

IGV tutorial

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Step0: Download software

- **Prerequisite:** IGV 2.4.x releases require Java 8
- **Support operating system:** Mac, Window or Linux/MacOS
(<http://software.broadinstitute.org/software/igv/download>)
- **# of hosted genomes:** 155



Install IGV

Download IGV Mac App

Download and unzip the Mac App Archive, then double-click the IGV application to run it. The application can be moved to the *Applications* folder, or anywhere else



Download IGV on Windows

Download and unzip the Archive, then double-click the *igv.bat* file to run IGV. See *readme.txt* to run IGV from the command line



For high DPI screens: Use Java 10 and the [development snapshot build of IGV](#).

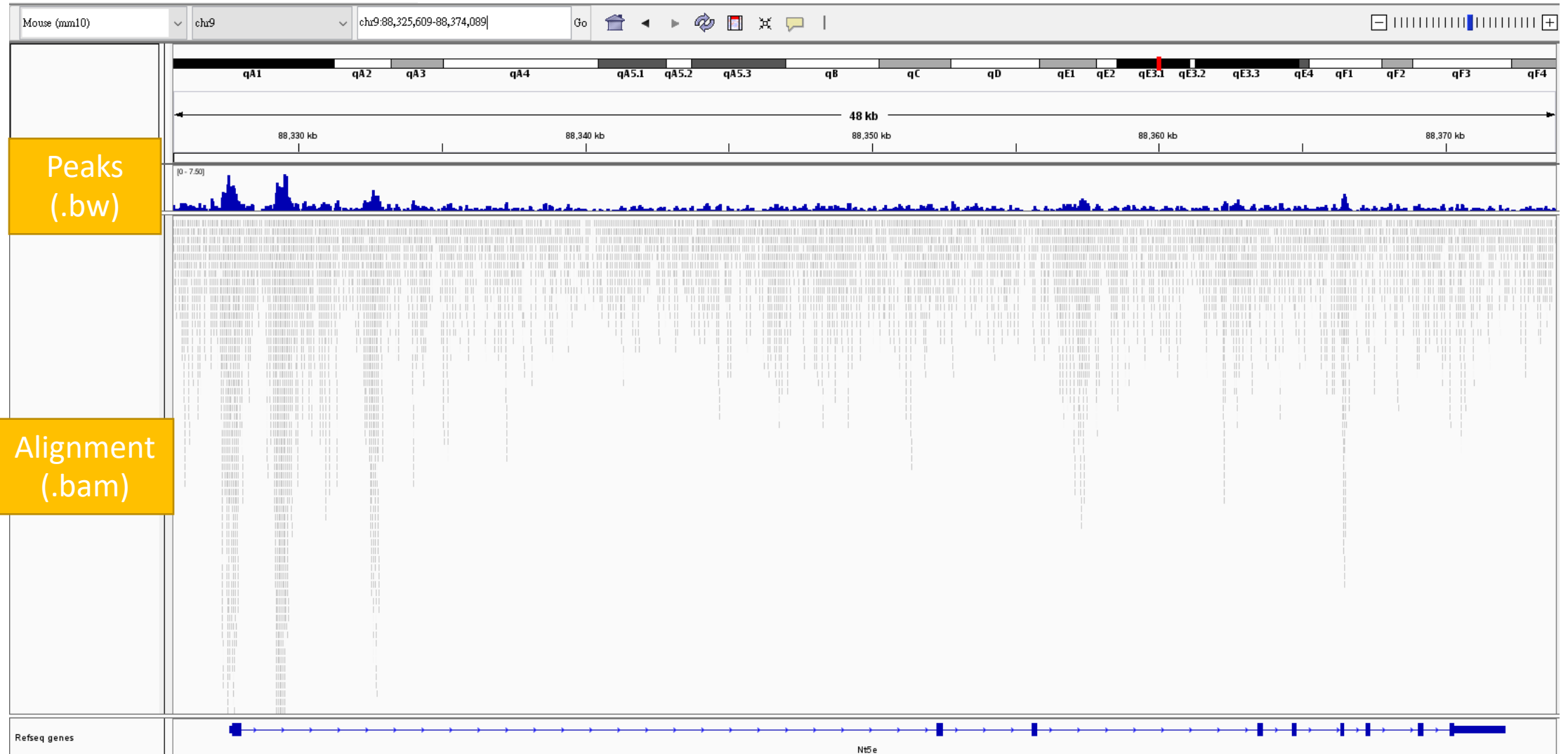
Step0: Launch IGV and its main interface

The screenshot displays the IGV main interface with the following components:

- Menu Bar:** File, Genomes, View, Tracks, Regions, Tools, GenomeSpace, Help.
- Header:** Human hg19, a dropdown menu set to "All", a "Go" button, and navigation icons.
- Genome Track:** A horizontal ruler showing all 22 chromosomes, X, and Y. This track is highlighted with a red border.
- Track(s) Panel:** A large empty area for displaying genomic tracks.
- Annotation Track:** A track labeled "RefSeq Genes" showing gene annotations as blue bars.
- Footer:** "2 tracks", "chr1:22,723,540", and "254M of 567M".

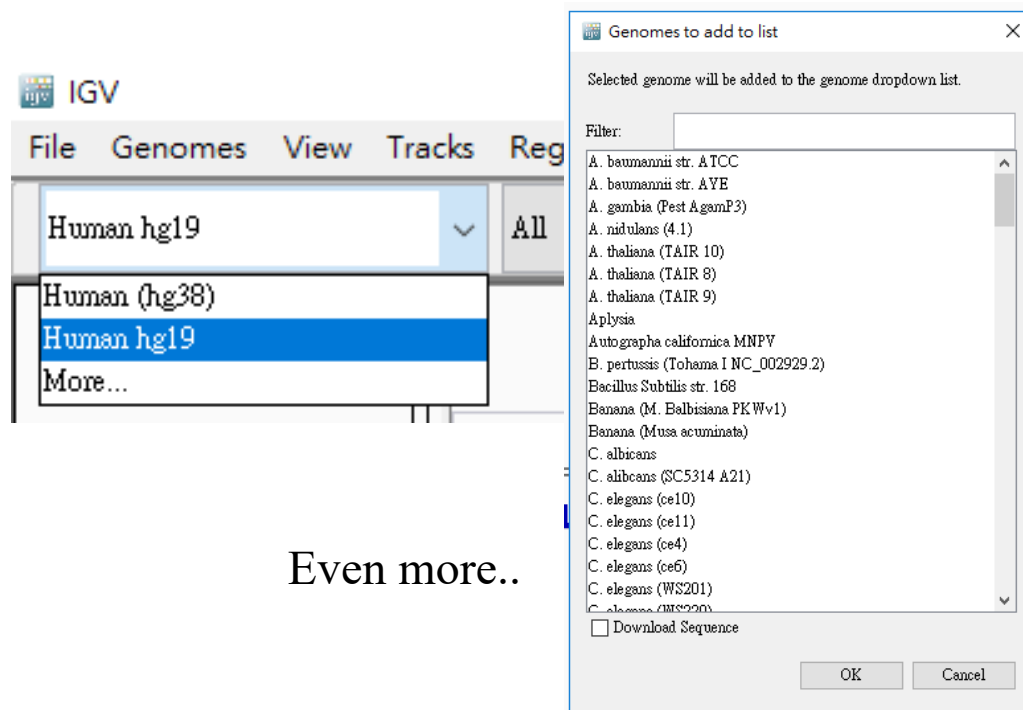
>>> Ruler displays all the chromosomes

Interface with ChIP-seq peaks & alignment



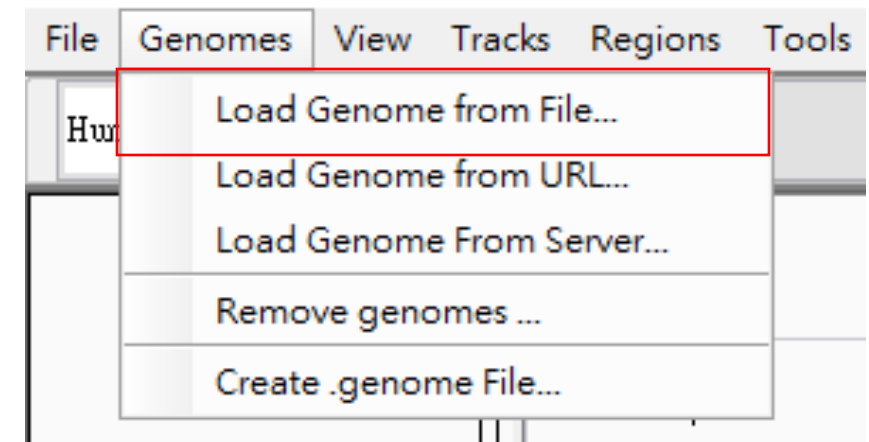
Step1: Select reference genome

- Choose one **already available** in the Reference Genome Selector
- Load your **own genome** with the indexed FASTA format (.fa or .fasta)
 - select **Genomes** > Load *Genome from File*



Even more..

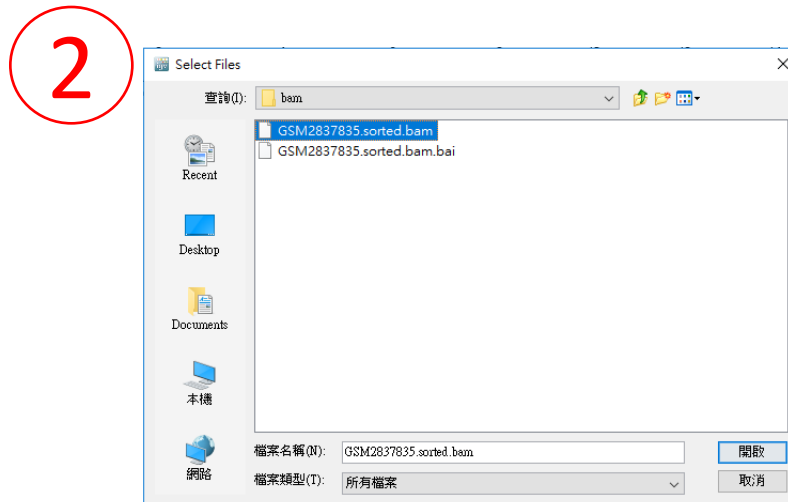
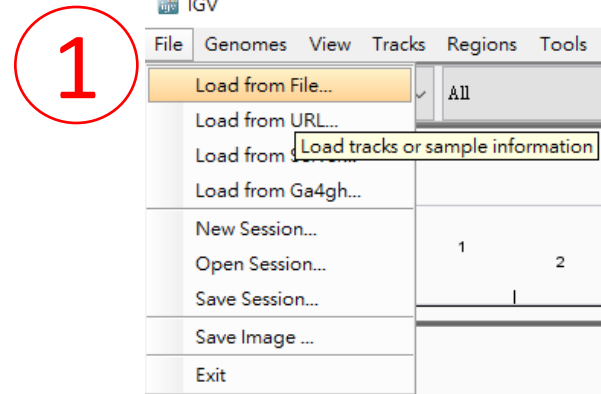
OR



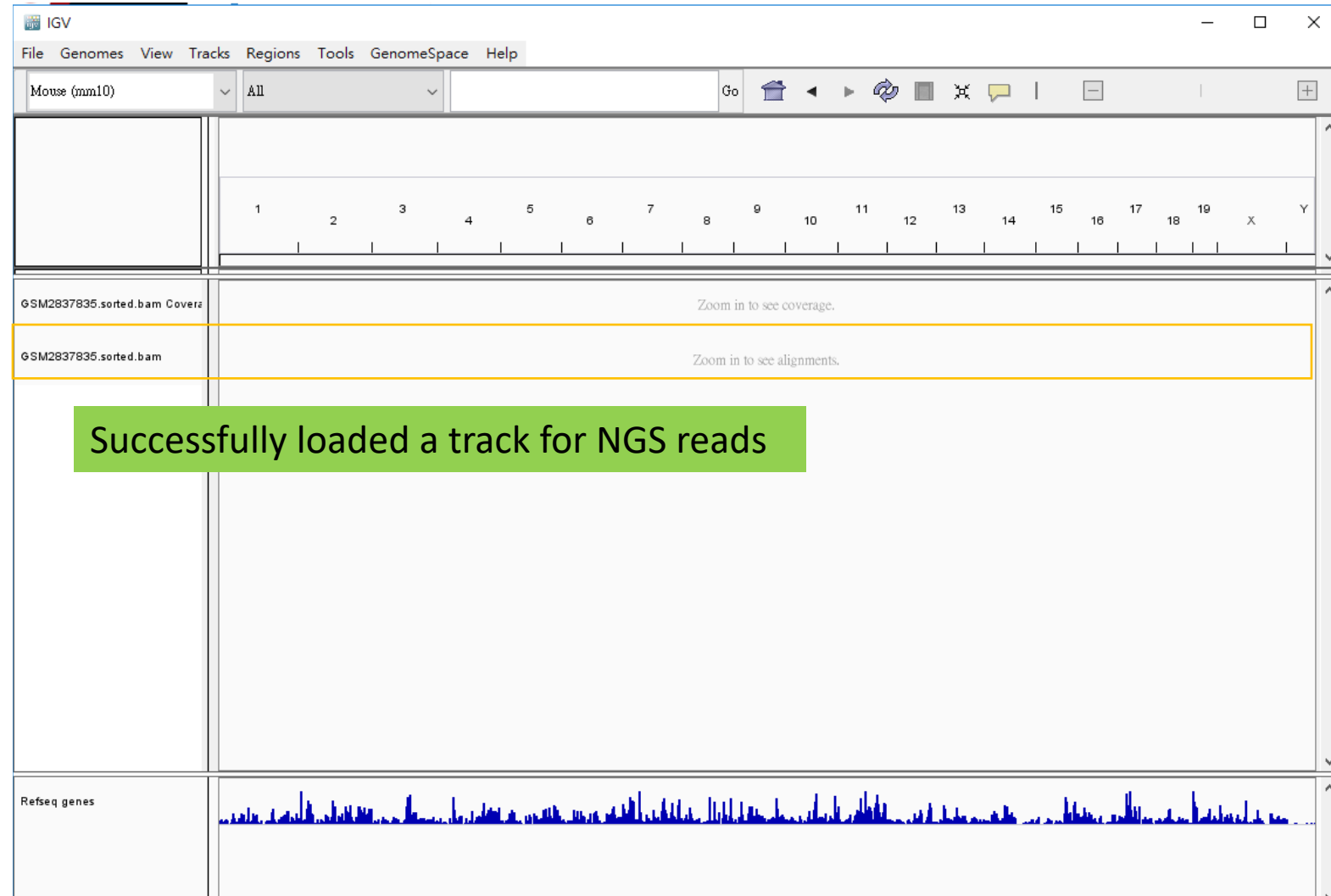
(Build-in Reference)

Step2: Load data from files

- *NGS reads*



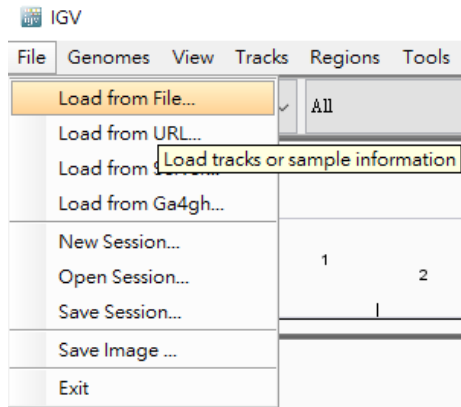
3



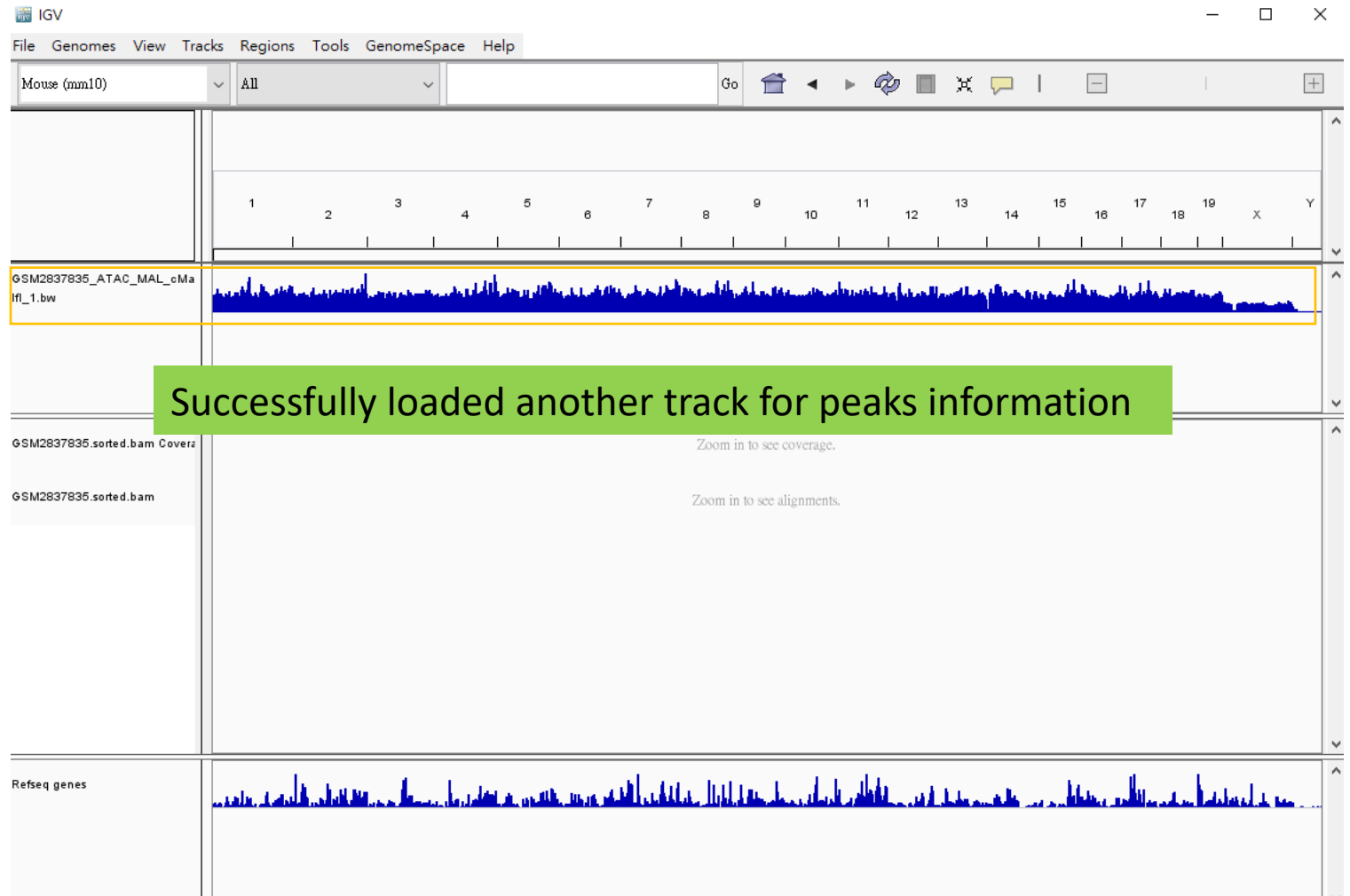
Step2: Load data from Files

- ChIP-/ATAC-seq data

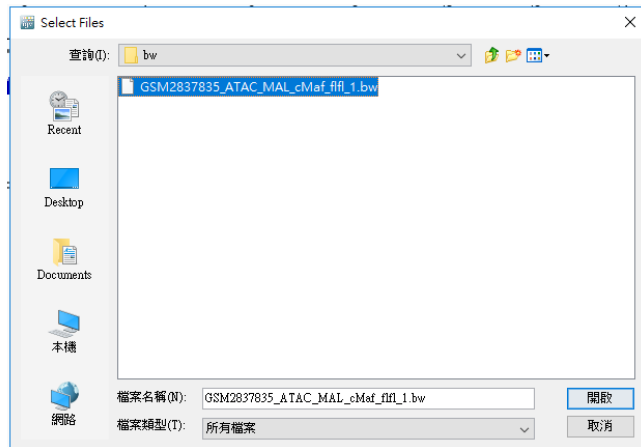
1



3



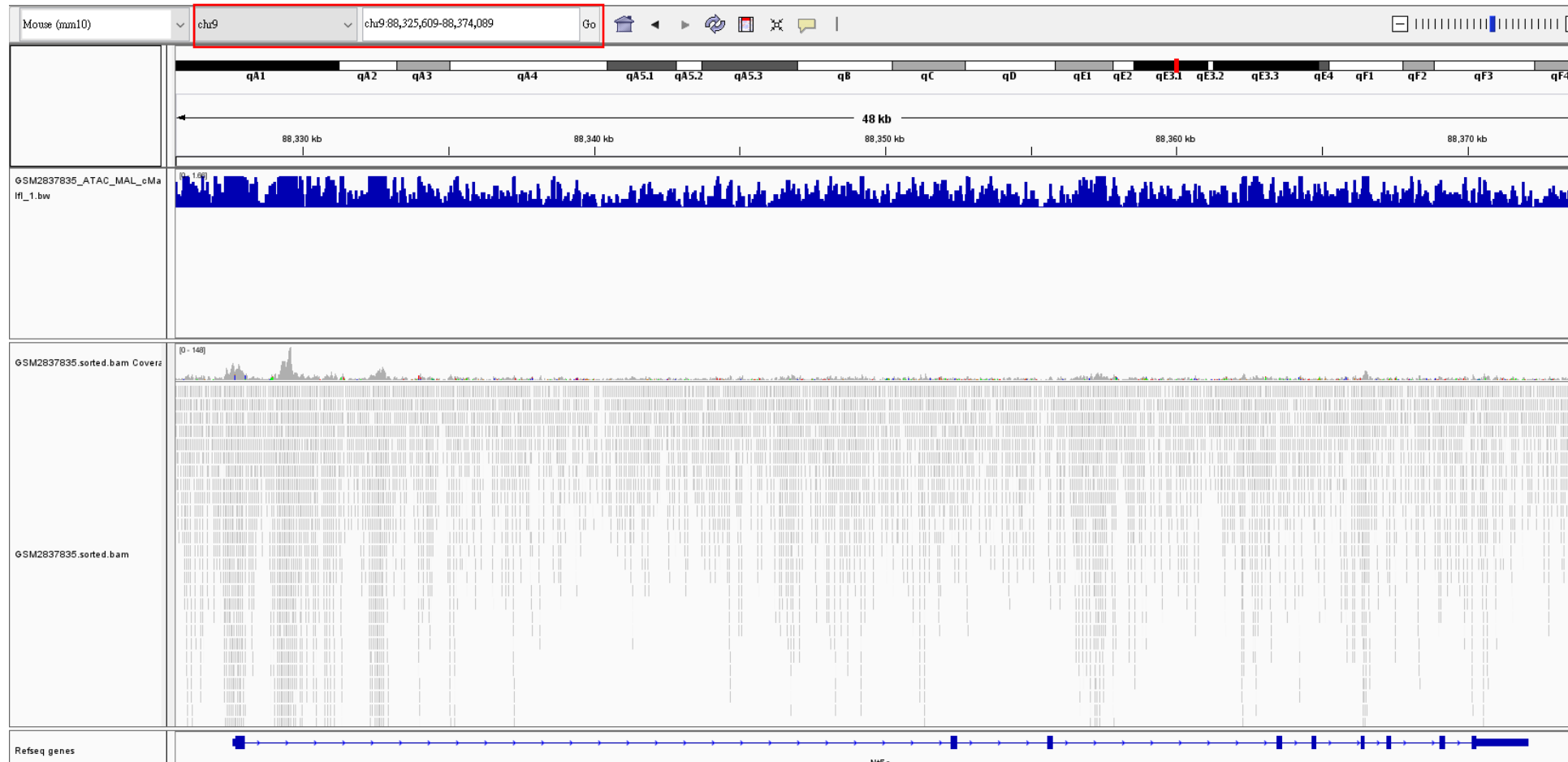
2



Step3: Navigate to **specific locus** or **gene** on any chromosome

> i.e. chr9:88,325,609-88,374,089 or Nt5e

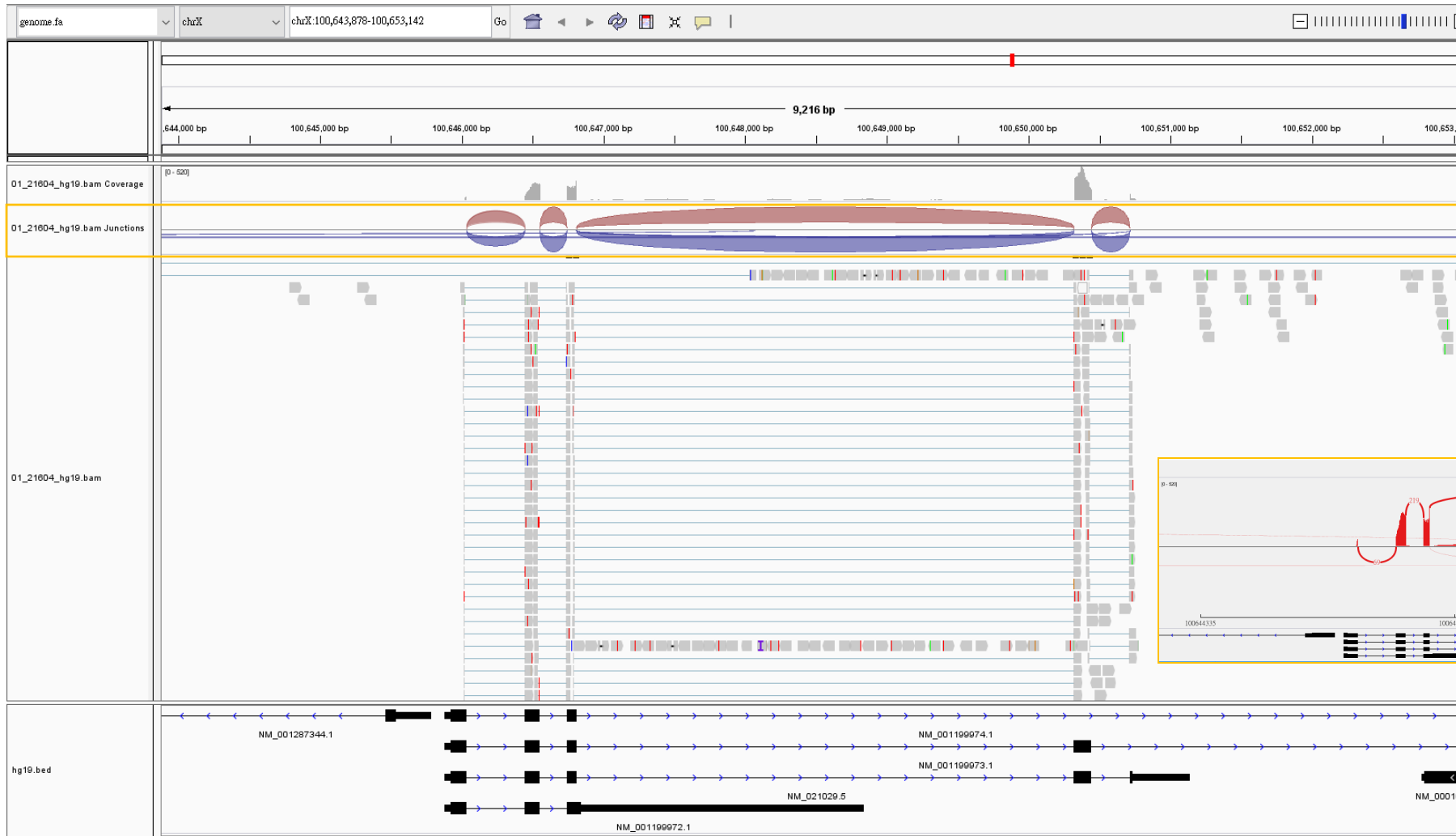
Search bar



Step4: Junctions and isoforms

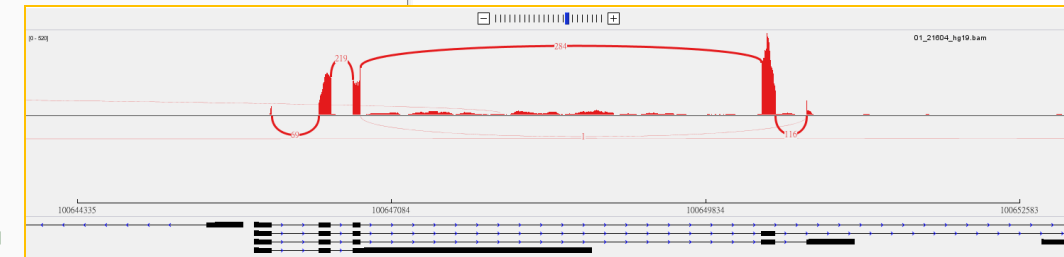
- *Sashimi plot*

Take NM_021029 as an example



Before loading data

- Click *View > Preferences*
- Select *Alignments* tab
- Check *Splice Junction Track*



Some useful options

- show details on click

- **Reads Information**

```
Read name = D9RF08P1:295:C16HVACXX:3:1104:10838:29062
Read length = 81bp
-----
Mapping = Primary @ MAPQ 60
Reference span = chrX:100,650,249-100,650,329 (+) = 81bp
Cigar = 81M
Clipping = None
-----
Mate is mapped = yes
Mate start = chrX:100650283 (-)
Insert size = 116
First in pair
Pair orientation = F1R2
-----
XG = 0
NH = 1
NM = 0
XM = 0
XN = 0
XO = 0
AS = 0
XS = -
YS = -5
YT = CP
Hidden tags: MD
-----
Location = chrX:100,650,295
Base = T @ QV 41
```

- **Coverage Information**

```
chrX:100,646,812
-----
Total count: 2
A : 0
C : 0
G : 0
T : 2 (100%, 1+, 1-)
N : 0
-----
```