```
awk '{if ($1 ~ /^@.*/) {print $1, "\t", $3}}' exampleR1.fastq > exampleR1.nl.tsv
```

```
awk '{if ($1 ~ /^@.*/) {print substr($1, 2), "\t", substr($3, 8)}}' exampleR1.fastq > exampleR1.nl.tsv
```

Sample problem 1

Download "`exampleR1.fastq`" and "`exampleR2.fastq`"

Write an awk command that prints the name and length of each read in `exampleR1.fastq`. Write output to `exampleR1.nl.tsv`

```
awk '{if ($1 ~ /^@.*/) {print $1, "\t", $3}}' exampleR1.fastq > exampleR1.nl.tsv
```

Now alter it so that you make sure to strip off the "`@`" at the beginning of each read, and exclude the "`length=`".

```
awk '{if ($1 ~ /^@.*/) {print substr($1, 2), "\t", substr($3, 8)}}' exampleR1.fastq > exampleR1.nl.tsv
```

join