This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Family-based genome analysis to identify disease-associated variants	<p>Genetic studies suggest that whole-genome sequencing of families could help identify genes associated with disease. Compared with individual genome sequencing, family-based sequencing allowed researchers to more accurately assess recombination sites. In two healthy parents and two children who had Miller syndrome and primary ciliary dyskinesia, family-based whole-genome sequencing identified <i>dihydroorotate dehydrogenase (DHODH)</i> as the primary causal gene for Miller syndrome and <i>dynexin axonemal heavy chain 5 (DNAH5)</i> as the main causal gene for primary ciliary dyskinesia. Next steps could include using the method to identify other disease-causing genes.</p> <p>SciBX 3(13); doi:10.1038/scibx.2010.415 Published online April 1, 2010</p>	Patent and licensing status unavailable	<p>Roach, J. <i>et al. Science</i>; published online March 11, 2010; doi:10.1126/science.1186802</p> <p>Contact: David J. Galas, Institute for Systems Biology, Seattle, Wash. e-mail: dgalas@systemsbiology.org</p> <p>Contact: Leroy Hood, same affiliation as above e-mail: lhoo@systemsbiology.org</p>