Custom Track - Displaying your own annotations in the Genome Browser

The Genome Browser provides dozens of aligned annotation tracks that have been computed at UCSC or have been provided by outside collaborators. In addition to these standard tracks, it is also possible for users to upload their own annotation data for temporary display in the browser. These custom annotation tracks are viewable only on the machine from which they were uploaded and are automatically discarded 48 hours after the last time they are accessed, unless they are saved in a Session. Optionally, users can make custom annotations viewable by others as well.

Custom tracks are a wonderful tool for research scientists using the Genome Browser. Because space is limited in the Genome Browser track window, many excellent genome-wide tracks cannot be included in the standard set of tracks packaged with the browser. Other tracks of interest may be excluded from distribution because the annotation track data is too specific to be of general interest or can't be shared until journal publication. Many individuals and labs have contributed custom tracks to the Genome Browser website for use by others.

Custom annotation tracks are similar to standard tracks, but never become part of the MySQL genome database. Each track has its own controller and persists even when not displayed in the Genome Browser window, e.g. if the position changes to a range that no longer includes the track. Typically, custom annotation tracks are aligned under corresponding genomic sequence, but they can also be completely unrelated to the data. For example, a track can be displayed under a long sequence consisting of millions of *N*s.

Genome Browser annotation tracks are based on files in line-oriented format. Each line in the file defines a display characteristic for the track or defines a data item within the track. Annotation files contain three types of lines: browser lines, track lines, and data lines. Empty lines and those starting with "#" are ignored.

To construct an annotation file and display it in the Genome Browser, follow these steps:

Step 1. Format the data set

Formulate your data set as a tab-separated file using one of the formats supported by the Genome Browser. Annotation data can be in standard GFF format or in a format designed specifically for the Human Genome Project or UCSC Genome Browser,
including bedGraph, GTF, PSL, BED, bigBed, WIG, bigWig, BAM, VCF, MAF, BED detail,Personal Genome SNP, broadPeak, narrowPeak, and microarray (BED15). GFF and GTF files *must* be tab-delimited rather than space-delimited to display correctly. Chromosome references must be of the form *chrN* (the parsing of chromosome names ***is*** case-sensitive). You may include more than one data set in your annotation file; these need not be in the same format.

Step 2. Define the Genome Browser display characteristics

Add one or more optional browser lines to the beginning of your formatted data file to configure the overall display of the Genome Browser when it initially shows your annotation data. Browser lines allow you to configure such things as the genome position that the Genome Browser will initially open to, the width of the display, and the configuration of the other annotation tracks that are shown (or hidden) in the initial display.
NOTE: If the browser position is not explicitly set in the annotation file, the initial display will default to the position setting most recently used by the user, which may not be an appropriate position for viewing the annotation track.

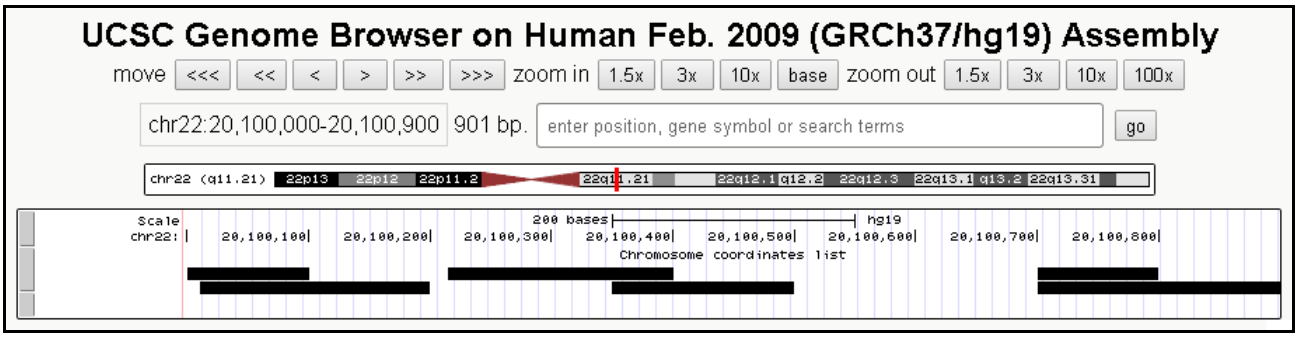
Step 3. Define the annotation track display characteristics

Following the browser lines--and immediately preceding the formatted data--add a track line to define the display attributes for your annotation data set. Track lines enable you to define annotation track characteristics such as the name, description, colors, initial display mode, use score, etc. The track type=<*track_type*> attribute is required for some tracks. If you have included more than one data set in your annotation file, insert a track line at the beginning of each new set of data.

Example 1:
Here is an example of a simple annotation file that contains a list of chromosome coordinates.

```
browser position chr22:20100000-20100900
track name=coords description="Chromosome coordinates list" visibility=2
chr22   20100000 20100100
chr22   20100011 20100200
chr22   20100215 20100400
chr22   20100350 20100500
chr22   20100700 20100800
chr22   20100700 20100900
```

Click here to view this track in the Genome Browser (see the picture down below).



UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr22:20,100,000-20,100,900 901 bp.

Example 2:

Here is an example of an annotation file that defines 2 separate annotation tracks in BED format. The first track displays blue one-base tick marks every 10000 bases on chr 22. The second track displays red 100-base features alternating with blank space in the same region of chr 22.

```
browser position chr22:20100000-20140000
track name=spacer description="Blue ticks every 10000 bases" color=0,0,255,
chr22   20100000 20100001
chr22   20110000 20110001
chr22   20120000 20120001
track name=even description="Red ticks every 100 bases, skip 100" color=255,0,0
chr22   20100000 20100100       first
chr22   20100200 20100300       second
chr22   20100400 20100500       third
```

Click here to view this track in the Genome Browser.

Example 3A:

This example shows an annotation file containing one data set in BED format. The track displays features with multiple blocks, a thick end and thin end, and hatch marks indicating the direction of transcription. The track labels display in green (0,128,0), and the gray level of the each feature reflects the score value of that line. NOTE: The track name line in this example has been split over 2 lines for documentation purposes. If you paste this example into the Genome Browser, you must remove the line break to display the track successfully. Click here for a copy of this example that can be pasted into the browser without editing.

```
browser position chr22:1000-10000
browser hide all
track name="BED track" description="BED format custom track example" visibility=2
color=0,128,0 useScore=1
chr22 1000 5000 itemA 960 + 1100 4700 0 2 1567,1488, 0,2512
chr22 2000 7000 itemB 200 - 2200 6950 0 4 433,100,550,1500 0,500,2000,3500
```

Click here to view this track in the Genome Browser.

Example 3B:

This example shows a simple annotation file containing one data set in the bigBed format. This track displays random sized blocks across chr21 in the human genome. The big data formats, such as the bigBed format, must be uploaded using a bigDataUrl that is specified in the track line. For more information on these track line parameters, refer to the Track Lines section.
You may paste these two lines directly into the "Add Custom Tracks" page to view this example in the browser:

```
browser position chr21:33,031,597-33,041,570


track type=bigBed name="bigBed Example One" description="A bigBed file"
bigDataUrl=http://genome.ucsc.edu/goldenPath/help/examples/bigBedExample.bb
```

Step 4. Display your annotation track in the Genome Browser
To view your annotation data in the Genome Browser, open the Genome Browser home page and click the Genome Browser link in the top menu bar. On the Gateway pagethat displays, select the genome and assembly on which your annotation data is based, then click the "add custom tracks" button. (Note: if the Gateway displays the "manage custom tracks" button instead, see Displaying and Managing Custom Tracks for information on how to display your track.)

On the Add Custom Tracks page, load the annotation track data or URL for your custom track into the upper text box and the track documentation (optional) into the lower text box, then click the Submit button. Tracks may be loaded by entering text, a URL, or a pathname on your local computer. The track type=<*track_type*> attribute is required for some tracks. For more information on these methods, as well as information on creating and adding track documentation, see Loading a Custom Track into the Genome Browser.

If you encounter difficulties displaying your annotation, read the section Troubleshooting Annotation Display Problems.

Step 5. (Optional) Add details pages for individual track features
After you've constructed your track and have successfully displayed it in the Genome Browser, you may wish to customize the details pages for individual track features. The Genome Browser automatically creates a default details page for each feature in the track containing the feature's name, position information, and a link to the corresponding DNA sequence. To view the details page for a feature in your custom annotation track (in full, pack, or squish display mode), click on the item's label in the annotation track window.

You can add a link from a details page to an external web page containing additional information about the feature by using the track line *url* attribute. In the annotation file, set the *url* attribute in the track line to point to a publicly available page on a web server. The *url* attribute substitutes each occurrence of '$$' in the URL string with the name defined by the *name* attribute. You can take advantage of this feature to provide individualized information for each feature in your track by creating HTML anchors that correspond to the feature names in your web page.

Example 4:
Here is an example of a file in which the *url* attribute has been set to point to the file http://genome.ucsc.edu/goldenPath/help/clones.html. The '#$$' appended to the end of the file name in the example points to the HTML NAME tag within the file that matches the name of the feature (cloneA, cloneB, etc.). NOTE: The track line in this example has been split over 2 lines for documentation purposes. If you paste this example into the browser, you must remove the line break to display the track successfully. Click here for a copy of this example that can be pasted into the browser without editing.

```
browser position chr22:10000000-10020000
browser hide all
track name=clones description="Clones" visibility=2
color=0,128,0 useScore=1
url="http://genome.ucsc.edu/goldenPath/help/clones.html#$$"
chr22 10000000 10004000 cloneA 960
chr22 10002000 10006000 cloneB 200
chr22 10005000 10009000 cloneC 700
chr22 10006000 10010000 cloneD 600
chr22 10011000 10015000 cloneE 300
chr22 10012000 10017000 cloneF 100
```

Click here to display this track in the Genome Browser.

Step 6. (Optional) Share your annotation track with others
The previous steps showed you how to upload annotation data for your own use on your own machine. However, many users would like to share their annotation data with members of their research group on different machines or with colleagues at other sites. To learn how to make your Genome Browser annotation track viewable by others, read the section Sharing Your Annotation Track with Others.

Loading a Custom Track into the Genome Browser

Using the Genome Browser's custom track upload and management utility, annotation tracks may be added for display in the Genome Browser, deleted from the Genome Browser, or updated with new data and/or display options. You may also use this interface to upload and manage custom track sets for multiple genome assemblies.

To load a custom track into the Genome Browser:

Step 1. Open the Add Custom Tracks page

Click the "add custom tracks" button on the Genome Browser Gateway page. (Note: if one or more tracks have already been uploaded during the current Browser session, additional tracks may be loaded on the Manage Custom Tracks page. In this case, the button on the Gateway page will be labeled "manage custom tracks" and will automatically direct you to the track management page. See Displaying and Managing Custom Tracks for more information).

Step 2. Load the custom track data

The Add Custom Tracks page contains separate sections for uploading custom track data and optional custom track descriptive documentation. Load the annotation data into the upper section by one of the following methods:

- Enter one or more URLs for custom tracks (one per line) in the data text box. The Genome Browser supports both the HTTP and FTP (passive-only) protocols.
- Data provided by a URL may need to be proceeded by a separate line defining type=<*track_type*> required for some tracks, for example such as "track type=broadPeak".
- Click the "Browse" button directly above the data text box, then choose a custom track file from your local computer, or type the pathname of the file into the "upload" text box adjacent to the "Browse" button. The custom track data may be compressed by any of the following programs: gzip (*.gz*), compress (*.Z*), or bzip2 (*.bz2*). Files containing compressed data must include the appropriate suffix in their names.
- Paste or type the custom track data directly into the data box. Because the text in this box will not be saved to a file, this method is not recommended unless you have a copy of the data elsewhere.

Multiple custom tracks may be uploaded at one time on the Add Custom Tracks page through one of the following methods:

- Put all the tracks into the same file (rather than separate files), then load the file via the Browse button.
- Place your track files in a web-accessible location on your server, then load them into the Genome Browser by pasting their URLs into the data box.

NOTE: Please limit the number of custom tracks that you upload and maintain to less than 1000 tracks. If you have more than this suggested limit of 1000 tracks, please consider setting up a track hub instead.

Step 3. (Optional) Load the custom track description page

If desired, you can provide optional descriptive text (in plain or HTML format) to accompany your custom track. This text will be displayed when a user clicks the track's description button on the Genome Browser annotation tracks page. Descriptive text may be loaded by one of the following methods:

- Click the "Browse" button directly above the documentation text box, then choose a text file from your local computer, or type the pathname of the file into the "upload" text box adjacent to the "Browse" button.
- Paste or type the custom track data directly into the data box. Note that the text in this box will not be saved to a file; therefore, this method is not recommended except for temporary documentation purposes.
- If your descriptive text is located on a website, you can reference it from your custom track file by defining the track line attribute "htmlUrl": **htmlUrl=<*external_url*>**. In this case, there is no need to insert anything into the documentation text box.

To format your description page in a style that is consistent with standard Genome Browser tracks, click the template link below the documentation text box for an HTMLtemplate that may be copied and pasted into a file for editing.

If you load multiple custom tracks simultaneously using one of the methods described in Step 2, a track description can be associated only with the last custom track loaded, unless you upload the descriptive text using the track line "htmlUrl" attribute described above.

Step 4. Upload the track
Click the *Submit* button to load your custom track data and documentation into the Genome Browser. If the track uploads successfully, you will be directed to the custom track management page where you can display your track, update an uploaded track, add more tracks, or delete uploaded tracks. If the Genome Browser encounters a problem while loading your track, it will display an error. See the section Troubleshooting Annotation Display Problems for help in diagnosing custom track problems.

NOTE: Please limit the number of custom tracks that you upload and maintain to less than 1000 tracks. If you have more than this suggested limit of 1000 tracks, please consider setting up a track hub instead.

BED FILE for custom track UCSC Genome Browser

BED format provides a flexible way to define the data lines that are displayed in an annotation track. BED lines have three required fields and nine additional optional fields. The number of fields per line must be consistent throughout any single set of data in an annotation track. The order of the optional fields is binding: lower-numbered fields must always be populated if higher-numbered fields are used.

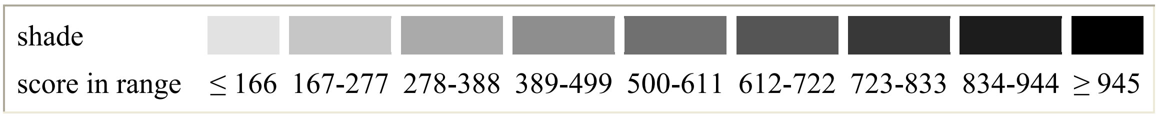
If your data set is BED-like, but it is very large and you would like to keep it on your own server, you should use the bigBed data format.

The first three required BED fields are:

1. **chrom** - The name of the chromosome (e.g. chr3, chrY, chr2_random) or scaffold (e.g. scaffold10671).
2. **chromStart** - The starting position of the feature in the chromosome or scaffold. The first base in a chromosome is numbered 0.
3. **chromEnd** - The ending position of the feature in the chromosome or scaffold. The *chromEnd* base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as *chromStart=0, chromEnd=100*, and span the bases numbered 0-99.

The 9 additional optional BED fields are:

4. **name** - Defines the name of the BED line. This label is displayed to the left of the BED line in the Genome Browser window when the track is open to full display mode or directly to the left of the item in pack mode.
5. **score** - A score between 0 and 1000. If the track line *useScore* attribute is set to 1 for this annotation data set, the *score* value will determine the level of gray in which this feature is displayed (higher numbers = darker gray). This table shows the Genome Browser's translation of BED score values into shades of gray:



shade	■	■	■	■	■	■	■	■	■
score in range	≤ 166	167-277	278-388	389-499	500-611	612-722	723-833	834-944	≥ 945

6. **strand** - Defines the strand - either '+' or '-'.
7. **thickStart** - The starting position at which the feature is drawn thickly (for example, the start codon in gene displays).
8. **thickEnd** - The ending position at which the feature is drawn thickly (for example, the stop codon in gene displays).
9. **itemRgb** - An RGB value of the form R,G,B (e.g. 255,0,0). If the track line *itemRgb* attribute is set to "On", this RBG value will determine the display color of the data contained in this BED line. NOTE: It is recommended that a simple color scheme (eight colors or less) be used with this attribute to avoid overwhelming the color resources of the Genome Browser and your Internet browser.
10. **blockCount** - The number of blocks (exons) in the BED line.
11. **blockSizes** - A comma-separated list of the block sizes. The number of items in this list should correspond to *blockCount*.
12. **blockStarts** - A comma-separated list of block starts. All of the *blockStart* positions should be calculated relative to *chromStart*. The number of items in this list should correspond to *blockCount*.

Example:

Here's an example of an annotation track that uses a complete BED definition:

```
track name=pairedReads description="Clone Paired Reads" useScore=1
chr22 1000 5000 cloneA 960 + 1000 5000 0 2 567,488, 0,3512
chr22 2000 6000 cloneB 900 - 2000 6000 0 2 433,399, 0,3601
```

Example:
This example shows an annotation track that uses the itemRgb attribute to individually color each data line. In this track, the color scheme distinguishes between items named "Pos*" and those named "Neg*". See the usage note in the *itemRgb* description above for color palette restrictions. NOTE: The track and data lines in this example have been reformatted for documentation purposes. This example can be pasted into the browser without editing.

```
browser position chr7:127471196-127495720
browser hide all
track name="ItemRGBDemo" description="Item RGB demonstration" visibility=2
itemRgb="On"
chr7    127471196  127472363  Pos1  0  +  127471196  127472363  255,0,0
chr7    127472363  127473530  Pos2  0  +  127472363  127473530  255,0,0
chr7    127473530  127474697  Pos3  0  +  127473530  127474697  255,0,0
chr7    127474697  127475864  Pos4  0  +  127474697  127475864  255,0,0
chr7    127475864  127477031  Neg1  0  -  127475864  127477031  0,0,255
chr7    127477031  127478198  Neg2  0  -  127477031  127478198  0,0,255
chr7    127478198  127479365  Neg3  0  -  127478198  127479365  0,0,255
chr7    127479365  127480532  Pos5  0  +  127479365  127480532  255,0,0
chr7    127480532  127481699  Neg4  0  -  127480532  127481699  0,0,255
```

Click here to display this track in the Genome Browser.

Example:
It is also possible to color items by strand in a BED track using the *colorByStrand* attribute in the track line as shown below. For BED tracks, this attribute functions only for custom tracks with 6 to 8 fields (i.e. BED6 through BED8). NOTE: The track and data lines in this example have been reformatted for documentation purposes. This example can be pasted into the browser without editing.

```
browser position chr7:127471196-127495720
browser hide all
track name="ColorByStrandDemo" description="Color by strand demonstration"
visibility=2 colorByStrand="255,0,0 0,0,255"
chr7    127471196  127472363  Pos1  0  +
chr7    127472363  127473530  Pos2  0  +
chr7    127473530  127474697  Pos3  0  +
chr7    127474697  127475864  Pos4  0  +
chr7    127475864  127477031  Neg1  0  -
chr7    127477031  127478198  Neg2  0  -
chr7    127478198  127479365  Neg3  0  -
chr7    127479365  127480532  Pos5  0  +
chr7    127480532  127481699  Neg4  0  -
```

Click here to display this track in the Genome Browser.

Custom Track – Different colors for displaying your own annotations

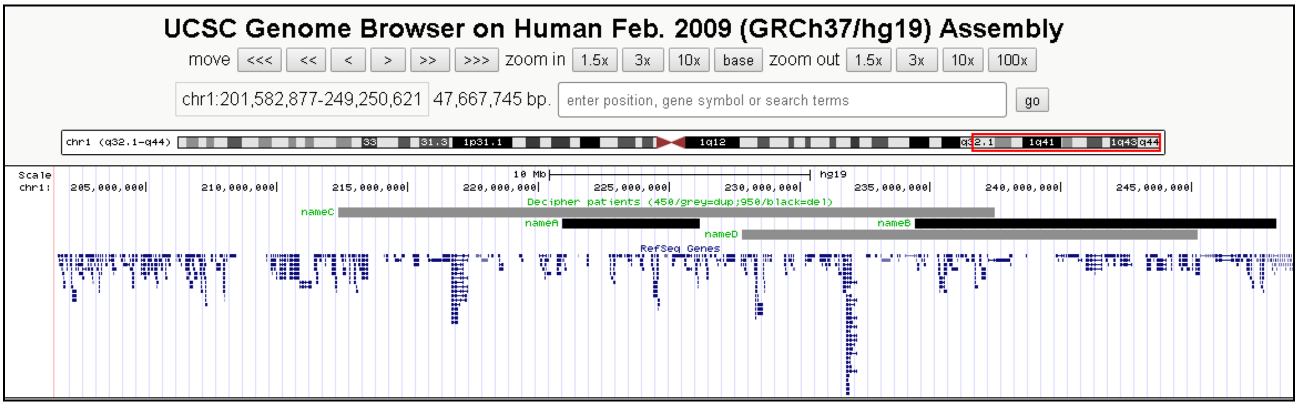
1) Different colors (shades of grey) for features present in the same BED file

In your BED file you can insert a score to display your annotations using different shades of gray (from white to black). In this case you just need to write a specific number near each annotation in your BED file (these score number represent the fifth column in your BED file).
In this case, in the first row of your file, *Genome Browser display characteristics*, insert "*useScore=1*".

Example:
If you have some deletions and duplications and you want to display them differently, you can indicate the first group using black color and the second group using grey color. For example, you can write near each duplication the number '450' (middle shade of grey) and near each deletion the number '950' (black) [*check the color intervals at step 5 of chapter "BED FILE for custom track UCSC Genome Browser"*].

```
browser position chr1:1-200000000
track name="Decipher patients affected by OFCs" description="Decipher patients
(450/grey=dup;950/black=del)" visibility=2 useScore=1
chr1   220916999    226162869    nameA  950
chr1   234413268    248220098    nameB  950
chr1   212374942    237468576    nameC  450
chr1   227778741    245226841    nameD  450
```

Result:



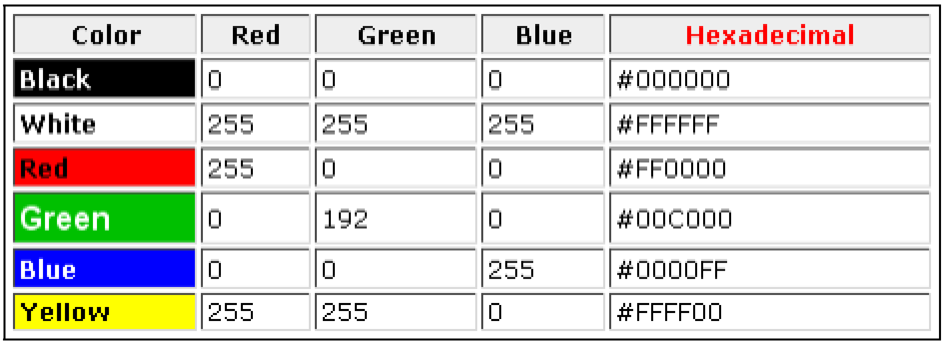
UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr1:201,582,877-249,250,621 47,667,745 bp.

2) Different colors (RGB colors) for features present in two or more BED files

There is also another way to highlight your features with different colors: using RGB color convention.
NOTE: in this case you can use just one color for displaying all the features contained in your BED file! In this case you cannot distinguish the features present in the same file because all of them will be highlighted with the same color. So, considering the last example, to use different colors for indicating deletions and duplications, they have to be split in two different BED file (one for deletions only and the other one for duplications only). Otherwise, you cannot distinguish them!

In your BED file you can insert a code to display all your track (you features included) using a specific color (RGB colors). In this case, to specify the colors you just need to type "*color=0,0,0*" (change '0' to modify the color!) in the first row of your file, *Genome Browser display characteristics*.
You can insert three numbers and, setting different combination of them, you can get different nuances of colors numbers.
The principle combinations to get the more important colors are:



Color	Red	Green	Blue	Hexadecimal
Black	0	0	0	#000000
White	255	255	255	#FFFFFF
Red	255	0	0	#FF0000
Green	0	192	0	#00C000
Blue	0	0	255	#0000FF
Yellow	255	255	0	#FFFF00

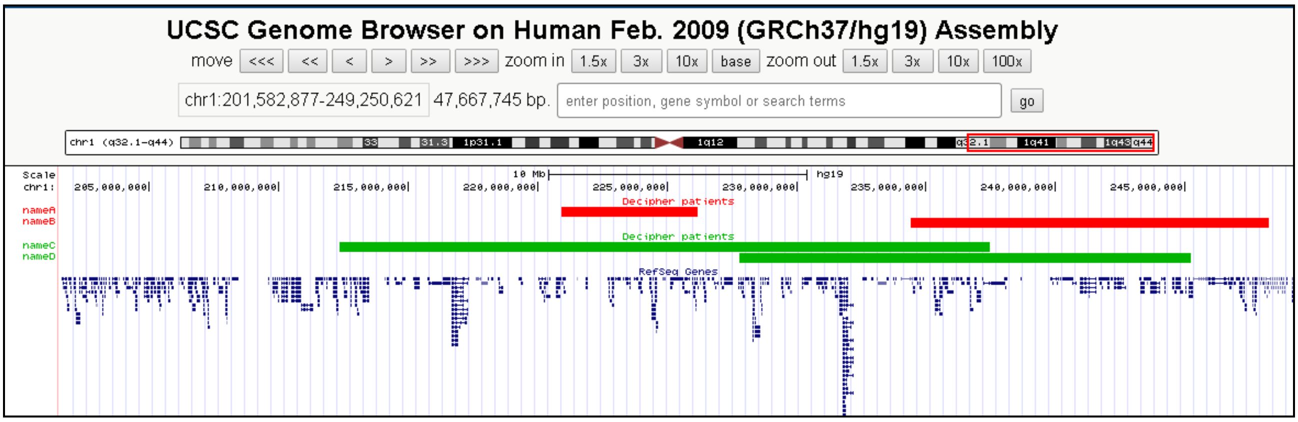
Usually, all colors are specified by some combination of values of red, green and blue, from 0 to 255 but, actually, you can also set numbers higher than 255 to get different nuances.

Example:
If you want to display with different colors some deletions and duplications, firstly you have to split them creating two BED files (one for deletions and one for duplications).Then, you have to write in the row *Genome Browser display characteristics* the code for the color you want for each BED file. For example, you can write “color=0,180,0” in the row of *display characteristics* of the BED file containing the duplications for visualizing them in green, and “color=255,0,0” in the row of *display characteristics* of the BED file containing deletions for visualizing them in green color.
Then, using UCSC Custom Track, you can display both deletions and duplications at the same time, or display just one type of CNV (only deletions or only duplications), because you are working with two separated files.

```
browser position chr1:1-200000000
track name="DELETIONS" description="Decipher patients" visibility=2 color=255,0,0
chr1   220916999     226162869     nameA
chr1   234413268     248220098     nameB

browser position chr1:1-200000000
track name="DUPLICATIONS" description="Decipher patients" visibility=2 color=0,180,0
chr1   212374942     237468576     nameC
chr1   227778741     245226841     nameD
```

Result:



chr1:201,582,877-249,250,621 47,667,745 bp.