SciBX
Science-Business eXchange

THE DISTILLERY

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
High-coverage, single-cell genome and exome sequencing at base-pair resolution to aid biomarker identification	A single-cell sequencing method with base-pair resolution, dubbed Nuc-seq, could be used to explore heterogeneity in cancer and other diseases to aid biomarker identification and guide therapeutic development. The approach relies on sequencing DNA from cells in the G2/M phase, after the genome has been replicated but before cells have divided. In a cancer cell line, about 90% sequence coverage could be attained from a single cell. In a triple-negative breast cancer sample, many mutations were only found in small subpopulations of the tumor, and the mutation rate was shown to be higher than that in an estrogen receptor–positive breast cancer sample. Next steps could include applying this technique to additional cancer types. *SciBX* 7(33); doi:10.1038/scibx.2014.993 Published online Aug. 28, 2014	Patent and licensing status unavailable	Wang, Y. *et al. Nature*; published online July 30, 2014; doi:10.1038/nature13600 **Contact:** Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, Texas e-mail: nnavin@mdanderson.org