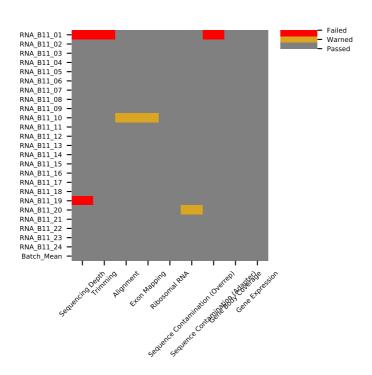
## QC Plotter Input Summary

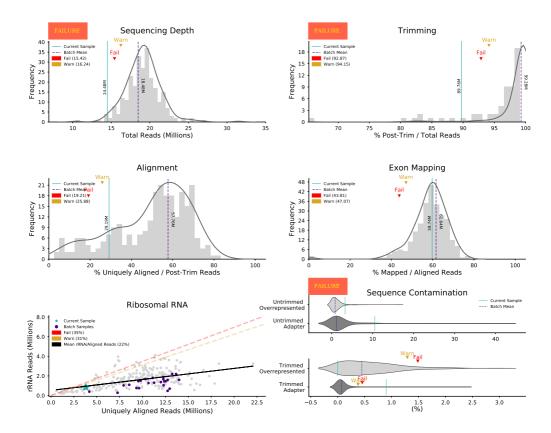
Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/USER\_testData\_B11.csv
Output location = /projects/b1063/Gaurav/pyRetroPlotter/SCRIPTB11\_defaultcutoffs\_6panel.pdf
Background table = data/SCRIPTretro\_masterStatistics\_allBatches.csv
Gene Body Coverage file = None
Gene read depth distribution histogram file = None
Cutoff file = False

Warn cutoffs: Default alpha =0.9| Sequencing Depth = 16.241| Trimming = 94.146| Alignment = 25.883| Gene Exon Mapping = 47.068
| Ribosomal RNA = 0.312| Adapter Contamination = 0.378| Overrep. Seg. Contamination = 1.292| Gene Body Coverage = 0.9| Distribution of Gene Expression = None

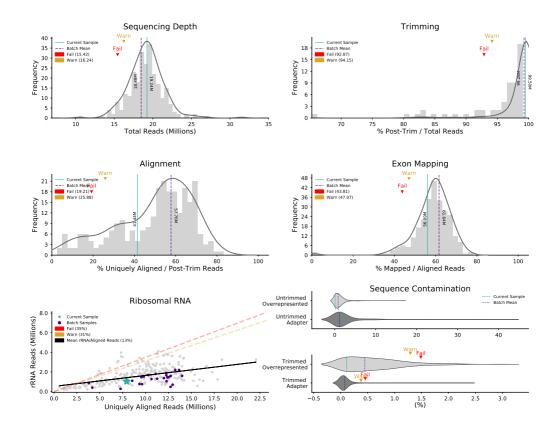
## Summary of QC Metrics



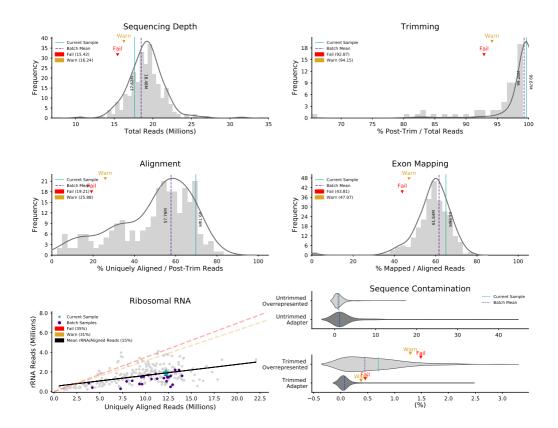
Sample: RNA B11 01 Batch: batch 11



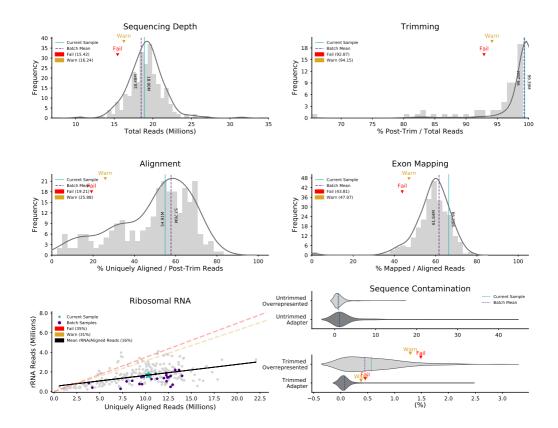
Sample: RNA\_B11\_02 Batch: batch\_11



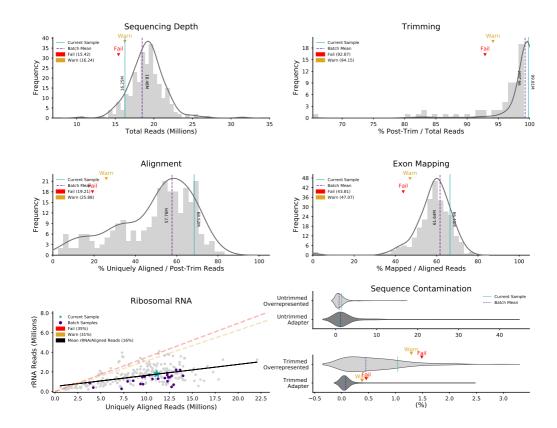
Sample: RNA\_B11\_03 Batch: batch\_11



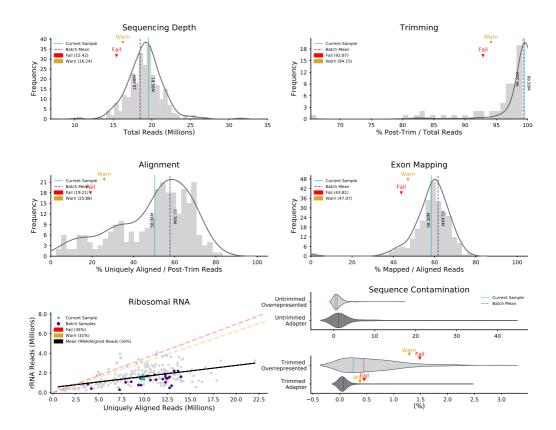
Sample: RNA\_B11\_04 Batch: batch\_11



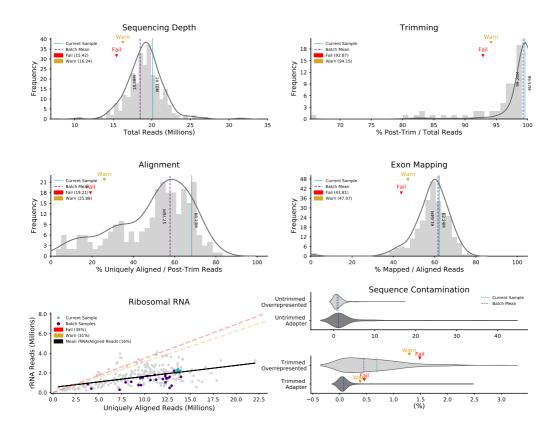
Sample: RNA\_B11\_05 Batch: batch\_11



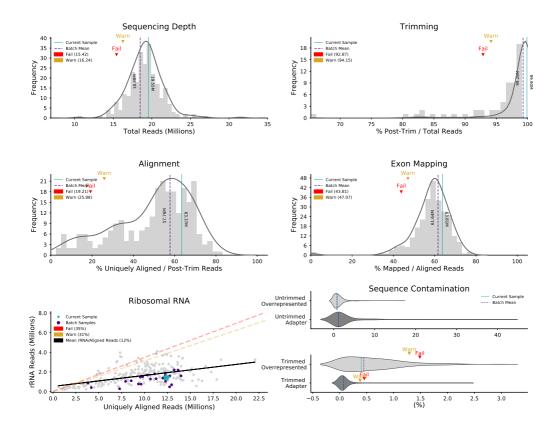
Sample: RNA\_B11\_06 Batch: batch\_11



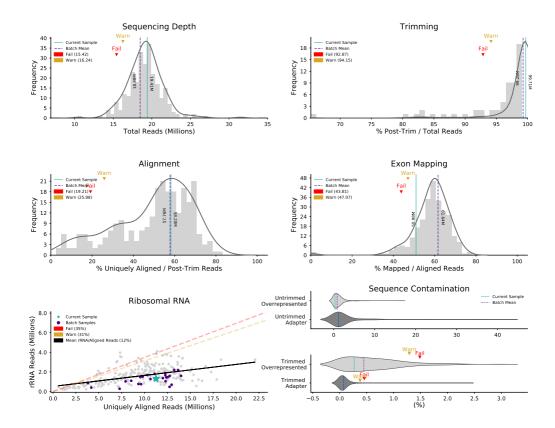
Sample: RNA\_B11\_07 Batch: batch\_11



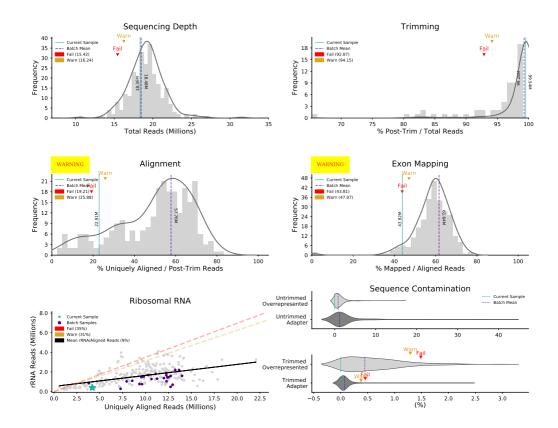
Sample: RNA\_B11\_08 Batch: batch\_11



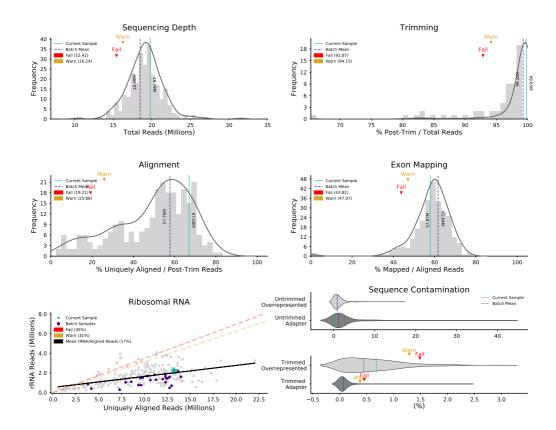
Sample: RNA\_B11\_09 Batch: batch\_11



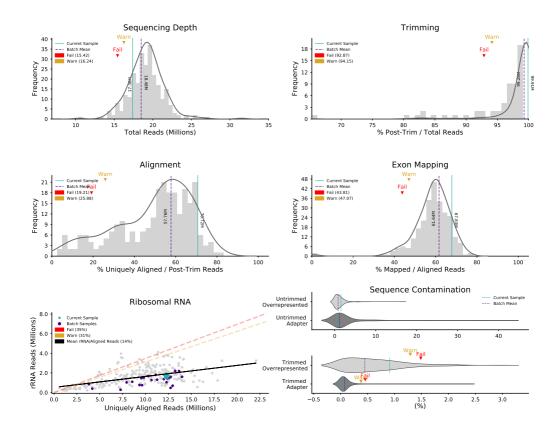
Sample: RNA\_B11\_10 Batch: batch\_11



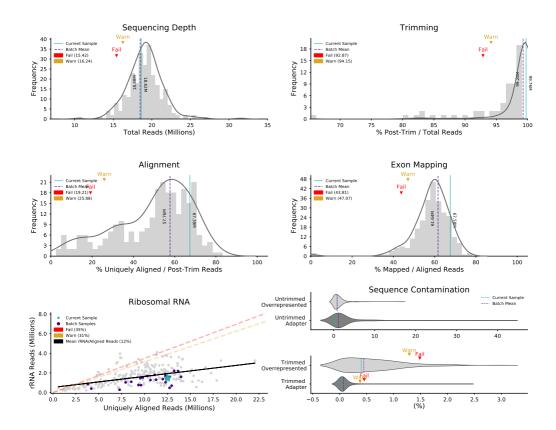
Sample: RNA\_B11\_11 Batch: batch\_11



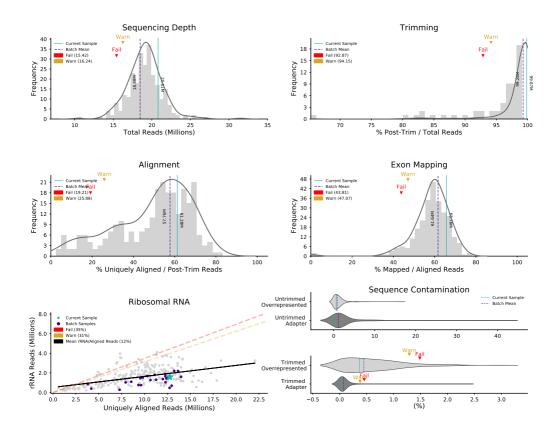
Sample: RNA\_B11\_12 Batch: batch\_11



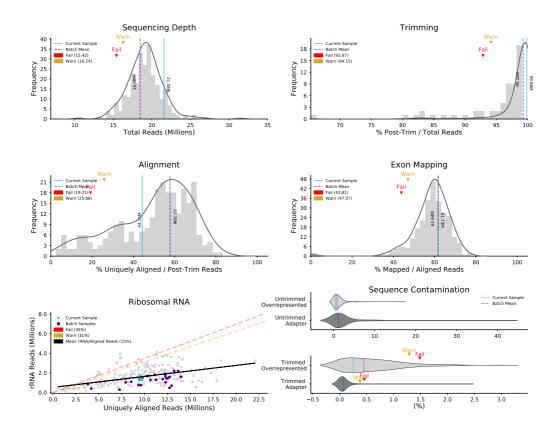
Sample: RNA\_B11\_13 Batch: batch\_11



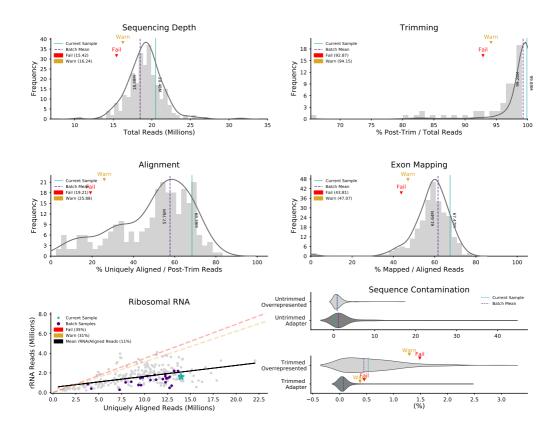
Sample: RNA\_B11\_14 Batch: batch\_11



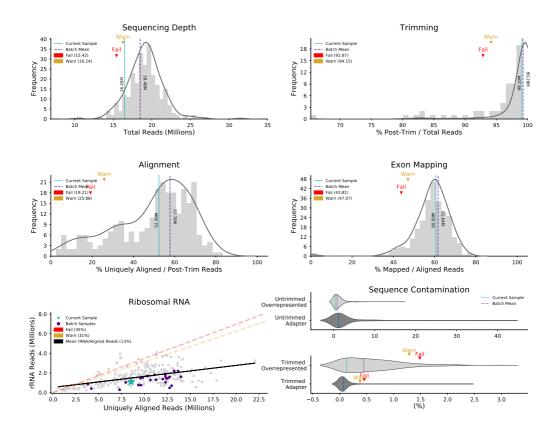
Sample: RNA\_B11\_15 Batch: batch\_11



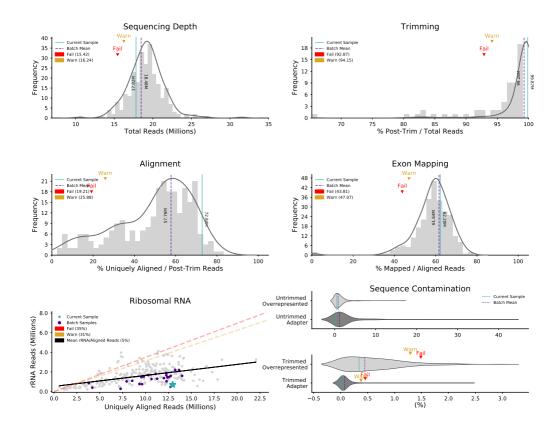
Sample: RNA\_B11\_16 Batch: batch\_11



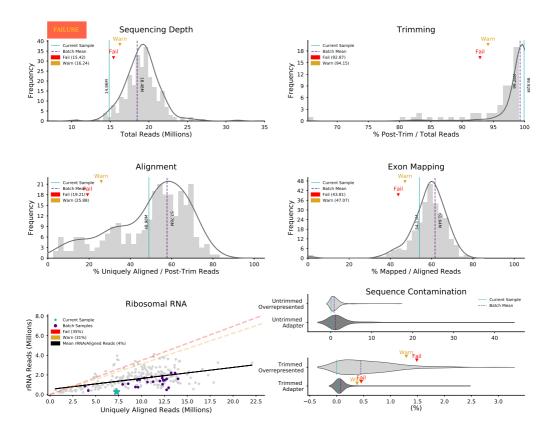
Sample: RNA\_B11\_17 Batch: batch\_11



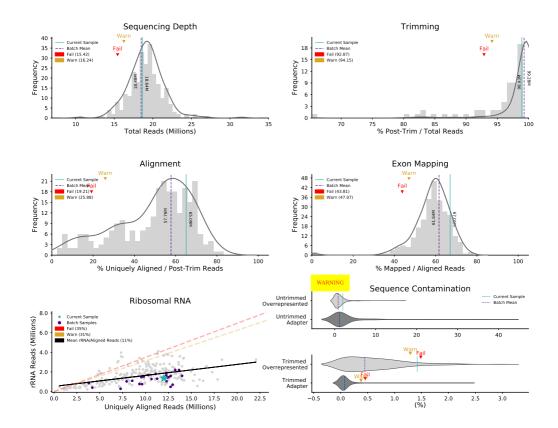
Sample: RNA B11 18 Batch: batch 11



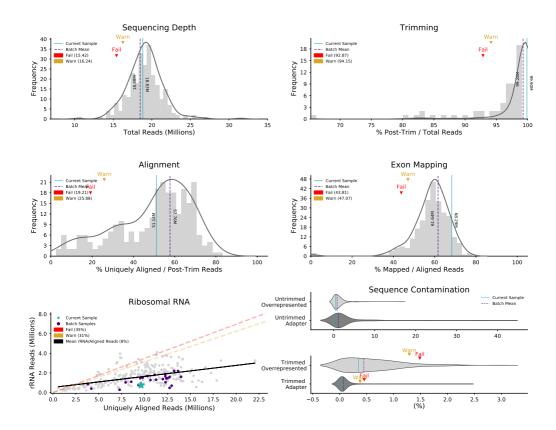
Sample: RNA B11 19 Batch: batch 11



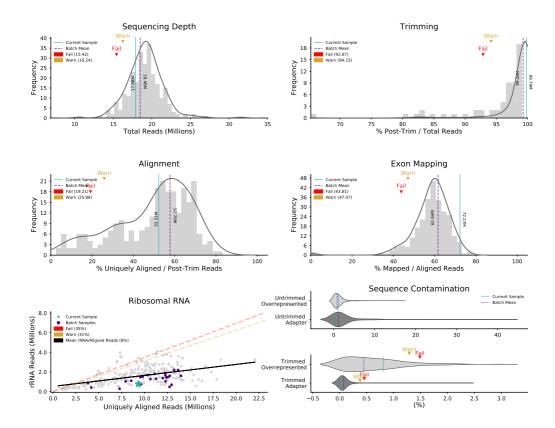
Sample: RNA B11 20 Batch: batch 11



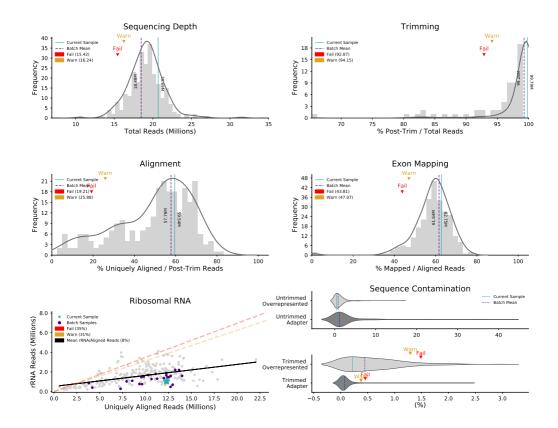
Sample: RNA\_B11\_21 Batch: batch\_11



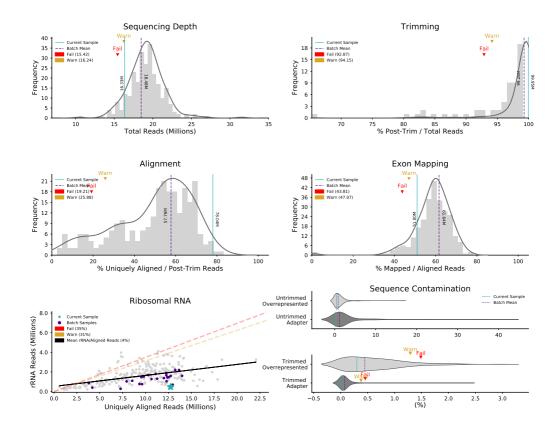
Sample: RNA\_B11\_22 Batch: batch\_11



Sample: RNA\_B11\_23 Batch: batch\_11



Sample: RNA\_B11\_24 Batch: batch\_11



Sample: Batch Mean Batch: batch 11

