One of every twenty Americans will be affected with Colorectal Cancer (CRC) with Hereditary Non-Polyposis Colorectal Cancer being the most common (HNPCC). This type of cancer is a hereditary gene caused by a missense mutation on the 2nd chromosome of the human DNA. To conduct our research, we used *Saccharomyces cerevisiae* cells, specifically the msh2 strain. These yeast cells serve as a model for understanding human MSH2 mutations, which is a tumor suppressor. The purpose is to manipulate the yeast MSH2 gene to determine which missense mutation is likely to be benign or pathogenic. We examined the defects at a molecular level to determine what MSH2 variants are dysfunctional by using a DNA mismatch pair and the reporter plasmid, pSH44, fused with URA3. The mismatch repair efﬁciencies were determined qualitatively using the 5-ﬂuororotic acid monohydrate (FOA) dinucleotide instability plate assays resulting in the formation of 5-FU. With the occurrence of 5-FU, the yeast cells should die; however, the ability of yeast cells to survive in the presence of 5-FOA reveals a dysfunction in mismatch repair. Defining the consequences of missense mutation within the MSH2 gene could result in the development of biomarkers for early detection of HNPCC.