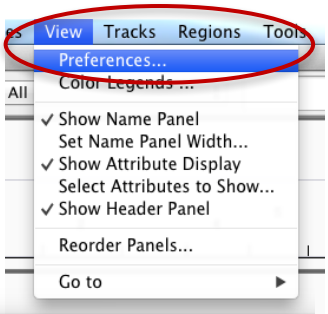
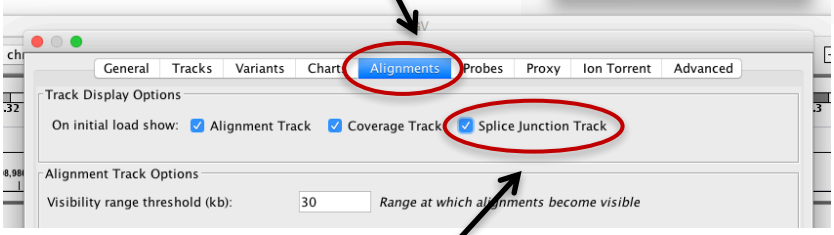
IGV Hands-on Exercise | Compute coverage track

1. Set preferences for viewing RNA-seq data

Click *View > Preferences*



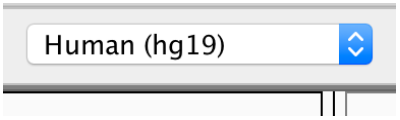
Select *Alignments* tab



Check *Splice Junction Track*

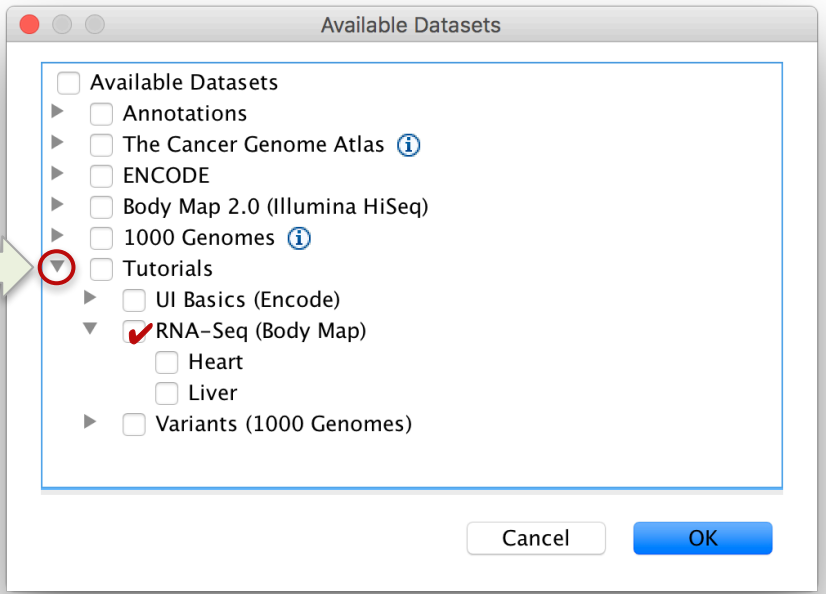
2. Load data

Select *Human hg19* from the genome dropdown menu



Click *File > Load from Server*

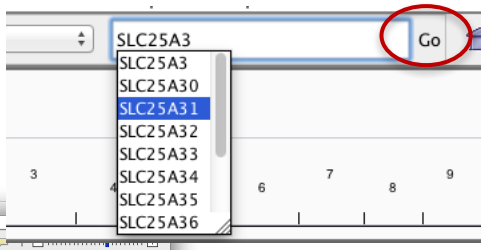
Open the *Tutorials* menu (Use ▶ on Mac, and + on Windows)
and click on *RNA-Seq (Body Map)*
and then click on *OK*

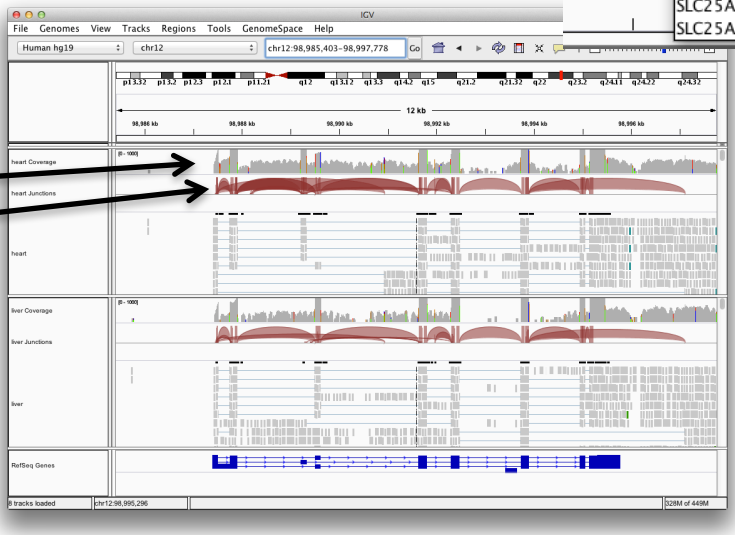


Make sure you only **open** the *Tutorials* menu. Do **not** check the box next to *Tutorials.* That will select everything under *Tutorials,* but we only want *RNA-Seq* for this exercise.

3. Jump to gene SLC25A3

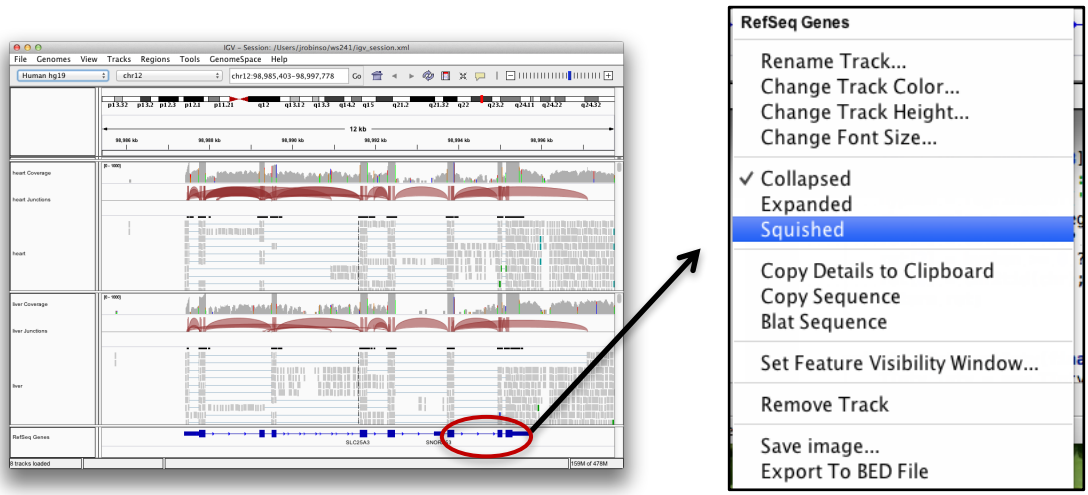
Type *SLC25A3* in the search box and click ***Go***





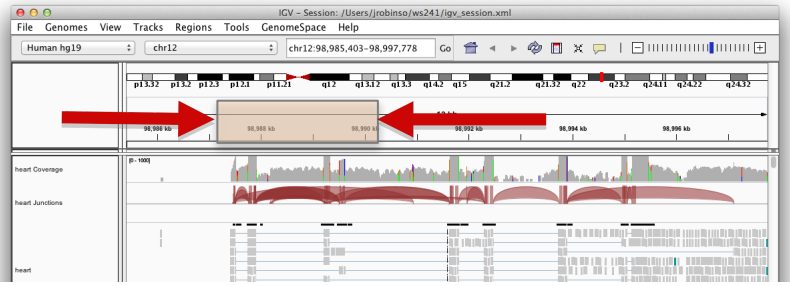
4. Expand gene track to see isoforms

Right-click over the *RefSeq Genes* track, and select ***Squished***



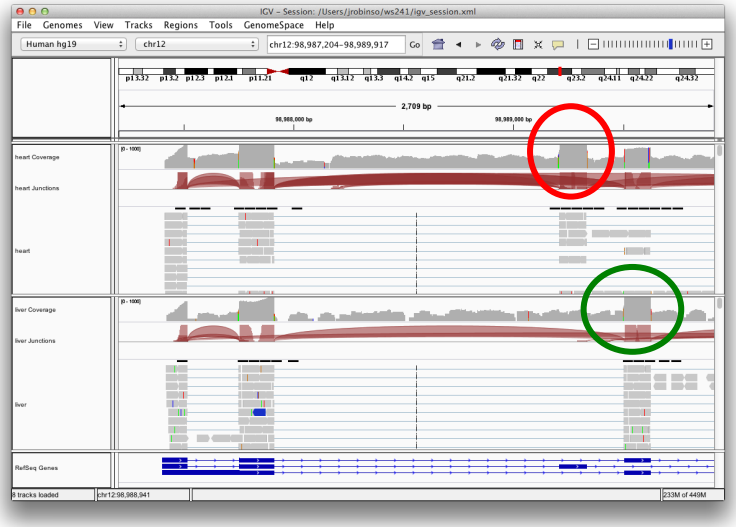
5. Zoom in on first 3 exons

Click and drag in ruler region over area shown



6. Note evidence of alternative splicing.

Observe which isoforms in the RefSeq track are expressed in each tissue.

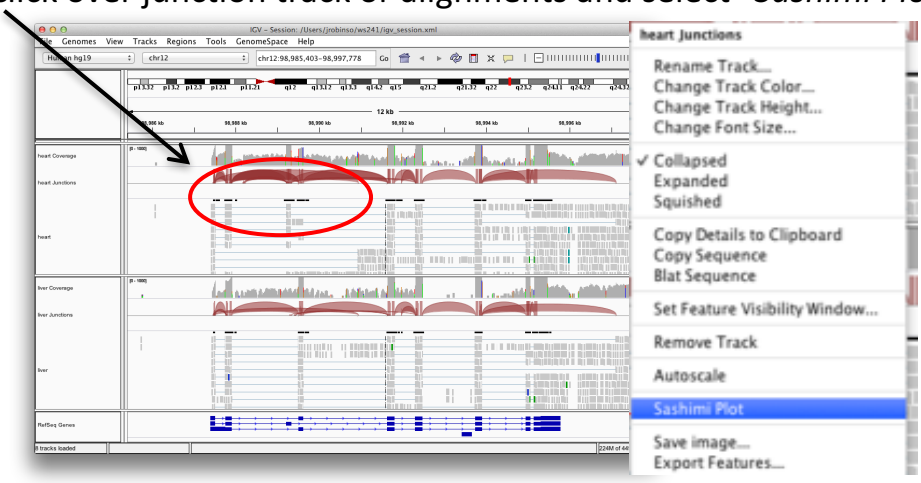


7. Zoom back out to view whole gene

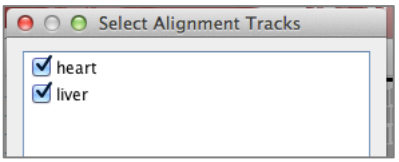
Click the back button in the command bar to zoom out to previous view

8. Open Sashimi plot

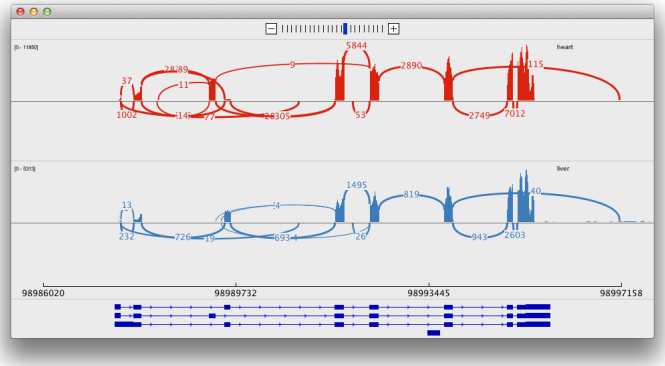
Right-click over junction track or alignments and select *"Sashimi Plot"*



Verify both *heart* and *liver* are checked, and click *OK*



9. Examine Sashimi plot



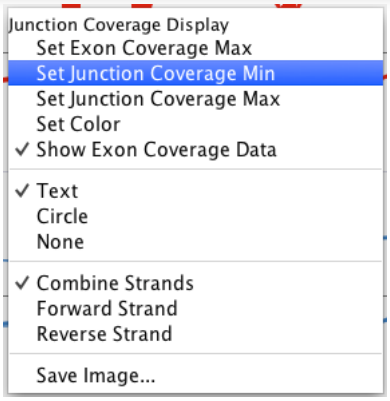
Note:

- Arcs represent reads spanning exon junctions
- Peaks represent exon coverage

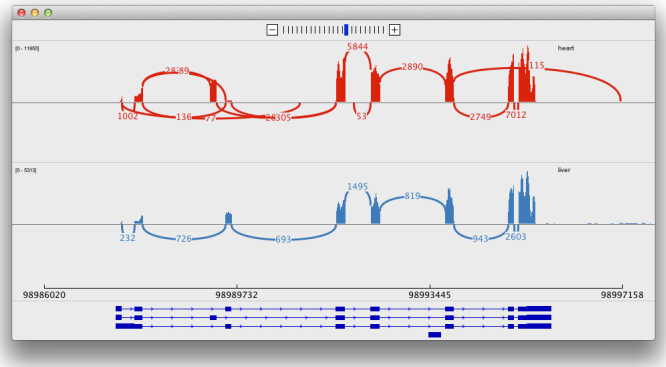
10. Filter out low-count splicing events

Right click over red (heart) track and select ***Set Junction Coverage Min***. Enter **50** and click ***OK***.

Repeat for blue (liver) track.



11. Compare with non-filtered view



12. Zoom in on 5' end

Click "+" button 2 times

Click-and-drag tracks to the right to bring the first 3 exons in view.

13. Observe the alternative splicing of the 3rd exon

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END OF EXERCISE