# uliCUT&RUN maps protein binding on chromatin in single cells and single embryos

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Groundbreaking research by Sarah Hainer, an assistant professor of gene expression and cell fate in the University of Pittsburgh Department of Biological Sciences, and Thomas G. Fazzio of the University of Massachusetts Medical School has adapted the CUT&RUN method to examine mapping of transcription factor and other DNA binding protein occupancies on chromatin using a low number of cells, including single cells, and individual pre-implantation embryos.

CUT&RUN is similar to the broadly used chromatin immunoprecipitation (ChIP) technique, in that it determines protein localization on chromatin. However, current methods for genome-wide mapping of DNA binding proteins require tens of thousands to millions of cells. Consequently, in vivo mapping of DNA binding proteins has been severely limited, as many biologically important populations of cells are present in low cell numbers.

Originally adapted in 2017, CUT&RUN has since been successfully applied to populations of more than 1,000 cells. Hainer and Fazzio sought to further adapt this technology and in this paper describe, for the first time, the genome-wide mapping of factor occupancy from single cells and individual pre-implantation mouse embryos.

The paper, "Profiling of Pluripotency Factors in Single Cells and Early Embryos," published April 4 online in *Cell*.

Experiments conducted using the new technique, known as ultra-low

input CUT&RUN (uliCUT&RUN,) have revealed that only a fraction of transcription factor binding sites are occupied in most cells, which confirms measurements taken through multi-cell studies. It also showed that uliCUT&RUN allows for examination of transcription factor binding from rare cell populations that are key in cell development or disease.

"By advancing localization studies to single cells and individual embryos, future studies can focus on cell heterogeneity and studies from limited biological samples,' said Hainer. "Typically, a tradeoff between cell number and cell purity in tissue samples prevents use of ChIP-seq to profile purified populations of tissue-specific cells. The ability of uliCUT&RUN to obtain maps of factor binding from 50 cells that are highly overlapping with maps from high cell numbers enables mapping from virtually any available specimen. "

Provided by University of Pittsburgh

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