1. Make sure you have NXF\_SINGULARITY\_CACHEDIR specified
2. Create conda environment with Nextflow

`salloc -c 4 –mem=32G -t 4:00:00`

`module load miniconda`

`conda config –add channels bioconda`

`conda config –add channels conda-forge`

`conda create -c conda-forge -c bioconda –name nfcore nextflow nf-core python=3.12`

1. Download nf-core pipeline and its dependencies (singularity images)

`conda activate nfcore`

`nf-core download chipseq -r 2.0.0 –outdir nf\_chipseq -x none -s singularity -p 4 -d

Outdir cannot already exist!

Unclear if it is a good idea to set -x to some form of compression to save space