

This week in techniques

| Approach | Summary | Licensing status | Publication and contact information |
|---|---|---|---|
| Markers | | | |
| Comprehensive high throughput array-based methylation analysis to identify variably methylated regions (VMRs) associated with disease risks | Genetic studies suggest that methylation signatures of certain genes could help predict disease susceptibility. A longitudinal analysis of 74 patients over 11 years identified 227 regions in which DNA methylation was highly variable. Of those, 119 had stable methylation patterns in the individuals over the course of the study. Four of the stable regions were associated with body mass index and were located near obesity-related genes, suggesting that variability in methylation could be used to determine disease risk. Next steps include replicating the findings. SciBX 3(38); doi:10.1038/scibx.2010.1165 Published online Sept. 30, 2010 | Patent pending covering findings; will be available for licensing | Feinberg, A.P. <i>et al. Sci. Transl. Med.</i> ; published online Sept. 15, 2010; doi:10.1126/scitranslmed.3001262 Contact: M. Daniele Fallin, The Johns Hopkins University School of Medicine, Baltimore, Md. e-mail: dfallin@jhsph.edu Contact: Andrew P. Feinberg, same affiliation as above e-mail: afeinberg@jhu.edu |