

## Question 9

### Are there ways to customize displays and designate preferences? Can tracks or features be added to displays by users on the basis of their own research?

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In this example, the UCSC browser will be used to view particular tracks. Start at the UCSC home page (<http://genome.ucsc.edu>), click on *Browser* in the blue sidebar on the left-hand side of the page, and set the Genome Browser Gateway to a region of interest. For example, one could set the *genome* to *Human* and the *assembly* to *Nov. 2002*, type *chr22:38496887-39496866* into the *position* box, and click *Submit* to display a representative region of the November 2002 assembly of human chromosome 22. A number of tracks are already displayed in dense format (Fig. 9.1). Below the graphic showing the specified region are pull-down menus that allow the user to change the appearance of the graphic (Fig. 9.2). There are five options in each of these pull-down menus:

- *Hide*, which allows the user to eliminate that particular track from the display.
- *Dense*, which displays all annotations or features for that track on a single line.
- *Squish*, which displays all annotations or features for that track on a single line, but at 50% the height of full mode
- *Pack*, which displays all annotations or features for that track separately, but not necessarily on a separate line. The *Known Genes* track is shown in this mode.
- *Full*, which displays each annotation or feature for that track on a separate line; this is the 'exploded view' that is illustrated in a number of the questions in this guide.

Once the desired selections have been made, the user clicks on

the *refresh* button to redraw the graphic. Further customization of individual tracks can be achieved by clicking on the track name. The user can, for example, customize the EST track to color red all ESTs from a certain library that contain a particular keyword in their GenBank entry or to eliminate all such ESTs from the display. The browser retains these selections for all subsequent sessions; the default settings can be restored by clicking on the *reset all* button.

One of the attractive features of the UCSC system is that users can add their own annotations, features or tracks to their local displays. These changes are not written or saved in any way to the original data held at UCSC. To customize the display, the user returns to the Human Genome Browser Gateway page and scrolls down to the *Add Your Own Tracks* section. Here, the user is presented with a large text box into which properly formatted text can be typed or pasted. Alternatively, the specifications can be in a text file, which the user can select by using the *Browse* button above the large text box. As another option, if the text file is posted on the user's local web page, the user can share the custom track of annotations with other colleagues simply by telling them the URL of the file. Colleagues can then view the custom annotation by starting the UCSC browser and entering this URL into the large text box.

For the purposes of this example, enter the following text file into the entry field (Fig. 9.3) and click *Submit* at the top of the page:

```
browser position chr22:38496887-39496866
browser hide cytoBand
browser hide stsMap
browser hide gap
browser hide clonePos
browser full refGene
browser dense mrna
track name="scale" description="our peak"
chr22 38996887 38996888 peak
track name="Microsatellites" description="Microsatellites" color=0,128,0
chr22 38627059 38627060 D22S276
chr22 39005417 39005418 D22S307
track name="Genotyped SNPs" description="Genotyped SNPs" color=0,0,255
chr22 38518342 38518343 ss146131
chr22 38705963 38705964 ss2941443
chr22 38884157 38884158 ss141110
chr22 39171390 39171391 ss22916
chr22 39438769 39438770 ss1479794
track name="Upcoming SNPs" description="Upcoming SNPs" color=0,128,192
chr22 38615712 38615713 ss86855
chr22 38804838 38804839 ss85533
chr22 39077895 39077896 ss141190
chr22 39305065 39305066 ss137027
```

At Ensembl, the user can customize the *Detailed View* section of the ContigView, adding annotations and changing colors, by selecting options under the *Features* link (Fig. 1.12, center yellow bar). Users can visualize their own custom data on Ensembl's ContigView displays and even share that data with other users by following the instructions under the *DAS Sources* link (Fig. 1.12, center yellow bar). At the NCBI, Map Viewer displays are changed in the *Maps & Options* window (Fig. 3.9).

The browser will ignore any entries in the *position* box and look only to the file pasted in the *Add Your Own Tracks* field. The results of this customized display are shown in Fig. 9.4.

Lines that begin with the word 'browser' control the overall browser display. Lines beginning with 'track' create new tracks. Lines following track lines provide positional information for each item to be displayed on that track. Therefore:

- the first line of the above format sets the browser to position 38496887–39496866 on chromosome 22.
- the next six 'browser' lines change the overall browser display for the *Chromosome Band*, *STS Markers*, *Gap*, *Coverage*, *Known Genes* and *Human mRNAs* tracks. The formatted text must contain the symbolic name for each track rather than the name listed on the web page display. Symbolic names used by the UCSC browser are listed in Table 9.1. Compared with the default settings (Fig. 9.1), the *Chromosome Band*, *STS Markers*, *Gap* and *Coverage* tracks have all been hidden, and *Human mRNAs* is dense rather than full (Fig. 9.4).
- the remaining lines instruct the browser to create four new tracks named *scale*, *Microsatellites*, *Genotyped SNPs* and *Upcoming SNPs*, respectively. Names are listed on the left side of the browser display. The lines beginning with the word 'track' name the tracks, as listed above, and also set the descriptions (*our peak*, *Microsatellites*, *Genotyped SNPs* and *Upcoming SNPs*) and colors [default (black), green, blue, and light blue] to be used to display those tracks (Fig. 9.4). The descriptions appear as a center label in the browser and colors are determined by the three RGB values provided. All lines following a 'track' line provide position information for the tick marks corresponding to the individual items. For example, 'peak' is displayed at position 38996887–38996888 on chromosome 22.

This is but one example using only some of many options to the *Add Your Own Tracks* feature. A full description, information on input format and additional examples are available at <http://genome.ucsc.edu/goldenPath/help/customTrack.html>.

Table 9.1 Symbolic Names for UCSC Browser Tracks

Track	Symbolic name
Acembly Genes	<i>acembly</i>
Assembly	<i>gold</i>
BAC End Pairs	<i>bacEndPairs</i>
Base position	<i>ruler</i>
Chromosome Band	<i>cytoBank</i>
Coverage	<i>clonePos</i>
CpG Islands	<i>cpgIsland</i>
Duplications	<i>genomicDups</i>
Ensembl Genes	<i>ensGene</i>
Exofish Ecores	<i>exoFish</i>
Fgenesh++ Genes	<i>softberryGene</i>
Fish Blat	<i>blatFish</i>
FISH Clones	<i>fishClones</i>
Gap	<i>gap</i>
GC Percent	<i>gcPercent</i>
Geneid Genes	<i>geneid</i>
Genscan Genes	<i>genscan</i>
GNF Ratio	<i>affyRatio</i>
Human Blat	<i>blatHuman</i>
Human ESTs	<i>est</i>
Human mRNAs	<i>mrna</i>
Known Genes	<i>refGene</i>
Map Contigs	<i>ctgPos</i>
Mouse Blat	<i>blatMouse</i>
Mouse ESTs	<i>est</i>
Mouse mRNA	<i>mrna</i>
Mouse Synteny	<i>mouseSyn</i>
NCI60	<i>nci60</i>
Nonhuman EST	<i>xenoEst</i>
Nonhuman mRNA	<i>xenoMrna</i>
Nonmouse mRNA	<i>xenoMrna</i>
Overlap SNPs	<i>snpNih</i>
Random SNPs	<i>snpTsc</i>
RepeatMasker	<i>rmsk</i>
Rosetta	<i>rosetta</i>
Sanger 22	<i>sanger22</i>
Simple Repeats	<i>simpleRepeat</i>
Spliced ESTs	<i>intronEst</i>
STS Markers	<i>stsMap</i>
Tigr Gene Index	<i>tigrGeneIndex</i>
UniGene	<i>uniGene</i>



Figure 9.1

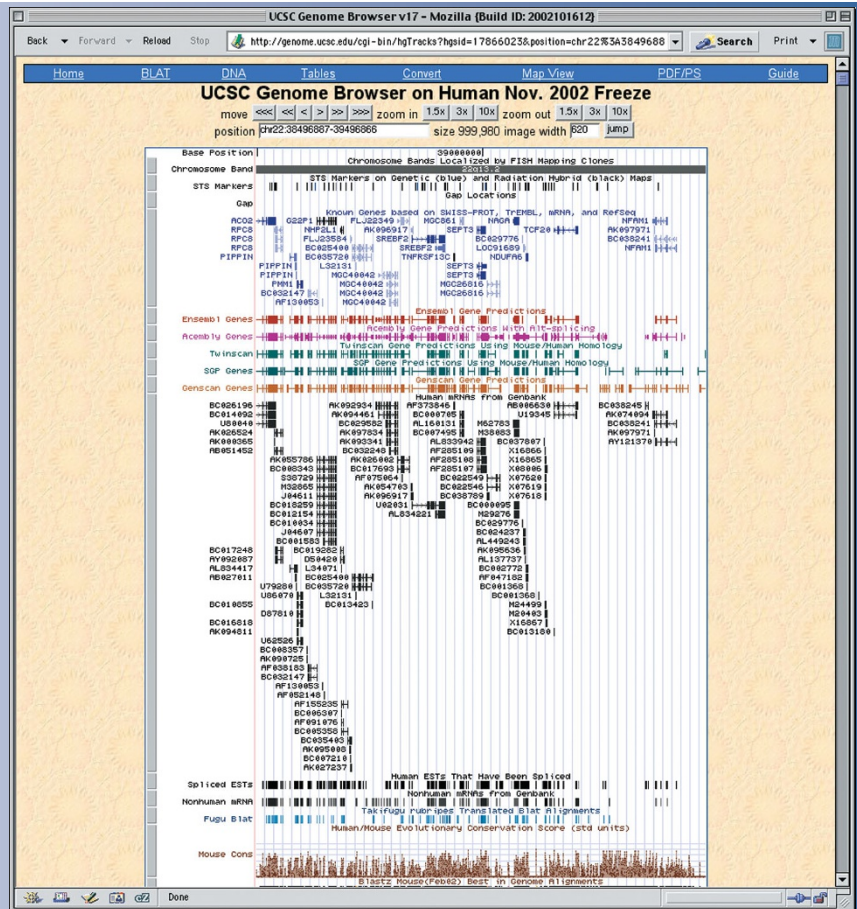


Figure 9.2

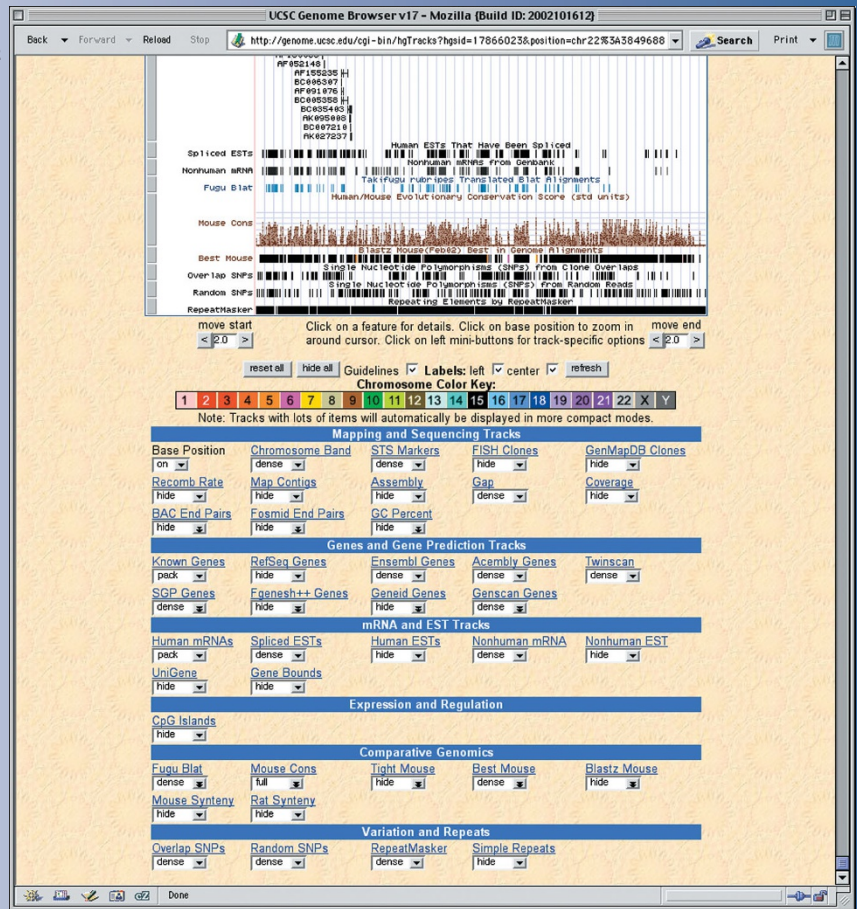




Figure 9.3

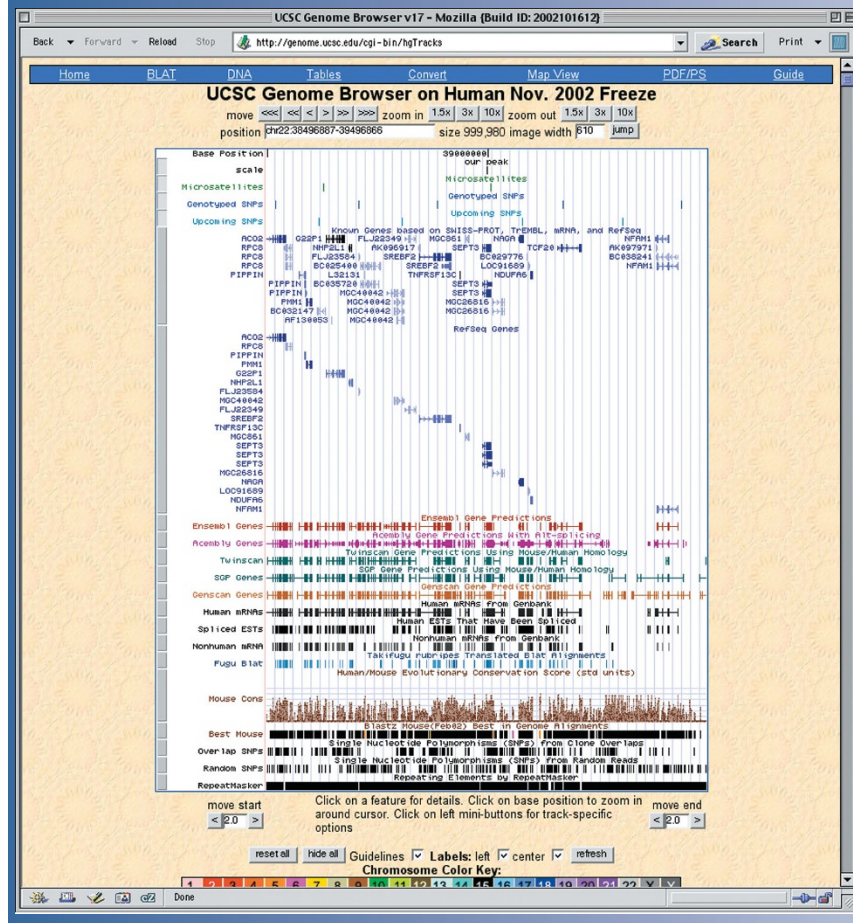


Figure 9.4