# concatenated\_host\_viral

### FRIDAY, 4/5/2019

### Concatenating host and viral genome

cat Macaca\_fascicularis.Macaca\_fascicularis\_5.0.dna.toplevel.fa Makona\_genome.fasta > Cynomolgus\_Makona.fasta

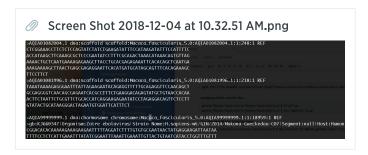
### Open fasta file

#### nano Cynomolgus\_Makona.fasta

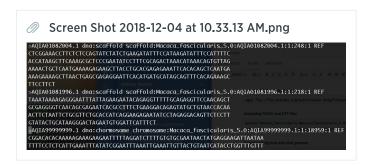
- Scroll to end and find where Makona genome starts



- annotate header of the Makona genome to look similar to Cynomolgus
- choose an identifier that follows Cynomolgus format but is also unique from all other identifiers (use command/ctrl find)



-Final should look like this



## Open GTF file and add additional information at the end.

- Mannually annotate information about the viral genome/gene
- Make sure to follow Cynomolgus macaque format (9 columns of information)
- based on whether you are annotating the viral gene as a gene, exon or CDS, follow the same format of the last column



- Final should look like this
- Save as a new name that incorporates viral name.

