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' , 12), ('AGCTC', 2), ('GCATC', 71), ('CTATT', 23), ('TGCAT', 15), ('GCAGA', 17), ('TACCA', 7), ('TACCC', 6), ('TAGTT', 34), ('GGCCT', 3), ('GGATG', 3), ('CCCGT', 2), ('AGAGG', 1), ('AGGGT', 6), ('CATCT', 19), ('AGAGC', 1), ('GGCGA', 1), ('TAACT', 8), ('AGAGT', 4), ('CCCGG', 1), ('CATCC', 7), ('CCCGA', 2), ('AGGGA', 1), ('CATCG', 2), ('CACGG', 4), ('CACGC', 4), ('CACGA', 4), ('CACGT', 1), ('TNAGA', 4), ('GTGTT', 14), ('TCCGT', 3), ('CTGTA', 60), ('TTCTC', 3), ('CTGTC', 36), ('TTCTA', 1), ('CTCCT', 4), ('GTCAT', 4), ('CTGTG', 64), ('TCCGA', 3), ('TCCGG', 3), ('CTCCA', 6), ('CTCCC', 12), ('CTGTT', 47), ('TTCTT', 2), ('ATCAC', 4), ('TGCTC', 7), ('CTACG', 37), ('TGCTA', 7), ('GAAAT', 38), ('TGCTG', 10), ('CTACC', 11), ('AAACA', 8), ('CTACA', 33), ('GCAAT', 22), ('CCCGG', 2), ('ACACG', 1), ('CTACT', 26), ('AAACT', 9), ('TGCTT', 38), ('CCAC', 4), ('GCAAG', 18), ('GCAAA', 11), ('GCAAC', 6), ('ACACC', 4), ('ACATG', 8), ('TCTTA', 5), ('ATATG', 9), ('CGGG', 9), ('CGAGT', 55), ('CGGGA', 8), ('CAGAT', 49), ('CGGGC', 12), ('GGTTT', 86), ('CGCTA', 15), ('CGCTC', 3), ('TCAT', 17), ('CGCTG', 4), ('CAGAA', 24), ('CGGGT', 41), ('CAGAC', 8), ('TTTCC', 1), ('CGAGC', 5), ('CGAGA', 35), ('TCAAC', 15), ('TCAAA', 20), ('CGCTT', 5), ('TCAAG', 39), ('ATAGG', 43), ('ATAGA', 1), ('TATTT', 23), ('ATAGC', 4), ('GNATC', 1), ('GACCT', 30), ('ATAGT', 6), ('TATTC', 3), ('TATTA', 8), ('TATTG', 5), ('GACCG', 3), ('CGGAC', 2), ('GACCC', 4), ('GNATT', 16), ('GACCA', 6)]
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There were 234072 number of good reads out of 250000 total reads
* Good reads = 80.0 percent of nucleotides in a read had a phred score > 50
15928 were bad reads and would be dropped
^[[0;ib50l_stud12@compute-0-19:~/shell$g^[[01;31m^B09:25:30 ^[[01;32m^Bib501_stud12 ^[[02;36m^Bcompute-0-19 ^[[01;34m^B/
home/a-m/ib50l_stud12/shell ^[[00;33m^B^[[00m
```

```
$ exit
exit
```

Script done on Sun Sep 25 09:25:38 2016