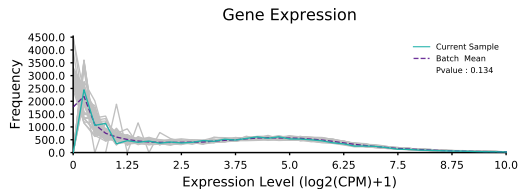
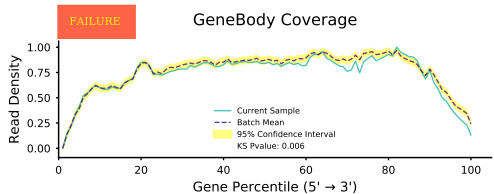
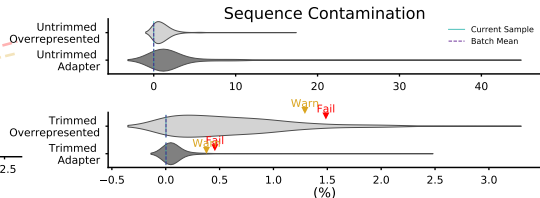
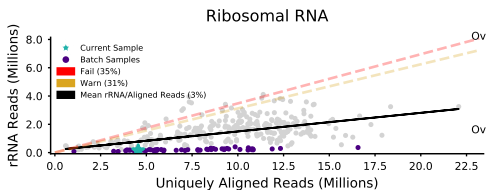
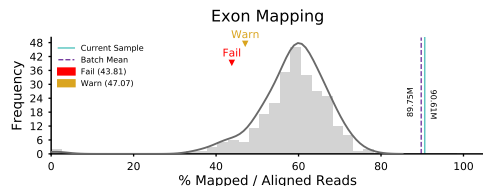
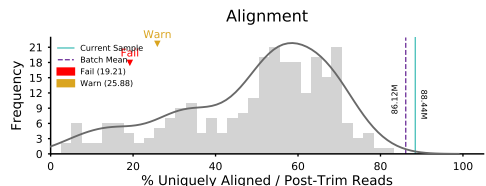
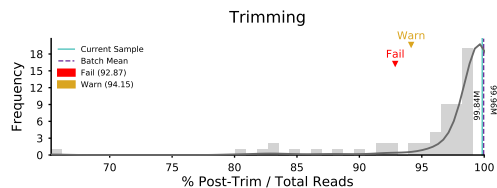
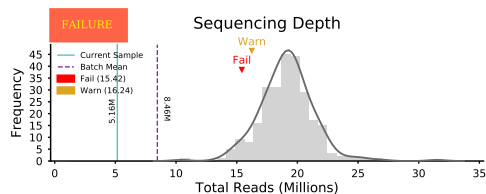


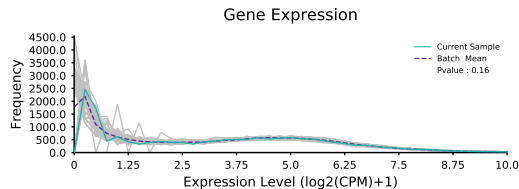
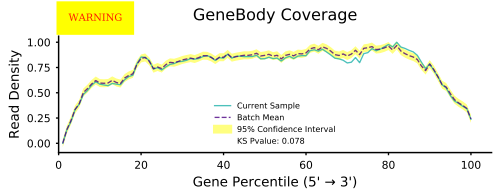
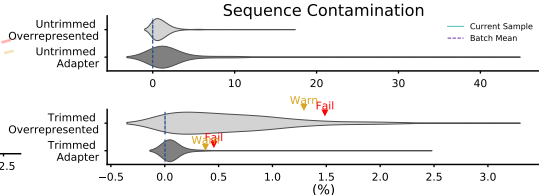
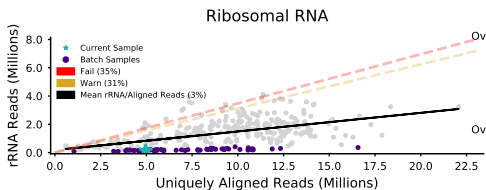
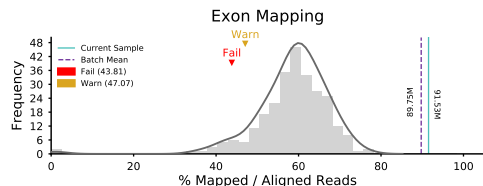
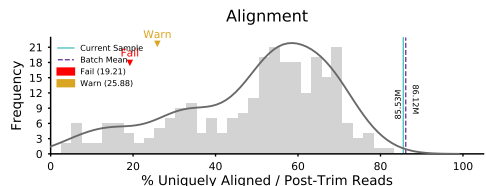
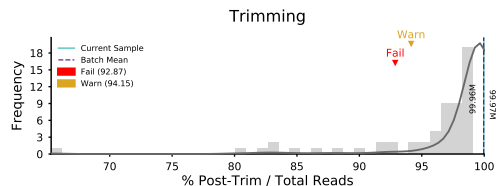
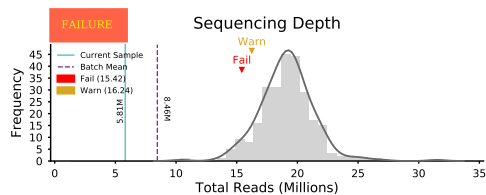
QC Plotter Input Summary

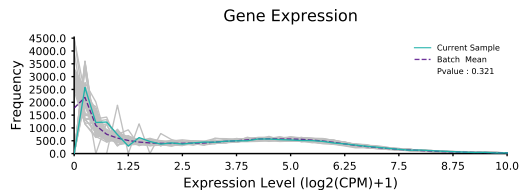
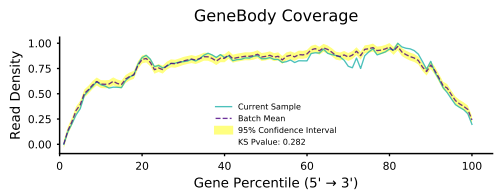
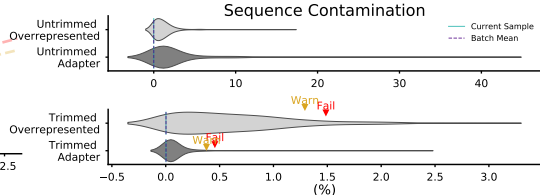
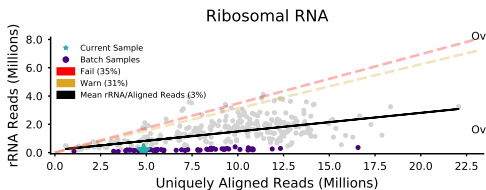
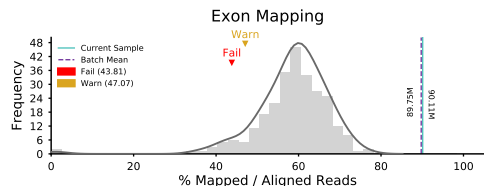
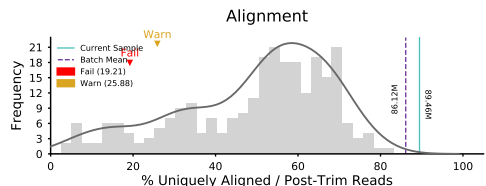
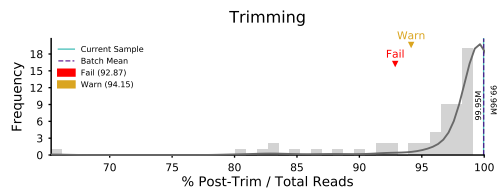
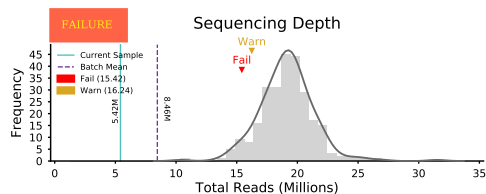
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Output location = /projects/b1063/Gaurav/pyRetroPlotter/fib_with_SCRIPT_background.pdf
Background table = data/SCRIPTretro_masterStatistics_allBatches.csv
Gene Body Coverage file = data/fibGBC_output.csv
Gene read depth distribution histogram file = data/fibhist.254pltr.csv
Cutoff file = False

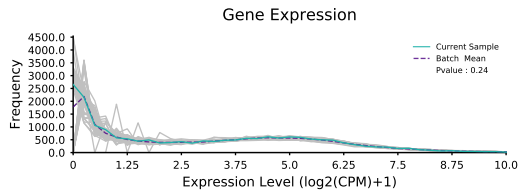
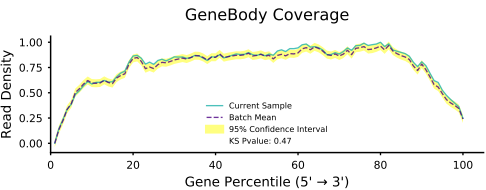
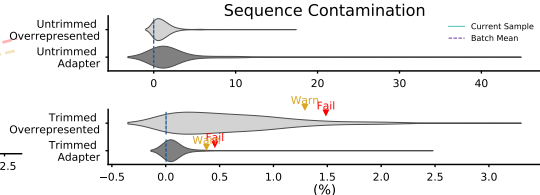
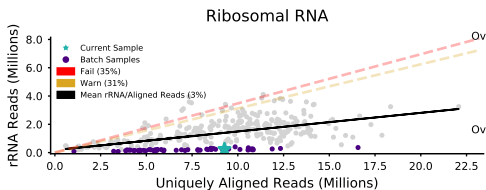
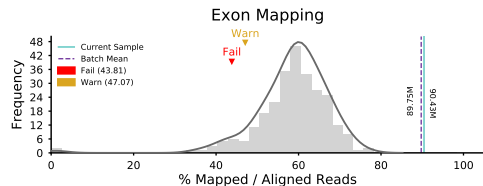
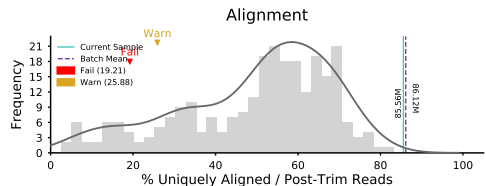
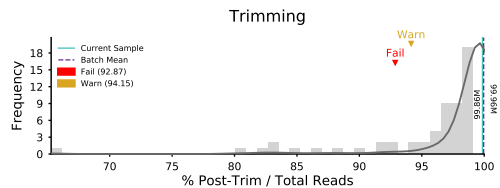
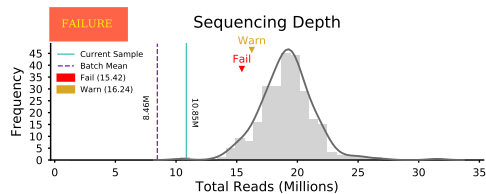
*Warn cutoffs: Default alpha =0.9| Sequencing Depth = 16.241| Trimming = 94.146| Alignment = 25.883| Gene Exon Mapping = 47.068
| Ribosomal RNA = 0.312| Adapter Contamination = 0.378| Overrep. Seq Contamination = 1.292| Gene Body Coverage = 0.9| Distribution of Gene Expression = 15732*

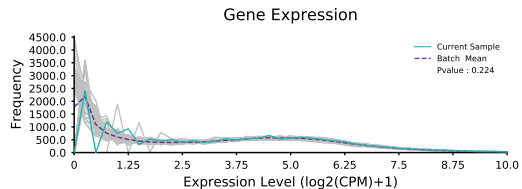
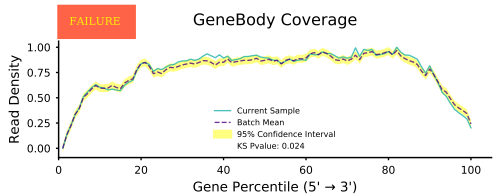
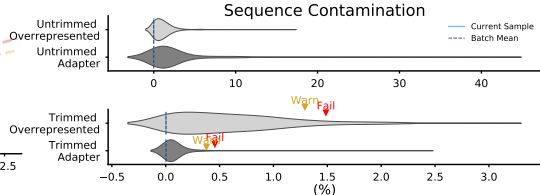
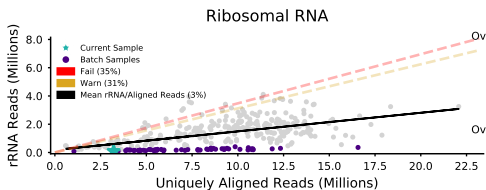
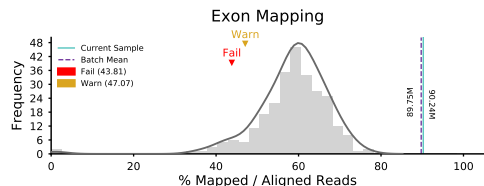
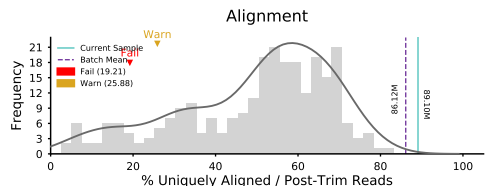
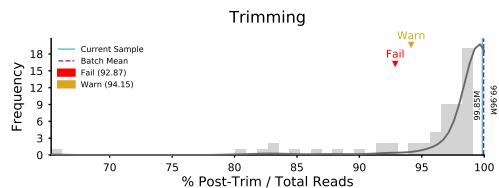
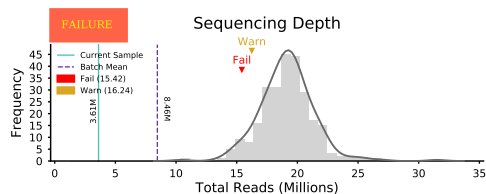
*Fail cutoffs: Default alpha =0.95| Sequencing Depth = 15.422| Trimming = 92.869| Alignment = 19.211| Gene Exon Mapping = 43.814
| Ribosomal RNA = 0.348| Adapter Contamination = 0.456| Overrep. Seq Contamination = 1.487| Gene Body Coverage = 0.95| Distribution of Gene Expression = 16320*

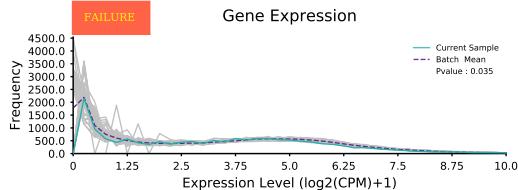
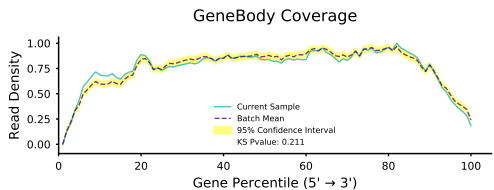
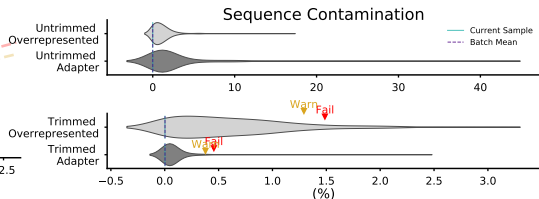
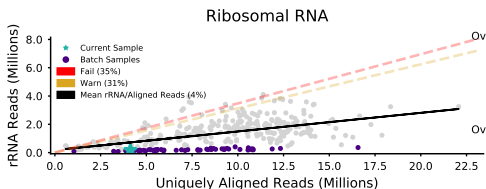
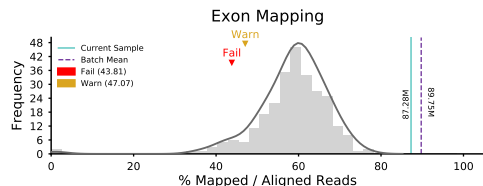
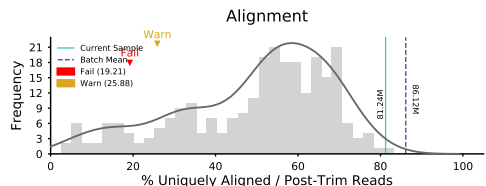
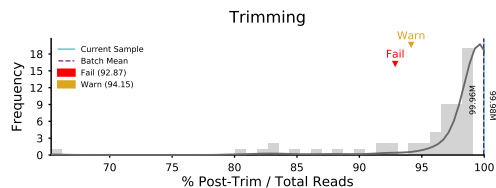
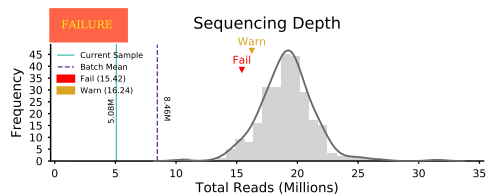




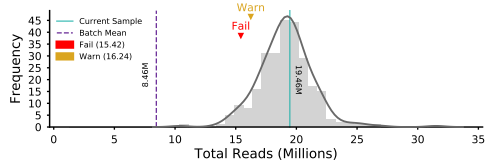




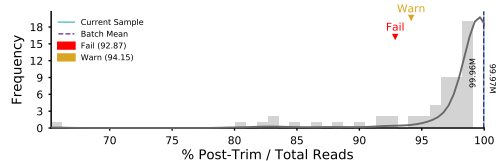




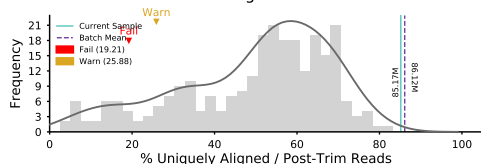
Sequencing Depth



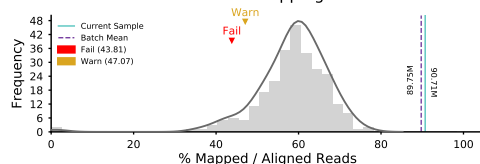
Trimming



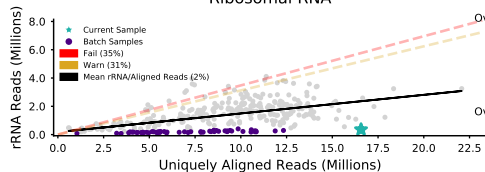
Alignment



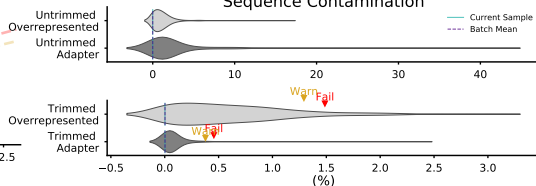
Exon Mapping



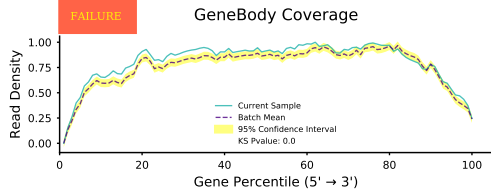
Ribosomal RNA



Sequence Contamination



GeneBody Coverage



Gene Expression

