WashU Epigenome Browser - Issues

#	Tracker	Status	Priority	Subject	Assignee	Updated
251	Feature	Closed	Normal	support location following		03/10/2015 04:17 pm
241	Bug	Closed	Normal	cannot choose region from gene set view		10/28/2014 06:47 am
229	Support	Closed	Normal	IMR90 cell line incorrectly classified	Daofeng Li	10/14/2014 02:11 pm
228	Support	Closed	Normal	Samples without data		10/14/2014 02:11 pm
225	Bug	Closed	Normal	genome snapshot of categorical track error		09/19/2014 11:20 am
223	Bug	Closed	Normal	custom bam track error		09/11/2014 04:25 pm
222	Bug	Closed	Normal	methyC track combine error?		09/10/2014 02:42 pm
221	Bug	Closed	Normal	missing mouse over event?		09/10/2014 01:12 am
220	Bug	Closed	Normal	Uncaught TypeError: Cannot read property 'dim1' of null		08/28/2014 12:25 am
218	Bug	Closed	Normal	track detail information missed		08/21/2014 11:55 pm
217	Bug	Closed	Normal	metadata term show up repeatedly in metadata colormap		08/21/2014 11:55 pm
215	Bug	Closed	Normal	making svg of genome snapshot error		08/07/2014 02:58 pm
213	Bug	Closed	Normal	fixed scale for matplot not work?		08/03/2014 12:38 am
207	Bug	Closed	Normal	fixed scale for bam track error		07/31/2014 12:21 am
206	Bug	Closed	Normal	matplot error after split panel		08/01/2014 11:54 pm
205	Bug	Rejected	Normal	custom BAM track could not be used for Genome Snapshot?		07/18/2014 12:31 pm
203	Bug	Closed	Normal	hidden methylC track not saved in session		07/07/2014 01:59 pm
202	Bug	Closed	Normal	private metadata vocabulary cannot be saved with session		07/07/2014 01:58 pm
201	Bug	Closed	Normal	session save error		07/07/2014 01:58 pm
200	Bug	Closed	Normal	making screenshot error		07/02/2014 03:53 pm
199	Bug	Closed	Normal	juxtaposition error when there is long range track		06/18/2014 03:22 pm
197	Bug	Closed	Normal	js TypeError for danRer7		06/15/2014 11:40 pm
196	Bug	Closed	Normal	embedded browser JS error		06/06/2014 12:47 am
195	Bug	Closed	Normal	genome snapshot not working		06/05/2014 12:31 am
192	Bug	Closed	Normal	circlet plot JS error		06/15/2014 11:41 pm
191	Bug	Closed	Normal	js TypeError when operating methyC tracks		05/02/2014 11:26 am
189	Bug	Closed	Normal	track and barplot background didn't apply to splitted panel		05/25/2014 12:10 am
188	Bug	Closed	Normal	showing wrong reference sequence for a split read		05/25/2014 12:12 am
187	Bug	Closed	Normal	wrong display of a minimum methylC track		05/25/2014 12:10 am
185	Bug	Closed	Normal	crashes upon a broken hammock track		05/25/2014 12:12 am
184	Bug	Closed	Normal	reorder gene set list error		04/06/2014 12:31 am
183	Bug	Closed	Normal	share y-scale vs 'apply to all'		04/06/2014 12:32 am

182	Bug	Rejected	Normal	circlet plot panel cannot hide when there is no plot displaying		04/05/2014 09:28 am
181	Bug	Closed	Normal	empty geneplot results		03/29/2014 01:58 am
180	Bug	Closed	Normal	overlap display of gene sets and gene plot panel		03/27/2014 01:36 am
178	Bug	Closed	Normal	gear button in embedded browser not work		03/12/2014 11:12 am
177	Bug	Closed	Normal	refGene color change not kept in session		03/12/2014 11:11 am
176	Bug	Rejected	Normal	browser is not drag-move when there is no track in central canvas		03/07/2014 07:26 am
175	Bug	Closed	Normal	alignment issue with 2nd panel		03/13/2014 11:59 pm
174	Bug	Closed	Normal	2nd panel background color issue		03/06/2014 11:27 pm
173	Bug	Closed	Normal	coordinates jumping not working after modifying		03/12/2014 11:12 am
172	Bug	Closed	Normal	methylC tracks cannot added back to secondary panels		03/14/2014 12:04 am
171	Bug	Rejected	Normal	cannot load hub while showing secondary panels		03/14/2014 10:48 am
170	Bug	Closed	Normal	methylC track cannot be hidden by default		03/12/2014 11:14 am
169	Bug	Closed	Normal	long range tracks not appeared in 2nd panel and also freeze 2nd panel		03/03/2014 11:16 pm
167	Bug	Closed	Normal	metadata color map change not saved in session		03/03/2014 11:18 pm
166	Bug	Rejected	Normal	submit default gene set error		02/27/2014 07:01 am
165	Bug	Closed	Normal	browser frozen when panning of BAM tracks		02/19/2014 11:19 am
164	Bug	Closed	Normal	UI frozen when click 'remove all' from json hub		02/19/2014 10:13 am
162	Feature	Closed	Normal	Tooltip information		03/13/2014 11:59 pm
160	Bug	Closed	Normal	Custom PE BAM files unstable	Xin Zhou	05/25/2014 12:12 am
159	Bug	Closed	Normal	Session not saving		02/14/2014 04:46 pm
155	Bug	Rejected	Normal	browser url parameter for coordinate not working	Xin Zhou	02/14/2014 04:45 pm
154	Bug	Closed	Normal	Cannot search for gene in embedded browser		03/03/2014 11:22 pm
153	Bug	Closed	Normal	track information display error		03/03/2014 11:19 pm
152	Bug	Closed	Normal	clicking "zoom in" button makes browser unresponsive		02/11/2014 10:52 pm
150	Bug	Closed	Normal	js error and clickable 'None yet'		01/31/2014 08:40 am
149	Bug	Rejected	Normal	possible coordinate issue	Xin Zhou	01/30/2014 06:50 am
148	Bug	Closed	Normal	add geneset to genome snapshot error		02/11/2014 10:51 pm
147	Bug	Closed	Normal	crash when track file not exist in json hub		02/14/2014 10:18 pm
145	Feature	Closed	Normal	loose format requirement for coordinates format		02/11/2014 10:52 pm
144	Bug	Closed	Normal	mouse over event for meta data header (in track table) disappear		01/31/2014 08:40 am
143	Bug	Closed	Normal	error when switching from intra- to inter-chromosomal display	Xin Zhou	03/14/2014 12:00 am
142	Bug	Closed	Normal	typo "Unselect All"		01/22/2014 08:37 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
138	Bug	Closed	Normal	track display outside of canvas		01/17/2014 06:09 pm

137	Bug	Rejected	Normal	cutsom BED track not displayed	Xin Zhou	01/16/2014 07:48 am
136	Support	Closed	Normal	Collecting new Hi-C data sets	Daofeng Li	01/24/2014 05:21 pm
133	Bug	Rejected	Normal	custom bed submit error		12/26/2013 04:43 pm
132	Bug	Closed	Normal	default tracks were not be able to be added to genome snapshot		12/26/2013 03:55 pm
131	Bug	Closed	Normal	new genome have no 'Tracks' button		12/22/2013 09:15 pm
130	Bug	Closed	Normal	chromosome sequence display error		03/14/2014 12:01 am
129	Bug	Rejected	Normal	native tracks not shown in public hub		12/20/2013 09:03 am
128	Bug	Rejected	Normal	upload a session didn't show the status list		12/19/2013 08:22 am
127	Bug	Closed	Normal	could not select track for scatter plot		12/19/2013 10:18 pm
126	Bug	Closed	Normal	genome snapshot error		12/19/2013 10:20 pm
125	Bug	Closed	Normal	could not select numerical track from geneplot		12/19/2013 10:20 pm
124	Bug	Closed	Normal	Querying for SOX2 but got SOX21 when adding gene set		12/19/2013 10:23 pm
123	Bug	Closed	Normal	embedded browser cannot handle hidden tracks		02/11/2014 10:52 pm
122	Bug	Rejected	Normal	defaultcontent=on behavior differently since v30.2		12/18/2013 07:21 am
121	Bug	Closed	Normal	duplicated display of meta colormap		12/10/2013 01:40 pm
120	Bug	Closed	Normal	custom bed track strand issue		12/06/2013 12:55 pm
119	Bug	Closed	Normal	fixedscale and track height probem in json hub		01/31/2014 08:41 am
116	Bug	Closed	Normal	chromHMM tracks cannot be found by "chromhmm" keyword		12/06/2013 12:29 am
114	Bug	Rejected	Normal	Cannot read property 'cigar' of undefined		04/05/2014 09:32 am
113	Bug	Closed	Normal	retrieve session which contains USCS hub error		11/24/2013 09:13 pm
112	Bug	Closed	Normal	bam display as 'density' when specified as 'full' in UCSC hub		11/24/2013 09:17 pm
109	Bug	Closed	Normal	Problem saving session		05/25/2014 12:13 am
107	Bug	Closed	Normal	handling of hub file errors		03/14/2014 12:00 am
106	Bug	Closed	Normal	gencodeV17 track cannot be saved in session		11/18/2013 09:47 pm
105	Bug	Rejected	Normal	'Remove all' button in Facet of public hub was not working		11/18/2013 07:25 am
104	Bug	Closed	Normal	configuration of long range track missing height adjustment		11/18/2013 09:51 pm
103	Bug	Rejected	Normal	taking screen shot of genome snapshot		11/18/2013 07:19 am
102	Bug	Closed	Normal	problem loading a datahub with no tracks shown by default		11/18/2013 09:51 pm
101	Bug	Closed	Normal	json syntax error when retrieving session		04/08/2014 01:14 pm
100	Bug	Closed	Normal	geneplot (lines plot) error		11/10/2013 12:08 am
98	Feature	Closed	Normal	multiple selection of tracks		11/18/2013 09:53 pm
96	Bug	Rejected	Normal	location jumping was not accurate		11/08/2013 06:46 am
95	Bug	Closed	Normal	crashed when loading a hub with wrong metadata vocabulary		11/18/2013 09:54 pm
94	Bug	Closed	Normal	Crashed when creating gene set on mm9		11/18/2013 09:55 pm
93	Bug	Closed	Normal	new genecode v17 track not work with genome snapshot		11/09/2013 12:05 am

92	Bug	Closed	Normal	configuration of category track not 'apply to all' and 'apply background'		11/18/2013 09:56 pm
91	Bug	Closed	Normal	crashed when loading bam track		11/18/2013 09:58 pm
90	Bug	Closed	Normal	long range track display runs into error		11/21/2013 12:08 am
89	Bug	Closed	Normal	mCRF tracks not recognized	Xin Zhou	03/14/2014 12:05 am
88	Bug	Closed	Normal	gene tracks are omitted in restored sessions		11/18/2013 09:59 pm
87	Bug	Closed	Normal	SNP track showing all SNPs to be on reverse strand		11/18/2013 10:33 pm
86	Bug	Closed	Normal	2nd panel didn't align top with main panel		04/01/2014 11:32 pm
85	Bug	Closed	Normal	rmsk track configuration not available for subfamily tracks		10/31/2013 09:35 am
84	Bug	Closed	Normal	background in 2nd panel didn't apply to main panel automatically		10/31/2013 09:35 am
83	Bug	Closed	Normal	oversize text in SVG on Firefox		12/06/2013 12:30 am
82	Bug	Closed	Normal	crashed when restoring session		11/18/2013 10:28 pm
81	Bug	Rejected	Normal	lineplot information not contain in 'making url'		10/28/2013 11:07 am
76	Bug	Closed	Normal	circlet view not work at test		10/25/2013 08:36 am
75	Bug	Closed	Normal	smoothing window doesn't work well on tracks in secondary panel		10/25/2013 08:36 am
74	Bug	Closed	Normal	circlet plot generates wrong graph		11/18/2013 10:27 pm
73	Bug	Closed	Normal	bam track in json hub set to show cause syntax error		11/18/2013 10:01 pm
72	Bug	Closed	Normal	error when click 'smooth window' after check 'apply to all'		10/23/2013 04:00 pm
71	Bug	Closed	Normal	cannot handle irregularity in custom metadata		11/18/2013 10:22 pm
70	Bug	Closed	Normal	right click caused background color disappear		10/10/2013 11:23 pm
69	Bug	Rejected	Normal	track name in svg		11/18/2013 12:04 pm
67	Feature	Closed	Normal	change background color		11/18/2013 10:00 pm
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
64	Bug	Rejected	Normal	json hub not show custom meta colormap		10/07/2013 07:29 am
63	Bug	Closed	Normal	Gene plot by Google Chart seems not working		10/01/2013 11:32 pm
61	Bug	Closed	Normal	error embedding browser		09/30/2013 09:59 pm
60	Feature	Closed	Normal	"file type" category for custom facet table		11/18/2013 10:17 pm
59	Bug	Closed	Normal	error filling contents for facet table of 2nd datahub		11/18/2013 12:05 pm
58	Feature	Closed	Normal	make publichubs for ENCODE tracks	Daofeng Li	05/25/2014 12:13 am
57	Bug	Closed	Normal	Can not import encode data. Just stop at importing...		09/27/2013 11:23 pm
56	Bug	Closed	Normal	error handling with failed custom tracks	Xin Zhou	05/25/2014 12:14 am
54	Bug	Rejected	Normal	upload bigWig error		09/26/2013 09:27 am
53	Bug	Rejected	Normal	virus gene info display problem		09/24/2013 07:25 am
47	Bug	Closed	Normal	wrong Y axis range display	Xin Zhou	09/18/2013 10:54 pm
45	Bug	Closed	Normal	mappability track display issue		09/18/2013 08:18 am

44	Bug	Closed	Normal	long range track display weird in SVG output		05/25/2014 12:15 am
43	Bug	Closed	Normal	screenshot error on hub		09/18/2013 08:21 am
42	Bug	Closed	Normal	json hub load error		09/13/2013 09:57 pm
41	Bug	Closed	Normal	scatter plot json error		09/13/2013 09:57 pm
40	Bug	Closed	Normal	gene plot crashed on gene set of json hub		09/13/2013 09:58 pm
39	Bug	Closed	Normal	json syntax error when running gene set view		09/13/2013 09:58 pm
38	Bug	Closed	Normal	new hub Turn off Gene Set View not work		09/13/2013 09:58 pm
36	Feature	Closed	Normal	add Brassica Rapa genome	Daofeng Li	09/13/2013 09:06 am
31	Bug	Closed	Normal	Cannot refresh Tabix index file	Xin Zhou	09/17/2013 08:50 am
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
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
14	Feature	Closed	Normal	Custom categorical track	Xin Zhou	09/13/2013 09:07 am
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