**General 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