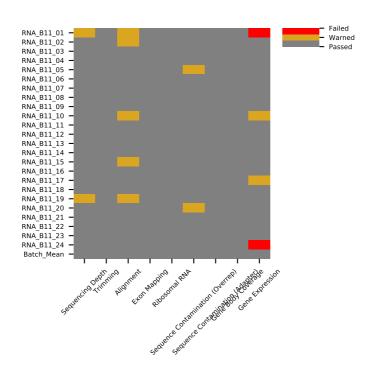
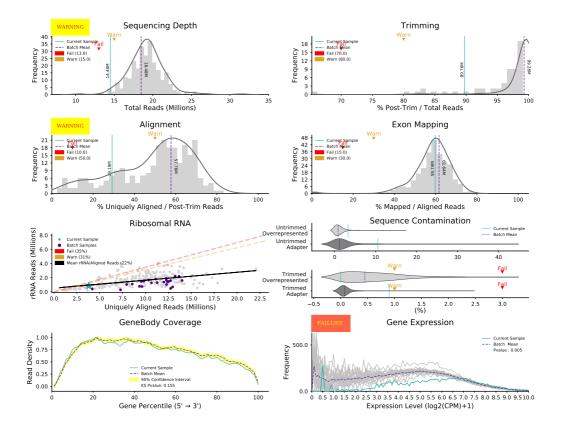
## QC Plotter Input Summary

| Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/USER\_testData\_B11.csv
| Output location = /projects/b1063/Gaurav/pyRetroPlotter/SCRIPTB11\_mancLotffs.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 = data/Man | Input Cutoff test.xlsx

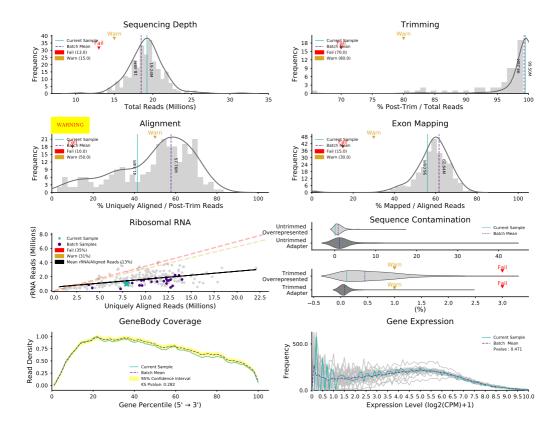
## Summary of QC Metrics



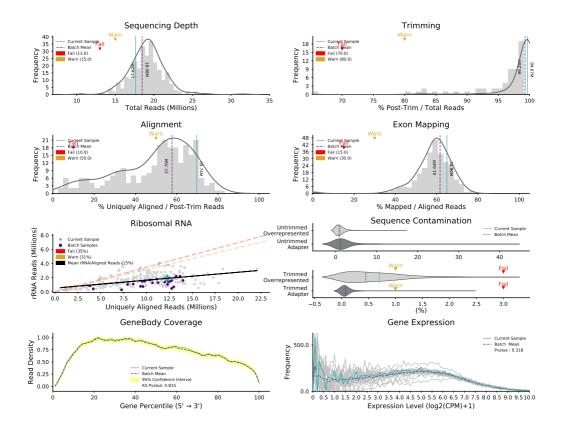
Sample: RNA B11 01 Batch: batch 11



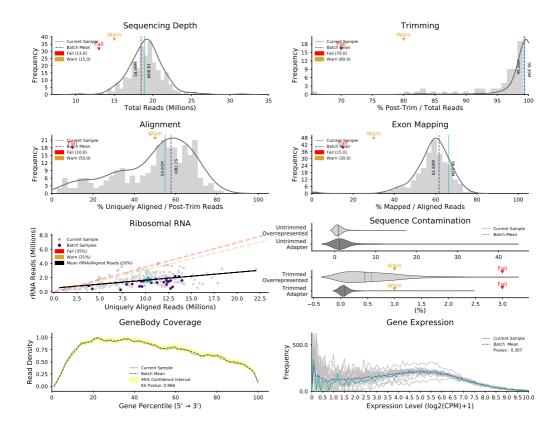
Sample: RNA B11 02 Batch: batch 11



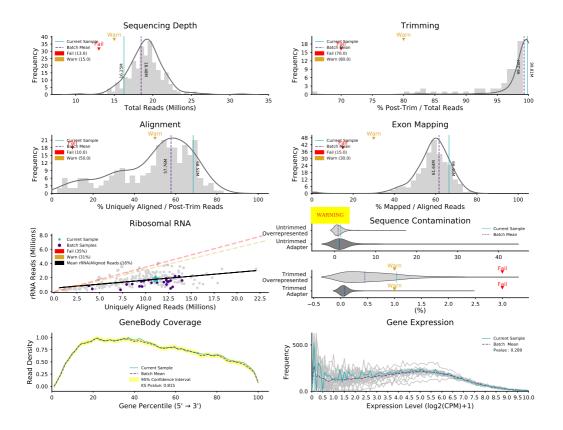
Sample: RNA B11 03 Batch: batch 11



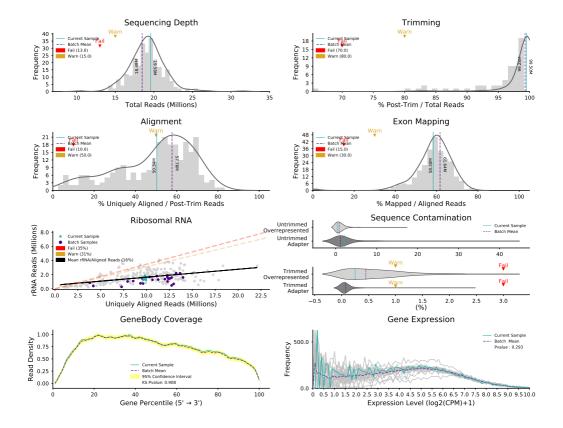
Sample: RNA B11 04 Batch: batch 11



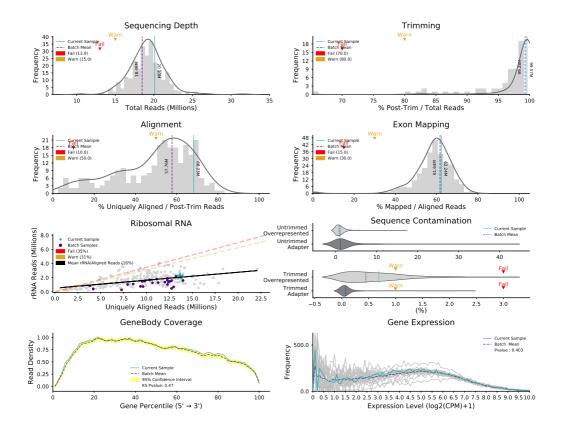
Sample: RNA B11 05 Batch: batch 11



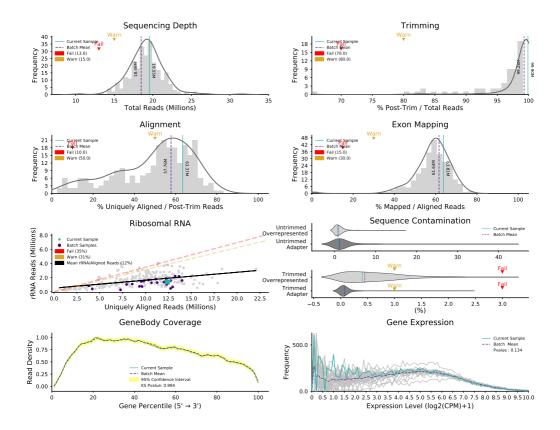
Sample: RNA\_B11\_06 Batch: batch\_11



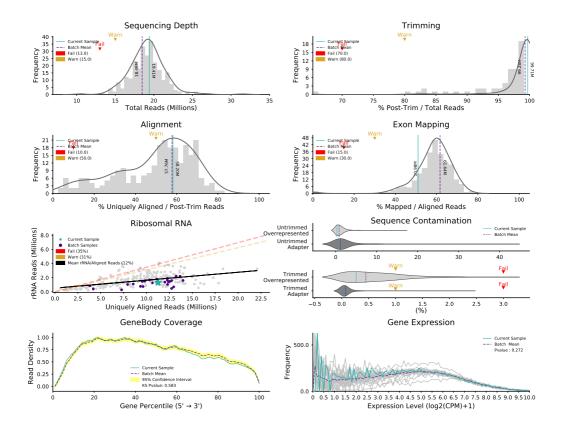
Sample: RNA B11 07 Batch: batch 11



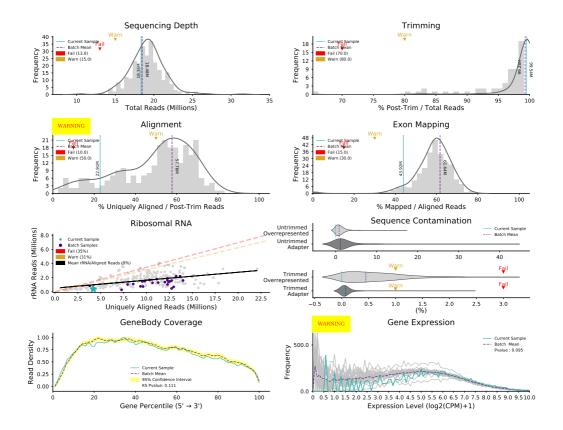
Sample: RNA\_B11\_08 Batch: batch\_11



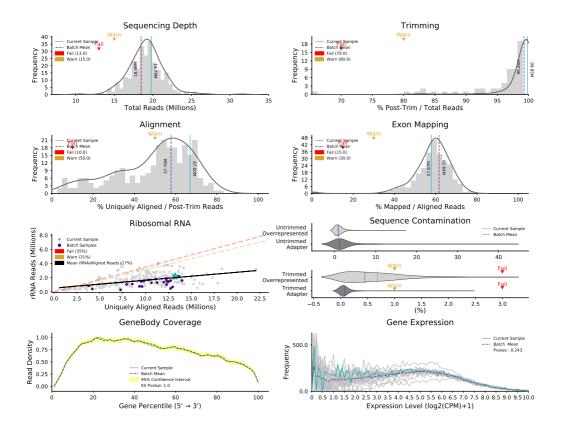
Sample: RNA\_B11\_09 Batch: batch\_11



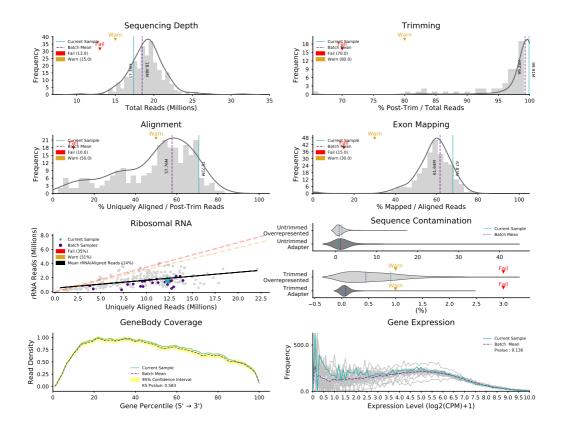
Sample: RNA\_B11\_10 Batch: batch\_11



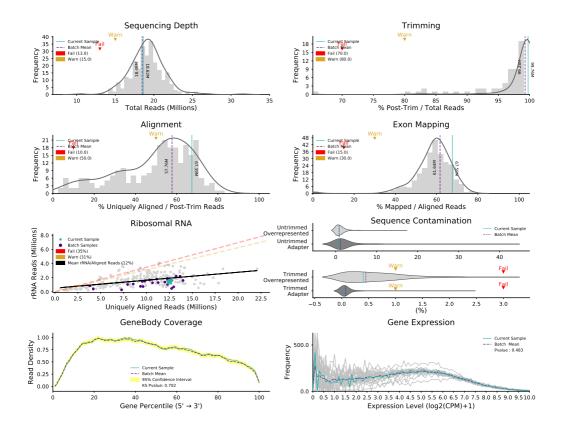
Sample: RNA\_B11\_11 Batch: batch\_11



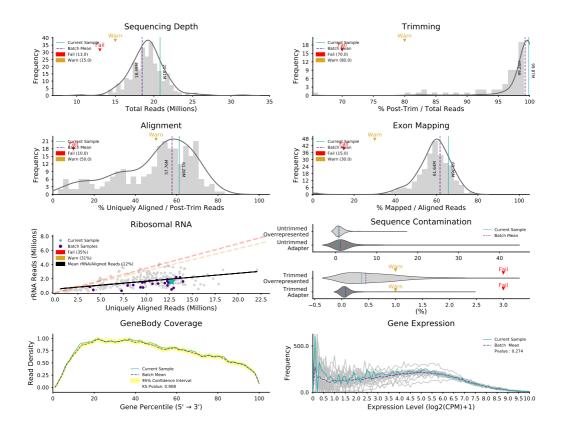
Sample: RNA B11 12 Batch: batch 11



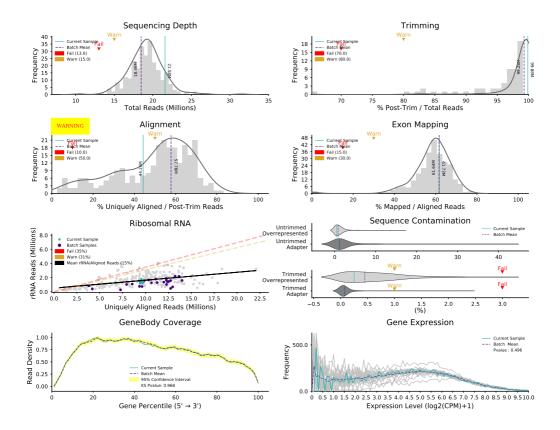
Sample: RNA B11 13 Batch: batch 11



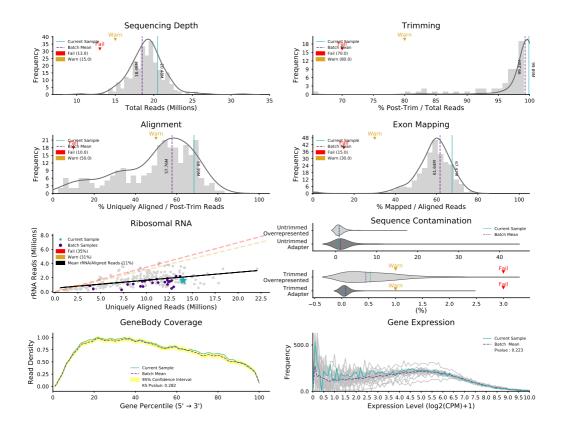
Sample: RNA B11 14 Batch: batch 11



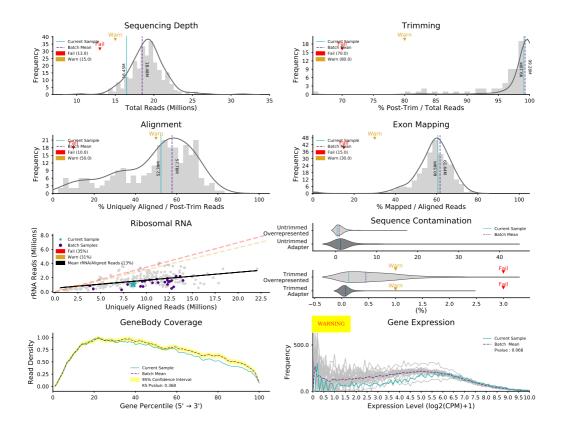
Sample: RNA B11 15 Batch: batch 11



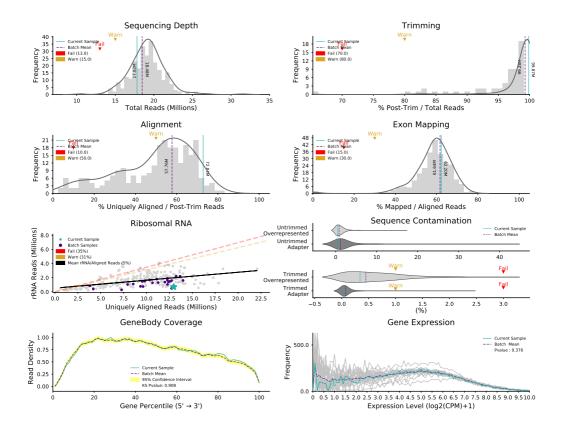
Sample: RNA\_B11\_16 Batch: batch\_11



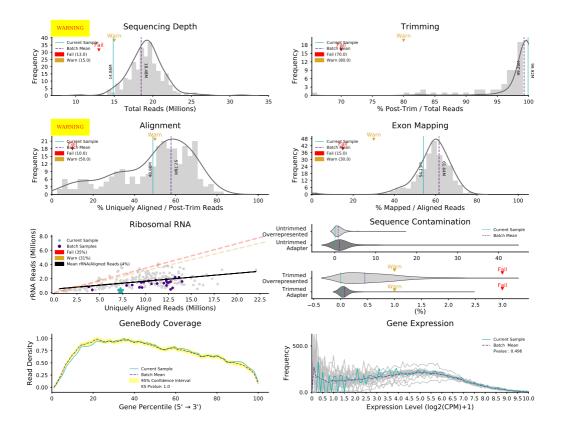
Sample: RNA\_B11\_17 Batch: batch\_11



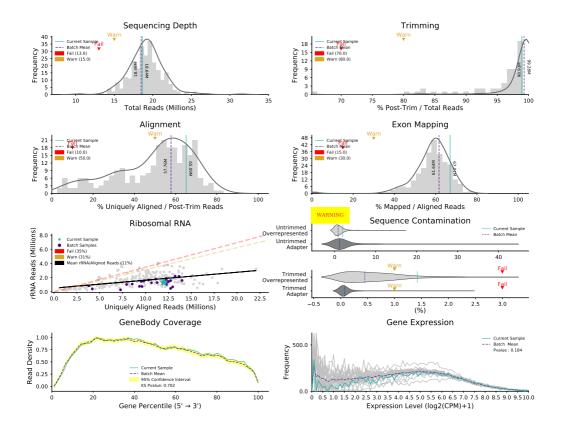
Sample: RNA\_B11\_18 Batch: batch\_11



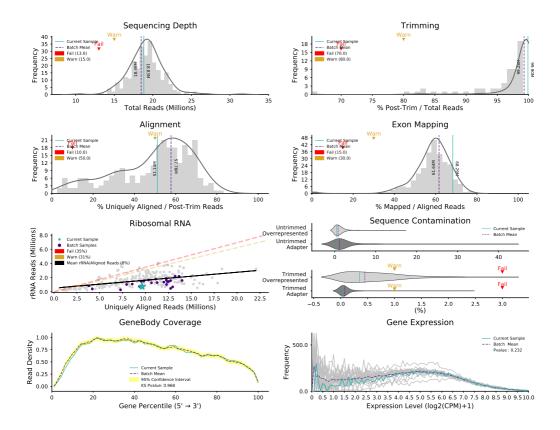
Sample: RNA\_B11\_19 Batch: batch\_11



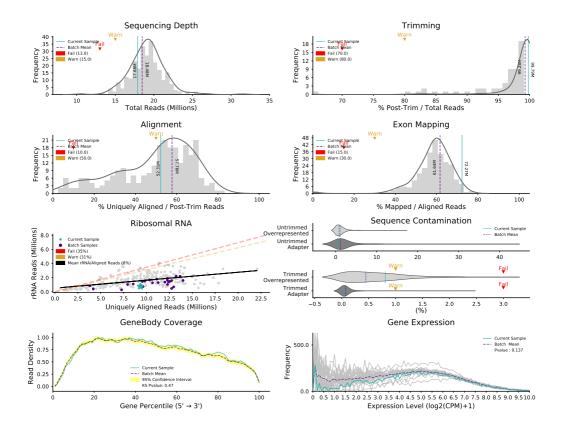
Sample: RNA\_B11\_20 Batch: batch\_11



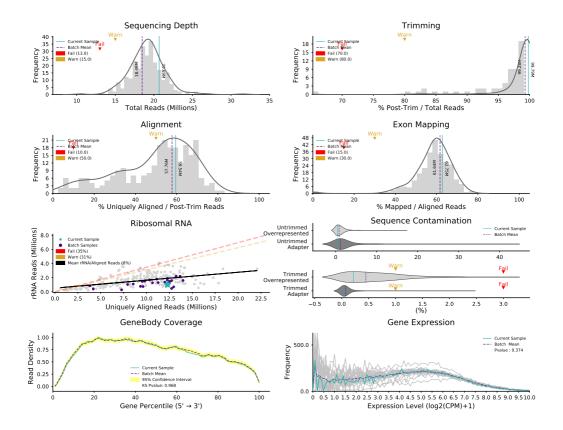
Sample: RNA B11 21 Batch: batch 11



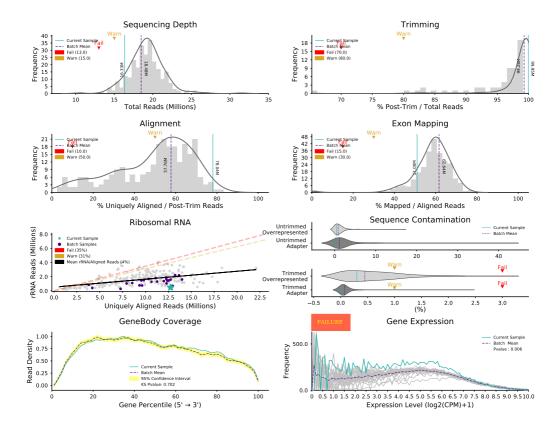
Sample: RNA B11 22 Batch: batch 11



Sample: RNA B11 23 Batch: batch 11



Sample: RNA B11 24 Batch: batch 11



Sample: Batch\_Mean Batch: batch\_11

