

# WashU Epigenome Browser

	2024-8				2024-9				2024-10				2024-11				2024-12				2025-1							
	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	1	2	3	4			
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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