

### This week in techniques

Approach	Summary	Licensing status	Publication and contact information
<b>Assays &amp; screens</b>			
<i>In situ</i> RNA sequencing in fixed cells and tissues	<p><i>In situ</i> RNA sequencing could help reveal genetic heterogeneity in complex samples for clinical diagnostics. In fresh-frozen cells or tissues, single-cell RNA sequence information was derived from sequencing by ligation after padlock probing and rolling-circle amplification. Control <i>in situ</i> experiments on the human <math>\beta</math>-actin transcript showed an average accuracy of 98.6%. In sections of frozen tissue from breast cancer biopsies, 39 probes, including 21 from a prognostic gene panel, were combined in a single multiplex reaction, and the results were validated by comparison to published RNA-sequencing data.</p> <p>Next steps could include optimization of the workflow for handling large numbers of samples and comparison of this method directly with bulk expression profiling for prognostic evaluation.</p> <p><b>SciBX 6(31); doi:10.1038/scibx.2013.834</b>  <b>Published online Aug. 15, 2013</b></p>	Patent and licensing status undisclosed	<p>Ke, R. <i>et al. Nat. Methods</i>; published online July 14, 2013; doi:10.1038/nmeth.2563</p> <p><b>Contact:</b> Mats Nilsson, Stockholm University, Stockholm, Sweden  e-mail: <a href="mailto:mats.nilsson@scilifelab.se">mats.nilsson@scilifelab.se</a></p> <p><b>Contact:</b> Carolina Wählby, Broad Institute of MIT and Harvard, Cambridge, Mass.  e-mail: <a href="mailto:carolina@broadinstitute.org">carolina@broadinstitute.org</a></p>