

**Part B****Case 4 – Genetic Drift:**

Initial Class Frequencies:	AA: _____	Aa: _____	aa: _____
My initial Genotype: _____			
F <sub>1</sub> Genotype: _____			
F <sub>2</sub> Genotype: _____			
F <sub>3</sub> Genotype: _____			
F <sub>4</sub> Genotype: _____			
F <sub>5</sub> Genotype: _____			
Final Class Frequencies:	AA: _____	Aa: _____	aa: _____
Total # of A alleles: _____		Total # of a alleles: _____	

**Analysis:**

1. Using the PTC paper results for the entire class, how close were the frequencies of each phenotype (taster vs. non-taster) to those found in the North American population (approximately 70% tasters)? If your class results were different, what could have caused this?
2. In the first exercise in Part B (case 1), what would you expect the values of A and a alleles to be after 5 generations?
3. How close were your class results to an ideal population? What do you think would happen if you carried out this simulation for another 10 generations?