講演会のお知らせ

日時： 2022 年 11 月 25 日 10 時～
場所：薬学部本館 南講義室

Imaging genome-wide nuclear compartmentalization across diverse cell types in the mouse brain

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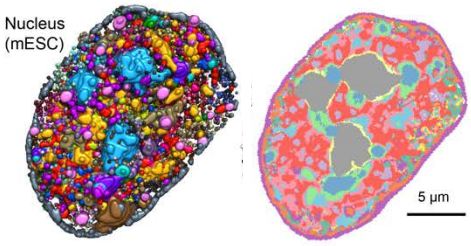
Imaging the genome and transcriptome along with diverse subnuclear structures is pivotal to decipher the relationships between three-dimensional chromatin organization and gene regulation in single cells. Here, we performed imaging-based single-cell multi-modal profiling, characterizing genomic loci across the mouse genome by DNA seqFISH+ together with mature and nascent transcriptome by mRNA and intron seqFISH as well as subnuclear structures and epigenetic marks by sequential immunofluorescence. We applied this integrated genomics approach to mouse embryonic stem cells and diverse cell types in the mouse brain. In the naive tissue sections of the mouse brain, we spatially resolved distinct organization of active and repressive chromatin subcompartment, which can encode a functionally distinct set of genes and pathways. Together, our results demonstrate that imaging-based single-cell multi-modal approaches can derive new spatial insights of nuclear compartmentalization in a discovery-driven fashion.

***The talk is based on PhD work in Long Cai's lab at Caltech.**



Reference

Takei, Y. *et al.* (2021) *Science*. 374, 586–594.

Takei, Y. *et al.* (2021) *Nature*. 590, 344-350.

Shah, S., **Takei, Y.**, Zhou, W. *et al.* (2018) *Cell*. 174, 363-376.

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