The relationship between transcription pre-initiation complexes and gene expression variability in *S. cerevisiae*

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Abstract

Understanding the variability of gene expression at molecular level is a major challenge in biology. Expression variability can be defined as stochastic noise, responsiveness and expression divergence based on the source of variation.Variation of gene expression is due to intrinsic properties (DNA sequence and transcription factors/ regulators) as well as extrinsic features (such as environment). Transcription initiation is the first and very essential process in the regulation and variability of gene expression. The relationship between the occupancy of general transcription machinery and gene expression is not yet understood. Recent study provided a comprehensive occupancy map of general transcription factors (GTFs) and RNA polymerase II on whole genome scale for *S. cerevisiae.* In our study, we have attempted to understand the positional organization of different GTFs and their relationship with gene expression. For this purpose we have considered genes with highest and lowest variability in their gene expression and compared their GTFs and RNAPII occupancy in genomic region flanking the Transcription start sites (TSS). We observed that the GTF and RNAPII occupancy of highly variable and lowly variable genes differ both in level and position of occupancy. The genes with high expression variability have greater occupancy of TBP, TFIIA, B, E, F, H, K compared to the genes with less expression variability. Further, we observed distinct patterns of RNAPII and

nucleosome occupancy in genes with low and high expression variability. The difference in the GTF, RNAPII or nucleosome occupancy of the genes may arise due to differences in the DNA sequence or related structural features, in their core promoter region.