This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Markers			
Identification of tumor markers and targets through integrative genomic analysis of cancer transcriptomes	<p>An integrated approach to cancer transcriptome analysis could help identify mutations and other genetic aberrations that serve as disease markers and therapeutic targets. In proof-of-concept experiments using 10 patient-derived melanoma samples, transcriptome analysis identified and validated 11 new gene fusions caused by genomic rearrangements. The analysis also validated 27 missense mutations that were present in tumor DNA but not in matched healthy germline DNA. Next steps include analyzing whether the identified gene fusions are recurrent in melanoma patients and applying the approach to other tumor types.</p> <p>SciBX 3(10); doi:10.1038/scibx.2010.327 Published online March 11, 2010</p>	Work unpatented; licensing status not applicable	<p>Berger, M.F. <i>et al. Genome Res.</i>; published online Feb. 23, 2010; doi:10.1101/gr.103697.109</p> <p>Contact: Levi A. Garraway, Dana-Farber Cancer Institute, Harvard Medical School, Cambridge, Mass. e-mail: Levi_Garraway@dfci.harvard.edu</p>