

Integrative Alignments of DNA Elements for Transcriptional Regulation in Swine Epigenome

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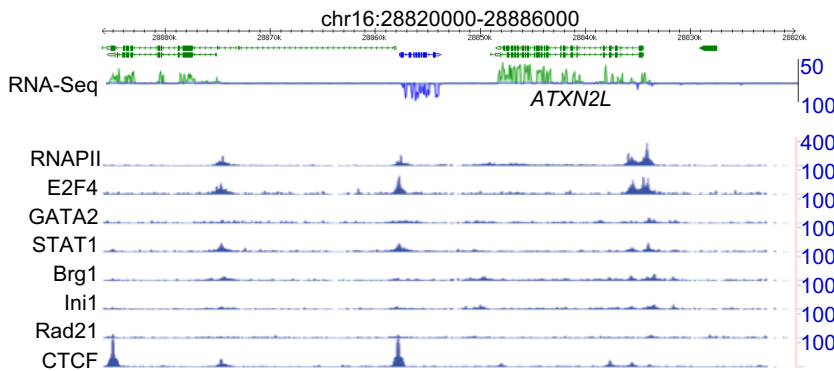
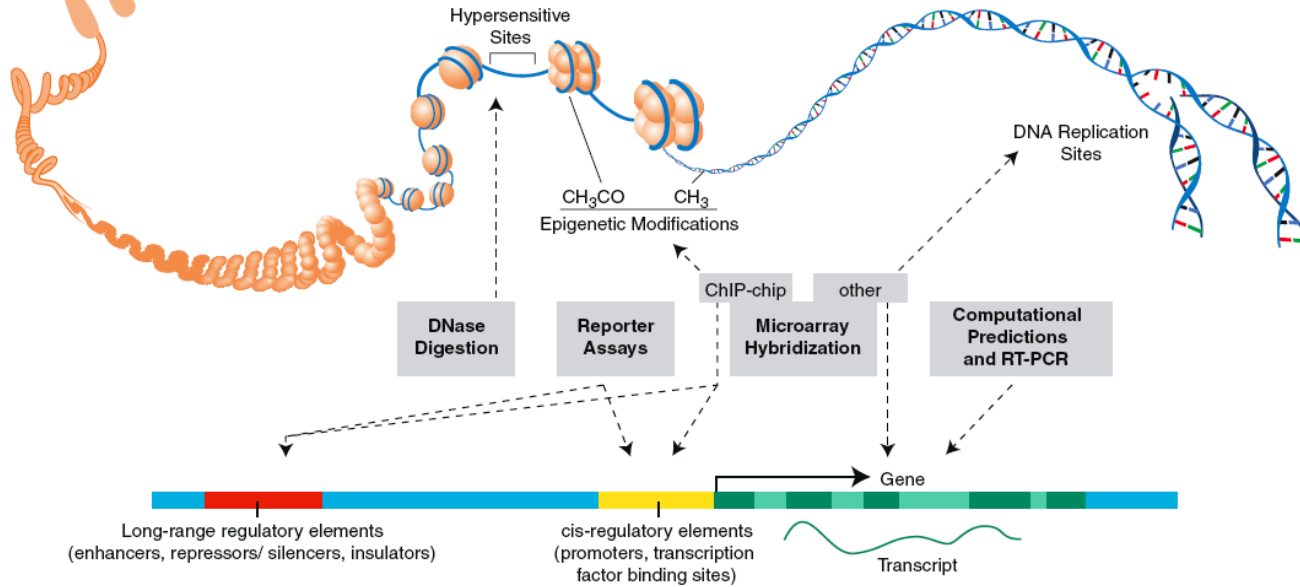
Key Laboratory of Agricultural Animal Genetics, Breeding
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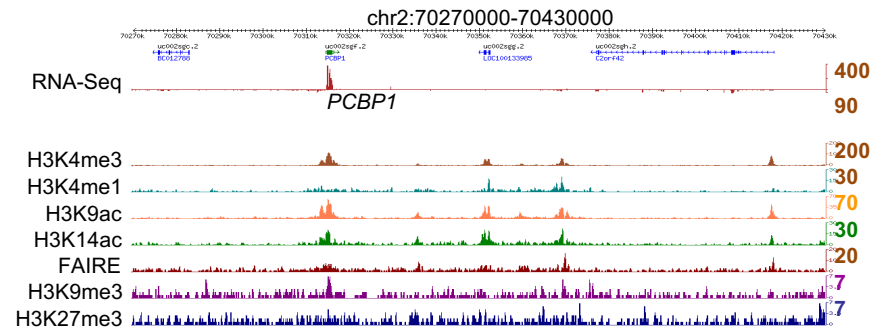
Outlines

- Introduction
- Data presentation
- Results(data quality; main output; examples)
- Conclusion

Human ENCODE project

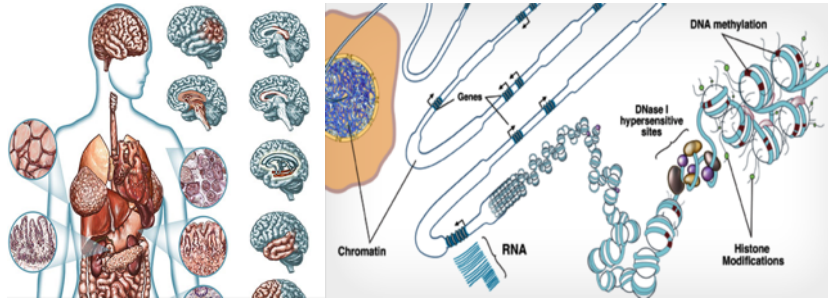


TF binding



Histone modification

“An integrated encyclopedia of DNA elements in the human genome”, *Nature*, 2012

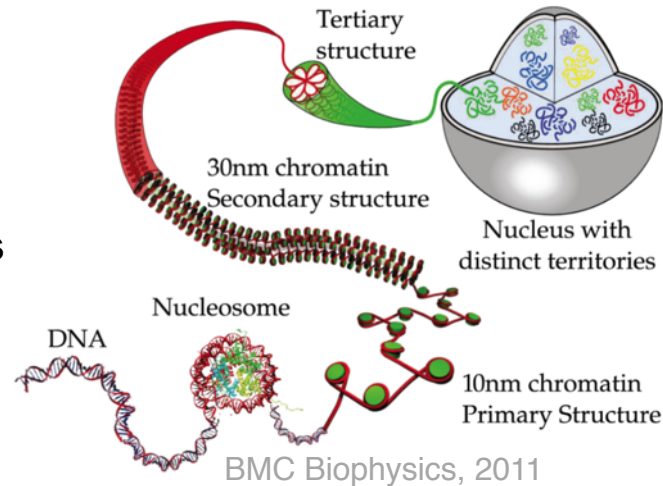


Roadmap Epigenomics Consortium, *Nature*, 2015

ENCODE/ Roadmap

Structure

- ❖ Massively packaged
- ❖ non-randomly organized
- ❖ Coiled/looped in high level orders
- ❖ Fluid and dynamic

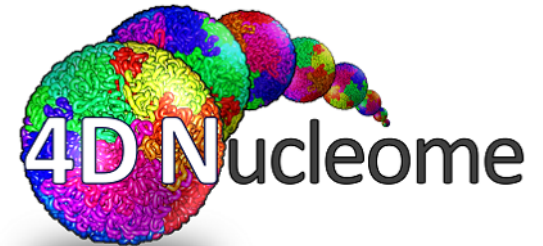


3D Genome

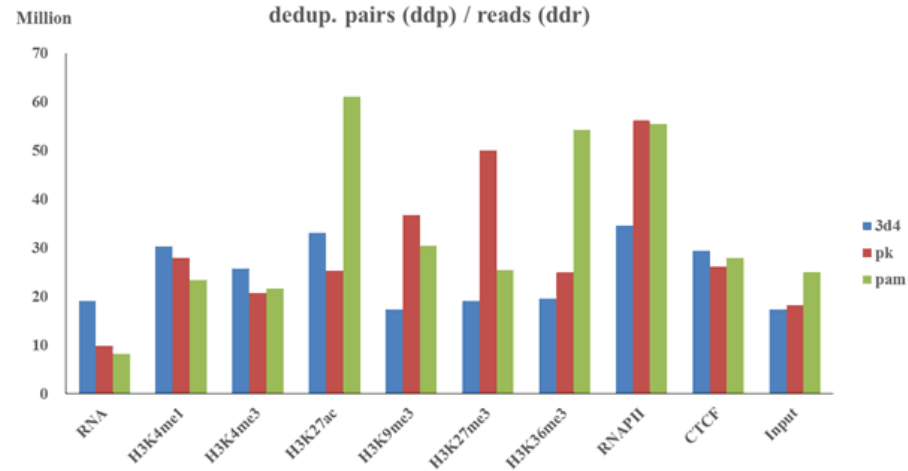
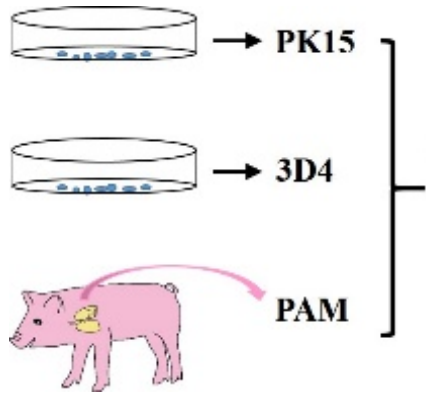
BMC Biophysics, 2011

Function

- ❖ Gene transcription regulation
- ❖ DNA replication
- ❖ Genome translocation
- ❖ DNA repair



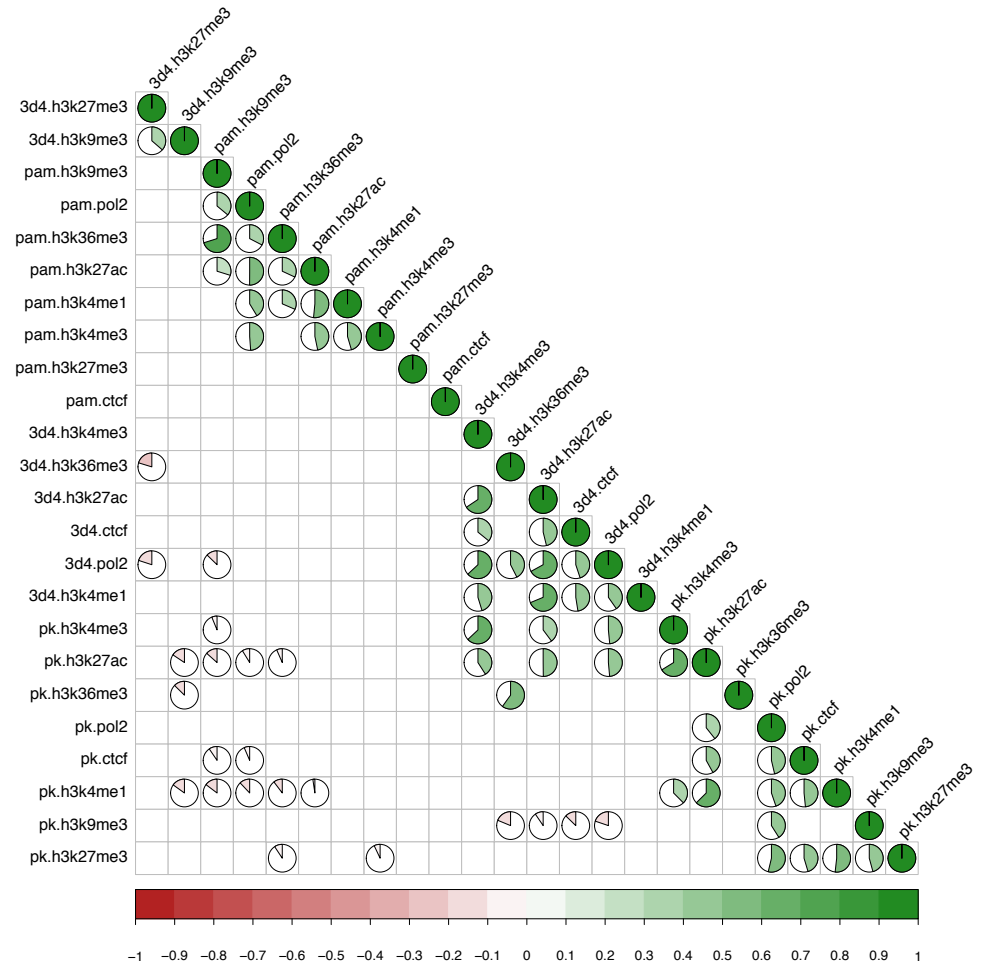
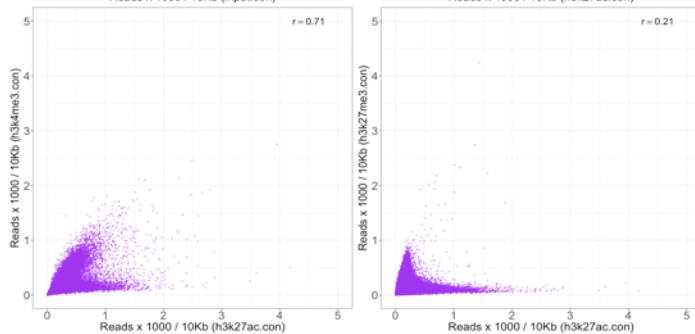
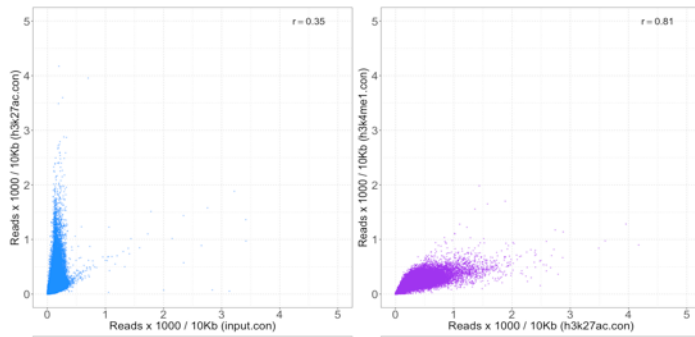
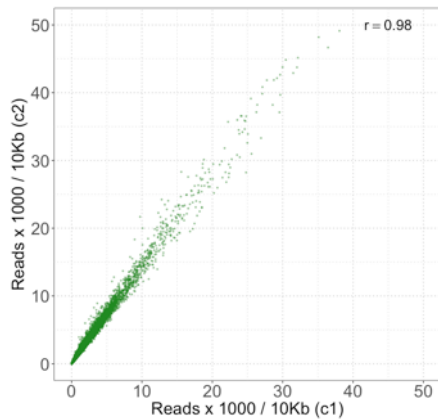
ChIP/RNA-Seq data of porcine cells/tissue



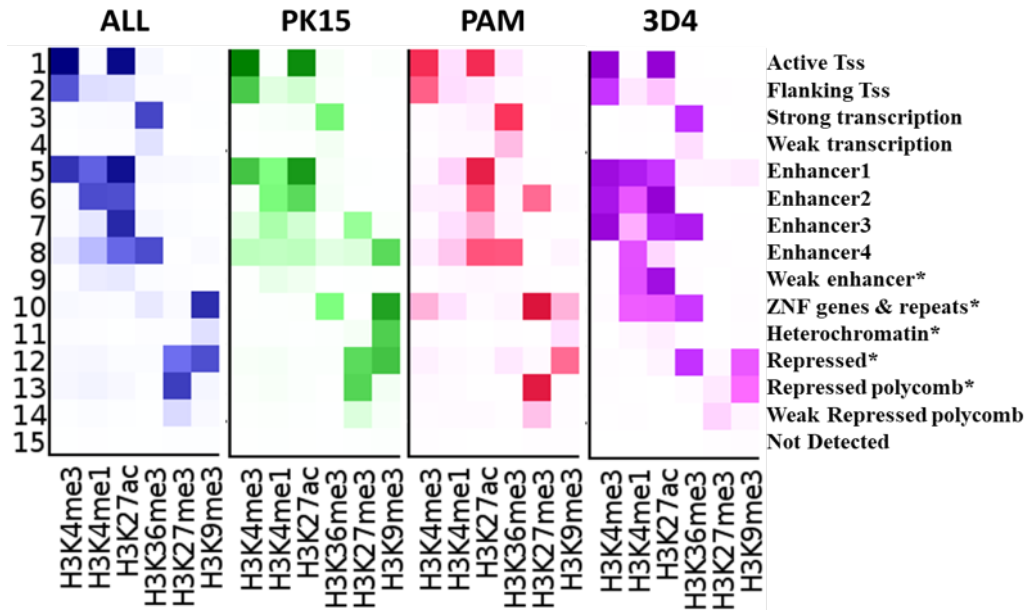
	3D4/21	PAM	PK-15	LDM
H3K4me1	✓	✓	✓✓	✓
H3K4me3	✓	✓✓	✓	✓✓
H3K9me3	✓	✓	✓	✓
H3K27ac	✓	✓✓	✓✓	✓
H3K27me3	✓✓	✓✓	✓✓	✓
H3K36me3	✓	✓	✓	✓
CTCF	✓	✓	✓	✓
POL2	✓✓	✓	✓	✓✓
INPUT	✓	✓	✓	✓

- Over **15,000** peaks for narrow peak
- ~**10,000** enriched region for broad peak
- PAMs have better performance on **H3K27me3**.

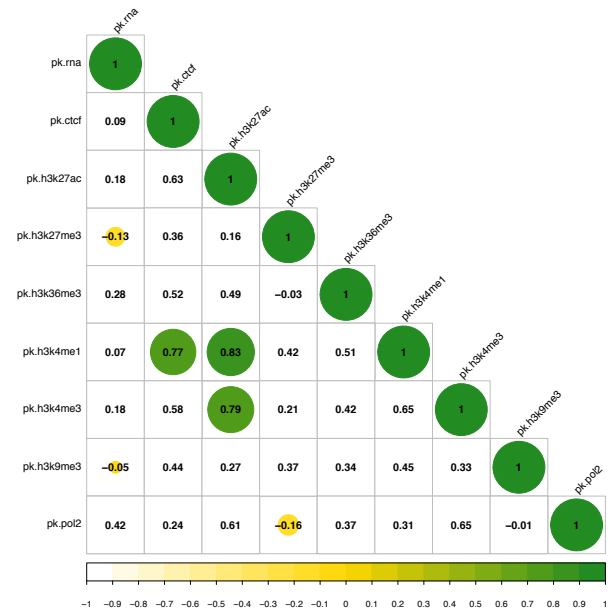
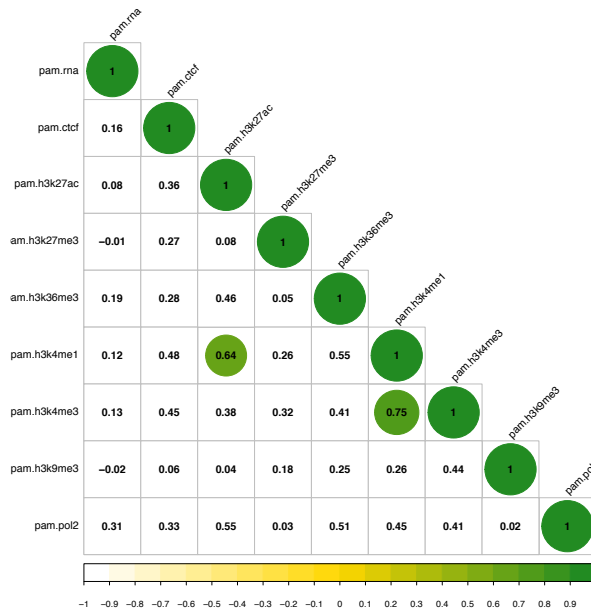
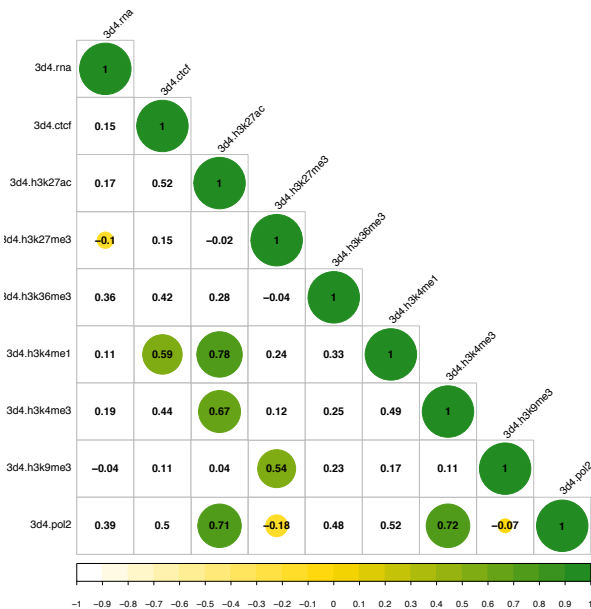
Data quality assessments: RNA-Seq Reproducibility and ChIP-Seq Correlations



chromHMM: chromatin states assignments

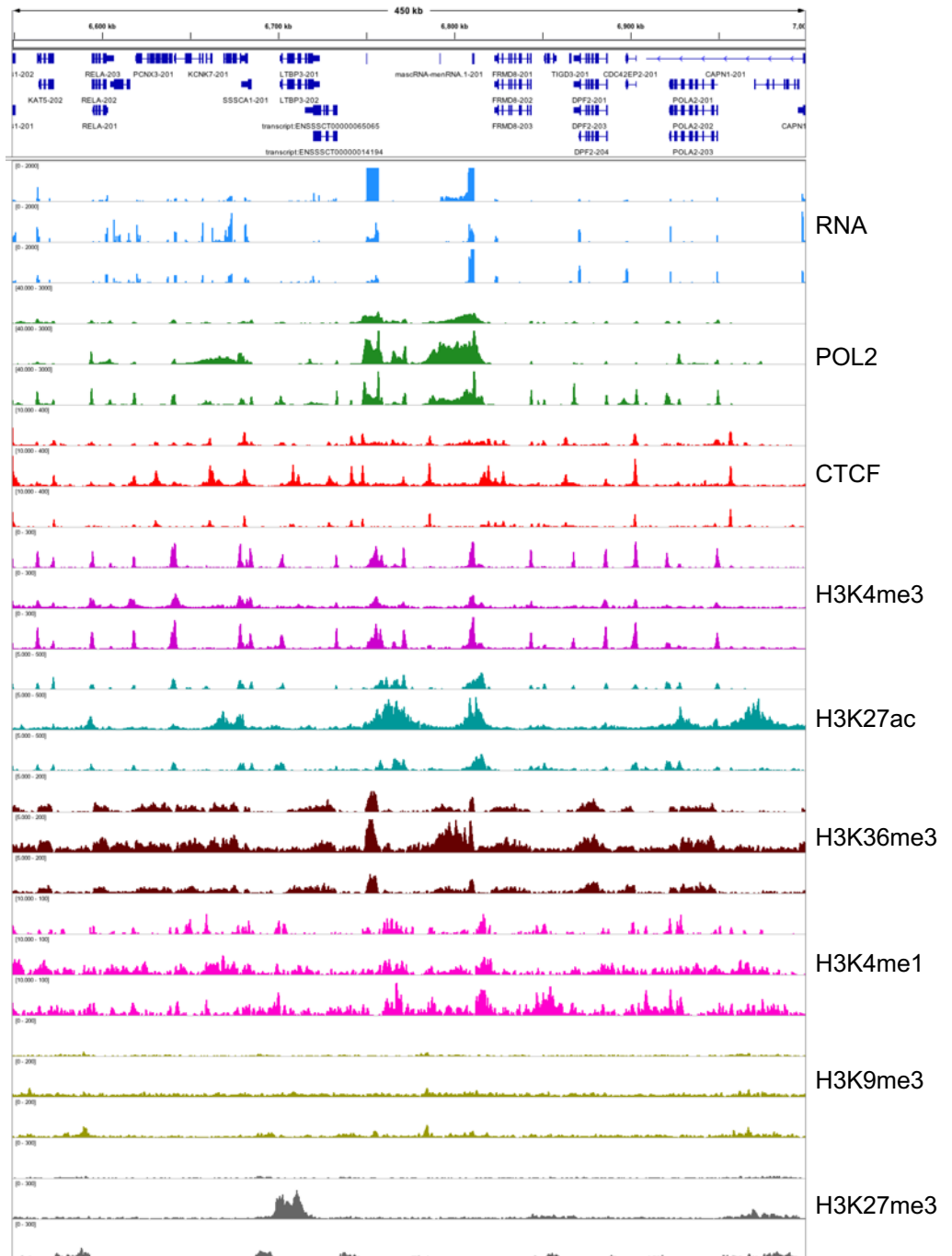


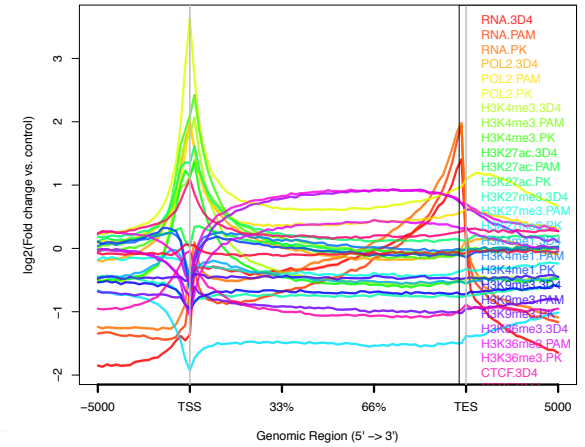
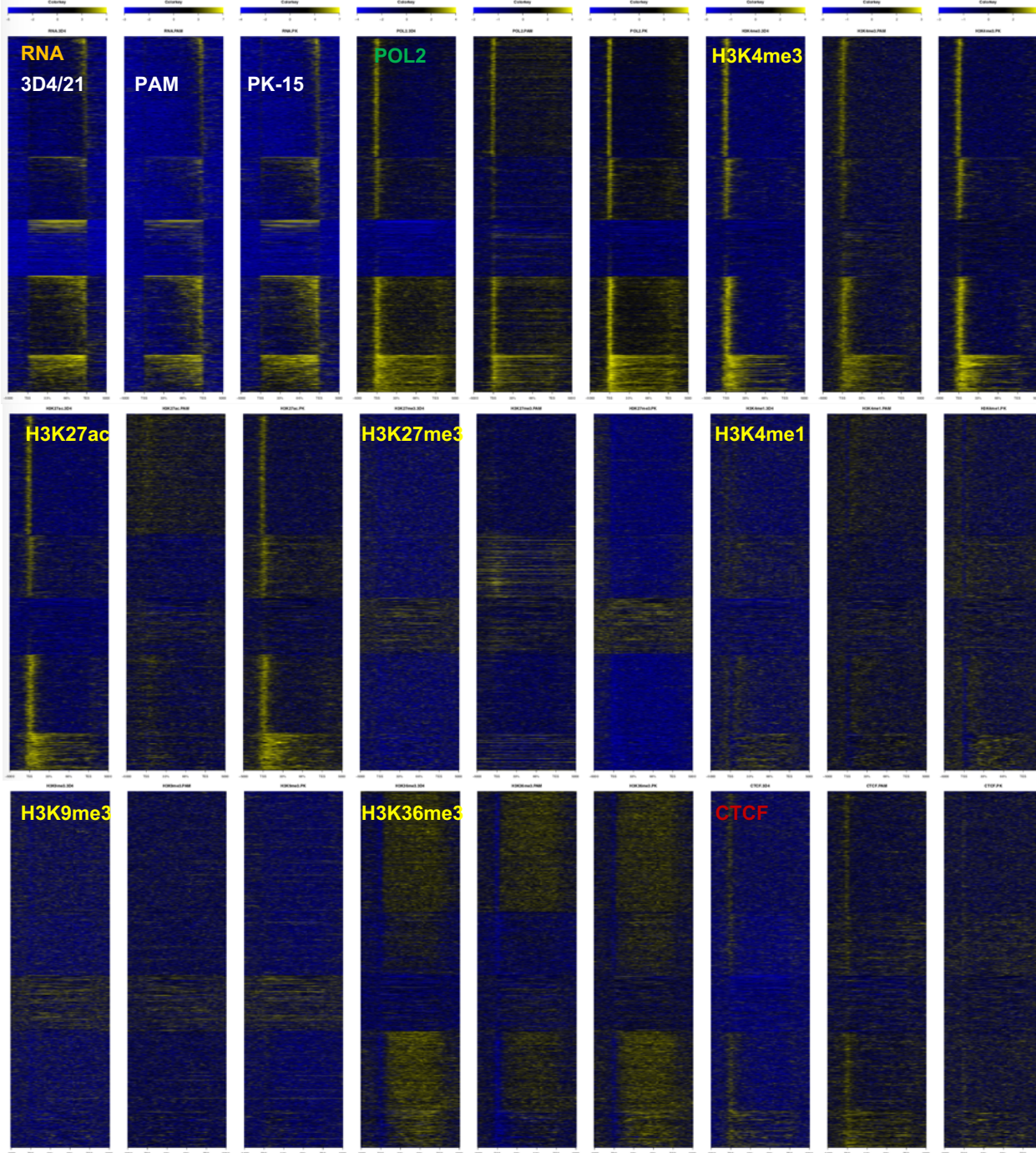
- Assigned 15 chromatin states based on 6 histone markers.
- Markers within a state have more correlation.
- Primary PAM cells have lower correlations between markers.



Overview of ChIP-Seq and RNA-Seq data

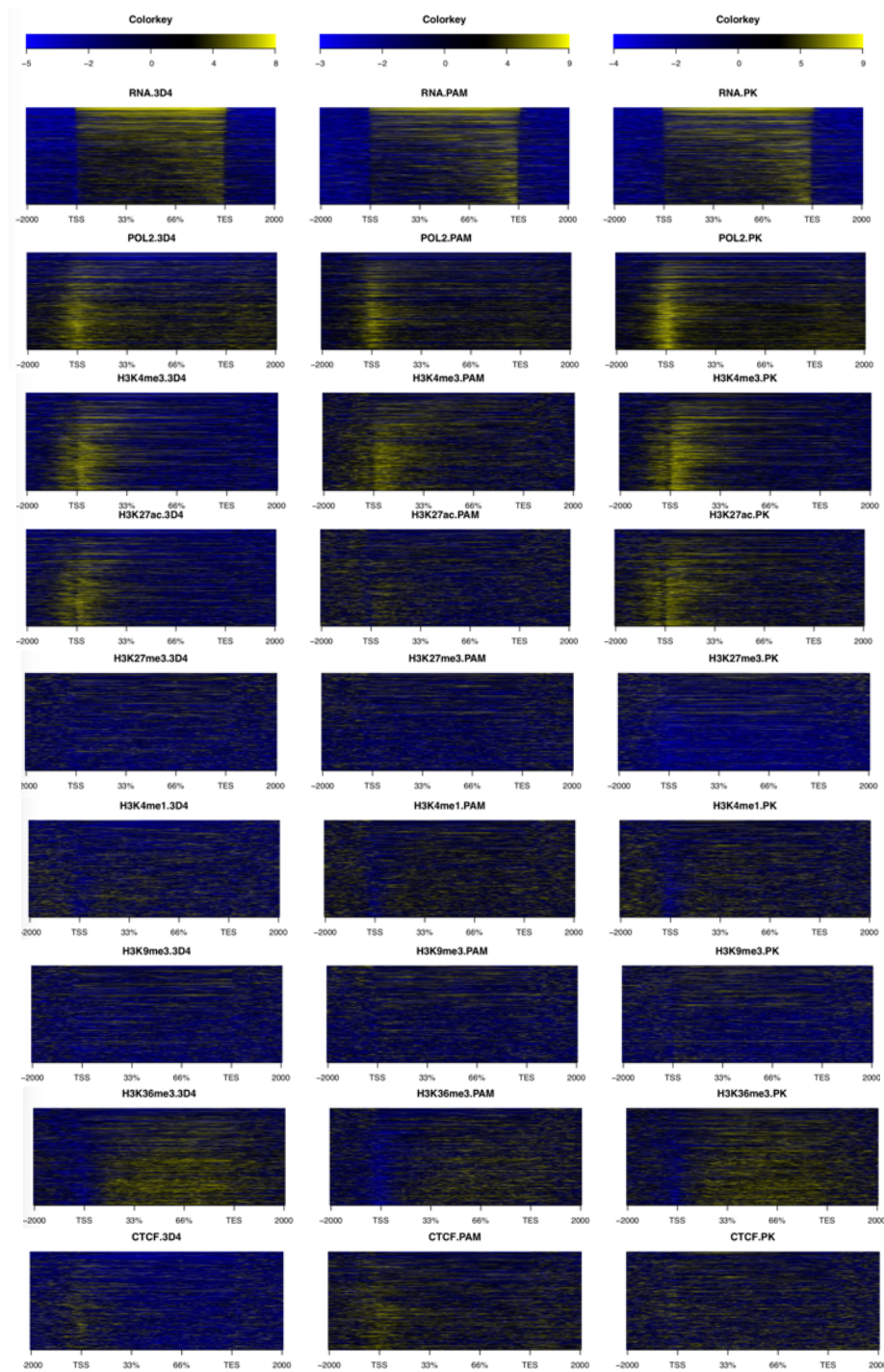
- MALAT1 and NEAT1 sites
- RNAPII and CTCF factor work well in swine genome
- 6 Histone markers are also work well.





Integrative Alignments of DNA Elements for Transcriptional Regulation in Swine Epigenome

- RNAPII (POL2), transcriptional factor
- CTCF, insulator for 3D genomics
- PAM with unique characters at H3K27ac/me3 profiling



RNA

POL2

H3K4me3

H3K27ac

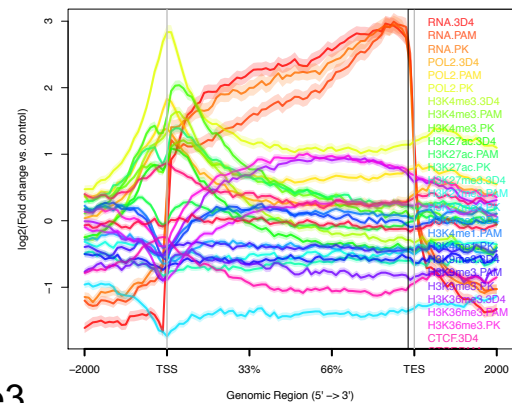
H3K27me3

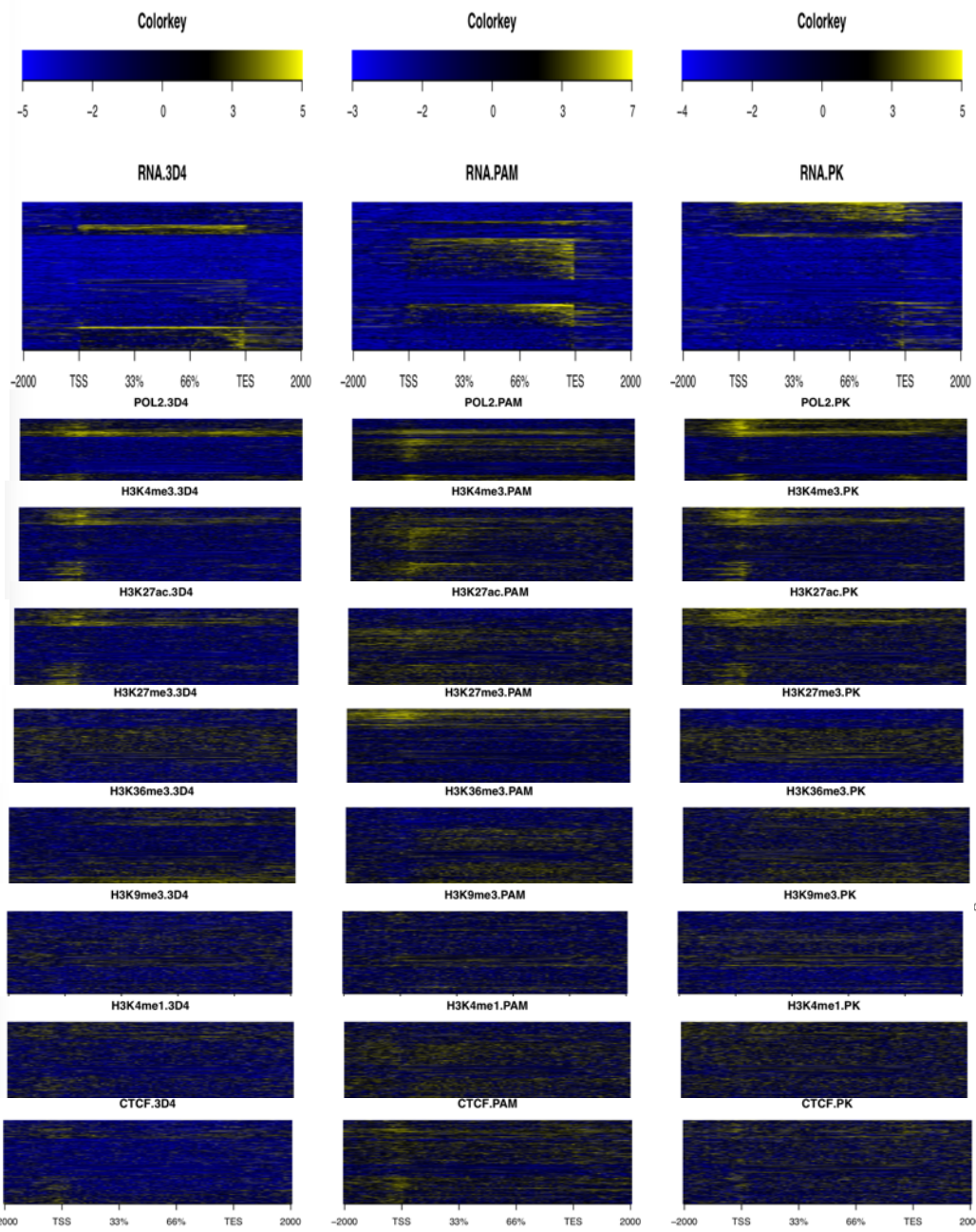
H3K4me1

H3K9me3

H3K36me3

CTCF





SOX17

PK-15

RNA

POL2

H3K4me3

H3K27ac

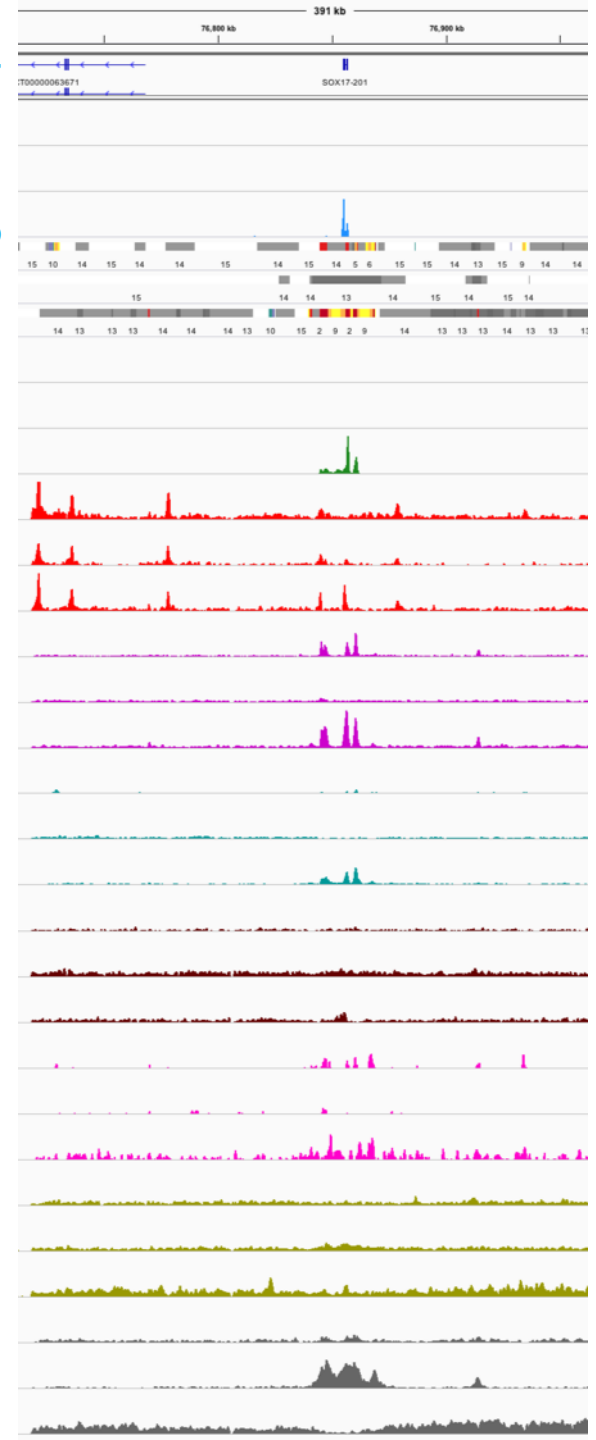
H3K27me3

H3K4me1

H3K9me3

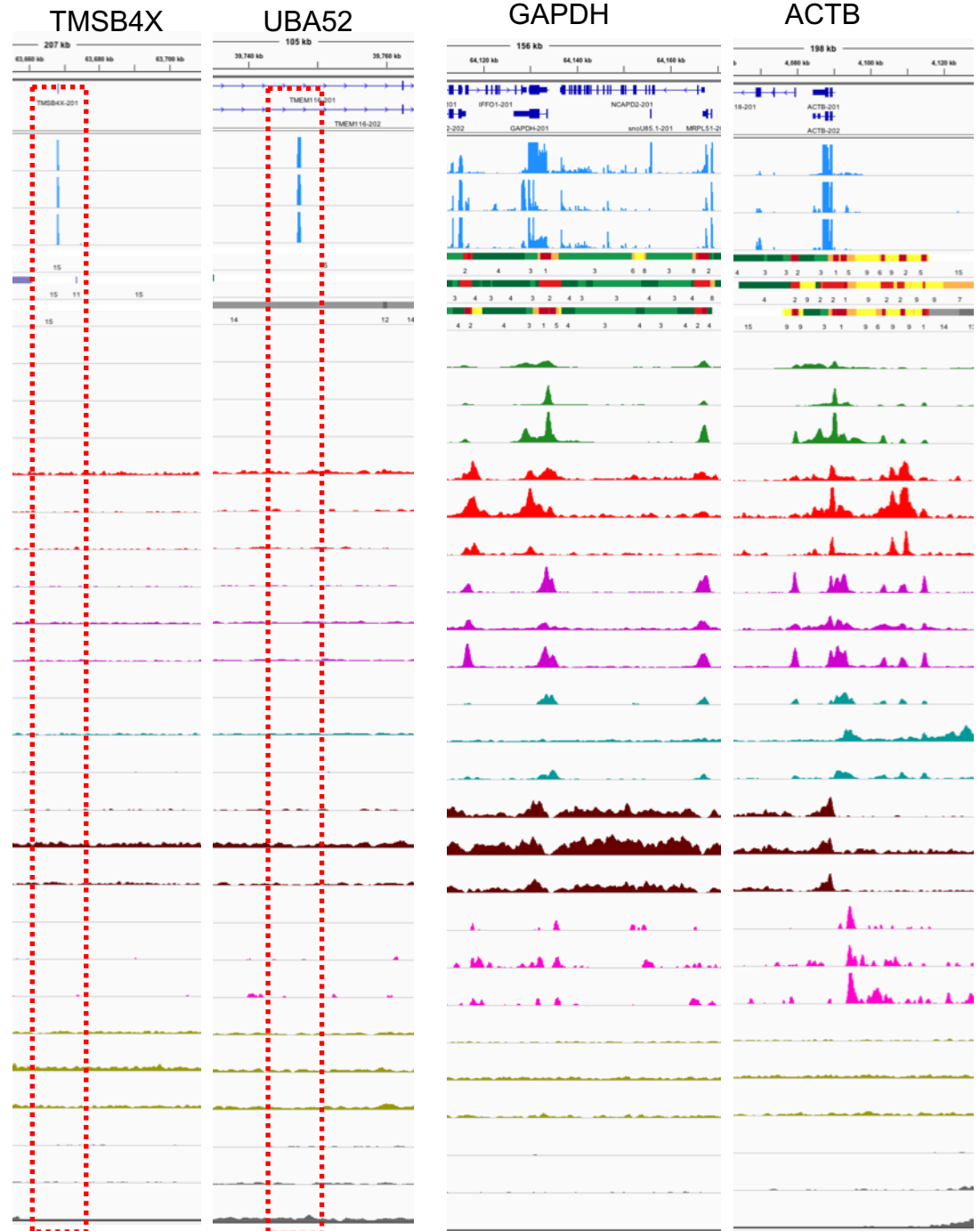
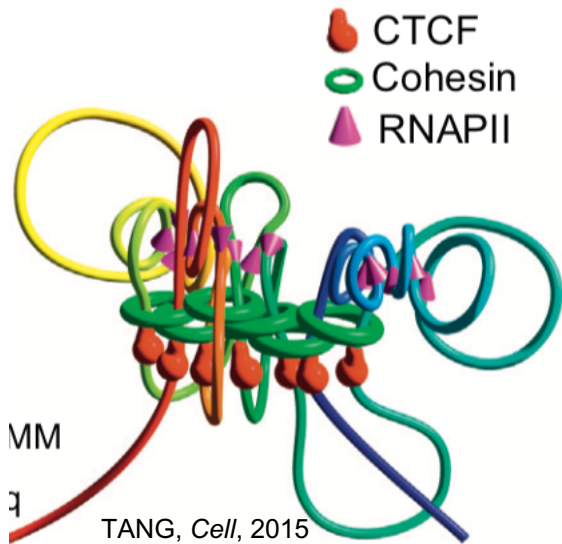
H3K36me3

CTCF



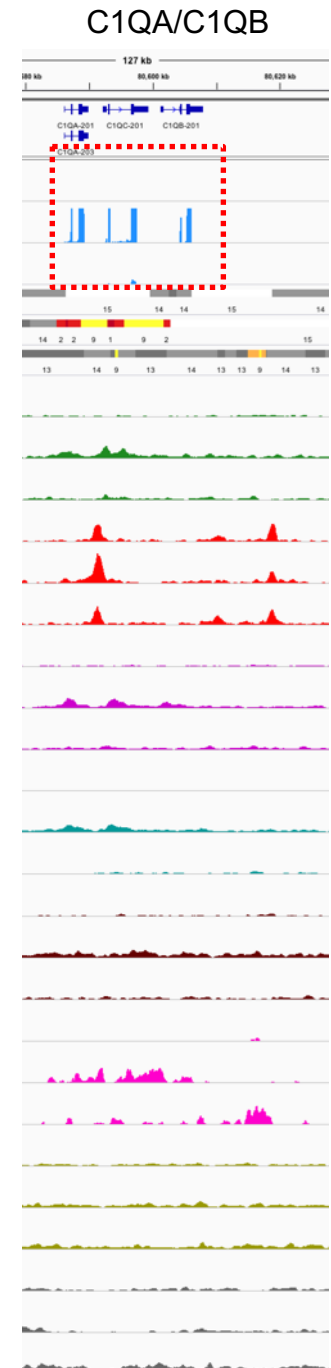
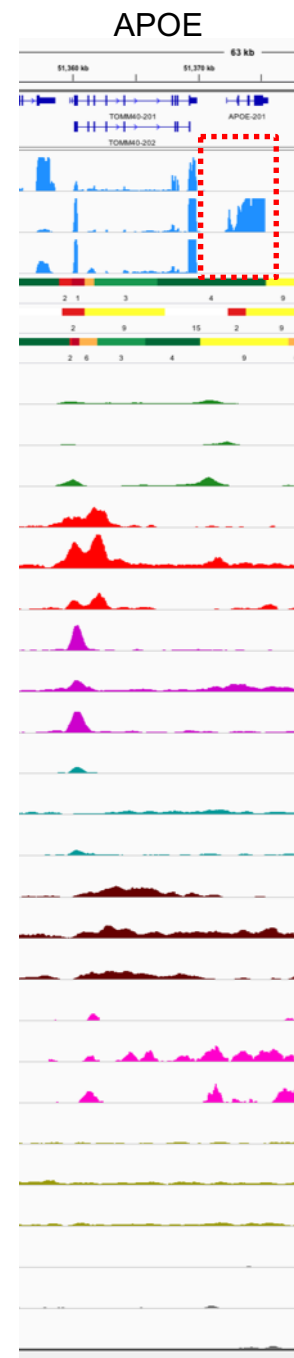
Constantly high expressed genes

- Two categories:
 - Chromatin state free
 - Chromatin state related
- Extension discussion:
 - Conserved “transcription factory”
 - “loop” genes

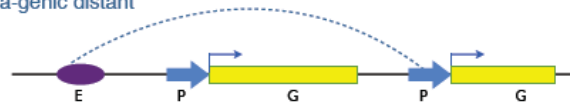


Primary Porcine Alveolar Macrophages Specific expressed genes

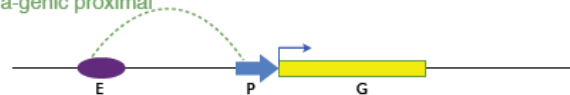
- APOE: CTCF binding motif
- C1QA/C1QB: long-range interactions or enhancers



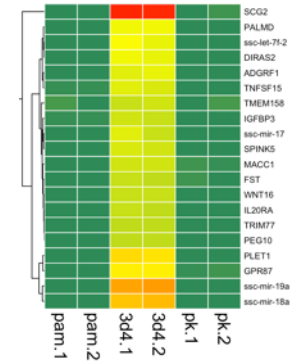
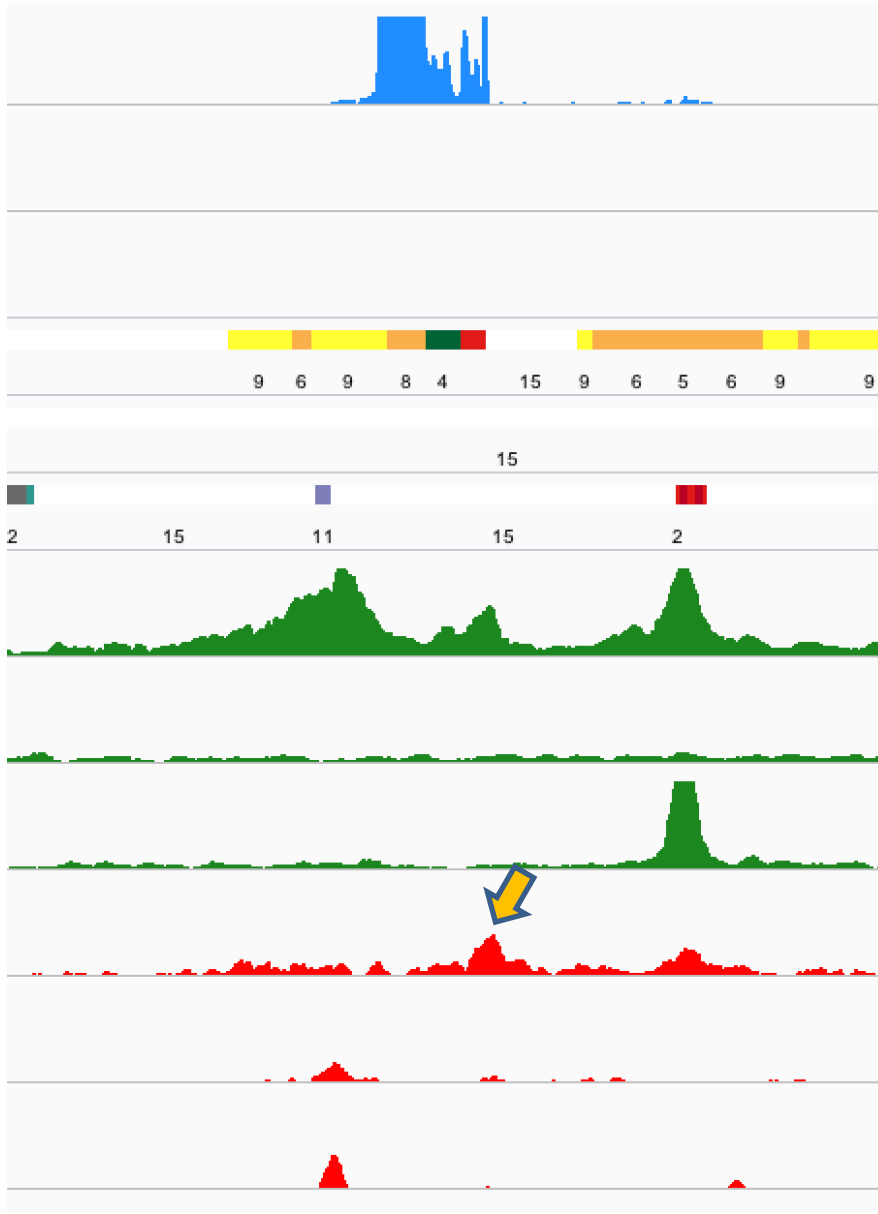
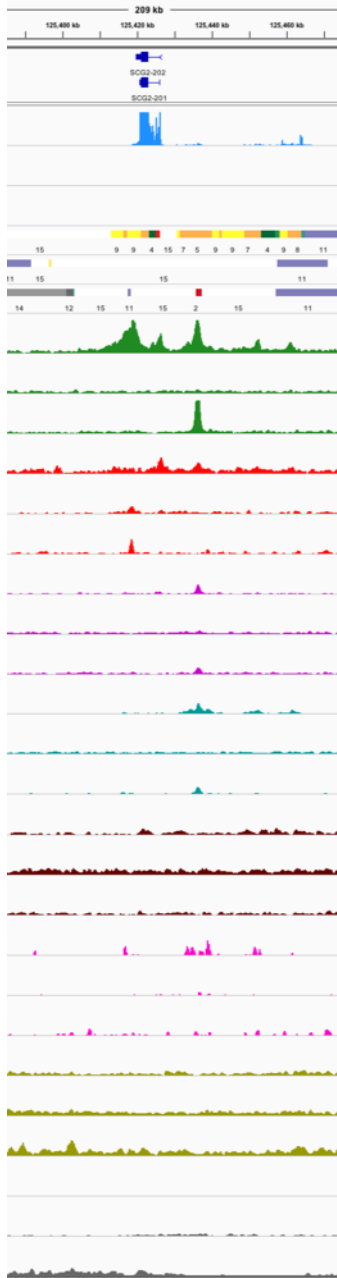
Extra-genic distant



Extra-genic proximal



SCG2



3D4/21 cell line specific highly expressed

CTCF binding motif



CTCF TAD



POL2 transcription factory formed



SCG2 gene transcription



Summary and perspectives

- 8 epigenomic markers on 3 cell types were surveyed chromatin states to explore DNA elements modifications in swine epigenomes.
- Integrative analysis was used to elucidate the relationship between gene transcription and proximal modifications by using RNA-Seq and ChIP-Seq data.
- Purposefully using **RNAPII** and **CTCF** factor in this study to peep the **3D** chromatin conformation organizations and dynamics in swine genome.

Acknowledgements



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