Running CZI pipeline

1. CD into working directory (not home directory)

```
cd /mnt/ajung/ARTIC/
```

2. Download Kraken database

```
mkdir kraken2_db
wget https://genome-idx.s3.amazonaws.com/kraken/k2_viral_20210517.tar.gz
tar –xf k2_viral_20210517.tar.gz
```

https://benlangmead.github.io/aws-indexes/k2

Running CZI pipeline

3. Run command

nextflow run czbiohub/sc2-illumina-pipeline -profile artic,docker --reads '/mnt/atlantis1/ajung/tutorial/ARTIC_tutorial/WUSTL_data/*_R{1,2}.fastq.gz*' **--primers** 'SARS-CoV-2.dna_manifest.20200408.bed'
--kraken2_db '/mnt/atlantis1/ajung/tutorial/ARTIC_tutorial/WUSTL_data/kraken2_db' --outdir '/mnt/atlantis1/ajung/tutorial/ARTIC_tutorial/WUSTL_data/outdir'

Post CZI analysis

- Full workflow

```
nextflow run anajung/CZI_addon --combinedfa 'combined.fa' --vcf 'sample-variants/*.vcf.gz' --outdir './out'
```

- Variant annotation

```
nextflow run anajung/variant_annotation --vcf 'sample-variants/*.vcf.gz' --outdir './out'
```

- Lineage and tree generation

```
nextflow run anajung/lineage --combinedfa 'combined.fa' --outdir './out'
```

https://github.com/anajung/CZI_addon

Tree generation

- https://microreact.org/upload