Name: Tao Wu Email: tao.wu@bcm.edu

Quantitative Profiling of DNA N6-methyladenine at single-base resolution with NAME-Seq

Xuwen Li, Tao P. Wu

Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX 77030

DNA N6-methyladenine (6mA) is prokaryotes' most prevalent type of DNA methylation. Recently, DNA 6mA has been identified in eukaryotic genomes. However, the prevalence and existence of 6mA in eukaryotic genomes have been debated due to the limitation of 6mA genomic profiling and quantification methods. To solve this challenge, we develop a chemical-based sequencing method, Nitrite-Assisted Amino MEthylation sequencing (NAME-Seq), for whole genome profiling and single-base quantification of 6mA mathylation rate. NAME-Seq workflow combines nitrite conversion in the acid condition of 6mA to nitrosylated-6mA with Klenow fragment (exo-) mediated DNA synthesis to achieve the 6mA-to-T transversion. Tested in several bacterial and eukaryotic genomes, we demonstrated that NAME-Seq can accurately map the 6mA in genome and quantify the methylation ratio at single-base resolution. Furthermore, we combine the NAME-Seq with 6mA MeDIP-Seq and apply 6mA MeDIP-NAME-Seq to map 6mA in human genome; the result indicated that NAME-Seq can significantly improve the accuracy of MeDIP-Seq. Moreover, we are applying this cutting-edge method to human brain samples and uncovering new biology of this non-canonical mammalian DNA methylation. We will be glad to share our new method and open for any type of collaboration.