

### This week in techniques

Approach	Summary	Licensing status	Publication and contact information
<b>Computational models</b>			
Driver-gene inference by genetic-genomics and information theory (DIGGIT) algorithm to identify disease driver mutations	<p><i>In vitro</i> studies suggest network-based analysis with DIGGIT could help identify disease driver mutations. DIGGIT is an algorithm that identifies driver mutations by analyzing known disease master regulators and their upstream genes. In a cohort of mesenchymal subtype glioblastoma samples from patients, deletions in <i>kelch-like 9 (KLHL9)</i> were identified as potential driver mutations. In mice grafted with these primary glioblastoma cells, restoring <i>KLHL9</i> expression led to decreased tumor growth compared with that seen in mice given uncorrected cells. Next steps could include using DIGGIT to identify additional driver mutations in other diseases and validating such mutations in additional models and patient samples.</p> <p><b>SciBX 7(43); doi:10.1038/scibx.2014.1271</b>  <b>Published online Nov. 6, 2014</b></p>	Patent and licensing status unavailable	<p>Chen, J.C. <i>et al. Cell</i>; published online Oct. 9, 2014;            doi:10.1016/j.cell.2014.09.021  <b>Contact:</b> Andrea Califano, Columbia University, New York, N.Y.            e-mail:  <a href="mailto:califano@c2b2.columbia.edu">califano@c2b2.columbia.edu</a></p>