

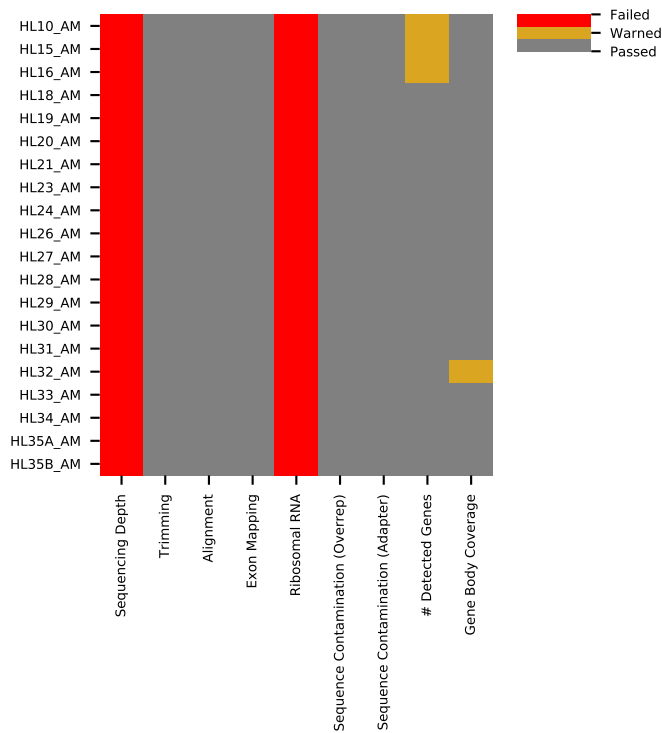
# QC Plotter Input Summary

Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/fib4pyRetroplotter\_2023\_5\_5.csv  
Output location = /projects/b1063/Gaurav/pyRetroPlotter/fib\_with\_SCRIPT\_background.pdf  
Background table = data/SCRIPTretro\_masterStatistics\_allBatches\_2023\_5\_5.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 = 0.003| 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 = 0.002| 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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