# eDentity Sequencer Qc

## 01/11/24

### 1.1.1 Percantage of bases >= Q30

Metric: Calculate the fraction of bases whose Phred score are greater or equal to Q30.

| Illumina | Elements |
|---|---|
| 0.92 | 0.93 |

### 1.1.2 Read Length Retension after Q30 Trimming (Percentage).

Metric: (Average length after trimming / original read length ) * 100

| Illumina | Elements |
|---|---|
| 94.67 | 94.46 |

### 1.2.1 Hommopolymer Accuracy

Metric: Average Q score decay per additional base in homopolymer runs (e.g AAAA, TTTT)

| Illumina | Elements |
|---|---|
| 0.05 | -0.01 |

### 1.2.2 Demultiplexing Efficiency (Percentage)

Metric: (Number of reads successfully demultiplexed / Total number of reads)* 100

N/B: The data from Elements was missing unsuccessfully demultiplexed reads thus we could not calculate its demultiplexing efficiency

|  | **Illumina** | **Element** |
|---|---|---|
| Total Reads | 885,110,280 | |
| Demultiplexed Reads | 608,699,786 | 361,464,384 (?) |
| Demultiplexing Efficiency | 68.77 | NA |

### 1.2.3 PhiX Control performance

Metric: Assess sequencing quality using spiked-in Phix control

|  | Illumina | Element |
|---|---|---|
| PhiX Error Rate | 0.005588 | 0.022586 |
| PhiX Alignment Rate | 0.2520 | 0.0000 |
| **PhiX Coverage Uniformity:** | | |
| - Coefficient of Variation: | 0.1554 | 0.4593 |
| - Percentage within ±20% of mean coverage: | 0.9332 | 0.4330 |
| **Additional Information:** | | |
| - Total Reads: | 885,110,280 | 361,464,384 |
| - Mapped Reads: | 223,075,671 | 482 |
| - Mean Coverage: | 12,410,202.48 | 26.73 |
| - Coverage Range: | 12,54,247 - 14,897,715 | 1 - 70 |

### 1.2.4 Duplicate Read Rate (Percentage)

Metrics: Percentage of duplicate reads in a standard non-amplified library.

Only reads mapping to Phix were used here under the assumption that Phix is a "standard non-amplified library"

but it appears Phix reads from Illumina were amplified therefore they may not be a good measure of duplication rate.

|  | Illumina | Element |
|---|---|---|
| Mapped Reads: | 223,075,671 | 482 |
| Duplicate reads: | 219,577,678 | 27 |
| Duplicate rate | 0.9843 | 0.0560 |

### 1.2.5 GC Bias

Metric: Deviation of coverage in GC-rich regions compared to AT-rich regions

Only reads mapping to Phix were used to compute GC Bias

| Illumina | Elements |
|---|---|
| 3074930 | 6.24 |