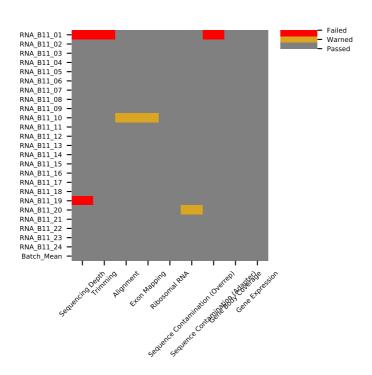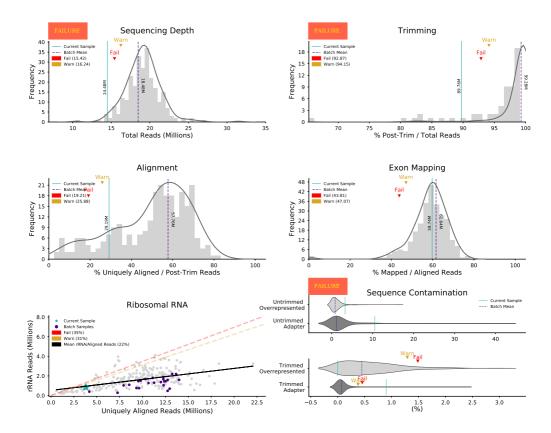# QC Plotter Input Summary

Input table =   /projects/b1063/Gaurav/pyRetroPlotter/data/USER_testData_B11.csv
Output location =   /projects/b1063/Gaurav/pyRetroPlotter/test_SCRIPT11_wbgd.pdf
Background table =   data/SCRIPTretro_masterStatistics_allBatches.csv
Gene Body Coverage file =   None
Gene read depth distribution histogram file =   None
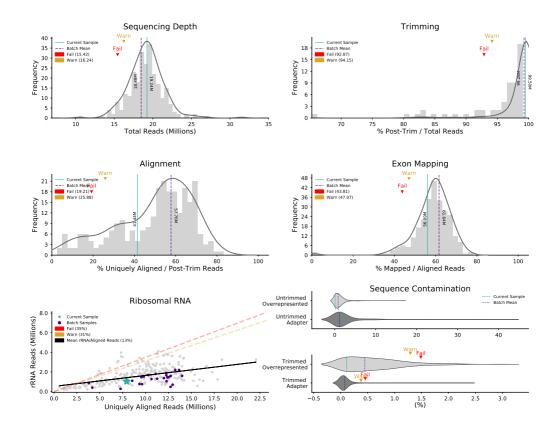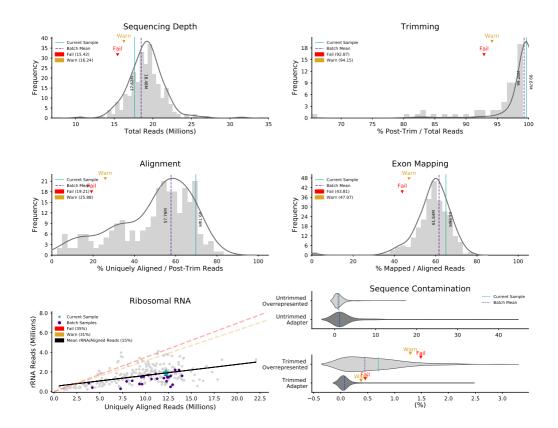Cutoff file =   False

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 = None

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 = None

Summary of QC Metrics

Sequencing Depth

FAILURE

- Current Sample
- Batch Mean
- Fail (15.42)
- Warn (16.24)

Warn ▼
Fail ▼

14.48M
18.48M

Frequency
Total Reads (Millions)

Trimming

FAILURE

- Current Sample
- Batch Mean
- Fail (92.87)
- Warn (94.15)

Warn ▼
Fail ▼

89.76M
99.28M

Frequency
% Post-Trim / Total Reads

Alignment

- Current Sample
- Batch Mean
- Fail (19.21)
- Warn (25.88)

Warn ▼
Fail ▼

29.19M
57.76M

Frequency
% Uniquely Aligned / Post-Trim Reads

Exon Mapping

- Current Sample
- Batch Mean
- Fail (43.81)
- Warn (47.07)

Warn ▼
Fail ▼

59.74M
61.96M

Frequency
% Mapped / Aligned Reads

Ribosomal RNA

- ★ Current Sample
- Batch Samples
- Fail (35%)
- Warn (31%)
- Mean rRNA/Aligned Reads (22%)

rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

Sequence Contamination

FAILURE

- Current Sample
- Batch Mean

Untrimmed Overrepresented
Untrimmed Adapter

Trimmed Overrepresented
Trimmed Adapter

Warn Fail
W.Fail

(%)

Sequencing Depth

Trimming

Alignment

Exon Mapping

Ribosomal RNA

Sequence Contamination

Sequencing Depth

Current Sample
Batch Mean
Fail (15.42)
Warn (16.24)

Warn
Fail

18.48M
20.10M

Frequency
Total Reads (Millions)

Trimming

Current Sample
Batch Mean
Fail (92.87)
Warn (94.15)

Warn
Fail

98.79M
99.57M

Frequency
% Post-Trim / Total Reads

Alignment

Current Sample
Batch Mean
Fail (19.21)
Warn (25.88)

Warn
Fail

57.76M
68.23M

Frequency
% Uniquely Aligned / Post-Trim Reads

Exon Mapping

Current Sample
Batch Mean
Fail (43.81)
Warn (47.07)

Warn
Fail

61.19M
62.24M

Frequency
% Mapped / Aligned Reads

Ribosomal RNA

Current Sample
Batch Samples
Fail (35%)
Warn (31%)
Mean rRNA/Aligned Reads (16%)

rRNA Reads (Millions)
Uniquely Aligned Reads (Millions)

Sequence Contamination

Current Sample
Batch Mean

Untrimmed Overrepresented
Untrimmed Adapter

Trimmed Overrepresented
Trimmed Adapter

Warn Fail
Warn Fail

(%)

Sequencing Depth

Trimming

Alignment

Exon Mapping

Ribosomal RNA

Sequence Contamination

Sequencing Depth

Trimming

Alignment

Exon Mapping

Ribosomal RNA

Sequence Contamination

Sequencing Depth

Trimming

Alignment

Exon Mapping

Ribosomal RNA

Sequence Contamination