**MATERIALS**

The following materials were used to gather sequences, align said sequences, and create and manipulate phylogenetic trees:

1. Modern computer with proper software downloaded and access to internet
2. A Nucleotide Database: ncbi.nlm.nih.giv OR hiv.lanl.gov
3. Version Control
   1. Required in order to recover old files
   2. Used *GitHub*
4. Software
   1. Sequence Manipulation
      1. *Komodo Edit, SeaView, Mafft, Mesquite, Linsi*
   2. Phylogenetic Analysis Using Parsimony
      1. *PAUP\**
   3. Bayesian Analysis / BEAST Suite
      1. *BEAST, BEAUTi, Tree Annotator, Tracer*
   4. Tree Viewing
      1. *FigTree*