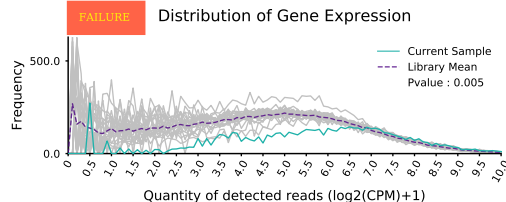
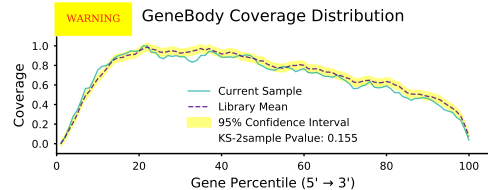
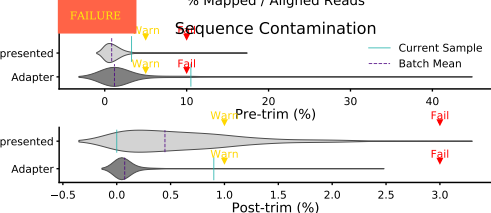
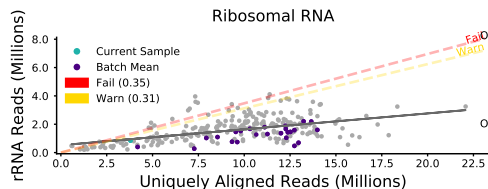
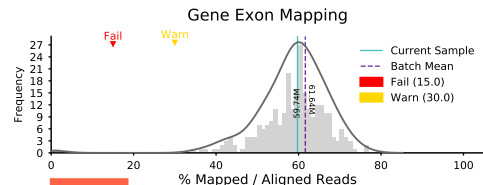
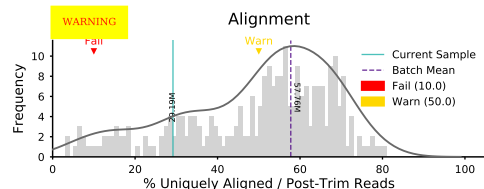
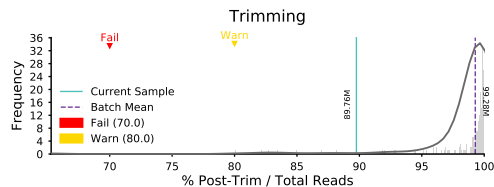
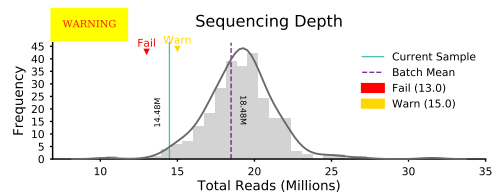


# Sample : RNA\_B11\_01 Batch\_11

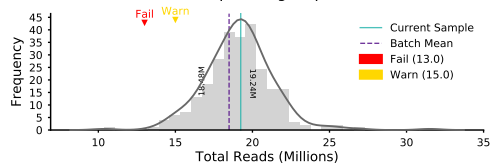
1

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

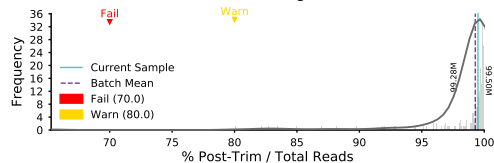


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

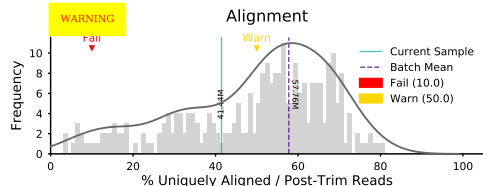
## Sequencing Depth



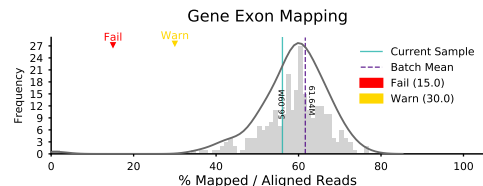
## Trimming



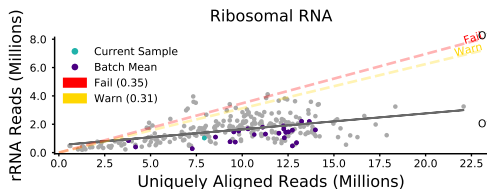
## Alignment



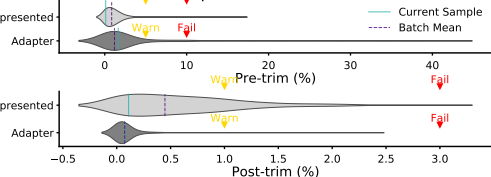
## Gene Exon Mapping



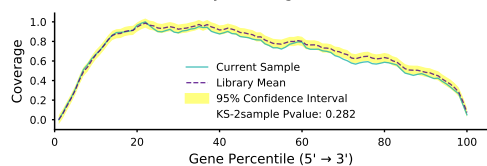
## Ribosomal RNA



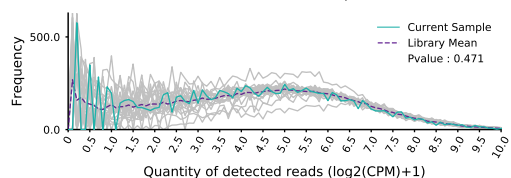
## Sequence Contamination



## GeneBody Coverage Distribution



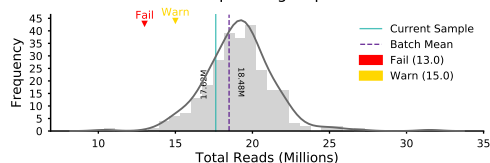
## Distribution of Gene Expression



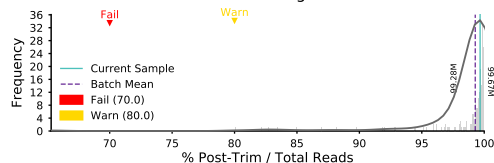
# Sample : RNA\_B11\_03 Batch : batch\_11

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

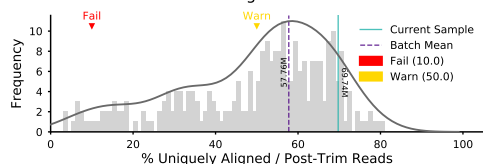
## Sequencing Depth



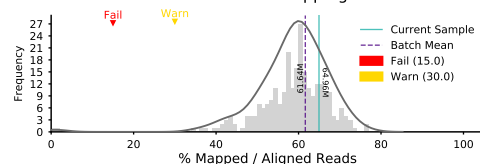
## Trimming



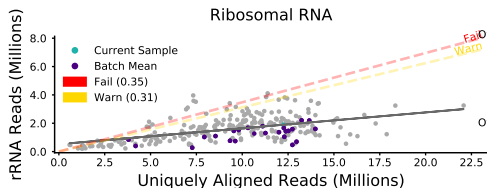
## Alignment



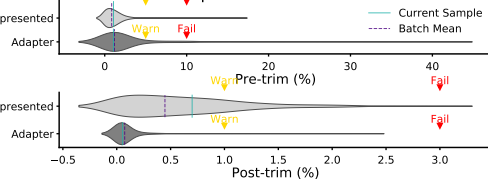
## Gene Exon Mapping



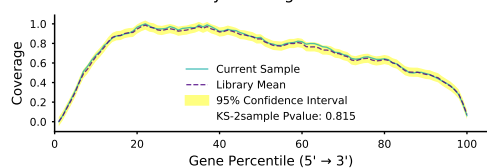
## Ribosomal RNA



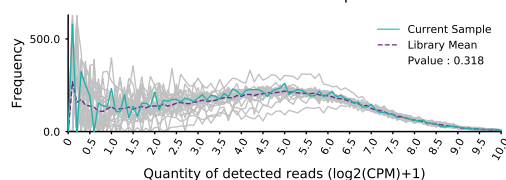
## Sequence Contamination



## GeneBody Coverage Distribution



## Distribution of Gene Expression

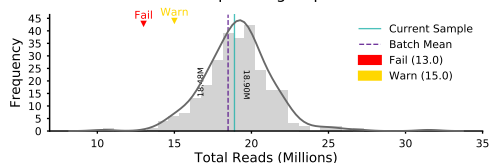


# Sample : RNA\_B11\_04 Batch : batch\_11

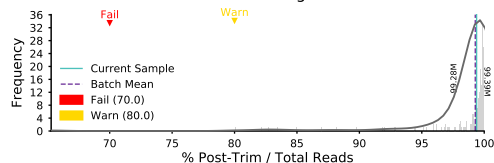
4

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

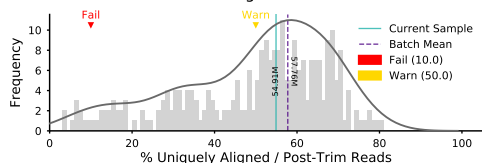
## Sequencing Depth



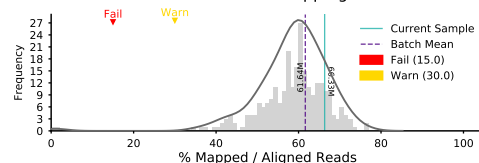
## Trimming



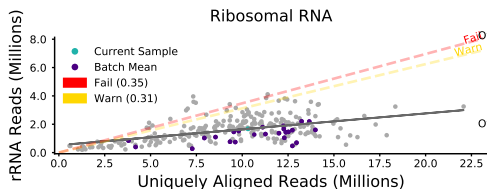
## Alignment



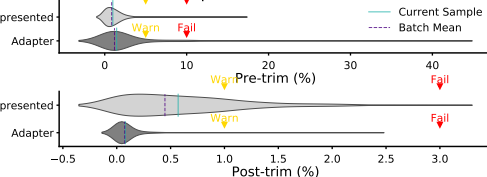
## Gene Exon Mapping



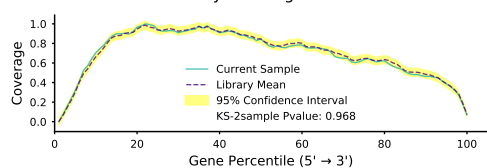
## Ribosomal RNA



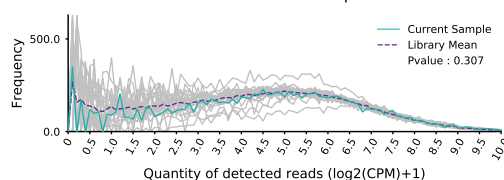
## Sequence Contamination



## GeneBody Coverage Distribution



## Distribution of Gene Expression

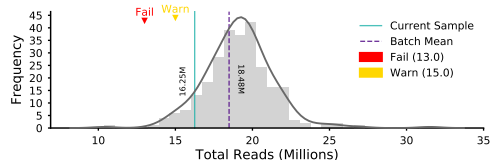


# Sample : RNA\_B11\_05 Batch : batch\_11

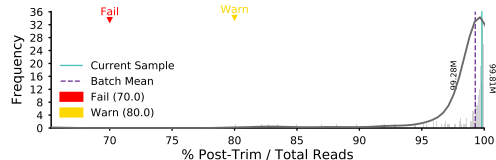
5

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

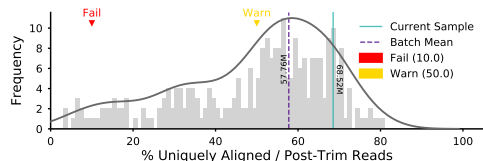
## Sequencing Depth



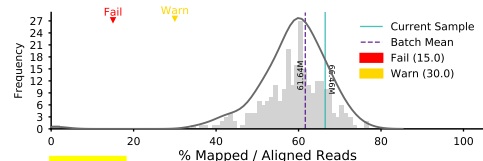
## Trimming



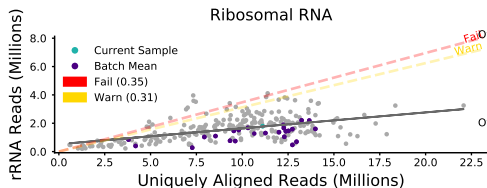
## Alignment



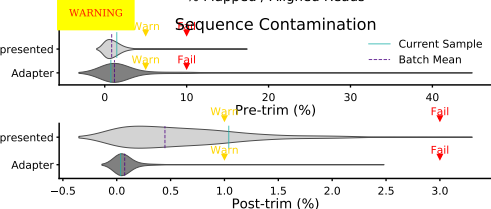
## Gene Exon Mapping



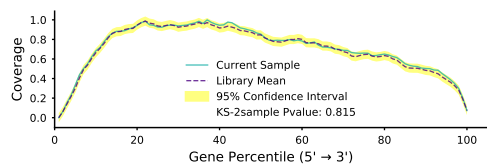
## Ribosomal RNA



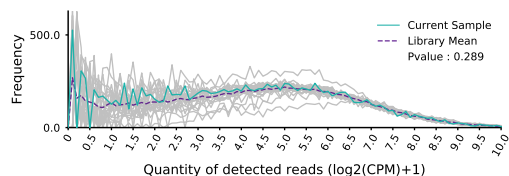
## Sequence Contamination



## GeneBody Coverage Distribution



## Distribution of Gene Expression

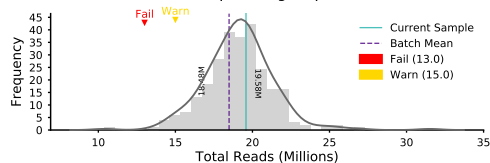


# Sample : RNA\_B11\_06 Batch : batch\_11

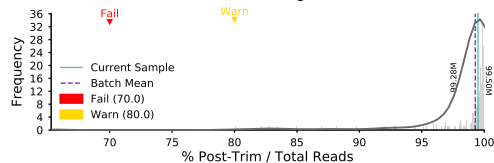
6

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

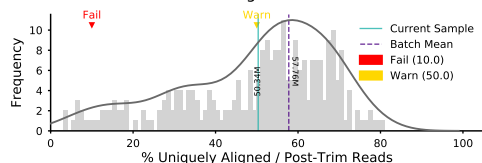
## Sequencing Depth



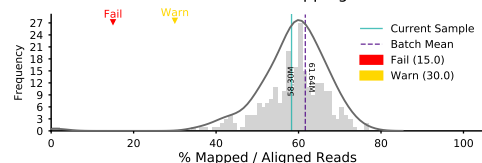
## Trimming



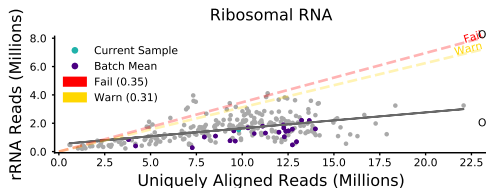
## Alignment



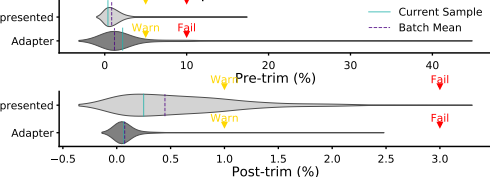
## Gene Exon Mapping



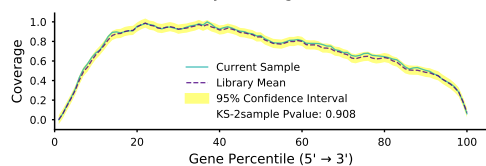
## Ribosomal RNA



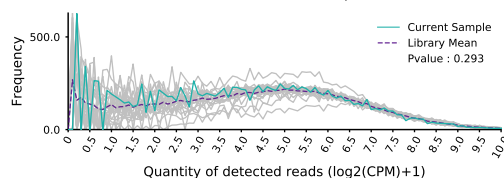
## Sequence Contamination



## GeneBody Coverage Distribution

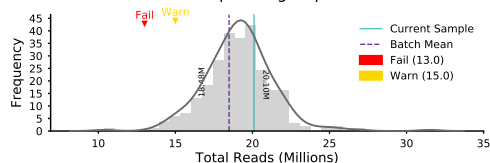


## Distribution of Gene Expression

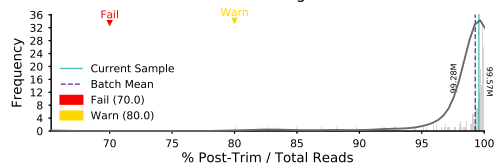


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

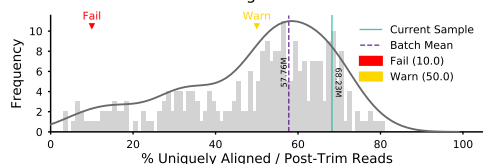
### Sequencing Depth



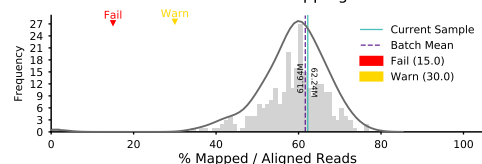
### Trimming



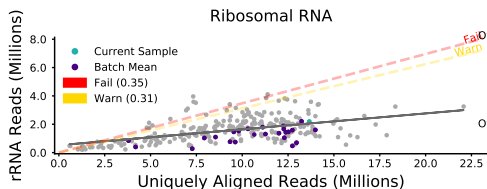
### Alignment



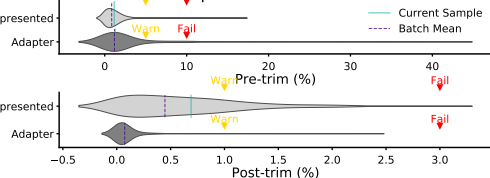
### Gene Exon Mapping



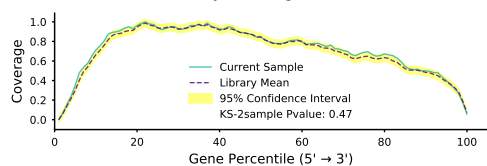
### Ribosomal RNA



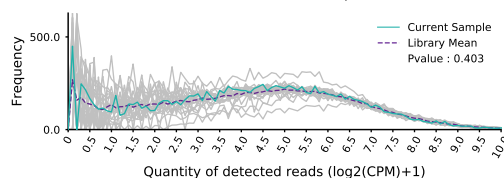
### Sequence Contamination



### GeneBody Coverage Distribution



### Distribution of Gene Expression

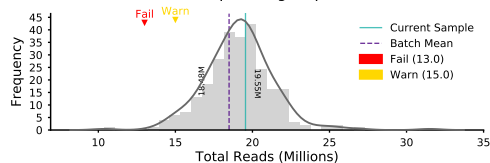


# Sample : RNA\_B11\_08 Batch : batch\_11

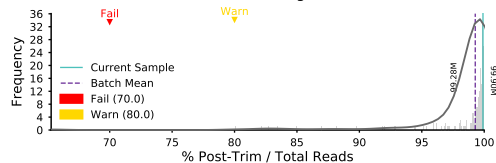
8

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

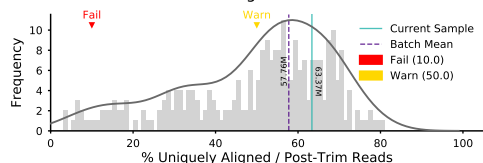
## Sequencing Depth



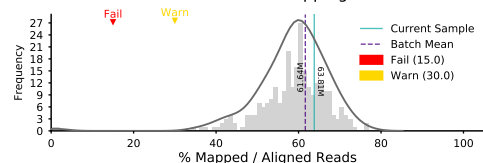
## Trimming



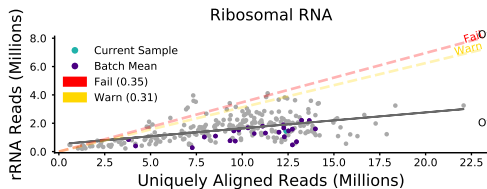
## Alignment



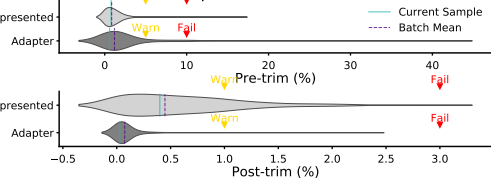
## Gene Exon Mapping



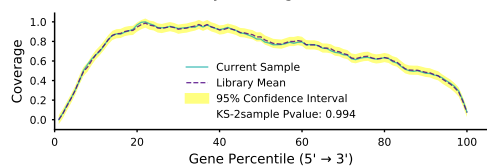
## Ribosomal RNA



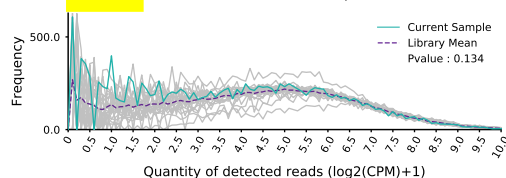
## Sequence Contamination



## GeneBody Coverage Distribution



## Distribution of Gene Expression



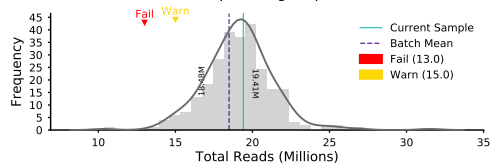


# Sample : RNA\_B11\_09 Batch : batch\_11

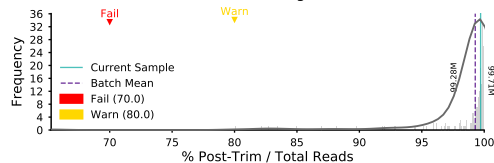
9

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

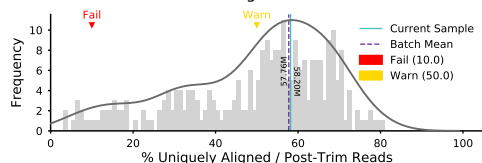
## Sequencing Depth



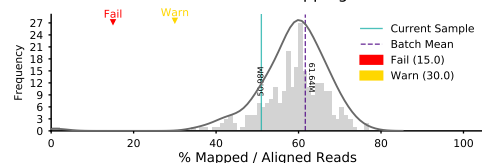
## Trimming



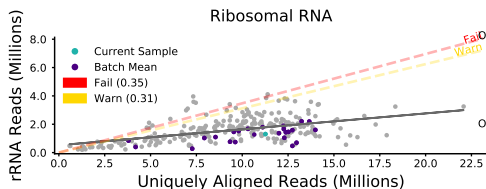
## Alignment



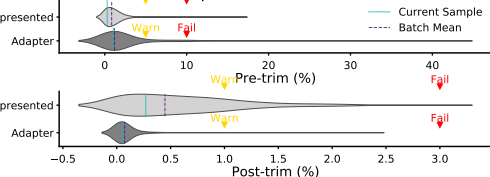
## Gene Exon Mapping



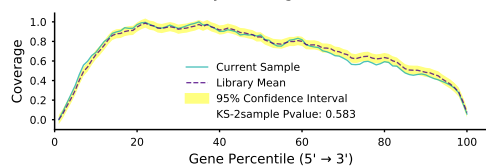
## Ribosomal RNA



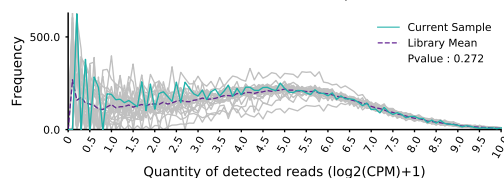
## Sequence Contamination



## GeneBody Coverage Distribution



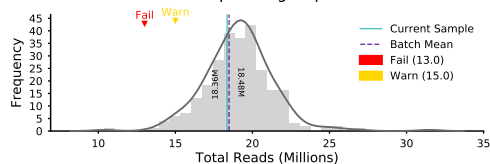
## Distribution of Gene Expression



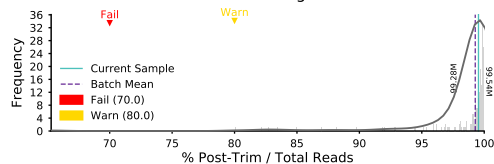
# Sample : RNA\_B11\_10 Batch : batch\_11

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

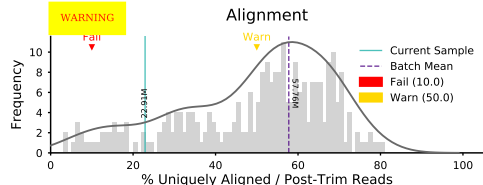
## Sequencing Depth



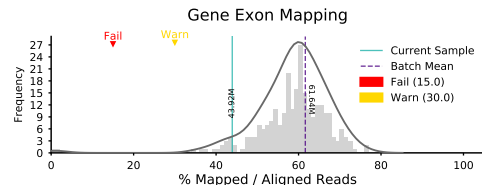
## Trimming



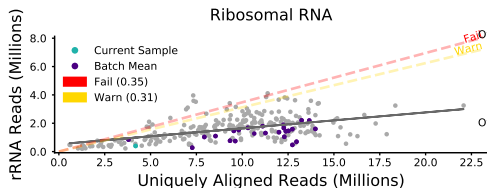
## Alignment



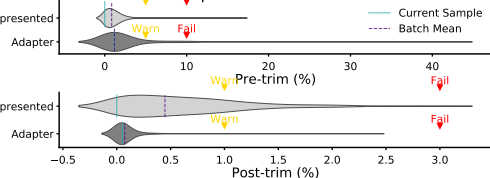
## Gene Exon Mapping



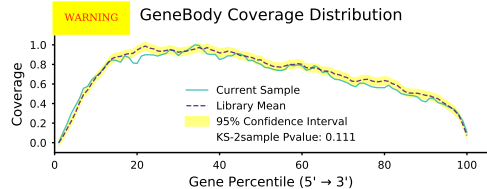
## Ribosomal RNA



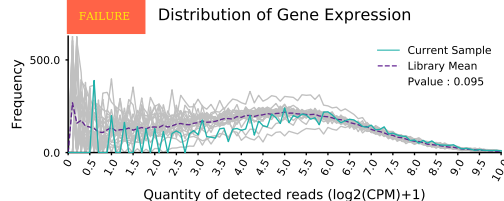
## Sequence Contamination



## GeneBody Coverage Distribution

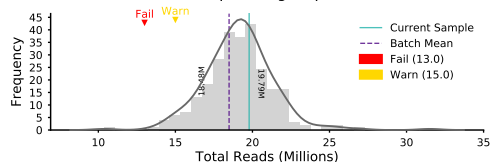


## Distribution of Gene Expression

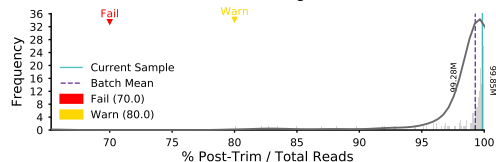


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

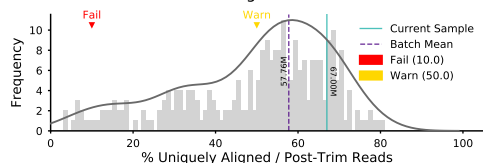
Sequencing Depth



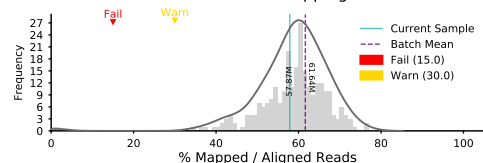
Trimming



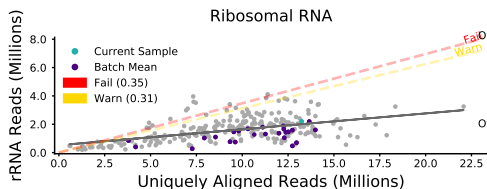
Alignment



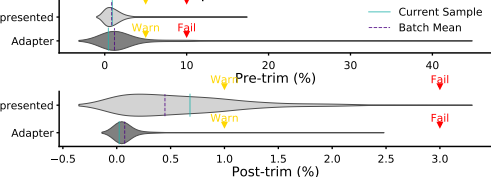
Gene Exon Mapping



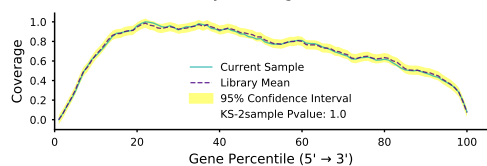
Ribosomal RNA



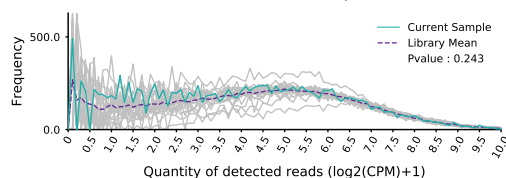
Sequence Contamination



GeneBody Coverage Distribution

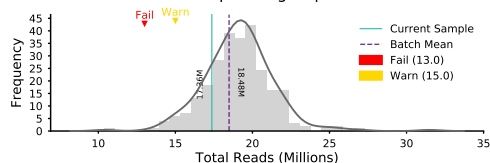


Distribution of Gene Expression

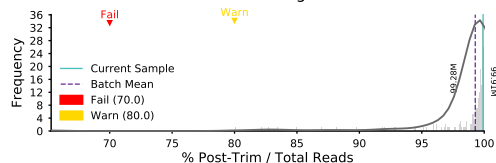


Warn cutoffs: Default alpha = 0.8| Sequencing Depth = 15.0| Trimming = 80.0| Alignment = 50.0| Gene Exon Mapping = 30.0| Ribosomal RNA = 0.312| Sequence Contamination = 5.0| Gene Body Coverage = 0.8| Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9| Sequencing Depth = 13.0|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

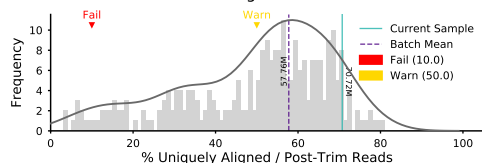
## Sequencing Depth



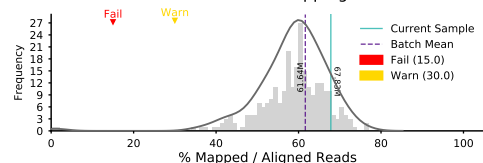
## Trimming



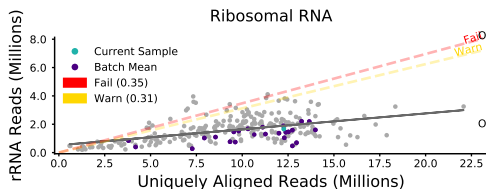
## Alignment



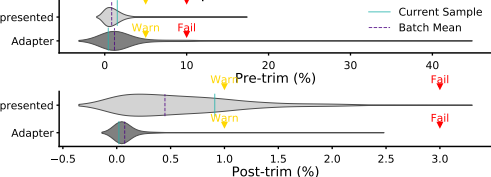
## Gene Exon Mapping



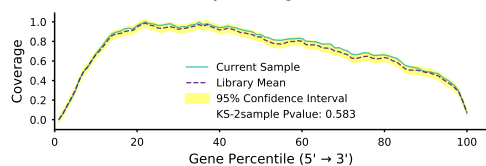
## Ribosomal RNA



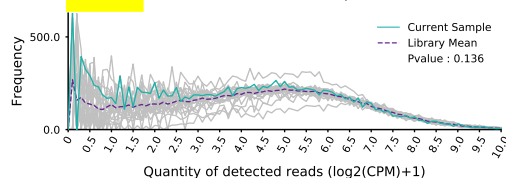
## Sequence Contamination



## GeneBody Coverage Distribution

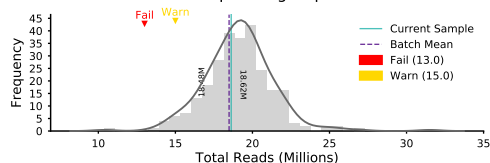


## Distribution of Gene Expression

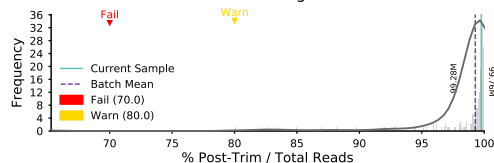


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

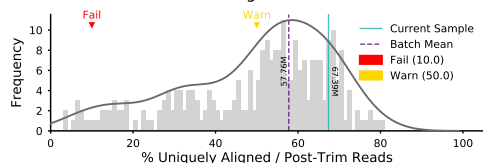
## Sequencing Depth



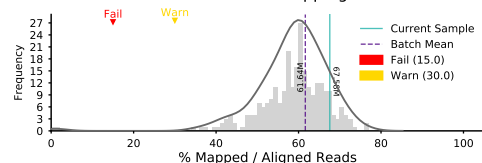
## Trimming



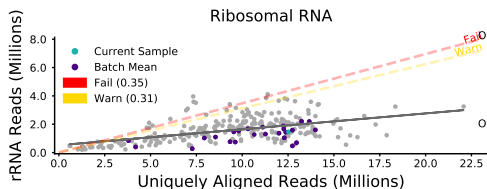
## Alignment



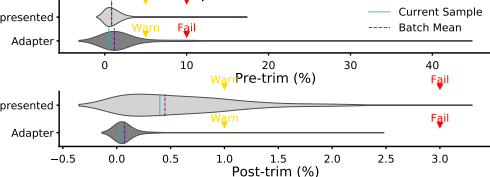
## Gene Exon Mapping



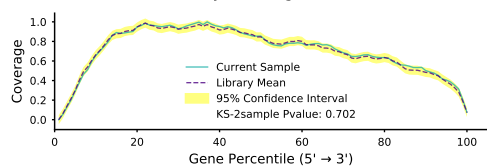
## Ribosomal RNA



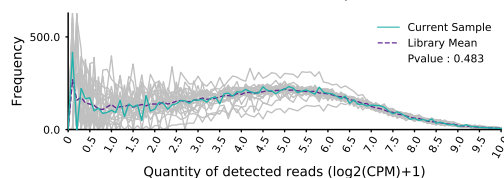
## Sequence Contamination



## GeneBody Coverage Distribution



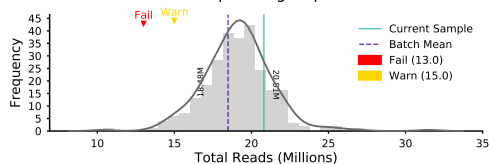
## Distribution of Gene Expression



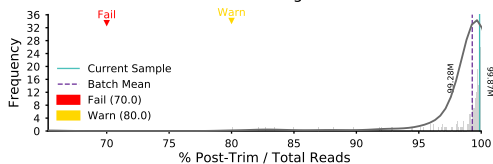
# Sample : RNA\_B11\_14 Batch : batch\_11

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

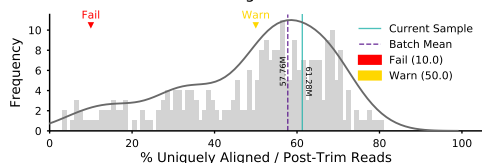
## Sequencing Depth



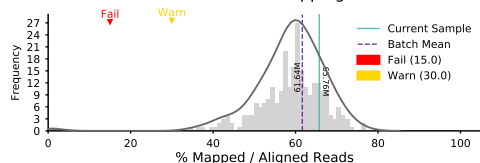
## Trimming



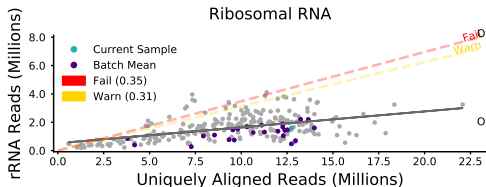
## Alignment



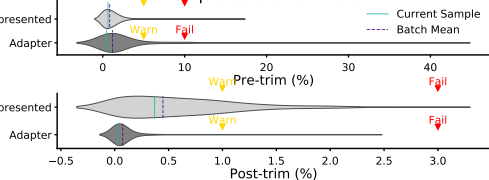
## Gene Exon Mapping



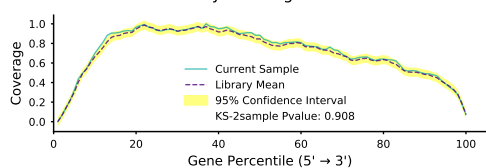
## Ribosomal RNA



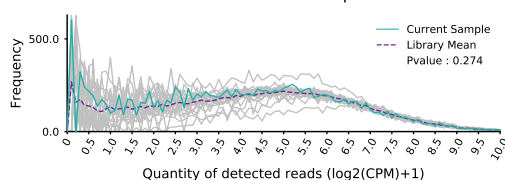
## Sequence Contamination



## GeneBody Coverage Distribution

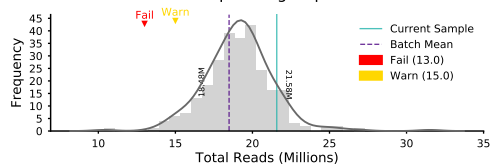


## Distribution of Gene Expression

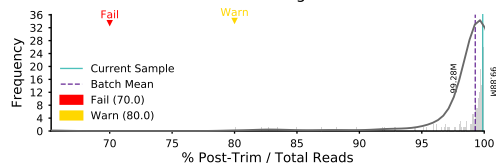


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

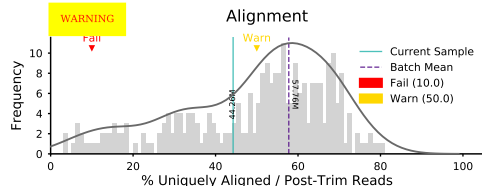
## Sequencing Depth



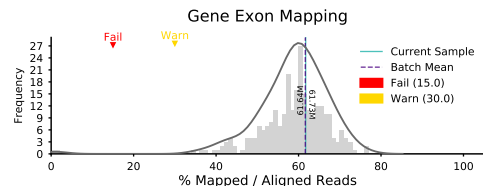
## Trimming



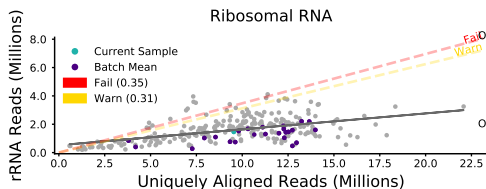
## Alignment



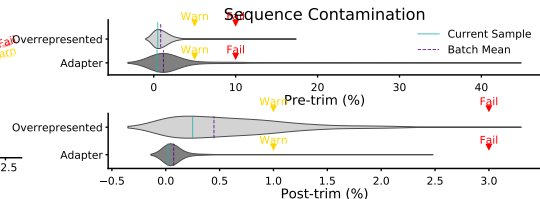
## Gene Exon Mapping



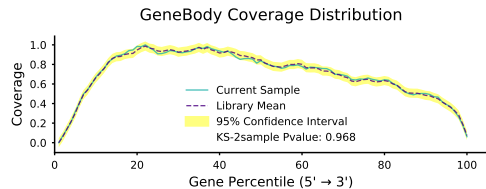
## Ribosomal RNA



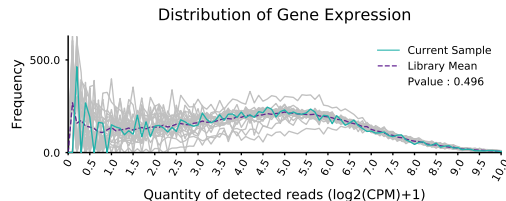
## Sequence Contamination



## GeneBody Coverage Distribution

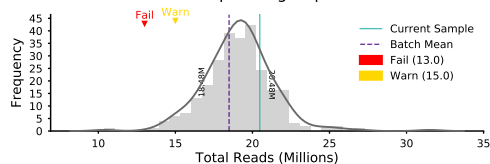


## Distribution of Gene Expression

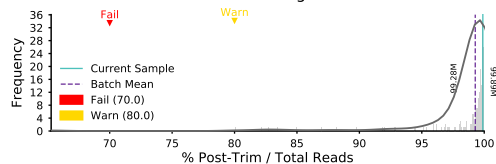


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

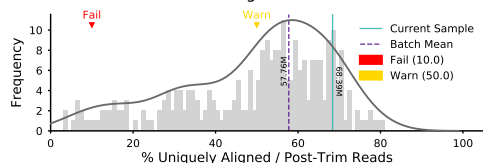
Sequencing Depth



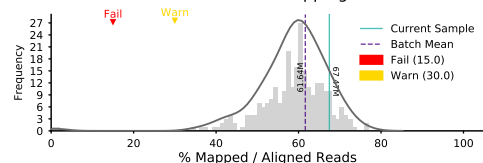
Trimming



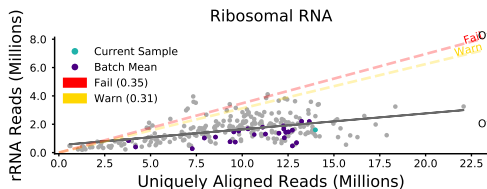
Alignment



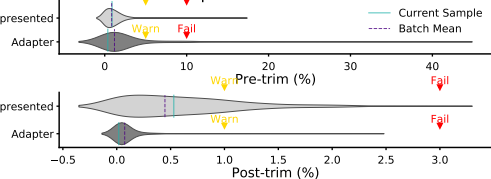
Gene Exon Mapping



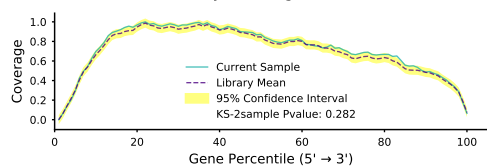
Ribosomal RNA



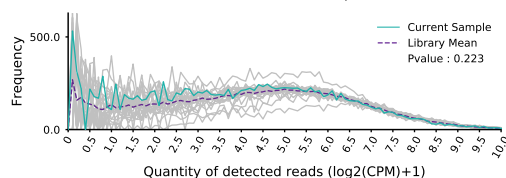
Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression



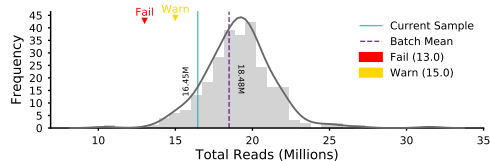


# Sample : RNA\_B11\_17 Batch\_11

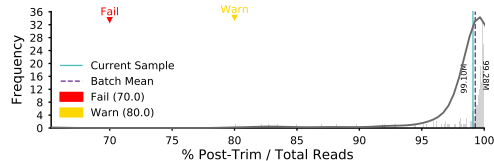
17

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

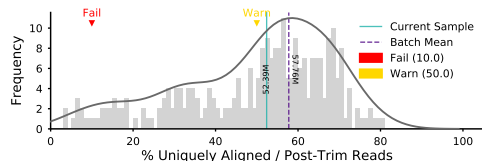
## Sequencing Depth



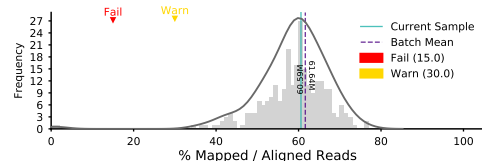
## Trimming



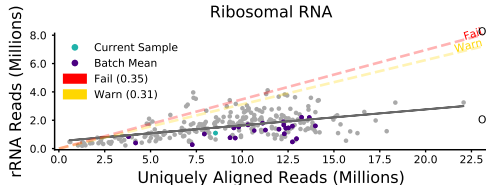
## Alignment



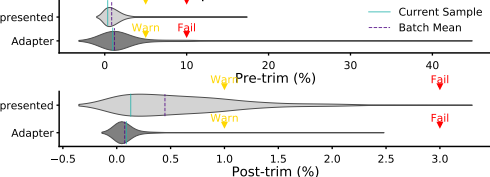
## Gene Exon Mapping



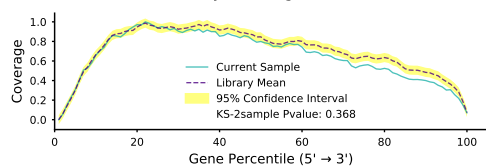
## Ribosomal RNA



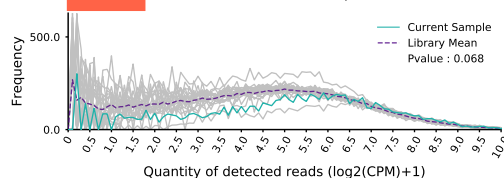
## Sequence Contamination



## GeneBody Coverage Distribution

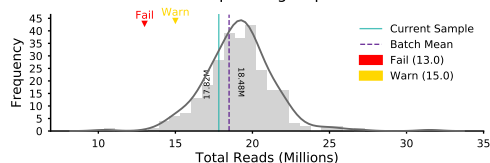


## Distribution of Gene Expression

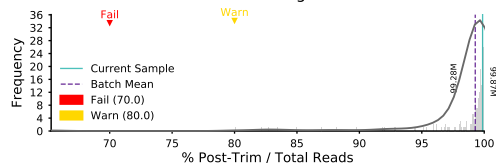


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

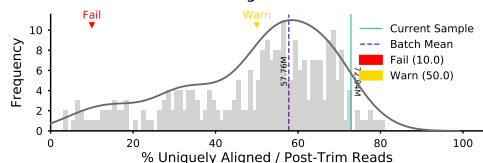
Sequencing Depth



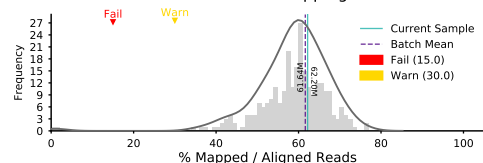
Trimming



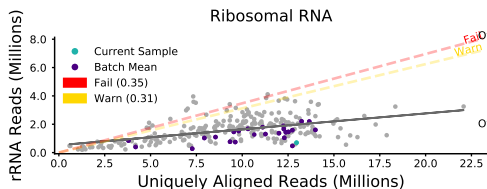
Alignment



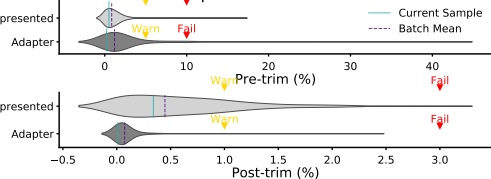
Gene Exon Mapping



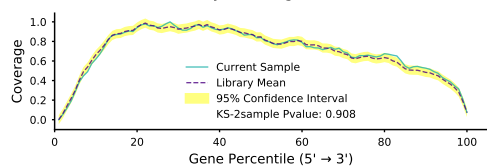
Ribosomal RNA



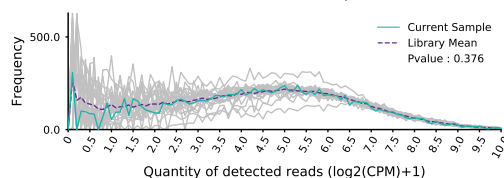
Sequence Contamination



GeneBody Coverage Distribution



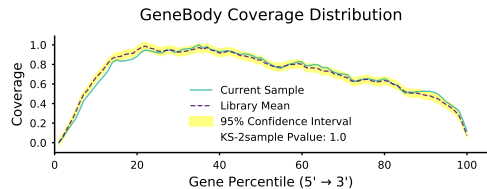
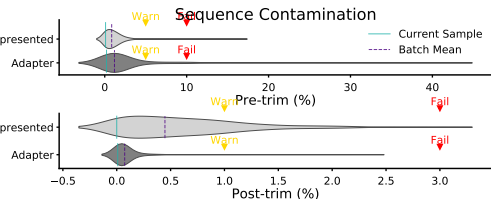
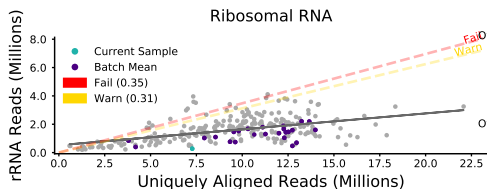
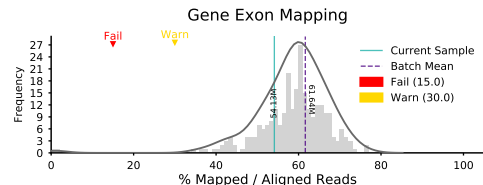
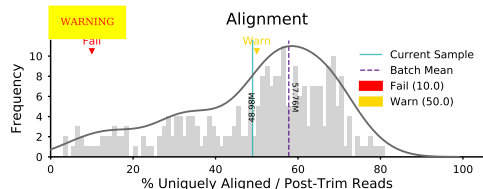
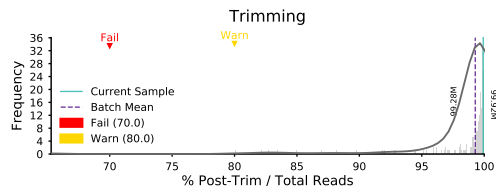
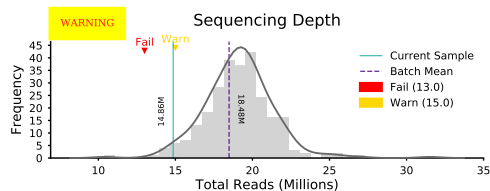
Distribution of Gene Expression



# Sample : RNA\_B11\_19 Batch\_11

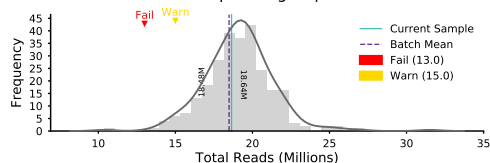
19

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

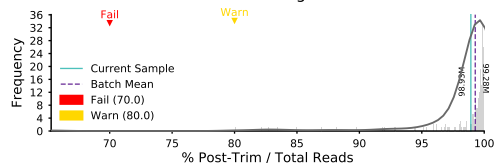


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

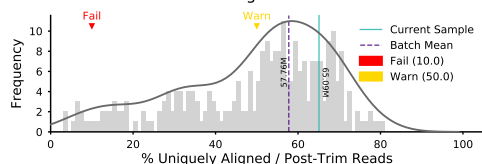
## Sequencing Depth



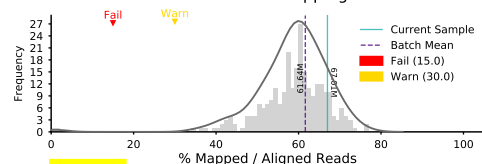
## Trimming



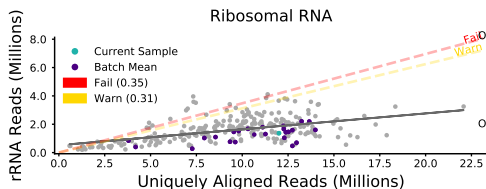
## Alignment



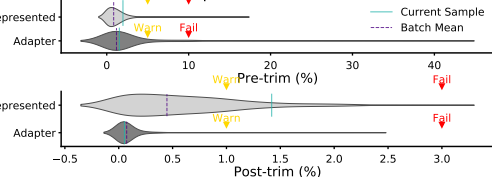
## Gene Exon Mapping



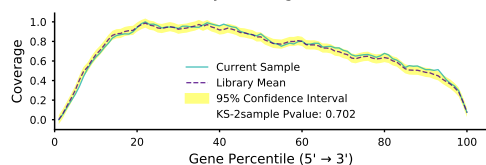
## Ribosomal RNA



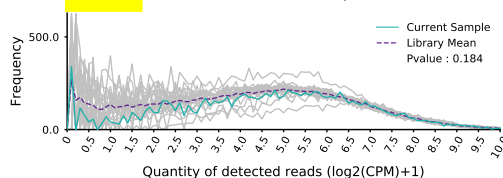
## Sequence Contamination



## GeneBody Coverage Distribution

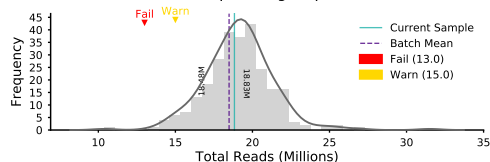


## Distribution of Gene Expression

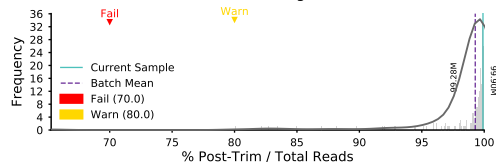


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

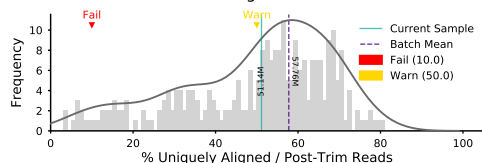
Sequencing Depth



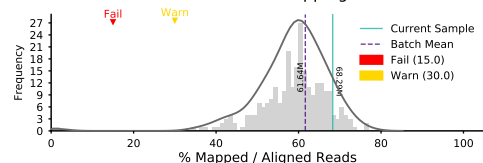
Trimming



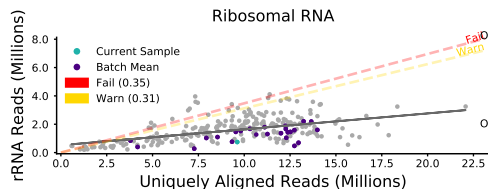
Alignment



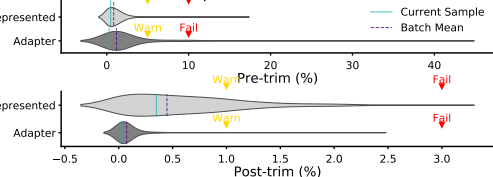
Gene Exon Mapping



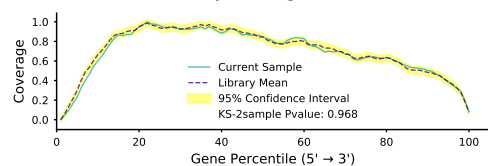
Ribosomal RNA



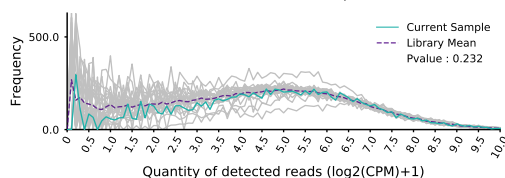
Sequence Contamination



GeneBody Coverage Distribution

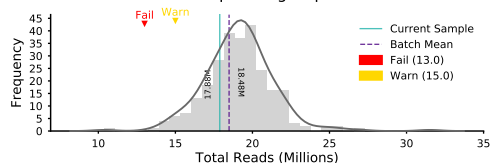


Distribution of Gene Expression

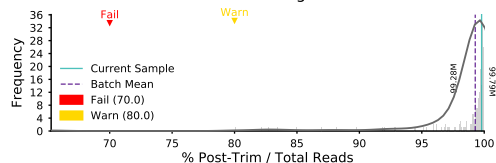


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

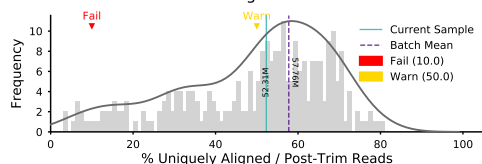
### Sequencing Depth



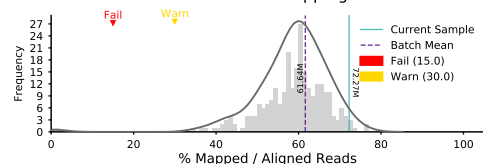
### Trimming



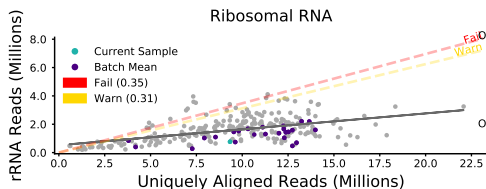
### Alignment



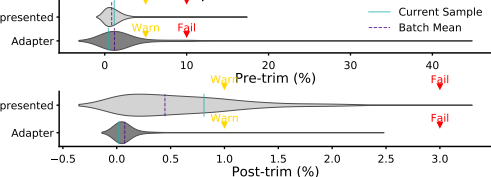
### Gene Exon Mapping



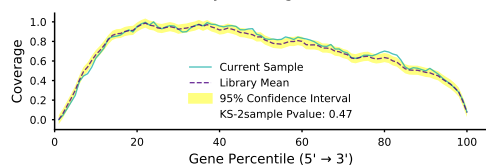
### Ribosomal RNA



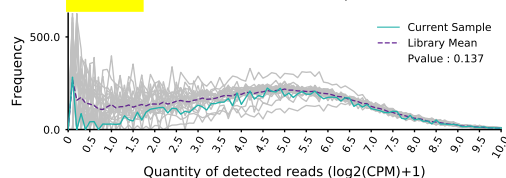
### Sequence Contamination



### GeneBody Coverage Distribution

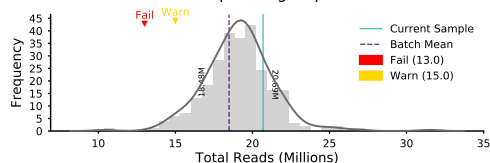


### Distribution of Gene Expression

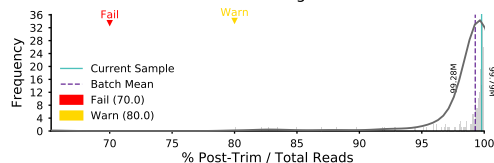


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
 Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

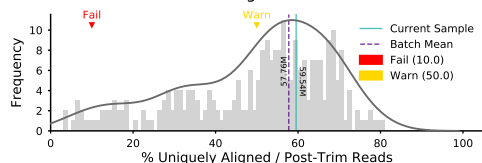
Sequencing Depth



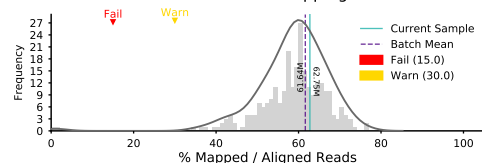
Trimming



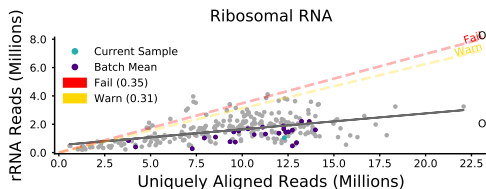
Alignment



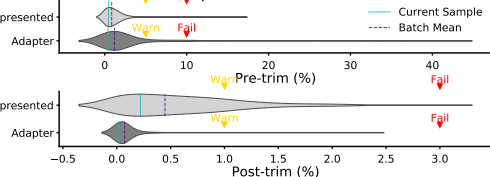
Gene Exon Mapping



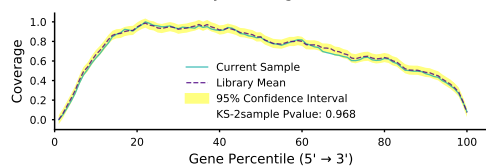
Ribosomal RNA



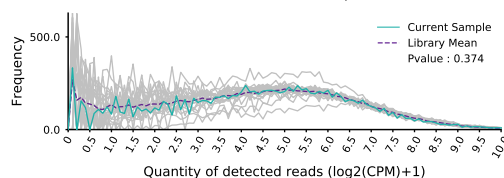
Sequence Contamination



GeneBody Coverage Distribution



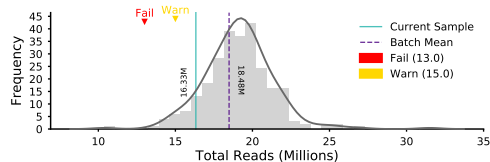
Distribution of Gene Expression



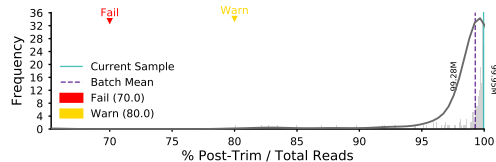
Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8

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

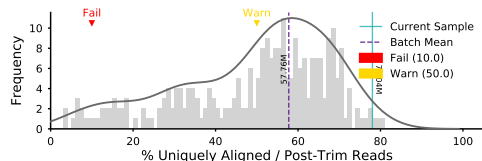
Sequencing Depth



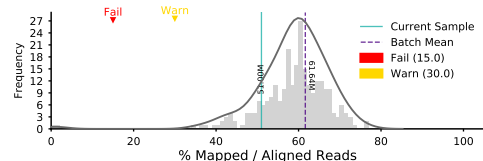
Trimming



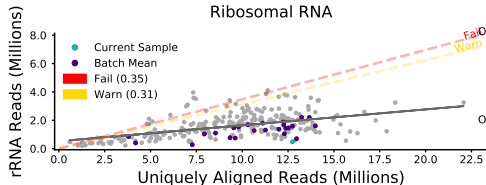
Alignment



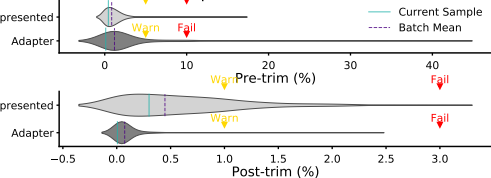
Gene Exon Mapping



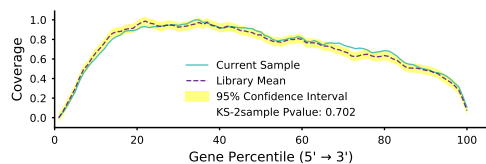
Ribosomal RNA



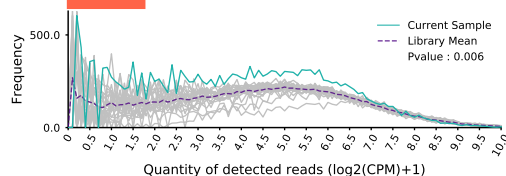
Sequence Contamination



GeneBody Coverage Distribution



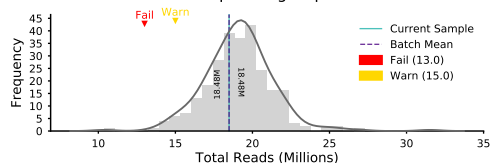
Distribution of Gene Expression



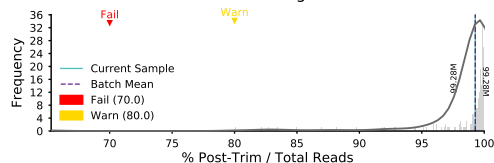


Warn cutoffs: Default alpha = 0.8 | Sequencing Depth = 15.0 | Trimming = 80.0 | Alignment = 50.0 | Gene Exon Mapping = 30.0 | Ribosomal RNA = 0.312 | Sequence Contamination = 5.0 | Gene Body Coverage = 0.8 | Distribution of Gene Expression = 0.8  
Fail cutoffs: Default alpha = 0.9 | Sequencing Depth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

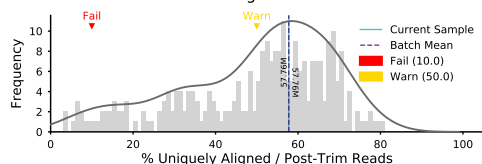
Sequencing Depth



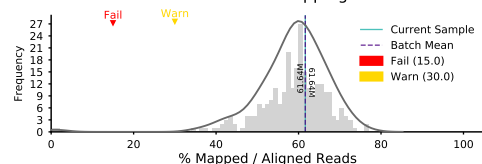
Trimming



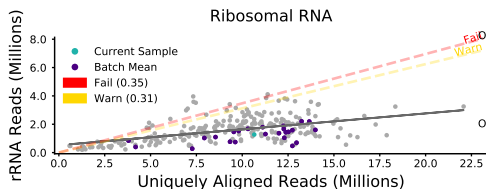
Alignment



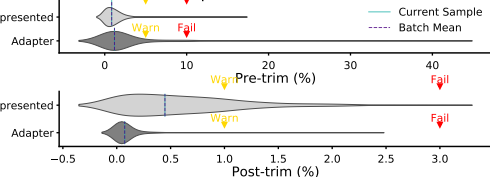
Gene Exon Mapping



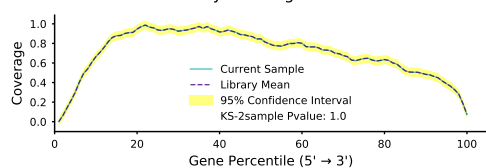
Ribosomal RNA



Sequence Contamination



GeneBody Coverage Distribution



Distribution of Gene Expression

