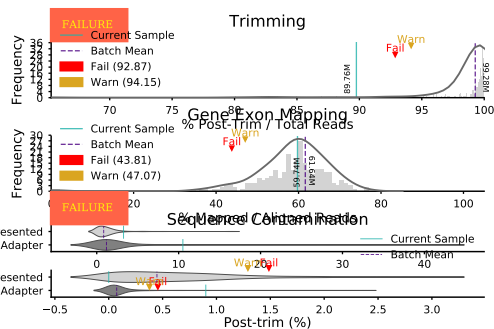
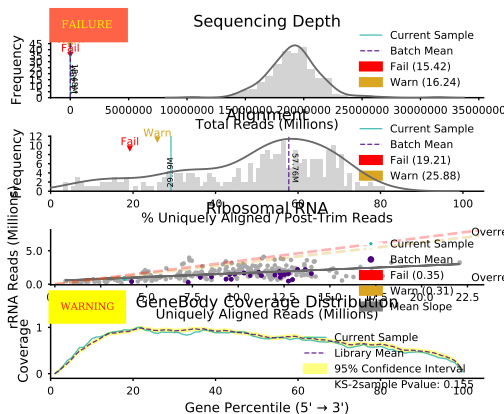


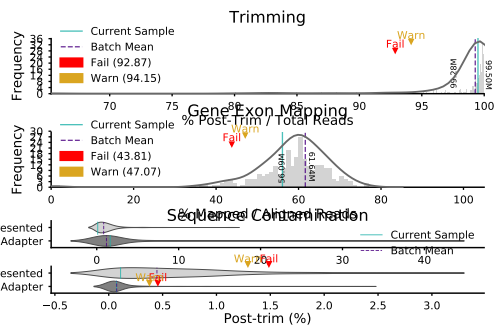
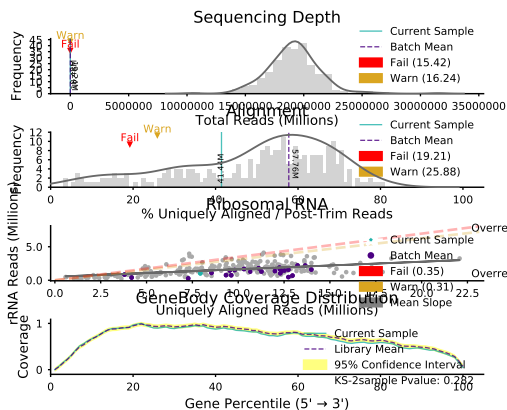
Sample : RNA_B11_01 Batch : batch_11

Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.21411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9



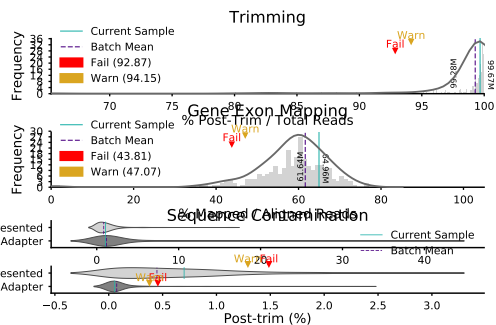
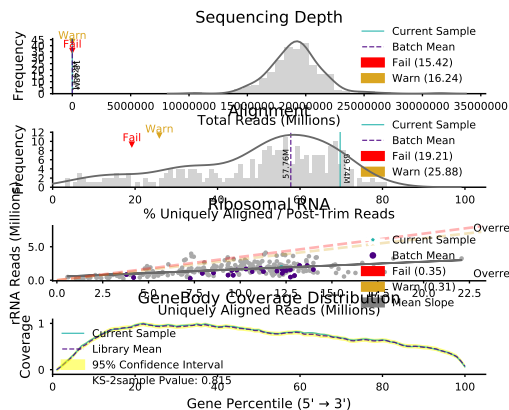
Sample : RNA_B11_02 Batch : batch_11

Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883432206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8|
 Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9|

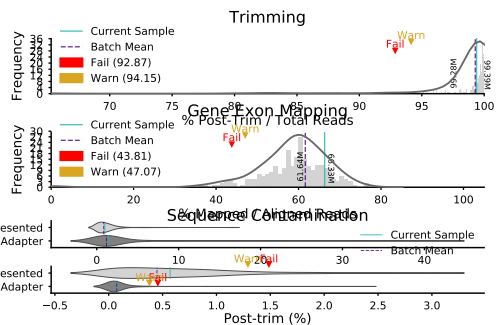
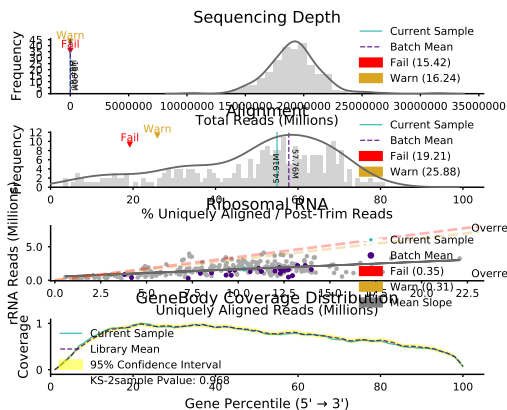


Warn cutoffs: Default alpha = 0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage = 0.91 Dis

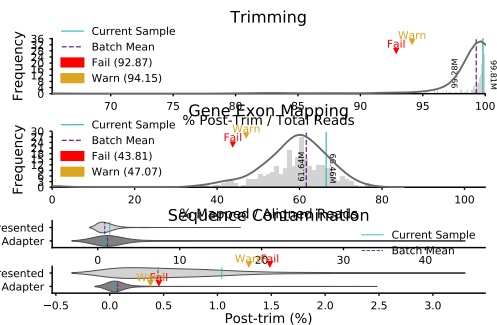
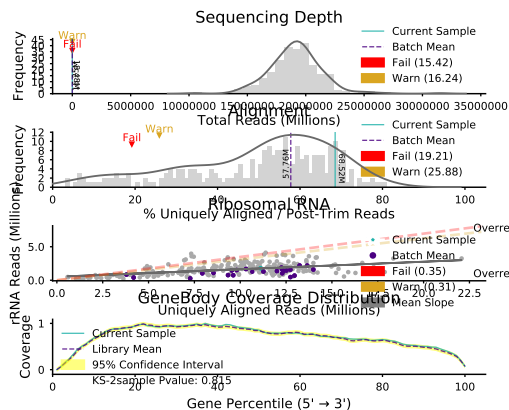
Fail cutoffs: Default alpha = 0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.91 Dis



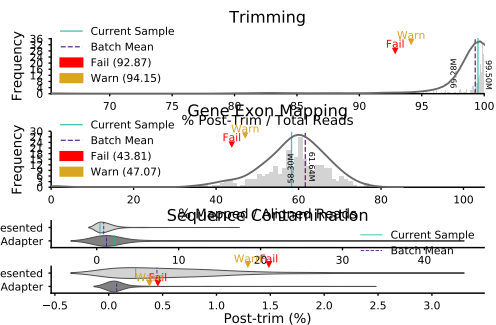
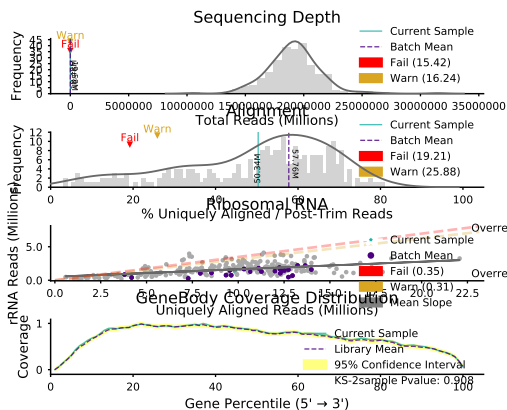
Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 [Dis]
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9 [Dis]



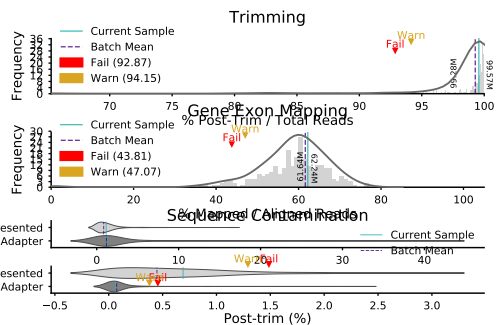
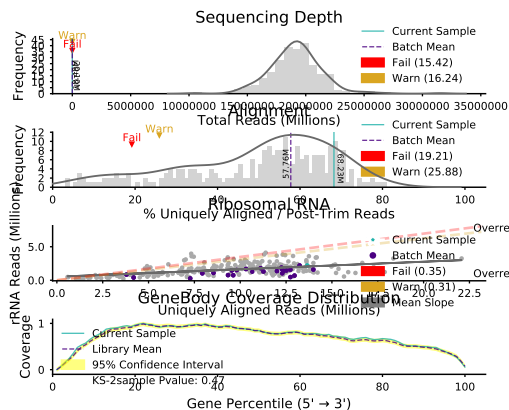
Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883423206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8| Dis
Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9| Dis



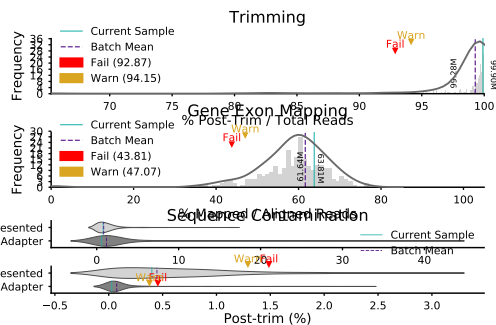
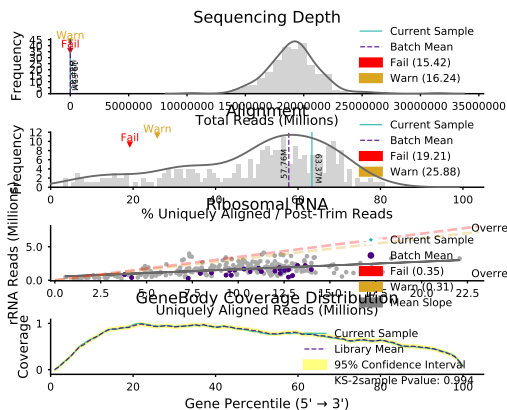
Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883432206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8|
 Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9|



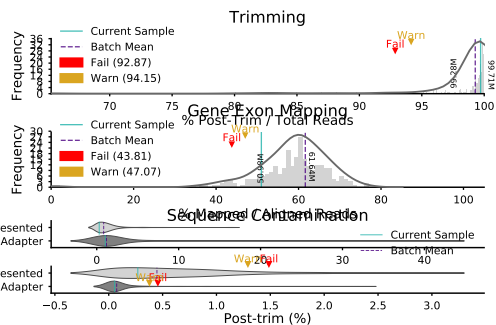
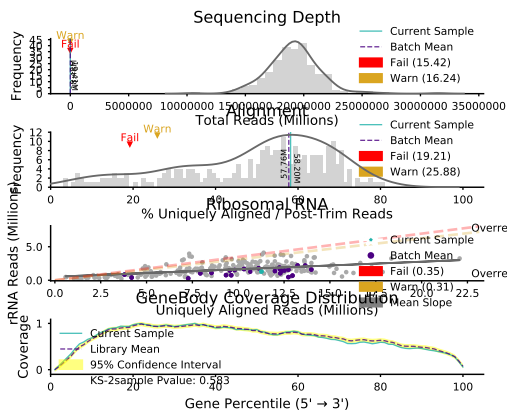
Warn cutoffs: Default alpha = 0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 [0.77, 0.83] Fail cutoffs: Default alpha = 0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9 [0.82, 0.98]



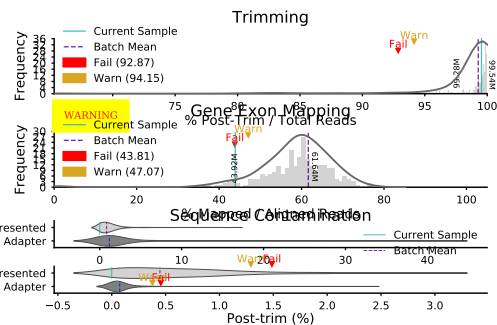
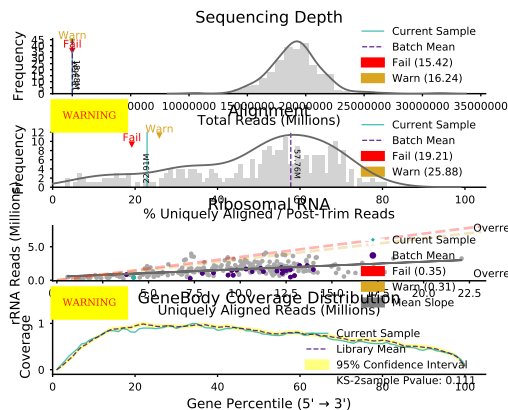
Warn cutoffs: Default alpha = 0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 [0.8] D
 Fail cutoffs: Default alpha = 0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9 [0.9] D



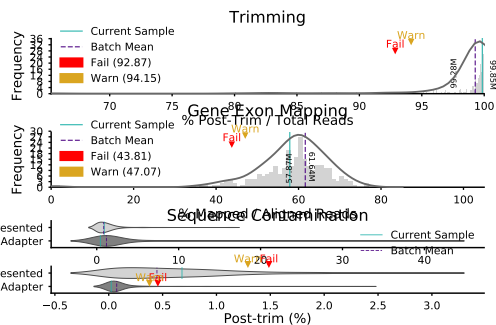
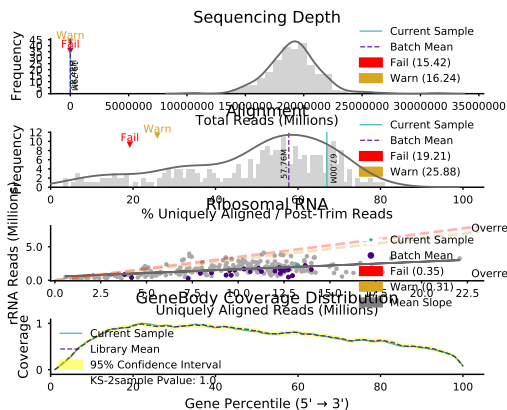
Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883432206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8| Dis
 Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9| Dis



Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883432206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8| D
Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9| D

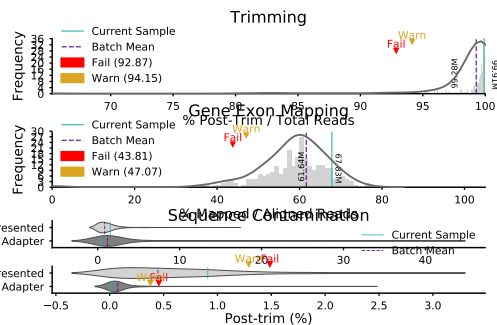
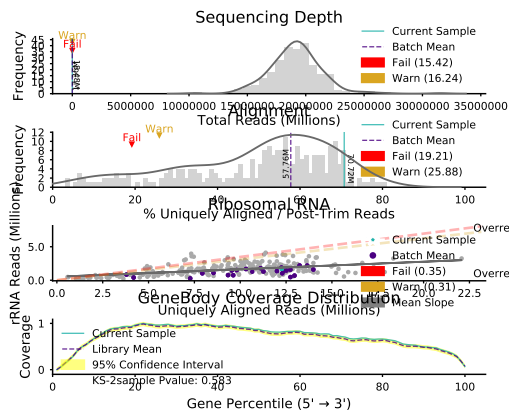


Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883432206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8| Dis
 Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9| Dis

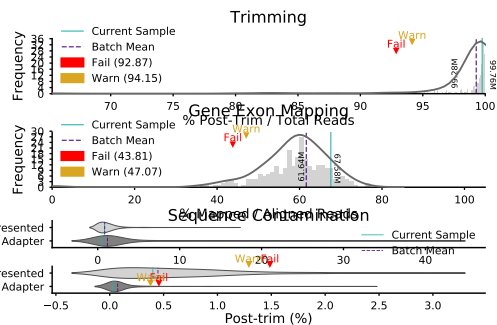
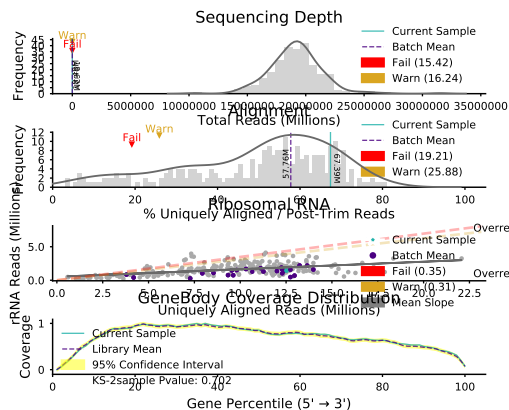


Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage = 0.91 Dis

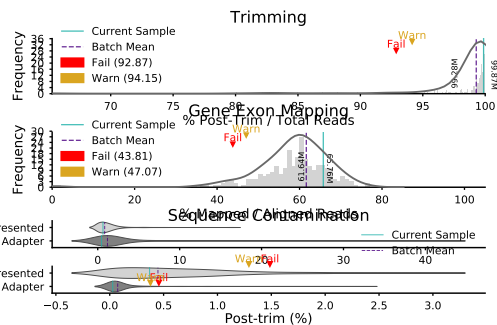
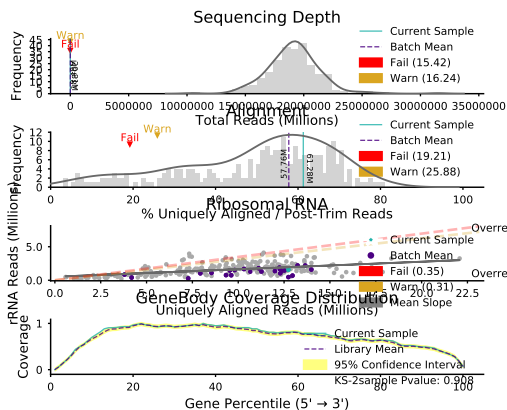
Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.91 Dis



Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution Mean Slope = 20.0 KS-2sample Pvalue = 0.402
Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.21411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9



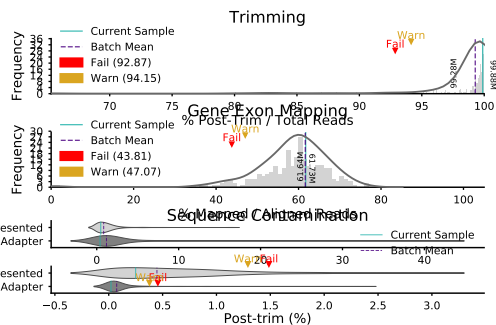
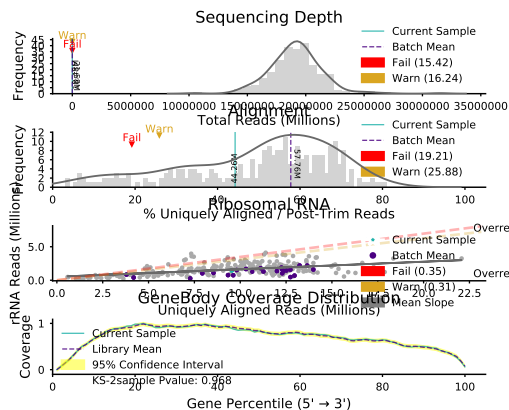
Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution Mean Slope = 20.0 KS-2sample Pvalue: 0.908
Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9



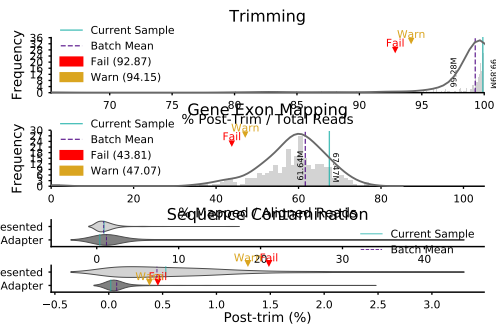
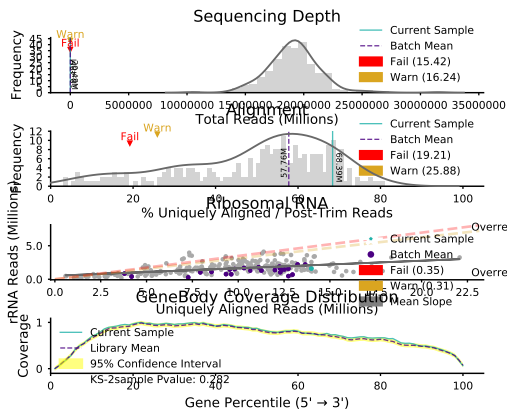
Sample : RNA_B11_15 Batch : batch_11

Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution Mean Slope = 20.0 KS-2sample Pvalue = 0.368

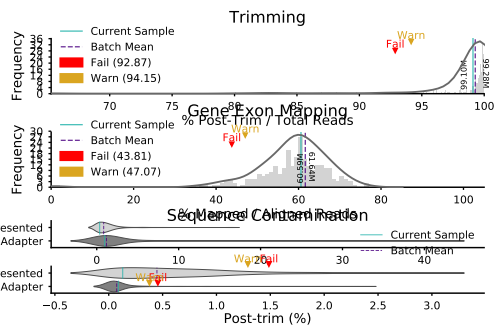
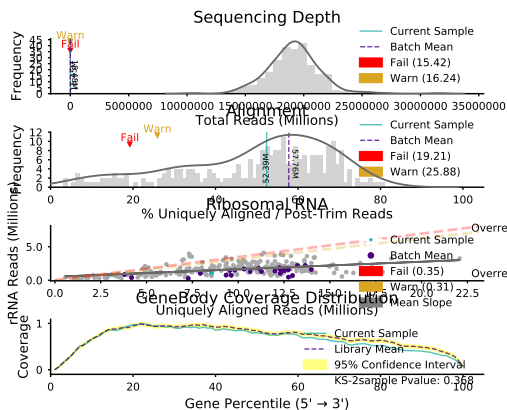
Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9



Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution = 0.282
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.21411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9 Gene Body Coverage Distribution = 0.282

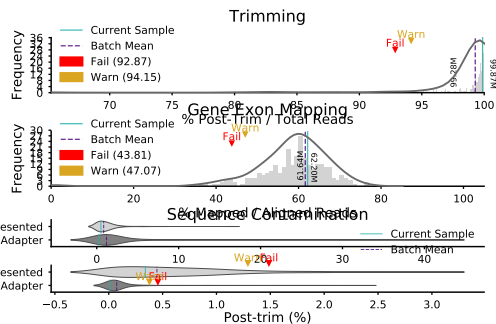
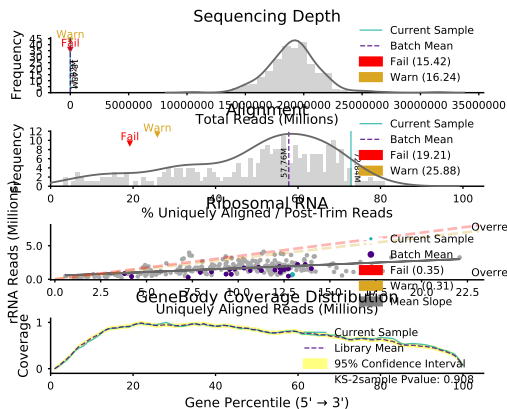


Warn cutoffs: Default alpha =0.8| Sequencing Depth = 16.241476381729186| Trimming = 94.1462290640725| Alignment = 25.883432206791934| Gene Exon Mapping = 47.068386642306564| Ribosomal RNA = 0.312| Sequence Contamination = 0.37816525422038655| Gene Body Coverage = 0.8|
 Fail cutoffs: Default alpha =0.9| Sequencing Depth = 15.422129911096862| Trimming = 92.86918155320676| Alignment = 19.211411756396192| Gene Exon Mapping = 43.813950731314556| Ribosomal RNA = 0.348| Sequence Contamination = 10.860615219281971| Gene Body Coverage = 0.9|



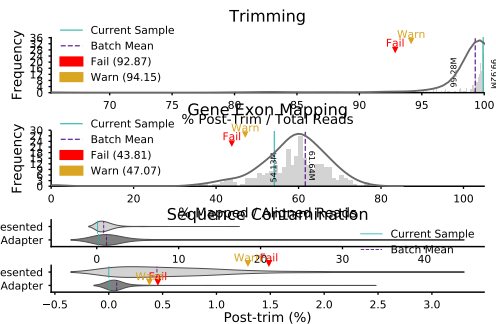
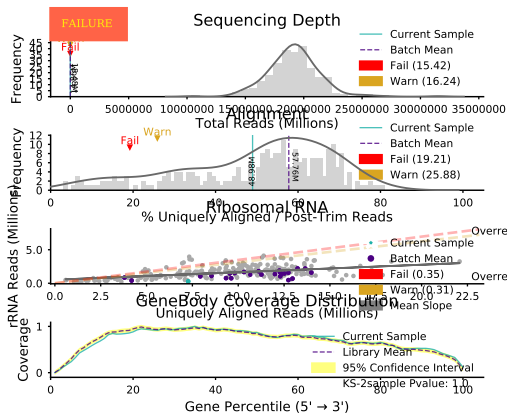
Sample : RNA_B11_18 Batch : batch_11

Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage = 0.91
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.91

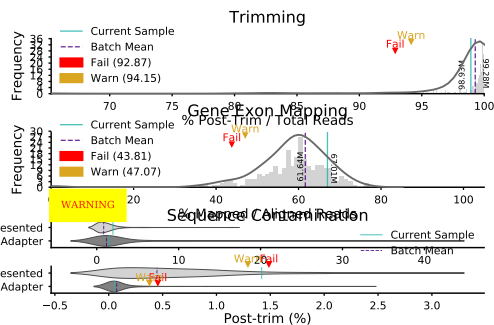
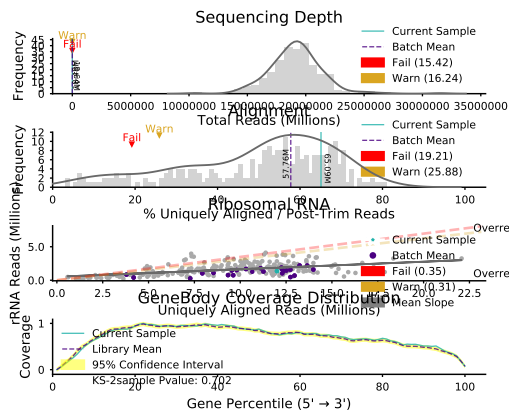


Sample : RNA_B11_19 Batch : batch_11

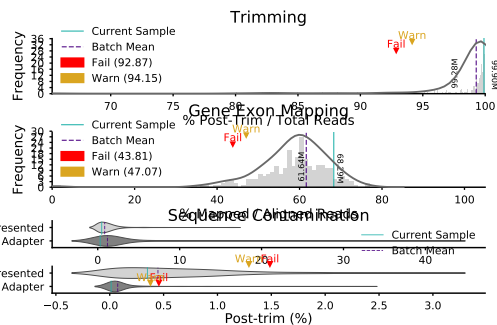
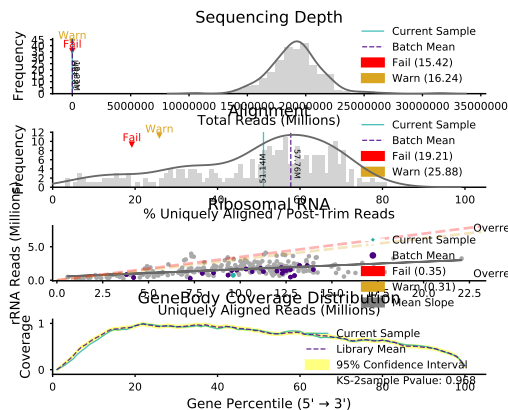
Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution Mean Slope = 20.0 KS-2sample Pvalue: 1.0
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9



Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8122222222222222
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9122222222222222

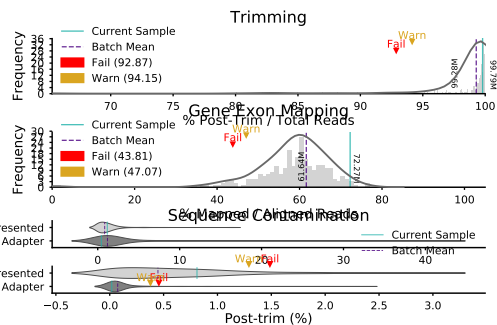
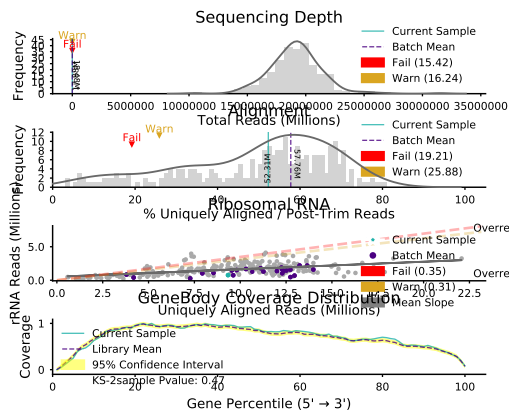


Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage = 0.9
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9

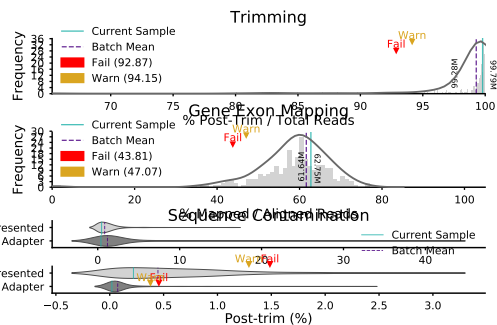
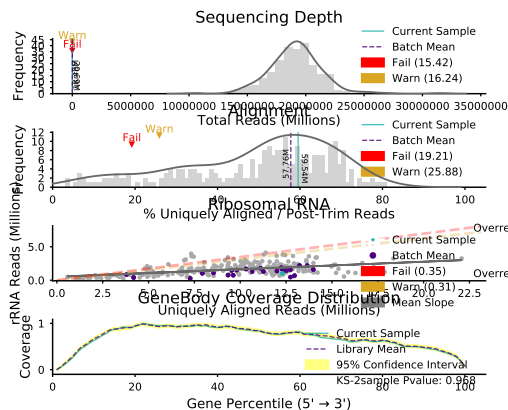


Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution = 20.0 KS-2sample Pvalue = 0.47

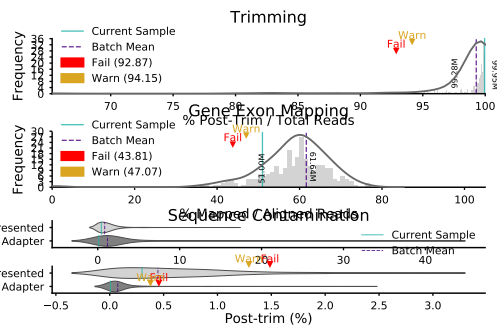
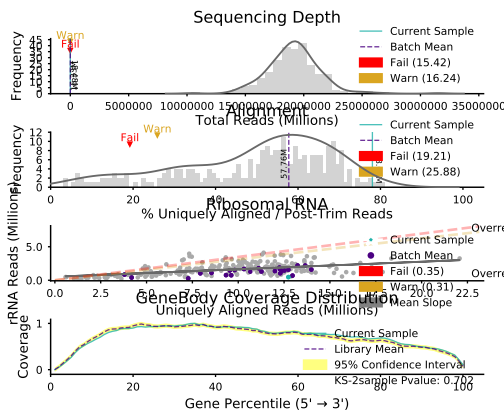
Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.21411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9 Gene Body Coverage Distribution = 22.5



Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution Mean Slope = 20.0 KS-2sample Pvalue = 0.958
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9



Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 [0.7, 0.9] Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9 [0.7, 0.9]



Sample : Batch_Mean Batch : batch_11

Warn cutoffs: Default alpha =0.8 Sequencing Depth = 16.241476381729186 Trimming = 94.1462290640725 Alignment = 25.883432206791934 Gene Exon Mapping = 47.068386642306564 Ribosomal RNA = 0.312 Sequence Contamination = 0.37816525422038655 Gene Body Coverage = 0.8 Gene Body Coverage Distribution Mean Slope = 20.0 KS-2sample Pvalue: 1.0
 Fail cutoffs: Default alpha =0.9 Sequencing Depth = 15.422129911096862 Trimming = 92.86918155320676 Alignment = 19.211411756396192 Gene Exon Mapping = 43.813950731314556 Ribosomal RNA = 0.348 Sequence Contamination = 10.860615219281971 Gene Body Coverage = 0.9

