



# CALIFORNIA SCIENCE & ENGINEERING FAIR 2019 PROJECT SUMMARY

<b>Name(s)</b> <b>Heather Lee; Dilan Patel</b>	<b>Project Number</b> <b>S0515</b>
<b>Project Title</b> <b>Supporting the Notion that Nanopipette Injection Is an Accurate and Reliable Method for Multiplexed Genetic Editing</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives</b> The uses of nanopipette surgery in genomic editing and DNA extraction are vast. Before it can be used and trusted it must be verified as a reliable and accurate tool. The purpose of this research is to test if nanopipettes are an accurate tool for extracting and injecting genetic material and if scientists can rely on nanopipettes. We analyzed the gene expression of two breast cancer cell types referred to as MBL and MCL, as well as HeLa and Neuron cells, in a heatmap. In the process of analyzing the accuracy of nanopipettes, we used the coding platform R studio, as well as Terminal. By examining four different cell lines extracted by the nanopipettes and comparing them to the human genome, we were able to conclude that nanopipettes are an accurate and reliable way of extracting genomic information.</p> <p><b>Methods</b> Methods and Materials: R programming software, Mac terminal, nanopipettes, Human reference genome, human DNA extracted using nanopipettes</p> <p>Obtain Human DNA sequences extracted using nanopipettes Download the human reference genome Access DNA files in Mac OS terminal Run htseq count in order to convert trimmed files to counts files that show the number of times a gene is expressed Sort the counts files by the amount of gene expression using the sort command Pick out the top 20 recurring genes from the sorted file Use the grep command to paste the new 20 genes into one file Open this file in a vim table and organize the data in order to be analyzed Export the organized data as a .text file Open data in R studio and run through the code to synthesize the heatmap Analyze heatmap to look for correlation in gene expression</p> <p>The goal of this project was to analyze the use of nanopipettes as a genetic tool. In order to do this, we created data analysis charts such as heatmaps and PCA to figure out the accuracy. Throughout our project, we studied the extraction of DNA from MBL, MCL, HeLa, and Neuron cells.</p> <p><b>Results</b></p>	
<b>Summary Statement</b> Supporting the Notion that Nanopipette Injection is an Accurate and Reliable Method for Multiplexed Genetic Editing	
<b>Help Received</b> We would also like to thank our mentors Geo Chaves and Gonca Bulbul at UCSC.	