

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Comprehensive cell-line panel for predicting responses to cancer therapies	<p>A collection of hundreds of cancer cell lines could help predict responses to cancer therapies. The panel consisted of 639 human tumor cell lines representing a range of adult and childhood cancers of epithelial, mesenchymal and hematopoietic origin. In each of the cell lines, multiple genomic technology platforms were used to determine the mutational status of 64 commonly mutated cancer genes and characterize copy number variation and profile the expression of 14,500 genes. The sensitivity of the cell lines to 132 cancer therapeutics also was measured. As proof of principle, the platform identified a previously unknown sensitivity of <i>Ewing sarcoma breakpoint region 1 (EWSR1; EWS)</i>-<i>Friend leukemia virus integration 1 (FLI1)</i>-mutant Ewing sarcoma cells to poly(ADP-ribose) polymerase (PARP) inhibitors. Next steps include characterizing some of the cell lines at the epigenetic level and studying cell responses to drug combinations.</p> <p>SciBX 5(17); doi:10.1038/scibx.2012.448 Published online April 26, 2012</p>	Unpatented; licensing status not applicable	<p>Garnett, M.J. <i>et al. Nature</i>; published online March 28, 2012; doi:10.1038/nature11005 Contact: Ultan McDermott, Wellcome Trust Sanger Institute, Hinxton, U.K. e-mail: um1@sanger.ac.uk Contact: Cyril H. Benes, Harvard Medical School, Boston, Mass. e-mail: cbenes@partners.org</p>