WashU Epigenome Browser - Issues

#	Tracker	Status	Priority	Subject	Assignee	Updated
252	Bug	New	Normal	json syntax error when loading genome comparison tracks		03/10/2015 04:21 pm
250	Bug	New	Normal	slow loading of big hub		12/19/2014 03:45 pm
249	Feature	New	Normal	track hub include feature		12/18/2014 05:24 pm
248	Bug	New	Normal	Custom track can not be submitted again after removal		12/17/2014 04:21 pm
247	Feature	New	Low	Multiple upload of custom tracks		12/17/2014 04:16 pm
246	Feature	New	Low	Change names of custom tracks		12/17/2014 04:14 pm
245	Bug	Resolved	Normal	Missing display of 0% methylated Cs in methylC track		11/24/2014 01:40 pm
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
242	Feature	New	Normal	Please add the option to remove genome comparison track		11/07/2014 09:37 am
240	Bug	Resolved	Normal	can't zoom out in gene set view in mm9	Xin Zhou	10/28/2014 06:46 am
239	Bug	New	Normal	zooming in on a genomic region doesn't give the right region		10/27/2014 01:57 pm
237	Bug	New	Normal	Potential bug in the json hub name?	Xin Zhou	10/17/2014 06:08 pm
236	Support	New	Normal	Roadmap analysis hub crashes		10/16/2014 02:48 pm
235	Bug	New	Normal	Gene shading feature inconsistent and needs to be made optional		10/16/2014 09:55 am
234	Support	New	Normal	Error in SE paper datahub	Daofeng Li	10/16/2014 10:02 am
233	Bug	Resolved	Normal	dbSNP track crashes		10/15/2014 08:04 pm
232	Bug	Resolved	Normal	Matplot not working with sessions		10/15/2014 02:09 pm
231	Bug	Resolved	Normal	load hub and session issue		10/15/2014 11:15 am
227	Bug	New	Normal	missing 0% methylated CpG display in methylC track		10/03/2014 01:02 pm
204	Bug	In Progress	Normal	gene set view not working		07/07/2014 03:04 pm
198	Bug	New	Normal	refresh cache issue		06/18/2014 09:51 am
194	Bug	New	Normal	juxtaposition issue on genome align tracks		05/25/2014 12:09 am
193	Bug	New	Normal	Json syntax error when trying to jump to a new location	Xin Zhou	05/14/2014 12:42 pm
190	Bug	New	Normal	geneplot on methylC track		04/28/2014 12:11 am
186	Bug	New	Normal	MCM (metadata colormap) shows blank when splitting panel		04/05/2014 09:40 am
179	Bug	New	Normal	refGene track automatically be put to bottom when split panel		03/19/2014 11:39 pm
168	Bug	New	Normal	'pack and hide' status not saved in session		03/01/2014 12:59 am
163	Bug	New	Normal	long responsive time while track missed in hub		02/18/2014 03:39 pm
161	Feature	New	Normal	Include scaffolds on genome snapshot	Xin Zhou	02/13/2014 03:32 pm
158	Feature	New	Low	wrapping for tooltip read information		02/13/2014 05:59 pm
157	Bug	New	Normal	refSeq gene position didn't keep in session		02/14/2014 04:43 pm

156	Bug	New	Normal	WUGB popup link get blocked		02/07/2014 11:32 pm
146	Bug	New	Normal	Session cannot save more than 1 custom metadata vocabularies		01/23/2014 07:37 am
135	Feature	New	Normal	adjust track order in genome snapshot		01/05/2014 11:11 pm
134	Feature	New	Normal	Track configuration on ipad		01/01/2014 10:09 pm
118	Feature	New	Normal	search auto completion by right clicking from gene tracks		11/29/2013 11:11 pm
117	Feature	New	Normal	add track name to genome snapshot		11/29/2013 11:10 pm
115	Bug	New	Normal	tracks do not relocate and some disappear in GSV	Xin Zhou	11/23/2013 04:19 pm
111	Bug	New	Normal	Tracks disappear when using config panel		11/24/2013 03:25 pm
110	Feature	New	Normal	hub check button		11/20/2013 03:13 pm
108	Feature	New	Normal	compute pearson correlation in scatterplot		11/19/2013 08:06 am
99	Feature	New	Normal	function that move track(s) to top or bottom		11/07/2013 05:36 pm
97	Feature	New	Normal	user defined track color		11/07/2013 05:33 pm
80	Bug	New	Normal	session with lineplot TypeError		10/26/2013 11:45 pm
79	Bug	New	Normal	browser background color		10/26/2013 11:40 pm
78	Bug	New	Normal	2nd panel lineplot not applied to main panel		10/26/2013 11:30 pm
77	Bug	New	Normal	track background color not applied on 2nd panel of line plot		10/26/2013 11:25 pm
62	Support	New	Normal	"donor" terms in hg19 metadata	Daofeng Li	10/01/2013 08:34 am
55	Feature	New	Normal	[System] killing subtleKnife process which had been stucked longer than 10min		09/26/2013 09:14 am
52	Feature	New	Normal	Improve gene set view		09/21/2013 07:14 pm
51	Feature	New	Normal	Improve gene search function		09/21/2013 07:14 pm
50	Feature	New	Normal	Improve session?		09/21/2013 07:13 pm
49	Feature	New	Normal	general suggestions from UCSF		09/21/2013 07:13 pm
48	Feature	New	Normal	automatically refresh cache		09/18/2013 10:59 pm
46	Bug	New	Normal	Coordinate issue in hg19	Xin Zhou	09/19/2013 10:16 am
33	Feature	New	Low	batch GEO id output		08/20/2013 10:57 pm
30	Feature	New	Low	bam track (full) view range limit	Xin Zhou	08/05/2013 04:50 pm
28	Feature	New	Low	add time information for session and status	Xin Zhou	08/03/2013 11:43 pm
25	Feature	New	Normal	Quick capture of the central canvas	Daofeng Li	08/02/2013 07:49 am
21	Feature	New	Low	operation history	Xin Zhou	07/26/2013 02:47 pm
17	Feature	New	Low	public datahub unload button?	Xin Zhou	07/25/2013 09:42 pm
13	Feature	New	Normal	Line plot	Xin Zhou	09/22/2013 02:50 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
3	Bug	New	Normal	Safari 5 navigation display disorder		07/18/2013 01:34 pm