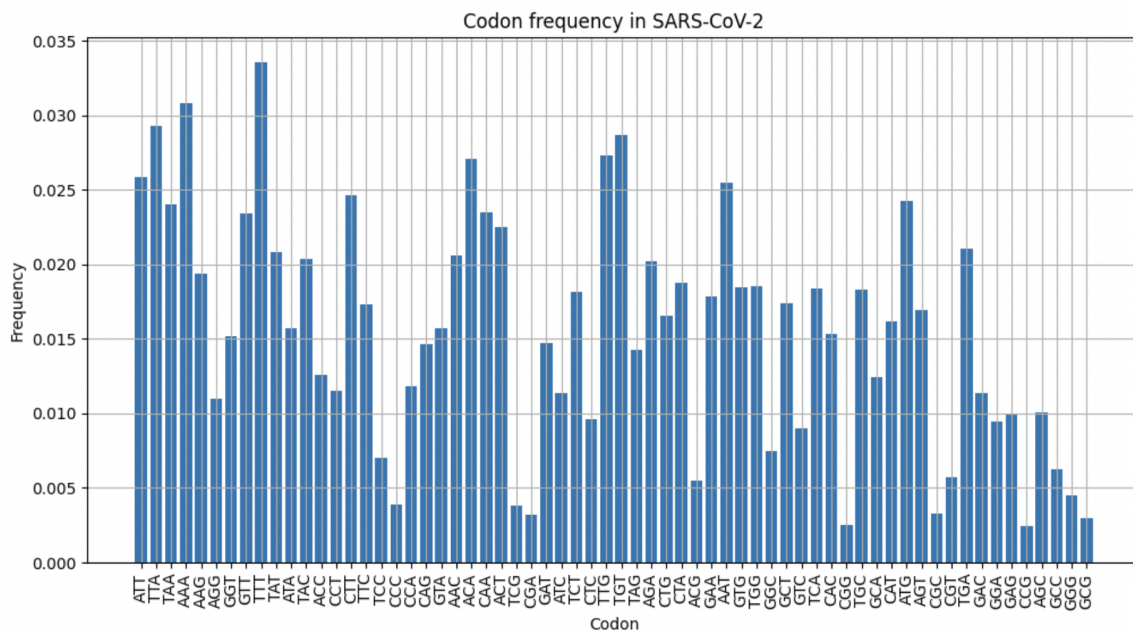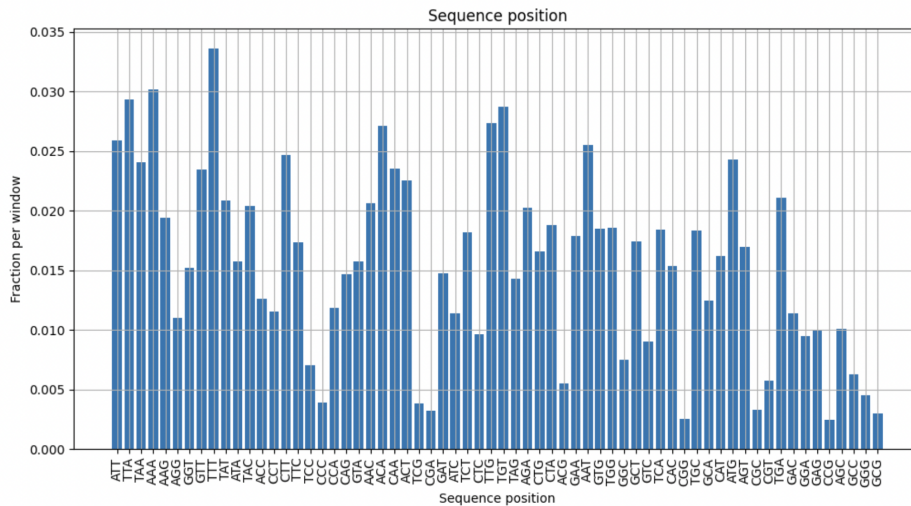Your report should comment on and include the following items:

1. Include all generated histogram plots and the base pair density plot as figures
   - Ensure that the window width you've used for the base pair density is clearly stated

2. Report on the KL divergences between the additional sequences and the reference SARS-Cov-2 sequence
3. Decide whether `seqA.txt` or `seqB.txt` is more likely to be the Covid variant, and justify this both qualitatively and quantitatively
4. We used the `count` method to generate the base pair density plot. Why didn't we use this for the codon histograms (e.g. `geneStr.count('ATA')`)?
   ○ What problems does the dictionary approach solve?
5. What effect does changing the window width have on the base pair density plot?