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# exported downloaded SRR_Acc_List.txt from local to HPC directory ~/ RNAseq
# converting the accession numbers to sra formatted files using SRA toolkit

# -----
# 1) List and load available versions of sra-tools to the environment
# -----
module avail sra-tools/3.0.3-gcc-13.2.0
module load sra-tools/3.0.3-gcc-13.2.0

# -----
# 2) Create output directories
# -----
mkdir sra          # .sra downloads will be stored
mkdir fastq        # Directory where FASTQ outputs will be written
# -----
# 3) Download .sra files using prefetch
# -----
prefetch --option-file SRR_Acc_List.txt --output-directory sra/

# -----
# 4) Convert downloaded .sra files to FASTQ using fasterq-dump
# -----
fasterq-dump sra/*/*.sra --split-files --threads 4 -O fastq/

# -----
# 5) Running quality check on the FASTQ files
# -----
# running fastqc from the directory where my FASTQ files are (if not specify the path to the
FASTQ files/direcotry)
module load fastqc
fastqc *.fastq -o /scratch/grp/msc_appbio/Group2_ABCC/RNAseq/trial/QC

# *.fastq runs FastQC on all FASTQ files in the current directory.
# -O Specifies the output directory where FastQC results will be written.
# Output: For each FASTQ file, FastQC generates:
#   an HTML report (<sample_number>_fastqc.html),
#   a compressed results archive (<sample_number>_fastqc.zip).

```