The budding yeast \textit{Saccharomyces cerevisiae} (\textit{S.cerevisiae}) is a single-celled lower eukaryote belonging to the kingdom of fungi. Ever since its discovery, \textit{S.cerevisae} has nourished human advancements in the field of fermented food products, alcoholic beverages, and nowadays, the production of biofuel. Beyond its contributions to industrial fermentation, \textit{S.cerevisiae} has become one of the most popular model organism in eukaryotic biology, due to its simple cellular architecture, cheap maintenance cost, fast growth, and homologies to human cells \cite{botstein\_yeast\_2011}. The haploid genome of \textit{S.cerevisiae} consists of 16 linear chromosomes containing 6604 genes encoded within 12 megabase-pairs (Mbp)\cite{belda\_saccharomyces\_2019}. Since the genome of \textit{S.cerevisiae} is fully sequenced, relatively small, virtually free of intronic DNA, this microorganism is ideally suited for genetic analyses.\\

\noindent In this project, we focused on identifying novel mutations that may suppress the phenotypic alteration caused by the deletion of the gene Trigger of mitosis, abbreviated *TOM1*. *TOM1* is a gene located on chromosome 4 and codes for a large protein of 380 kDa that belongs to the group of Hect-domain E3 ubiquitin ligases \cite{utsugi\_yeast\_1999}. Utsugi and colleagues found that mutations in the Hect-domain of *TOM1*, which is necessary for thioester-bond formation with ubiquitin, or the entire deletion of the gene rendered \textit{S.cerevisiae} unable to grow at high temperatures \cite{utsugi\_yeast\_1999}. The authors found that \textit{S.cerevisiae} with mutated *TOM1* exhibited an abnormally large nucleus containing duplicated DNA, fragmented nucleoli, accumulation of poly(A)+RNA in the nucleus, and cell cycle arrest at G2/M, suggesting that the disruption of TOM1 had a severe impact on nuclear transport and cell division. Later it was shown that TOM1 was targeting DIA2 and CDC6 for proteasomal degradation during G1 and G2/M phases (Kim et al., Mol Biol Cell, 2012), confirming that TOM1 is involved in the regulation of the cell cycle.\\

\noindent Furthermore, TOM1 has been found to plays an integral role in the regulation of proteostasis by ubiquitinating highly basic histone proteins (Singh et al., Nat Cell Biol, 2009) and various unassembled ribosomal proteins of the large and small subunit (RPL and RPS, respectively)(Sung et al., eLife, 2016). This demonstrates that the deletion of *TOM1* (termed *∆TOM1* in this study) has a highly pleiotropic effect on the phenotype of \textit{S.cerevisiae} under heat stress. To date, several extragenic suppressors of *∆TOM1* have been identified that restore the ability of \textit{S.cerevisiae} to grow at high temperatures, such as deletion of DIA2, (Kim et al., Mol Biol Cell, 2012), overexpression of STM1, \cite{utsugi\_high\_1995} as well as genes that are linked to down-regulation of the cAMP/PKA pathway(Sasaki et al., Mol Gen Genet, 2000).

The aim of this study was to identify potential new extragenic suppressors of *∆TOM1* in six strains of \textit{S.cerevisiae} that were derived from YDK1364. While YDK1364 is unable to grow under heat stress due to the deletion of *TOM1*, the tested strains partially regained the ability to grow at high temperatures due to the accumulation of random mutations. The six strains were sequenced using Illumina Technology and potential mutations associated with the revertant phenotype were identified using a bioinformatic pipeline. We found several known suppressors of *∆TOM1* as well as some new candidates that were mostly associated with the RPL and RPS gene family. \\