**Project Timeline**

1. Convert available Zaninifile.Csv into .fasta with Convert\_Zanini\_to\_geneious.R
2. Use Geneious to cut and align sequences
3. Export new data as .fasta
4. Use Gap\_Deletion\_col1.R to delete “-“ from consensus sequence and create 5UTRSeqs.csv
5. Use 5UTR\_Freqs.R to analyze frequencies in 5UTRSeqs.csv