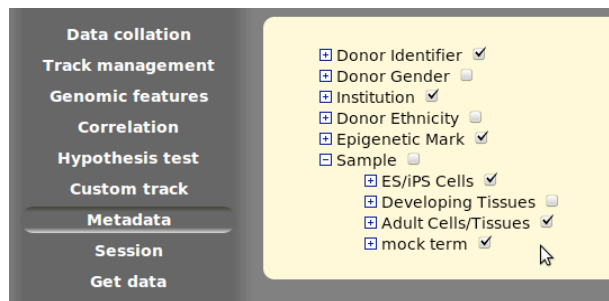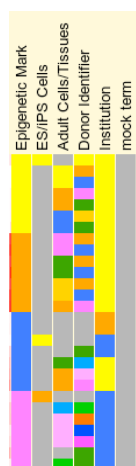## Step-by-step Instruction for Adding a Custom Track

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:

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

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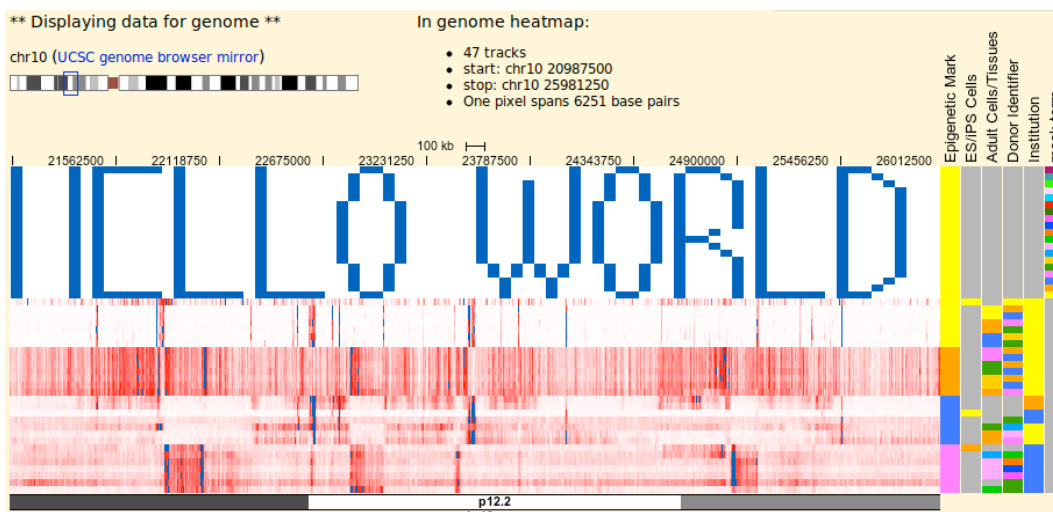
Seems that we still miss something... go to the custom bigWig track submission panel, enter following URL into the text field: http://remc.wustl.edu/xzhou/mock10.bigWig, enter a random track name, then open the "use our metadata vocabulary" panel, at "Sample > mock term", choose value 10 from the

drop-down menu:

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