



Integrative Alignments of DNA Elements for Transcriptional Regulation in Swine Epigenome

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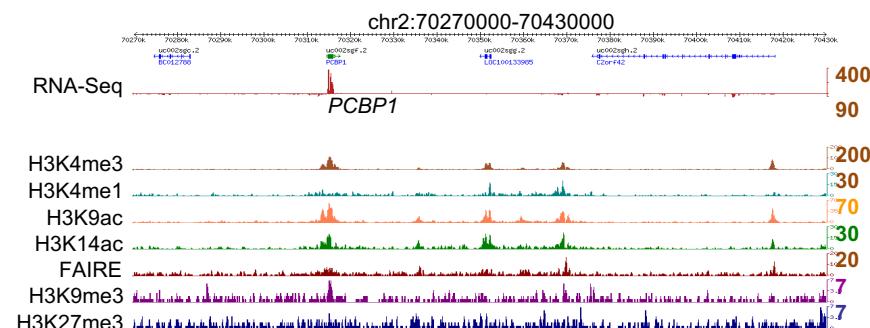
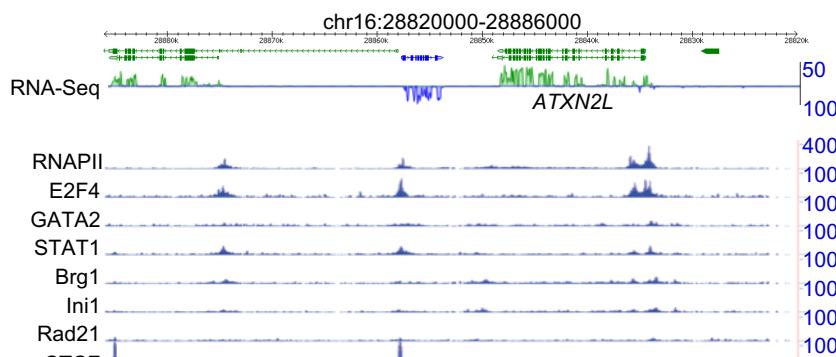
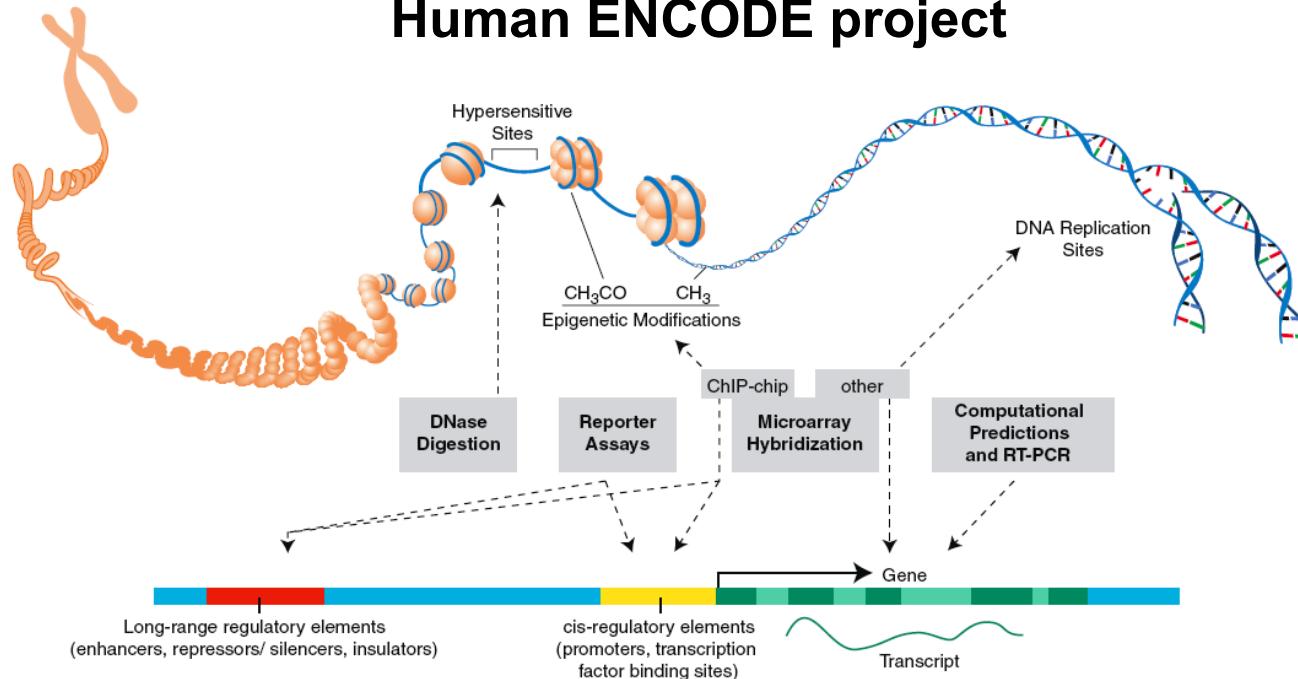
Key Laboratory of Agricultural Animal Genetics, Breeding
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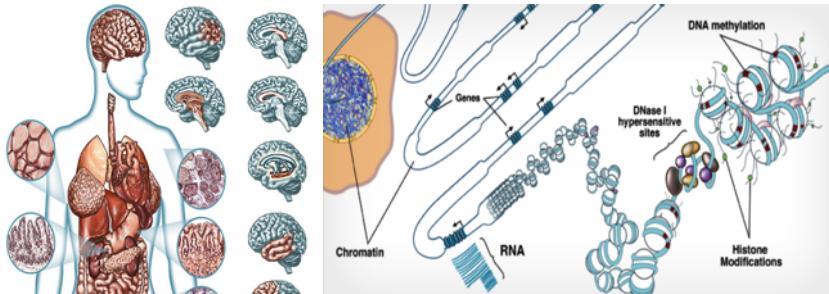


Outlines

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

Human ENCODE project



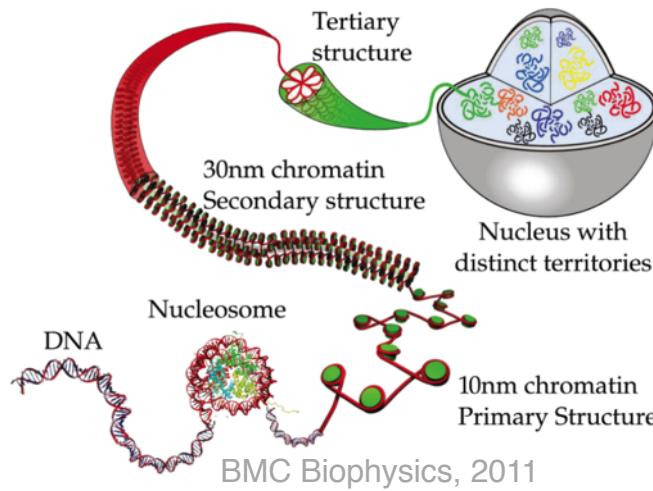


Roadmap Epigenomics Consortium, *Nature*, 2015

ENCODE/ Roadmap

Structure

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



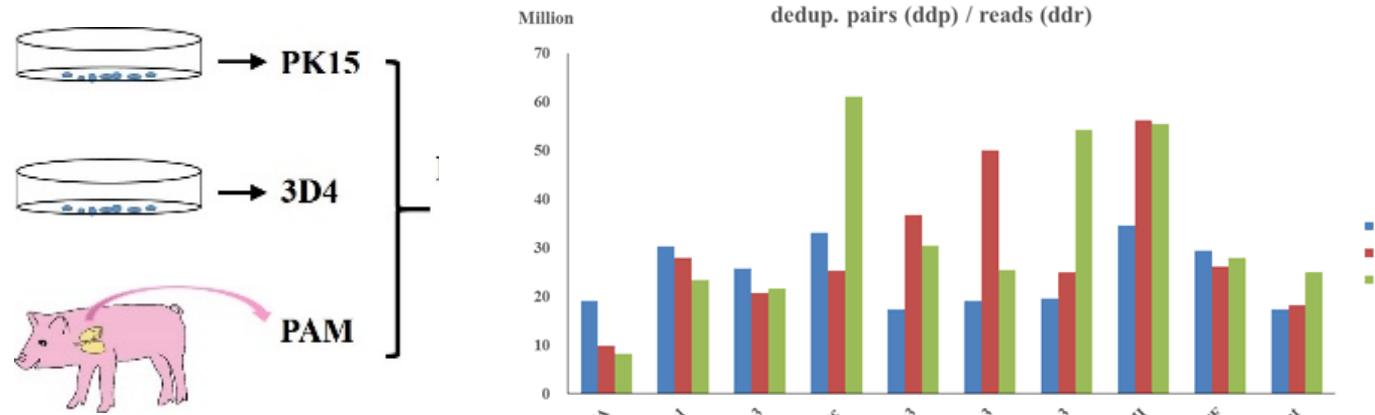
3D Genome

Function

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



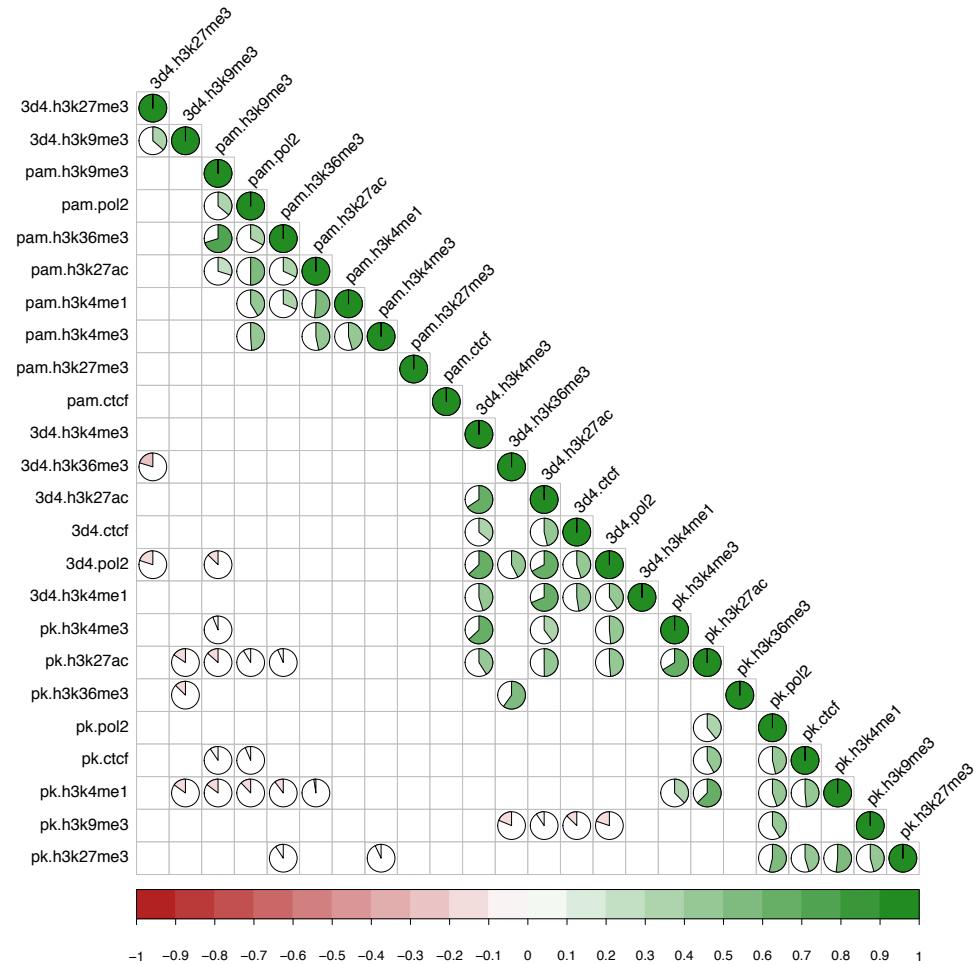
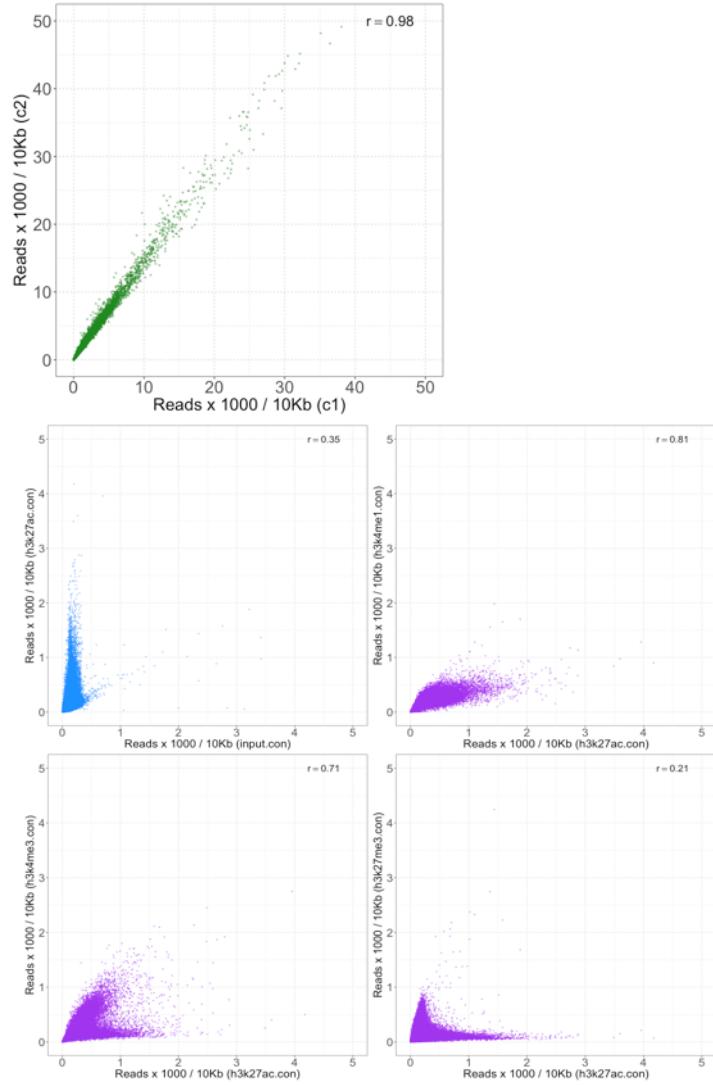
ChIP/RNA-Seq data of porcine cells/tissue



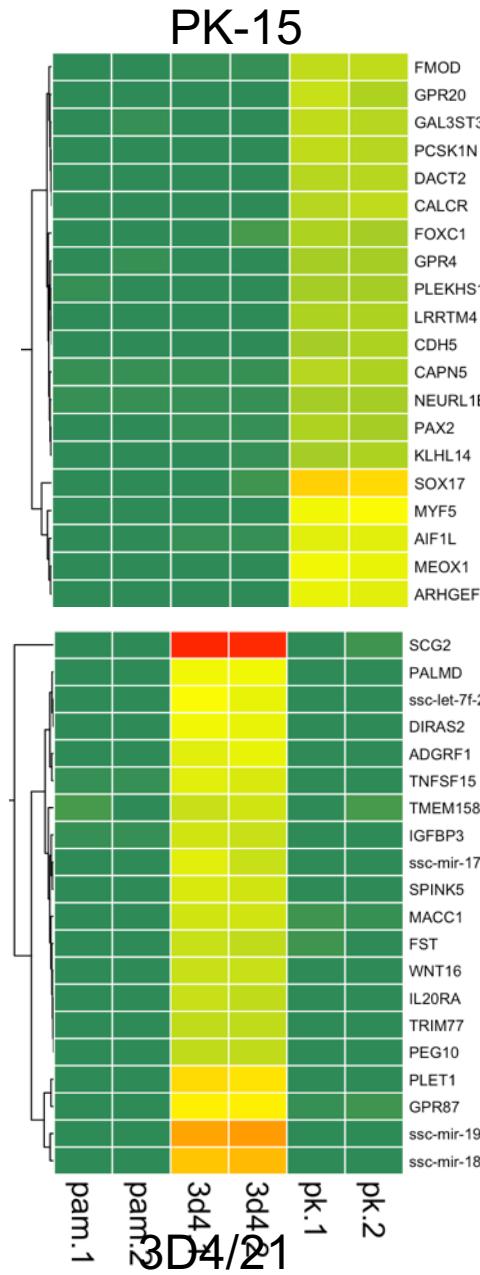
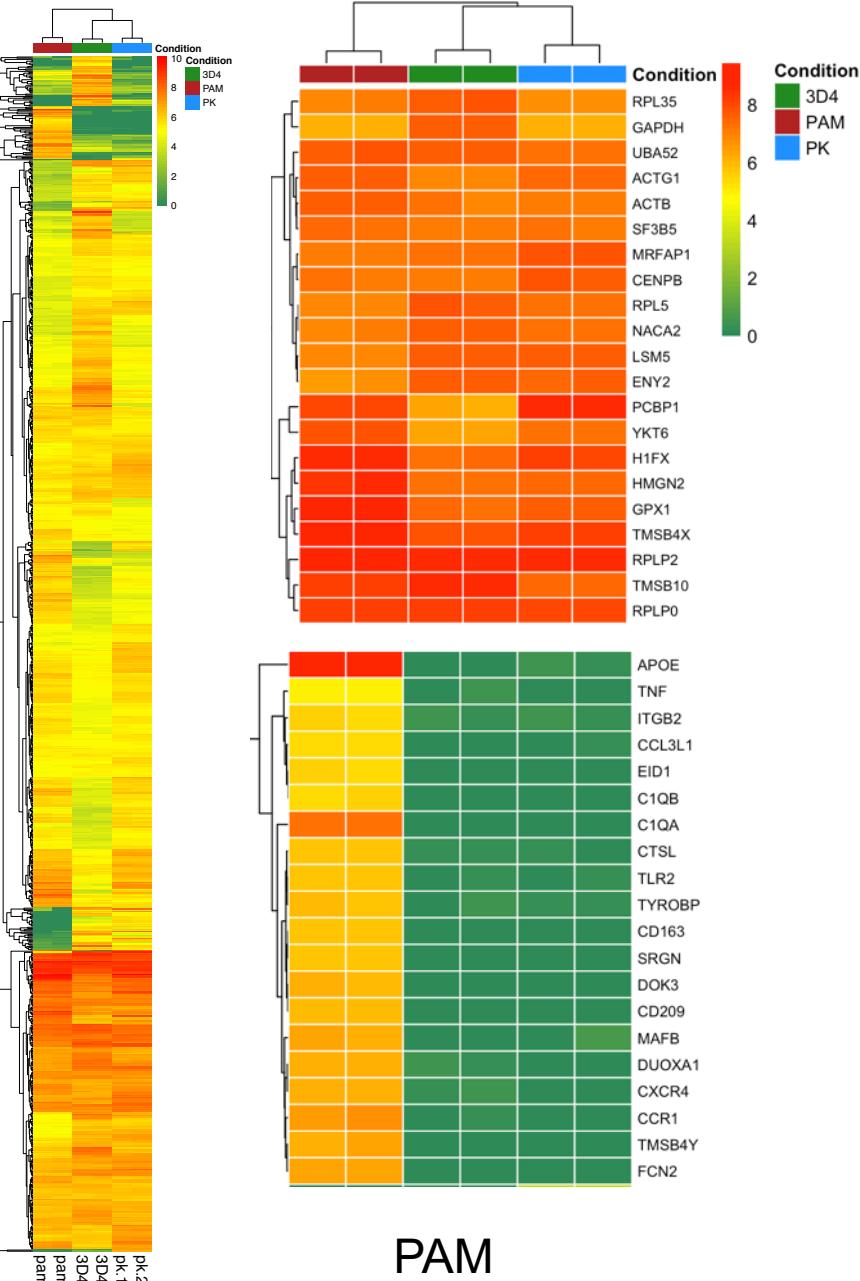
	3D4/21	PAM	PK-15	LDM
H3K4me1	✓	✓	✓✓	✓
H3K4me3	✓	✓✓	✓	✓✓
H3K9me3	✓	✓	✓	✓
H3K27ac	✓	✓✓	✓✓	✓
H3K27me3	✓✓	✓✓	✓✓	✓
H3K36me3	✓	✓	✓	✓
CTCF	✓	✓	✓	✓
POL2	✓✓	✓	✓	✓✓
INPUT	✓	✓	✓	✓

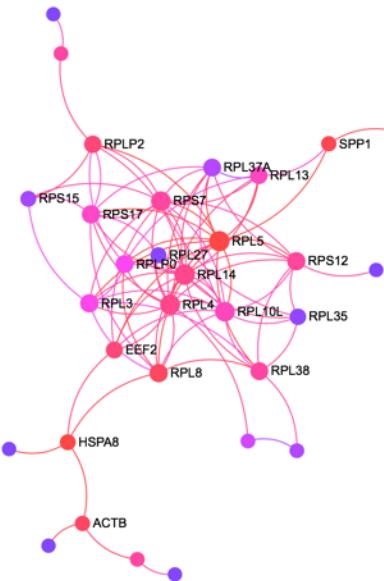
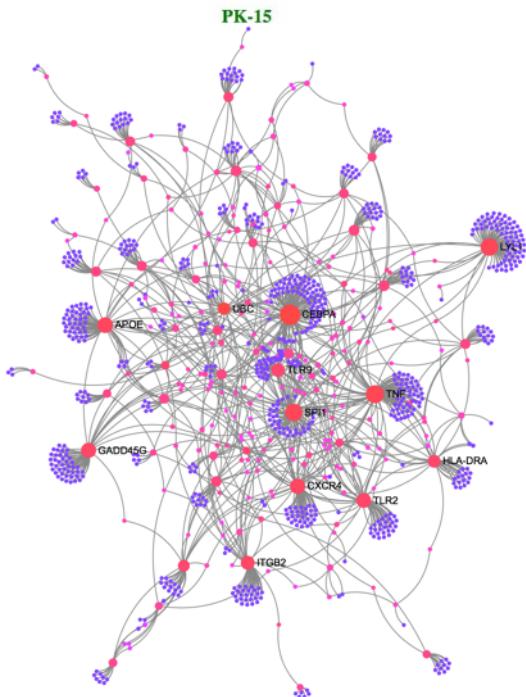
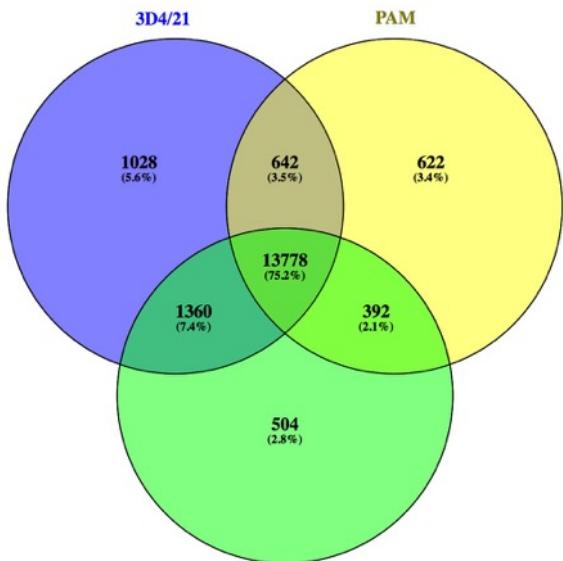
- Over 15,000 peaks for narrow peak
- ~10,000 enriched region for broad peak
- PAMs have better performance on H3K27me3.

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



RNA-Seq data characterization on 3 types of cells





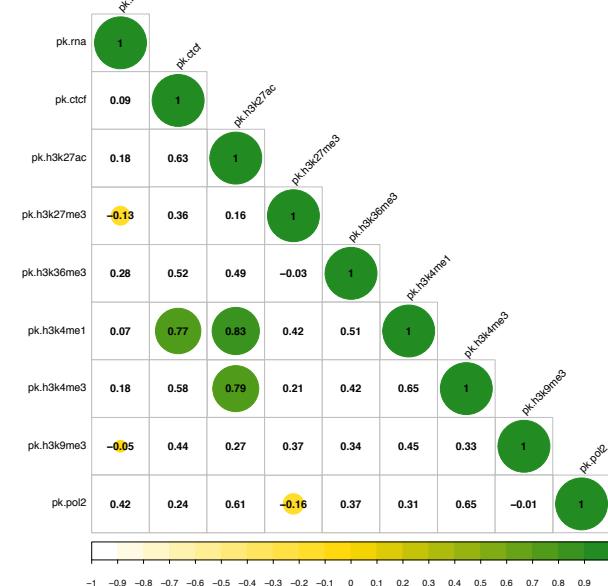
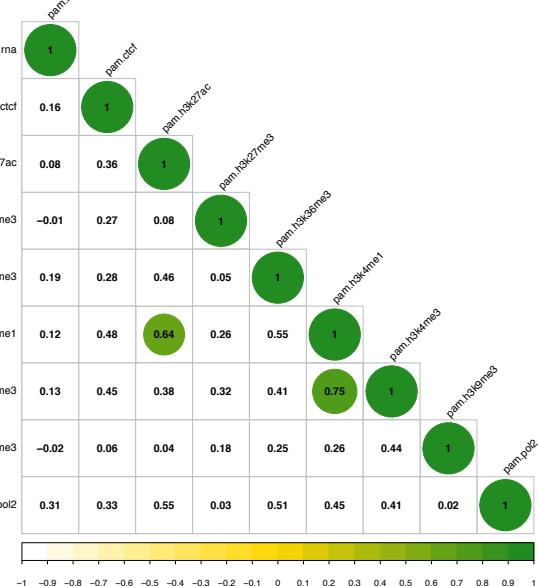
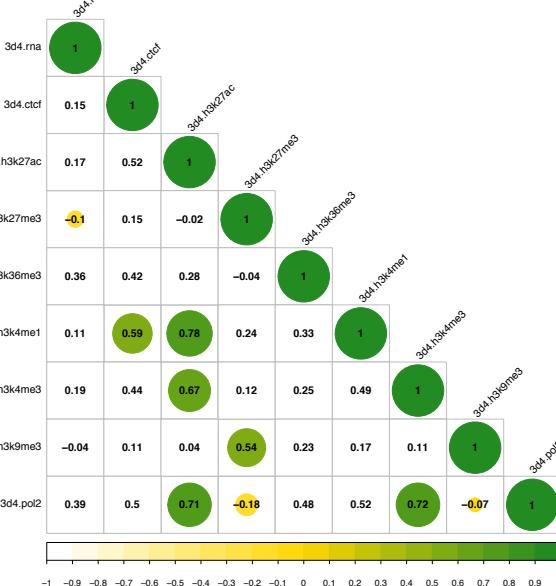
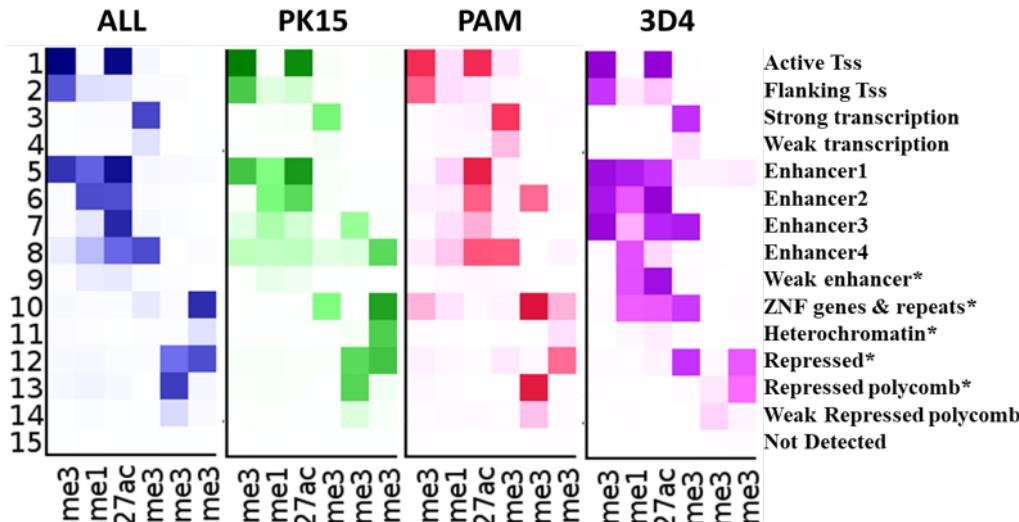
structural constituent of ribosome	18	9.24e-1
structural molecule activity	20	7.15e-1
RNA binding	15	2.62e-1
transport	21	0.0000
structural constituent of cytoskeleton	2	0.012
mRNA binding	2	0.0189
double-stranded DNA binding	2	0.0403
hydrolase activity, hydrolyzing N-glycosyl compound	1	0.0461
structure-specific DNA binding	2	0.0943
oxidoreductase activity, acting on the aldehyde or ox	1	0.096

Gene networks and GO functional annotations

Immune System	218	1.3e-38
Innate Immune System	134	6.86e-3
Signaling by Interleukins	50	2.16e-2
Toll-Like Receptors Cascades	51	6.52e-2
Cytokine Signaling in Immune sys	80	1.22e-2
Toll Like Receptor 4 (TLR4) Casc	44	2.2e-21
Activated TLR4 signalling	42	4.07e-2
TRIF-mediated TLR3/TLR4 signa	37	4.51e-1
MyD88-independent cascade	37	7.19e-1
Toll Like Receptor 3 (TLR3) Casc	37	7.19e-1
Hemostasis	101	1.83e-1
MyD88:Mal cascade initiated on p	33	1.42e-1
Toll Like Receptor TLR1:TLR2 C	33	1.42e-1
Toll Like Receptor TLR6:TLR2 C	33	1.42e-1
Toll Like Receptor 2 (TLR2) Casc	33	1.42e-1
Interleukin-3, 5 and GM-CSF sign	25	2.29e-1

- Over 75% genes are common transcriptional.
- COM genes are responsible for cell structure, metabolism,...
- SP genes are more dependents on cell types

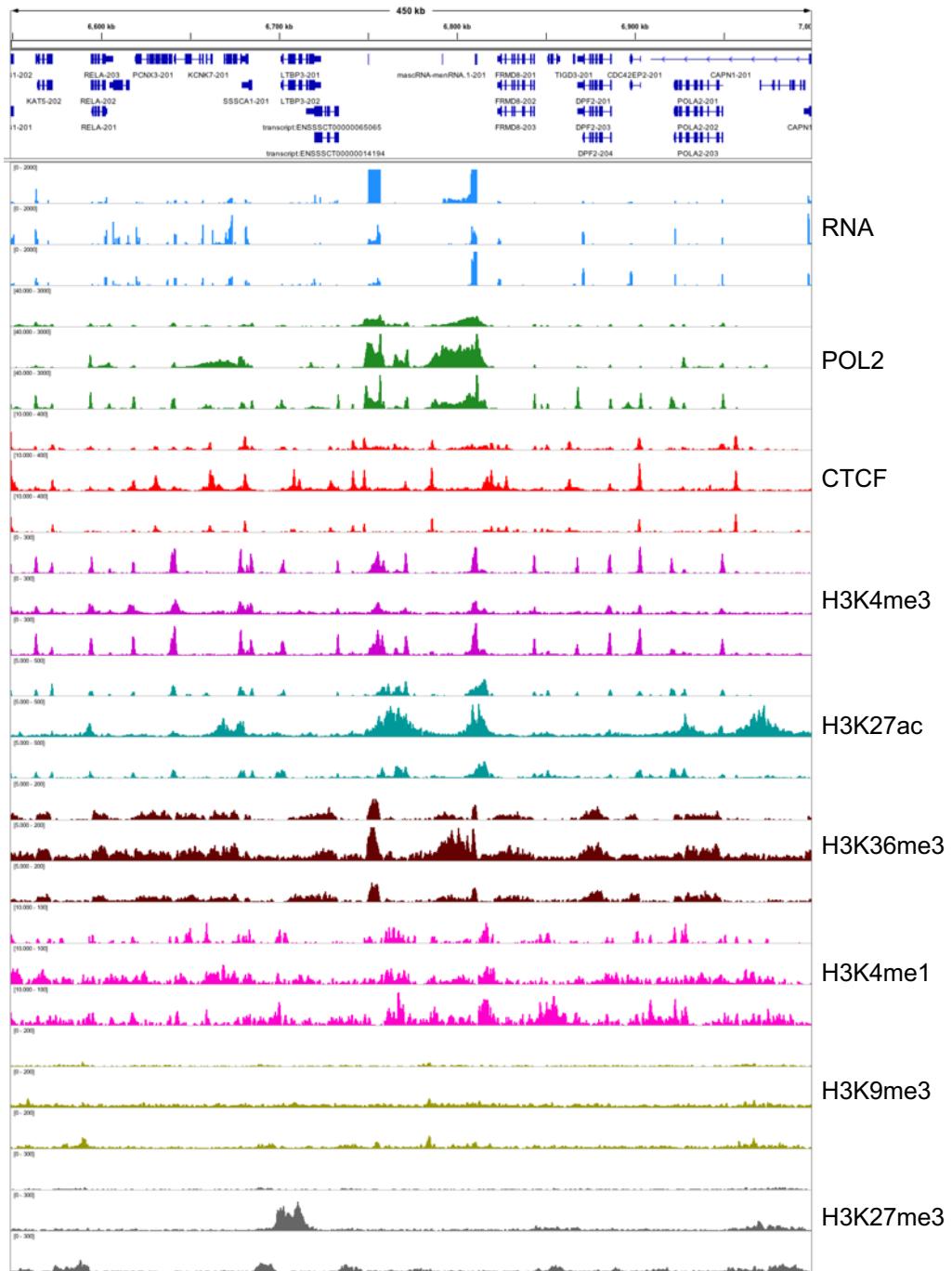
chromHMM: chromatin states assignments

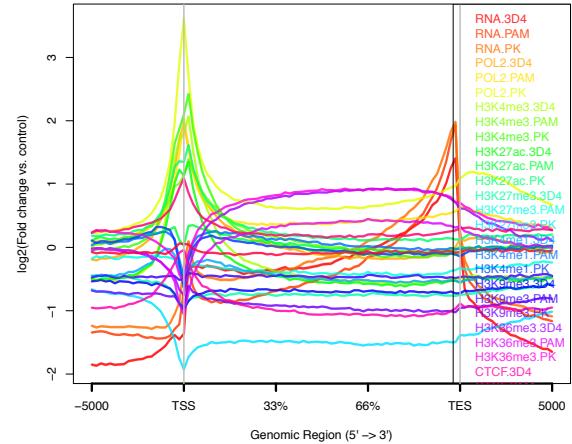
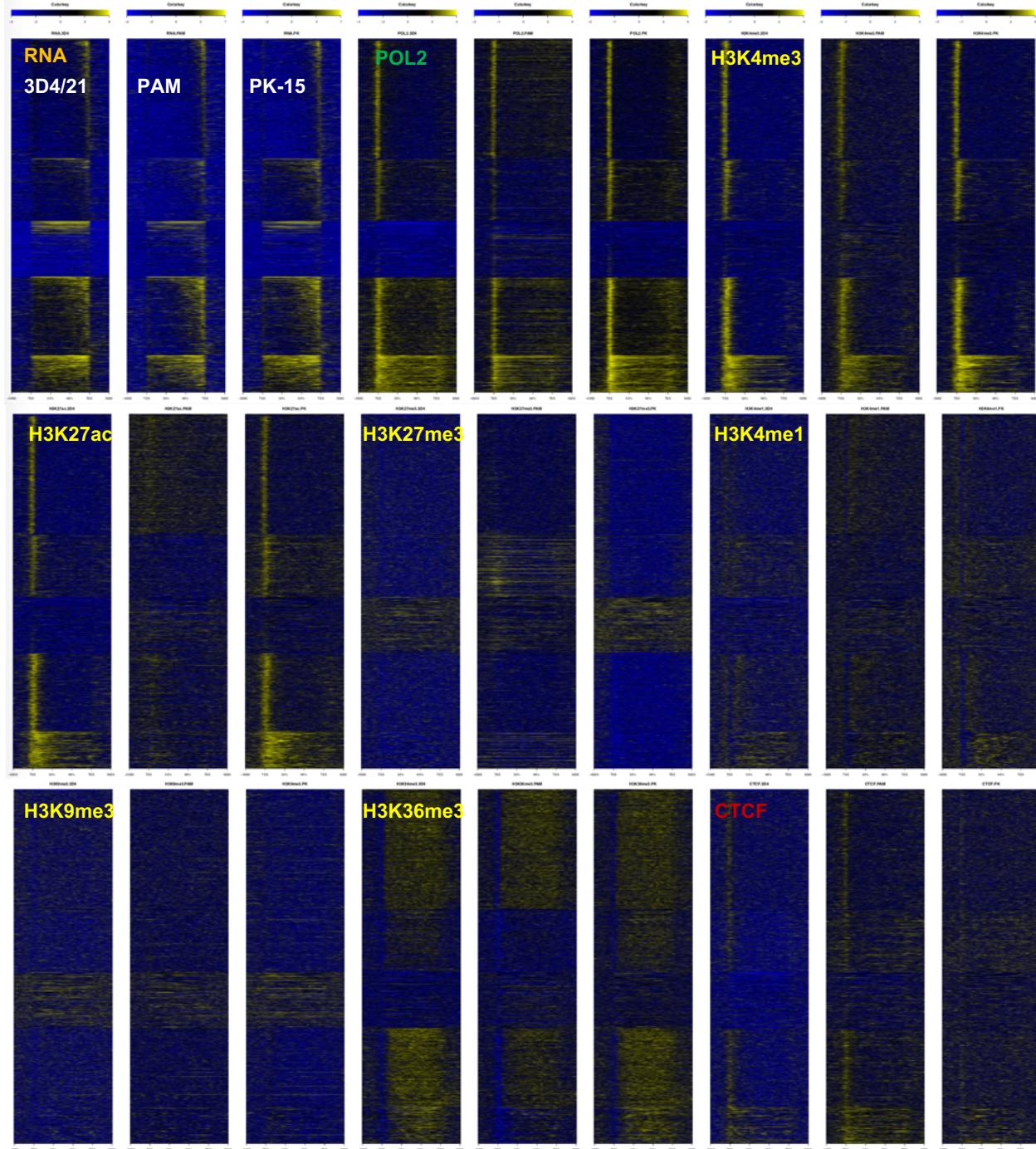


- Assigned 15 chromatin states based on 6 histone markers.
- Markers within a state have more correlation.
- Primary PAM cells have lower correlations between markers.

Overview of ChIP-Seq and RNA-Seq data

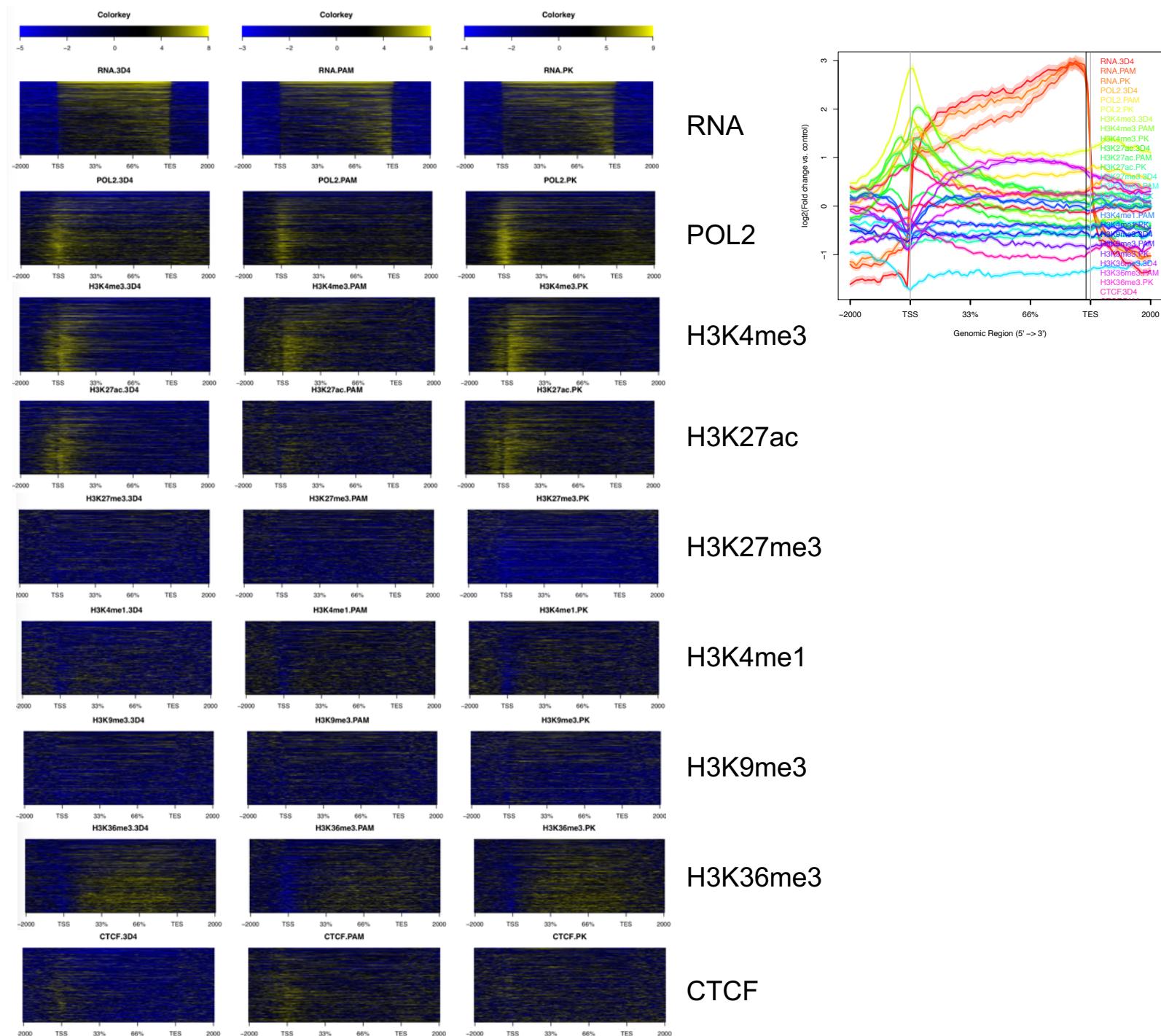
- MALAT1 and NEAT1 sites
- RNAPII and CTCF factor work well in swine genome
- 6 Histone markers are also work well.

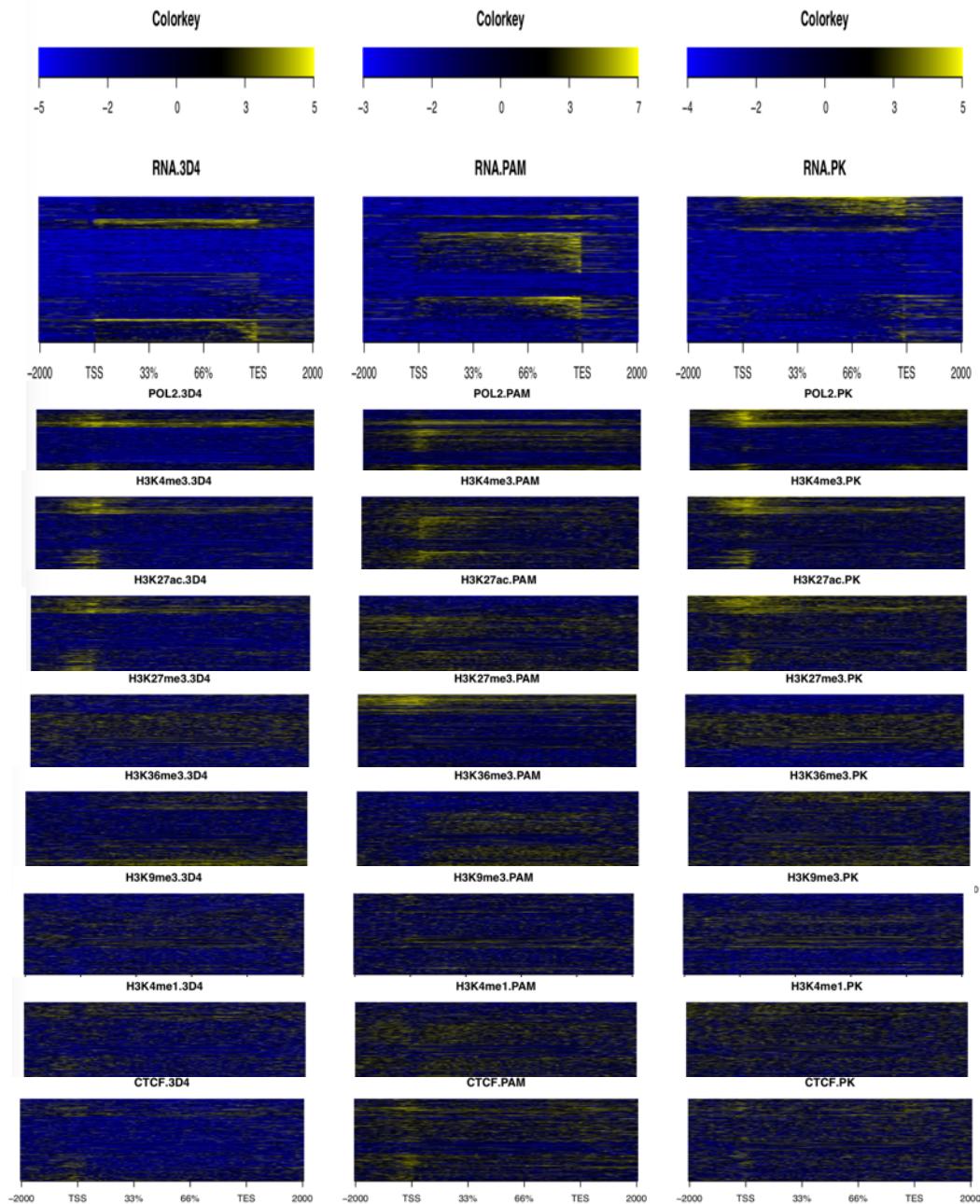




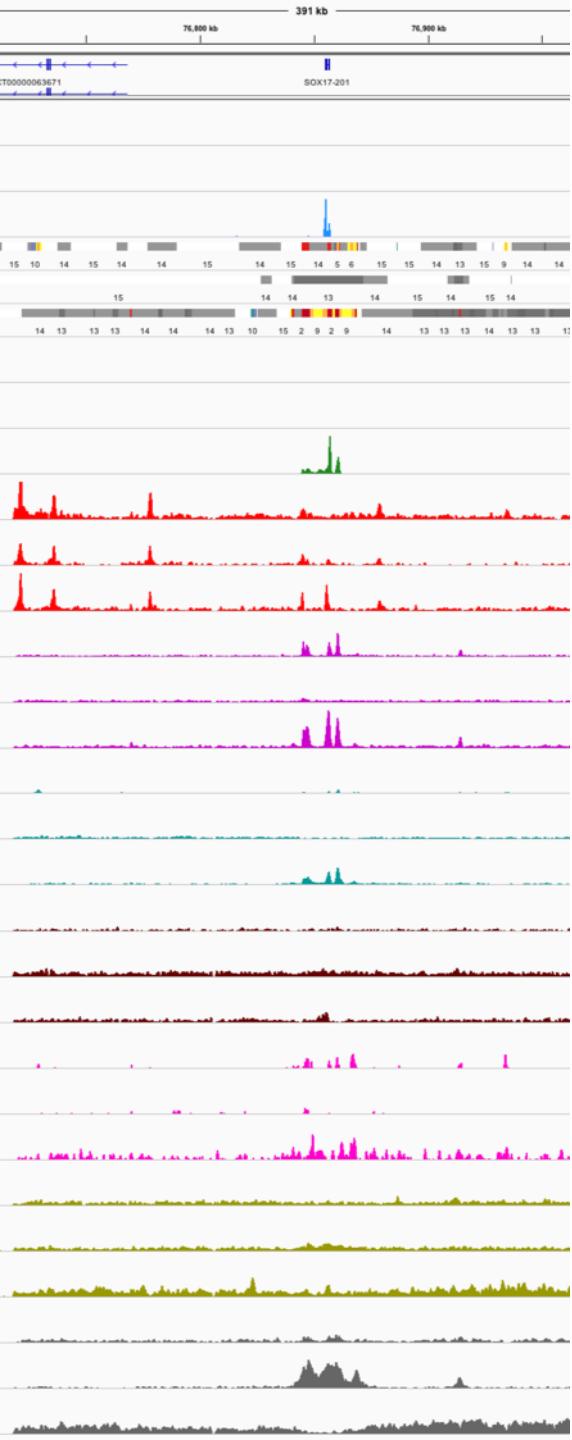
Integrative Alignments of DNA Elements for Transcriptional Regulation in Swine Epigenome

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



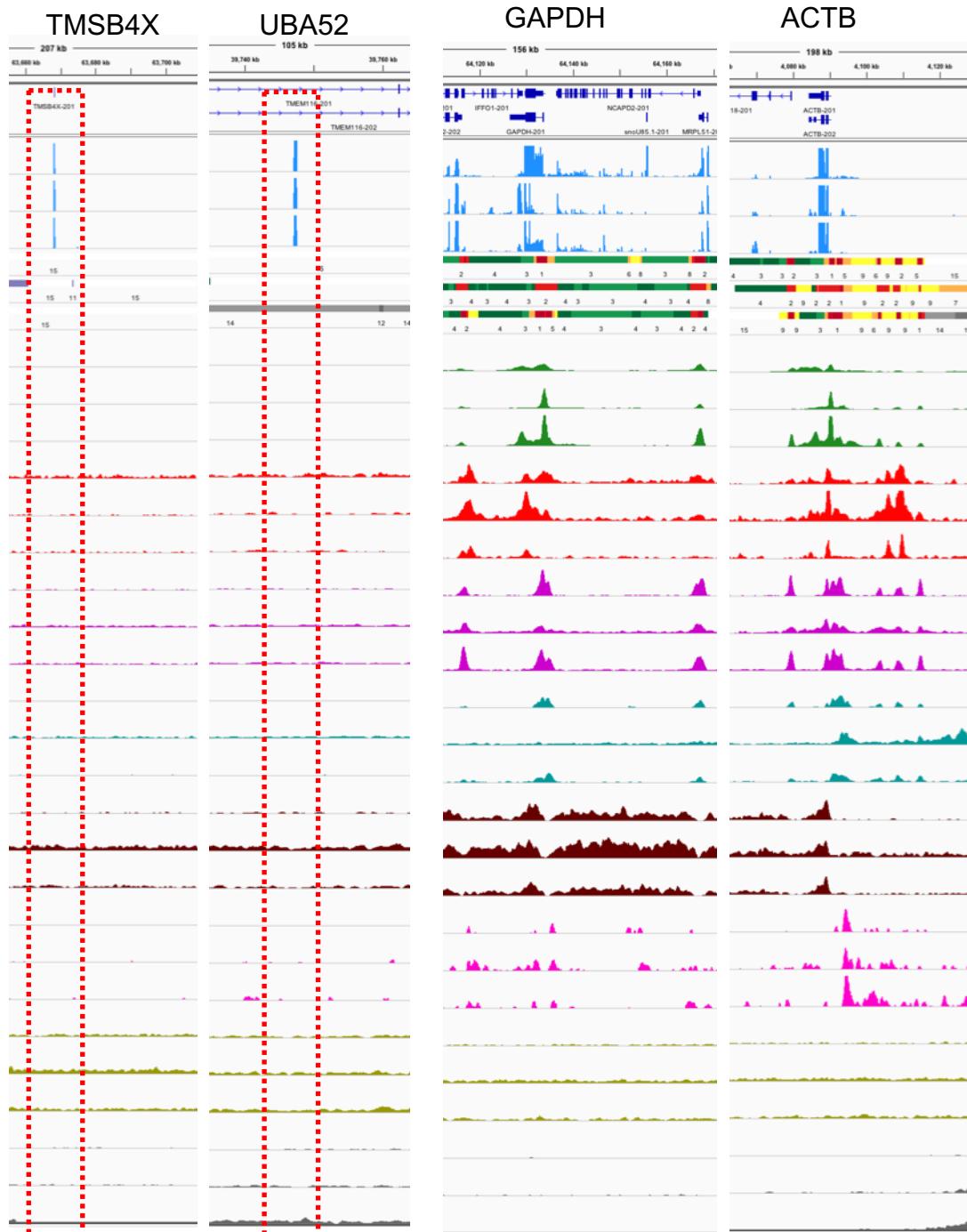
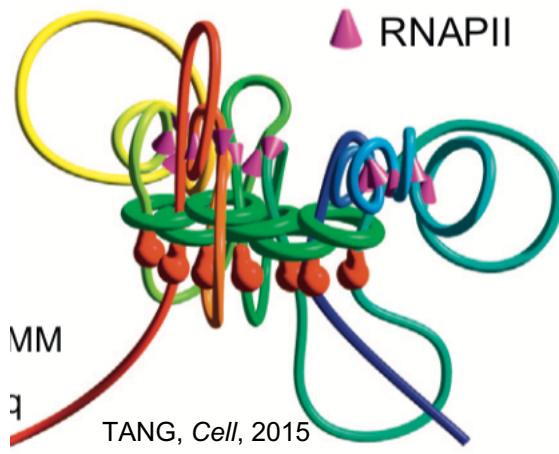


SOX17



Constantly high expressed genes

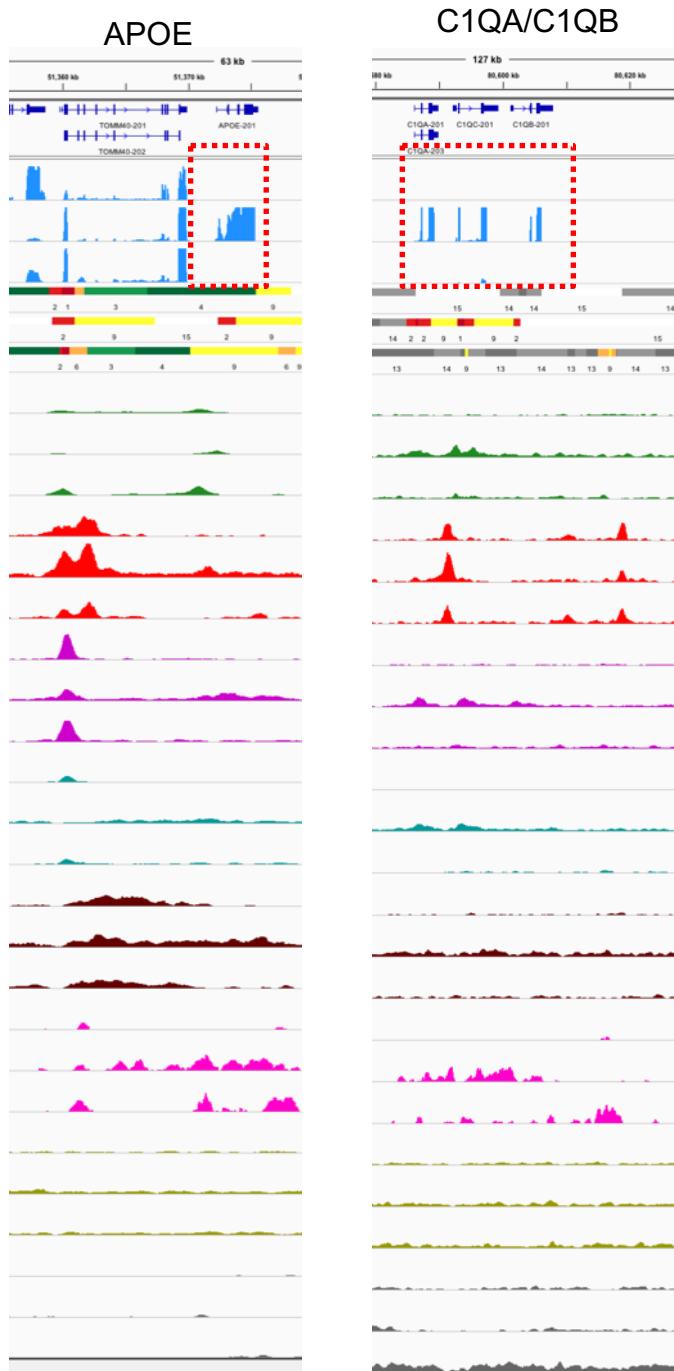
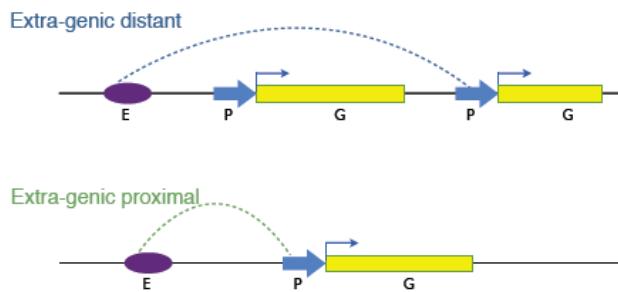
- Two categories:
 - Chromatin state free
 - Chromatin state related
- Extension discussion:
 - Conserved “transcription factory”
 - “loop” genes



Primary Porcine Alveolar Macrophages

Specific expressed genes

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



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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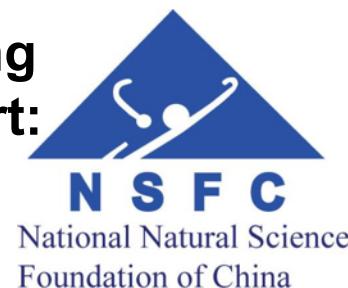
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