

Exon and Intron Structure of a Gene

CACGTGGAC | GTAAAC -----TTCCCTTAG | GTAGCCAAAA

When aligning the mRNA to genome using e.g. BLAT:

CACGTGGAC GTAGCCAAAA

Many possible alignments have equal score:

CACGTGGAC | GTAAAC -----TTCCCTTAG | GTAGCCAAAA
CACGTGGAC GTAGCCAAAA

CACGTGGAC | GTAAAC -----TTCCCTTAG | GTAGCCAAAA
CACGTGGAC G TAGCCAAAA

CACGTGGAC | GTAAAC -----TTCCCTTAG | GTAGCCAAAA
CACGTGGAC GT AGCCAAAA

CACGTGGAC | GTAAAC -----TTCCCTTAG | GTAGCCAAAA
CACGTGGAC GTA GCCAAAA

Therefore, alignments in Genome Browser can often differ by one or a few positions at exon / intron junctions.