

[Genome] Too many items to display – RNA-Seq reads

Dear UCSC Developer and Support Team,

I am trying to visualize in the UCSC Genome Browser RNA-Seq reads that were mapped through the Galaxy Toolkit and sent to UCSC Genome browser to the Galaxy tool.

The difficulty I have is the following: when I have more than 1000 reads mapping to a given SNP, UCSC Browser does not display the reads above that limit. It just shows a bar indicating the position of the mapped reads (1st and 2nd custom tracks below the retroposed gene *DGKZP1* (in pink) in the attached print screen) and a “Too many items to display in the full/pack mode”.

How can I get the Browser to exhibit all the reads?

Best regard,

Enrique

Full mode

The image shows a screenshot of the UCSC Genome Browser interface. At the top, there is a navigation bar with links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. The main title is "UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly". Below the title, there are navigation controls for moving and zooming, and a search bar containing the coordinates "chr13:44,542,560-44,545,335" and "2,776 bp.". A chromosome ideogram for chromosome 13 is visible above the tracks. The tracks include a scale for chromosome 13, a track for "hg19" with coordinates 44,544,500 and 44,545,000, a track for the gene "DGKZP1" highlighted in purple, and a track for "BAM on data 42 bam" showing sorted reads. A modal dialog box is overlaid on the tracks, displaying the message "There are too many items to display the track in full mode." with an "OK" button.

Pack mode

The image shows a screenshot of the UCSC Genome Browser interface. At the top, there is a navigation bar with links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. The main title is "UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly". Below the title, there are navigation controls including "move" buttons (left and right arrows) and "zoom in" buttons (1.5x, 3x, 10x, base) and "zoom out" buttons (1.5x, 3x, 10x, 100x). A search bar contains the coordinates "chr13:44,542,560-44,545,335" and "2,776 bp." with a "go" button. The main content area displays a genomic track for chromosome 13 (q14.11) with a purple bar representing the gene DGKZP1. A white dialog box with the text "There are too many items to display the track in pack mode." and an "OK" button is overlaid on the track. The track shows a dense collection of reads, with a vertical orange line indicating the current position. The track is labeled "BAM on data 42: bam" and "d reads (sorted BAM)".