WashU Epigenome Browser - Issues

#	Tracker	Status	Priority	Subject	Assignee	Updated
244	Feature	New	Normal	Pop-up window for confirming zooming in on a region	Xin Zhou	11/09/2014 11:39 pm
243	Bug	New	Normal	Incorrect SNP coordinate based on SNP ID	Xin Zhou	11/07/2014 10:43 am
240	Bug	Resolved	Normal	can't zoom out in gene set view in mm9	Xin Zhou	10/28/2014 06:46 am
237	Bug	New	Normal	Potential bug in the json hub name?	Xin Zhou	10/17/2014 06:08 pm
193	Bug	New	Normal	Json syntax error when trying to jump to a new location	Xin Zhou	05/14/2014 12:42 pm
161	Feature	New	Normal	Include scaffolds on genome snapshot	Xin Zhou	02/13/2014 03:32 pm
160	Bug	Closed	Normal	Custom PE BAM files unstable	Xin Zhou	05/25/2014 12:12 am
155	Bug	Rejected	Normal	browser url parameter for coordinate not working	Xin Zhou	02/14/2014 04:45 pm
149	Bug	Rejected	Normal	possible coordinate issue	Xin Zhou	01/30/2014 06:50 am
143	Bug	Closed	Normal	error when switching from intra- to inter-chromosomal display	Xin Zhou	03/14/2014 12:00 am
141	Bug	Closed	Normal	improper view range in session-restored gene set view	Xin Zhou	03/03/2014 11:20 pm
140	Bug	Closed	Normal	error with tracks of same file URL	Xin Zhou	03/03/2014 11:19 pm
137	Bug	Rejected	Normal	cutsom BED track not displayed	Xin Zhou	01/16/2014 07:48 am
115	Bug	New	Normal	tracks do not relocate and some disappear in GSV	Xin Zhou	11/23/2013 04:19 pm
89	Bug	Closed	Normal	mCRF tracks not recognized	Xin Zhou	03/14/2014 12:05 am
66	Bug	Closed	Normal	Save custom metadata vocabulary into session	Xin Zhou	11/18/2013 10:15 pm
65	Bug	Closed	Normal	Error rendering RRBS track	Xin Zhou	11/18/2013 10:06 pm
56	Bug	Closed	Normal	error handling with failed custom tracks	Xin Zhou	05/25/2014 12:14 am
47	Bug	Closed	Normal	wrong Y axis range display	Xin Zhou	09/18/2013 10:54 pm
46	Bug	New	Normal	Coordinate issue in hg19	Xin Zhou	09/19/2013 10:16 am
32	Bug	Closed	Low	right click twice caused background color change	Xin Zhou	08/07/2013 09:32 am
31	Bug	Closed	Normal	Cannot refresh Tabix index file	Xin Zhou	09/17/2013 08:50 am
30	Feature	New	Low	bam track (full) view range limit	Xin Zhou	08/05/2013 04:50 pm
29	Bug	Closed	Low	make url didn't save secondary panel	Xin Zhou	08/04/2013 09:39 pm
28	Feature	New	Low	add time information for session and status	Xin Zhou	08/03/2013 11:43 pm
27	Bug	Closed	Normal	retrieve session with custom categorical track error	Xin Zhou	08/03/2013 11:38 pm
26	Bug	Closed	Normal	categorical track submit json error	Xin Zhou	08/02/2013 10:17 am
24	Bug	Closed	Low	rule display problem when open secondary panel	Xin Zhou	08/03/2013 11:37 pm
23	Bug	Closed	Normal	metadata colormap not added for public hub by url parameter	Xin Zhou	07/29/2013 12:13 pm
22	Bug	Closed	Normal	no thing happens when click information after right click on refgene track	Xin Zhou	07/29/2013 12:13 pm
21	Feature	New	Low	operation history	Xin Zhou	07/26/2013 02:47 pm
20	Bug	Closed	Low	track information display problem	Xin Zhou	07/29/2013 12:13 pm

19	Feature	Closed	Low	new url parameter for public hub	Xin Zhou	07/29/2013 12:14 pm
18	Bug	Closed	Low	embed example 2 from test not working	Xin Zhou	07/29/2013 12:15 pm
17	Feature	New	Low	public datahub unload button?	Xin Zhou	07/25/2013 09:42 pm
14	Feature	Closed	Normal	Custom categorical track	Xin Zhou	09/13/2013 09:07 am
13	Feature	New	Normal	Line plot	Xin Zhou	09/22/2013 02:50 pm
12	Bug	Closed	Low	message after datahub submission confusion	Xin Zhou	07/29/2013 12:14 pm
11	Feature	New	Low	ability to cancel a super-enhancer job	Xin Zhou	07/22/2013 05:40 pm
10	Feature	New	Low	gene set list in hub support url	Xin Zhou	07/22/2013 05:35 pm
9	Bug	Closed	Low	no necessary 'Go Back' button after datahub submission	Xin Zhou	07/22/2013 02:08 pm
8	Bug	Closed	Normal	Datahub submission Json error	Xin Zhou	07/22/2013 02:09 pm
7	Feature	Closed	Normal	store gene set info in datahub descriptor file	Xin Zhou	07/26/2013 10:47 am
6	Bug	Closed	Normal	scatter plot shared between genomes and caused Json syntax error	Xin Zhou	07/22/2013 02:09 pm