This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Predicting disease progression by measuring the evolution of mutational heterogeneity in cancer samples	Computational analysis of patient whole-exome sequencing data could be used to measure the evolution of tumor heterogeneity and help predict disease progression. Whole-exome sequencing and subsequent computational analysis of 149 samples from patients with chronic lymphocytic leukemia (CLL) identified more than 3,000 mutations in total and quantified the prevalence of mutations in each cancer sample. In 12 matched patient samples taken before and after chemotherapy, sequence analysis identified driver mutations that expanded in prevalence after treatment and predicted poor survival. Next steps include determining whether the presence of these driver mutations or the measurement of chemotherapy-induced tumor evolution can predict patient outcomes in prospective clinical trials. *SciBX* 6(10); doi:10.1038/scibx.2013.251 Published online March 14, 2013	Patent applications filed; available for licensing and freely available for academic and not-for-profit organizations	Landau, D.A. *et al. Cell*; published online Feb. 14, 2013; doi:10.1016/j.cell.2013.01.019 **Contact:** Catherine J. Wu, Dana-Farber Cancer Institute, Boston, Mass. e-mail: cwu@partners.org **Contact:** Gad Getz, Broad Institute of MIT and Harvard, Cambridge, Mass. e-mail: gadgetz@broadinstitute.org