This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Tissue-selective motifs for microRNA (miRNA) identification	<p>A computational analysis of the 3' untranslated regions (UTRs) of genes expressed in selected tissues may be useful for identifying disease-related miRNAs. Using overrepresented nucleotide motifs as potential target sites of miRNAs, the analysis identified over two-thirds of known miRNAs and predicted the existence of 36 new miRNA genes. Functional validation confirmed the potential gene targets for two of the new miRNAs. Next steps include assessing the effect of the identified miRNAs on the cell cycle and cell proliferation, and studying the effects of the miRNAs in animal models.</p> <p>SciBX 1(40); doi:10.1038/scibx.2008.986 Published online Nov. 6, 2008</p>	Unpatented; licensing status not applicable	<p>Chang, Y.-M. <i>et al. Proc. Natl. Acad. Sci. USA</i>; published online Oct. 20, 2008; doi:10.1073/pnas.0809151105 Contact: Arthur Chun-Chieh Shih, Academia Sinica, Nankang, Taipei, Taiwan e-mail: arthur@iis.sinica.edu.tw Contact: Wen-Hsiung Li, University of Chicago, Chicago, Ill. e-mail: whli@uchicago.edu</p>