eDentity Sequencer Qc

13/11/24

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.

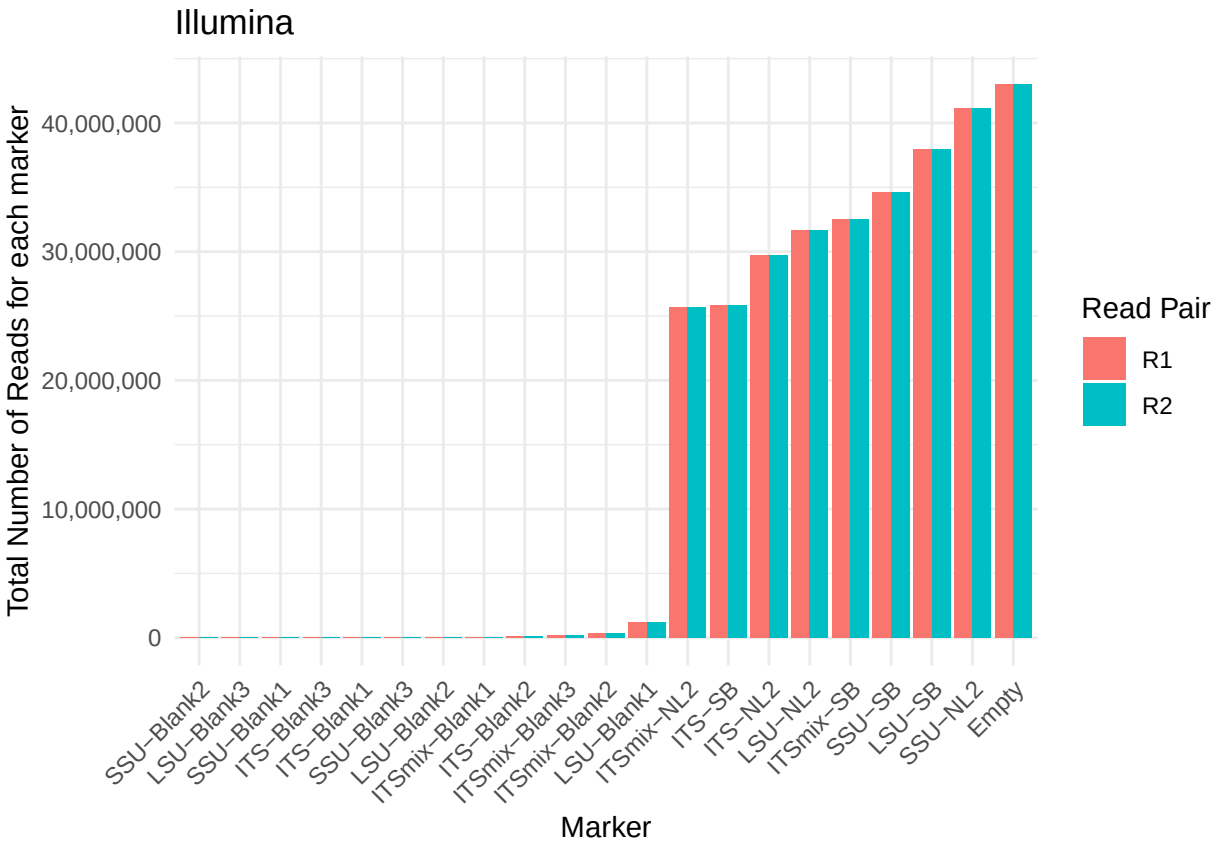
This section looks at the total number of reads as received from the sequencer.

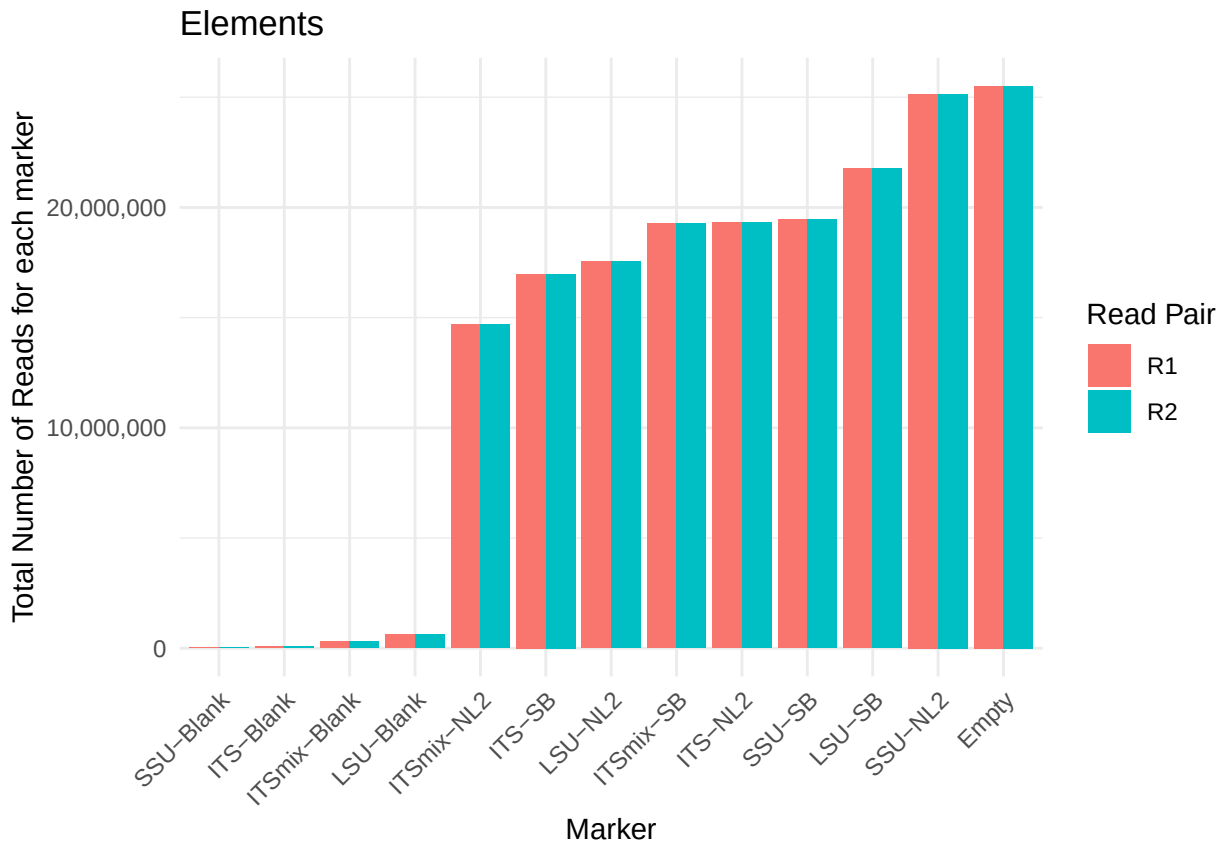
N/B: Illumina used a flow cell with a higher yield capacity (240 GB) compared to the yield capacity used by Elements (160 GB).

Therefore a more comparable number is the `scaled_proportion`, which is computed by scaling the total number of reads by the yield capacity.

total_reads	total_files	average_reads	yield_capacity	scaled_proportion	sequencer
885,110,280	3,074	287,934.4	240	0.53	Illumina
520,004,986	3,082	168,723.2	160	0.47	Elements

Total number of reads per marker





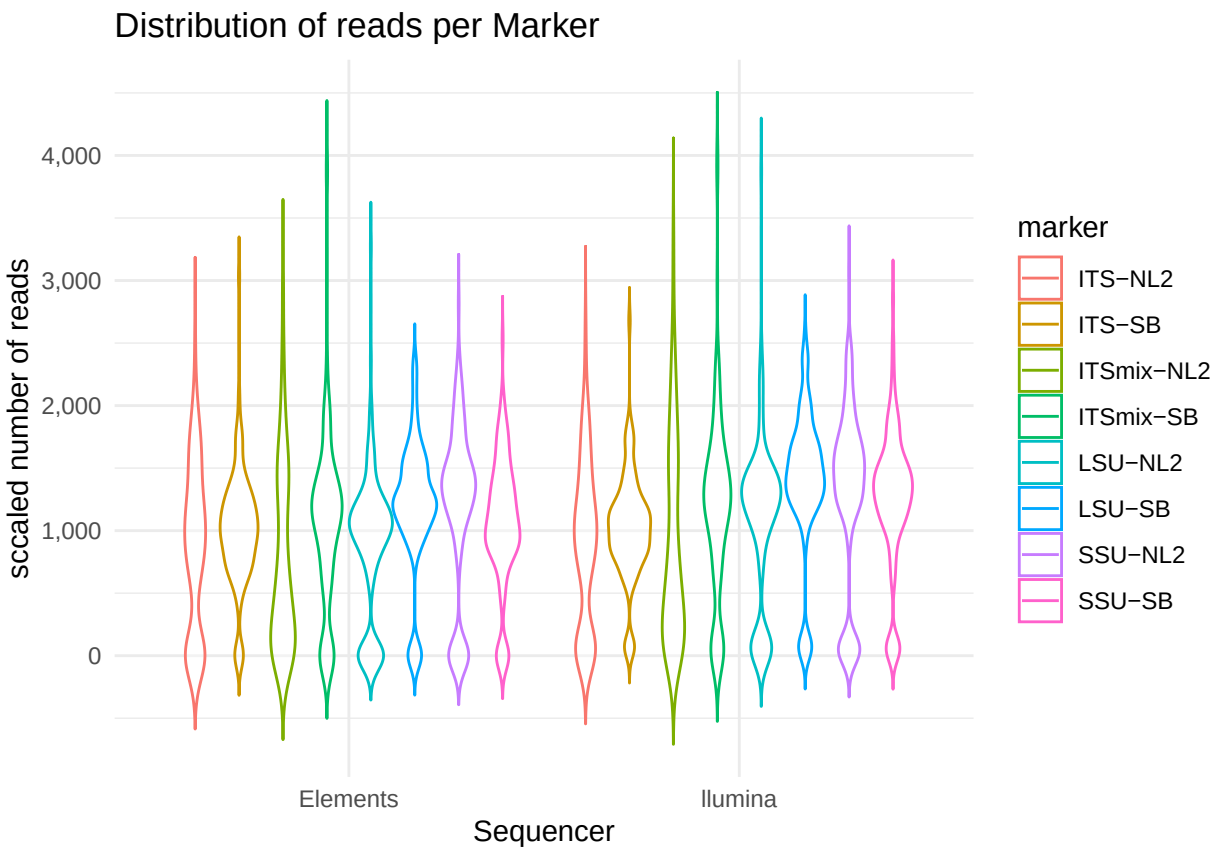
Filter out the Empty, Phix and undetermined reads.

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

Then we look at the number of reads after filtering.

total_reads	total_files	average_reads	yield_capacity	scaled_proportion
518,441,730	1,916	270,585.5	240	0.53
308,357,648	1,916	160,938.2	160	0.47

What is the distribution of reads per marker after filtering?



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	942,836 - 9,820,668

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