

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Microarray monitoring of genomic instability to predict disease progression in chronic lymphocytic leukemia (CLL)	A SNP microarray study of lymphocyte DNA from CLL patients suggests that allelic losses may predict the rate of disease progression. Untreated patients with a large number of allelic losses (a high genomic complexity score) had a shorter time until first treatment than patients with low scores. Among patients who had already received treatment, those with high genomic complexity scores needed a second round of treatment sooner than patients with low scores. Next steps include both validating the prognostic method in patients who received uniform treatment and testing whether genomic complexity scores predict survival.	Patent status undisclosed; high-density SNP microarrays commercially available from Affymetrix Inc.; software available for licensing from the University of Michigan	Kujawski, L. <i>et al. Blood</i> ; published online April 24, 2008; doi:10.1182/blood-2007-07-099432 Contact: Sami N. Malek, University of Michigan, Ann Arbor, Mich. e-mail: smalek@med.umich.edu