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### **Title**

Transcriptional Interactome in Mouse Genome

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# Transcriptional Interactome in Mouse Genome

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# Transcriptional Interactome in Mouse Genome

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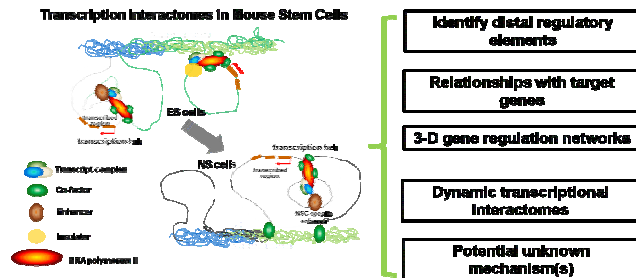
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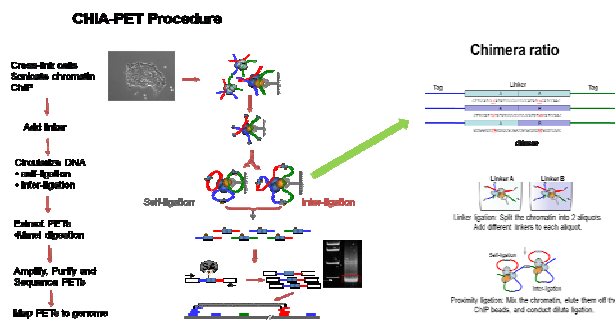
## Abstract

Distant regulatory elements have been shown to influence gene function *via* long-range chromatin interactions. In this study, we depict the dynamic transcriptional interactomes mediated by RNA polymerase II (RNAPII) with the newly developed Chromatin Interaction Analysis by Pair End diTag (ChIA-PET) to define the chromatin organizations pertinent to transcription regulation and epigenetic control in pluripotent embryonic stem cells (mES), neural stem cells (mNS) and neurosphere cells (mNP). With over 150 million ChIA-PET sequencing, thousands of *cis*- and *trans*- chromatin interactions tethered by RNAPII are defined. We plan to integrate the transcription interactome maps with global transcription expression changes, promoter activities, gene activities and major epigenomic features to define spatial distribution and temporal regulation of transcription networks.

## 1. Project goal



## 2. approaches used

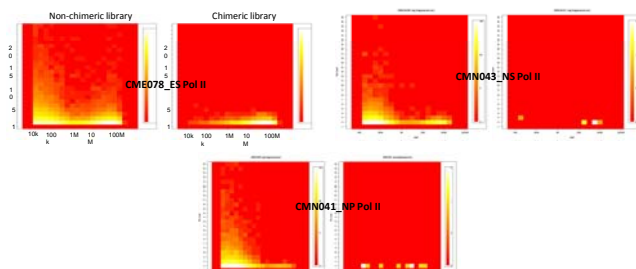


## Result

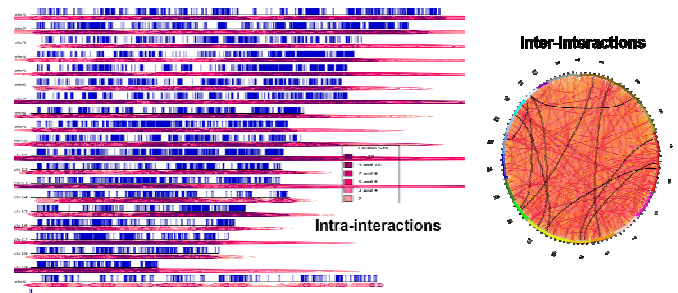
### 1. CHIA-PET sequencing and mapping summary

Library ID	ES_CME078	NS_CMN043	NP_CMN041
<b>Total PETs</b>	160.98M	152.6M	166.7M
<b>Unique mapped PETs</b>	94.6M (58.8%)	72.1M (47.3%)	79.8M (47.9%)
<b>Merged Unique PETs (&gt;2bp)</b>	68.9M (41.6%)	38.7M (25.4%)	8.1M (4.9%)
<b>Self-ligation PETs</b>	26.9M (40.3%)	5.6M (3.3)	722K (0.9%)
<b>Intra-chromosomal PETs</b>	3.0M (4.5%)	2.3M (3.5%)	765K (9.4%)
<b>Inter-chromosomal PETs</b>	72,427	9,671	6,581
<b>Inter-chromosomal Interactions (2+)</b>	36.1M (54.6%)	30.1M (79.7%)	6.5M (79.8%)
<b>Inter-chromosomal Interactions (2+)</b>	278,606	59,152	1,700

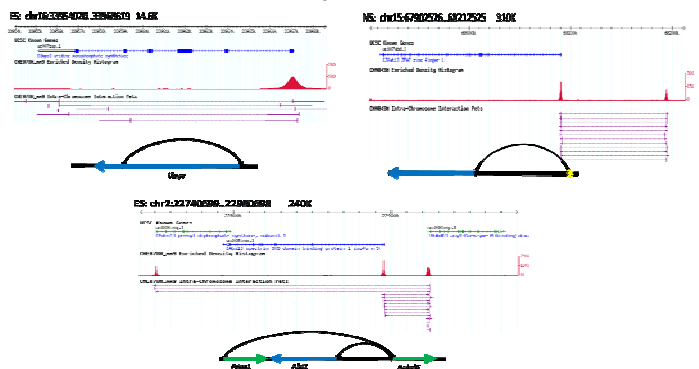
### 2. Evaluation noise level via chimera library



## 3. Overview of the mES Interactome across Genome

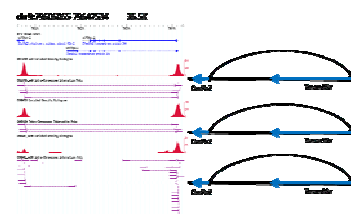


## 4. Interactions identified by CHIA-PET in mES

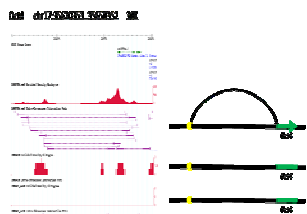


## 5. Specific Interactions

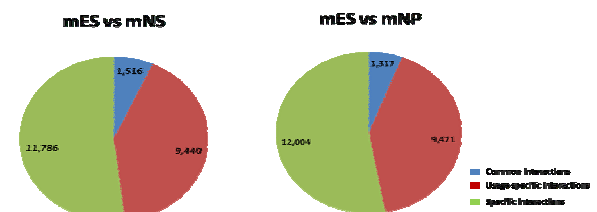
### a. Common Interactions identified



### b. Tissue specific interactions



## 6. Dynamic interactome across three cell lines



## Ongoing works

1. Validation our dataset via various experiments, such as 3C, FISH
2. integrating with other genomic datasets, CHIP-Seq, RNA-Seq, RIP-Seq, methylome
3. Dynamic interactome analysis across the mouse genome
4. Modeling the 3-D gene regulation networks

## References

Fullwood. M et al., Nature 462, 58-64, 2009  
 Li. G et al., Genome Biology, 11(2):R22, 2010  
 Handoko. L et al., Nature Genetics 43, 630-638, 2011