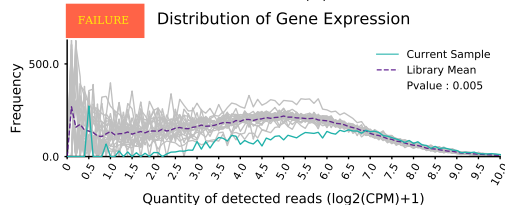
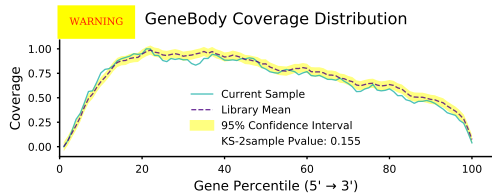
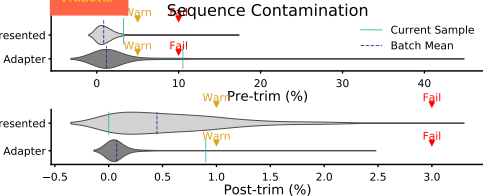
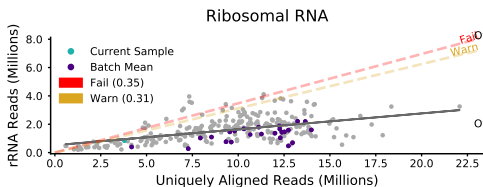
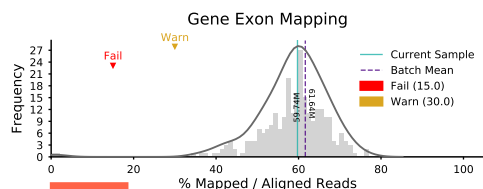
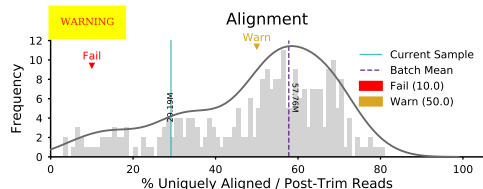
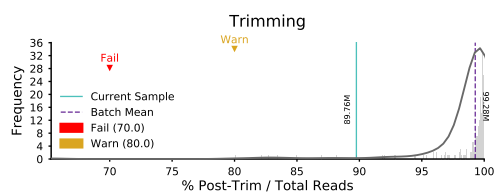
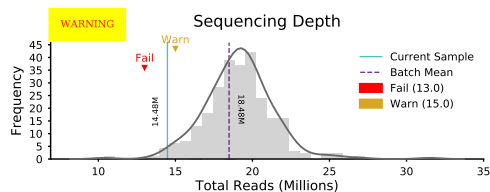
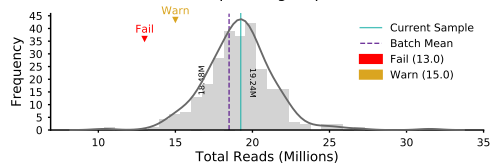


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

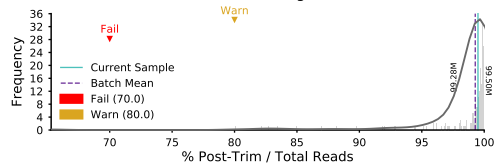


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

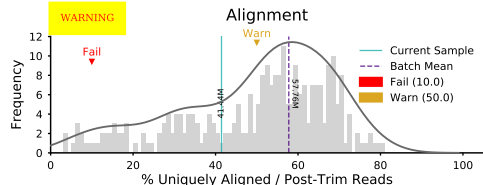
Sequencing Depth



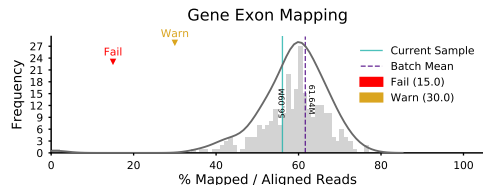
Trimming



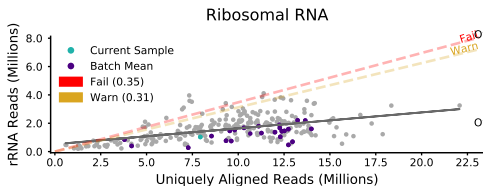
Alignment



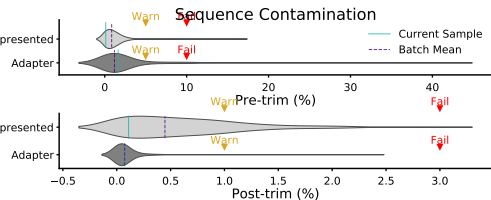
Gene Exon Mapping



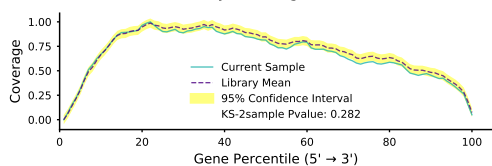
Ribosomal RNA



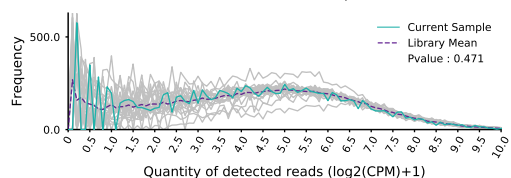
Sequence Contamination



GeneBody Coverage Distribution

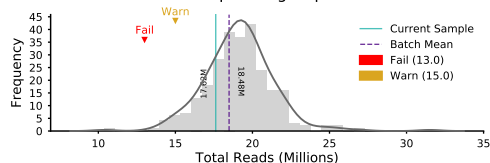


Distribution of Gene Expression

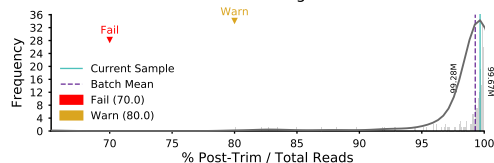


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

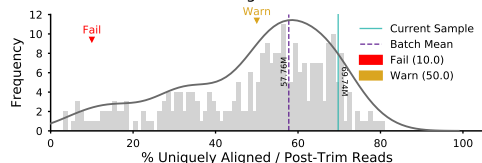
Sequencing Depth



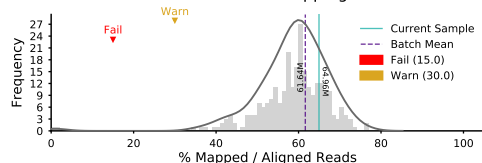
Trimming



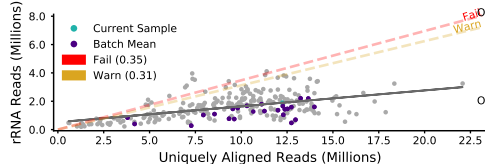
Alignment



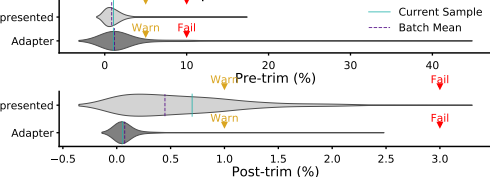
Gene Exon Mapping



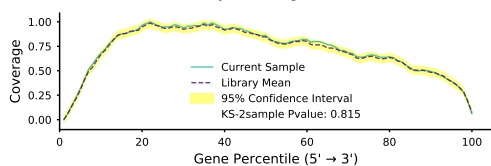
Ribosomal RNA



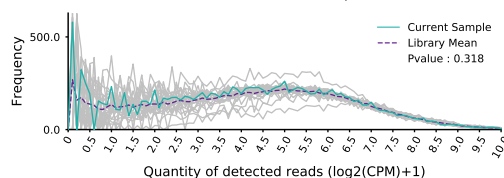
Sequence Contamination



GeneBody Coverage Distribution



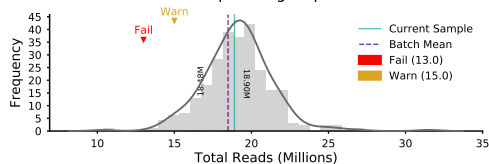
Distribution of Gene Expression



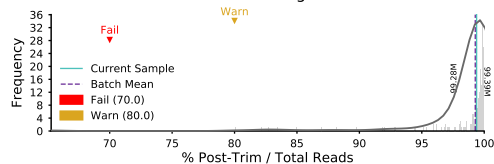
Sample : RNA_B11_04 Batch : batch_11

Warn cutoffs: Default alpha = 0.8| Sequencing Depth = 15.0| Trimming = 80.0| Alignment = 50.0| Gene Exon Mapping = 30.0| Ribosomal RNA = 0.312| Sequence Contamination = 5.0| Gene Body Coverage = 0.8| Distribution of Gene Expression = 0.8
Fail cutoffs: Default alpha = 0.9| Sequencing Depth = 13.0| Trimming = 70.0| Alignment = 10.0| Gene Exon Mapping = 15.0| Ribosomal RNA = 0.348| Sequence Contamination = 10.0| Gene Body Coverage = 0.9| Distribution of Gene Expression = 0.9

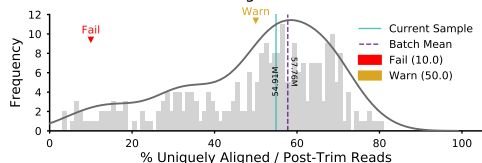
Sequencing Depth



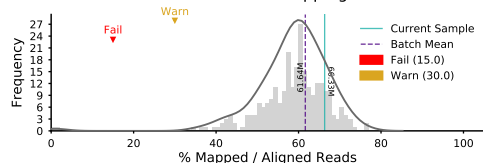
Trimming



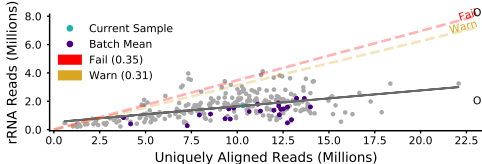
Alignment



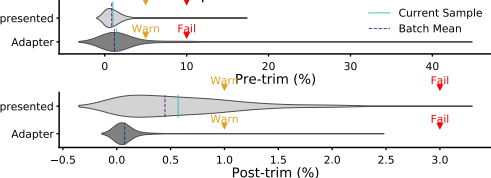
Gene Exon Mapping



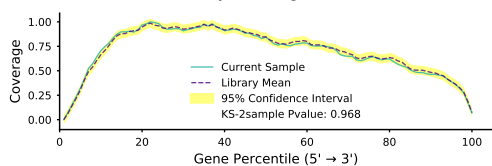
Ribosomal RNA



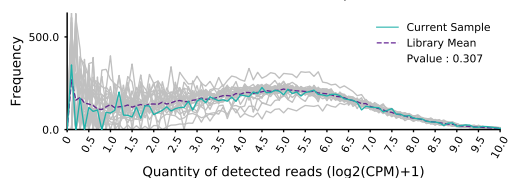
Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression

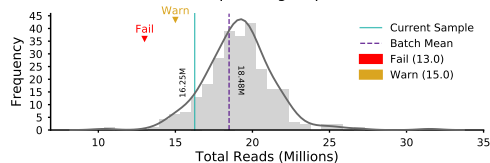


Sample : RNA_B11_05 Batch_11

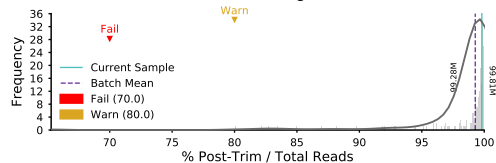
5

Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

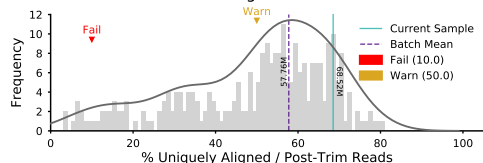
Sequencing Depth



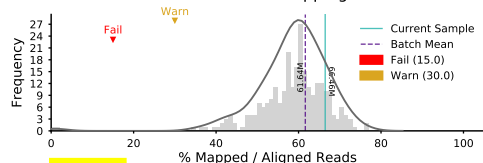
Trimming



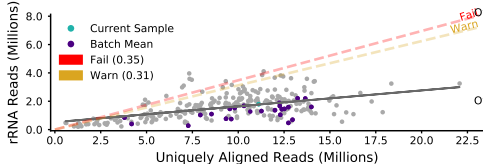
Alignment



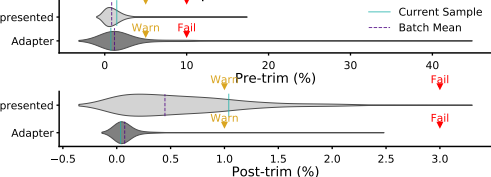
Gene Exon Mapping



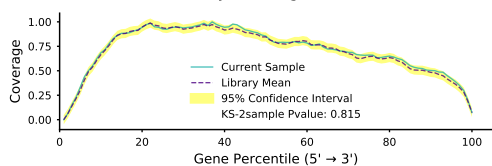
Ribosomal RNA



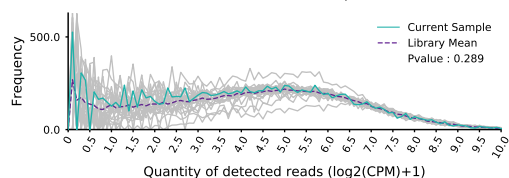
Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression

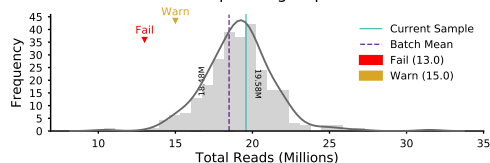


Sample : RNA_B11_06 Batch : batch_11

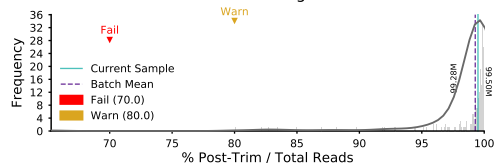
6

Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

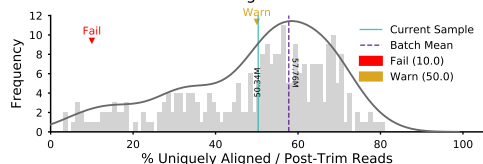
Sequencing Depth



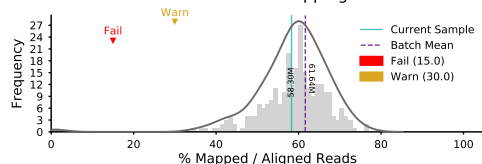
Trimming



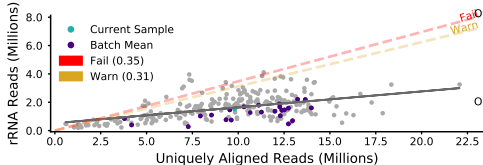
Alignment



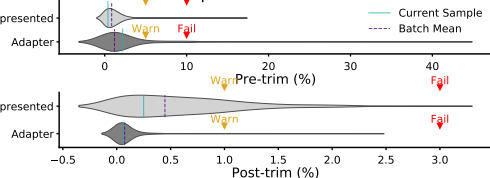
Gene Exon Mapping



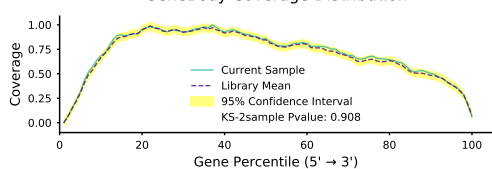
Ribosomal RNA



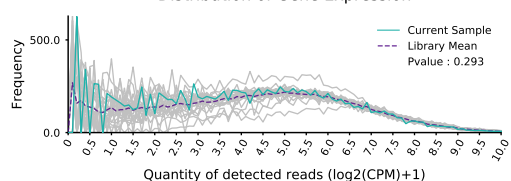
Sequence Contamination



GeneBody Coverage Distribution



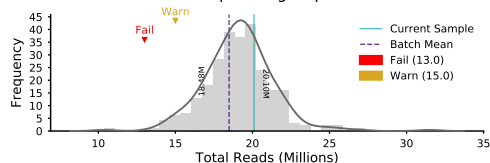
Distribution of Gene Expression



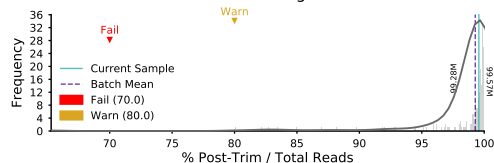
Sample : RNA_B11_07 Batch : batch_11

Warn cutoffs: Default alpha = 0.8| Sequencing Depth = 15.0| Trimming = 80.0| Alignment = 50.0| Gene Exon Mapping = 30.0| Ribosomal RNA = 0.312| Sequence Contamination = 5.0| Gene Body Coverage = 0.8| Distribution of Gene Expression = 0.8
Fail cutoffs: Default alpha = 0.9| Sequencing Depth = 13.0| Trimming = 70.0| Alignment = 10.0| Gene Exon Mapping = 15.0| Ribosomal RNA = 0.348| Sequence Contamination = 10.0| Gene Body Coverage = 0.9| Distribution of Gene Expression = 0.9

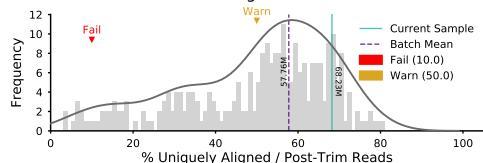
Sequencing Depth



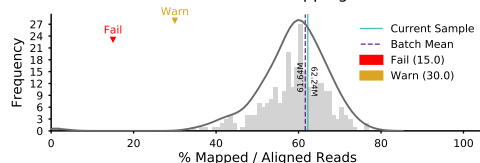
Trimming



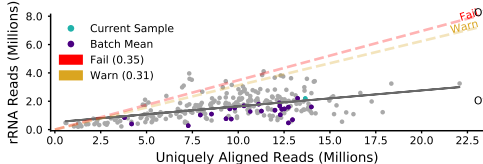
Alignment



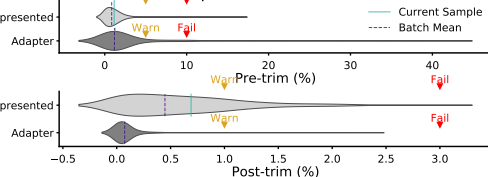
Gene Exon Mapping



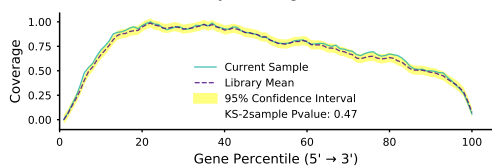
Ribosomal RNA



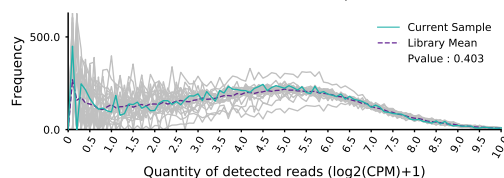
Sequence Contamination



GeneBody Coverage Distribution

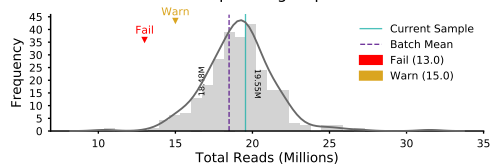


Distribution of Gene Expression

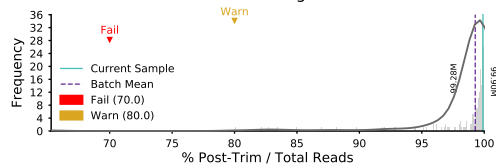


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

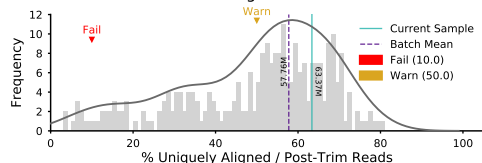
Sequencing Depth



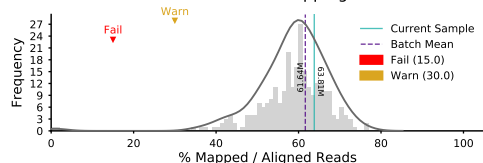
Trimming



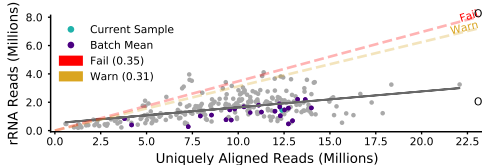
Alignment



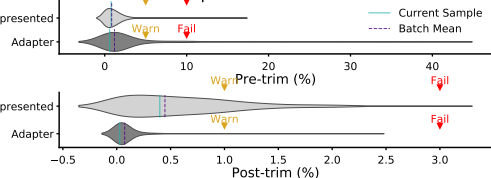
Gene Exon Mapping



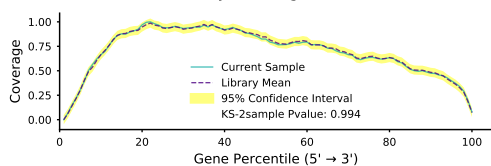
Ribosomal RNA



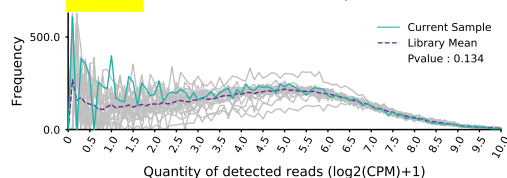
Sequence Contamination



GeneBody Coverage Distribution



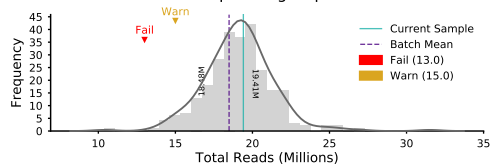
Distribution of Gene Expression



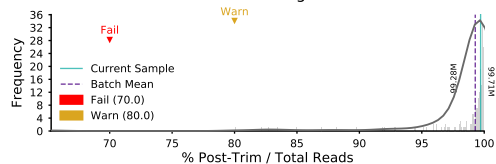
Sample : RNA_B11_09 Batch : batch_11

Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

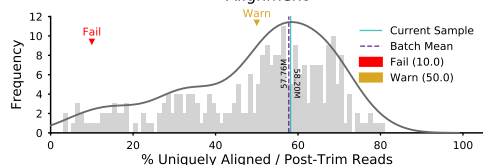
Sequencing Depth



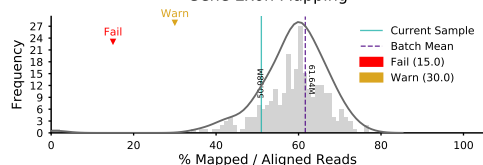
Trimming



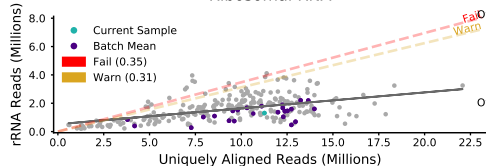
Alignment



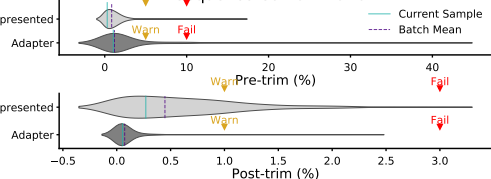
Gene Exon Mapping



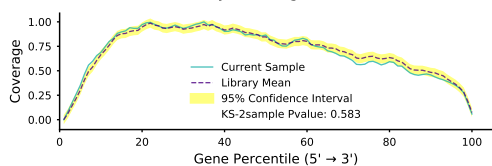
Ribosomal RNA



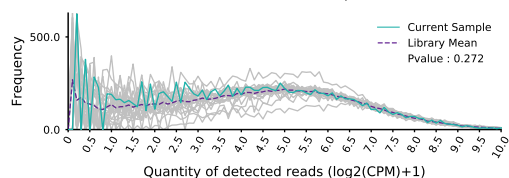
Sequence Contamination



GeneBody Coverage Distribution



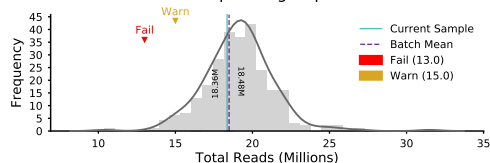
Distribution of Gene Expression



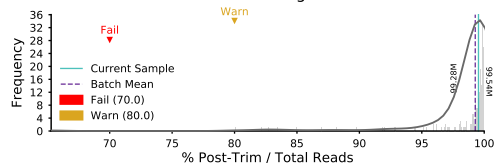
Sample : RNA_B11_10 Batch : batch_11

Warn cutoffs: Default alpha = 0.8 Sequencing Depth = 15.0 Trimming = 80.0 Alignment = 50.0 Gene Exon Mapping = 30.0 Ribosomal RNA = 0.312 Sequence Contamination = 5.0 Gene Body Coverage = 0.8 Distribution of Gene Expression = 0.8
Fail cutoffs: Default alpha = 0.9 Sequencing Depth = 13.0 Trimming = 70.0 Alignment = 10.0 Gene Exon Mapping = 15.0 Ribosomal RNA = 0.348 Sequence Contamination = 10.0 Gene Body Coverage = 0.9 Distribution of Gene Expression = 0.9

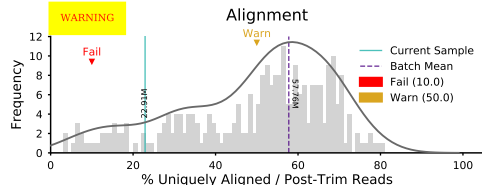
Sequencing Depth



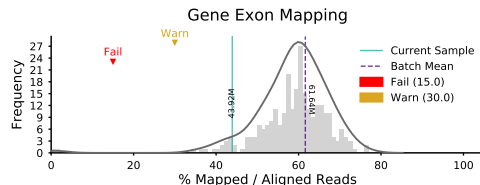
Trimming



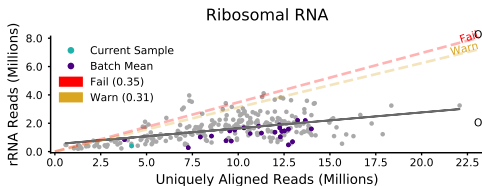
Alignment



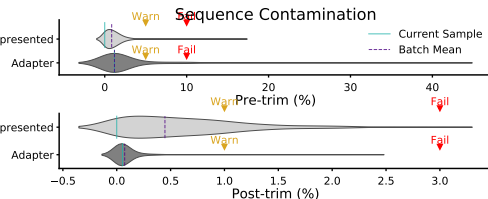
Gene Exon Mapping



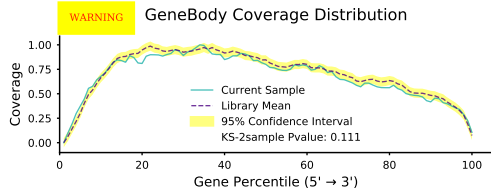
Ribosomal RNA



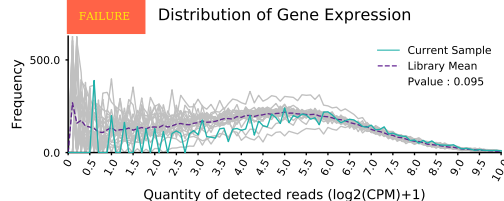
Sequence Contamination



GeneBody Coverage Distribution

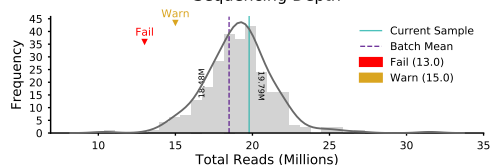


Distribution of Gene Expression

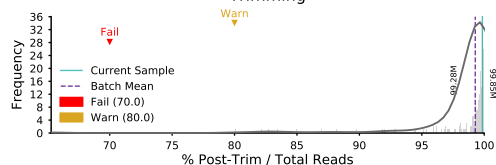


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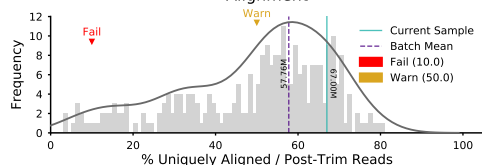
Sequencing Depth



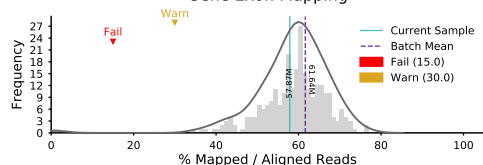
Trimming



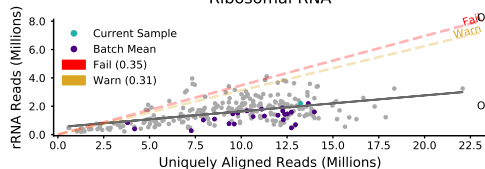
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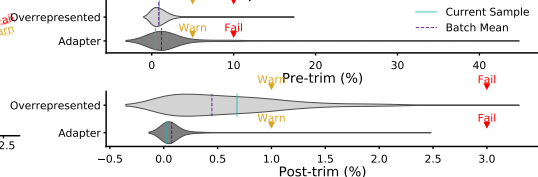
Gene Exon Mapping



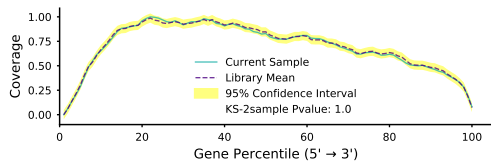
Ribosomal RNA



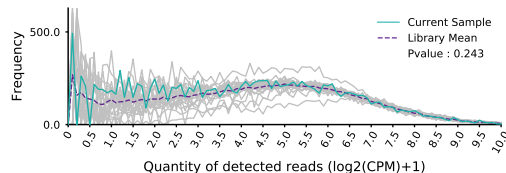
Sequence Contamination



GeneBody Coverage Distribution

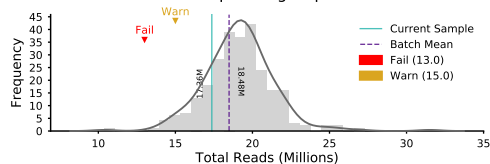


Distribution of Gene Expression

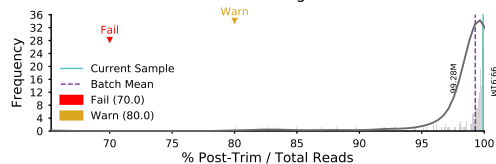


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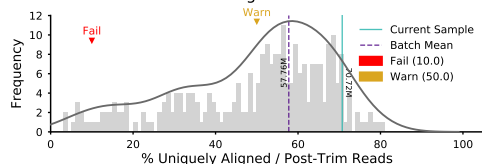
Sequencing Depth



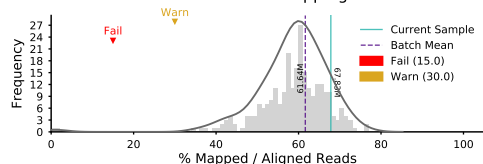
Trimming



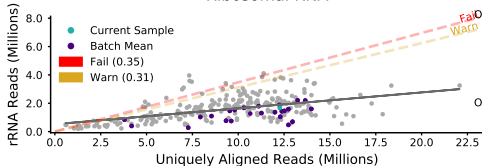
Alignment



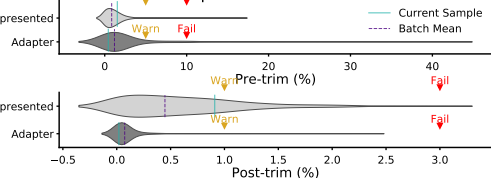
Gene Exon Mapping



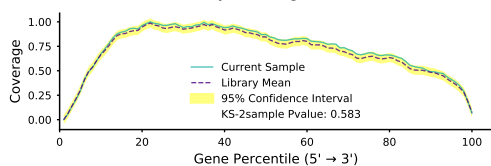
Ribosomal RNA



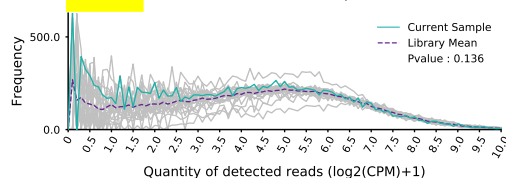
Sequence Contamination



GeneBody Coverage Distribution

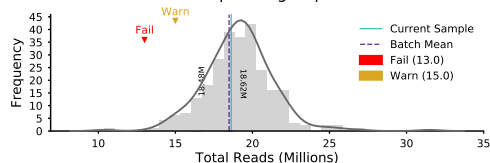


Distribution of Gene Expression

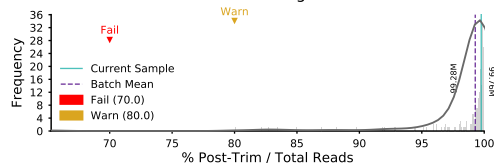


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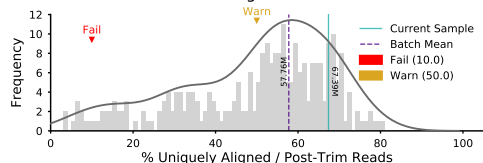
Sequencing Depth



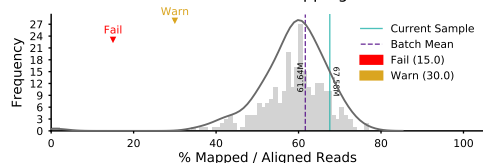
Trimming



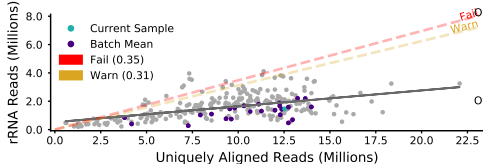
Alignment



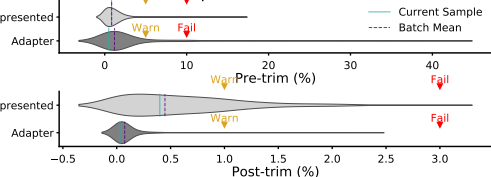
Gene Exon Mapping



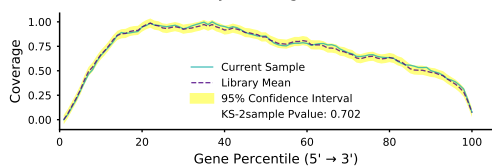
Ribosomal RNA



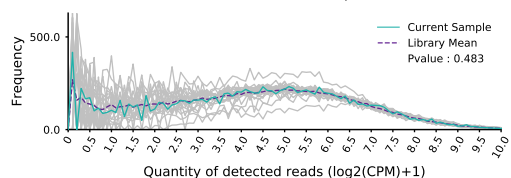
Sequence Contamination



GeneBody Coverage Distribution

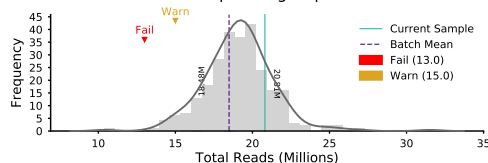


Distribution of Gene Expression

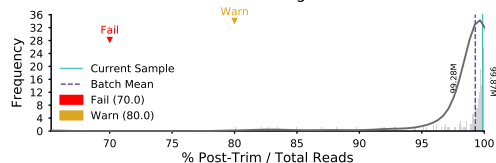


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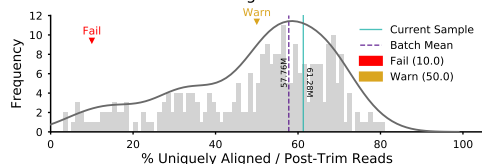
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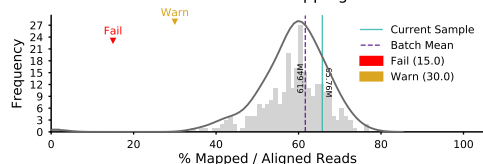
Trimming



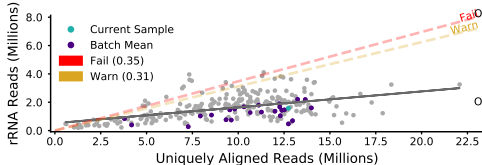
Alignment



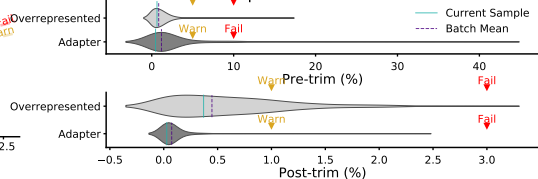
Gene Exon Mapping



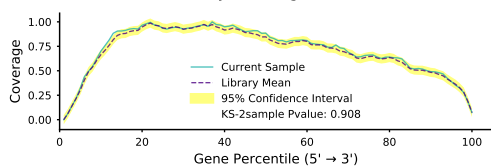
Ribosomal RNA



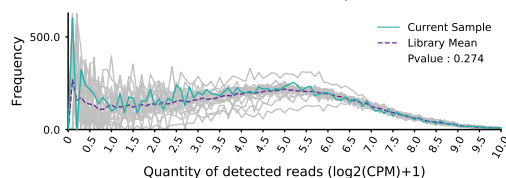
Sequence Contamination



GeneBody Coverage Distribution

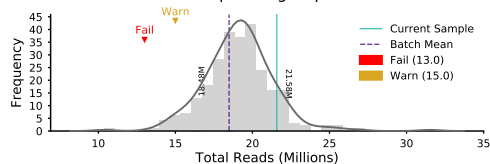


Distribution of Gene Expression

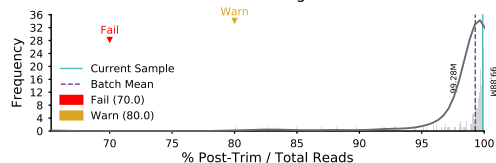


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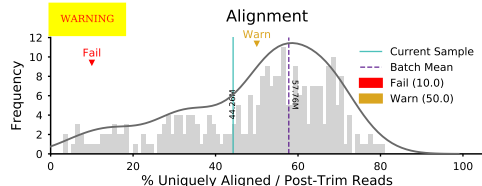
Sequencing Depth



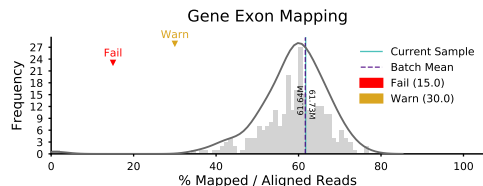
Trimming



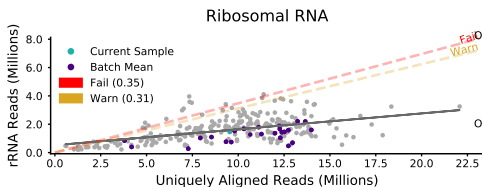
Alignment



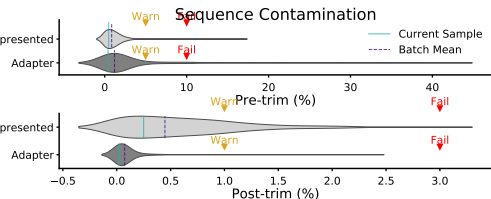
Gene Exon Mapping



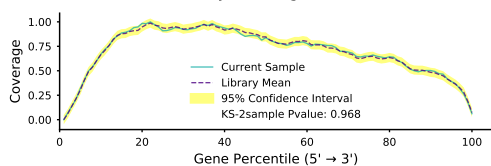
Ribosomal RNA



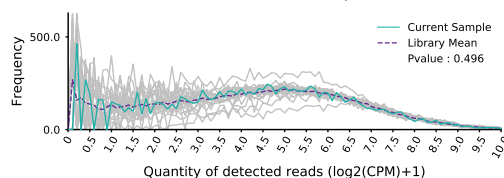
Sequence Contamination



GeneBody Coverage Distribution

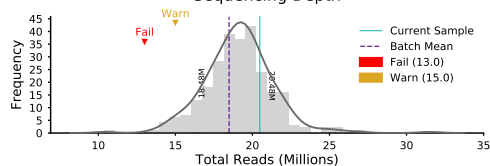


Distribution of Gene Expression

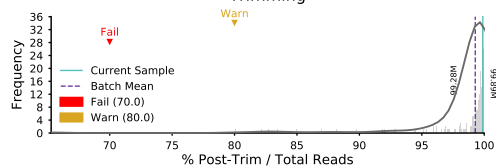


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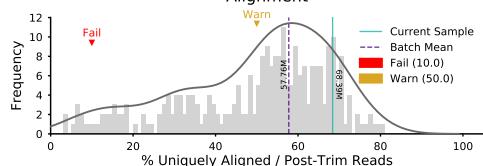
Sequencing Depth



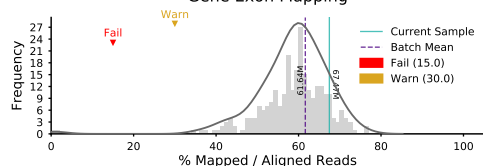
Trimming



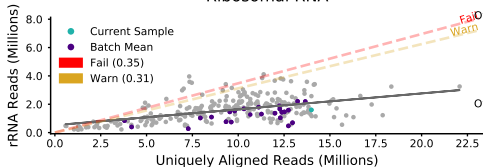
Alignment



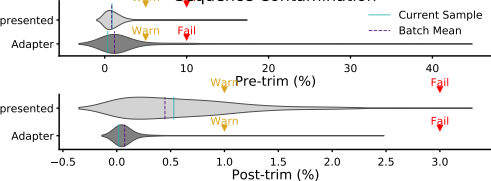
Gene Exon Mapping



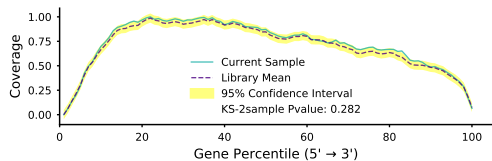
Ribosomal RNA



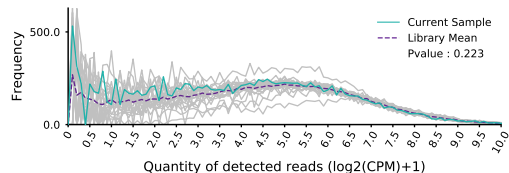
Sequence Contamination



GeneBody Coverage Distribution

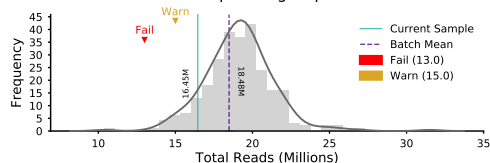


Distribution of Gene Expression

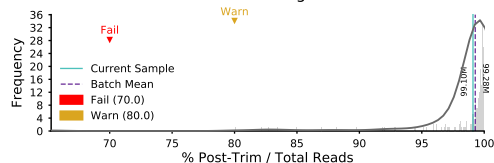


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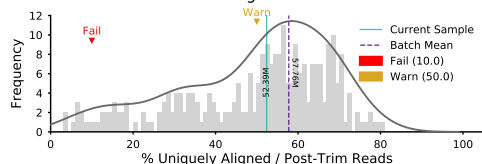
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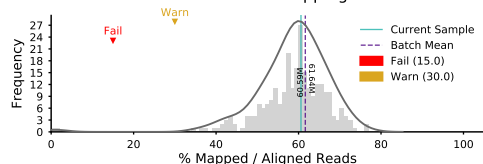
Trimming



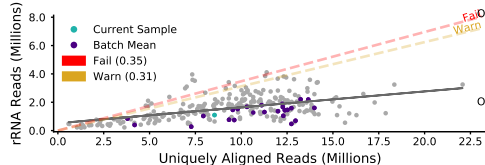
Alignment



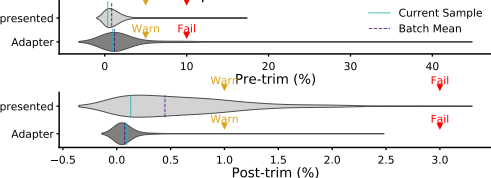
Gene Exon Mapping



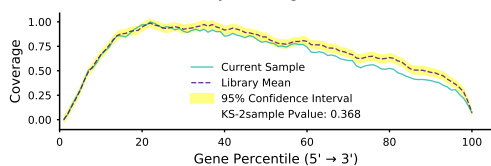
Ribosomal RNA



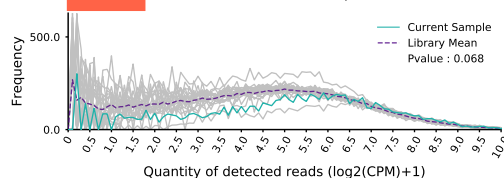
Sequence Contamination



GeneBody Coverage Distribution

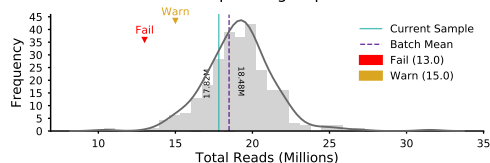


Distribution of Gene Expression

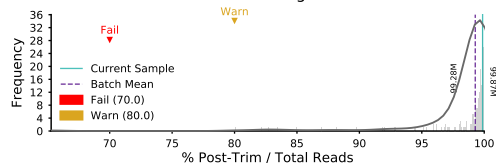


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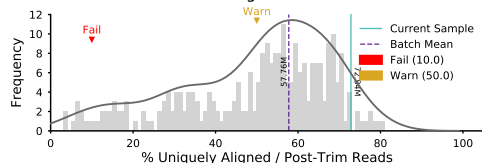
Sequencing Depth



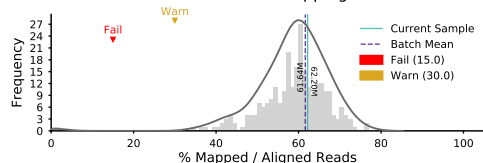
Trimming



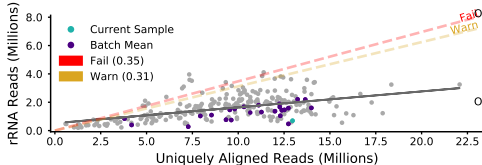
Alignment



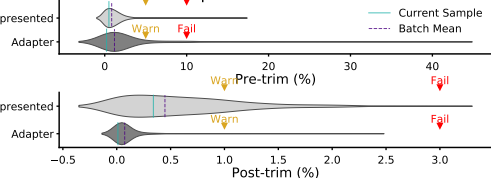
Gene Exon Mapping



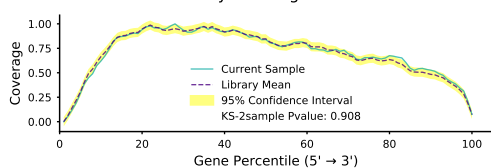
Ribosomal RNA



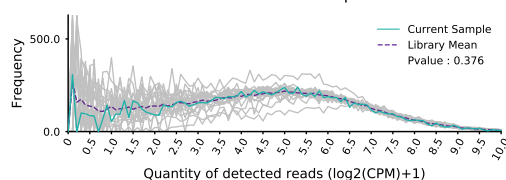
Sequence Contamination



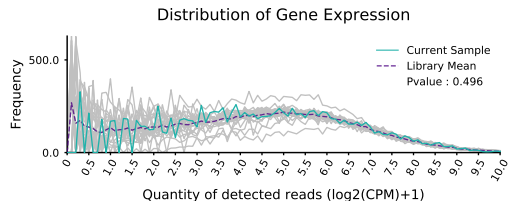
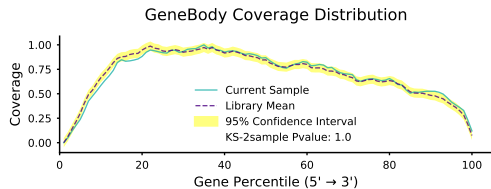
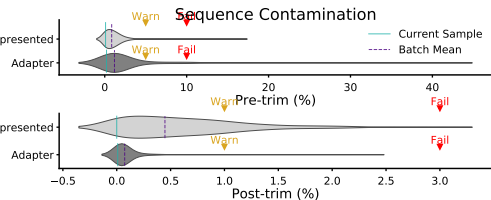
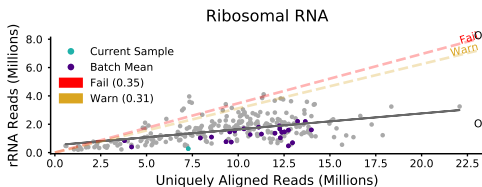
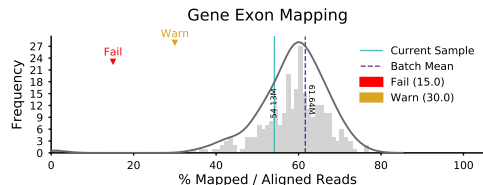
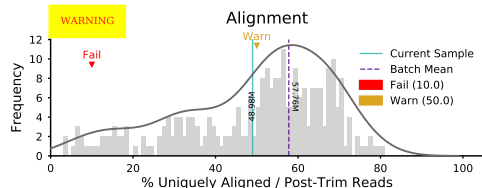
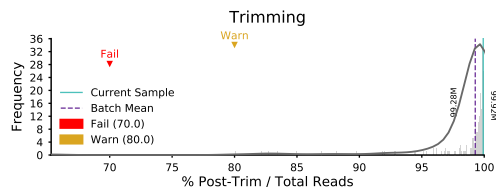
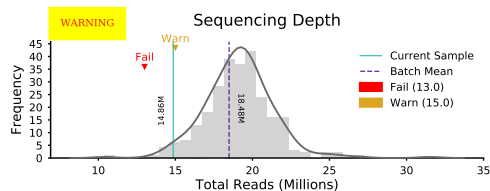
GeneBody Coverage Distribution



Distribution of Gene Expression

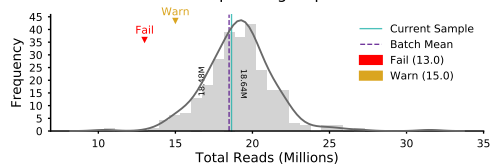


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

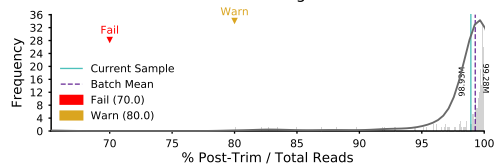


Warn cutoffs: Default alpha = 0.8| Sequencing Depth = 15.0| Trimming = 80.0| Alignment = 50.0| Gene Exon Mapping = 30.0| Ribosomal RNA = 0.312| Sequence Contamination = 5.0| Gene Body Coverage = 0.8| Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9| Sequencing Depth = 13.0| Trimming = 70.0| Alignment = 10.0| Gene Exon Mapping = 15.0| Ribosomal RNA = 0.348| Sequence Contamination = 10.0| Gene Body Coverage = 0.9| Distribution of Gene Expression = 0.9

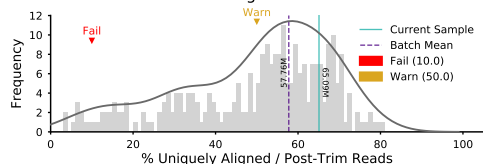
Sequencing Depth



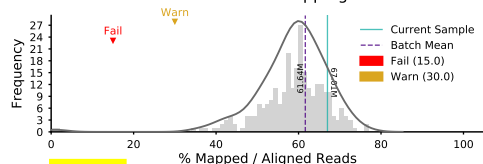
Trimming



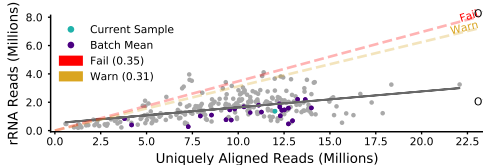
Alignment



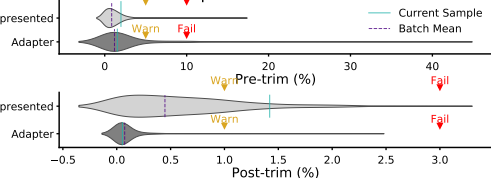
Gene Exon Mapping



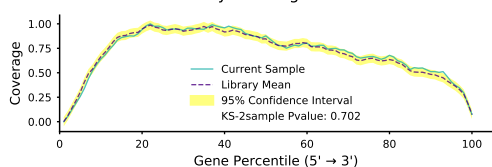
Ribosomal RNA



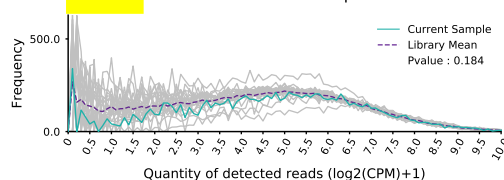
Sequence Contamination



GeneBody Coverage Distribution

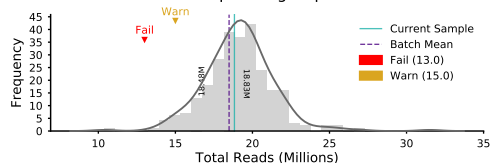


Distribution of Gene Expression

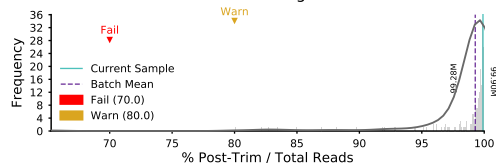


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

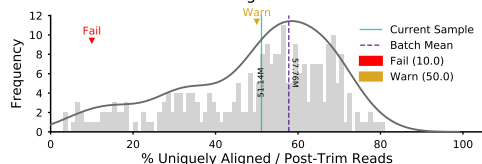
Sequencing Depth



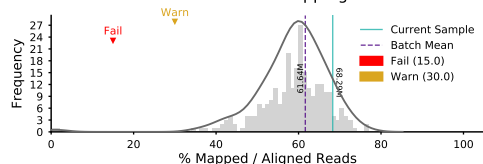
Trimming



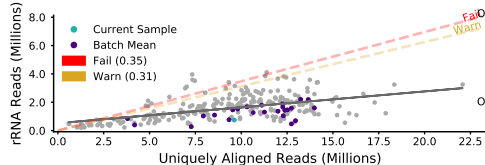
Alignment



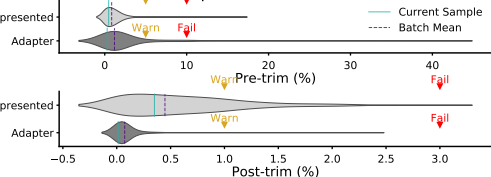
Gene Exon Mapping



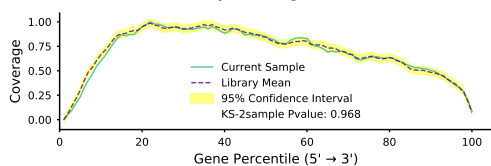
Ribosomal RNA



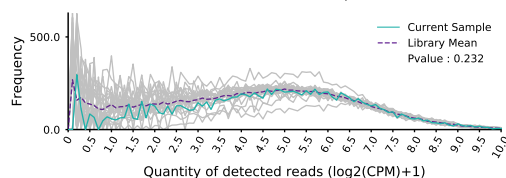
Sequence Contamination



GeneBody Coverage Distribution

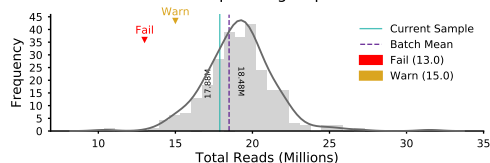


Distribution of Gene Expression

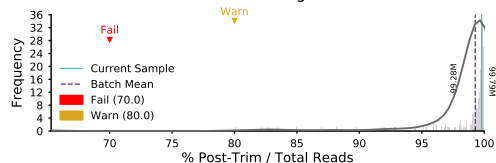


Warn cutoffs: Default alpha = 0.8| Sequencing Depth = 15.0| Trimming = 80.0| Alignment = 50.0| Gene Exon Mapping = 30.0| Ribosomal RNA = 0.312| Sequence Contamination = 5.0| Gene Body Coverage = 0.8| Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9| Sequencing Depth = 13.0| Trimming = 70.0| Alignment = 10.0| Gene Exon Mapping = 15.0| Ribosomal RNA = 0.348| Sequence Contamination = 10.0| Gene Body Coverage = 0.9| Distribution of Gene Expression = 0.9

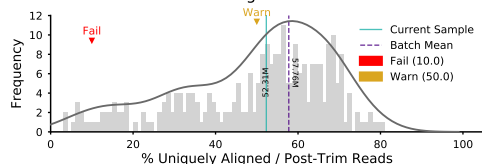
Sequencing Depth



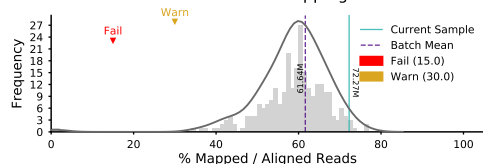
Trimming



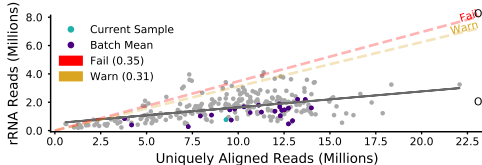
Alignment



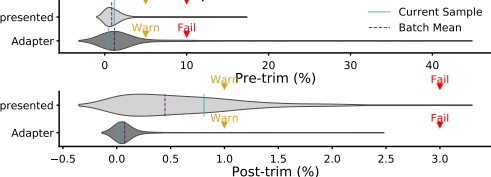
Gene Exon Mapping



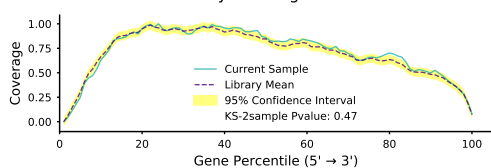
Ribosomal RNA



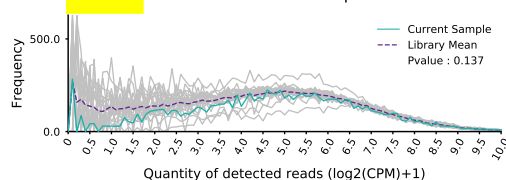
Sequence Contamination



GeneBody Coverage Distribution

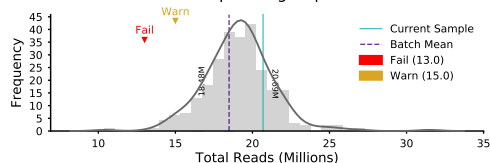


Distribution of Gene Expression

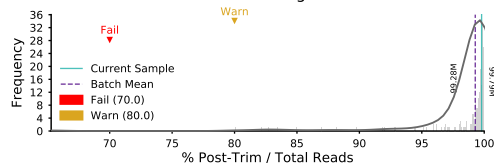


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth = 13.0 | Trimming = 70.0 | Alignment = 10.0 | Gene Exon Mapping = 15.0 | Ribosomal RNA = 0.348 | Sequence Contamination = 10.0 | Gene Body Coverage = 0.9 | Distribution of Gene Expression = 0.9

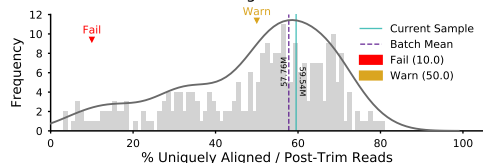
Sequencing Depth



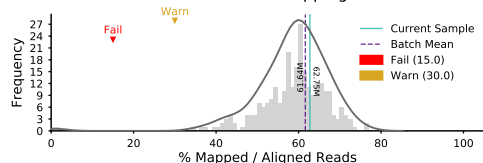
Trimming



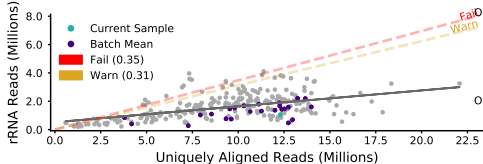
Alignment



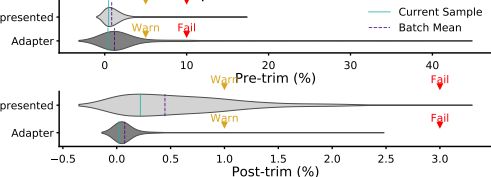
Gene Exon Mapping



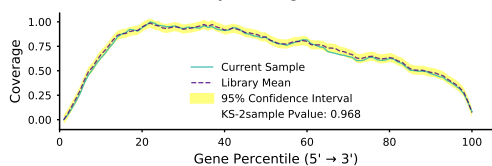
Ribosomal RNA



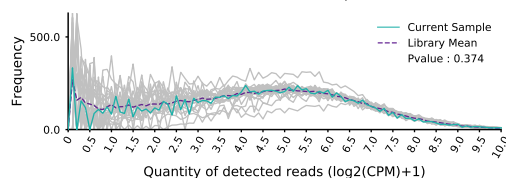
Sequence Contamination



GeneBody Coverage Distribution

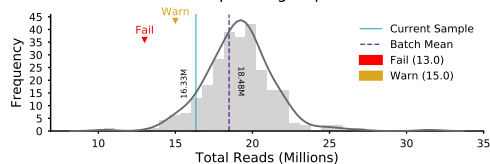


Distribution of Gene Expression

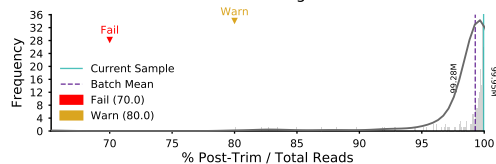


Warn cutoffs: Default alpha = 0.8| Sequencing Depth = 15.0| Trimming = 80.0| Alignment = 50.0| Gene Exon Mapping = 30.0| Ribosomal RNA = 0.312| Sequence Contamination = 5.0| Gene Body Coverage = 0.8| Distribution of Gene Expression = 0.8
 Fail cutoffs: Default alpha = 0.9| Sequencing Depth = 13.0| Trimming = 70.0| Alignment = 10.0| Gene Exon Mapping = 15.0| Ribosomal RNA = 0.348| Sequence Contamination = 10.0| Gene Body Coverage = 0.9| Distribution of Gene Expression = 0.9

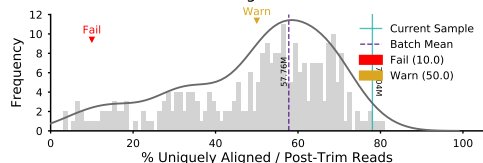
Sequencing Depth



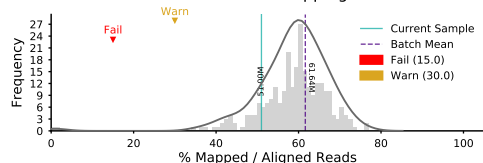
Trimming



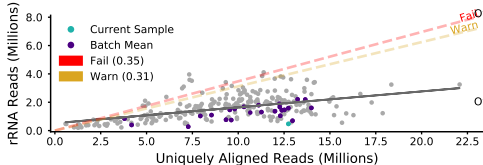
Alignment



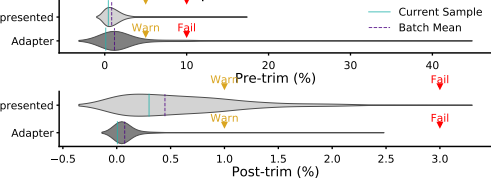
Gene Exon Mapping



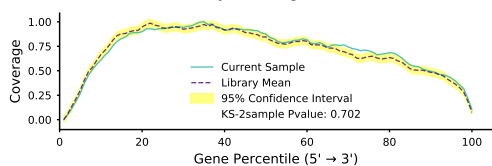
Ribosomal RNA



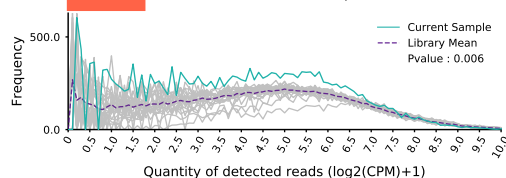
Sequence Contamination



GeneBody Coverage Distribution

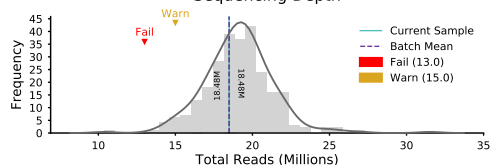


Distribution of Gene Expression

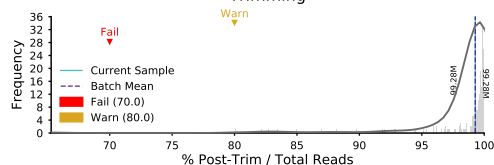


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8
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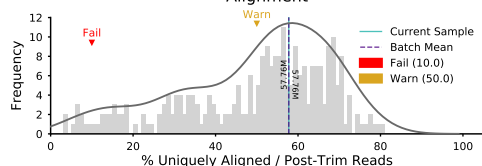
Sequencing Depth



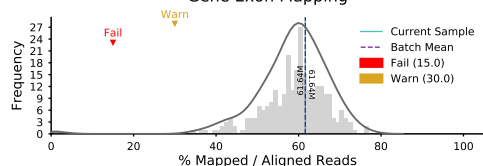
Trimming



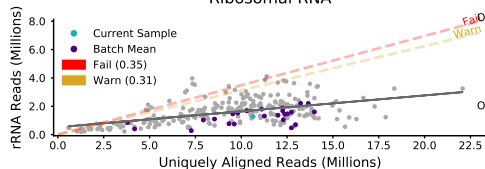
Alignment



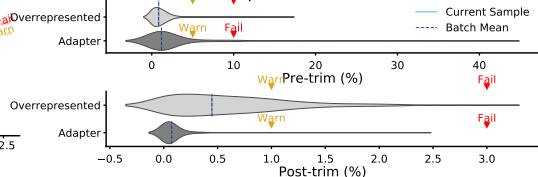
Gene Exon Mapping



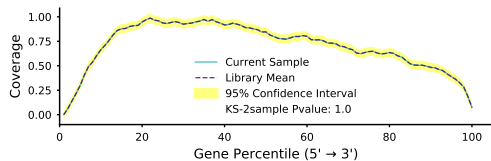
Ribosomal RNA



Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression

