How do I identify exon number with the UCSC Genome Browser

How do I identify exon numbers using the UCSC Genome Browser?

Let's visit the browser at genome.ucsc.edu.

We will start at this main page and in the upper left-hand corner we will find a couple of links that take us to a location where we can choose our genome of interest. We will click here to reset to set the browser to the default genome assembly which is the human hg19 assembly at the present time. The [submit] button takes us into the main browser viewer with a large number of data tracks turned on. The [hide all] button below the browser graphic allows us to turn all of these data tracks off and start with a clean page. We will turn on the UCSC Genes track to "pack," but you can see we can use other genes for this purpose as well. We can use the RefSeq or the GENCODE gene tracks. The [refresh] button then will turn on the UCSC genes track to the default location. This is the SOD1 gene and it is easy to see that there are 5 exons in this gene.

[1:11] If you're interested to know which exon you are at if you are in a zoomed position where you can only see one or a few exons, let's go there first by clicking on the region and dragging it to the right or left to highlight the area. We will zoom into this region and now we can see by the stripes the scale, and we can see any individual codons in alternating light and dark colors. So if you were zoomed into such an exon and you were interested to know what the exon number was, you could put your mouse over the double headed arrows to the right or the left of the screen. The previous exon is number 1 and next exon is number 3.

[1:55] As that is off the screen in this configuration, let's configure it to make the graphic a little bit narrower, and we will make it 880 pixels wide. Now you can see that on the right-hand side of the screen the arrows are a little bit further over and the mouseover shows us that the next exon is number 3 of 5.

[2:20] We can highlight these as well by putting the cursor in the same configuration as before by dragging it across the top and using the highlight button. Now it's possible, for example, to zoom out and put this in the middle of the screen.

[2:39] And then using the right and left exon arrows we can move to the next exon or back to the exon where we were just looking. It's a little bit more complicated if you are in the middle of an exon such as this demonstration right here. At this resolution we can see the amino acid names and once again on the right-hand side of the screen the next exon is number 3 out of 5. However, because this exon actually runs off the screen when you put your mouse over the arrow here it tells you that the next exon is 2 out of 5 so the best way to think about this is that its pointing to the next edge of an exon. If you are in the middle

of an exon it will point to the end of the current exon; if you're between exons in the middle of an intron it will tell you the number of the next exon over. So let's pick another gene that's a little more complicated, the FGFR1 gene and choose the gene from the menu and hit the [go] button. It puts the gene in the middle of the screen and you can see that there are multiple isoforms here, some of which contain this large exon and some of which do not. In the center of the screen you can see several large exons that are in some isoforms and not others and so let's zoom into the region just downstream from that exon which is to the left because this gene is transcribed from the right to the left. The [zoom in] button then takes us into these exons we have just selected and we can use the mouse-over to see that the next exon off-screen will be number 7 out of 19 on this isoform, number 6 out of 18 on this isoform and number 5 out of 17 on this isoform.