QC Plotter Input Summary

Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/USER_testData_B11_2023_5_5.csv

Output location = /projects/b1063/Gaurav/pyRetroPlotter/SCRIPTB11_mancutoffs.pdf

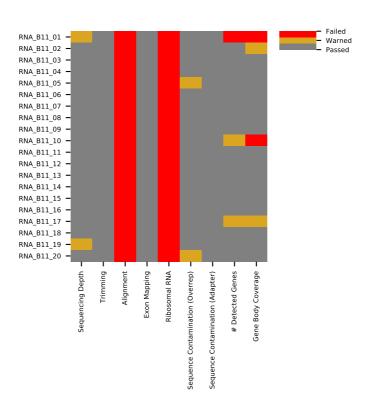
Background table = data/SCRIPTretro_masterStatistics_allBatches_2023_5_5.csv

Gene Body Coverage file = data/SCRIPT_RNAseq_Batch_11_GeneCoverageData.csv

Gene read depth distribution histogram file =data/CPM_SCRIPT_RNAseq_Batch_11_final_count_bincounts_0.5.csv

Cutoff file = data/man_cutoffs_2023_5_5.xlsx

Summary of QC Metrics



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