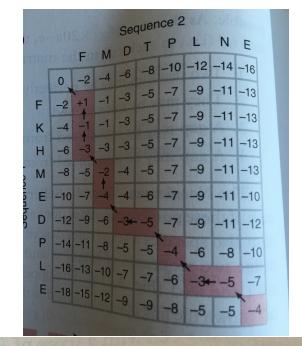
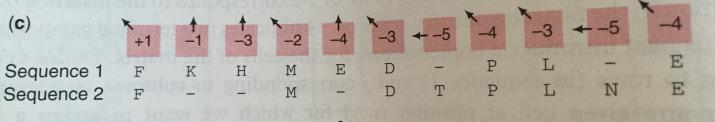
# FASTQ AND ILLUMINA 23 SEPT 15

# **ANNOUNCEMENTS**

# ALIGNMENT FLASHBACK

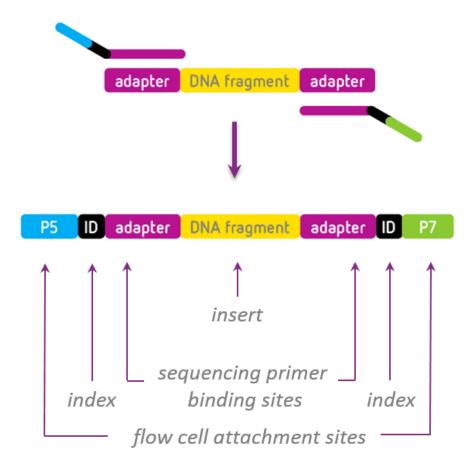




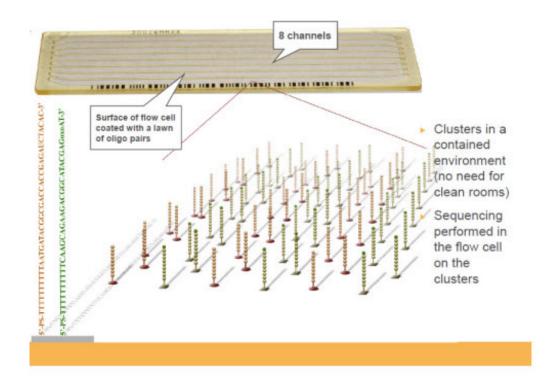
# fastQ -> Illumina Seq

https://youtu.be/womKfikWlxM

#### Illumina Seq



# **Illumina Seq**



# **Illumina Seq**

@HSQ-7001360:67:H88RHADXX:1:1101:1448:2158 1:N:0:CAGATO

- 1101=tile number
- 1448= x coordinate
- 2158= y coordinate

#### fastq Quality Scores

+

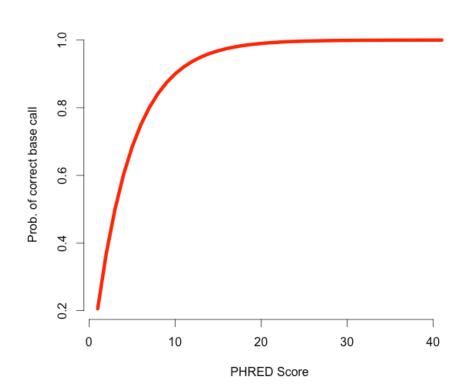
@HSQ-7001360:67:H88RHADXX:1:1101:1448:2158 1:N:0:CAGATC ATCTATCTGAGACTGATACGCCTTCGGCTTAATTTATACAAG

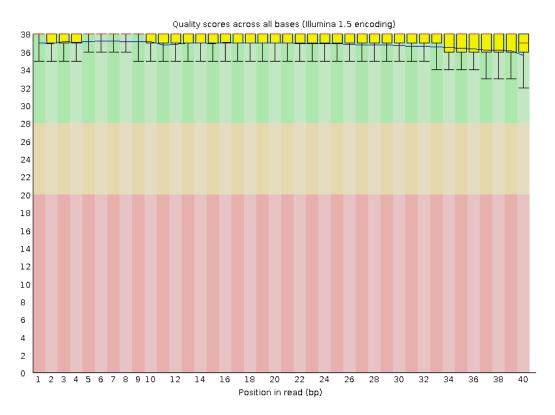
#### Quality Scores https://en.wikipedia.org/wiki/FASTQ\_format

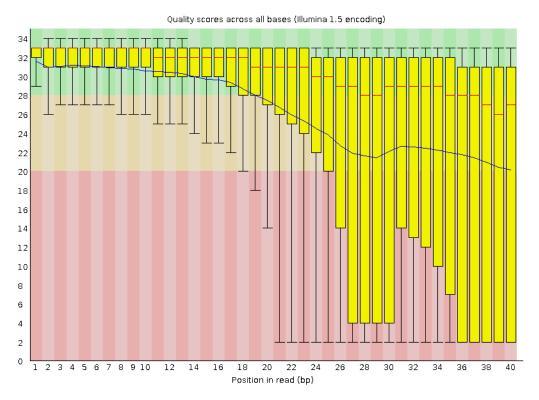
```
LIBERTADE BELLEBERT B
!"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[\]^ `abcdefghijklmnopqrstuvwxyz{|}~
33
                                     104
                                                 126
3.....40
0.2.....41
S - Sanger
     Phred+33, raw reads typically (0, 40)
X - Solexa
        Solexa+64, raw reads typically (-5, 40)
I - Illumina 1.3+ Phred+64, raw reads typically (0, 40)
J - Illumina 1.5+ Phred+64, raw reads typically (3, 40)
  with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)
  (Note: See discussion above).
L - Illumina 1.8+ Phred+33, raw reads typically (0, 41)
```

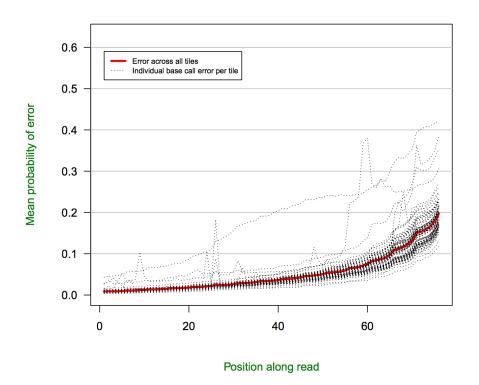
```
L - Illumina 1.8+ Phred+33, raw reads typically (0, 41)
```

$$p_{correct} = 1 - [10^{-\left(\frac{Q}{10}\right)}]$$
 Q=Phred score









What should we do about this?

