This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Single-cell PCR analysis of tumor samples to identify prognostic gene expression signatures	A method to measure gene expression in individual tumor cells could help identify new cancer biomarkers and targets. Xenograft mouse tumors generated from a single colon cancer cell were surgically extracted, separated and sorted. Expression of selected genes was then measured by microfluidic single-cell PCR. Identification of genes expressed in specific subsets of tumor cells led to the discovery of a two-gene prognostic signature that could predict disease-free survival for patients with colorectal cancer. Next steps could include application of this methodology to clinical tumor samples. Stephen Quake and Michael Clarke, co-senior authors of the publication, are founders of Quanticel Pharmaceuticals Inc., which uses single-cell genomic analysis of patient tumor samples to identify predictive biomarkers. The company declined to comment on the licensing status of this work. *SciBX* 4(46); doi:10.1038/scibx.2011.1305 Published online Dec. 1, 2011	Patent application filed; licensing status unavailable	Dalerba, P. *et al. Nat. Biotechnol.*; published online Nov. 13, 2011; doi:10.1038/nbt.2038 **Contact:** Stephen R. Quake, Stanford University, Stanford, Calif. e-mail: quake@stanford.edu **Contact:** Michael F. Clarke, same affiliation as above e-mail: mfclarke@stanford.edu