This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Census-based, whole-exome sequencing of circulating tumor cells (CTCs)	<p>Census-based, whole-exome sequencing of CTCs could be used for blood-based diagnosis and monitoring of cancer metastasis. Census-based sequencing involves sequencing multiple DNA libraries generated from the same sample of CTCs and using variants present in more than one library to distinguish somatic mutations from sequencing errors. In 19 CTC libraries from a patient with metastatic castration-resistant prostate cancer (CRPC), census-based sequencing detected 73 somatic single-nucleotide variants (SSNVs), with 51 of them also detected in the primary tumor. In the same patient, among 93 SSVNs found in a sample from a lymph node metastasis, 47 were also detected in CTCs. Next steps include optimizing the method to decrease cost and increase throughput.</p> <p>SciBX 7(20); doi:10.1038/scibx.2014.595 Published online May 22, 2014</p>	Patent and licensing status unavailable	<p>Lohr, J.G. <i>et al. Nat. Biotechnol.</i>; published online April 20, 2014; doi:10.1038/nbt.2892 Contact: J. Christopher Love, Broad Institute of MIT and Harvard, Cambridge, Mass. e-mail: clove@mit.edu Contact: Jesse S. Boehm, same affiliation as above e-mail: boehm@broadinstitute.org Contact: Gad Getz, same affiliation as above e-mail: gadgetz@broadinstitute.org</p>