

WashU Epigenome Browser

	2023-10					2023-11					2023-12					2024-1					2024-2					2024-3				
	40	41	42	43	44	45	46	47	48	49	50	51	52	1	2	3	4	5	6	7	8	9	10	11	12	13				
WashU Epigenome Browser	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																														

<p>tracks do not relocate and some disappear (...)</p> <p>add track name to genome snapshot</p> <p>search auto completion by right clicking (...)</p> <p>Track configuration on ipad</p> <p>adjust track order in genome snapshot</p> <p>Session cannot save more than 1 custom metadata (...)</p> <p>refSeq gene position didn't keep in session</p> <p>wrapping for tooltip read information</p> <p>Include scaffolds on genome snapshot</p> <p>long responsive time while track missed in (...)</p> <p>'pack and hide' status not saved in session</p> <p>refGene track automatically be put to bottom (...)</p> <p>MCM (metadata colormap) shows blank when (...)</p> <p>geneplot on methylC track</p> <p>Json syntax error when trying to jump to (...)</p> <p>juxtaposition issue on genome align tracks</p> <p>refresh cache issue</p> <p>gene set view not working</p> <p>missing 0% methylated CpG display in methylC (...)</p> <p>load hub and session issue</p> <p>Matplot not working with sessions</p> <p>dbSNP track crashes</p> <p>Error in SE paper datahub</p> <p>Gene shading feature inconsistent and needs (...)</p> <p>Roadmap analysis hub crashes</p> <p>Potential bug in the json hub name?</p> <p>zooming in on a genomic region doesn't give (...)</p> <p>can't zoom out in gene set view in mm9</p> <p>Please add the option to remove genome comparison (...)</p> <p>Incorrect SNP coordinate based on SNP ID</p> <p>Pop-up window for confirming zooming in on (...)</p> <p>Missing display of 0% methylated Cs in methylC (...)</p> <p>Change names of custom tracks</p> <p>Multiple upload of custom tracks</p>	
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<p>Custom track can not be submitted again after (...)</p> <p>track hub include feature</p> <p>slow loading of big hub</p> <p>json syntax error when loading genome comparison (...)</p> <p>Complete Epigenome Browser</p> <p>WUGB popup link get blocked</p>	
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