# ASHBi SEMINAR

## Exploring The Epigenomic Impacts of Non-Coding Sequences on Gene Regulation


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**Date** Friday, 8 November 2024

**Time** 13:00 – 14:00 [JST]

**Venue** Conference Room Onsite Only*
B1F, Faculty of Medicine Bldg. B

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**Abstract**

While the genome serves as the instruction manual encoding all biological functions within our cells, the epigenome acts as the annotations and footnotes that dictate how our DNA is correctly interpreted. Cellular functions necessitate appropriate transcriptional activation and repression through chemical modifications on DNA, as well as their associated histone proteins. These epigenetic marks modulate various non-coding sequences to give rise to cell-type specific transcriptional programs. Our research focuses on understanding how such molecular mechanisms alter gene expression during development and diseases. Specifically, we are interested in how non-coding DNA, including cis-regulatory elements and retrotransposons, impact the transcriptome. Here, I will describe instances of how these genomic sequences impact the epigenome and higher-order chromatin structures in mammalian cells. Through a combination of epigenomic assays, genome engineering, and cellular and molecular biology techniques, we have discovered non-coding elements that serve as enhancers for genes and binding sites for chromatin factors that regulate the three-dimensional "shape" of the genome. Elucidating these processes allows for a better understanding of the functions of repetitive elements in both physiological processes and pathologies.



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