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Drupal.behaviors.print = function(context) {window.print();window.close();}>
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This Week in Genome Biology

November 09, 2011

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In a paper published online in advance in *Genome Biology* this week, the Centre for Genomic Regulation's Andre Minoche, Juliane Dohm, and Heinz Himmelbauer report their evaluation of sequencing data generated using Illumina's HiSeq and Genome Analyzer systems. In the team's experience, "GAllx and HiSeq data sets show slightly different error profiles," and "quality filtering is essential to minimize downstream analysis artifacts" for both systems.

Yale University's Mark Gerstein and his team this week present a genome-wide analysis of chromatin features in yeast, through which the researchers identified histone modification-sensitive and -insensitive yeast transcription factors. The team says its method predicts "yeast transcription factor targets by integrating histone modification profiles with transcription factor binding motif information." This, the authors add, "shows improved predictive power compared to a binding motif-only method."