

Analysis of the yeast transcriptome using RNAseq

BIOL 426/626
Approaches to Molecular Biology



Reading

- Nagalakshmi U, Wang Z, Waern K, Shou C, Raha D, Gerstein M, Snyder M. The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science* 2008 320:1344



Five minute writing

- Given that much about the structure of the yeast transcriptome appears to have already been worked out using other techniques but with less general accuracy, what was the larger purpose of the authors doing this work and why did *Science* think it was worthy of publication?



Figure 1

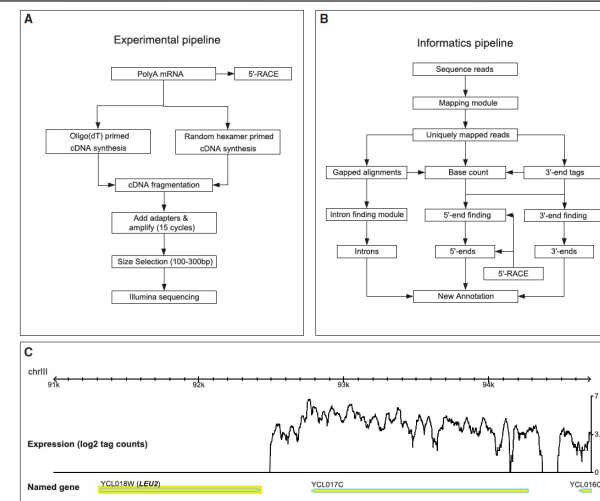


Fig. 1. (A and B) Flowcharts of the RNA-Seq method. (C) RNA-Seq signals are not evident at a deleted gene (LEU2) but are abundant at an expressed neighboring gene (YCL017C).

Figure 2

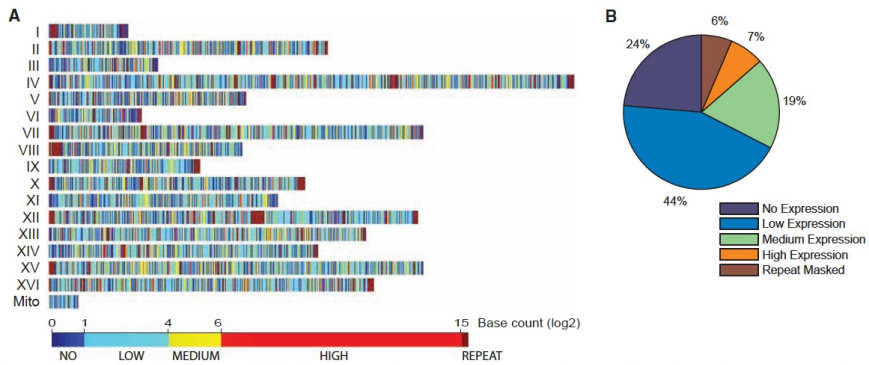


Fig. 2. (A) The genome distribution of transcribed regions in yeast. Colors represent different transcription levels for each base (log2 tag count). Numbers of chromosome regions are shown on the left. Mito, mitochondria. **(B)** A summary of the transcription level of the transcriptome.

Figure 3

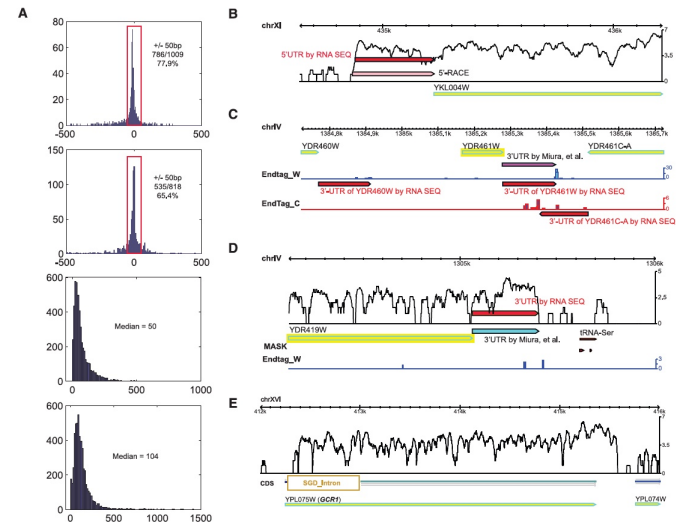


Figure 4

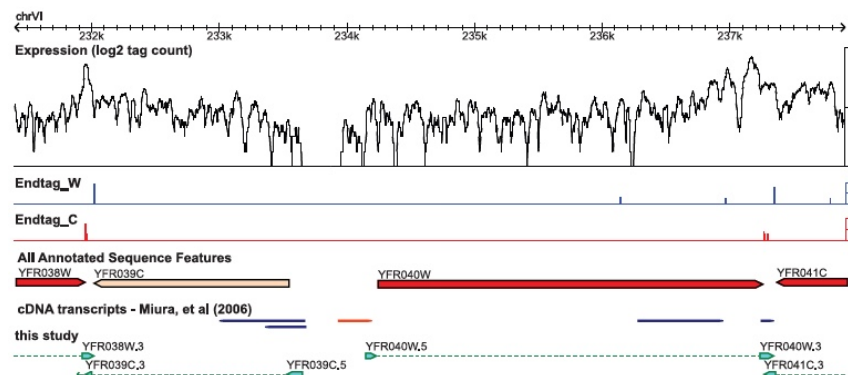


Fig. 4. New annotations of UTRs in a relatively poorly annotated chrVI region. ORFs identified by this study are denoted by dotted lines, and arrows denote the transcription direction. Green-shaded boxes are UTRs. cDNA transcripts in red are of high confidence and those in blue are of low confidence [defined in (9)].

Figure 5 A-C

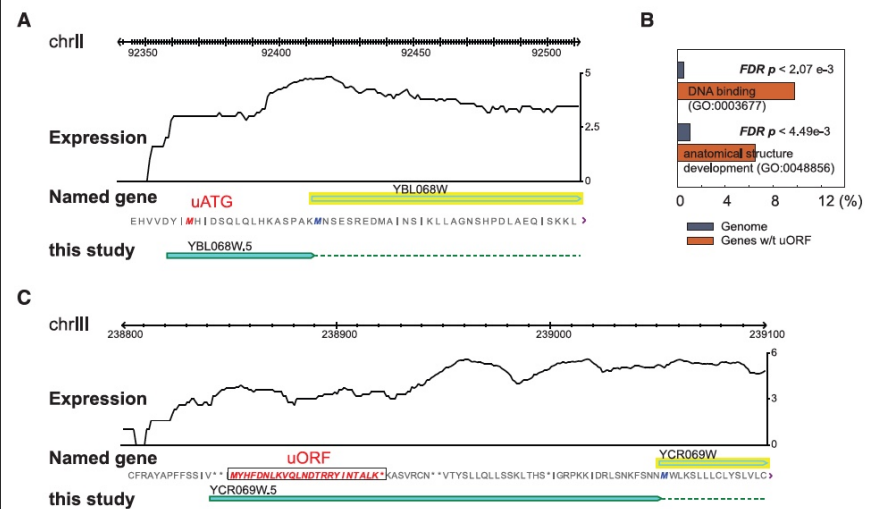
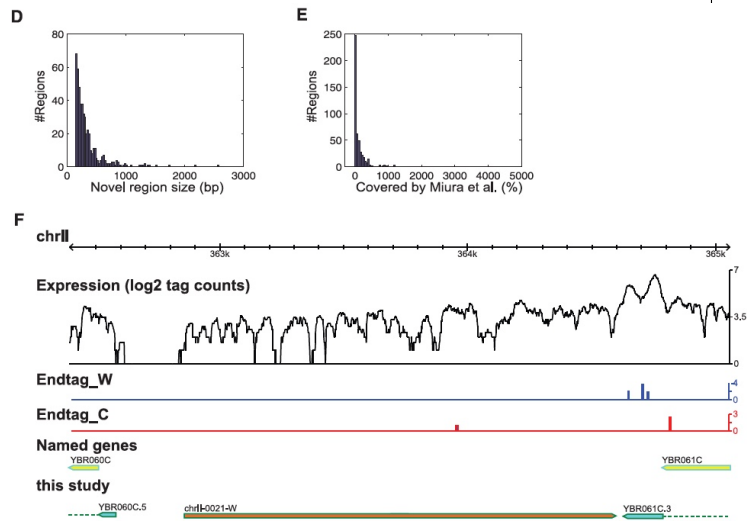


Figure 5 D-F



Reading for next time:



- Smith ZD, Chan MM, Mikkelsen TS, Gu H, Gnirke A, Regev A, Meissner A. A unique regulatory phase of DNA methylation in the early mammalian embryo. *Nature*. 2012 484:339