UCSC Genome Browser Basics. Part Three: Configuration + DNA Navigation

Welcome to Part Three of the Basic Browser video series. In Part One of the series, we focused on the use of accession names – the many ways that identifiers of various kinds can be used to locate genomic locations and annotations. We also saw a few configuration options for setting up the Browser.

In Part Two, we featured more ways to set up the Browser to your liking, as well as several options for exporting images to use in posters, papers and presentations.

In this installment, we will continue the conversation about configuring the Browser and show how to use DNA sequence as a device for finding a location.

At the end of Part One, we found ourselves on chromosome 11, with several datasets turned on. That's a convenient location to begin this installment as well. To make it easy to find that location again, we saved the configuration for easy access.

[0:55] Load Saved Session

The Saved Sessions feature is the subject of a separate tutorial in the UCSC Browser video collection, so it will not be repeated here.

The session was saved under the username, videoDemo1, and the session name, hg19_nav1. The session can be accessed directly in any browser using this url:

https://genome.ucsc.edu/s/videoDemo1/hg19_nav1

This returns us to the same location with all the configuration options intact. Note that the following tracks are turned on: Alternate Haplotypes (but there are no data for this track at this location in the Browser), Chromosome Bands, UCSC Genes and OMIM Genes and we are at a 5.5 megabase region of chromosome 11.

[1:55] Get DNA sequence from an mRNA

A good way to get around in the Browser is to use DNA sequences. So let's get some DNA from a gene to use as starting material. Let's click into the details page of SLC6A5 and find out what it is. Turns out it's "Homo sapiens solute carrier family six (neurotransmitter transporter, glycine)." A lot of other details are provided here as well. But for the moment, let's just get some DNA sequence. We'll scroll down the page just a little bit and we'll get the mRNA

sequence and then grab a chunk of mRNA right out of the middle of it. I will copy that.

[2:37] Paste DNA into the Position Box

Then we'll go back to the Browser and just paste the DNA into the Position Box. If that DNA is unique, or *not*, BLAT will show us a page of matches where we can go to that location on the Browser. So here we are on a page with a single match. And if we hit the "browser" link there, then we'll go to a 52-nucleotide location.

[3:02] Run BLAT with mismatches

BLAT is tolerant of some mismatches. So if I paste this 52 nucleotides back in and just remove a couple of G's here and maybe insert a couple of C's right here and hit [go], BLAT will still find it, but now it finds several smaller hits for the segments that are uninterrupted on other chromosomes as well. But the biggest hit, the one with the highest score that spans the full 52, is still on chromosome 11. And if I go to the Browser using that link, here's our two-base deletion. And here's our insertion over here where I added a couple of bases, shown as a little tickmark between the bases where it was inserted.

[3:51] Short Match track

BLAT will work well when you have a nucleotide probe to put in the box of 22 bases or more. And it works a little bit as you get smaller down to around 16, but below that it doesn't work at all. In that case, there's a feature of the Browser that will let you find strings of nucleotides in the current Browser window. It won't find them all over the genome, but if you go into the mapping and sequencing blue bar group the below the Browser graphic, there is a track called Short Match. If you click into Short Match, it tells you that you can use anything between 2 and 30 nucleotides. And let's just put it in GCG. You'll see also that the IUPAC ambiguity codes are supported, so R is for puRine (G or A), Y is for pYrimidine (C or T), and so forth. So if we just hit [submit] and we'll find any occurrences of GCG and it'll also find it such occurrences on the opposite strand. So a CGC here on the minus strand is also a match. It'll find all stretches of that particular nucleotide string in the current Browser window. It is not possible, however, to export a list of all of the occurrences of this string via the Table Browser as it is for other tracks.

[5:15] Drag-N-Highlight

Another useful feature of the Browser is Drag-N-Zoom or Drag-N-Highlight, depending on which choice you make in the menu that appears. If you put your mouse up in the scale bar near the top of the Browser graphic and drag it to the

right or left it will highlight a region. Let's highlight the region around this two-base deletion in the BLAT track that we made. We'll put a single highlight here. And let's zoom out by a factor of 3.

[5:48] Set highlight color

Let's select a region next to it and highlight and change the color. Let's make the color much darker and add a second highlight.

So you have two highlights side by side and you can see how the colors stand up when you zoom out. If you zoom out by a factor of 10 or more, the lighter color starts to get more difficult to see as you get farther and farther out. So it's a good idea to use a darker color if you're going to zoom out.

[6:21] Remove highlight

You can put your right mouse button over the highlight and you have the option to remove a particular highlight by using the option in that popup.

[6:34] Drag-rearrange tracks

Another feature of the Browser that can help when you're configuring it to your liking is your ability to drag tracks up and down and rearrange them on the screen. Ordinarily, the tracks appear in the same order that the options appear among the pulldown menus below the Browser graphic, but you are not constrained to using that ordering on the screen. If you put your mouse over the text space on the left side of the Browser graphic for any track, you can drag tracks up and down and put them in any order that you choose.

[7:05] Drag-N-Zoom

Another option that you get when you put your mouse over the region in the scale bar near the top of the screen is to zoom in. You can zoom into any specific region that you select.

[7:21] Right-click menu: Zoom to an item

On any spot of the Browser, there is a context-sensitive right click menu. If you put your mouse over a specific item in the Browser graphic and use the right mouse button, you get a menu that lets you zoom to the full length of the item. In this case, we selected a gene. You can highlight the entire gene. You can get the DNA. You can click into the details page that we've been to before where it shows you all of the information about the gene itself.

And you can go to the configuration page where you can turn off the splice variants. This has the same effect as using the small button on the left side of the track in the image. So let's just zoom to the gene and observe the full-sized gene filling the entire window.

[8:11] Scale bar / Base Position configuration

Let's turn off some of the data tracks and leave just the gene set on. So we'll turn off the All Haplotypes track, the Cytobands track, the OMIM track, and the Short Match track. We'll also turn off the BLAT track. That leaves us with just our gene in the window. Let's zoom in to the exon right here in the middle of the screen by selecting it from the top of the window and we'll zoom in even a little further to get down to the amino acid level.

And let's look at configuring the scale bar at the top of the page. You can see that we have the scale bar in roughly the middle third of the page and the genome assembly is listed next to it in the Browser graphic, although it can be removed using the configuration button that we visited in Part Two of this Browser Basics series.

[9:07] Add title in graphic

Let's click into the scale bar configuration button on the left side and you can decorate the graphic just a little bit by putting in a title such as "this is my title" and then you can add an assembly and a position to the Browser graphic and [submit] that. So now you have a new row at the top where it says "this is my title" and the assembly and the position are listed here in another row of text.

[9:33] Display three reading frames

Let's go back to the configuration window, and we'll turn off the title, assembly and position and switch the display mode from "dense" to "full." You can see now that we have the amino acids of all three reading frames showing in the Browser below the DNA sequence, so you can see that one of the three reading frames is going to match the amino acid sequence of the exon we have in the window: YVVLV and YVVLV.

[10:11] Reverse-strand DNA sequence

If your gene was being transcribed on the opposite strand, you can reverse the orientation by clicking on the little arrow on the left. Of course, in this orientation, the translation does not match the reading frame of the gene we have in the window currently.

[10:27] View in other genomes by homology

Let's turn the DNA base sequence back to the plus strand and we'll go back into the position bar configuration and turn it from “full” back to “dense” and [submit] that and we'll look at one other way to navigate in the Genome Browser.

You see here we're at a 48-base window in the SLC6A5 gene. And one option is to use DNA sequence homology to jump to the same location in other genomes. So if you go to “View in other genomes… Convert” in the top bluebar menu, you see that the default is to go to another human genome. You can go to the hg38 assembly or back to hg18 or you can go to other animals. Human and mouse are the most widely used on the Browser, so they come up at the top. Let's just accept the default and go to the hg38 genome assembly and hit [submit].

For a small region, especially an exon, this is likely to be a really good single hit. If you’re zoomed out and have a much larger region or if you're going to an animal that's more distantly related than one human genome assembly to another, you're likely to have multiple hits on this window here, because of rearrangements in one lineage or the other since the last common ancestor. So let's just click into this link and you'll see that here we are, in the same region of SLC6A5 amino acids YVVLV is still in the window.

[12:00] Jump to previous settings in human, mouse

It's possible then to get back to hg19 two different ways. You can use the “View, In Other Genomes… Convert” using homology again. Or, if you have navigated to a different location, you have another option. Let’s go to a different location by dragging the window off to the left. For the last two human and the last two mouse genomes you have the option to return to your previous location on the other assembly.

Go over here to “Genomes” and choose the hg19 assembly. In this case, the Browser just remembers your last location. So it's not using homology, it's using memory and it's essentially setting up the Browser just the way it was the last time you were on that genome. So if I click on hg19, you see we're back at the 48-basepair window at the same region of SLC6A5 we were at before.

So that concludes our conversation about how to get around in the Browser, and how to configure the Browser to display the image the way you like it.

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http://genome.ucsc.edu/training/

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