Skills Assessment Quiz Answers

TAs ask the following:

- **Move to the QUIZ directory, have them show the current directory, list the contents**

```bash
$ cd /mnt/scratch Nobackup/tobiasm/Workshop/QUIZ/
$ ls -l
```

```
total 0
drwxr-x-x 2 tobiasm bioSequencing 1 Jun 10 08:44 Day5
drwxr-xr-x 2 tobiasm bioSequencing 4 Jun 10 09:23 FastQC
drwxr-xr-x 2 tobiasm bioSequencing 7 Jun 10 09:22 PBS
-rw-r--r-- 1 tobiasm bioSequencing 125 Jun 10 08:53 README.txt
drwxr-xr-x 2 tobiasm bioSequencing 1 Jun 10 09:05 Trimmed
```

- **Open the first FastQC, check**
- **Open the second FastQC, check**

**Before trimming**

**After trimming**

Overrepresented Sequences

**TruSeq Adapter Index 1**

Overrepresented Sequences

**GA, G, GAT**
- Open the README, check

### Run my commands, or whatever else IN SCRATCH
rsync -r /mnt/scratch_nobackup/sread2016/Workshop/FASTQ/Day5
/mnt/scratch_nobackup/$USER/Workshop/QUIZ

### Load modules
module load fastqc_0.11.2

### Run my commands, or whatever else IN SCRATCH
fastqc -o /mnt/scratch_nobackup/$USER/Workshop/QUIZ/FastQC
/mnt/scratch_nobackup/$USER/Workshop/QUIZ/Day5/Day5_assessment.fastq

### Run my commands, or whatever else IN SCRATCH
java -jar /opt/trimmomatic/0.32/trimmomatic-0.32.jar SE -phred33
/mnt/scratch_nobackup/$USER/Workshop/QUIZ/Day5/Day5_assessment.fastq
/mnt/scratch_nobackup/$USER/Workshop/QUIZ/Trimmed/Day5_assessment_out.fastq
ILLUMINACLIP:/opt/trimmomatic/0.32/adapters/TruSeq2-PE.fa:2:30:10

fastqc -o /mnt/scratch_nobackup/$USER/Workshop/QUIZ/FastQC
/mnt/scratch_nobackup/$USER/Workshop/QUIZ/Trimmed/Day5_assessment_out.fastq

---

**Quiz Answers**

3. There are 4,000,000 reads in Day5_assessment.fastq

4a. Adapter dimer
4b. 101

5a. 3,994,371
5b. 1-101