This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Statistical genomic analysis approach to determine driver mutations in melanoma	<p>A statistical genomic analysis approach to determine driver mutations in melanoma could help identify new targets to treat the disease. Driver mutations in melanoma are difficult to identify due to the large number of random mutations induced by UV damage. Using genomic sequence data from paired tumor and normal tissues of patients with melanoma, a baseline mutation rate was defined and used to help identify five new candidate genes that could drive the disease: <i>protein phosphatase 6 catalytic subunit (PPP6C)</i>, <i>ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1; RAC1)</i>, <i>sorting nexin 31 (SNX31)</i>, <i>transforming acidic coiled-coil containing protein 1 (TACC1)</i> and <i>serine/threonine kinase 19 (STK19)</i>. Next steps include applying the strategy to a larger cohort of patients with melanoma as well as to patients with lung cancer.</p> <p>SciBX 5(32); doi:10.1038/scibx.2012.849 Published online Aug. 16, 2012</p>	Patent application filed; available for licensing	<p>Hodis, E. <i>et al. Cell</i>; published online July 20, 2012; doi:10.1016/j.cell.2012.06.024 Contact: Lynda Chin, The University of Texas MD Anderson Cancer Center, Houston, Texas e-mail: lchin@mdanderson.org Contact: Levi A. Garraway, Broad Institute of MIT and Harvard, Cambridge, Mass. e-mail: levi_garraway@dfci.harvard.edu</p>