This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Massively parallel sequencing of genome protein-coding regions (exomes)	<p>Massively parallel sequencing of exomes could help accelerate discovery of disease-associated genetic variance while reducing sequencing costs. A microarray-based hybridization protocol was used to enrich for exomes. As proof of principle, analysis of four genomes from individuals with Freeman-Sheldon syndrome, an inherited form of cranial dysplasia, correctly identified known genes associated with the disorder. Next steps include optimizing the approach for its application to complex and heterogeneous diseases and scaling up the method to accommodate larger sample populations.</p> <p>SciBX 2(33); doi:10.1038/scibx.2009.1290 Published online Aug. 27, 2009</p>	Method unpatented; licensing status not applicable	<p>Ng, S. <i>et al. Nature</i>; published online Aug. 16, 2009; doi:10.1038/nature08250</p> <p>Contact: Jay Shendure, University of Washington, Seattle, Wash. e-mail: shendure@u.washington.edu</p>