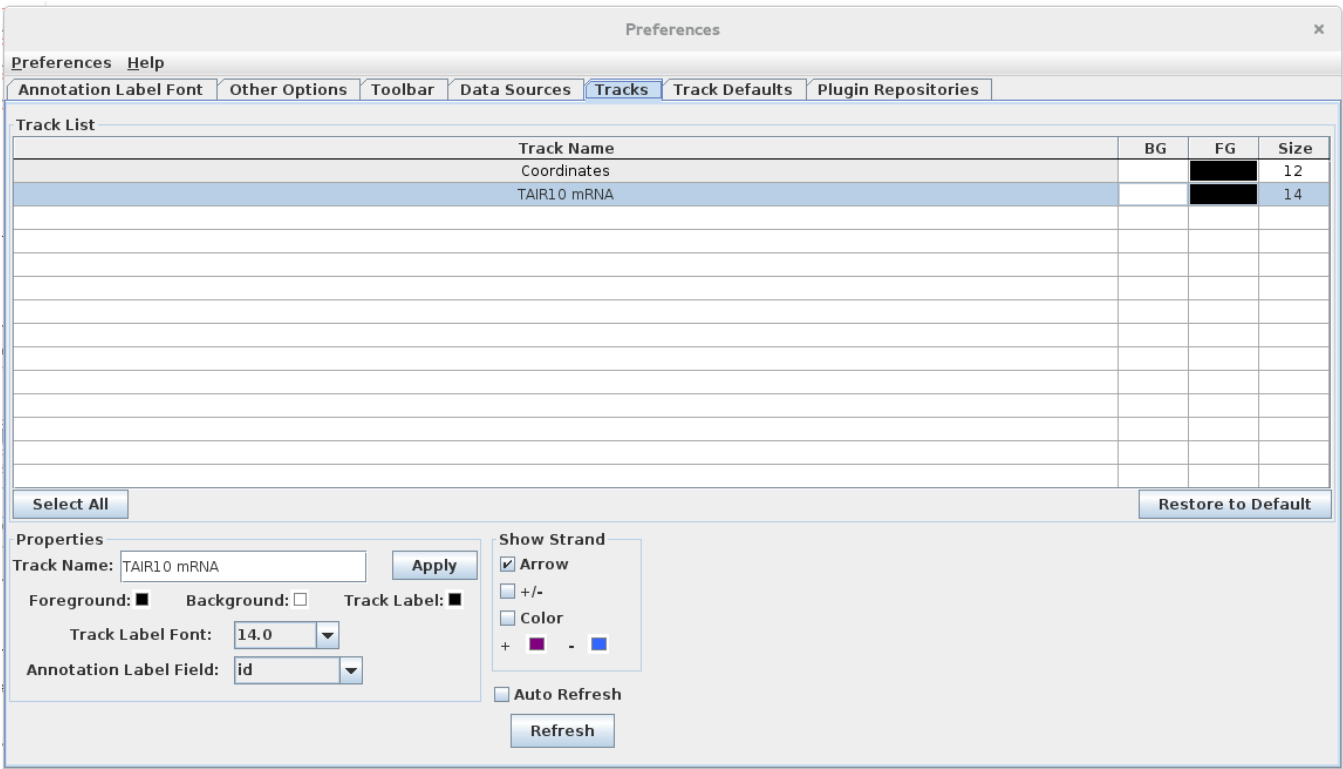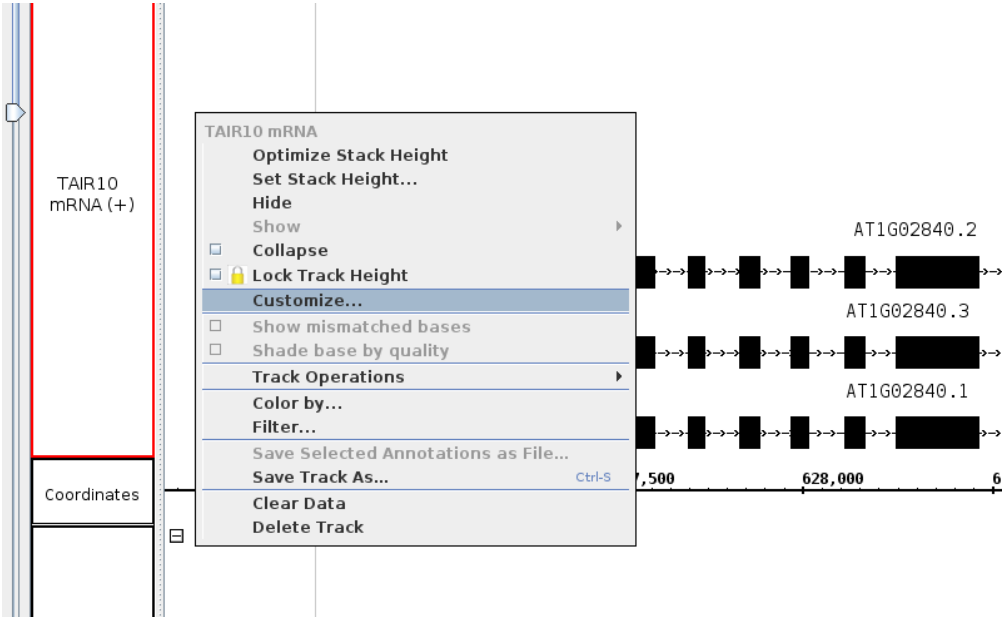# Track View

General Function Checklist

Validating Track Preference Changes

1. Open the **A_thaliana_Jun_2009** genome.
2. Navigate to the following coordinates: **Chr1:635,037-637,360**
3. Right click on the track label and select **Optimize Stack Height**.
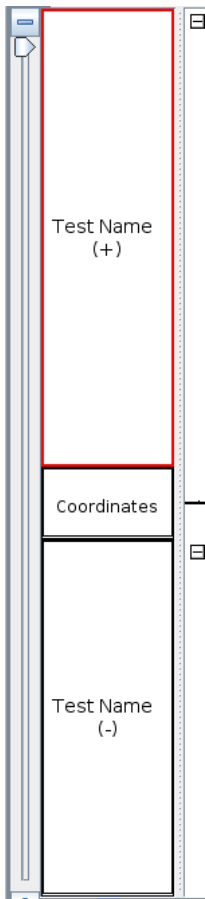4. Right click on the white space within a track.
5. Select **Customize...**

- This action opened the **Track Preferences** tab with the selected track highlighted.

- [ ] mac
- [ ] linux
- [ ] windows

Change the **Track Name** to **Test Name**, then select **Apply**.
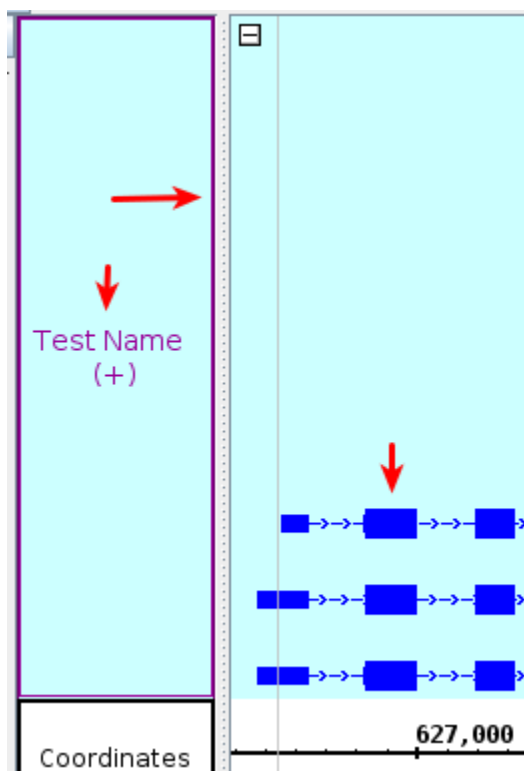

- The track names were updated.

- [ ] mac
- [ ] linux
- [ ] windows

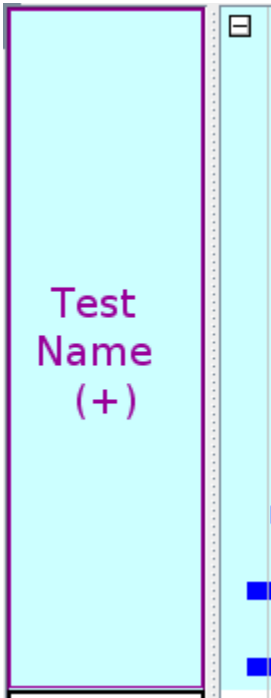Change the foreground, background, and track label colors to match the following image:

- The main view of IGB is now colored correctly with the three colors you chose.

☐ mac

☐ linux
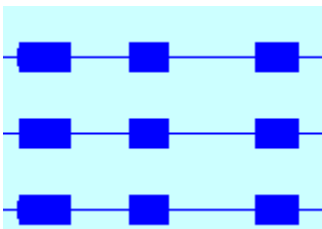
☐ windows

Change the track label font size to **20.0**.

- The font increased appropriately.

	mac
	linux
	windows

Uncheck the **Arrow** option in the **Show Strand** box.

- The barbed wire disappeared from the intron sections of gene models.

	mac
	linux
	windows

Check the **+/-** option in the **Show Strand** box to combine the plus and minus strands.
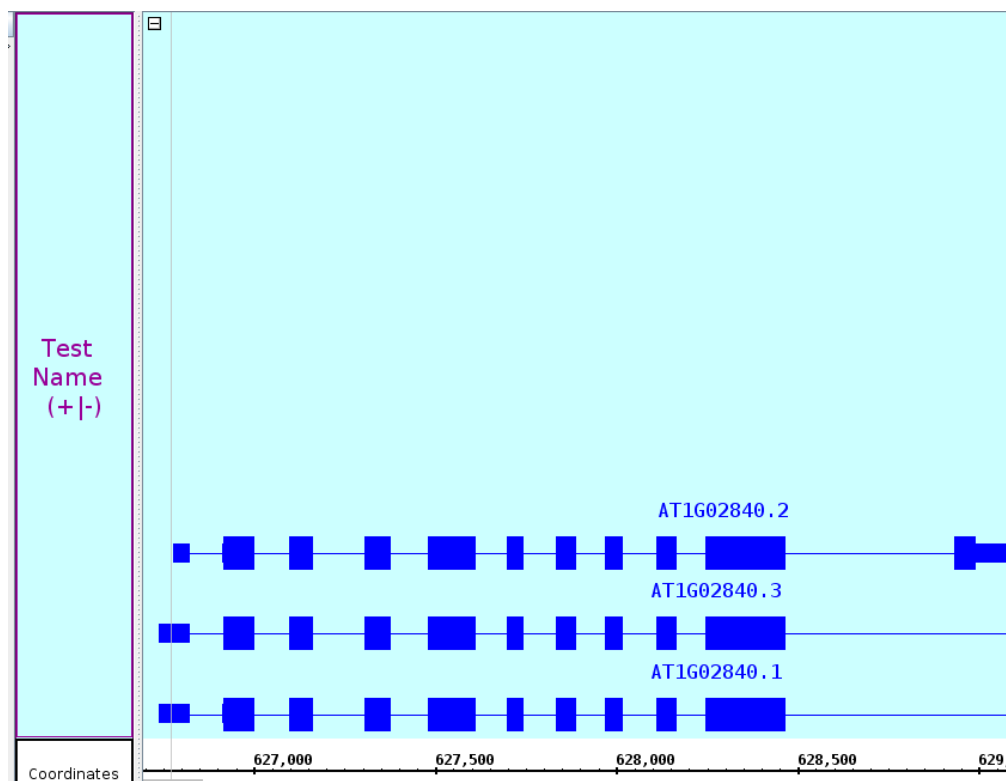

- The two strands are now one.

☐ mac

☐ linux

☐ windows

Check the **Color** option in the **Show Strand** box.

AT1G02860.2

AT1G02860.1

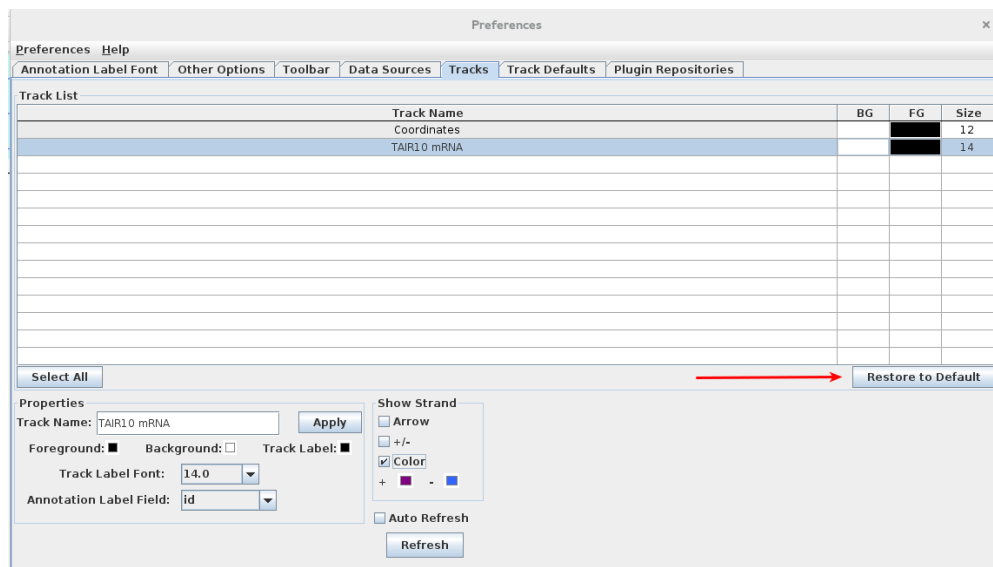635,000

AT1G0287…

- The gene models updated to the colors indicated.

☐ mac

☐ linux

☐ windows

Click **Restore to Default** in the **Tracks** tab in **Preferences**.

- All settings changed in the **Tracks** tab are restored to their original values
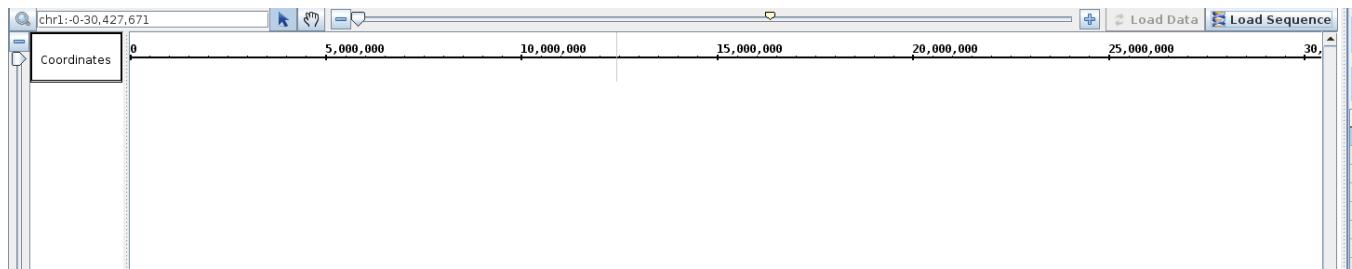
☐ mac

☐ linux

☐ windows

Adding and Removing Tracks

Right click on the white space surrounding the gene models.
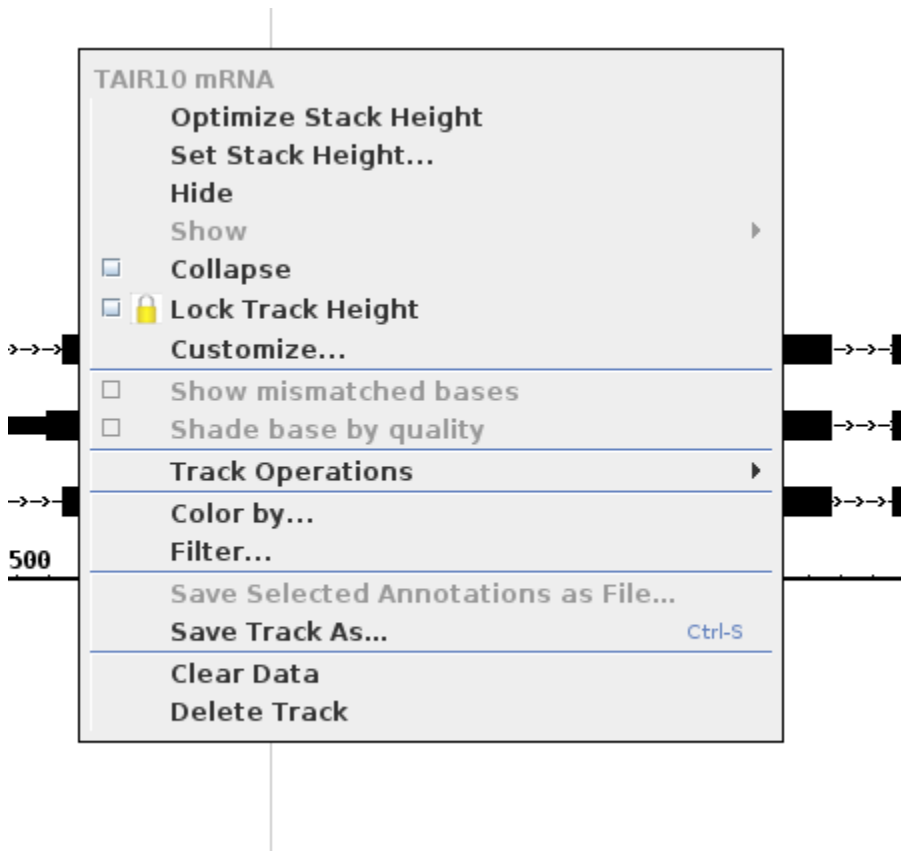
- The context menu looks like the one pictured above.

☐ mac

☐ linux

☐ windows
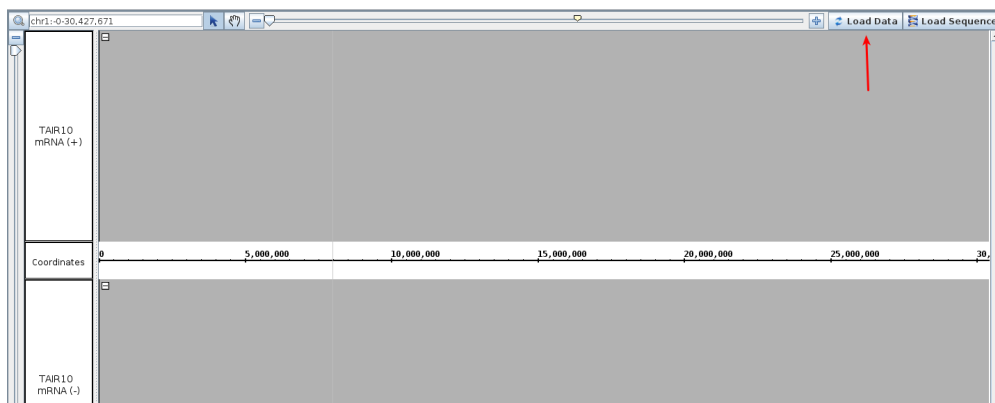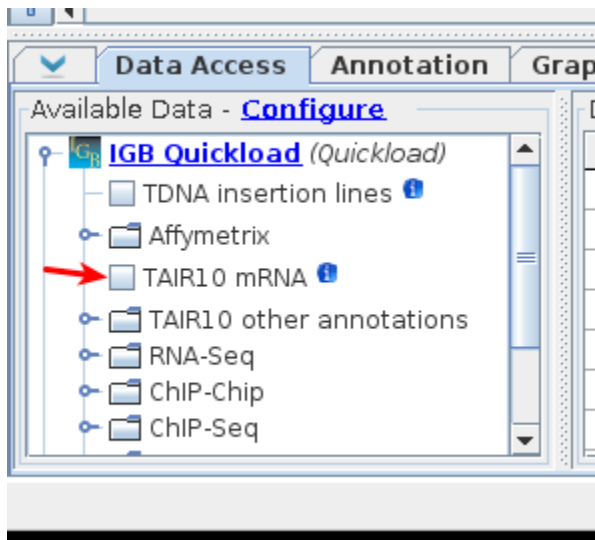
Select **Delete Track**.

- The track disappeared.

☐ mac

☐ linux

☐ windows

Add the **TAIR10 mRNA** track back in via the **Available Data** section.

- The track reappeared with no data loaded.

☐ mac

☐ linux

☐ windows