Correlation of RNA-seq and ChIP-seq data

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Exercise

- 1. We want to know how many up-regulated genes contain a peak for MITF
  - Compare Gene names 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 peaks are used (annotated with Homer)
  - 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 named RNAseq_seqminer.txt located in the directory Correlation on your computer
  - Use MITF peak summits (second MACS2 run) as reference coordinates). Download the file from GalaxEast.