

Right-click (context) menus

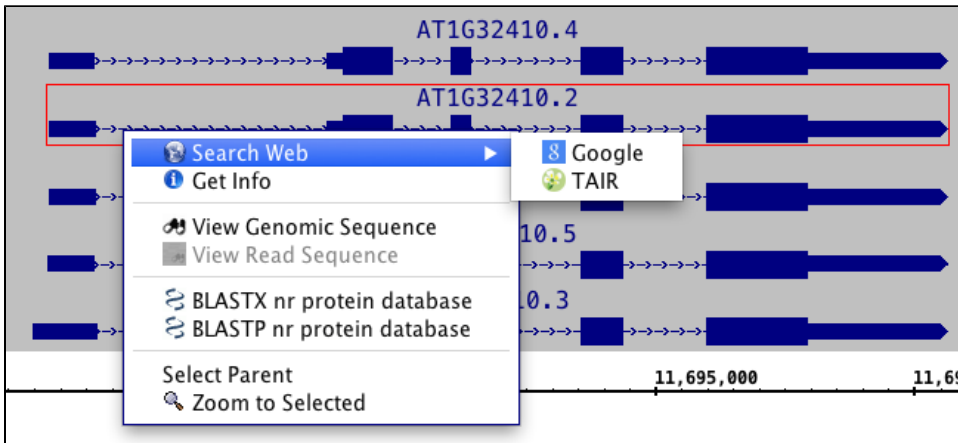
IGB displays context menus when you right-click track labels or items in the data display area. These menus are called "context menus" because the menu options you'll see depend on what you clicked.

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Right-clicking annotations

When you right-click an annotation, you'll see a context menu with the following options:

- **Select Parent** selects the feature of which the right-clicked item is a part. For example, if you right-click an exon and choose **Select Parent**, the entire gene model is selected.
- **Zoom to Selected** zooms to the right-clicked item. Choosing this option is the same as double-clicking.
- **View Genomic Sequence** loads genomic sequence (if not already loaded) and displays it in a new **Sequence Viewer** window.
- **Search Web** opens your web browser to Web pages that have more information about the selected model.
- **Get Info** displays the **Selection Info** panel containing information relevant to your selection.
- **BLASTX nr protein database** searches a non-redundant **protein** database using a **translated nucleotide** query.
- **BLASTP nr protein database** searches a non-redundant **protein** database using a **protein** query.



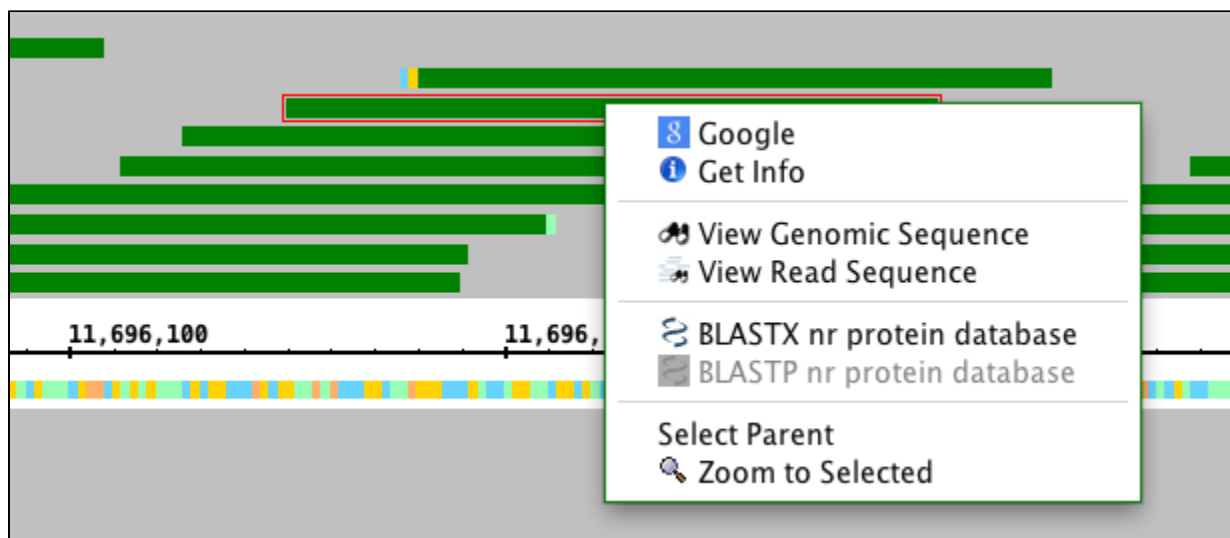
Right-clicking alignments

When you right-click an alignment, you'll see the same options as in the preceding section plus new options specific to alignments. Context menu items for alignments include:

View Read Sequence opens the aligned sequence in the **Sequence Viewer**.

Restore Read sequence superimposes the read sequence on the alignment blocks. Ordinarily, if the genomic sequence has been loaded, only mismatched bases are drawn.

For more information about alignments, see [Visualizing read alignments](#).

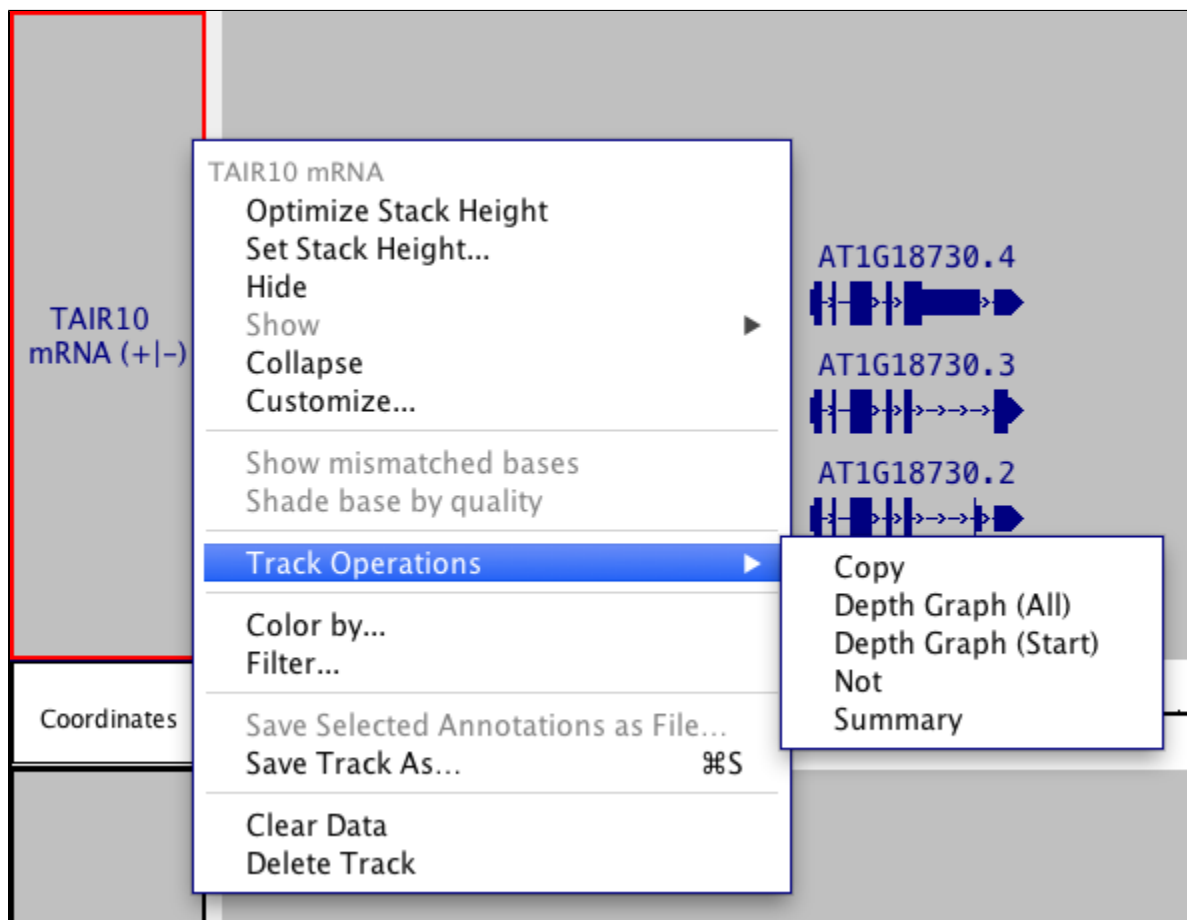


Track labels

Right click a track label to view options and operations.

The menu you see will vary depending on the track type.

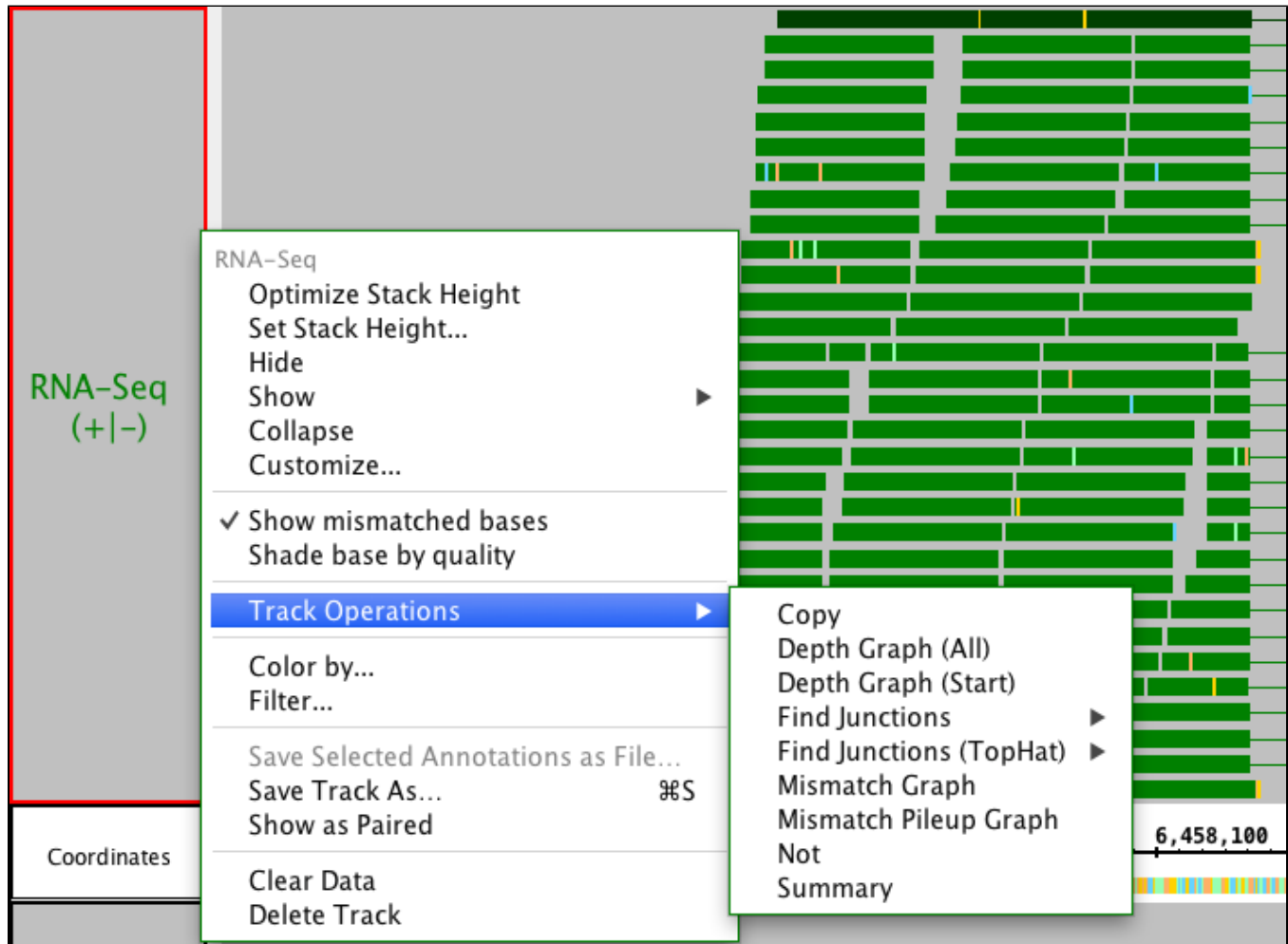
Annotation track right-click menu



- **Optimize Stack Height** Set stack height so that all available annotations in the currently visible region are shown.
- **Set Stack Height** Open a window that allows you to set the stack height.

- **Hide** Hide the track.
- **Show** Show hidden tracks.
- **Collapse** Compress the track so that all annotations occupy a single row.
- **Customize** Open the **Preferences > Tracks tab** window.
- **Track Operations** Perform operations on a track. See [Annotation track operations](#)
- **Color by Score** Change annotation color depending on score
- **Set Range of Color by Score** Configure color options.
- **Save Selected Annotations as File...** Saves selected annotations to a file
- **Save Track As...** Save all the data in the track as a file.

Short read (alignment) track right-click menu



Graph track right-click menu

