

```
sci-RNA-seq.pipeline.elegans.sh
```

```
set -euo pipefail
```

```
WORKING_DIR=$HOME/output-clean
```

```
CONFIG_DIR=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/config
```

```
SCRIPTS_DIR=./sci-RNA-seq-pipeline-scripts
```

```
READS_DIR=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/reads
```

```
LOG_DIR=$WORKING_DIR/cluster-logs
```

```
DATAMASH_PATH=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/datamash
```

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Extract RT barcode
& UMI from R2

```
#-----  
# Put read 1 info (RT well, UMI) into read 2 read name  
#-----  
echo "Moving read 1 info into read 2 name"  
  
cd $WORKING_DIR  
  
mkdir combined-fastq  
mkdir file-lists-for-r1-info-munging  
mkdir put-r1-info-in-r2-logs  
  
ls $READS_DIR/fastq | grep _R1_ | grep -v Undetermined | split -l 25 -d - file-lists-for-r1-info-munging/
```