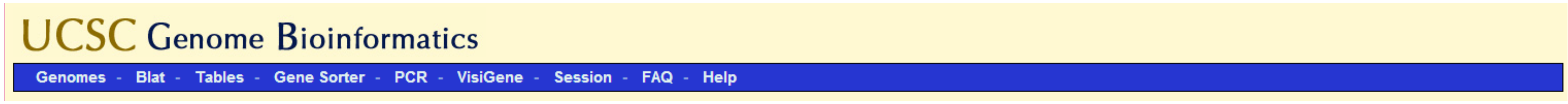
UCSC data hubs

How to use them ?

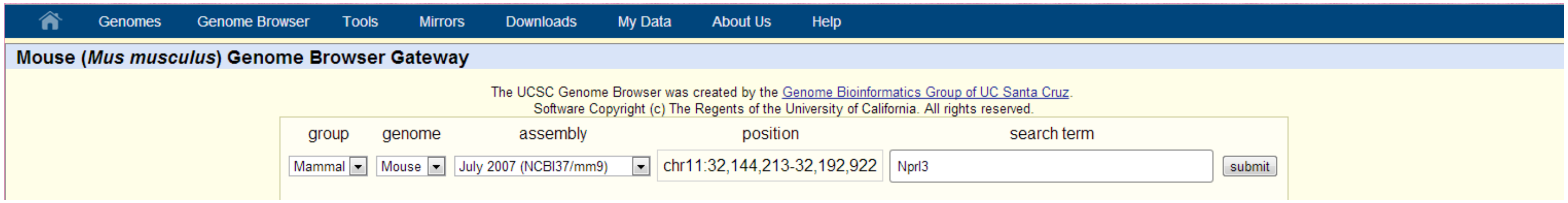
1.10.2013

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



Mouse (*Mus musculus*) Genome Browser Gateway

The UCSC Genome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
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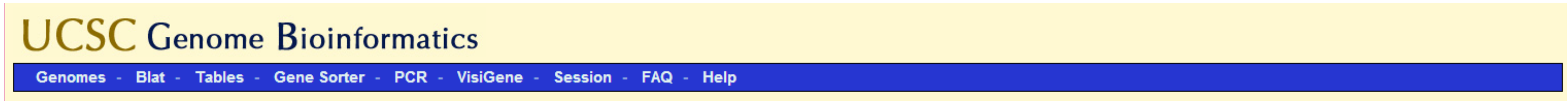
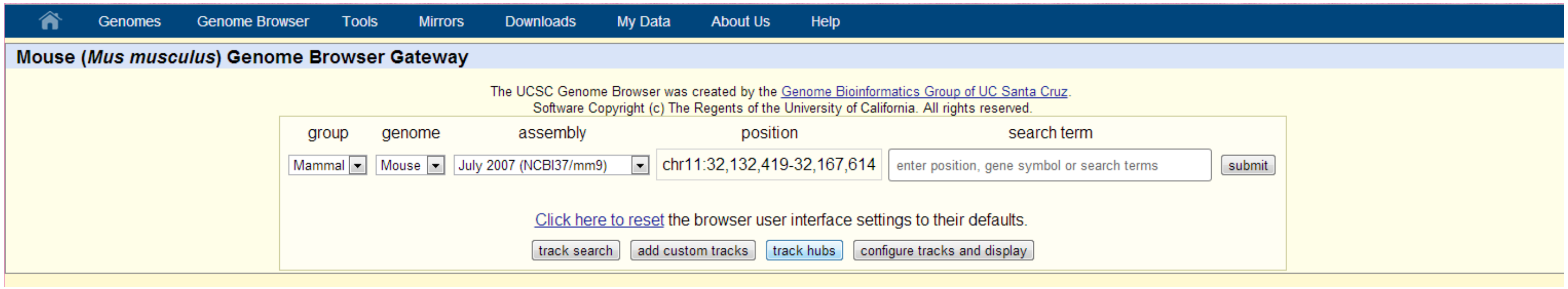
group	genome	assembly	position	search term
Mammal	Mouse	July 2007 (NCBI37/mm9)	chr11:32,144,213-32,192,922	Nprl3

2) Press “submit”



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



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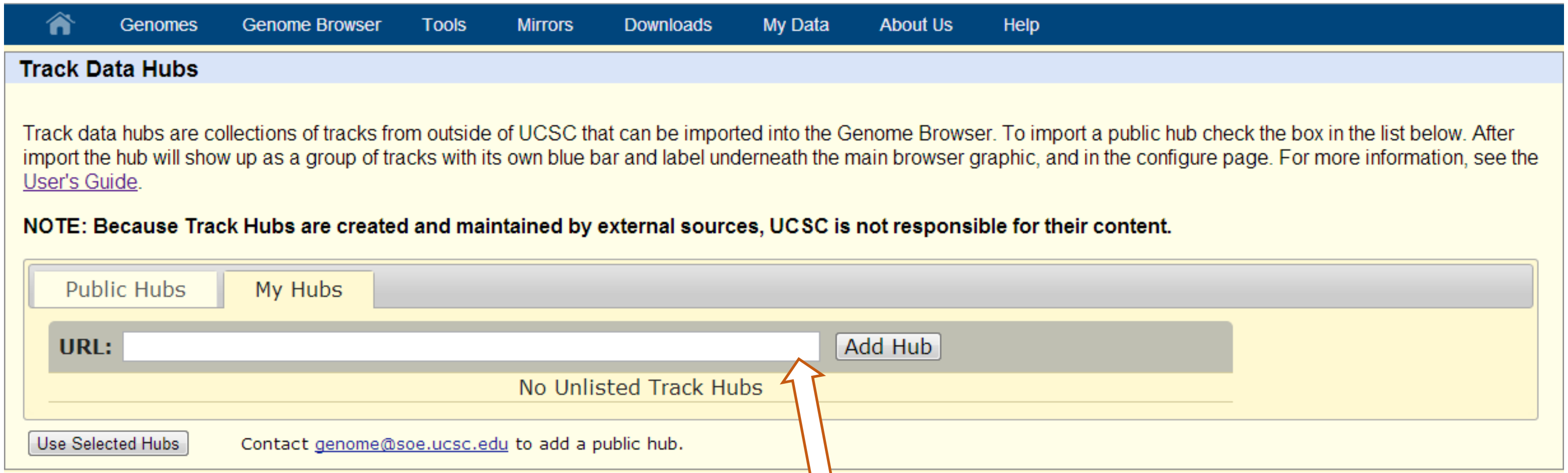
group	genome	assembly	position	search term
Mammal	Mouse	July 2007 (NCBI37/mm9)	chr11:32,132,419-32,167,614	enter position, gene symbol or search terms

Click here to reset the browser user interface settings to their defaults.

4) Click “track hubs” to add a hub !



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.

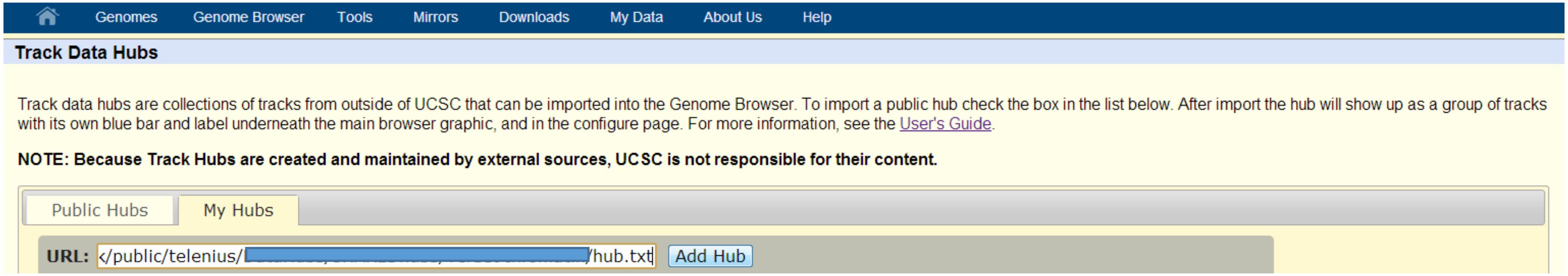
NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.

No Unlisted Track Hubs

Contact 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



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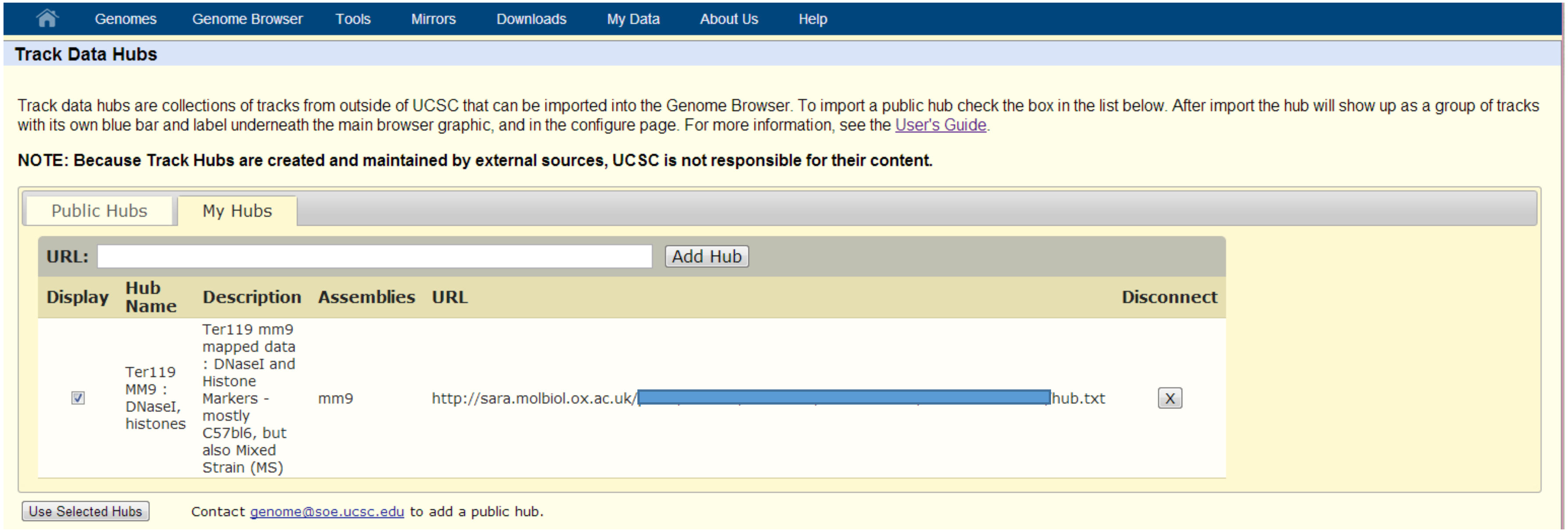
URL: </public/telenius/[redacted]/hub.txt

6) Click “Add Hub”



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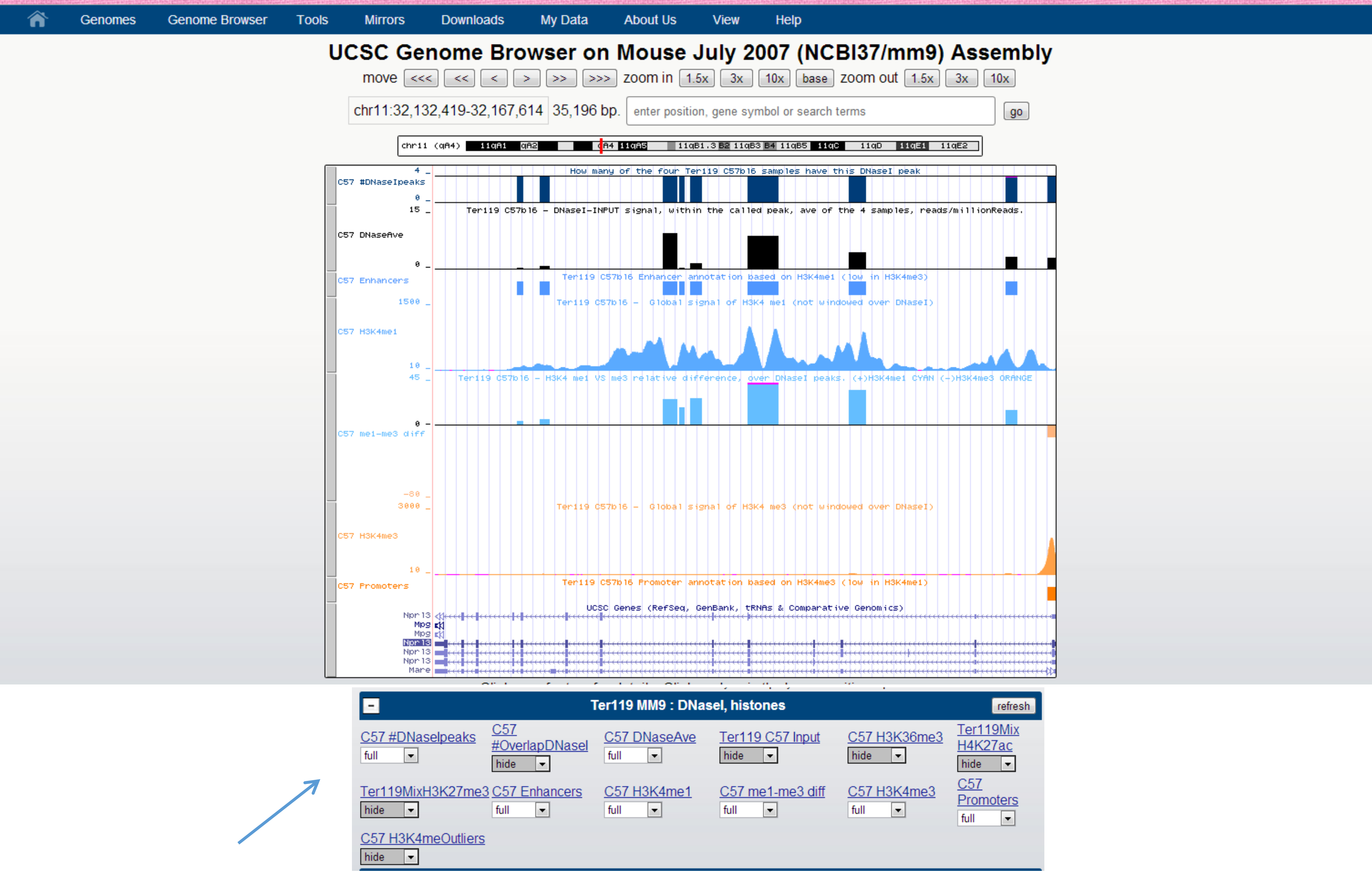
URL:

Display	Hub Name	Description	Assemblies	URL	Disconnect
☑	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	X

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

7) Click “Use Selected Hubs”



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

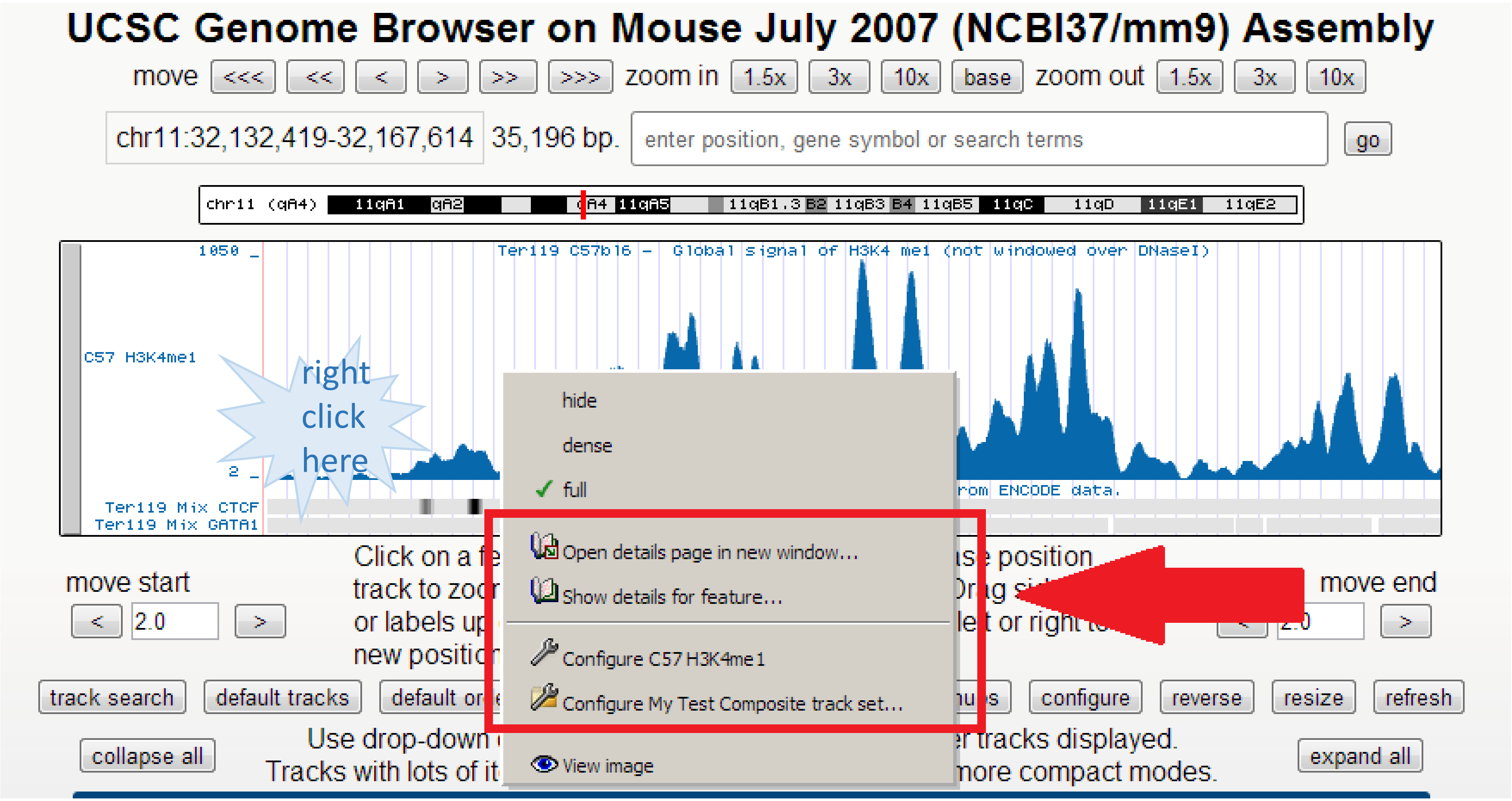
chr11:32,132,419-32,167,614 35,196 bp.

Ter119 MM9 : DNaseI, histones

- C57 #DNaseIpeaks: full
- C57 #OverlapDNaseI: hide
- C57 DNaseAve: full
- Ter119 C57 Input: hide
- C57 H3K36me3: hide
- Ter119Mix H4K27ac: hide
- Ter119MixH3K27me3: hide
- C57 Enhancers: full
- C57 H3K4me1: full
- C57 me1-me3 diff: full
- C57 H3K4me3: full
- C57 Promoters: full
- C57 H3K4meOutliers: hide

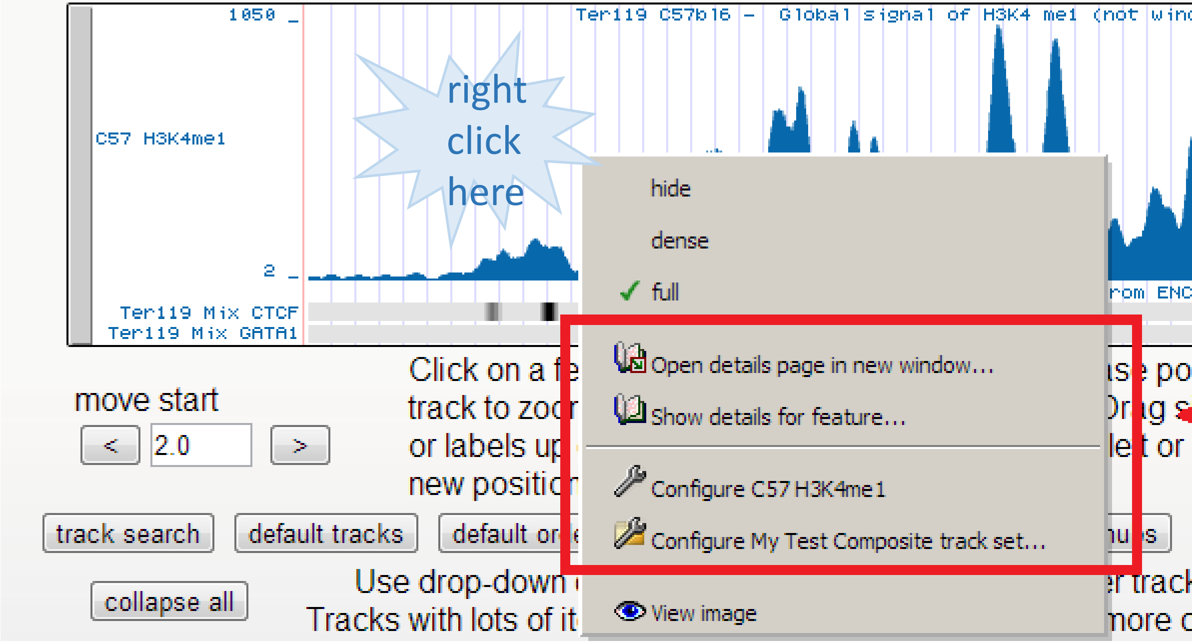
8) All the tracks of the hub show in standard UCSC way below the visualisation. Just click and play with them like you would have normal UCSC tracks !

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 !

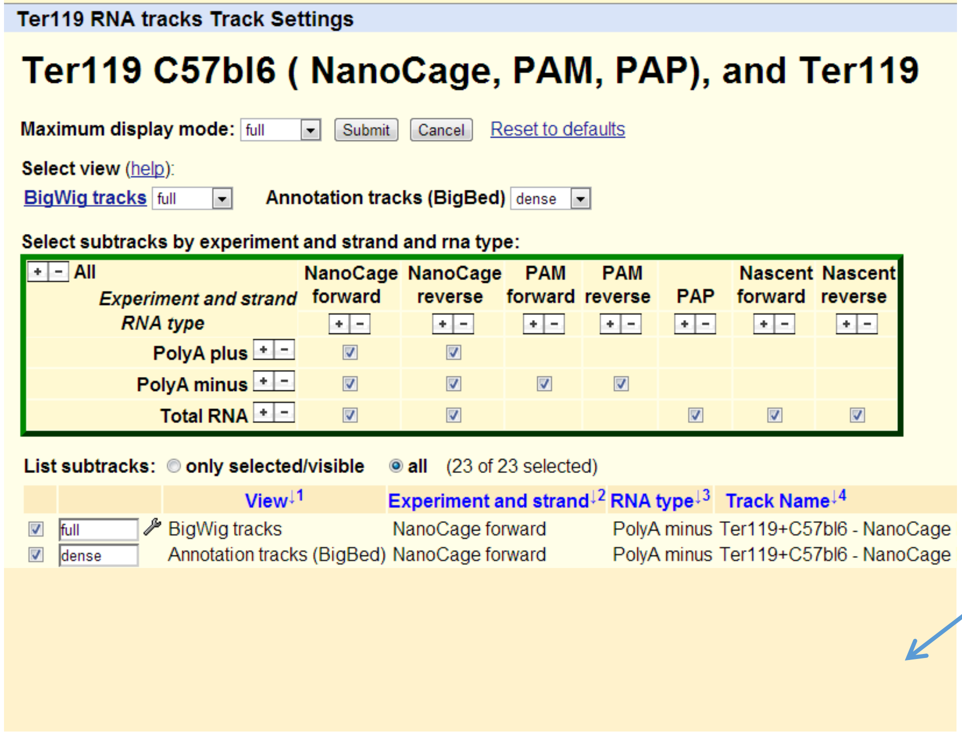

UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

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: full ▾ Submit Cancel Reset to defaults

Select view (help):

BigWig tracks full ▾ **Annotation tracks (BigBed)** dense ▾

Select subtracks by experiment and strand and rna type:

+ − All *Experiment and strand* *RNA type*	NanoCage forward + −	NanoCage reverse + −	PAM forward + −	PAM reverse + −	PAP + −	Nascent forward + −	Nascent reverse + −
PolyA plus + −	☑	☑					
PolyA minus + −	☑	☑	☑	☑			
Total RNA + −	☑	☑			☑	☑	☑

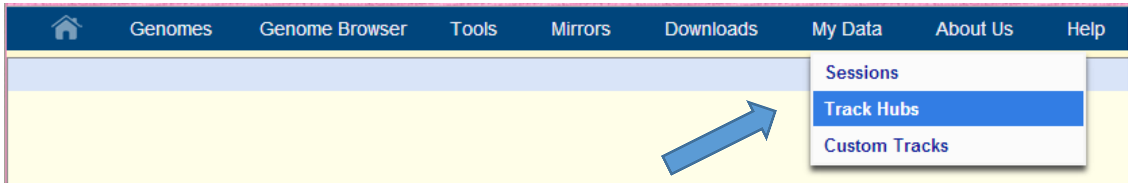
List subtracks: ○ only selected/visible ● all (23 of 23 selected)

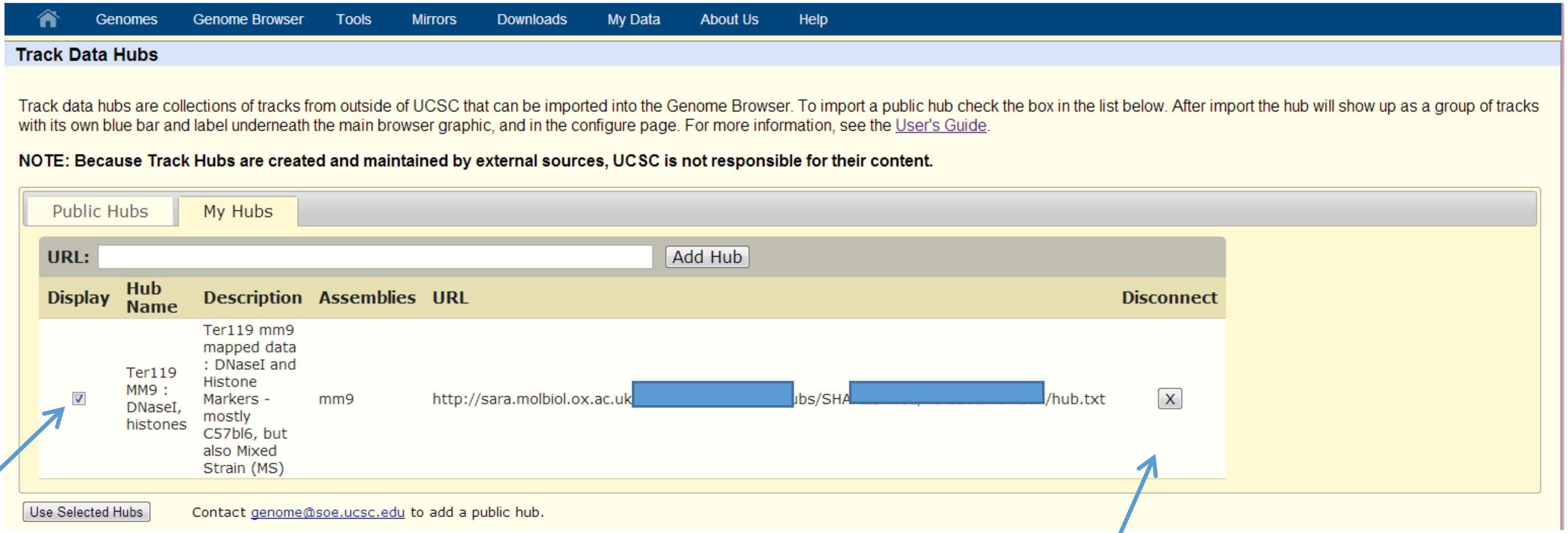
		View↓1	Experiment and strand↓2	RNA type↓3	Track Name↓4
☑	full	BigWig tracks	NanoCage forward	PolyA minus	Ter119+C57bl6 - NanoCage
☑	dense	Annotation tracks (BigBed)	NanoCage forward	PolyA minus	Ter119+C57bl6 - NanoCage

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 ..





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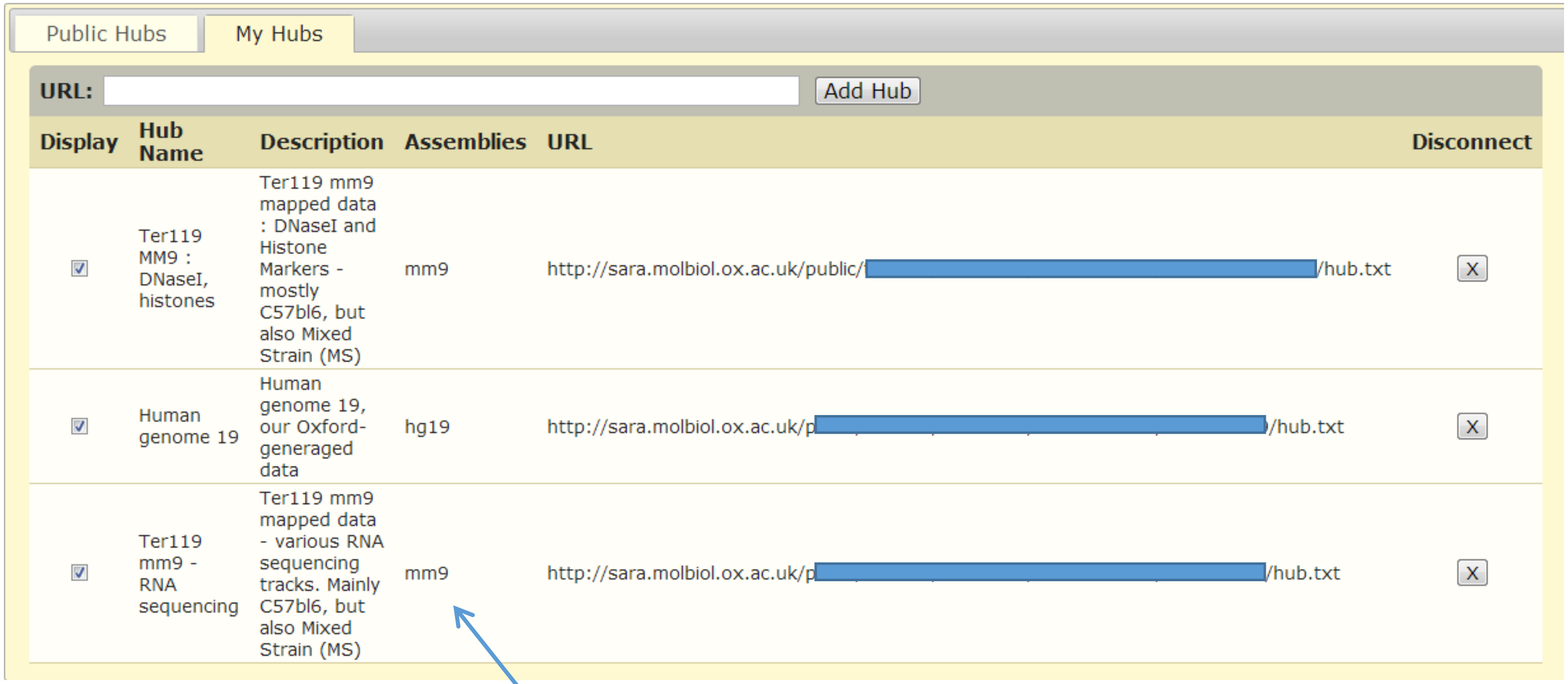
Contact genome@soe.ucsc.edu to add a public hub.

Hides the hub

Removes the hub

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



Display	Hub Name	Description	Assemblies	URL	Disconnect
☑	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
☑	Human genome 19	Human genome 19, our Oxford-generaged data	hg19	http://sara.molbiol.ox.ac.uk/p[redacted]/hub.txt	X
☑	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