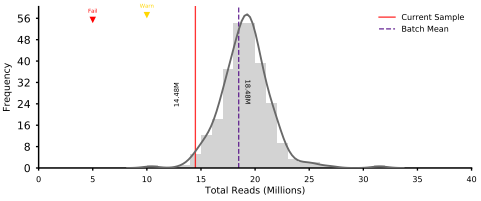
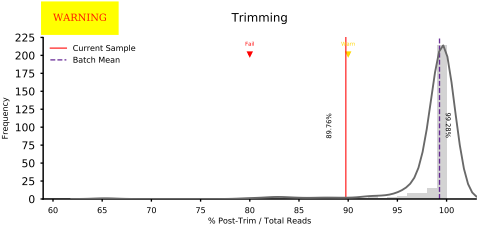
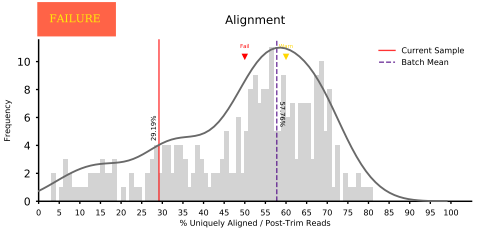
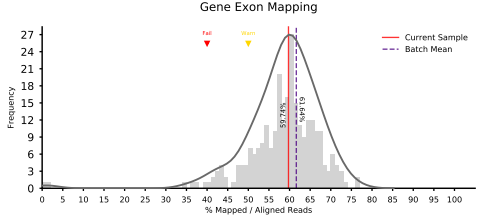
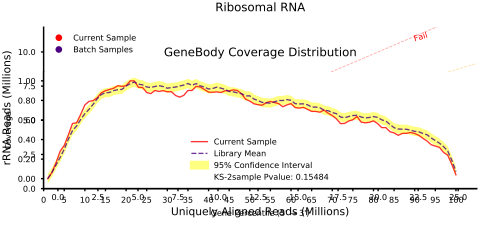
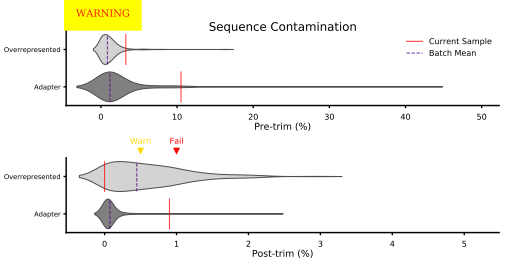

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
14.48M
18.93M
Total Reads (Millions)


WARNING
Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
89.76%
99.36%
% Post-Trim / Total Reads

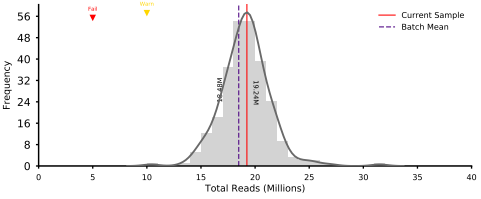

FAILURE
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
29.19%
56.47%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
59.74%
61.44%
% Mapped / Aligned Reads

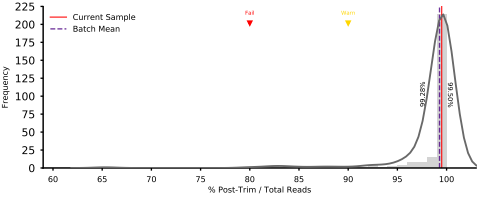

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.15484
Uniquely Aligned Reads (Millions)


WARNING
Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

Sequencing Depth

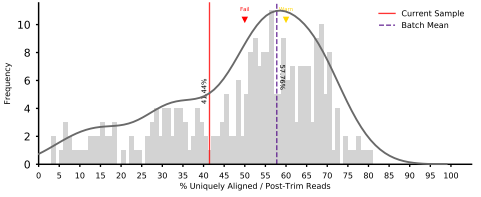


Trimming

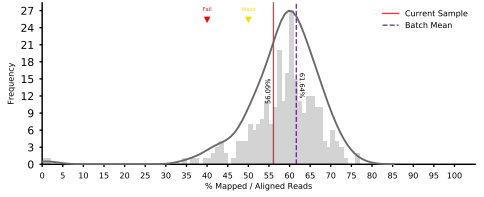


FAILURE

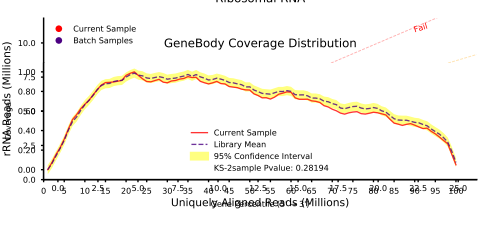
Alignment



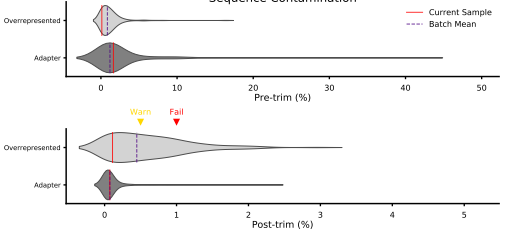
Gene Exon Mapping



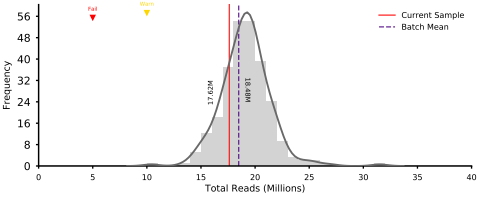
Ribosomal RNA



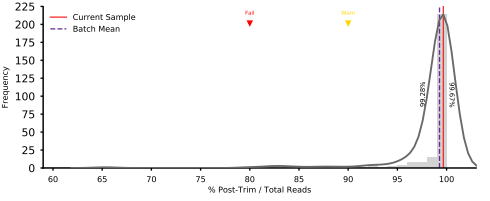
Sequence Contamination



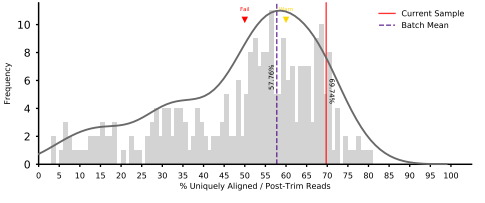
Sequencing Depth



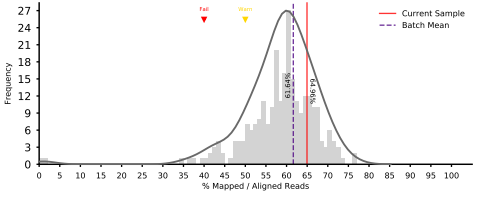
Trimming



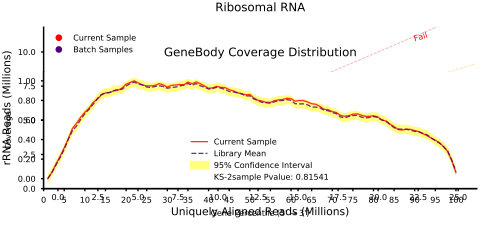
Alignment



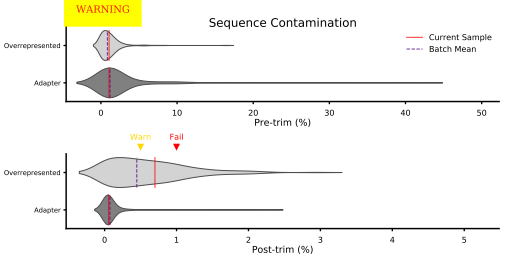
Gene Exon Mapping



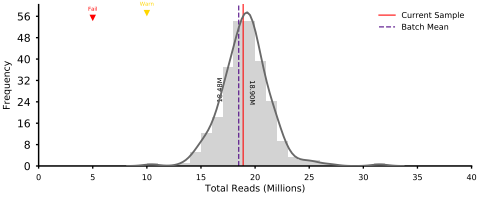
Ribosomal RNA



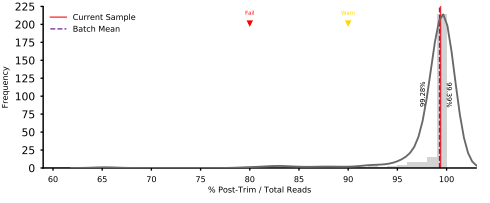
Sequence Contamination



Sequencing Depth

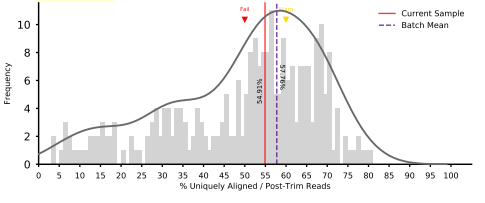


Trimming

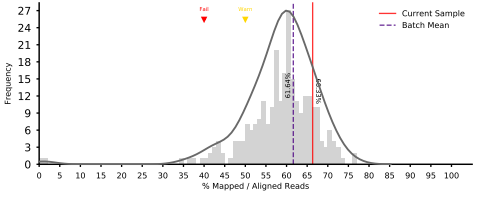


WARNING

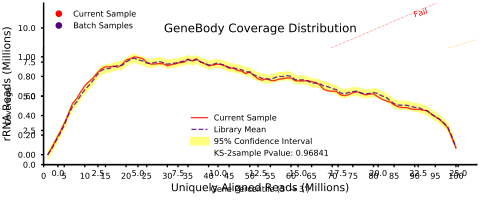
Alignment



Gene Exon Mapping

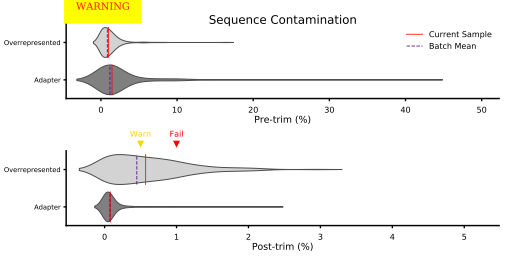


Ribosomal RNA

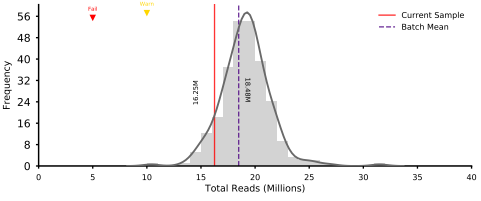


WARNING

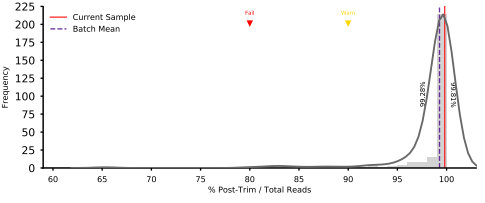
Sequence Contamination



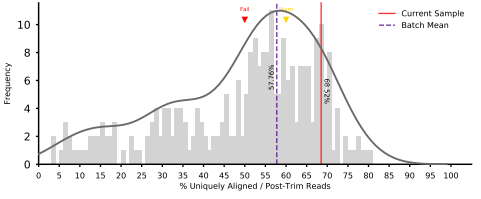
Sequencing Depth



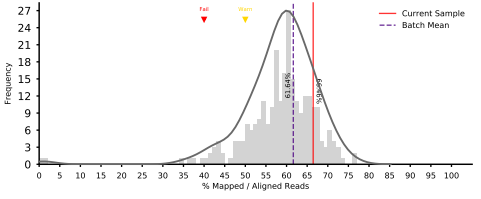
Trimming



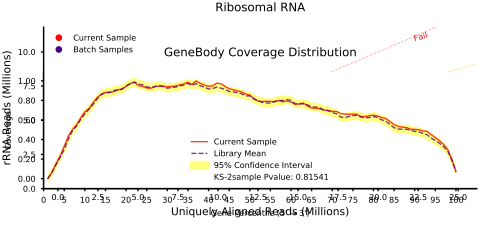
Alignment



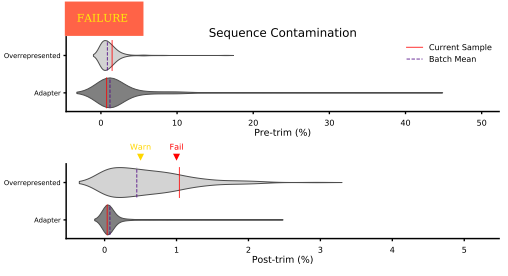
Gene Exon Mapping



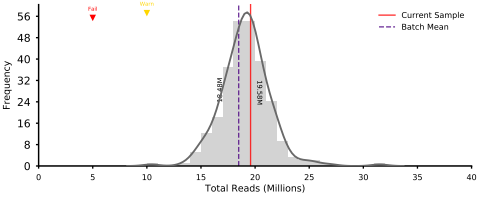
Ribosomal RNA



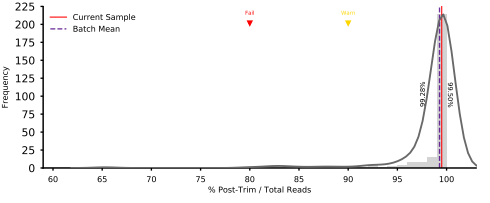
Sequence Contamination



Sequencing Depth

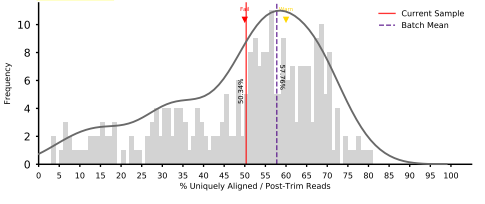


Trimming

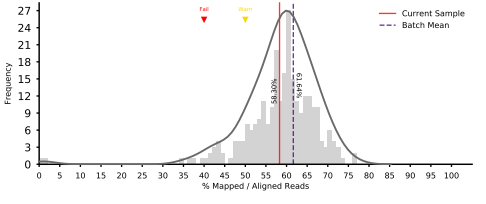


WARNING

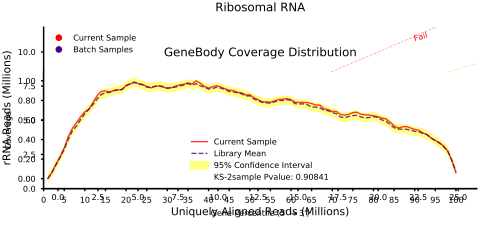
Alignment



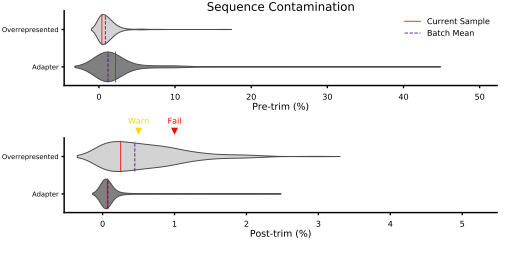
Gene Exon Mapping



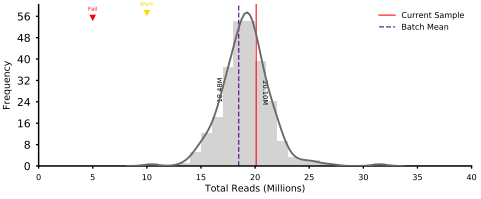
Ribosomal RNA



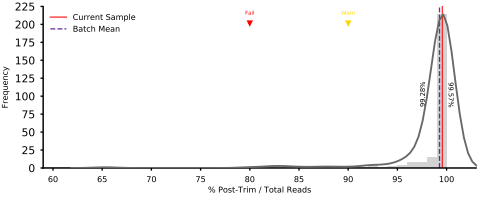
Sequence Contamination



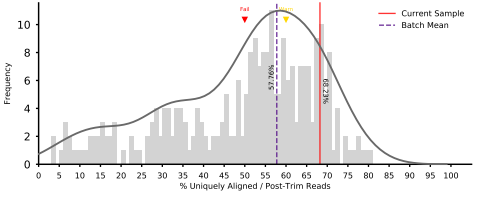
Sequencing Depth



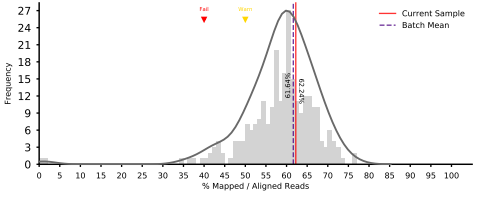
Trimming



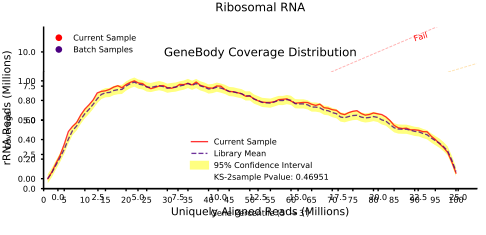
Alignment



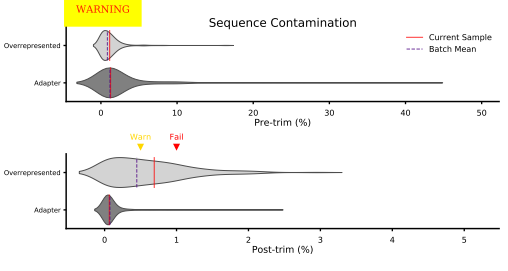
Gene Exon Mapping



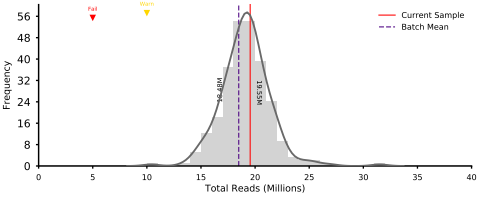
Ribosomal RNA



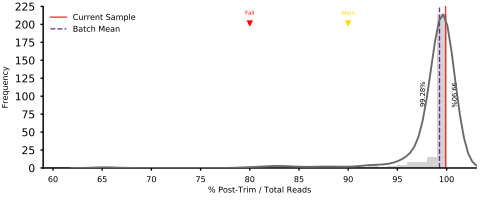
Sequence Contamination



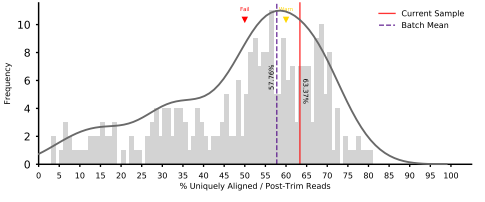
Sequencing Depth



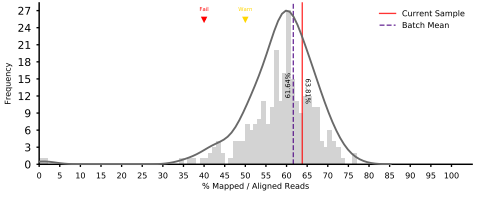
Trimming



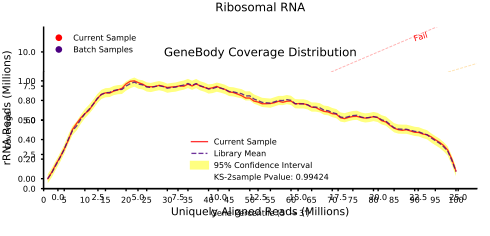
Alignment



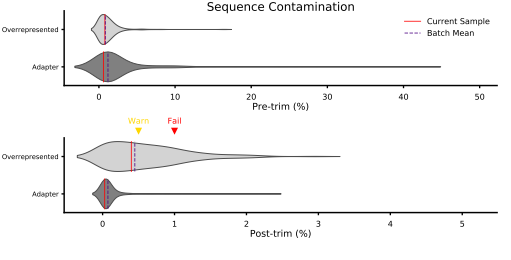
Gene Exon Mapping

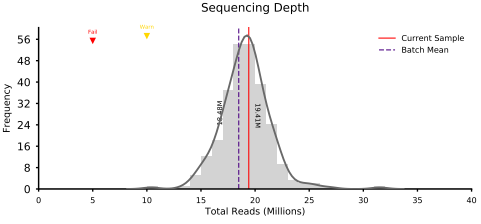


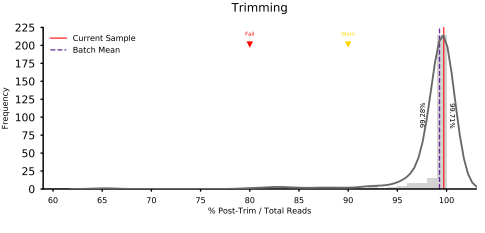
Ribosomal RNA

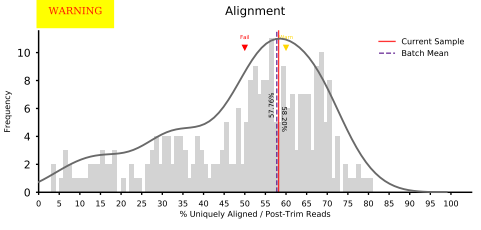


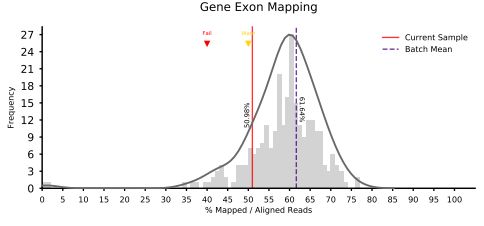
Sequence Contamination

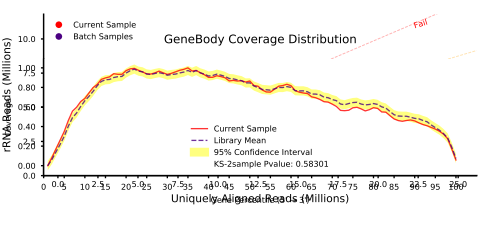


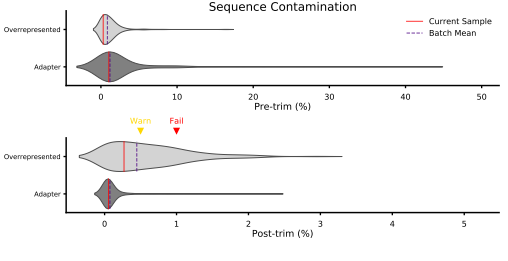

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
Total Reads (Millions)
16.68M
19.41M


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
% Post-Trim / Total Reads
99.28%
99.71%

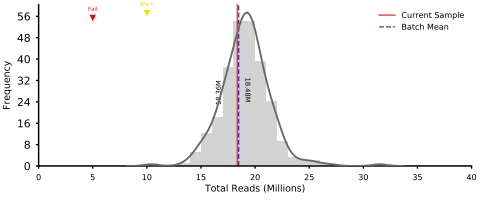

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
% Uniquely Aligned / Post-Trim Reads
57.76%
58.23%


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
% Mapped / Aligned Reads
50.98%
61.54%

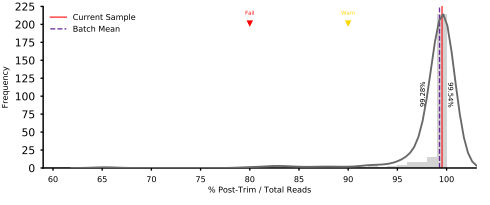

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.58301
Uniquely Aligned Reads (Millions)


Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Post-trim (%)

Sequencing Depth

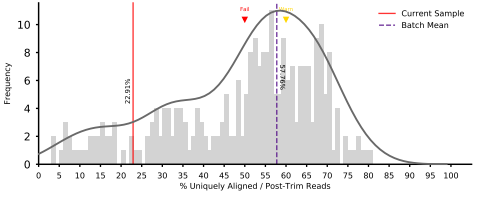


Trimming



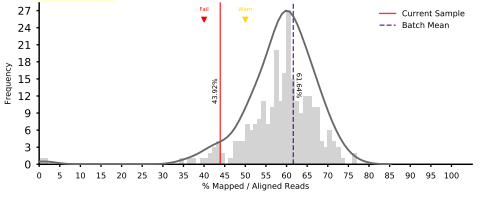
FAILURE

Alignment

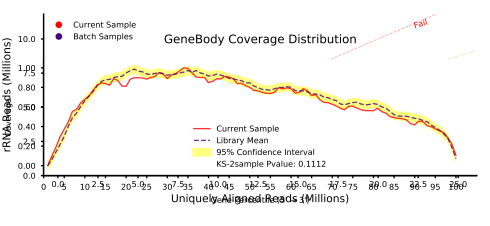


WARNING

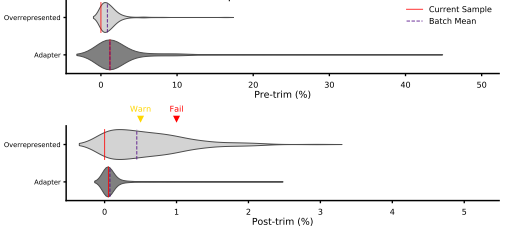
Gene Exon Mapping

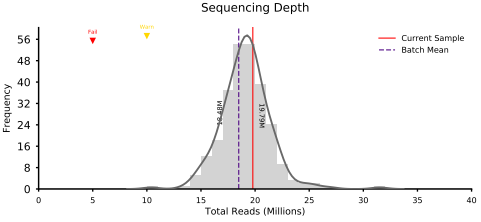


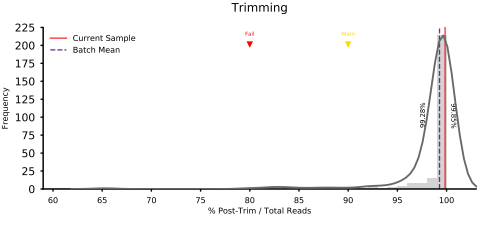
Ribosomal RNA

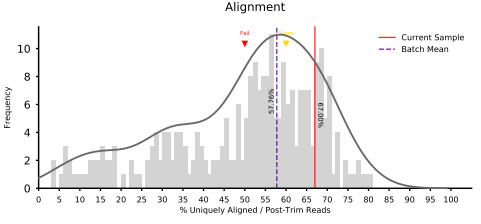


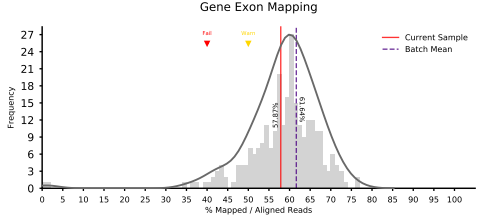
Sequence Contamination

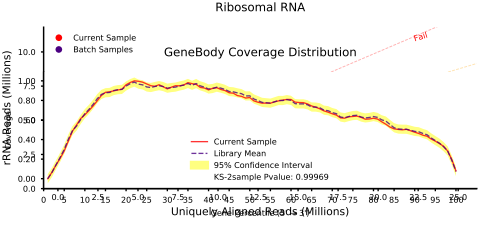


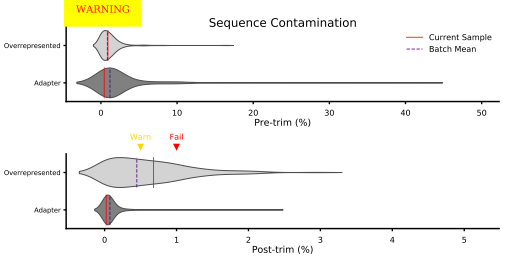

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
%6.68M
%6.61
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
%97.89
%98.66
% Post-Trim / Total Reads

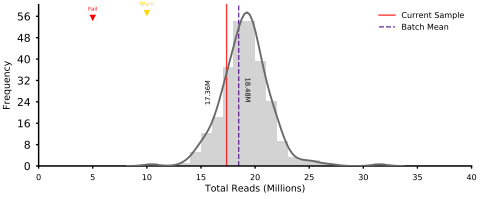

Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
%57.76
%67.49
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
%57.87
%61.44
% Mapped / Aligned Reads

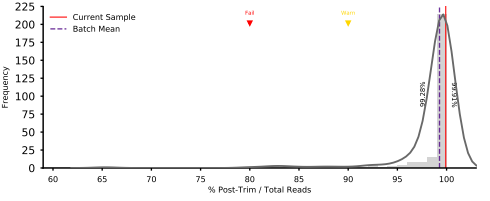

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.99969
Uniquely Aligned Reads (Millions)


WARNING
Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

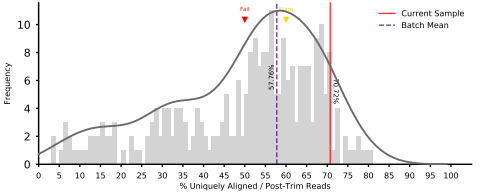
Sequencing Depth



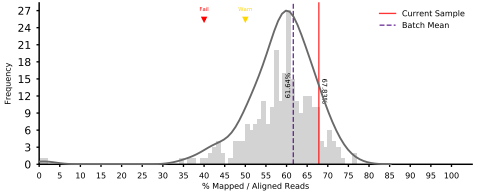
Trimming



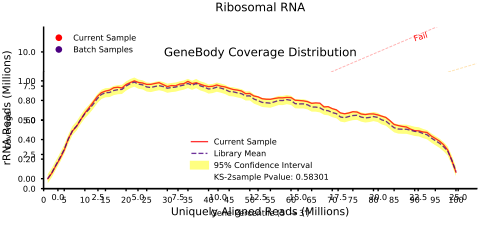
Alignment



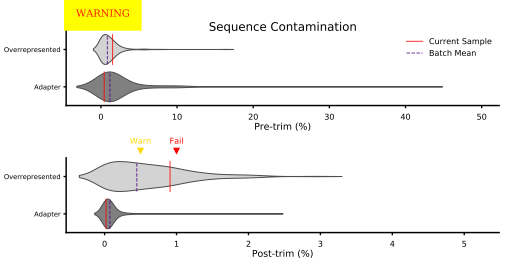
Gene Exon Mapping

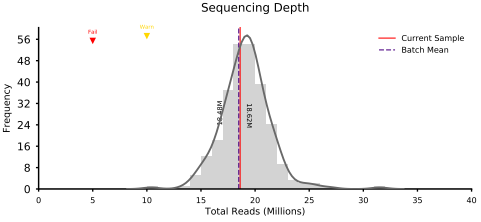


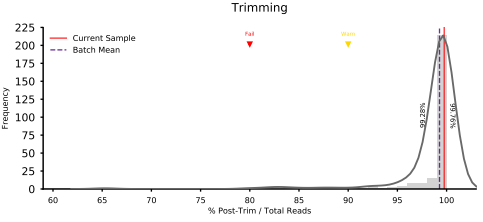
Ribosomal RNA

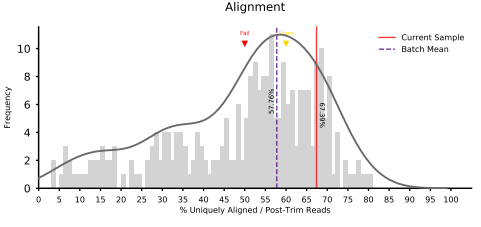


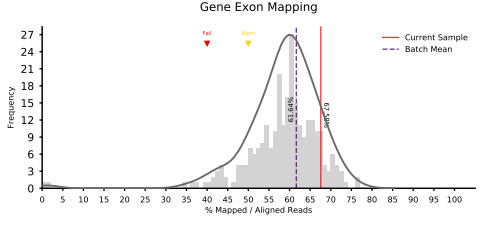
Sequence Contamination

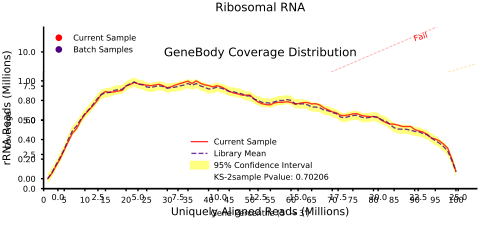


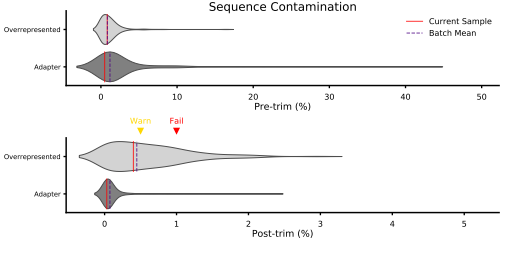

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
18.63M
16.48M
Frequency
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
99.28%
99.76%
Frequency
% Post-Trim / Total Reads

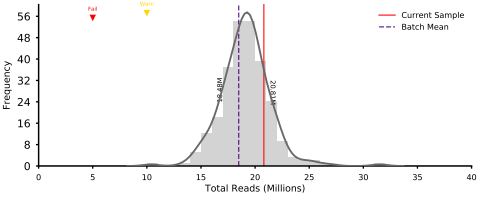

Alignment
Fail
Warn
Current Sample
Batch Mean
57.76%
68.39%
Frequency
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
61.64%
67.39%
Frequency
% Mapped / Aligned Reads

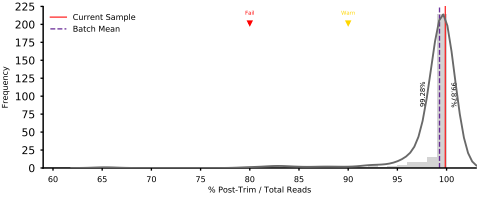

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.70206
Uniquely Aligned Reads (Millions)


Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

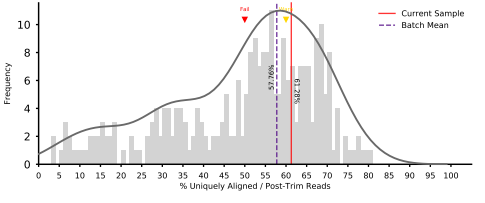
Sequencing Depth



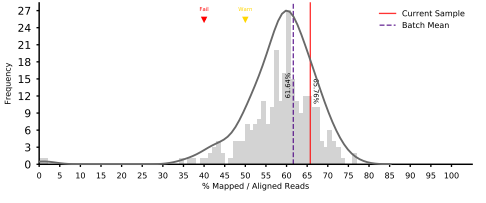
Trimming



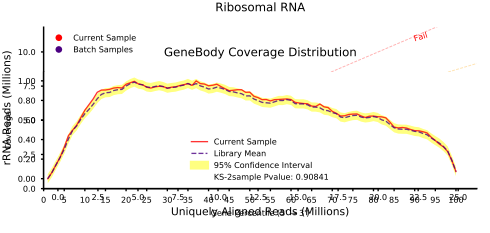
Alignment



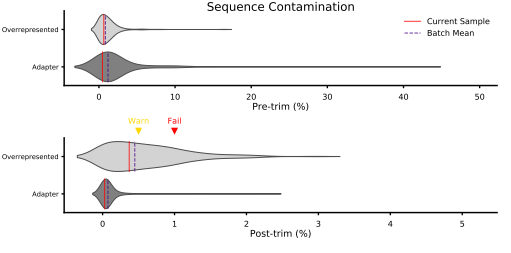
Gene Exon Mapping

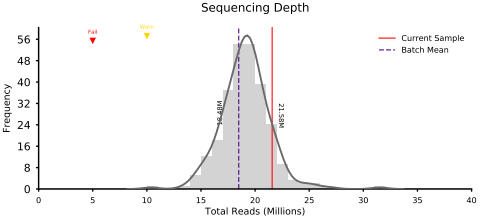


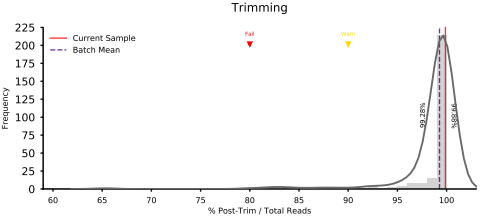
Ribosomal RNA

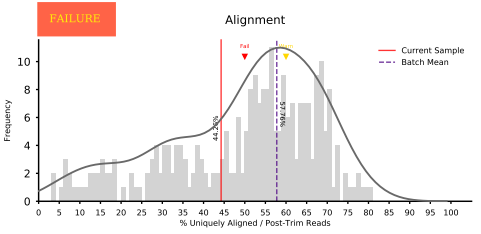


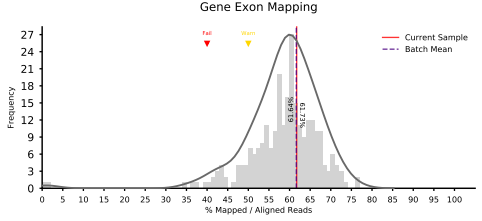
Sequence Contamination

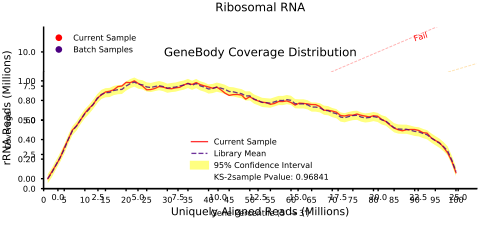


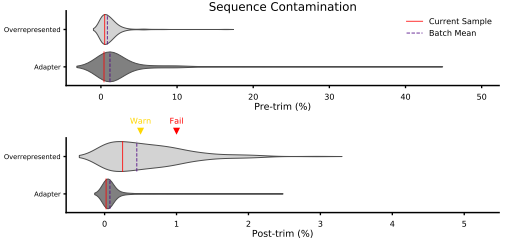

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
18.48M
21.58M
Frequency
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
99.28%
99.88%
Frequency
% Post-Trim / Total Reads

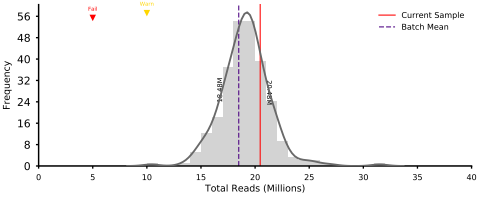

FAILURE
Alignment
Fail
Warn
Current Sample
Batch Mean
44.24%
57.76%
Frequency
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
61.64%
61.73%
Frequency
% Mapped / Aligned Reads

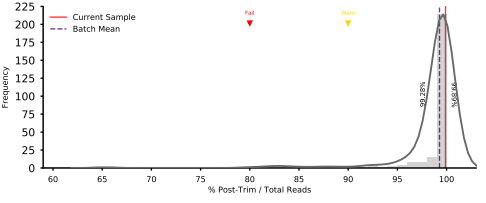

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.96841
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


Sequence Contamination
Current Sample
Batch Mean
Overrepresented
Adapter
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

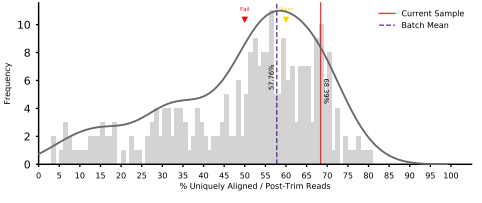
Sequencing Depth



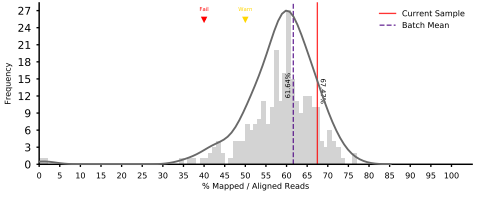
Trimming



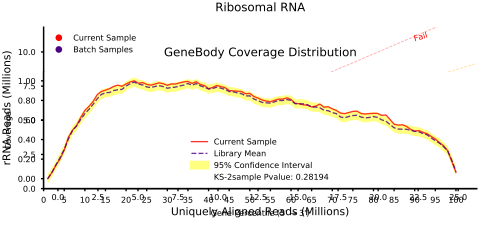
Alignment



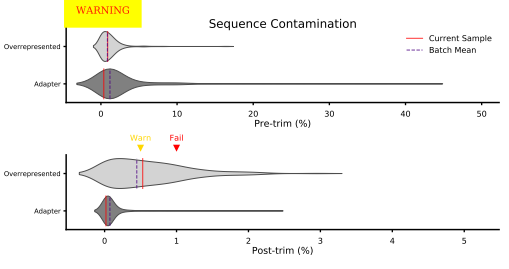
Gene Exon Mapping

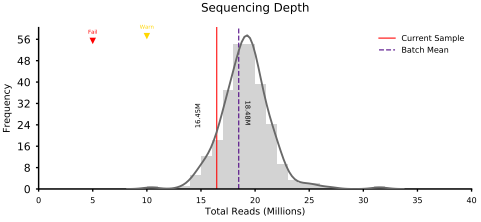


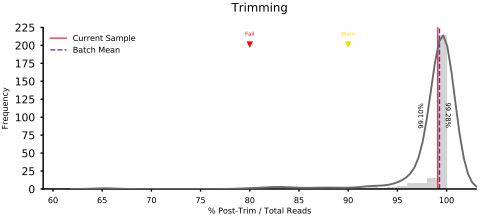
Ribosomal RNA

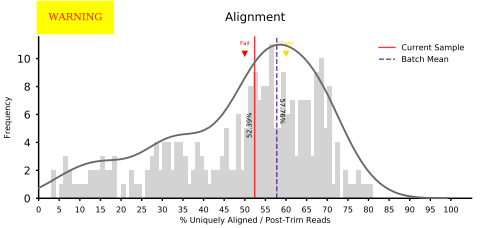


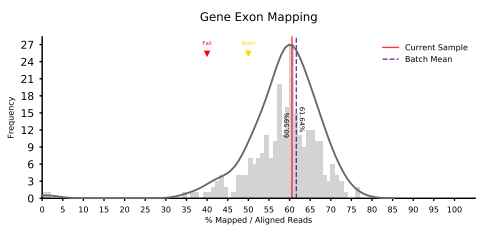
Sequence Contamination

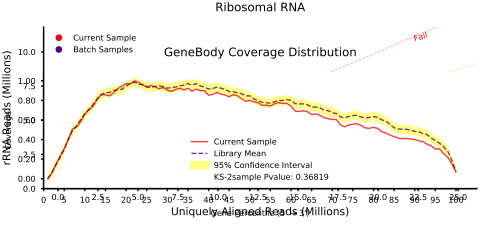


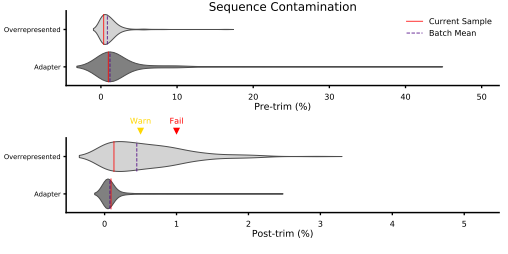

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
16.45M
18.48M
Frequency
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
99.10%
99.33%
Frequency
% Post-Trim / Total Reads

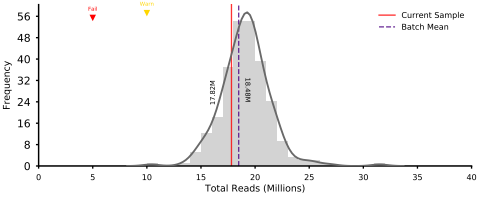

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
52.39%
57.76%
Frequency
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
60.59%
61.54%
Frequency
% Mapped / Aligned Reads

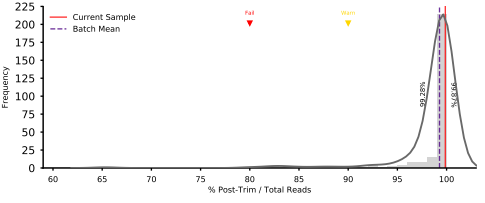

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.36819
Uniquely Aligned Reads (Millions)


Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

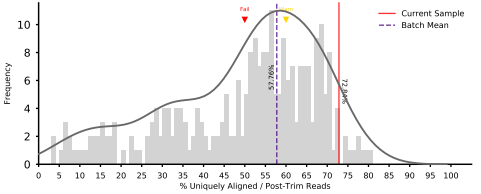
Sequencing Depth



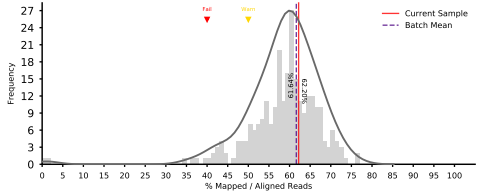
Trimming



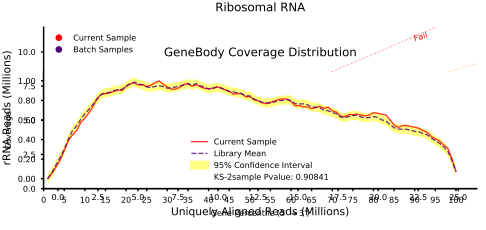
Alignment



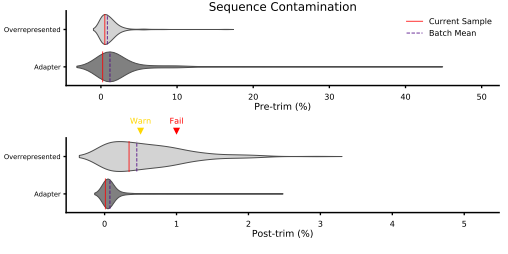
Gene Exon Mapping



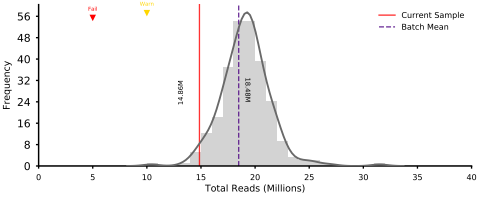
Ribosomal RNA



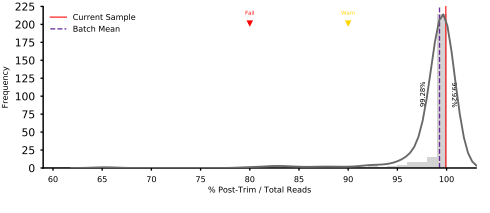
Sequence Contamination



Sequencing Depth

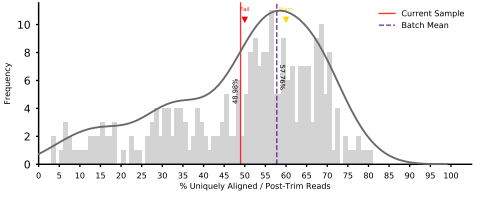


Trimming

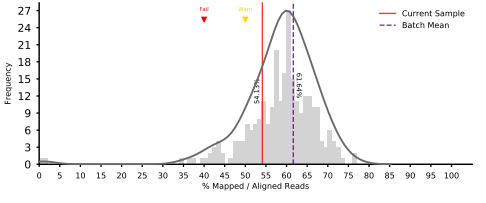


FAILURE

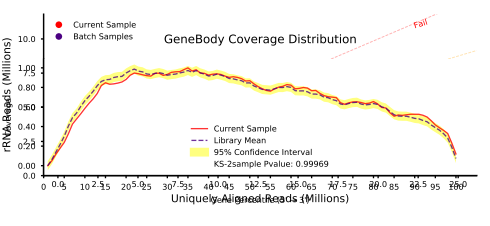
Alignment



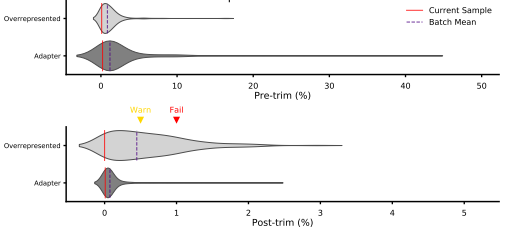
Gene Exon Mapping



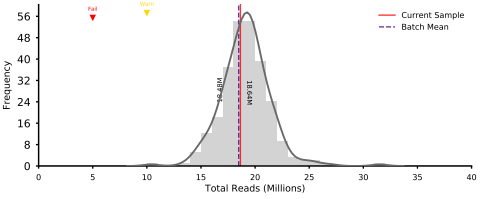
Ribosomal RNA



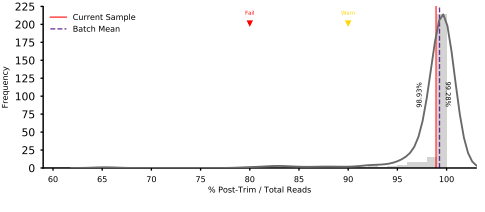
Sequence Contamination



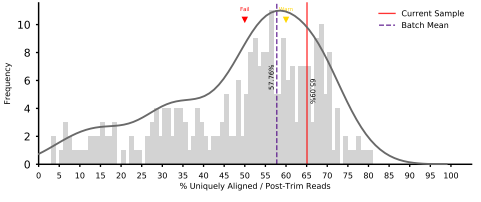
Sequencing Depth



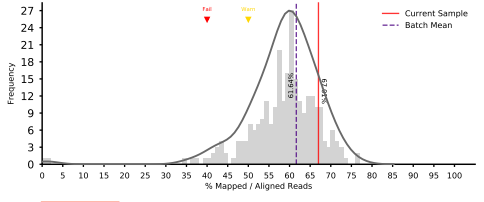
Trimming



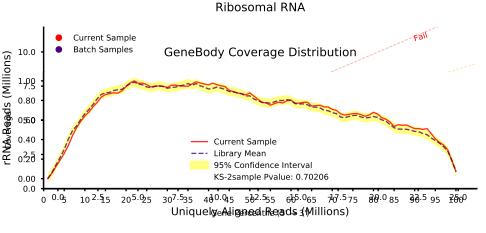
Alignment



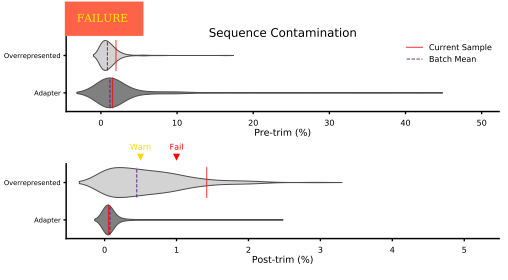
Gene Exon Mapping

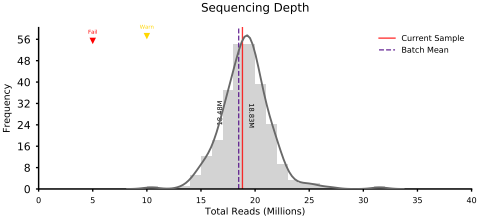


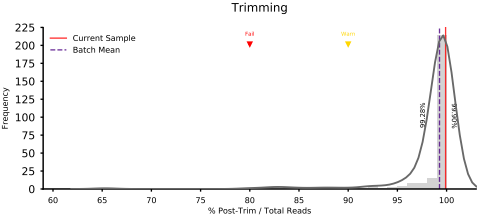
Ribosomal RNA

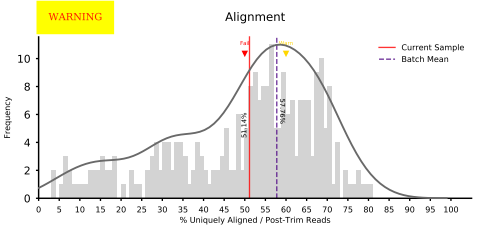


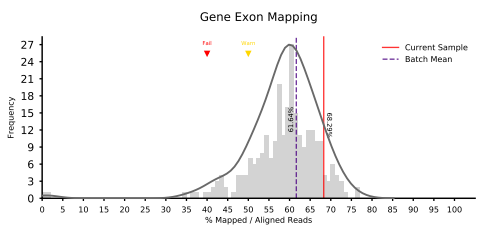
Sequence Contamination

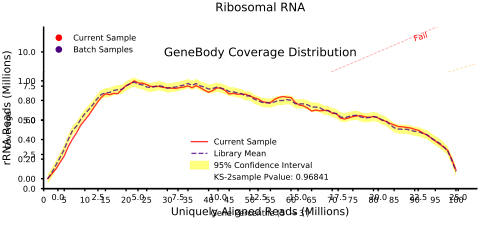


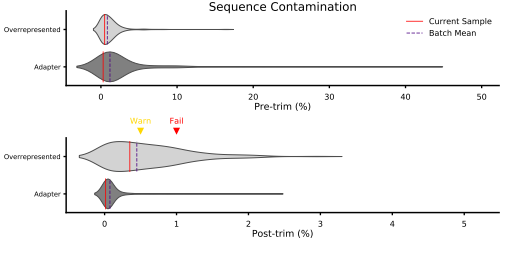

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.68M
18.83M
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
99.28%
100.0%
% Post-Trim / Total Reads

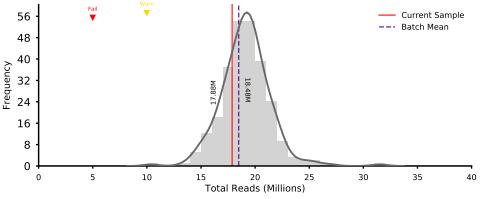

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
51.14%
57.76%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
61.64%
68.29%
% Mapped / Aligned Reads

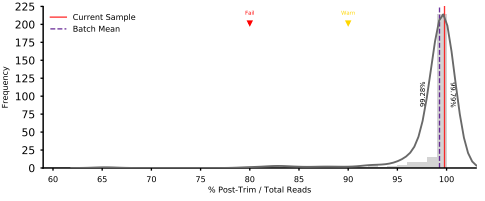

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.96841
Uniquely Aligned Reads (Millions)


Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

Sequencing Depth

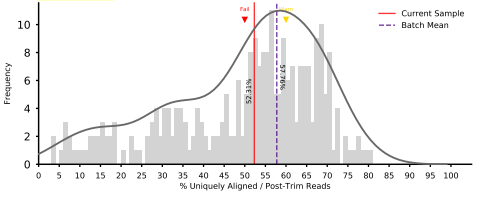


Trimming

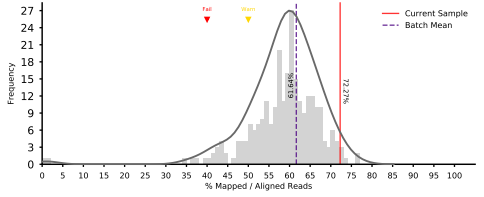


WARNING

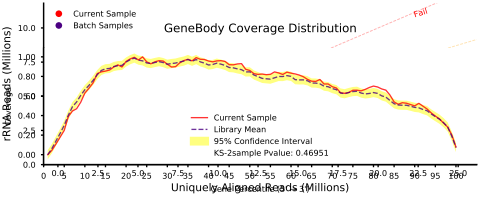
Alignment



Gene Exon Mapping

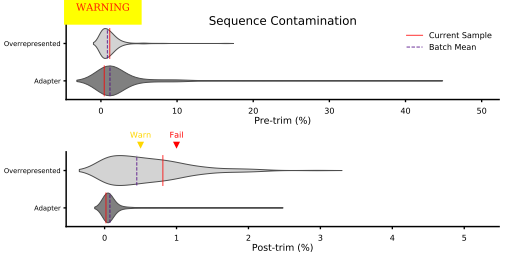


Ribosomal RNA

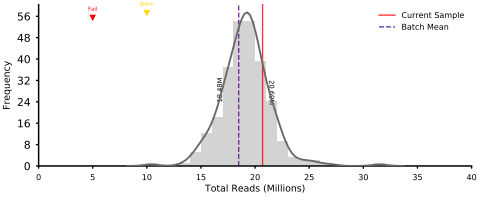


WARNING

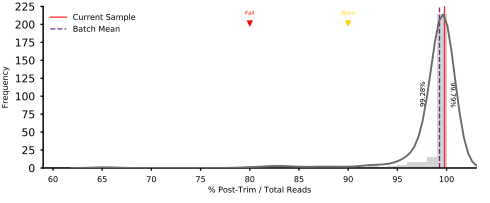
Sequence Contamination



Sequencing Depth

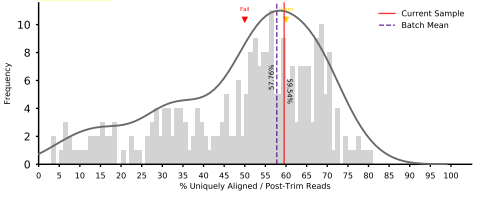


Trimming

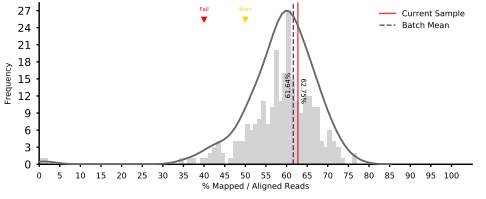


WARNING

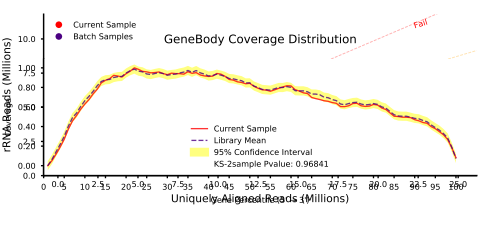
Alignment



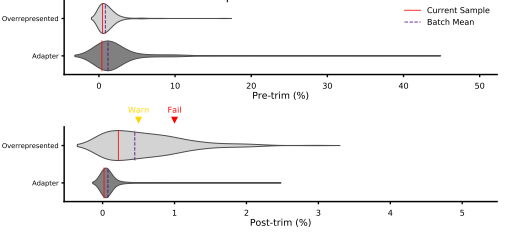
Gene Exon Mapping

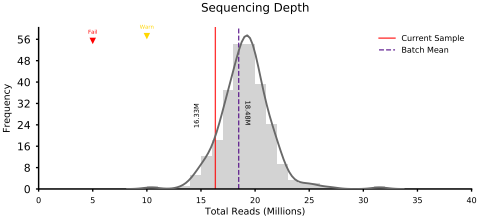


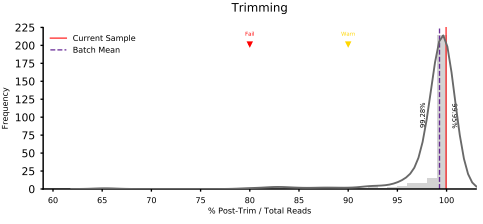
Ribosomal RNA

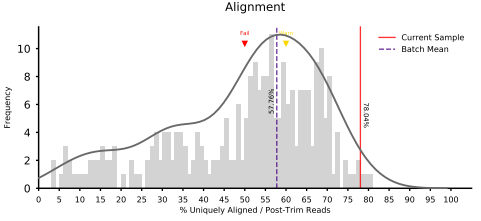


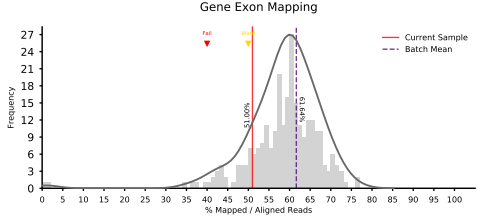
Sequence Contamination

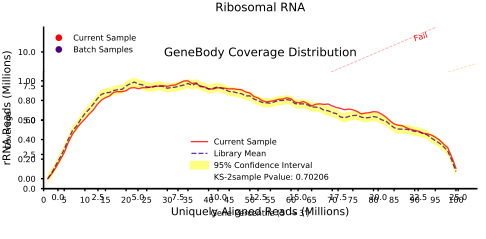


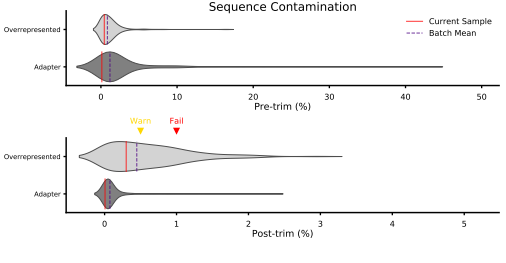

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
16.33M
18.98M
Frequency
Total Reads (Millions)

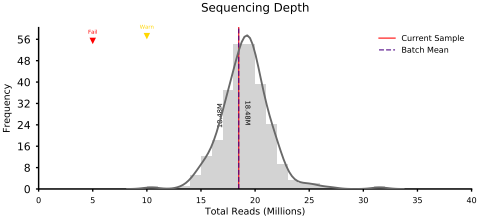

Trimming
Current Sample
Batch Mean
Fail
Warn
97.28%
99.66%
Frequency
% Post-Trim / Total Reads

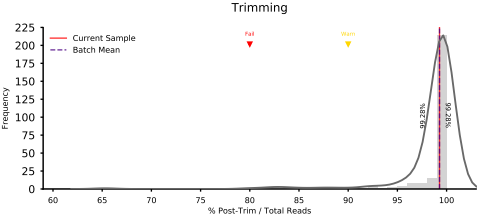

Alignment
Fail
Warn
Current Sample
Batch Mean
57.76%
78.04%
Frequency
% Uniquely Aligned / Post-Trim Reads

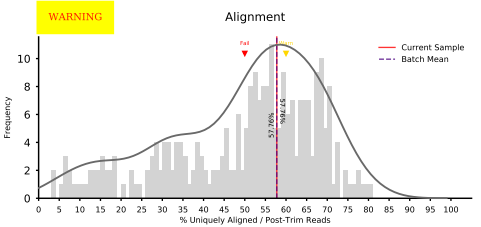

Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
51.00%
61.44%
Frequency
% Mapped / Aligned Reads

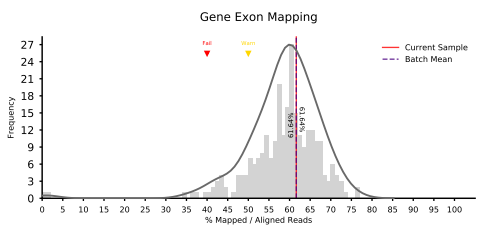

Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.70206
Uniquely Aligned Reads (Millions)

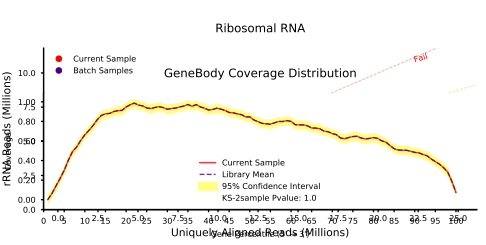

Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

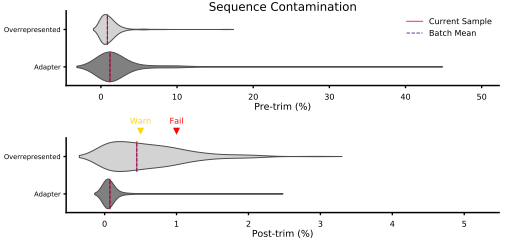

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.48M
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
99.28%
% Post-Trim / Total Reads


WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
57.76%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
61.64%
% Mapped / Aligned Reads


Ribosomal RNA
Current Sample
Batch Samples
GeneBody Coverage Distribution
Fail
rRNA Reads (Millions)
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 1.0
Uniquely Aligned Reads (Millions)


Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)