Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

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Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sample : HL15_AM

Sequencing Depth

FAILURE

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

WARNING

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

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Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth — FAILURE. Frequency vs Total Reads (Millions). Current Sample 6.31M, Batch Mean 8.46M. Fail/Warn markers.

Trimming — Frequency vs % Post-Trim / Total Reads. Current Sample, Batch Mean. 99.99%, W66.66. Fail/Warn markers.

Alignment — Frequency vs % Uniquely Aligned / Post-Trim Reads. Current Sample, Batch Mean 86.12%, W90.88. Fail/Warn markers.

Gene Exon Mapping — Frequency vs % Mapped / Aligned Reads. Current Sample, Batch Mean 89.75%, W96.16. Fail/Warn markers.

Ribosomal RNA — rRNA Reads (Millions) vs Uniquely Aligned Reads (Millions). Current Sample, Batch Samples. Fail/Warn.

Sequence Contamination — Pre-trim (%): Overrepresented, Adapter. Post-trim (%): Overrepresented, Adapter. Current Sample, Batch Mean. Warn/Fail markers.

GeneBody Coverage Distribution — FAILURE. Coverage vs Gene Percentile (5' → 3'). Current Sample, Library Mean, 95% Confidence Interval, KS-2sample Pvalue: 0.0.

Distribution of Gene Expression — Frequency vs Quantity of detected reads (log2(CPM)+1). Current Sample, Library Mean, ZTest Pvalue : 0.252.

Sequencing Depth — FAILURE. Frequency vs Total Reads (Millions). Current Sample, Batch Mean. Fail/Warn markers. 5.87M, 8.46M.

Trimming — Frequency vs % Post-Trim / Total Reads. Current Sample, Batch Mean. Fail/Warn. 99.93M, 99.96M.

Alignment — Frequency vs % Uniquely Aligned / Post-Trim Reads. Fail/Warn. Current Sample, Batch Mean. 86.12M, 87.84M.

Gene Exon Mapping — Frequency vs % Mapped / Aligned Reads. Fail/Warn. Current Sample, Batch Mean. 89.75M, 91.7M.

Ribosomal RNA — rRNA Reads (Millions) vs Uniquely Aligned Reads (Millions). Current Sample, Batch Samples. Fail/Warn.

Sequence Contamination — Pre-trim (%): Overrepresented, Adapter. Post-trim (%): Overrepresented, Adapter. Current Sample, Batch Mean. W/Fail, Warn/Fail.

GeneBody Coverage Distribution — FAILURE. Coverage vs Gene Percentile (5' → 3'). Current Sample, Library Mean, 95% Confidence Interval. KS-2sample Pvalue: 0.0.

Distribution of Gene Expression — Frequency vs Quantity of detected reads (log2(CPM)+1). Current Sample, Library Mean, ZTest Pvalue : 0.3.

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth — Frequency vs Total Reads (Millions); FAILURE; Current Sample; Batch Mean; Fail Warn

Trimming — Frequency vs % Post-Trim / Total Reads; Current Sample; Batch Mean; Fail Warn

Alignment — Frequency vs % Uniquely Aligned / Post-Trim Reads; Fail Warn; Current Sample; Batch Mean

Gene Exon Mapping — Frequency vs % Mapped / Aligned Reads; Fail Warn; Current Sample; Batch Mean

Ribosomal RNA — rRNA Reads (Millions) vs Uniquely Aligned Reads (Millions); Current Sample; Batch Samples; Fail; Warn

Sequence Contamination — Overrepresented; Adapter; Pre-trim (%); Post-trim (%); Current Sample; Batch Mean; W Fail; Warn Fail

GeneBody Coverage Distribution — Coverage vs Gene Percentile (5' → 3'); Current Sample; Library Mean; 95% Confidence Interval; KS-2sample Pvalue: 0.211

Distribution of Gene Expression — Frequency vs Quantity of detected reads (log2(CPM)+1); Current Sample; Library Mean; ZTest Pvalue : 0.319

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression

Sequencing Depth

FAILURE

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

FAILURE

Distribution of Gene Expression

Sequencing Depth — FAILURE. Frequency vs Total Reads (Millions). Current Sample (11.68M), Batch Mean. Fail/Warn markers.

Trimming — Frequency vs % Post-Trim / Total Reads. Current Sample, Batch Mean. Fail/Warn markers. W90.99, W86.96.

Alignment — Frequency vs % Uniquely Aligned / Post-Trim Reads. Current Sample (86.12M), Batch Mean (86.90M). Fail/Warn markers.

Gene Exon Mapping — Frequency vs % Mapped / Aligned Reads. Current Sample (87.42M), Batch Mean (89.75M). Fail/Warn markers.

Ribosomal RNA — rRNA Reads (Millions) vs Uniquely Aligned Reads (Millions). Current Sample, Batch Samples. Fail/Warn markers.

Sequence Contamination — Overrepresented and Adapter. Pre-trim (%) and Post-trim (%). Current Sample, Batch Mean. Warn/Fail markers.

GeneBody Coverage Distribution — Coverage vs Gene Percentile (5' → 3'). Current Sample, Library Mean, 95% Confidence Interval. KS-2sample Pvalue: 0.908.

Distribution of Gene Expression — FAILURE. Frequency vs Quantity of detected reads (log2(CPM)+1). Current Sample, Library Mean. ZTest Pvalue : 0.046.

Sequencing Depth — FAILURE

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution — FAILURE

Distribution of Gene Expression — WARNING

Sequencing Depth

Trimming

Alignment

Gene Exon Mapping

Ribosomal RNA

Sequence Contamination

GeneBody Coverage Distribution

Distribution of Gene Expression