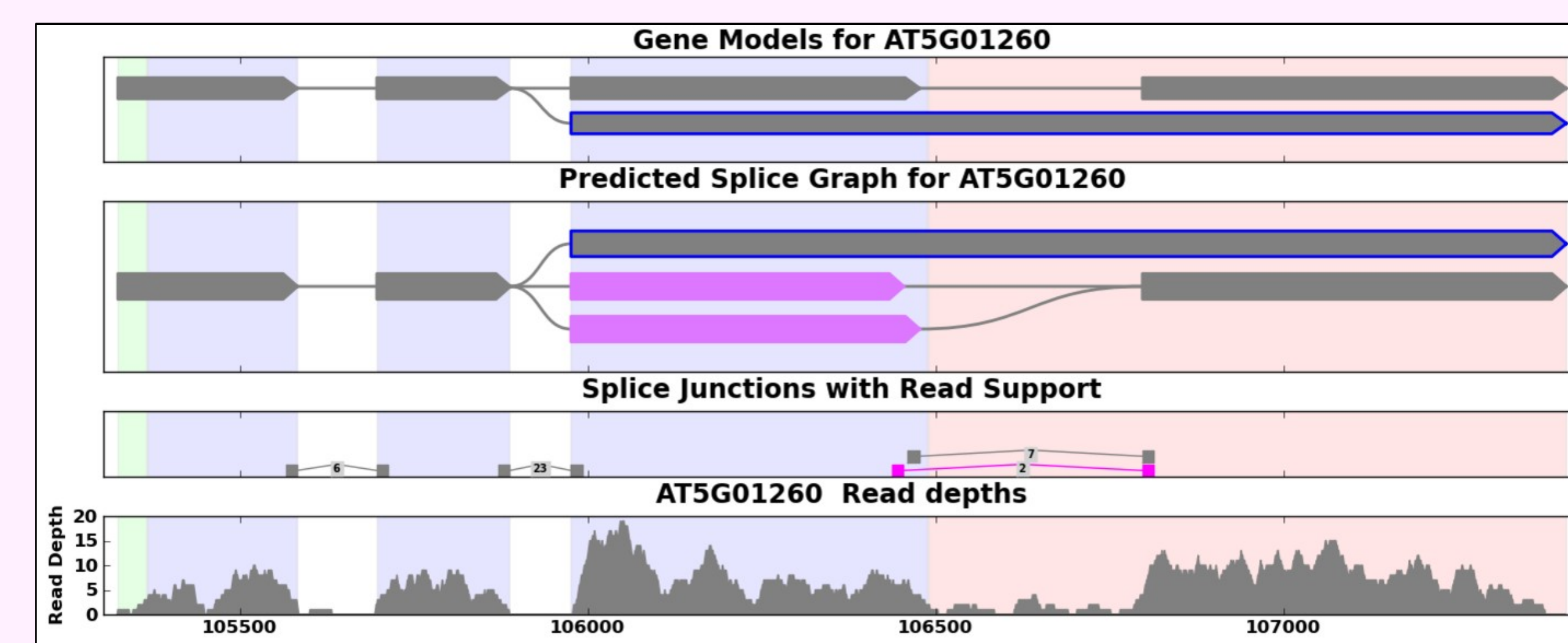
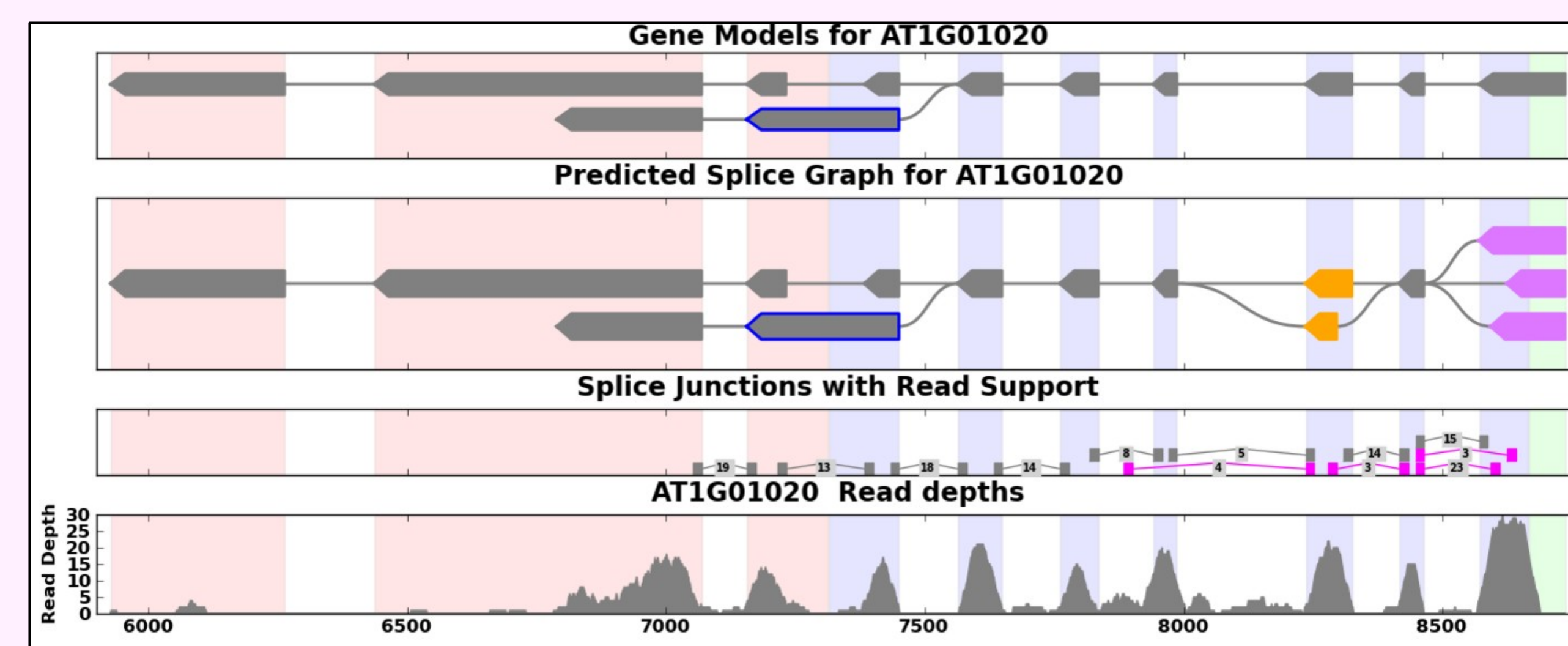
Our objective is to predict alternative splicing events using **annotated gene models, EST/cDNA transcripts and RNA-Seq** data.

Challenges with RNA-Seq



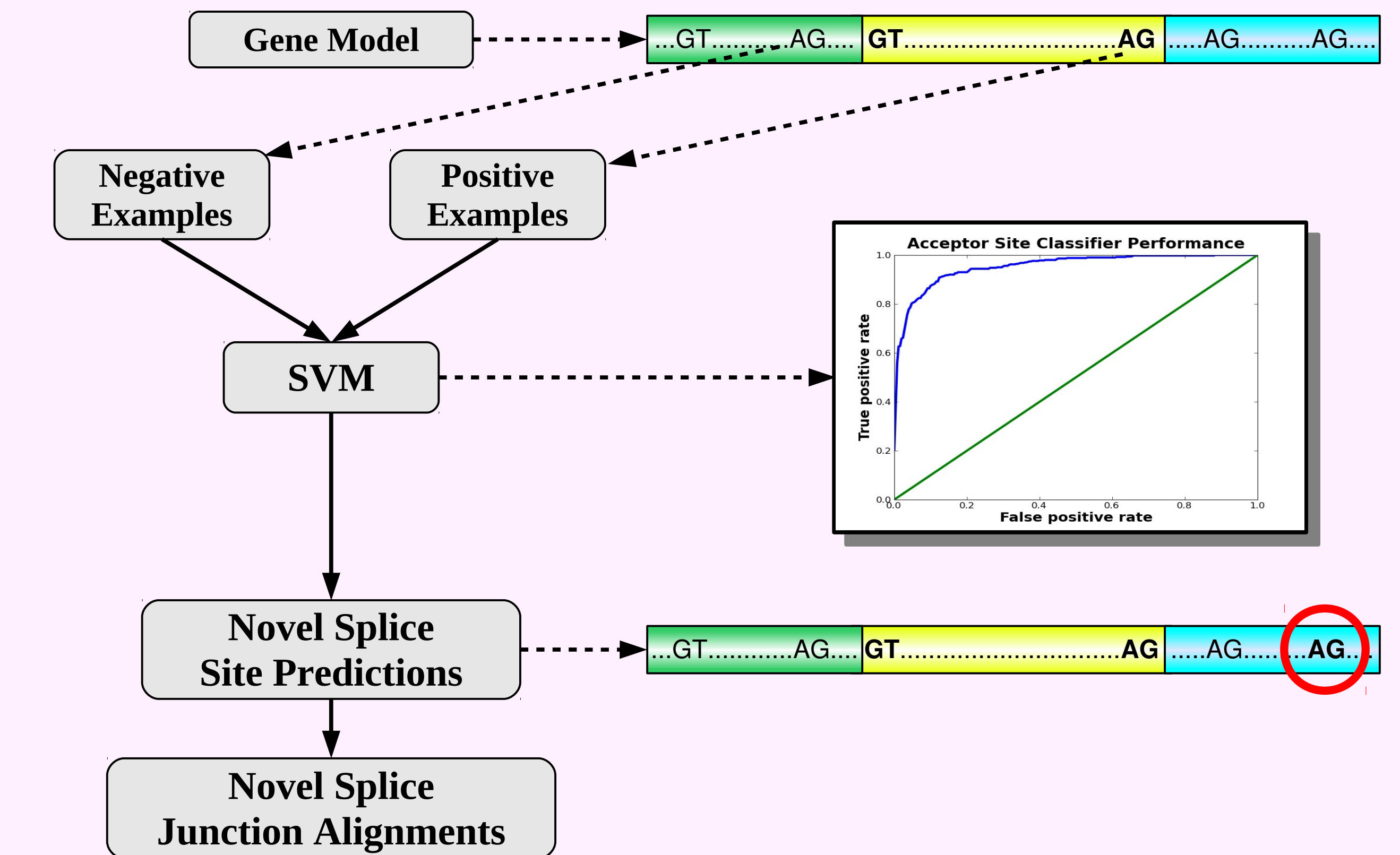
- Reads are short (~40nt), leading to possible spurious alignments
- Not as informative as ESTs
- Uneven coverage within genes
- Volume of reads (~10⁶ - 10⁸)

Splice Graphs



Predicting Novel Splice Junctions

SpliceGrapher includes tools that accurately predict novel splice sites by using known splice sites.

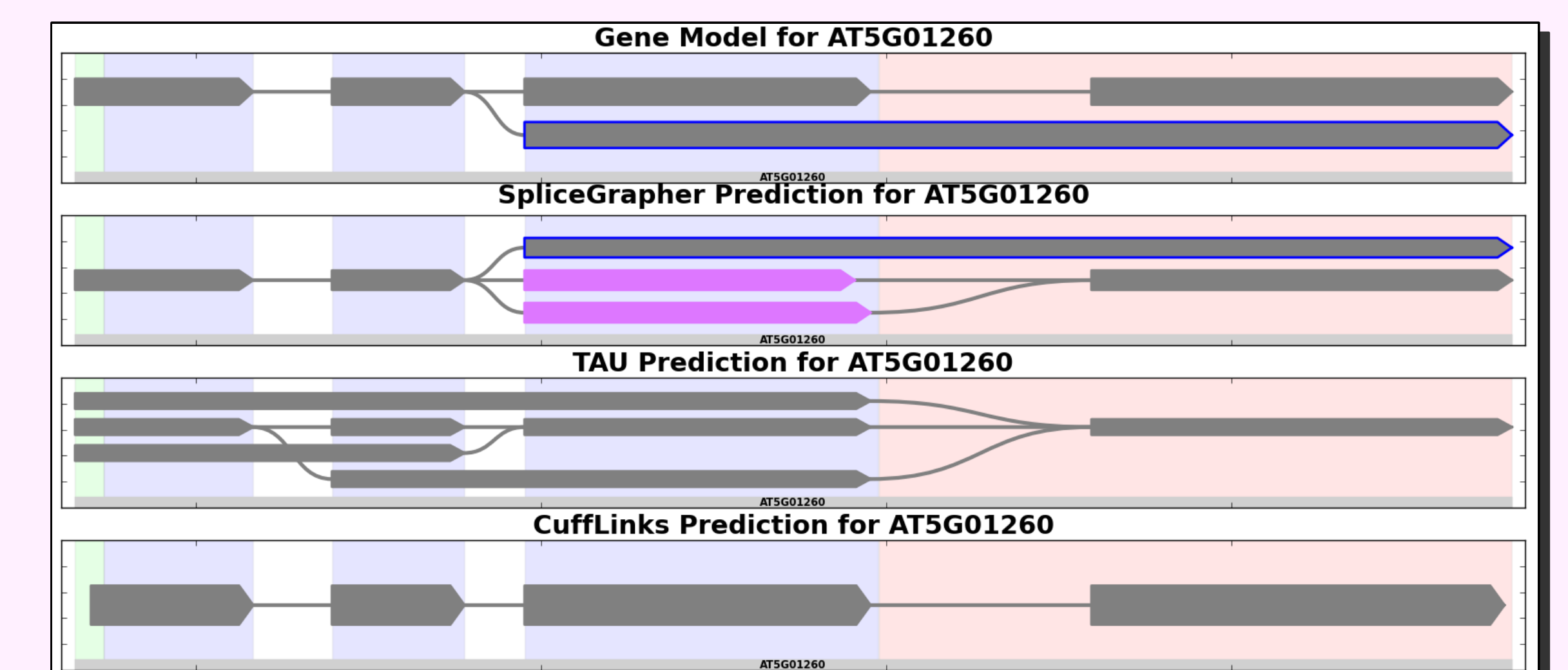
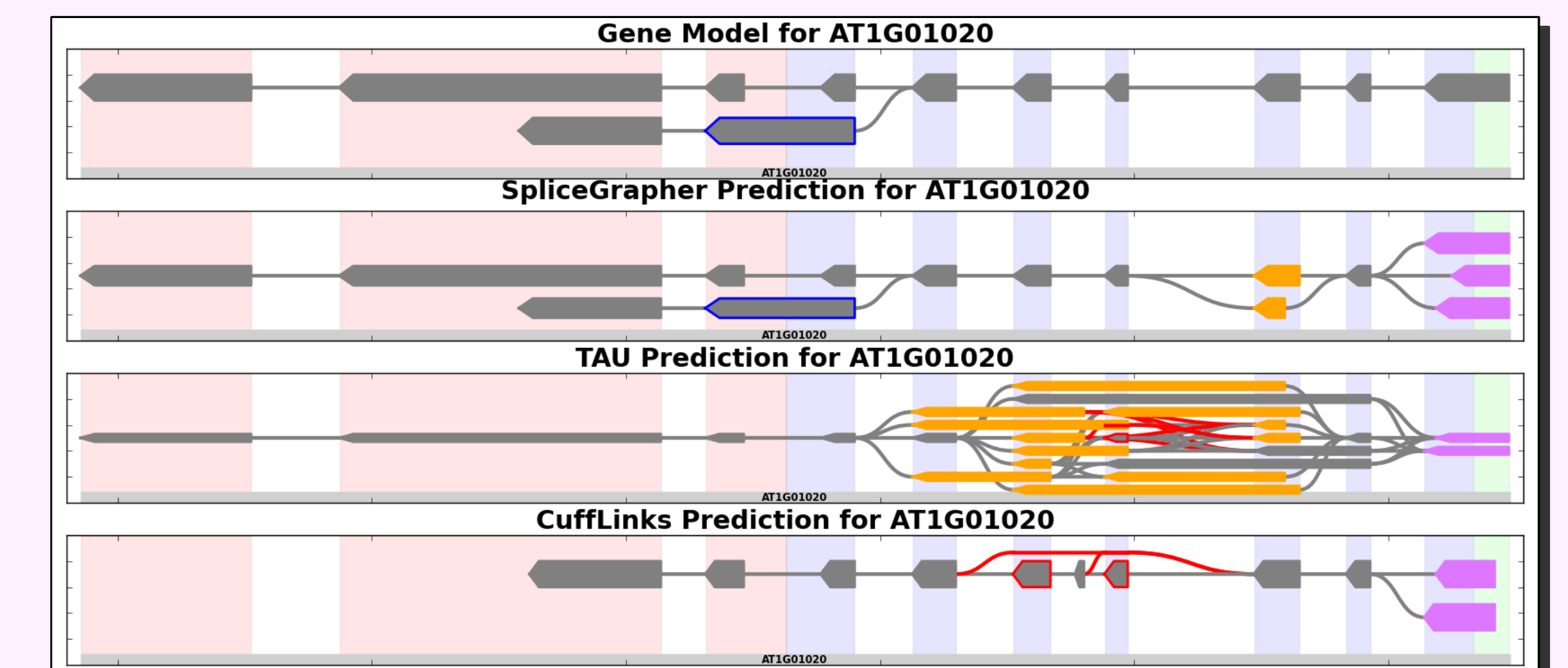


Arabidopsis thaliana junctions validated by short reads:

Junction	Known	Novel	
		Recombined	Predicted
GT-AG	87,086	1,224	13,252
GC-AG	884	15	541

Comparisons

SpliceGrapher predictions are more consistent with known gene models than those of TAU or Cufflinks.



For details, see: http://combi.cs.colostate.edu/splice_graphs/