

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:

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.

Chromosome 1 (Homo sapiens (Dec 2013) human being (GRCh38/hg38)) - Integrated Genome Browser 9.1.0

Selection Info: Click the map below to select annotations

chr1:9,971-10,034

Bam - PacBio with softclipping (binary alignment with index) (+/-)

Coordinates

Available Data - Configure

- smokeTesting (Quickload)
 - Bam
 - Bam (binary alignment with index) (+/-)
 - ☒ Bam - PacBio with softclipping
 - Bed
 - BedGraph
 - BigBed

FG	BG	+/-	Load Mode	Track Name
☒	☒	☒	Manual	Bam - PacBio with softclipping (binary alignment with index) (+/-)

Species: Homo sapiens

Genome Version: H_sapiens...

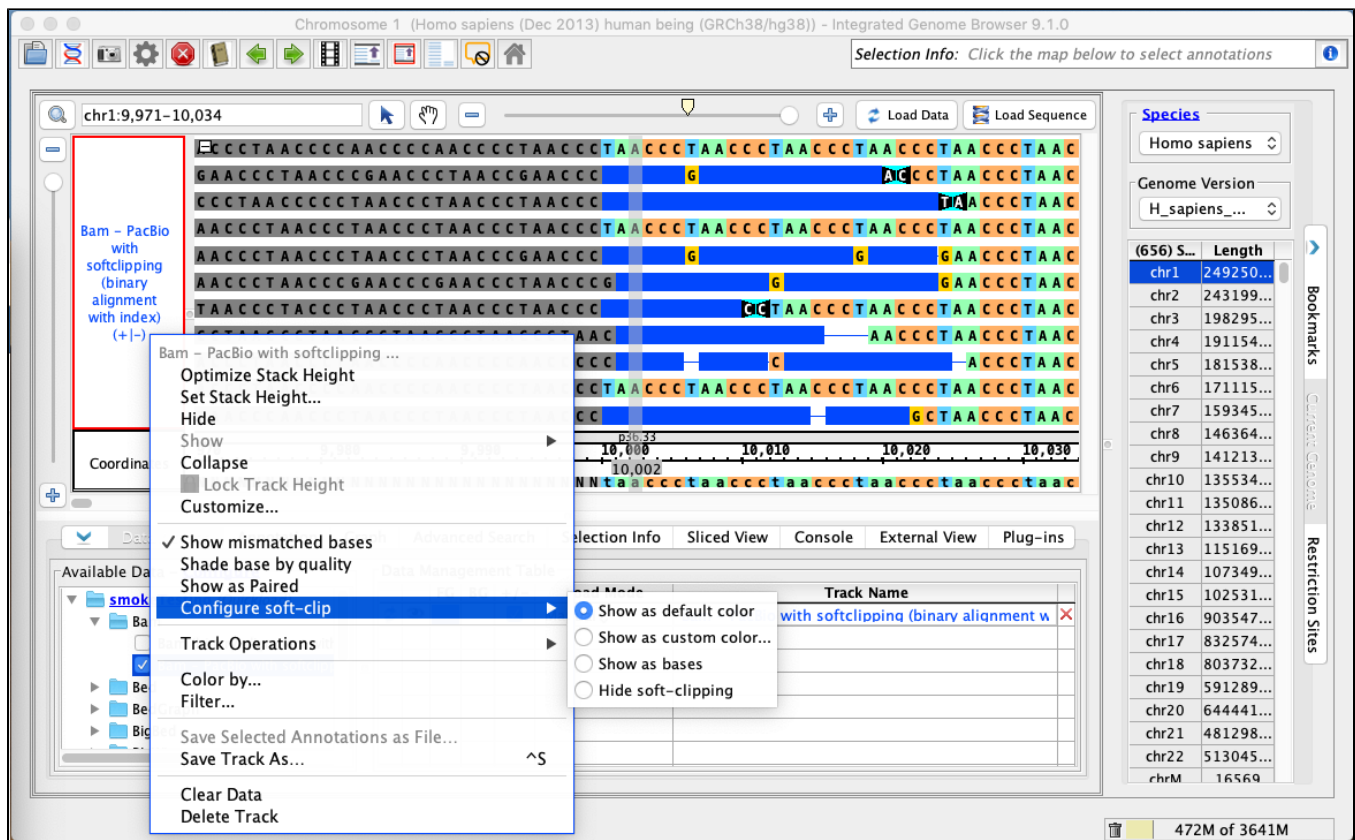
(656) S... Length

chr	Length
chr1	249250...
chr2	243199...
chr3	198295...
chr4	191154...
chr5	181538...
chr6	171115...
chr7	159345...
chr8	146364...
chr9	141213...
chr10	135534...
chr11	135086...
chr12	133851...
chr13	115169...
chr14	107349...
chr15	102531...
chr16	903547...
chr17	832574...
chr18	803732...
chr19	591289...
chr20	644441...
chr21	481298...
chr22	513045...
chrM	16569...

444M of 3641M

- 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

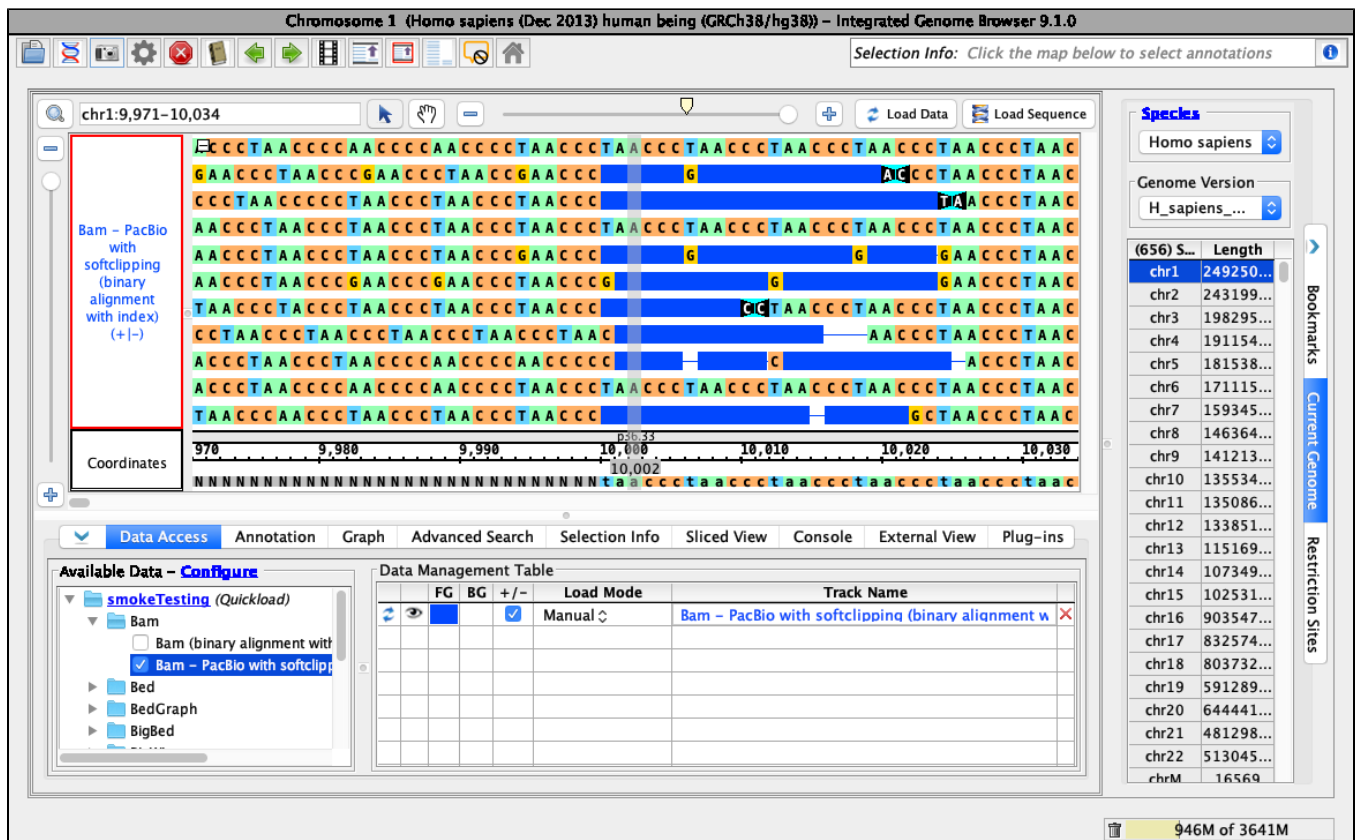
1. Right-click on the bam track and select: **Configure soft-clip** -> **Show as custom color**.
2. Choose a **red** color from the color picker.



- Your IGB looks like the above image.

- ☐ mac
- ☐ linux
- ☐ windows

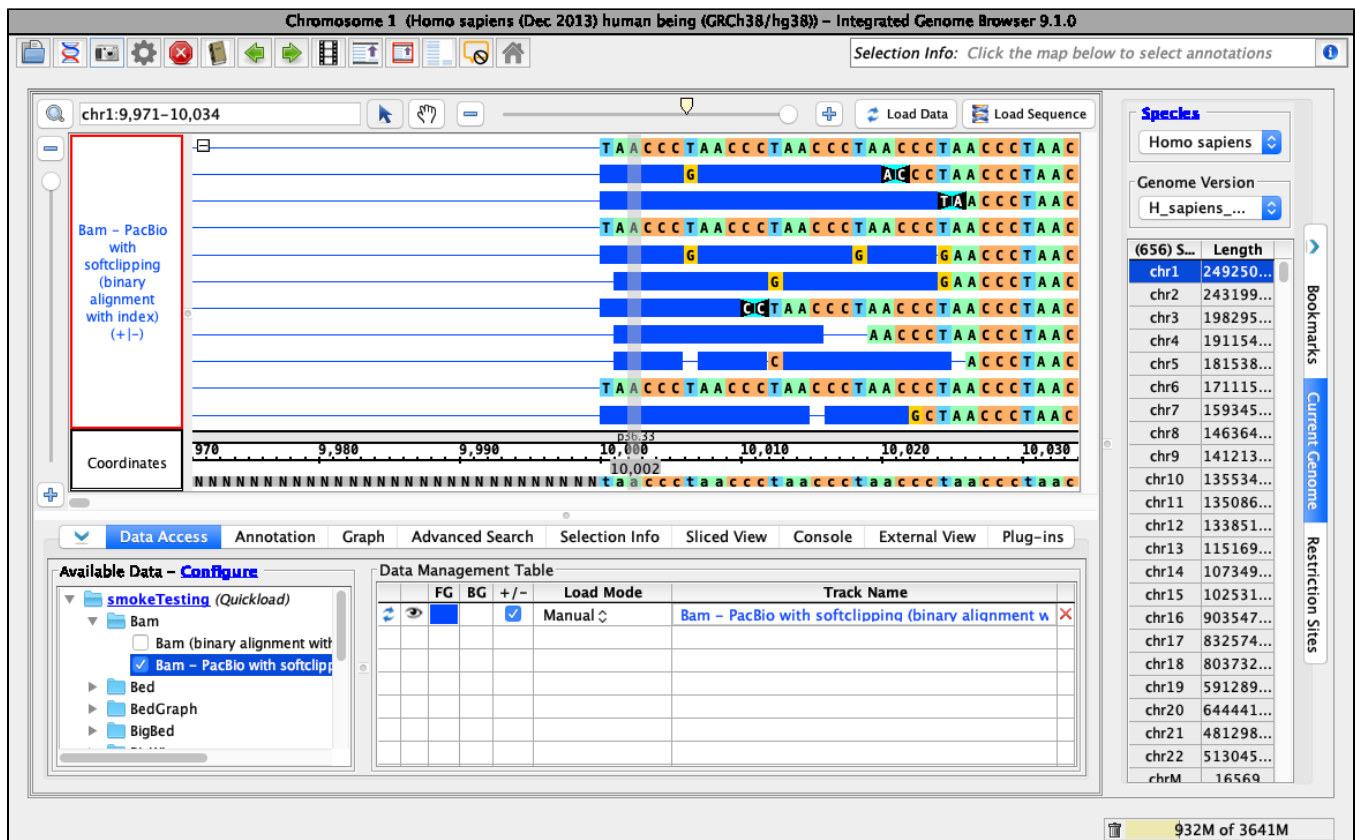
Right-click on the bam track and select: **Configure soft-clip** -> **Show as bases**.



- 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

