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.

The example in this tutorial shows monocyte and neutrophil data from the September 2015 release. This release contains signal and region data from RNA-Seq, ChIP-Seq and WGS Bisulfite sequencing from across the haematopoetic lineage.

The latest track hub is available from

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

Note: This tutorial is based on Blueprint trackhub for human genome build GRCh38. Trackhub and tutorial based on GRCh37 can be found from January 2015 release. ftp://ftp.ebi.ac.uk/pub/databases/blueprint/releases/20150128/
Attaching Hubs to Ensembl

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

1. Paste this link into your browser
   http://ensembl.org/Homo_sapiens/Location/View?g=ENSG00000130544;contigviewbottom=url:http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/current_release/homo_sapiens/hub/hub.txt;format=DATAHUB;menu=Blueprint_data

   This will take you to the region 19: 7,069,455-7,087,979 focused on ZNF557 with the trackhub loaded under your data. You can change the track hub display settings using “Configure this page” option.

2. Or from your region of interest such as:
   http://ensembl.org/Homo_sapiens/Location/View?g=ENSG00000130544;r=19:7069444-7087968

   Click on the Add your data menu item on the left hand menu [Fig. 1]. Add a name for your track in the Name for this data box; e.g. “Blueprint”. Select Trackhub from the dropdown menu [Fig. 2]. This will make a box for your url appear, paste in the hub url:
   http://ftp.ebi.ac.uk/pub/databases/blueprint/releases/current_release/homo_sapiens/hub/hub.txt

   Hit the Attach button to attach the hub to the page.
Configuring your trackhub in Ensembl

By default Ensembl does not switch on any elements of a loaded track hub. When you first load a hub you will be presented with a link to “Configure your hub” which takes you straight to the configuration menu [Fig.3].

Fig. 3

Alternatively you can use the configure this page menu item in the left hand menu [Fig. 4]

Fig. 4
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 [Fig. 5].

Fig. 5

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.
When the Blueprint Signal track is selected. This is what the configuration menu looks like [Fig. 6].

![Blueprint Signal Menu](image)

**Fig. 6**
If you click on one of the boxes (The greyed out boxes have no data), this shows you the tracks available for this category [Fig. 7].

![Blueprint Hub](image)

**Fig. 7**
If you click on the C000S5 monocyte BS-Seq box you should set this menu pop up and list the data available for this sample/cell type combination [Fig. 8].
If you click on the C0005 CPG call signal track you then get the option to switch the track on and choose the display options, Choose the wiggle plot [Fig. 9].
Also turn on the CPG call signal track for the C000S5 mature neutrophil data [Fig. 10].

Fig. 10

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 [Fig. 11].

![Fig. 11](image1)

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 [Fig. 12].

![Fig. 12](image2)
Attaching Hubs to UCSC

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

1. Paste this link into your browser


   This will take you to the last place in UCSC hg38 that you browsed. This examples work from chr19: 7,069,455-7,087,979

2. Go to your location of interest in the UCSC Browser and click on the track hubs button in the bottom menu [Fig. 13].

   http://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38

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Fig. 13
Select “Blueprint Hub” from Public Hubs and connect [Fig. 14]
Or select the “My Hubs” tab and paste the link into the hub URL box and select “Add Hub” to load selected hub return to your region of interest [Fig. 15].

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

Fig. 15
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 16 tracks. These are region and signal tracks of all available assay types from monocyte samples from a single donor (C0010K).

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.

If you click on the name of Blueprint you will be taken to a more detailed configuration menu [Fig. 16].
Configuration panel view of Blueprint trackhub in UCSC [Fig. 17]
Here BS-Seq CPG call signal tracks from monocyte and neutrophil samples are selected [Fig. 18 & 19]. 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 genome view on UCSC browser [Fig. 18].

Tracks associated with specific samples can be selected from the “Sample barcode” drop down list [Fig. 19]
Now at the top of the view you can see just the tracks that you have selected are now switched on [Fig. 20].

Fig. 20

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