

## WashU Epigenome Browser - Issues

| #   | Tracker | Status | Priority | Subject   | Assignee   | Updated             |
|-----|---------|--------|----------|---|------------|---------------------|
| 249 | Feature | New    | Normal   | track hub include feature   |            | 12/18/2014 05:24 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 |
| 244 | Feature | New    | Normal   | Pop-up window for confirming zooming in on a region                           | Xin Zhou   | 11/09/2014 11:39 pm |
| 242 | Feature | New    | Normal   | Please add the option to remove genome comparison track                       |            | 11/07/2014 09:37 am |
| 161 | Feature | New    | Normal   | Include scaffolds on genome snapshot  | Xin Zhou   | 02/13/2014 03:32 pm |
| 158 | Feature | New    | Low      | wrapping for tooltip read information   |            | 02/13/2014 05:59 pm |
| 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 |
| 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 |
| 55  | Feature | New    | Normal   | [System] killing subtleKnife process which had been stucked 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 |
| 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 |
| 25  | Feature | New    | Normal   | Quick capture of the central canvas   | Daofeng Li | 08/02/2013 07:49 am |
| 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 |