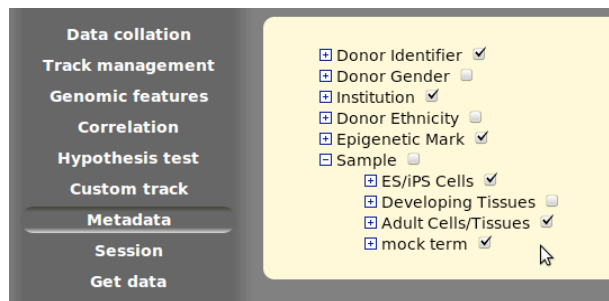
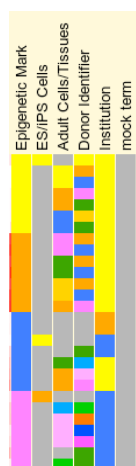


Step-by-step Instruction for Adding a Custom Track

Go to the control panel, click “Metadata”, check the “Sample > mock term” check box:



The “mock term” should be added as a new column to the metadata heatmap:



Go to the “Track management” tab of control panel. Make sure the track selection table is organized by “Sample” and “Epigenetic Mark” as below (if not, change the organization using “advanced options” above this table). The “mock term” can be found in “Sample” category:

		Epigenetic Mark														
		DNA Methylation	MRE	RRBS	MeDIP	BisulfiteSeq	Histone Mark	ChIP-Seq Input	H2A	H2B	H3	H4	Other Epigenetic Mark	Chromatin Accessibility	mRNA-Seq	smRNA-Seq
Sample	ES/iPS Cells	3/1	55/0	2/0	8/0	26/0	4/0	13/0	139/2	10/0	4/0	1/0	1/0			
	Developing Tissues	2/0	none	2/0	1/0	12/0	2/0	10/0	61/4	10/0	54/0	none	none			
	Adult Cells/Tissues	30/6	19/0	30/7	none	58/0	none	none	309/8	none	22/0	10/0	1/0			
	mock term	19/0	none	none	none	none	none	none	none	none	none	none	none	none	none	none

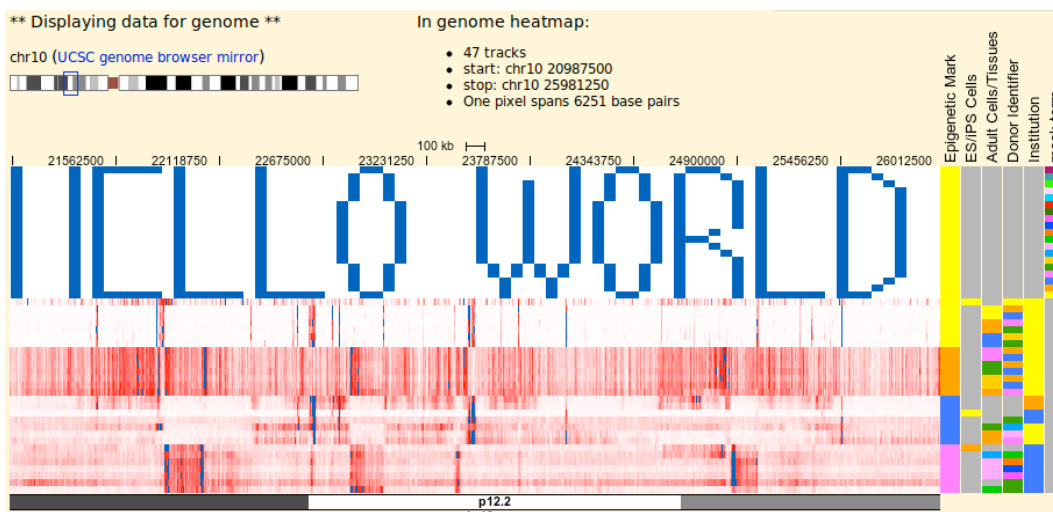
Move mouse over the “mock term” and click “select all” option:

Epigenetic Mark													
	DNA Methylation				Histone Mark				Other Epigenetic Mark				
	MRE	RRBS	MeDIP	BisulfiteSeq	ChIP-Seq Input	H2A	H2B	H3	H4	Chromatin Accessibility	mRNA-Seq	smRNA-Seq	
Sample	ES/iPS Cells	3/1	55/0	2/0	8/0	26/0	4/0	13/0	139/2	10/0	4/0	1/0	1/0
	Developing Tissues	2/0	none	2/0	1/0	12/0	2/0	10/0	61/4	10/0	54/0	none	none
	Adult Cells/Tissues	30/6	19/0	30/7	none	58/0	none	none	309/8	none	22/0	10/0	1/0
	mock term												

As a result of this step, 19 mock tracks will be added (if you could not see below pattern, jump to region chr10:21000000-26000000, make sure the browser is not in data collation or gene set viewing mode):



Click on the vertical “mock term”, sort tracks:



Seems that we still miss something... go to the custom bigWig track submission panel, enter following URL into the text field: <http://remc.wustl.edu/xzhou/mock10.bigWig>, enter a random track name, then open the “use our metadata vocabulary” panel, at “Sample > mock term”, choose value 10 from the

drop-down menu:

Submit a bigWig track

Enter bigWig file URL

Track name

(Optional) annotate bigWig track using metadata:

[\[-\] hide](#)

- for metadata terms relevant to your custom track, select a value from the drop-down menu,
- don't make selection for irrelevant terms,
- for terms with additional detail, click / to show/hide details.

|----Donor Identifier

|----Donor Gender

|----Institution

|----Donor Ethnicity

Epigenetic Mark

Sample

 | ES/iPS Cells

 |----Developing Tissues

 | Adult Cells/Tissues

 |----mock term

[\[+\] create & use custom metadata](#)

Submit this custom track, and you'll see following pattern on genome heatmap:

