

Instructions for displaying examples of mapped read distributions in Santa Cruz Genome Browser.

1. Download the bedGraph.gz files from Supplementary Files.
2. Go to UCSC Browser at <https://genome.ucsc.edu/> .
3. Choose from Genomes: GRCh38/mm10
4. Choose “Add custom tracks”.
5. Choose “Choose file”
6. Click on appropriate file.
7. Click “Submit”

These steps have been followed to set up as a temporarily link displaying one example of data from vehicle-treated mpkCCD cells and one example of data from dDAVP-treated cells at

https://genome.ucsc.edu/cgi-bin/hgTracks?hgS_doOtherUser=submit&hgS_otherUserName=chen119&hgS_otherUserSessionName=Pablo_RNA_seq

Note: The display has been set to “Autoscale”, which adjusts y-axis for optimal display of reads. For direct vehicle vs. dDAVP comparisons, this setting can be changed to “Fixed” by right clicking on track and choosing “Configure”.