

WashU Epigenome Browser - Bug # 89

<b>Status:</b>	Closed	<b>Priority:</b>	Normal
<b>Author:</b>	Rebecca Lowdon	<b>Category:</b>	
<b>Created:</b>	11/05/2013	<b>Assignee:</b>	Xin Zhou
<b>Updated:</b>	03/14/2014	<b>Due date:</b>	
<b>Subject:</b>	mCRF tracks not recognized		
<b>Description</b>			
<p>When I load my dataHub, some of the mCRF tracks are not recognized by the browser. They are set to mode:"full" to appear when loading, but they do not appear. They are also not found in the facet browser.</p> <p>DataHub: <a href="http://cgs.wustl.edu/~rlowdon/skinProjHub.json">http://cgs.wustl.edu/~rlowdon/skinProjHub.json</a></p> <p>The 3 skin cell type mCRF tracks load fine. It is the two breast cell type mCRF (at the bottom of the file) that are not loading.</p> <p>Thanks!</p>			

History

#1 - 11/05/2013 11:53 am - Xin Zhou

- File 59.png added
- Status changed from New to Resolved

Thanks for the report, following issues have been fixed.

- numerical hub tracks (bigwig or bedgraph) will be shown by default if their mode is labeled as "full" (legitimate mode is "show").
- browser is made more tolerant for datahub track mode assignment (you can assign "show" for a bed track and it will be automatically turned to "full" mode)
- updated facet cell prints track number as "red/green" (but not "green/red")

Two tracks are found to have invalid file URL and warning msg is given but is hard to see (need to drag down the message box to see, in screenshot). I will try to make the warning more evident.

#2 - 11/05/2013 01:26 pm - Xin Zhou

Did a quick fix and added the error-reporting function, see this:

[http://epgg-test.wustl.edu/browser/?genome=hg19&#38;datahub\\_jsonfile=http://vizhub.wustl.edu/hubSample/hg19/hub.error](http://epgg-test.wustl.edu/browser/?genome=hg19&#38;datahub_jsonfile=http://vizhub.wustl.edu/hubSample/hg19/hub.error)

#3 - 03/14/2014 12:05 am - Daofeng Li

- Status changed from Resolved to Closed

Files

59.png	221.5 kB	11/05/2013	Xin Zhou
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