

WashU Epigenome Browser - Issues

| # | Tracker | Status | Priority | Subject | Assignee | Updated |
|-----|---------|--------|----------|---|----------|---------------------|
| 252 | Bug | New | Normal | json syntax error when loading genome comparison tracks | | 03/10/2015 04:21 pm |
| 250 | Bug | New | Normal | slow loading of big hub | | 12/19/2014 03:45 pm |
| 249 | Feature | New | Normal | track hub include feature | | 12/18/2014 05:24 pm |
| 248 | Bug | New | Normal | Custom track can not be submitted again after removal | | 12/17/2014 04:21 pm |
| 247 | Feature | New | Low | Multiple upload of custom tracks | | 12/17/2014 04:16 pm |
| 246 | Feature | New | Low | Change names of custom tracks | | 12/17/2014 04:14 pm |
| 242 | Feature | New | Normal | Please add the option to remove genome comparison track | | 11/07/2014 09:37 am |
| 239 | Bug | New | Normal | zooming in on a genomic region doesn't give the right region | | 10/27/2014 01:57 pm |
| 236 | Support | New | Normal | Roadmap analysis hub crashes | | 10/16/2014 02:48 pm |
| 235 | Bug | New | Normal | Gene shading feature inconsistent and needs to be made optional | | 10/16/2014 09:55 am |
| 227 | Bug | New | Normal | missing 0% methylated CpG display in methylC track | | 10/03/2014 01:02 pm |
| 198 | Bug | New | Normal | refresh cache issue | | 06/18/2014 09:51 am |
| 194 | Bug | New | Normal | juxtaposition issue on genome align tracks | | 05/25/2014 12:09 am |
| 190 | Bug | New | Normal | geneplot on methylC track | | 04/28/2014 12:11 am |
| 186 | Bug | New | Normal | MCM (metadata colormap) shows blank when splitting panel | | 04/05/2014 09:40 am |
| 179 | Bug | New | Normal | refGene track automatically be put to bottom when split panel | | 03/19/2014 11:39 pm |
| 168 | Bug | New | Normal | 'pack and hide' status not saved in session | | 03/01/2014 12:59 am |
| 163 | Bug | New | Normal | long responsive time while track missed in hub | | 02/18/2014 03:39 pm |
| 158 | Feature | New | Low | wrapping for tooltip read information | | 02/13/2014 05:59 pm |
| 157 | Bug | New | Normal | refSeq gene position didn't keep in session | | 02/14/2014 04:43 pm |
| 156 | Bug | New | Normal | WUGB popup link get blocked | | 02/07/2014 11:32 pm |
| 146 | Bug | New | Normal | Session cannot save more than 1 custom metadata vocabularies | | 01/23/2014 07:37 am |
| 135 | Feature | New | Normal | adjust track order in genome snapshot | | 01/05/2014 11:11 pm |
| 134 | Feature | New | Normal | Track configuration on ipad | | 01/01/2014 10:09 pm |
| 118 | Feature | New | Normal | search auto completion by right clicking from gene tracks | | 11/29/2013 11:11 pm |
| 117 | Feature | New | Normal | add track name to genome snapshot | | 11/29/2013 11:10 pm |
| 111 | Bug | New | Normal | Tracks disappear when using config panel | | 11/24/2013 03:25 pm |
| 110 | Feature | New | Normal | hub check button | | 11/20/2013 03:13 pm |
| 108 | Feature | New | Normal | compute pearson correlation in scatterplot | | 11/19/2013 08:06 am |
| 99 | Feature | New | Normal | function that move track(s) to top or bottom | | 11/07/2013 05:36 pm |
| 97 | Feature | New | Normal | user defined track color | | 11/07/2013 05:33 pm |
| 80 | Bug | New | Normal | session with lineplot TypeError | | 10/26/2013 11:45 pm |

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|-----|---------|-------------|--------|---|------------|---------------------|
| 79 | Bug | New | Normal | browser background color | | 10/26/2013 11:40 pm |
| 78 | Bug | New | Normal | 2nd panel lineplot not applied to main panel | | 10/26/2013 11:30 pm |
| 77 | Bug | New | Normal | track background color not applied on 2nd panel of line plot | | 10/26/2013 11:25 pm |
| 55 | Feature | New | Normal | [System] killing subtleKnife process which had been stuck longer than 10min | | 09/26/2013 09:14 am |
| 52 | Feature | New | Normal | Improve gene set view | | 09/21/2013 07:14 pm |
| 51 | Feature | New | Normal | Improve gene search function | | 09/21/2013 07:14 pm |
| 50 | Feature | New | Normal | Improve session? | | 09/21/2013 07:13 pm |
| 49 | Feature | New | Normal | general suggestions from UCSF | | 09/21/2013 07:13 pm |
| 48 | Feature | New | Normal | automatically refresh cache | | 09/18/2013 10:59 pm |
| 33 | Feature | New | Low | batch GEO id output | | 08/20/2013 10:57 pm |
| 3 | Bug | New | Normal | Safari 5 navigation display disorder | | 07/18/2013 01:34 pm |
| 204 | Bug | In Progress | Normal | gene set view not working | | 07/07/2014 03:04 pm |
| 245 | Bug | Resolved | Normal | Missing display of 0% methylated Cs in methylC track | | 11/24/2014 01:40 pm |
| 233 | Bug | Resolved | Normal | dbSNP track crashes | | 10/15/2014 08:04 pm |
| 232 | Bug | Resolved | Normal | Matplot not working with sessions | | 10/15/2014 02:09 pm |
| 231 | Bug | Resolved | Normal | load hub and session issue | | 10/15/2014 11:15 am |
| 234 | Support | New | Normal | Error in SE paper datahub | Daofeng Li | 10/16/2014 10:02 am |
| 62 | Support | New | Normal | "donor" terms in hg19 metadata | Daofeng Li | 10/01/2013 08:34 am |
| 25 | Feature | New | Normal | Quick capture of the central canvas | Daofeng Li | 08/02/2013 07:49 am |
| 244 | Feature | New | Normal | Pop-up window for confirming zooming in on a region | Xin Zhou | 11/09/2014 11:39 pm |
| 243 | Bug | New | Normal | Incorrect SNP coordinate based on SNP ID | Xin Zhou | 11/07/2014 10:43 am |
| 237 | Bug | New | Normal | Potential bug in the json hub name? | Xin Zhou | 10/17/2014 06:08 pm |
| 193 | Bug | New | Normal | Json syntax error when trying to jump to a new location | Xin Zhou | 05/14/2014 12:42 pm |
| 161 | Feature | New | Normal | Include scaffolds on genome snapshot | Xin Zhou | 02/13/2014 03:32 pm |
| 115 | Bug | New | Normal | tracks do not relocate and some disappear in GSV | Xin Zhou | 11/23/2013 04:19 pm |
| 46 | Bug | New | Normal | Coordinate issue in hg19 | Xin Zhou | 09/19/2013 10:16 am |
| 30 | Feature | New | Low | bam track (full) view range limit | Xin Zhou | 08/05/2013 04:50 pm |
| 28 | Feature | New | Low | add time information for session and status | Xin Zhou | 08/03/2013 11:43 pm |
| 21 | Feature | New | Low | operation history | Xin Zhou | 07/26/2013 02:47 pm |
| 17 | Feature | New | Low | public datahub unload button? | Xin Zhou | 07/25/2013 09:42 pm |
| 13 | Feature | New | Normal | Line plot | Xin Zhou | 09/22/2013 02:50 pm |
| 11 | Feature | New | Low | ability to cancel a super-enhancer job | Xin Zhou | 07/22/2013 05:40 pm |
| 10 | Feature | New | Low | gene set list in hub support url | Xin Zhou | 07/22/2013 05:35 pm |
| 240 | Bug | Resolved | Normal | can't zoom out in gene set view in mm9 | Xin Zhou | 10/28/2014 06:46 am |