



Using the Blueprint Track Hubs

Blueprint is providing Track Hubs to enable our users to view our data in both the Ensembl and UCSC genome browsers.

This document shows you how to attach these hubs to the browsers and configure them.

This example uses our monocyte and neutrophil release from March 2013

http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20130301/homo_sapiens/hub/hub.txt

This release contains signal from RNASeq, ChipSeq and WGS Bisulphite sequencing of Adult Monocyte and Neutrophil samples and Region calls for the ChipSeq experiments.

Attaching Hubs to Ensembl

You can view these hubs in Ensembl in two different ways.

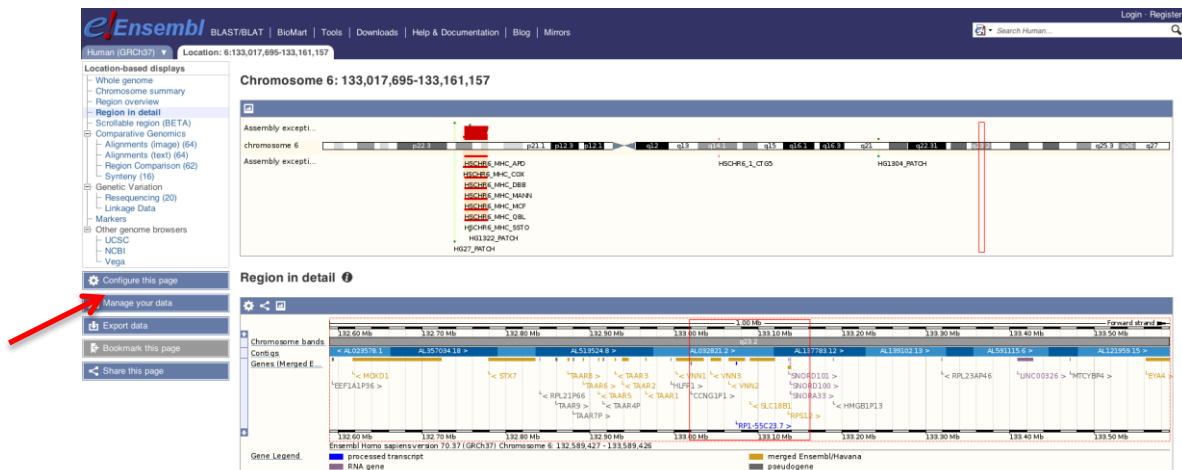
1. Paste this link into your browser

http://www.ensembl.org/Homo_sapiens/Location/View?g=ENSG00000130544;contigviewbottom=url:http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20130301/homo_sapiens/hub/hub.txt;format=DATAHUB;menu=Blueprint data

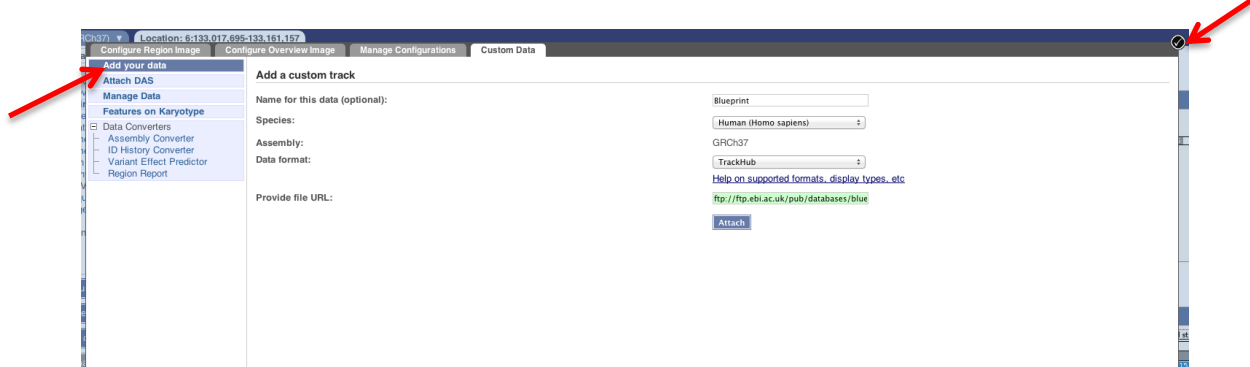
This will take you to the region 19:7069455-7087979 focused on ZNF557

2. From your region of interest

e.g http://www.ensembl.org/Homo_sapiens/Location/View?r=6:133017695-133161157



Click on the Manage your data menu item in the left hand menu



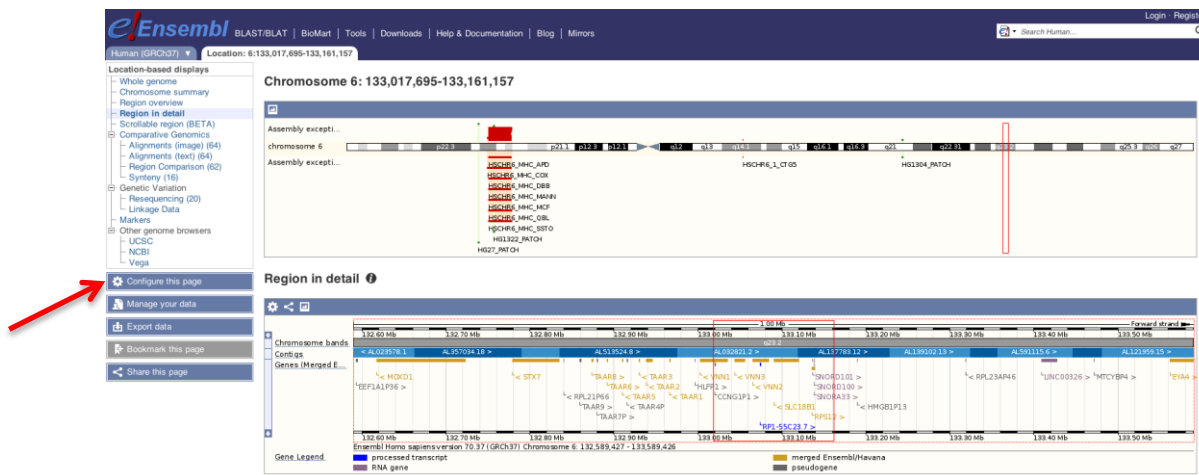
Click on the Add your data menu item on the left hand menu. Name your track; here I used Blueprint and select Trackhub from the dropdown menu. This will make a box for your url appear, paste in the hub url:

http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20130301/homo_sapiens/hub/hub.txt

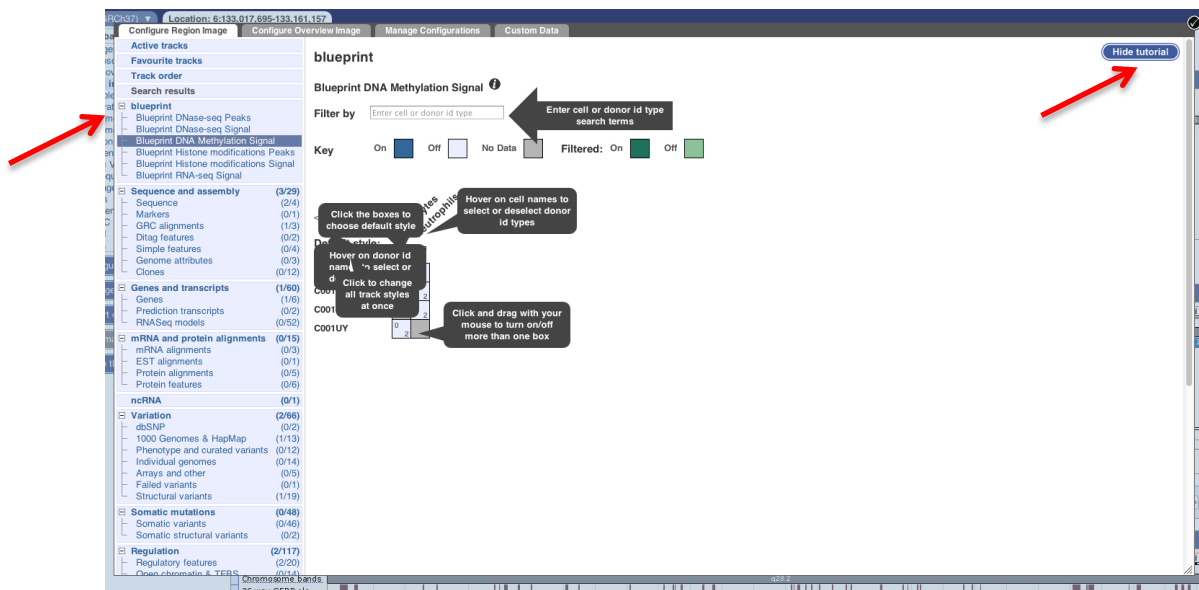
Then close this menu by clicking the tick on the top right hand corner of the box. This will return you to your previously selected location view.

Configuring your trackhub in Ensembl

By default Ensembl does not switch on any elements of a loaded track hub. To configure which aspects of the hub you switch on you need to click on the configure this page menu item in the left hand menu



You should see a menu item named in the same way as you labelled your hub when you loaded it. In this instance we used the name blueprint



The first time you load a track hub Ensembl has the tutorial flags for the configuration menu switched on. You can switch these off by clicking on the hide tutorial button in the top right hand corner. This button remains labelled as show tutorial if you wish to see them again.

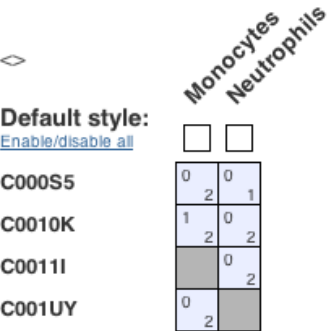
We have selected the Blueprint DNA Methylation Signal tracks. This is what the configuration menu looks like.

blueprint

Blueprint DNA Methylation Signal

Filter by

Key On  Off  No Data  Filtered: On  Off 



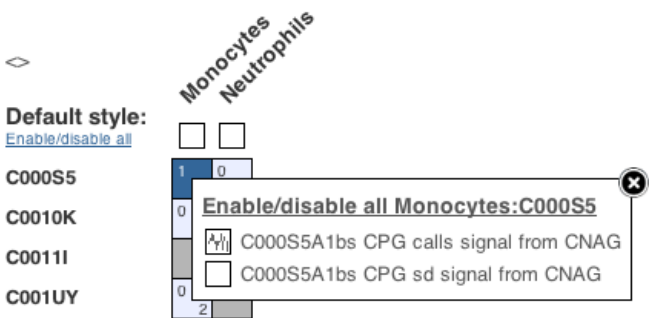
If you click on one of the boxes (The greyed out boxes have no data), this shows you the tracks available for this catagory.

blueprint

Blueprint DNA Methylation Signal

Filter by

Key On  Off  No Data  Filtered: On  Off 



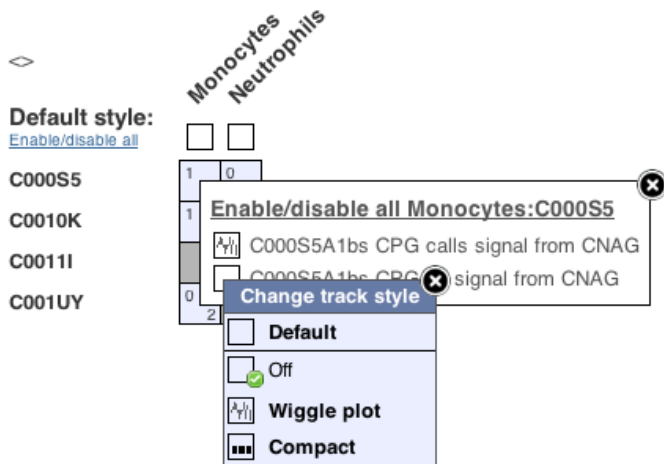
If you click on the C000S5 monocyte box you should seet this menu pop up and list the data available for this sample/cell type combination.

blueprint

Blueprint DNA Methylation Signal

Filter by

Key On  Off  No Data  Filtered: On  Off 



If you click on the C000S5A CPG call signal track you then get the option to switch the track on and choose the display options, I choose wiggle plot.

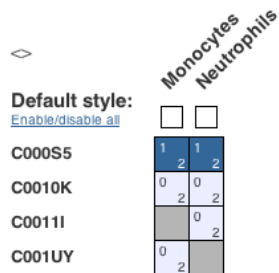
Active tracks	
Favourite tracks	
Track order	
Search results	
[+] blueprint data	
[-] Blueprint DNase-seq Peaks	
[-] Blueprint DNase-seq Signal	
[-] Blueprint DNA Methylation Signal	
[-] Blueprint Histone modifications Peaks	
[-] Blueprint Histone modifications Signal	
[-] Blueprint RNA-seq Signal	
[+] Sequence and assembly (3/29)	
[-] Sequence (2/4)	
[-] Markers (0/1)	
[-] GRC alignments (1/3)	
[-] Ditag features (0/2)	
[-] Simple features (0/4)	
[-] Genome attributes (0/3)	
[-] Clones (0/12)	
[+] Genes and transcripts (1/60)	
[-] Genes (1/6)	
[-] Prediction transcripts (0/2)	
[-] RNASeq models (0/52)	
[+] mRNA and protein alignments (0/15)	
[-] mRNA alignments (0/3)	
[-] EST alignments (0/1)	
[-] Protein alignments (0/5)	
[-] Protein features (0/6)	

blueprint data

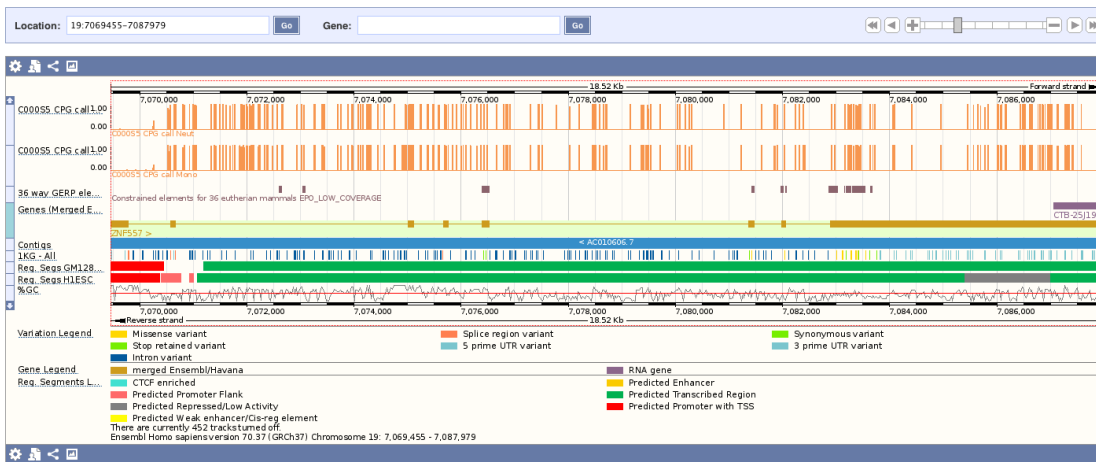
Blueprint DNA Methylation Signal

Filter by

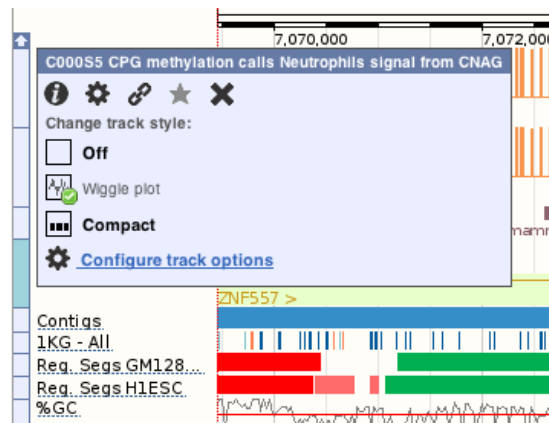
Key On  Off  No Data  Filtered: On  Off 



This is also done for the neutrophil data available for C000S5 and then the tick in the top right hand corner is used to close the menu and this data should load in the display.



Once you close your menu the data you selected will be displayed in location view. You can also configure this display by hovering over the name of the track and a series of options that allow you to change the style of display and find out more information about the track



Attaching Hubs to UCSC

You can view these hubs in Ensembl in two different ways.

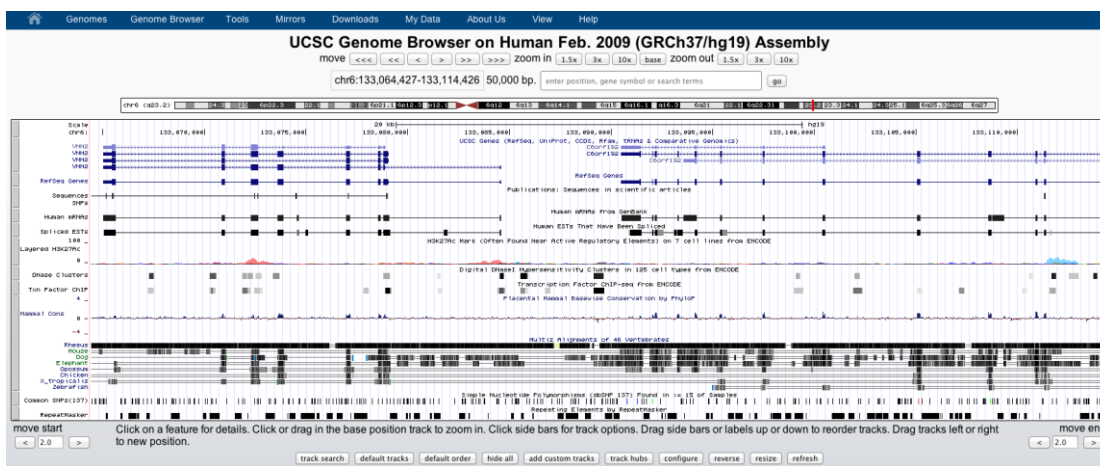
1. Paste this link into your browser

<http://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&hubUrl=http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20130301/hub/hub.txt>

This will take you to the last place in UCSC hg19 that you browsed. My examples work from chr6:133,064,427-133,114,426

2. Go to your location of interest in the UCSC Browser

<http://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19>



And click on the track hubs button in the bottom menu.

Track Data Hubs

Track data hubs are collections of tracks from outside of UCSC that can be imported into the Genome Browser. To import a public hub check the box in the list below. After import you will see a blue bar and label underneath the main browser graphic, and in the configure page. For more information, see the [User's Guide](#).

NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.

Public Hubs

My Hubs

URL:

Display	Hub Name	Description	Assemblies	URL	Disconnect
☒	Blueprint 20130301	Blueprint Epigenomics Data Hub	hg19	http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20130301/homo_sapiens/hub/hub.txt	X

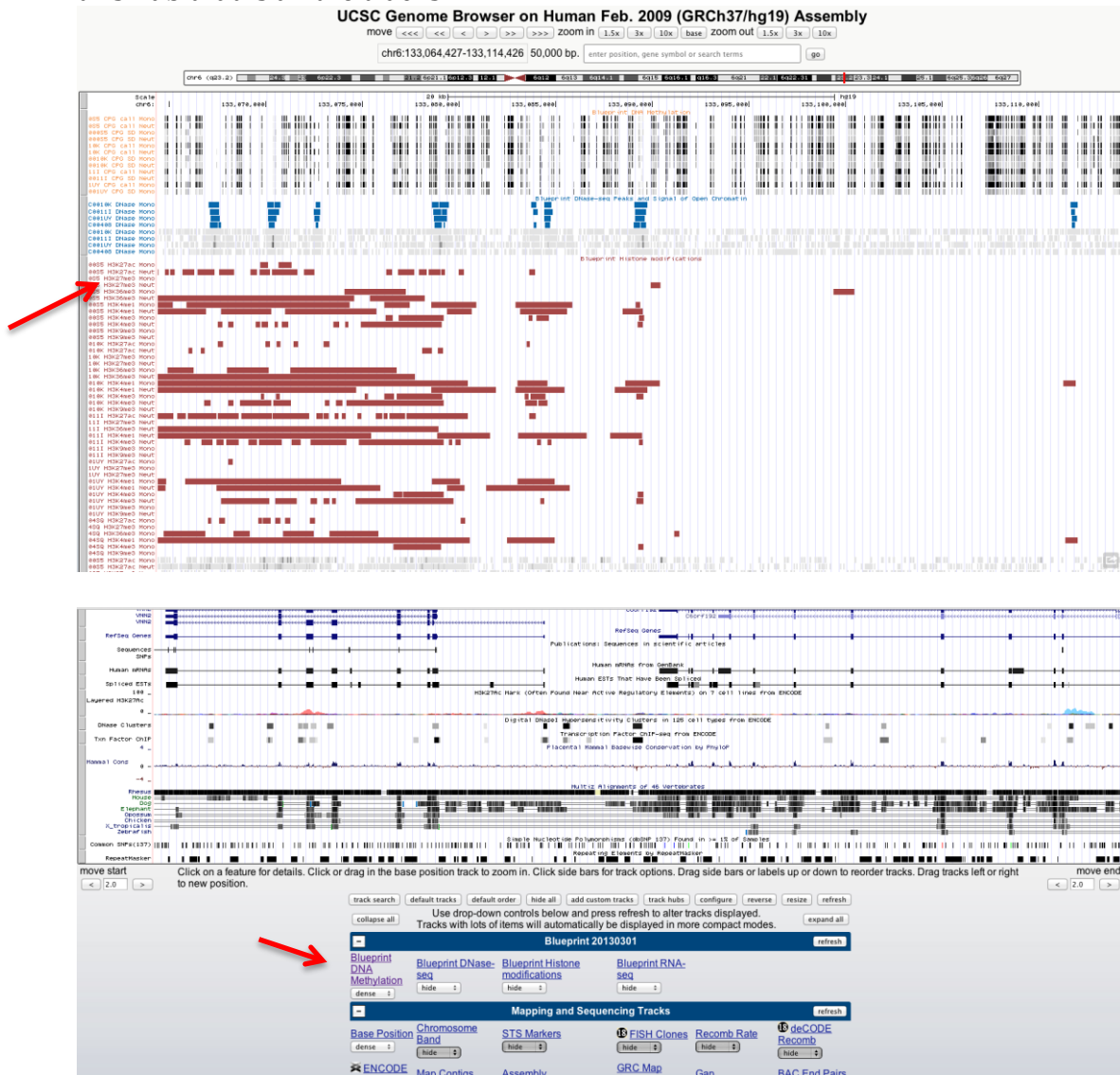
Contact genome@soe.ucsc.edu to add a public hub.

You will need to select the my hubs tab and paste:

http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20130301/homo_sapiens/hub/hub.txt into the hub URL box. Once loaded you click the load selected hubs button at the bottom of the page to return to your region of interest.

Configuring Hubs in UCSC

By default all hub tracks that the hub declares as on are switched on in the UCSC browser, for this hub that is all the tracks.



You can see the hub configuration menu at the top of configuration for the UCSC Browser. By default all these tracks are set to display type dense. I have switched all the tracks that are not DNA Methylation to hide to reduce the amount of data on screen. After making these changes you need to click the refresh button in the top right hand corner of the menu set.

If you click on the name of Blueprint DNA Methylation you will be taken to a more detailed configuration menu.

Blueprint DNA Methylation Track Settings

Blueprint DNA Methylation

Maximum display mode: [Reset to defaults](#)

Select view ([help](#)):
[Signal](#)

Select subtracks by cell type and donor id:

	All	Cell type	Monocytes	Neutrophils
Donor id	☐	☐	☐	☐
C000S5	☒	☒	☒	☒
C0010K	☐	☐	☐	☐
C0011I	☐	☐	☐	☐
C001UY	☐	☐	☐	☐

Select subtracks further by: (select multiple categories and items - [help](#))

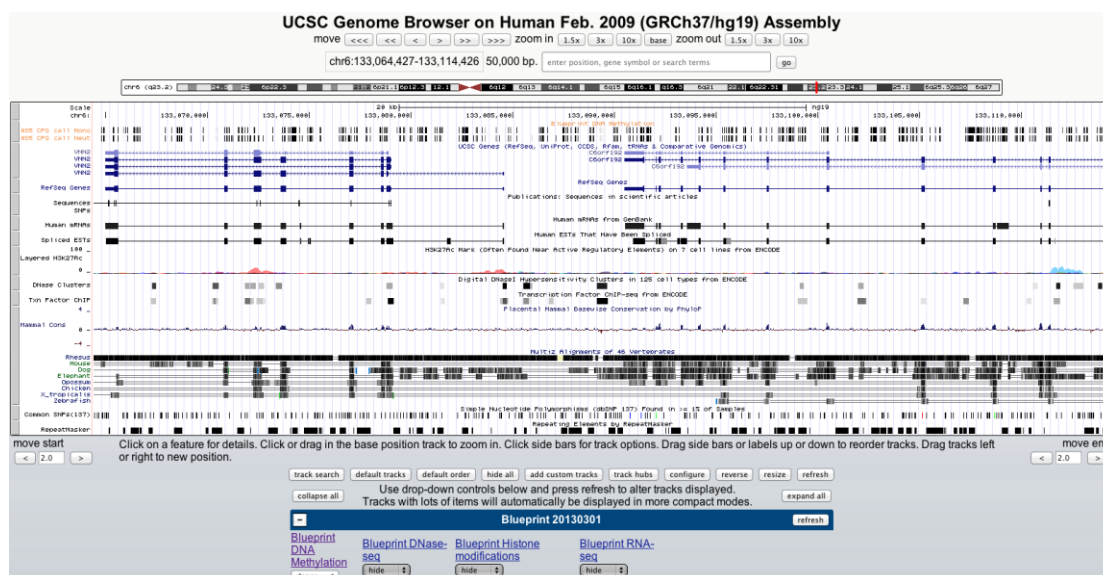
View:

List subtracks: ☐ only selected/visible ☒ all (2 of 11 selected)

	View ¹	Donor id ²	Mark ³	Cell type ⁴	Track Name ⁵
☒	dense	Signal C000S5	CPG methylation calls	Monocytes	C000S5A1bs CPG_calls signal from CNAG
☐	dense	Signal C000S5	CPG methylation sd	Monocytes	C000S5A1bs CPG_sd signal from CNAG
☒	dense	Signal C000S5	CPG methylation calls	Neutrophils	C000S5A2bs CPG_calls signal from CNAG
☐	dense	Signal C0010K	CPG methylation calls	Neutrophils	C0010KA1bs CPG_calls signal from CNAG
☐	dense	Signal C0010K	CPG methylation sd	Neutrophils	C0010KA1bs CPG_sd signal from CNAG
☐	dense	Signal C0010K	CPG methylation calls	Monocytes	C0010KA2bs CPG_calls signal from CNAG
☐	dense	Signal C0010K	CPG methylation sd	Monocytes	C0010KA2bs CPG_sd signal from CNAG
☐	dense	Signal C0011I	CPG methylation calls	Neutrophils	C0011IA3bs CPG_calls signal from CNAG
☐	dense	Signal C0011I	CPG methylation sd	Neutrophils	C0011IA3bs CPG_sd signal from CNAG
☐	dense	Signal C001UY	CPG methylation calls	Monocytes	C001UYA3bs CPG_calls signal from CNAG
☐	dense	Signal C001UY	CPG methylation sd	Monocytes	C001UYA3bs CPG_sd signal from CNAG

2 of 11 selected

Here I have switched off everything that is not associated with C000S5. Again you hit the submit button which is found both at the top and bottom of this configuration page to take you back to your starting point.



Now at the top of the view you can see just the tracks that you have switched on.

If you have any questions about these track hubs or other aspects of the Blueprint project please email blueprint-info@ebi.ac.uk.