eDentity Sequencer Qc

05/11/24

1.1.1 Percentage 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) \times 100

Illumina	Elements
94.67	94.46

1.2.1 Hommopolymer Accuracy

Homopolymer sequence: A series of consecutive identical bases— in this case four or more consecutive repeats of the same base.

Metric: Average Q score decay per additional base in homopolymer runs (e.g AAAA, TTTT) compared to the Phix reference genome.

Illumina	Elements
0.05	-0.01

1.2.2 Demultiplexing Efficiency (Percentage)

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

	Illumina	Element
Total Reads (without Phix reads) Demultiplexed Reads Demultiplexing Efficiency	662,034,609 608,699,786 91.94	361,464,384 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 $\pm 20\%$ 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:	1,254,247 - 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: Duplicate rate	219,577,678 0.9843	$\frac{27}{0.0560}$

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
0.32	0.3