

New UCSC Genome Browser Views: Exon-Only, Gene-Only, Alternate Haplotypes, and Custom Regions

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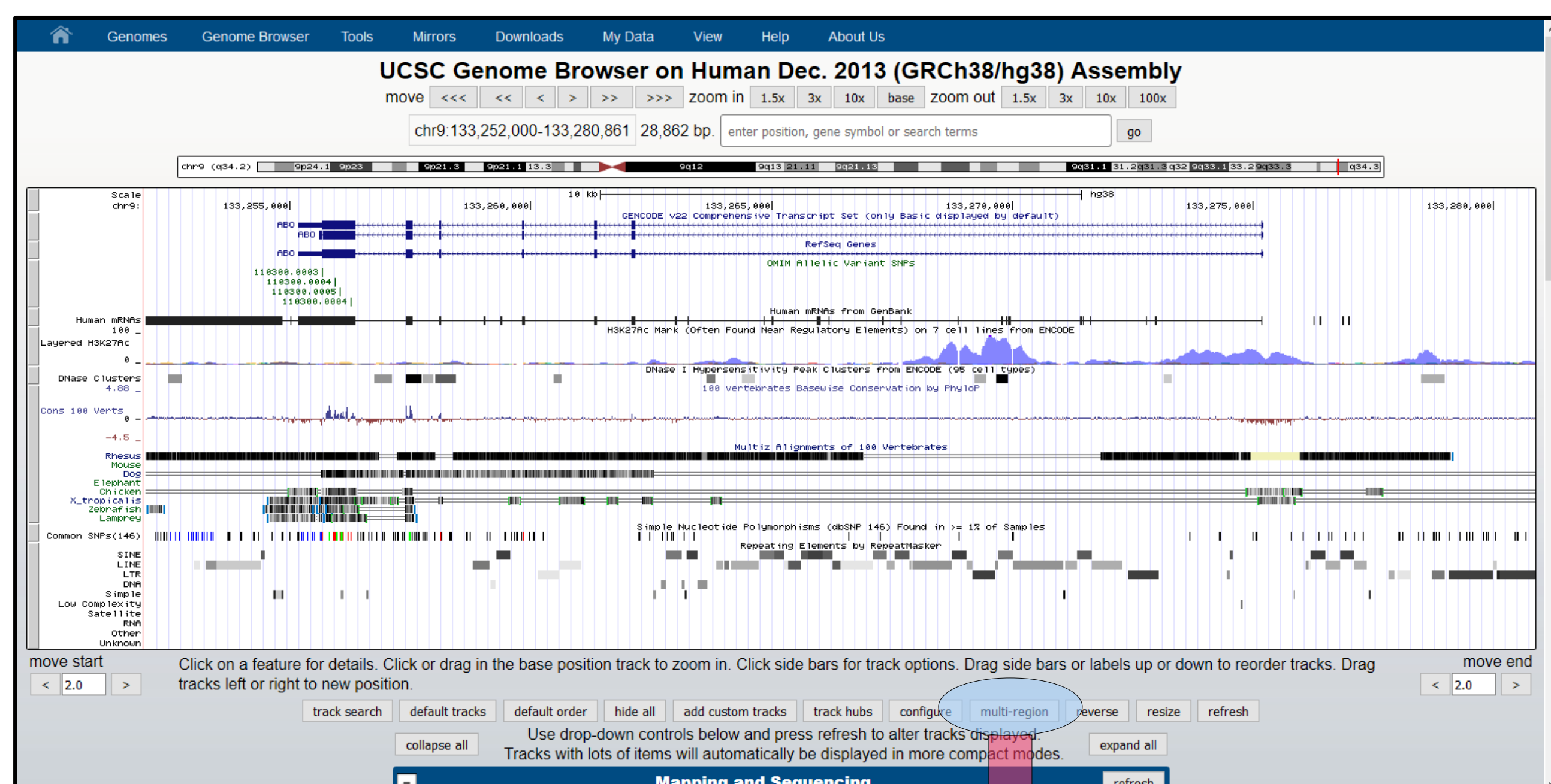
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The University of California, Santa Cruz

(UCSC) Genome Browser (<http://genome.ucsc.edu>)

is a public, freely available web-based graphical viewer for the display of genomic sequences and their annotations with links to external public databases.

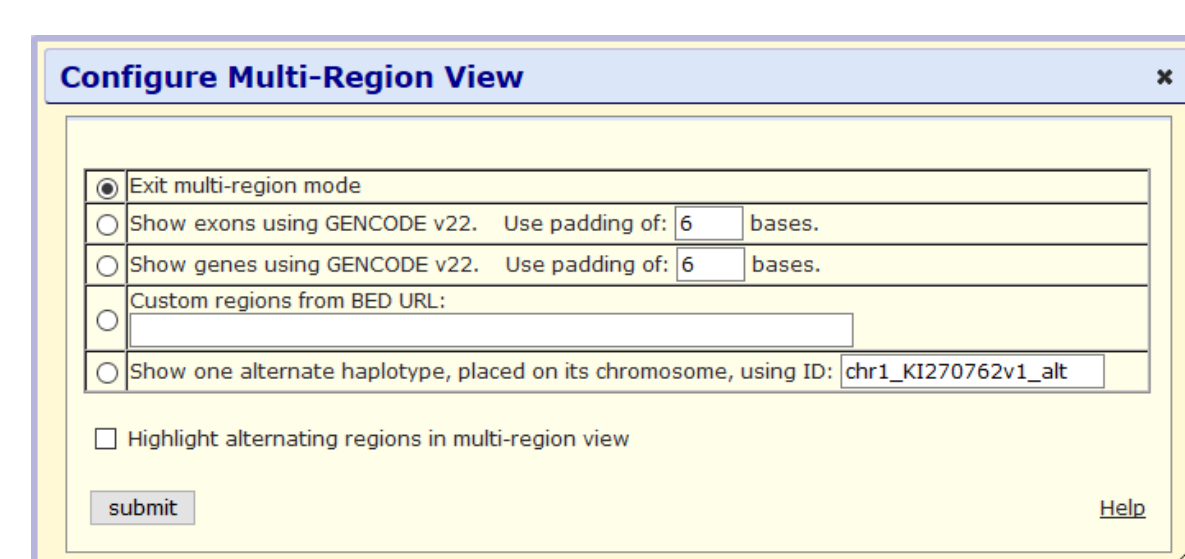
Default Genome Browser view



Browser users have long asked for the ability to remove intronic and intergenic regions from the display, leaving only the exons on view. These intronic and intergenic regions are often extremely large and can occupy much of the visual field in the browser display. Removing them allows the user to focus on the annotations in exonic regions in greater detail.

The Genome Browser now offers a **multi-region** configuration option that supports an **"exon-only"** display mode, and more! Simply click the new multi-region button, or select it from the view-menu. Shortcut keys "ev" are even quicker!

Multi-Region Configuration Box

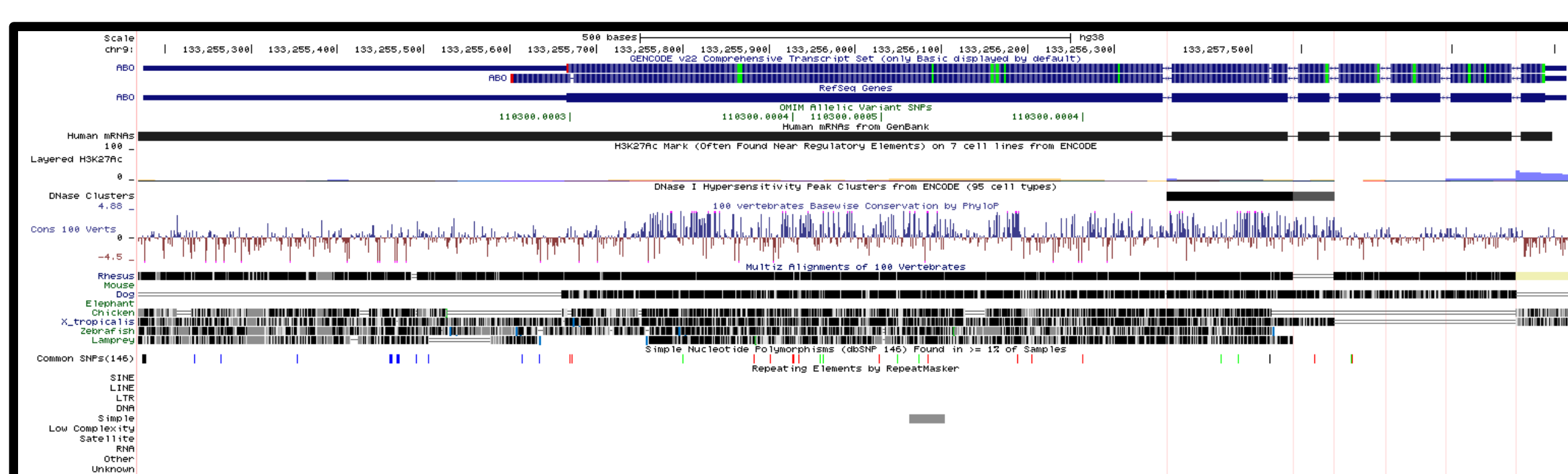


Choose your multi-region view. For exon and gene views, choose the number of bases to use for padding between exons or genes. The default is 6 bases. There is a link to the help page in the lower right-hand corner of the dialog.

(<http://genome.ucsc.edu/goldenPath/help/multiRegionHelp.html>)

When many regions are present, an option to highlight regions with an alternating blue and white background may be helpful.

Exon View shows only exons from the gene set



As we see here, there is much more space devoted to exons which appear larger and more detailed. The **exon-only** display is especially useful for looking at protein-coding regions and variants. The exon and gene regions are defined by a preset gene track optimized for the selected genome assembly. The view responds dynamically to gene track settings, such as options to include non-coding or alternatively spliced transcripts.

Acknowledgments

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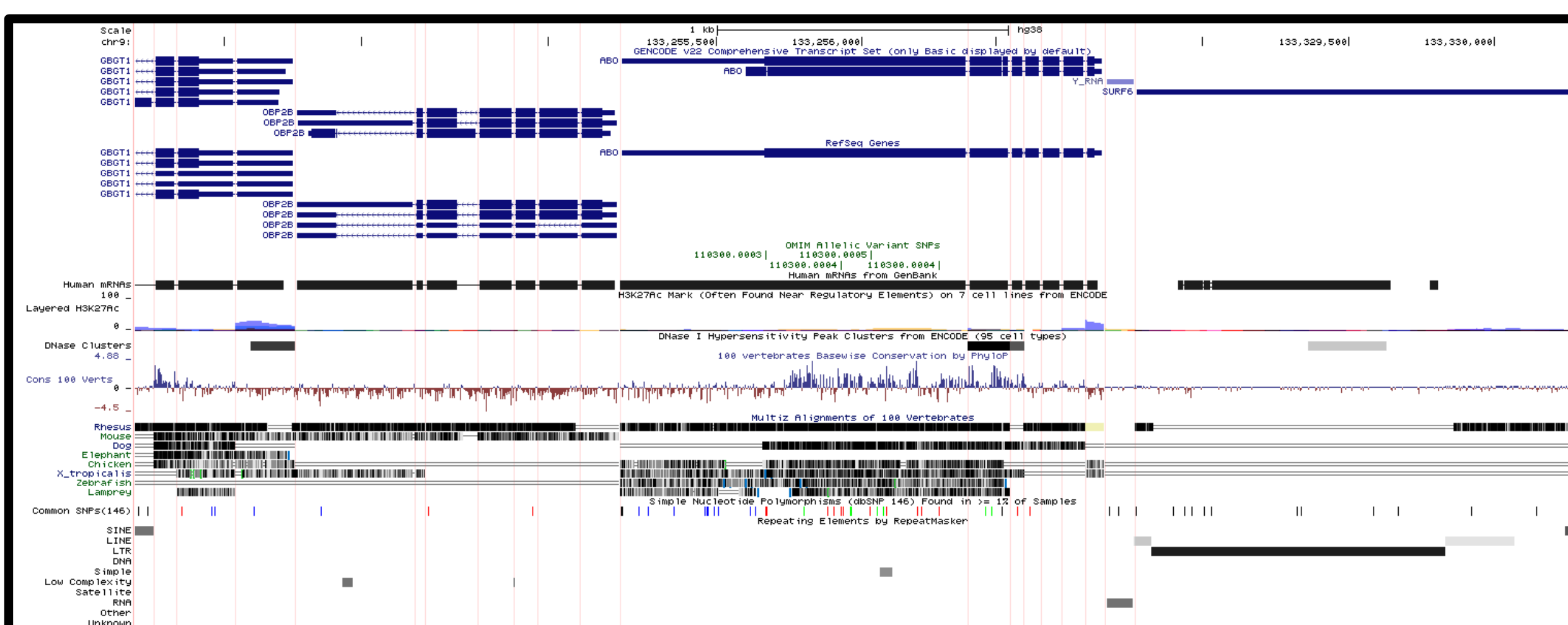
Reference:

The UCSC Genome Browser database: 2016 update. Speir ML, Zweig AS, Rosenbloom KR, Raney BJ, Paten B, Nejad P, Lee BT, Learned K, Karolchik D, Hinrichs AS, Heitner S, Harte RA, Haeussler M, Guruvadoo L, Fujita PA, Eisenhart C, Diekhans M, Clawson H, Casper J, Barber GP, Haussler D, Kuhn RM, Kent WJ. Nucleic Acids Res. 2016 Jan 4;44(D1):D717-25. PMID: 26590259; PMC: PMC4702902

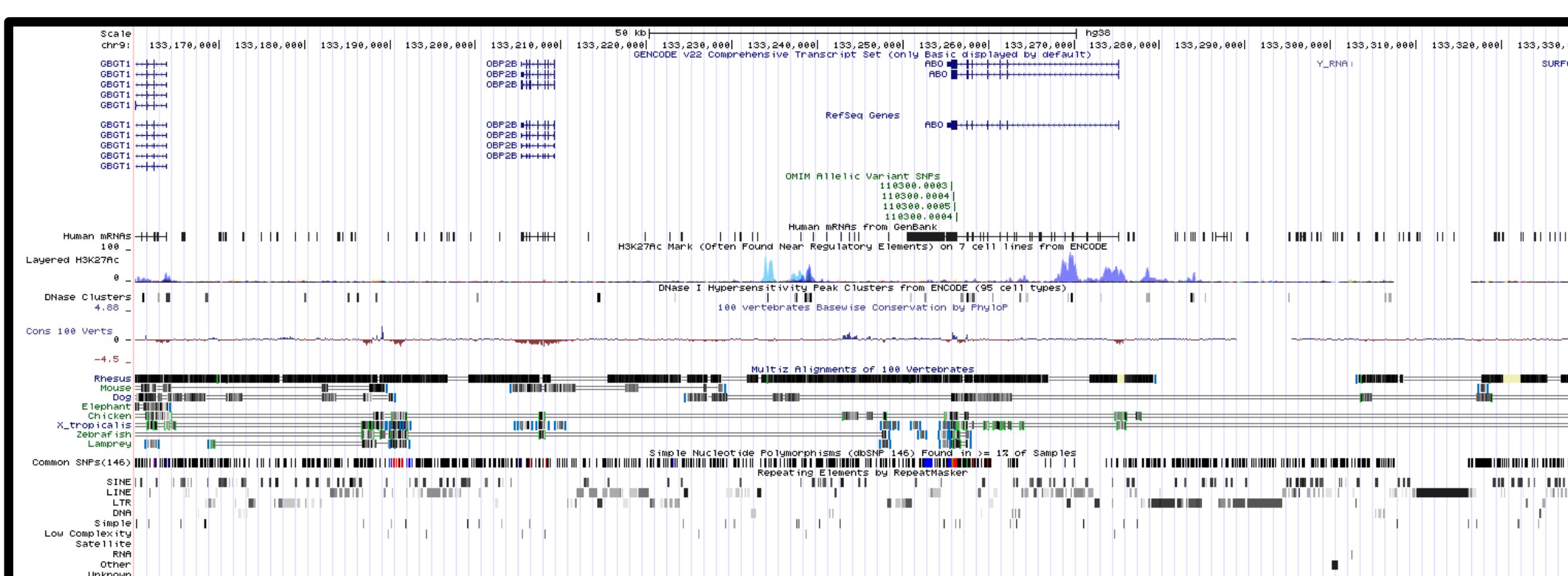
All the standard navigation works with multi-region. Users are free to move the view about, zooming in and out with buttons, dragging, selecting, clicking the ruler at the top of the window, next/prev exon/item arrows, or entering a chromosome position or search. Since regions can become quite small when zoomed out, the region position is now shown when hovering over the ruler. The position of each region within the chromosome is indicated by a red box on the chromosome ideogram above the tracks window.

Let's zoom out now by 3X, so that we can see multiple genes on the screen at the same time. This is a common operation, and shows the nearby gene neighborhood. We will also use this same location in several views below, showing them together, one above the other, for easy comparison.

Exon View zoomed out 3X, showing multiple genes



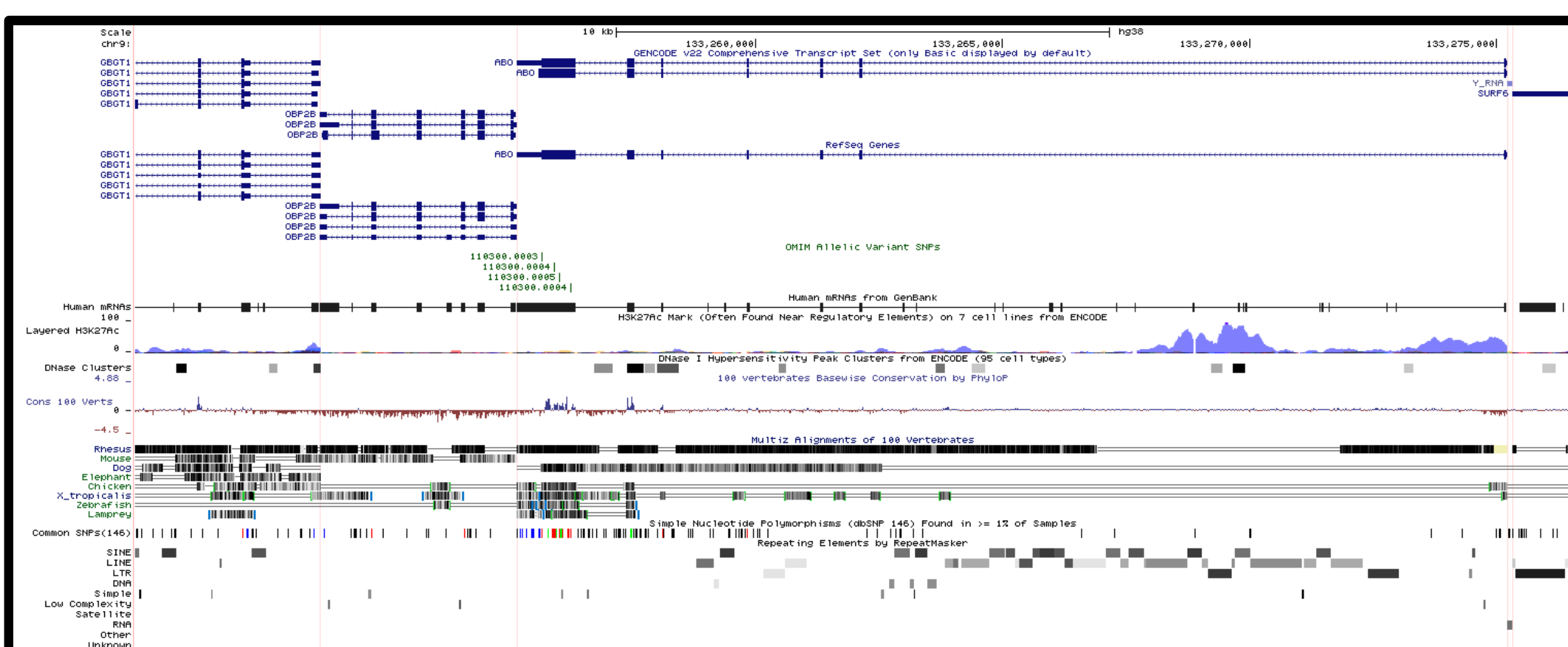
Default View at same location, for comparison



Easily return to default non-multi-region view pressing shortcut keys "dv". Here we see the same genes, but much more space is devoted to introns and intergenic regions, so the coding regions look small by comparison.

In addition to exon-only mode, the Genome Browser supports three **other display modes** that allow users to view multiple regions alongside one another in the same browser window. Let's see what Gene View looks like now at this same location:

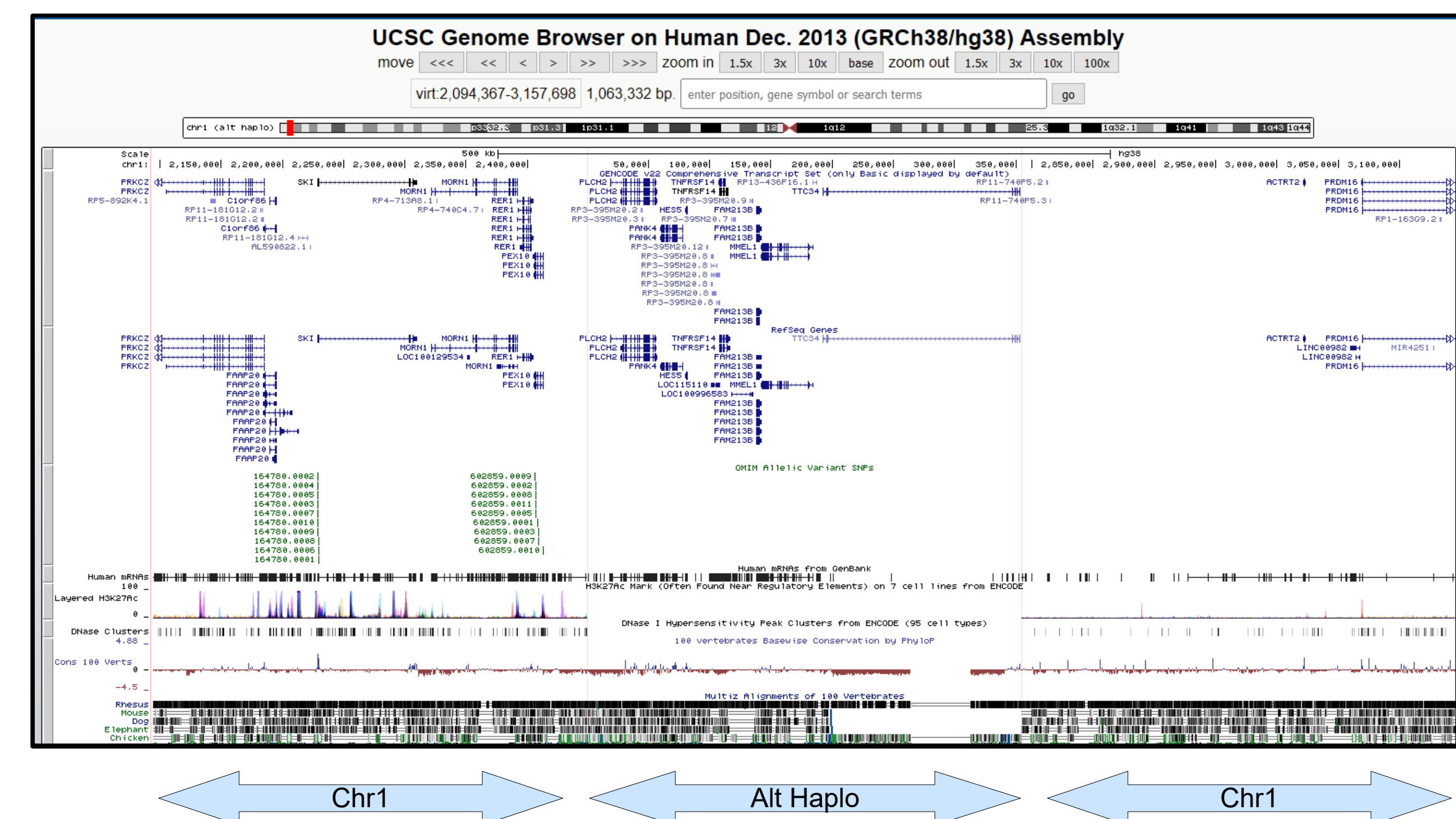
Gene View leaves out intergenic regions



In the **gene-only** view, the intergenic spaces are removed from the display, but introns remain. Gene deserts and other non-genic regions will not be visible in this view.

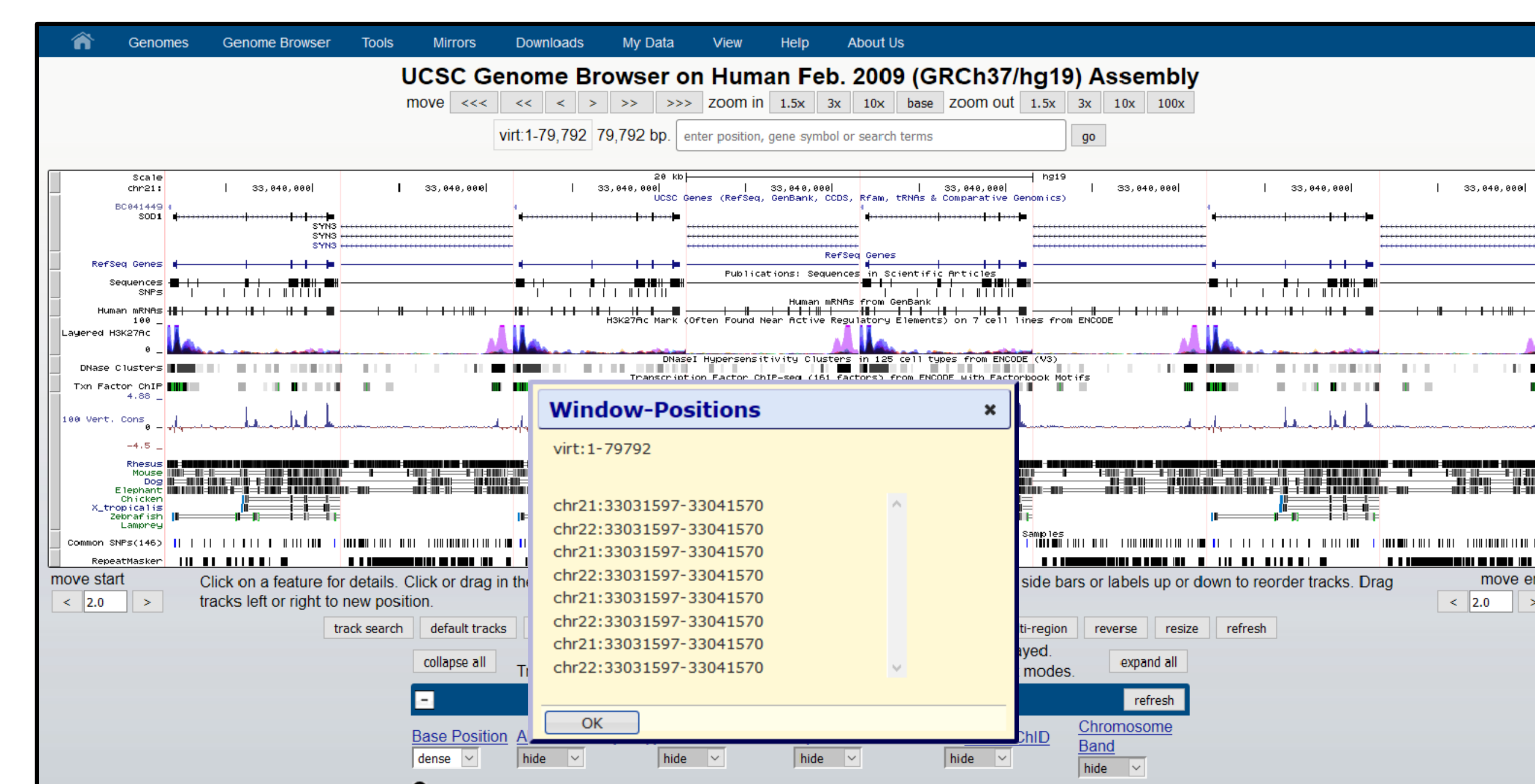
An **alternate haplotype** view (on newer human assemblies) shows a user-selected alternate haplotype placed in context on its reference chromosome. Here, the alternate haplotype is placed in the middle region with the neighboring regions from the reference genome visible on either side of it. Genes near the alternate-haplotype's borders are easily seen.

Alternate Haplotype View



The **custom regions** view allows the user to create a customized view of regions specified in a BED file URL. The user can then scroll around the large virtual chromosome made from the custom regions list. This simple example models 2 regions on 2 different chromosomes repeated 4 times. Custom regions allow a list of arbitrary regions from different chromosomes to be placed side-by-side. In the image below, the pop-up box shows the list of individual chromosome regions, as well as the span of the virtual chromosome that results when the regions are combined into a multi-region view. The custom regions can be genes, exons, alignments, enhancers, centromere models, favorite spots, etc.

Custom Regions View – Roll your own!



Multi-region works well with the Browser's new data tracks from the Genotype-Tissue Expression (GTEx) project, a resource to study human tissue-specific gene expression and regulation and its relationship to genetic variation. Each bar in the graph corresponds to a tissue, and the bar height represents the gene expression level in that tissue. We see a variety of them here. The left side of the bar-graph is anchored to the left side of the gene, however the right side of the bar-graph does **NOT** correspond to the span of the gene. This is a special new non-proportional browser screen element. For each gene, the bar-graph will have the same tissues in the same order, with the same total width, so that comparing graphs is easy.

GTEx and multi-region together

