IGV Quick Start

1 Install java

Download and install java: https://java.com/download

2 Install IGV

2.1 Brief registration is required:

http://www.broadinstitute.org/software/igv/?q=registration

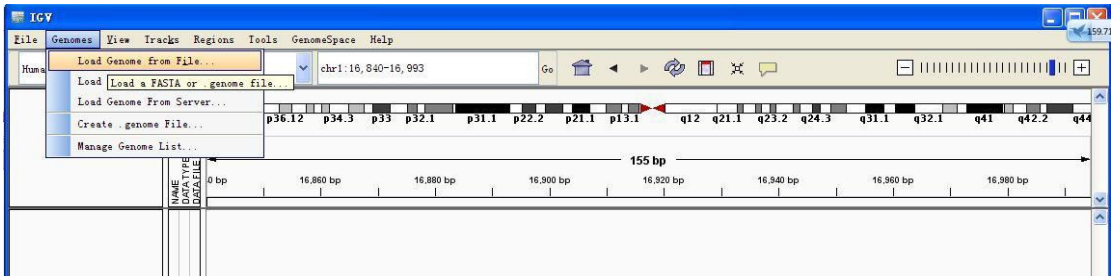
2.2 Download and install:

http://www.broadinstitute.org/software/igv/download

3 Starting IGV

3.1 Loading a Genome:

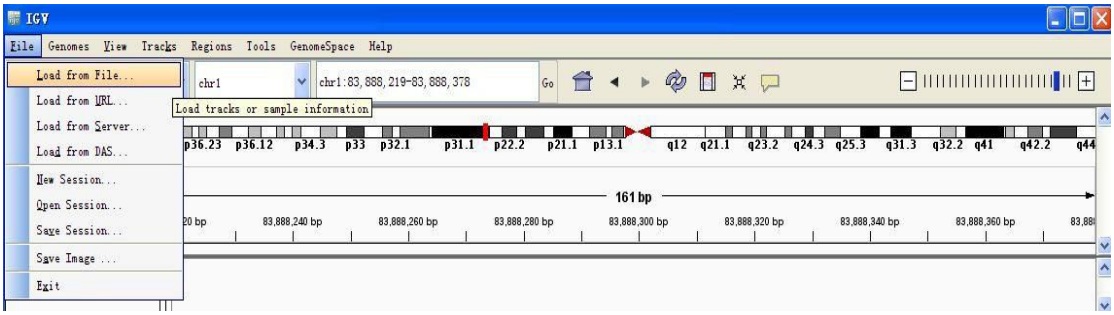
Genomes → load genomes from file → select your target organism genome in fasta format.



3.2 Loading annotation file:

File→ load from File →select annotation file in gtf(gff/bed) format.

An annotation file, which IGV uses to display the reference gene track. The file can be in BED format, GTF format, GFF format, or any variation of the genePred table format.



3.3 Visualize sequence read alignment data (BAM or SAM) on IGV

File→ load from File →select alignment file in *.sort.bam format.

4 User Interface

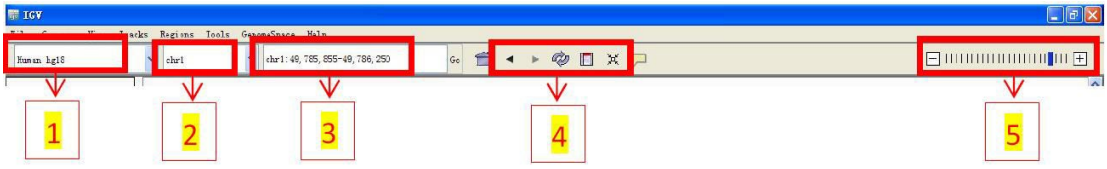
4.1 Menu Bar:

View→Choose 1,2.

1) Show name Panel: Shows the track name panel (like exm.gtf).

2) Show Header Panel: Shows the chromosome location header panel (like the chromosome ideogram or location).

4.2 Tool Bar:



1) Genome drop-down box: Loads a genome.

2) Chromosome drop-down box: Zooms to a chromosome.

3) Search box: Displays the chromosome location being shown. To scroll to a different location, enter the gene name, locus, or track name and click Go.

4) Genome view:

Zooms to whole genome view;

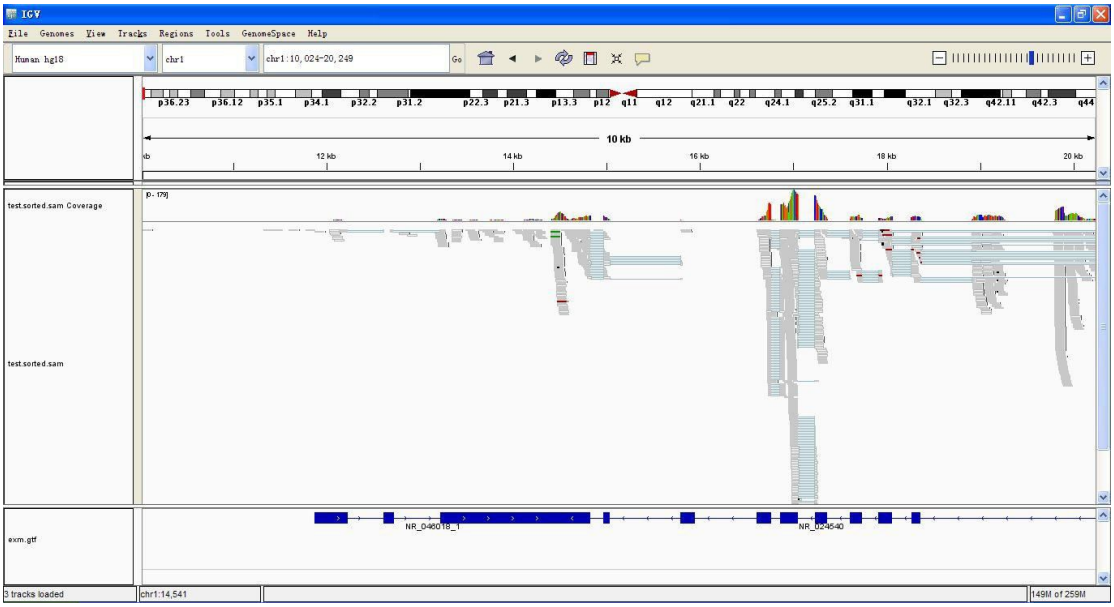
Moves backward and forward through views of the genome like the back and forward buttons in a web browser;

Refreshes the display;

Defines a region of interest on the chromosome;

Reduces the row height on all tracks to fit all data for the region in view into the window; will also expand tracks (to their maximum preferred size) to fill the view, if needed.

5) Zoom slider: Zooms in and out on a chromosome. Sometimes referred to as the "railroad track."



5 Viewing Alignments

Loading a BAM file creates up to 3 associated tracks:

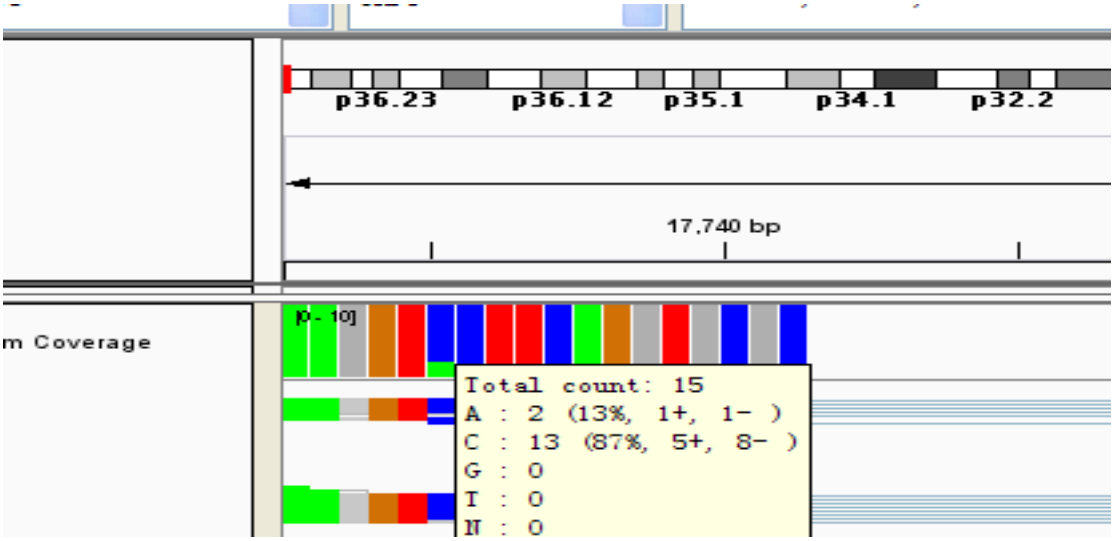
Alignment track to view individual aligned reads;

Coverage track to view depth of coverage;

Annotation track to view the gene that these reads lie on.

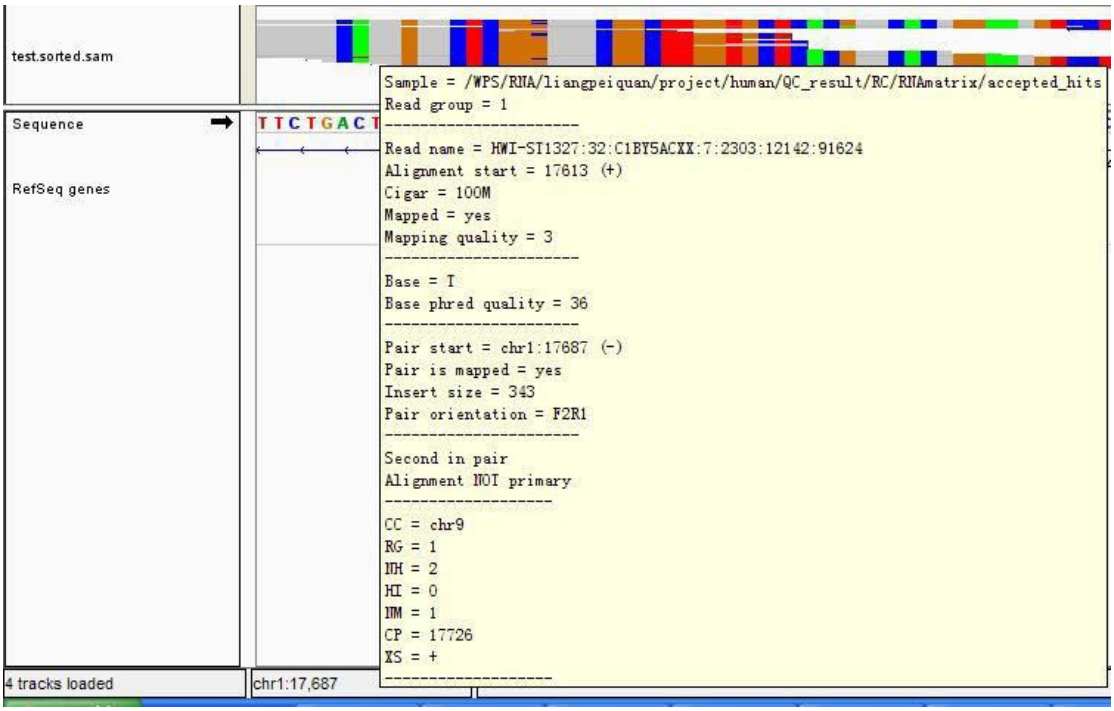
5.1 Coverage track

The coverage track displays the depth of the reads displayed at each locus as a gray bar chart. If a nucleotide differs from the reference sequence in greater than 20% of quality weighted reads, IGV colors the bar in proportion to the read count of each base (green= A; blue= C; brown= G; red=T). View count details by hovering the mouse over a coverage bar.



5.2 Alignment track

In the alignments, each sequence read is shown as a very thin gray line, stacked densely on top of one another. In many regions of the alignment where coverage is very deep, IGV displays only a subset of reads for enhanced visibility. IGV shows positions in each sequence read that do not match the consensus sequence as small colored tick marks, color coded (green=A; blue=C; brown=G; red=T; black=deletion; purple=insertion).



5.3 Annotation track

In the annotation track on IGV, Genes are represented as blue lines and boxes. Lines represent intronic regions, and boxes represent exonic regions. The arrows indicate the direction/strand of transcription for the gene.