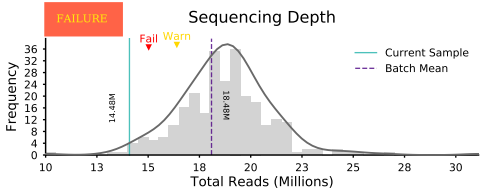
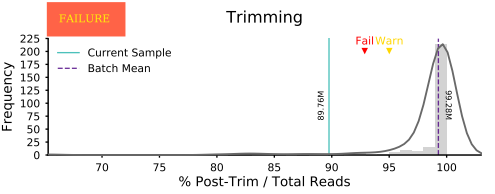
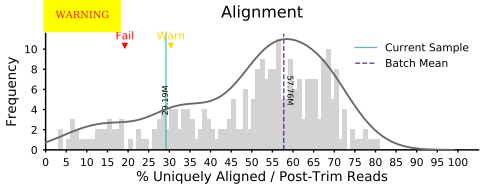
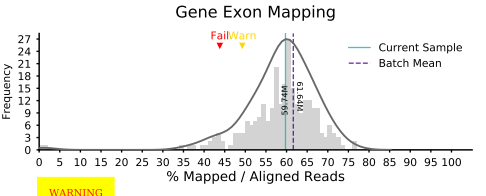
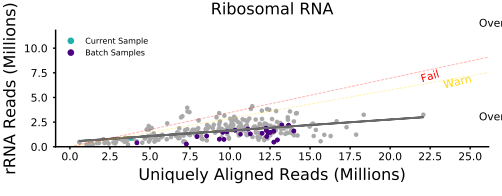
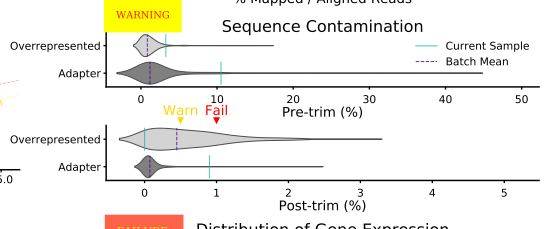

FAILURE
Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
14.48M
18.48M
Total Reads (Millions)

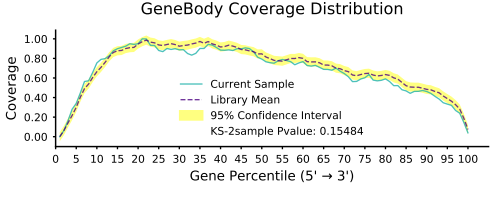

FAILURE
Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
89.76M
99.28M
% Post-Trim / Total Reads

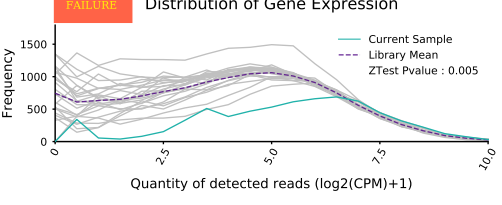

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
29.19M
57.76M
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
59.74M
61.64M
% Mapped / Aligned Reads

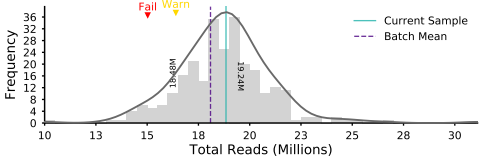

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

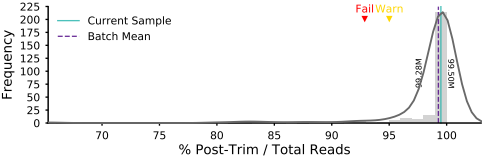

GeneBody Coverage Distribution
Coverage
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.15484
Gene Percentile (5' → 3')


FAILURE
Distribution of Gene Expression
Current Sample
Library Mean
ZTest Pvalue : 0.005
Frequency
Quantity of detected reads (log2(CPM)+1)

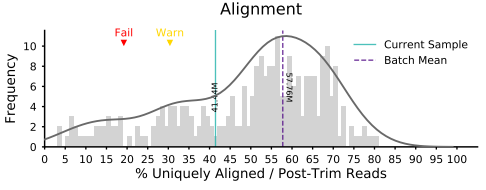
Sequencing Depth



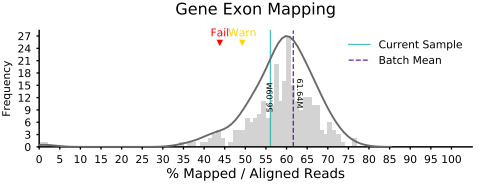
Trimming



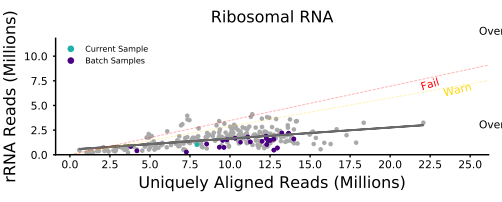
Alignment



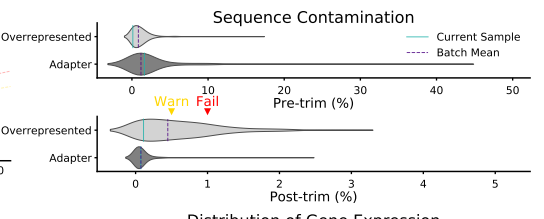
Gene Exon Mapping



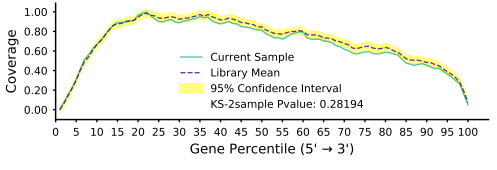
Ribosomal RNA



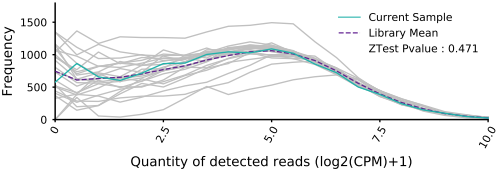
Sequence Contamination



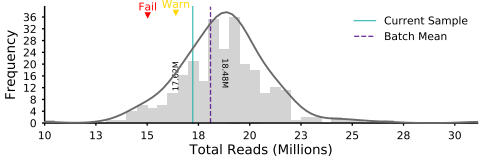
GeneBody Coverage Distribution



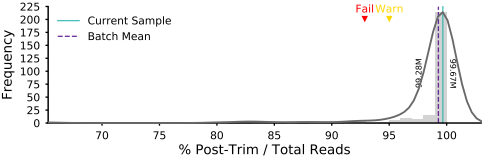
Distribution of Gene Expression



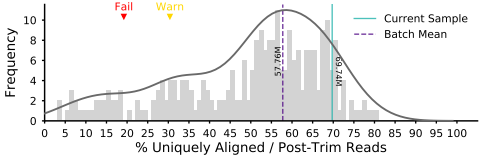
Sequencing Depth



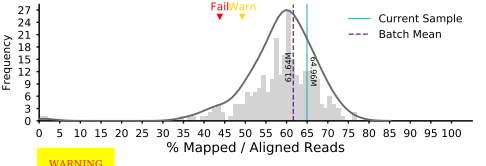
Trimming



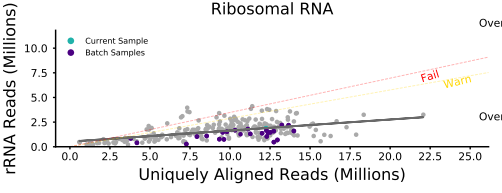
Alignment



Gene Exon Mapping

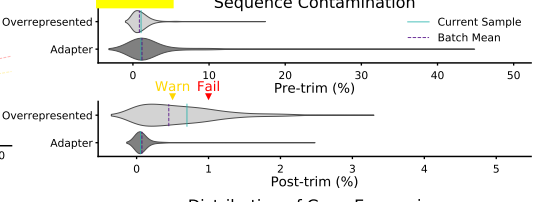


Ribosomal RNA

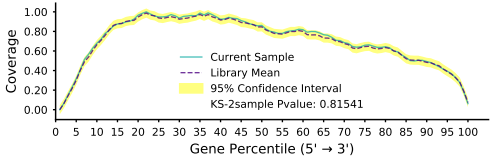


Sequence Contamination

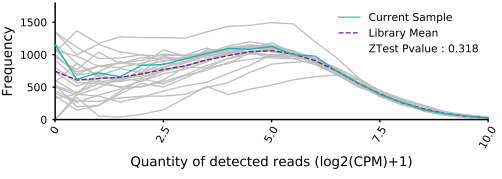
WARNING



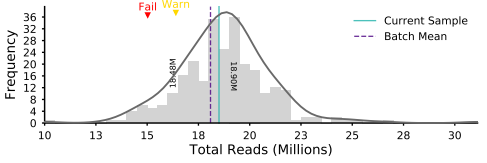
GeneBody Coverage Distribution



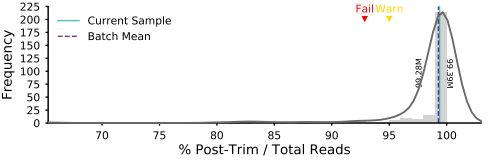
Distribution of Gene Expression



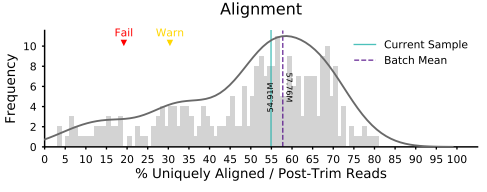
Sequencing Depth



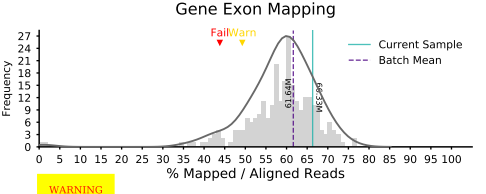
Trimming



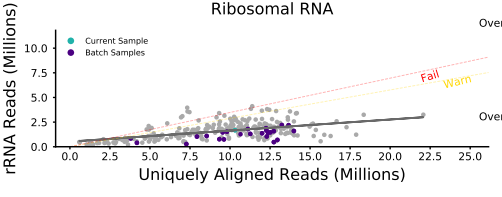
Alignment



Gene Exon Mapping

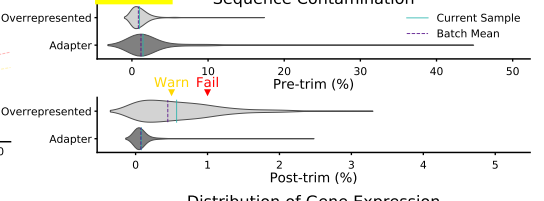


Ribosomal RNA

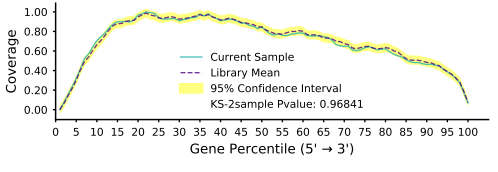


Sequence Contamination

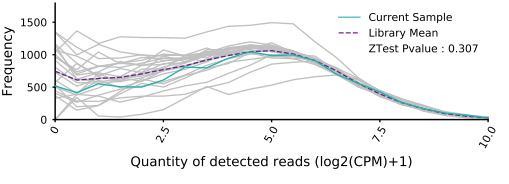
WARNING



GeneBody Coverage Distribution

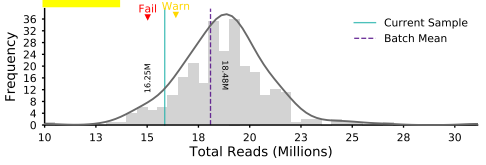


Distribution of Gene Expression

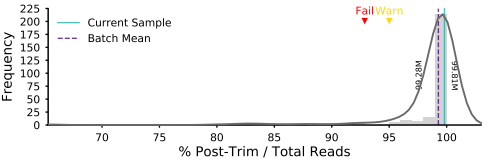


WARNING

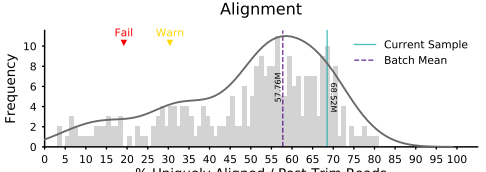
Sequencing Depth



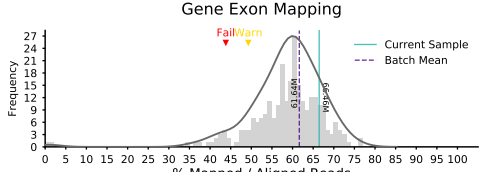
Trimming



Alignment

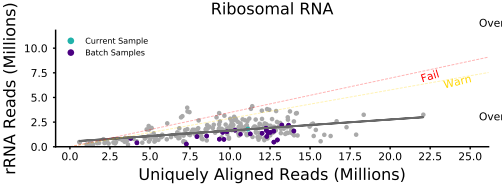


Gene Exon Mapping

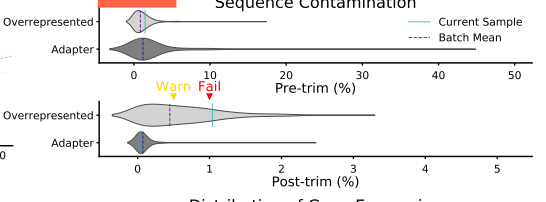


FAILURE

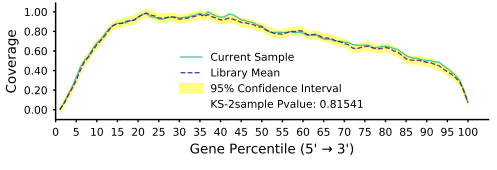
Ribosomal RNA



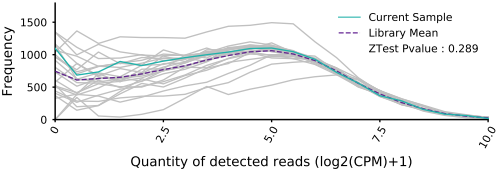
Sequence Contamination



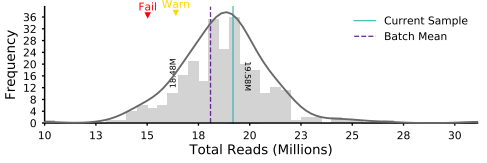
GeneBody Coverage Distribution



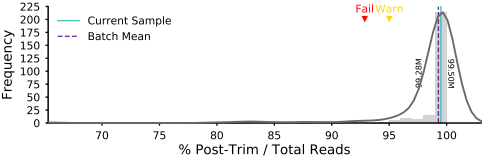
Distribution of Gene Expression



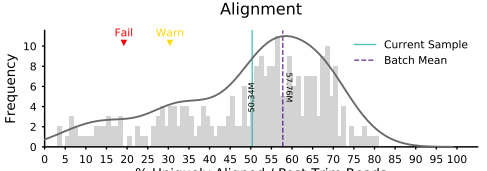
Sequencing Depth



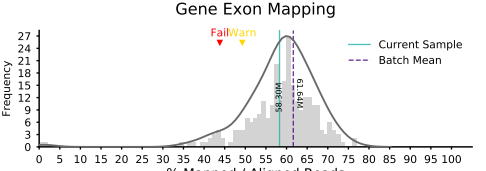
Trimming



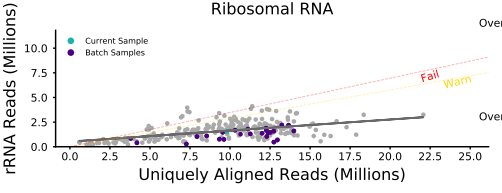
Alignment



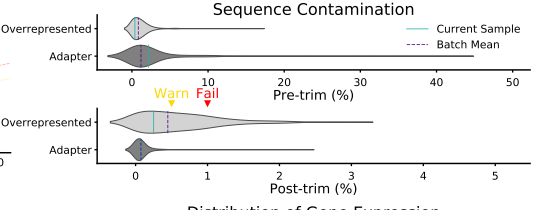
Gene Exon Mapping



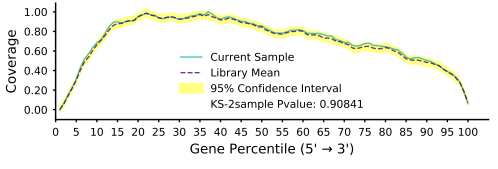
Ribosomal RNA



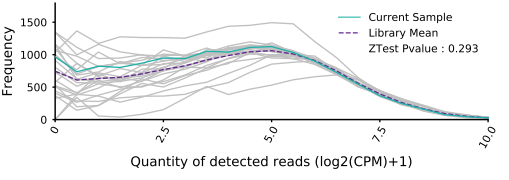
Sequence Contamination



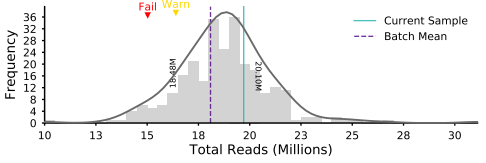
GeneBody Coverage Distribution



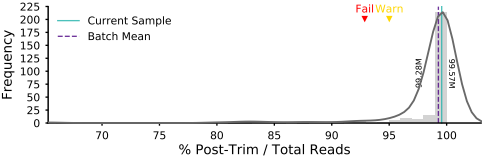
Distribution of Gene Expression



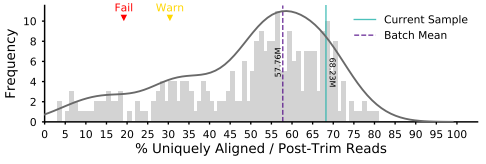
Sequencing Depth



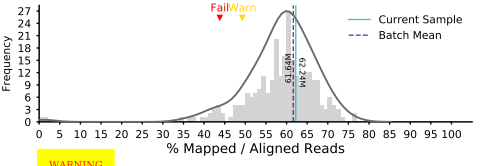
Trimming



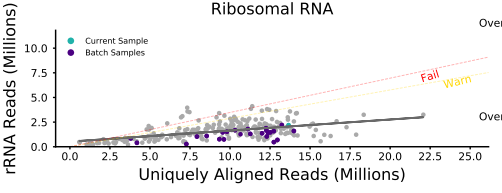
Alignment



Gene Exon Mapping

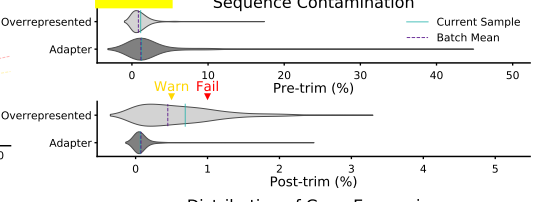


Ribosomal RNA

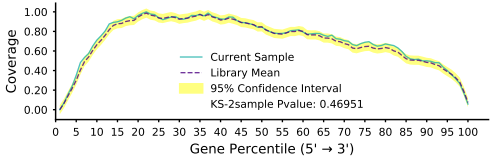


Sequence Contamination

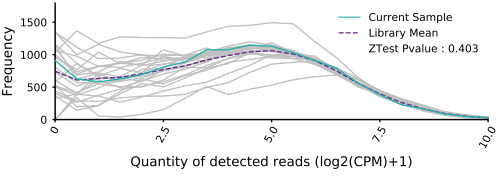
WARNING



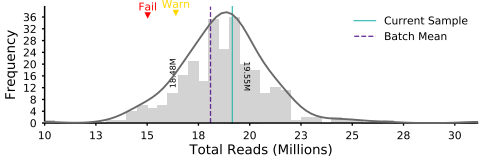
GeneBody Coverage Distribution



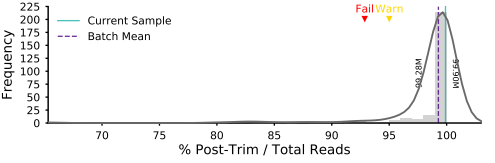
Distribution of Gene Expression



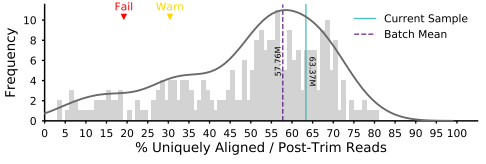
Sequencing Depth



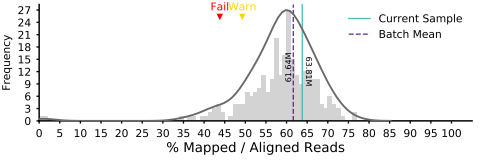
Trimming



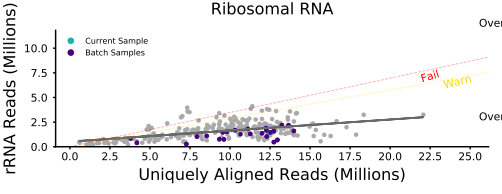
Alignment



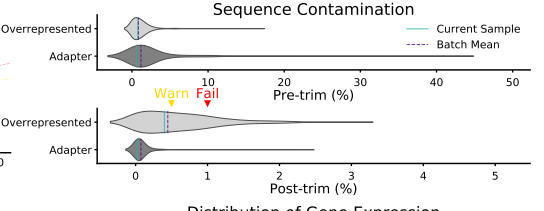
Gene Exon Mapping



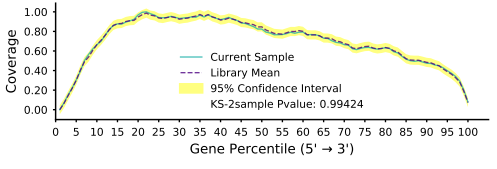
Ribosomal RNA



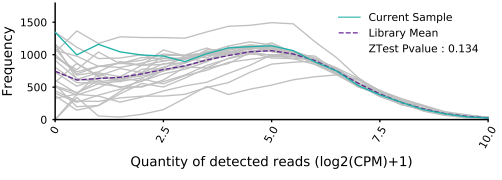
Sequence Contamination



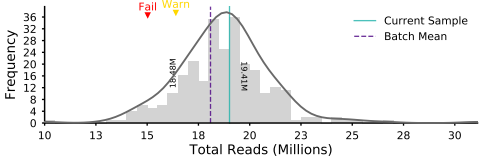
GeneBody Coverage Distribution



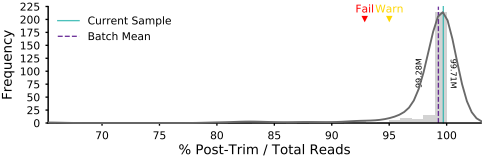
Distribution of Gene Expression



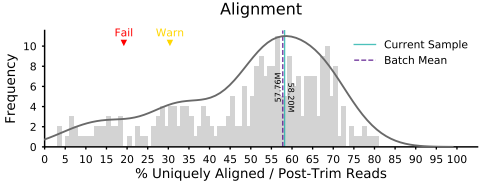
Sequencing Depth



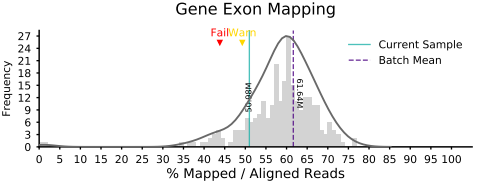
Trimming



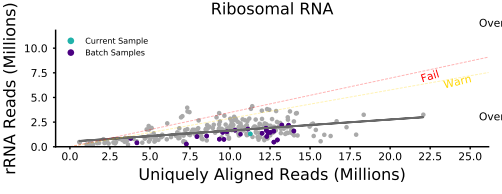
Alignment



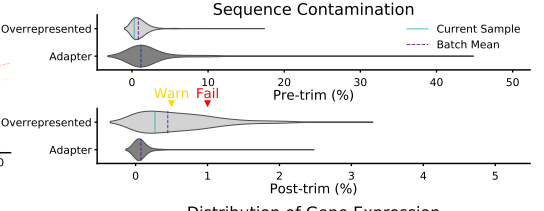
Gene Exon Mapping



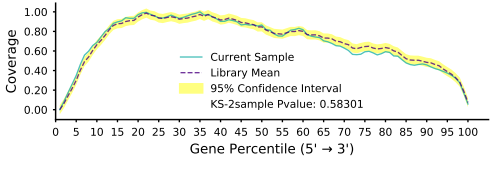
Ribosomal RNA



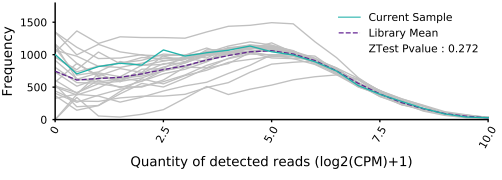
Sequence Contamination

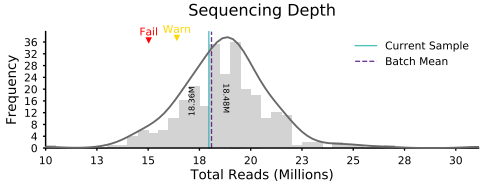


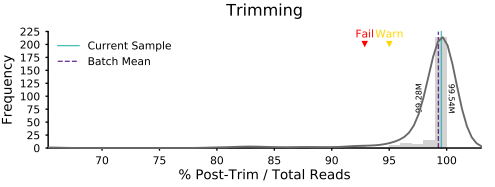
GeneBody Coverage Distribution

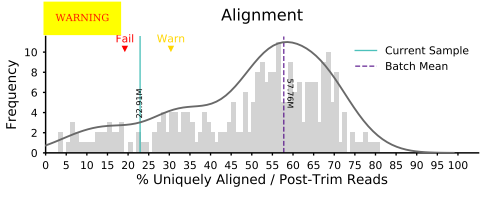


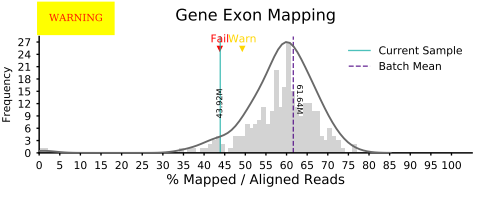
Distribution of Gene Expression

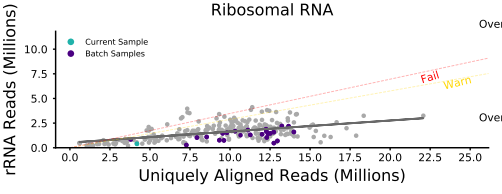


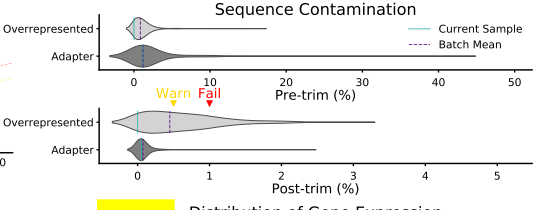

Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
18.36M
18.48M
Total Reads (Millions)

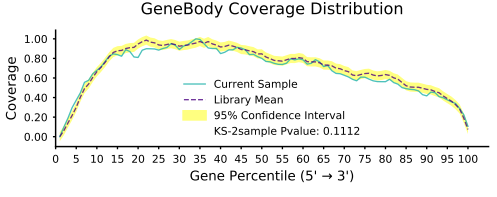

Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
98.28M
99.54M
% Post-Trim / Total Reads

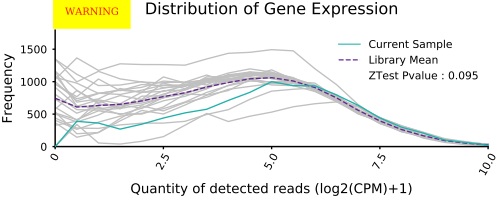

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
22.91M
57.76M
% Uniquely Aligned / Post-Trim Reads


WARNING
Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
43.92M
61.64M
% Mapped / Aligned Reads

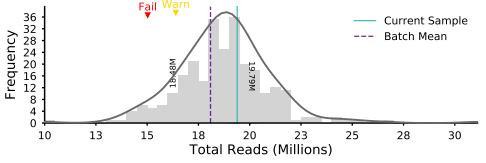

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

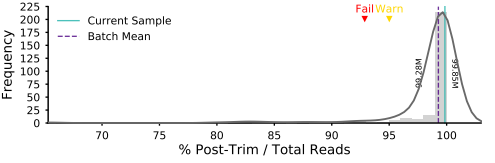

GeneBody Coverage Distribution
Coverage
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.1112
Gene Percentile (5' → 3')


WARNING
Distribution of Gene Expression
Current Sample
Library Mean
ZTest Pvalue : 0.095
Frequency
Quantity of detected reads (log2(CPM)+1)

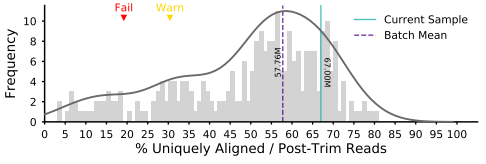
Sequencing Depth



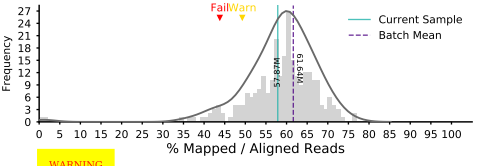
Trimming



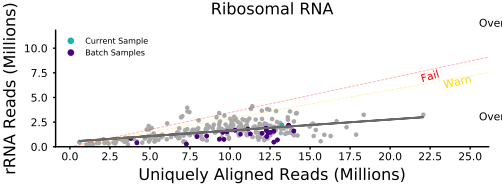
Alignment



Gene Exon Mapping

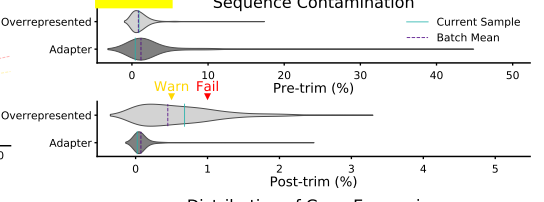


Ribosomal RNA

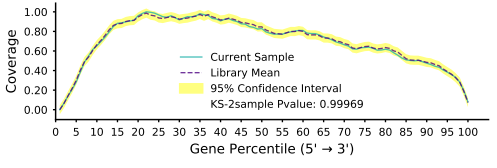


Sequence Contamination

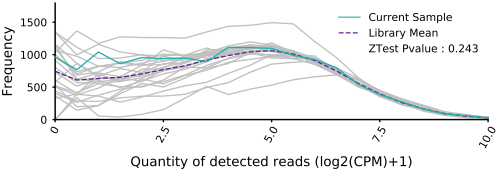
WARNING



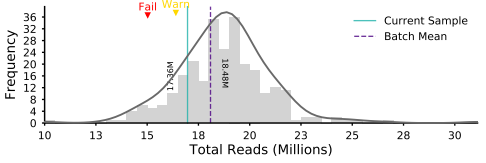
GeneBody Coverage Distribution



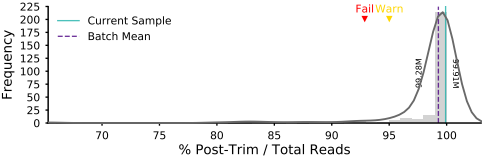
Distribution of Gene Expression



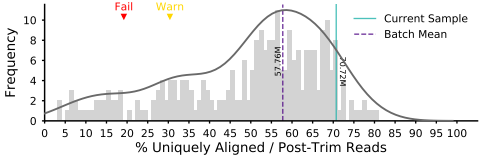
Sequencing Depth



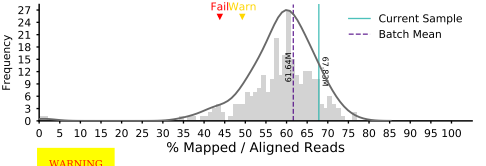
Trimming



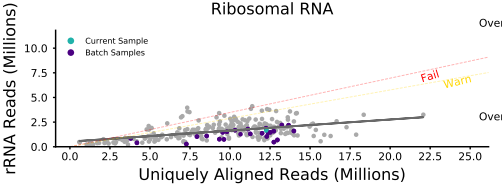
Alignment



Gene Exon Mapping

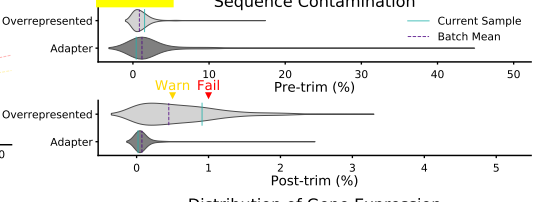


Ribosomal RNA

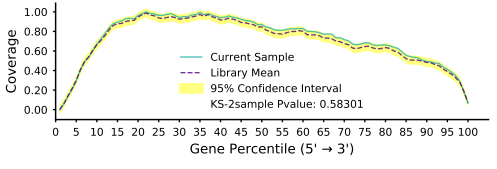


Sequence Contamination

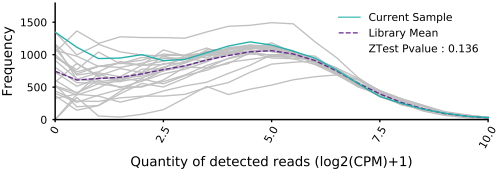
WARNING



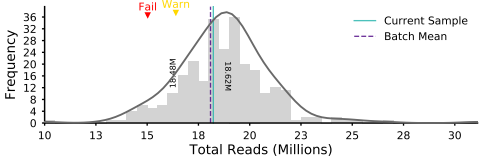
GeneBody Coverage Distribution



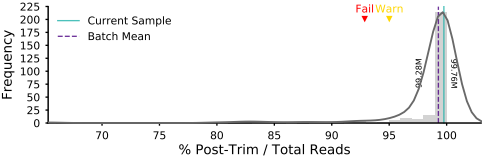
Distribution of Gene Expression



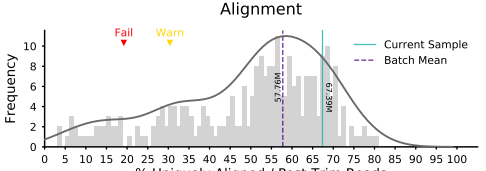
Sequencing Depth



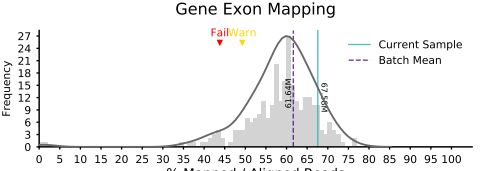
Trimming



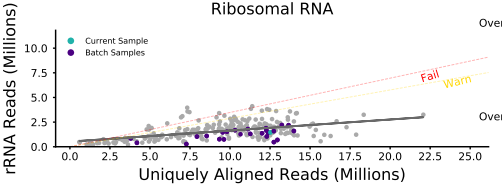
Alignment



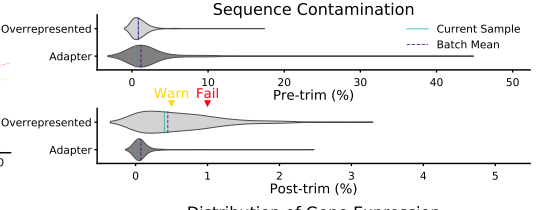
Gene Exon Mapping



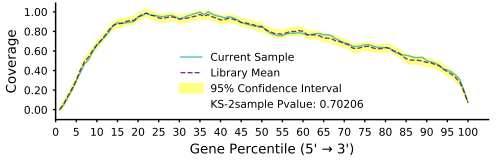
Ribosomal RNA



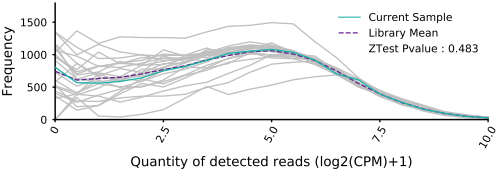
Sequence Contamination



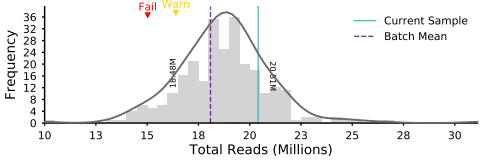
GeneBody Coverage Distribution



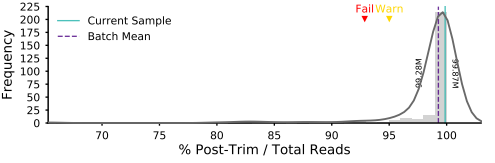
Distribution of Gene Expression



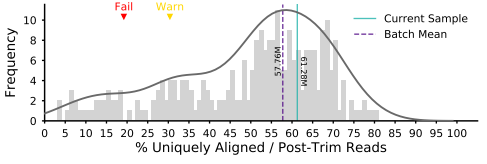
Sequencing Depth



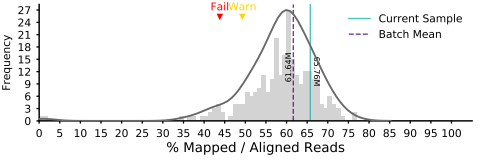
Trimming



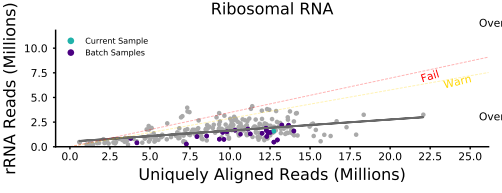
Alignment



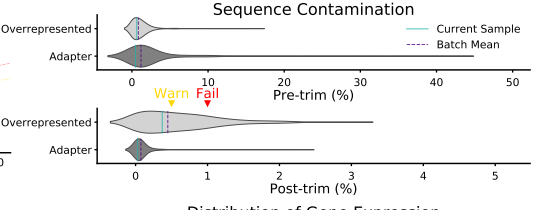
Gene Exon Mapping



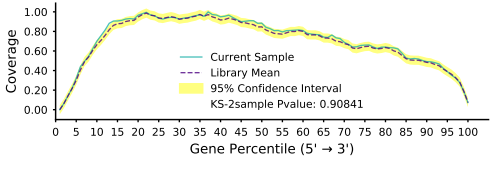
Ribosomal RNA



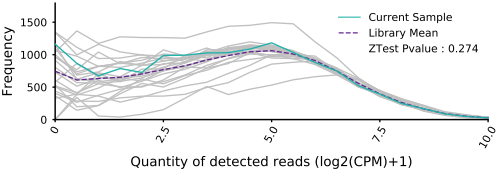
Sequence Contamination



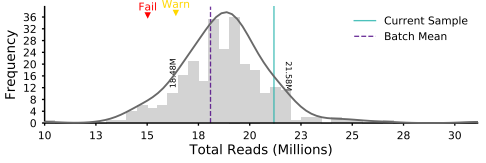
GeneBody Coverage Distribution



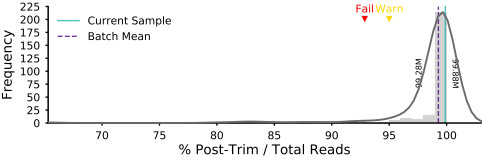
Distribution of Gene Expression



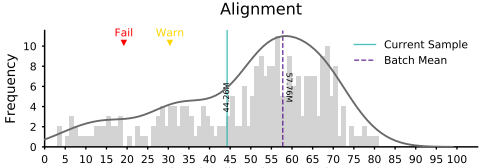
Sequencing Depth



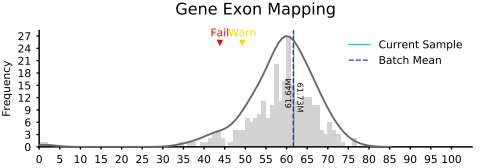
Trimming



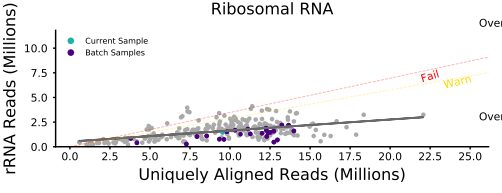
Alignment



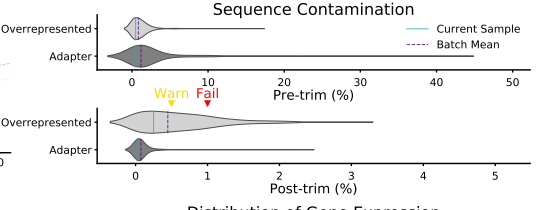
Gene Exon Mapping



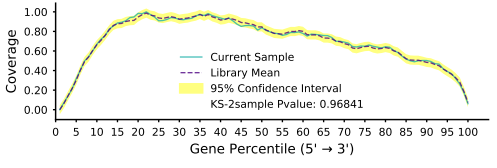
Ribosomal RNA



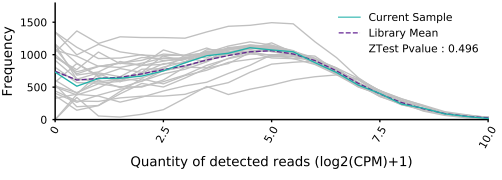
Sequence Contamination



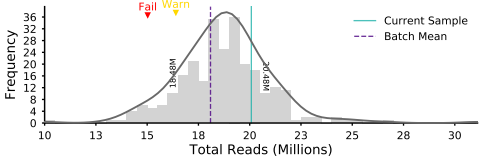
GeneBody Coverage Distribution



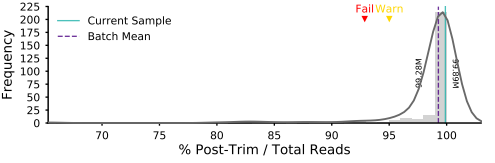
Distribution of Gene Expression



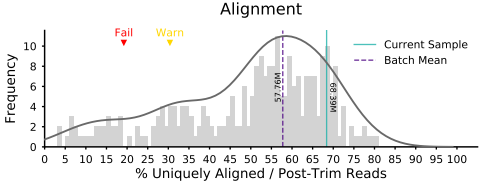
Sequencing Depth



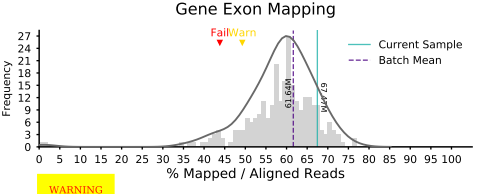
Trimming



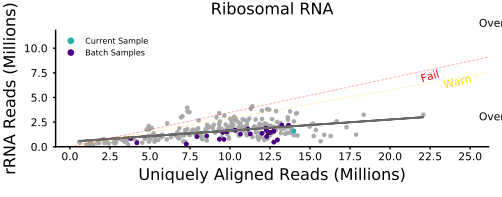
Alignment



Gene Exon Mapping

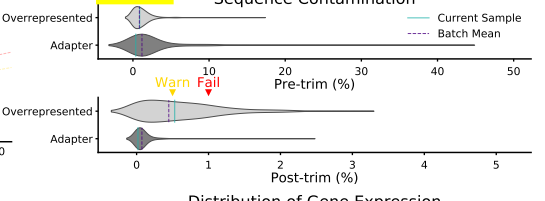


Ribosomal RNA

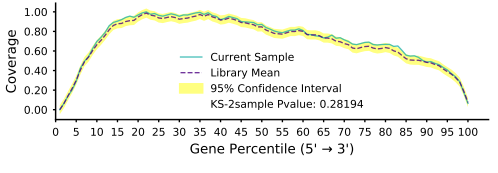


WARNING

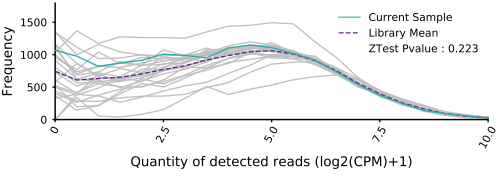
Sequence Contamination

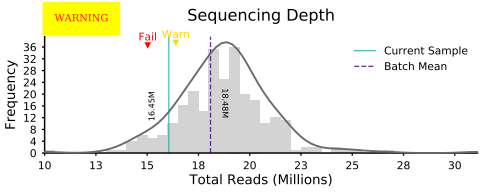


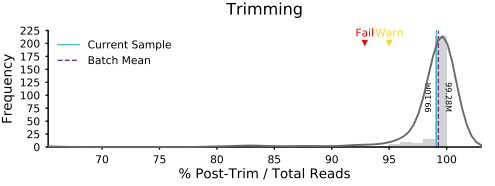
GeneBody Coverage Distribution

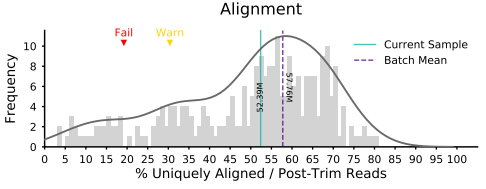


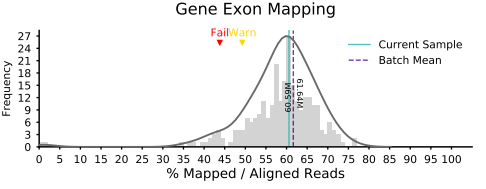
Distribution of Gene Expression

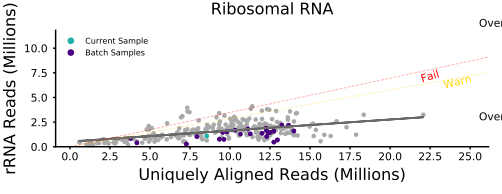


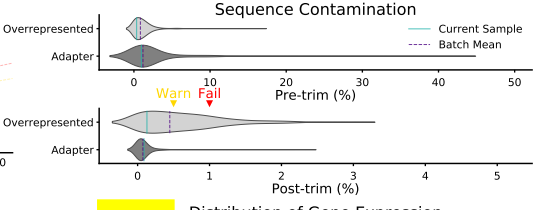

WARNING
Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
16.45M
18.48M
Total Reads (Millions)

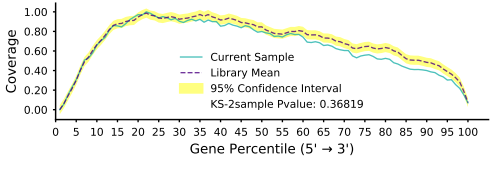

Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
99.10M
99.28M
% Post-Trim / Total Reads

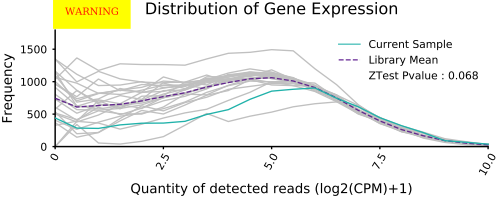

Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
52.38M
57.70M
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
60.69M
61.41M
% Mapped / Aligned Reads

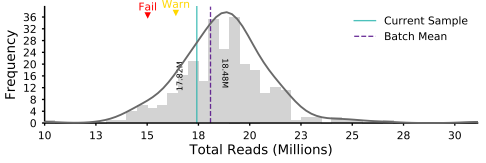

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

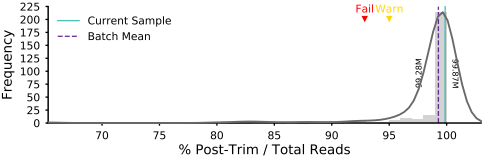

GeneBody Coverage Distribution
Coverage
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.36819
Gene Percentile (5' → 3')


WARNING
Distribution of Gene Expression
Current Sample
Library Mean
ZTest Pvalue : 0.068
Frequency
Quantity of detected reads (log2(CPM)+1)

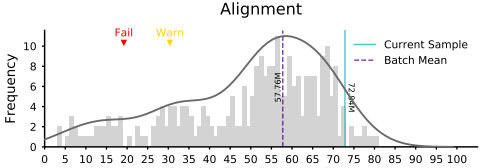
Sequencing Depth



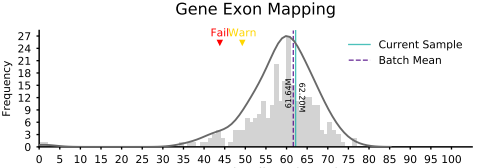
Trimming



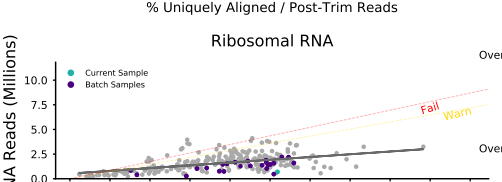
Alignment



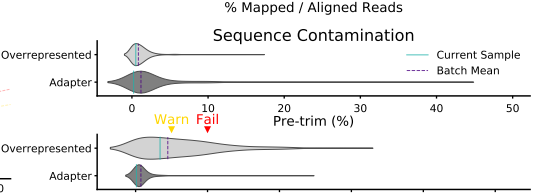
Gene Exon Mapping



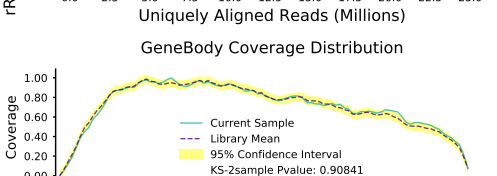
Ribosomal RNA



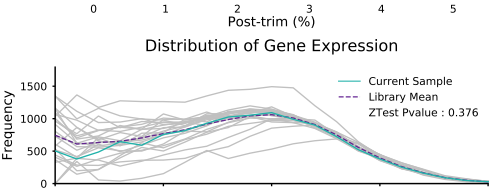
Sequence Contamination

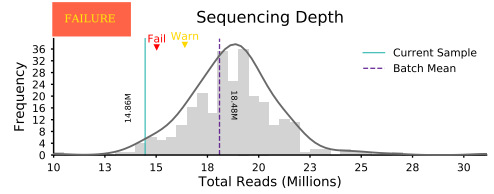


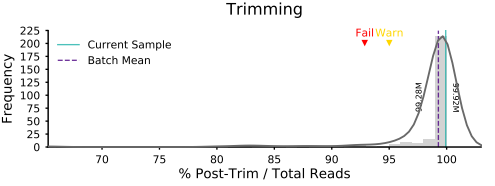
GeneBody Coverage Distribution

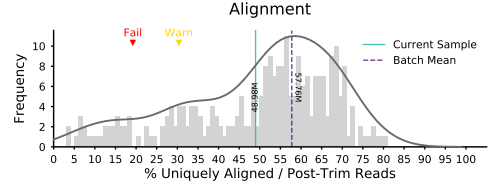


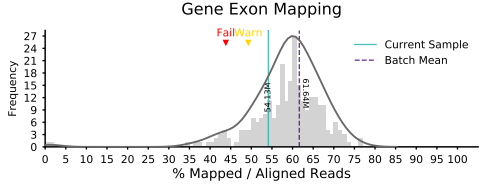
Distribution of Gene Expression

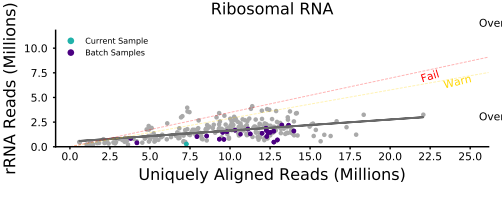


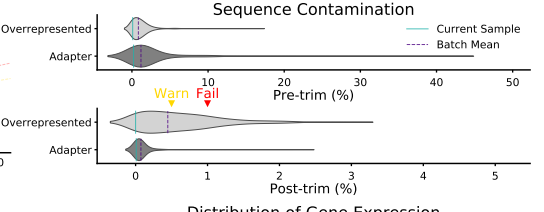

FAILURE
Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
14.86M
18.48M
Total Reads (Millions)

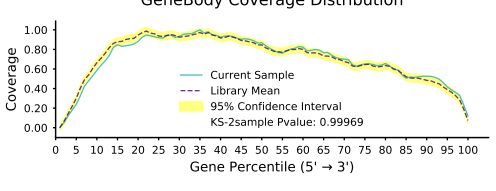

Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
98.28M
99.93M
% Post-Trim / Total Reads

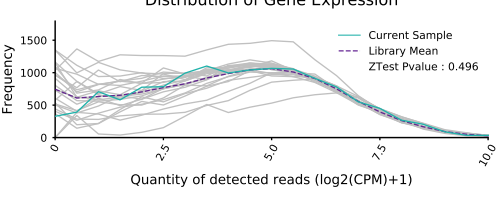

Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
48.98M
57.76M
% Uniquely Aligned / Post-Trim Reads


Gene Exon Mapping
Fail
Warn
Current Sample
Batch Mean
Frequency
54.13M
61.64M
% Mapped / Aligned Reads

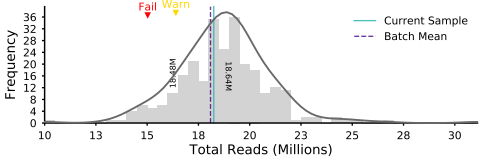

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

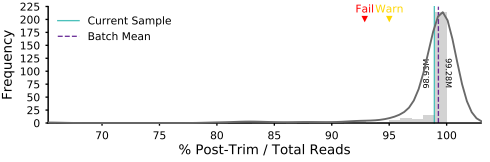

GeneBody Coverage Distribution
Coverage
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.99969
Gene Percentile (5' → 3')


Distribution of Gene Expression
Frequency
Current Sample
Library Mean
ZTest Pvalue : 0.496
Quantity of detected reads (log2(CPM)+1)

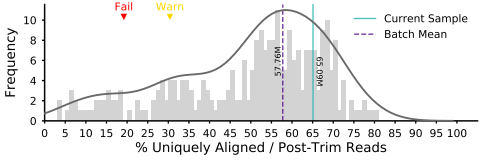
Sequencing Depth



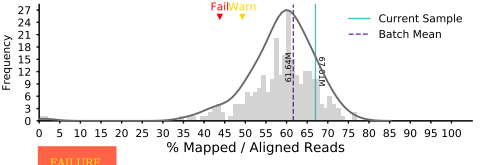
Trimming



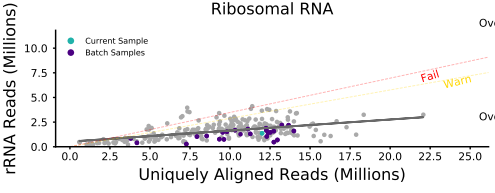
Alignment



Gene Exon Mapping

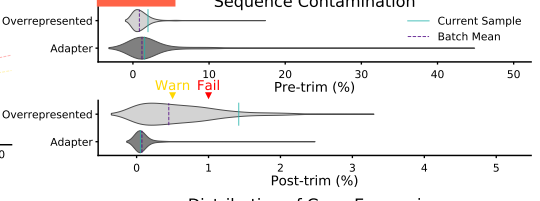


Ribosomal RNA

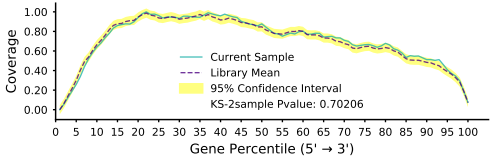


FAILURE

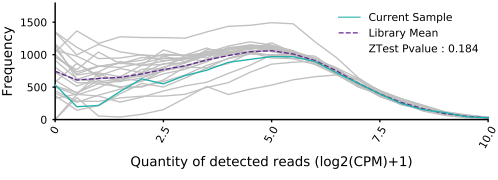
Sequence Contamination



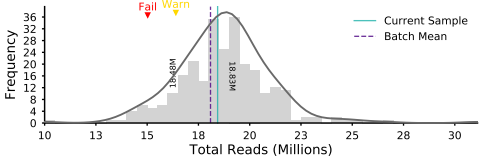
GeneBody Coverage Distribution



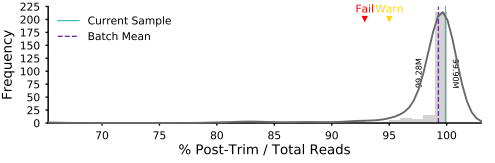
Distribution of Gene Expression



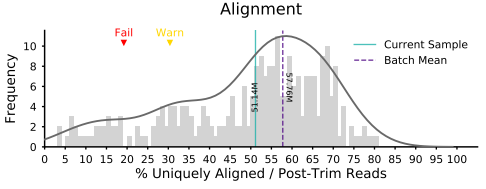
Sequencing Depth



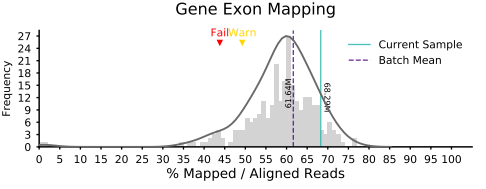
Trimming



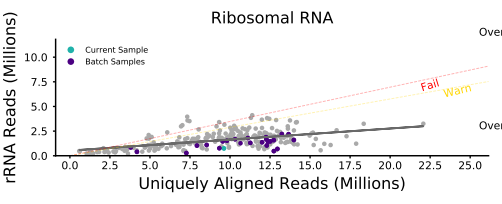
Alignment



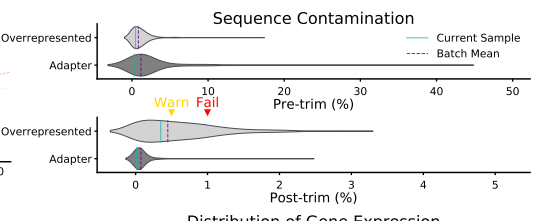
Gene Exon Mapping



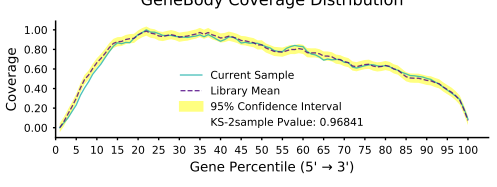
Ribosomal RNA



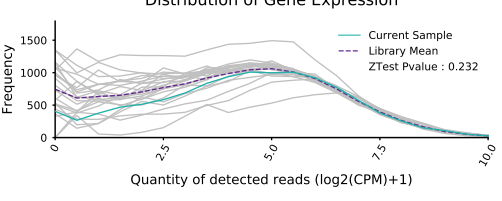
Sequence Contamination



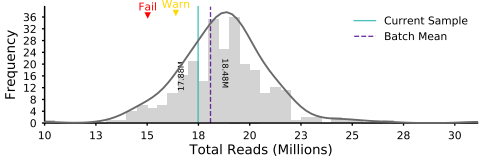
GeneBody Coverage Distribution



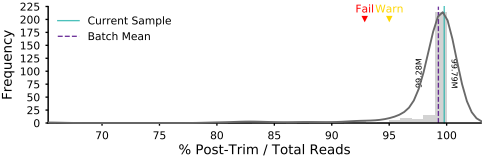
Distribution of Gene Expression



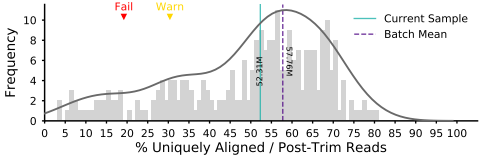
Sequencing Depth



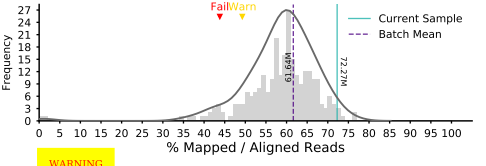
Trimming



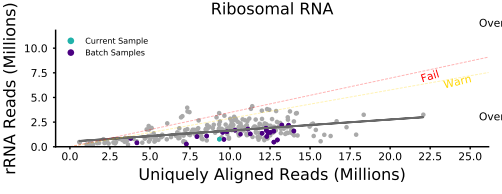
Alignment



Gene Exon Mapping

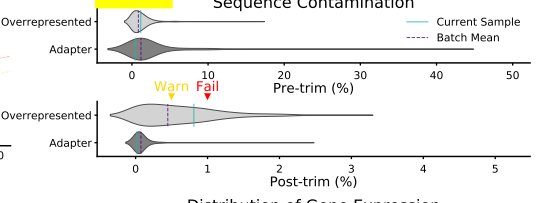


Ribosomal RNA

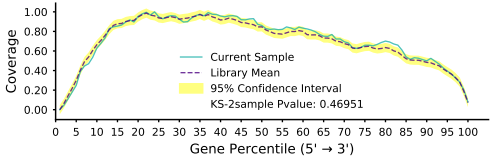


Sequence Contamination

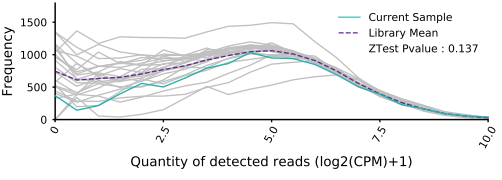
WARNING



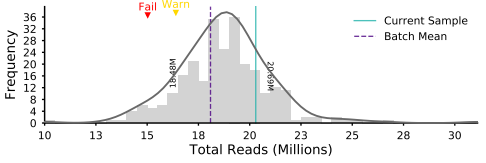
GeneBody Coverage Distribution



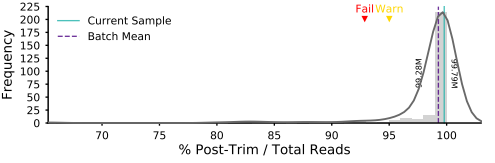
Distribution of Gene Expression



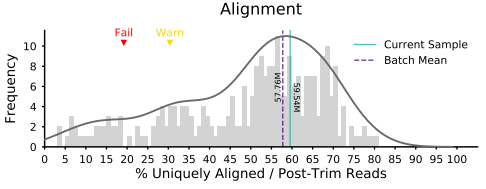
Sequencing Depth



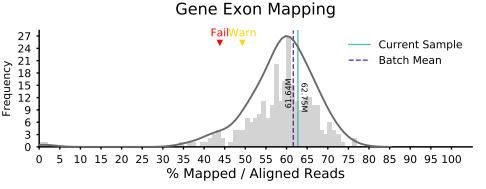
Trimming



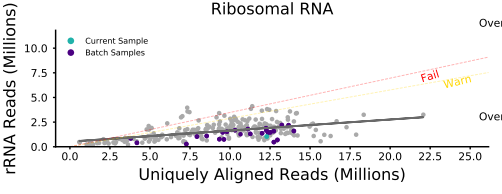
Alignment



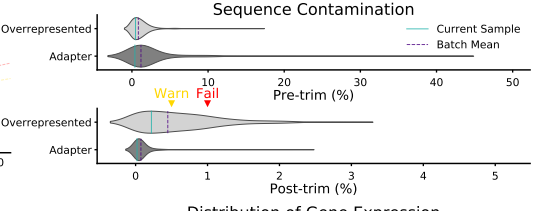
Gene Exon Mapping



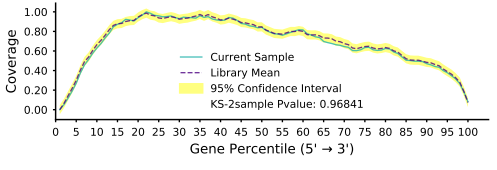
Ribosomal RNA



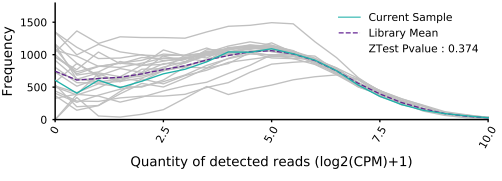
Sequence Contamination



GeneBody Coverage Distribution

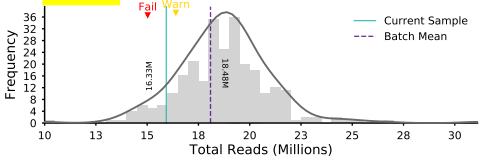


Distribution of Gene Expression

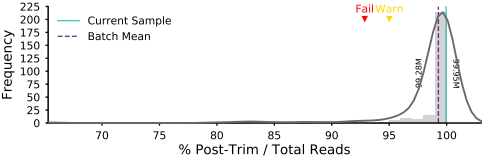


WARNING

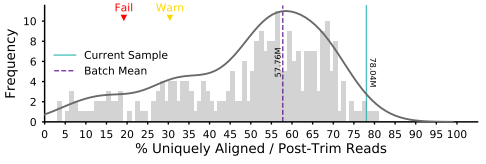
Sequencing Depth



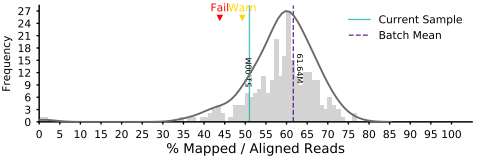
Trimming



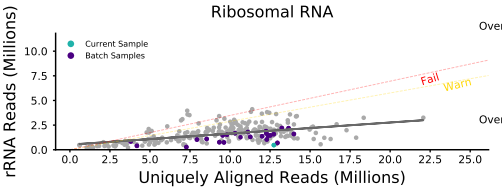
Alignment



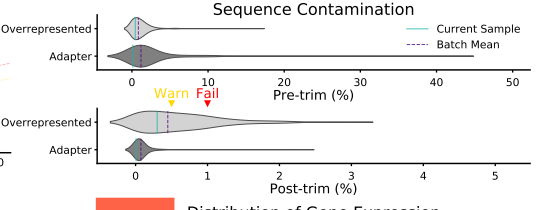
Gene Exon Mapping



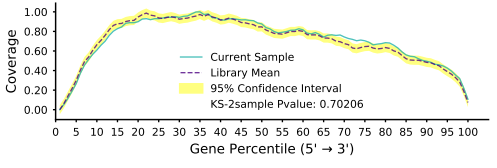
Ribosomal RNA



Sequence Contamination

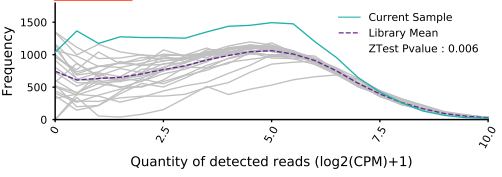


GeneBody Coverage Distribution

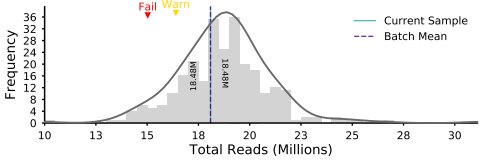


FAILURE

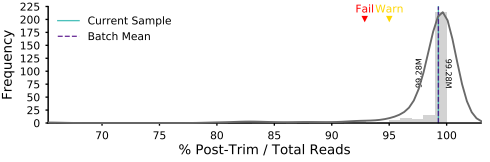
Distribution of Gene Expression



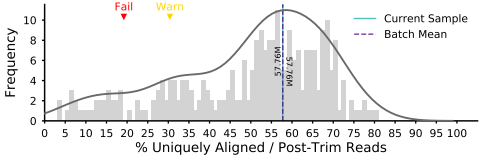
Sequencing Depth



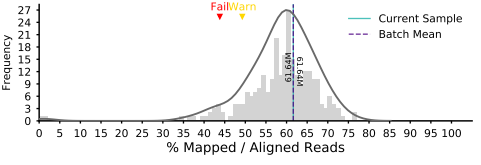
Trimming



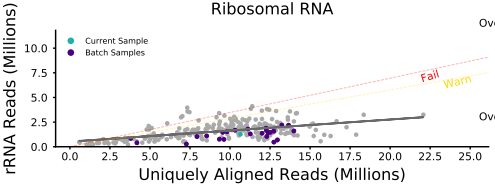
Alignment



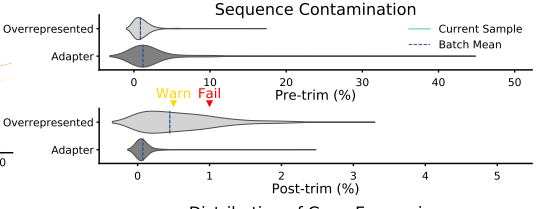
Gene Exon Mapping



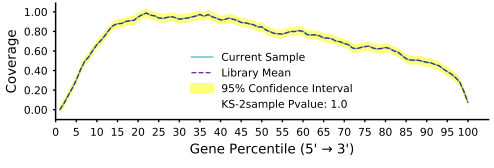
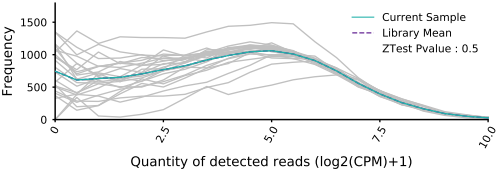
Ribosomal RNA



Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression