

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)

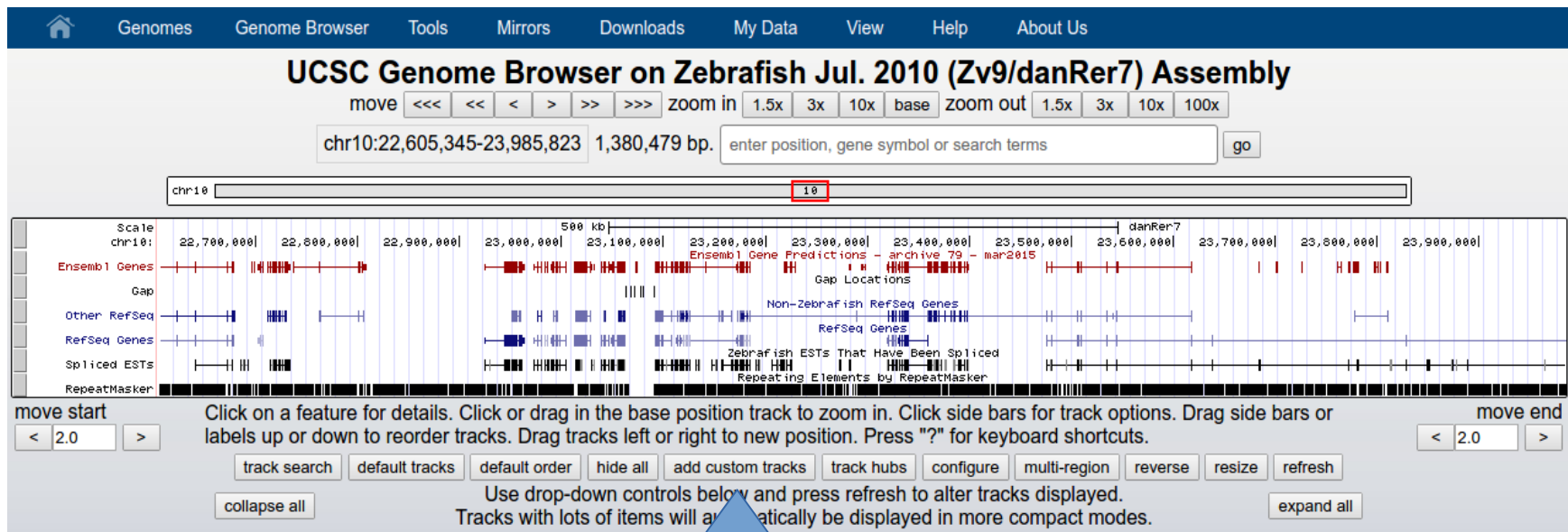
```
awk -FSO="\t" '{ $1="chr"$1; print $ _ }' novel_genes.transcript.gtf > novel_genes.transcript.chr.gtf
```

(to add the characters “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 button: "add custom tracks"



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



The screenshot shows the 'Add Custom Tracks' page of the UCSC Genome Browser. At the top is a navigation bar with links: Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. Below the navigation bar, there are dropdown menus for 'clade' (set to Vertebrate), 'genome' (set to Zebrafish), and 'assembly' (set to Jul. 2010 (Zv9/danRer7)). A paragraph of text explains that users can display their own data as custom annotation tracks, listing various data formats like bigBed, bigChain, bigGenePred, bigMaf, bigPsl, bigWig, barChart, bigBarChart, BAM, VCF, BED, BED detail, bedGraph, broadPeak, CRAM, GFF, GTF, MAF, narrowPeak, Personal Genome SNP, PSL, or WIG. It also mentions that data can be provided via a URL or embedded in a track line. Below this text, there are two input sections. The first section is labeled 'Paste URLs or data:' and has a 'Submit' button. The second section is labeled 'Optional track documentation:' and has a 'Clear' button. A blue arrow points to the 'Choose File' button in the 'Or upload:' section of the first input section.

clade Vertebrate genome Zebrafish assembly Jul. 2010 (Zv9/danRer7)

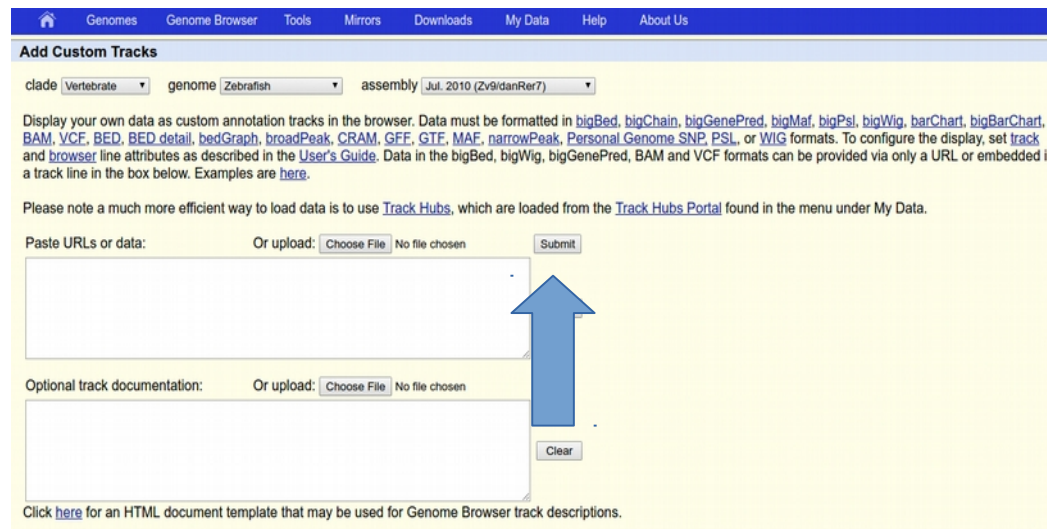
Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigChain](#), [bigGenePred](#), [bigMaf](#), [bigPsl](#), [bigWig](#), [barChart](#), [bigBarChart](#), [BAM](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [CRAM](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

Please note a much more efficient way to load data is to use [Track Hubs](#), which are loaded from the [Track Hubs Portal](#) found in the menu under My Data.

Paste URLs or data: Or upload: Choose File No file chosen Submit

Optional track documentation: Or upload: Choose File No file chosen Clear

Click [here](#) for an HTML document template that may be used for Genome Browser track descriptions.



This screenshot is identical to the one above, showing the 'Add Custom Tracks' page. However, a blue arrow points to the 'Submit' button in the 'Paste URLs or data:' section.

clade Vertebrate genome Zebrafish assembly Jul. 2010 (Zv9/danRer7)

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigChain](#), [bigGenePred](#), [bigMaf](#), [bigPsl](#), [bigWig](#), [barChart](#), [bigBarChart](#), [BAM](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [CRAM](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

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Paste URLs or data: Or upload: Choose File No file chosen Submit

Optional track documentation: Or upload: Choose File No file chosen Clear

Click [here](#) for an HTML document template that may be used for Genome Browser track descriptions.

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



The screenshot shows the 'Update Custom Track' configuration page for 'Cuffdiff results for 2cells [danRer7]'. It includes instructions on data formats (bigBed, bigChain, etc.) and a configuration box. A blue arrow points to the 'Submit' button.

Update your custom track configuration, data, and/or documentation. Data must be formatted in [bigBed](#), [bigChain](#), [bigGenePred](#), [bigMaf](#), [bigPsl](#), [bigWig](#), [barChart](#), [bigBarChart](#), [BAM](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [CRAM](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

Please note a much more efficient way to load data is to use [Track Hubs](#), which are loaded from the [Track Hubs Portal](#) found in the menu under My Data.

Edit configuration:

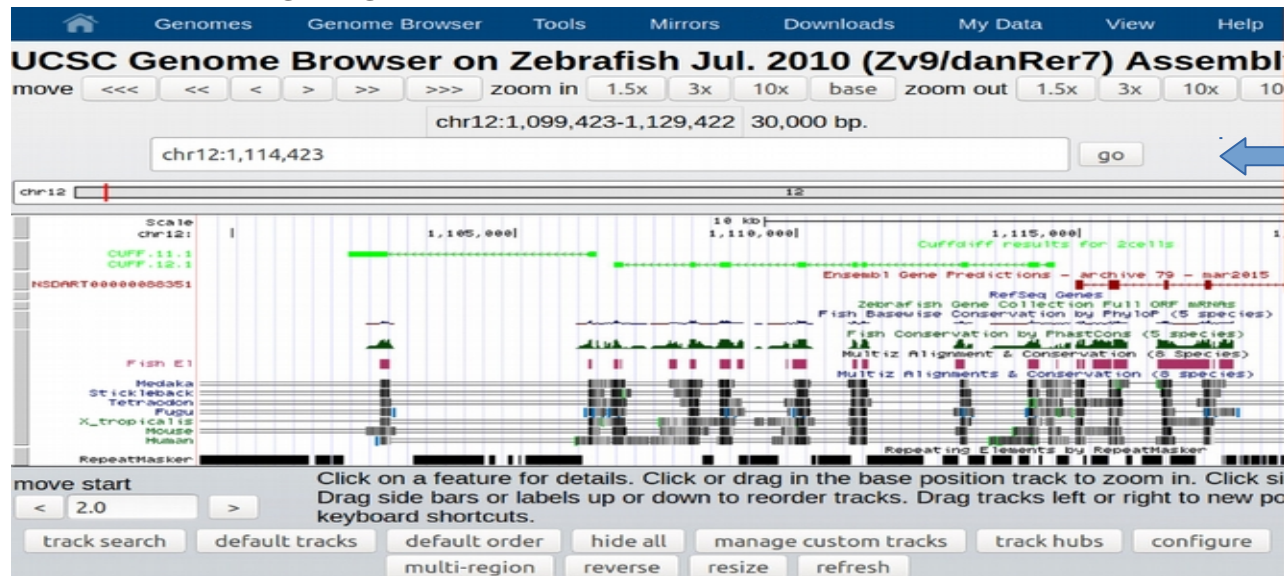
```
track name='Novel genes' description='Cuffdiff results for 2cells'
color='0,255,0'
```

Submit

Paste in replacement data: Or upload: [Sfoglia...](#) Nessun file selezionato.

Clear

8. your Results (in light green):



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