

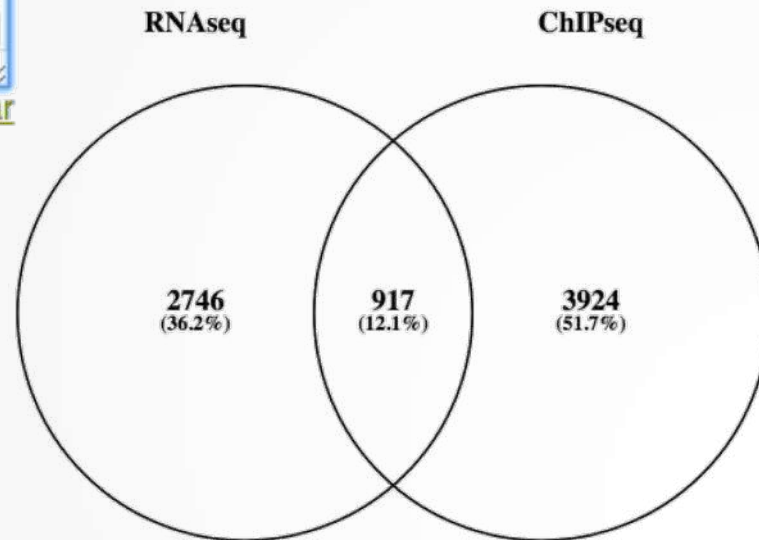
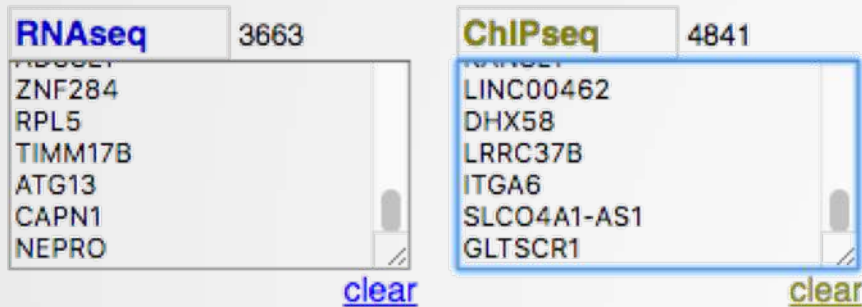
# RNA-seq and ChIP-seq data integration

(answer to questions)

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# Exercise

- 1.
  - Retrieve Gene symbols of up-regulated genes (use the file siMitfvssiLuc.up.txt you annotated with BioMart )
  - Download the annotated peaks (dataset generated with HOMER). Use the Gene Name column.



# Exercise

- 2.
  - Download MITF peaks (Output of MACS2 narrow peaks) -> Use it as reference coordinates in seqMINER

The screenshot shows the seqMINER web interface with the following components:

- File Tools Help** menu at the top.
- Method tabs: **Density Array Method**, **Enrichment Based Method**, and **Advance(RNA-Seq)**.
- Step 1: Load data**
  - Load reference coordinates (i.e. peaks) button.
  - Select assembly dropdown: **hg38\_ense...** (Ensembl 95 (hg38)).
  - Advanced button.
  - Load aligned reads section with a list of files: **mitf.sort.bam**, **H3K4me3.sort.bam**, and **poll.sort.bam** (ChIP-seq datasets).
  - Browse ... button.
  - Load file(s) >> button.
- Step 2: Data extraction**
  - Galaxy29-[MACS2\_callpeak\_or 7745 peaks. Peak length mean: 172] (MITF peaks).
  - RNA-Seq expression section with **RNAseq\_seqMINER.txt** selected (RNAseq data).
  - Selected datasets section with **mitf.sort.bam**, **H3K4me3.sort.bam**, and **poll.sort.bam**.
  - Delete button.
  - Extract data button.

Callouts in the image point to:

- Ensembl 95 (hg38)** pointing to the assembly dropdown.
- ChIP-seq datasets** pointing to the list of aligned reads.
- MITF peaks** pointing to the Galaxy29-[MACS2\_callpeak\_or 7745 peaks. Peak length mean: 172] text.
- RNAseq data** pointing to the RNAseq\_seqMINER.txt file.

100 %

# Exercise

- Go to Density Array Method (top tabs)
- Click on Extract data
- Click on Clustering

# Exercise

