ChIP-seq: Peak Calling (answers to questions)

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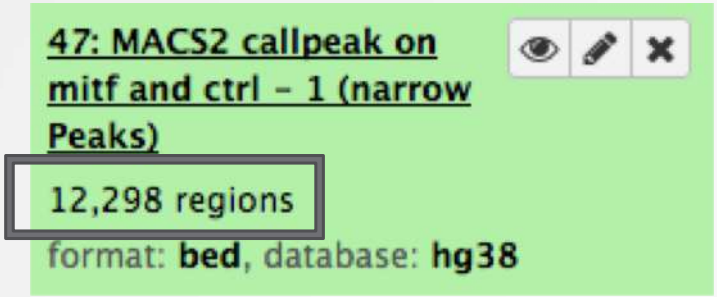
Exercise: peak calling

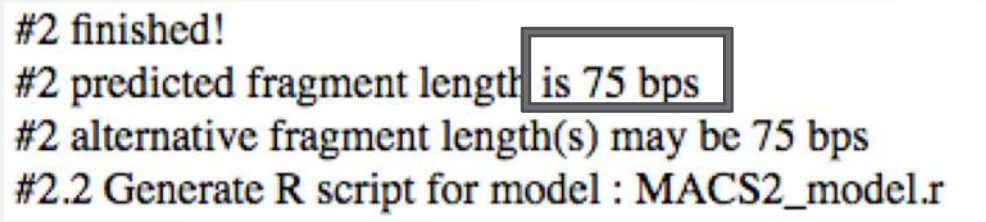
- 1.
  - Search for “macs2 callpeak” in the search field (tool panel)
  - Click on the name of the tool
  - Set parameters:
    - ChIP-Seq Treatment File: mitf.bam
    - ChIP-Seq Control File: ctrl.bam
    - Effective genome size: Human
    - Outputs: select Peaks as tabular file, summits, Summary page (html), Plot in PDF
    - Click on 

Exercise: peak calling

- 2.
  - There is 12,298 peaks



- 3. Look at the HTML dataset



  - The d value estimated by MACS seems a bit small. Let's try to re-run MACS with the expected fragment size : 200

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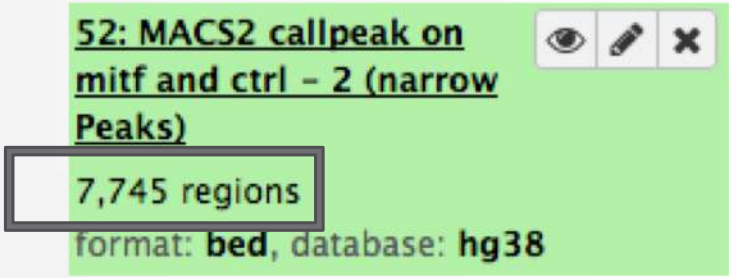
- 4.
  - Click on the name of one of the datasets generated by Macs2.
  - Click on ↻ to display Macs2 form with the same parameters as for the previous run of Macs2
  - In Build Model, select Do not build the shifting model (--nomodel)
  - Enter 100 in the text box "The arbitrary extension size in bp"
  - Click on ✔ Execute
- 5.
  - 7,745 peaks are now found



  - NOTE: the graphs (showing the d values estimate) are no longer generated