

# WashU Epigenome Browser

	2024-4					2024-5					2024-6					2024-7					2024-8					2024-9													
	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39													
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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