

## WashU Epigenome Browser

|  | 2024-6                  |    |    |    | 2024-7 |    |    |    | 2024-8 |    |    |    | 2024-9 |    |    |    | 2024-10 |    |    |    | 2024-11 |    |    |    |    |    |  |  |
|--|-------------------------|----|----|----|--------|----|----|----|--------|----|----|----|--------|----|----|----|---------|----|----|----|---------|----|----|----|----|----|--|--|
|  | 23                      | 24 | 25 | 26 | 27     | 28 | 29 | 30 | 31     | 32 | 33 | 34 | 35     | 36 | 37 | 38 | 39      | 40 | 41 | 42 | 43      | 44 | 45 | 46 | 47 | 48 |  |  |
| 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         |                         |    |    |    |        |    |    |    |        |    |    |    |        |    |    |    |         |    |    |    |         |    |    |    |    |    |  |  |

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

|  |  |
|--|--|
| <p><b>Custom track can not be submitted again after (...)</b><br/><b>track hub include feature</b><br/><b>slow loading of big hub</b><br/><b>json syntax error when loading genome comparison (...)</b><br/><b>Complete Epigenome Browser</b><br/><b>WUGB popup link get blocked</b></p> |  |
|--|--|