[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.

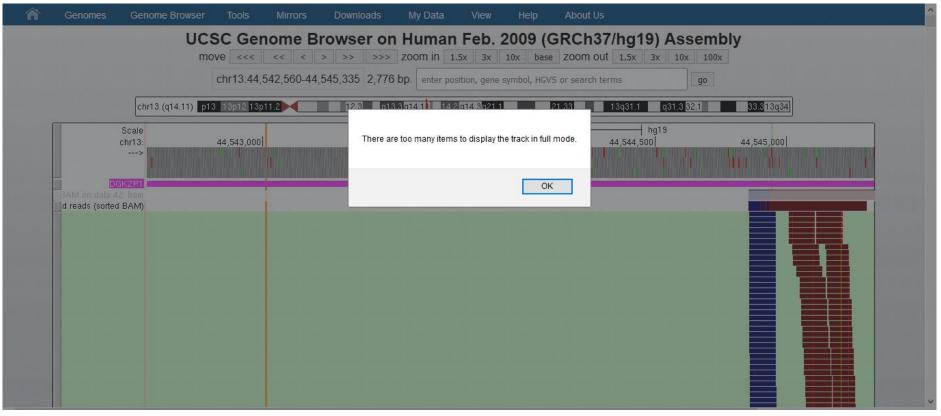
The difficulty I have is the following: when I have more than 1000 reads mapping to a given SNP, UCSC Browser does not display the reads above that limit. It just shows a bar indicating the position of the mapped reads (1<sup>st</sup> and 2<sup>nd</sup> custom tracks below the retroposed gene *DGKZP1* (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



## Pack mode

