1) Create directory "equcab3" in snpEff data directory:

mkdir /usr/bin/snpEff/data/equcab3

2) Moved the fasta and gff files to the equcab3 directory

3) Edited snpEff.config and inserted equcab3:

vi snpEff.config

# Horse genome, version 3

equcab3.genome : Horse

4) Built database:

cd /usr/bin/snpEff

java –Xmx8g -jar snpEff.jar build –gff3 -v equcab3