

`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"
```

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

Put-read1-into-read2.awk

Extract RT barcode  
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```
BEGIN {
    read_num = 0;
    hits = 0;

    bases[1] = "A";
    bases[2] = "C";
    bases[3] = "G";
    bases[4] = "T";

    p5_row = substr(PCR_COMB0, 1, 1);
    p5_col = substr(PCR_COMB0, 2, 2);
    p7_row = substr(PCR_COMB0, 4, 1);
    p7_col = substr(PCR_COMB0, 5, 2);

    single_sample = "";
} {

XXXXXXXXXXXX

} END {
    printf("%d\t%d\t%.3f\t(RT barcode matches, total reads, proportion)\n",
        hits, read_num, hits / read_num) > "/dev/stderr";
}
```