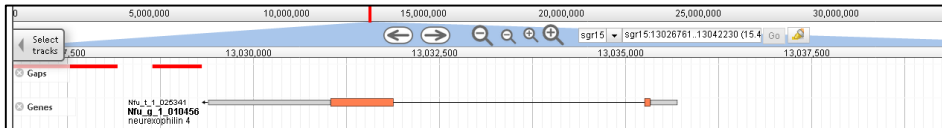


How to retrieve a sequence region of choice from the *N. furzeri* Genome Browser at nfingb.leibniz-fli.de

Example

Get the promoter region of a particular gene. Here we are interested in 2.5kb upstream of the gene Nfu_g_1_010456:

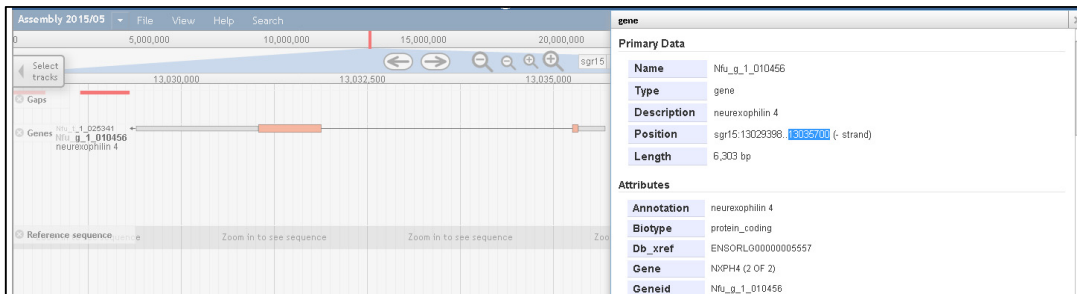


Step 1

Click on “Select Tracks” and activate the track “Reference sequence”

Step 2

Click on the gene and look for the starting coordinate:



Because this gene is on the minus strand, we start with the “right most” coordinate and add 2.5kb to 13,035,700 which is 13,038,200. Close the gene details window.

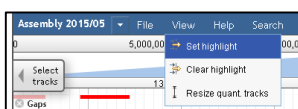
Construct this coordinates string from the numbers above and additionally add 1bp to both numbers. It will finally look like this:

```
sgr15:13035701..13038201
```

For a gene on the plus strand starting at position 12,345,678 you would define the coordinates string of a 2.5kb region like this: `sgr:12343177..12345677`

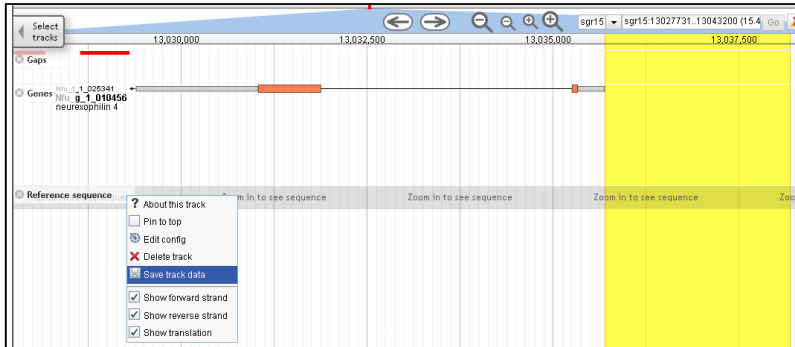
Step 3

Click on “View” and “Set highlight” and enter the coordinates string inside the appearing window. The 2.5kb are now highlighted.



Step 4

Click on the drop-down menu of the Reference sequence track name and hit “Save track data”.



Step 5

Select the “highlighted region” as “Region to save”. You can now directly view the sequence or store it in fasta format.

