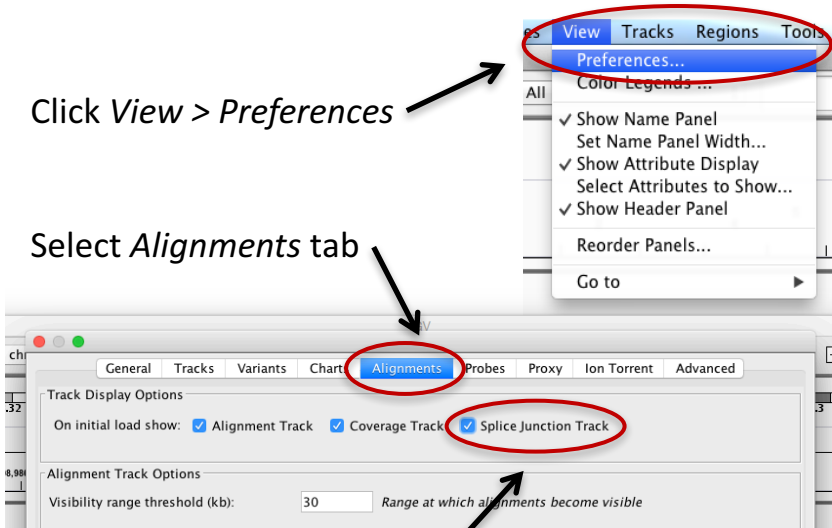**Introduction to the Integrative Genomics Viewer (IGV)**

Hands-on exercise: Viewing RNA-seq Data

1. Set preferences for viewing RNA-seq data

Click *View > Preferences*

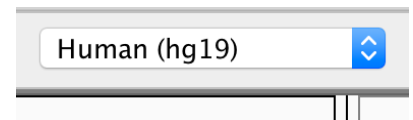Select *Alignments* tab

Check *Splice Junction Track*

2. Load data
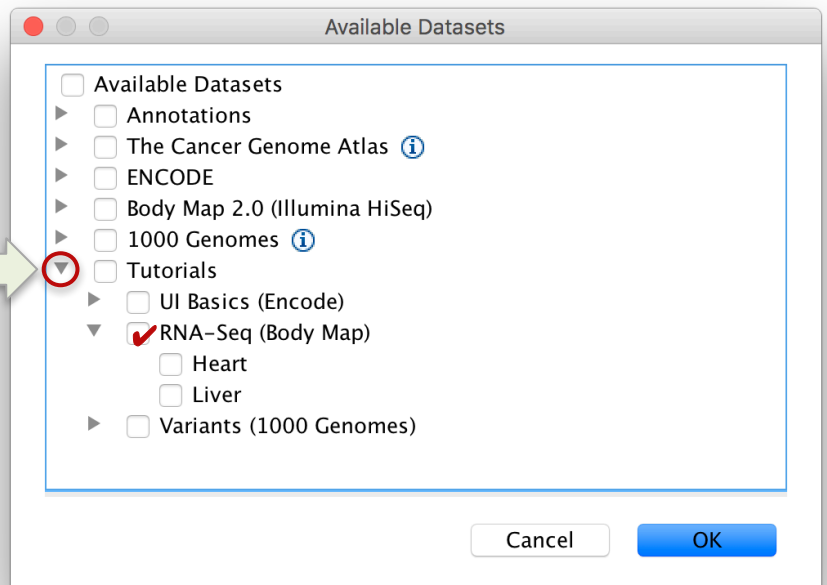
Select *Human hg19* from the genome dropdown menu
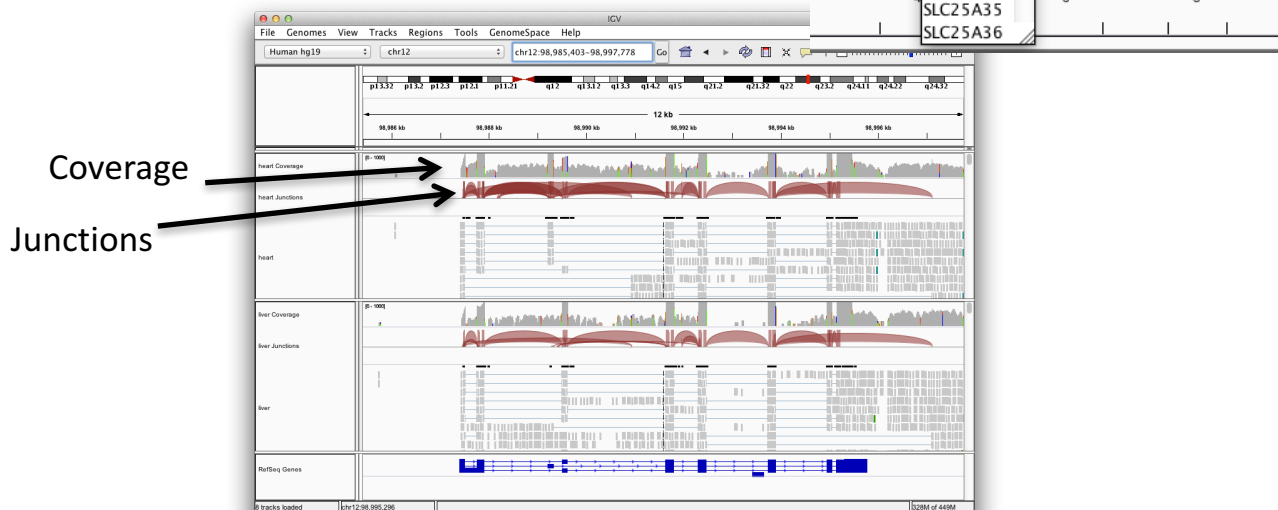
Human (hg19)

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.

Available Datasets

☐ Available Datasets
  ▶ ☐ Annotations
  ▶ ☐ The Cancer Genome Atlas ⓘ
  ▶ ☐ ENCODE
  ▶ ☐ Body Map 2.0 (Illumina HiSeq)
  ▶ ☐ 1000 Genomes ⓘ
  ▼ ☐ Tutorials
    ▶ ☐ UI Basics (Encode)
    ▼ ☑ RNA–Seq (Body Map)
        ☐ Heart
        ☐ Liver
    ▶ ☐ Variants (1000 Genomes)

Cancel   OK

3. Jump to gene SLC25A3

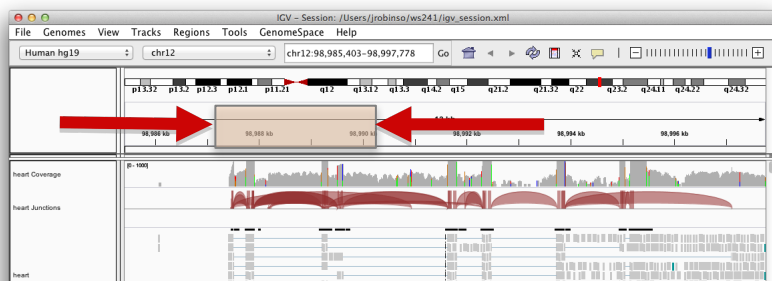Type *SLC25A3* in the search box and click *Go*

Coverage

Junctions

4. Expand gene track to see isoforms

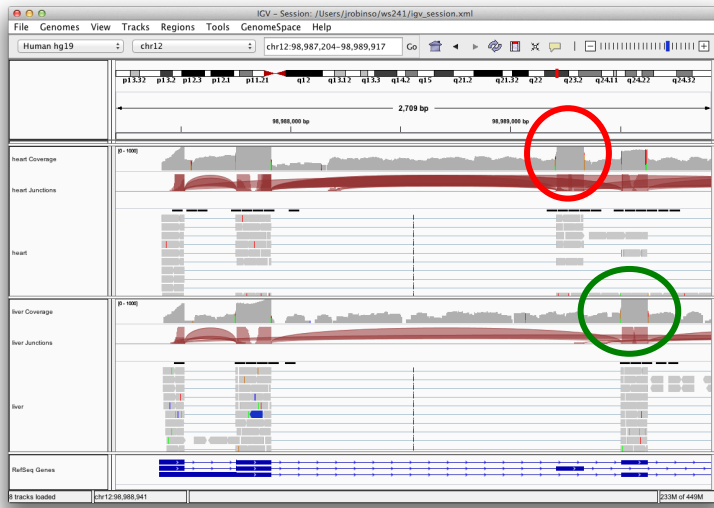Right-click over the *RefSeq Genes* track, and select *Squished*
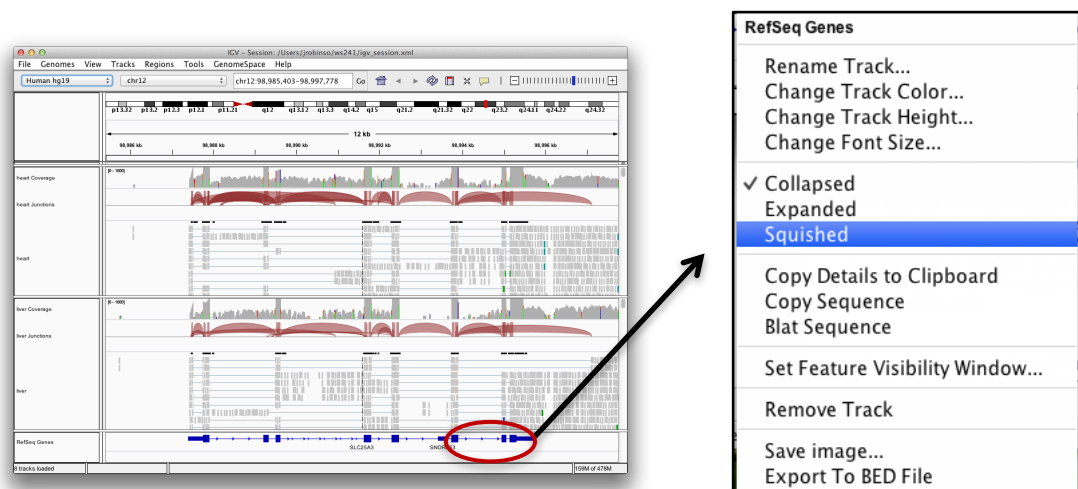
5. Zoom in on first 3 exons

Click and drag in ruler region over area shown

6. **Note evidence of alternative splicing**.

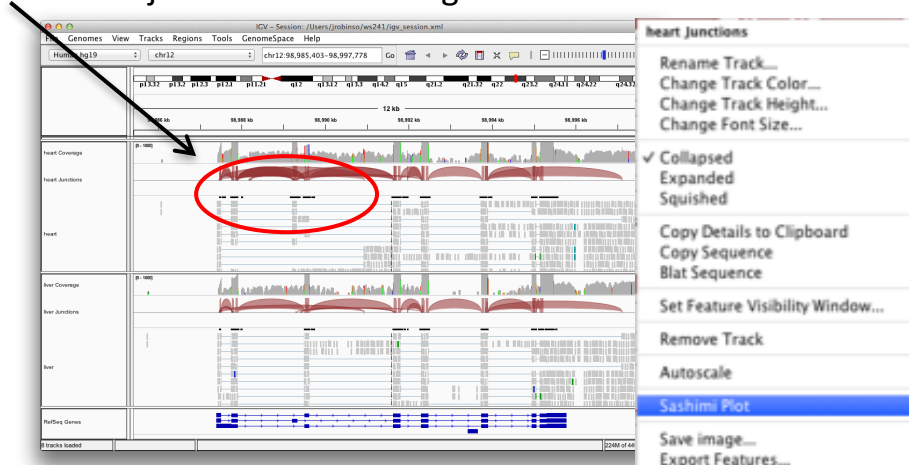Which isoforms in the RefSeq track are expressed in each tissue?

7. **Zoom back out to view whole gene**

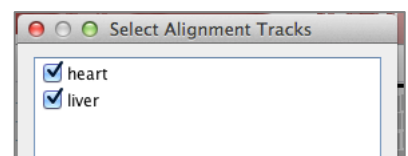Click the back button in the command bar to zoom out to previous view

8. **Open Sashimi plot**

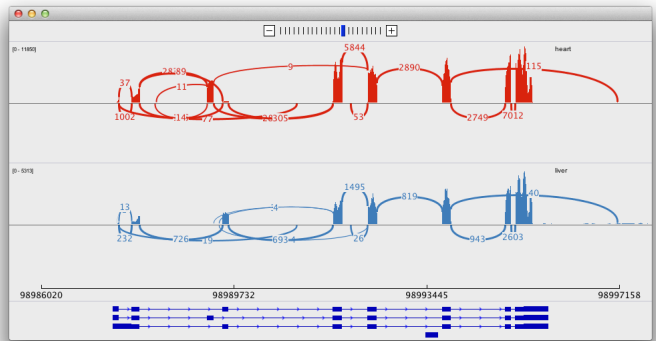Right-click over junction track or alignments and select *"Sashimi Plot"*

Verify both *heart* and *liver* are checked, and click *OK*
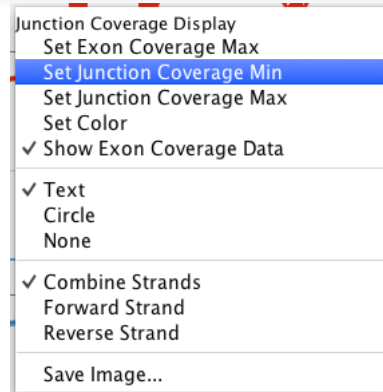
9. Examine Sashimi plot

Note:

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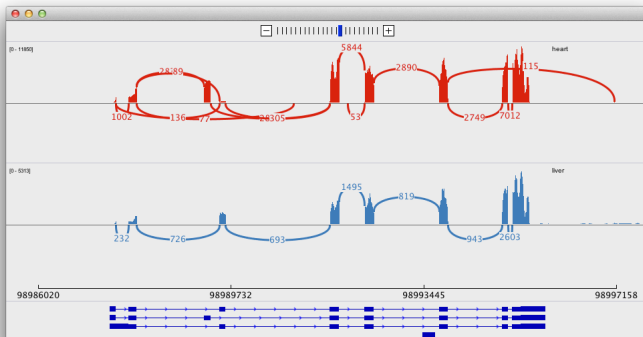- Peaks represent exon coverage

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. Note the alternative splicing
of the 3rd exon