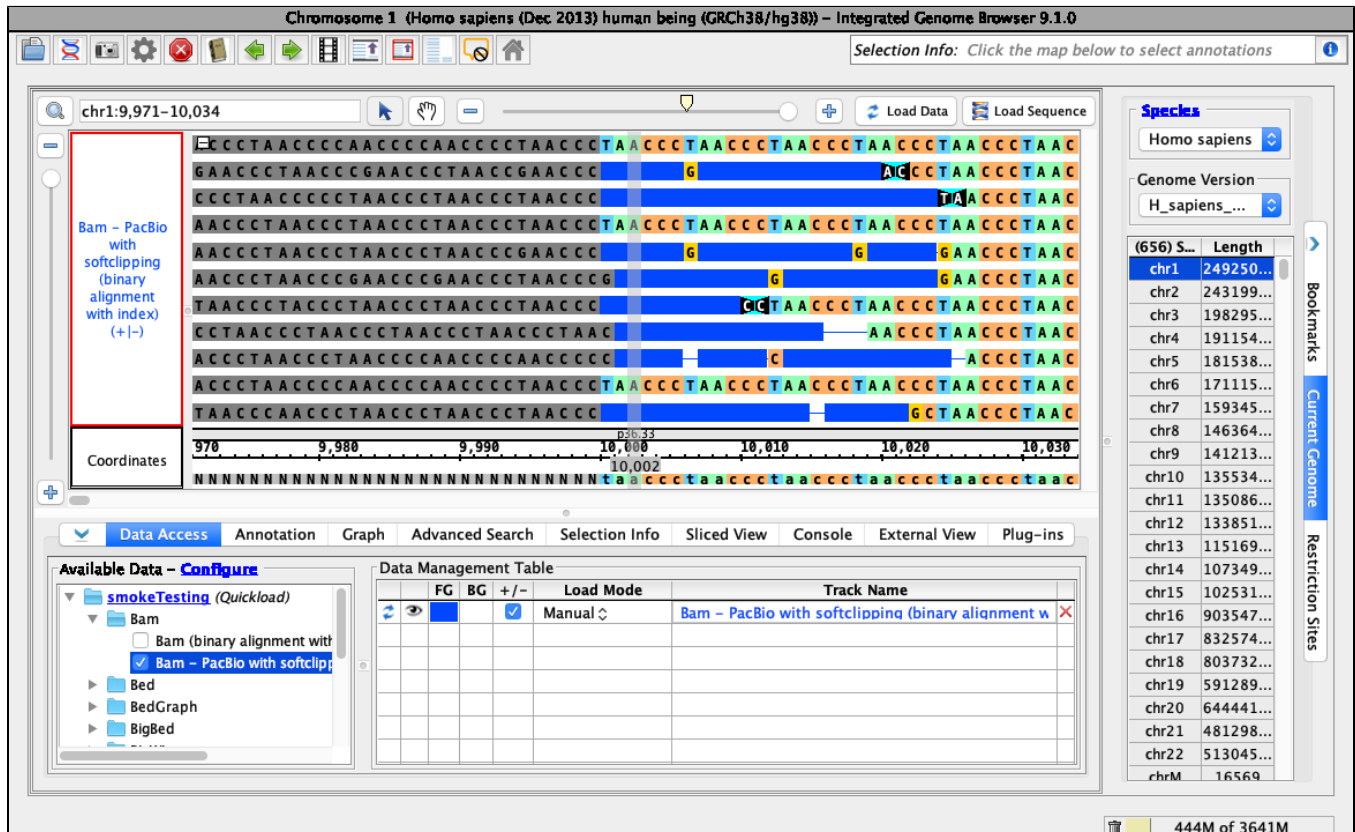


General Function Checklist

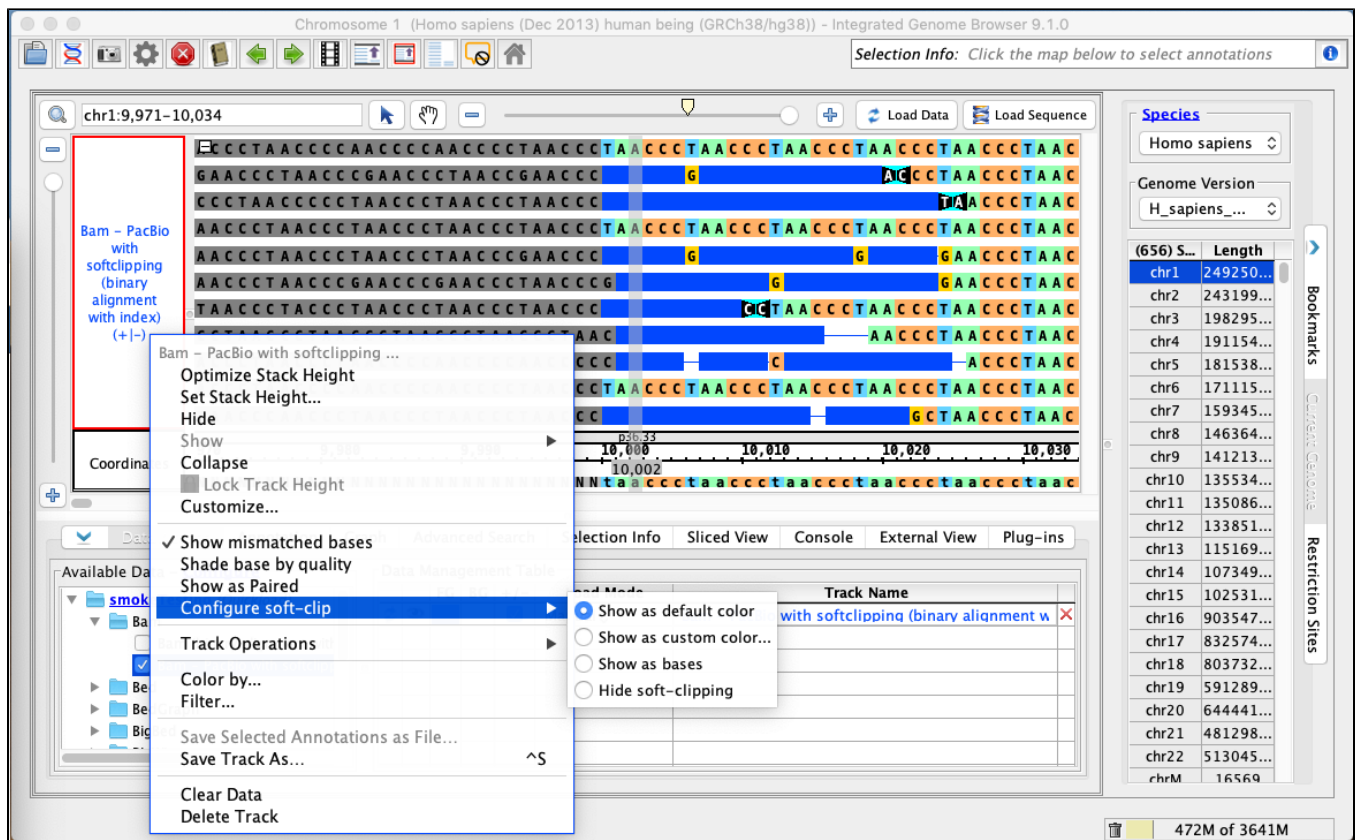
Objective: Validate that soft-clipping can be hidden and customized using the right-click menu of a bam track, as shown below:

1. In the **Data Sources** tab in **Preferences**, add the smoke test Data Provider to IGB using the following URL: <https://quickload-testing.s3.amazonaws.com/smokeTestingQuickload/>
2. Open the **H_Sapiens_Dec_2013** genome.
3. In the **Available Data** panel, add the **Bam - PacBio with softclipping** data from your newly added Quickload.
4. Navigate to: **chr1:9,971-10,034**
5. Click **Load Sequence** to load sequence data, then click **Load Data** to load data into it.



- Loading data looks like this (stack height set at 10, reads may be organized randomly):

- ☐ mac
- ☐ linux
- ☐ windows



- The **Configure soft-clip** submenu of the bam track right-click menu has **Show as default color** selected.

- ☐ mac
- ☐ linux
- ☐ windows

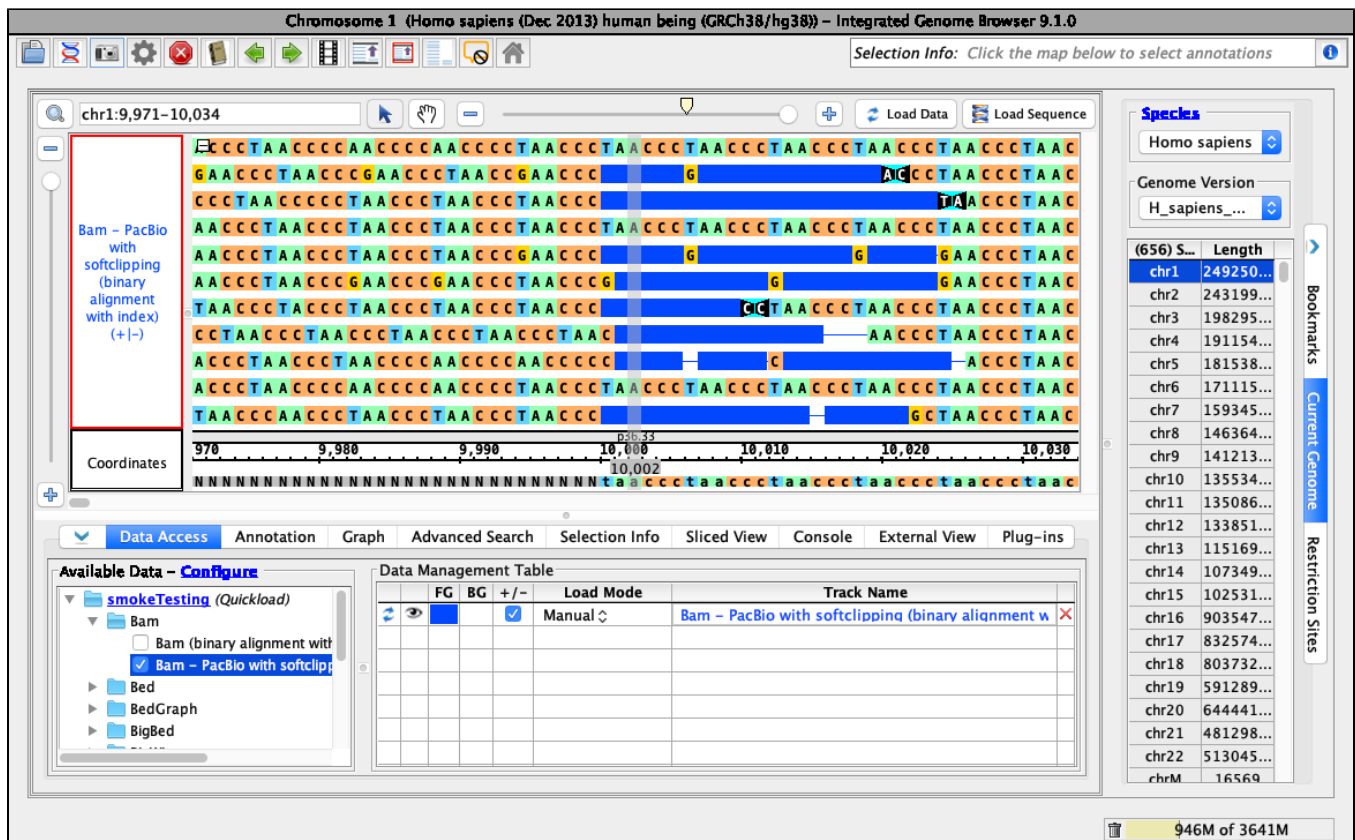
1. Right-click on the bam track and select: **Configure soft-clip** -> **Show as custom color**.
2. Choose a **red** color from the color picker.



- Your IGB looks like the above image.

- ☐ mac
- ☐ linux
- ☐ windows

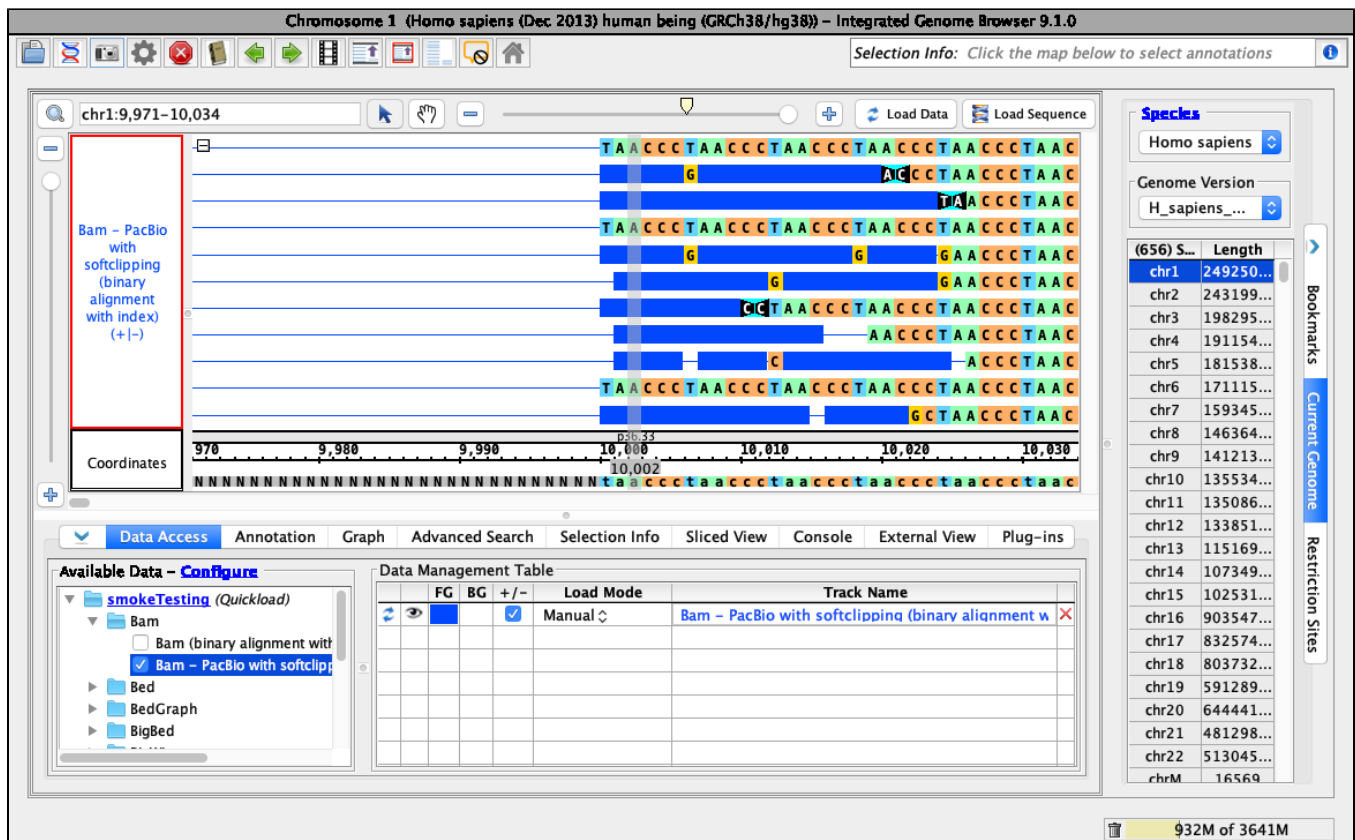
Right-click on the bam track and select: **Configure soft-clip** -> **Show as bases**.



- Your IGB looks like the above image.

- ☐ mac
- ☐ linux
- ☐ windows

Right-click on the bam track and select: **Configure soft-clip** -> **Hide softclipping**.



- Your IGB looks like the above image.

- ☐ mac
- ☐ linux
- ☐ windows

To test track operations are working correctly for soft-clipped data, right-click on the bam track and select the following:

1. Track Operations > Depth Graph (All)
2. Track Operations > Depth Graph (Start)
3. Track Operations > Mismatch Graph
4. Track Operations > Mismatch Pileup Graph
5. Collapse

