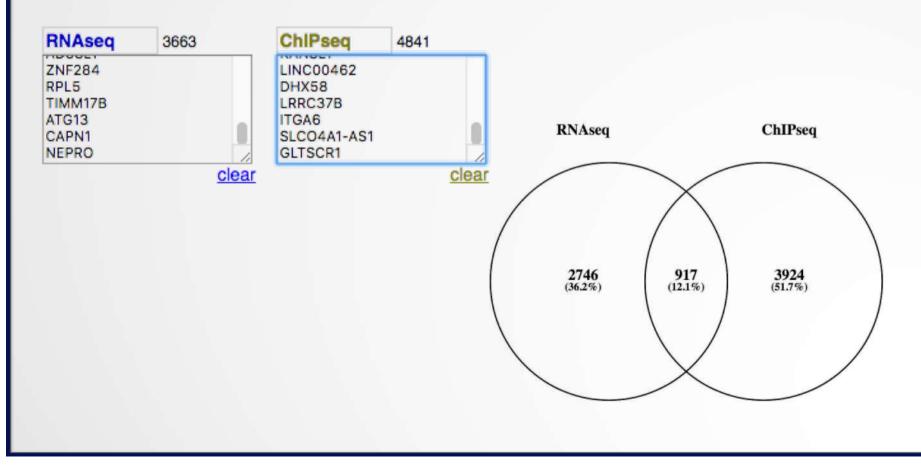
Correlation of RNA-seq and ChIP-seq data (answer to questions)

Stéphanie Le Gras (slegras@igbmc.fr)

• 1.

• Retrieve Gene symbols of up-regulated genes (use the file siMitfvssiLuc.up.txt you annotated with BioMart)

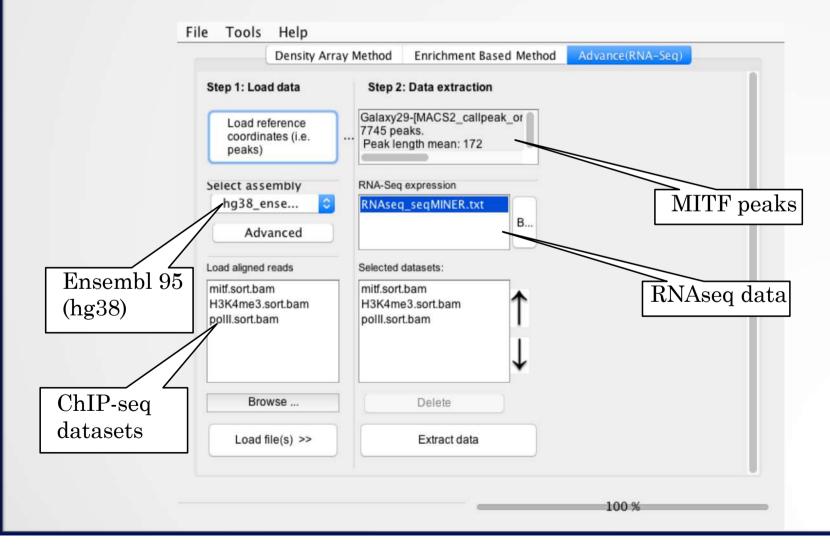
• Download the annotated peaks (dataset generated with HOMER). Use the Gene Name column.



 $\mathbf{2}$

• 2.

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



3

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

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