Introduction to NGS Visualization with the Integrative Genomics Viewer (IGV)

Programming for Biology 2014
Cold Spring Harbor

Jim Robinson

BROAD INSTITUTE

Integrative Genomics Viewer

Agenda

Integrative Genomics Viewer

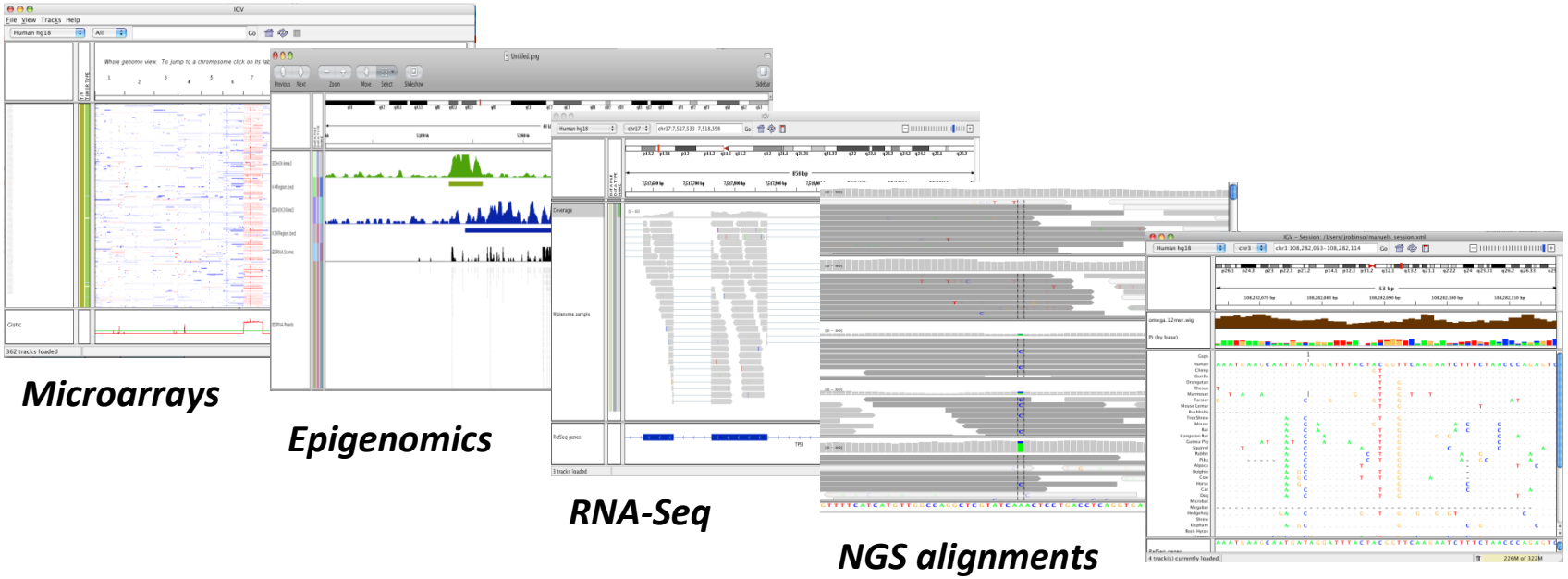
- Introduction
- Using IGV: The Basics
- Data Tracks and File Formats
- NGS Alignments
  - SNPs
  - Structural Events
  - RNA-seq
- igvtools
- Exercises

BROAD INSTITUTE

What is IGV

Integrative Genomics Viewer

A desktop application for integrated visualization of multiple data types and annotations in the context of the genome.



Microarrays

Epigenomics

RNA-Seq

NGS alignments

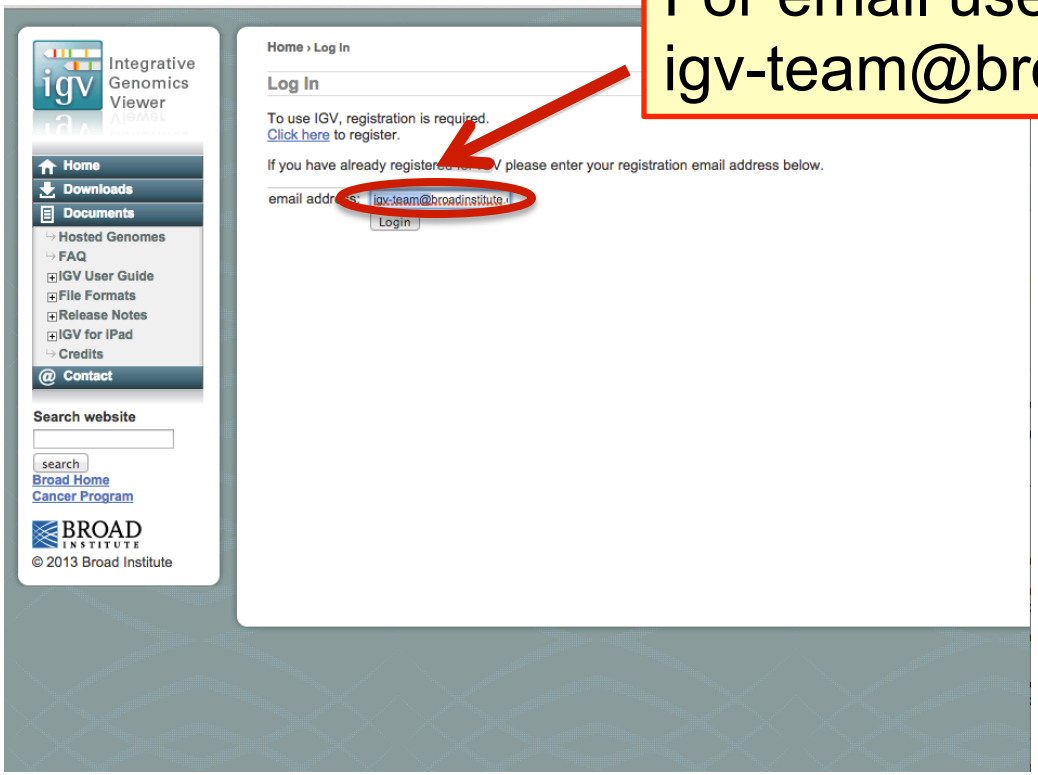
Comparative genomics

BROAD INSTITUTE

Installing IGV

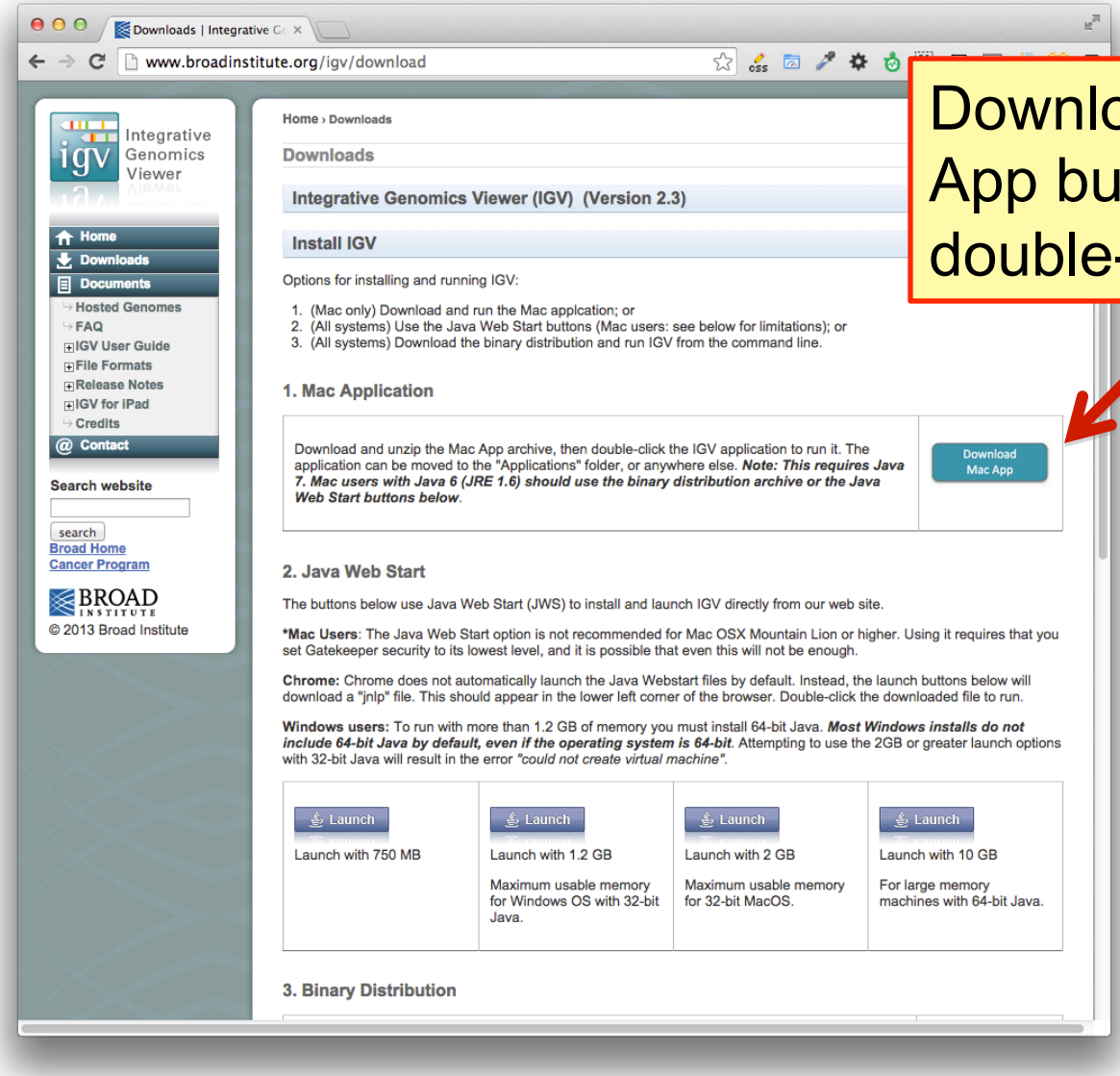
http://www.broadinstitute.org/igv

Installing IGV



For email use
igv-team@broadinstitue.org

Launch IGV



Download the Mac App bundle and double-click to unzip it.

Using IGV: The Basics

BROAD INSTITUTE

Integrative Genomics Viewer

Using IGV: the basics

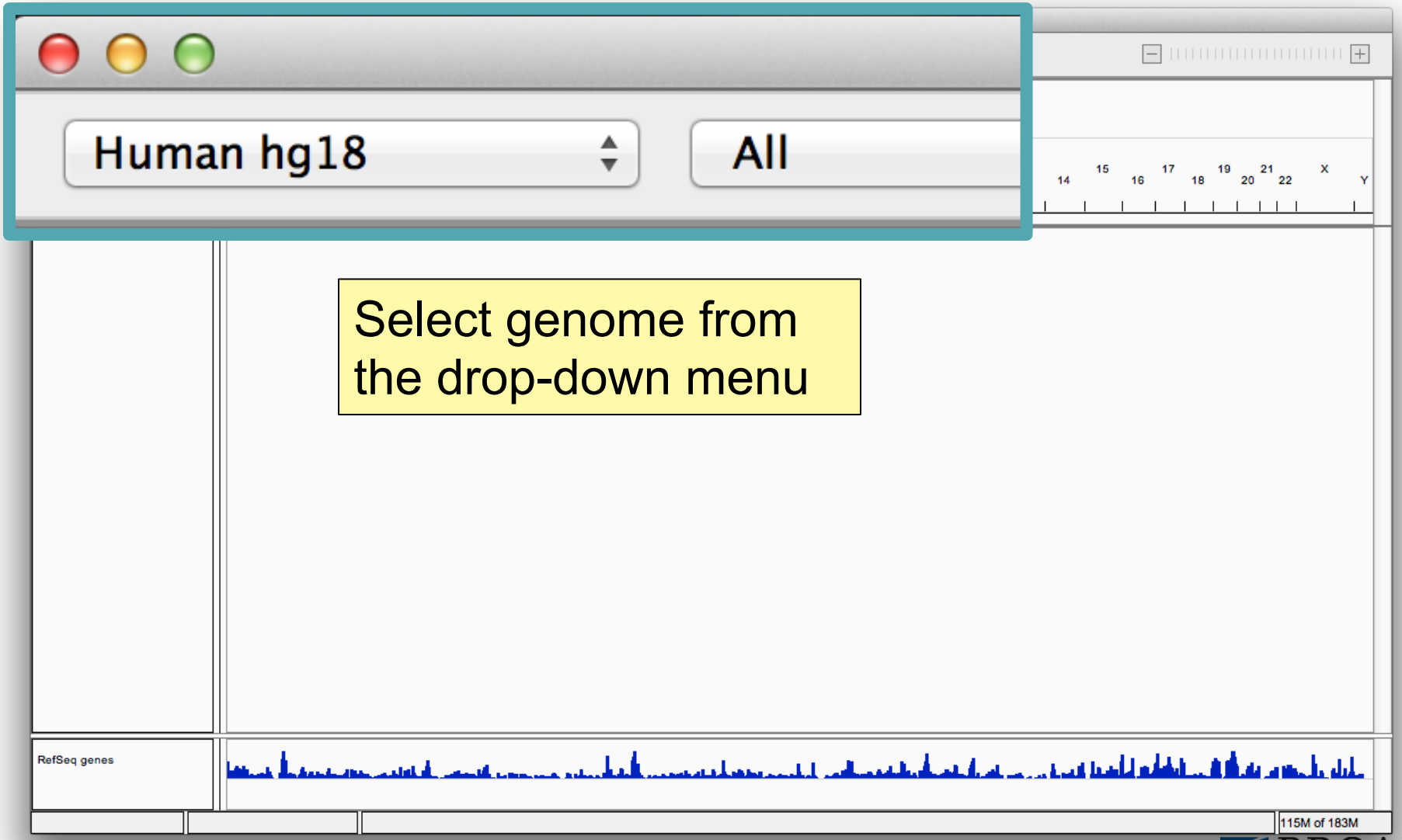
Integrative Genomics Viewer

Hands-on exercise

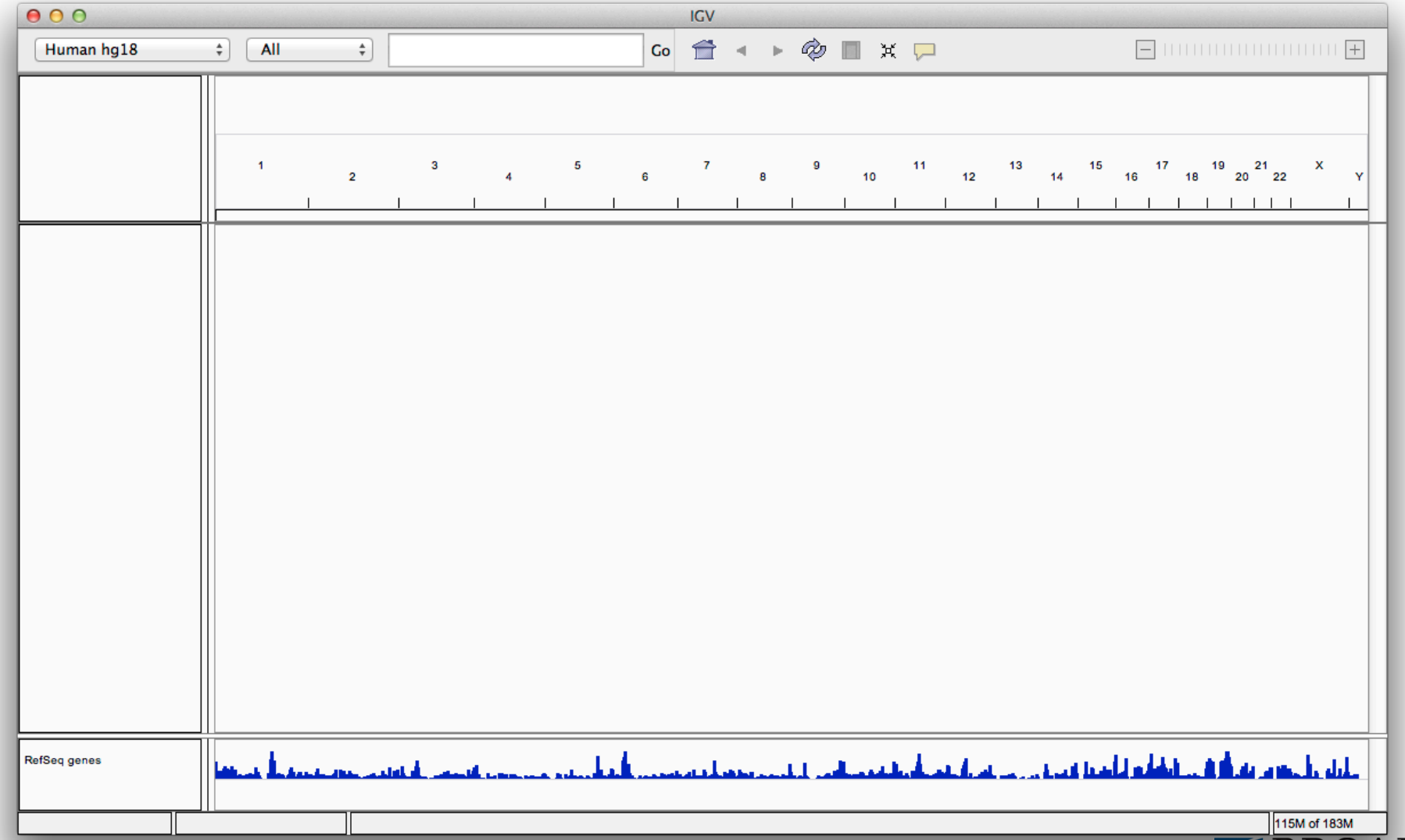
- Launch IGV
- Select a reference genome
- Load data
- Navigate through the data

BROAD INSTITUTE

Select the reference genome

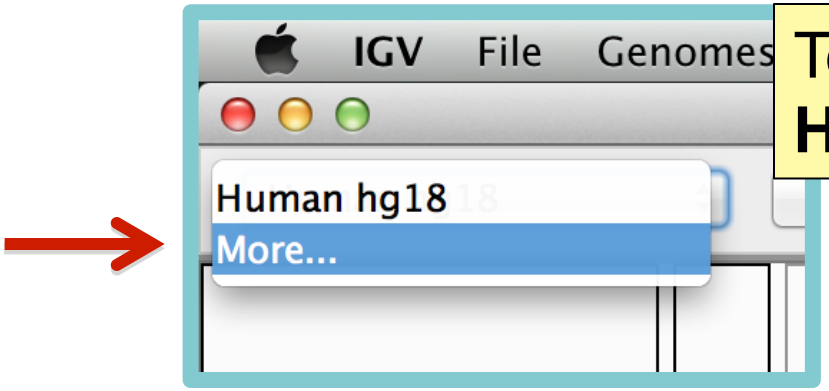


Integrative Genomics Viewer



BROAD INSTITUTE

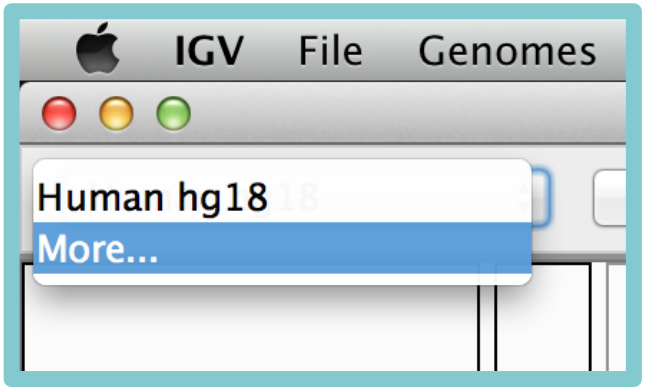
Select the reference genome

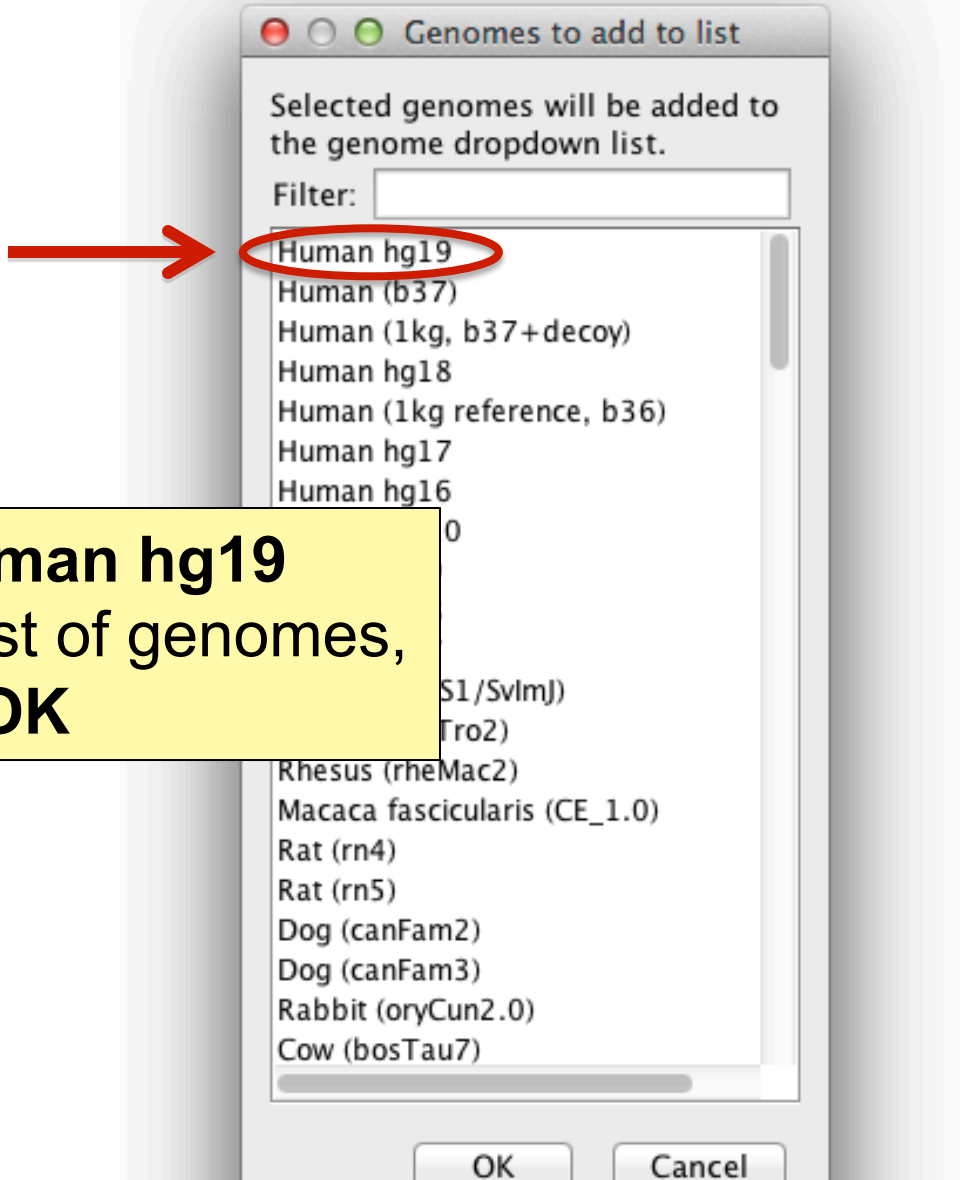


Today, we will use both **Human hg18** and **hg19**

If **Human hg19** is not in the menu, then click on ***More…***

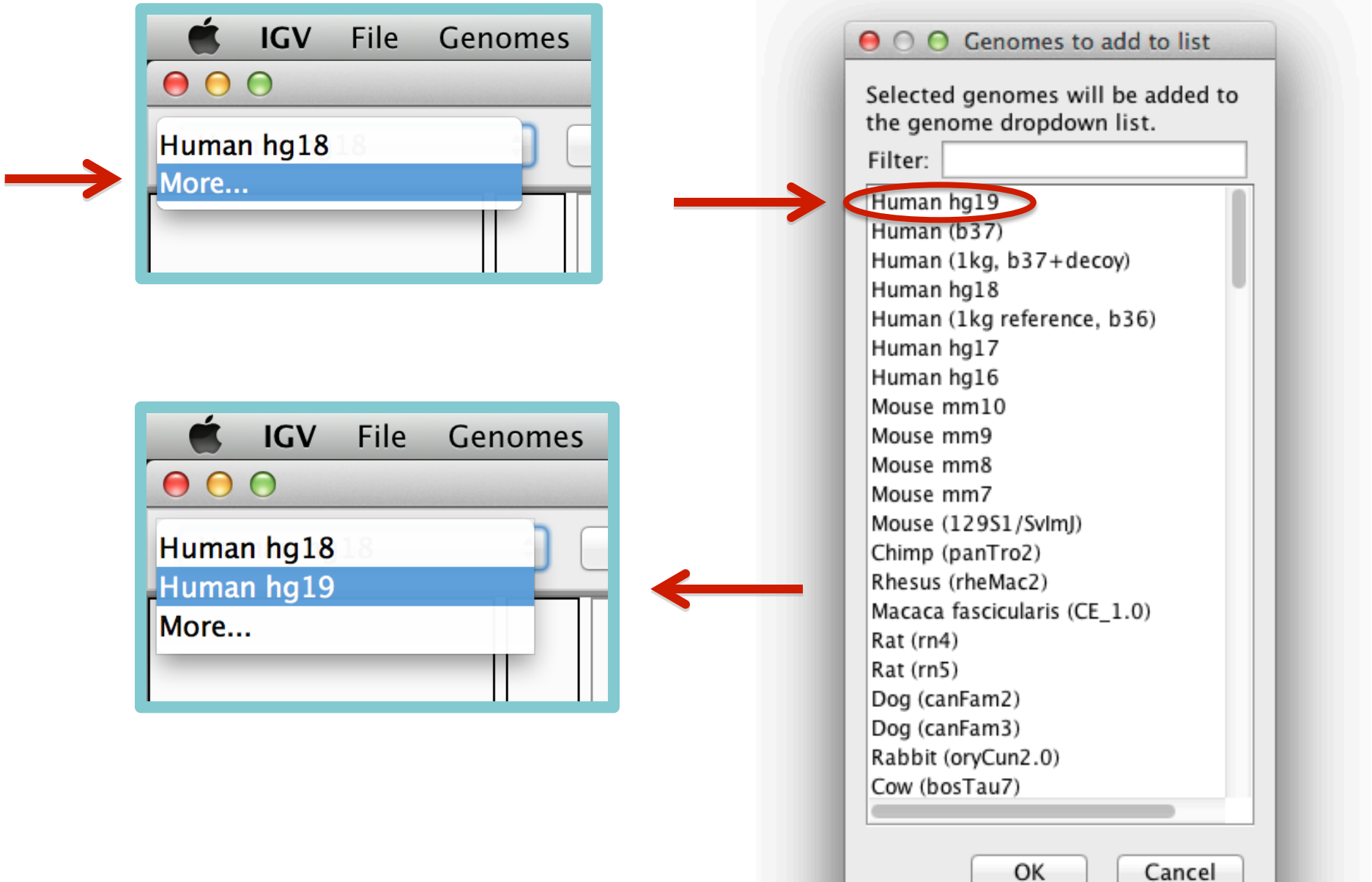
Select the reference genome





Select **Human hg19** from the list of genomes, and click **OK**

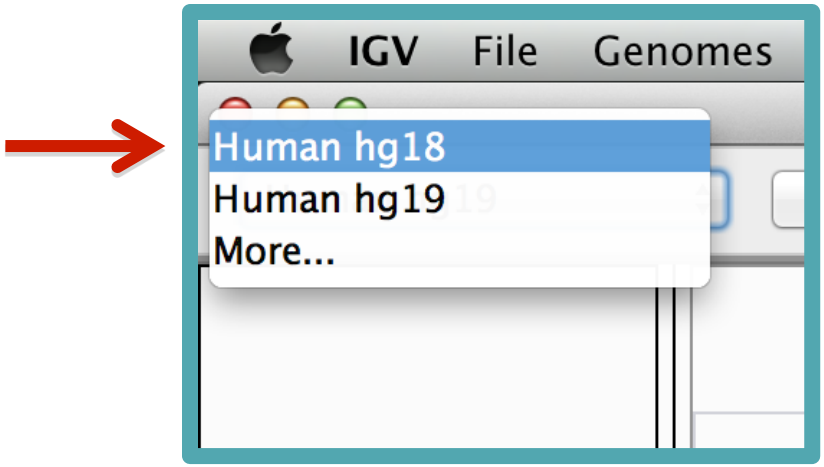
Select the reference genome



Select the reference genome

Integrative Genomics Viewer

Select **Human hg18**

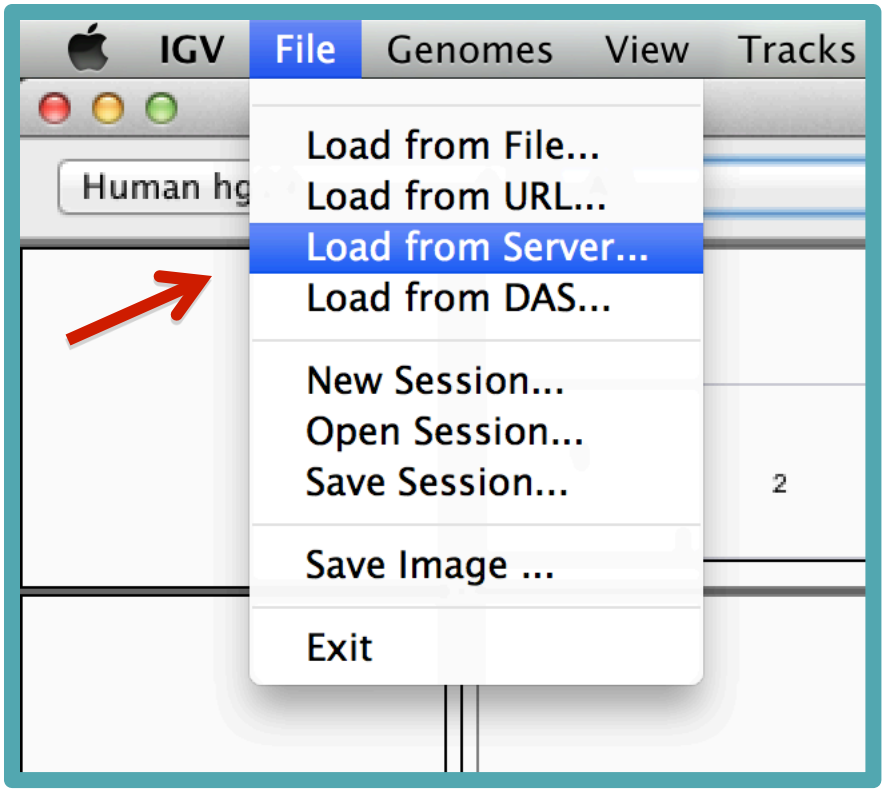


BROAD INSTITUTE

Load data

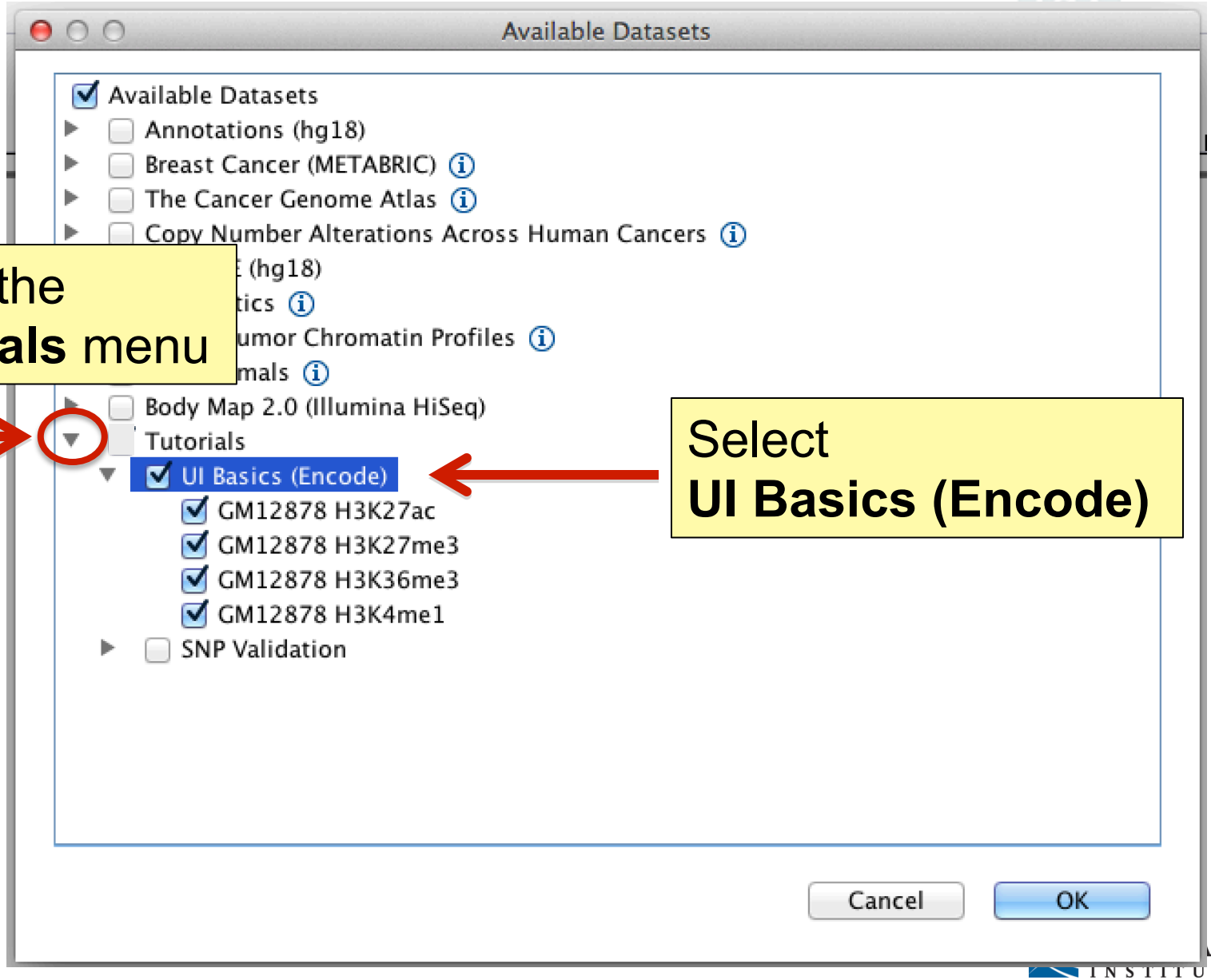
Integrative Genomics Viewer

Select **File > Load from Server…**



BROAD INSTITUTE

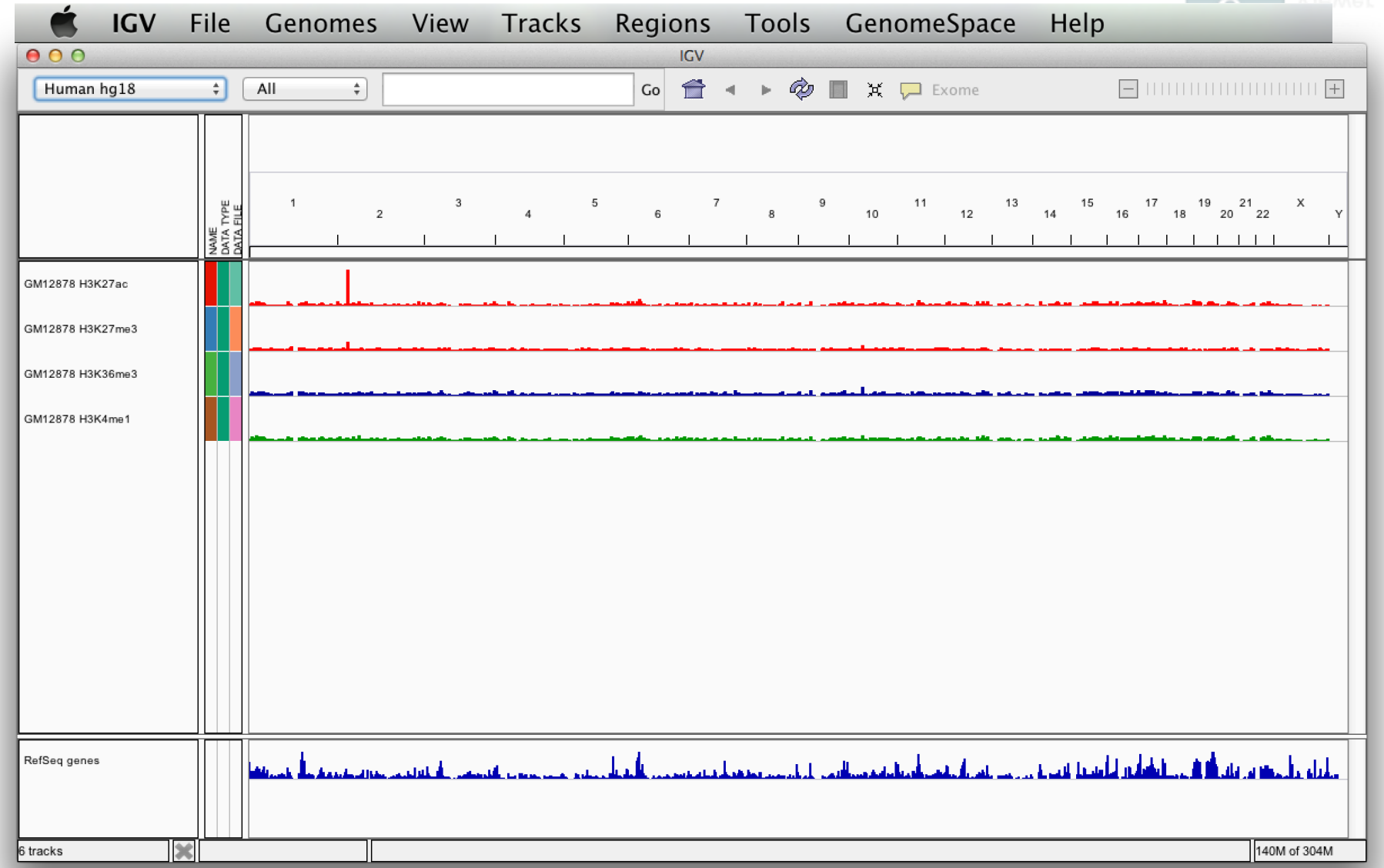
Load data



Open the **Tutorials** menu

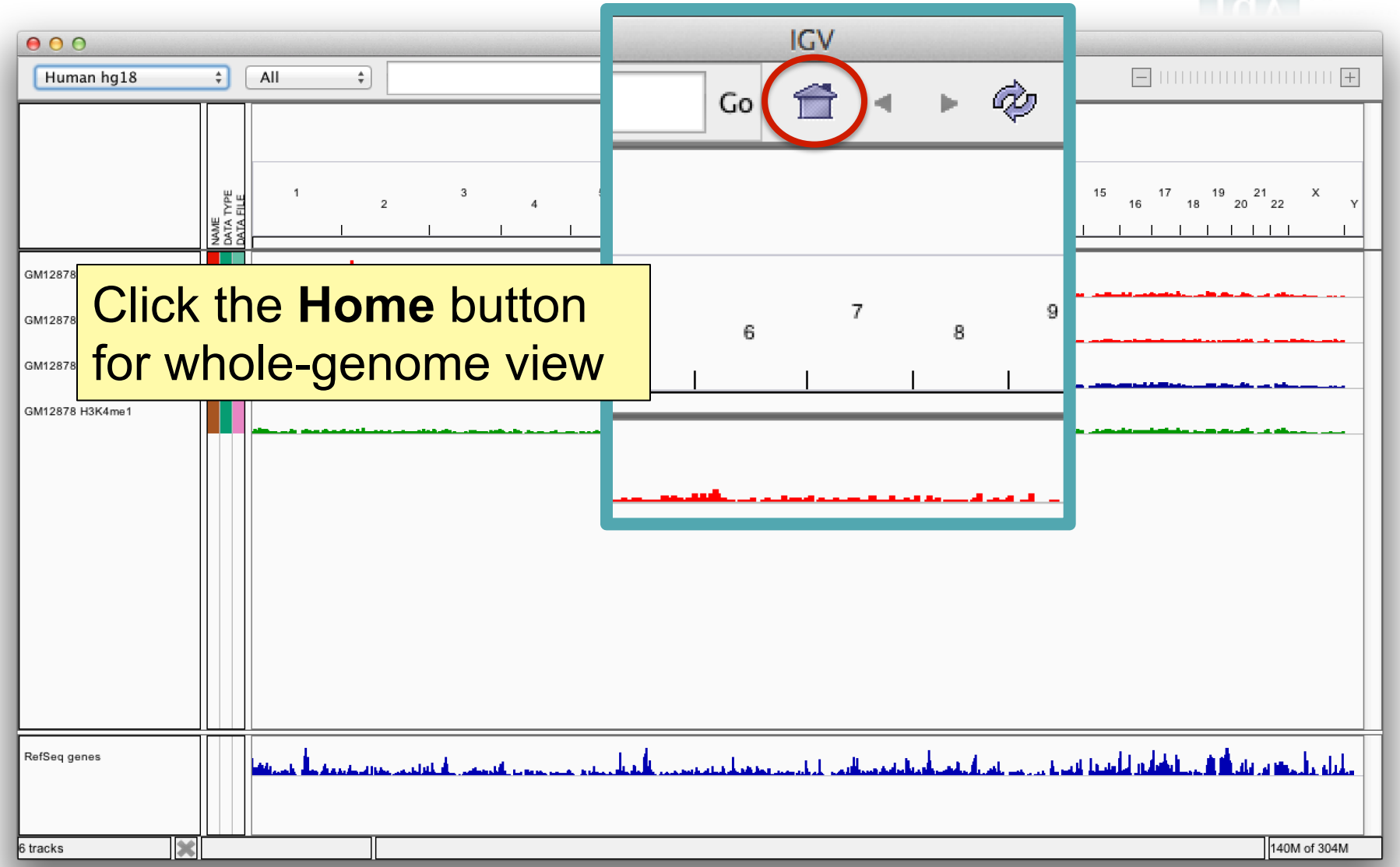
Select **UI Basics (Encode)**

Screen layout



Screen layout

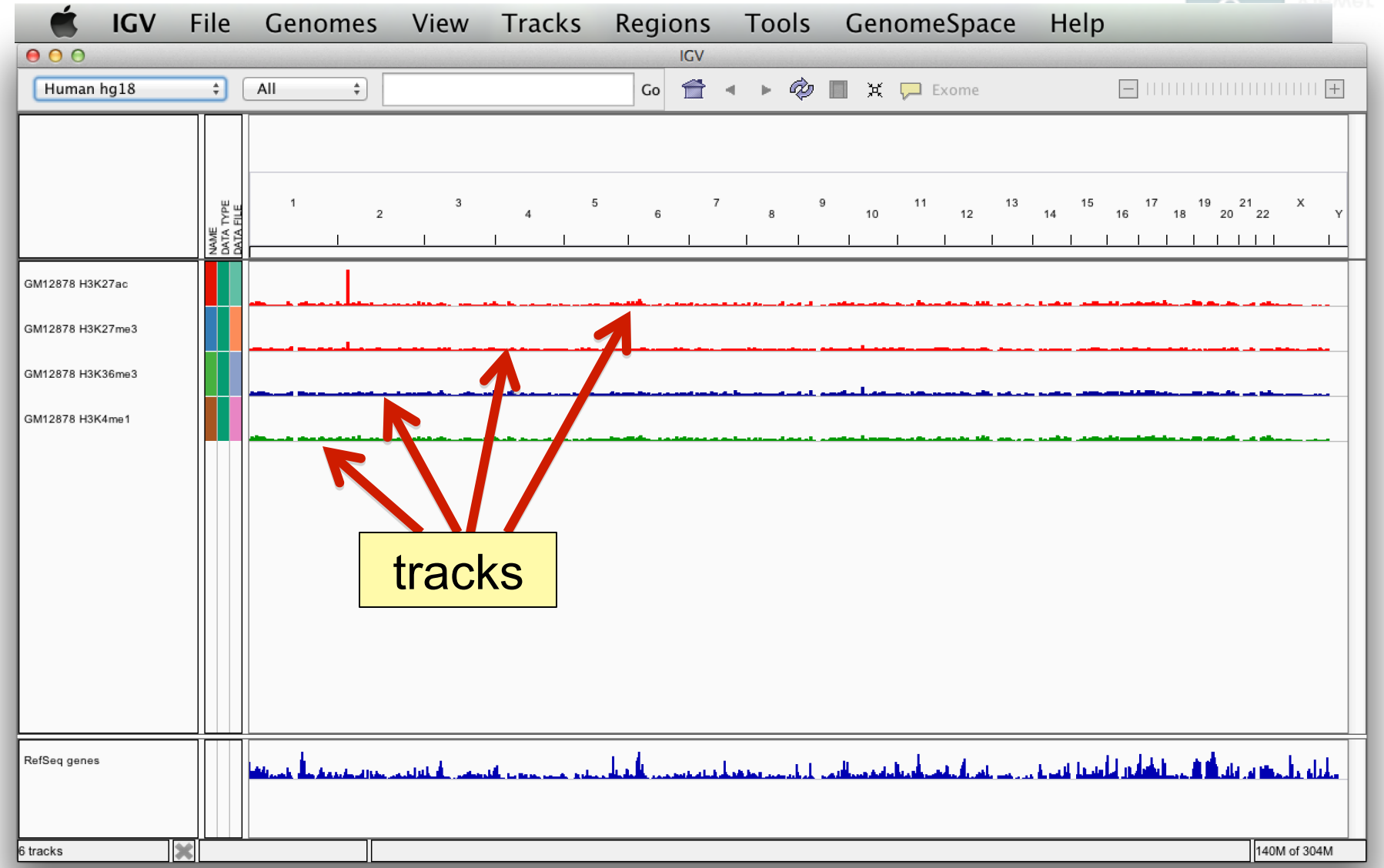
Integrative Genomics Viewer



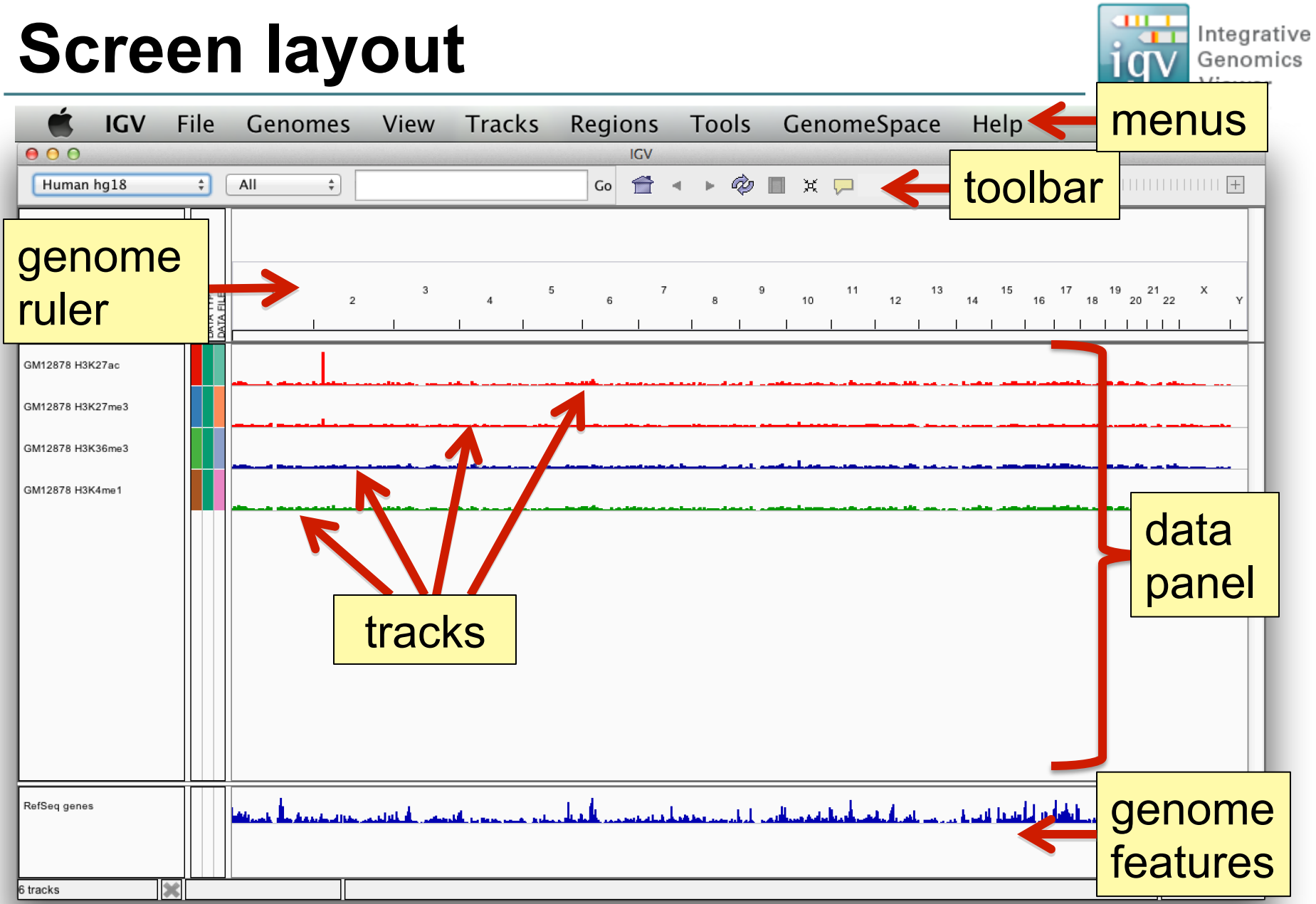
Click the **Home** button for whole-genome view

BROAD INSTITUTE

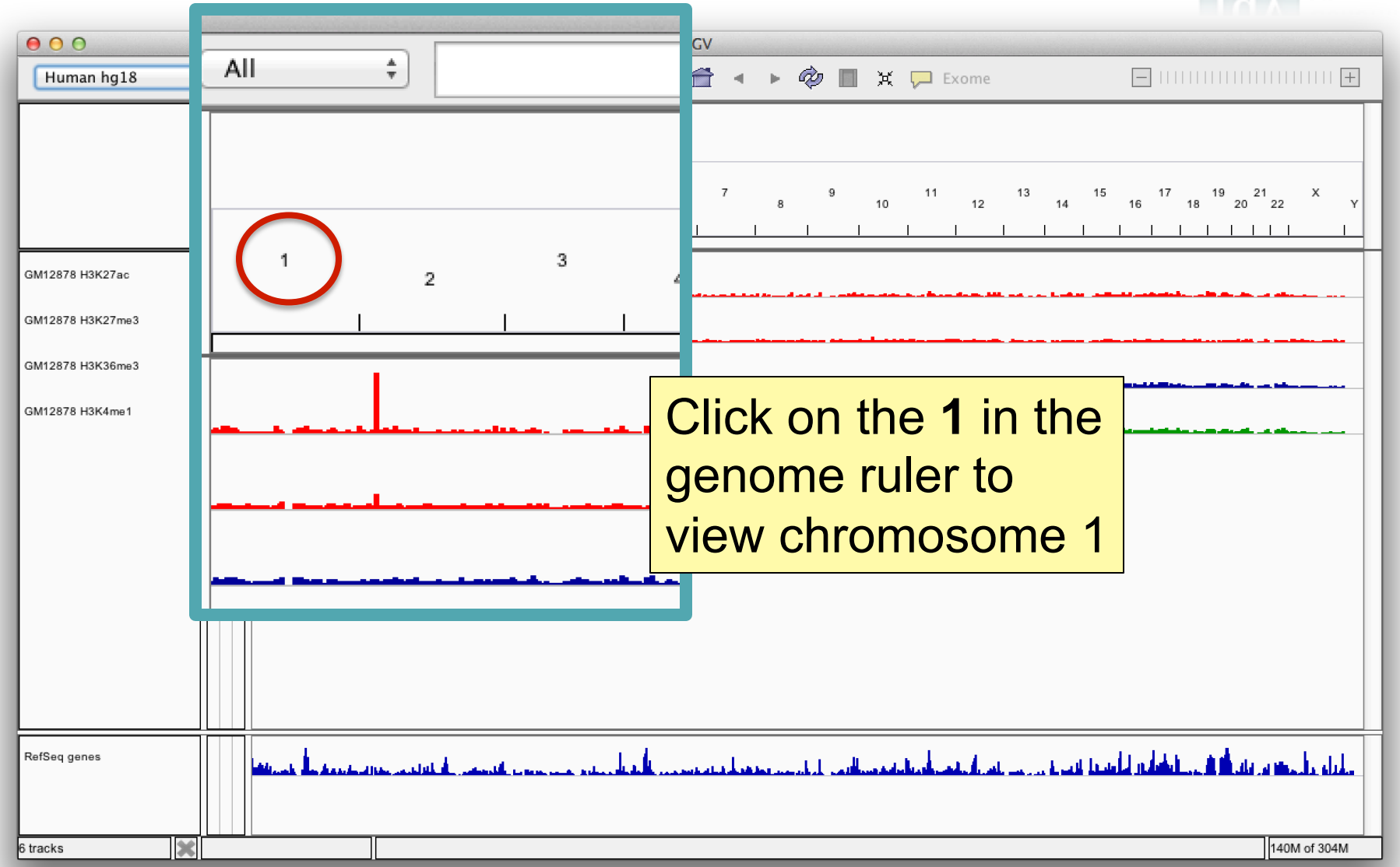
Screen layout



Screen layout

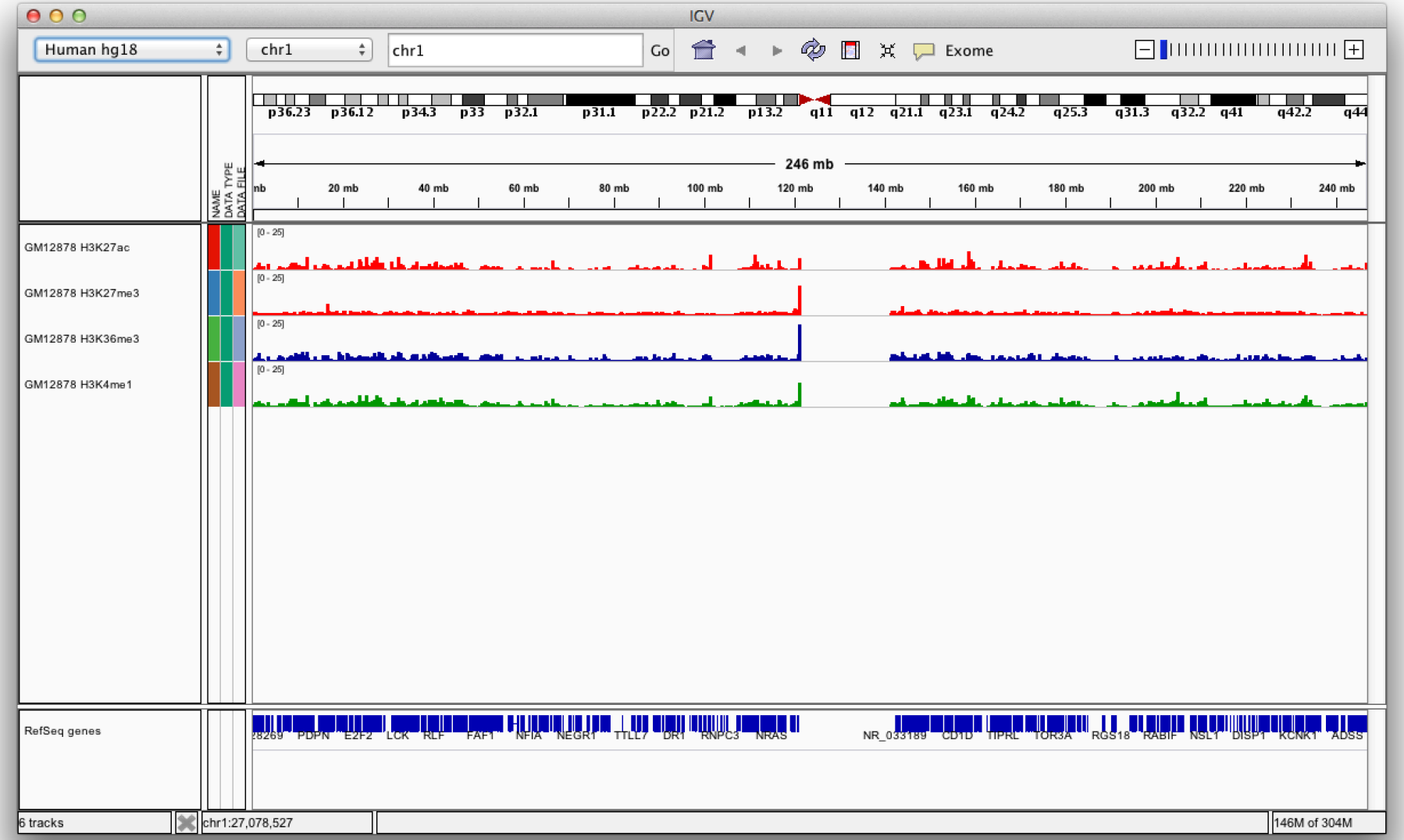


Navigate


Human hg18
All
GV
Exome
GM12878 H3K27ac
GM12878 H3K27me3
GM12878 H3K36me3
GM12878 H3K4me1
RefSeq genes
6 tracks
140M of 304M
Click on the 1 in the genome ruler to view chromosome 1

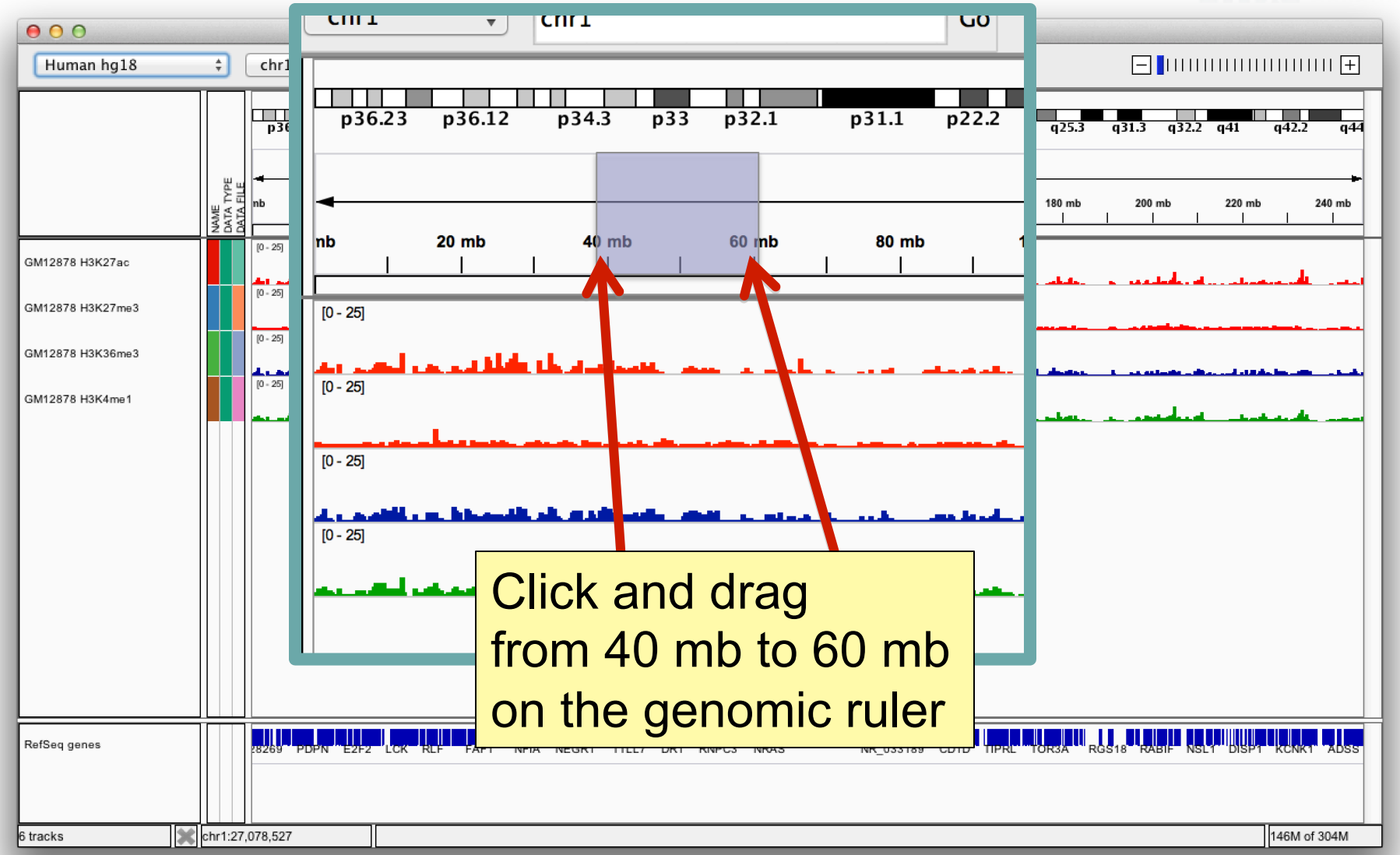
Navigate

Integrative Genomics Viewer



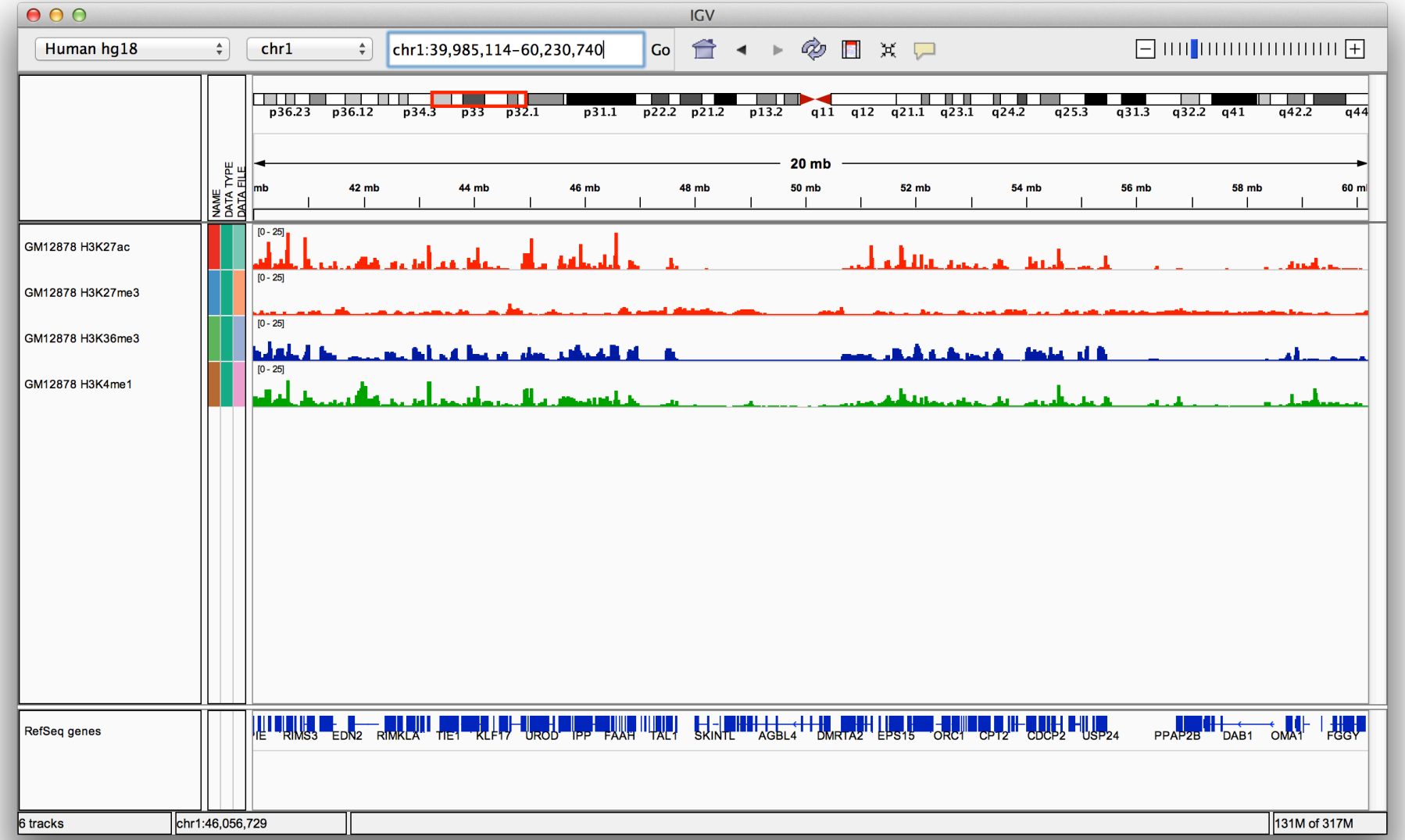
BROAD INSTITUTE

Navigate


Human hg18
chr1
Go
p36.23
p36.12
p34.3
p33
p32.1
p31.1
p22.2
q25.3
q31.3
q32.2
q41
q42.2
q44
20 mb
40 mb
60 mb
80 mb
180 mb
200 mb
220 mb
240 mb
GM12878 H3K27ac
GM12878 H3K27me3
GM12878 H3K36me3
GM12878 H3K4me1
[0 - 25]
RefSeq genes
6 tracks
chr1:27,078,527
146M of 304M
Click and drag
from 40 mb to 60 mb
on the genomic ruler

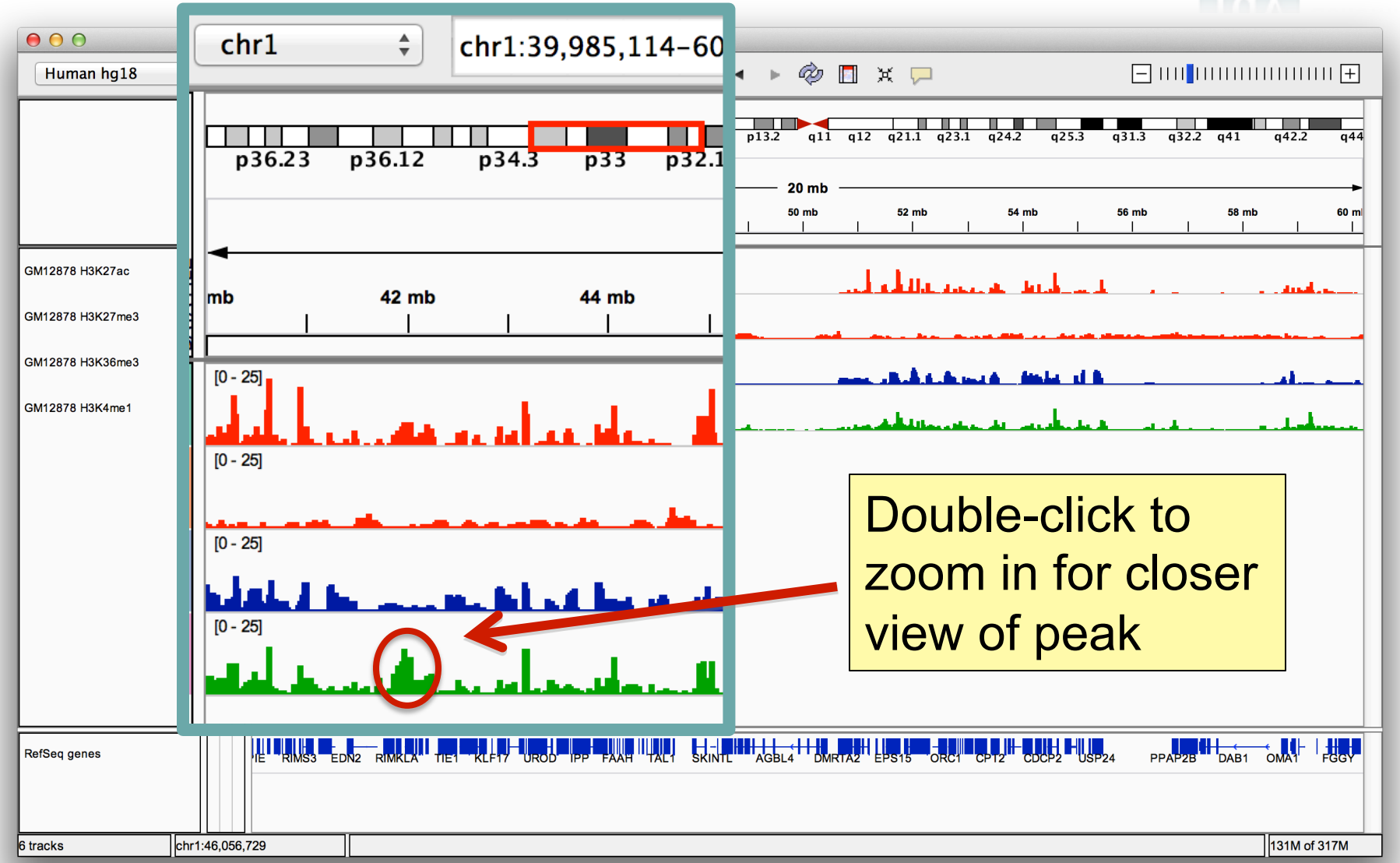
Navigate

Integrative Genomics Viewer



BROAD INSTITUTE

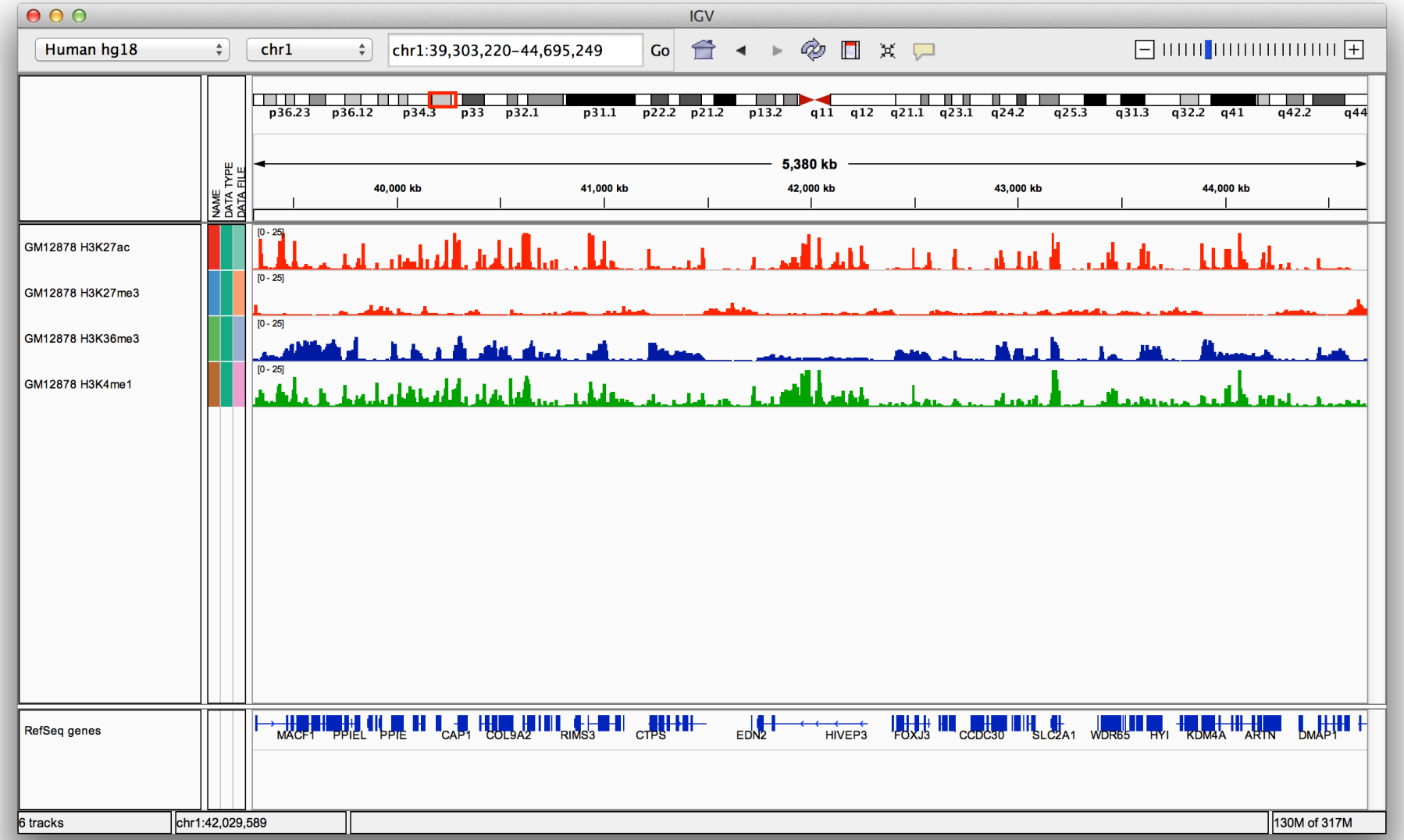
Navigate



Double-click to zoom in for closer view of peak

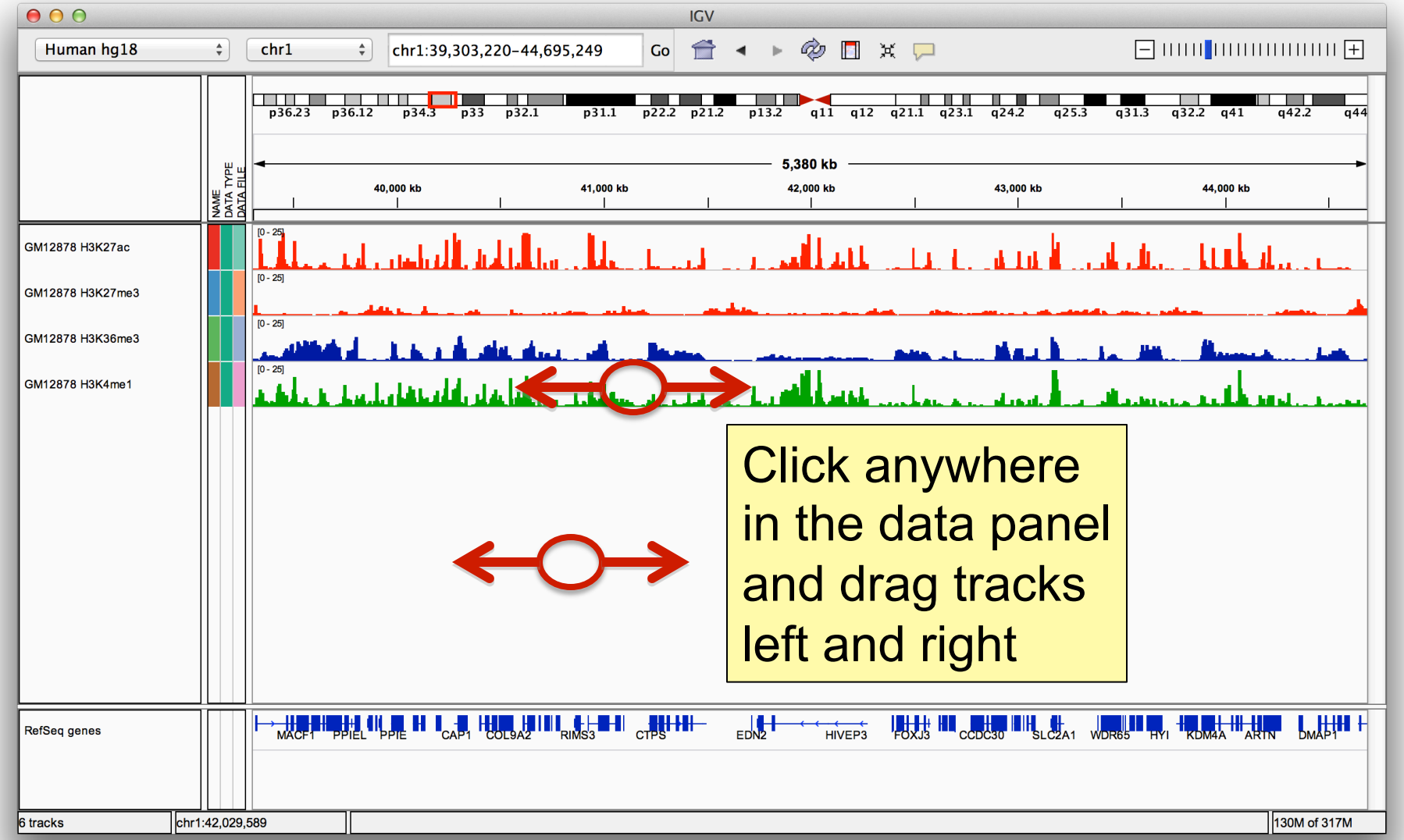
Navigate

Integrative Genomics Viewer

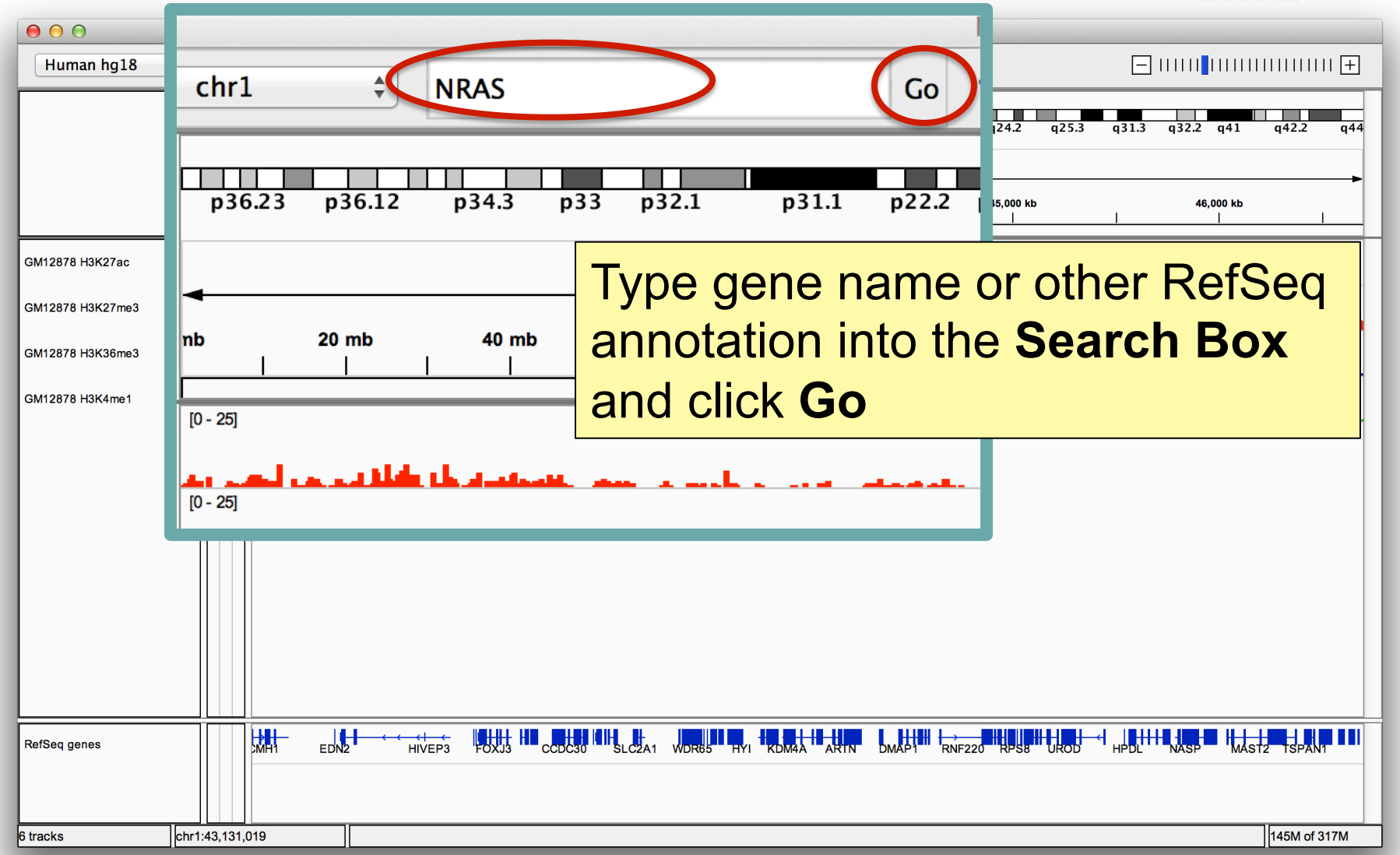


BROAD INSTITUTE

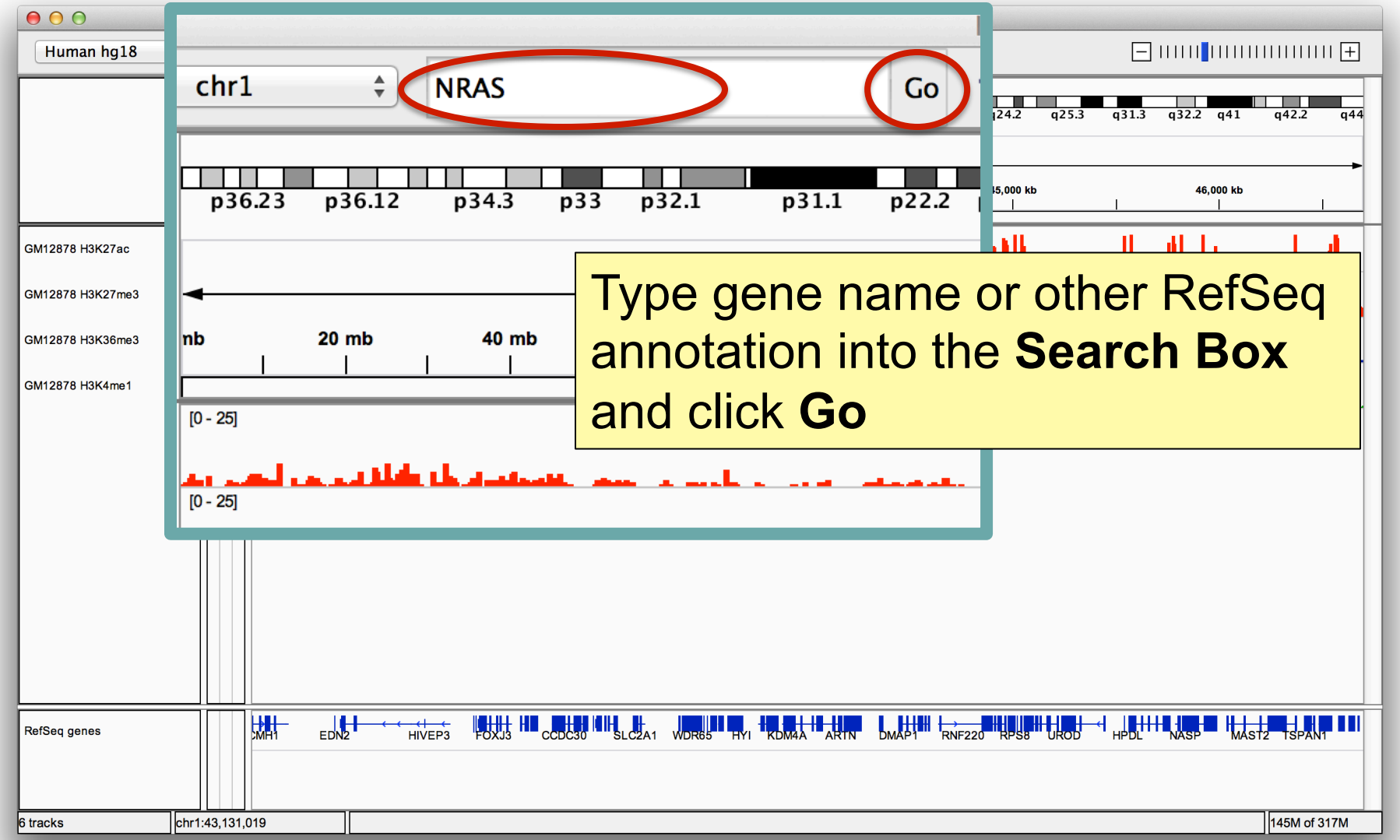
Navigate


IGV
Human hg18
chr1
chr1:39,303,220-44,695,249
Go
5,380 kb
40,000 kb
41,000 kb
42,000 kb
43,000 kb
44,000 kb
GM12878 H3K27ac
GM12878 H3K27me3
GM12878 H3K36me3
GM12878 H3K4me1
RefSeq genes
6 tracks
chr1:42,029,589
130M of 317M
Click anywhere in the data panel and drag tracks left and right

Navigate

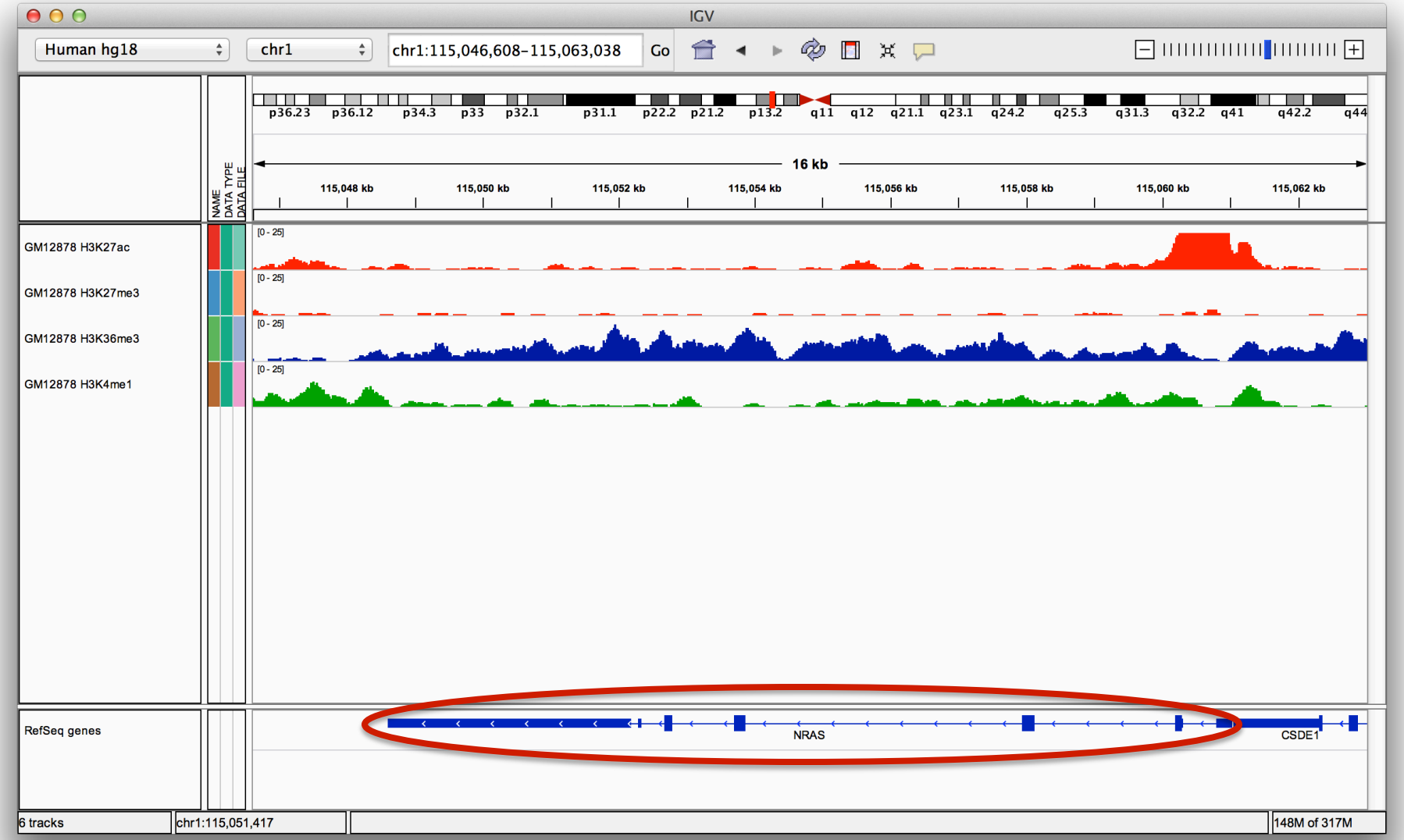

Human hg18
chr1
NRAS
Go
p36.23
p36.12
p34.3
p33
p32.1
p31.1
p22.2
GM12878 H3K27ac
GM12878 H3K27me3
GM12878 H3K36me3
GM12878 H3K4me1
20 mb
40 mb
[0 - 25]
[0 - 25]
Type gene name or other RefSeq annotation into the **Search Box** and click **Go**
RefSeq genes
EDN2
HIVEP3
FOXJ3
CCDC30
SLC2A1
WDR65
HYI
KDM4A
ARTN
DMAP1
RNF220
RPS8
UROD
HPDL
NASP
MAST2
TSPAN1
6 tracks
chr1:43,131,019
145M of 317M

Navigate


Human hg18
chr1
NRAS
Go
p36.23
p36.12
p34.3
p33
p32.1
p31.1
p22.2
GM12878 H3K27ac
GM12878 H3K27me3
GM12878 H3K36me3
GM12878 H3K4me1
20 mb
40 mb
[0 - 25]
[0 - 25]
Type gene name or other RefSeq annotation into the **Search Box** and click **Go**
RefSeq genes
EDN2
HIVEP3
FOXJ3
CCDC30
SLC2A1
WDR65
HYI
KDM4A
ARTN
DMAP1
RNF220
RPS8
UROD
HPDL
NASP
MAST2
TSPAN1
6 tracks
chr1:43,131,019
145M of 317M

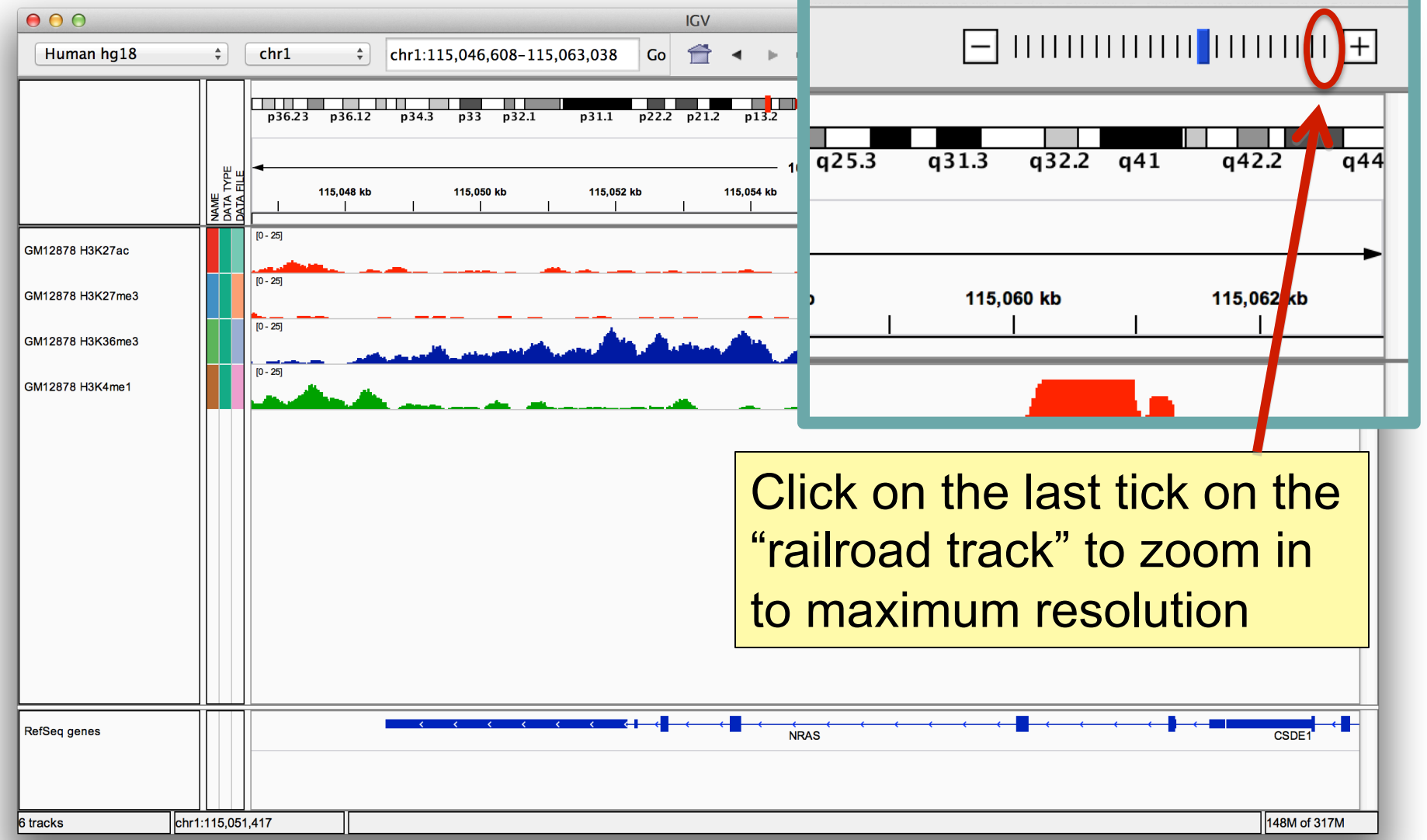
Navigate

Integrative Genomics Viewer



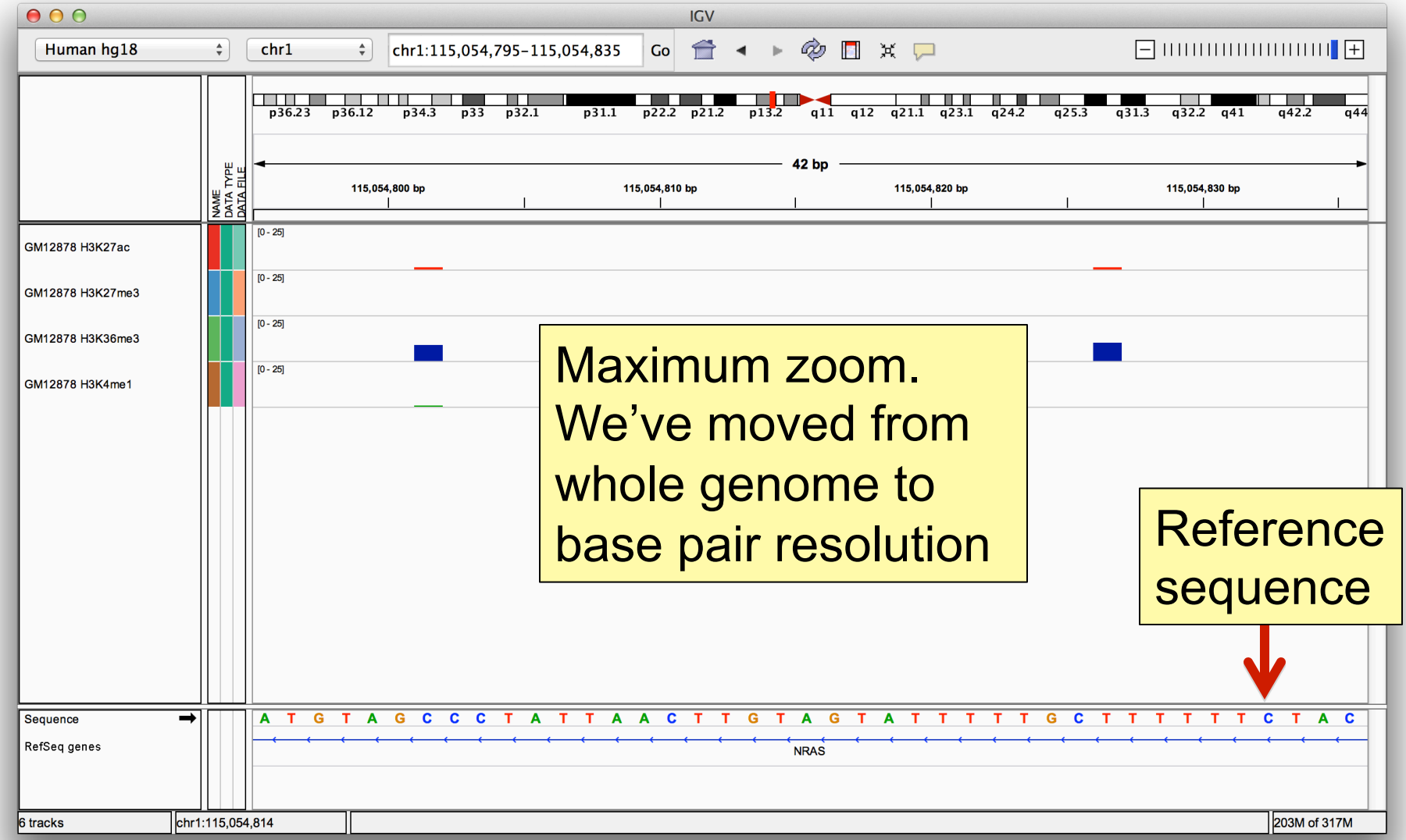
BROAD INSTITUTE

Navigate



Click on the last tick on the "railroad track" to zoom in to maximum resolution

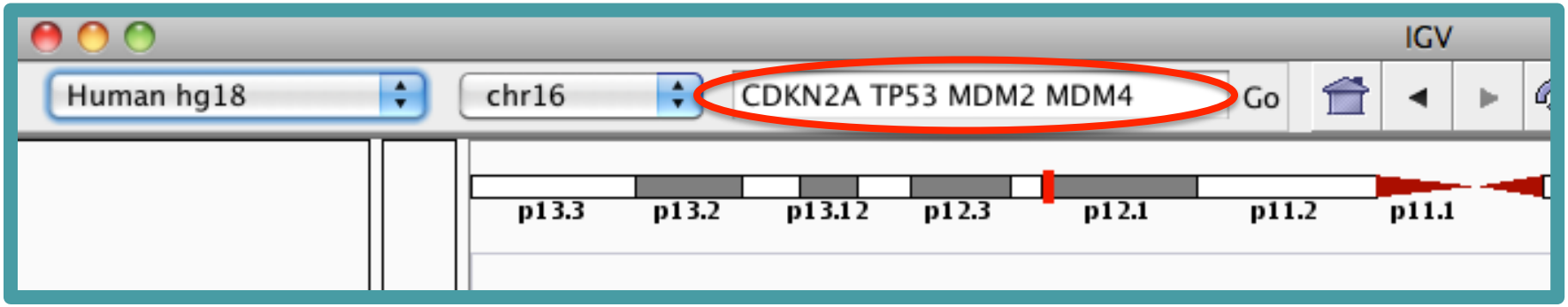
Navigate


IGV
Human hg18
chr1
chr1:115,054,795-115,054,835
Go
p36.23 p36.12 p34.3 p33 p32.1 p31.1 p22.2 p21.2 p13.2 q11 q12 q21.1 q23.1 q24.2 q25.3 q31.3 q32.2 q41 q42.2 q44
42 bp
115,054,800 bp
115,054,810 bp
115,054,820 bp
115,054,830 bp
NAME
DATA TYPE
DATA FILE
GM12878 H3K27ac
GM12878 H3K27me3
GM12878 H3K36me3
GM12878 H3K4me1
[0 - 25]
Maximum zoom. We've moved from whole genome to base pair resolution
Reference sequence
Sequence
RefSeq genes
A T G T A G C C C T A T T A A C T T G T A G T A T T T T T G C T T T T T T C T A C
NRAS
6 tracks
chr1:115,054,814
203M of 317M

Viewing multiple regions

- **Search box**

  Enter multiple loci or features in the search box



- **Regions > Gene Lists…**

  Select from a number of pre-defined gene lists, or

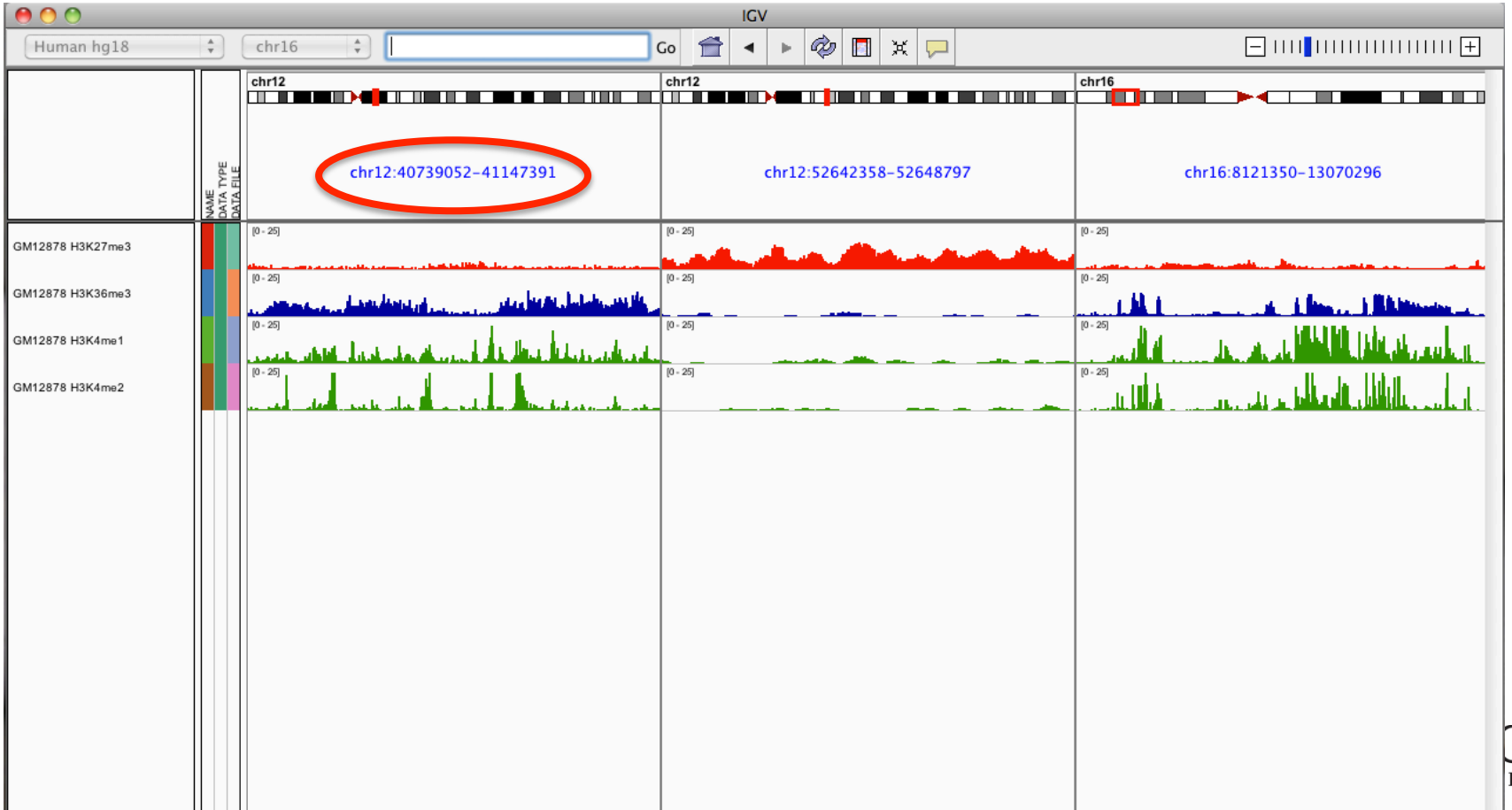
  Create your own persistent list

Viewing multiple regions

Viewing multiple regions

To go back to the standard, single-region view:

- *double-click* on a region label – or –
- *right-click* and select “Switch to standard view”



File formats and track types

Integrative Genomics Viewer

- The **file format** defines the track type.
- The **track type** determines the display options

BROAD INSTITUTE

File formats and track types

Integrative Genomics Viewer

- The **file format** defines the track type.
- The **track type** determines the display options
- IGV supports many different file formats.

  - BAM
  - BED
  - BedGraph
  - bigBed
  - bigWig
  - Birdsuite Files
  - broadPeak
  - CBS
  - CN
  - Cufflinks Files
  - Custom File Formats
  - Cytoband
  - FASTA
  - GCT
  - genePred
  - GFF
  - GISTIC
  - Goby
  - GWAS
  - IGV
  - LOH
  - MAF (Multiple Alignment Format)
  - MAF (Mutation Annotation Format)
  - Merged BAM File
  - MUT
  - narrowPeak
  - PSL
  - RES
  - SAM
  - Sample Information
  - SEG
  - SNP
  - TAB
  - TDF
  - Track Line
  - Type Line
  - VCF
  - WIG

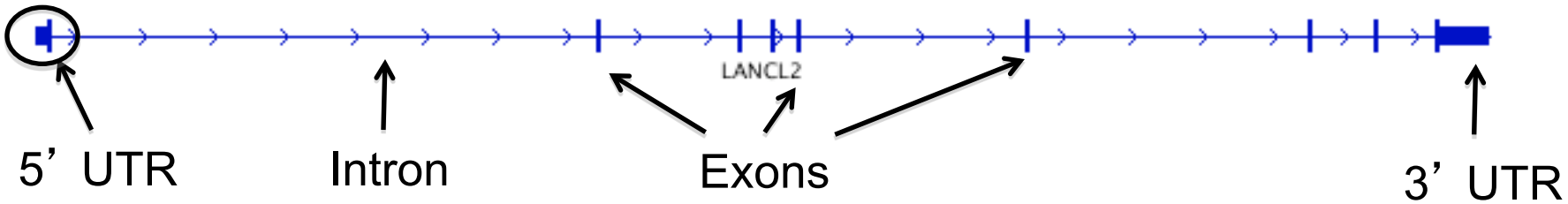
- For current list see: www.broadinstitute.org/igv/FileFormats

BROAD INSTITUTE

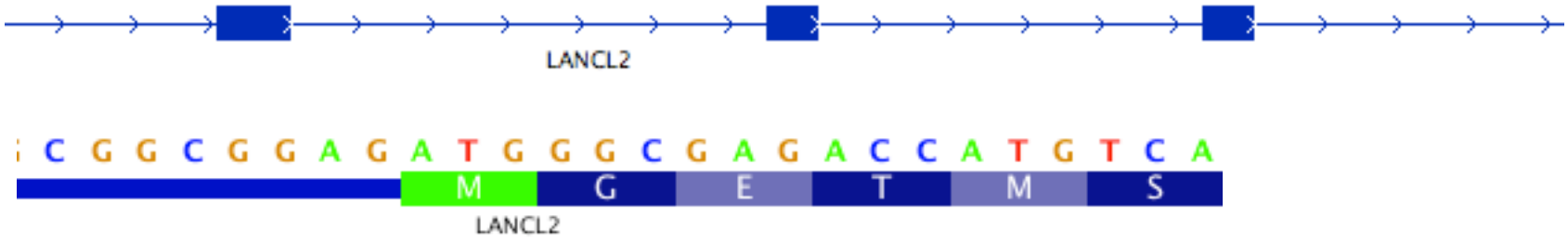
Genome annotation track

Integrative Genomics Viewer

UCSC style gene representation



Zoomed in views



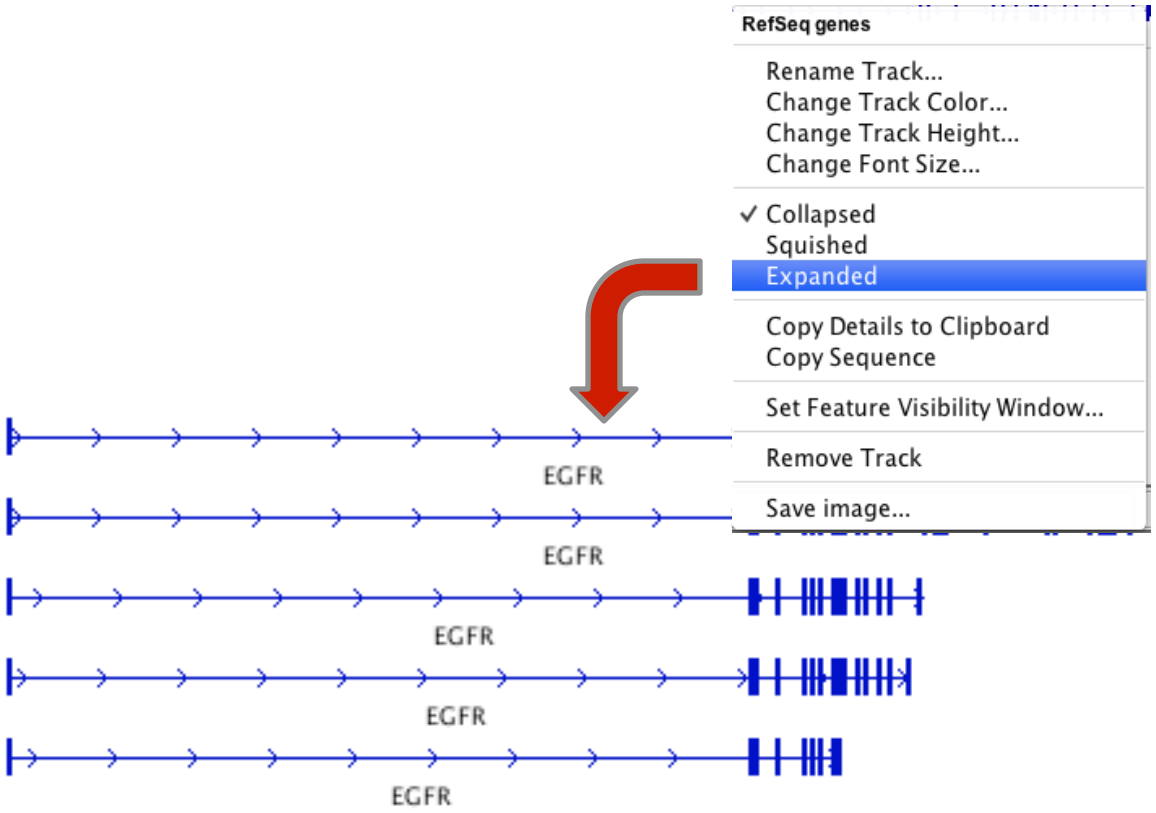
Zoomed out views

BROAD INSTITUTE

Annotation display mode

1. Features are drawn in a single row, by default

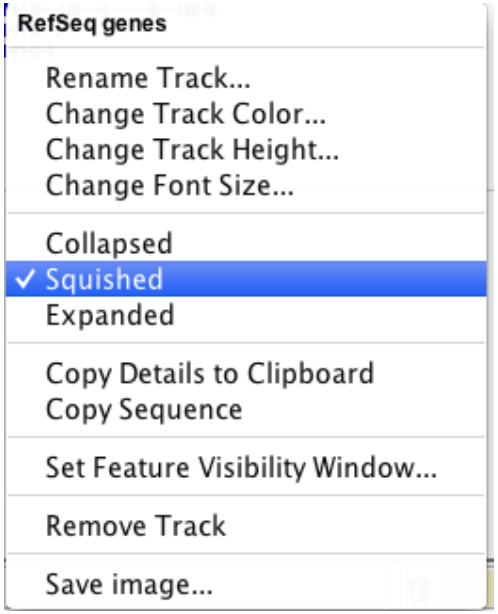
2. Expand the track using the popup menu

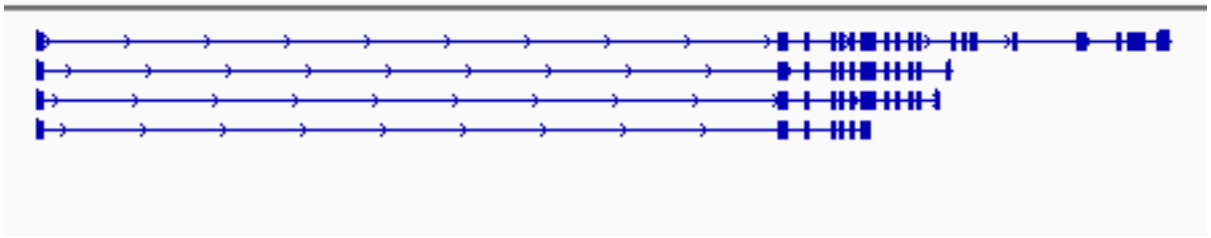


Annotation display mode

Integrative Genomics Viewer

3. For a compact view of all variants use “Squished”



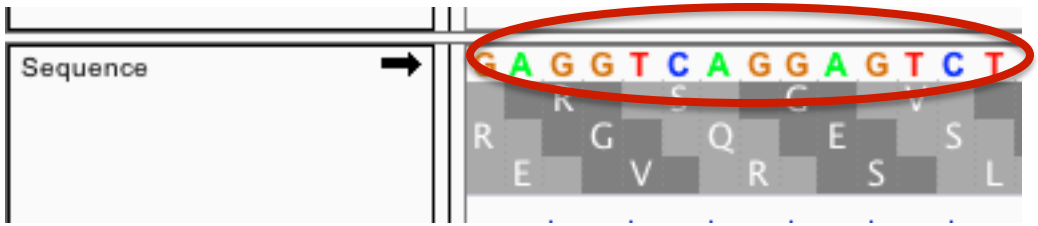


BROAD INSTITUTE

Reference sequence

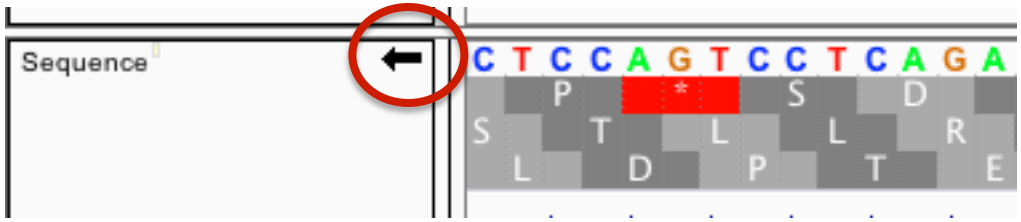
Integrative Genomics Viewer

Click anywhere on the sequence to see a 3 frame translation.



By default the sequence for the forward strand is shown.

Click the arrow on the left to reverse the strand.



BROAD INSTITUTE

Viewing NGS Data

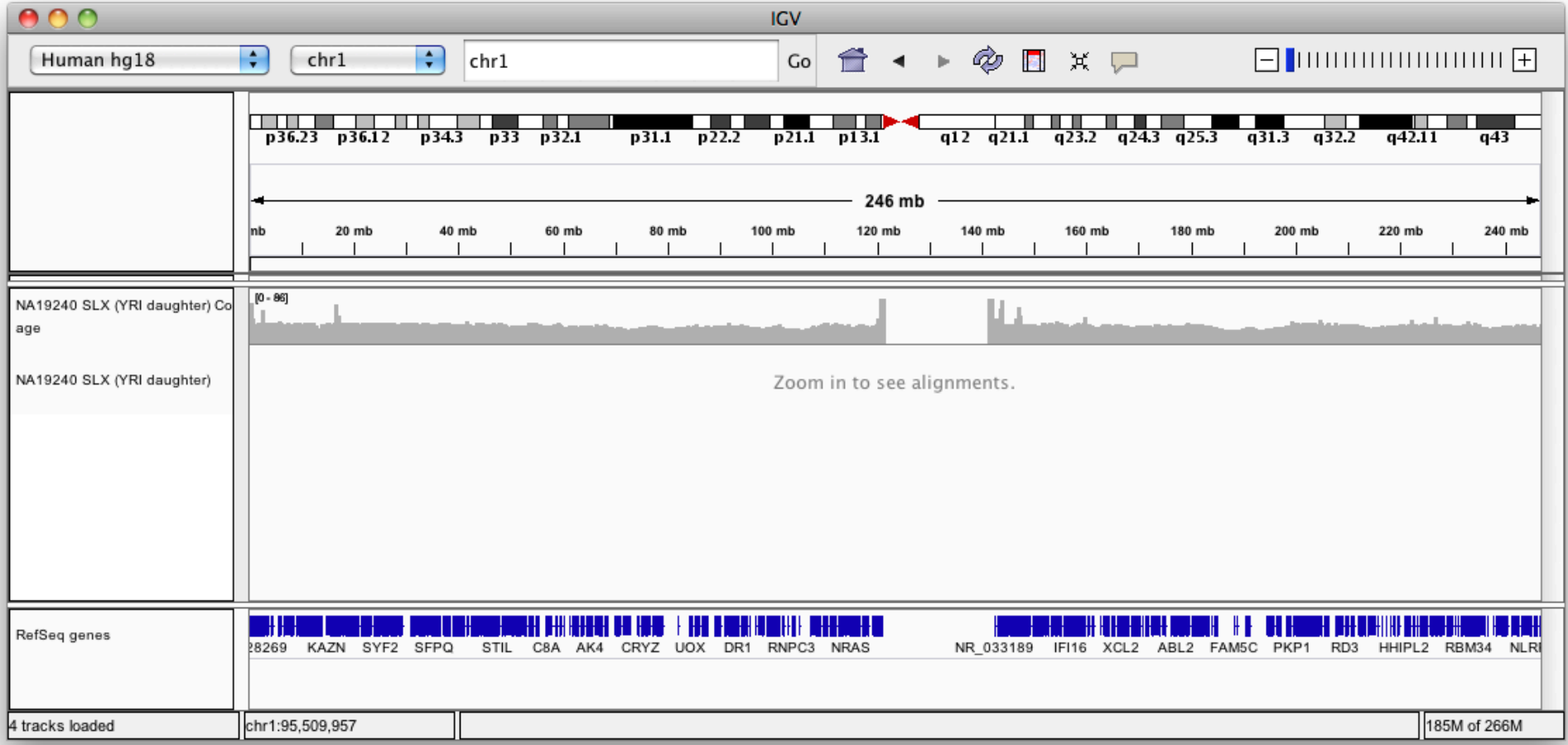
BROAD INSTITUTE

Integrative Genomics Viewer

Viewing alignments

Integrative Genomics Viewer

Whole chromosome view

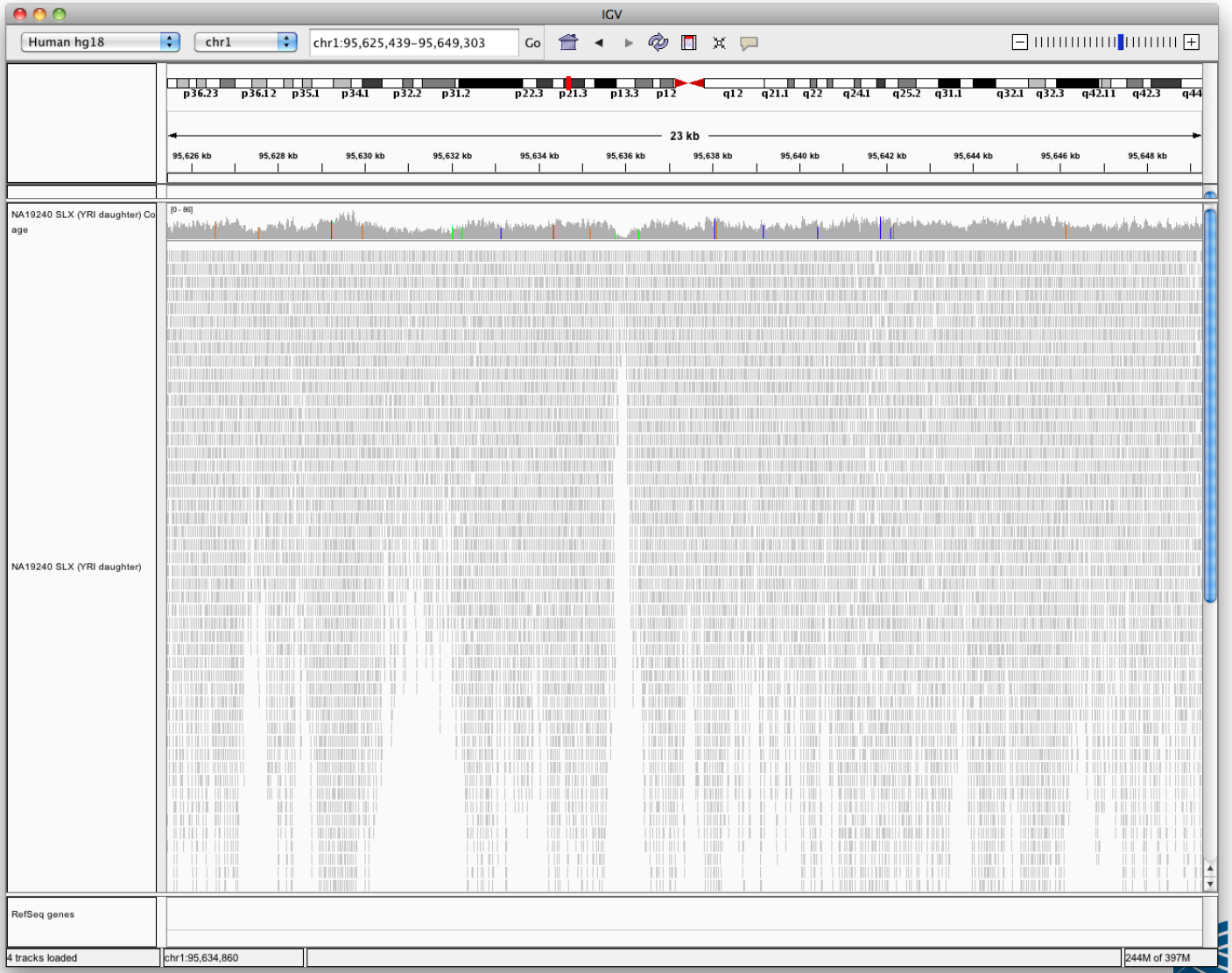


BROAD INSTITUTE

Viewing alignments

Integrative Genomics Viewer

Zoom in to view alignments

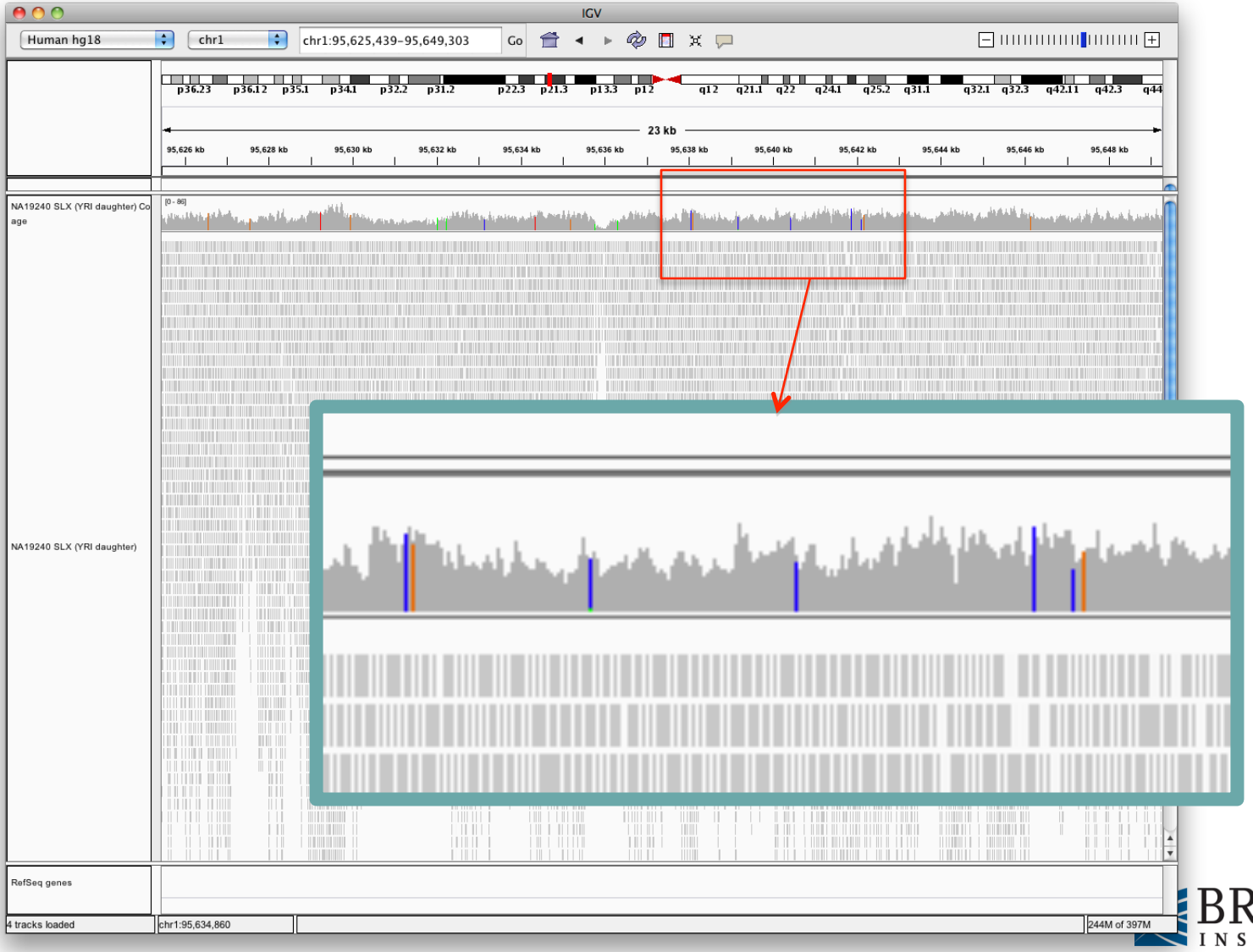


BROAD INSTITUTE

Viewing alignments

Integrative Genomics Viewer

Coverage track now has more detail

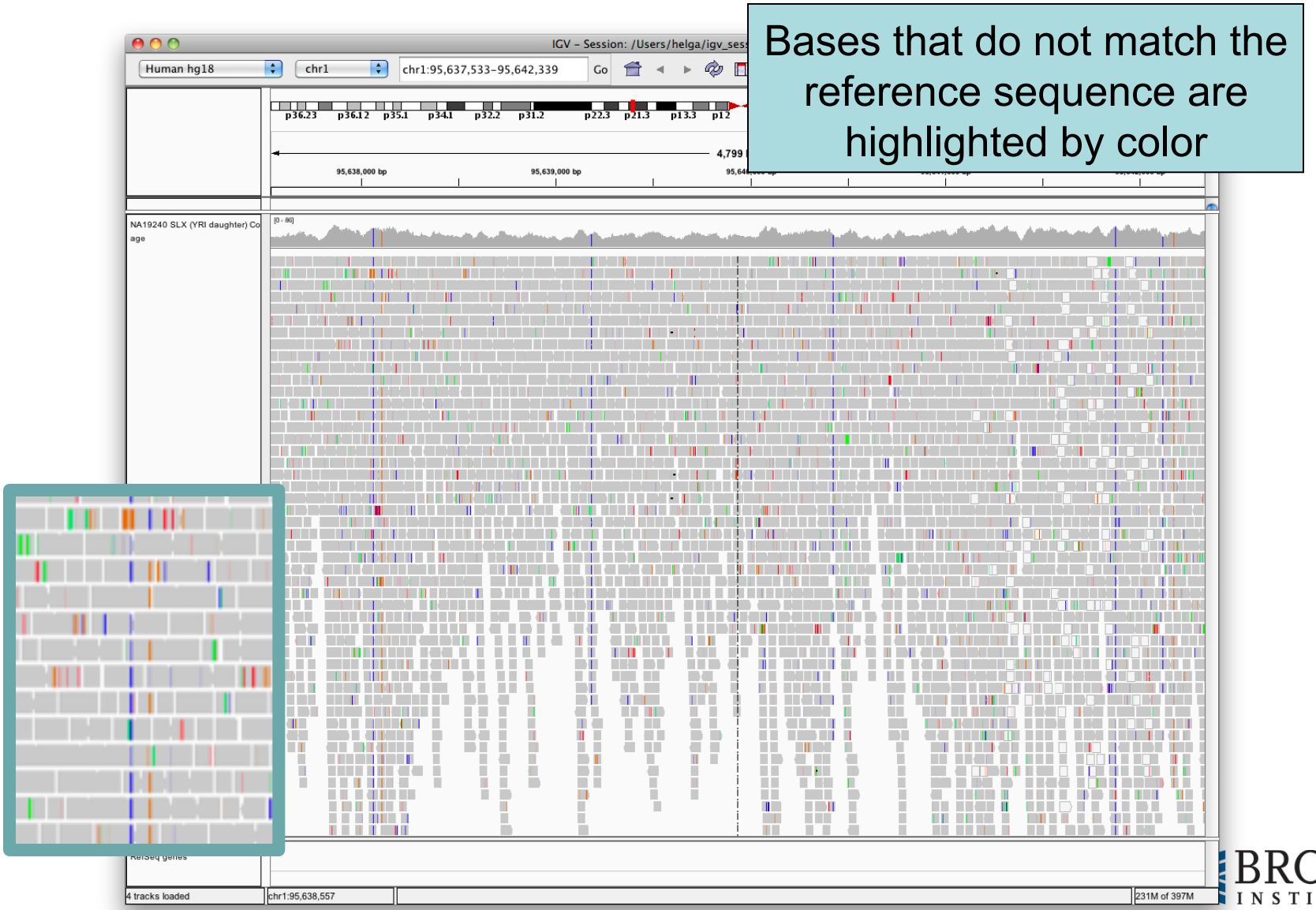


BROAD INSTITUTE

Viewing alignments

Integrative Genomics Viewer

Zoom in to see more detail

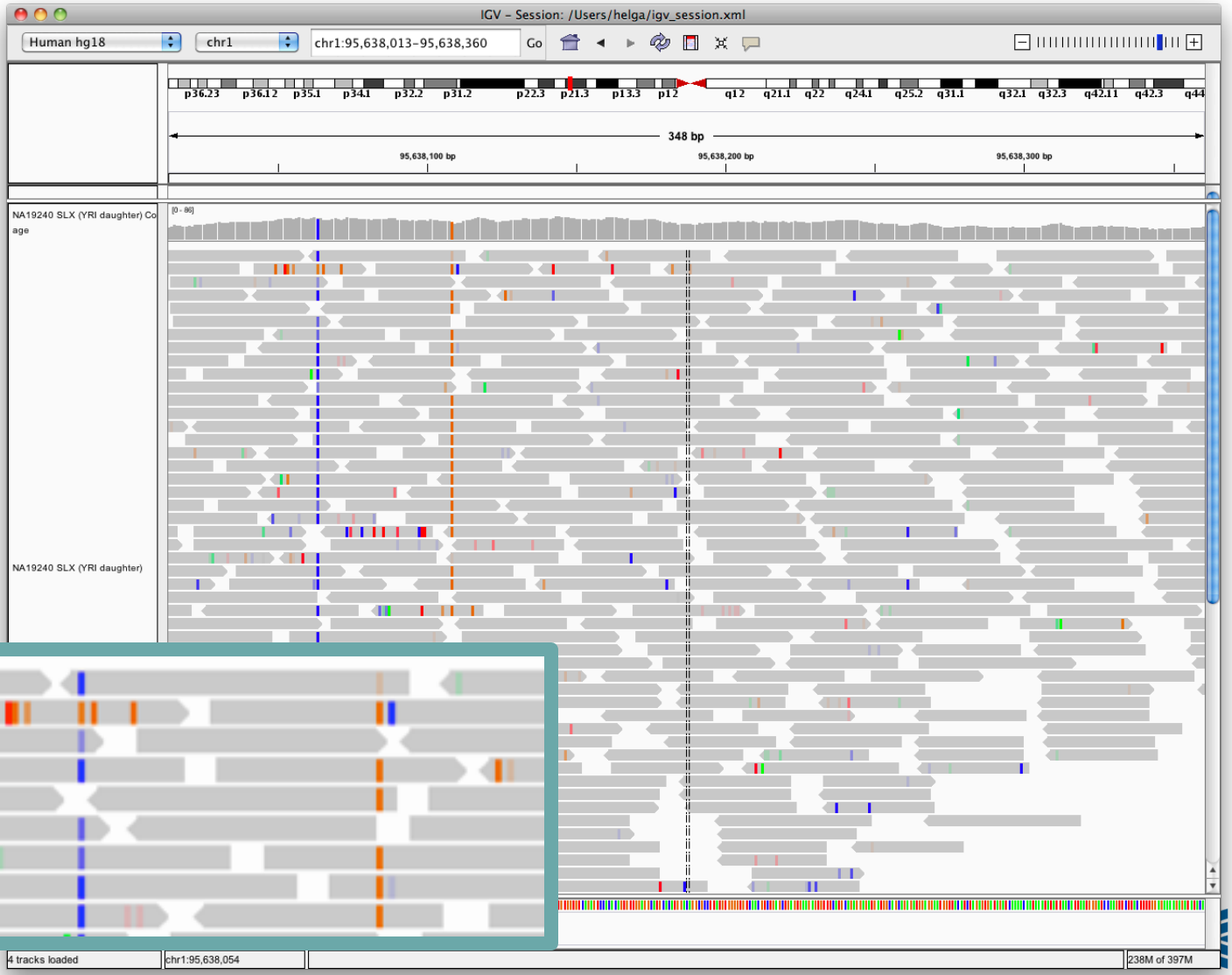


BROAD INSTITUTE

Viewing alignments

Integrative Genomics Viewer

Zoom in to see more detail



BROAD INSTITUTE

Viewing alignments

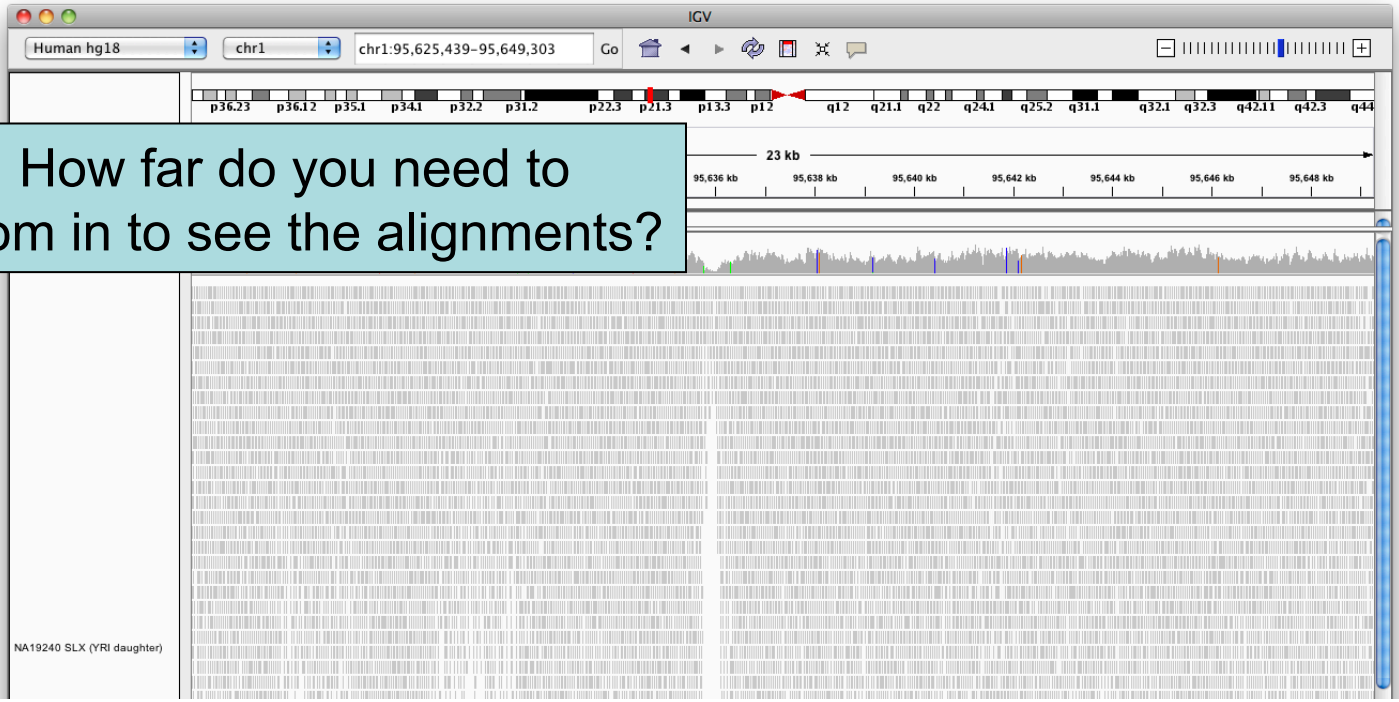
Integrative Genomics Viewer

Zoom in to see more detail

BROAD INSTITUTE

Viewing alignments

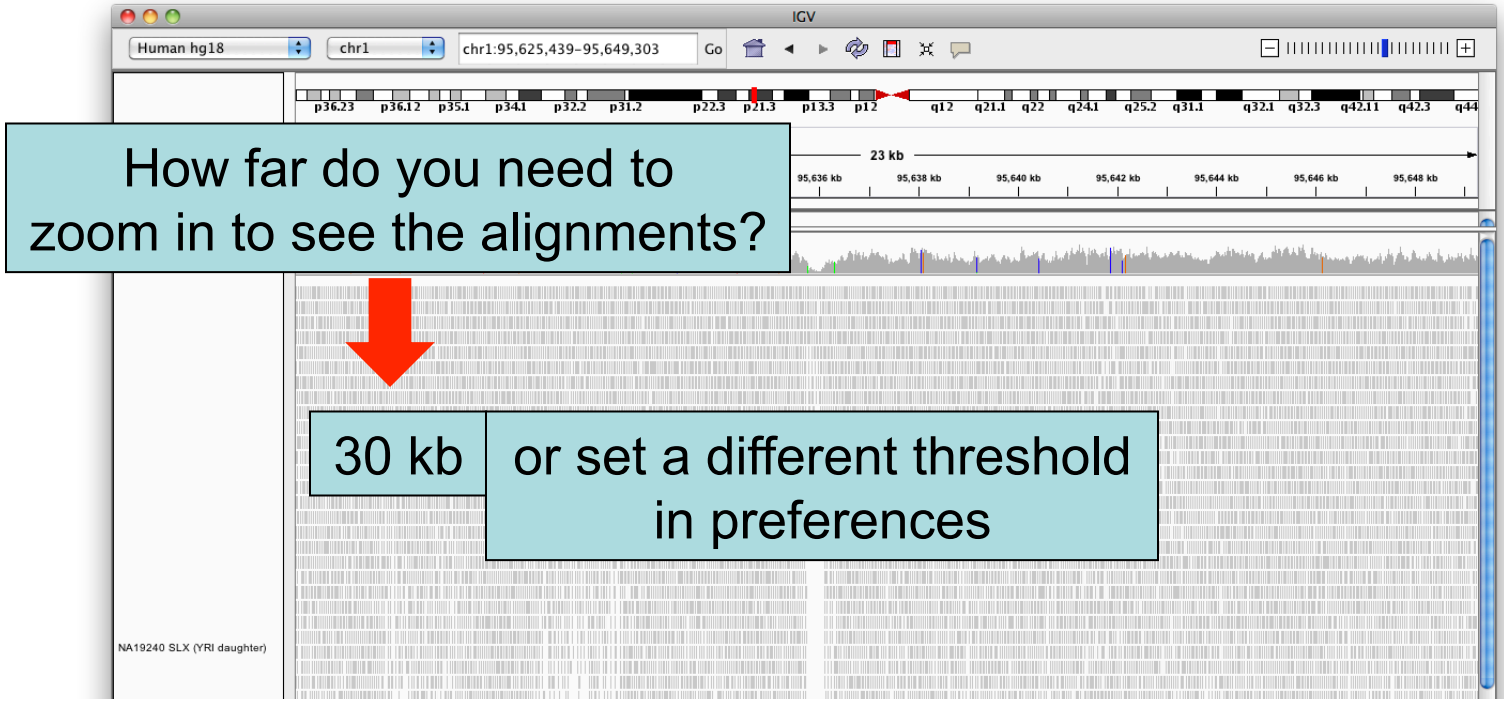
Integrative Genomics Viewer



How far do you need to zoom in to see the alignments?

BROAD INSTITUTE

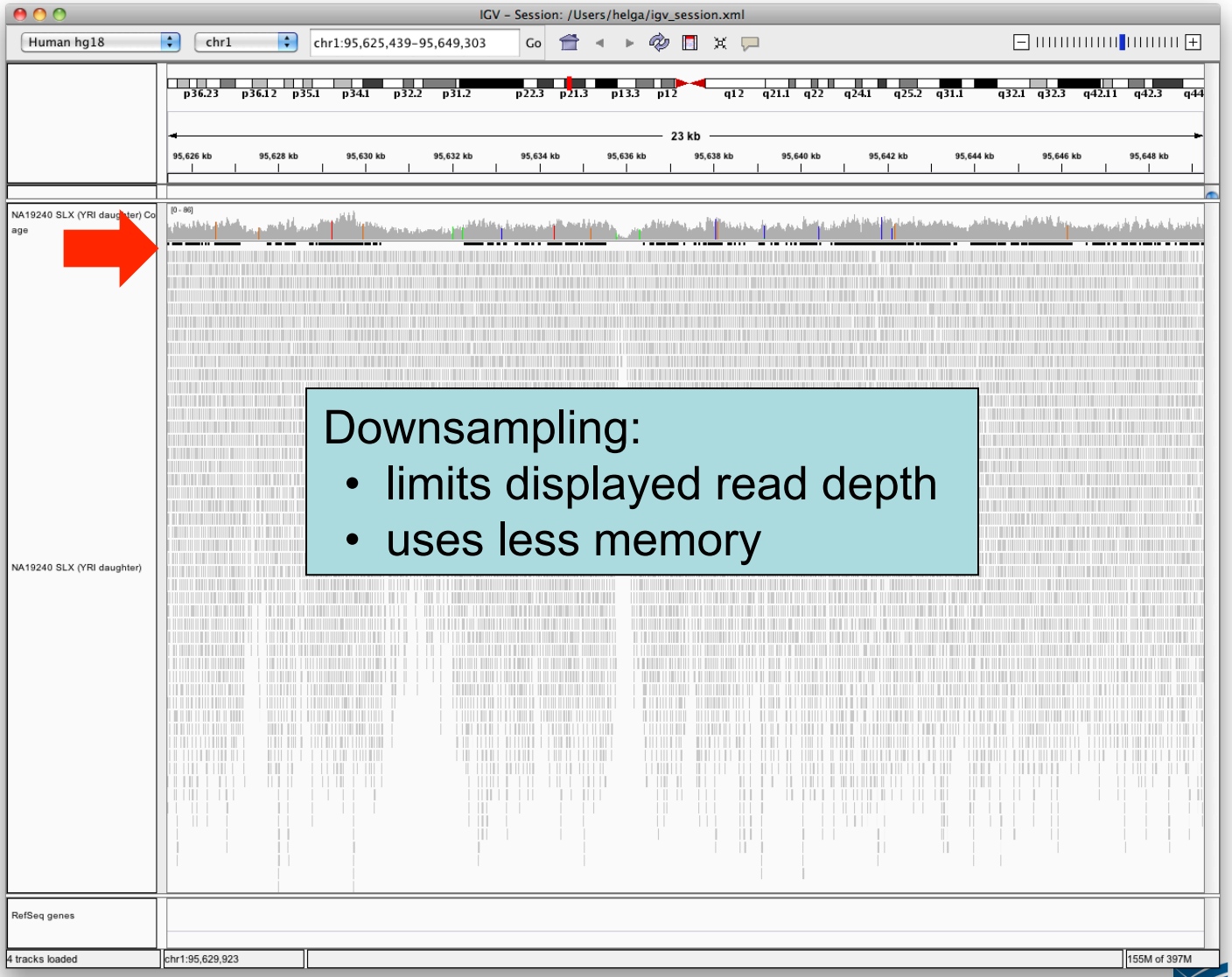
Viewing alignments



- Higher value (larger region) ➔ requires more memory
- Low coverage files ➔ ok to use higher value
- Very deep coverage files ➔ use lower value

Viewing alignments

Integrative Genomics Viewer



BROAD INSTITUTE

Viewing SNPs

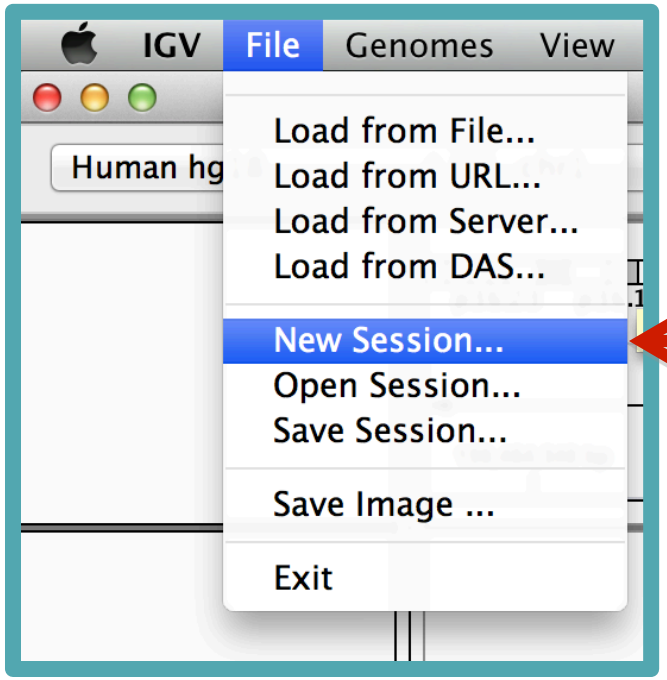
Integrative Genomics Viewer

Hands-on exercise

- Load alignments from whole genome sequencing
- View sites where SNPs were called
- Sort and color to highlight patterns

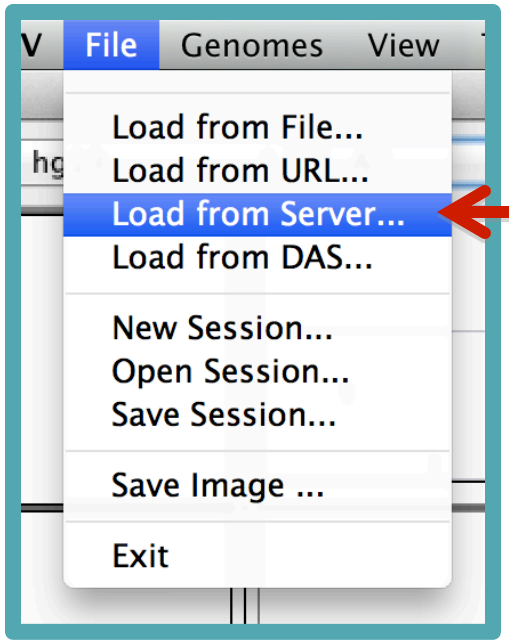
BROAD INSTITUTE

Viewing SNPs



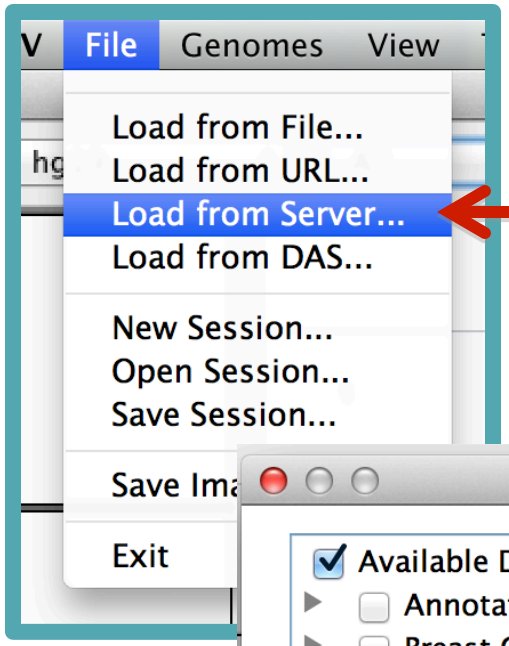
Before we start:
Select **File > New Session**
to clear IGV window

Viewing SNPs

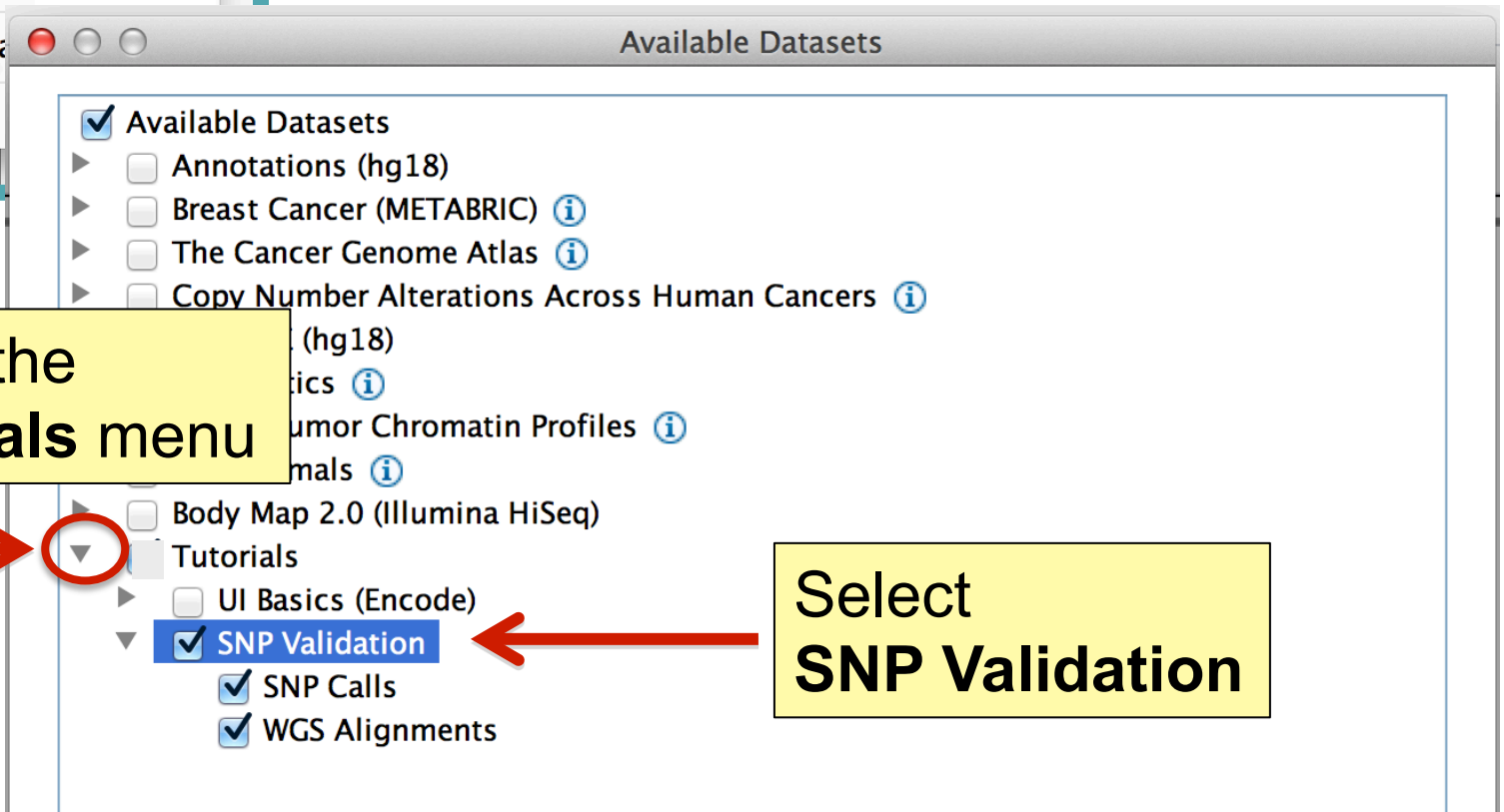


Select **File > Load from Server…**

Viewing SNPs



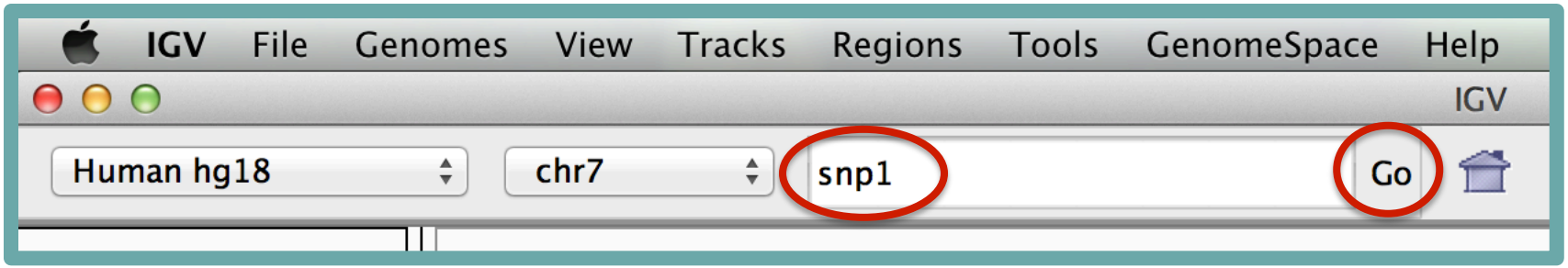
Select **File > Load from Server…**



Open the **Tutorials** menu

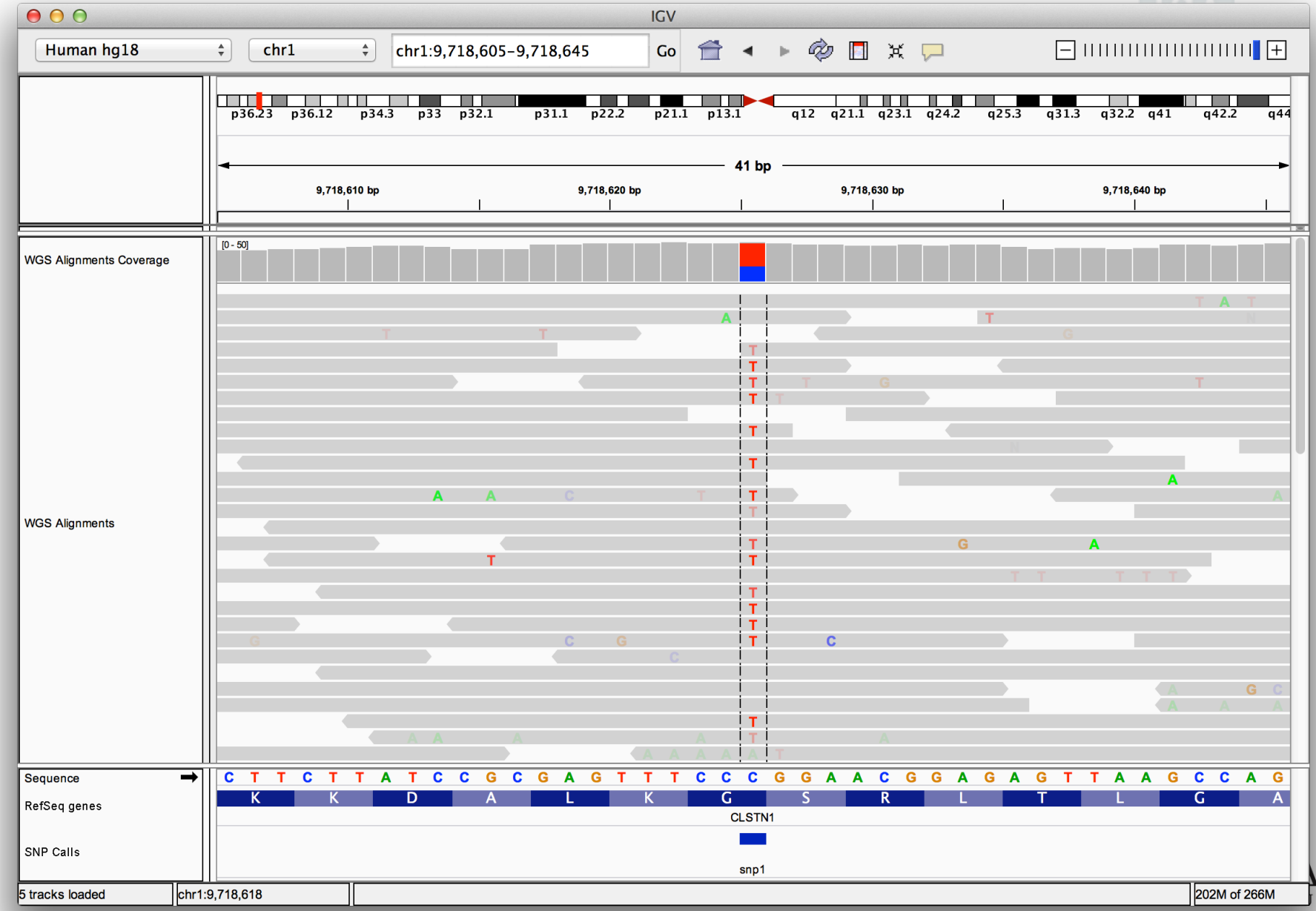
Select **SNP Validation**

Viewing SNPs

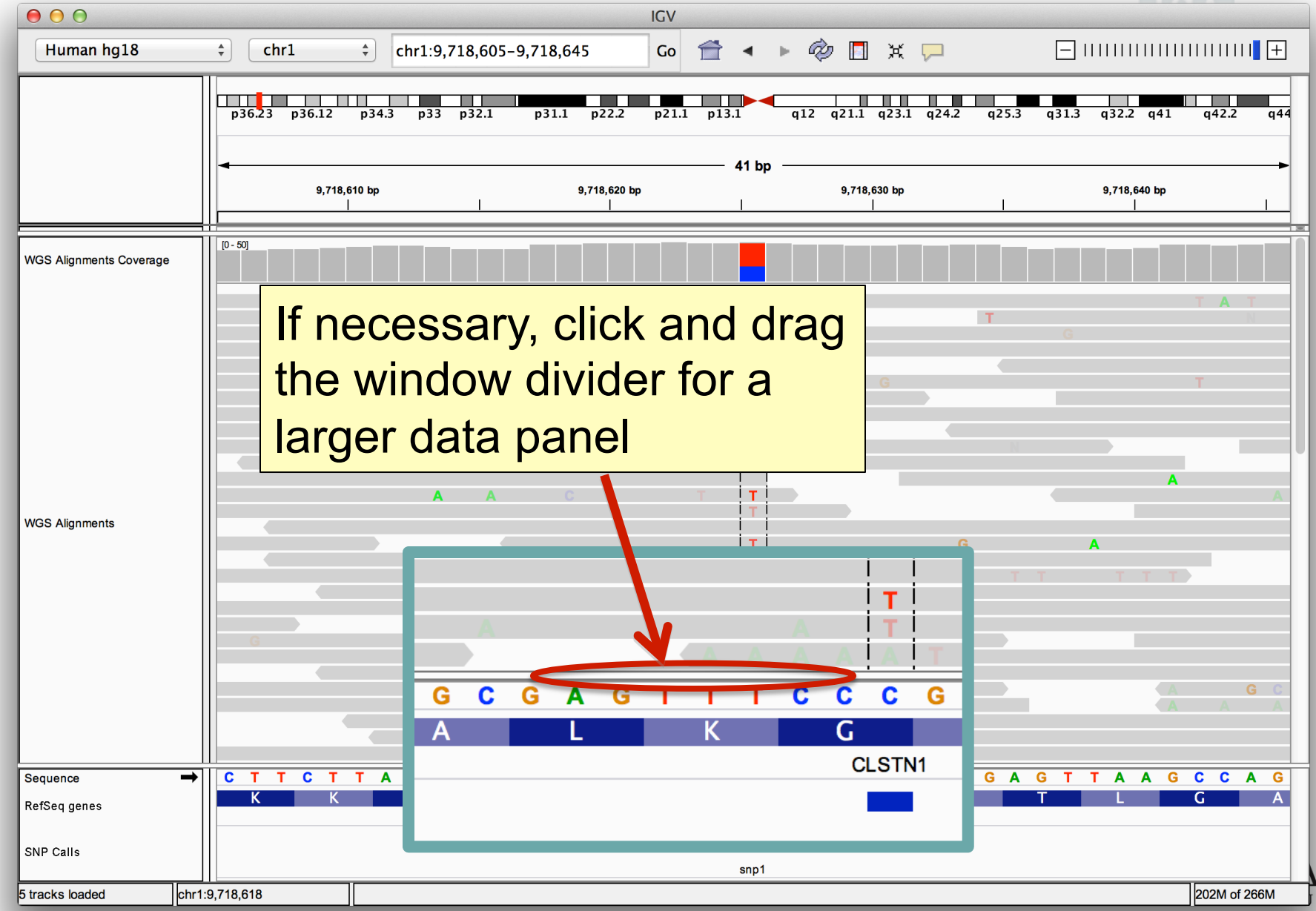


Type “snp1” in the **Search Box** and click **Go**

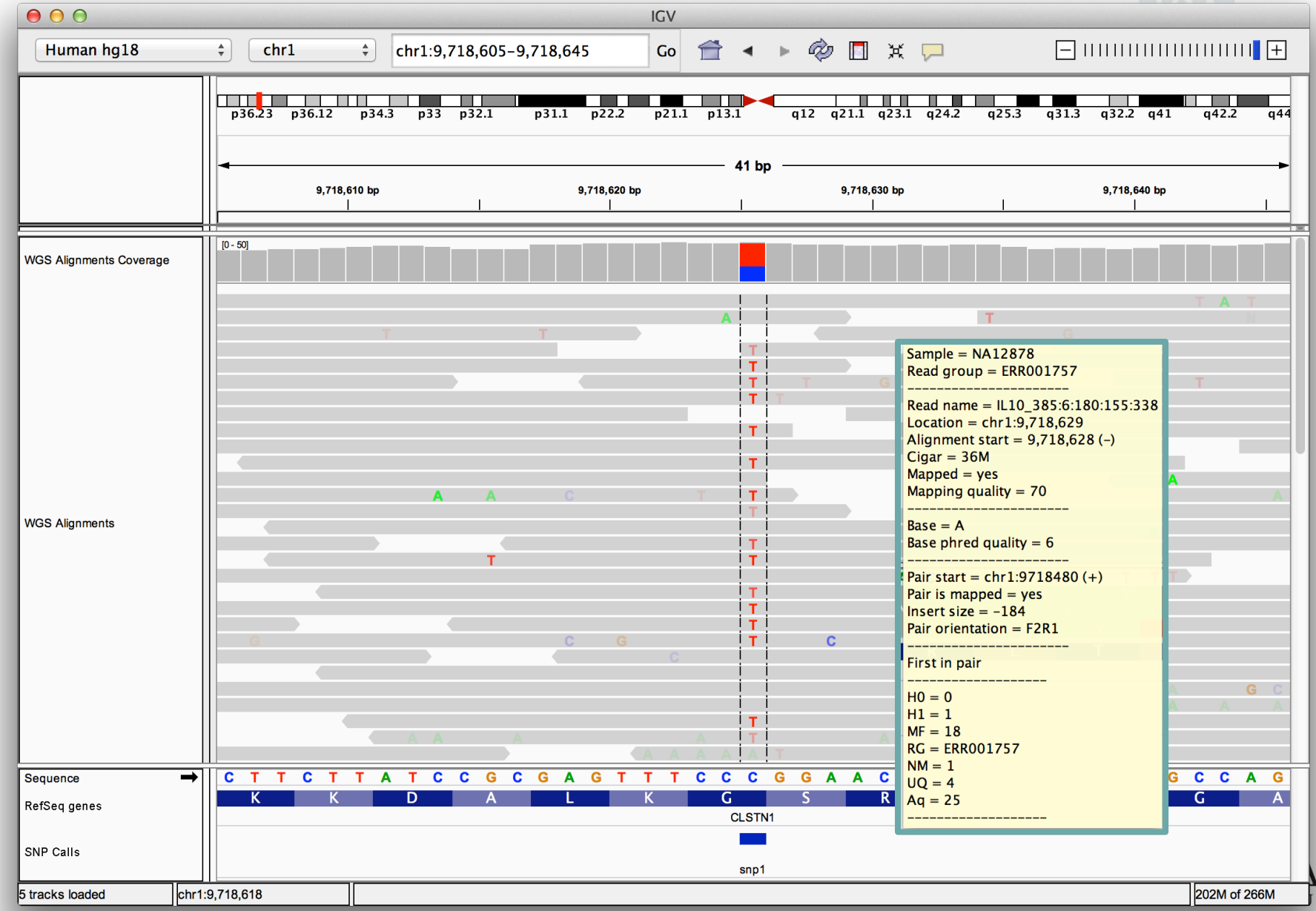
Viewing SNPs



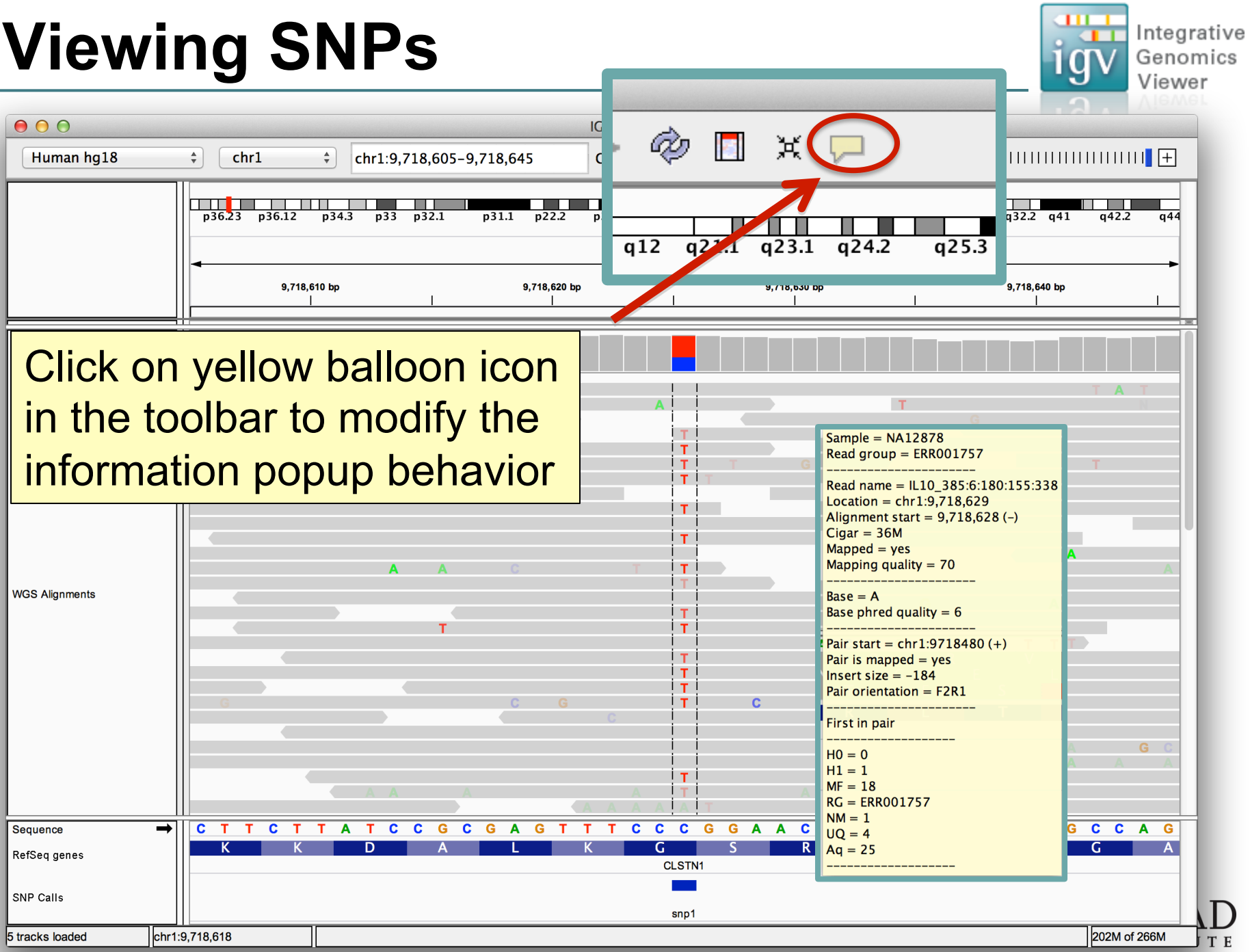
Viewing SNPs



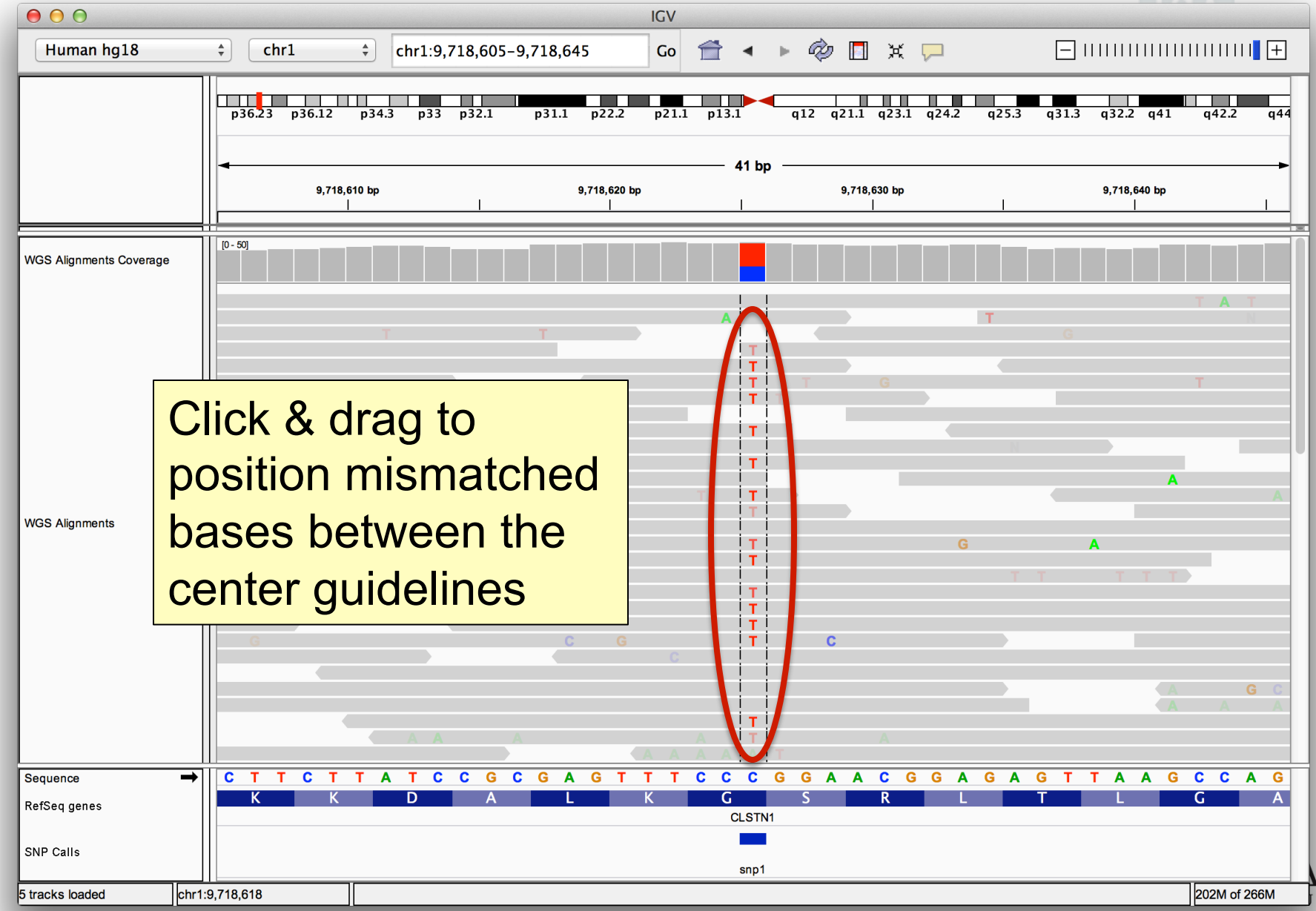
Viewing SNPs



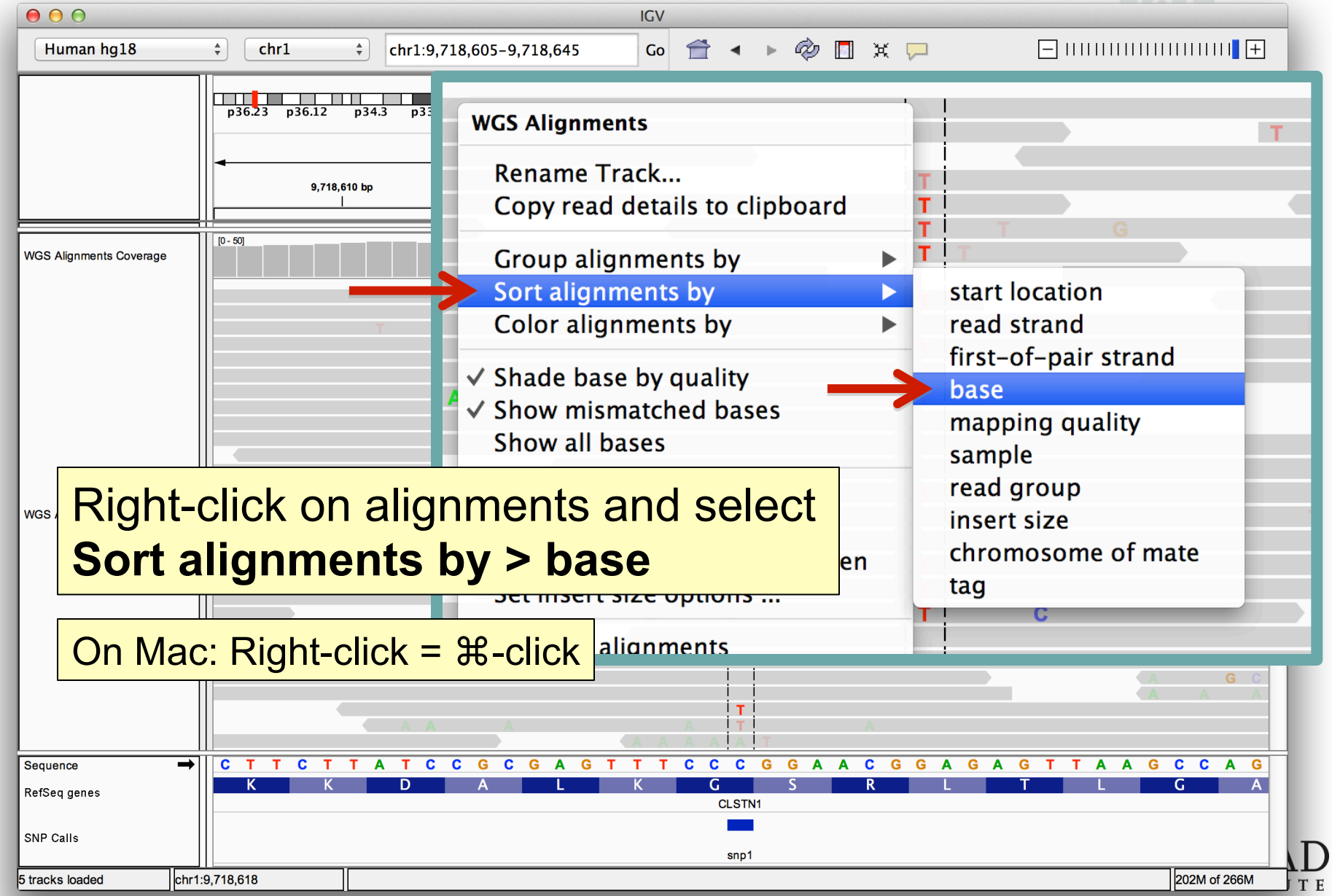
Viewing SNPs



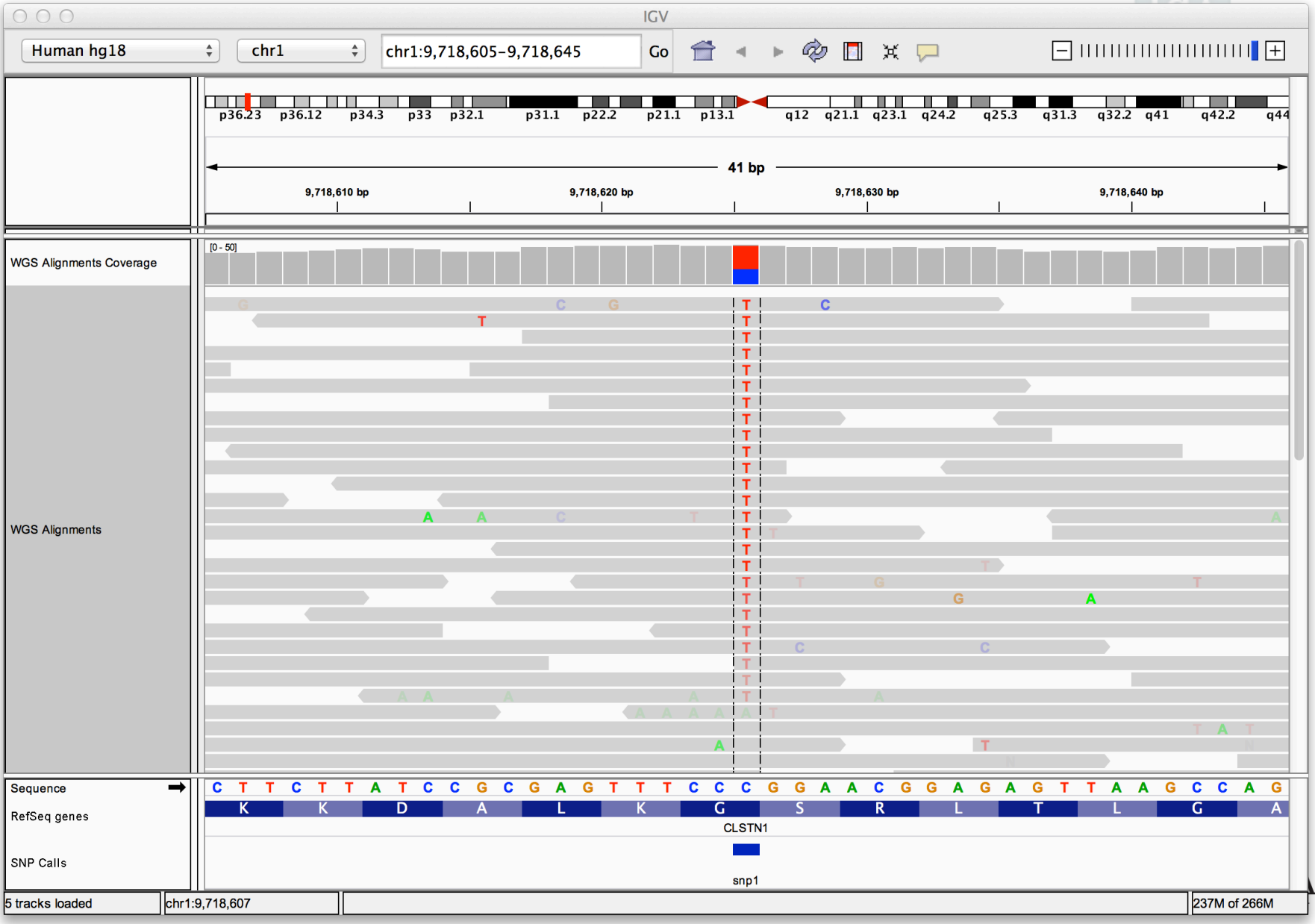
Viewing SNPs



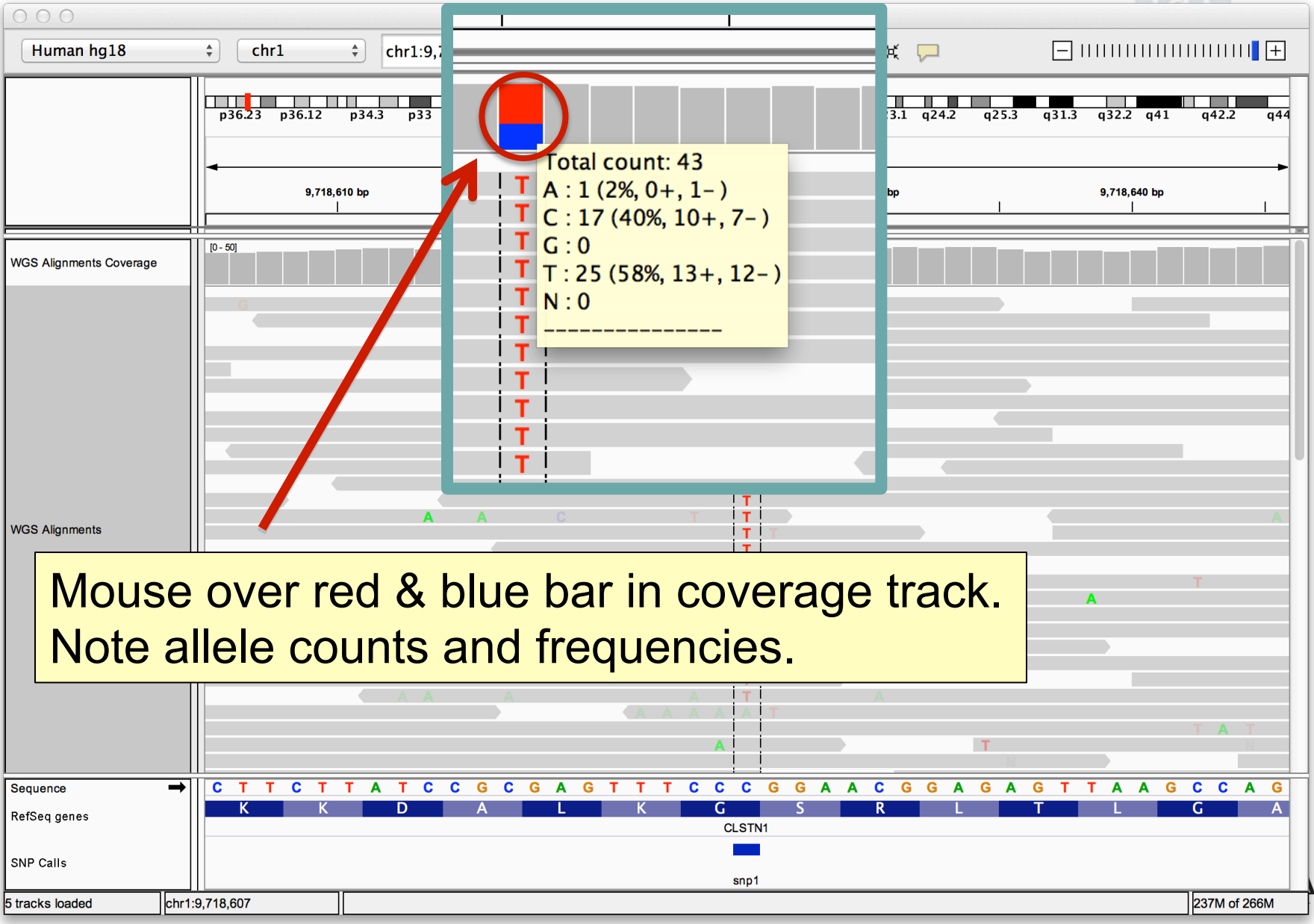
Viewing SNPs



Viewing SNPs

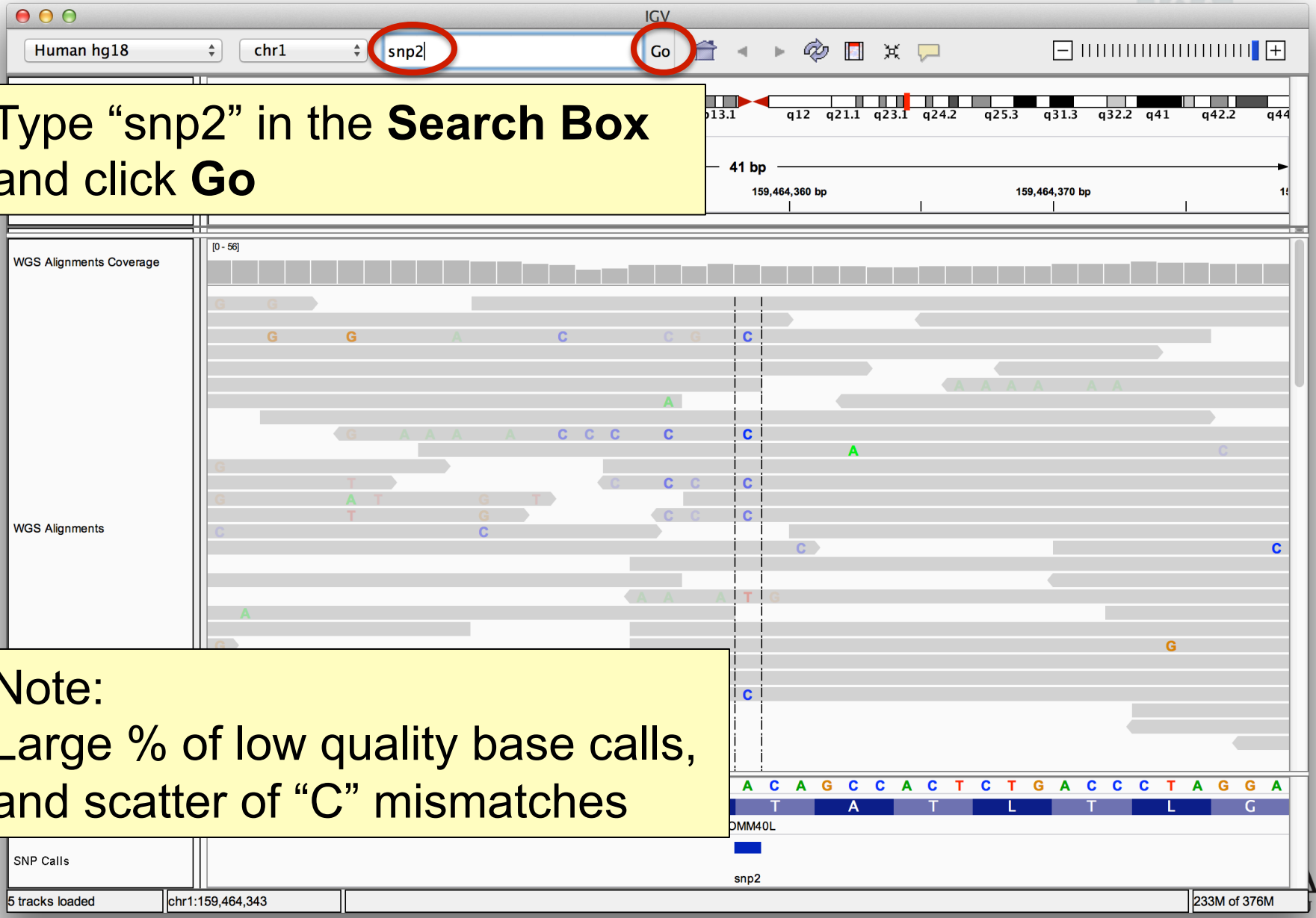


Viewing SNPs



Mouse over red & blue bar in coverage track.
Note allele counts and frequencies.

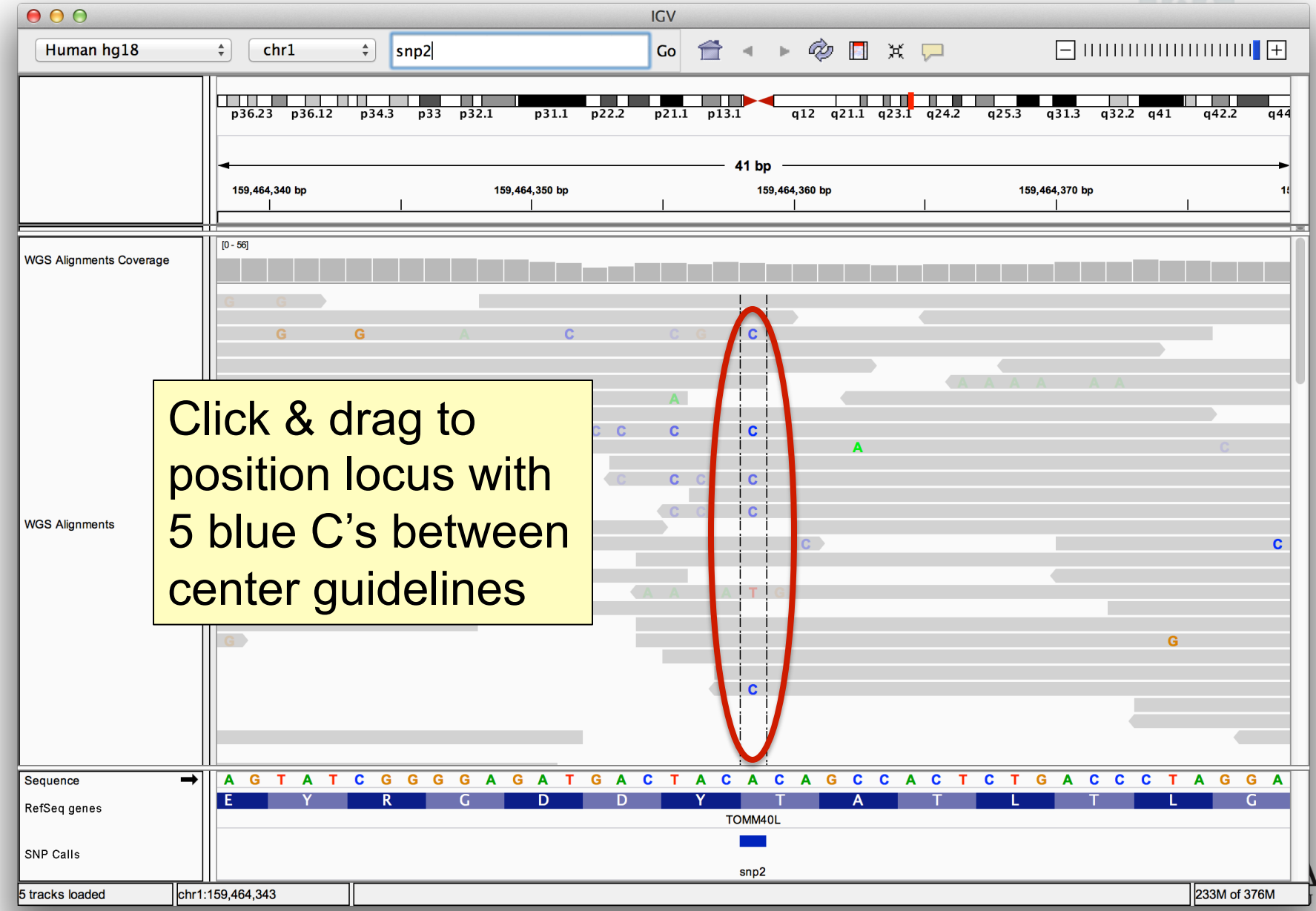
Viewing SNPs



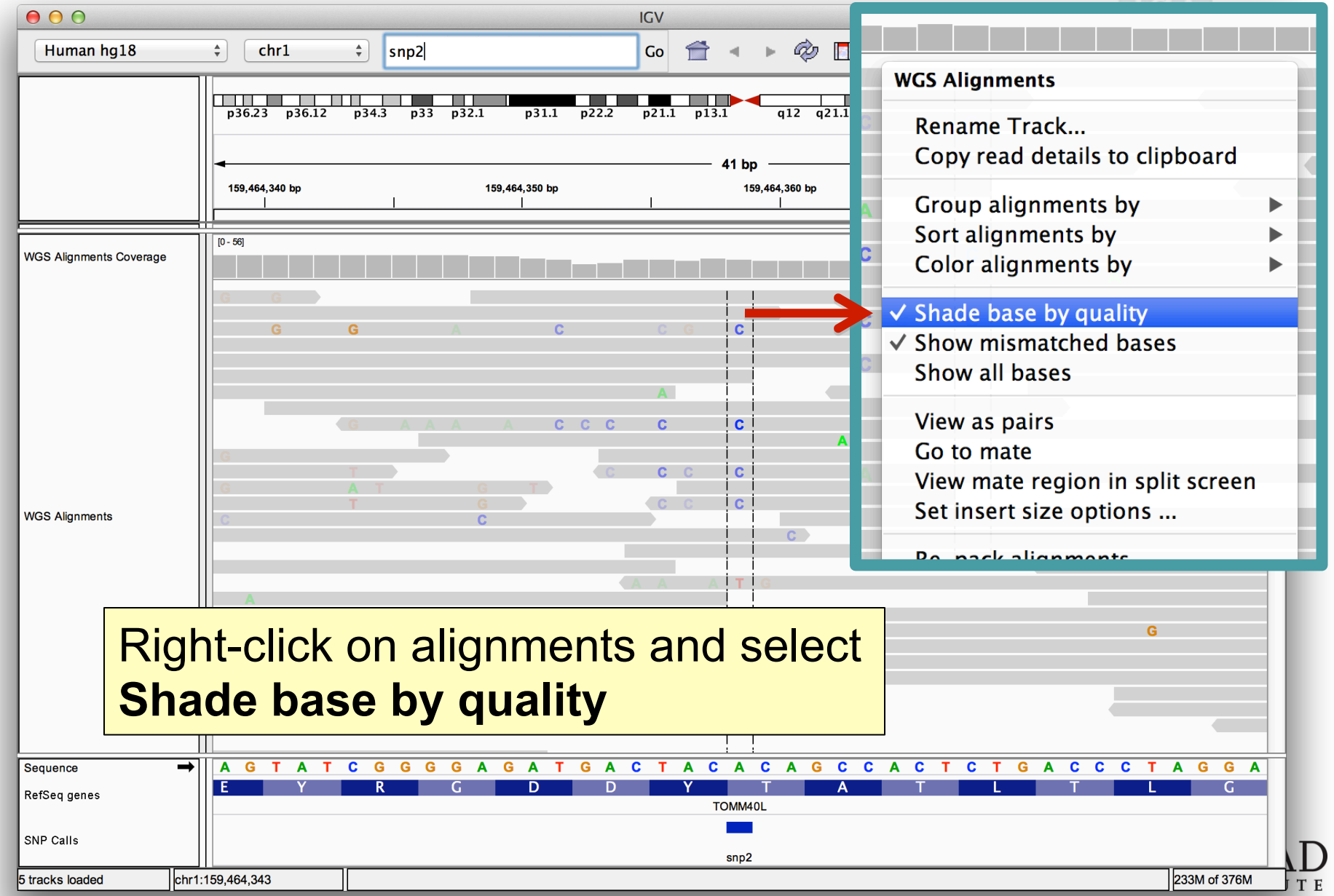
Type “snp2” in the **Search Box** and click **Go**

Note:
Large % of low quality base calls, and scatter of “C” mismatches

Viewing SNPs

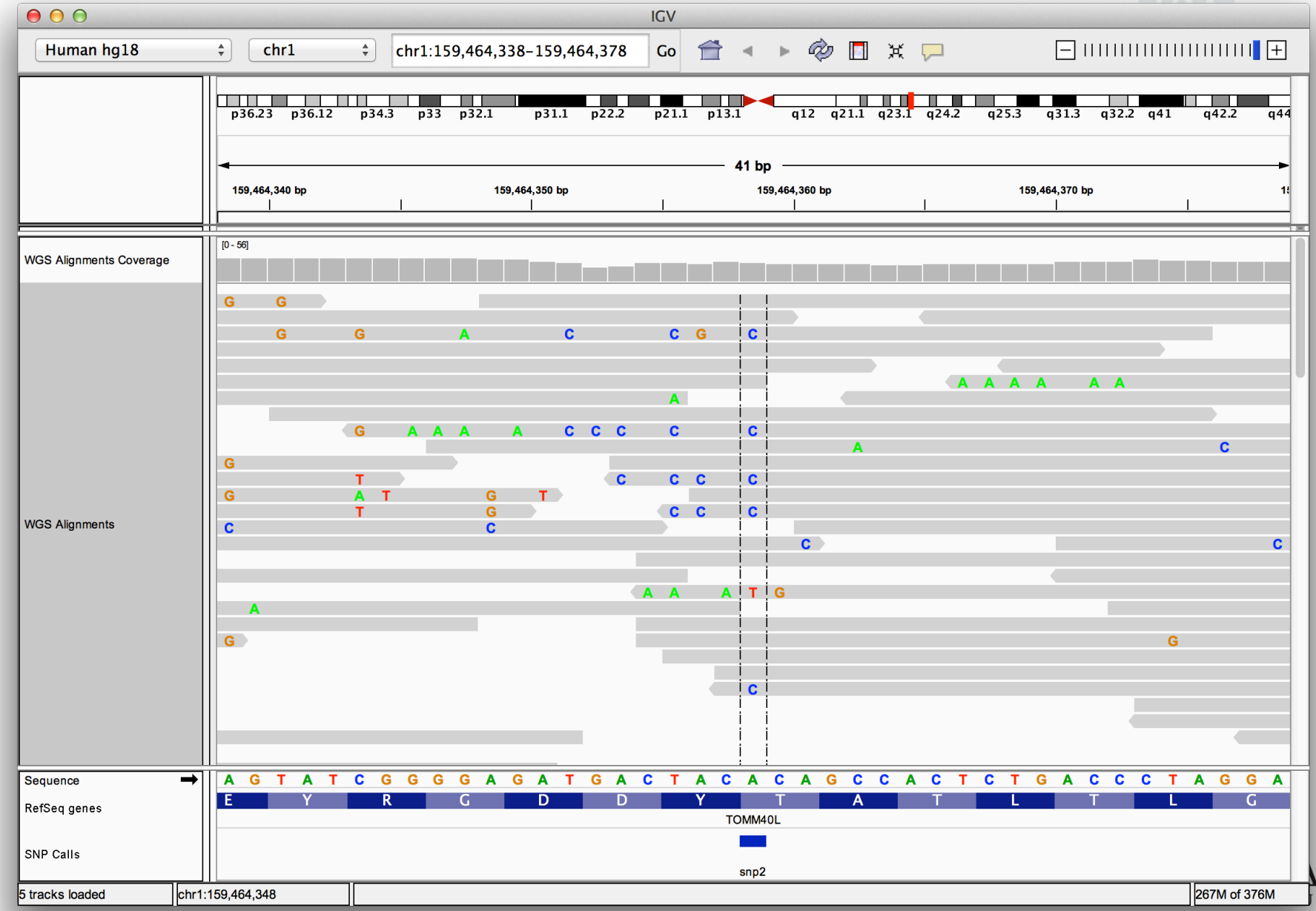


Viewing SNPs

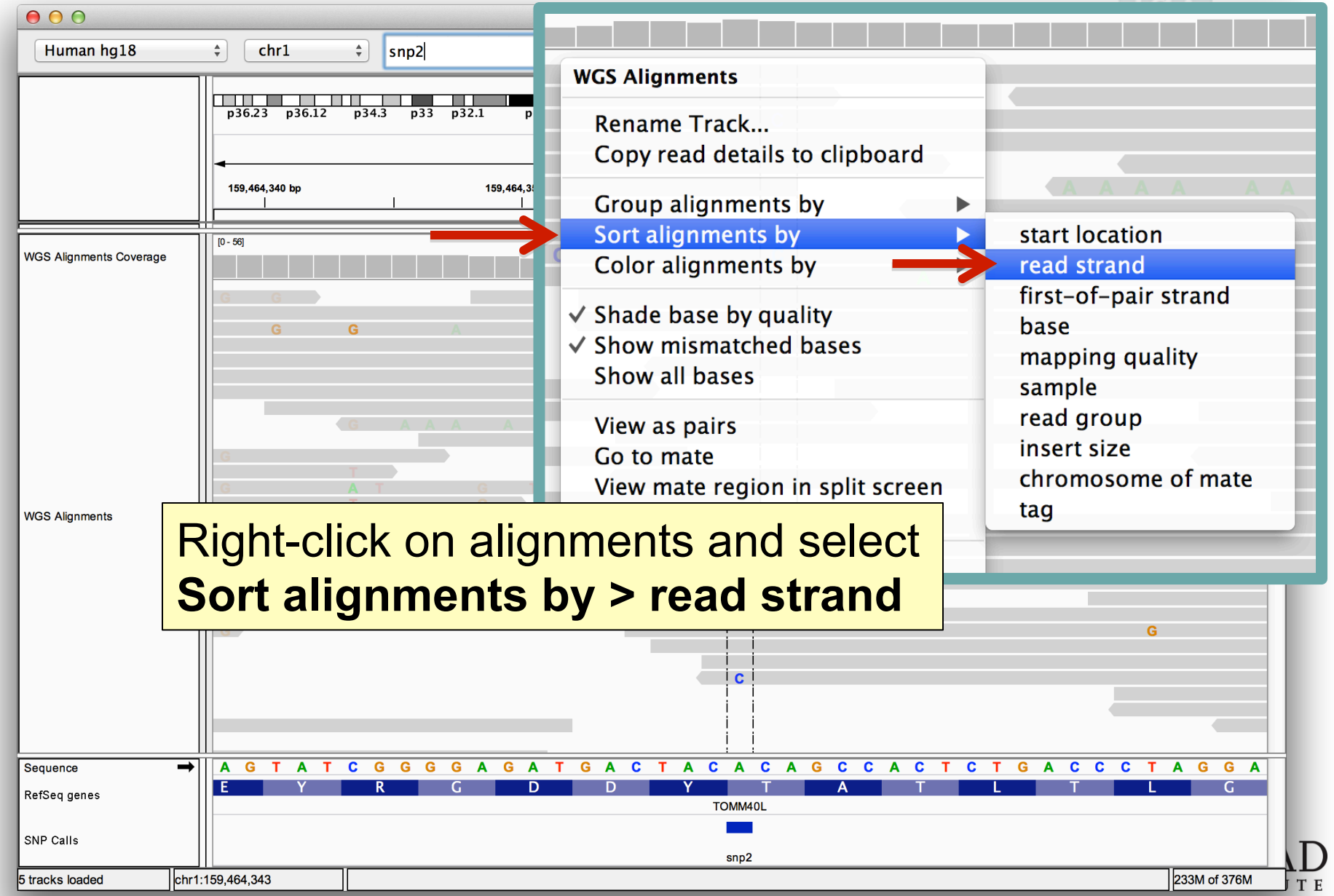


Right-click on alignments and select **Shade base by quality**

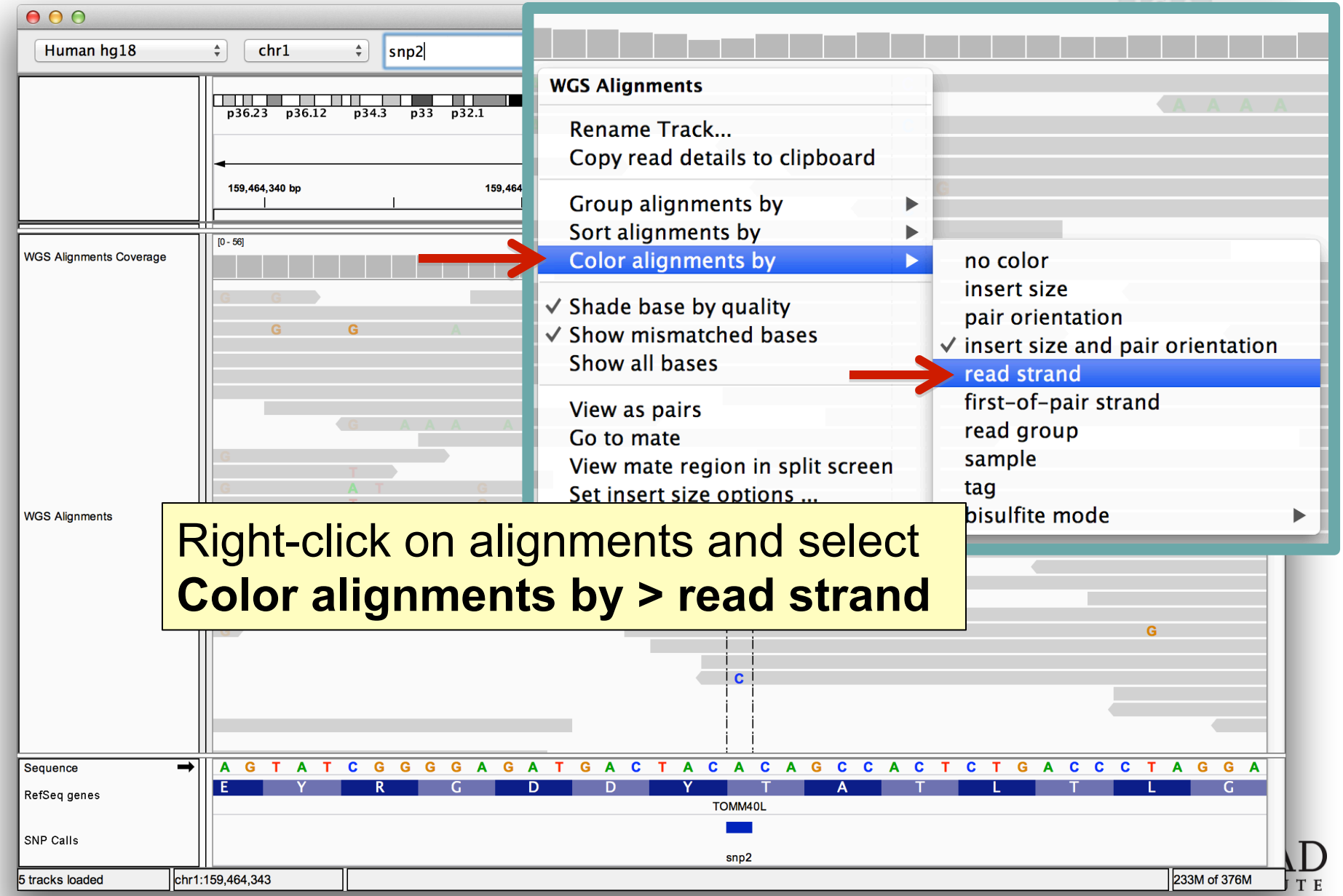
Viewing SNPs



Viewing SNPs



Viewing SNPs



Viewing SNPs

Viewing Structural Events

BROAD INSTITUTE

Integrative Genomics Viewer

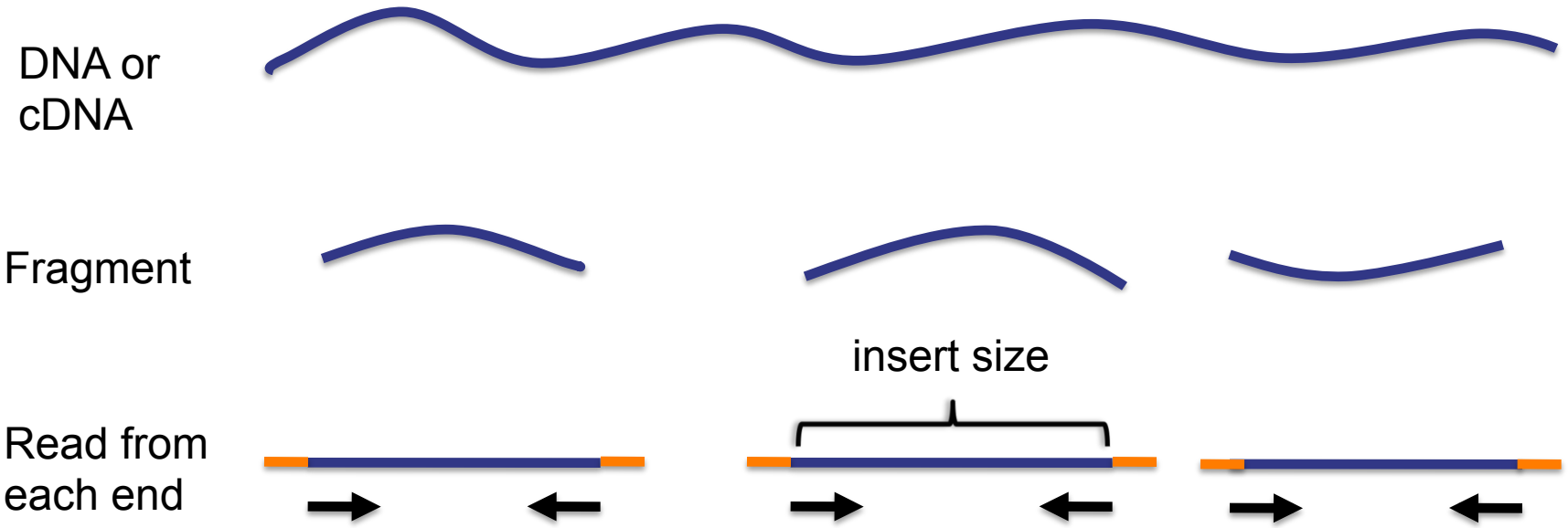
Structural events

Integrative Genomics Viewer

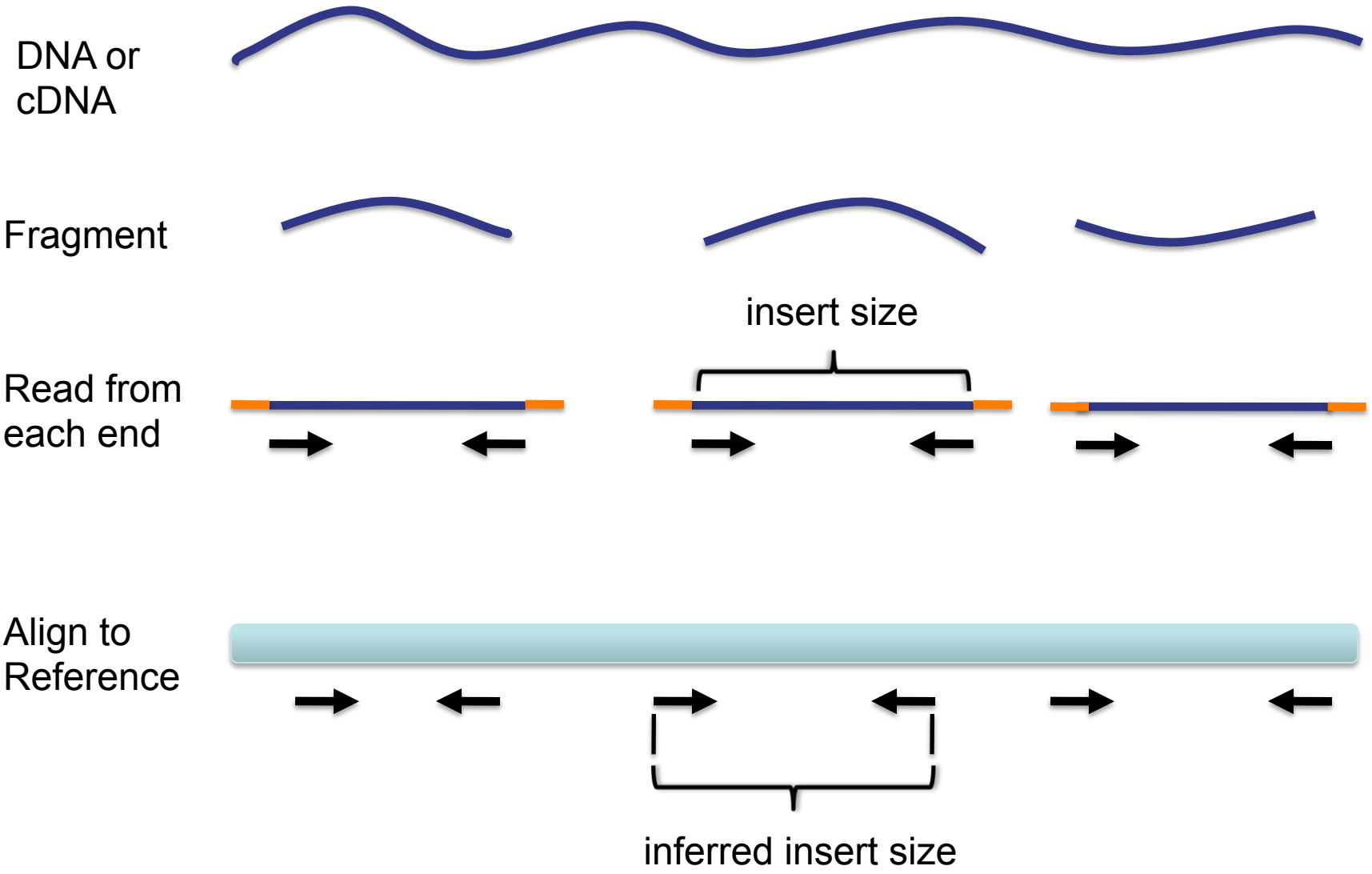
- Paired reads can yield evidence for genomic “structural events”, such as deletions, translocations, and inversions.
- Alignment coloring options help highlight these events based on:
  - Inferred insert size (template length)
  - Pair orientation (relative strand of pair)

BROAD INSTITUTE

Paired-end sequencing



Paired-end sequencing



Interpreting Insert Size

Interpreting inferred insert size

Integrative Genomics Viewer

The “inferred insert size” can be used to detect structural variants, including:

- Deletions
- Insertions
- Inter-chromosomal rearrangements: (Undefined insert size)

BROAD INSTITUTE

Deletion

What is the effect of a deletion on inferred insert size?

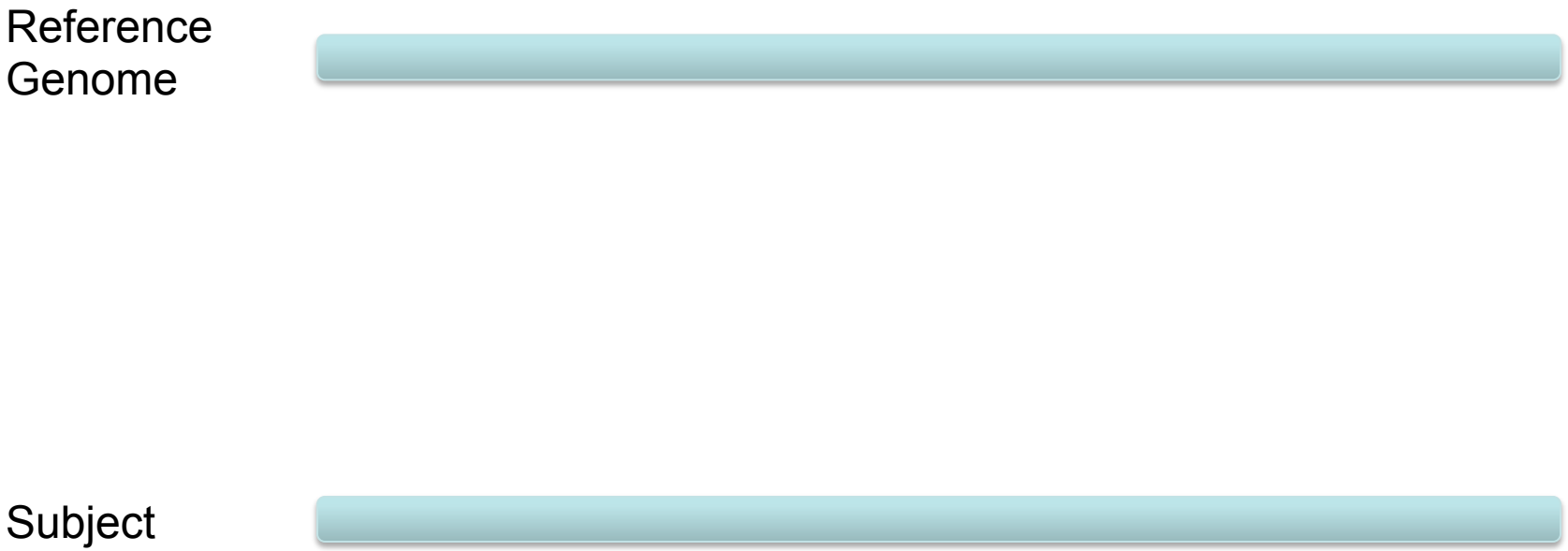
Deletion

Integrative Genomics Viewer

Reference Genome

BROAD INSTITUTE

Deletion

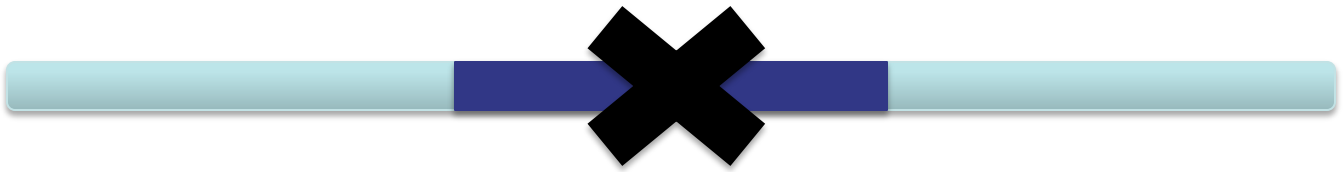


Deletion

Integrative Genomics Viewer

Reference Genome

Subject



BROAD INSTITUTE

Deletion

Integrative Genomics Viewer

Reference Genome

Subject

BROAD INSTITUTE

Deletion

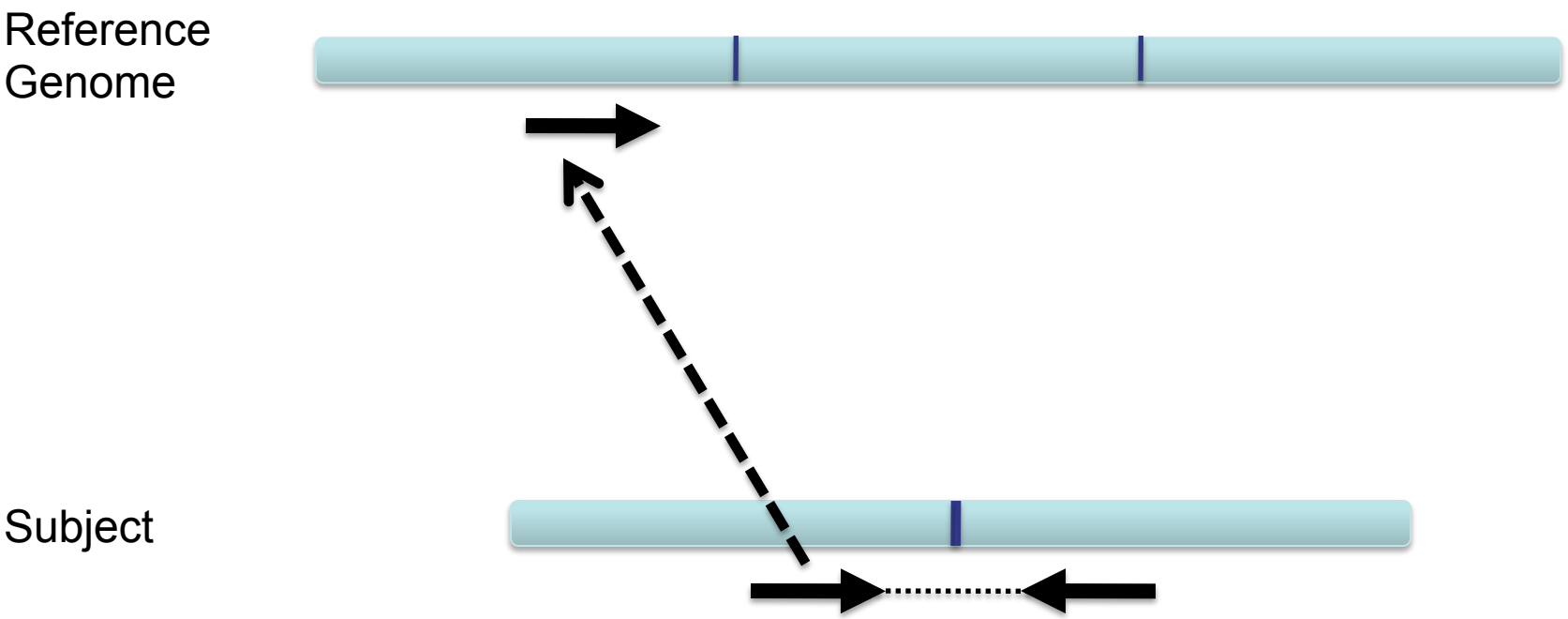
Integrative Genomics Viewer

Reference Genome

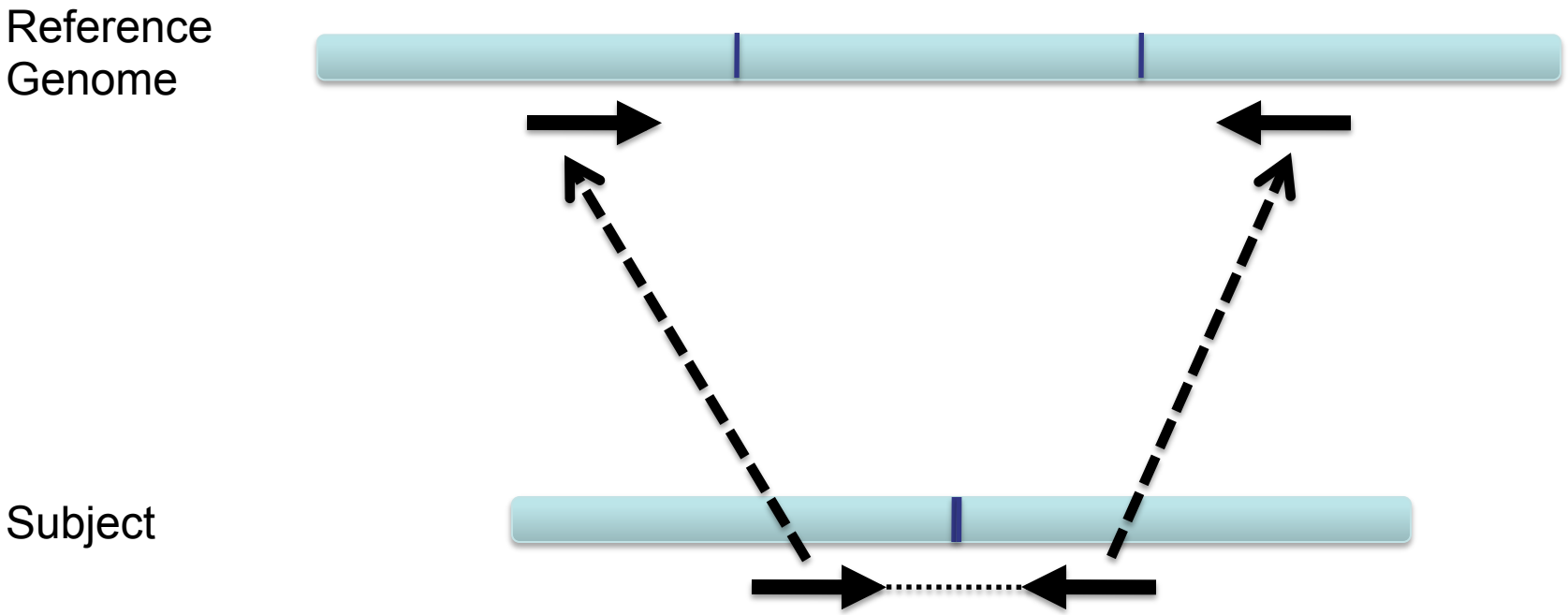
Subject

BROAD INSTITUTE

Deletion



Deletion



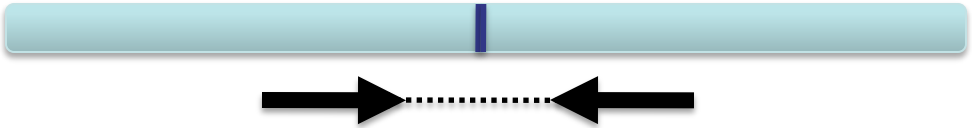
Deletion

Integrative Genomics Viewer

Reference Genome

inferred insert size

Subject



BROAD INSTITUTE

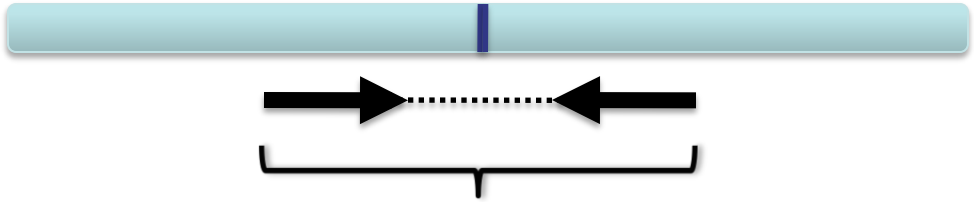
Deletion

Integrative Genomics Viewer

Reference Genome

inferred insert size

Subject



expected insert size

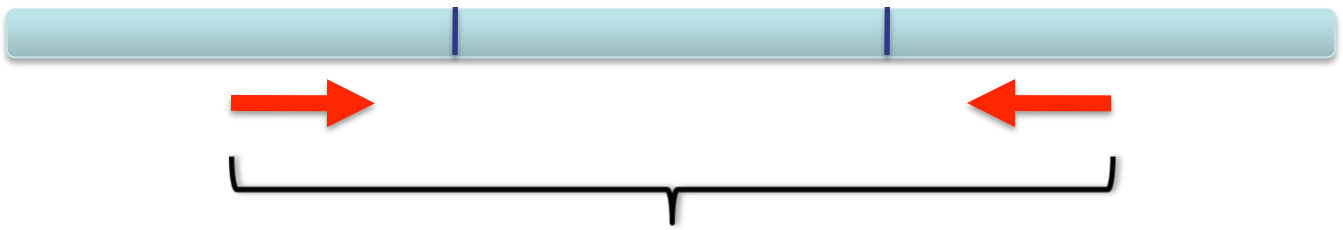
BROAD INSTITUTE

Deletion

Integrative Genomics Viewer

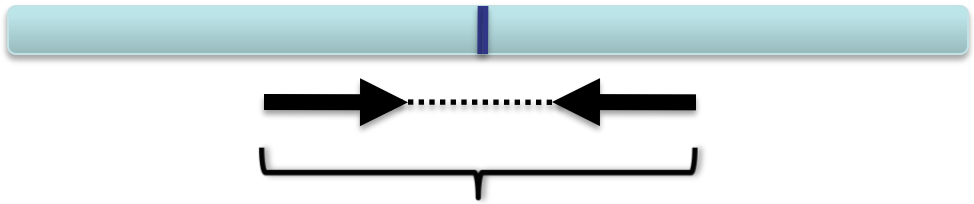
Inferred insert size is > expected value

Reference Genome



inferred insert size

Subject



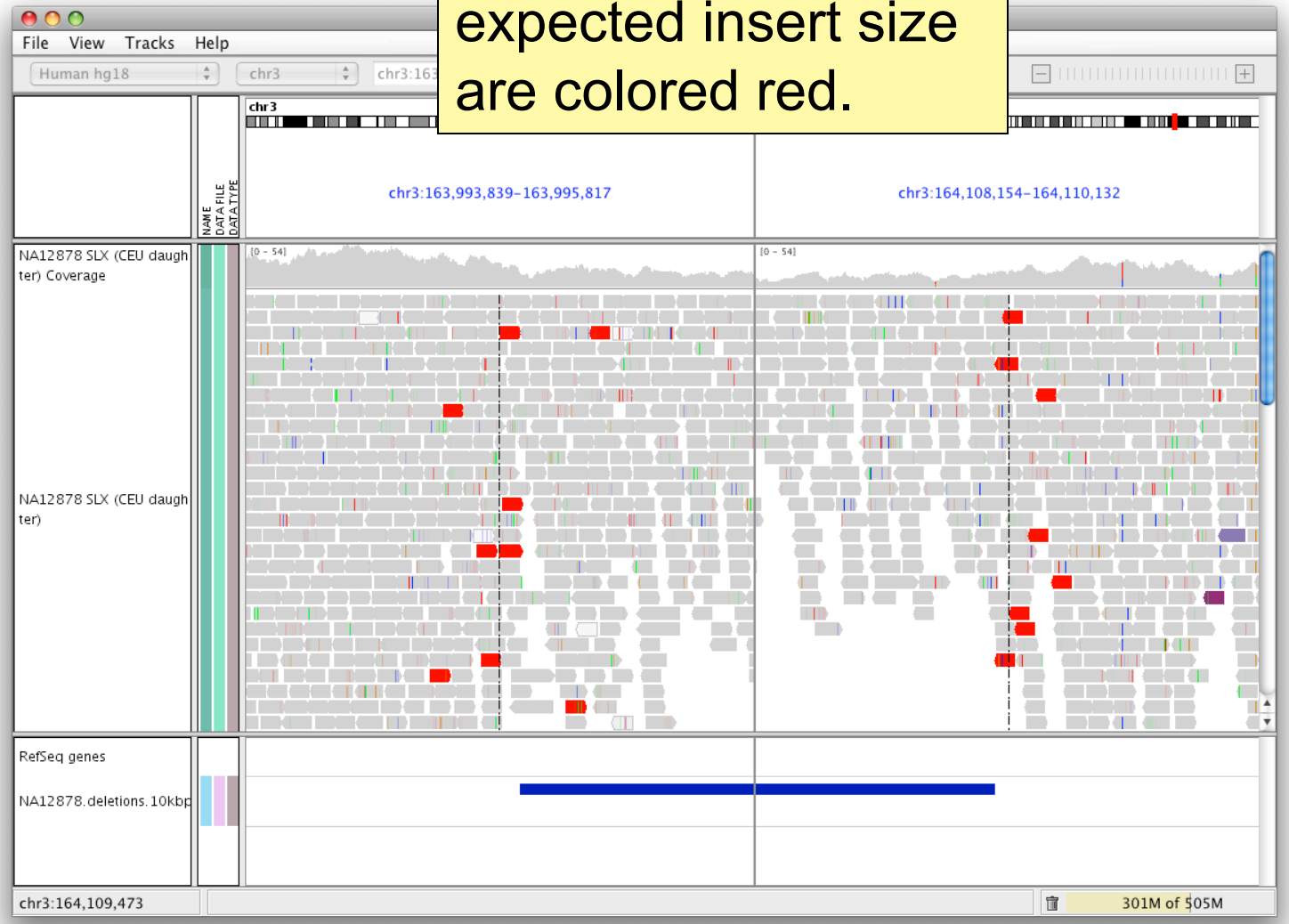
expected insert size

BROAD INSTITUTE

Deletion

Integrative Genomics Viewer

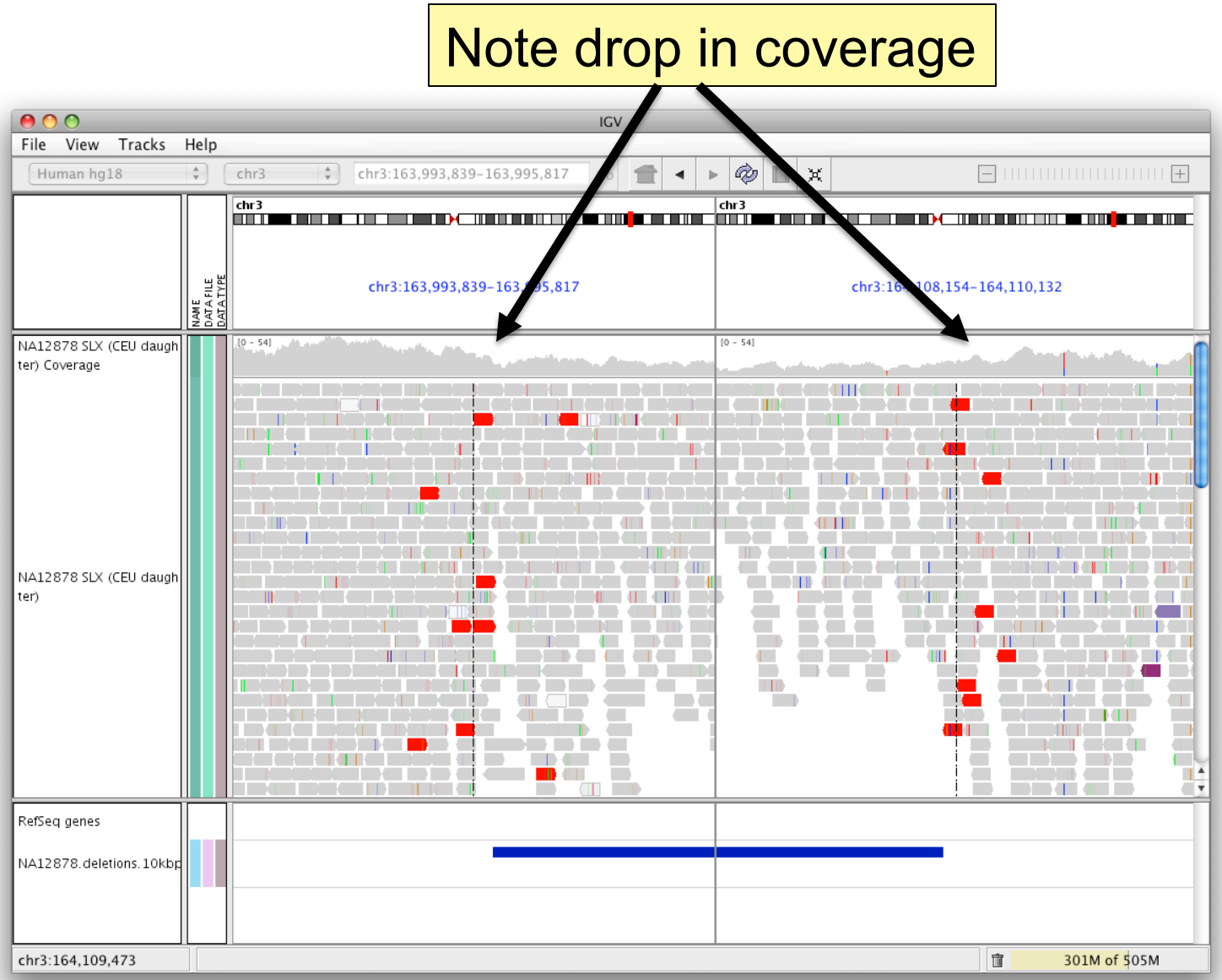
Pairs with larger than expected insert size are colored red.



BROAD INSTITUTE

Deletion

Integrative Genomics Viewer

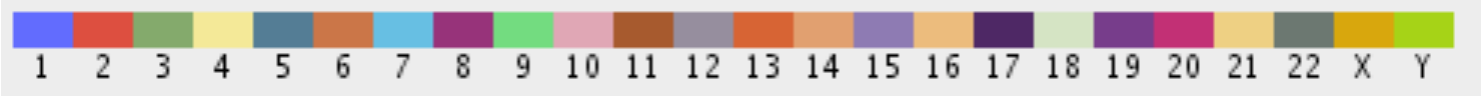


BROAD INSTITUTE

Insert size color scheme

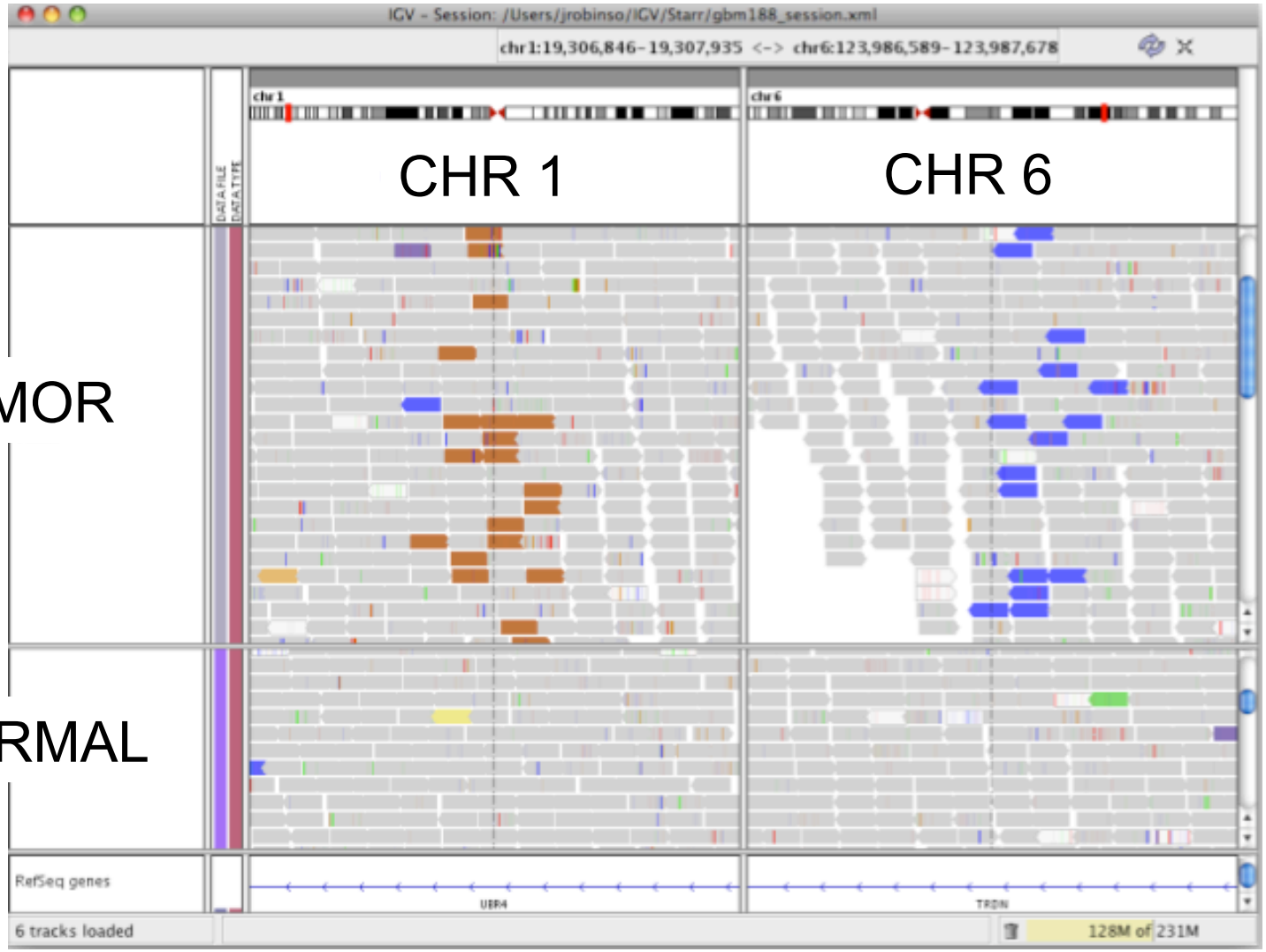
- Smaller than expected insert size: 
- Larger than expected insert size: 
- Pairs on different chromosomes

Each end colored by chromosome of its mate



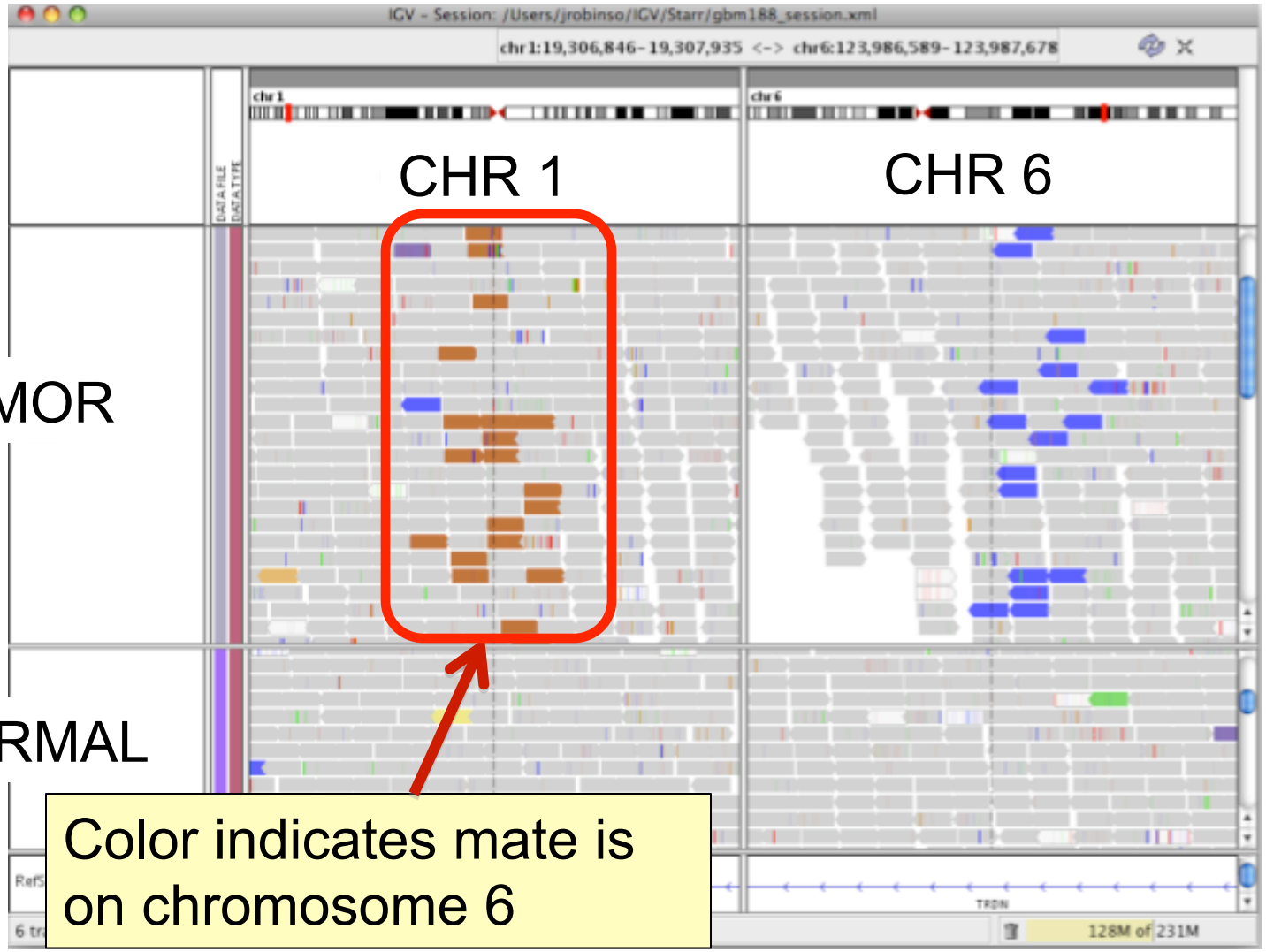
Rearrangement

Integrative Genomics Viewer



BROAD INSTITUTE

Rearrangement



Interpreting Pair Orientations

BROAD INSTITUTE

Integrative Genomics Viewer

Interpreting pair orientations

Integrative Genomics Viewer

Orientation of paired reads can reveal structural events, including:

- inversions
- duplications
- translocations

Orientation is defined in terms of

- read strand, left *vs* right, *and*
- read order, first *vs* second

BROAD INSTITUTE

Inversion

Integrative Genomics Viewer

Reference genome

BROAD INSTITUTE

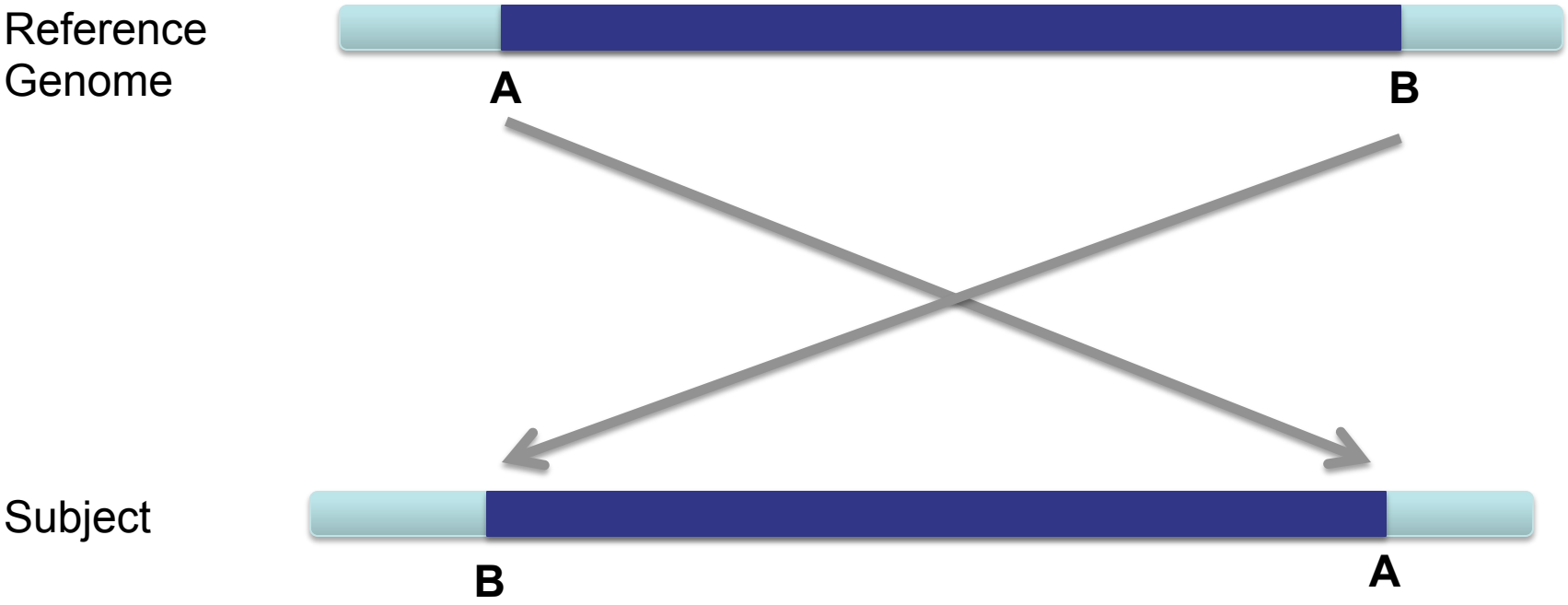
Inversion

Integrative Genomics Viewer

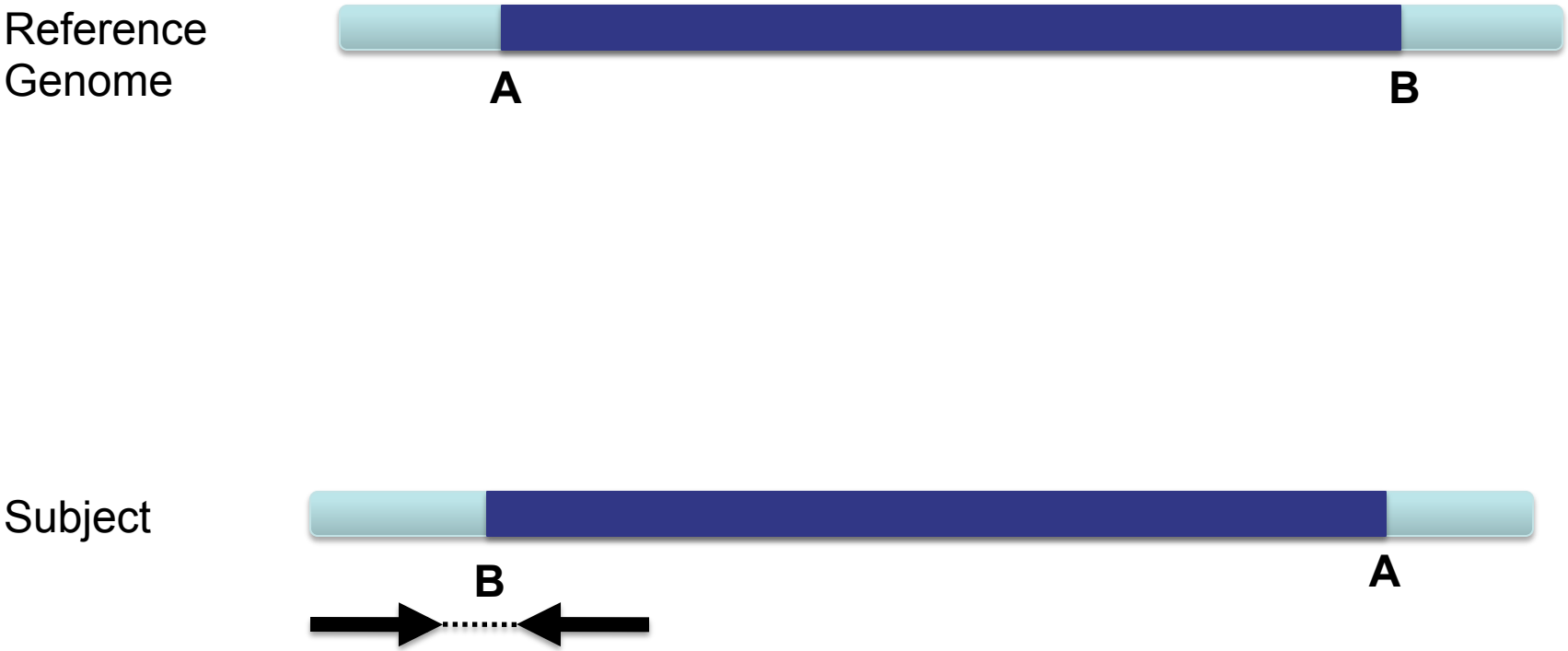
Reference genome

BROAD INSTITUTE

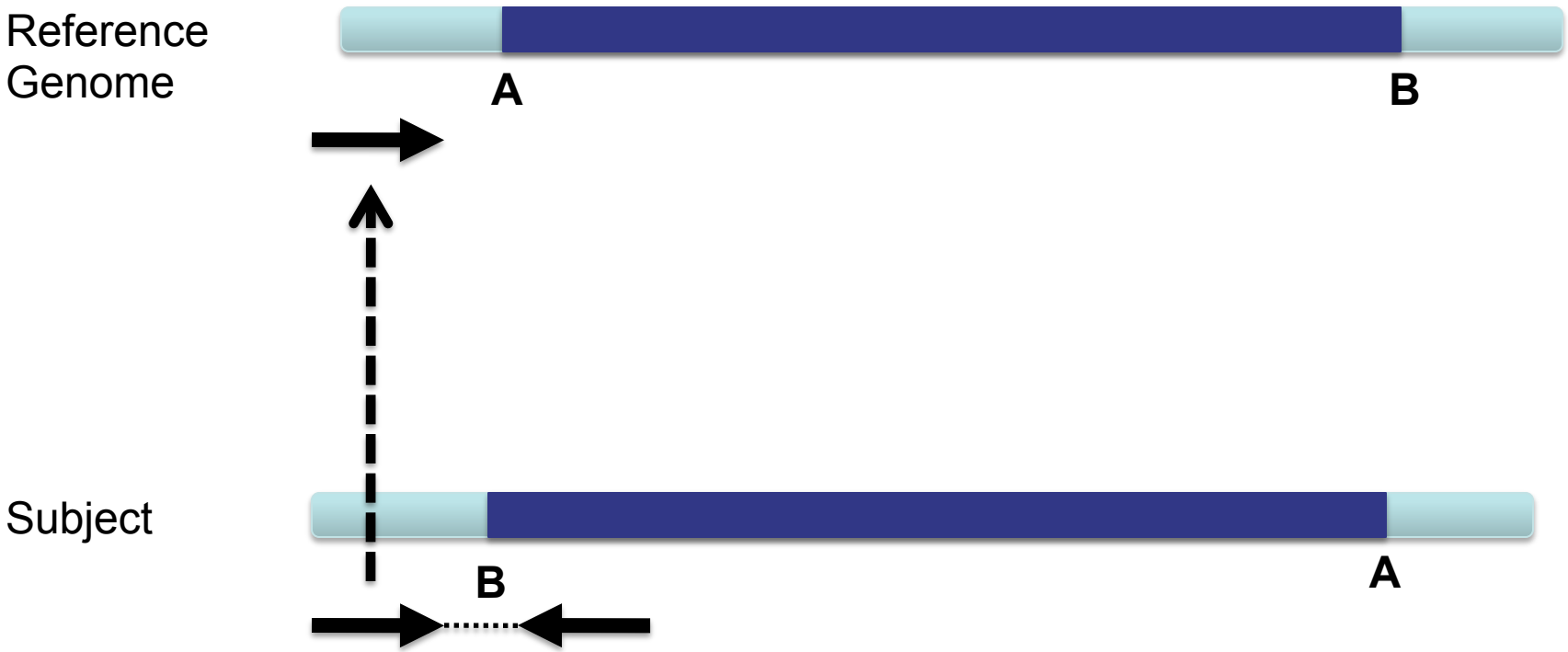
Inversion



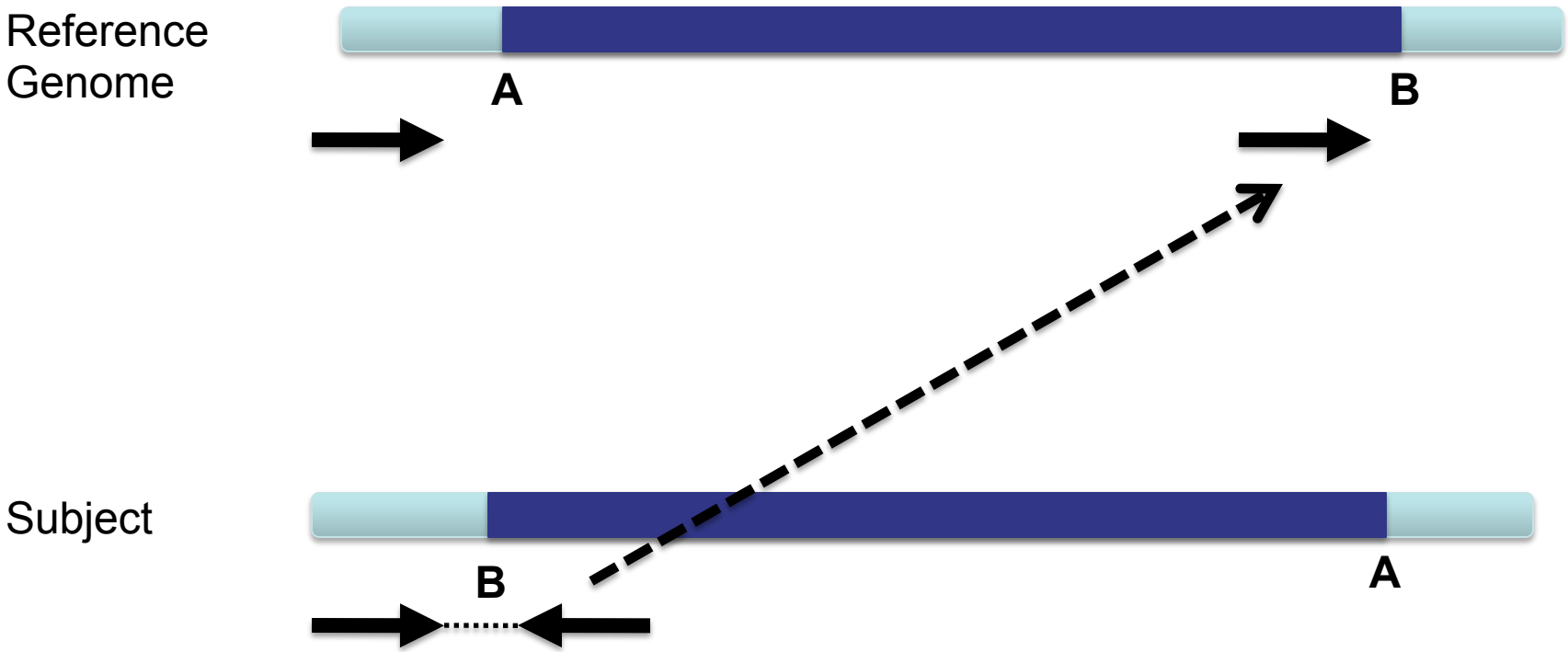
Inversion



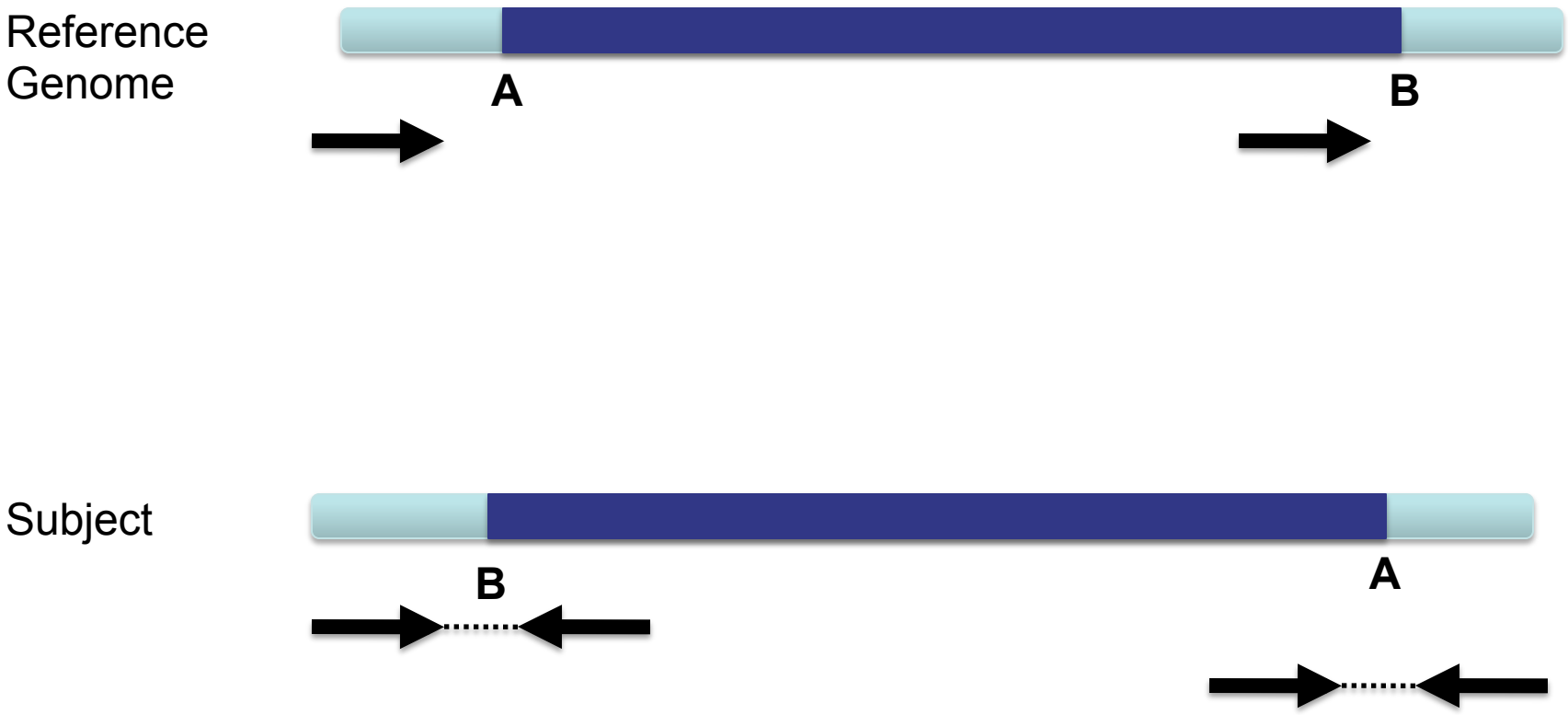
Inversion



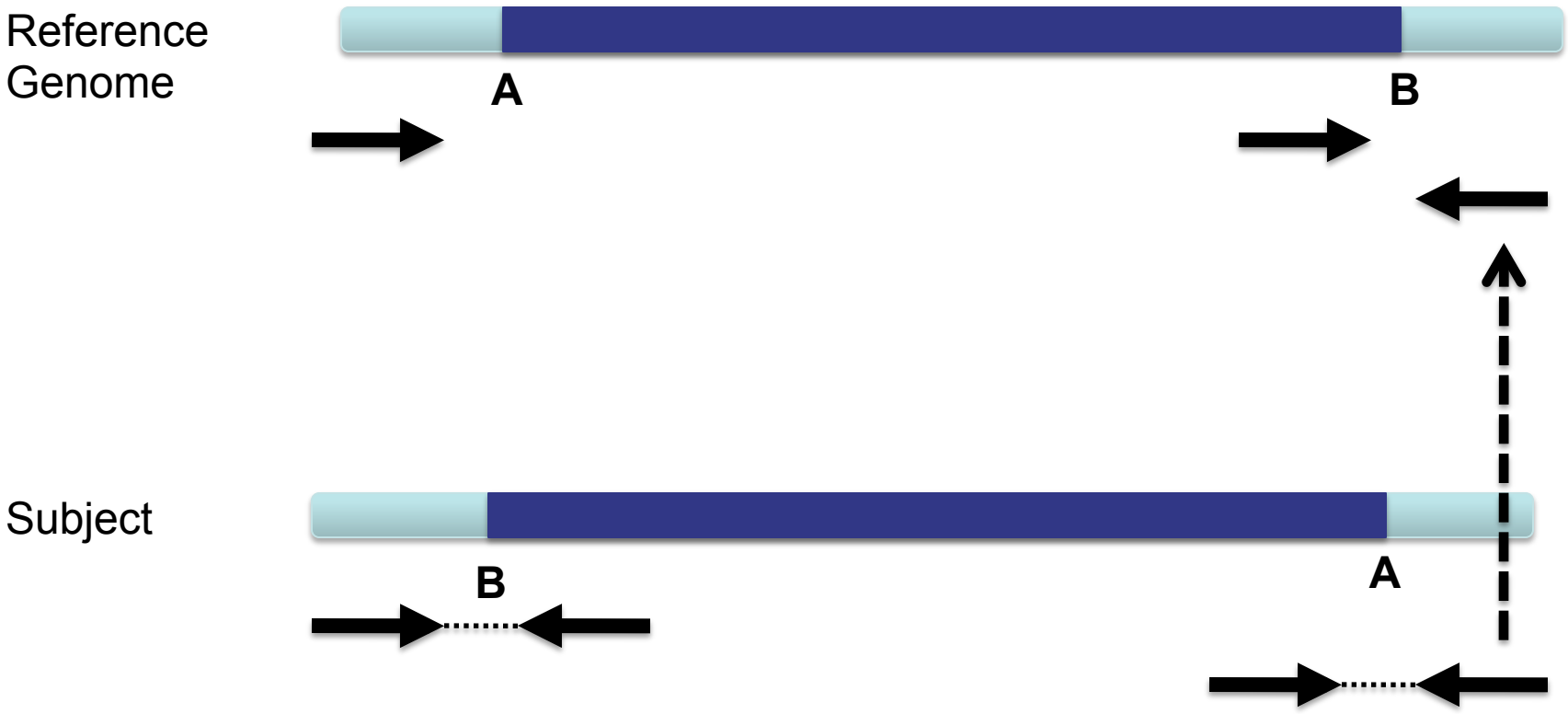
Inversion



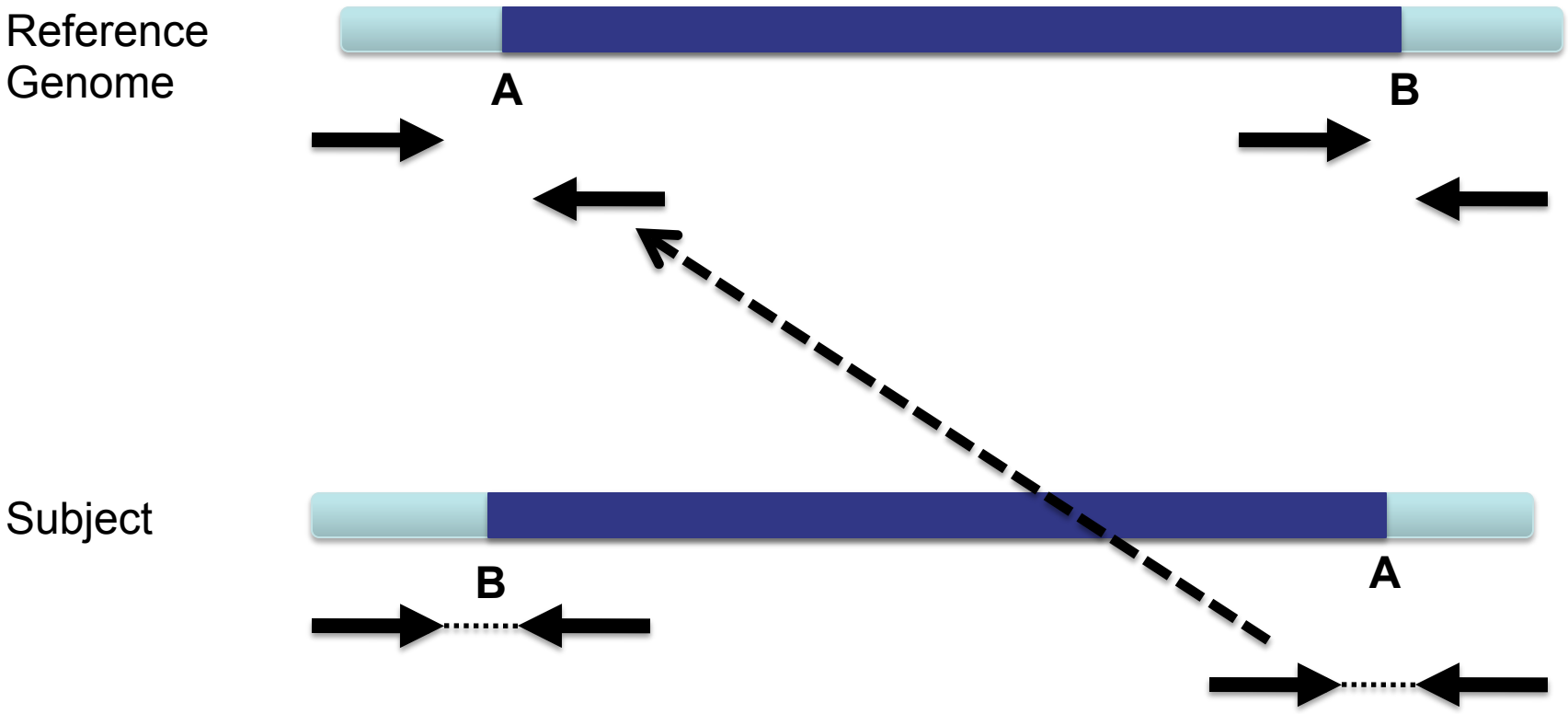
Inversion



Inversion



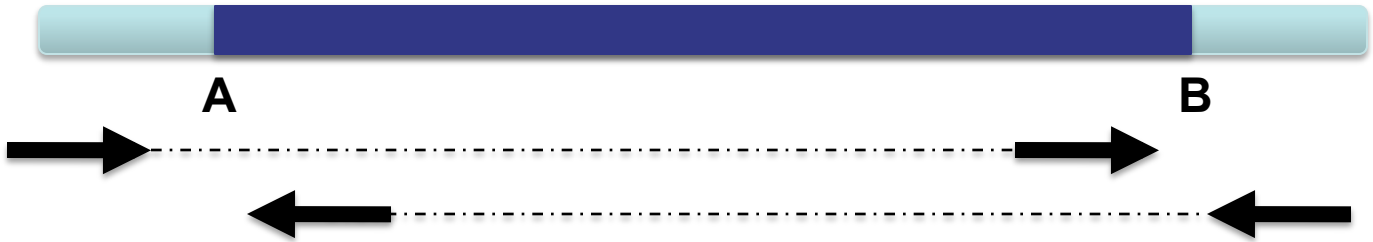
Inversion



Inversion

Integrative Genomics Viewer

Reference Genome

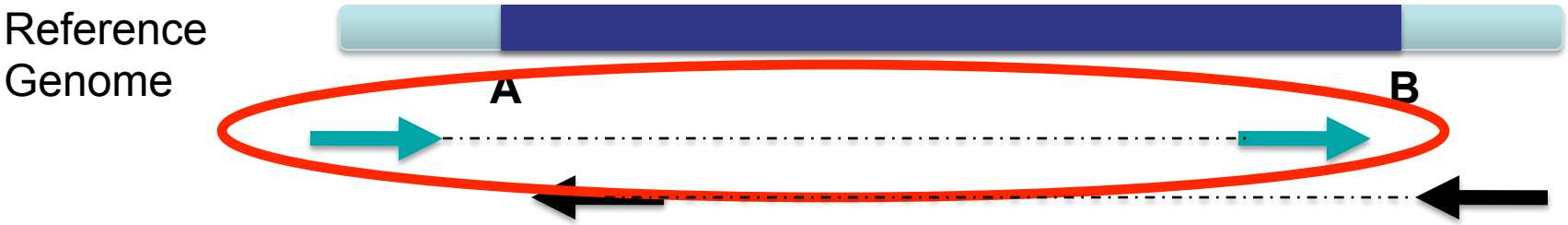


BROAD INSTITUTE

Inversion

Anomaly –
Expected pair orientation is inward facing (→ ←)

Inversion

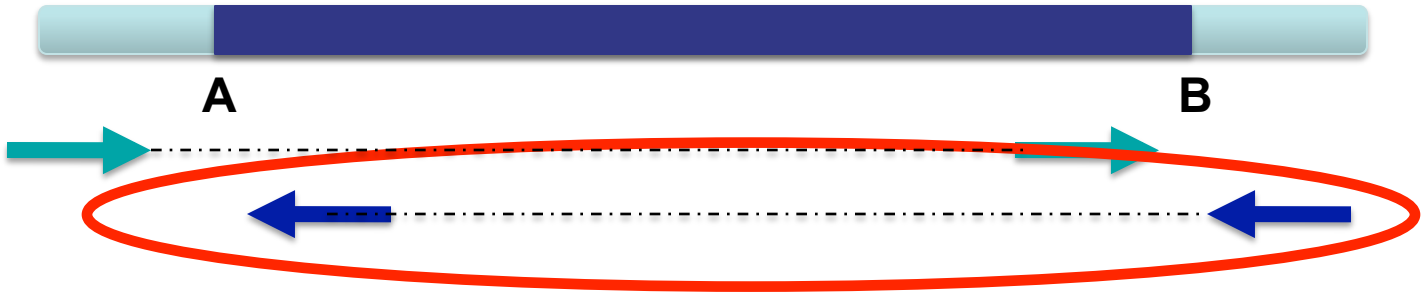


"Left" side pair

Inversion

Integrative Genomics Viewer

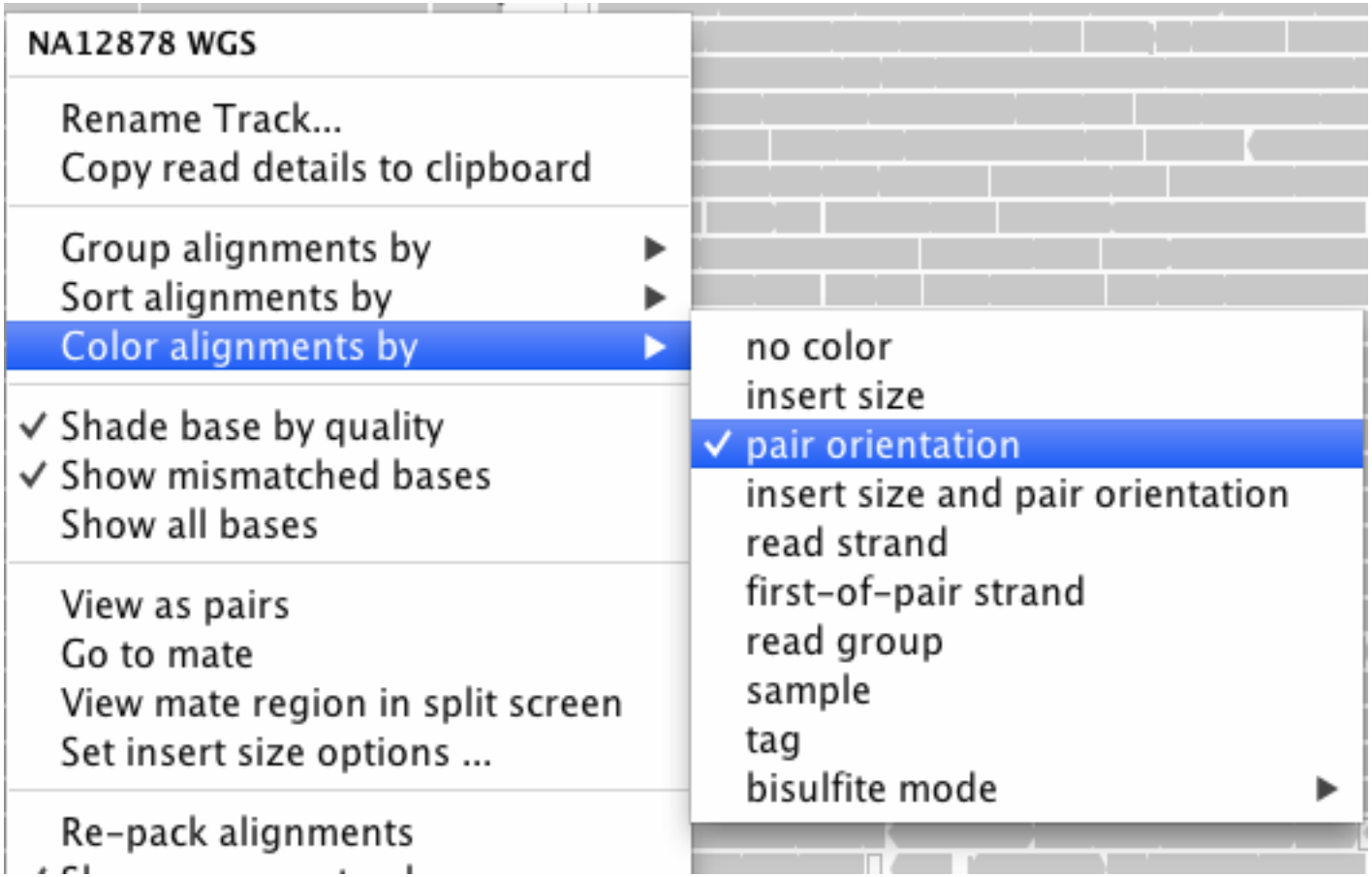
Reference Genome



“Right” side pair

BROAD INSTITUTE

Color by pair orientation



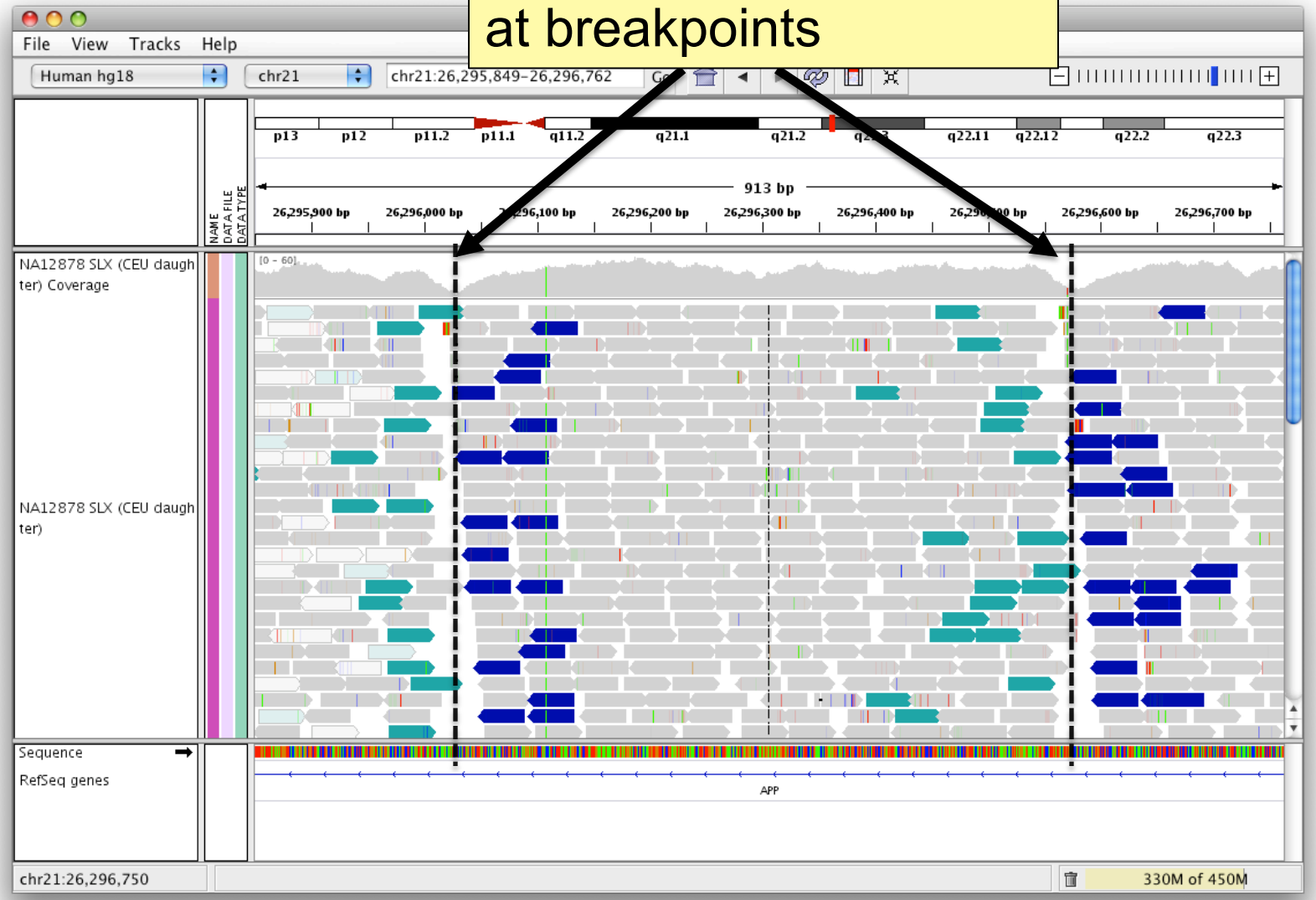
Inversion

Integrative Genomics Viewer

BROAD INSTITUTE

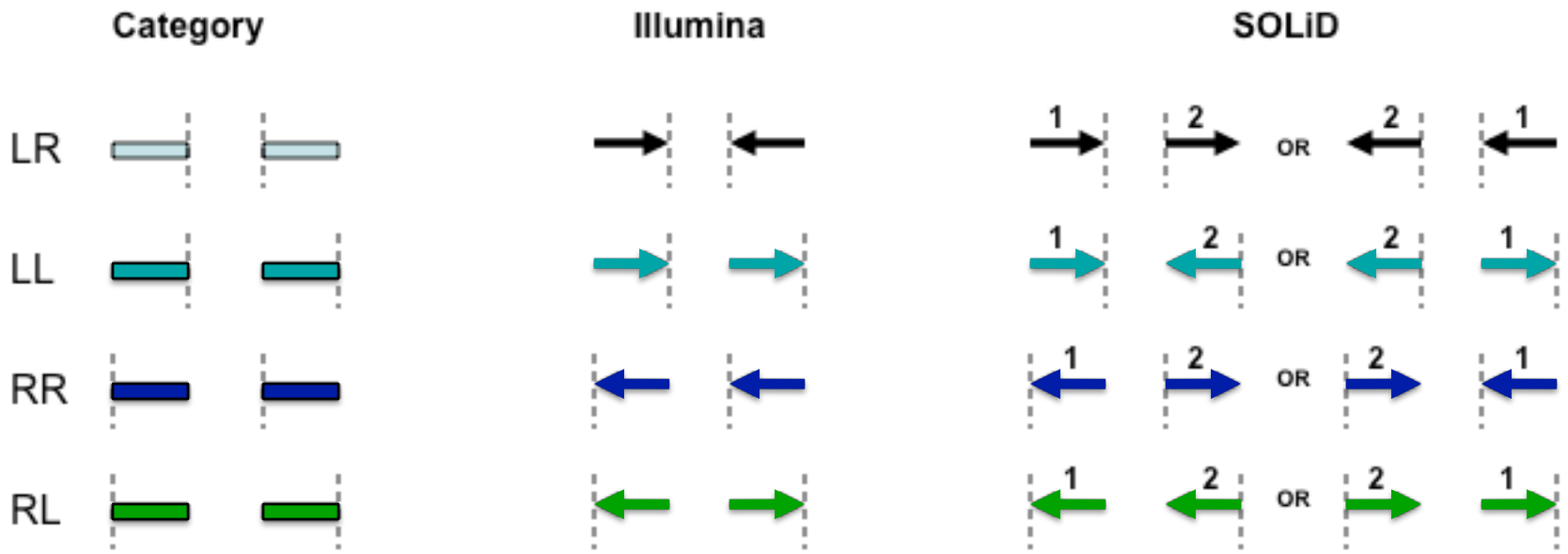
Inversion

Integrative Genomics Viewer



BROAD INSTITUTE

Interpretation of read pair orientations



LR Normal reads.
The reads are left and right (respectively) of the unsequenced part of the sequenced DNA fragment when aligned back to the reference genome.

LL,RR Implies inversion in sequenced DNA with respect to reference.

RL Implies duplication or translocation with respect to reference.

These categories only apply to reads where both mates map to the same chromosome.

Figure courtesy of Bob Handsaker

RNA-Seq

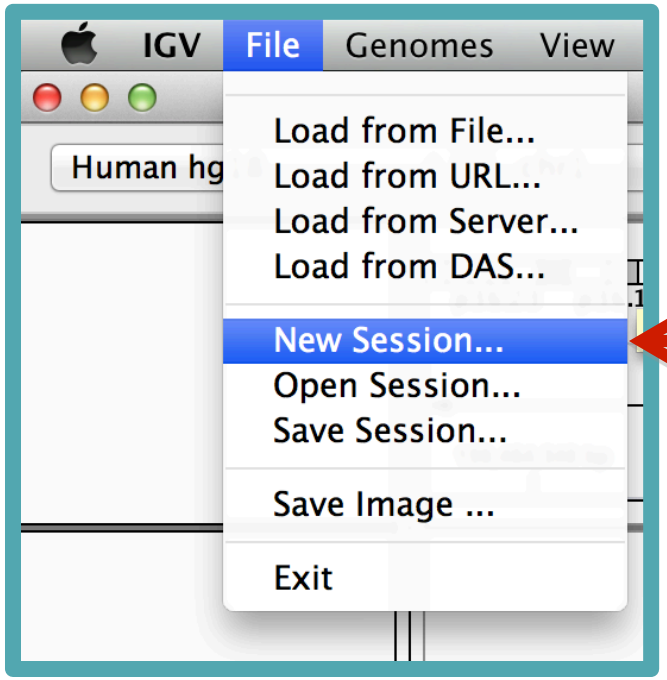
Integrative Genomics Viewer

Hands-on exercise

- Examine tissue-specific alternative splicing.
- Data: Illumina BodyMap 2.0

http://www.illumina.com/science/data_library.ilmn

BROAD INSTITUTE



Before we start:
Select **File > New Session**
to clear IGV window

RNA-Seq Setup

Integrative Genomics Viewer

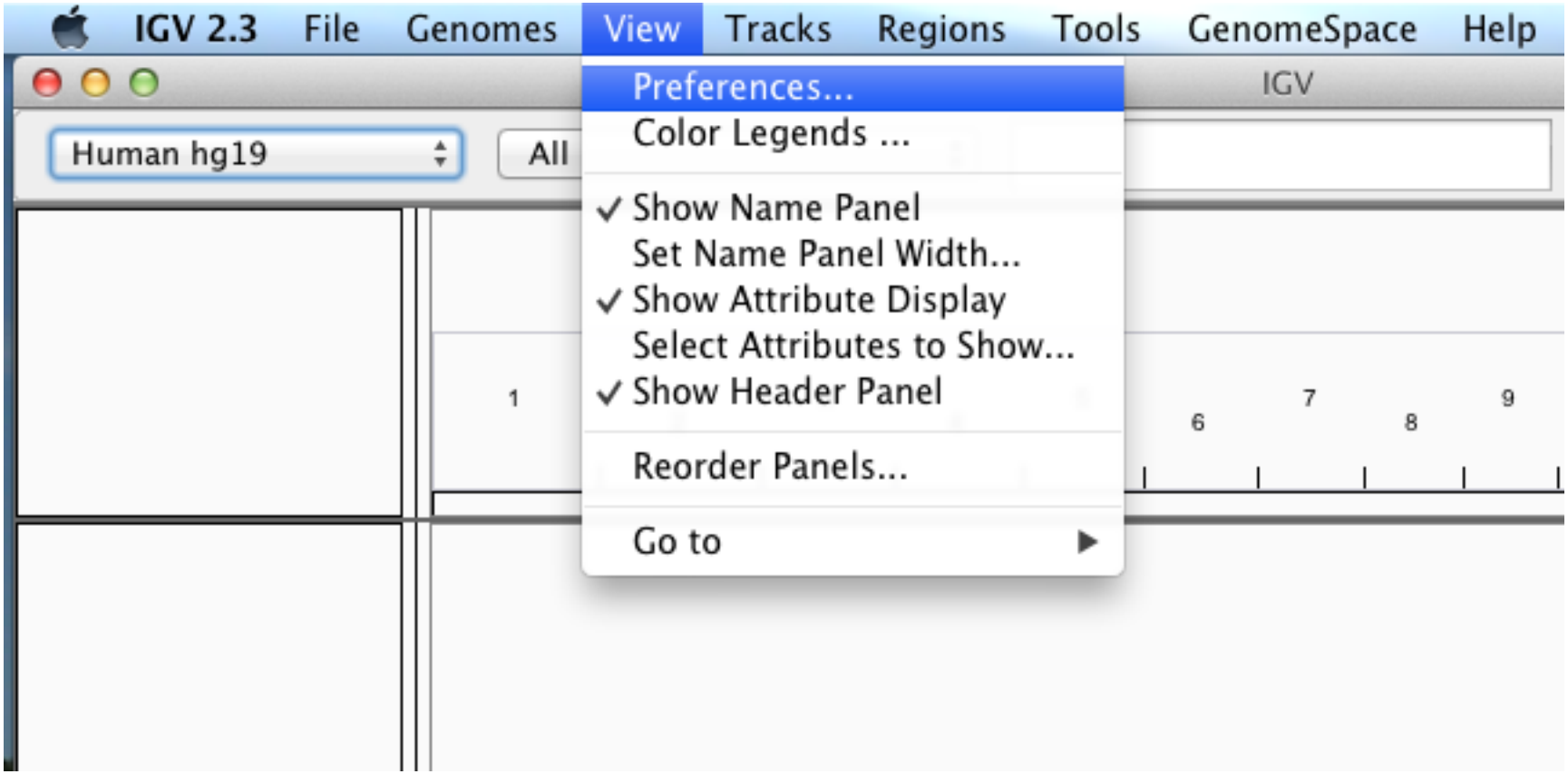
- Step 1: Tune settings for RNA.

BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer

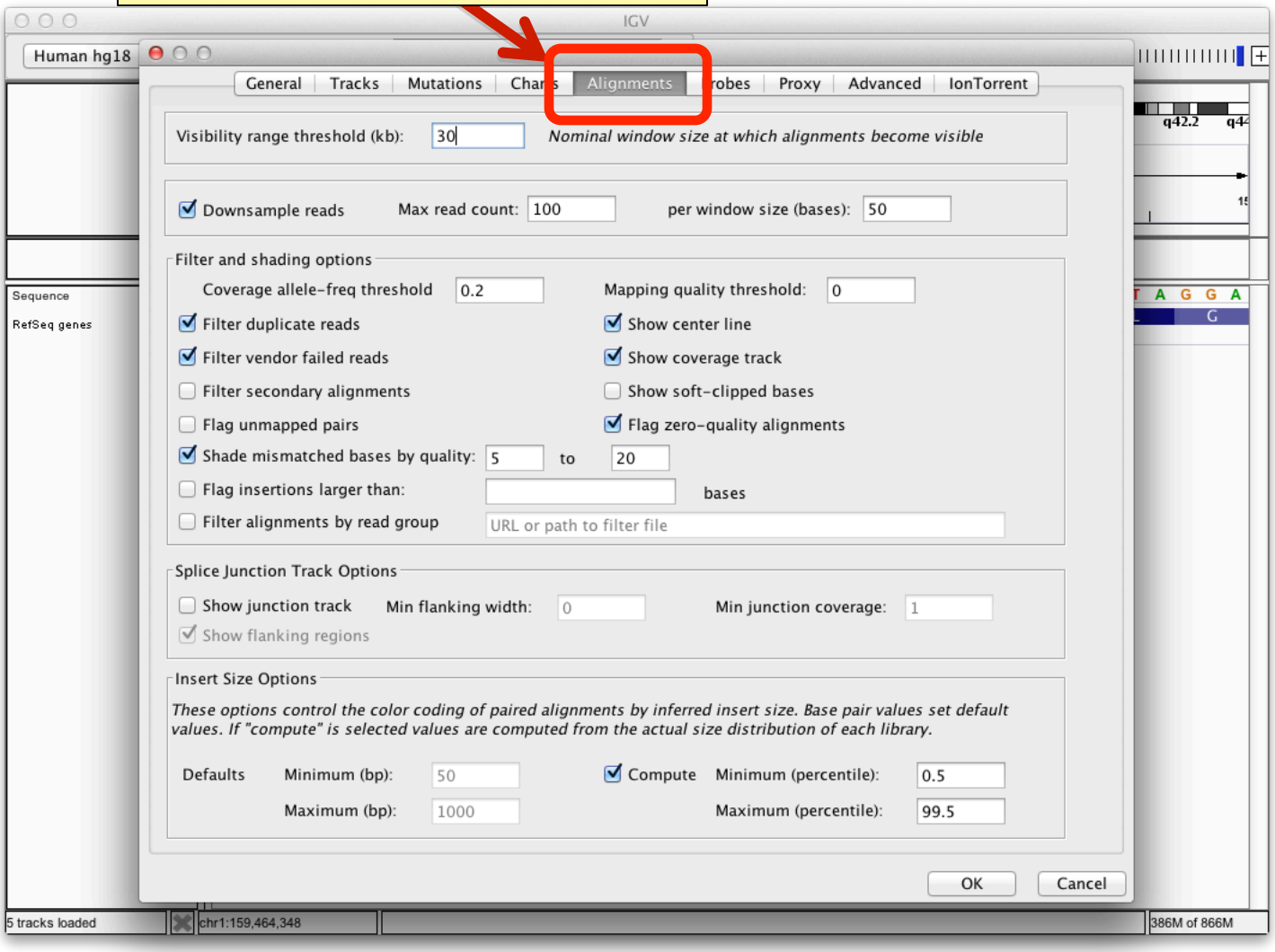
Select **View > Preferences…**



BROAD INSTITUTE

RNA-seq alignments

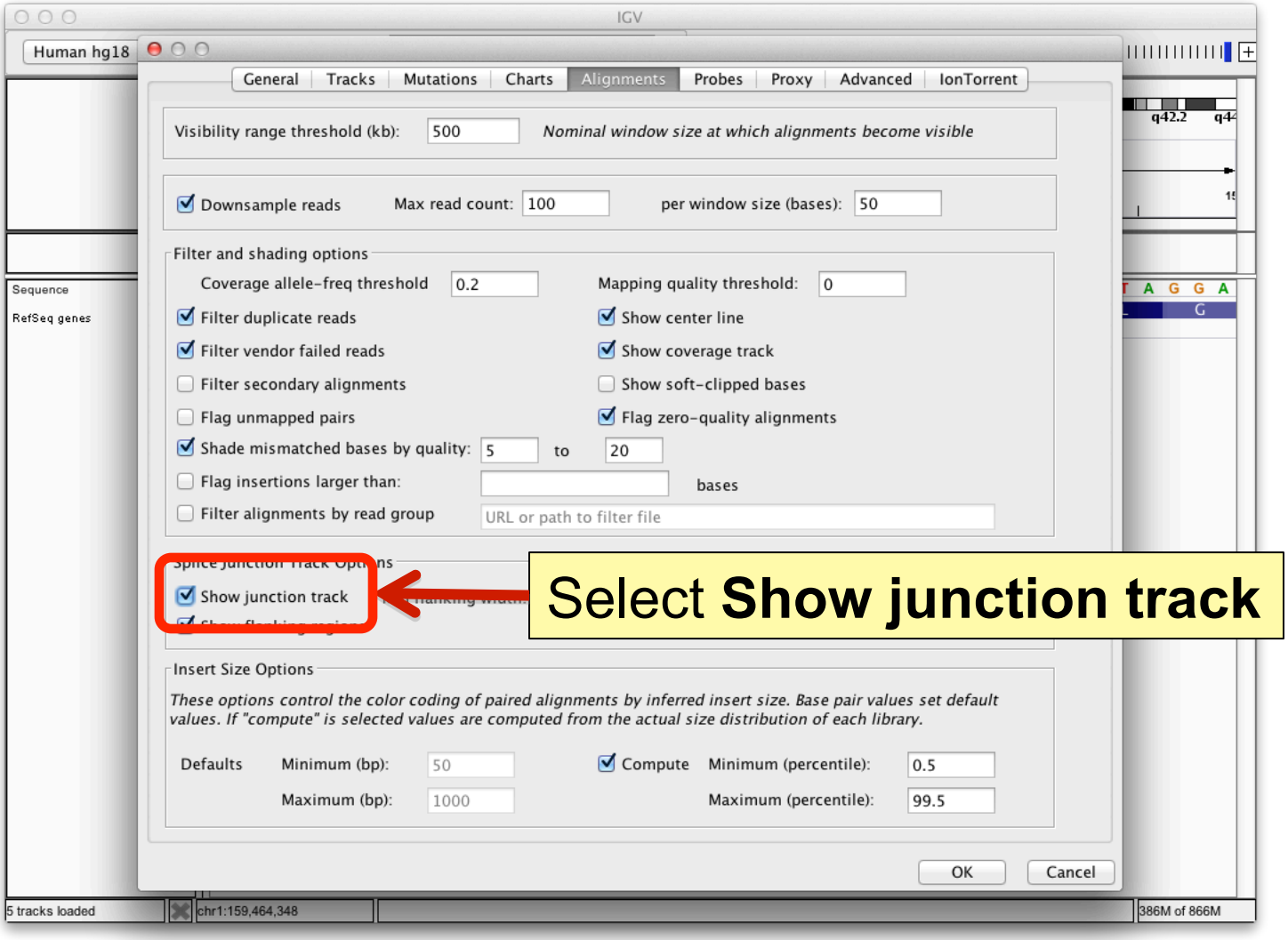
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

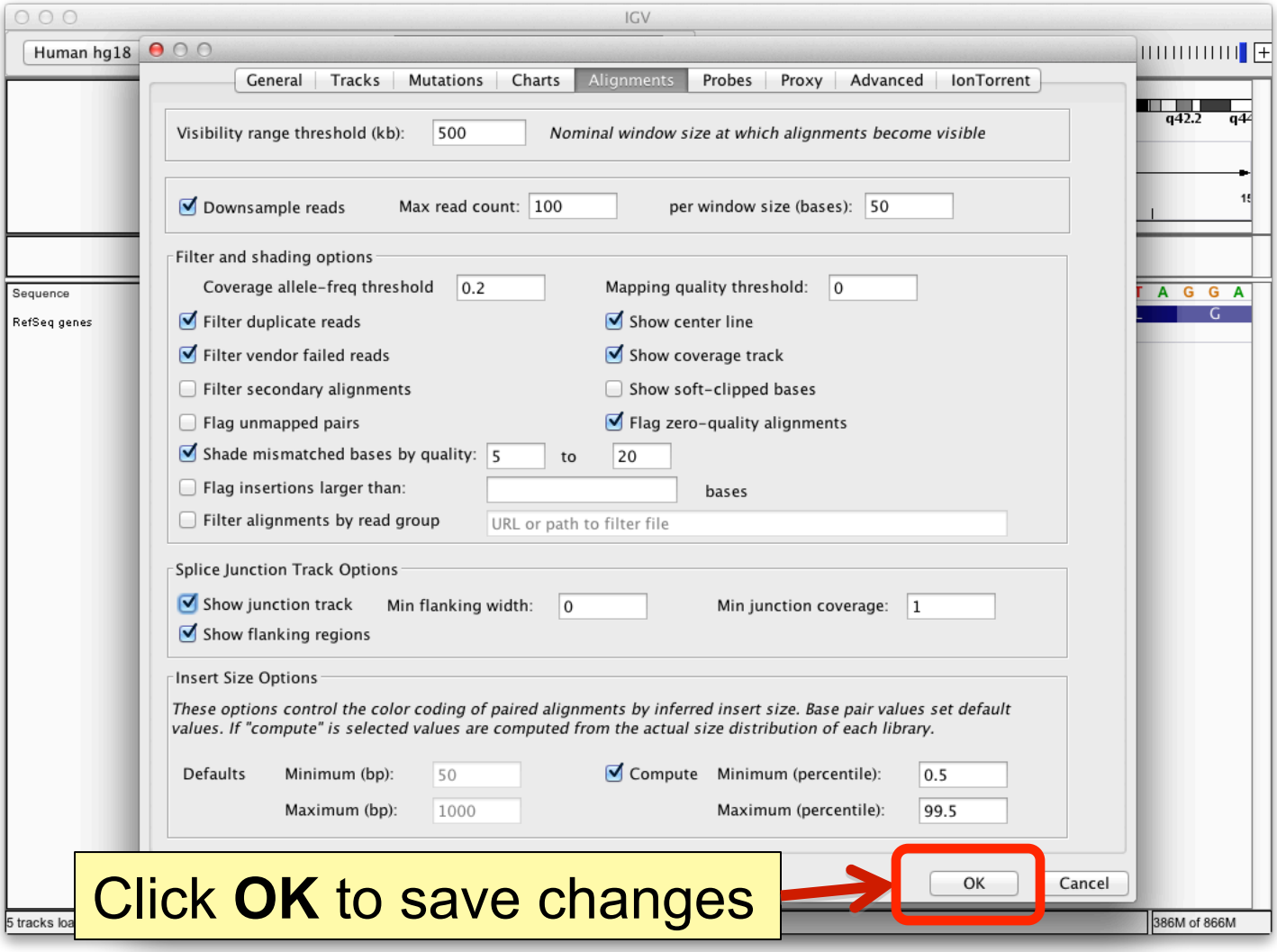
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

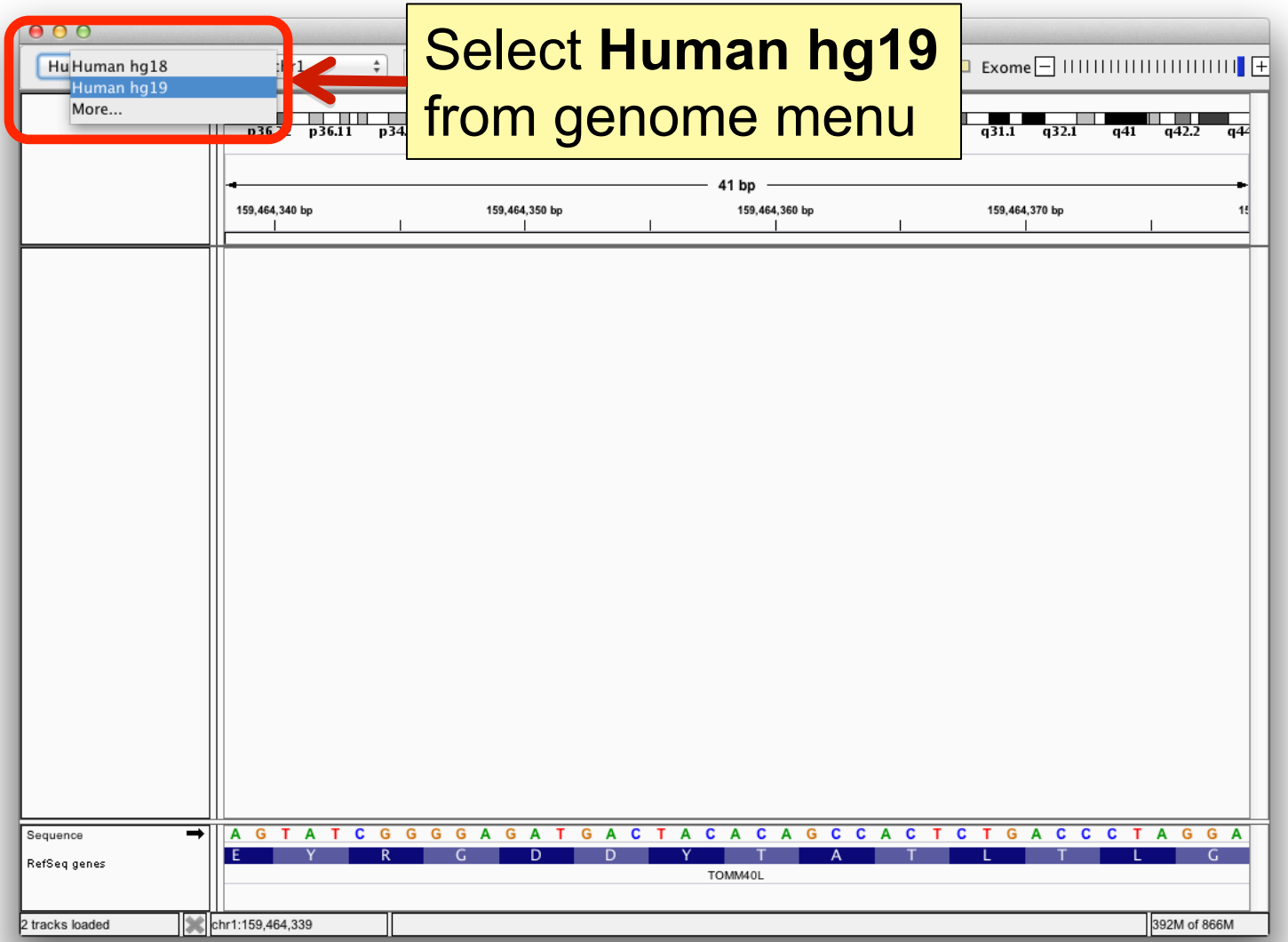
Integrative Genomics Viewer



BROAD INSTITUTE

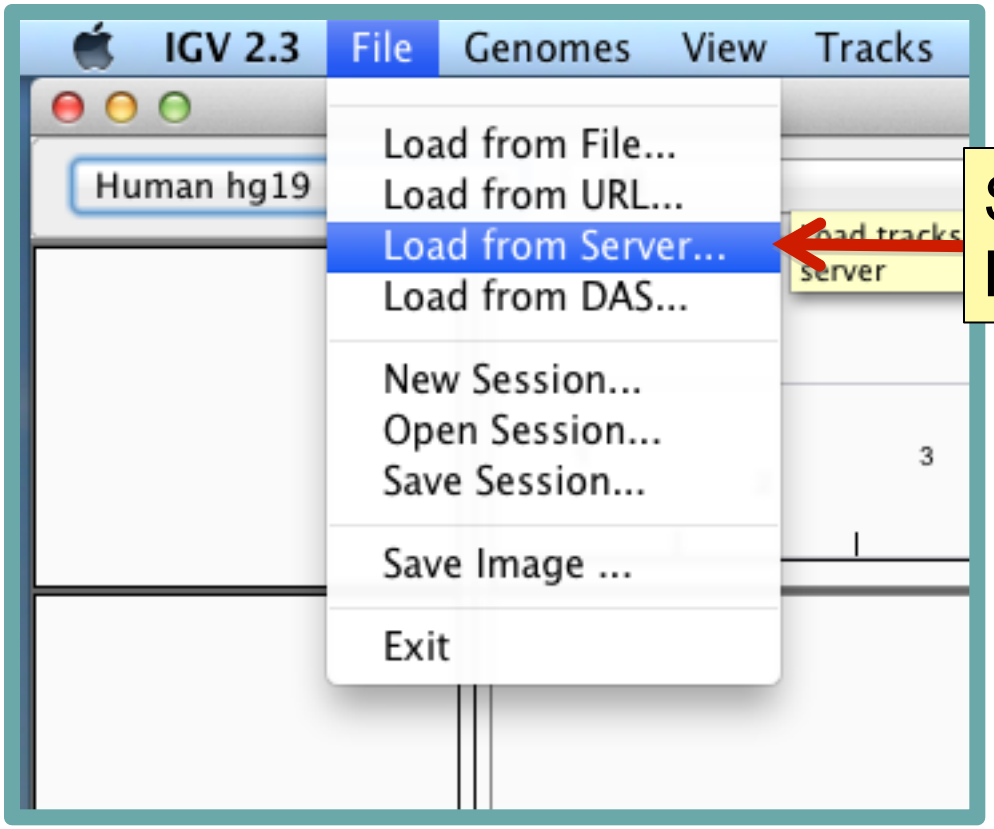
RNA-seq alignments

Integrative Genomics Viewer



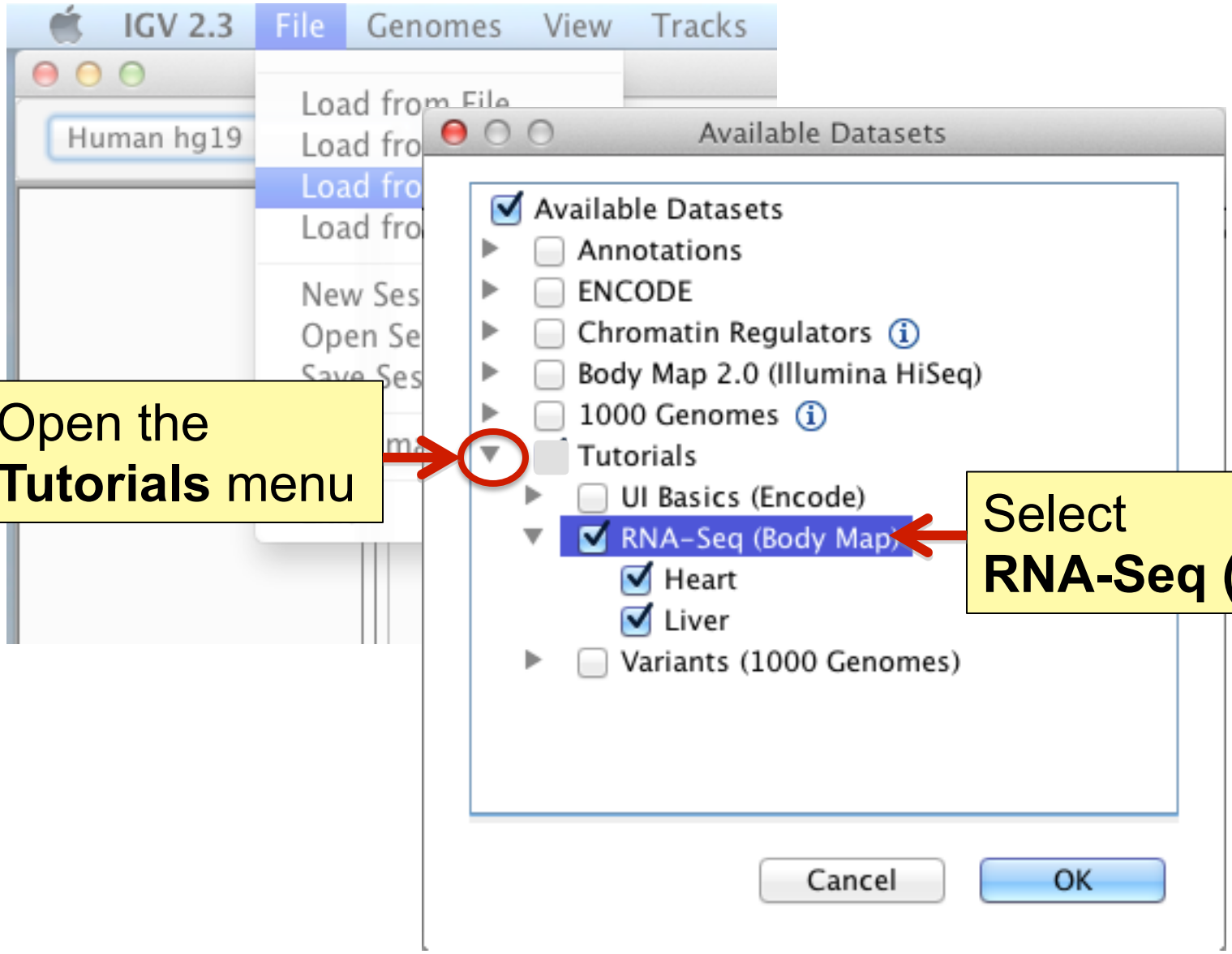
BROAD INSTITUTE

RNA-seq alignments



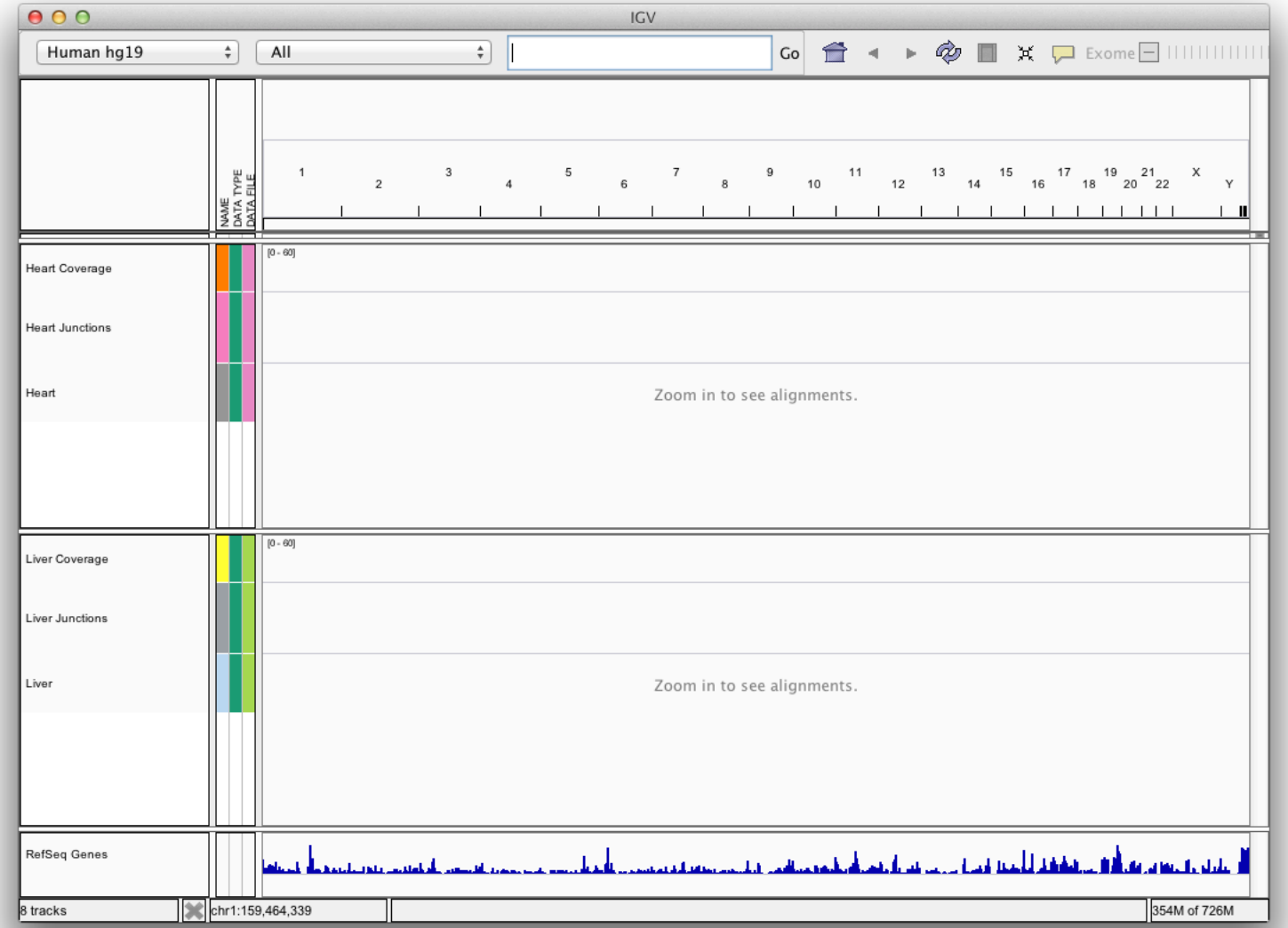
Select:
File > Load from Server…

RNA-seq alignments



RNA-seq alignments

Integrative Genomics Viewer

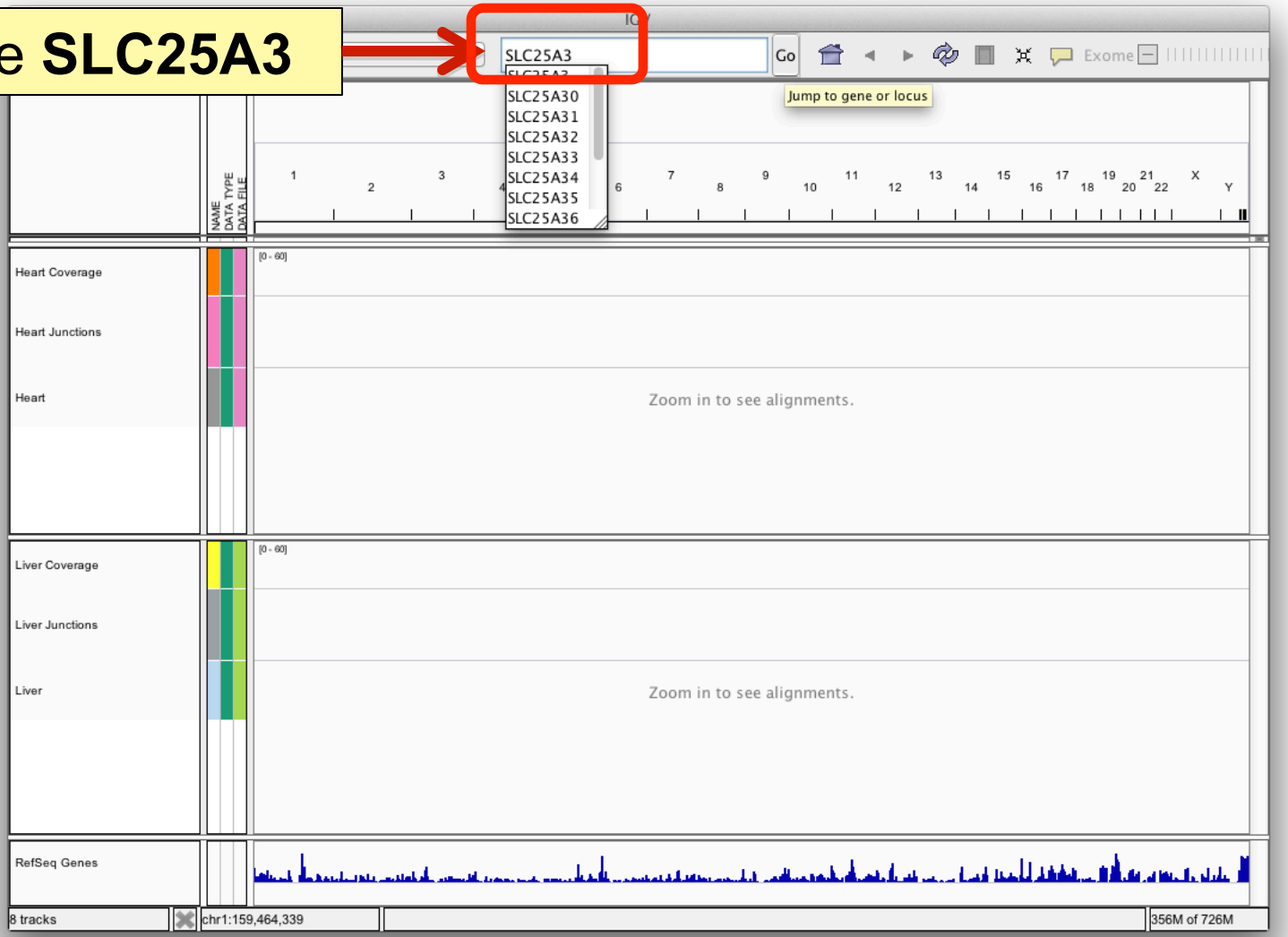


BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer

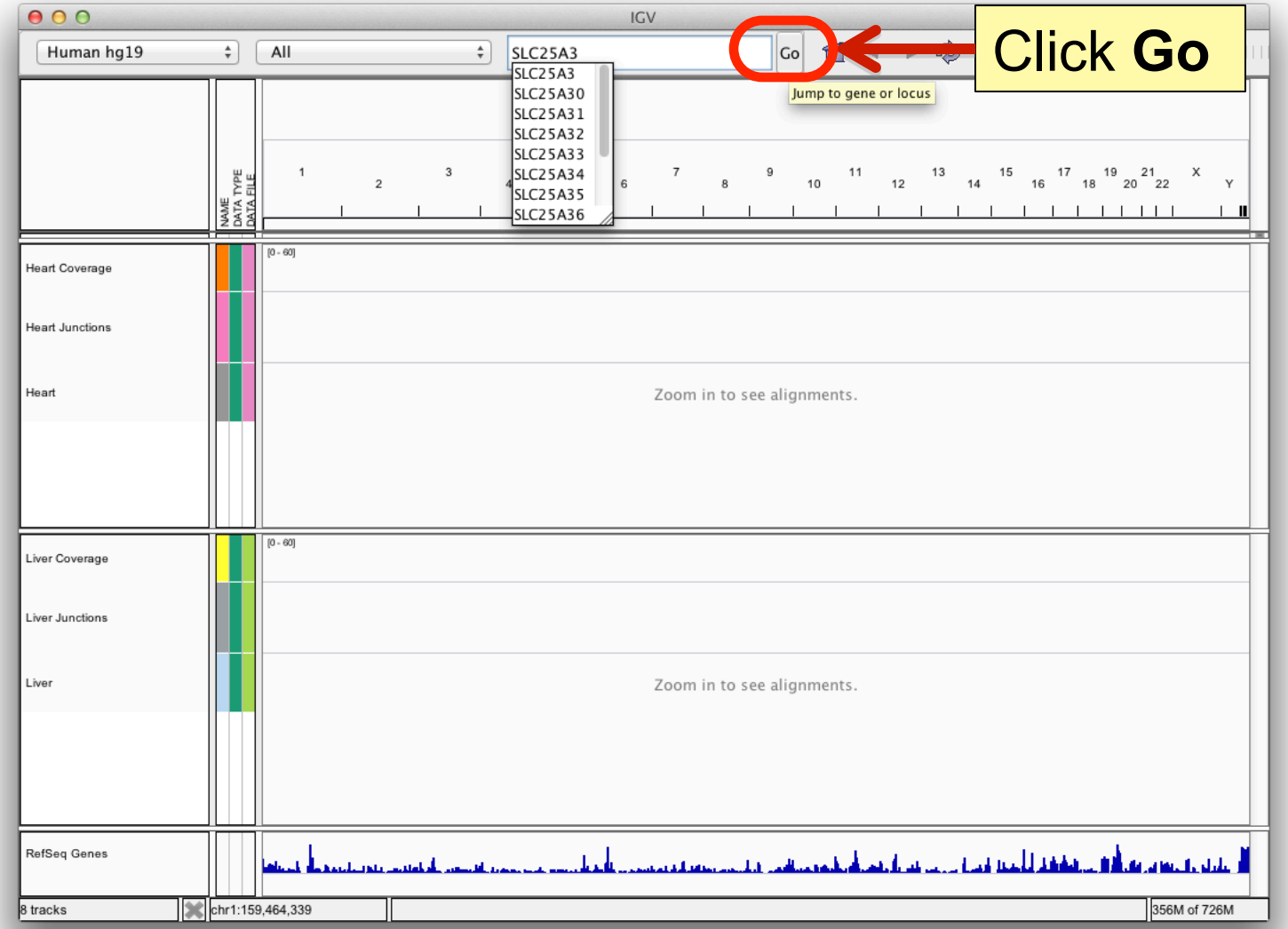
Type **SLC25A3**



BROAD INSTITUTE

RNA-seq alignments

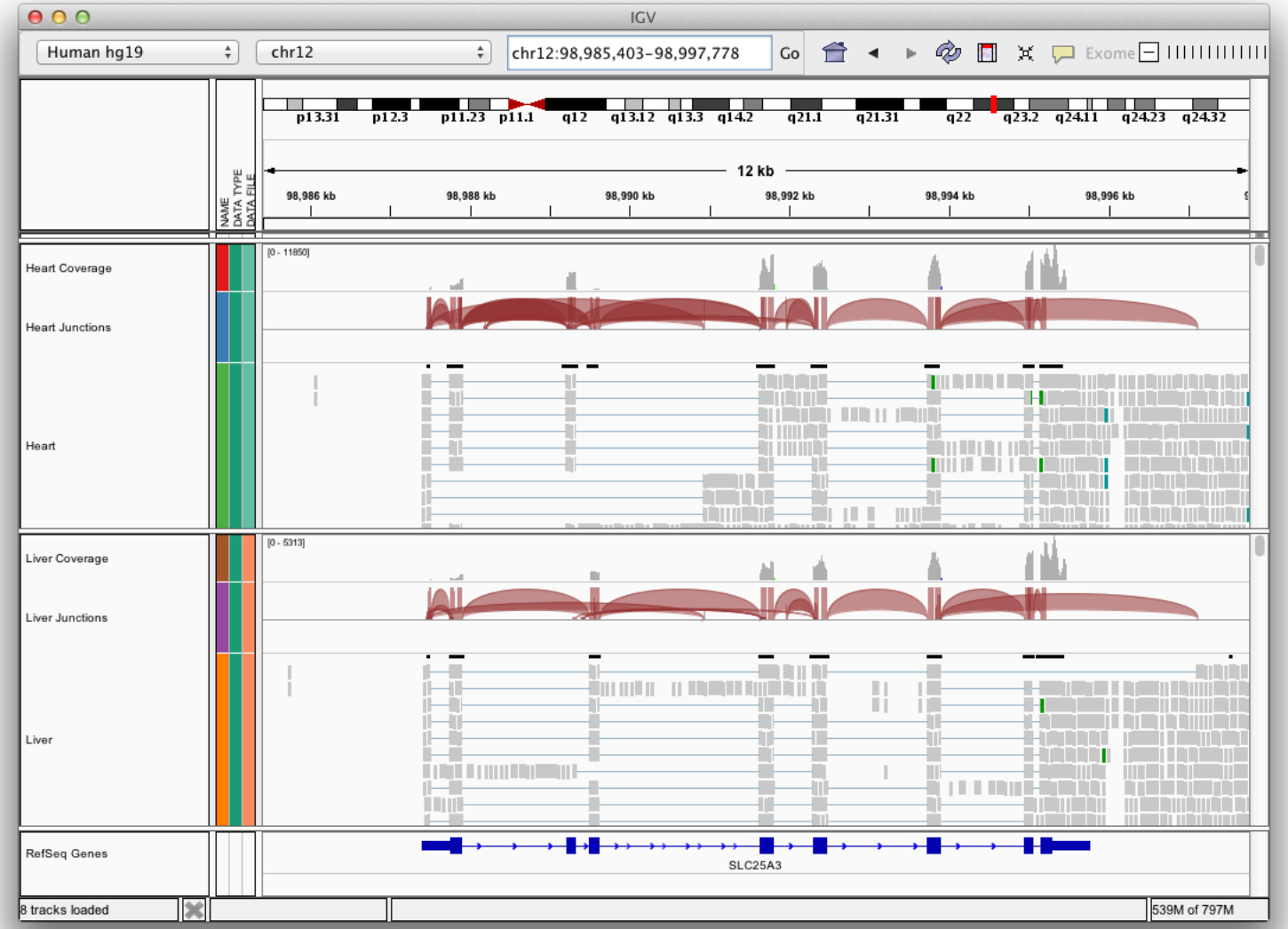
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

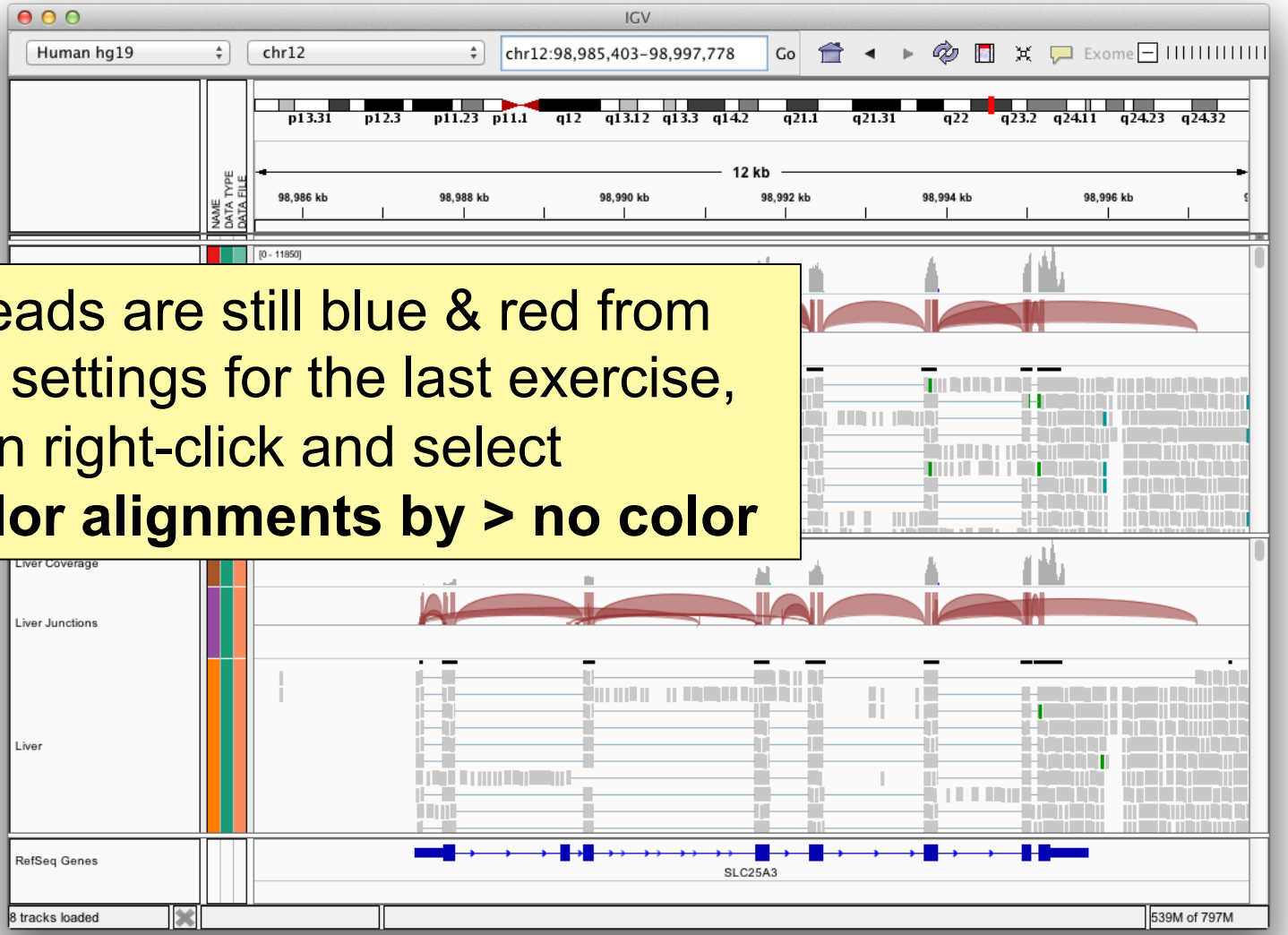
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer

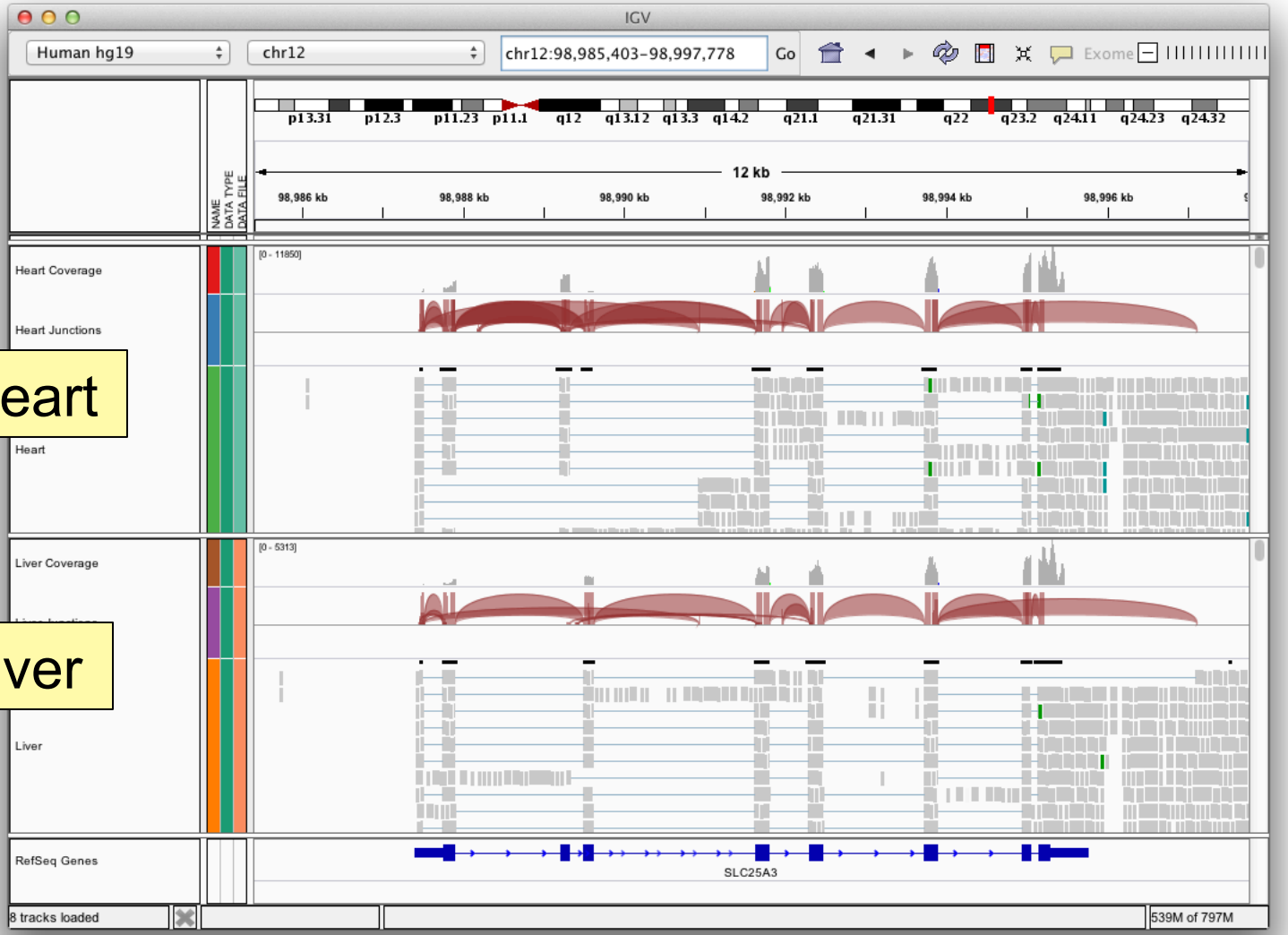


If reads are still blue & red from the settings for the last exercise, then right-click and select **Color alignments by > no color**

BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer



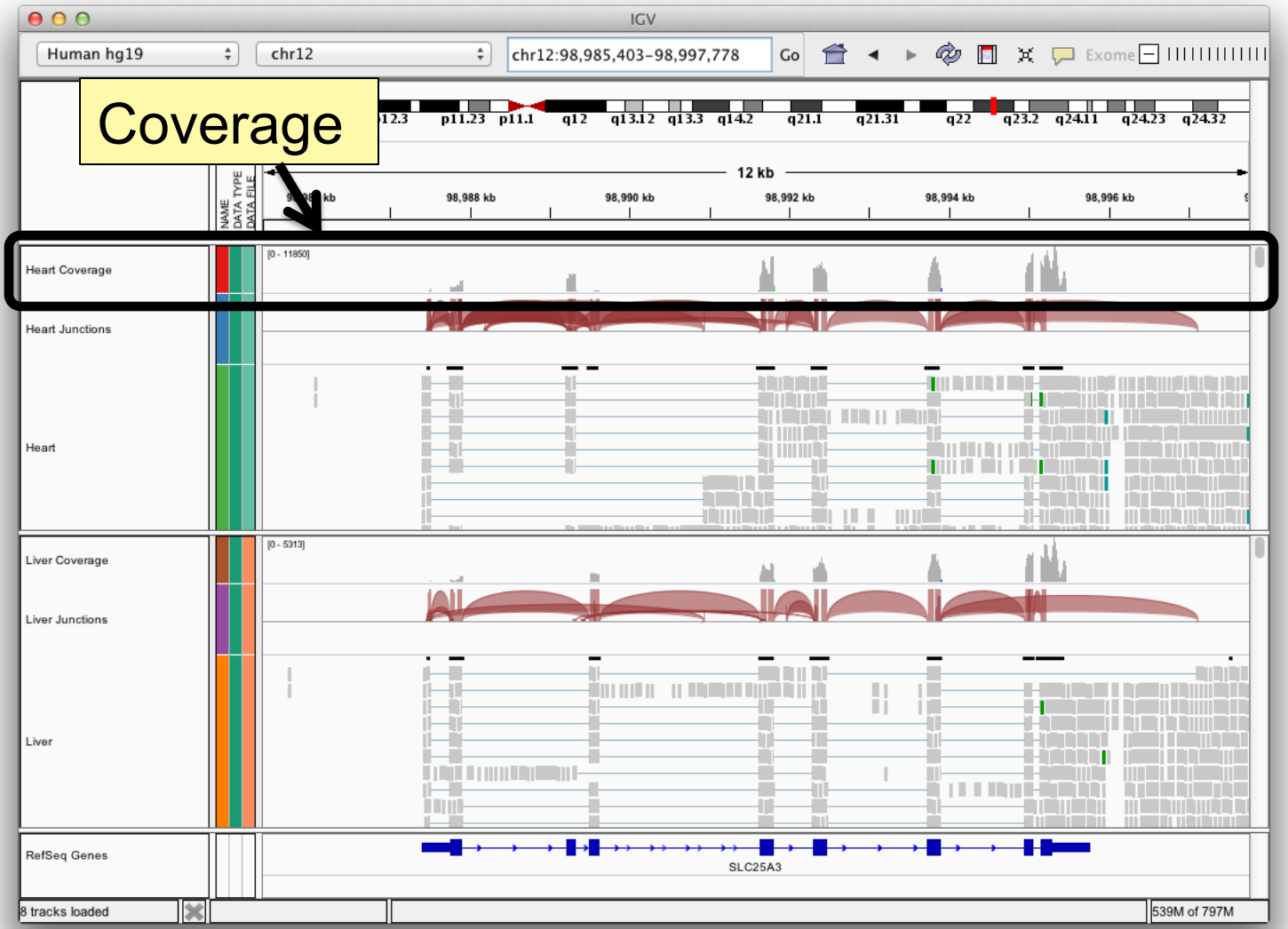
Heart

Liver

BROAD INSTITUTE

RNA-seq alignments

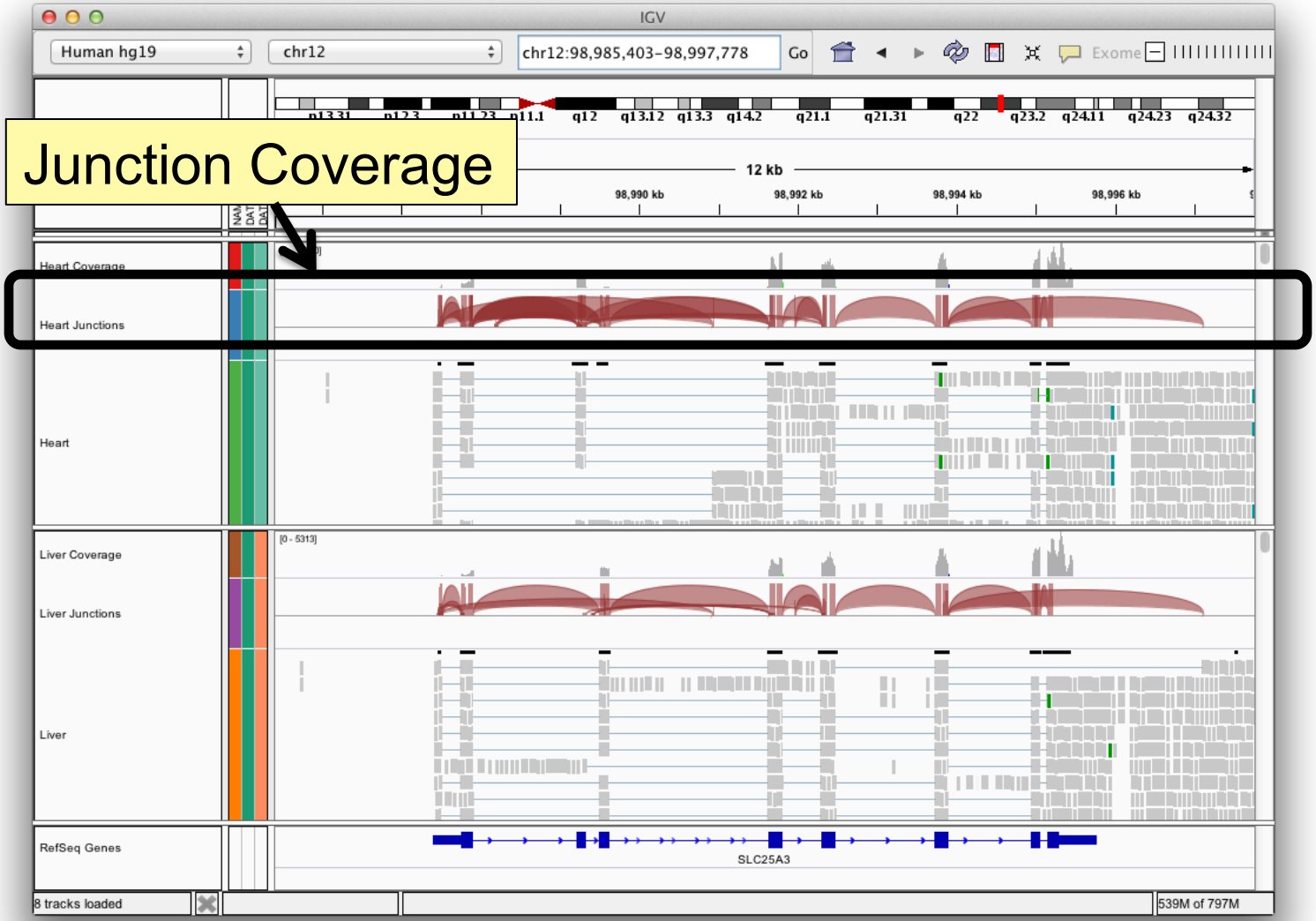
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

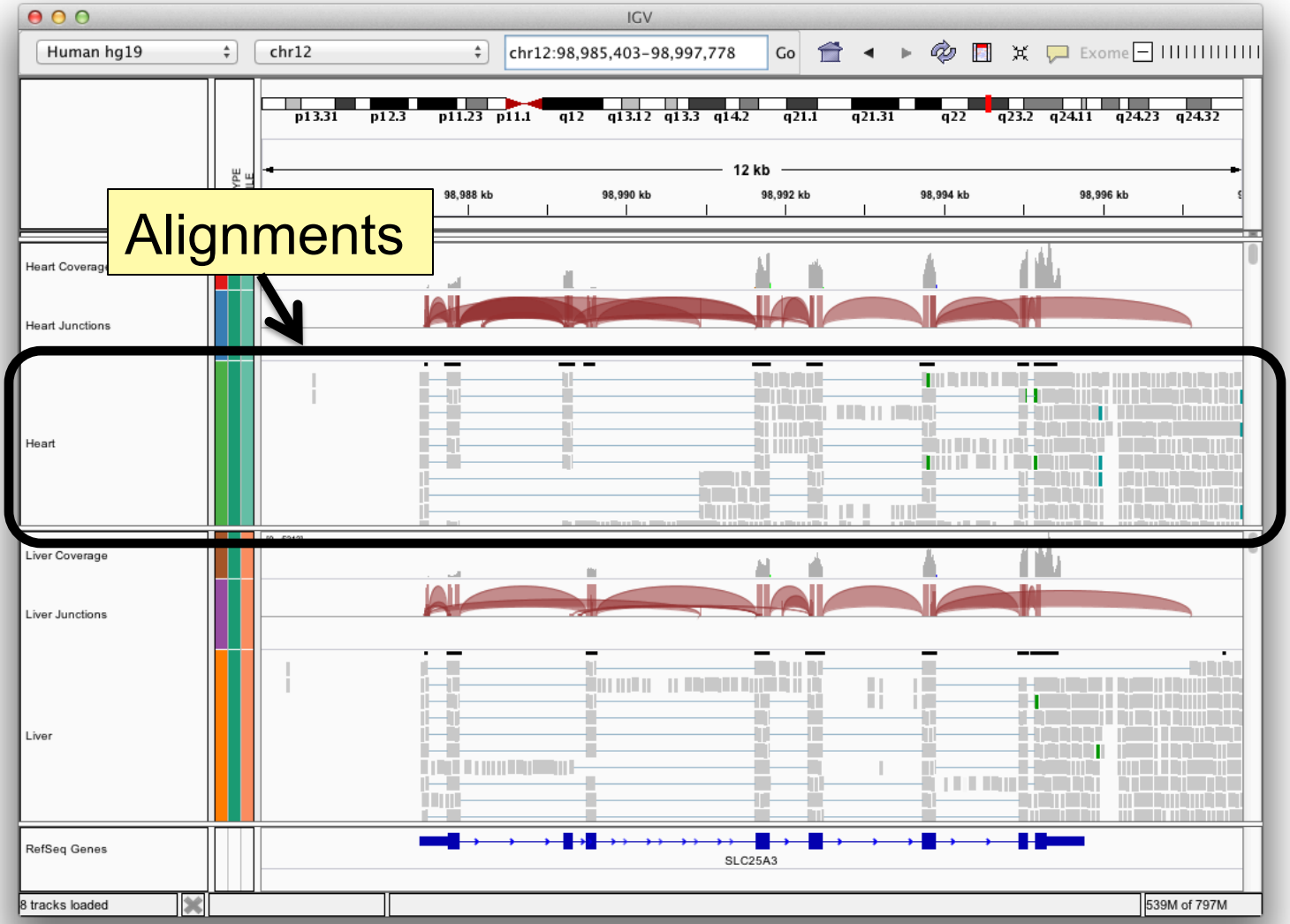
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

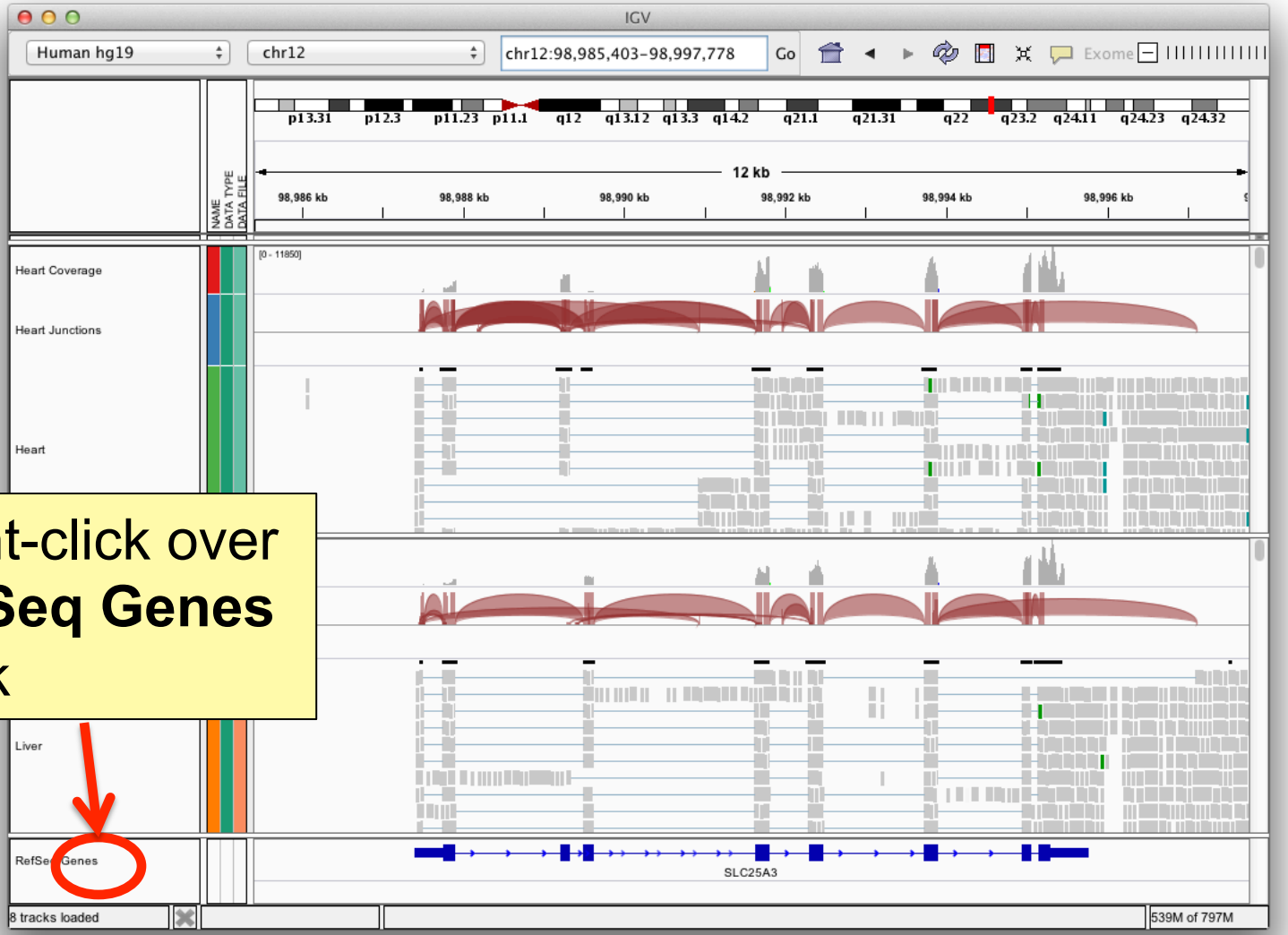
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer

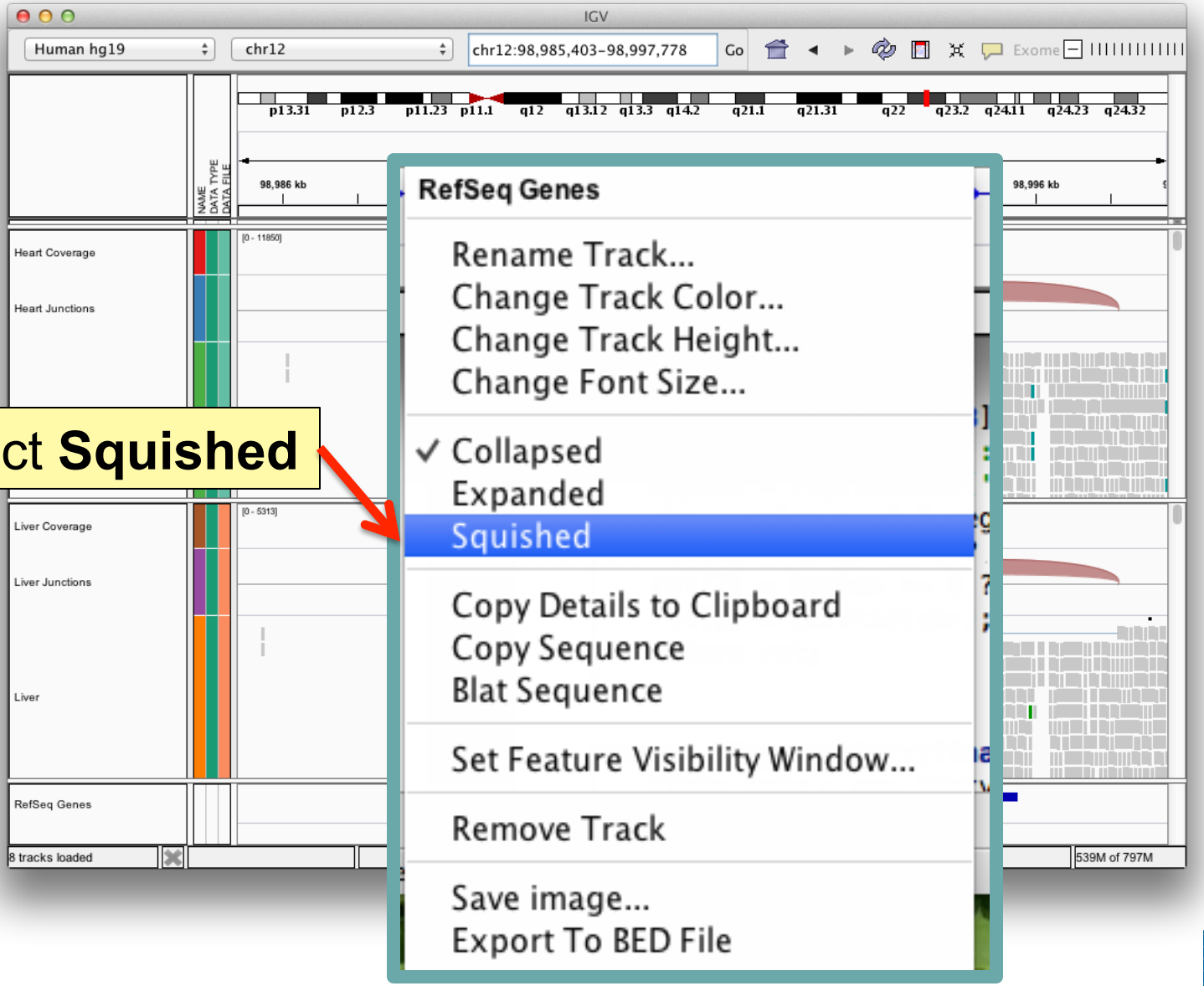


Right-click over **RefSeq Genes** track

BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer

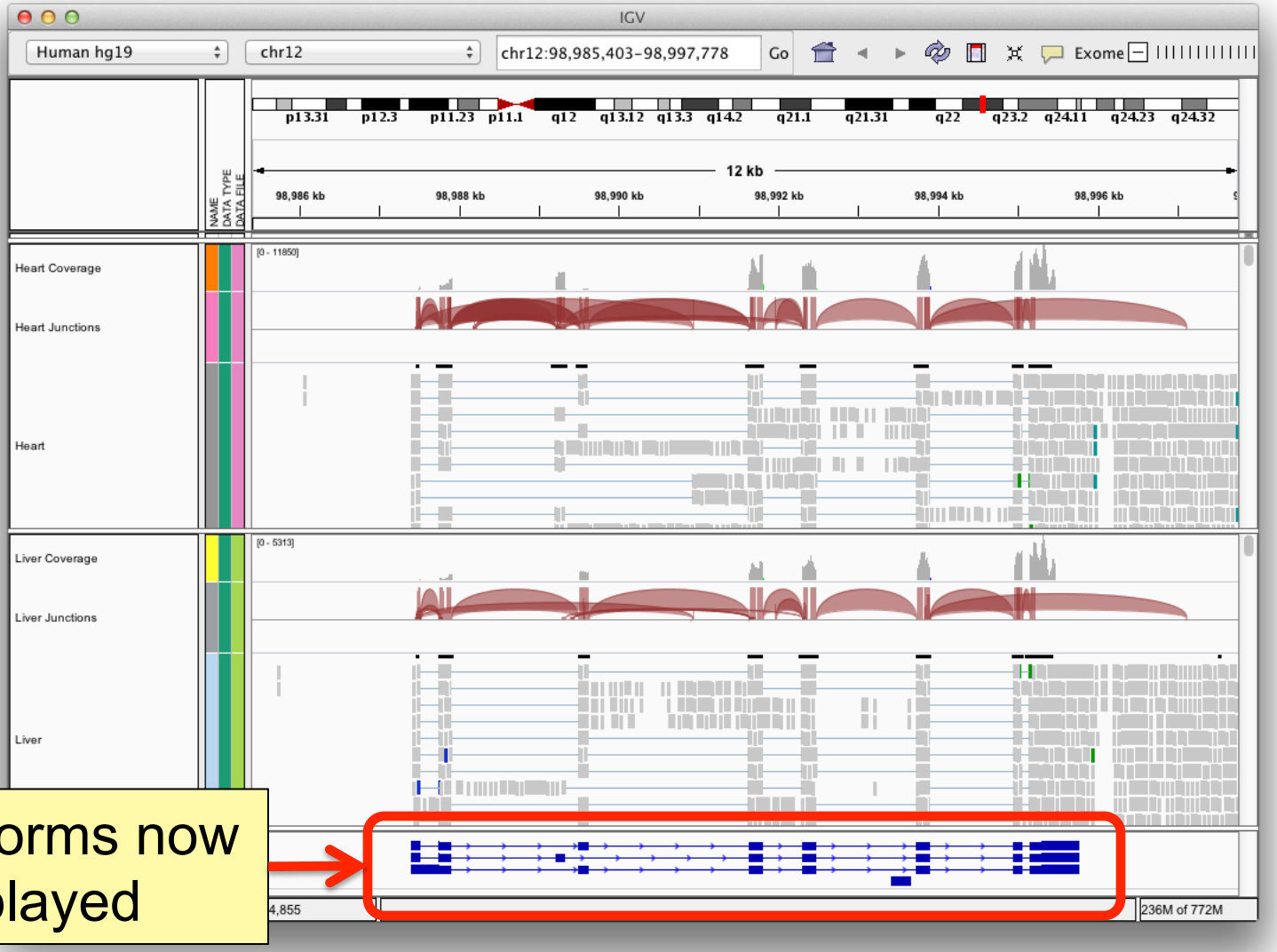


Select **Squished**

BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer

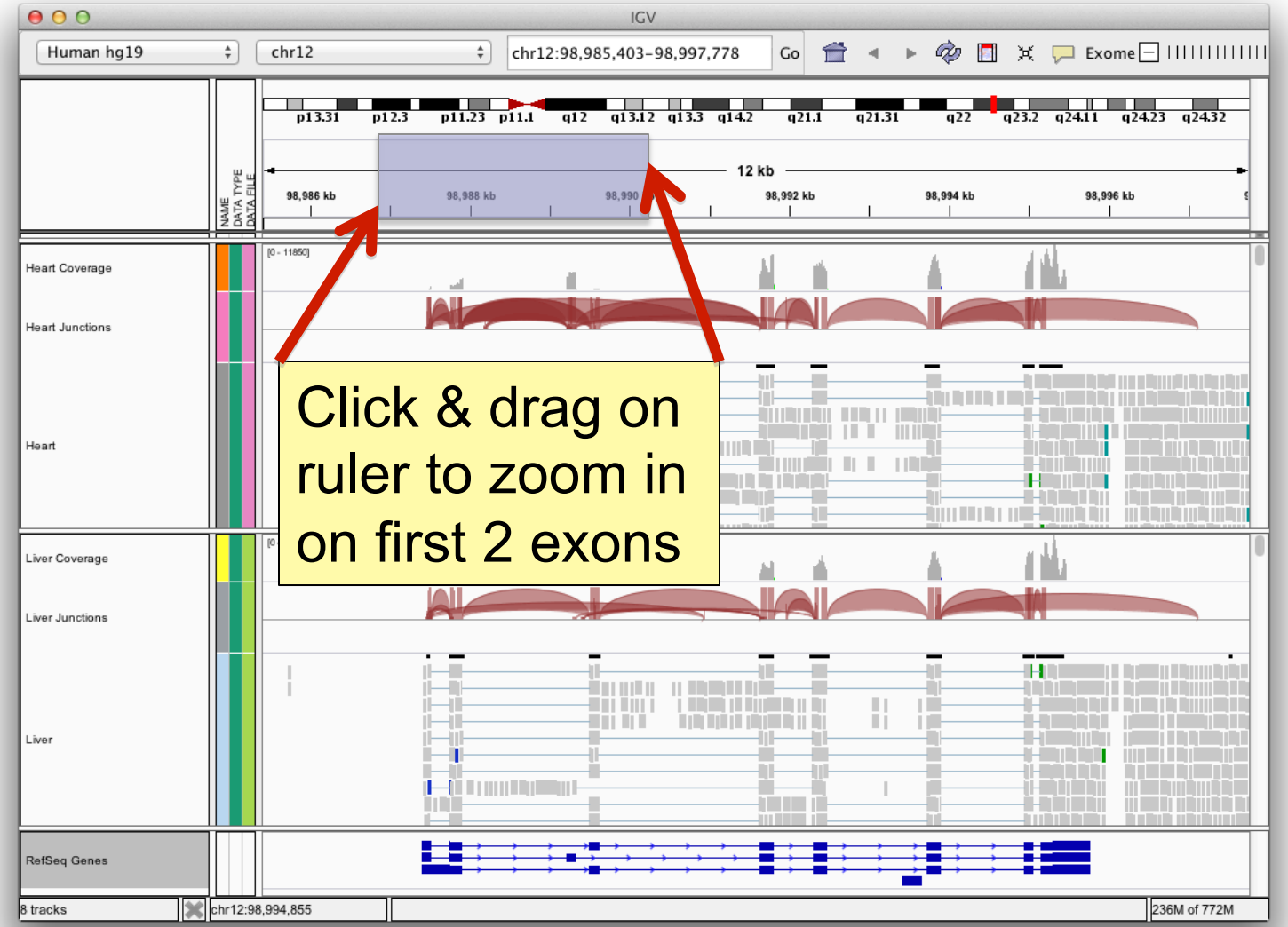


Isoforms now displayed

BROAD INSTITUTE

RNA-seq alignments

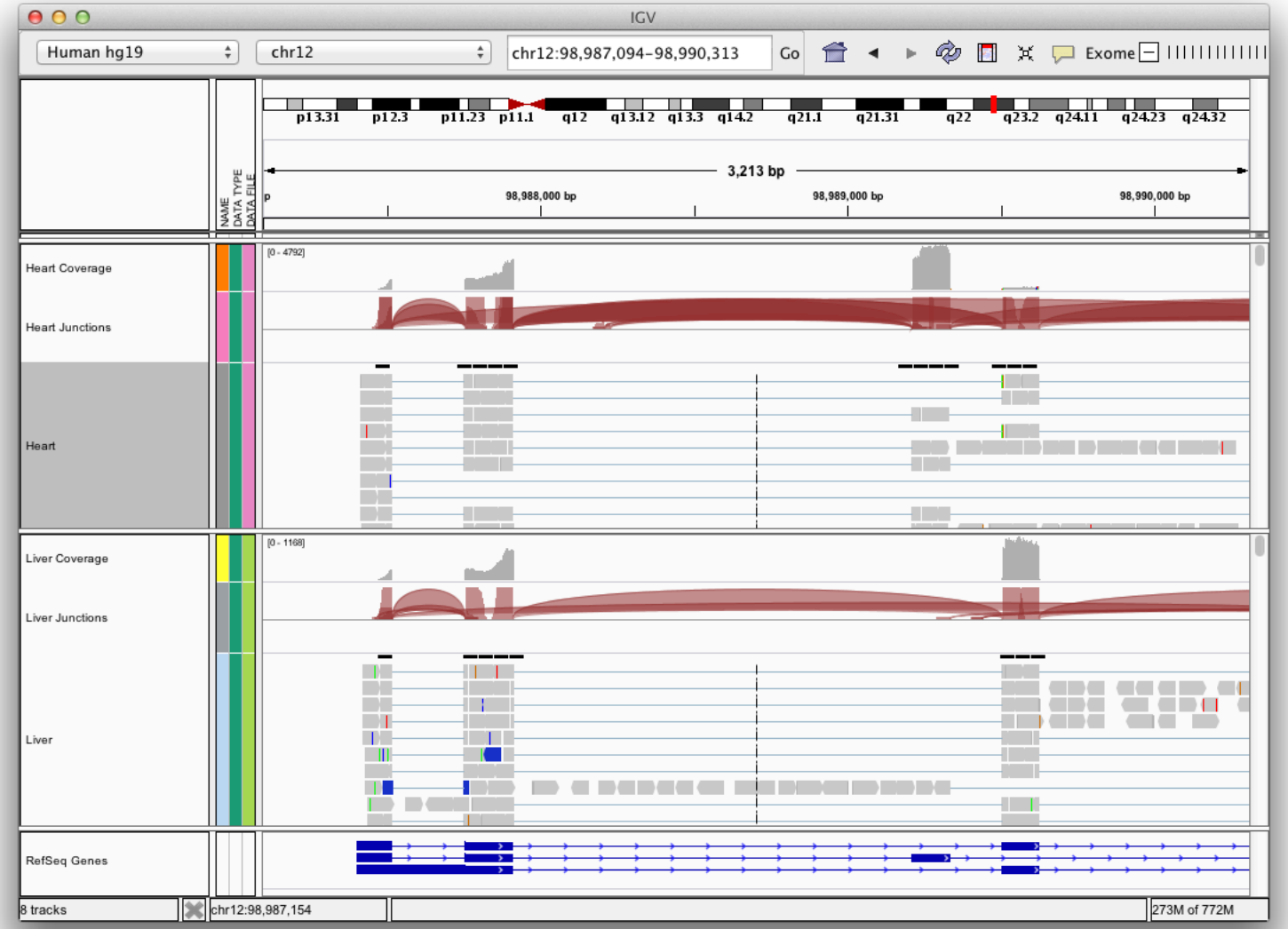
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

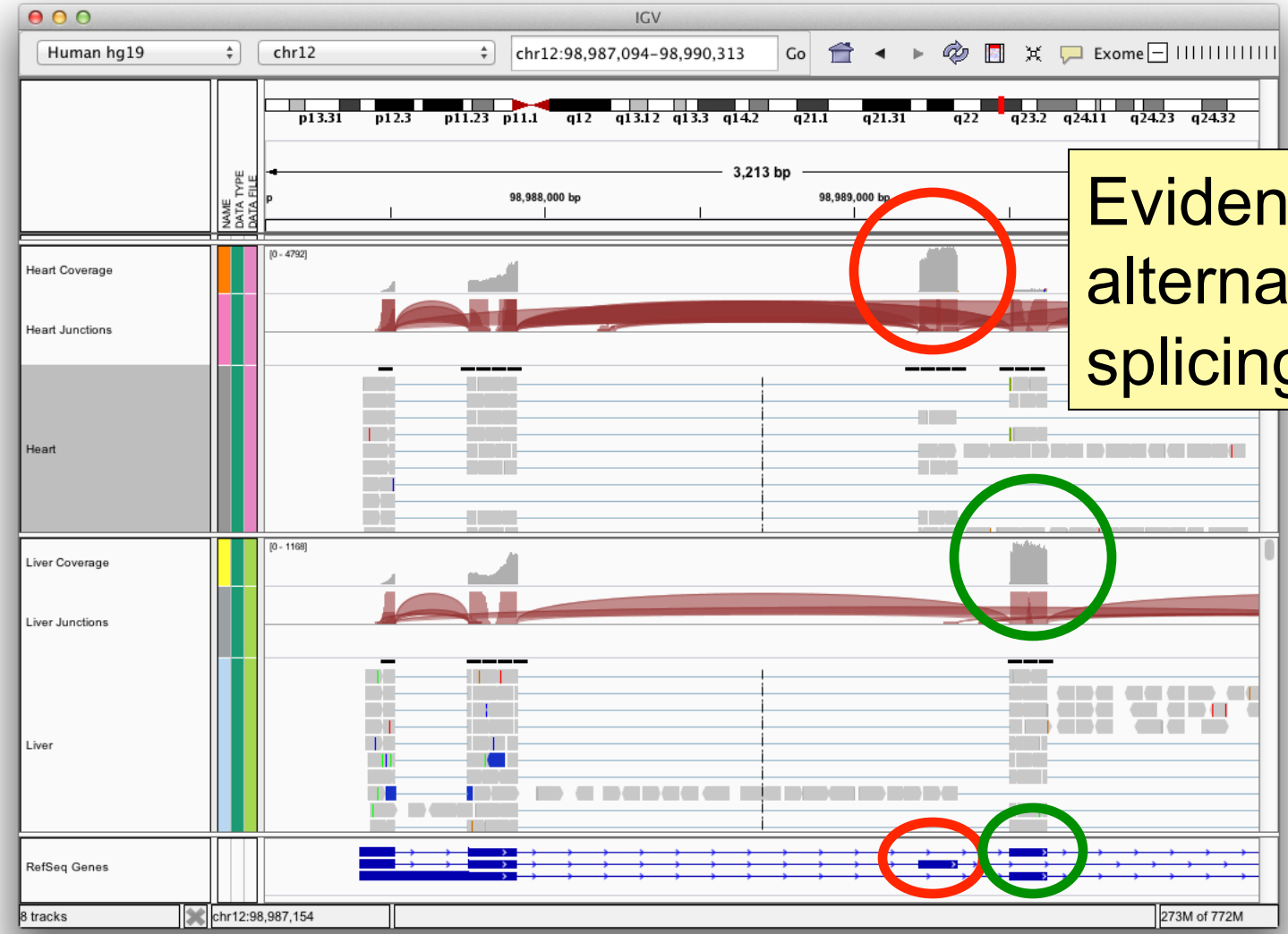
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer



Evidence of alternative splicing

BROAD INSTITUTE

Sashimi plot

Integrative Genomics Viewer

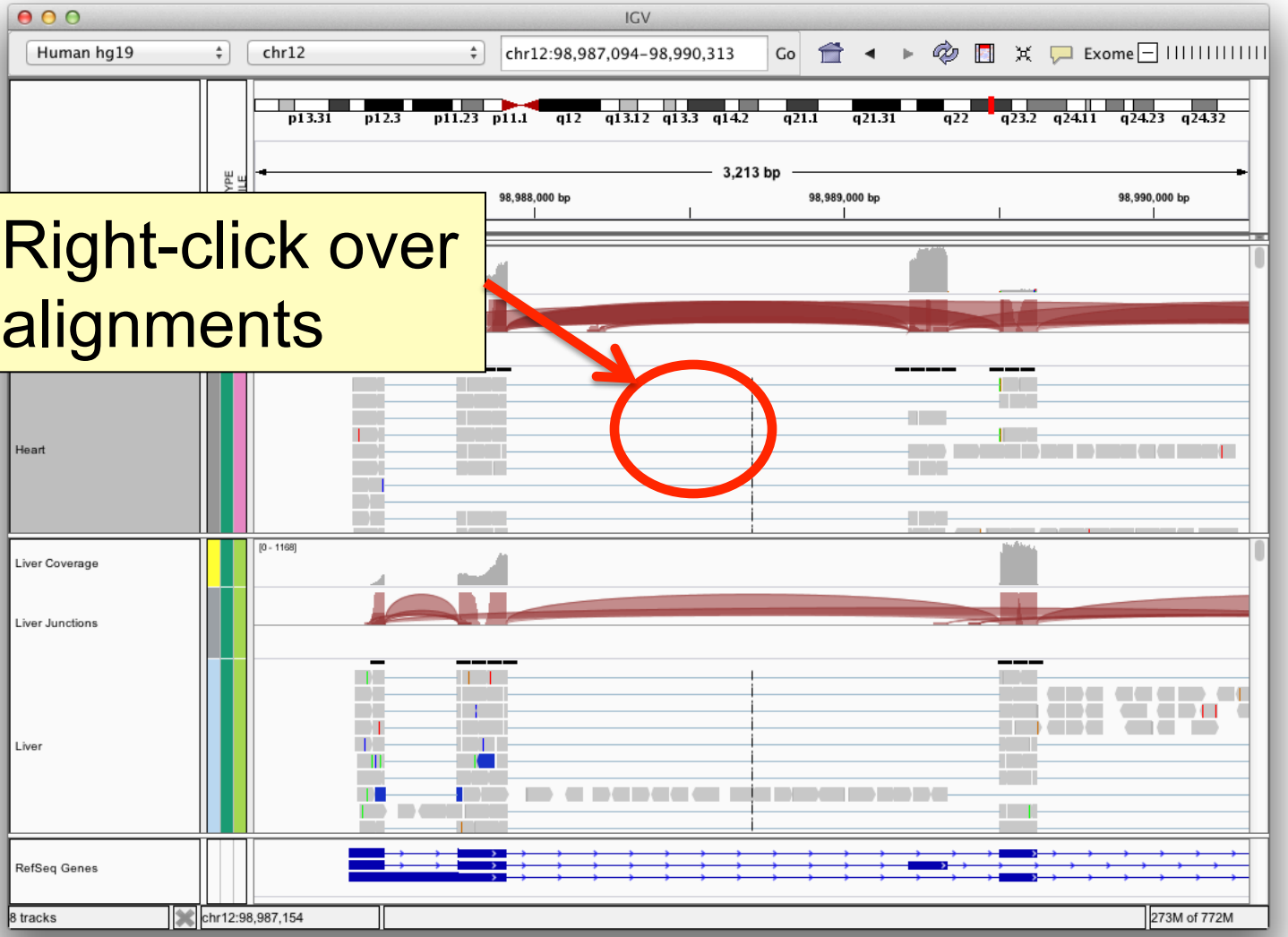
Viewing RNA splicing with Sashimi Plots

Reference: Katz Y, Wang ET, Silterra J, Schwartz S, Wong B, Mesirov JP, Airoldi EM, Burge, CB. ***Sashimi plots: Quantitative visualization of RNA sequencing read alignments.*** arXiv:1306.3466 [q-bio.GN], 2013

BROAD INSTITUTE

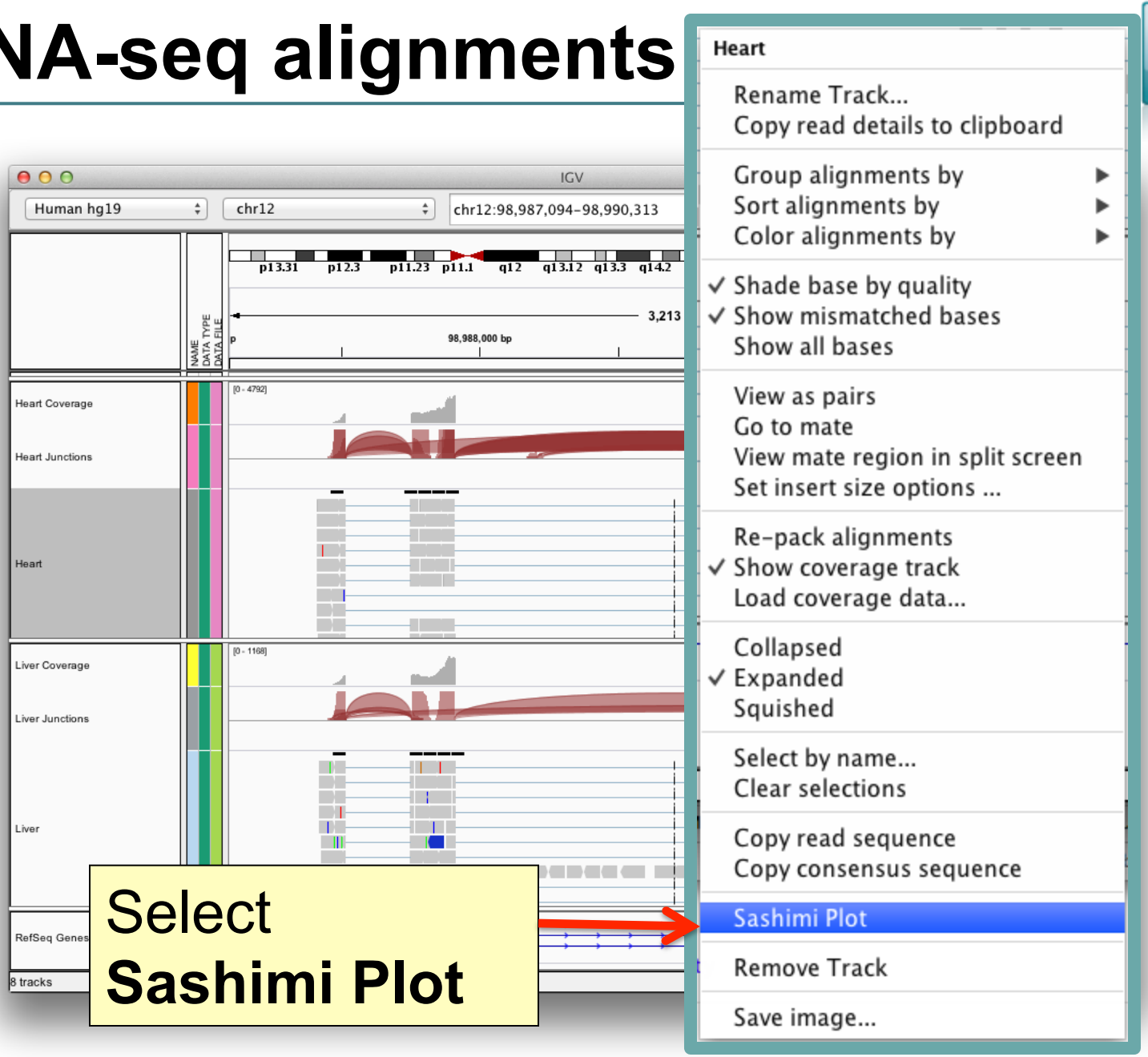
RNA-seq alignments

Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

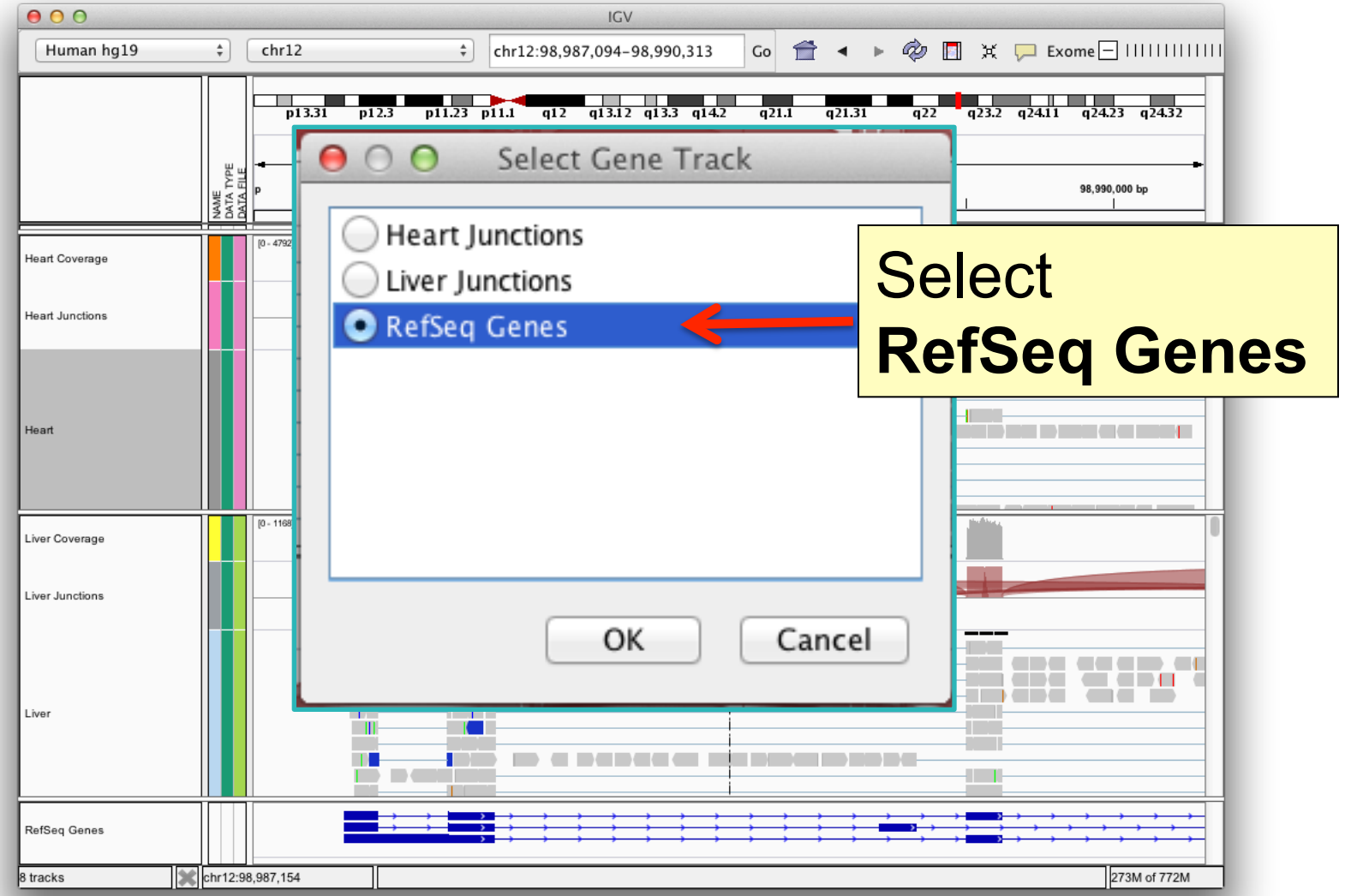


Integrative Genomics Viewer

BROAD INSTITUTE

RNA-seq alignments

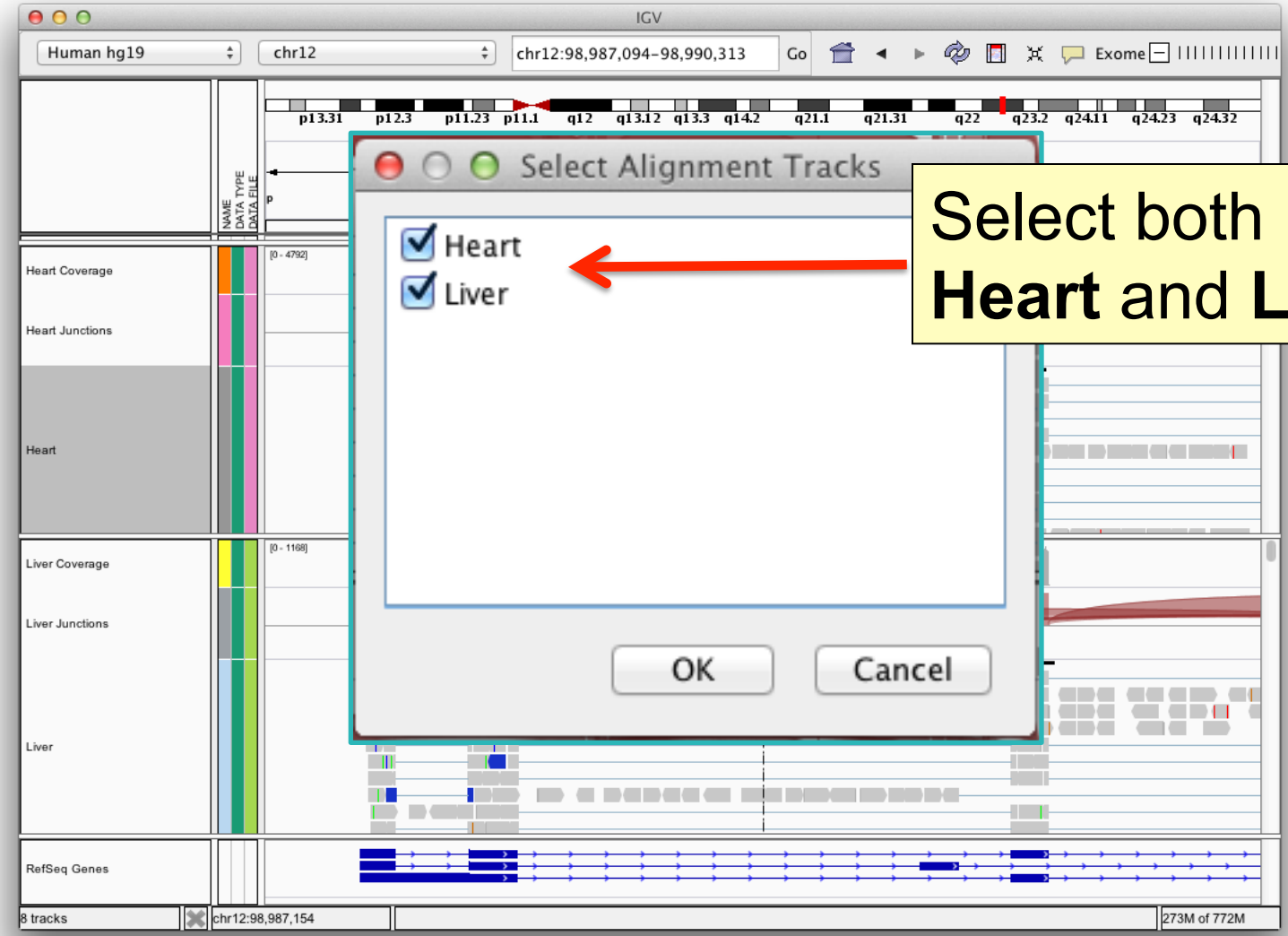
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer



BROAD INSTITUTE

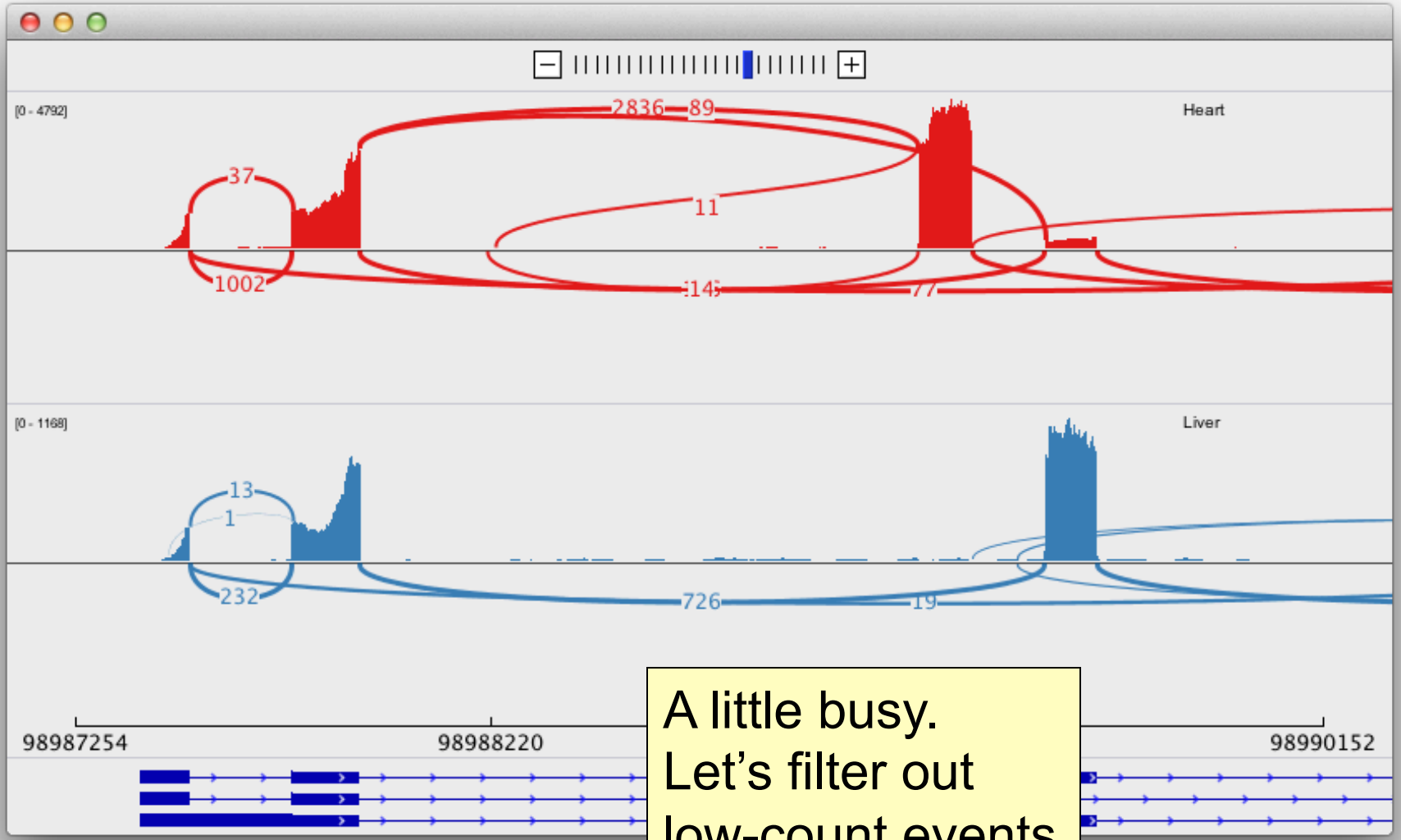
RNA-seq alignments

Integrative Genomics Viewer

BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer



A little busy.
Let's filter out
low-count events

BROAD INSTITUTE

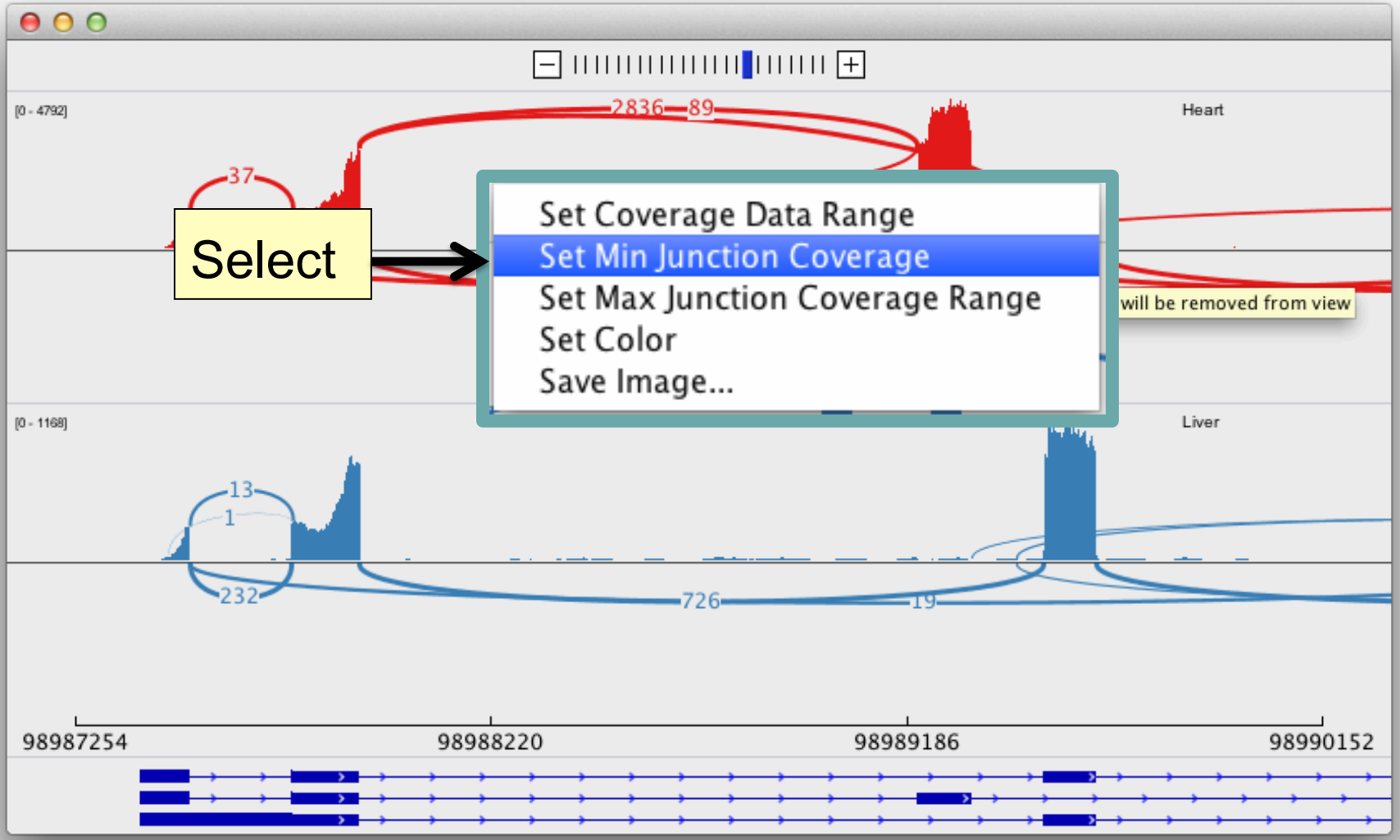
RNA-seq alignments

Integrative Genomics Viewer

BROAD INSTITUTE

RNA-seq alignments

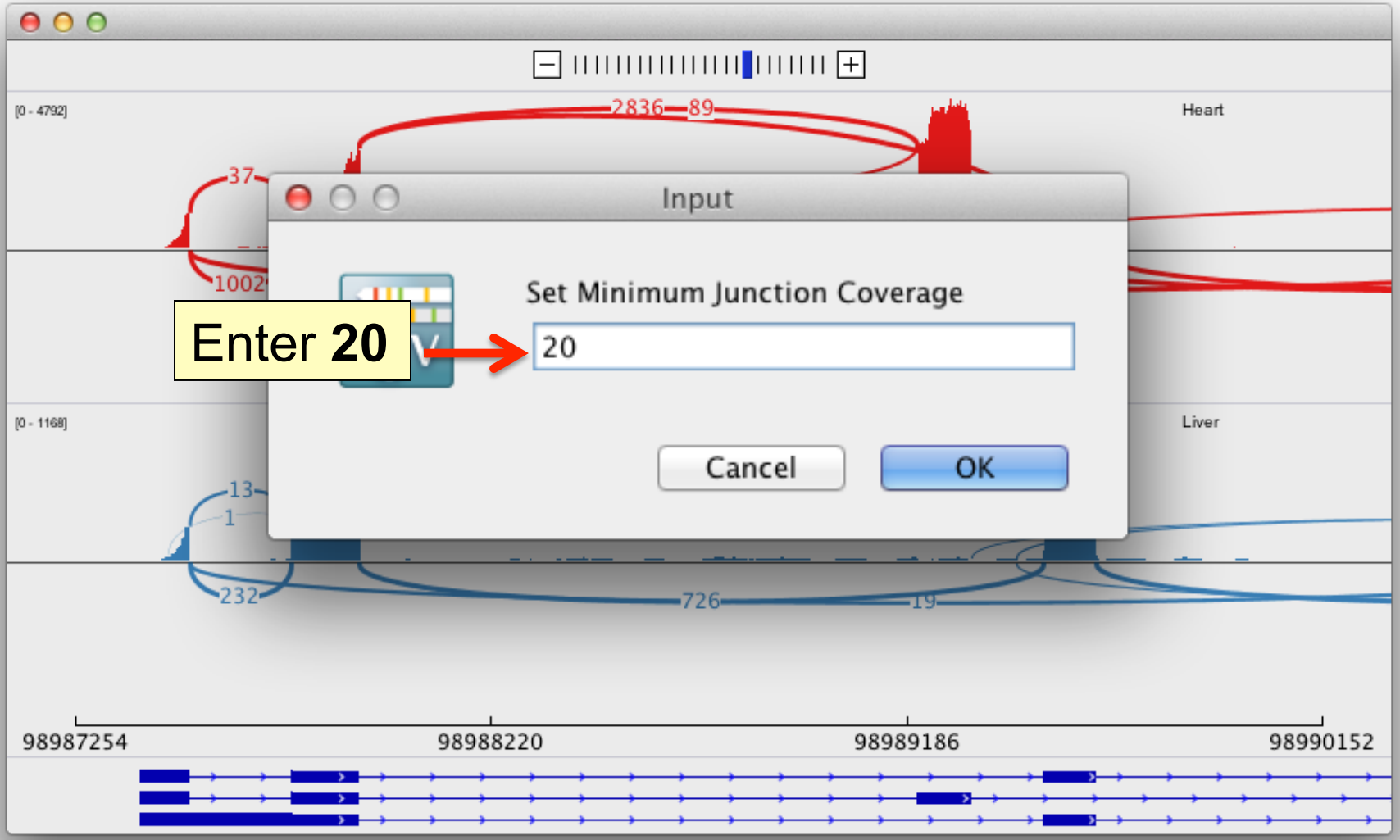
Integrative Genomics Viewer



BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer



BROAD INSTITUTE

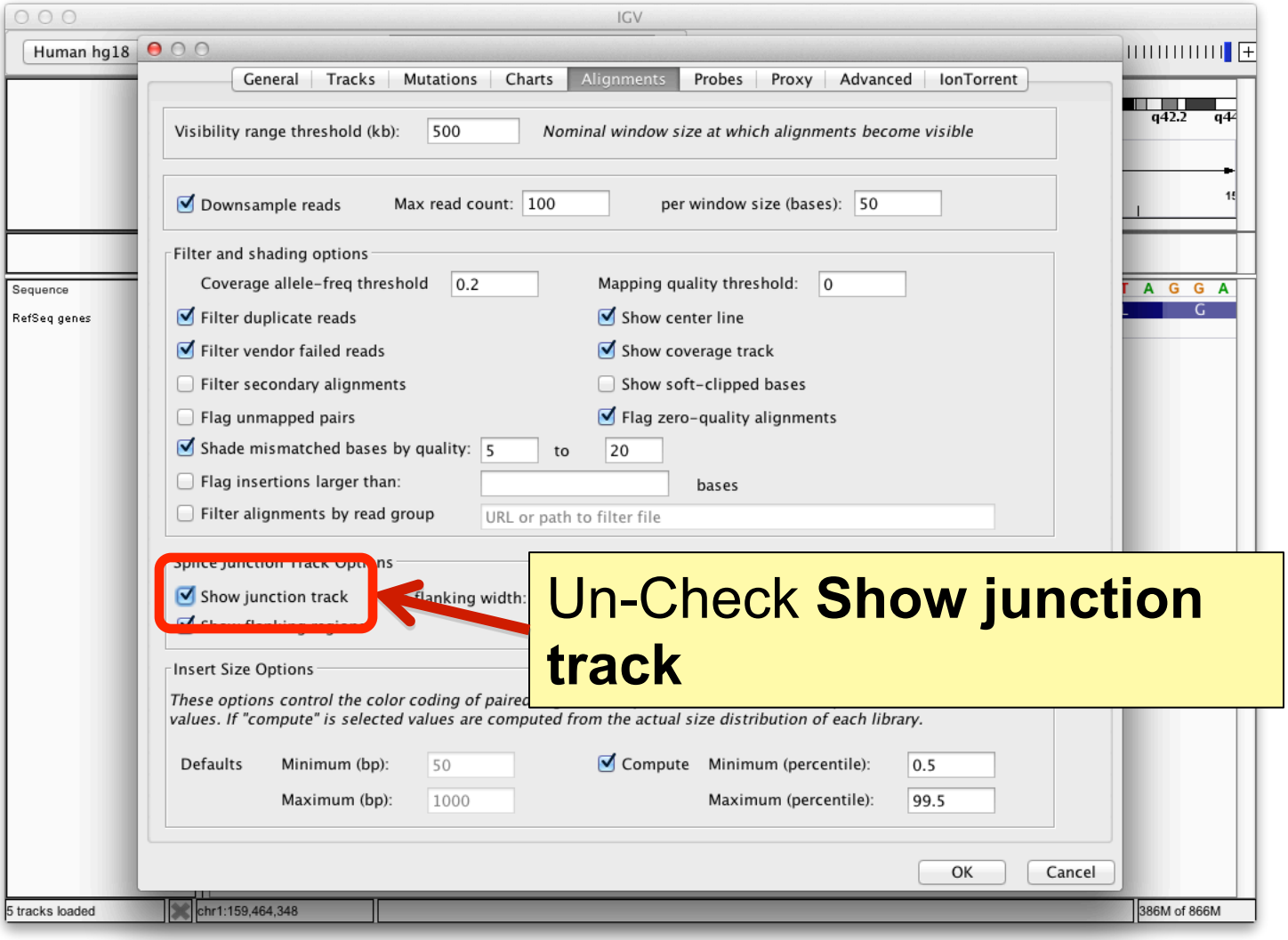
RNA-seq alignments

Integrative Genomics Viewer

BROAD INSTITUTE

RNA-seq alignments

Integrative Genomics Viewer



BROAD INSTITUTE

igvtools

igvtools

Integrative Genomics Viewer

A set of utilities for preparing files for efficient display.

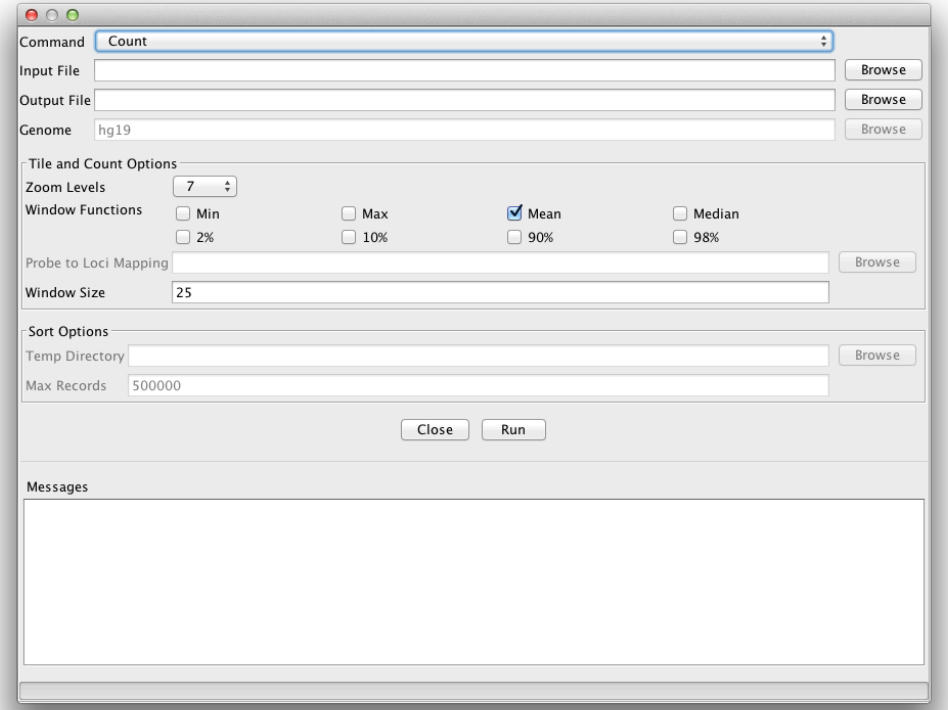
toTDF	• Converts sorted data file to a binary tiled data file (TDF). • Supported file formats: .wig, .cn, .snp, .igv, .gct
count	• Computes average alignment or feature density over a specified window size across the genome. • Supported file formats: .sam, .bam, .aligned, .sorted.txt, .bed
sort	• Sorts file by genomic start position. • Supported file formats: .cn, .igv, .sam, .aligned, .bed.
index	• Creates an index file for alignment or feature file. • Supported file formats: .sam, .aligned, .sorted.txt, .bed

BROAD INSTITUTE

igvtools

Integrative Genomics Viewer

- Can be launched from the IGV user interface *File > Run igvtools…*
- Or run from the command line



BROAD INSTITUTE

igvtools toTDF

Integrative Genomics Viewer

The **toTDF** utility converts large ASCII data files into tiled data format (.tdf) files.

TDF files have the following advantages:

- Data is indexed for efficient retrieval.
- Data is preprocessed for zoomed out views.
- TDF files are web friendly – large data files can be shared over the web. Only small slices of the file are actually transferred as needed.

BROAD INSTITUTE

igvtools count

Integrative Genomics Viewer

The **count** command is used to transform alignment files to read density TDF files, e.g. for ChIP-Seq, RNA-Seq, and similar alignment counting experiments.

Alignments

Alignments in bam/sam, .aligned, or bed format

Read Density

TDF format, indexed and optimized for fast retrieval at multiple resolution scales

BROAD INSTITUTE

igvtools sort

Integrative Genomics Viewer

- Sorts IGV-supported genomic formats by start position.
- The index command requires sorted files.

Example:
igvtools sort -m 1000000 –t ~/myTmpDir inputFile.sam outputFile.sorted.sam

- Uses combination of memory and disk to handle large files.

  -m = maximum # of lines to hold in memory. When this number is exceeded a temporary file is created.

  -t = directory used to create temporary files during sorting.

BROAD INSTITUTE

igvtools index

Integrative Genomics Viewer

Creates an index file for viewing large files in bed, gff, or vcf formats. An index is optional for bed or gff files, but required for vcf files.

An alternative indexing tool is “tabix”. Tabix both compresses and indexes genomic files. IGV can read either type of index (igvtools or tabix).

Example: igvtools index myFeatures.bed

The index file must remain in the same directory as the input file

BROAD INSTITUTE

Exercises

Integrative Genomics Viewer

- Computing total and strand specific coverage with igvtools
- IGV batch scripting
- Controlling IGV from a web page

BROAD INSTITUTE

Acknowledgments

IGV Team

Jim Robinson, Helga Thorvaldsdóttir, Jill Mesirov (PI)

Funding

IGV development has been made possible with funding from:

- National Cancer Institute (NCI) http://cancer.gov/
- Starr Cancer Consortium http://www.starrcancer.org/
- National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health http://www.nigms.nih.gov/
- IGV participates in GenomeSpace http://genomespace.org/, which is funded by the the National Human Genome Research Institute (NHGRI) http://www.genome.gov/

For further information and help:

http://www.broadinstitute.org/igv

http://groups.google.com/group/igv-help

Cite:

Robinson et al.
Integrative Genomics Viewer.
Nature Biotechnology 29, 24–26 (2011).

Thorvaldsdóttir, Robinson, and Mesirov.
Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration.
Briefings in Bioinformatics (2012).

BROAD INSTITUTE

Integrative Genomics Viewer