

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Microarray-based method for high-throughput analysis of CpG methylation	<p>A microarray-based method for high-throughput analysis of CpG methylation patterns could help identify new disease biomarkers. Aberrant methylation of CpG sites on the genome is associated with cancer and other diseases. The method measured the methylation status of 145,148 CpG sites in 5,472 genes and generated reproducible data that correlated with standard sequencing results. Next steps could include using the method to compare CpG methylation patterns in genomes from normal and diseased cells.</p> <p>SciBX 3(27); doi:10.1038/scibx.2010.838 Published online July 15, 2010</p>	Patent and licensing status unavailable	<p>Nautiyal, S. <i>et al. Proc. Natl. Acad. Sci. USA</i>; published online June 21, 2010; doi:10.1073/pnas.1005173107 Contact: Malek Faham, Mlc Dx Inc., Menlo Park, Calif. e-mail: malek.faham@mlcdx.com</p>