**********
Note: this process assumes you've got Homer (http://biowhat.ucsd.edu/homer/) installed and Homer's PATH information in your .bashrc
**********

Working from the directory that contains your read file (file.fastq):

```
$ cat file.fastq | perl -e '$i=0;while(<>){if(/^\@/&&$i==0){s/^\@/\>/;print;}elsif($i==1){print;$i=-3}$i++;}' > file.fasta

$ homerTools trim -3 CAGC file.fasta

$ homerTools trim -3 CTGC file.fasta.trimmed

$ awk '0 == NR % 2'  file.fasta.trimmed.trimmed  > barcodes.txt
#removes fasta identifiers and keeps only the barcode seqs

$ sed '/.\{9\}/d' barcodes.txt >barcodes_final.txt
#this drops "barcodes" longer than 8 characters - which are likely artifacts

$ cat barcodes_final.txt |sort |uniq -c > barcode_counts
```