**# Build custom database for Kraken2**

**kraken2-build** --download-taxonomy --db $DBNAME

**kraken2-build -**-add-to-library strain.fa --db $DBNAME

**kraken2-build** --build --db $DBNAME

**# Run Kraken2 to identify strains**

**kraken2 –**db $ DBNAME –report result.txt $sample\_1.fastq $sample\_2.fastq

**# Build custom database for Krakenuniq**

**krakenuniq-build** --db Krakenuniq\_DB --taxids-for-genomes --taxids-for-sequences

**# Run Krakenuniq to identify strains**

**krakenuniq** --db Kraken\_DB --threads 8 --fastq-input --paired $sample\_1.fastq $sample\_2.fastq --report\_file result.tsv> result.report

**# Build custom database for Centrifuge**

**centrifuge-build** --conversion-table $prefix.conv --taxonomy-tree $prefix.tree --name-table $prefix.name $prefix.fasta $prefix

**# Run Centrifuge to identify strains**

**centrifuge** -x $prefix -1 $sample\_1.fastq -2 $sample\_2.fastq --report\_file report.txt -S result.txt -p 8

**# Build custom database for Sigma**

**sigma-index-genomes** -c config.cfg -p 8

**# Run Sigma to identify strains**

**sigma-align-reads** -c config.cfg -p 8

**sigma** -c config.cfg -t 8

**# Run Sigma to identify strains**

**python pathoscope2.py** MAP -1 $sample\_1.fastq -2 $sample\_2.fastq -targetRefFiles Ref.fasta -filterRefFiles Human.fasta -outDir Results -outAlign out.sam -expTag tutorial

**python pathoscope2.py** ID -alignFile Results/out.sam -fileType sam -outDir Results -expTag tutorial

**# Run VirStrain to identify strains**

**python VirStrain.py** -d VirStrain\_DB -i $sample\_1.fastq -p $sample\_2.fastq -o Results

**# Build MegaBLAST index for strain genomes**

**makeblastdb** -in strains.fasta -out $INDEX -dbtype nucl

**# Run MegaBLAST to find the closest relative**

**blastn** -query strain.fasta -db $INDEX -outfmt "7 qseqid sseqid pident length mismatch evalue" -out Blast\_Out

**# Assembly for Washington data**

**megahit** -r $sample.fastq -o assembly\_result

**# Run bowtie2 to align reads to reference genome obtained by megahit**

**bowtie2-build** reference.fasta reference

**bowtie2** -p 6 -x reference -U reads.fastq -N 0 --no-unal --end-to-end -S result.sam