This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Automated, massively parallel RNA single-cell sequencing framework (MARS-Seq) for analyzing transcriptional states in thousands of single cells	<i>In vitro</i> studies suggest MARS-Seq can be applied to understand tissue heterogeneity in disease. Fluorescence-activated cell sorting was used to pool homogenous cell populations. RNA sequencing on the pooled samples yielded transcriptional profiles for 200–1,500 RNA molecules per cell, and unsupervised clustering distinguished heterogeneous transcriptional profiles. In a proof-of-concept application, the method distinguished between B cells, NK cells, macrophages, monocytes, plasmacytoid dendritic cells and other subtypes of dendritic cells derived from 4,000 mouse spleen cells. Next steps include improving RNA extraction efficiency and increasing multiplexing capacity from 1,600 to 10,000 cells per sequencing lane. SciBX 7(9); doi:10.1038/scibx.2014.267 Published online March 6, 2014	Patent filed; available for licensing from the Weizmann Institute of Science through Yeda Research and Development Company Ltd.	Jaitin, D.A. <i>et al. Science</i>; published online Feb. 14, 2014; doi:10.1126/science.1247651 Contact: Ido Amit, Weizmann Institute of Science, Rehovot, Israel e-mail: ido.amit@weizmann.ac.il Contact: Amos Tanay, same affiliation as above e-mail: amos.tanay@weizmann.ac.il