## **Soft-Clipping**

## **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:

- 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/
   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.

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- The Configure soft-clip submenu of the bam track right-click menu has Show as default color selected.
- mac
- linux
- windows
  - Right-click on the bam track and select: Configure soft-clip -> Show as custom color.
     Choose a red color from the color picker.

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- Your IGB looks like the above image.
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- Your IGB looks like the above image.
- mac
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Right-click on the bam track and select: Configure soft-clip -> Hide softclipping.

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- Your IGB looks like the above image.
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To test track operations are working correctly for soft-clipped data, right-click on the barn track and select the following:

- Track Operations > Depth Graph (All)
   Track Operations > Depth Graph (Start)
   Track Operations > Mismatch Graph
   Track Operations > Mismatch Pileup Graph
   Collapse

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- Your IGB looks like the above image.
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