eDentity Sequencer Qc

08/11/24

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

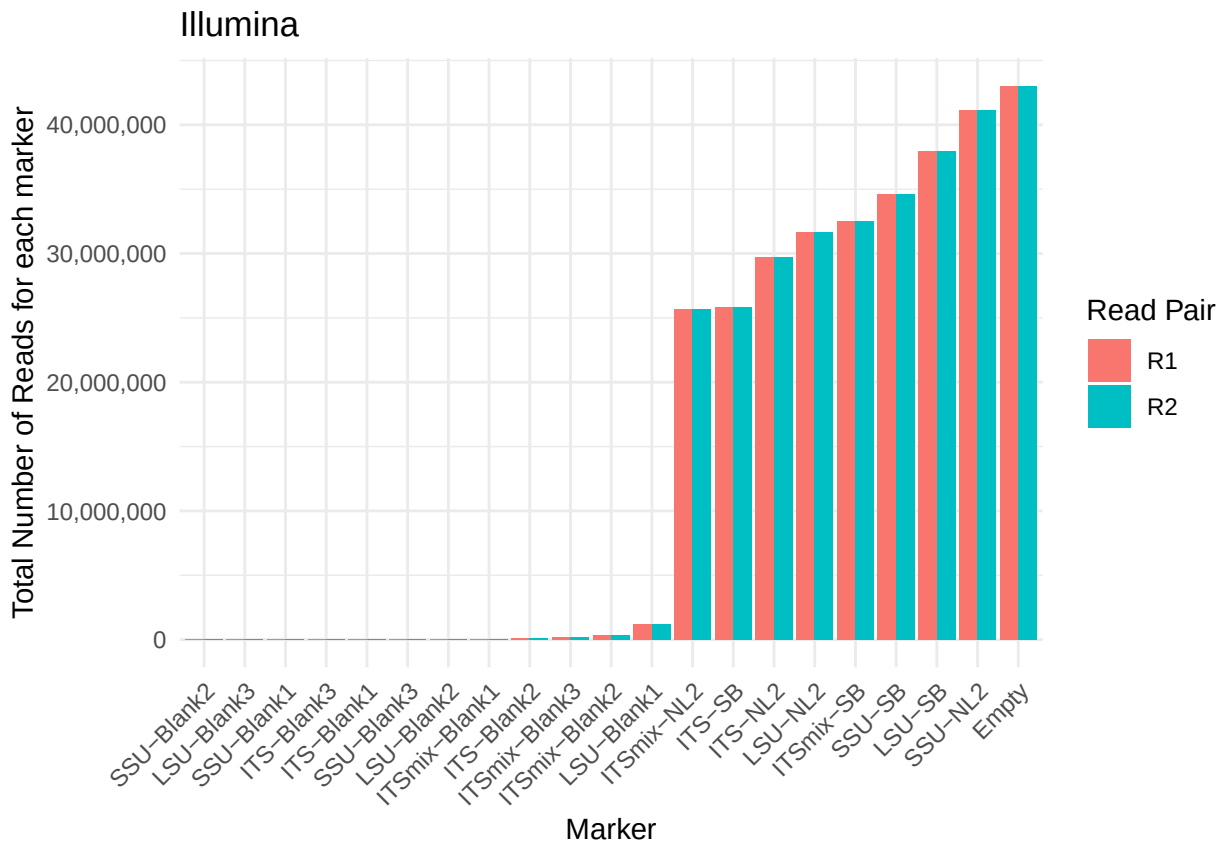
1.1.2 Read Length Retension after Q30 Trimming (Percentage).

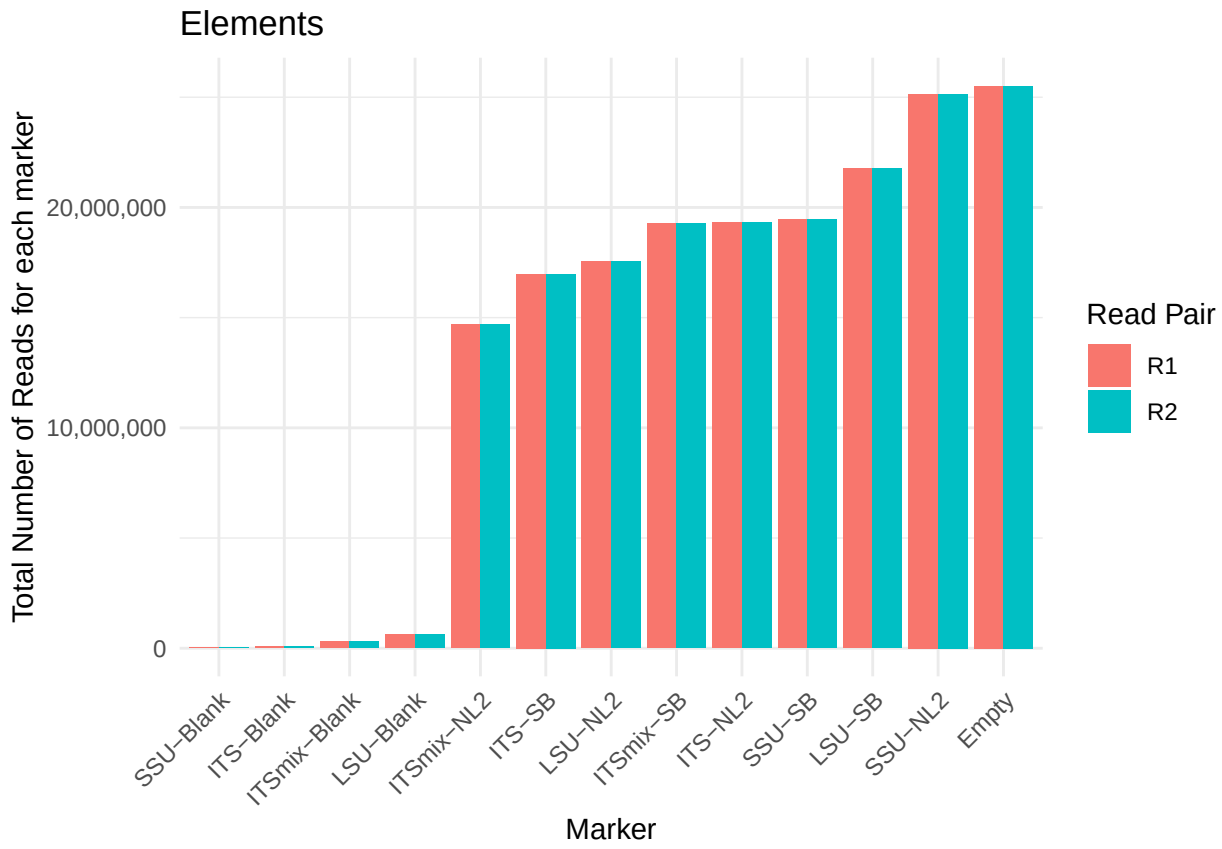
Metric: (Average length after trimming / original read length) × 100

Illumina	Elements
94.67	94.47

Total Number of reads per marker.

This section looks at the total number of reads per marker





Filter out the Empty, Phix and undetermined reads.

Next we exclude the empty , unassigned as well as sample with “Blank” markers.

Then we look at the average number of reads per marker

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) × 100

	Illumina	**Element**
Total Reads (without Phix reads)	662,034,609	376,486,325
Demultiplexed Reads	608,699,786	361,464,384
Demultiplexing Efficiency	91.94	96.01

1.2.3 PhiX Control performance

Metric: Assess sequencing quality using spiked-in Phix control

	Illumina	**Element**
PhiX Error Rate	0.005588	0.007656
PhiX Alignment Rate	0.2520	0.2760
PhiX Coverage Uniformity:		
- Coefficient of Variation:	0.1554	0.1631
- Percentage within ±20% of mean coverage:	0.9332	0.9081
Additional Information:		
- Total Reads:	885,110,280	520,004,986
- Mapped Reads:	223,075,671	143,518,661
- Mean Coverage:	12,410,202.48	7,927,615.76
- Coverage Range:	1,254,247 - 14,897,715	942836 - 9820668

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 were amplified therefore they may not be a good measure of duplication rate.

	Illumina	**Element**
Mapped Reads:	223,075,671	143,518,661
Duplicate reads:	219,577,678	138,553,627
Duplicate rate	0.9843	0.9654

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