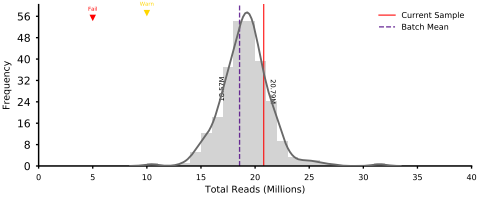
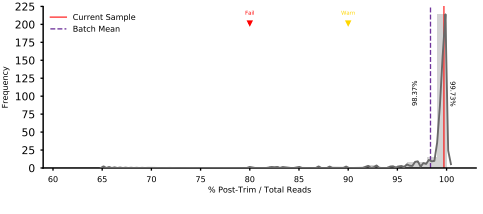
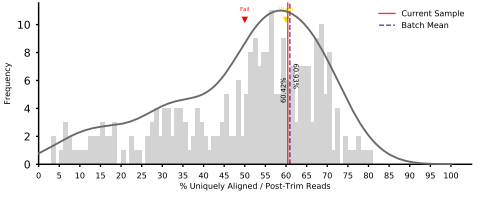
Sequencing Depth



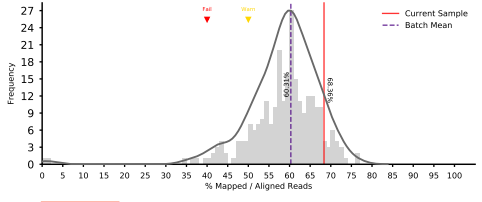
Trimming



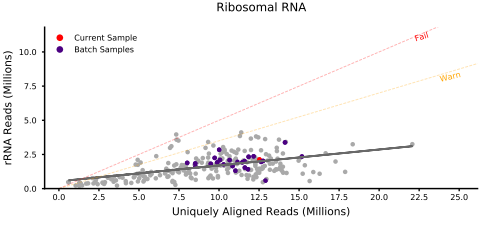
Alignment



Gene Exon Mapping

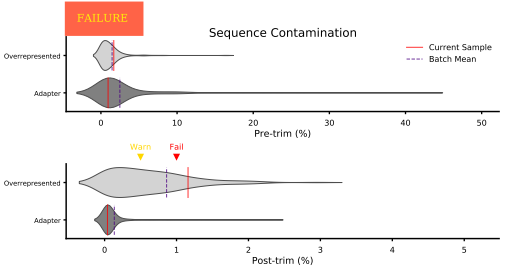


Ribosomal RNA

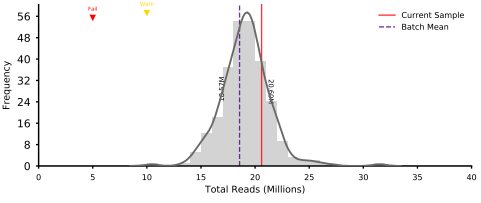


Sequence Contamination

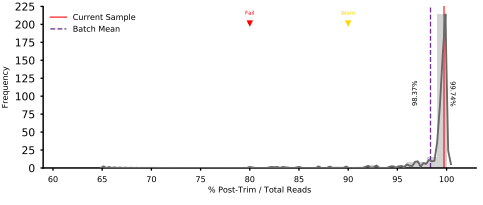
FAILURE



Sequencing Depth

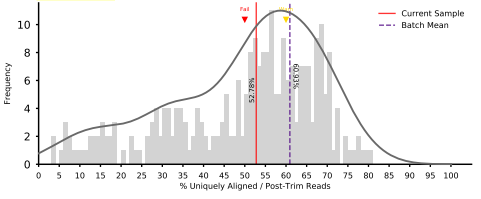


Trimming

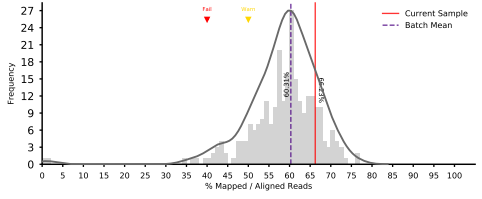


WARNING

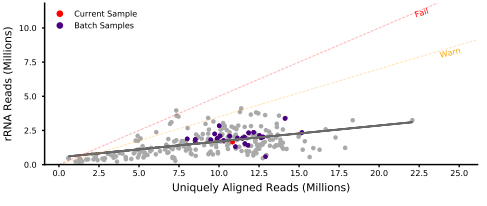
Alignment



Gene Exon Mapping

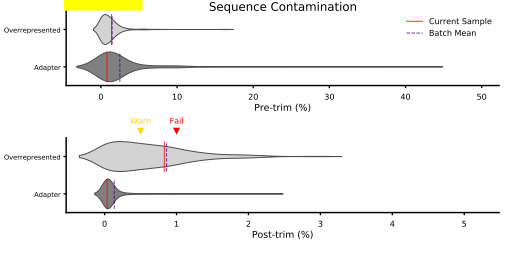


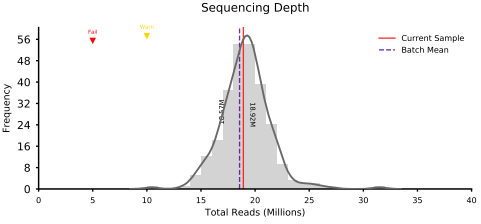
Ribosomal RNA

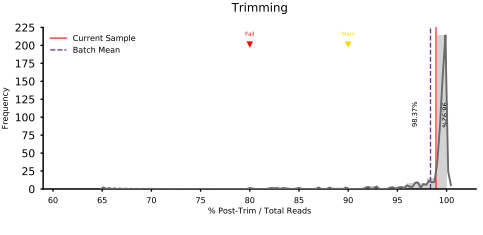


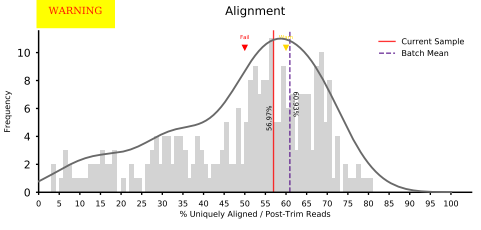
WARNING

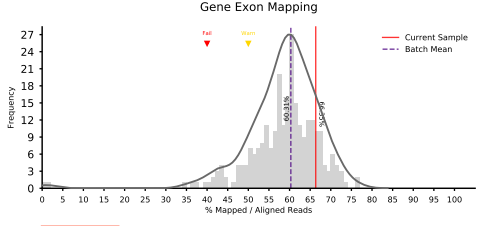
Sequence Contamination

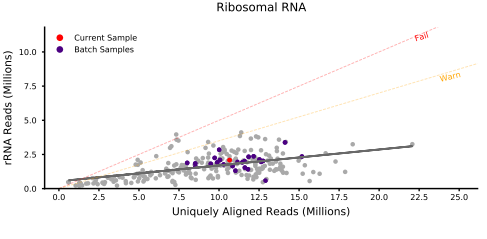


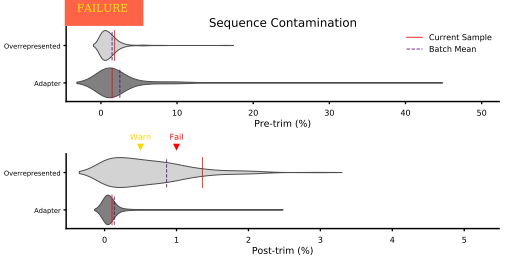

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
16.43M
18.92M
Total Reads (Millions)

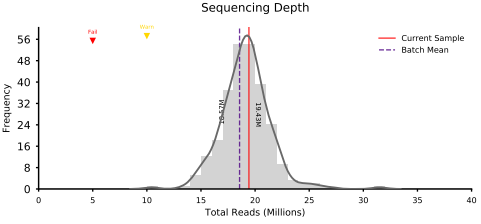

Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
98.27%
96.08%
% Post-Trim / Total Reads

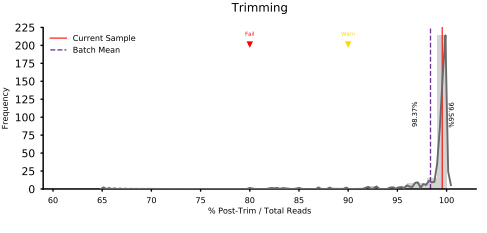

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
56.97%
60.09%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
60.31%
56.49%
% Mapped / Aligned Reads

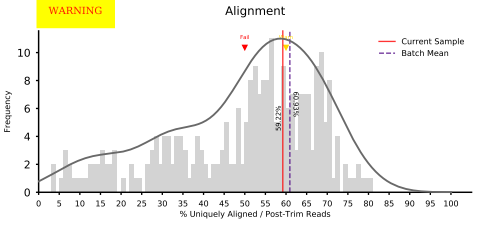

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

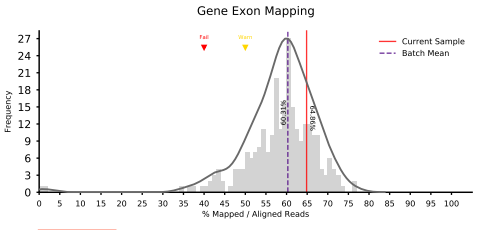

FAILURE
Sequence Contamination
Current Sample
Batch Mean
Overrepresented
Adapter
Pre-trim (%)
Warn
Fail
Post-trim (%)



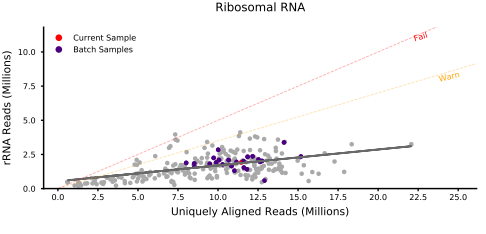


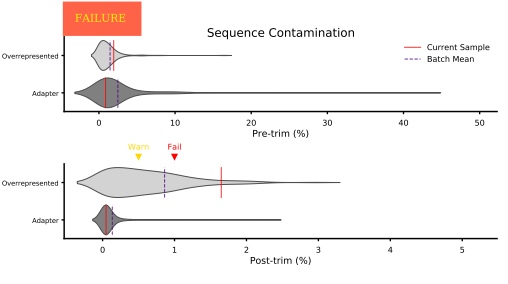
WARNING



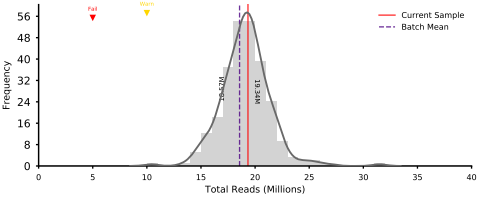


FAILURE

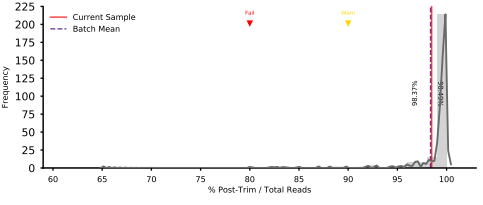




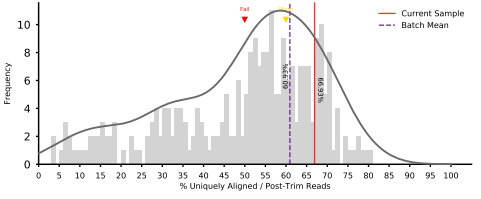
Sequencing Depth



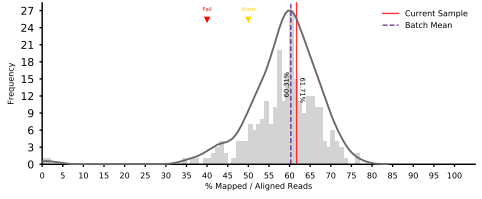
Trimming



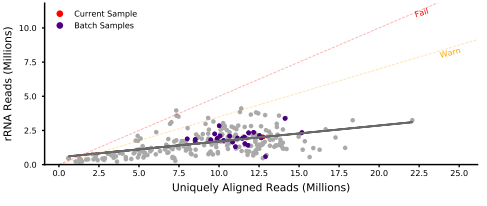
Alignment



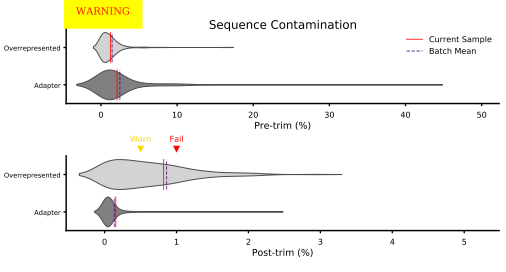
Gene Exon Mapping

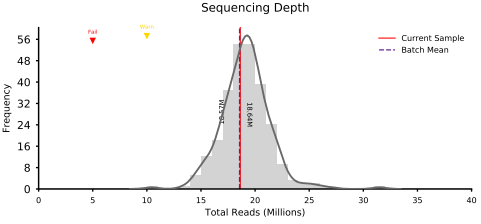


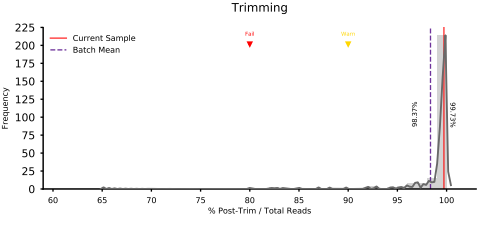
Ribosomal RNA

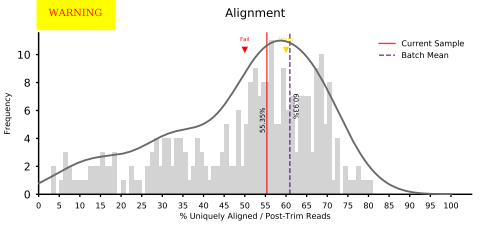


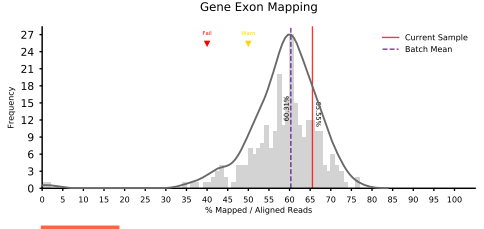
Sequence Contamination

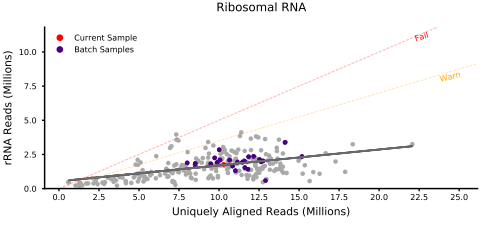


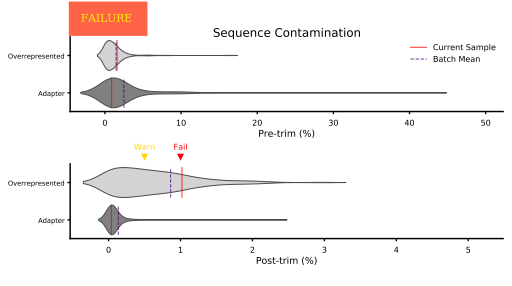

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.45M
18.44M
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
98.27%
97.66%
% Post-Trim / Total Reads

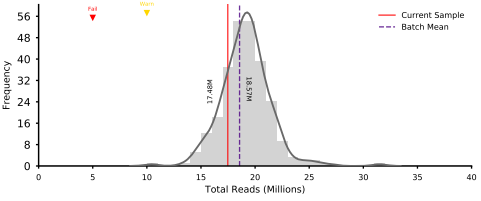

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
55.39%
60.09%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
60.31%
65.58%
% Mapped / Aligned Reads

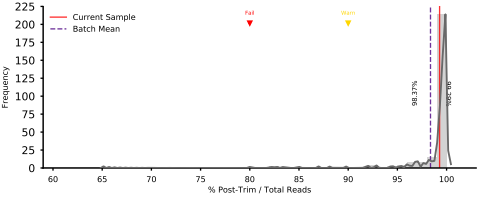

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

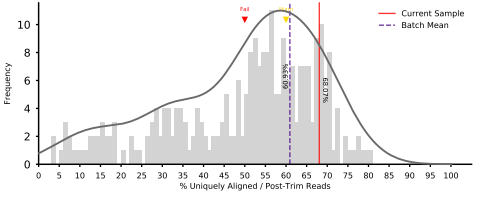
Sequencing Depth



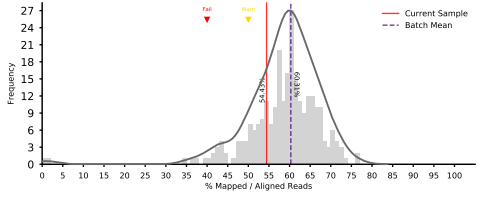
Trimming



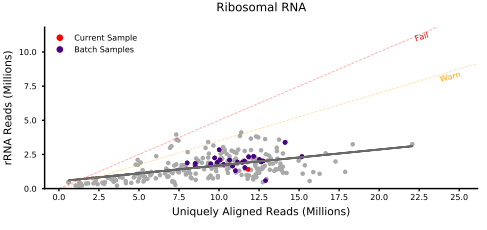
Alignment



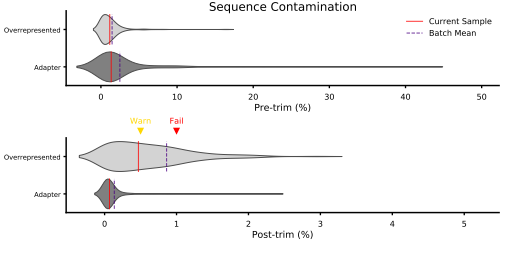
Gene Exon Mapping



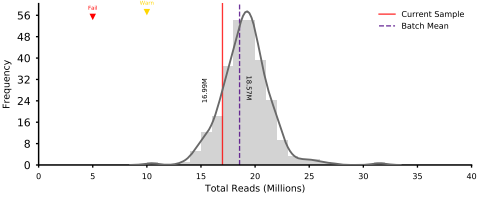
Ribosomal RNA



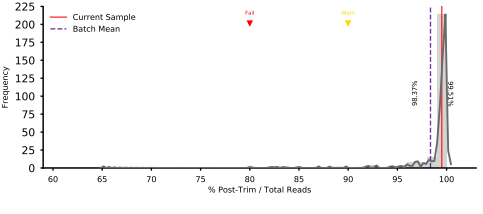
Sequence Contamination



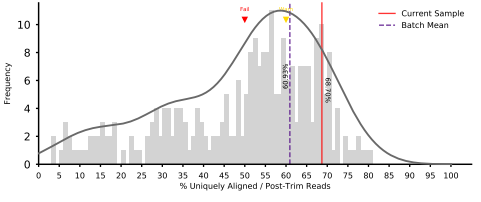
Sequencing Depth



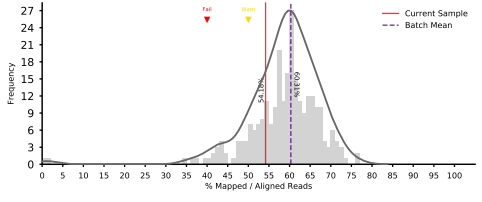
Trimming



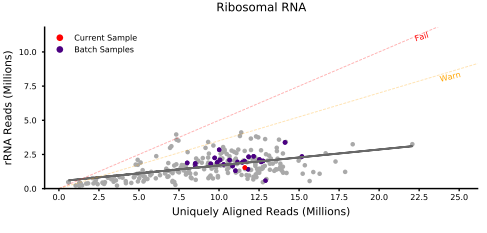
Alignment



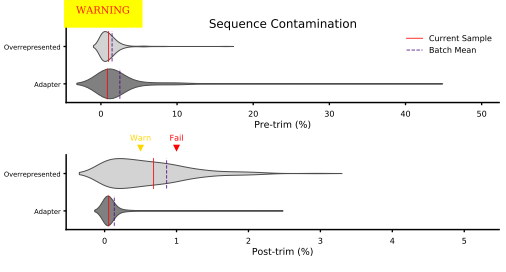
Gene Exon Mapping

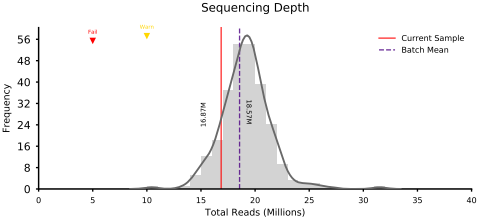


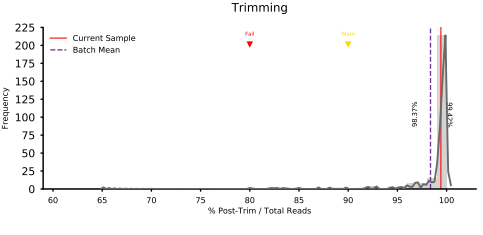
Ribosomal RNA

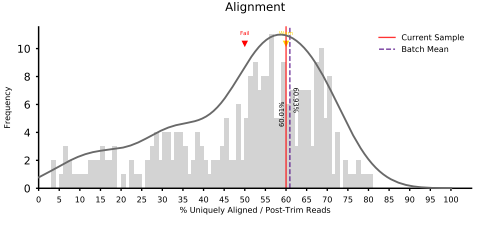


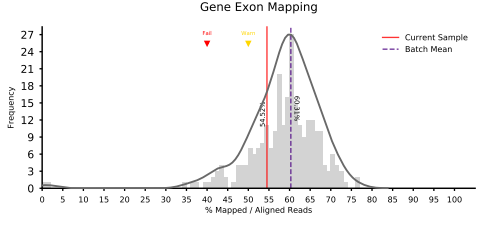
Sequence Contamination

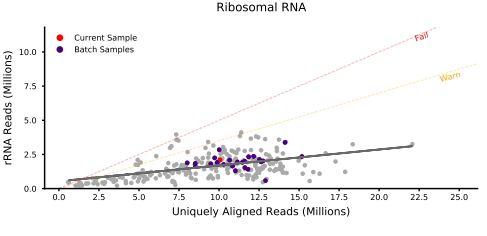


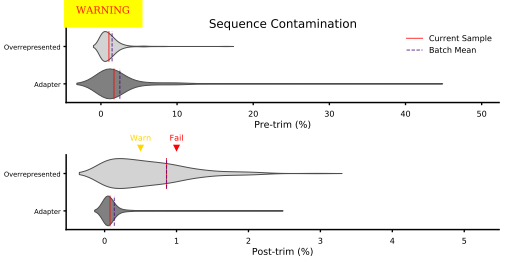

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
16.87M
18.53M
Frequency
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
98.27%
98.42%
Frequency
% Post-Trim / Total Reads

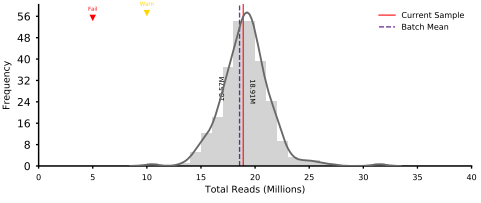

Alignment
Fail
Warn
Current Sample
Batch Mean
60.01%
60.69%
Frequency
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
54.29%
60.16%
Frequency
% Mapped / Aligned Reads

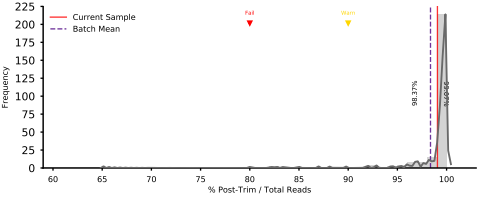

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

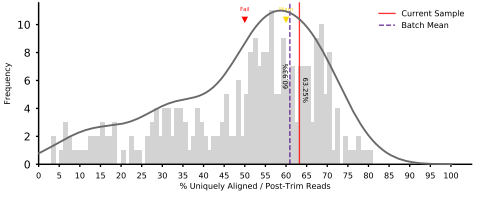
Sequencing Depth



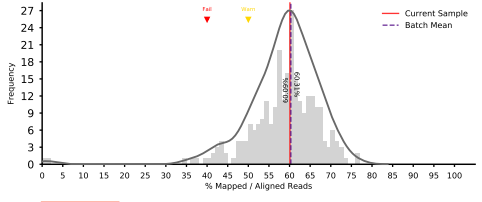
Trimming



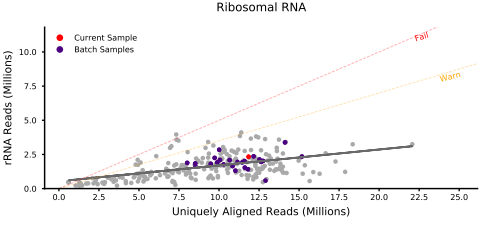
Alignment



Gene Exon Mapping

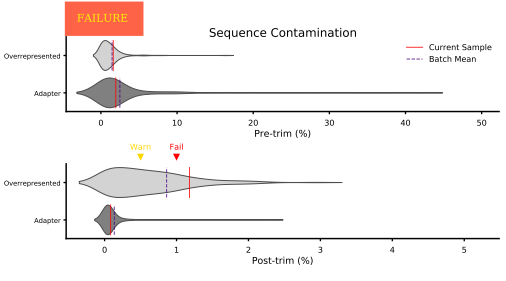


Ribosomal RNA

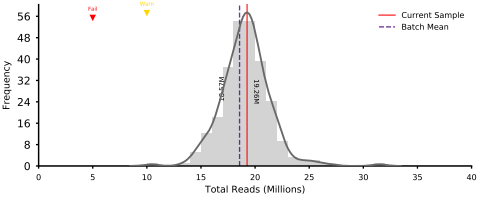


Sequence Contamination

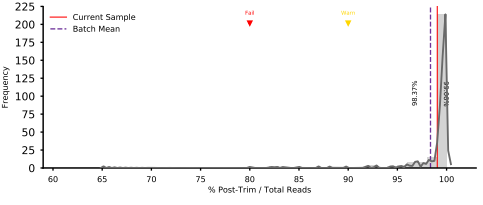
FAILURE



Sequencing Depth

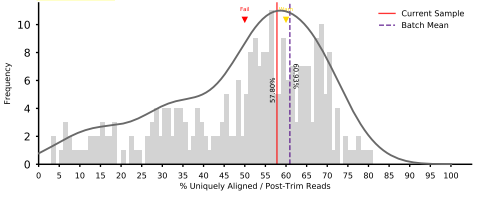


Trimming

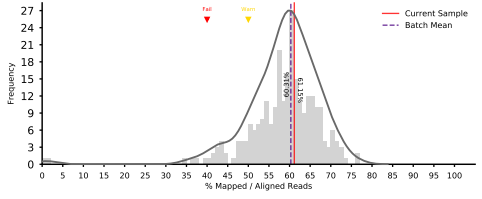


WARNING

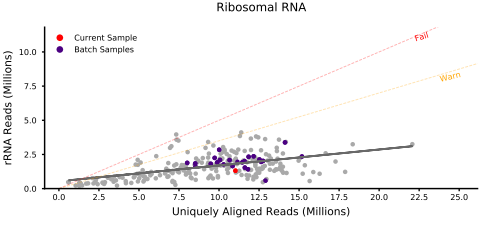
Alignment



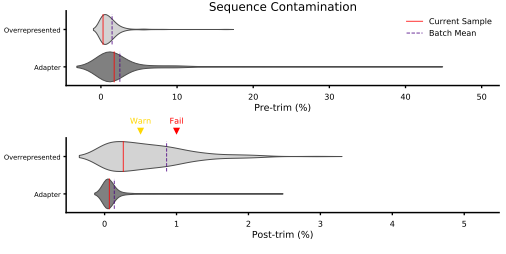
Gene Exon Mapping



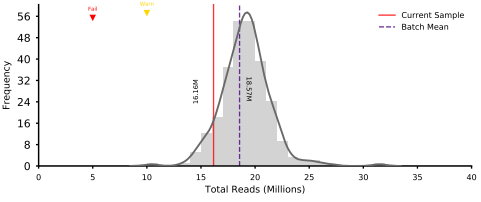
Ribosomal RNA



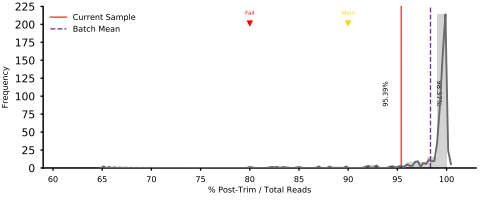
Sequence Contamination



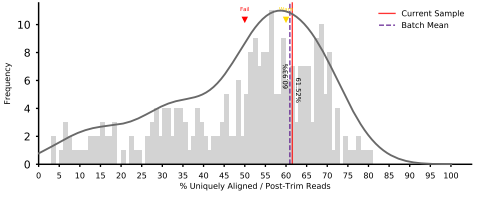
Sequencing Depth



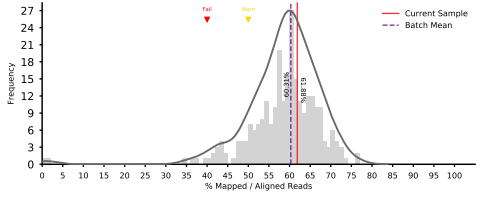
Trimming



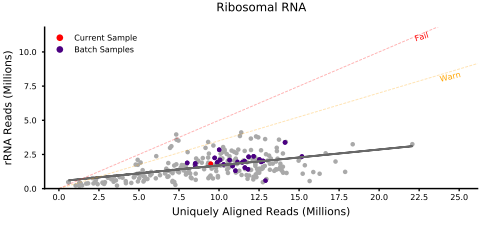
Alignment



Gene Exon Mapping

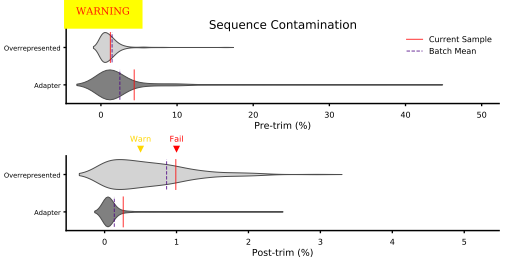


Ribosomal RNA

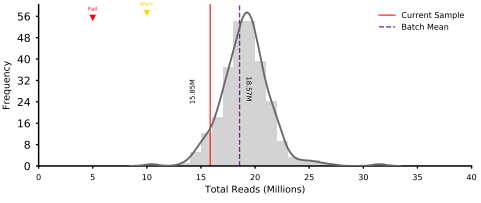


Sequence Contamination

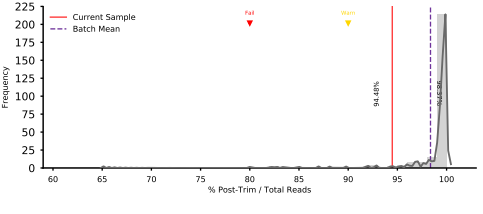
WARNING



Sequencing Depth

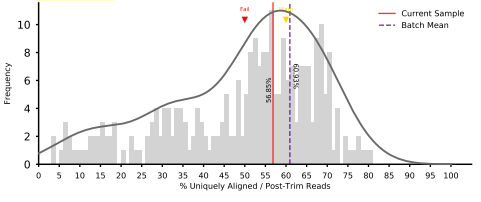


Trimming

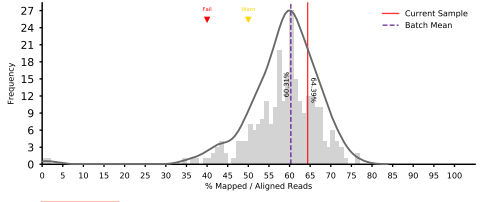


WARNING

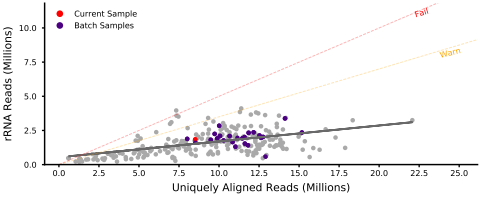
Alignment



Gene Exon Mapping

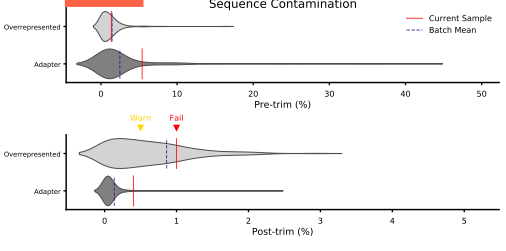


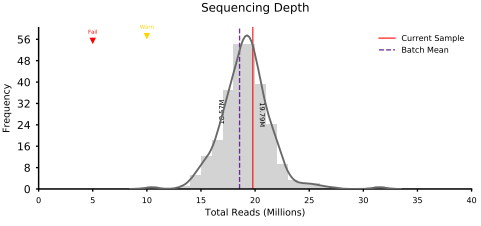
Ribosomal RNA

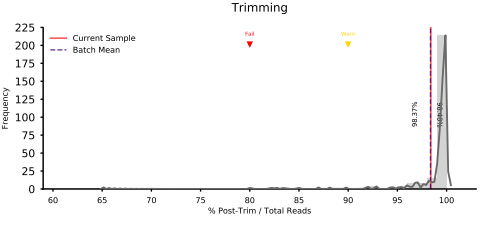


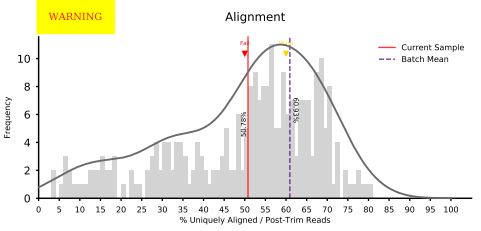
FAILURE

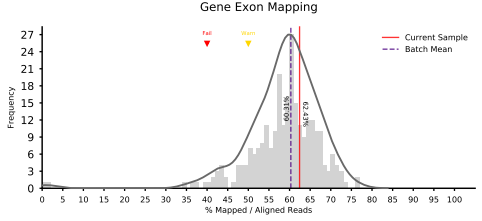
Sequence Contamination

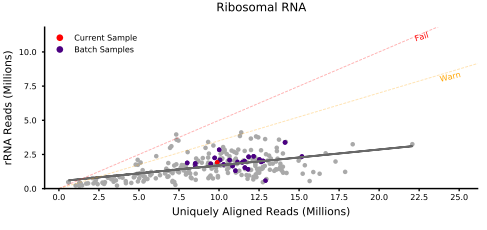


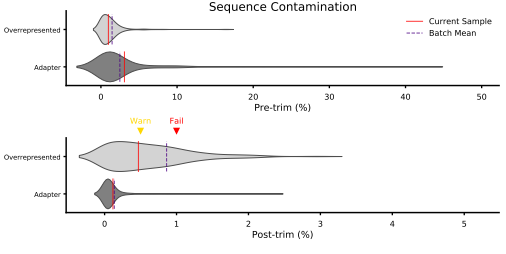

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
Total Reads (Millions)
19.57M
19.79M

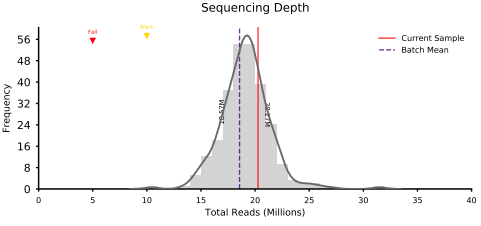

Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
% Post-Trim / Total Reads
98.37%
99.96%

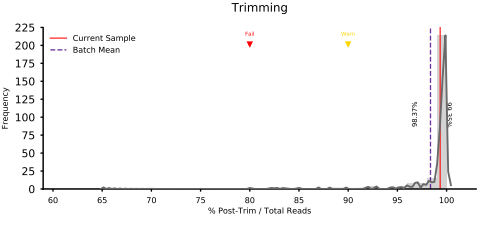

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
% Uniquely Aligned / Post-Trim Reads
50.78%
60.03%

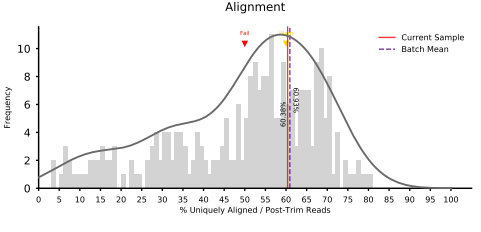

Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
% Mapped / Aligned Reads
60.31%
62.43%

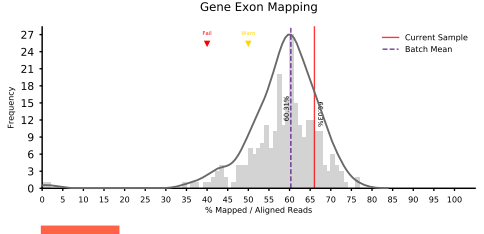

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

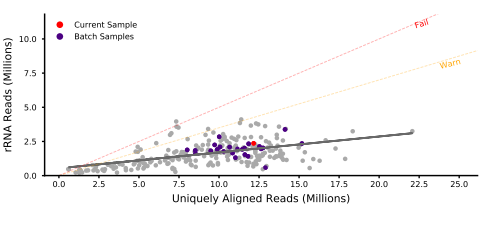

Sequence Contamination
Current Sample
Batch Mean
Overrepresented
Adapter
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

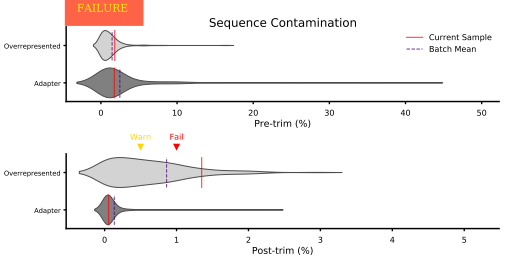

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.43M
20.24M
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
98.27%
99.55%
% Post-Trim / Total Reads

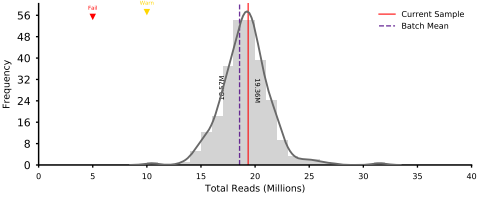

Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
60.38%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
60.31%
% Mapped / Aligned Reads

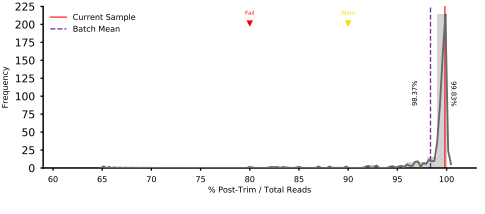

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

Sequencing Depth

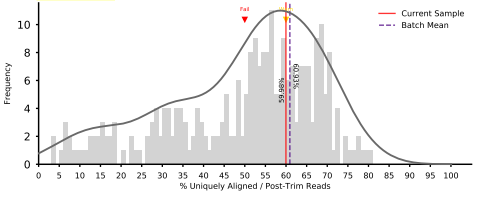


Trimming

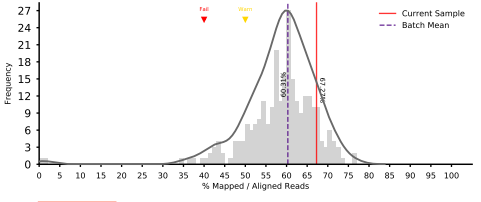


WARNING

Alignment

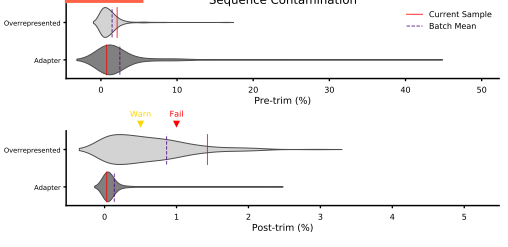


Gene Exon Mapping

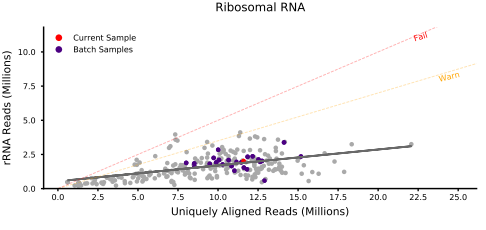


FAILURE

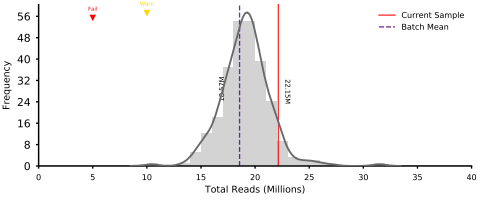
Sequence Contamination



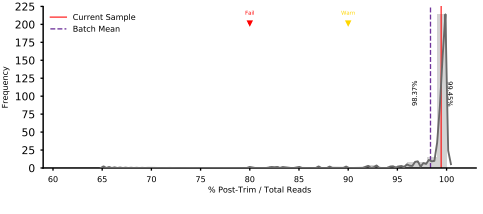
Ribosomal RNA



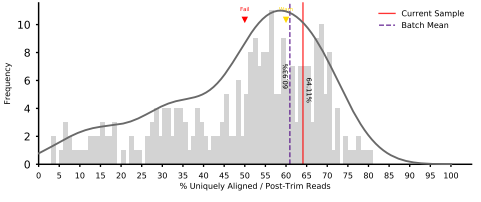
Sequencing Depth



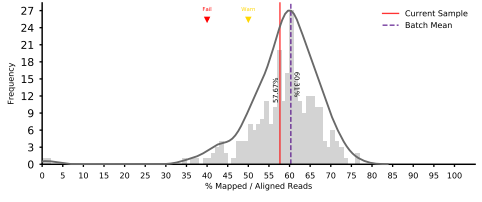
Trimming



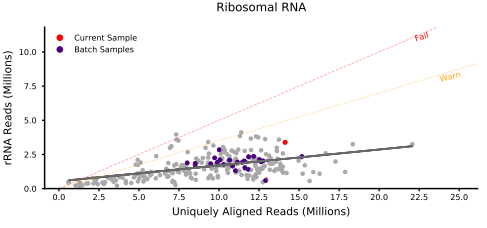
Alignment



Gene Exon Mapping

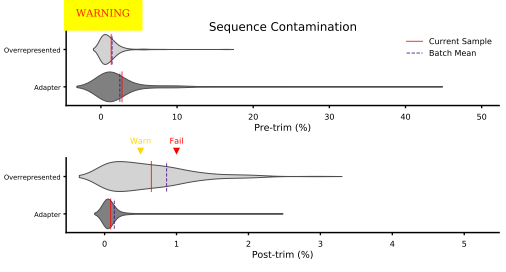


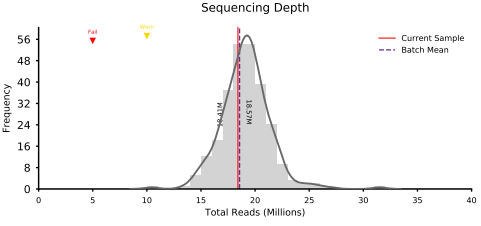
Ribosomal RNA

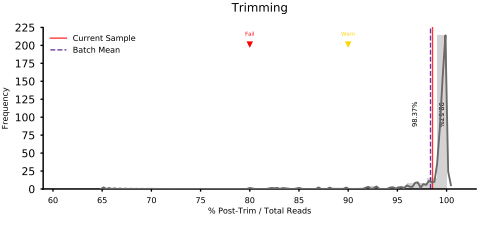


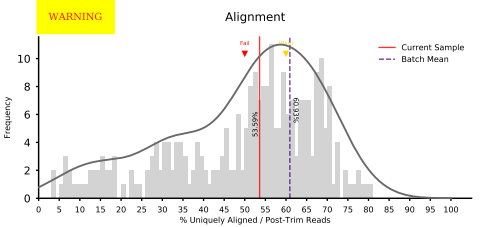
Sequence Contamination

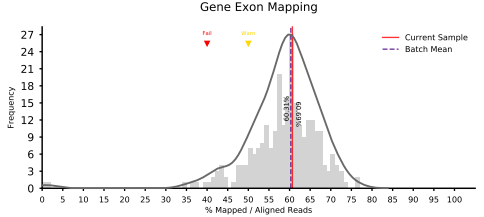
WARNING

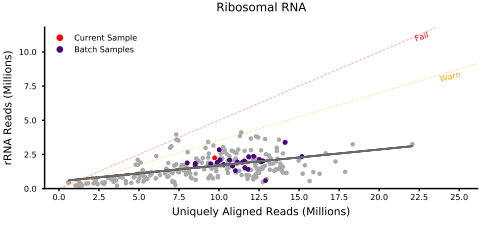


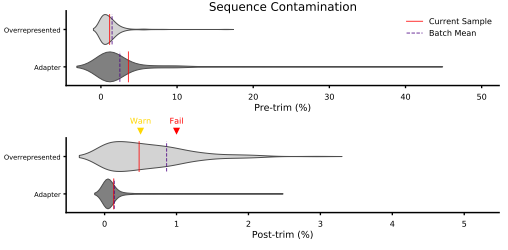

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.51M
18.51M
Total Reads (Millions)

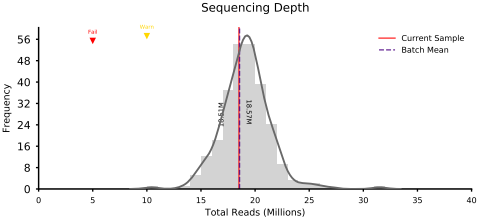

Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
98.27%
98.27%
% Post-Trim / Total Reads

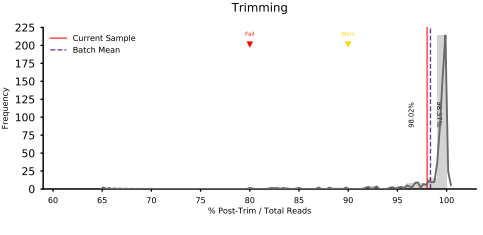

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
53.59%
60.09%
% Uniquely Aligned / Post-Trim Reads

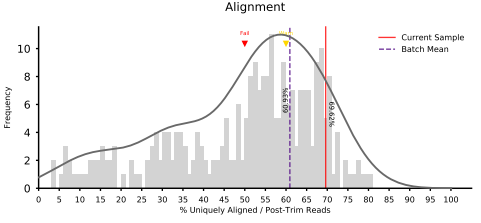

Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
60.31%
60.09%
% Mapped / Aligned Reads

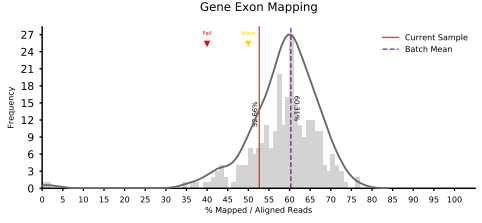

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

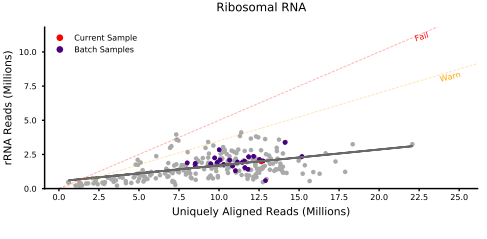

Sequence Contamination
Current Sample
Batch Mean
Overrepresented
Adapter
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

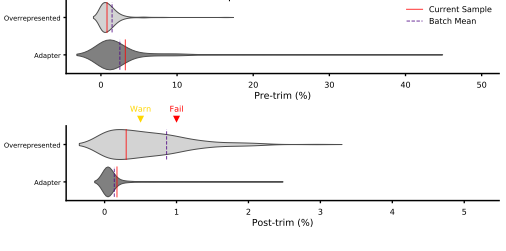

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.51M
Total Reads (Millions)

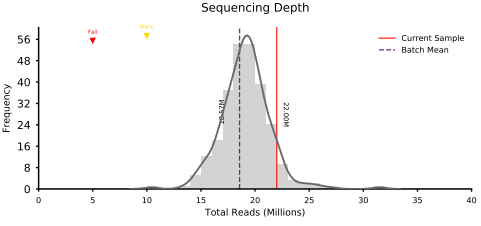

Trimming
Current Sample
Batch Mean
Fail
Warn
98.02%
% Post-Trim / Total Reads

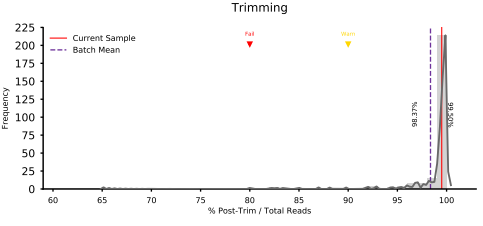

Alignment
Fail
Warn
Current Sample
Batch Mean
60.93%
69.49%
Frequency
% Uniquely Aligned / Post-Trim Reads

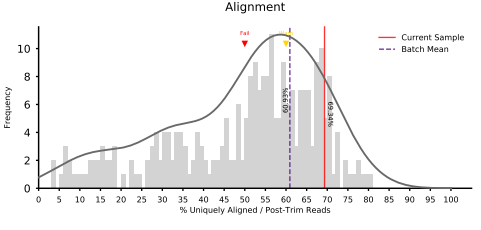

Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
59.60%
60.31%
Frequency
% Mapped / Aligned Reads

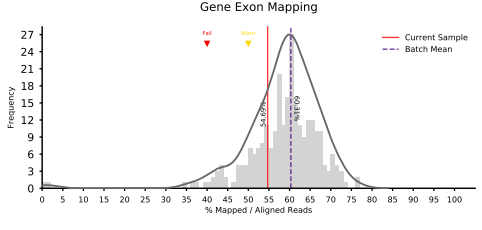

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

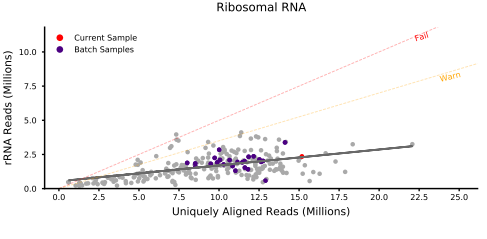

Sequence Contamination
Current Sample
Batch Mean
Overrepresented
Adapter
Pre-trim (%)
Warn
Fail
Overrepresented
Adapter
Post-trim (%)

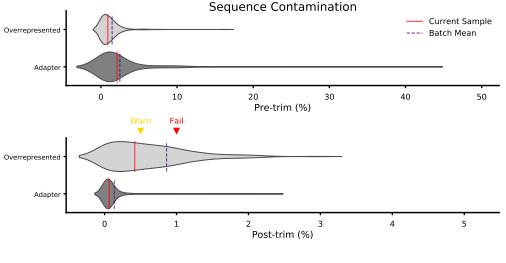

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.57M
22.00M
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
98.27%
98.90%
% Post-Trim / Total Reads

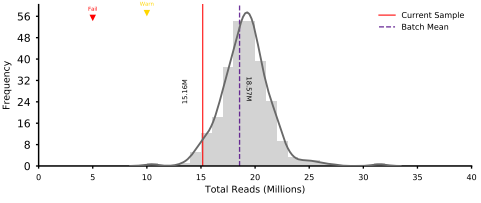

Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
60.96%
69.98%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
54.60%
59.31%
% Mapped / Aligned Reads

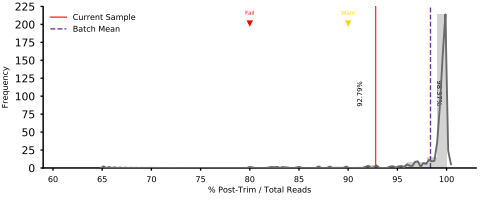

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

Sequencing Depth

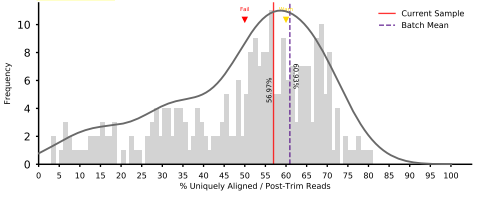


Trimming

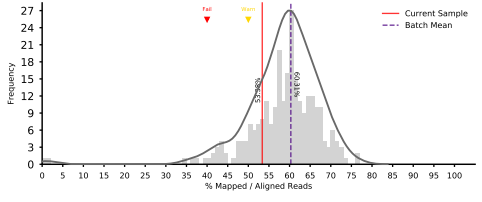


WARNING

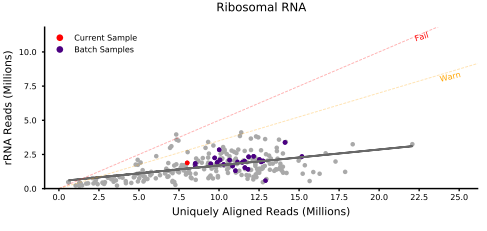
Alignment



Gene Exon Mapping

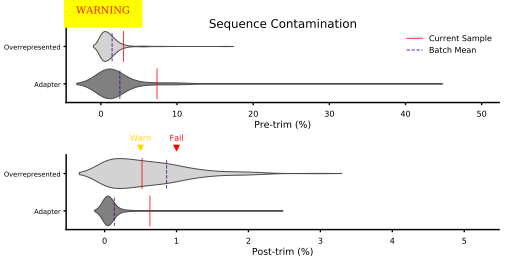


Ribosomal RNA

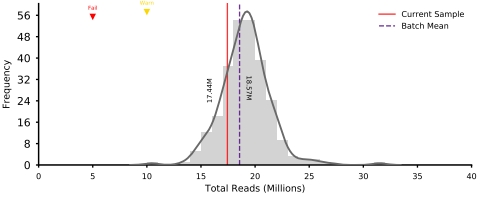


WARNING

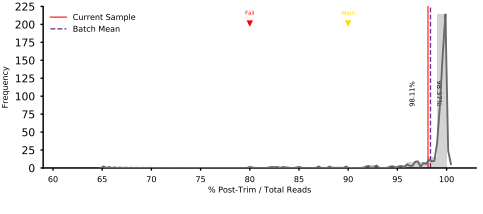
Sequence Contamination



Sequencing Depth

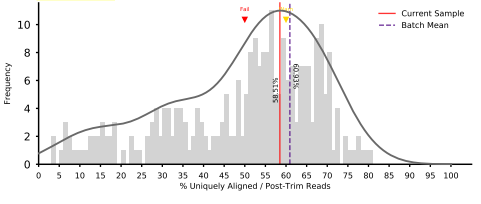


Trimming

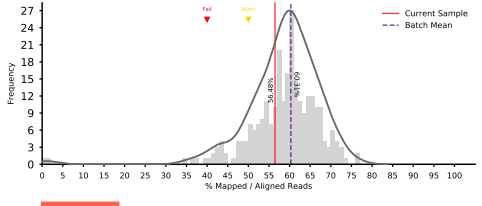


WARNING

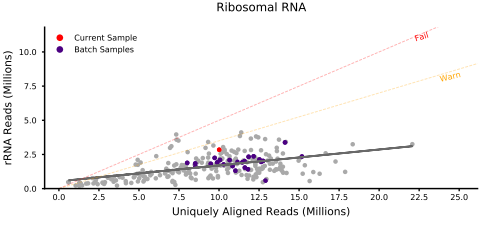
Alignment



Gene Exon Mapping

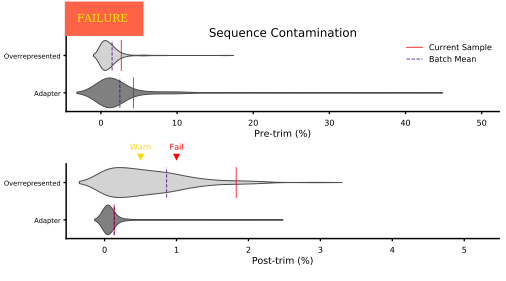


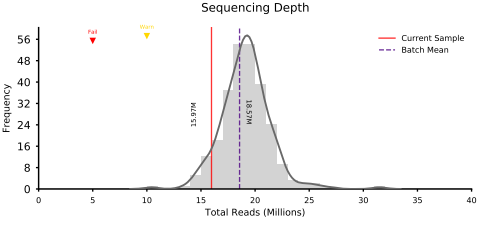
Ribosomal RNA

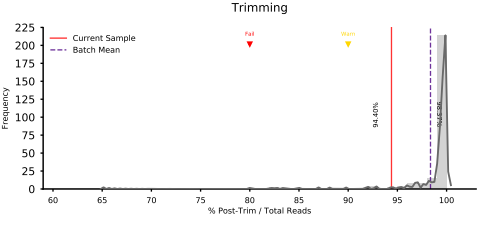


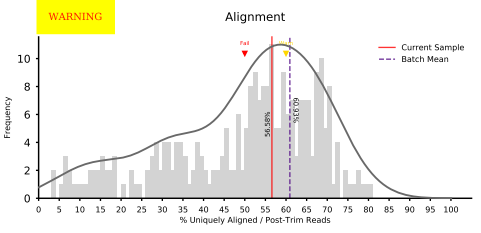
FAILURE

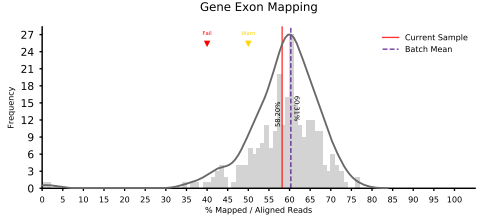
Sequence Contamination

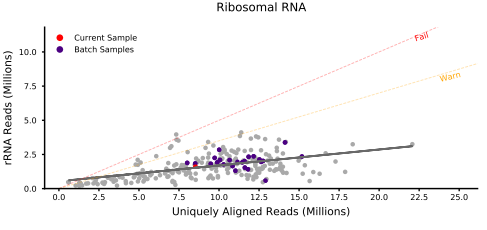


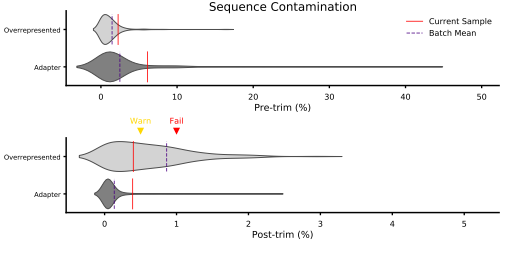

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
15.97M
18.57M
Frequency
Total Reads (Millions)

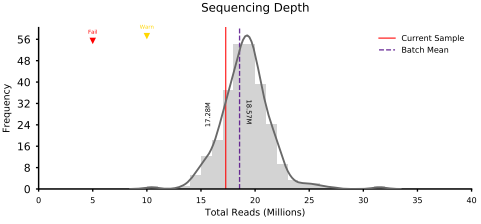

Trimming
Current Sample
Batch Mean
Fail
Warn
94.40%
98.38%
Frequency
% Post-Trim / Total Reads

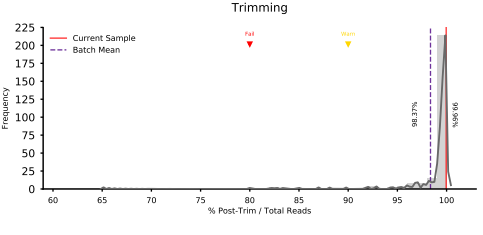

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
56.98%
60.09%
Frequency
% Uniquely Aligned / Post-Trim Reads

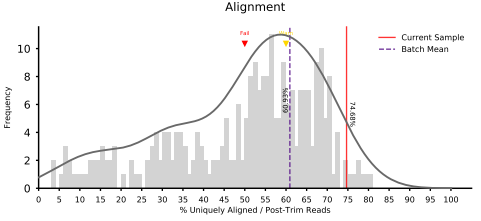

Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
58.20%
59.31%
Frequency
% Mapped / Aligned Reads

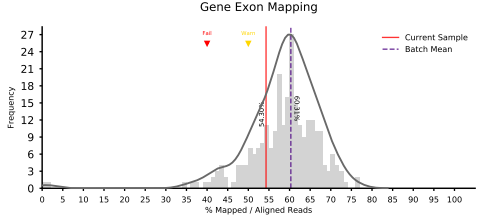

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

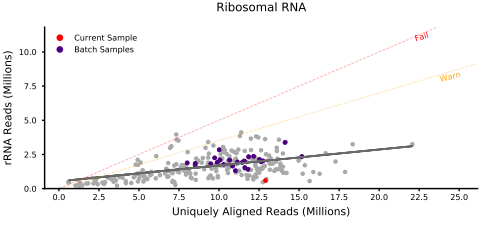

Sequence Contamination
Overrepresented
Adapter
Current Sample
Batch Mean
Pre-trim (%)
Warn
Fail
Post-trim (%)

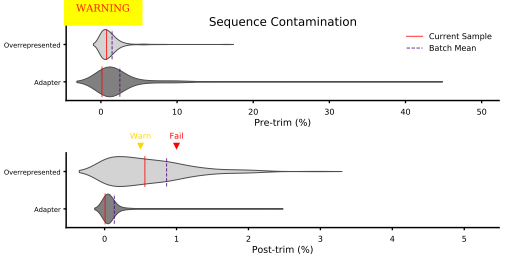

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
17.28M
18.57M
Total Reads (Millions)


Trimming
Current Sample
Batch Mean
Fail
Warn
Frequency
98.27%
% Post-Trim / Total Reads

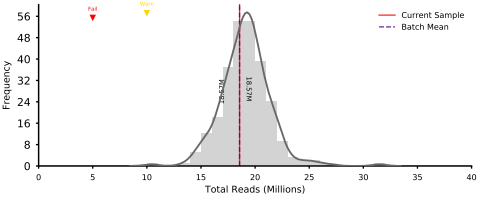

Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
60.99%
74.69%
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
54.20%
59.31%
% Mapped / Aligned Reads

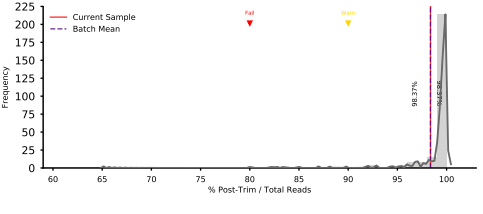

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

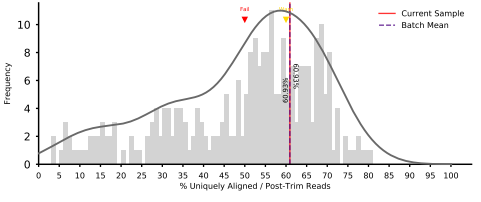
Sequencing Depth



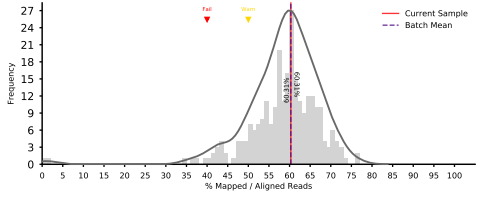
Trimming



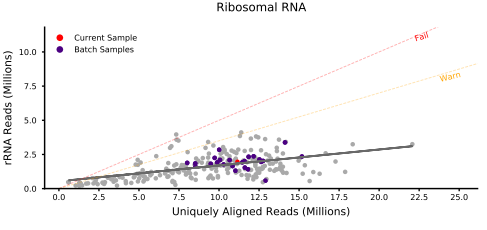
Alignment

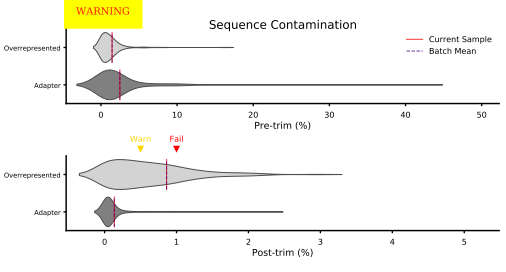


Gene Exon Mapping



Ribosomal RNA



Sequence Contamination

WARNING