

sci-RNA-seq.pipeline.elegans.sh

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/
```

“pipe”: sends the output of
one command into the next
command as input

grep: prints lines from the
input that match the regular
expression provided

split: split up a file into
chunks. In this case, chunks
of 25 lines

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qsub: submit a job to the SGE scheduler. In this case, the job script is “put-read1-info-in-read2.sh”

```
ls file-lists-for-r1-info-munging | while read BATCH; do  
  qsub -P $CLUSTER_ID -j y -o $LOG_DIR -N MOVER1R2.${BATCH} $SCRIPTS_DIR/put-read1-info-in-read2.sh \  
    $READS_DIR/fastq \\  
    $WORKING_DIR/file-lists-for-r1-info-munging/$BATCH \\  
    $SCRIPTS_DIR/ \\  
    $RT_BARCODES_FILE \\  
    $CONFIG_DIR/combinatorial.indexing.key \\  
    $WORKING_DIR/combined-fastq \\  
    $WORKING_DIR/put-r1-info-in-r2-logs  
done  
qsub -hold_jid "MOVER1R2*" -sync y -b y echo "DONE"
```

← This is a special way to call qsub so it waits for all
jobs named “MOVER1R2” to finish