**Commands for ADA Environment Setup**

**Download samtools**

// Download samtools from http://www.htslib.org/download/

wget <https://github.com/samtools/samtools/releases/download/1.13/samtools-1.13.tar.bz2>

tar xvjf samtools-1.13.tar.bz2

cd samtools-1.13

./configure

make

export PATH=$PATH: /home/qiwang/bin/samtools-1.13 // Added to .profile - modify it

**Download simulation data**

// Download the simulation data

wget https://bioinfo.uth.edu/VirusFinder/simulation-data.tgz?csrt=11929234083444165632

mv simulation-data.tgz\?csrt\=11929234083444165632 simu.tgz

tar xvfz simu.tgz

rm simu.tgz

**Download human reference genome**

wget <http://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz>

// Below is the version recommended by Heng Li to use

wget -m <ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/001/405/GCA_000001405.15_GRCh38/seqs_for_alignment_pipelines.ucsc_ids/GCA_000001405.15_GRCh38_no_alt_analysis_set.fna.gz>

gunzip GCA…\_set.fna.gz //The file name is too long 😊

bwa index GCA…\_set.fna

**Install sratoolkit**

wget --output-document sratoolkit.tar.gz <http://ftp-trace.ncbi.nlm.nih.gov/sra/sdk/current/sratoolkit.current-ubuntu64.tar.gz>

tar -vxzf sratoolkit.tar.gz

export PATH=$PATH:$PWD/sratoolkit.2.11.0-ubuntu64/bin

vi .bashrc //Add the command above to .bashrc

mkdir data process

vdb-config -i //Configure sratoolkit

// Download SRA data: <https://www.ncbi.nlm.nih.gov/sra/docs/sradownload/>

// https://www.ncbi.nlm.nih.gov/sra/docs/SRA-Google-Cloud/

prefetch SRR873430

Download other NGS data

// 1. RNS-seq

// Download SRA in SRA format from <https://www.ncbi.nlm.nih.gov/bioproject/206422>

prefetch SRR873430 //NOT USED <https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR873430>

// Download fastq from <https://trace.ddbj.nig.ac.jp/DRASearch/study?acc=SRP023539>

fastq-dump SRR873427

fastq-dump SRR873836

fastq-dump SRR873428

fastq-dump SRR873430

// 2. Targeted sequencing

Download 3rd party tools

//BWA (https://github.com/lh3/bwa)

wget <https://sourceforge.net/projects/bio-bwa/files/latest/download/bwa-0.7.17.tar.bz2>

tar xvjf bwa-0.7.17.tar.bz2

Make

export PATH=$PATH:/home/qiwang/bin/bwa-0.7.17 // Added to .profile - modify it