Practical: the UCSC Genome Browser

To interactively visualize genomic data.

The advantages of using UCSC Genome browser are:

- available from any computer, without having to install it

- you can compare your data with a lot of other annotations without having to download them

- all the tracks are always up-to-date

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We want to visualize the novel genes/transcripts (u) as a track into the Genome Browser

1. Prepare the Input file:

```
cd ~/tutorial/cufflinks_noref/2cells/

cut -f 5 novel_genes > novel_genes_codes.txt
(to extract only the transcript codes, the 5th field, from the novel_genes file)

grep -f novel_genes_codes.txt transcripts.gtf  > novel_genes.transcript.gtf
(to select only the novel transcripts among all the assembled transcripts; check the -f option of the grep command)

awk -FSO="\t" '{$1="chr"$1; print $_}' novel_genes.transcript.gtf > novel_genes.transcript.chr.gtf
(to add the characthers “chr” to the chromosome name, to be compatible with the reference genome format in the
UCSC Genome Browser)
```

The Input file is ready to be uploaded: novel_genes.transcript.chr.gtf
(it is a GTF file)

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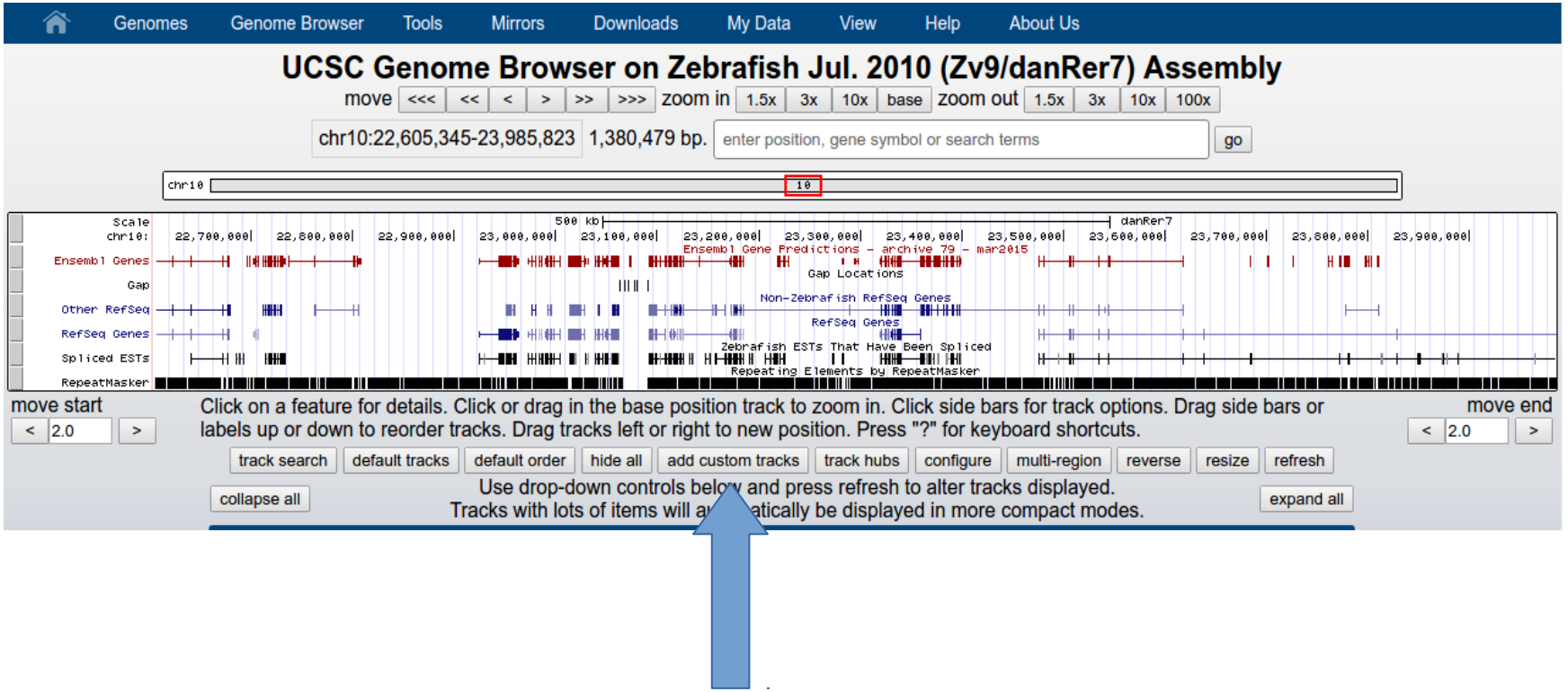
2. Open the UCSC genome browser https://genome.ucsc.edu/
3. Select: Genome Browser from the Tool list (on the right)
4. Select organism e genome assembly:
   Danio rerio
   Jul.2010 (Zv9/danrer7) (it is not the latest release)
   → GO
5. Click on the botton: "add custom tracks"



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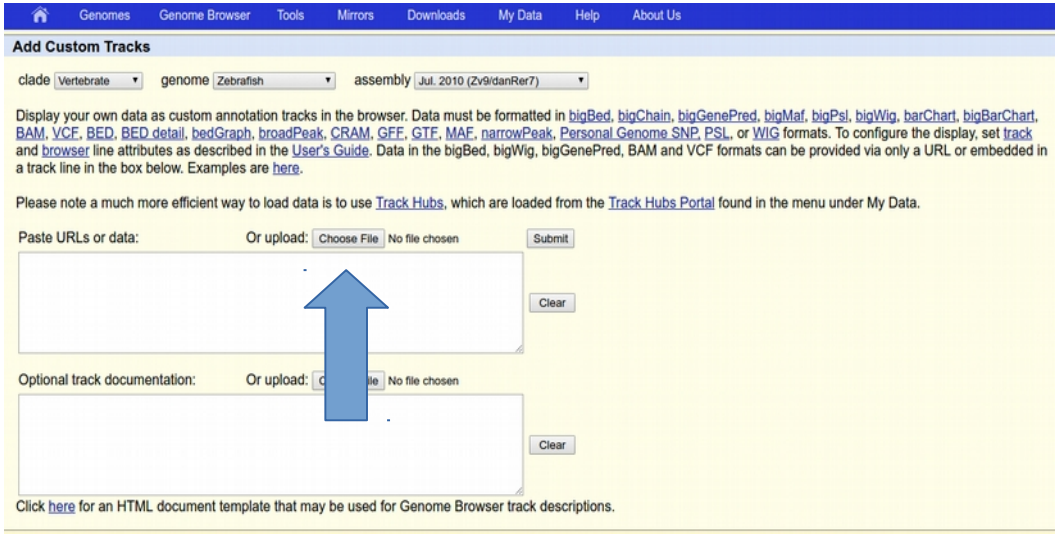
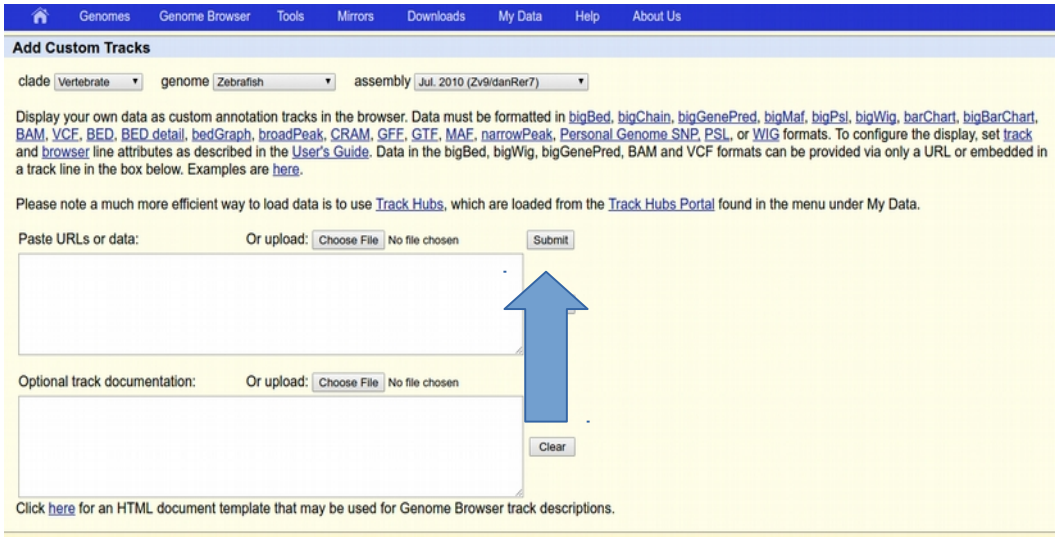
6. Click on Choose File and Upload your Input file, then click on Submit





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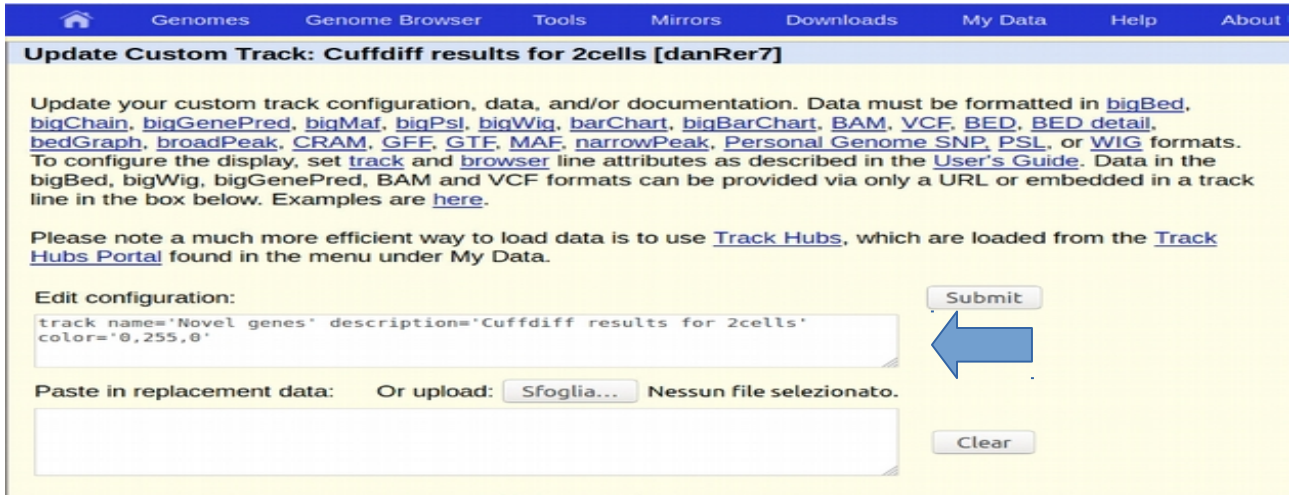
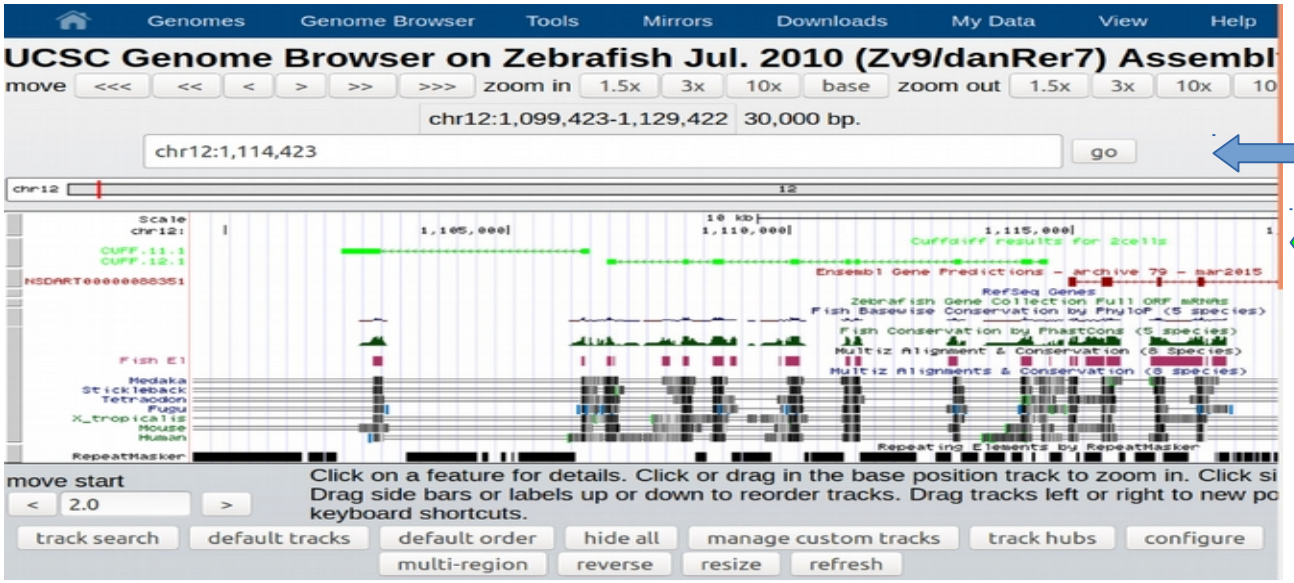
7. Click on the Name of the Track and you can insert: Name, description, color, ...



8. your Results (in light green):



enter chr12:1,114,423
to visualize this locus