1. Both the sequence letter and quality score are each encoded with a single ASCII character for brevity.

A FASTQ file normally uses four lines per sequence.

- Line 1 begins with a '@' character and is followed by a sequence identifier and an *optional* description (like a [FASTA](#) title line).
- Line 2 is the raw sequence letters.
- Line 3 begins with a '+' character and is *optionally* followed by the same sequence identifier (and any description) again.
- Line 4 encodes the quality values for the sequence in Line 2, and must contain the same number of symbols as letters in the sequence.

The byte representing quality runs from 0x21 (lowest quality; '!' in ASCII) to 0x7e (highest quality; '~' in ASCII). Here are the quality value characters in left-to-right increasing order of quality (ASCII):

```
!"#$%&'()*+,-
./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[\]^_`abcdefghijklmnopqrstuvw
xyz{|}~
```

The higher the quality value the higher the probability that the base is correct

2. **28+32=60; <**
3. The first 0x1f represent control codes, 0x20 is a space " ". And from 0x21 we have ! etc. (printable characters) with the last one ~ 0x7e

i. Sanger Phred+33 , raw reads typically (0, 40)

ii. Solexa Solexa+64, raw reads typically (-5, 40)

iii. Illumina 1.3+ Phred+64, raw reads typically (0, 40)
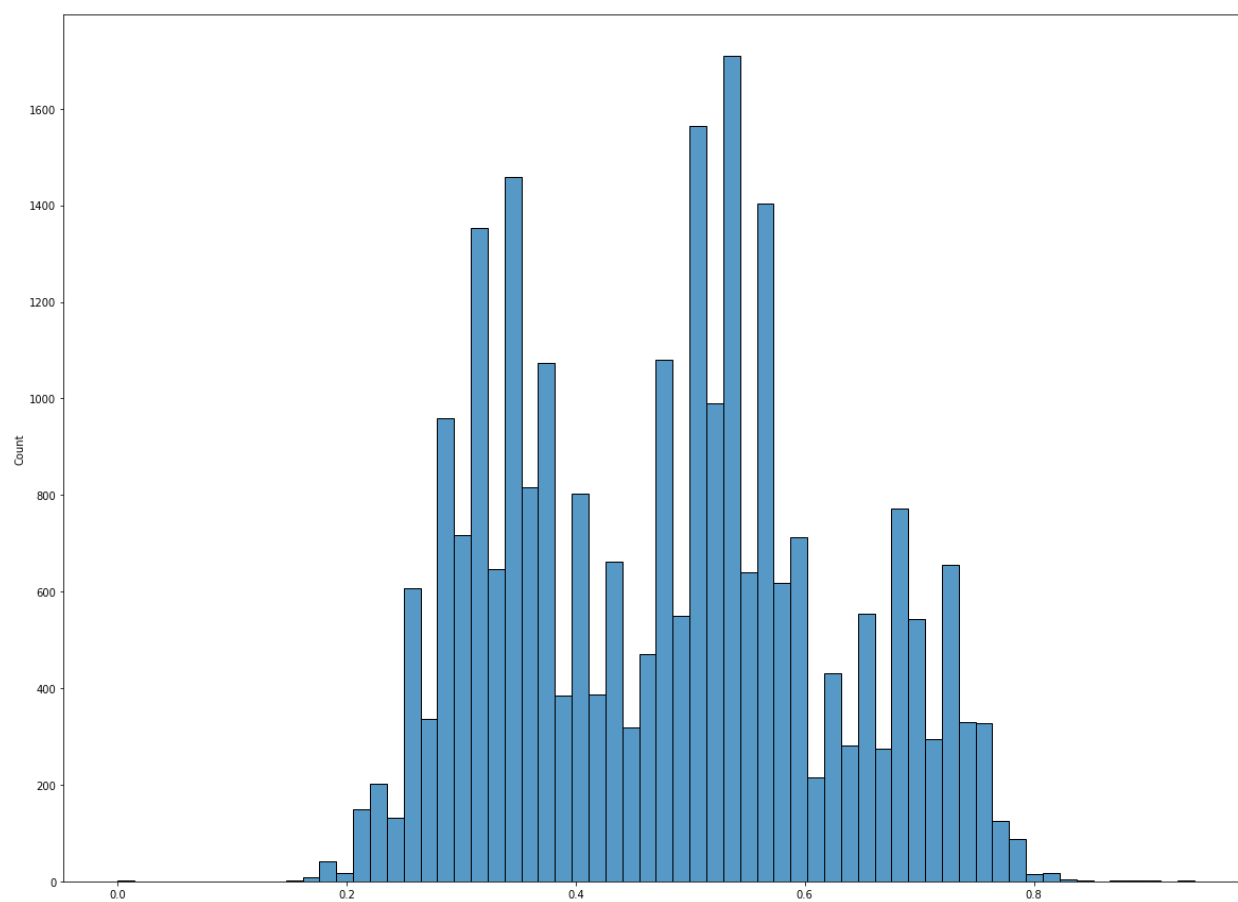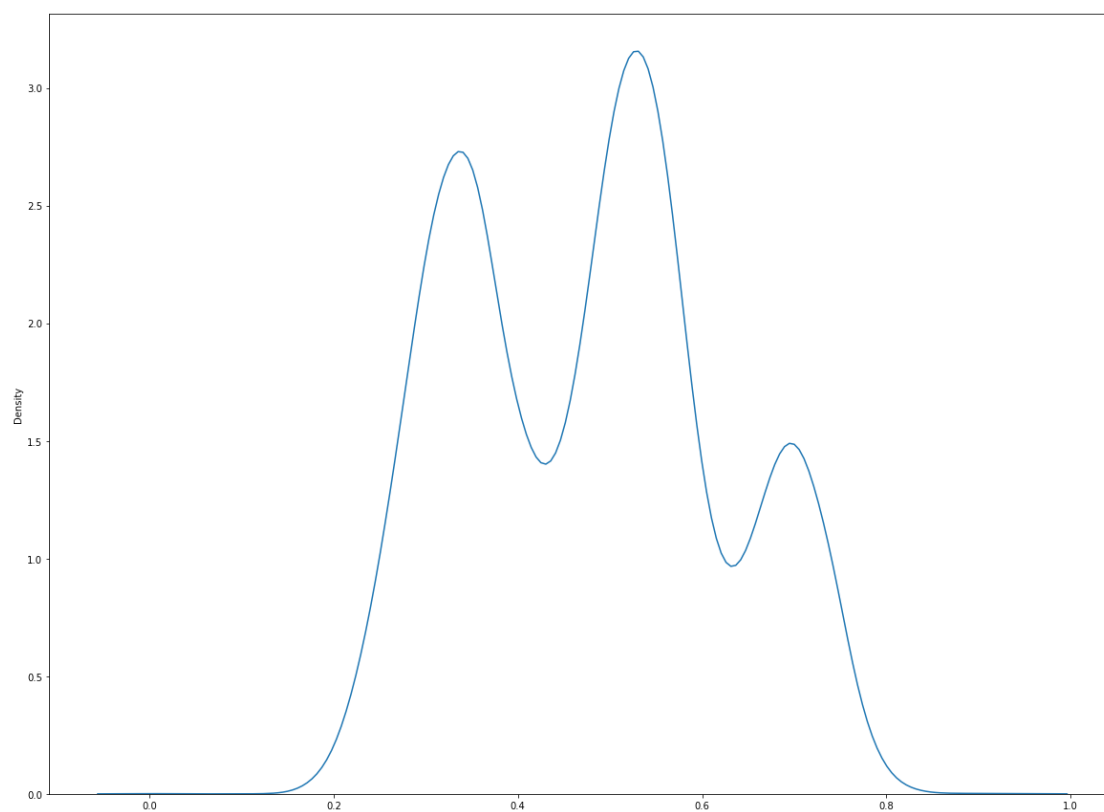
iv. Illumina 1.5+ Phred+64, raw reads typically (3, 41)

v. Illumina 1.8+ Phred+33, raw reads typically (0, 41)

4. A)The script shows that the quality codes range is [35, 73] or [#, I]

```
ranges = {
    'Sanger': (33, 73),
    'Illumina-1.8': (33, 74),
    'Solexa': (59, 104),
    'Illumina-1.3': (64, 104),
    'Illumina-1.5': (66, 105)
}
```
This means that it is either Sanger Phred+33 or Illumina-1.8+

4.B)**3**

Read ID	Microorganism Type
22457	Staphylococcus aureus strain PMB179-1 chromosome, complete genome
19791	Staphylococcus aureus strain K25C chromosome
4975	Staphylococcus aureus strain pt217 chromosome, complete genome
17423	Staphylococcus aureus TPS3156 DNA, complete genome
3695	Staphylococcus aureus strain B9-22D chromosome, complete genome
1024	Escherichia coli O152:H23 strain Res13-Lact-ER01-35 chromosome, complete genome
6157	Escherichia coli strain SCU-118 chromosome, complete genome
11980	Escherichia coli O112ab:H8 strain Res13-Lact-EA06-22 chromosome, complete genome
17638	Escherichia coli O152:H23 strain Res13-Lact-ER01-35 chromosome, complete genome
11403	Escherichia coli strain 18TN10VL01-EC chromosome, complete genome
22515	Thermus thermophilus HC11 DNA, complete genome
14898	Thermus thermophilus isolate TTHNAR1 genome assembly, chromosome: 1
8712	Thermus thermophilus HB8 genomic DNA, complete genome
21066	Thermus thermophilus HC11 DNA, complete genome
22696	Thermus thermophilus HC11 DNA, complete genome

Staphylococcus aureus

Escherichia coli

Thermus thermophilus