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

Example

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

0	5,000,000	10,000,000	15,000,000	20,000,	.000 25,000	000 30,000,000	
Select			$ \bigcirc $	Q Q Q Q	sgr15 👻 sgr15:1302676113	1042230 (15.4 Go 🍛	
tracks 7,500		13,030,000	13,032,500		13,035,000	13,037,500	
🖾 Gaps							
Genes	Nfu_t_1_026341 ← Nfu_g_1_010456 neurevonbilin 4						

Step 1

Click on "Select Tracks" and activate the track "Reference sequence"

Step 2

Click on the gene and look for the starting coordinate:

Assembly 2015/05 - File View Help Search		gene		×	
0 5,000,000 10,000,000	15,000,000 20,000,	000	Primary Data		^
Select 12.020.000		Q Q ⊕ ⊕ sgr15 13,035,000	Name	Nfu_g_1_010456	
13,030,000 13	13,033,000		Туре	gene	=
- odby			Description	neurexophilin 4	
© Genes Nru t_1_025341 ←			Position	sgr15:13029398 <mark>13035700</mark> (- strand)	
neurexophilin 4			Length	6,303 bp	
			Attributes		
			Annotation	neurexophilin 4	
Reference sequence Zoom in to real requence	Zoom in to see requence		Biotype	protein_coding	
			Db_xref	ENSORLG0000005557	
			Gene	NXPH4 (2 OF 2)	
			Geneid	Nfu_g_1_010456	

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.

