Khan Inan
Professor Truong
BI-GY 7683

1. Variable Allele frequency is essentially used to understand where a mutation came from and understand why it originated. VAF tells whether a mutation variant was inherited from parents or came from somatic cells. The percentage that VAF represents can represent whether or not it is a germline mutation if it is at 50 or 100 percent. After deriving from the generalized formula, zygosity, loss of zygosity and copy neutral loss of heterozygosity, I found that N was left after plugging in the known variables. which represents the population size

2. In a CRISPR experiment to study a tumor-suppressor gene that is inactivated by mutations in tumors, I would start by determining which mutations the suppressor gene is actually successful in preventing. Since CRISPR experiments allow us to flexibly manipulation genomes and create models using cells and animals, we would most likely need to induce mutations that would trigger the tumor-suppressing gene. Afterwards, we would need to induce a mutation in a tumor that does NOT trigger the suppressor gene. Lastly my experiment would conclude with comparing the mutation that did trigger the suppressing gene vs the one that did not.

   A CRISPR experiment to study an oncogene that is activated by mutations in tumors would be a bit different. Oncogenes are activated based on certain conditions and circumstances, so studying a specific oncogene successfully would involve finding out what a cell needs to do or have to transform into a tumor cell under the influence of an oncogene. Studying oncogenes by inducing mutations in cells and finding out what causes the cancer would involve too much trial and error, and instead a better and more intuitive approach would be to reverse the process and study tumors. We would just need to scan the genome of the tumor for segments of DNA that drove the cell towards cancerous behavior