RNA-seq and ChIP-seq data integration

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Exercise

- 1. We want to know how many up-regulated genes contain a peak for MITF
  - Compare Gene symbols of the chIPseq data (annotation step) and the RNAseq data (up-regulated genes).
    - Use the file siMitfvssiLuc.up.annot.txt (annotated with BioMart)
    - All chIPseq data are used
  - Use Venny (http://bioinfogp.cnb.csic.es/tools/venny/)
- 2. Use seqMINER to visualize at the same time chIP-seq data along with RNA-seq data
  - Use the Advance (RNAseq) tab to upload a 2-columns table: 1st column contains Ensembl Gene IDs and 2nd column contains normalized read counts of MITF divided by gene length in Kb
    - Use the file siMitfvssiLuc.up.annot.txt you annotated with BioMart and create a file which contains 2 columns (text file separated by tabs):
      - Gene IDs
      - Read counts divided by gene length in Kb