

QC Plotter Input Summary

```
Input table = /projects/b1063/Gaurav/pyRetroPlotter/data/SCRIPTretro_masterStatistics_allBatches.csv
Output location = /projects/b1063/Gaurav/pyRetroPlotter/test_script_all.pdf
Background table = /projects/b1063/Gaurav/pyRetroPlotter/data/SCRIPTretro_masterStatistics_allBatches.csv
                    Gene Body Coverage file = data/SCRIPT_GC_info.csv
Gene read depth distribution histogram file = data/SCRIPT_hist.25_info.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 = 8942*

*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 = 10059*















































































































































































































































































































































































































































































































































