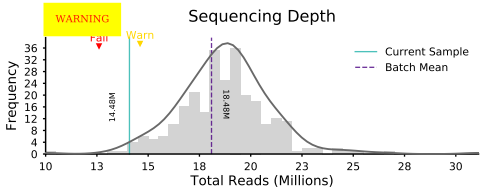
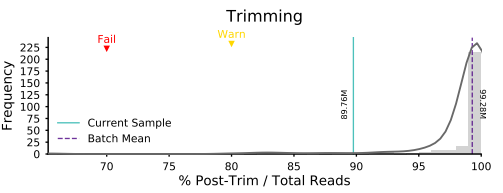
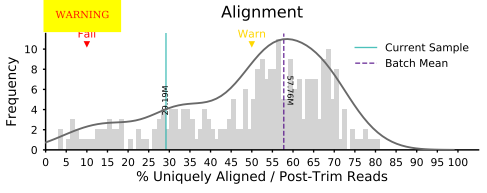
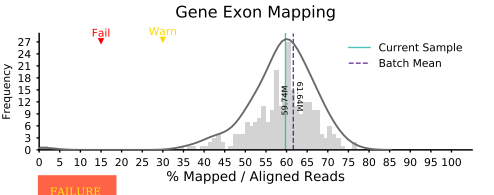
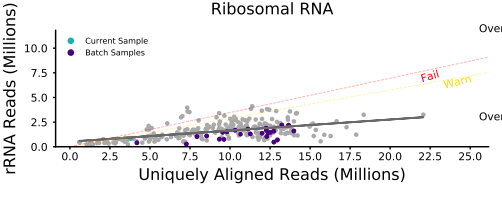
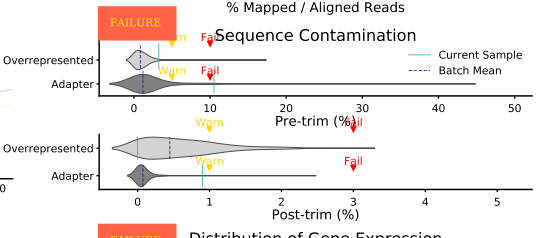

WARNING
Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
14.48M
18.48M
Total Reads (Millions)

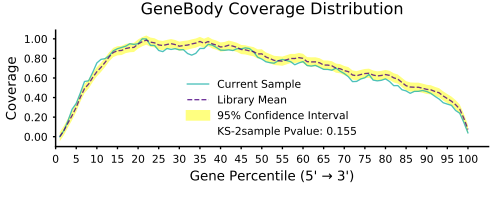

Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
89.76M
99.28M
% Post-Trim / Total Reads

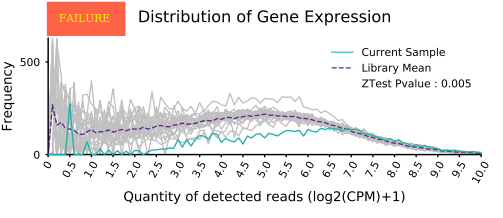

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
29.19M
57.76M
% Uniquely Aligned / Post-Trim Reads


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

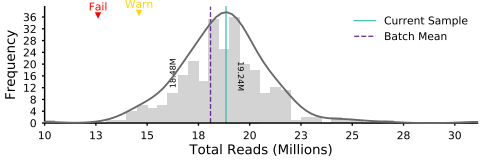

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

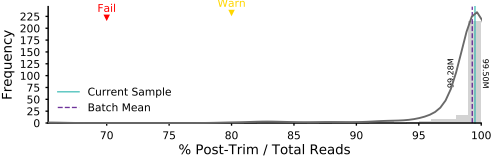

GeneBody Coverage Distribution
Coverage
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 0.155
Gene Percentile (5' → 3')


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

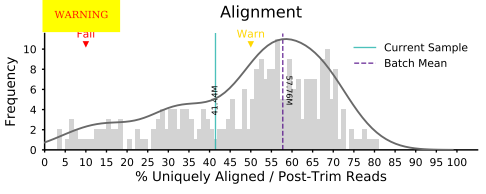
Sequencing Depth



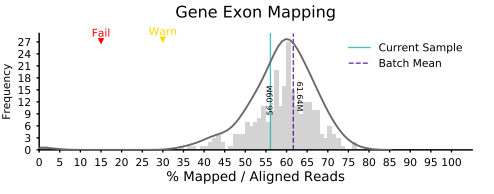
Trimming



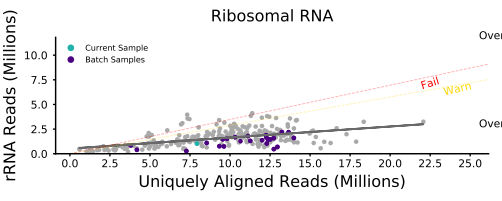
Alignment



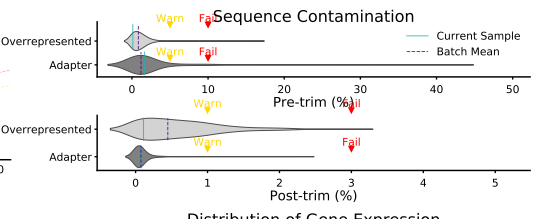
Gene Exon Mapping



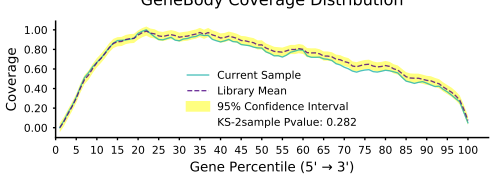
Ribosomal RNA



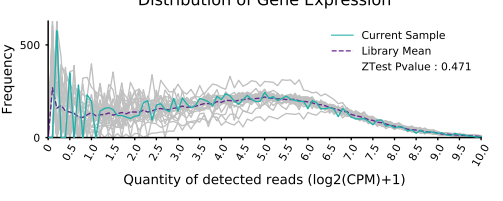
Sequence Contamination



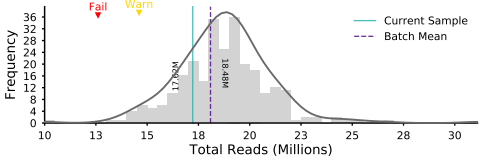
GeneBody Coverage Distribution



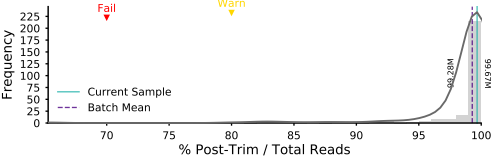
Distribution of Gene Expression



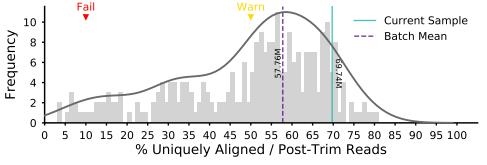
Sequencing Depth



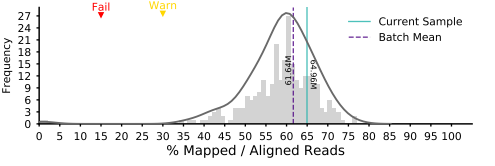
Trimming



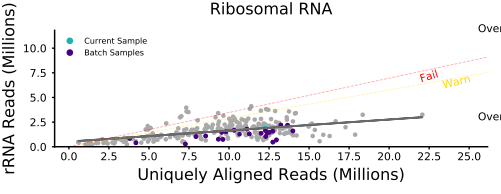
Alignment



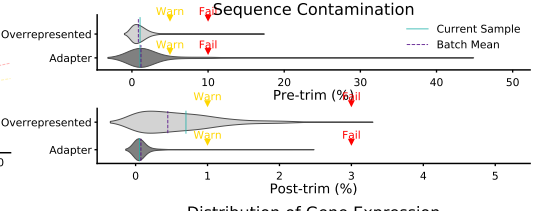
Gene Exon Mapping



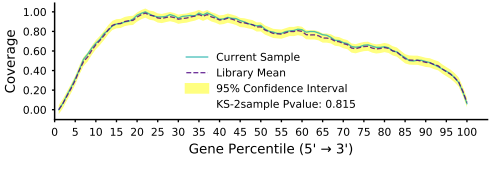
Ribosomal RNA



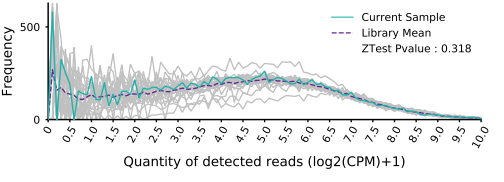
Sequence Contamination



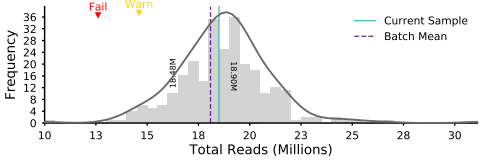
GeneBody Coverage Distribution



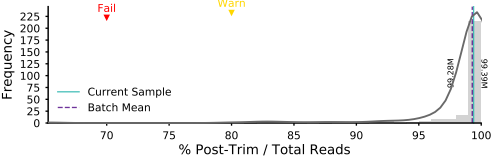
Distribution of Gene Expression



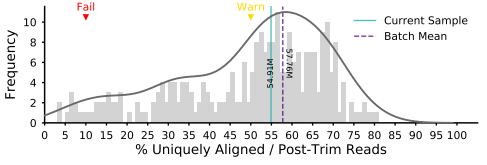
Sequencing Depth



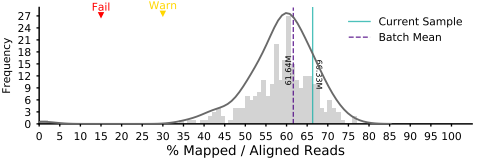
Trimming



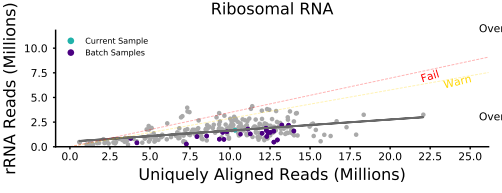
Alignment



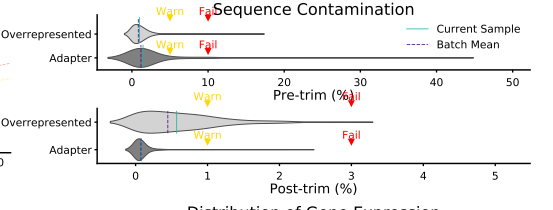
Gene Exon Mapping



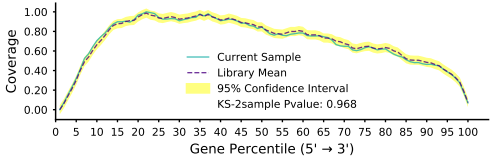
Ribosomal RNA



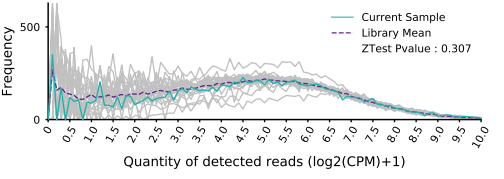
Sequence Contamination



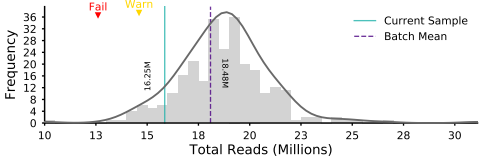
GeneBody Coverage Distribution



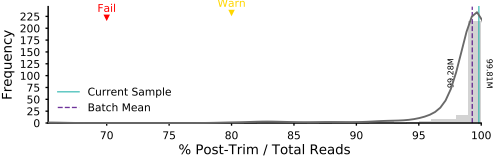
Distribution of Gene Expression



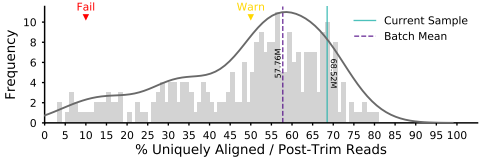
Sequencing Depth



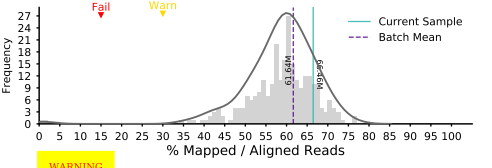
Trimming



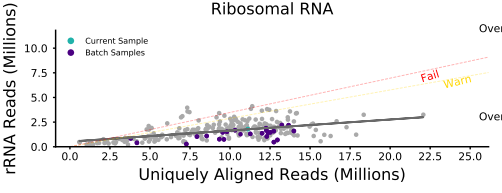
Alignment



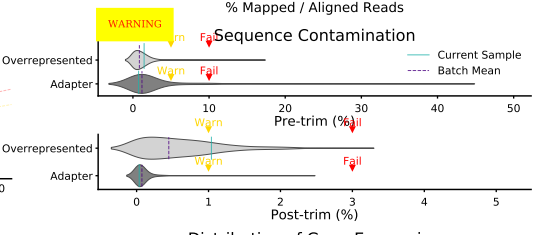
Gene Exon Mapping



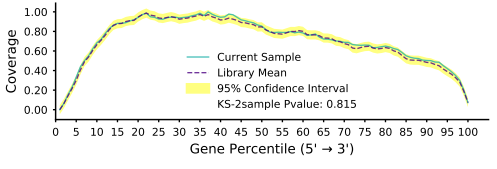
Ribosomal RNA



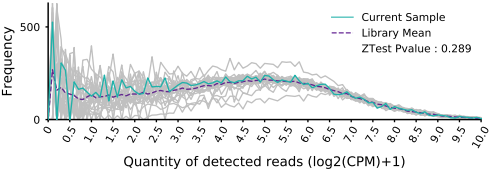
Sequence Contamination



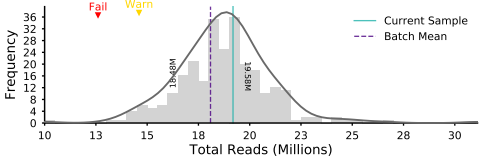
GeneBody Coverage Distribution



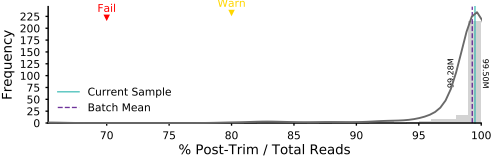
Distribution of Gene Expression



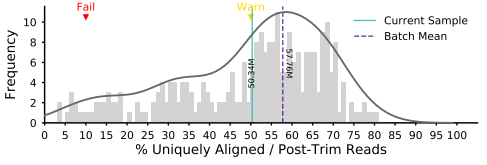
Sequencing Depth



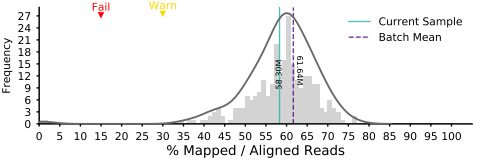
Trimming



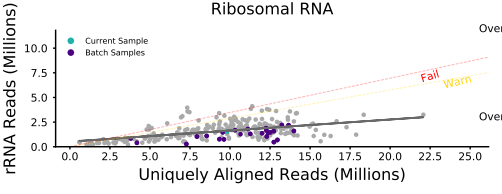
Alignment



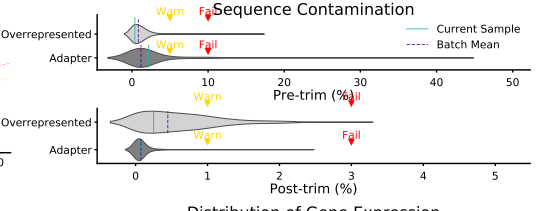
Gene Exon Mapping



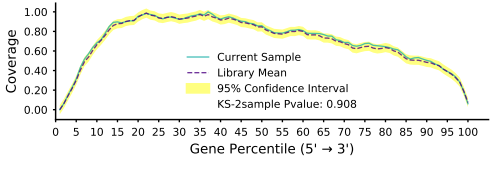
Ribosomal RNA



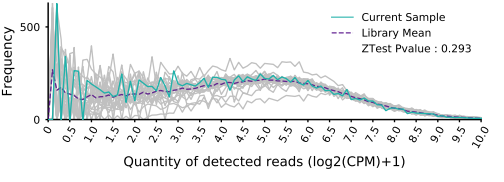
Sequence Contamination



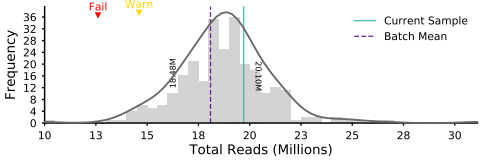
GeneBody Coverage Distribution



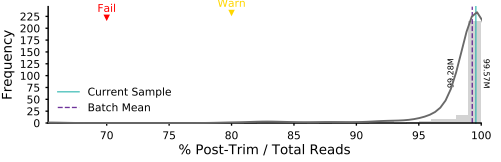
Distribution of Gene Expression



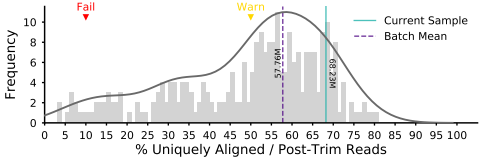
Sequencing Depth



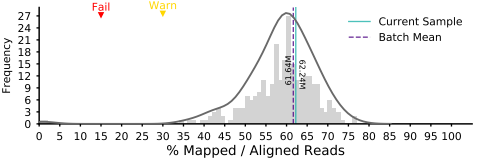
Trimming



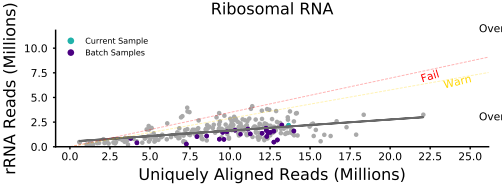
Alignment



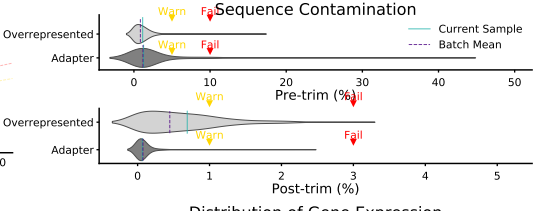
Gene Exon Mapping



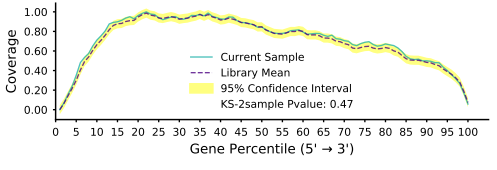
Ribosomal RNA



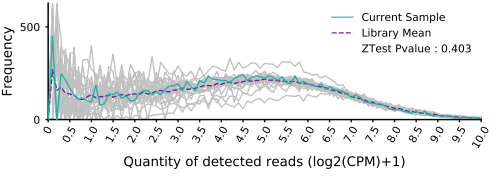
Sequence Contamination



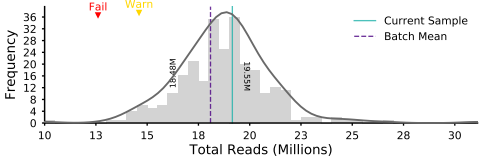
GeneBody Coverage Distribution



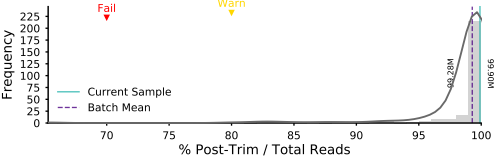
Distribution of Gene Expression



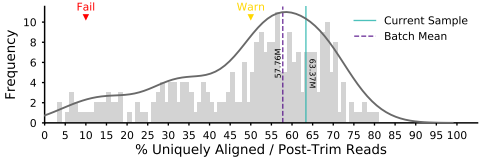
Sequencing Depth



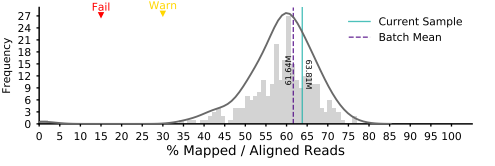
Trimming



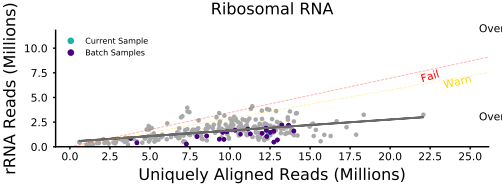
Alignment



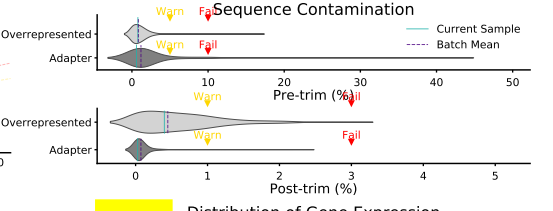
Gene Exon Mapping



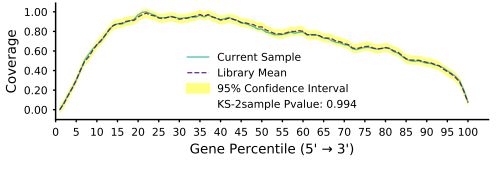
Ribosomal RNA



Sequence Contamination

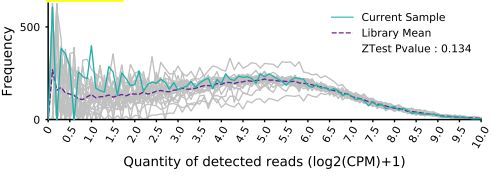


GeneBody Coverage Distribution

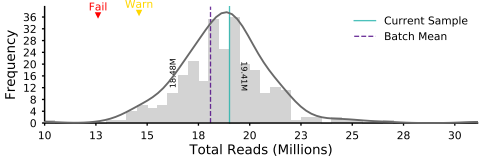


Distribution of Gene Expression

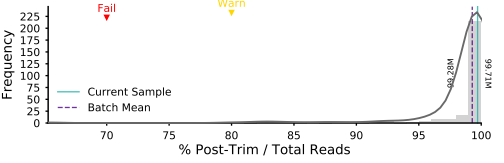
WARNING



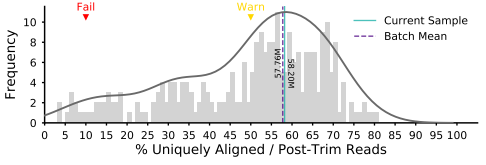
Sequencing Depth



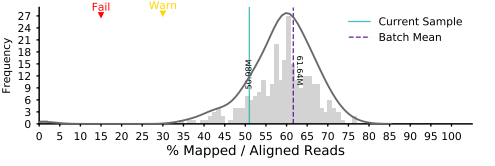
Trimming



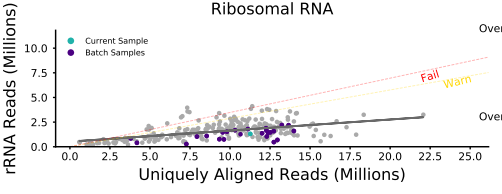
Alignment



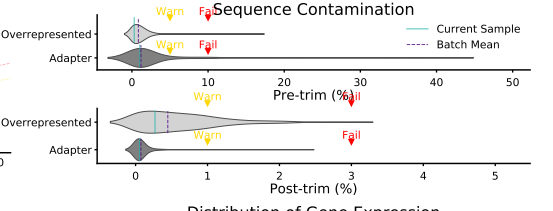
Gene Exon Mapping



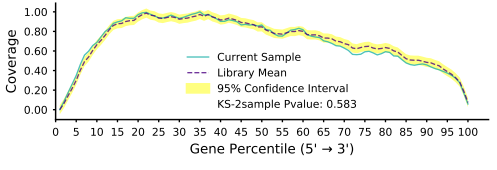
Ribosomal RNA



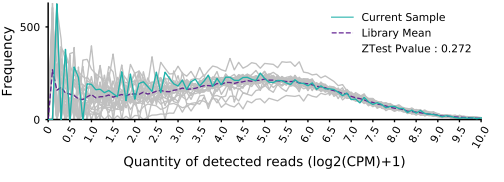
Sequence Contamination



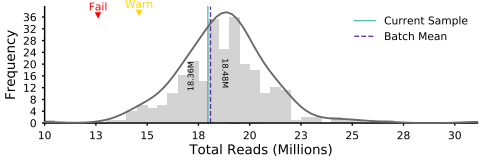
GeneBody Coverage Distribution



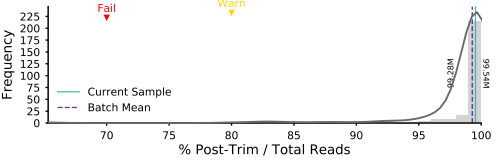
Distribution of Gene Expression



Sequencing Depth

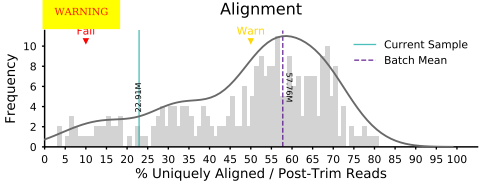


Trimming

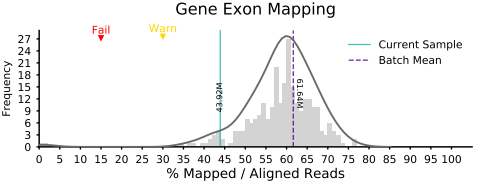


WARNING

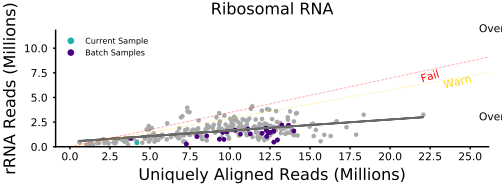
Alignment



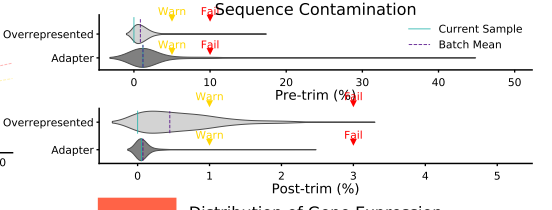
Gene Exon Mapping



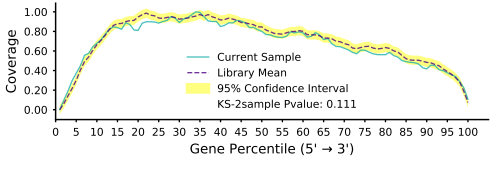
Ribosomal RNA



Sequence Contamination

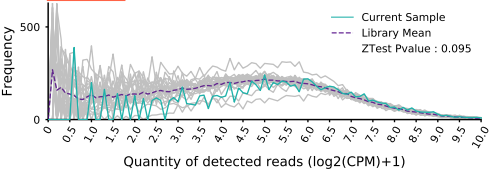


GeneBody Coverage Distribution

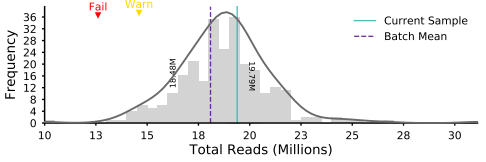


FAILURE

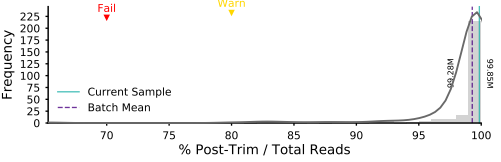
Distribution of Gene Expression



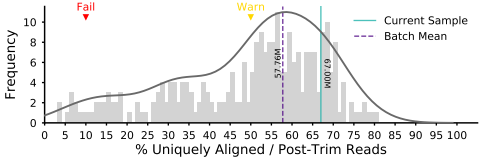
Sequencing Depth



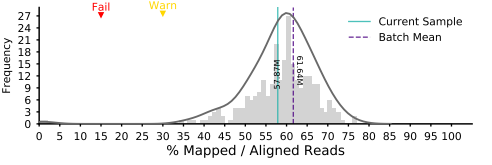
Trimming



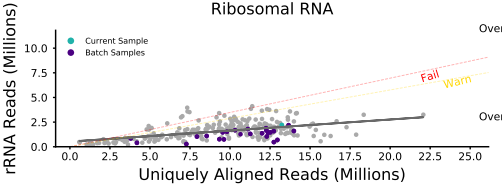
Alignment



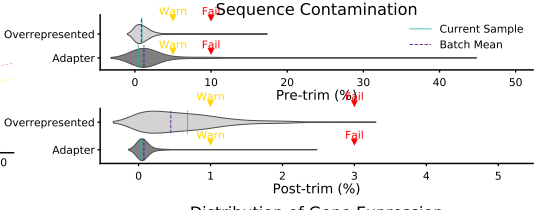
Gene Exon Mapping



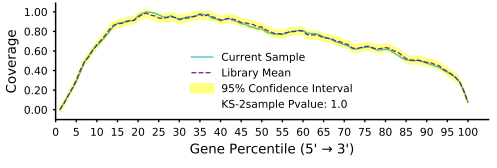
Ribosomal RNA



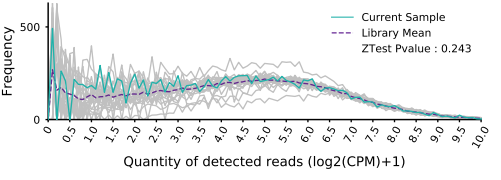
Sequence Contamination



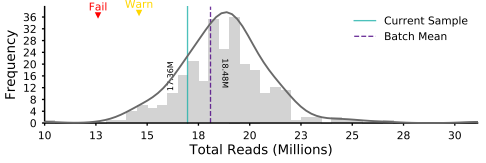
GeneBody Coverage Distribution



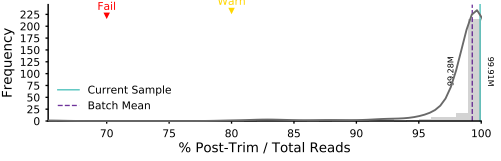
Distribution of Gene Expression



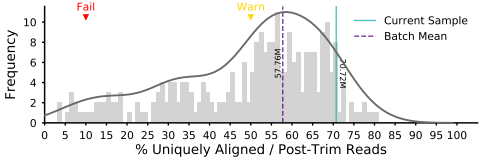
Sequencing Depth



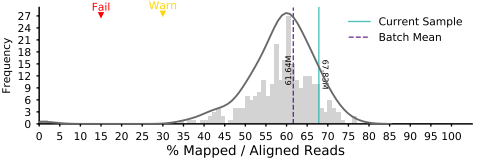
Trimming



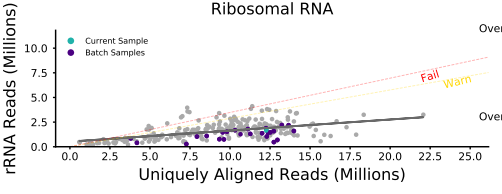
Alignment



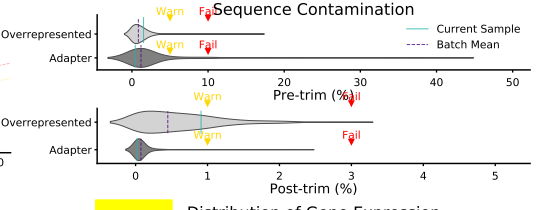
Gene Exon Mapping



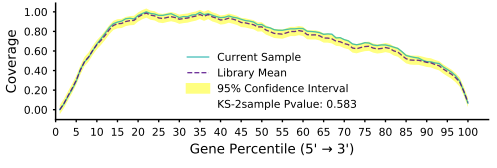
Ribosomal RNA



Sequence Contamination

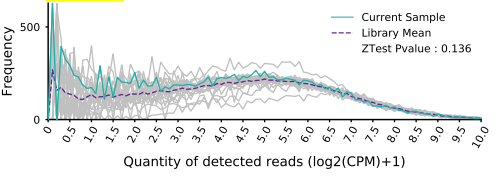


GeneBody Coverage Distribution

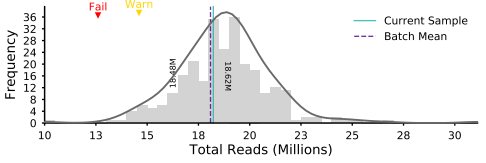


Distribution of Gene Expression

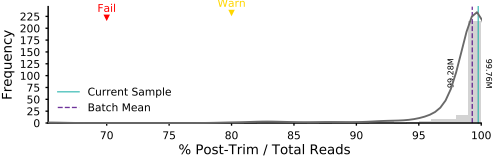
WARNING



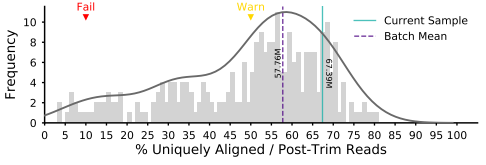
Sequencing Depth



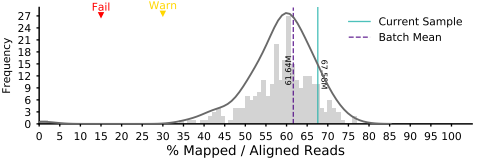
Trimming



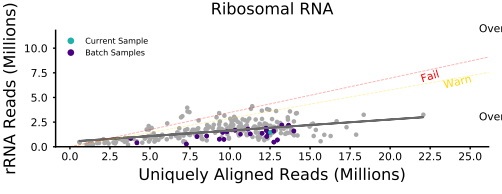
Alignment



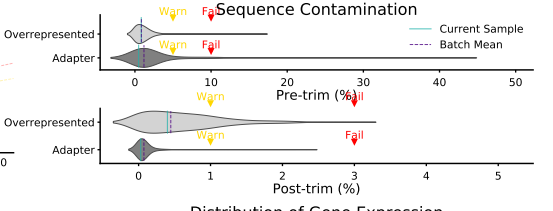
Gene Exon Mapping



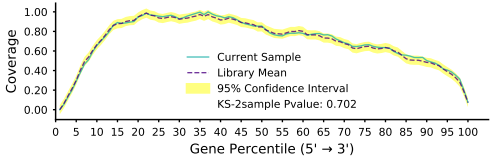
Ribosomal RNA



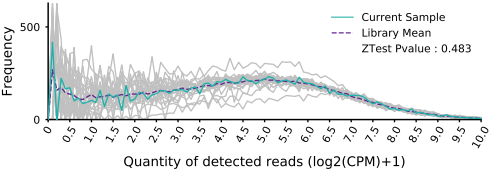
Sequence Contamination



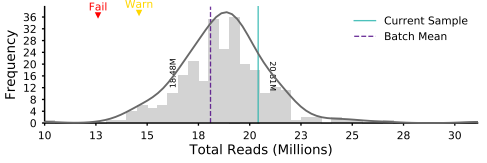
GeneBody Coverage Distribution



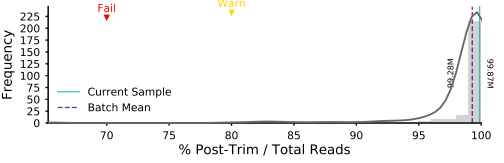
Distribution of Gene Expression



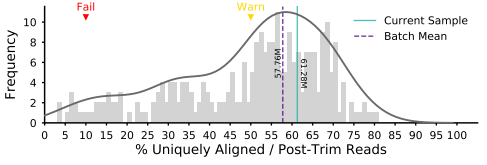
Sequencing Depth



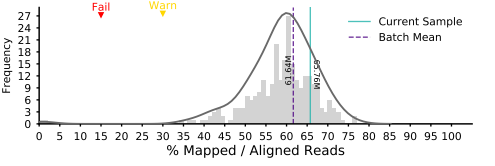
Trimming



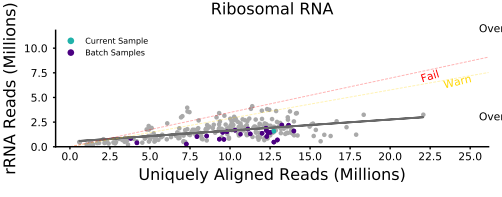
Alignment



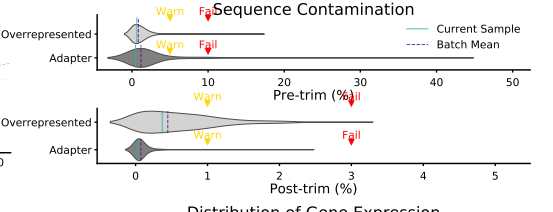
Gene Exon Mapping



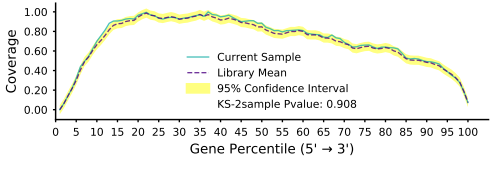
Ribosomal RNA



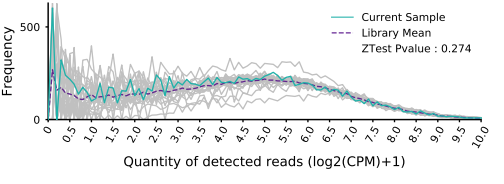
Sequence Contamination



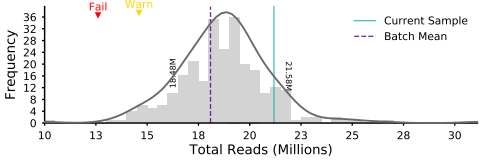
GeneBody Coverage Distribution



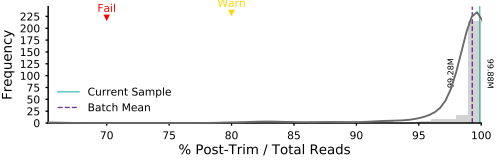
Distribution of Gene Expression



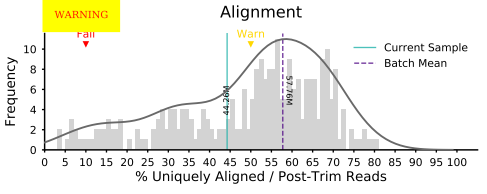
Sequencing Depth



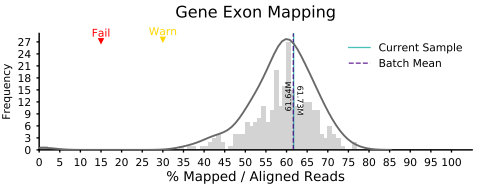
Trimming



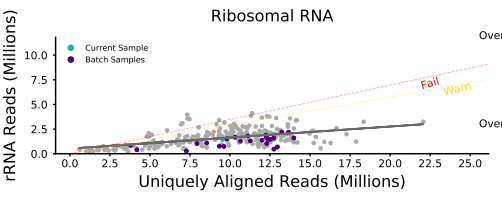
Alignment



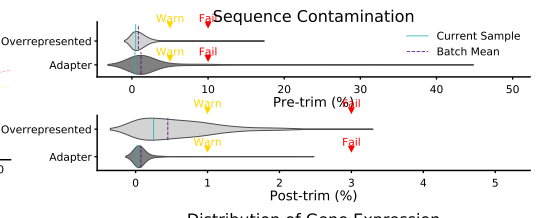
Gene Exon Mapping



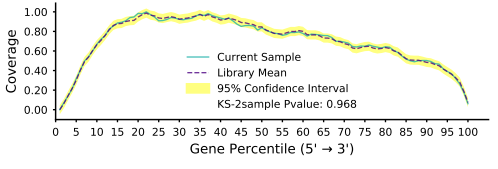
Ribosomal RNA



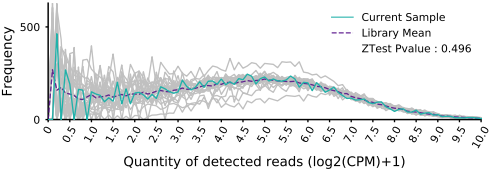
Sequence Contamination



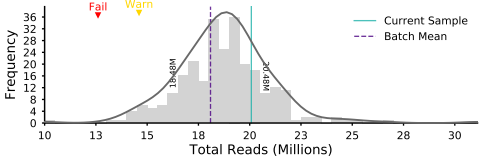
GeneBody Coverage Distribution



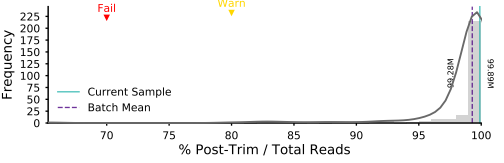
Distribution of Gene Expression



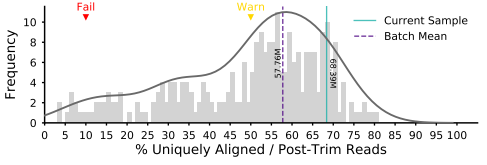
Sequencing Depth



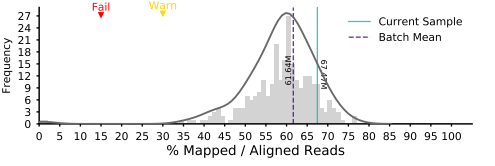
Trimming



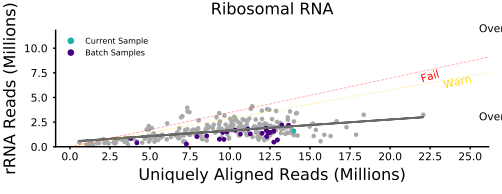
Alignment



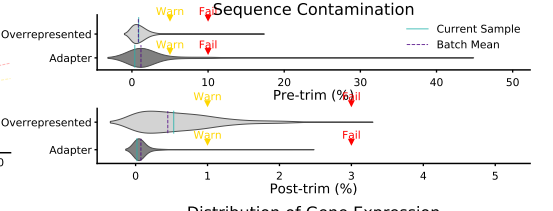
Gene Exon Mapping



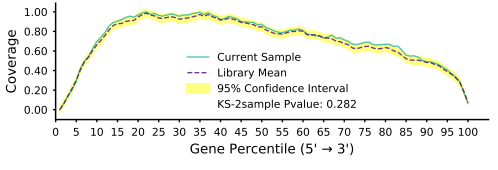
Ribosomal RNA



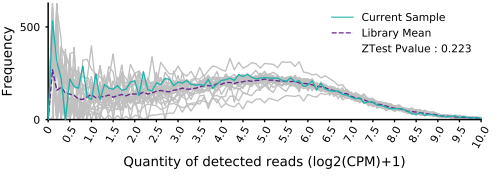
Sequence Contamination



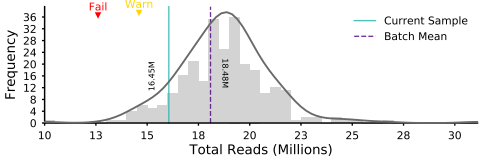
GeneBody Coverage Distribution



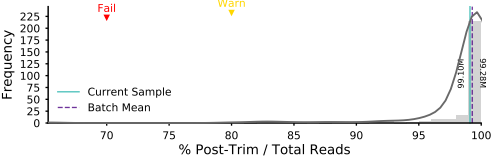
Distribution of Gene Expression



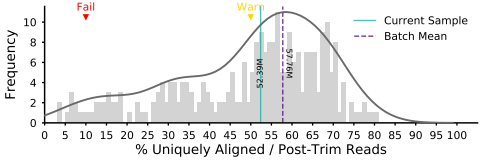
Sequencing Depth



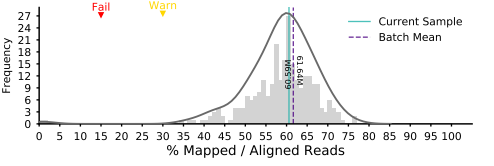
Trimming



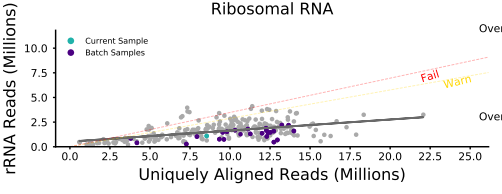
Alignment



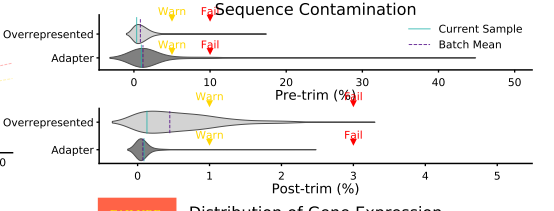
Gene Exon Mapping



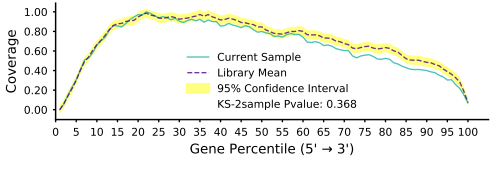
Ribosomal RNA



Sequence Contamination

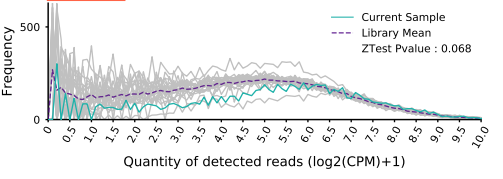


GeneBody Coverage Distribution

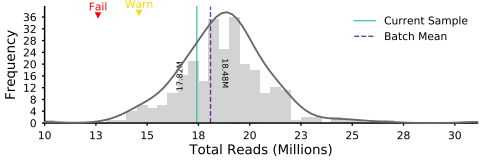


Distribution of Gene Expression

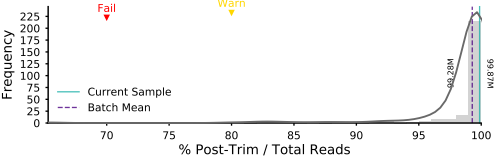
FAILURE



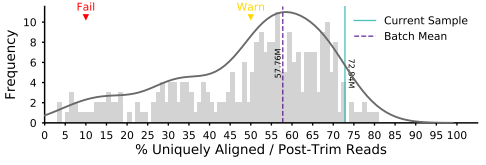
Sequencing Depth



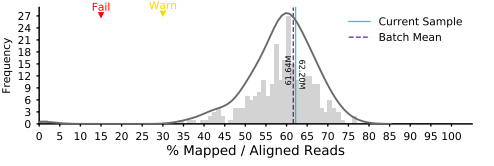
Trimming



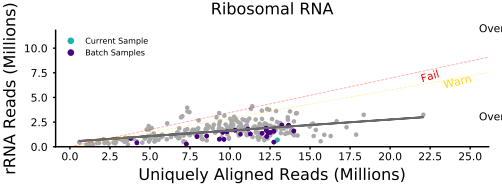
Alignment



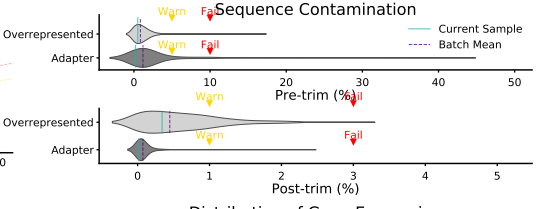
Gene Exon Mapping



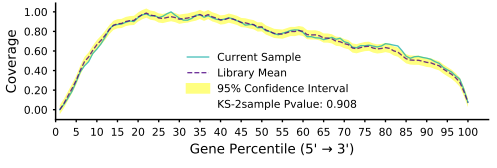
Ribosomal RNA



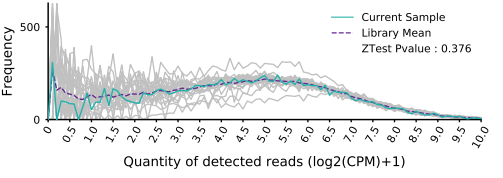
Sequence Contamination

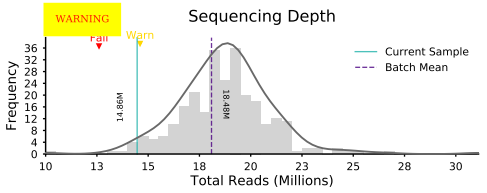


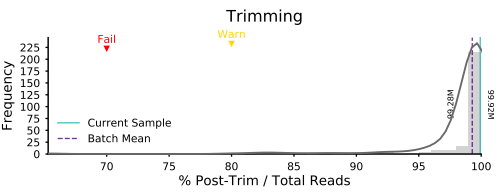
GeneBody Coverage Distribution

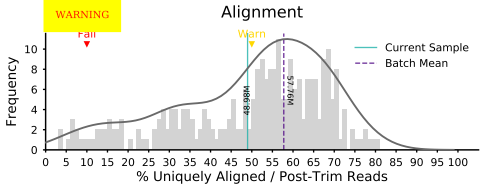


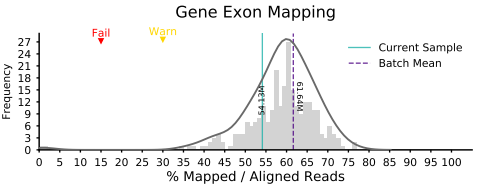
Distribution of Gene Expression

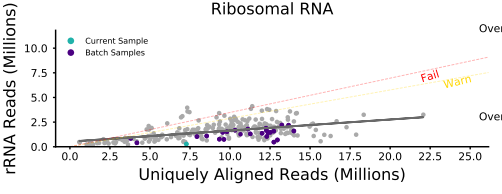


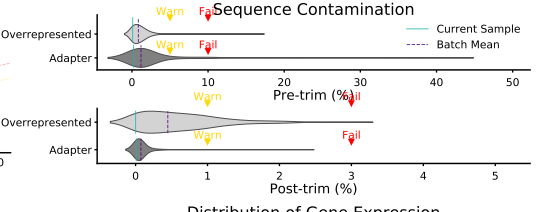

WARNING
Sequencing Depth
Fail
Warn
Current Sample
Batch Mean
Frequency
14.86M
18.48M
Total Reads (Millions)

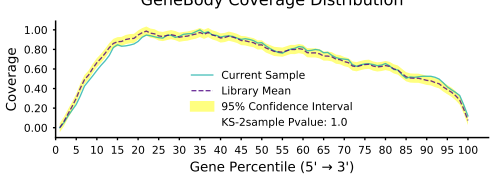

Trimming
Fail
Warn
Current Sample
Batch Mean
Frequency
90.28M
99.92M
% Post-Trim / Total Reads

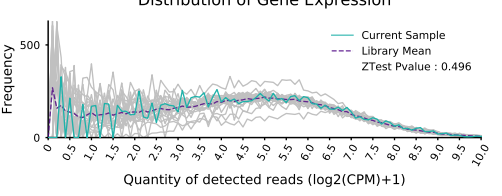

WARNING
Alignment
Fail
Warn
Current Sample
Batch Mean
Frequency
48.98M
57.76M
% Uniquely Aligned / Post-Trim Reads


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

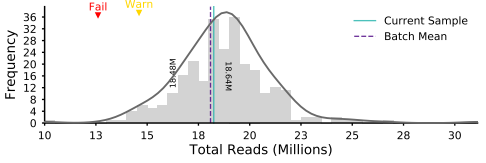

Ribosomal RNA
Current Sample
Batch Samples
Fail
Warn
rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)


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

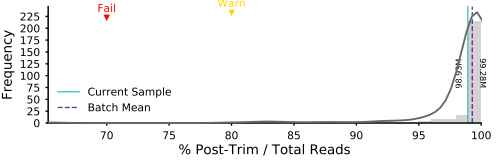

GeneBody Coverage Distribution
Coverage
Current Sample
Library Mean
95% Confidence Interval
KS-2sample Pvalue: 1.0
Gene Percentile (5' → 3')


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

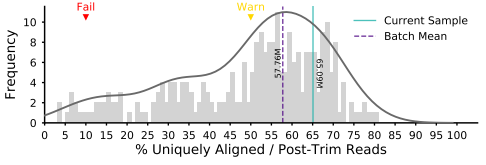
Sequencing Depth



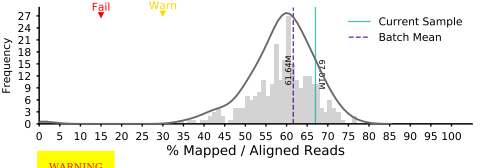
Trimming



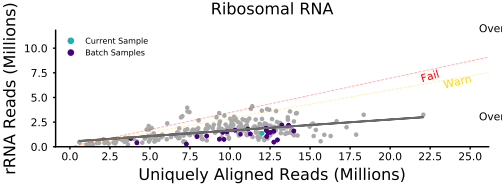
Alignment



Gene Exon Mapping

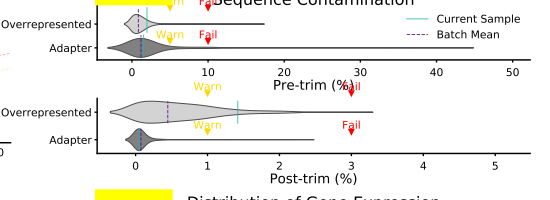


Ribosomal RNA

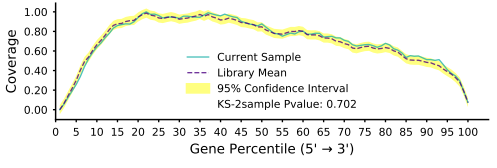


WARNING

Sequence Contamination

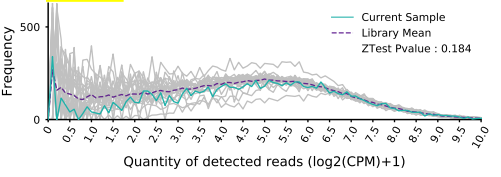


GeneBody Coverage Distribution

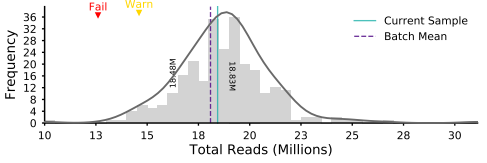


WARNING

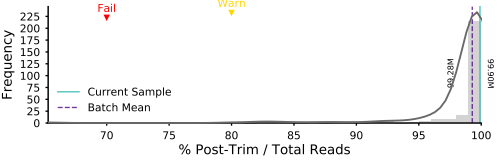
Distribution of Gene Expression



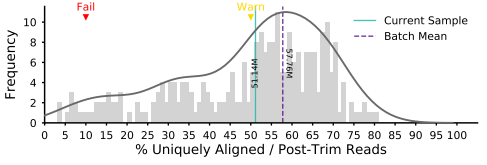
Sequencing Depth



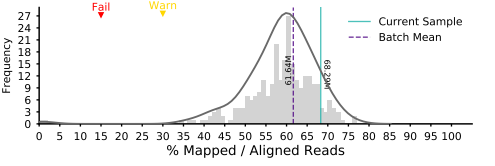
Trimming



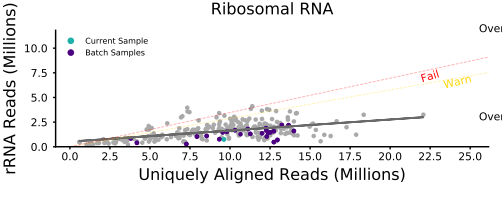
Alignment



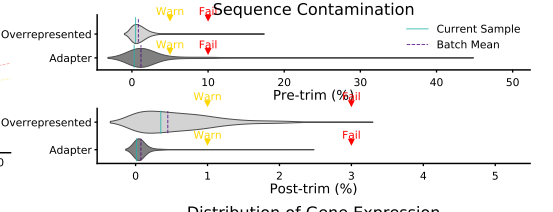
Gene Exon Mapping



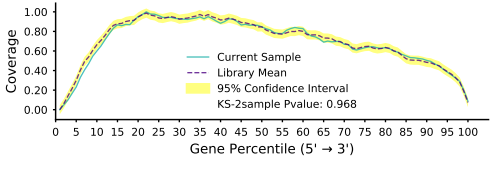
Ribosomal RNA



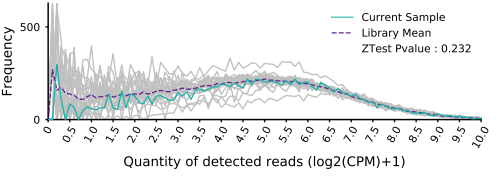
Sequence Contamination



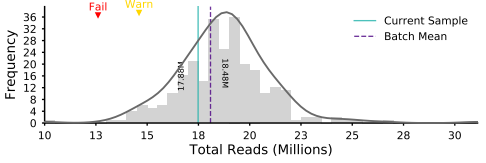
GeneBody Coverage Distribution



Distribution of Gene Expression



Sequencing Depth



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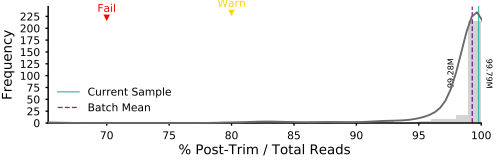
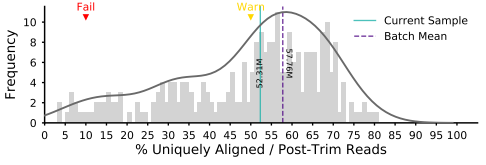
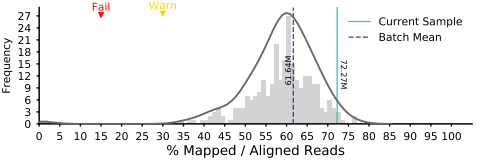


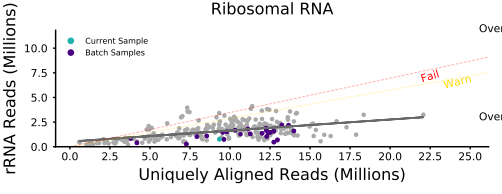
Alignment



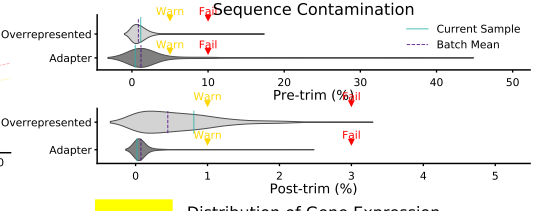
Gene Exon Mapping



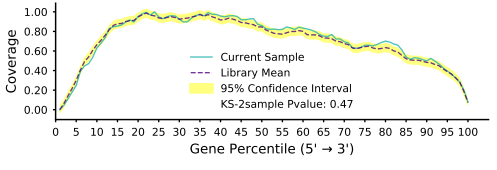
Ribosomal RNA



Sequence Contamination

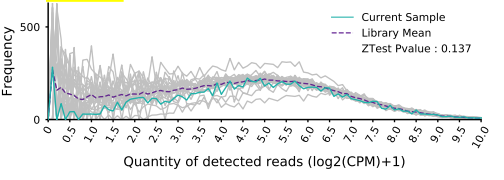


GeneBody Coverage Distribution

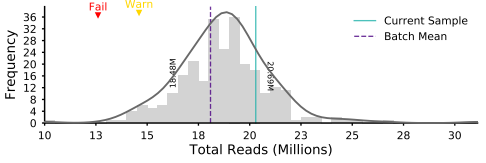


Distribution of Gene Expression

WARNING



Sequencing Depth



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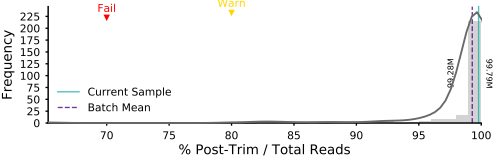
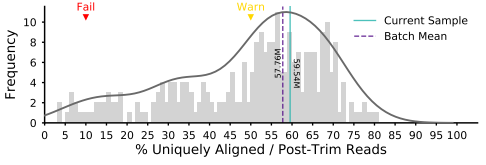
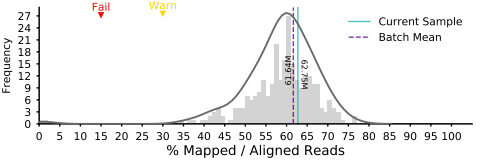


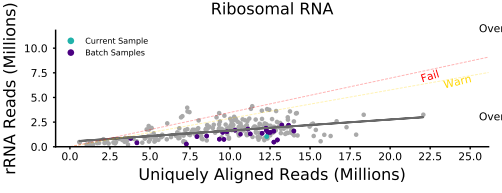
Alignment



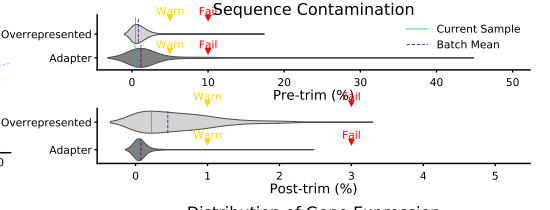
Gene Exon Mapping



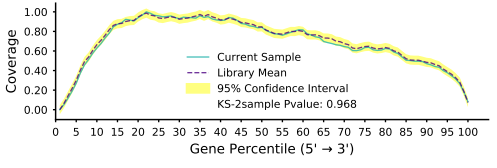
Ribosomal RNA



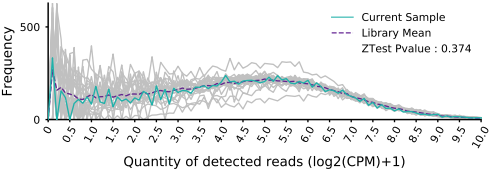
Sequence Contamination



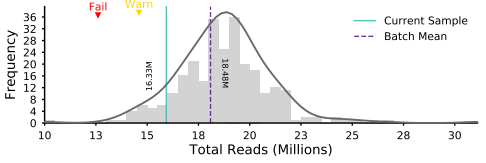
GeneBody Coverage Distribution



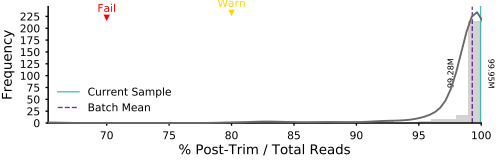
Distribution of Gene Expression



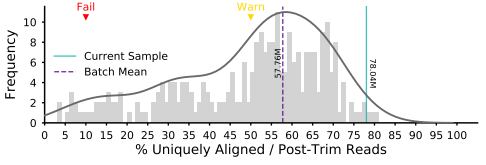
Sequencing Depth



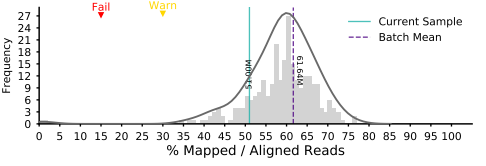
Trimming



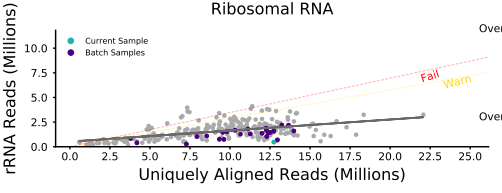
Alignment



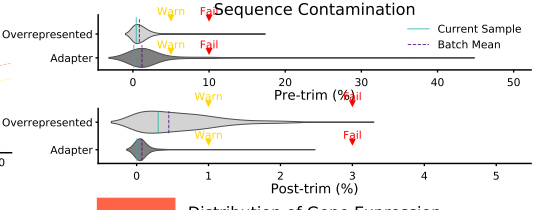
Gene Exon Mapping



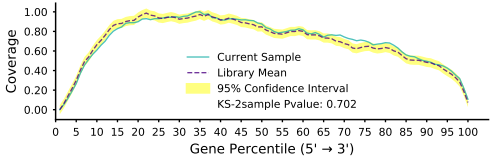
Ribosomal RNA



Sequence Contamination

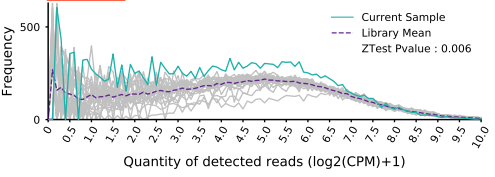


GeneBody Coverage Distribution

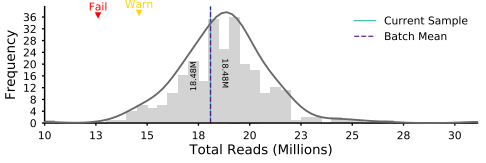


Distribution of Gene Expression

FAILURE



Sequencing Depth



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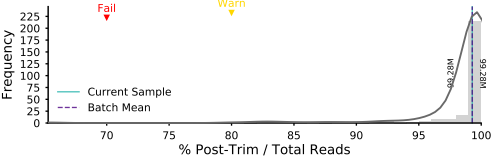
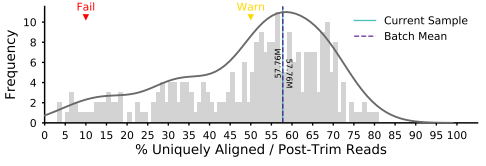
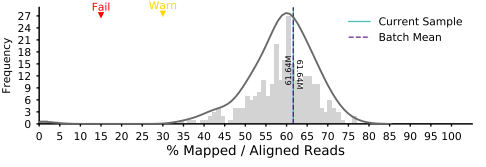


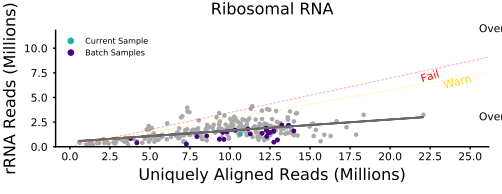
Alignment



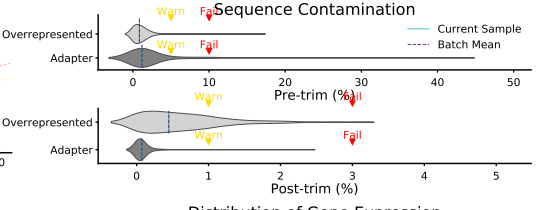
Gene Exon Mapping



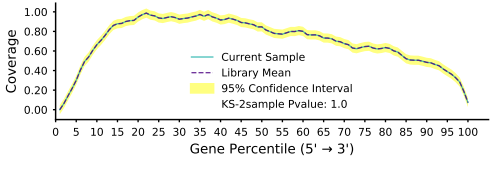
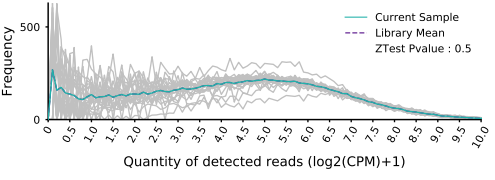
Ribosomal RNA



Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression