

# Present for Sally

MBL, from Ian, May 2014

# How to see Gert's data on UCSC

- Go to Gert's website:

## Genome assembly Xentr v7.1

The "tracks" file below is a bigWig file that can be used to visualize *H3K4me3*, *TBP*, *H3K4me1*, *RNAPII*, *H3K27me3*, *RNAseq*, *MethylCap* and *Input tracks* of multiple stages (stages 9, 12, 16 and 30) at the [genome browser at NIMR](#). Alternatively, browse genes for H3K4me3 and H3K27me3 profiles at our [gene profile page](#).

File Name:	Date Created:	File Size:
 <a href="#">mostconserved_gmap_k12.bed.gz</a>	7/17/2013	5,814 KB
 <a href="#">Veenstra_tracks_JGI-7-1__3.wig.gz</a>	7/15/2013	1 KB
 <a href="#">xtev_v3-4_JGI7-1_all.bed.gz</a>	12/4/2013	1,460 KB
 <a href="#">xtev_v3-4_JGI7-1_genename.bed.gz</a>	6/14/2013	999 KB

## Genome assembly [Joint Genome Institute Xentr v4.1](#) (xenTro2, August 2005).

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 <a href="#">DNAmE_St12_500mM_xenTro2.wg.gz</a>	3/23/2011	5,473 KB
 <a href="#">DNAmE_St12_700mM_xenTro2.wg.gz</a>	3/23/2011	5,561 KB

# How to see Gert's data on UCSC

Newer time-series data



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# How to see Gert's data on UCSC

- All his data are aligned already – wig files are a lot like bam files or bedgraph files
- The newer stuff is aligned to Trop genome v7.1, which is not available on the UCSC browser
- So instead you have to go to some other browser to see the reads – he links to it on his lab resources page. It's the NIMR link

# How to see Gert's data on UCSC

- NIMR link in the box:

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- Unfortunately the NIMR browser sucks, and there is something wrong with Gert's site such that you can't upload those newer tracks there.
- I just wrote him about it.

# How to see Gert's data on UCSC



Older data

## Genome assembly Xentr v7.1

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# How to see Gert's data on UCSC

- Older data are aligned to tropo v4.1

## Genome assembly Xentr v7.1

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# So go to UCSC trop

- Pick the v4.1 genome version:

Click here

## X. tropicalis (*Xenopus tropicalis*) Genome Browser Gateway

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

group	genome	assembly	position
Vertebrate ▾	X. tropicalis ▾	Aug. 2005 (JGI 4.1/xenTro2) ▾	scaffold_27:565,941-578,374

Pick  
This one

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group	genome	assembly	position
Vertebrate ▾	X. tropicalis ▾	Nov. 2009 (JGI 4.2/xenTro3) ✓ Aug. 2005 (JGI 4.1/xenTro2) Oct. 2004 (JGI 3.0/xenTro1)	scaffold_27:565,941-578,374

# So go to UCSC trop

- Pick the v4.1 genome version:
- Because Gert already aligned these, if you load them to the wrong genome build the numbers won't agree and it won't work
- For bedgraph and wig files, this mistake happens a lot. Pay attention to genome version!

Pick  
This one

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# Get the track links from Gert's site

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Right-click, "copy link address"

## Genome assembly [Joint Genome Institute Xentr v4.1](#) (xenTro2, August 2005).



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# Go back to the UCSC browser for tropis v4.1

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.

genome	assembly	position	search term	
<input type="text" value="X. tropicalis"/>	<input type="text" value="Aug. 2005 (JGI 4.1/xenTro2)"/>	<input type="text" value="scaffold_27:565,941-578,374"/>	<input type="text" value="enter position, gene symbol or search terms"/>	<input type="button" value="submit"/>
<p><a href="#">Click here to reset the browser user interface settings to their defaults.</a></p>				
<input type="button" value="track search"/>	<input type="button" value="add custom tracks"/>	<input type="button" value="track hubs"/>	<input type="button" value="configure tracks and display"/>	



Click "add custom tracks"

# Add track to browser

Paste track url in here

Go go go!

**Add Custom Tracks**

clade  genome  assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [BED](#), [VCF](#), [broadPeak](#), [narrowPeak](#), or [PSL](#) formats. To configure the display, set [track](#) and [browser](#) lines. Data can be provided via only a URL or embedded in a track line in the box below. Publicly available custom tracks are available in the [Track Hub](#).

Paste URLs or data: Or upload:  No file chosen

# You'll see this now

## Manage Custom Tracks

genome: X. tropicalis assembly: Aug. 2005 (JGI 4.1/xenTro2) [xenTro2]

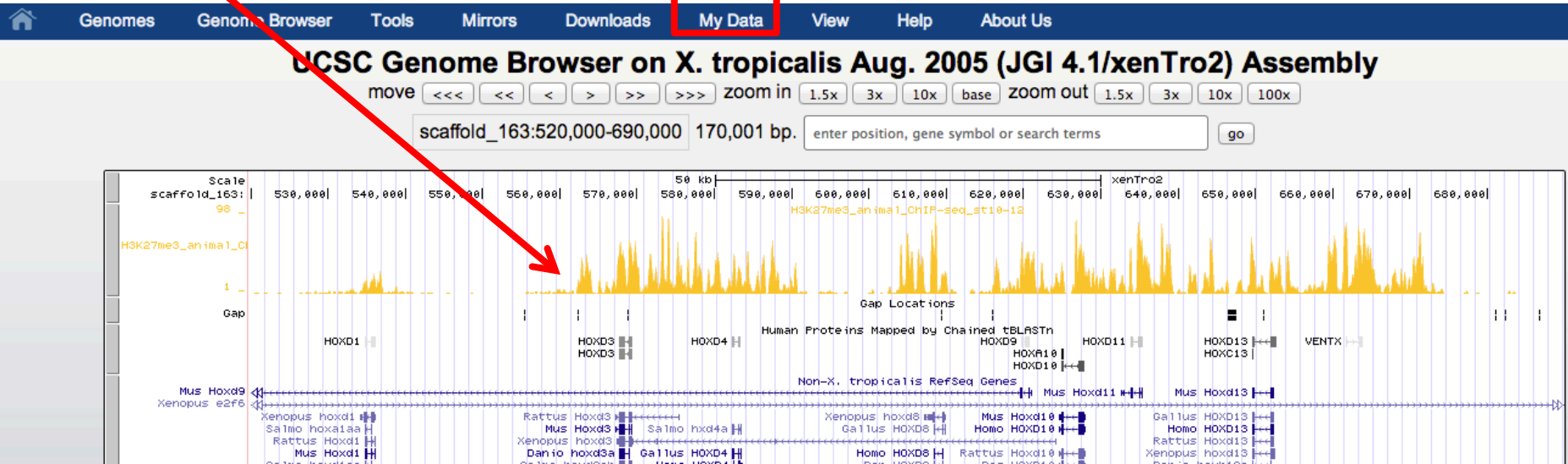
Name	Description	Type	Doc	Pos	delete	update	
<a href="#">H3K27me3_animal_ChIP-seq_st10-12</a>	H3K27me3_animal_ChIP-seq_st10-12	wiggle_0		<a href="#">scaffold_163:</a>	<input type="checkbox"/>	<input type="checkbox"/>	<a href="#">add custom tracks</a> <a href="#">go to genome browser</a> <a href="#">go to table browser</a> <a href="#">go to variant annotation integrator</a>

Go to browser



Track is here

Click "my data" to add more tracks the same way



Also in 'my data' you can save sessions to keep the same tracks for later so you don't have to keep reloading them. Very useful.

# Data from other sources

- You pretty much follow this for everything.
- After the course, you know how to map with bowtie2 and can download fastqs and map those yourself if you want, or just use the wigs/bedgraphs from somebody else



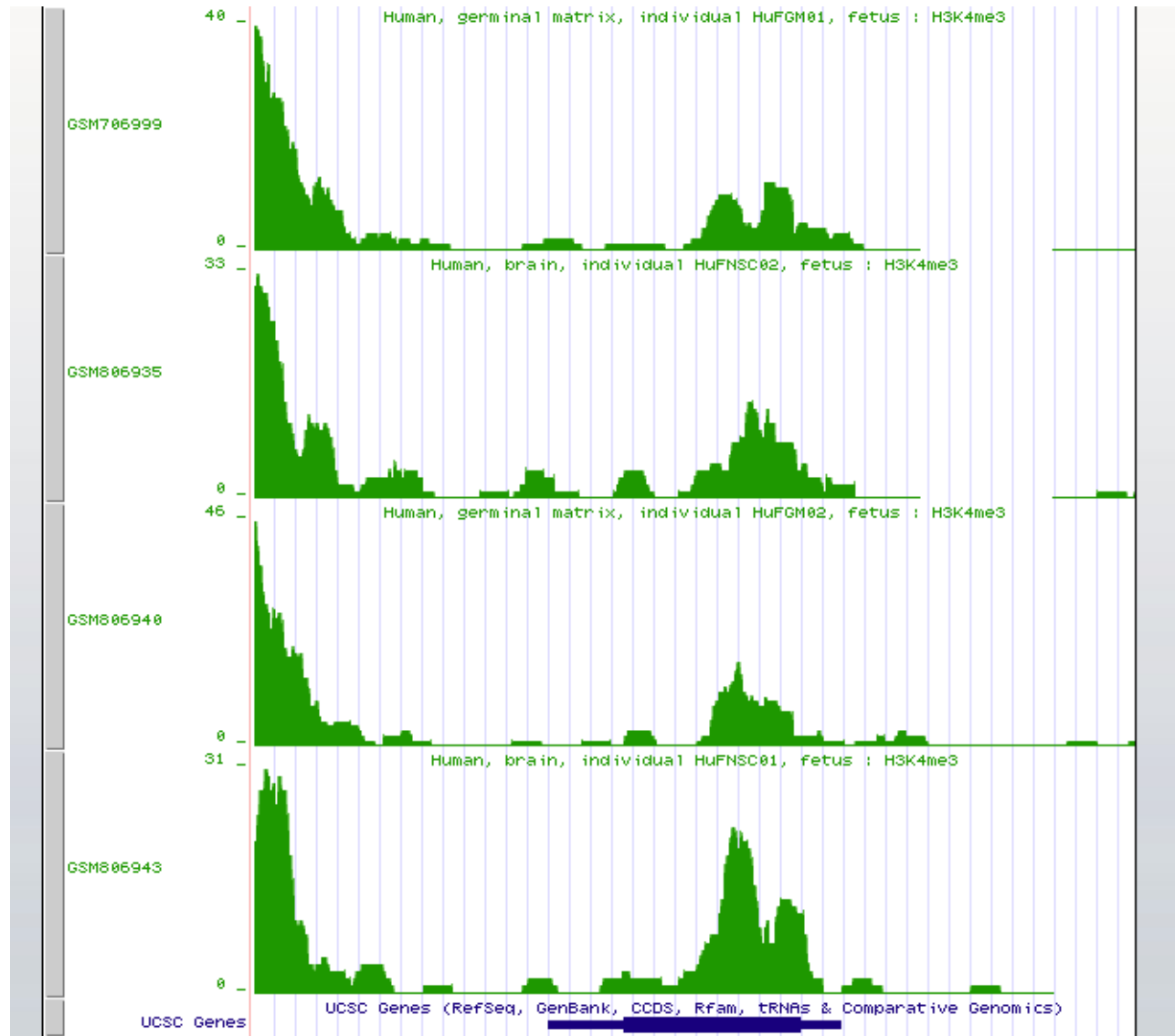
# Data from other sources

- NCBI geo often has wig or bedgraph files. Can also get fastq and align yourself
- UCSC has some nice collections:
- <http://genome.ucsc.edu/cgi-bin/hgHubConnect?db=hg19>
- Also encode project:
- <http://genome.ucsc.edu/ENCODE/dataMatrix/encodeDataMatrixMouse.html>

# Data from other sources

- Epigenetics roadmap:
- <http://www.ncbi.nlm.nih.gov/geo/roadmap/epigenomics/>
- Yeah, there sure is a lot there. Click on experimental matrix and you can click on samples that take you straight to browser.
- Each one, right-click track, get url, paste into UCSC custom tracks. Some have direct links too.

# Human fetal brain from roadmap



# Data from other sources

- Just remember the labs making these data are real factories. They're pretty good at it but don't have questions in mind, conditions and samples might be suboptimal. They also like cell lines because they can get lots of material.
- Have fun, there is a lot to discover. Good luck!