

INVITED SPEAKER PRESENTATION

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# Transcriptomics in a high throughput world

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*From* Beyond the Genome: The true gene count, human evolution and disease genomics  
Boston, MA, USA. 11-13 October 2010

Sequencing-based approaches are transforming our ability to investigate, interpret and define transcriptomes, which comprise the expressed elements in genomes. This is driven by innovations in all steps in the process, including sample preparation, cDNA library construction, increases in sequencing data yield and development of new computational approaches. I will describe the state of the art in the field as well as new approaches and results from current work in transcriptome analysis at the Broad Institute.

Published: 11 October 2010

doi:10.1186/gb-2010-11-S1-112

**Cite this article as:** Nusbaum: Transcriptomics in a high throughput world. *Genome Biology* 2010 **11**(Suppl 1):112.

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