Track Operators - Annotation Tracks

General Function Checklist

Annotation Track Operators

Note: Be sure to look at the user guide pages linked here. Skim them to make sure that the topics they cover are represented here (if not add points here as needed). Read enough to ensure that the instructions and explanations are clear, and the page has accurate information and generally appears up-to-date.

See Users Guide pages:

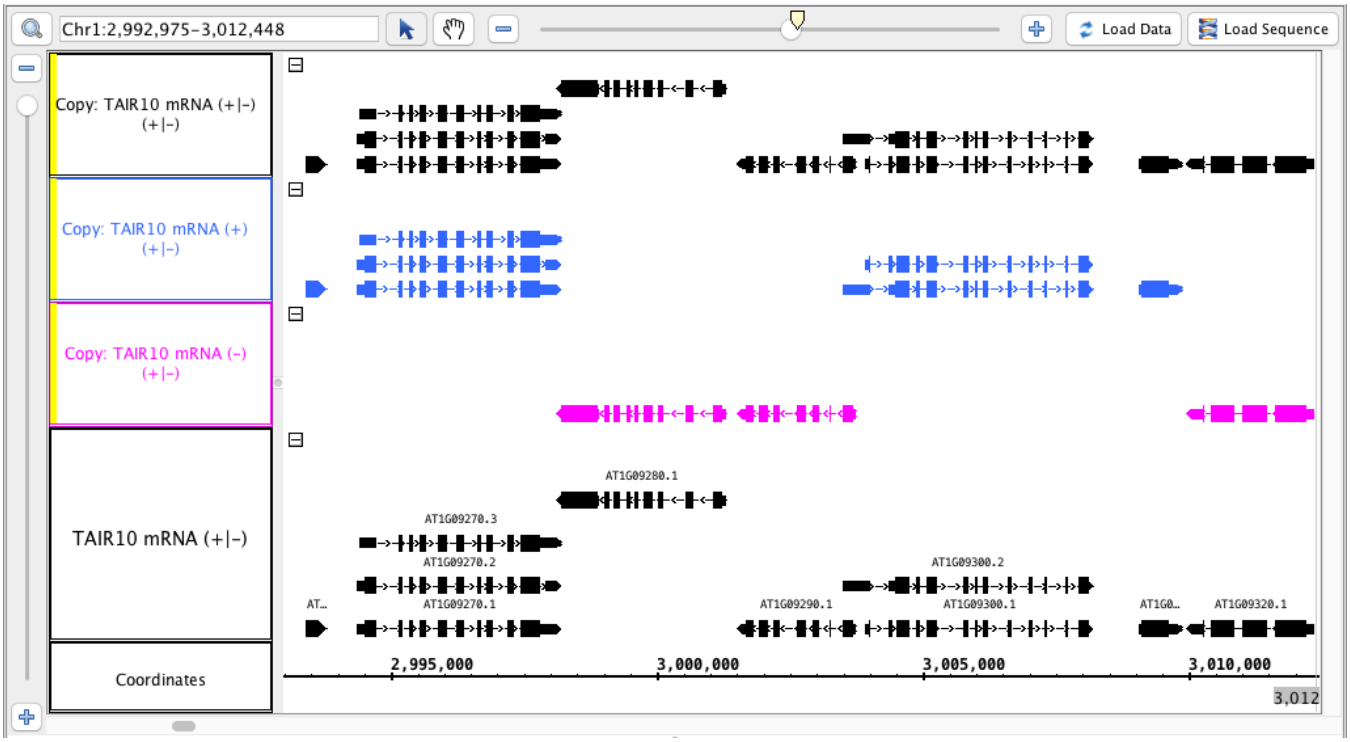
- [ ] Annotation track operations
- [ ] Creating graph tracks from annotations tracks

single track - output an annotation track

1. Open the **A_thaliana_Jun_2009** genome.
2. Go to this region: **Chr1:2,992,975-3,012,448**
3. Load the **TAIR10 mRNA** track via the **Available Data** section (**IGB Quickload** > **TAIR10 other annotations**).
4. Select the **Annotation** tab at the bottom of IGB, and look for the **Operations** box.

single track - copy

1. Select the (-) track and select **Copy**, hit **Go**.
2. Select the (+) track, select **Copy**, hit **Go**.
3. Combine the (-) and (+) tracks into one using the **+/-** checkbox.
4. Select the **+/-** track, select **Copy**, hit **Go**.
5. In the **Annotation** tab, use **Select All**, and under **Strand**, check the **Arrow** option (to make visual verification easier).



- The tracks produced match the image above (color matching is optional).

- [ ] Mac
- [ ] Linux
- [ ] Windows

- The track names for the new tracks indicate which track they were made from AND which strand (-, + or +/-)

- [ ] Mac
- [ ] Linux
- [ ] Windows

- The tracks made from only one strand have only the annotations from that strand.

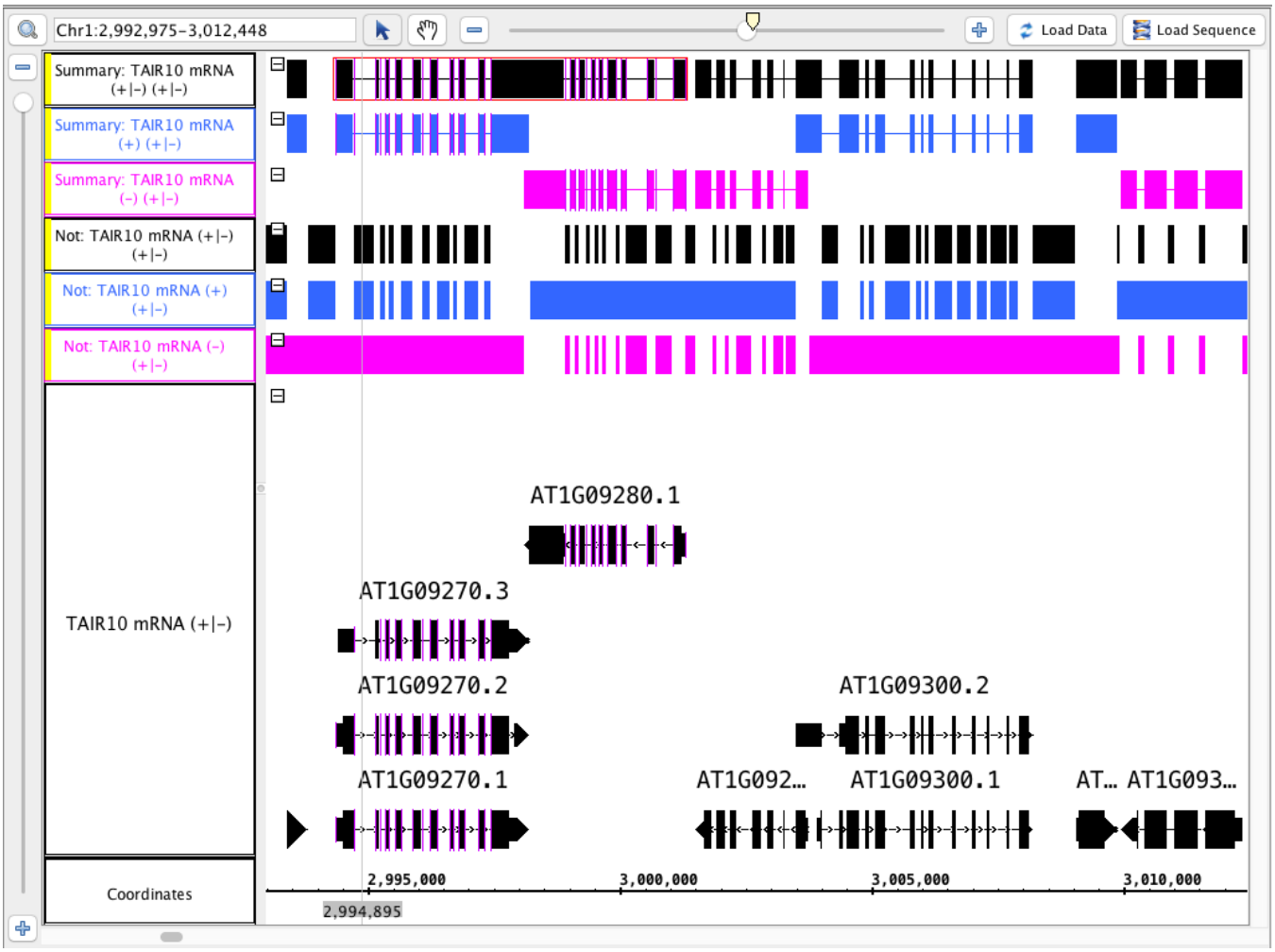
- [ ] Mac
- [ ] Linux
- [ ] Windows

- The track made from both strands has annotations from both strands.

- [ ] Mac
- [ ] Linux
- [ ] Windows

single track - not, summary

1. Delete the tracks you just created.
2. Split the **TAIR10 mRNA** track back into separate - and + tracks.
3. Select the (-) track, select **Not**, hit **Go**.
4. Select the (+) track, select **Not**, hit **Go**.
5. Recombine the - and + tracks.
6. Select the (+/-) track, select **Not**, hit **Go**.
7. Repeat all of the above for the **Summary** operation.
8. Color the tracks that were made from the (-) strand pink and the (+) blue for visual verification.



- Your IGB looks like the image above.

- [ ] Mac
- [ ] Linux
- [ ] Windows

multi track - output an annotation track

1. Using the combined (+/-) **TAIR10 mRNA** track, run the **Summary** operation and the **Not** operation.
2. Hide the original track and highlight the two newly created tracks (hold shift and click each one) --Select the **Not** track first.
3. Perform each of the multi-track operations:
    a. A not B
    b. B not A
    c. Intersection
    d. Union
    e. Xor

- Your IGB looks like the image above.

- [ ] Mac
- [ ] Linux
- [ ] Windows

- Track labels include the names of the operation and the input tracks.

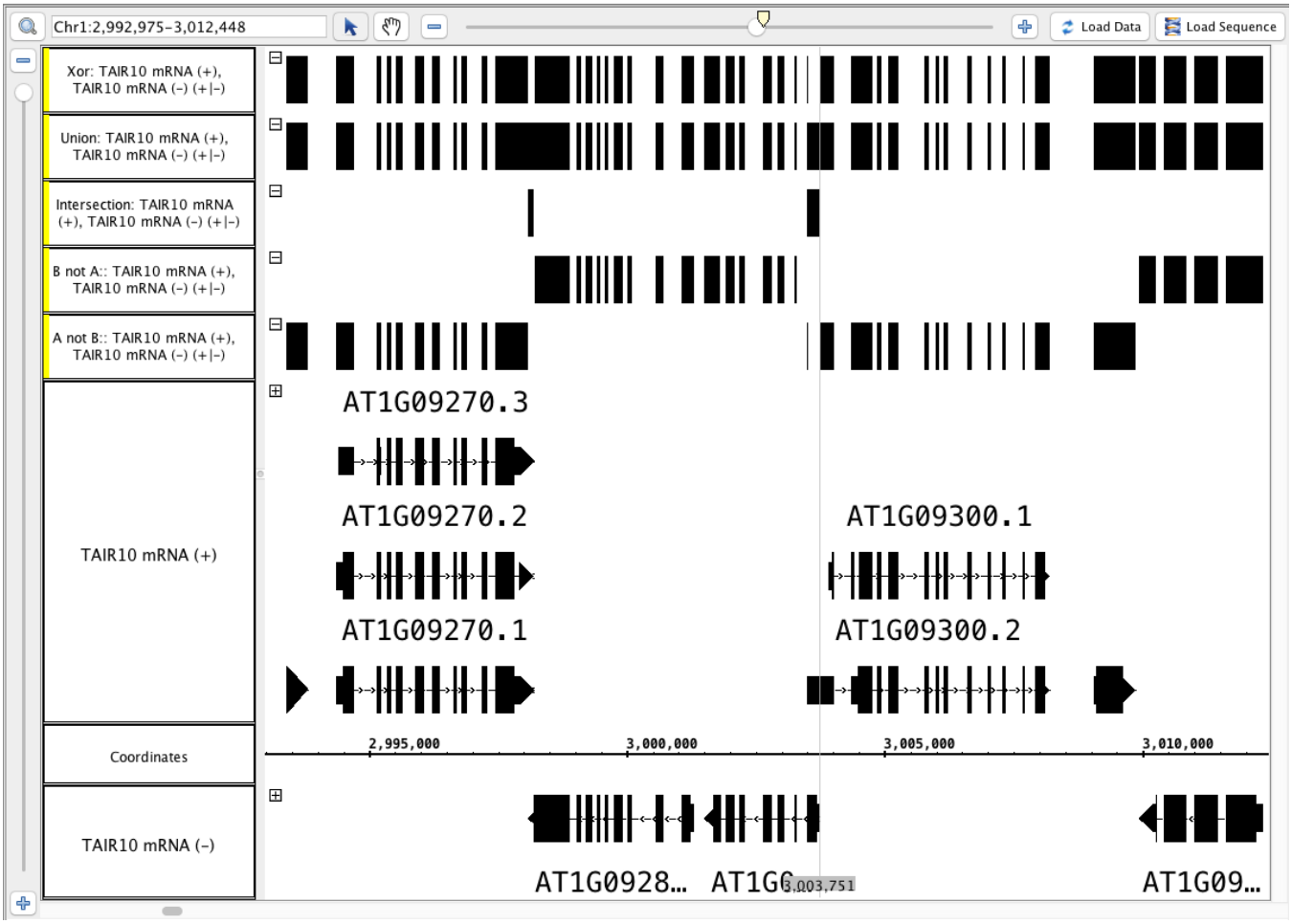
- [ ] Mac
- [ ] Linux
- [ ] Windows

- Each track is identical to the "Not" track, or identical to the "Summary" track, or completely solid, as appropriate.

- [ ] Mac
- [ ] Linux
- [ ] Windows

1. Delete the tracks you just created.

2. Using the split (-) and (+) **TAIR10 mRNA** track, perform each of the multi-track operations:
    a. A not B
    b. B not A
    c. Intersection
    d. Union
    e. Xor



- Your IGB looks like the image above (Particularly notice the area around the zoom stripe, it highlights the difference between Union and Xor.)

- [ ] Mac
- [ ] Linux
- [ ] Windows

single track - output a graph track from a bed file

1. Use the + and - tracks separately to run each of these operations (this produces 4 graph tracks).
    a. depth (all) (single track)
    b. depth (start) (single track)
2. Repeat this by selecting both the - and the + track at the same time (hold shift) and selecting the above single track operations.

- The results of step 1 and 2 above are identical.

- [ ] Mac
- [ ] Linux
- [ ] Windows

1. Select one of the **depth (all)** graphs.
2. In the **Graph** panel, choose **Thresholding...**
3. Set **Visibility** to **On**.
4. Slide the **By Value** slider back and forth.

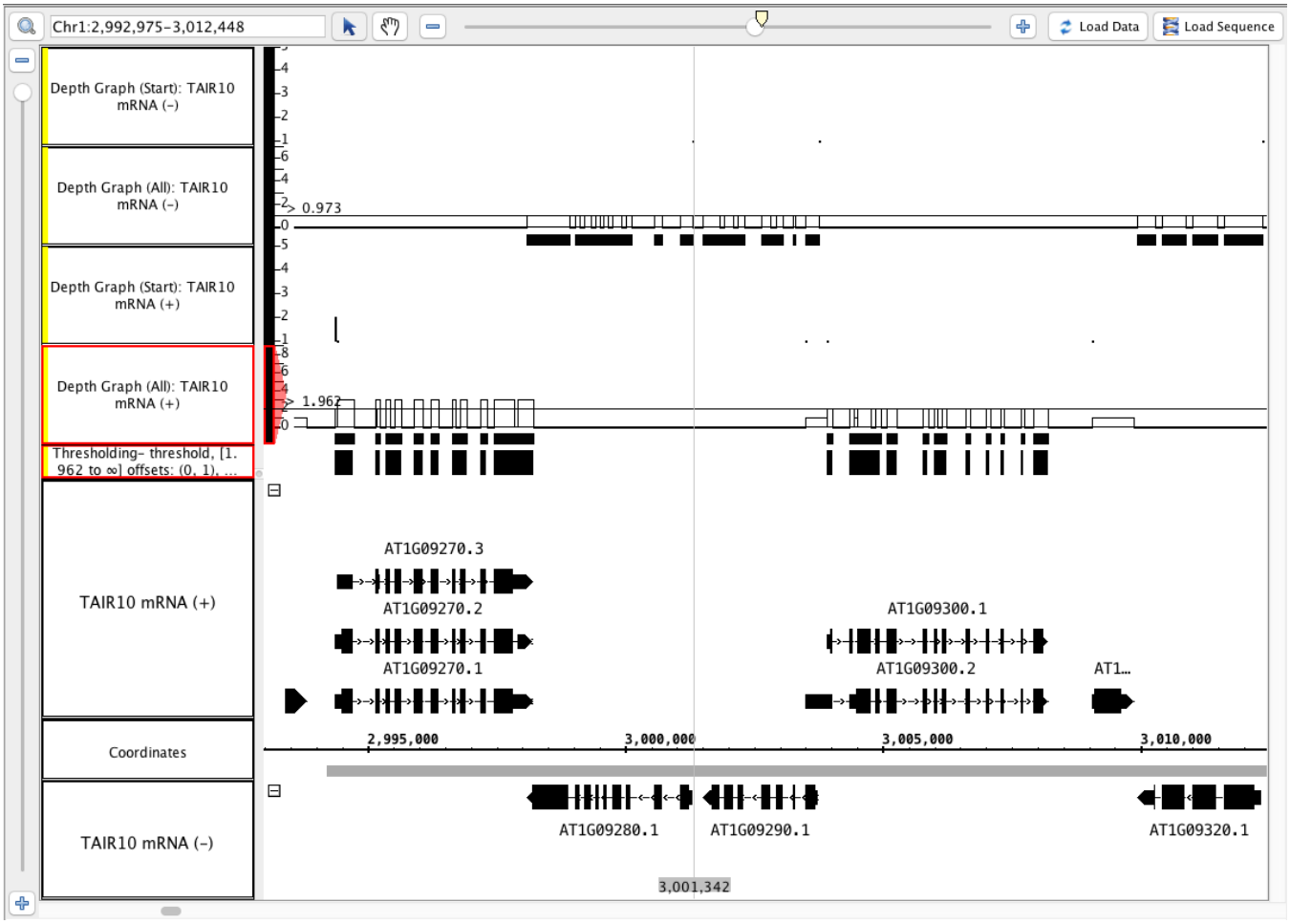
- The little blocks appear and disappear as the line touches the graph.

- [ ] Mac
- [ ] Linux
- [ ] Windows

- The values in the graph track correspond to counts of annotations that cover each location.

- [ ] Mac
- [ ] Linux
- [ ] Windows

Click **Make Track**.



- The new track looks correct based on the **By Value** threshold that you set.

- [ ] Mac
- [ ] Linux
- [ ] Windows

- The new track has an appropriate label that indicates what threshold was used to create it.

- [ ] Mac
- [ ] Linux
- [ ] Windows

- Your IGB looks similar to the image above (notice that the depth (start) graphs have data in a 1-base-wide area at the start of the annotations, and where there is only 1 annotation, the graph has a height of 1).

- [ ] Mac
- [ ] Linux
- [ ] Windows

single track - output a graph track from a bam file (part 1)

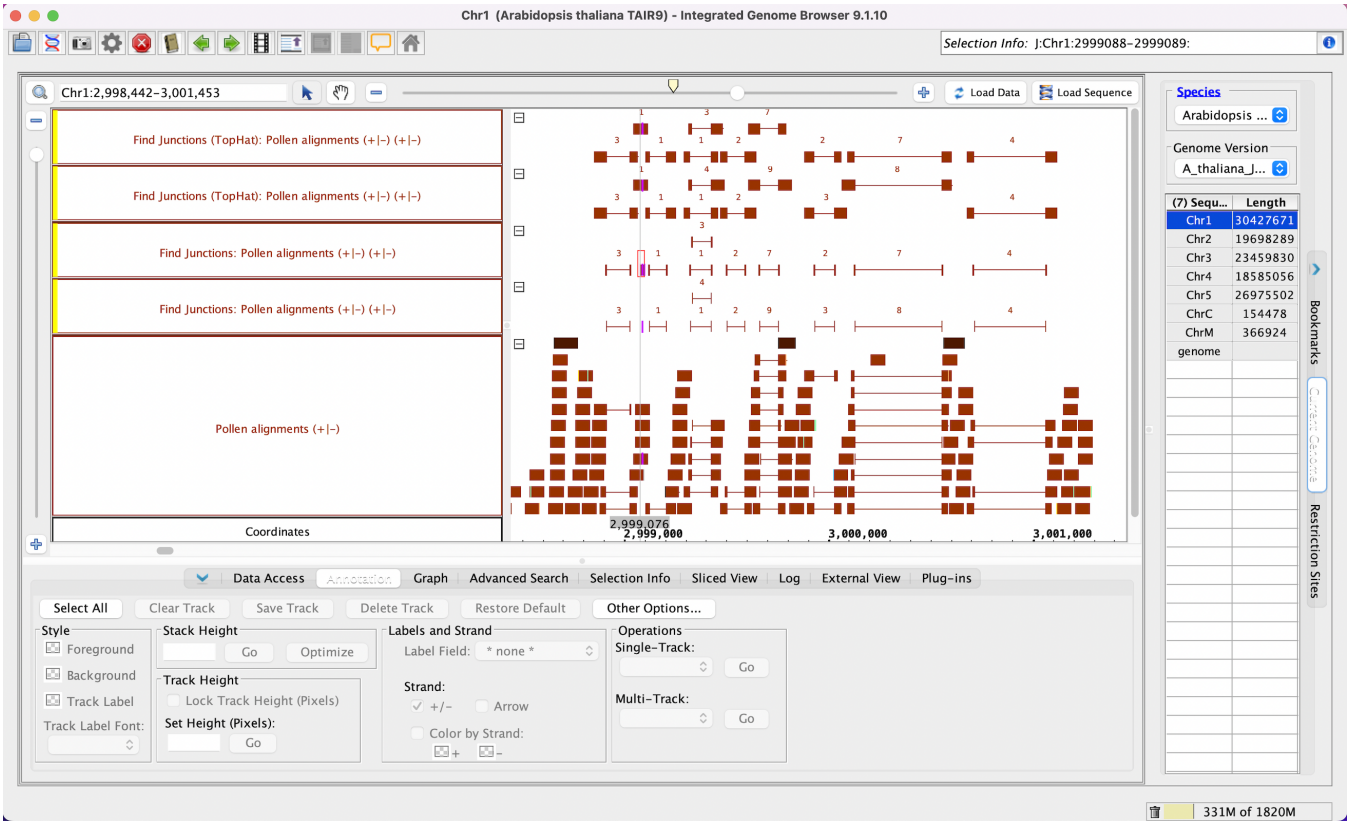
Go to this region: **Chr1:2,998,442-3,001,453**

From the **RNA-Seq Quickload** in the **Available Data** section, add the **RNA-Seq / Pollen SRP022162 / Reads / Pollen alignments** file.

Click **Load Data**, then **Load Sequence**.

Select the Pollen alignments track and run the following single track operations:

- Select **Find Junctions**, enter **5**, hit go.
- Select **Find Junctions**, enter **10**, hit go.
- Select **Find Junctions (tophat)**, enter **5**, hit go.
- Select **Find Junctions (tophat)**, enter **10**, hit go.



- Your IGB looks like the image above (*Read the junctions user guide **page** for more details).

- [ ] Mac
- [ ] Linux
- [ ] Windows

Right click blank space in any of the tracks, then click **Optimize Track Height**.

- The sizes of the blocks for the **Find Junctions** tracks match the value you entered; the **Find Junctions (tophat)** results will not all have the same block size.

- [ ] Mac
- [ ] Linux

- [ ] Windows

- The count above each junction is equal to the number of reads that matched that gap.

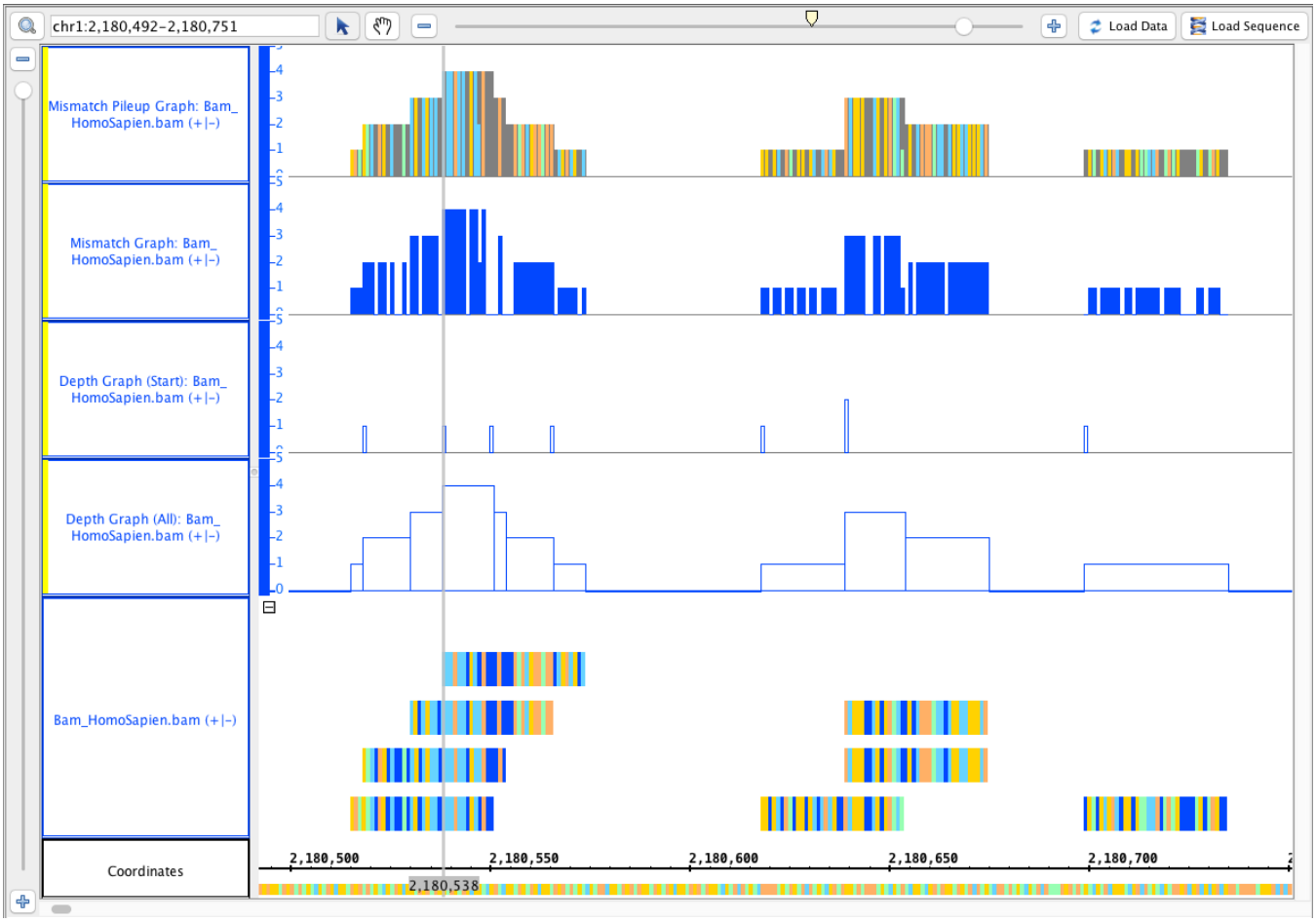
- [ ] Mac
- [ ] Linux
- [ ] Windows

- Find someplace where the matching Find Junctions operation using value 5 and value 10 have different scores. Identify the read(s) that matches that junction, and where where one side of the read is between 5 and 10 bases.

- [ ] Mac
- [ ] Linux
- [ ] Windows

single track - output a graph track from a bam file (part 2)

1. Open the **H_Sapiens_Dec_2013** genome.
2. Add the smoke testing Quickload using the **Available Data** section: http://igbquickload.org/smokeTestingQuickload/
3. Add the **Bam (binary alignment with index)** track to IGB.
4. Go to this region: **chr1:2,180,492-2,180,751**
5. Click **Load Data**, then click **Load Sequence**.
6. Select the **Bam (binary alignment with index)** track and do the following single track operations:
    a. **depth (all)** (single track)
    b. **depth (start)** (single track)
    c. **Mismatch Graph**
    d. **Mismatch Pileup Graph**



- Your IGB looks like the image above.

- [ ] Mac
- [ ] Linux

- [ ] Windows

1. Zoom out to the following coordinates: **chr1:2,180,361-2,180,883**
2. Click **Load Data** (do **not** load sequence). Load data a second time if needed, but not a third.

- The sequence loaded as needed after a max of two time clicking **Load Data**.

- [ ] Mac
- [ ] Linux
- [ ] Windows

Go to this region: **chr1:3,785,135-3,785,276**

- Your IGB looks like the image above.

- [ ] Mac
- [ ] Linux
- [ ] Windows

Users Guide

Review the users guide pages.

- Each page has accurate information and generally appears up-to-date.

- [ ] Mac
- [ ] Linux
- [ ] Windows