

## *Identification of Set1 Target Genes*

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The Set1 complex, a histone methyltransferase complex found in *S. cerevisiae* (budding yeast), is the only histone methyltransferase responsible for catalyzing methylation of histone H3 at Lysine 4. It possesses homologues in other species, humans included. While yeast only have the Set1 complex, the human homologues of the yeast Set1 complex include mixed-lineage leukemia family (MLL1-4), Set1 A, Set1 B, among others. MLL1-4 has been shown to play a role in transcription, cell type specification, and the development of leukemia. One application of characterizing the role of a protein is that the information gained can provide insight into the function of its homologues; possibly leading to treatments for mutations in those homologues.

This ongoing discovery-based project aims to characterize the role of Set1 in *Saccharomyces cerevisiae*, a model organism frequently used in genetics research commonly known as budding yeast. By utilizing a high-copy plasmid suppression screen, we aim to identify specific genes that are regulated by Set1. Set1's methylation (and activation of certain genes) has been shown by other studies to be necessary for cell wall integrity, and therefore colony growth, at high temperatures. This sensitivity was the basis of selection for this experiment. Plasmids from a library were transformed into the SET1 deletes to observe which, if any, rescued the cells. Plasmids from the library were extracted from *E. coli* using a standard miniprep protocol. Yeast was transformed using a long transformation protocol. The transformed cells were incubated for four to five days at 39.5°C.