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Example #5.

Browsing Genomic Position files.

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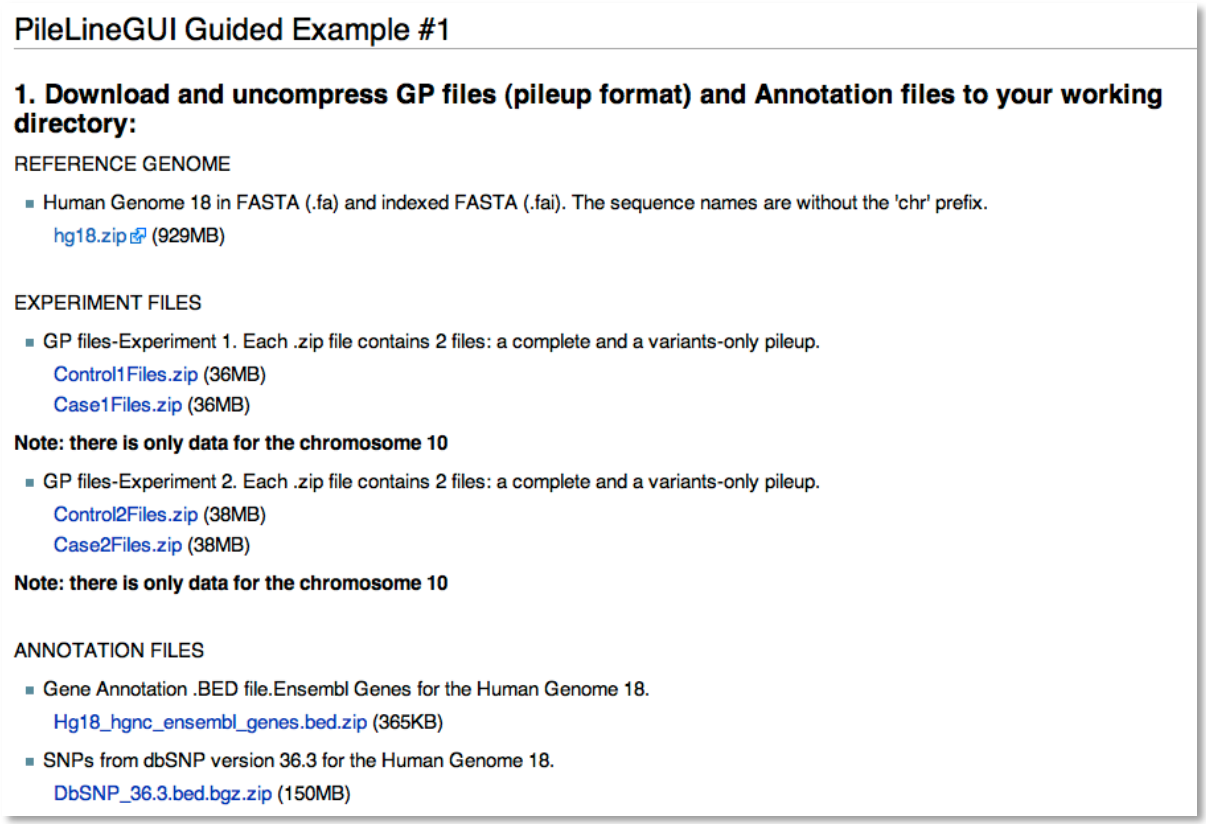
Step 1.

Download and uncompress the Genomic Position example files :



PileLineGUI Guided Example #1

1. Download and uncompress GP files (pileup format) and Annotation files to your working directory:

REFERENCE GENOME

- Human Genome 18 in FASTA (.fa) and indexed FASTA (.fai). The sequence names are without the 'chr' prefix.
  hg18.zip (929MB)

EXPERIMENT FILES

- GP files-Experiment 1. Each .zip file contains 2 files: a complete and a variants-only pileup.
  Control1Files.zip (36MB)
  Case1Files.zip (36MB)

Note: there is only data for the chromosome 10

- GP files-Experiment 2. Each .zip file contains 2 files: a complete and a variants-only pileup.
  Control2Files.zip (38MB)
  Case2Files.zip (38MB)

Note: there is only data for the chromosome 10

ANNOTATION FILES

- Gene Annotation .BED file.Ensembl Genes for the Human Genome 18.
  Hg18_hgnc_ensembl_genes.bed.zip (365KB)
- SNPs from dbSNP version 36.3 for the Human Genome 18.
  DbSNP_36.3.bed.bgz.zip (150MB)

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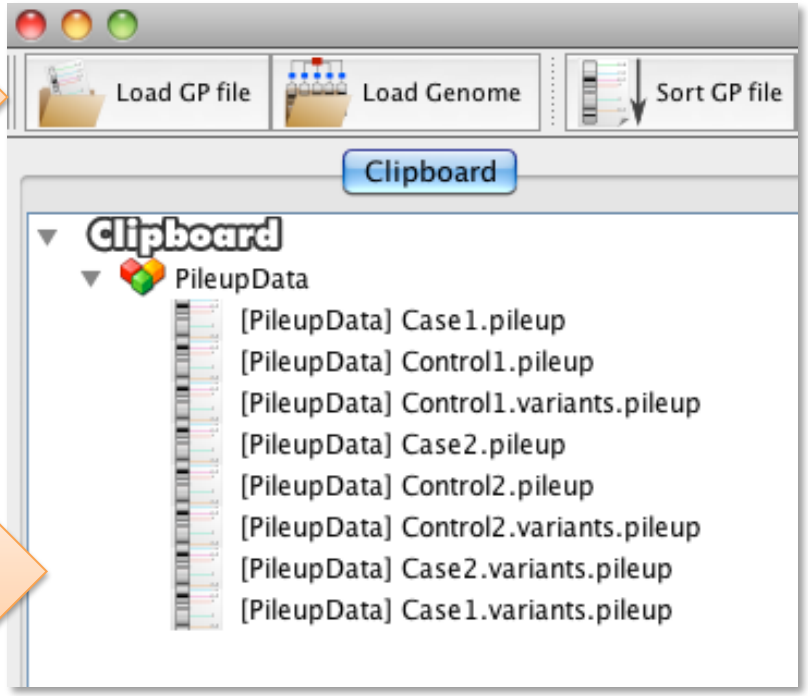
Step 2.

Load uncompressed Genomic Position files:

Case1.pileup
Case1.variants.pileup
Control1.pileup
Control1.variants.pileup

Click on 'Load GP' button



Find the loaded files in the clipboard

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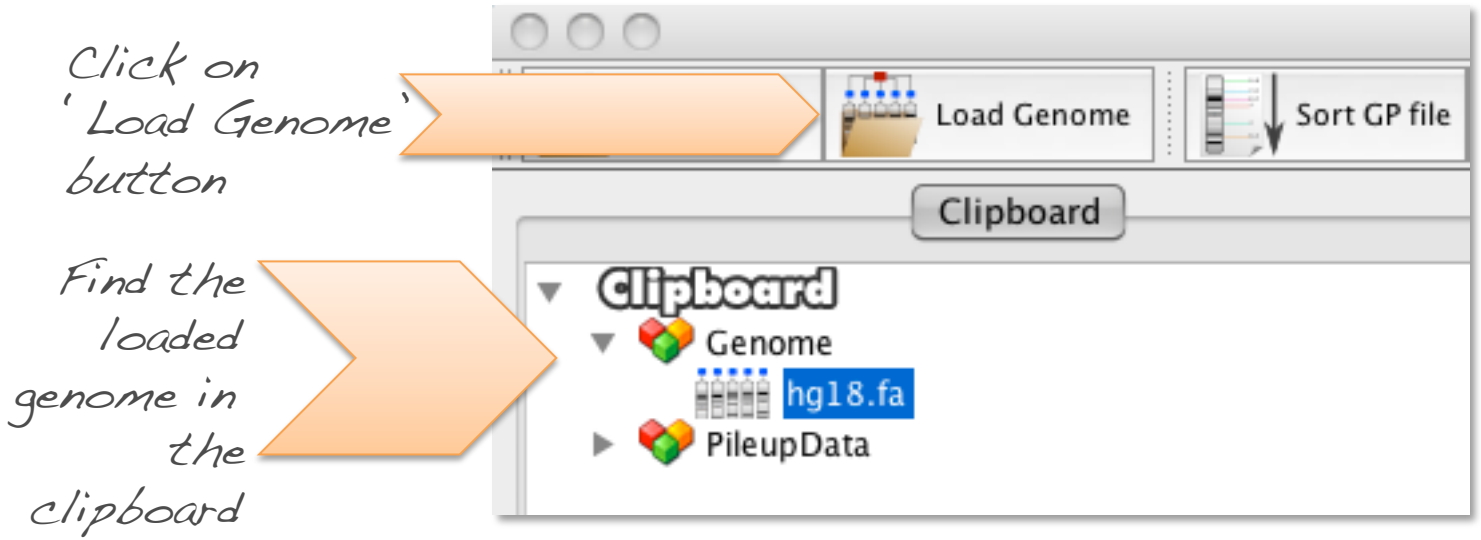
Step 3.

Load uncompressed Reference Genome FASTA file.

Note: Require .fai index



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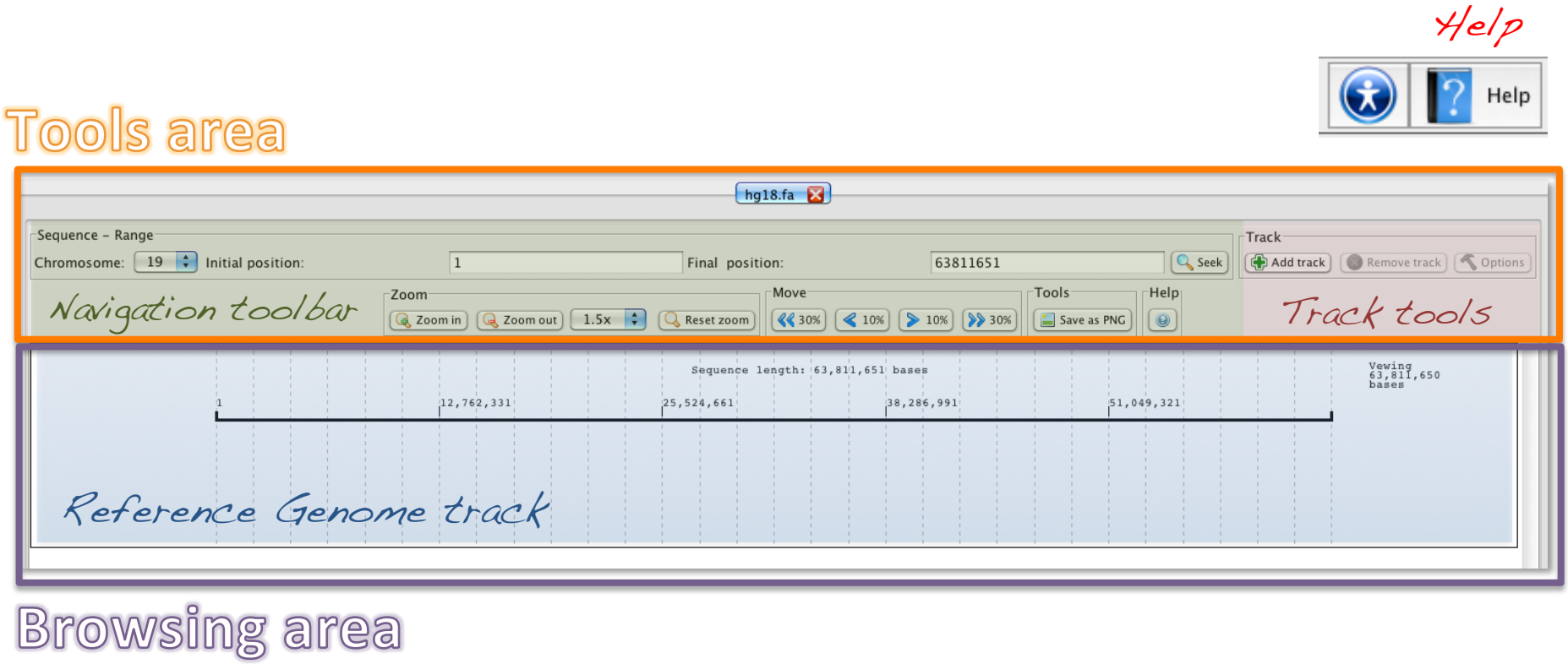
Step 4.

Summary of the the Browser interface .



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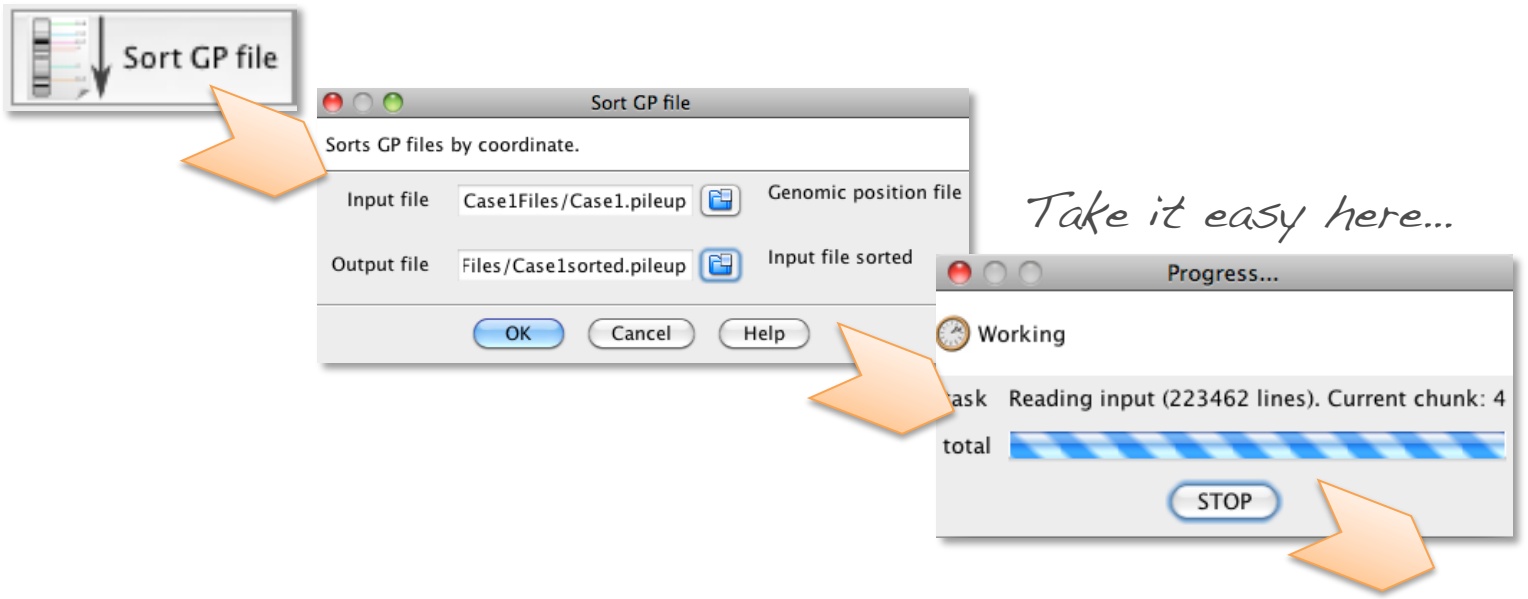
Step 5.

Adding new tracks I

IMPORTANT:
GP files MUST be sorted. Use ‘Sort GP file’ button to sort your Case1.pileup file.



Case1sorted.pileup file.

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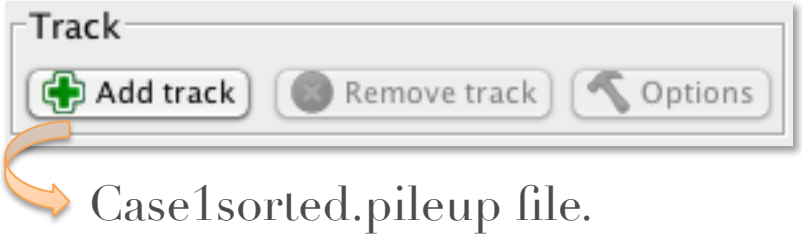
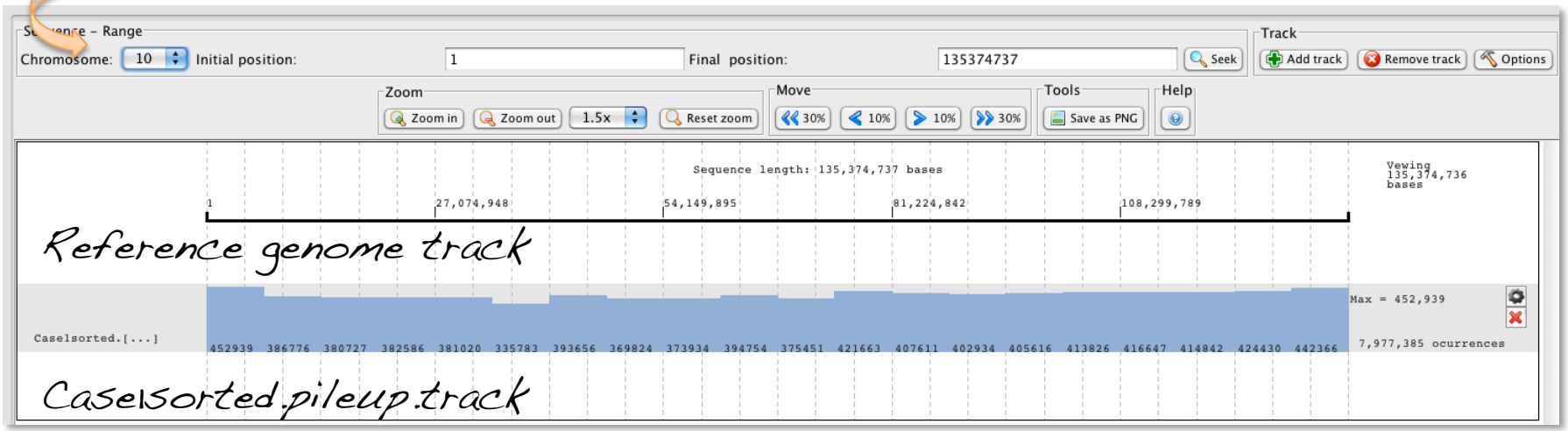
Step 6.

Adding new tracks II



Case1sorted.pileup file.



Reminder:
Example files only includes values for chromosome 10.

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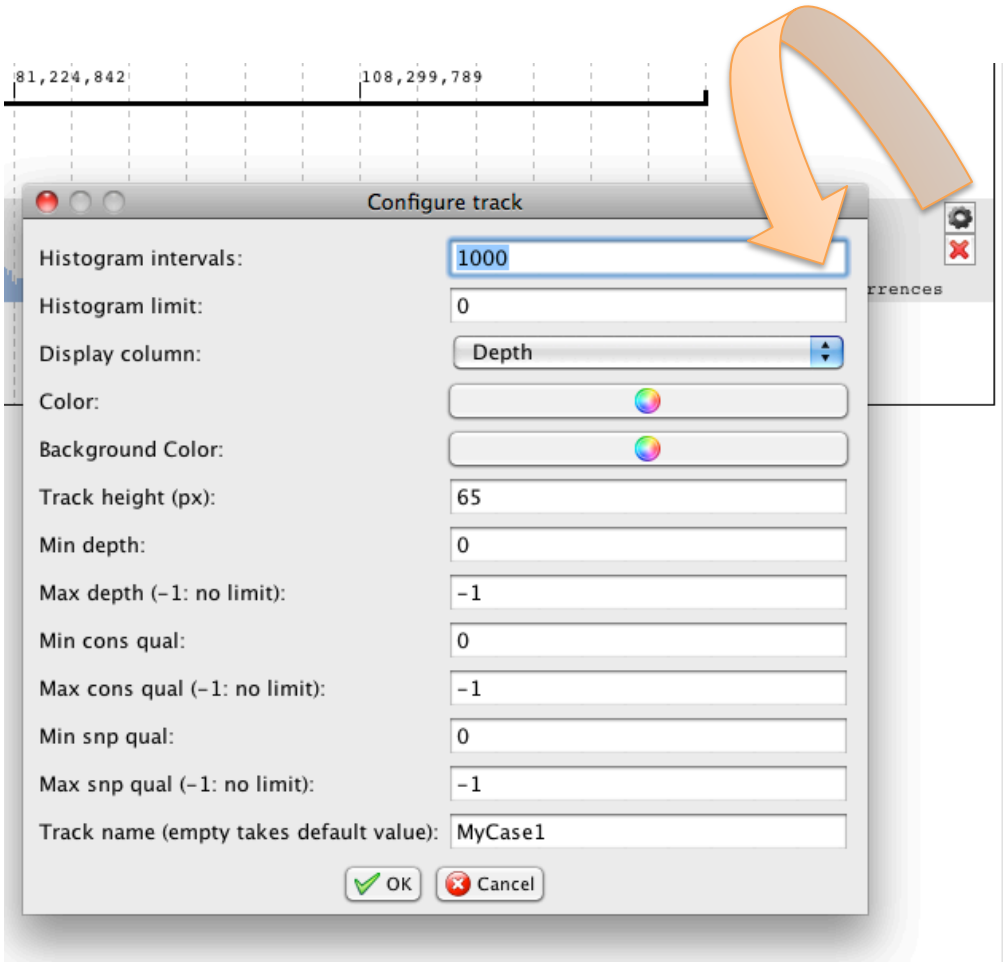
Step 7.

Configuring tracks



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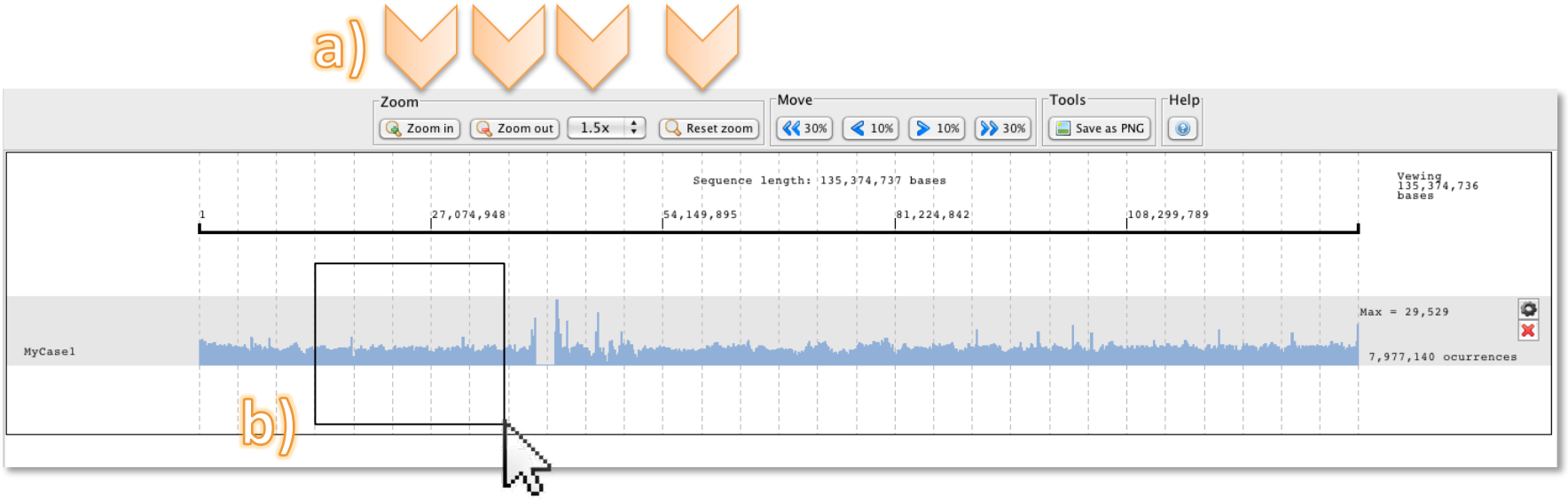
Step 8.

Zoom

Two ways to make zoom:
a) Use zoom buttons or b) roll over desired genomic region directly.



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For further info see PileLineGUI Documentation at:

http://sing.ei.uvigo.es/pileline/pilelineguihelp/