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Mapping chromatin modifications in nanochannels SHUANG FANG LIM, ALENA KARPUSENKO, ROBERT RIEHN, North Carolina State University — DNA and chromatin are elongated to a fixed fraction of their contour length when introduced into quasi-1d nanochannels. Because single molecules are analyzed, their hold great potential for the analysis for the genetic analysis of material from single cells. In this study, we have reconstituted chromatin with histones from a variety of sources, and mapped the modification profile of the chromatin. We monitored methylation and acetylation patterns of the histone tail protein residues using fluorescently labelled antibodies. Using those, we distinguished chromatin reconstituted from chicken erythrocytes, calf thymus, and HeLa cells. We discuss prospects for profiling histone modifications for whole chromosomes from single cells.

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