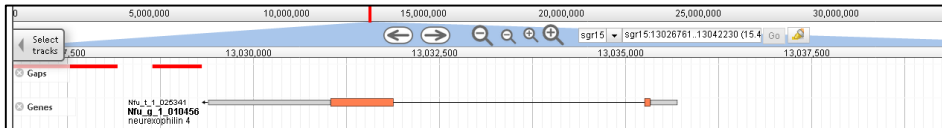# How to retrieve a sequence region of choice from the *N. furzeri* Genome Browser at nfingb.leibniz-fli.de

Example

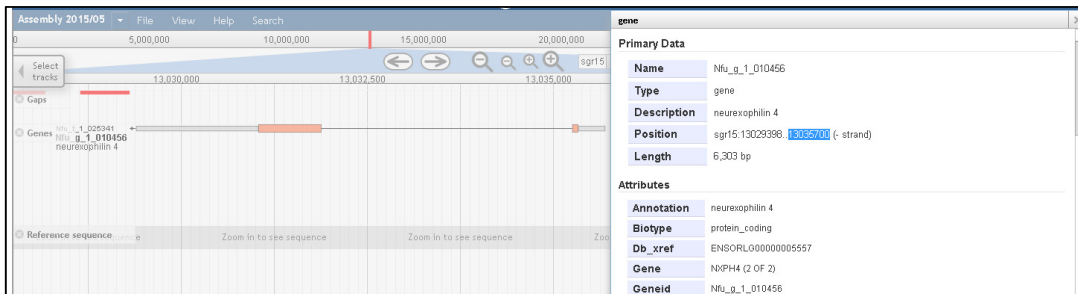Get the promoter region of a particular gene. Here we are interested in 2.5kb upstream of the gene Nfu_g_1_010456:

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`
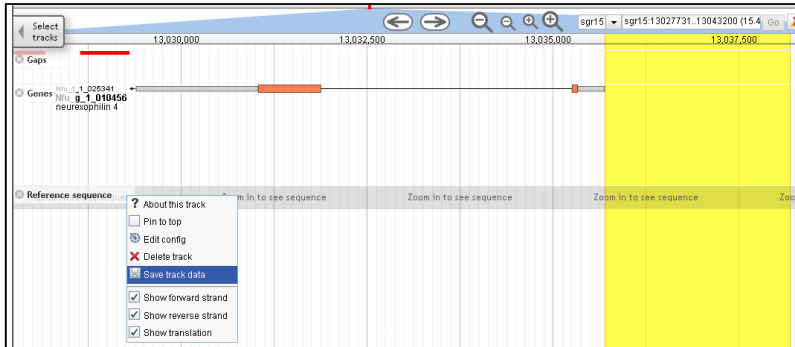
Step 3

Click on "View" and "Set highlight" and enter the coordinates string inside the appearing window. The 2.5kb are now highlighted.
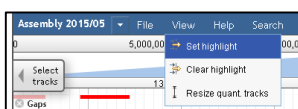
Step 4

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.