

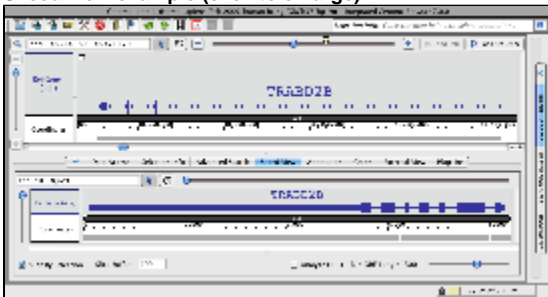
# Sliced View

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## Introduction

The **Sliced View** tab displays an alternative view of items from in the Main View. In the **Sliced View**, introns are shown as having the same size, set in the **Slice Buffer** box). The **Sliced View** also can show open reading frames (ORFs).

**Sliced view example (click to enlarge)**



## Display sliced view of a gene

To view a sliced view of a gene

- Click the Sliced View tab to make it the active bottom tab
- Open the Sliced View tab in a separate window (this is optional) **Tab > Open Current Bottom Tab in New Window**
- Click a gene model in the Main View
- Observe that the same gene model appears in the **Sliced View** but intronic regions are removed

## Sliced View options

The bottom row of the **Sliced View** panel shows options for controlling **Sliced View** appearance.

**Sliced View options (click to enlarge)**



### Slice by Selection

This option controls when the **Sliced View** updates. Check this option to ensure that whatever is selected in the Main View is shown in the **Sliced View** display.

### Slice Buffer

The **Slice Buffer** setting controls the size of introns drawn in the **Sliced View** display. The "buffer" consists of intronic sequence on the five and three prime ends of exons.

### Analyze ORFs

Check this option to activate display of ORFs (open reading frames) underneath the **Sliced View** coordinate axis track.

## Min ORF Length

This option controls the size of ORFs shown when Analyze ORFs is checked.

## Viewing deletions and insertions

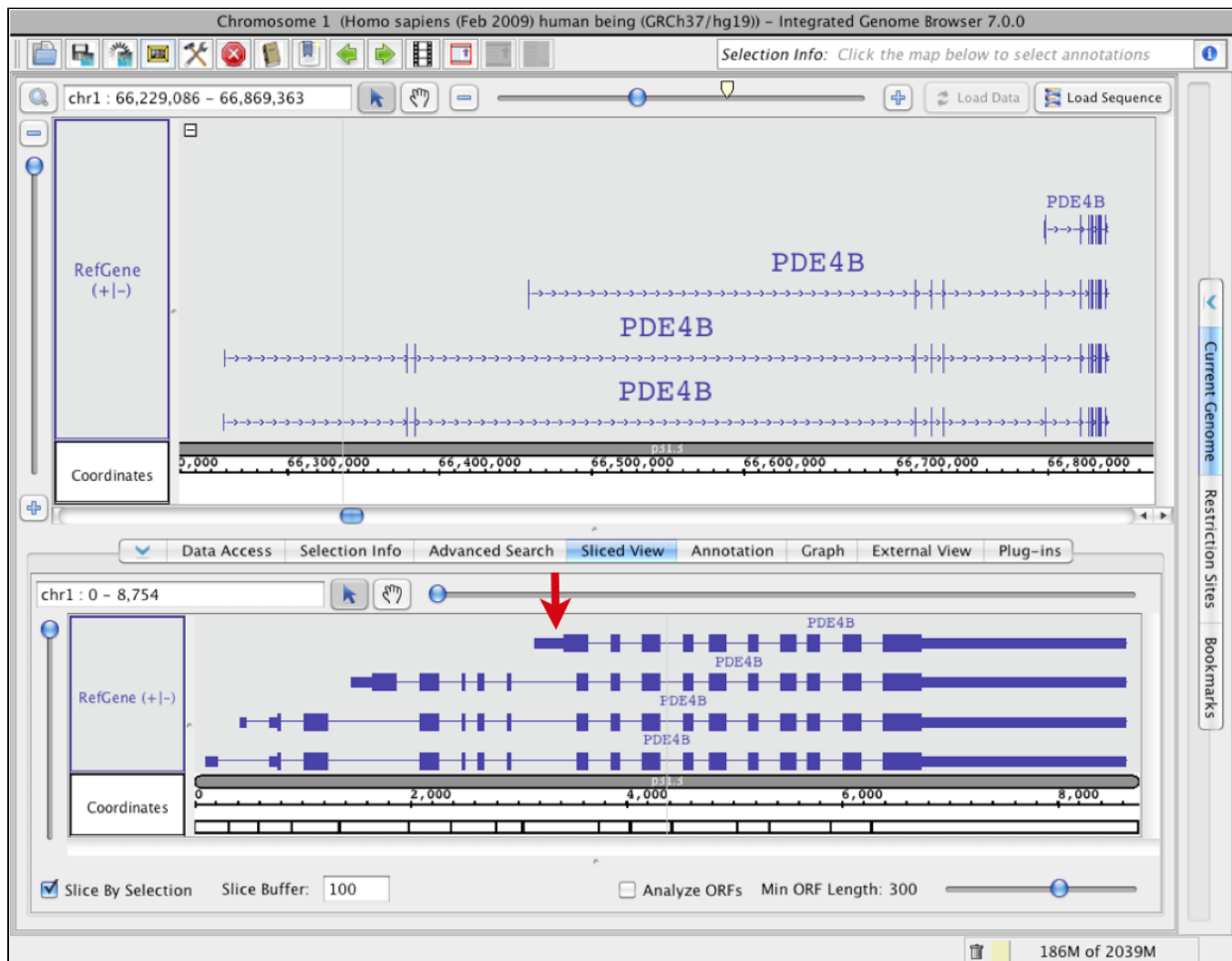
The **Sliced View** can help you see where sequences present in one transcript are absent from the others due to alternative splicing.

To examine alternate splicing using the **Sliced View**

- select one or more transcripts in the Main View
- deletion icons (X characters) IGB draws on the other transcripts
- insertions are shown as larger introns

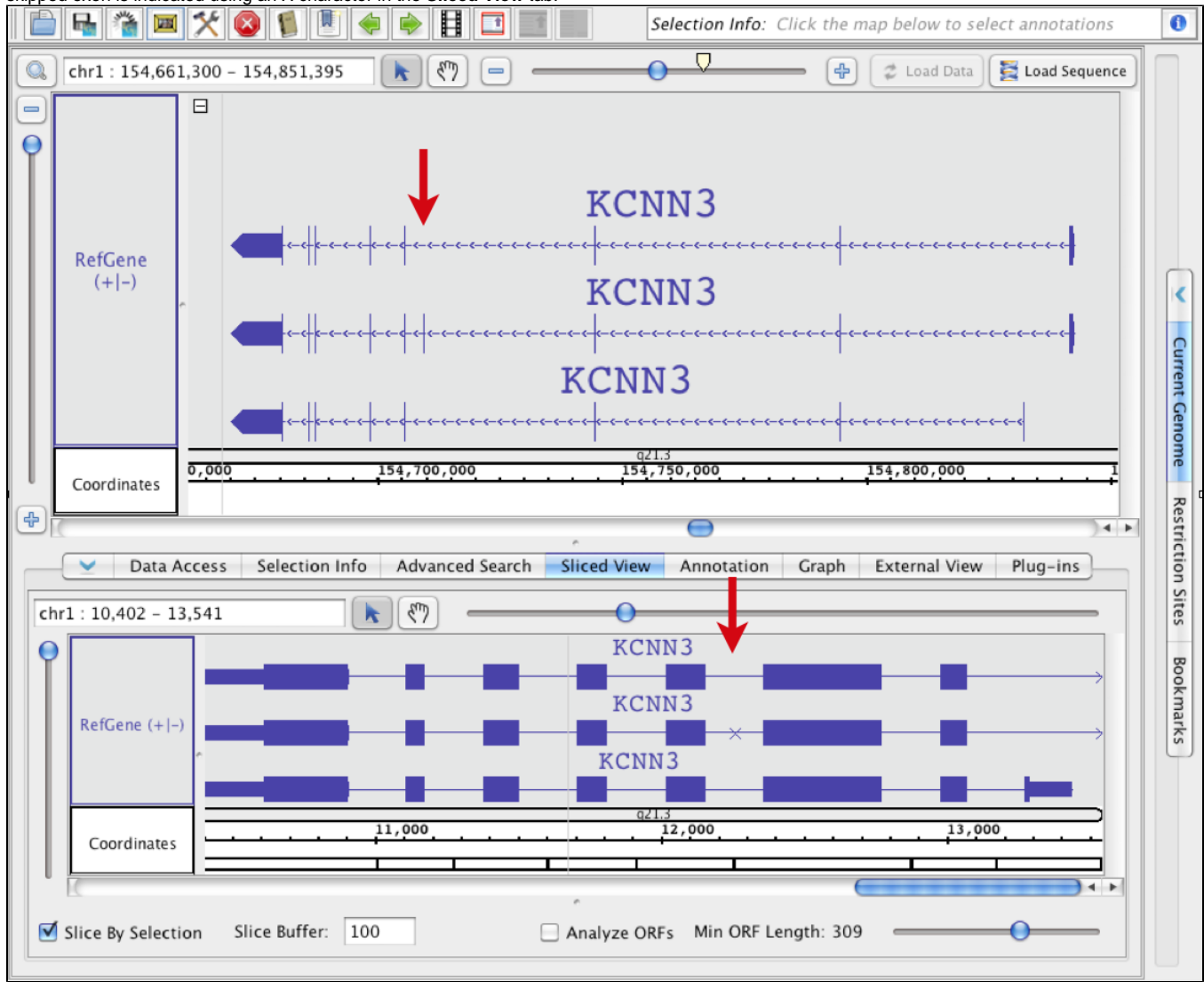
### Insertion example

In this example, all four gene models were selected in the main view when the sliced view was created. In the sliced view, an arrow points to an exon that is present in all four models but is larger in the first one. Introns overlapping this exon in the other three models are larger.



### Deletion example

In this example, the bottom gene was selected in the main view when the sliced view was created. An arrow points to an exon in the main view that is present in the middle gene model but absent in the other two. Since the third model which doesn't include this exon was used to create the sliced view, the skipped exon is indicated using an X character in the **Sliced View** tab.



## Showing ORFs and stop codons

The **Sliced View** panel can show open reading frames and stop codons.

To visualize open reading frames and stop codons

- Select an annotation in the Main View
- Click the **Sliced View** tab
- Check the **Analyze ORFs** checkbox
- Use the Min ORF slider to adjust the minimum length of ORFs to show (in base pairs)

ORFs will appear for all six translation frames. Stop codons are shown as red marks. ORFs that are as long as or longer than the minimum ORF setting will be shown as green lines. Stop codon and ORF colors can be set using **Preferences > Other Options**.

Sliced View ORF display.

