What is hidden in the darkness??

(scATAC in non-coding genome)

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Organism: Mus musculus

Genome assembly: mm10

Tissue: Cerebral cortex, adult mice p50

Dataset: 10x scATAC

Regions of interest:

Long non-coding RNAs

- LINEs (long interspersed nuclear elements)
- SINES (short interspersed nuclear elements)
- LTR (long terminal repeats)
- Retroposons
- Simple repeats
- Satellites
- Enhancers
- Promoters
- Protein coding

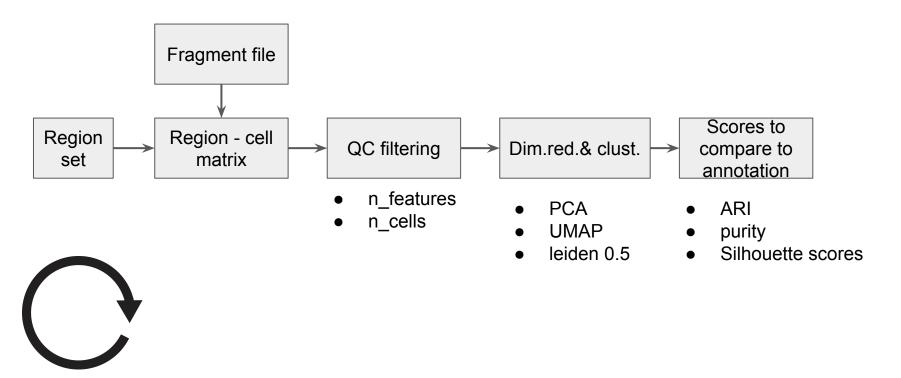


Gencode gtf file

Repeatmasker mm10

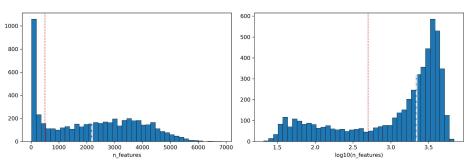
SCOG 2022 files

Data processing

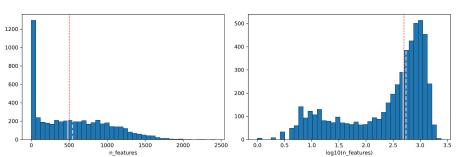


QC Distributions. Nr of peaks in features.

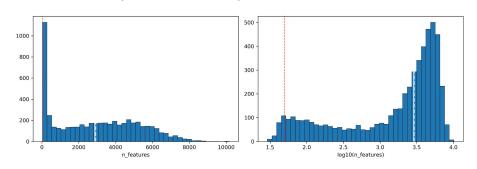
Protein coding (threshold 500)



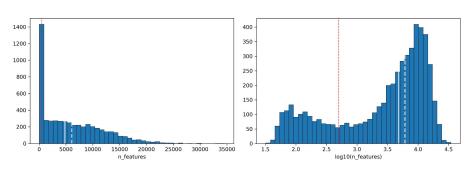
IncRNAs (threshold 500)



Promoters (threshold 500)

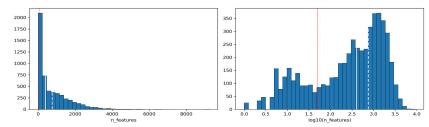


Enhancers (threshold 500)

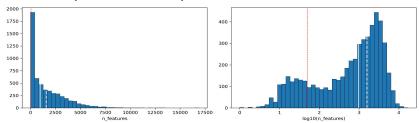


QC Distributions. Nr of peaks in features.

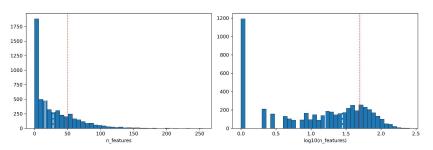
LINEs (threshold 50)



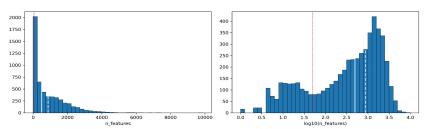
SINEs (threshold 50)



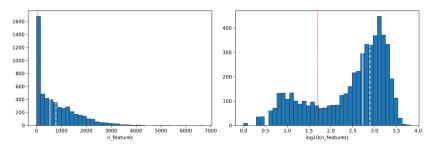
Satellite (threshold 50)



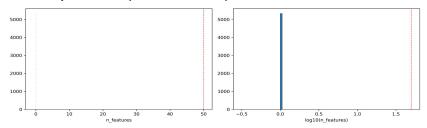
LTRs (threshold 50)

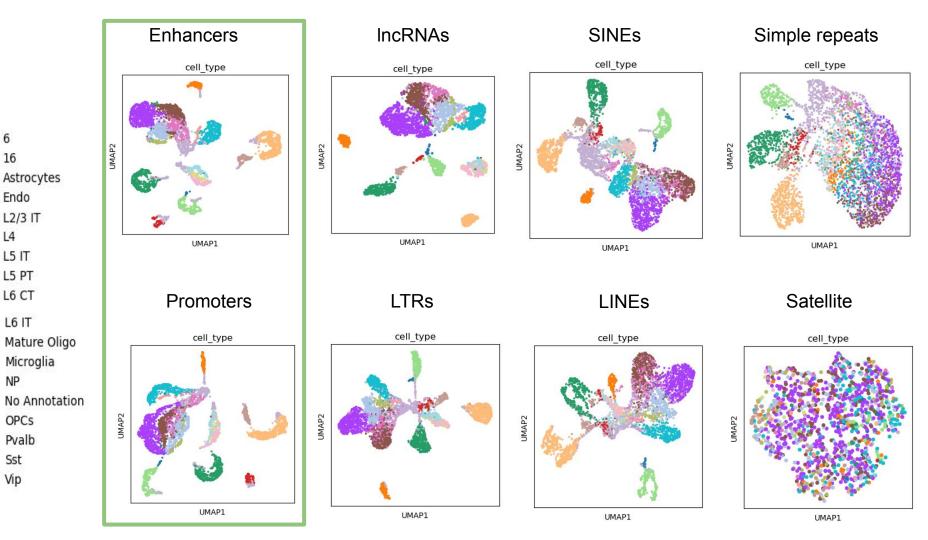


Simple repeats (threshold 50)

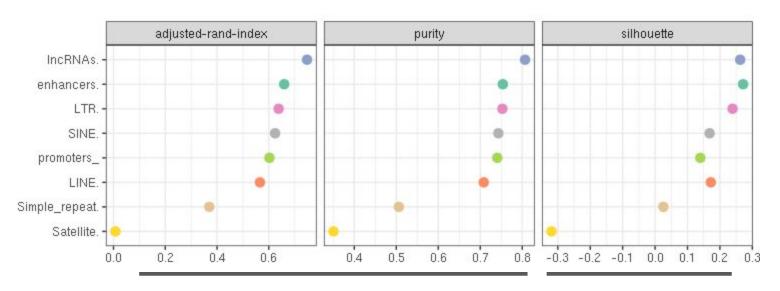


Retroposons (threshold 0)





Evaluation metrics

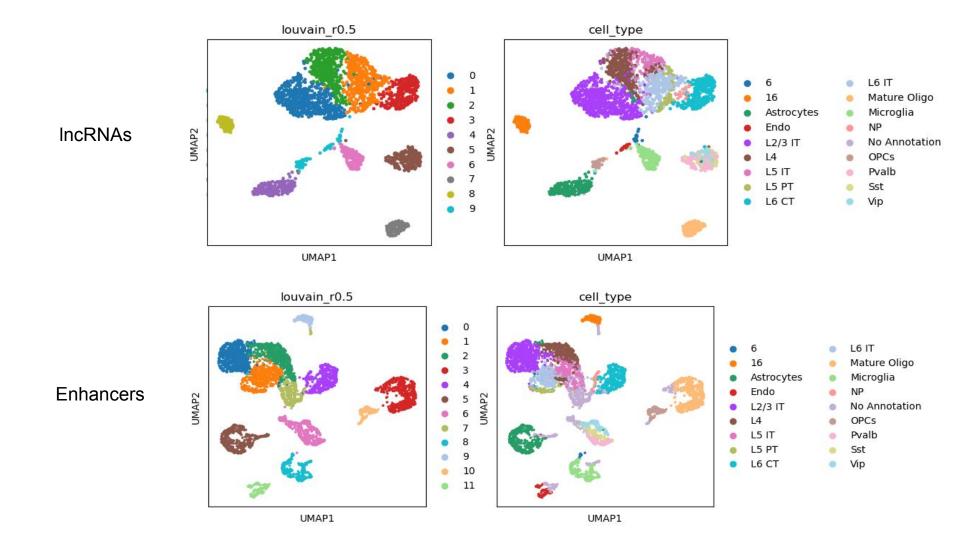


External evaluation:

Louvain clustering (res0.5) vs cell types (ground truth)

Internal evaluation:

Cell types (ground truth)



Summary

Chromatin accessibility in non coding region of the genome contains cell-type specific information.

- Enhancers and IncRNAs performs the best in separating two type of neurons and glial cells
- All repetitive elements are doing a good job in separating neuronal and glial cell types, but usually not able to separate glutamatergic and GABAergic neurons
- LTRs shows the best clustering for both neuronal and glial among all repetitive elements.
- Chromatin accessibility on satellite DNA does not seem to be cell type specific