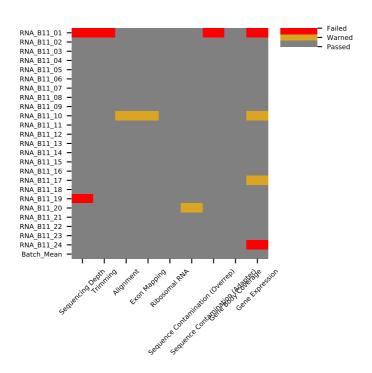
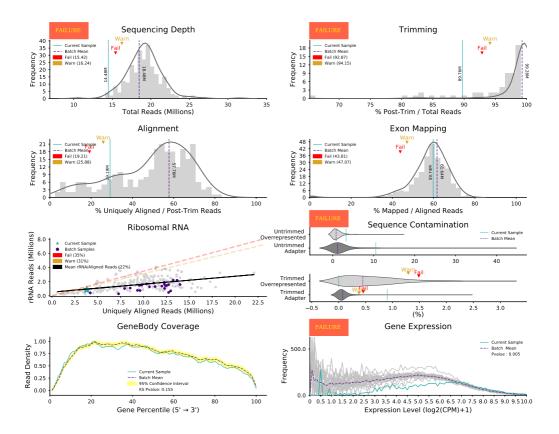
QC Plotter Input Summary

Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/USER_testData_B11.csv
Output location = /projects/b1063/Gaurav/pyRetroPlotter/SCRIPTB11_defaultcutoffs.pdf
Background table = data/SCRIPTretro_masterStatistics_allBatches.csv
Gene Body Coverage file = data/SCRIPT_RNAseq_Batch_11_GeneCoverageData.csv
Gene read depth distribution histogram file = data/sample11hist_data.csv
Cutoff file = False

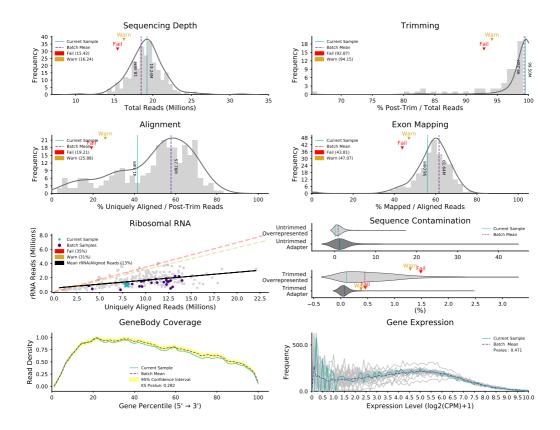
Summary of QC Metrics



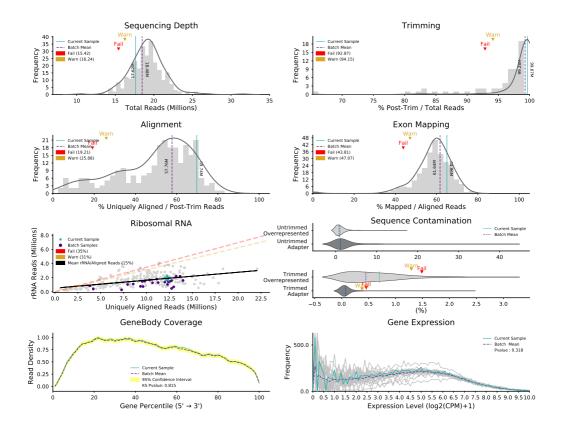
Sample: RNA B11 01 Batch: batch 11



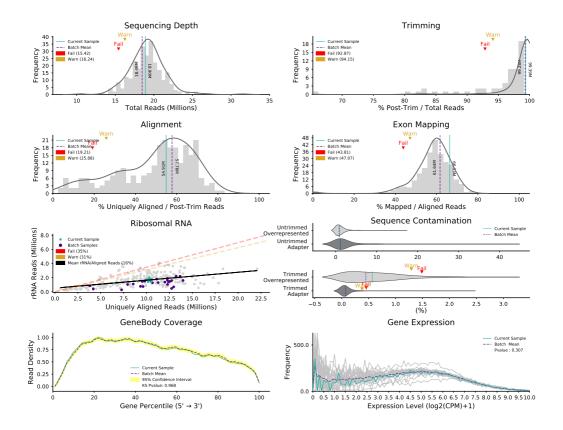
Sample: RNA B11 02 Batch: batch 11



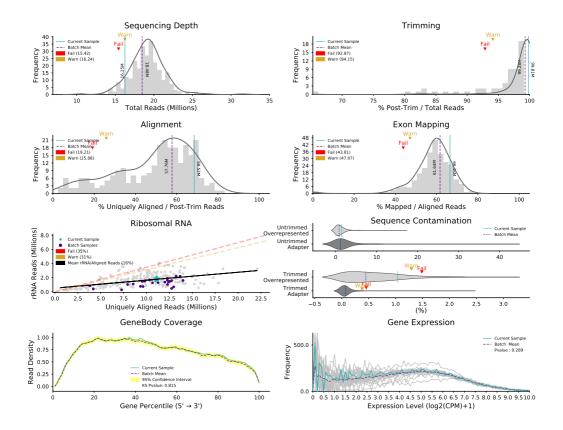
Sample: RNA B11 03 Batch: batch 11



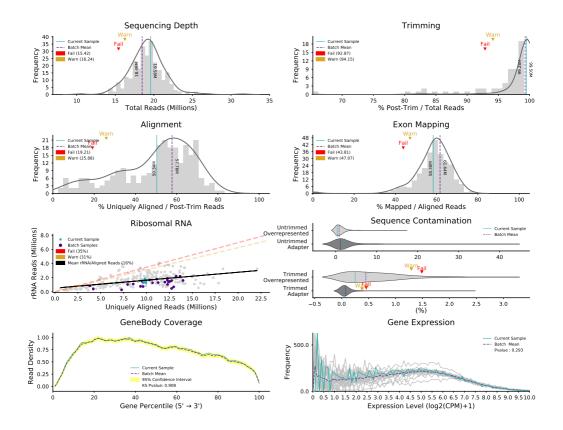
Sample: RNA B11 04 Batch: batch 11



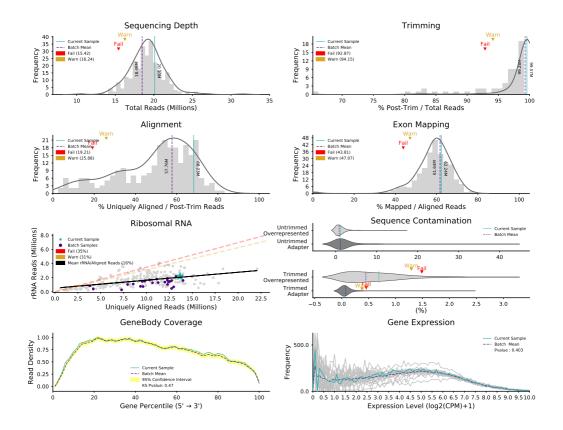
Sample: RNA B11 05 Batch: batch 11



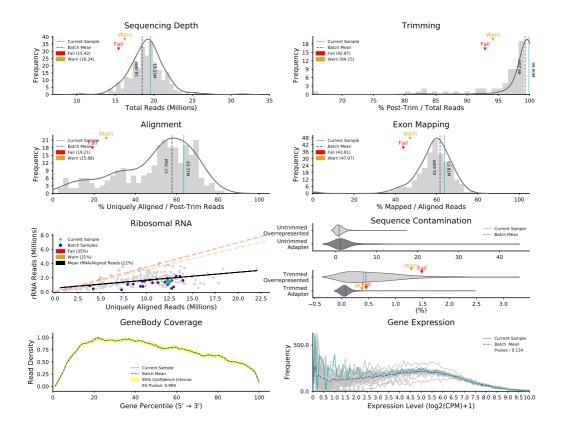
Sample: RNA B11 06 Batch: batch 11



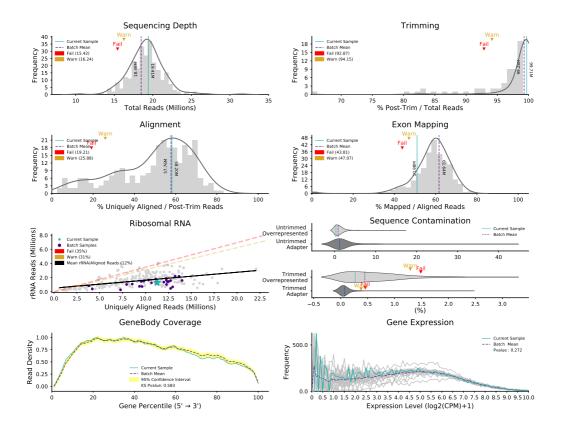
Sample: RNA B11 07 Batch: batch 11



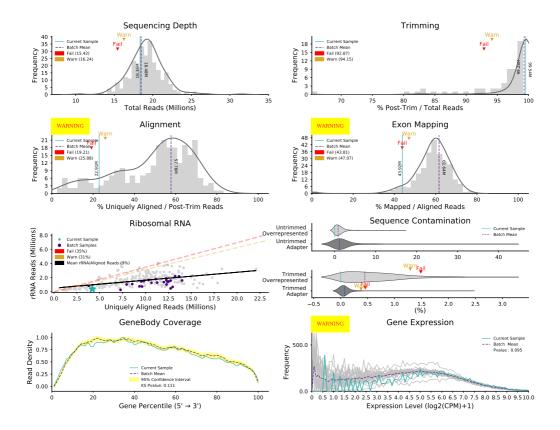
Sample: RNA B11 08 Batch: batch 11



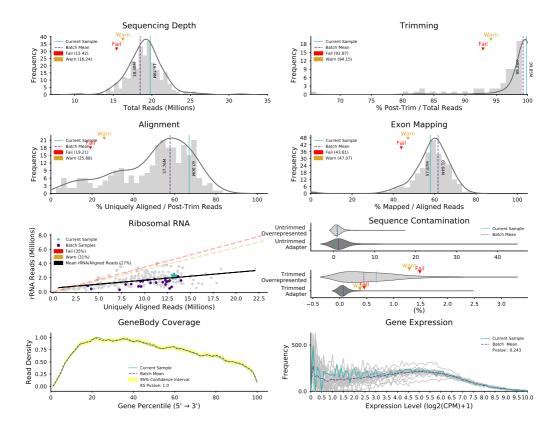
Sample: RNA B11 09 Batch: batch 11



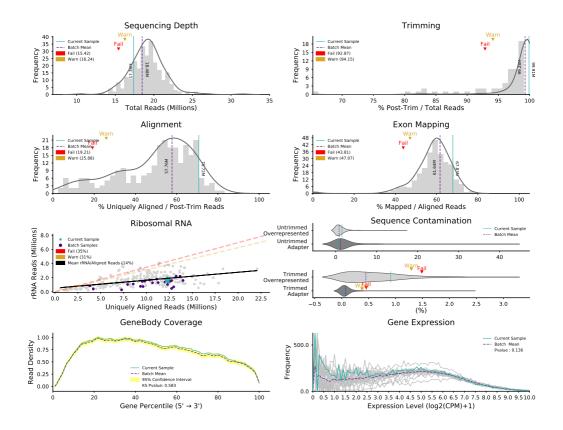
Sample: RNA_B11_10 Batch: batch_11



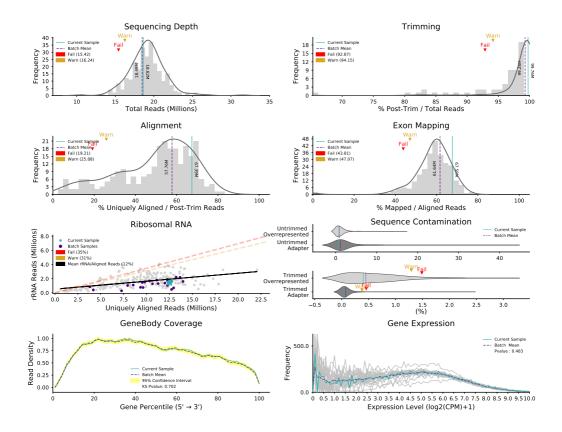
Sample: RNA B11 11 Batch: batch 11



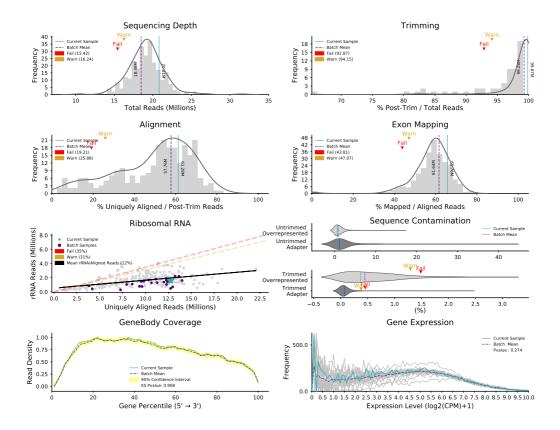
Sample: RNA B11 12 Batch: batch 11



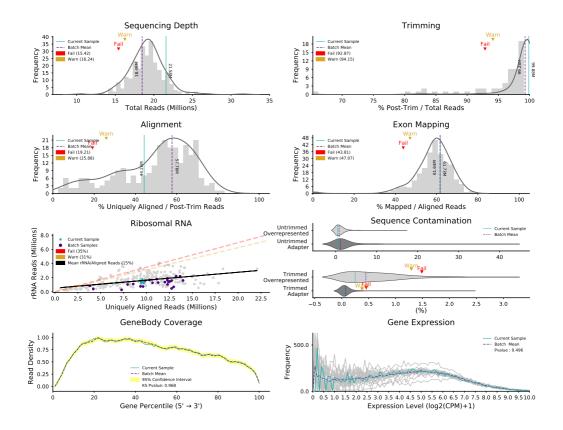
Sample: RNA B11 13 Batch: batch 11



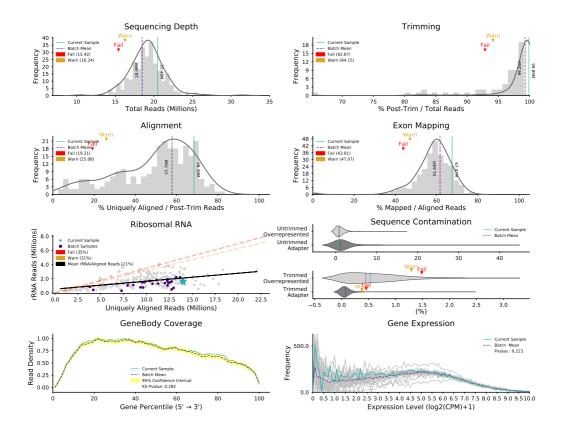
Sample: RNA B11 14 Batch: batch 11



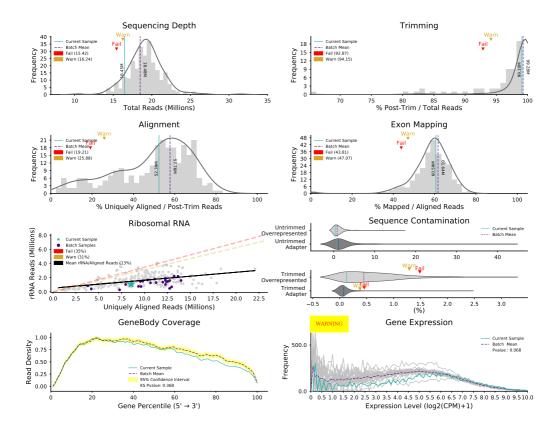
Sample: RNA B11 15 Batch: batch 11



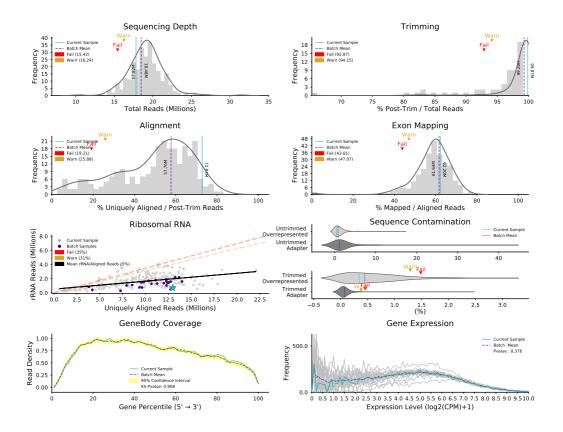
Sample: RNA B11 16 Batch: batch 11



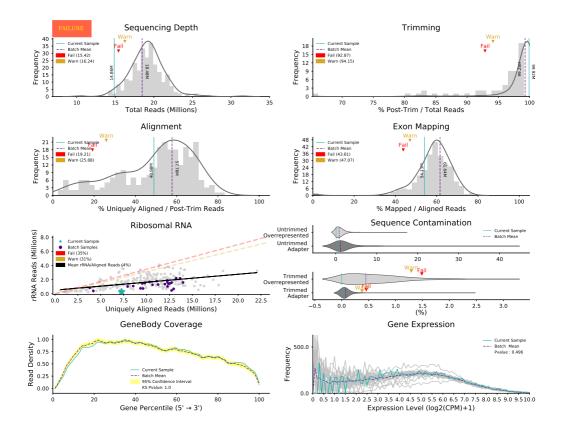
Sample: RNA B11 17 Batch: batch 11



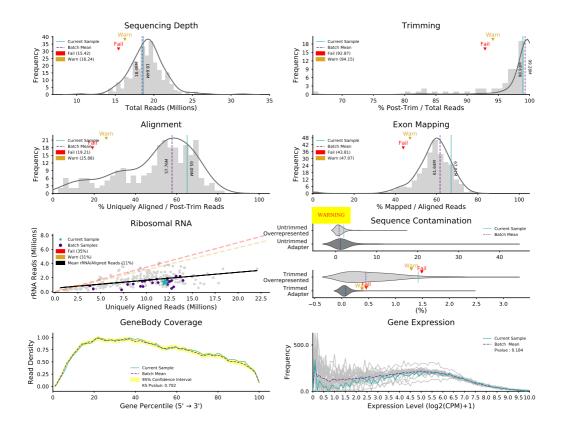
Sample: RNA_B11_18 Batch: batch_11



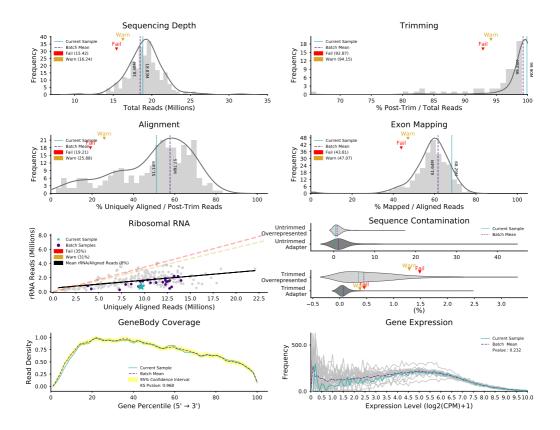
Sample: RNA B11 19 Batch: batch 11



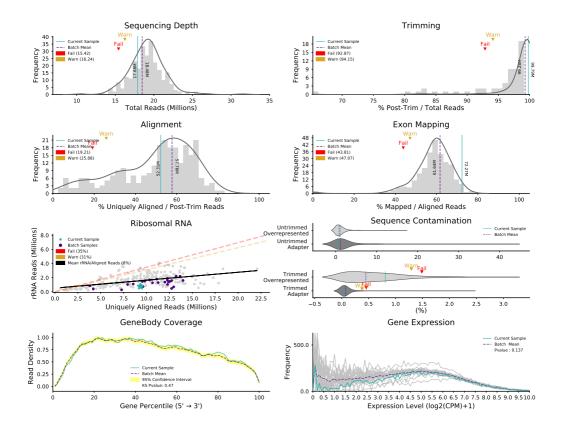
Sample: RNA B11 20 Batch: batch 11



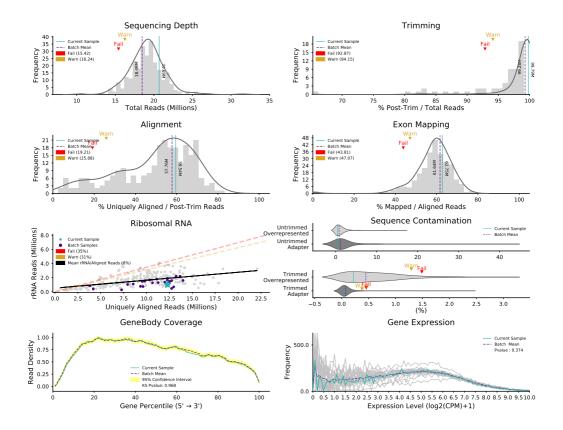
Sample: RNA B11 21 Batch: batch 11



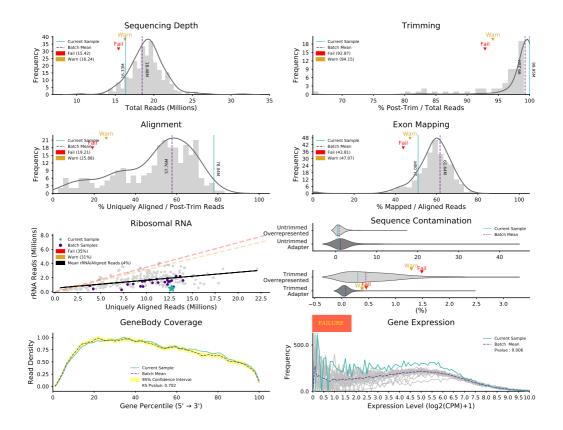
Sample: RNA B11 22 Batch: batch 11



Sample: RNA B11 23 Batch: batch 11



Sample: RNA B11 24 Batch: batch 11



Sample: Batch Mean Batch: batch 11

