

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Mass spectrometry profiling of histone modifications	<p>Mass spectrometry profiling of histone modifications could be used to discover new cancer targets that modify chromatin. Mass spectrometry analysis of 42 combinations of histone H3 modifications across 115 cancer cell lines enabled partitioning of cell subsets by chromatin state. Further DNA sequence analysis and gene expression profiling led to the identification of a subgroup of acute lymphoblastic leukemia (ALL) cells carrying E1099K activating mutations in the <i>nuclear SET domain-containing protein 2</i> (<i>NSD2</i>; <i>MMSET</i>; <i>WHSC1</i>) methyltransferase. In cell culture and mouse xenograft models carrying this mutation, small hairpin RNA knockdown of <i>NSD2</i> decreased growth compared with no knockdown. Next steps include expanding the method for use in patient stratification and selection.</p> <p>SciBX 6(39); doi:10.1038/scibx.2013.1105 Published online Oct. 10, 2013</p>	<p>Patent application filed covering discovery of oncogenic <i>NSD2-E1099K</i> mutations and molecular chromatin signatures that predict response to <i>NSD2</i> inhibition; licensing status undisclosed</p>	<p>Jaffe, J.D. <i>et al. Nat. Genet.</i>; published online Sept. 29, 2013; doi:10.1038/ng.2777 Contact: Frank Stegmeier, Novartis Institutes for BioMedical Research, Cambridge, Mass. e-mail: frank.stegmeier@novartis.com Contact: Levi A. Garraway, Broad Institute of MIT and Harvard, Cambridge, Mass. e-mail: levi_garraway@dfci.harvard.edu</p>