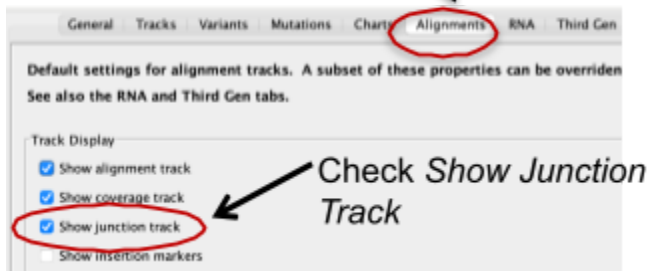
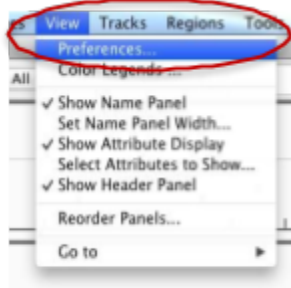


### 1. Set preferences for viewing RNA-seq data

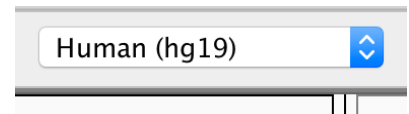
Click *View > Preferences*

Select *Alignments* tab





### 2. Load data

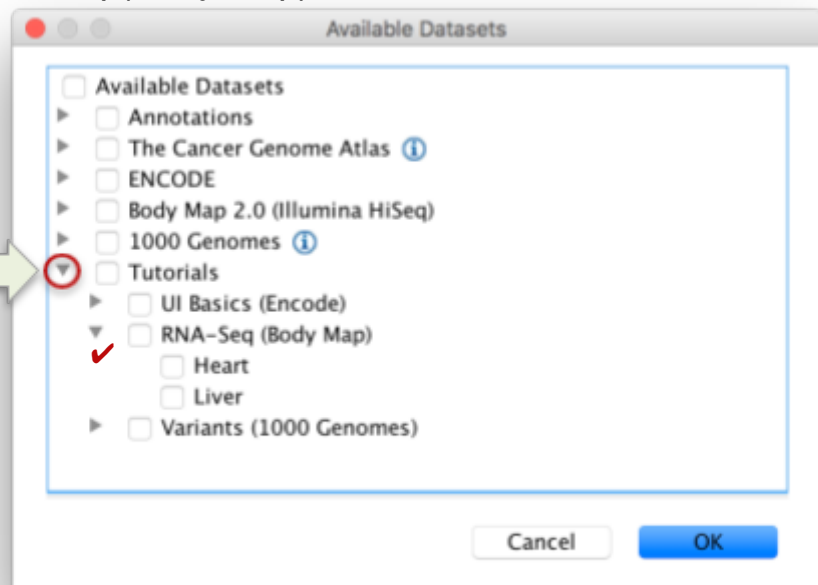
Select *Human hg19* from the genome dropdown



menu Click *File > Load from Server*

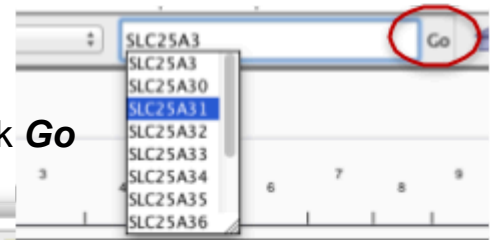
Open the *Tutorials* menu (Use  on Mac, and  on Windows) and click on *RNA-Seq (Body Map)* and then click on *OK*

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.

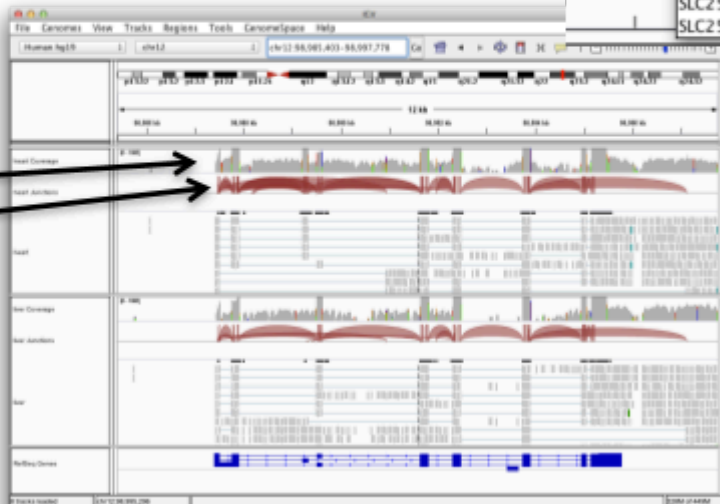


### 3. Jump to gene SLC25A3

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

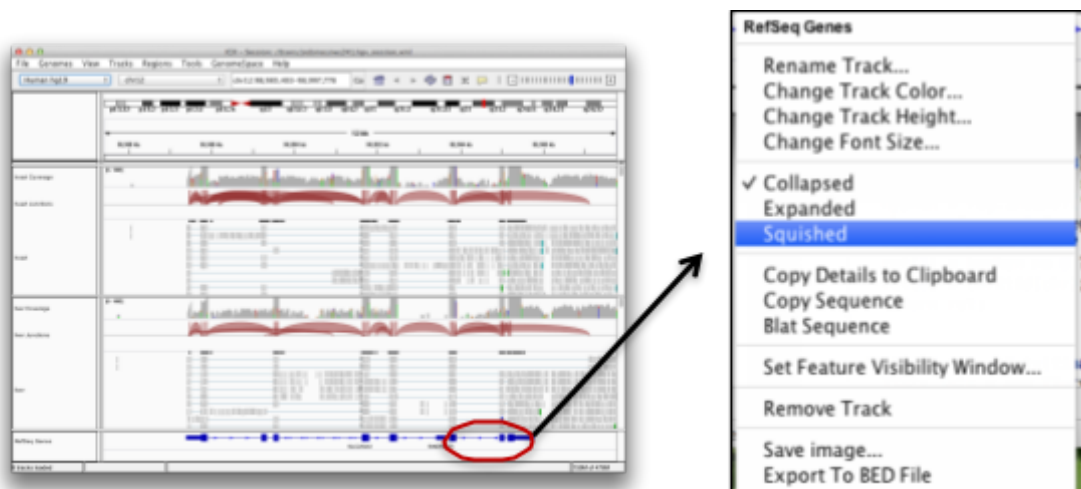


Coverage  
Junctions



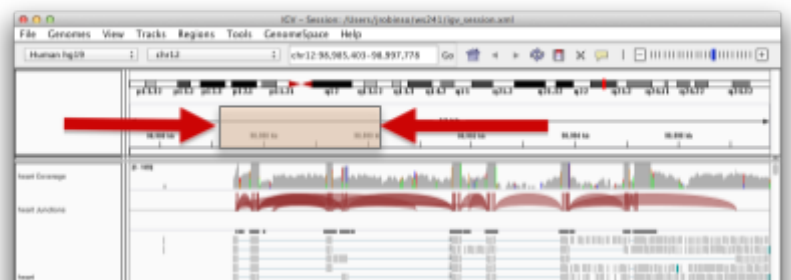
### 4. Expand gene track to see isoforms

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



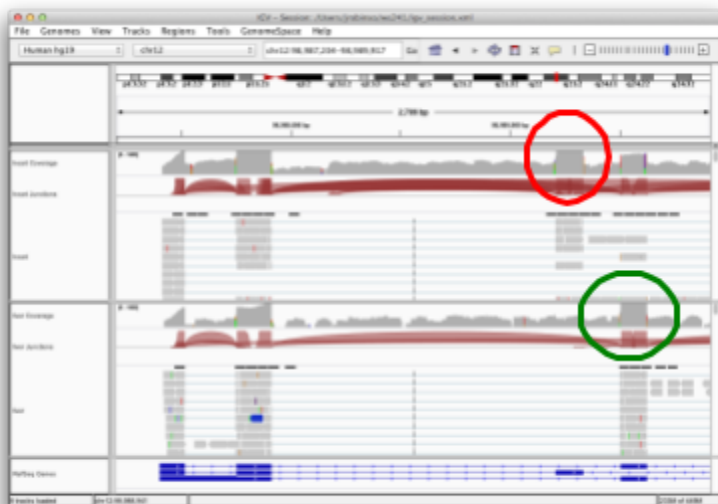
### 5. Zoom in on first 3 exons

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.



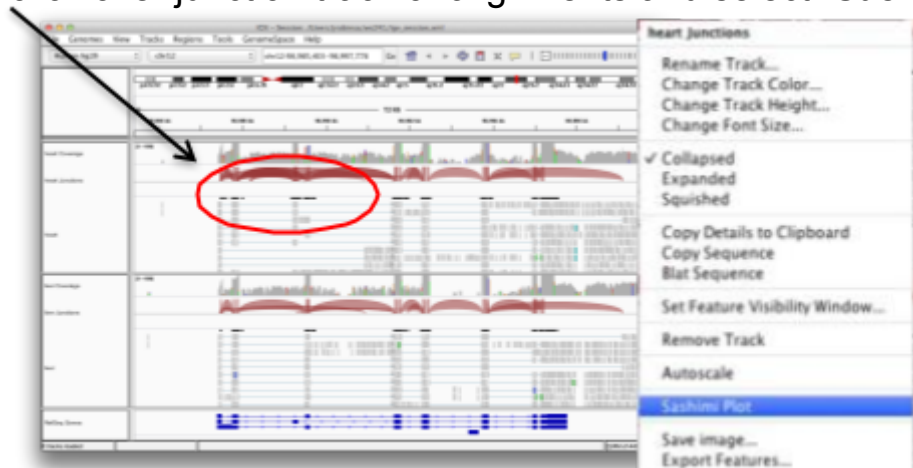
## 7. Zoom back out to view whole gene

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

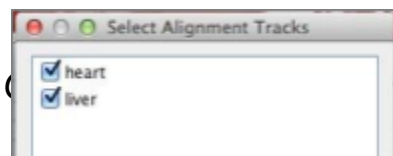


## 8. Open Sashimi plot

Right-click over junction track or alignments and select “Sashimi Plot”



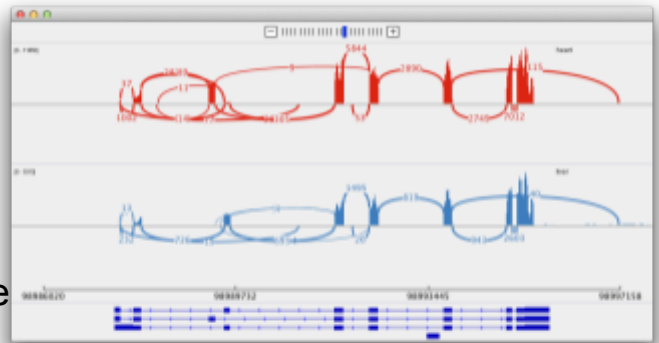
Verify both *heart* and *liver* are checked, and click



## 9. Examine Sashimi plot

Note:

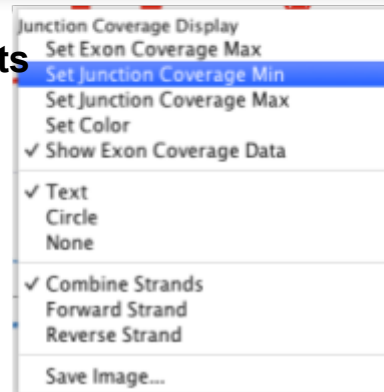
- Arcs represent reads spanning exon junctions
- Peaks represent exon coverage



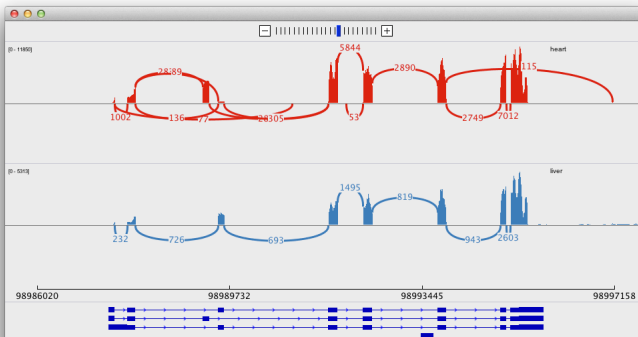
## 10. Filter out low-count splicing events

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



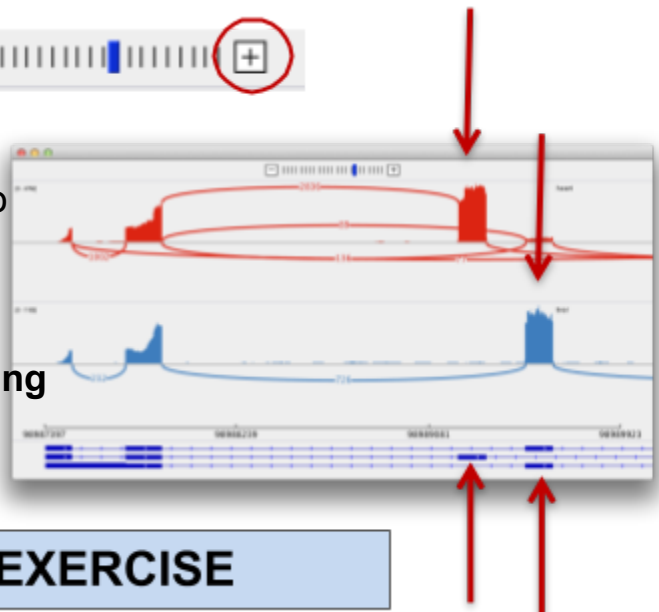
## 12. Zoom in on 5' end



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 3<sup>rd</sup> exon



Compute coverage

END OF EXERCISE