Budding Yeast Transcriptome and Nucleo-Protein Interactome

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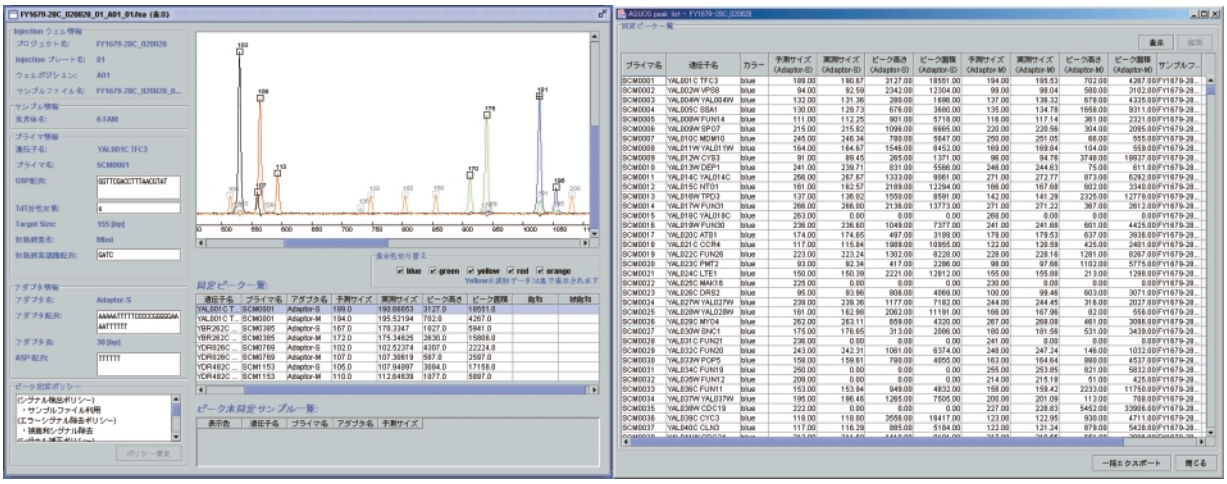
We developed a system for absolute quantification of every yeast mRNA, based on a unique method of adaptor-tagged competitive PCR using genomic DNA as a standard (GATC-PCR). The GATC-PCR system is composed of three modules, namely reaction, measurement, and data analysis (shown below). Using the system, we can describe the whole transcriptome on the basis of number of individual mRNA molecules per cell, thereby providing the most thorough and versatile description of transcriptome as well as novel points of view for the transcriptome analysis. We expect the absolute expression data to play an integral role in transcriptome analysis of nutritional stress response for cellular simulation. Furthermore, we pursue the potential use of this system in quantitative analysis of transcription factor-bound chromatin fragments, thereby improving genome-wide analysis of protein-DNA interactions.



To facilitate analysis of transcription network, we also develop a strategy for artificial activation of transcription factors, which would help us identify target genes for uncharacterized transcription factors with unknown upstream activating signals. The strategy is based on chimaerization of the DNA binding domain of transcription factor to be analyzed and a strong trans-activation domain. The power of this strategy was demonstrated in the comparative analysis of transcription factors presumably regulating multiple drug resistance of the budding yeast.