**The output files for pseudogene sequences were obtained using the following command for pseudofinder**

**Pseudofinder (Annotate)**

python3 pseudofinder.py annotate --genome GENOME.GBF --outprefix PREFIX --database /PATH/TO/NR/nr --threads 16

**Genral CRB-BLAST script used for comparing sequences**

**CRB BLAST SCRIPT**

module load ruby/2.4.3

crb-blast --query assembly.fna --target reference\_nucleotide.fna --threads 8 --output annotation.tsv

**To extract the subset of sequences from full sequences**

seqtk subseq file1.fasta file2.txt > output.fasta