The file **“Insertion_BAer_Pasteur_bpcheck.ipynb”** contains functions to assess whether inserted sequences from the Pasteur lineage match the Connaught reference sequence. These functions are used to identify nucleotide-level mutations within the inserted regions.

The file **“Insertion_BAer_Danish_bpcheck.ipynb”** contains functions to evaluate whether inserted sequences from the Danish lineage match the Connaught reference sequence, allowing for detection of nucleotide-level differences in the inserted regions.

The file **“Insertion_BAer_startstopcheck.ipynb”** contains functions to determine whether inserted sequences retain start and stop codons consistent with the Connaught reference sequence. These analyses assess whether mutations in the inserted regions disrupt the start codon or introduce premature stop codons.

The file **“Insertion_BAer_protein.ipynb”** contains functions to translate DNA sequences into protein sequences and to compare the resulting amino acid sequences with those from the Connaught reference, assessing whether protein products are conserved despite underlying nucleotide variation.

The file **“Deletion_BAer_bpcheck.ipynb”** contains functions to assess whether deleted sequences match the Connaught reference sequence, enabling identification of nucleotide-level mutations within deleted regions.

The file **“Deletion_BAer_startstopcheck.ipynb”** contains functions to determine whether deleted sequences retain start and stop codons consistent with the Connaught reference sequence, and to evaluate whether mutations result in loss of the start codon or introduction of premature stop codons.