Ubiquitous Genomics: Hackathon2

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Problem 1

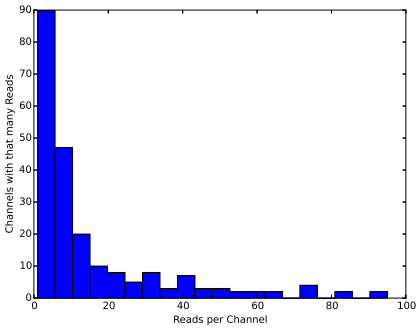
Number of 1D and 2D reads classified as failed: 265
Number of 1D and 2D reads classified as passed: 1082
Number of 2D reads classified as failed: 258
Number of 2D reads classified as passed: 1082
Fraction of 2D reads in failed folder: 0.97358490566
Fraction of 2D reads in passed folder: 1.0

Problem 2

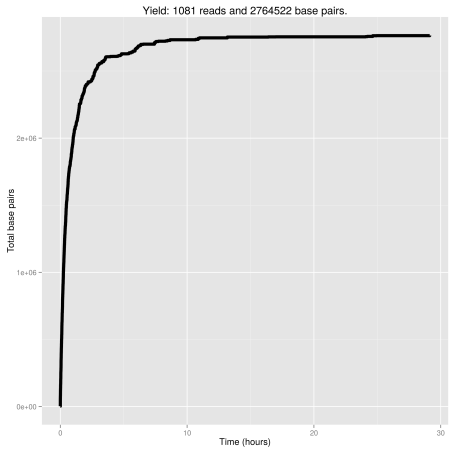
2 channels had at least one read, and 1 had at least five. This compares with 434 "active" channels during initialization, and 651 immediately after loading fuel

The average channel had 1262.0 reads. Channel 29 had 2520 reads, which was the most.

Just for fun, here's a histogram of reads per channel



Problem 3



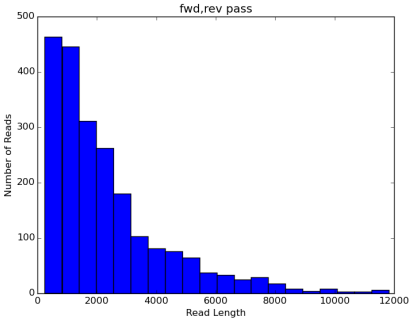
Passed Reads

Failed Reads

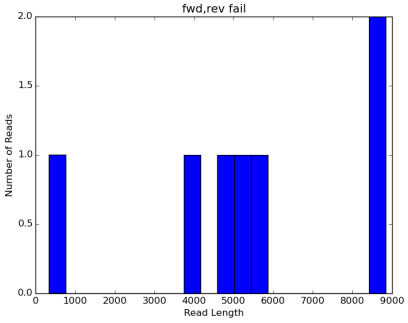
Problem 4

1D reads

The following histograms show the length distribution of 1D reads (both template and complement) for passes and fails.



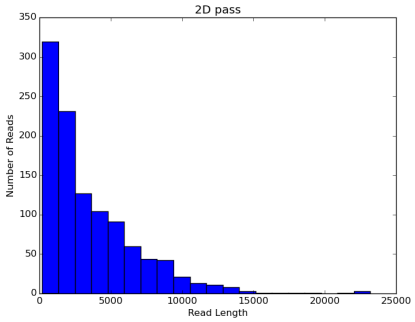
Passed Reads



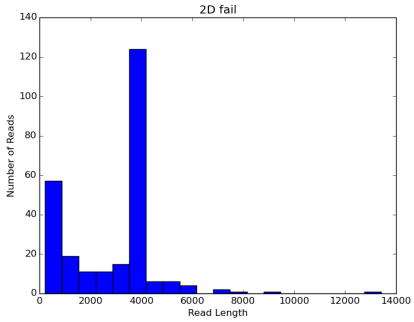
Failed Reads

2D reads

The following histograms show the length distribution of 2D reads for passes and fails.



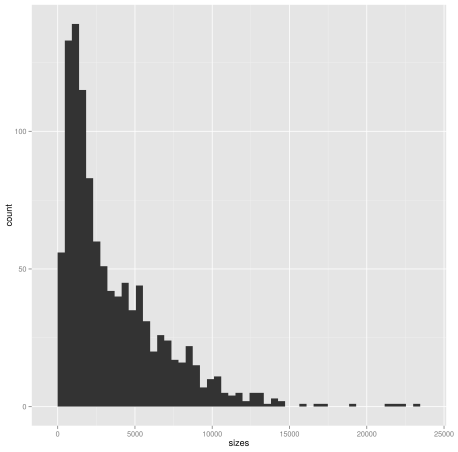
Passed Reads



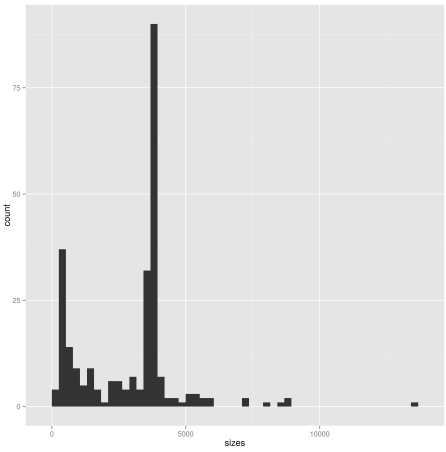
Failed Reads

1D and 2D reads

The following histogramss show the cumulative length distribution of both 1D and 2D reads for passes and fails.



Passed Reads



Failed Reads

Problem 5

LONGEST TEMPLATE READ
From file: .
Number of nucleotides: 5

LONGEST COMPLEMENT READ
From file: .
Number of nucleotides: 5

LONGEST 2D READ
From file: MINION02_Hackathon2_group4_TeamAWESOME_4029_1_ch9_file8_strand.fast5
Number of nucleotides: 23196