This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Computational algorithm to identify genes that drive cancer progression	<p>A computational algorithm that uses copy number and gene expression information could help identify genes that drive cancer progression. In 62 melanoma cell samples, the algorithm selected the 30 most likely tumor drivers, which included 10 previously known oncogenes and tumor suppressors. In melanoma cells, knockdown of two newly identified drivers decreased cell proliferation and confirmed their driver function. Next steps include using the program to identify cancer targets.</p> <p>SciBX 4(1); doi:10.1038/scibx.2011.25 Published online Jan. 6, 2011</p>	Findings unpatented; unavailable for licensing	<p>Akavia, U.D. <i>et al. Cell</i>; published online Dec. 2, 2010; doi:10.1016/j.cell.2010.11.013</p> <p>Contact: Dana Pe'er, Columbia University, New York, N.Y. e-mail: dpeer@biology.columbia.edu</p>