WashU Epigenome Browser

	2024-7				2024-8				2024-9				2024-10				2024-11				2024-12			
	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52
WashU Epigenome Browser	
Safari 5 navigation display disorder	
gene set list in hub support url	
ability to cancel a super-enhancer job	
Line plot	
public datahub unload button?	
operation history	
Quick capture of the central canvas	
add time information for session and status	
bam track (full) view range limit	
batch GEO id output	
Coordinate issue in hg19	
automatically refresh cache	
general suggestions from UCSF	
Improve session?	
Improve gene search function	
Improve gene set view	
[System] killing subtleKnife process which (...)	
"donor" terms in hg19 metadata	
track background color not applied on 2nd (...)	
2nd panel lineplot not applied to main panel	
browser background color	
session with lineplot TypeError	
user defined track color	
function that move track(s) to top or bottom	
compute pearson correlation in scatterplot	
hub check button	
Tracks disappear when using config panel	

tracks do not relocate and some disappear (...)

add track name to genome snapshot

search auto completion by right clicking (...)

Track configuration on ipad

adjust track order in genome snapshot

Session cannot save more than 1 custom metadata (...)

refSeq gene position didn't keep in session

wrapping for tooltip read information

Include scaffolds on genome snapshot

long responsive time while track missed in (...)

'pack and hide' status not saved in session

refGene track automatically be put to bottom (...)

MCM (metadata colormap) shows blank when (...)

geneplot on methylC track

Json syntax error when trying to jump to (...)

juxtaposition issue on genome align tracks

refresh cache issue

gene set view not working

missing 0% methylated CpG display in methylC (...)

load hub and session issue

Matplot not working with sessions

dbSNP track crashes

Error in SE paper datahub

Gene shading feature inconsistent and needs (...)

Roadmap analysis hub crashes

Potential bug in the json hub name?

zooming in on a genomic region doesn't give (...)

can't zoom out in gene set view in mm9

Please add the option to remove genome comparison (...)

Incorrect SNP coordinate based on SNP ID

Pop-up window for confirming zooming in on (...)

Missing display of 0% methylated Cs in methylC (...)

Change names of custom tracks

Multiple upload of custom tracks

Custom track can not be submitted again after (...) **track hub include feature** **slow loading of big hub** **json syntax error when loading genome comparison** **Complete Epigenome Browser** **WUGB popup link get blocked**	(...)