Data-driven and technical approaches to understand spatial gene regulation

Summary

Gene expression is precisely regulated by transcription factors (TFs) and chromatin structures, but their combinatorial actions for cell type-specific expression are not fully understood. Here, I developed a database designated ChIP-Atlas (https://chip-atlas.org), which integrates all of public ChIP-seq data including more than 120,000 experiments. The integrated data were further analyzed to identify TFs associated with tissue-specific gene expression and disease risk. In addition, I established a high-resolution spatial genomics technology, named photo-isolation chemistry, which allows to isolate gene expression profiles only from photo-irradiated regions out of whole tissues. This chemistry has a potential to be applied for other genomics technologies such as ATAC-seq and Bisulfite-seq. Combination of those data-driven and technical approaches will accelerate to gain deeper insight into the mechanisms of spatial gene regulation.

2) Shinya OKi*, et al., Integrative analysis of transcription factor occupancy at enhancers and disease risk loci in noncoding genomic regions. bioRxiv Rep, 262899