Recent studies have revealed a substantial variation in gene expression across different single cells, even within a homogeneous population of cells. In order to understand the underlying mechanisms of the cellular variation, we have developed single-cell techniques, including scDNase-seq and scMNase-seq, to analyze the epigenomic profiles at a single-cell level. Application of these techniques to various cell types revealed unexpected rules of chromatin organization and provided insights into the epigenetic basis of cellular heterogeneity in gene expression.

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Dr. Zhao’s research focuses on the epigenetic regulation of chromatin. Understanding how epigenetic patterns are established during development and how improper epigenetic signals contribute to disease is the long-term goal for his lab. His lab developed the ChIP-SAGE, ChIP-Seq, MNase-Seq, and scDNase-seq techniques and also developed corresponding algorithms to analyze these data. Using these approaches, Dr. Zhao’s lab has been pioneering whole-genome analyses of chromatin modifications in higher eukaryotic systems. By identifying these genome-wide epigenetic patterns, Dr. Zhao’s research has revealed numerous insights into the relationship between the epigenome, chromatin-modifying enzymes, and gene expression.