Supplementary Material (ESI) for Molecular BioSystems

# Supplementary Material

## Transcription factor (TF) regulation

To identify the transcription factors (TF) which regulate the genes of long lived and short lived group, the network of transcription factor and their regulated genes which have been obtained from Balaji *et al* [27] were used in this study. In brief, this network is comprised of 157 TF for 12589 promoter binding events covering 4406 genes. The sub-network for long lived and short lived genes was extracted using in house script written in Perl language. Further, list of common TF regulate genes of long lived and short lived group has been identified to know the extent of overlapping. Further, transcription factors which are unique for LL and SL are checked for their time course expression and hierarchical clustering was done using cluster software available at (http://rana.stanford.edu) and the resulting cluster was visualized using the program Tree View (available at http://rana.stanford.edu/software/).

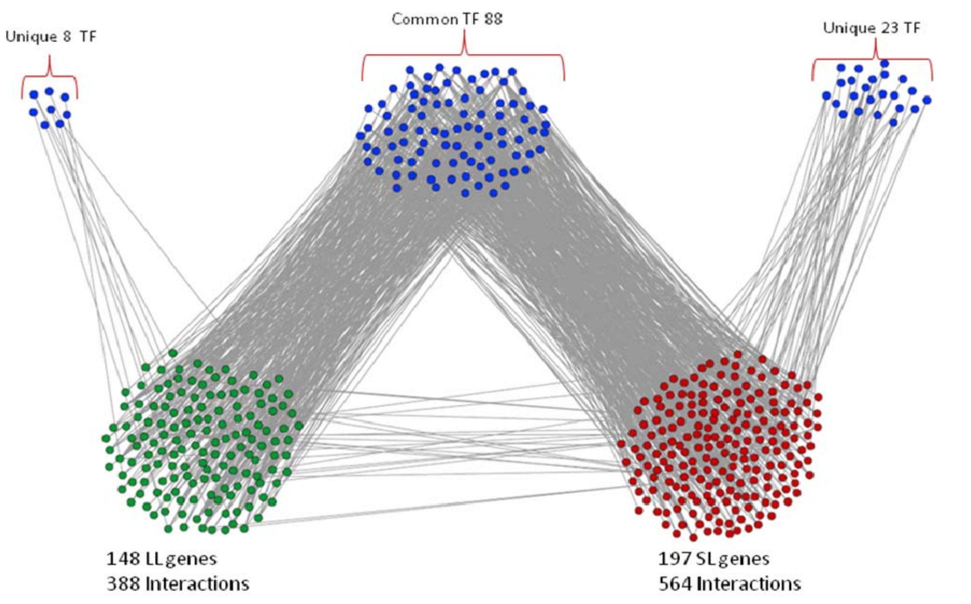

**Figure S1**: Transcriptional regulation of long lived and short lived genes. The green circles and red circles represent long lived and short lived genes respectively. Blue circles represent transcription factors (TF). Each circle corresponds to unique gene. The grey lines between circles represent the regulatory link between the two. The number shown in parenthesis represent transcription factors regulating long lived and short lived genes. The transcription factors, alone and in combination, show significant overlapping for two groups. This analysis suggests that the two groups are transcribed by the same transcription factors.

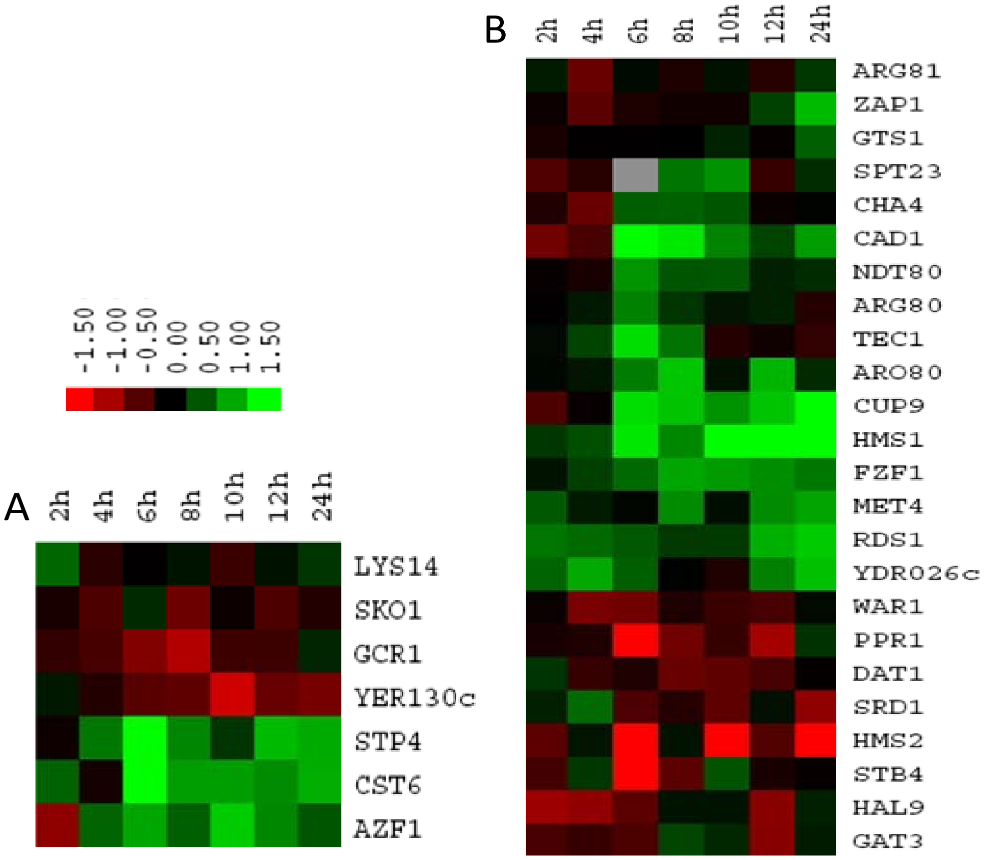

**Figure S2:** Time course expression of transcription factors which are found unique for the LL (A) and SL genes (B) for extended dataset. Figure shows the expression of transcription factors responsible for regulation of replicative lifespan, the expression of some TF increases (STP4, AZF1, HMS1) with time while expression of other TF decreases (SKO1, HMS2), certain TF remains unchanged (ARG80, ARG 81). Thus, indicating the role of TF in regulating the replicative life span associated genes.

## Chromosome localization of LL and SL gene

The chromosomal location of genes was obtained from http://www.yeastgenome.org/. In order to assess the distribution of replicative aging associated genes across the chromosomes two different types of statistical test were performed. The first one is a chi square test that has as a null hypothesis that the differentially expressed genes are distributed across the 16 yeast chromosomes in an unbiased manner. The second test computes the expected distribution of genes on the 16 chromosomes by repeatedly (1000 times) and randomly picking the same number of genes as the set of differentially expressed genes. This is compared to the observed distribution of the differentially expressed genes to obtain statistical significance for chromosomal preference (p-values and Z-scores). In order to assess whether the distribution of genes within chromosomes is random or clustered, we calculated the proximity index (PI) for the differentially expressed set of genes. The PI is defined as the ratio of proximal genes to the set of differentially expressed genes. Two genes are defined to be proximal, if they are separated by less than five genes on the chromosome. To assess statistical significance, the PI value was calculated from random sets of genes (1000 in this case) and compared to the observed value.

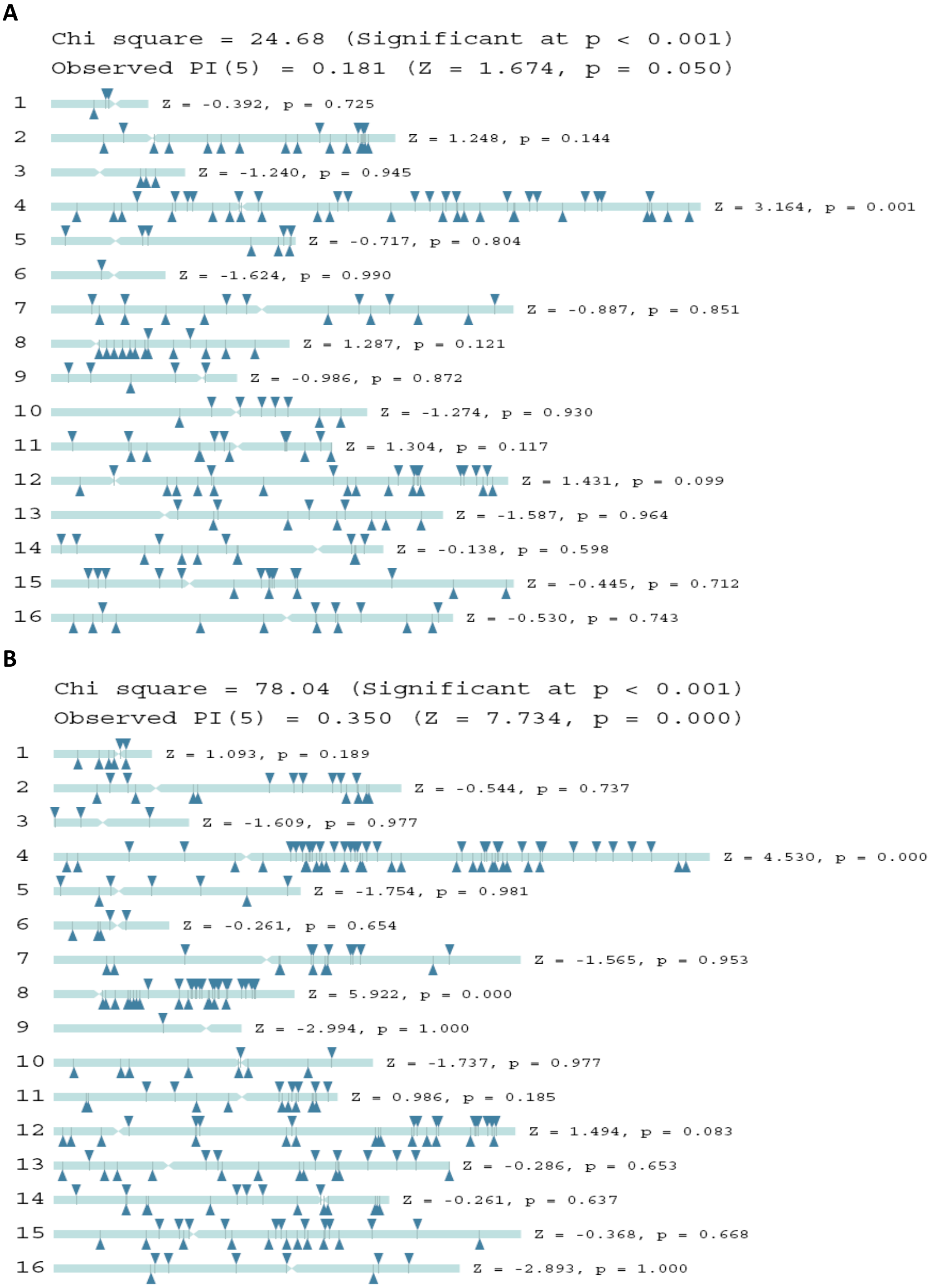

**Figure S3**: Figure showing the chromosome localization of replicative aging associated genes used in this study. (A) Shows the chromosomal location of long-lived genes while (B) Shows the chromosomal location of short-lived genes. It is from this analysis that almost all the aging associated genes are localized internally not in the telomeric and sub-telomeric region of the chromosome.