

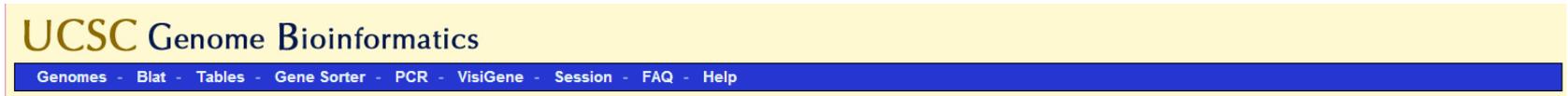
# UCSC data hubs

How to use them ?

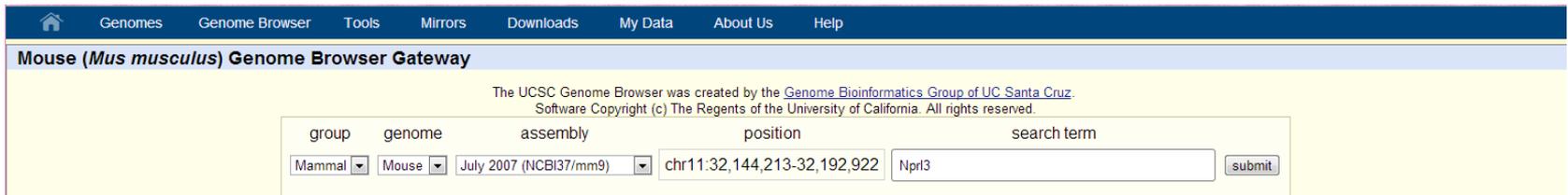
1.10.2013

Go to UCSC server – European mirror here  
<http://genome-euro.ucsc.edu/>

When clicking that, you should see following :



1) Go to the Genomes,  
And select the genome, and the gene you want to look at



2) Press “submit”

# UCSC Genome Bioinformatics

[Genomes](#) - [Blat](#) - [Tables](#) - [Gene Sorter](#) - [PCR](#) - [VisiGene](#) - [Session](#) - [FAQ](#) - [Help](#)



3) Now, go BACK to the Genomes – where you just were !

[Home](#) [Genomes](#) [Genome Browser](#) [Tools](#) [Mirrors](#) [Downloads](#) [My Data](#) [About Us](#) [Help](#)

## Mouse (*Mus musculus*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).  
Software Copyright (c) The Regents of the University of California. All rights reserved.

group	genome	assembly	position	search term
<input type="text" value="Mammal"/>	<input type="text" value="Mouse"/>	<input type="text" value="July 2007 (NCBI37/mm9)"/>	<input type="text" value="chr11:32,132,419-32,167,614"/>	<input type="text" value="enter position, gene symbol or search terms"/>

[Click here to reset](#) the browser user interface settings to their defaults.



4) Click “track hubs” to add a hub !

Genomes Genome Browser Tools Mirrors Downloads My Data About Us Help

### 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 the hub will show up as a group of tracks with its own blue bar and label underneath the main browser graphic, and in the configure page. For more information, see the [User's Guide](#).

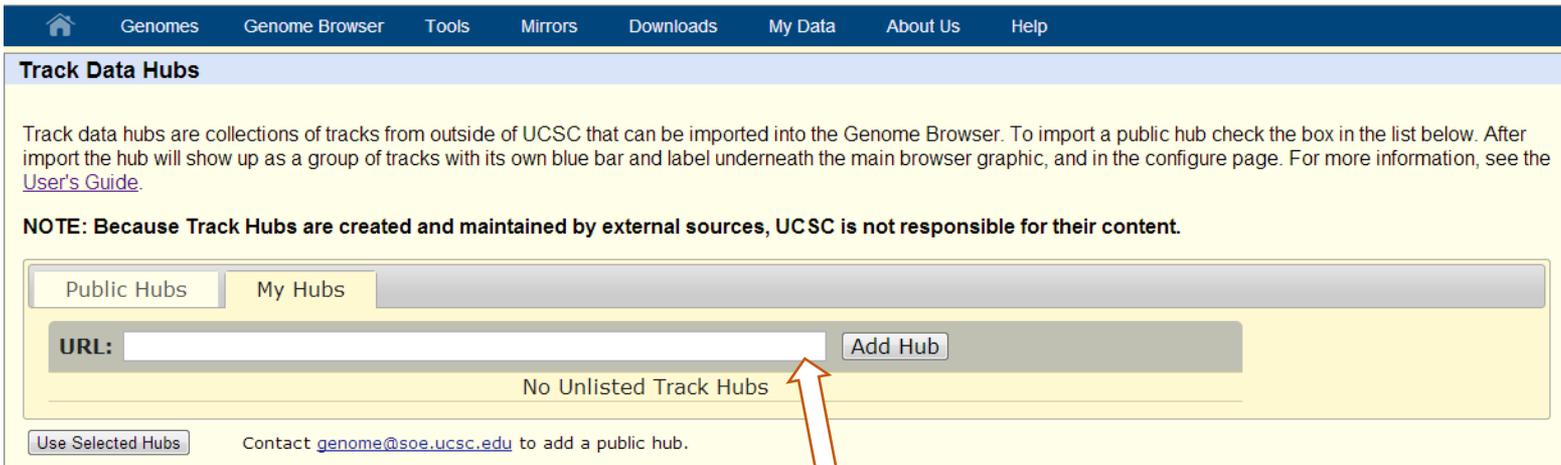
**NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.**

Public Hubs My Hubs

URL:  Add Hub

No Unlisted Track Hubs

Use Selected Hubs Contact [genome@soe.ucsc.edu](mailto:genome@soe.ucsc.edu) to add a public hub.



5) In here, copy+paste a hub address !

<http://sara.molbiol.ox.ac.uk/public/username/.../.../hub.txt>

### Track Data Hubs

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

Public Hubs My Hubs

URL: </public/telenius/[redacted]/hub.txt Add Hub

6) Click "Add Hub"



### Track Data Hubs

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

Public Hubs My Hubs

URL: Add Hub

Display	Hub Name	Description	Assemblies	URL	Disconnect
<input checked="" type="checkbox"/>	Ter119 MM9 : DNaseI, histones	Ter119 mm9 mapped data : DNaseI and Histone Markers - mostly C57bl6, but also Mixed Strain (MS)	mm9	http://sara.molbiol.ox.ac.uk/[redacted]hub.txt	<input type="checkbox"/>

Use Selected Hubs

Contact [genome@soe.ucsc.edu](mailto:genome@soe.ucsc.edu) to add a public hub.

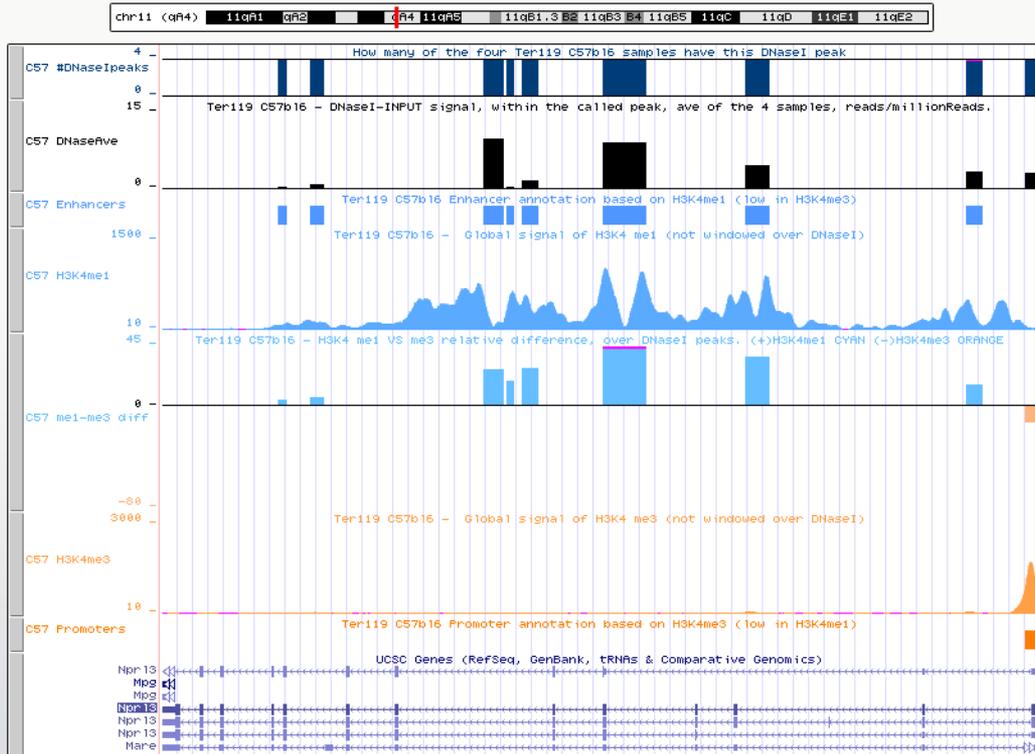


7) Click "Use Selected Hubs"

# UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

chr11:32,132,419-32,167,614 35,196 bp.  go



Ter119 MM9 : DNaseI, histones refresh

<a href="#">C57 #DNaseIpeaks</a> full	<a href="#">C57 #OverlapDNaseI</a> hide	<a href="#">C57 DNaseAve</a> full	<a href="#">Ter119 C57 Input</a> hide	<a href="#">C57 H3K36me3</a> hide	<a href="#">Ter119Mix H4K27ac</a> hide
<a href="#">Ter119MixH3K27me3</a> hide	<a href="#">C57 Enhancers</a> full	<a href="#">C57 H3K4me1</a> full	<a href="#">C57 me1-me3 diff</a> full	<a href="#">C57 H3K4me3</a> full	<a href="#">C57 Promoters</a> full
<a href="#">C57 H3K4meOutliers</a> hide					



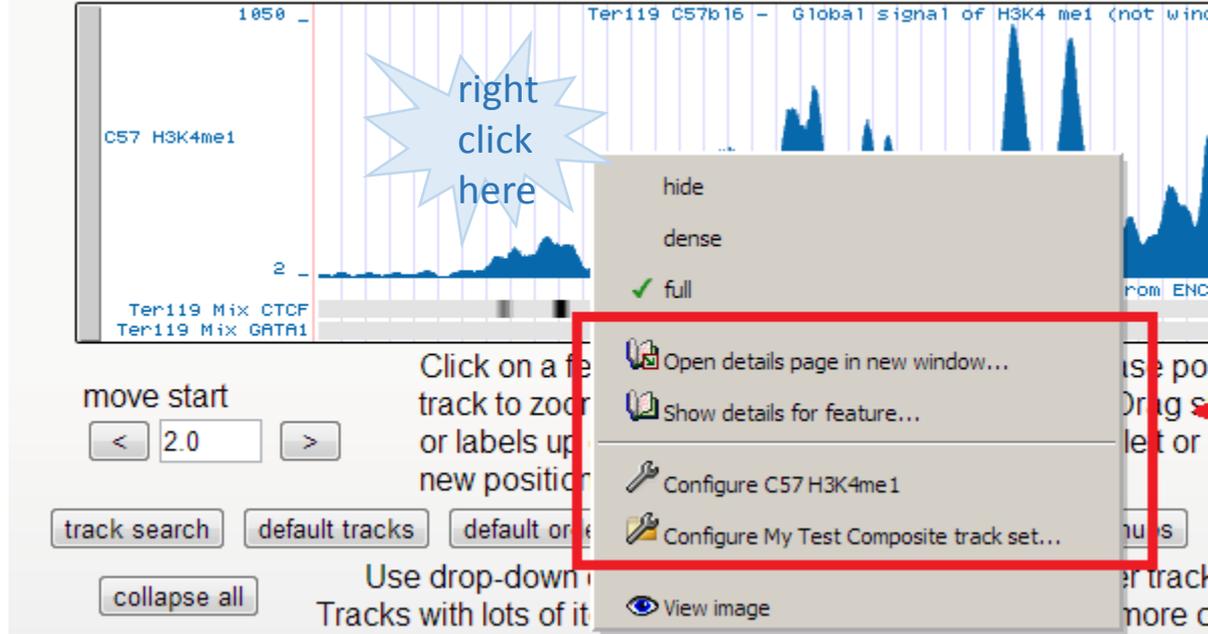
8) All the tracks of the hub show in standard UCSC way below the visualisation. Just click and play with them like you would have normal UCSC tracks !

- 10) Some hubs may have additional track information  
and options to change the visualisation style , coded into the hub  
→ Right click any track in the **graph area** !

The screenshot displays the UCSC Genome Browser interface for Mouse July 2007 (NCBI37/mm9) Assembly. The main track shown is 'C57 H3K4me1', with a blue signal plot. A right-click context menu is open over the track, listing options: 'hide', 'dense', 'full' (checked), 'Open details page in new window...', 'Show details for feature...', 'Configure C57 H3K4me1', 'Configure My Test Composite track set...', and 'View image'. A blue starburst graphic with the text 'right click here' points to the track. A red arrow points to the 'move end' control below the track. The interface includes navigation buttons (move, zoom in, zoom out), a search bar, and various track management options (collapse all, expand all, track search, default tracks, etc.).

Change visualisation style,  
check sample details

→ Right click any track in  
the **graph area** !



You can change the  
track visualisation :

Ter119 RNA tracks Track Settings

### Ter119 C57bl6 ( NanoCage, PAM, PAP), and Ter119

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

Select view ([help](#)):  
[BigWig tracks](#)  [Annotation tracks \(BigBed\)](#)

Select subtracks by experiment and strand and rna type:

		NanoCage forward	NanoCage reverse	PAM forward	PAM reverse	PAP	Nascent forward	Nascent reverse
<input type="checkbox"/> All								
	<i>Experiment and strand</i>							
	<i>RNA type</i>	<input type="checkbox"/>						
	PolyA plus	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
	PolyA minus	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>			
	Total RNA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>			<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

List subtracks:  only selected/visible  all (23 of 23 selected)

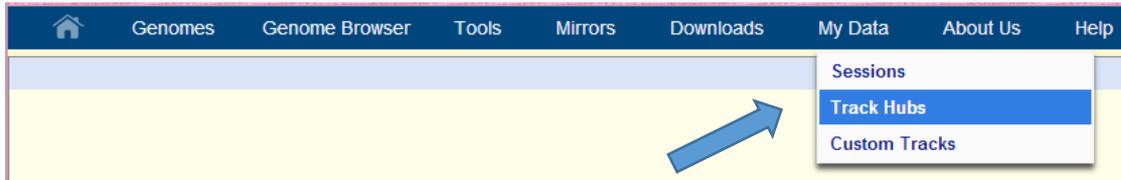
	View <sup>1</sup>	Experiment and strand <sup>2</sup>	RNA type <sup>3</sup>	Track Name <sup>4</sup>
<input checked="" type="checkbox"/>	<input type="text" value="full"/>	BigWig tracks	NanoCage forward	PolyA minus Ter119+C57bl6 - NanoCage
<input checked="" type="checkbox"/>	<input type="text" value="dense"/>	Annotation tracks (BigBed)	NanoCage forward	PolyA minus Ter119+C57bl6 - NanoCage

Many hubs have “extra  
information” under this  
(scroll down )

- Details of the sample
- Details of the bioinformatics of the sample



## 14) To see which hubs you have loaded ..



The 'Track Data Hubs' page in the UCSC Genome Browser. It includes a navigation menu at the top, a title 'Track Data Hubs', and a paragraph explaining that track data hubs are collections of tracks from outside of UCSC. A note states: "NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content." Below this is a section for 'Public Hubs' and 'My Hubs'. There is a 'URL:' input field and an 'Add Hub' button. A table lists the loaded hubs, with one hub selected. A blue arrow points to the 'Display' checkbox, and another blue arrow points to the 'Disconnect' button.

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 the hub will show up as a group of tracks with its own 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:  Add Hub

Display	Hub Name	Description	Assemblies	URL	Disconnect
<input checked="" type="checkbox"/>	Ter119 MM9 : DNaseI, histones	Ter119 mm9 mapped data : DNaseI and Histone Markers - mostly CS7bl6, but also Mixed Strain (MS)	mm9	<a href="http://sara.molbiol.ox.ac.uk/.../hub.txt">http://sara.molbiol.ox.ac.uk/.../hub.txt</a>	X

Use Selected Hubs Contact [genome@soe.ucsc.edu](mailto:genome@soe.ucsc.edu) to add a public hub.

Hides the hub

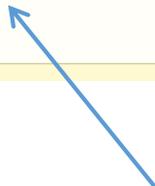
Removes the hub

### 13) You can use simultaneously many hubs, if you wish !

Public Hubs My Hubs

URL:  Add Hub

Display	Hub Name	Description	Assemblies	URL	Disconnect
<input checked="" type="checkbox"/>	Ter119 MM9 : DNaseI, histones	Ter119 mm9 mapped data : DNaseI and Histone Markers - mostly C57bl6, but also Mixed Strain (MS)	mm9	http://sara.molbiol.ox.ac.uk/public/[redacted]/hub.txt	X
<input checked="" type="checkbox"/>	Human genome 19	Human genome 19, our Oxford-generated data	hg19	http://sara.molbiol.ox.ac.uk/p[redacted]/hub.txt	X
<input checked="" type="checkbox"/>	Ter119 mm9 - RNA sequencing	Ter119 mm9 mapped data - various RNA sequencing tracks. Mainly C57bl6, but also Mixed Strain (MS)	mm9	http://sara.molbiol.ox.ac.uk/p[redacted]/hub.txt	X



UCSC will automatically select for visualisation only the hubs having the genome you selected in the "Genome" tab