IGV tutorial

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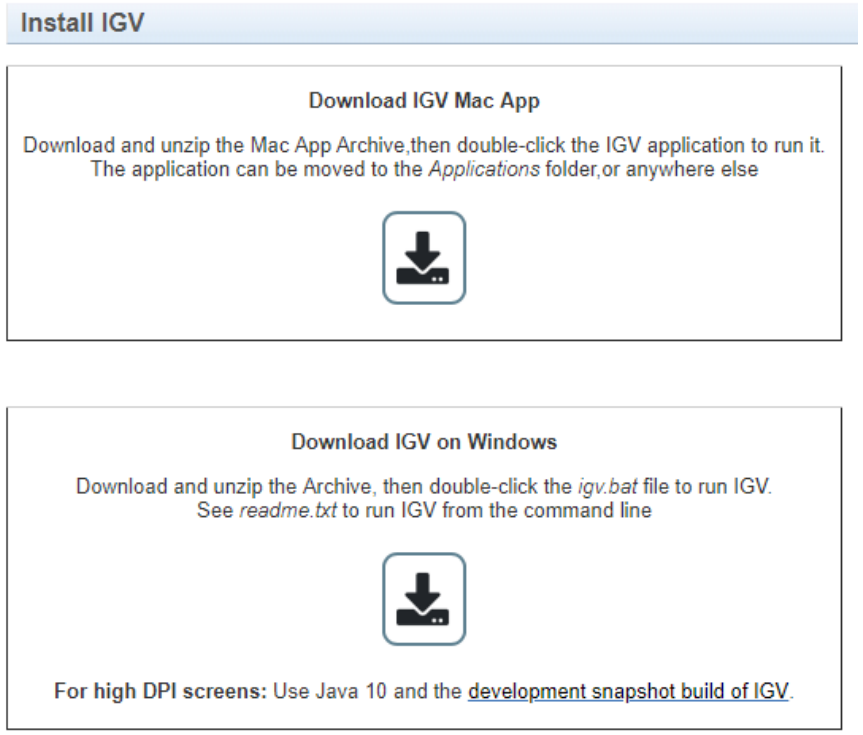
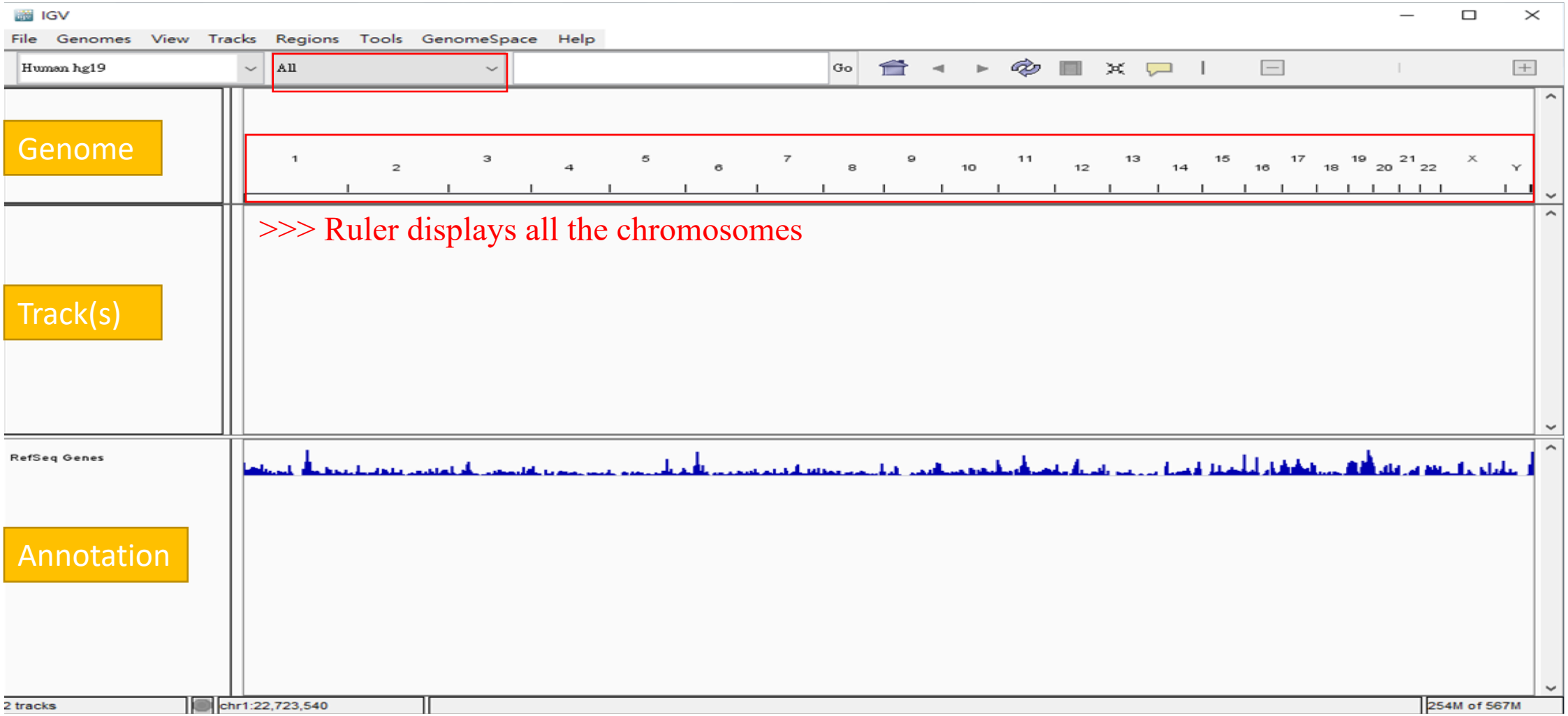
Step0: Download software

- **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

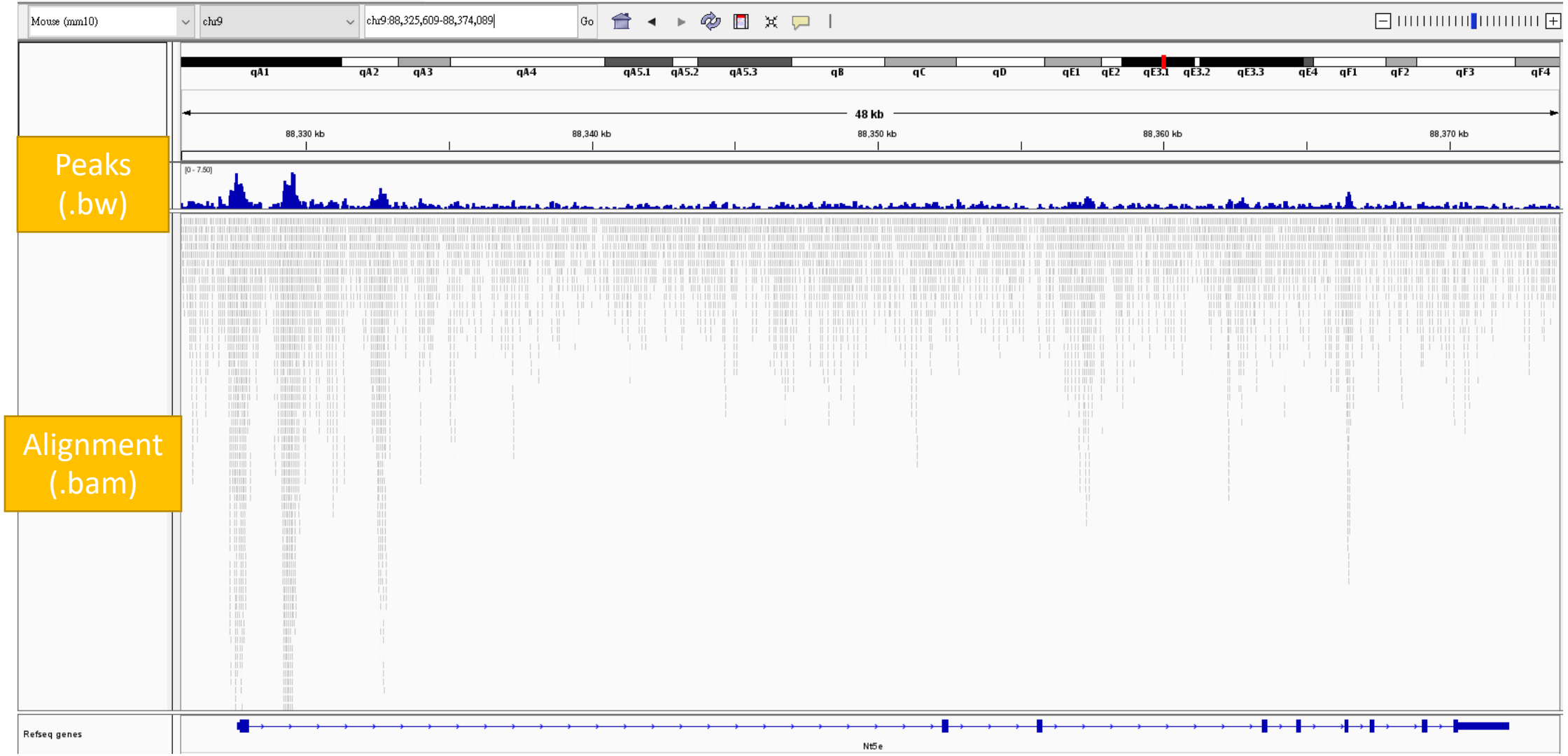
Integrative Genomics Viewer



Step0: Launch IGV and its main interface

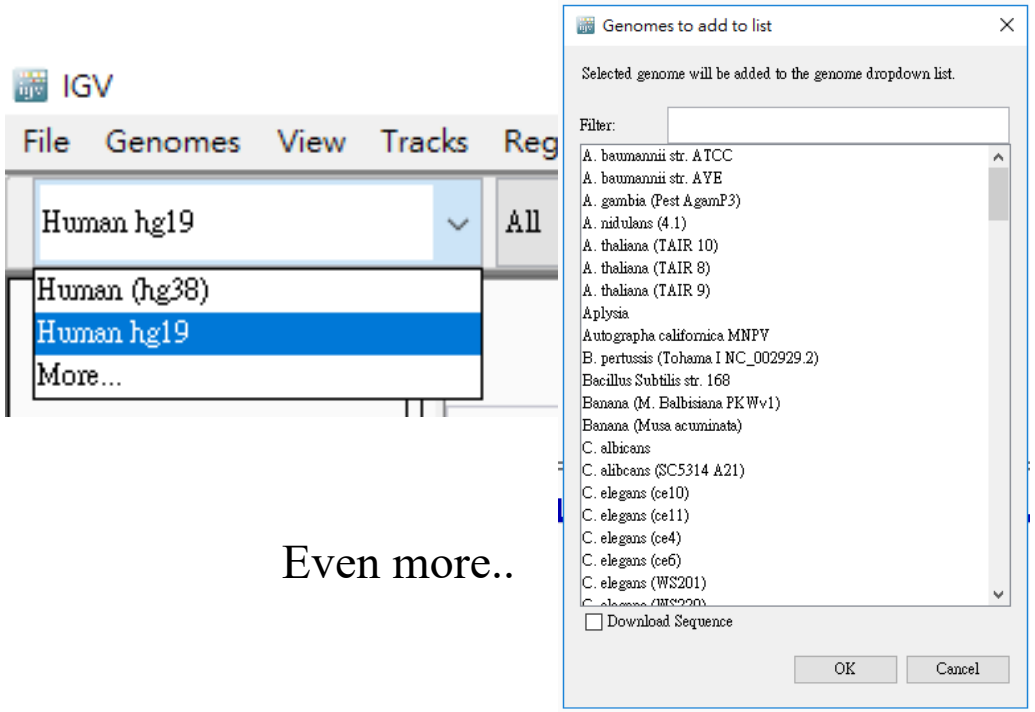


Interface with ChIP-seq peaks & alignment



Step1: Select reference genome

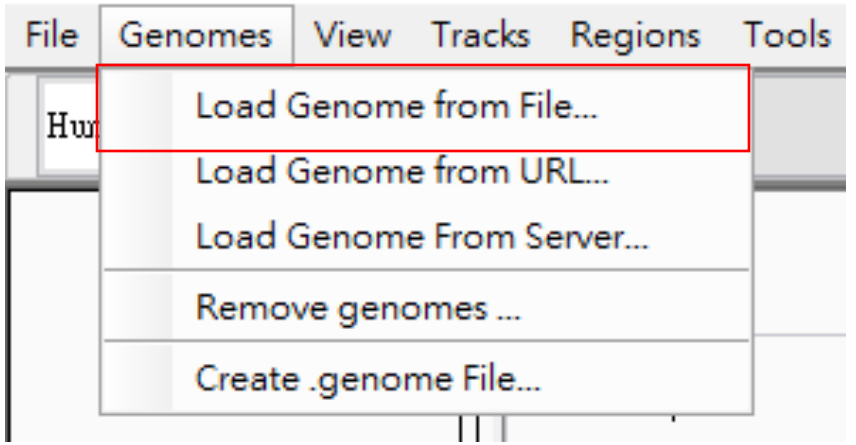
- Choose one **already available** in the Reference Genome Selector
- Load your **own genome** with the indexed FASTA format (.fa or .fasta)
  - select ***Genomes*** > Load *Genome from File*



Even more..

(Build-in Reference)

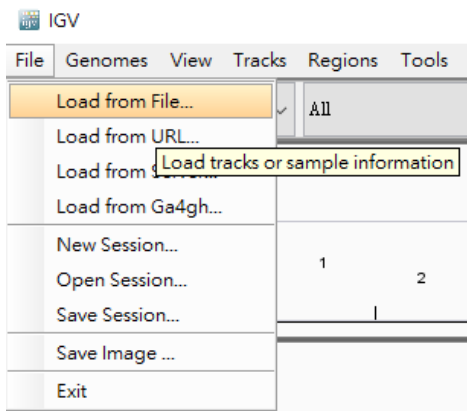
OR



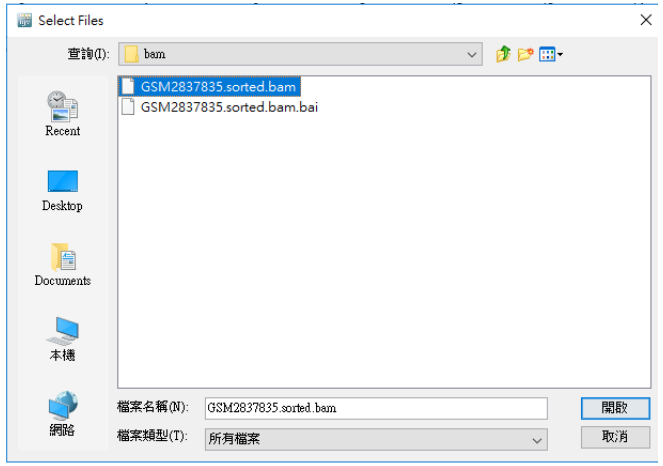
Step2: Load data from files

- *NGS reads*

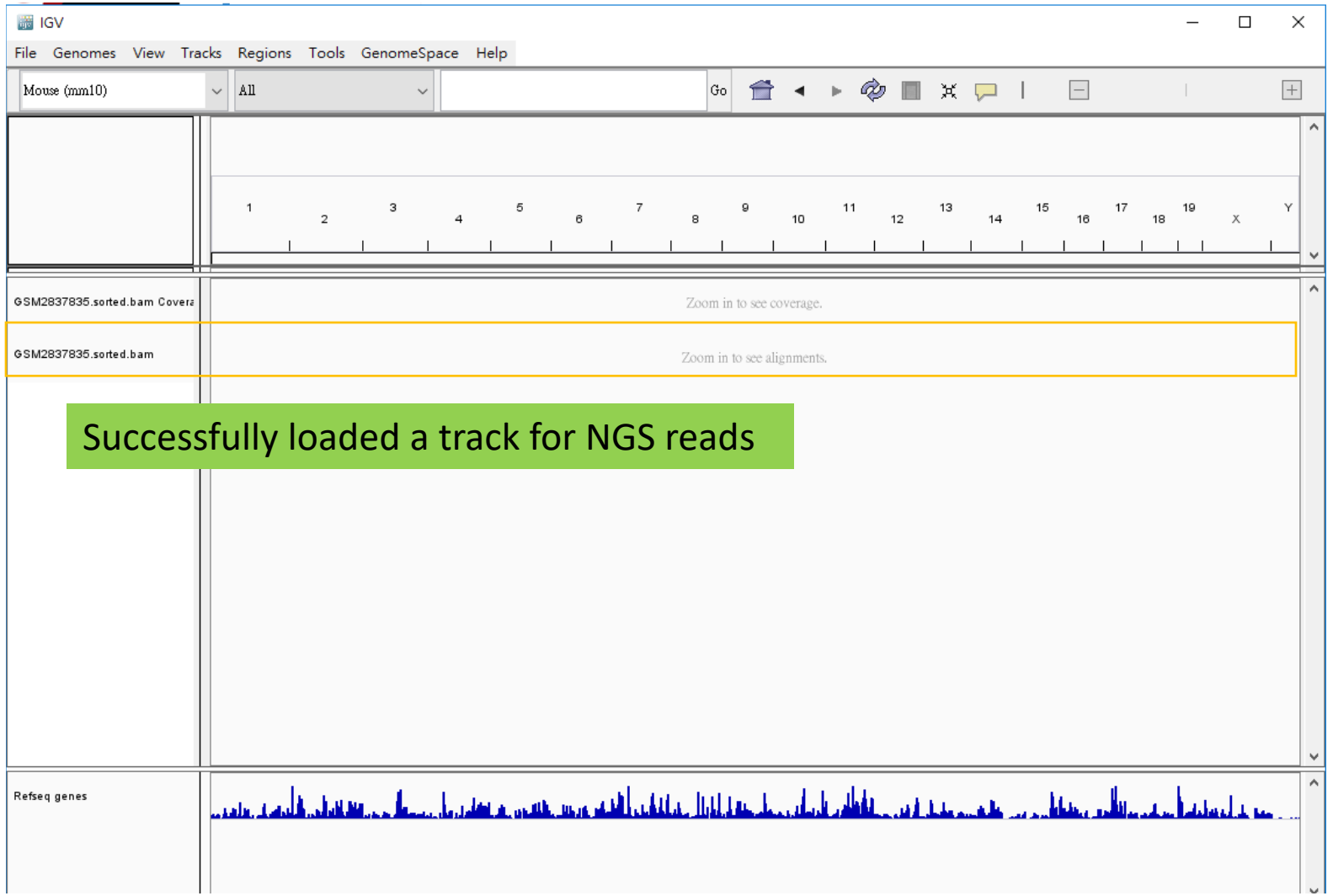
1



2



3

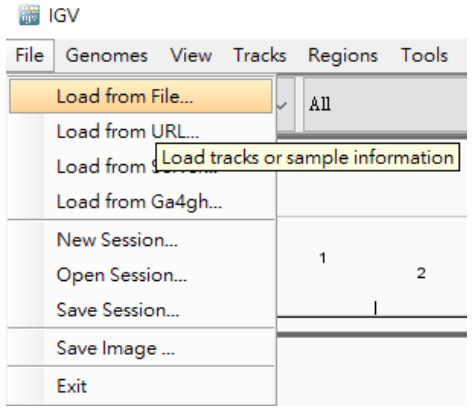


Successfully loaded a track for NGS reads

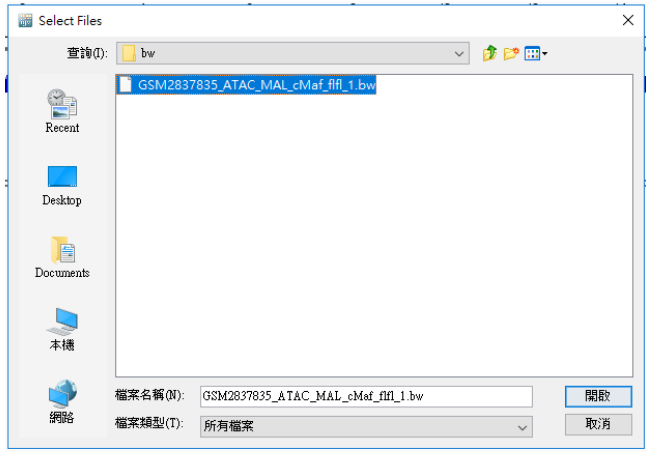
Step2: Load data from Files

- ChIP-/ATAC-seq data

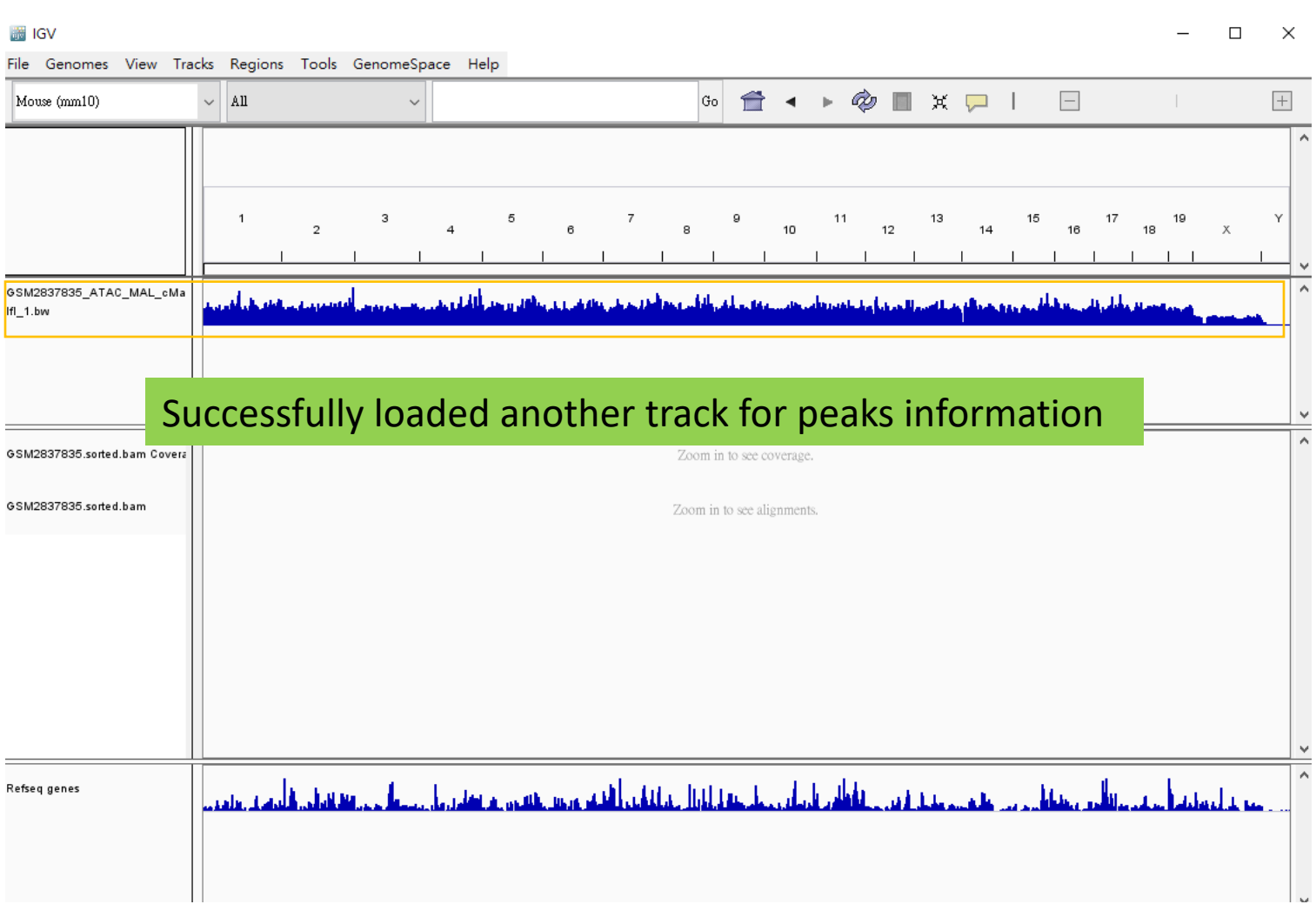
1



2



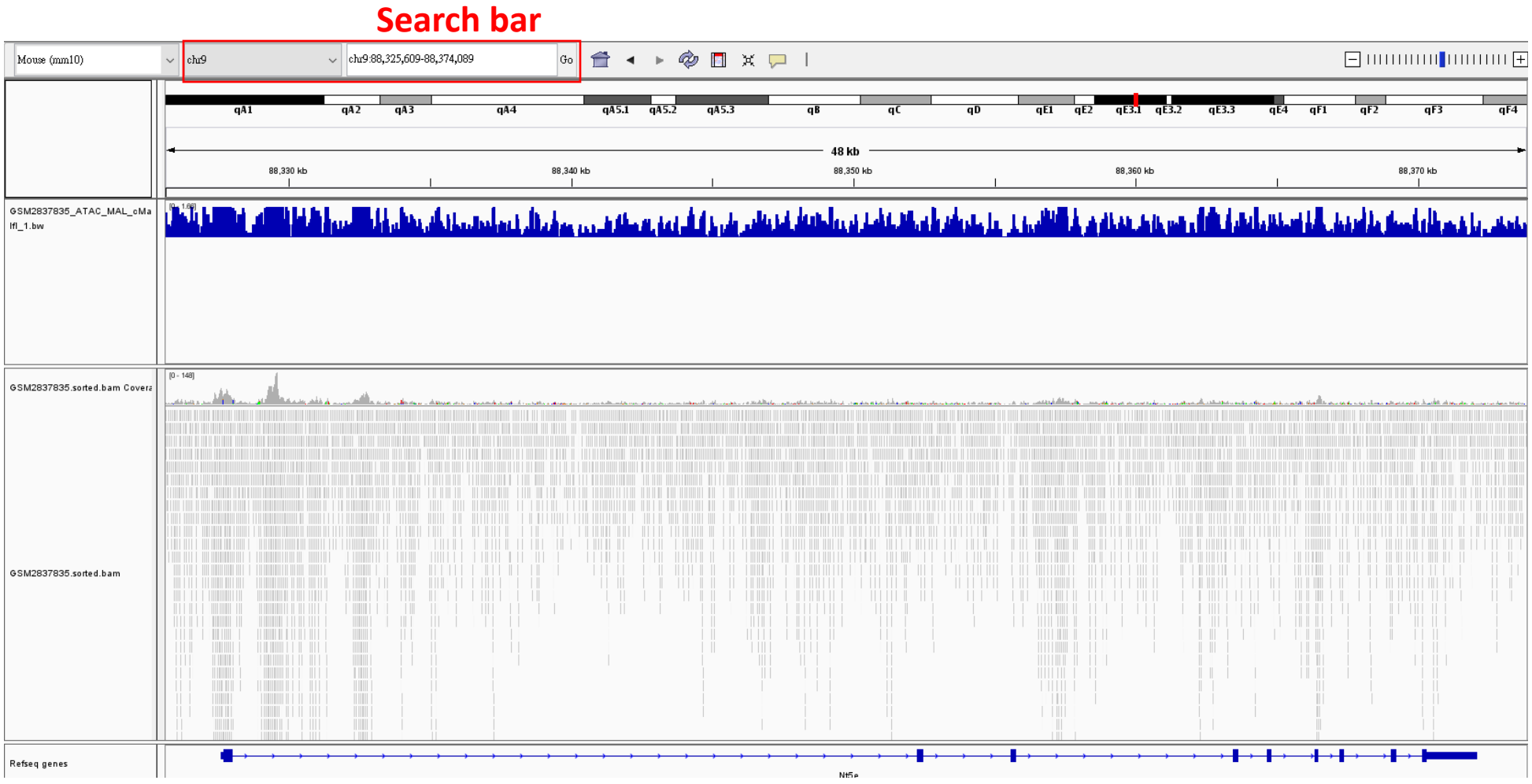
3



Successfully loaded another track for peaks information

Step3: Navigate to specific locus or gene on any chromosome

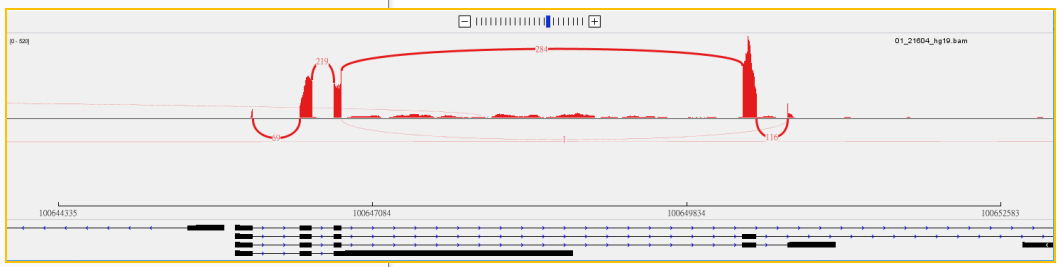
> i.e. chr9:88,325,609-88,374,089 or Nt5e



Step4: Junctions and isoforms

- *Sashimi plot*

Take NM_021029 as an example

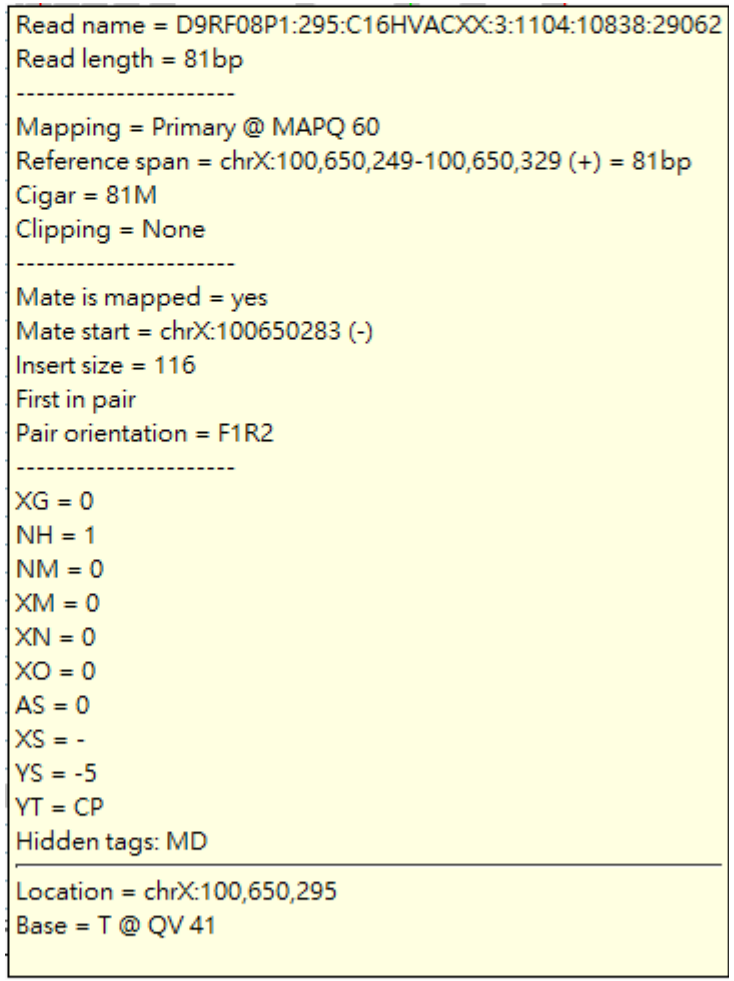


Before loading data

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

Some useful options
- show details on click

- **Reads Information**



- **Coverage Information**