Requirements:

1. Unmapped SmartSeq2 FASTQ files
2. SmartSeq2 demultiplex files (i.e. 1\_
3. mus\_index folder
4. barcode\_mapping.R
5. merge\_barcode.sh
6. qc\_align.sh
7. Conda environment for alignment. Required packages:
   1. Fastqc
   2. Multiqc
   3. Salmon

Workflow

1. Download or move all required files to project folder (ie. SN0189514)
2. Prepare demultiplex file to wells with barcode\_mapping.R
   1. Rscript barcode\_mapping.R -f [SmartSeq2 demultiplex text filename]
3. Create merged files with well identifiers using merge\_barcode.sh
   1. sh merge\_barcode.sh barcode\_map.txt
4. Activate conda alignment environment
   1. conda activate smartseq\_qc\_align
5. Conduct quality control and alignment with qc\_align.sh
   1. sh qc\_align.sh