

## WashU Epigenome Browser - Issues

#	Tracker	Status	Priority	Subject	Assignee	Updated
217	Bug	Closed	Normal	metadata term show up repeatedly in metadata colormap		08/21/2014 11:55 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
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
186	Bug	New	Normal	MCM (metadata colormap) shows blank when splitting panel		04/05/2014 09:40 am
185	Bug	Closed	Normal	crashes upon a broken hammock track		05/25/2014 12:12 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
154	Bug	Closed	Normal	Cannot search for gene in embedded browser		03/03/2014 11:22 pm
152	Bug	Closed	Normal	clicking "zoom in" button makes browser unresponsive		02/11/2014 10:52 pm
146	Bug	New	Normal	Session cannot save more than 1 custom metadata vocabularies		01/23/2014 07:37 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
136	Support	Closed	Normal	Collecting new Hi-C data sets	Daofeng Li	01/24/2014 05:21 pm
130	Bug	Closed	Normal	chromosome sequence display error		03/14/2014 12:01 am
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
116	Bug	Closed	Normal	chromHMM tracks cannot be found by "chromhmm" keyword		12/06/2013 12:29 am
108	Feature	New	Normal	compute pearson correlation in scatterplot		11/19/2013 08:06 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
102	Bug	Closed	Normal	problem loading a datahub with no tracks shown by default		11/18/2013 09:51 pm
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
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
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
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
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
71	Bug	Closed	Normal	cannot handle irregularity in custom metadata		11/18/2013 10:22 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
62	Support	New	Normal	"donor" terms in hg19 metadata	Daofeng Li	10/01/2013 08:34 am
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 public hubs for ENCODE tracks	Daofeng Li	05/25/2014 12:13 am
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
36	Feature	Closed	Normal	add Brassica Rapa genome	Daofeng Li	09/13/2013 09:06 am
35	Feature	Closed	High	add common bean genome	Daofeng Li	09/13/2013 09:06 am
34	Feature	Closed	High	add soybean 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
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
7	Feature	Closed	Normal	store gene set info in datahub descriptor file	Xin Zhou	07/26/2013 10:47 am