

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/
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“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