

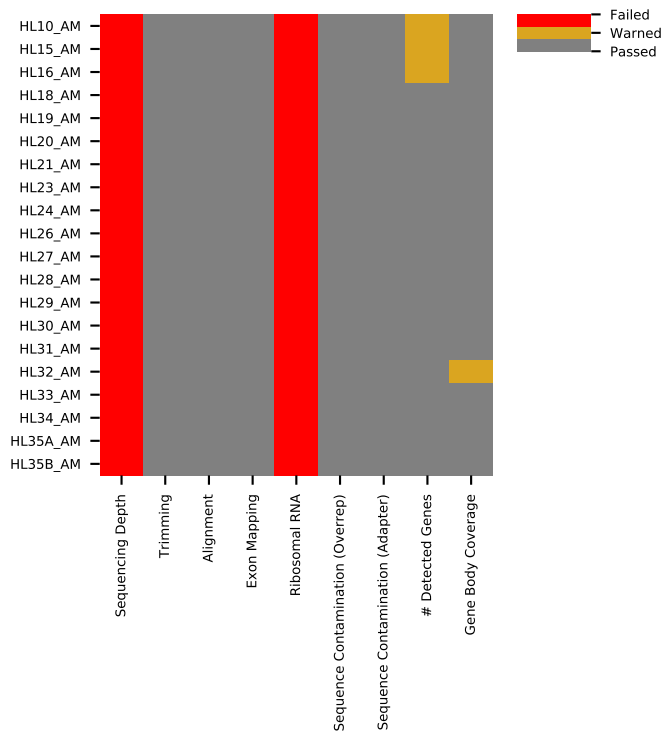
QC Plotter Input Summary

Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/fib4pyRetroplotter_2023_4_13.csv
Output location = /projects/b1063/Gaurav/pyRetroPlotter/fib_with_SCRIPT_background.pdf
Background table = data/SCRIPTretro_masterStatistics_allBatches_2023_4_13.csv
Gene Body Coverage file = data/fibGBC_output.csv
Gene read depth distribution histogram file = data/fib.5hist.csv
Cutoff file = False

*Warn cutoffs: Default alpha = 0.1 | 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 = 0.1 | Detected Genes = 16734*

*Fail cutoffs: Default alpha = 0.05 | 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 = 0.05 | Detected Genes = 16131*

Summary of QC Metrics



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