

ATAC-seq course Quiz

Goal: explore data, deepen understanding of the code and data

Judith Zaugg and Daria Bunina

Explore steroid hormone receptor Esrrg

- a steroid hormone receptor that stimulates proliferation

- Investigate the Esrrg **gene locus**, are there any cluster-specific putative enhancers?
- Compare Esrrg **gene activity** across your clusters, which cluster has the highest gene activity?
- Compare the Esrrg **footprint** across your clusters, which cluster has the highest footprint activity?
- How does Esrrg **TF activity** change across clusters, which cluster has the highest TF activity?
- How does Esrrg **TF activity** change across **pseudotime**?
- Do you think Esrrg is an activator or a repressor and why?

Hint: to find the motif name associated with Esrrg, go to the hocomoco database: <https://hocomoco11.autosome.org/>

Explore pluripotency transcription factor Nanog alternative: KLF4

- Investigate the Nanog **gene locus**, are there any cluster-specific putative enhancers?
- Compare Nanog **gene activity** across your clusters, which cluster has the highest gene activity?
- Compare the Nanog **footprint** across your clusters, which cluster has the highest footprint activity?
- How does Nanog **TF activity** change across clusters, which cluster has the highest TF activity?
- How does Nanog **TF activity** change across **pseudotime**?
- Do you think Nanog is an activator or a repressor and why?

Hint: to find the motif name associated with Nanog or KLF4, go to the hocomoco database: <https://hocomoco11.autosome.org/>

Explore transcription factor PITX1

an organ-development transcription factor

- Investigate the PITX1 **gene locus**, are there any cluster-specific putative enhancers?
- Compare PITX1 **gene activity** across your clusters, which cluster has the highest gene activity?
- Compare the PITX1 **footprint** across your clusters, which cluster has the highest footprint activity?
- How does PITX1 **TF activity** change across clusters, which cluster has the highest TF activity?
- How does PITX1 **TF activity** change across **pseudotime**?
- Do you think PITX1 is an activator or a repressor and why?

Hint: to find the motif name associated with PITX1, go to the hocomoco database: <https://hocomoco11.autosome.org/>

Explore repressor REST

repressing neuronal genes in non-neuronal cells

- Investigate the REST **gene locus**, are there any cluster-specific putative enhancers?
- Compare REST **gene activity** across your clusters, which cluster has the highest gene activity?
- Compare the REST **footprint** across your clusters, which cluster has the highest footprint activity?
- How does REST **TF activity** change across clusters, which cluster has the highest TF activity?
- How does REST **TF activity** change across **pseudotime**?
- Do you think REST is an activator or a repressor and why?

Hint: to find the motif name associated with REST, go to the hocomoco database: <https://hocomoco11.autosome.org/>

Explore chromatin structural factor CTCF involved in chromatin organisation

- Investigate the CTCF **gene locus**, are there any cluster-specific putative enhancers?
- Compare CTCF **gene activity** across your clusters, which cluster has the highest gene activity?
- Compare the CTCF **footprint** across your clusters, which cluster has the highest footprint activity?
- How does CTCF **TF activity** change across clusters, which cluster has the highest TF activity?
- How does CTCF **TF activity** change across **pseudotime**?
- Do you think CTCF is an activator or a repressor and why?

Hint: to find the motif name associated with CTCF, go to the hocomoco database: <https://hocomoco11.autosome.org/>

Advance: compare activity of different TFs

- compare the **gene activity** between two genes across cells
(e.g. Nanog vs Esrrg and PITX1 vs Esrrg - or choose your own)
- compare the **TF activity** between two TFs across cells
(e.g. Nanog vs Esrrg and PITX1 vs Esrrg - or choose your own)
- compare the **TF activity** and **gene activity** of a TF across cells
(e.g. Esrrg or PITX1 - or choose your own)

Hint: you need to extract the specific values from the seurat object. For visualisation you could start with scatterplot (e.g. `geom_point()`)