Open the HIV-1 genome in IGV (Genomes > Load Genome from Server). Create a BED file (0-based start) with the following three intervals:

- The gag gene located at positions 336 through 1838.
- The vif gene located at positions 4587 through 5165.
- A Gag protein potential epitope located at amino acid positions 271 through 285 of the Gag protein. The amino acid sequence is NKIVRMYSPTSILDI.
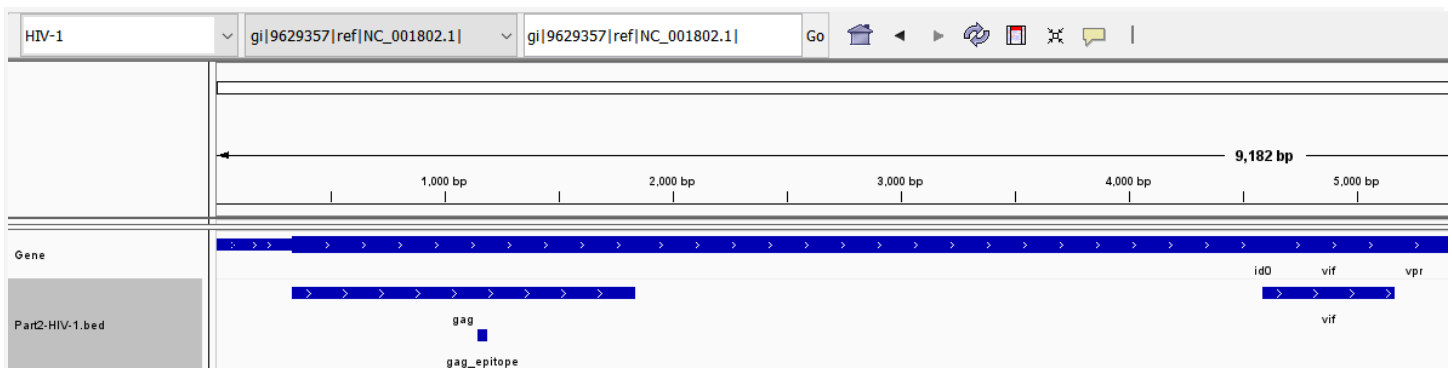
Create the BED file with NC_001802.1 in column one. Load it to IGV.

- (2 pts) Submit the BED file.

NC_001802.1 335   1838   gag   0   +
NC_001802.1 4586   5165   vif   0   +
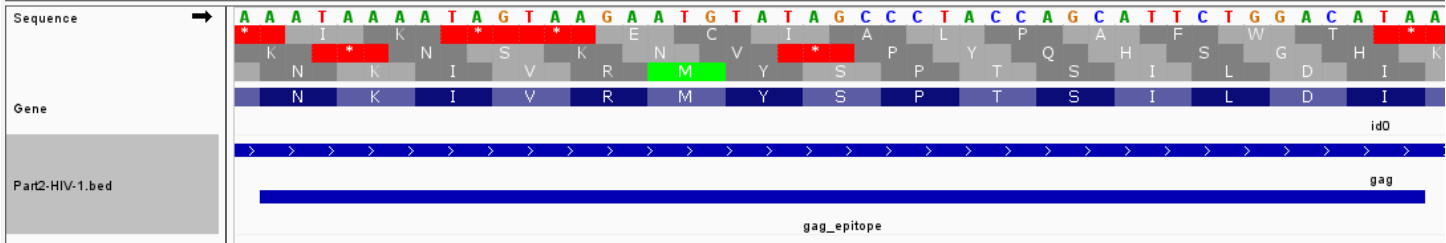NC_001802.1 1145   1190   gag_epitope 0   +

*Actual BED file is also attached

- (2 pts) Submit a screenshot that shows all three intervals in IGV.

*Expanded view also attached

- (2 pts) Submit a zoomed in screenshot that shows the epitope and the amino acid sequences.

*Expanded view also attached