

Genome Analysis Report

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1 Analysis Report

1.1 Alignment Statistics

Reports alignment summary statistics for CRAM files. Key metrics include total reads, mapped reads, duplicates, and properly paired reads. These statistics provide insights into sequencing quality and alignment efficiency.

1.1.1 Sample: NA12878_Statistics

- **320072124 + 0 mapped (95.42%: N/A)**
- **294504093 + 0 primary mapped (95.05%: N/A)**
- **287217566 + 0 properly paired (92.70%: N/A)**
- **3939296 + 0 singletons (1.27%: N/A)**

1.1.2 Sample: NA06994_Statistics

- **109338882 + 0 mapped (99.86%: N/A)**
- **99339182 + 0 primary mapped (99.84%: N/A)**
- **96020806 + 0 properly paired (96.51%: N/A)**
- **141032 + 0 singletons (0.14%: N/A)**

1.2 Sex Inference Based on Coverage

This section provides an analysis of sex inference based on genomic coverage data. The results are derived from coverage patterns across sex chromosomes, enabling the determination of the likely biological sex for each sample.

1.2.1 Sample: NA12878_Sex_Inference

Interpretation: The sample is likely biologically **Female**.

1.2.2 Sample: NA06994_Sex_Inference

Interpretation: The sample is likely biologically **Male**.

1.3 Genome Coverage

This section provides an analysis of coverage levels in the samples. The results are derived from depth files generated by Samtools, which quantify the number of reads aligned to each position in the genome.

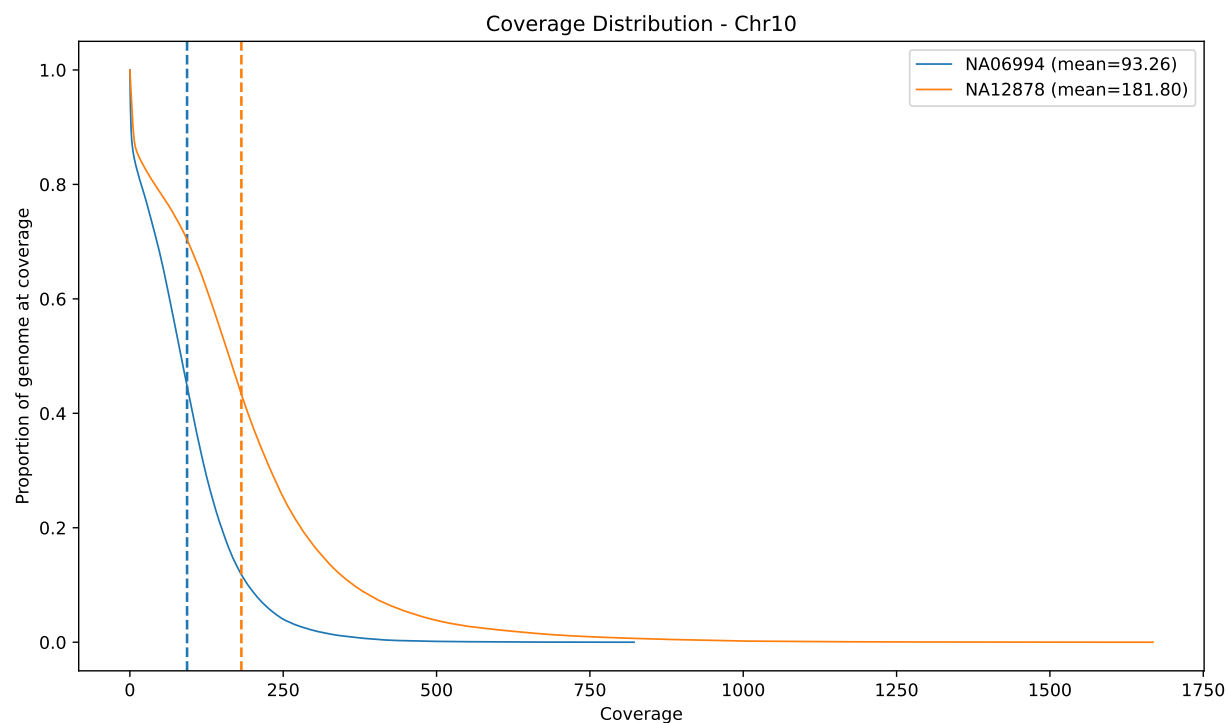


Figure: Genome Coverage for sample Chr10_coverage

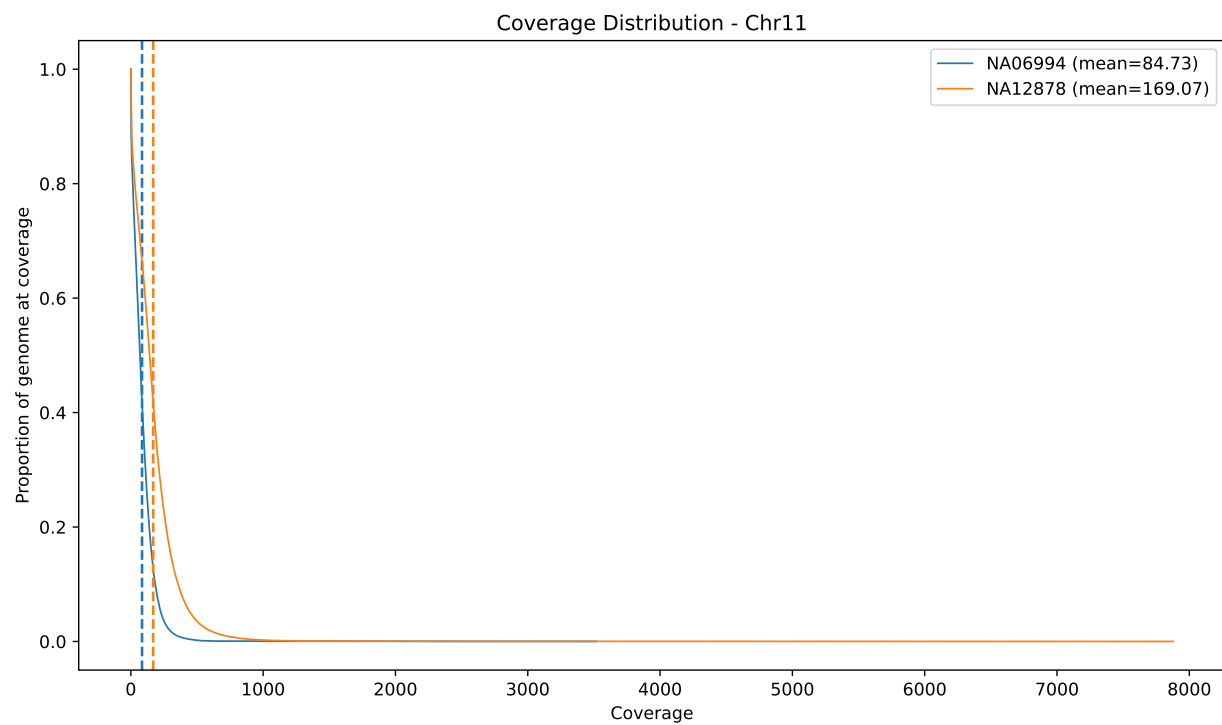


Figure: Genome Coverage for sample Chr11_coverage

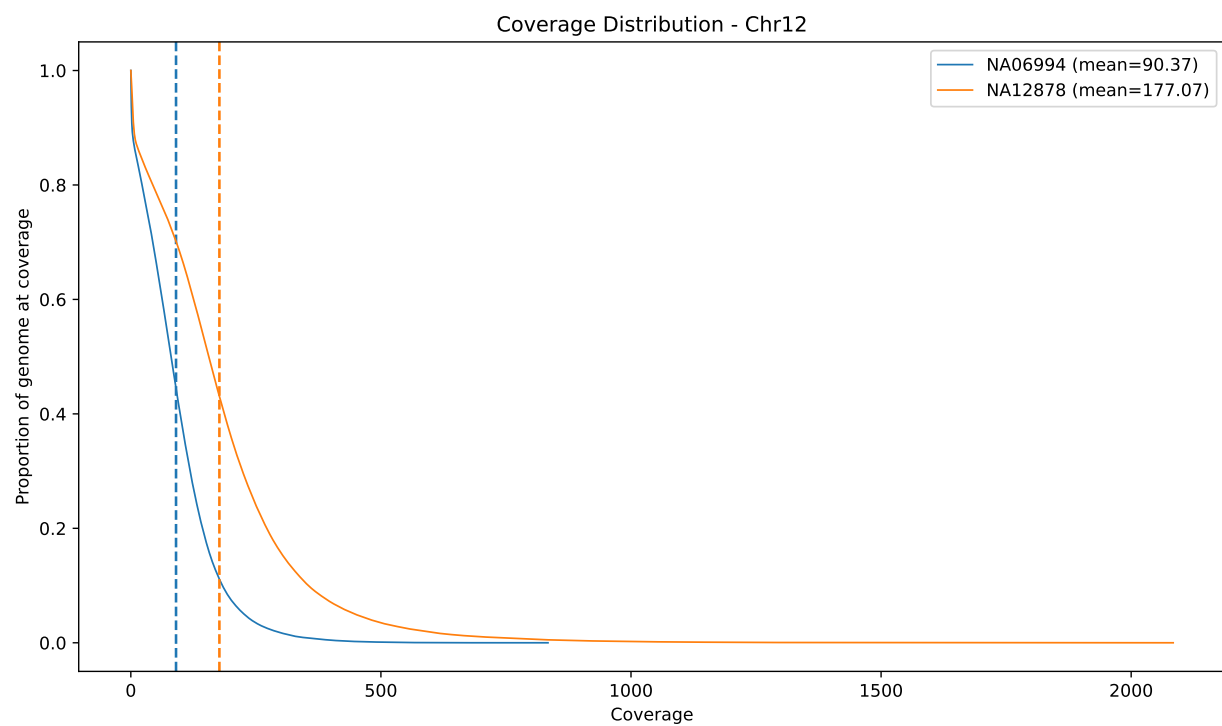


Figure: Genome Coverage for sample Chr12_coverage

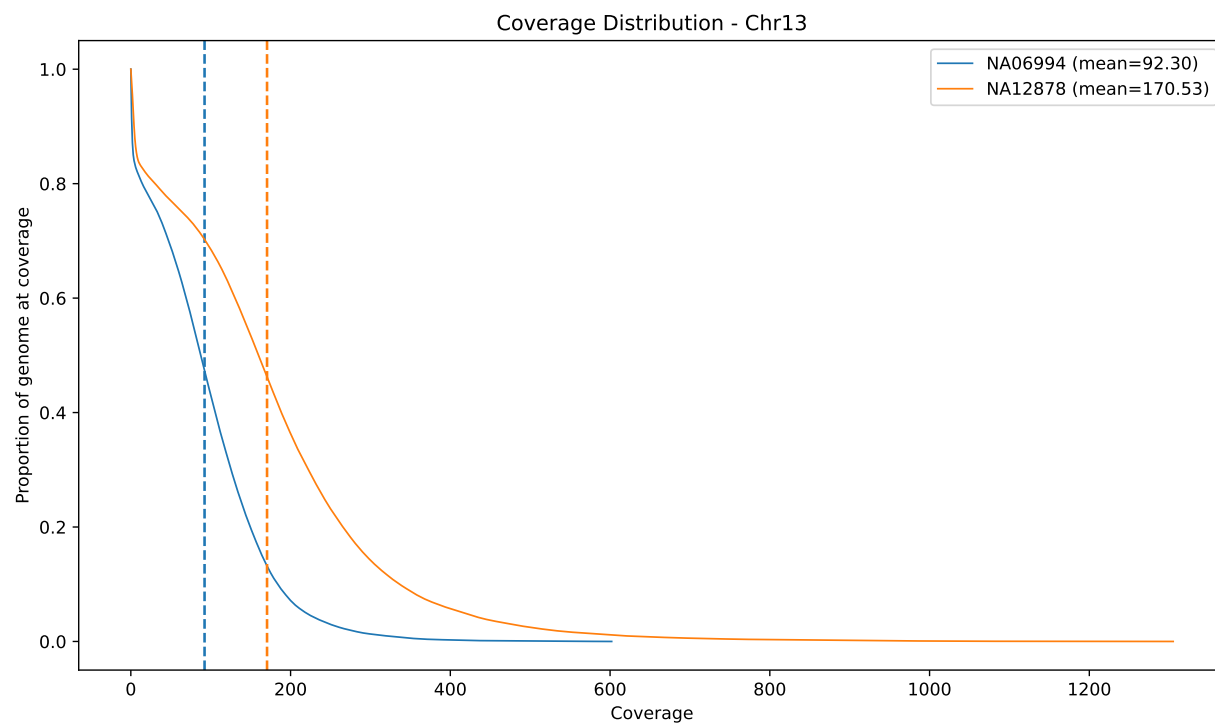


Figure: Genome Coverage for sample Chr13_coverage

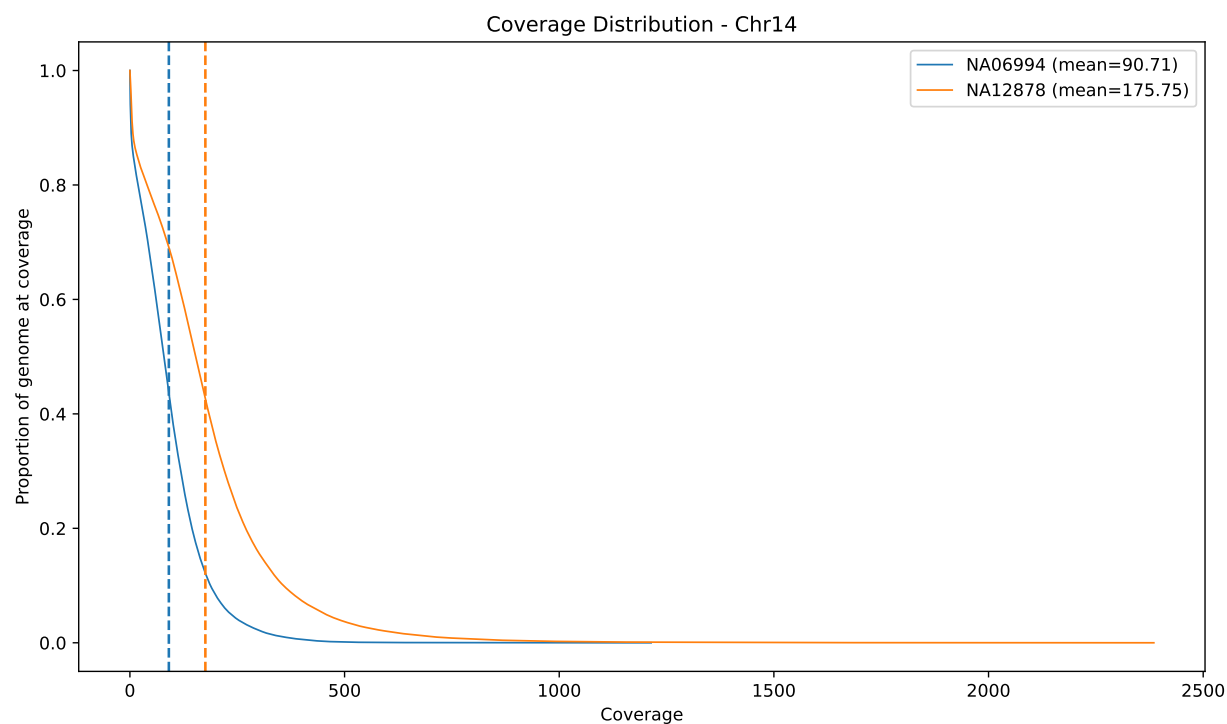


Figure: Genome Coverage for sample Chr14_coverage

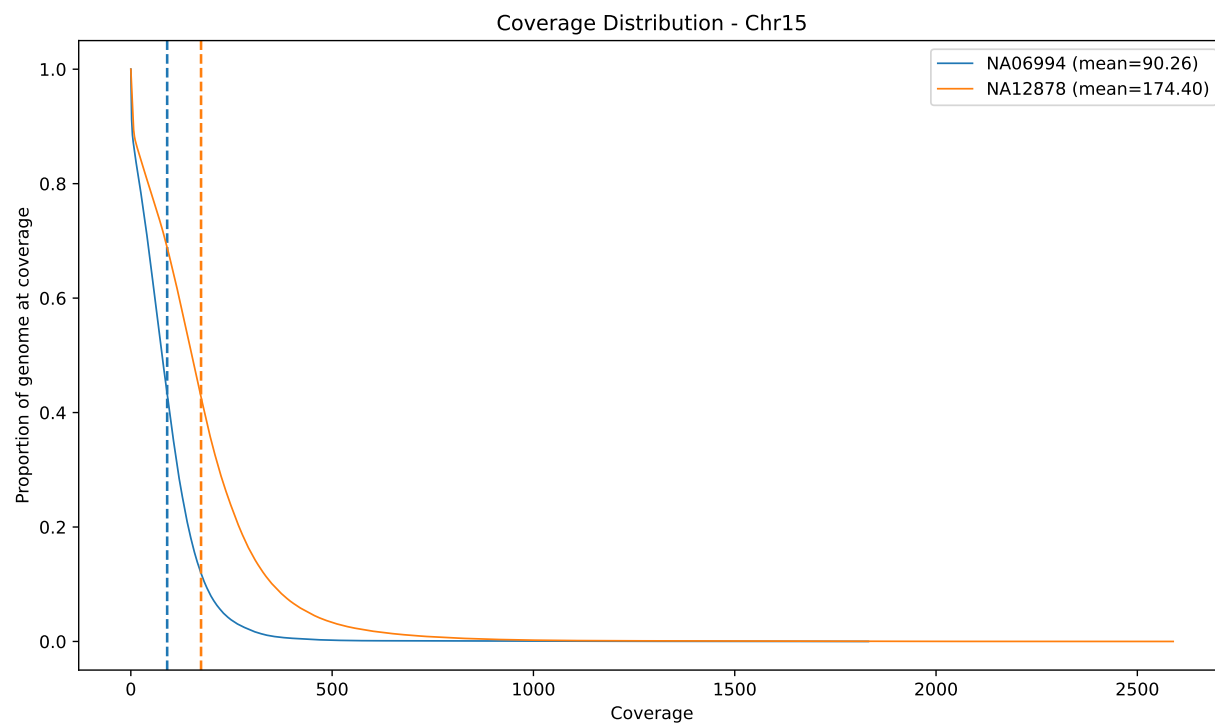


Figure: Genome Coverage for sample Chr15_coverage

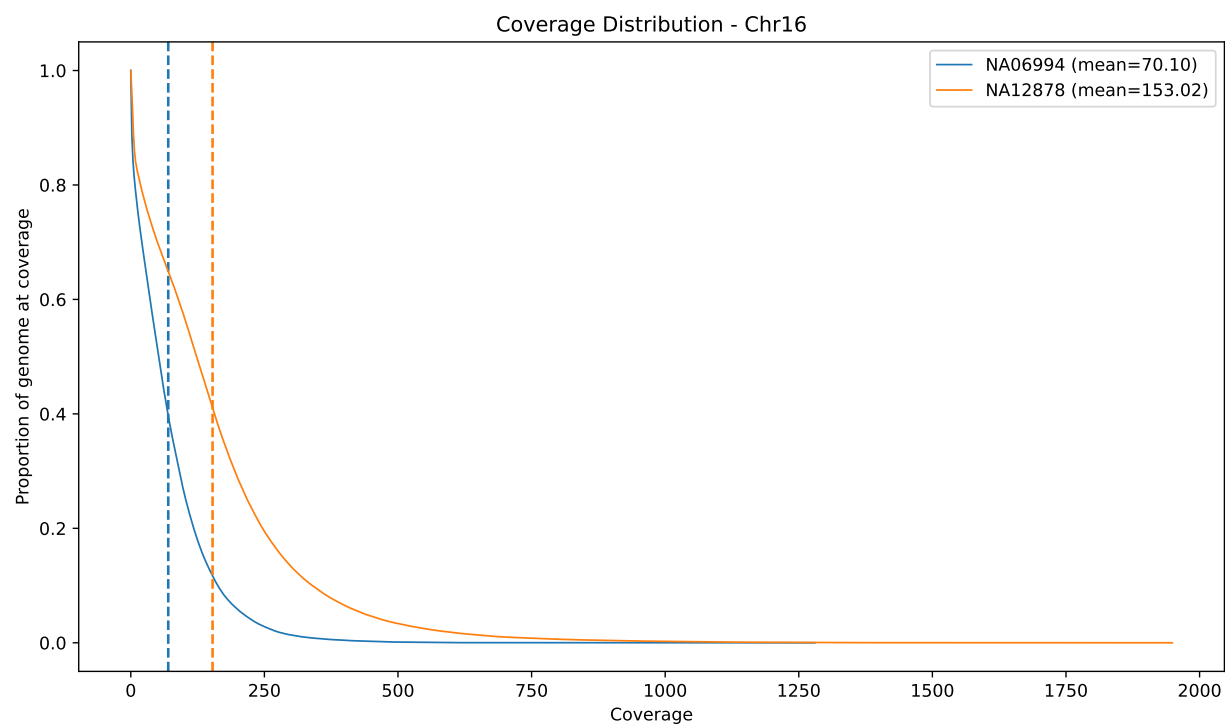


Figure: Genome Coverage for sample Chr16_coverage

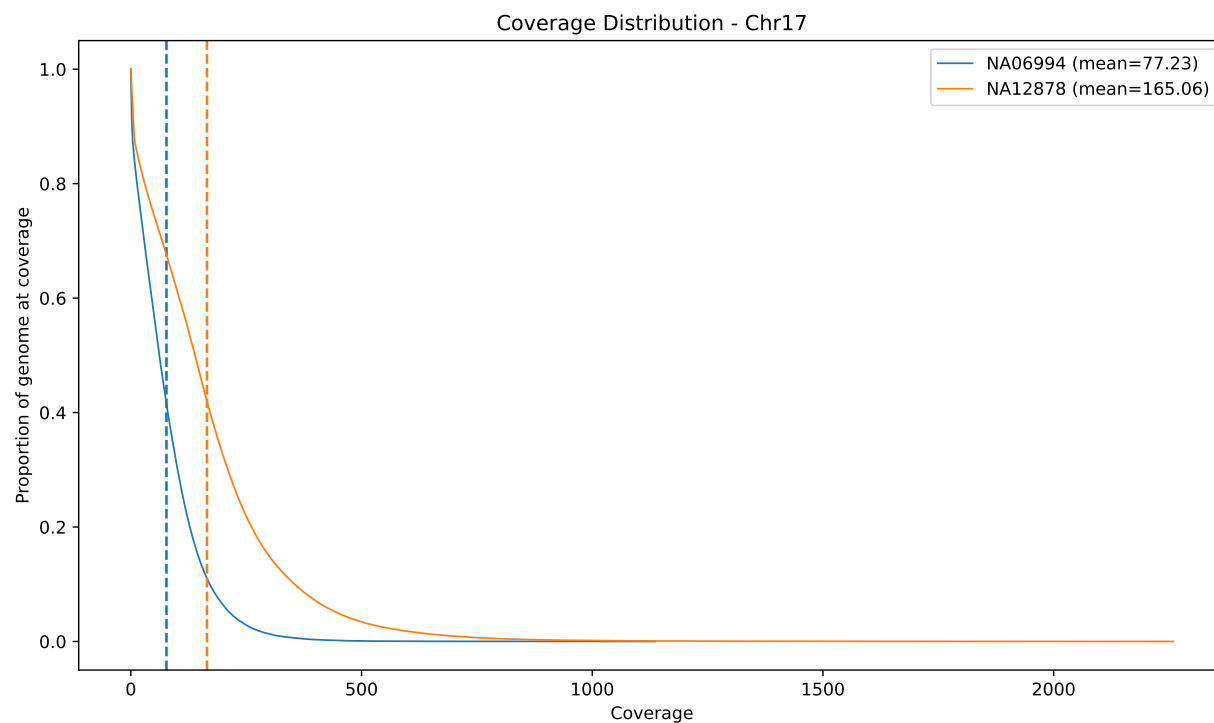


Figure: Genome Coverage for sample Chr17_coverage

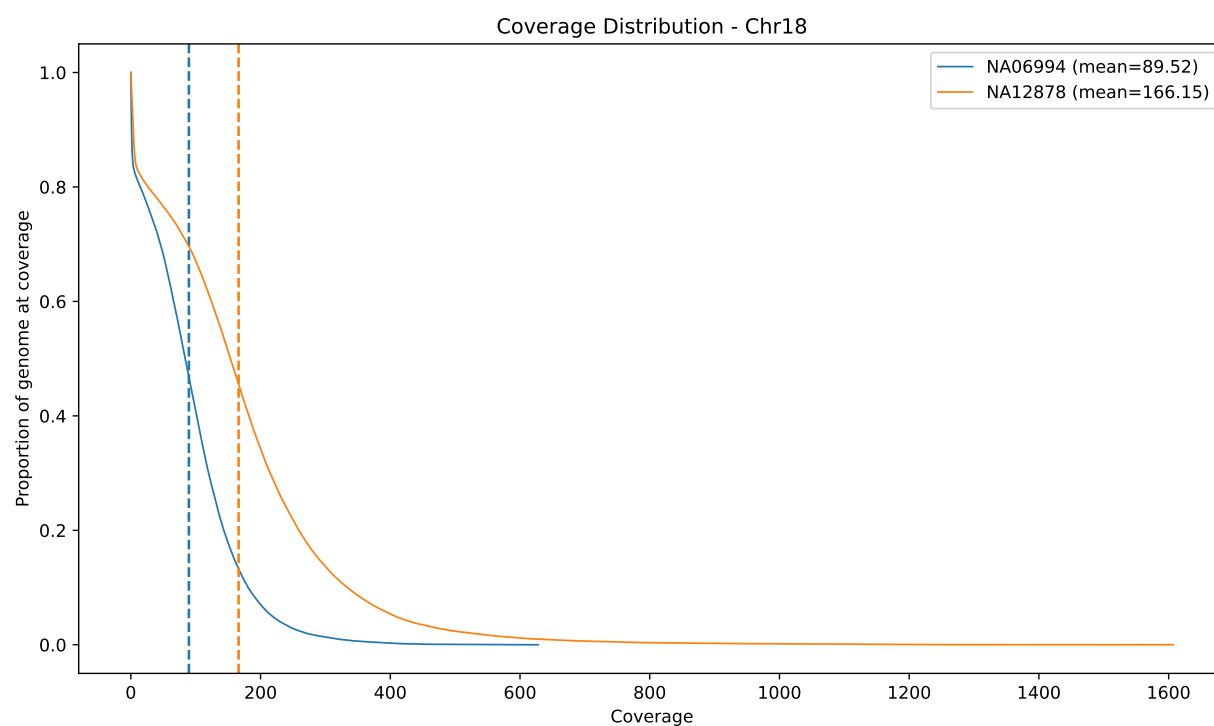


Figure: Genome Coverage for sample Chr18_coverage

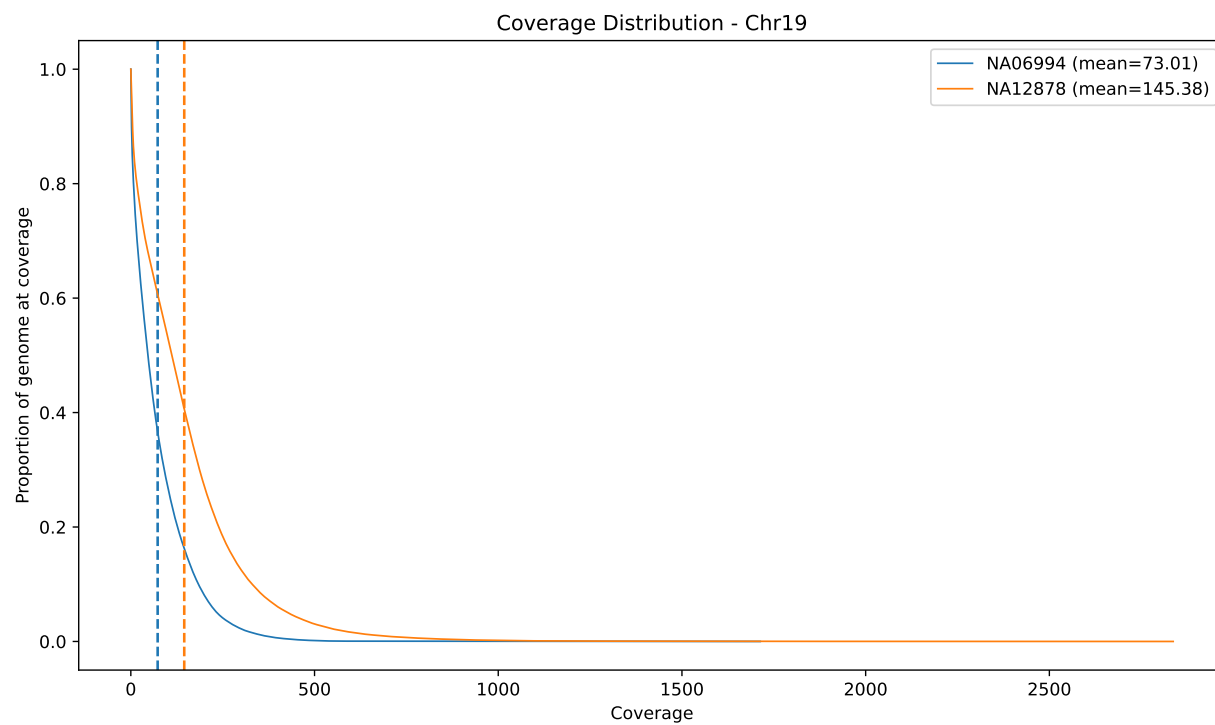


Figure: Genome Coverage for sample Chr19_coverage

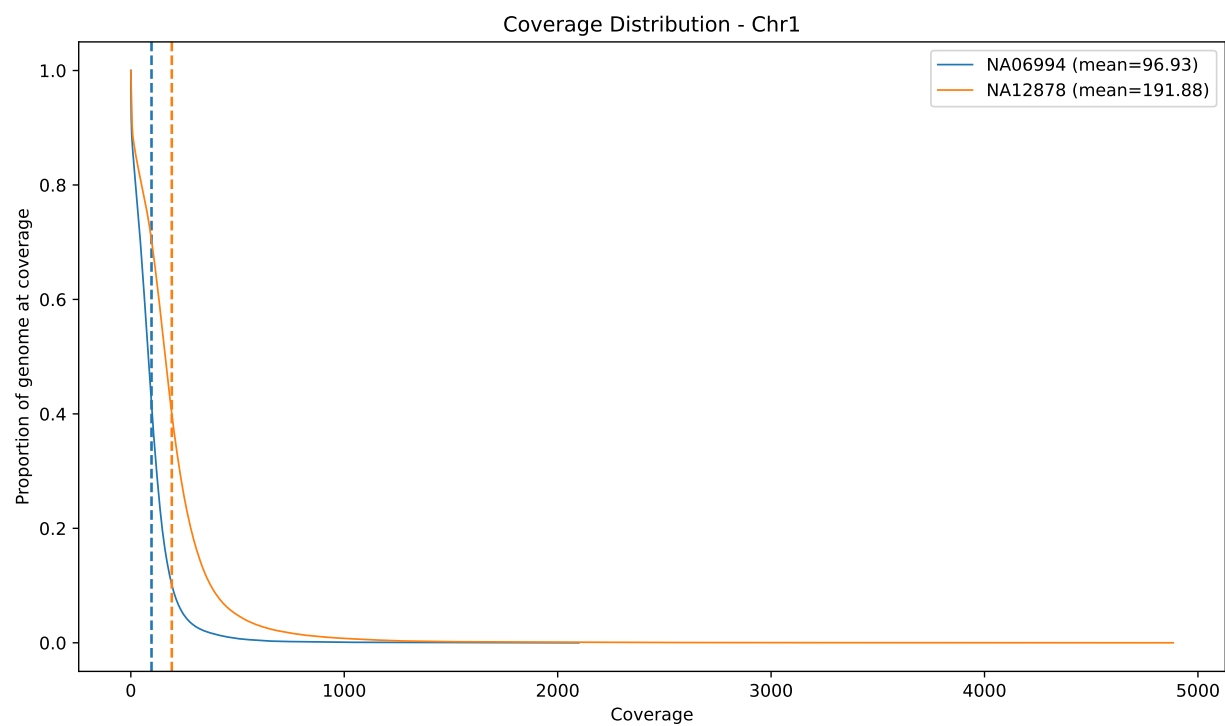


Figure: Genome Coverage for sample Chr1_coverage

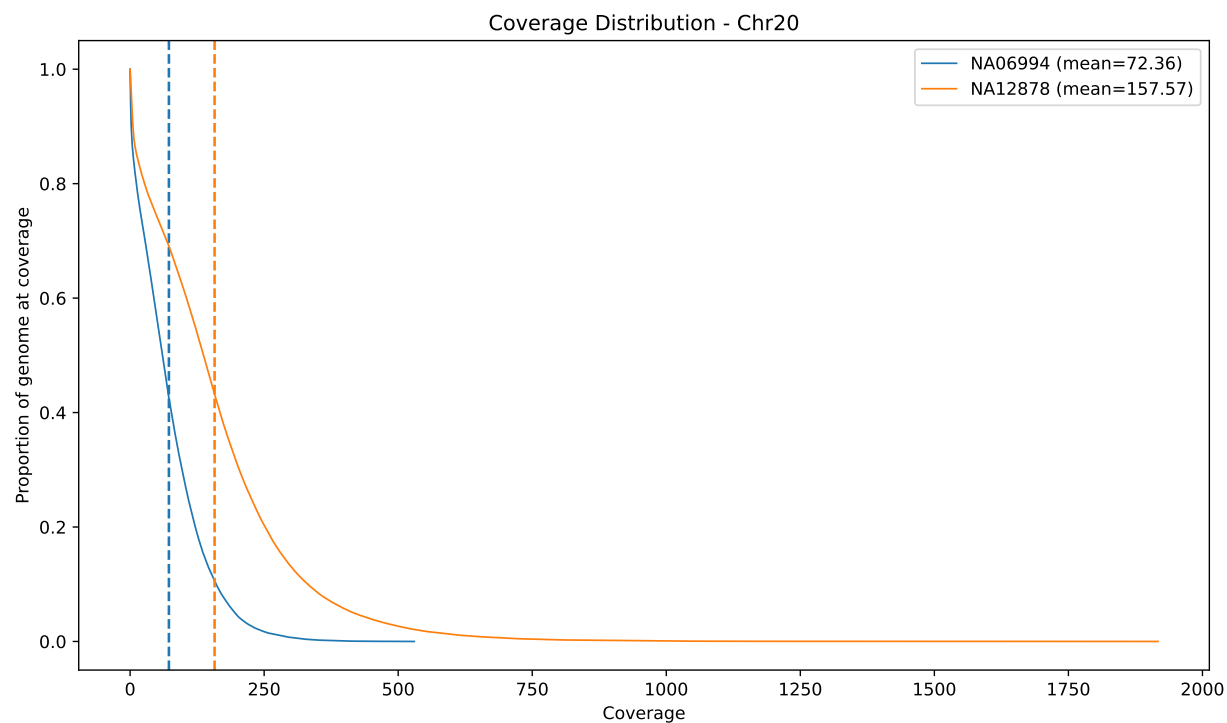


Figure: Genome Coverage for sample Chr20_coverage

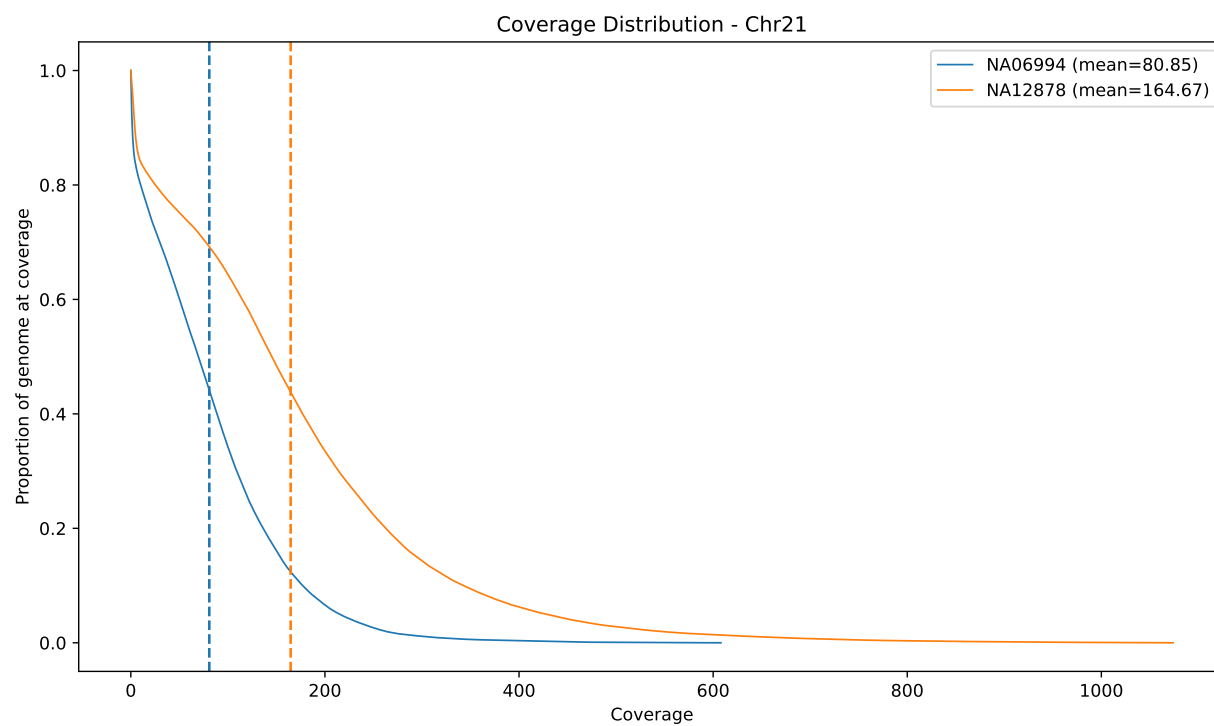


Figure: Genome Coverage for sample Chr21_coverage

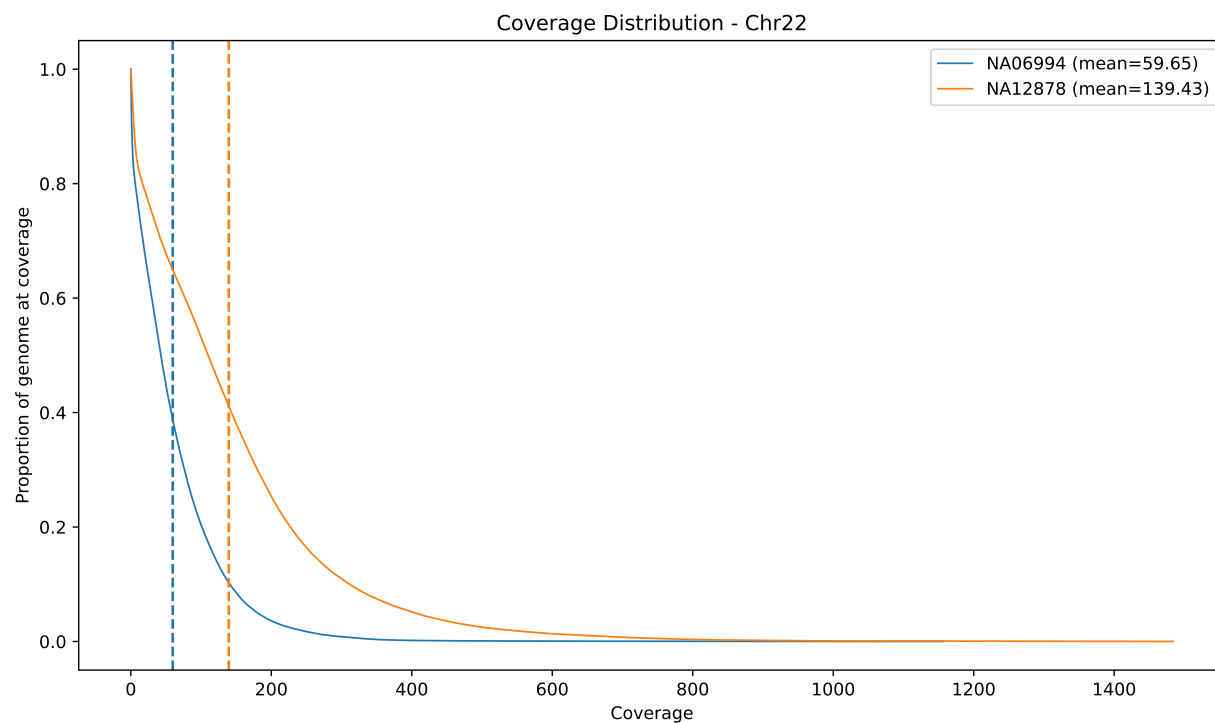


Figure: Genome Coverage for sample Chr22_coverage

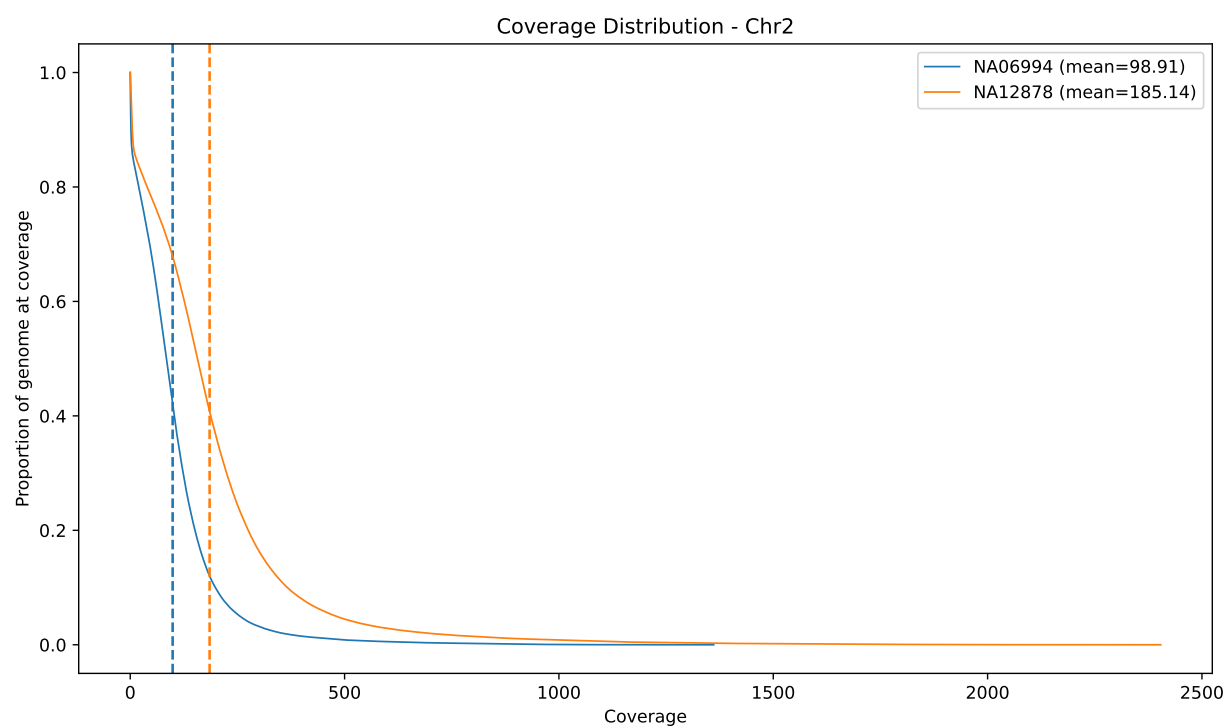


Figure: Genome Coverage for sample Chr2_coverage

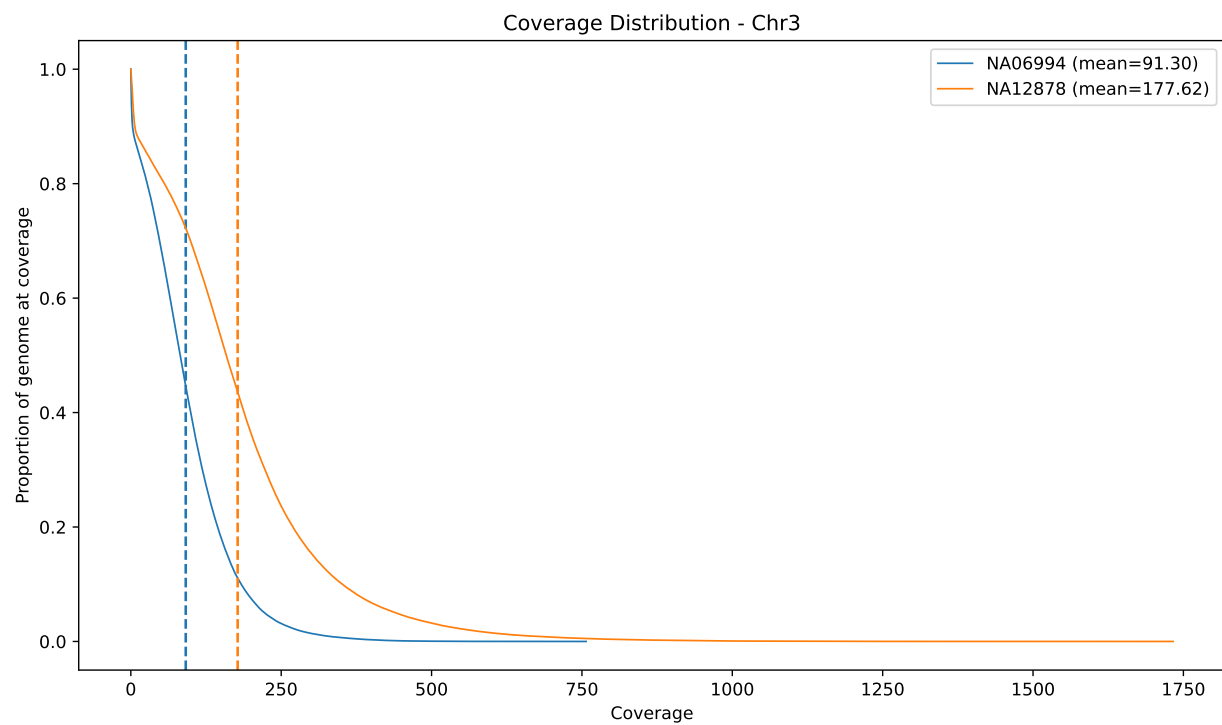


Figure: Genome Coverage for sample Chr3_coverage

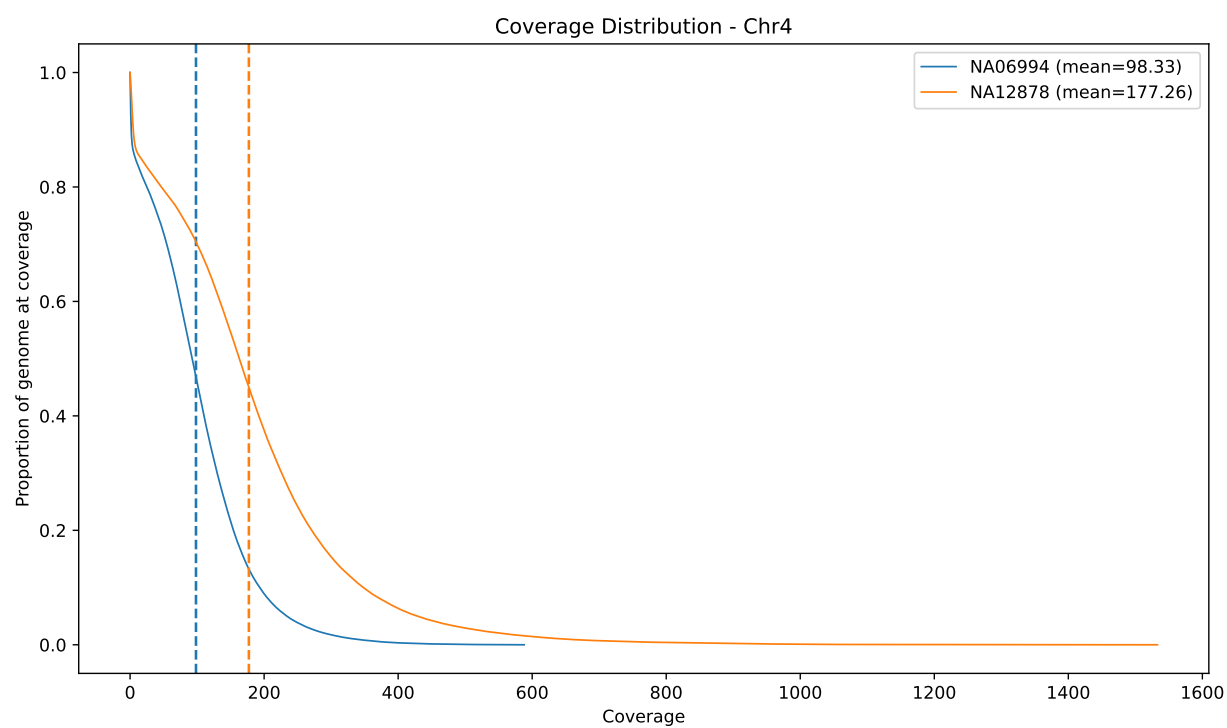


Figure: Genome Coverage for sample Chr4_coverage

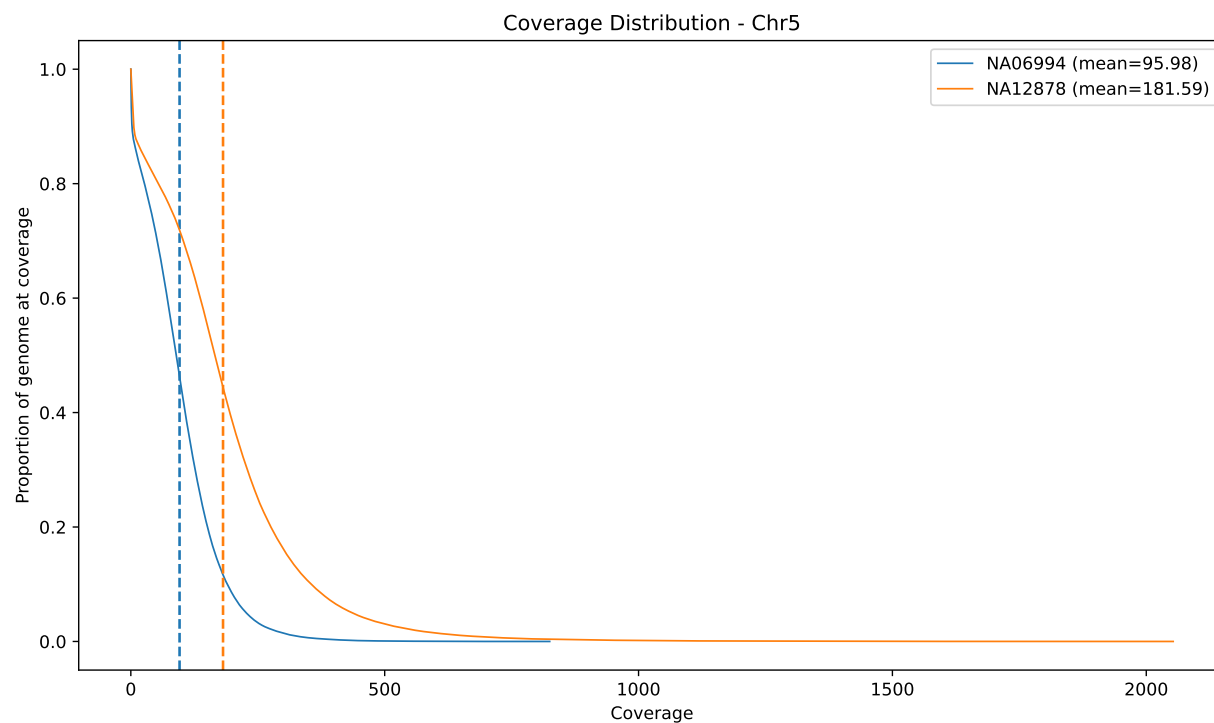


Figure: Genome Coverage for sample Chr5_coverage

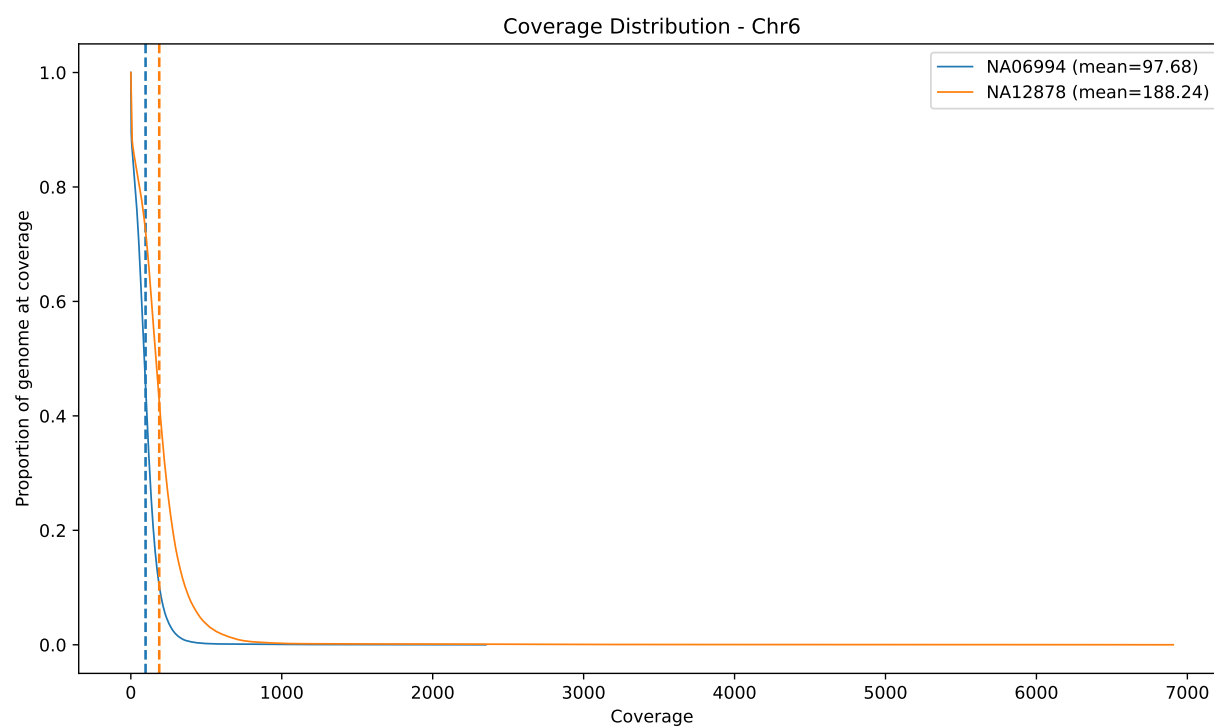


Figure: Genome Coverage for sample Chr6_coverage

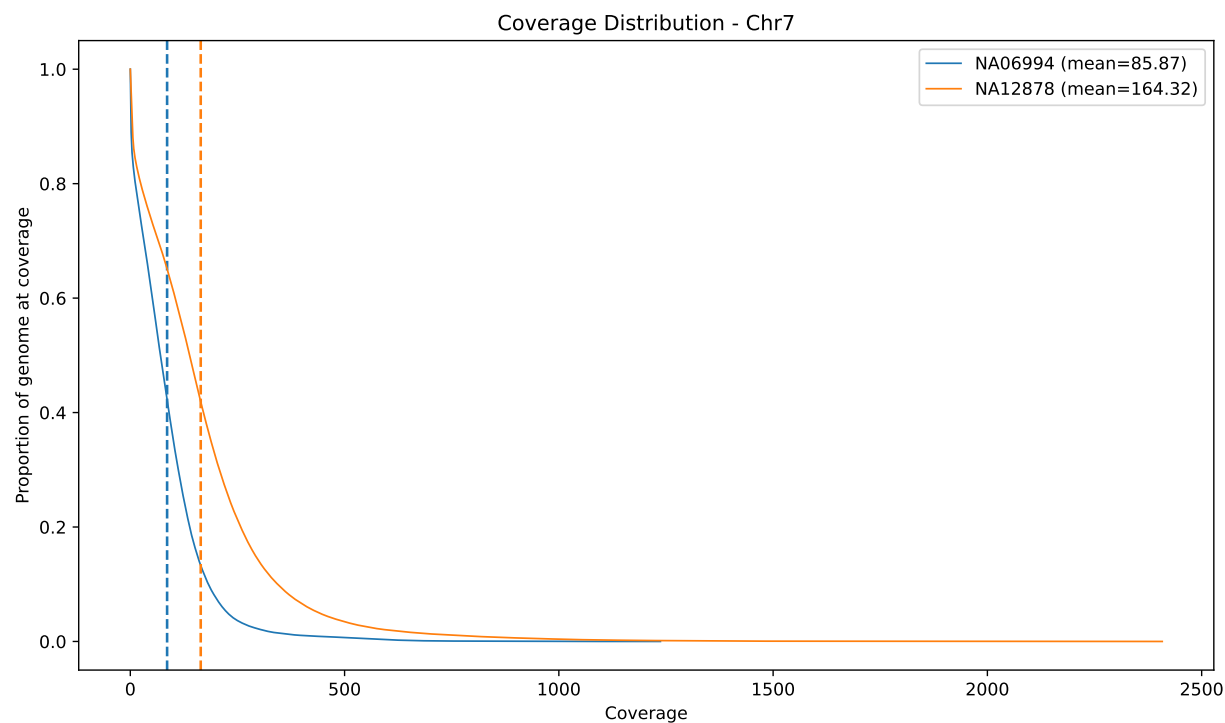


Figure: Genome Coverage for sample Chr7_coverage

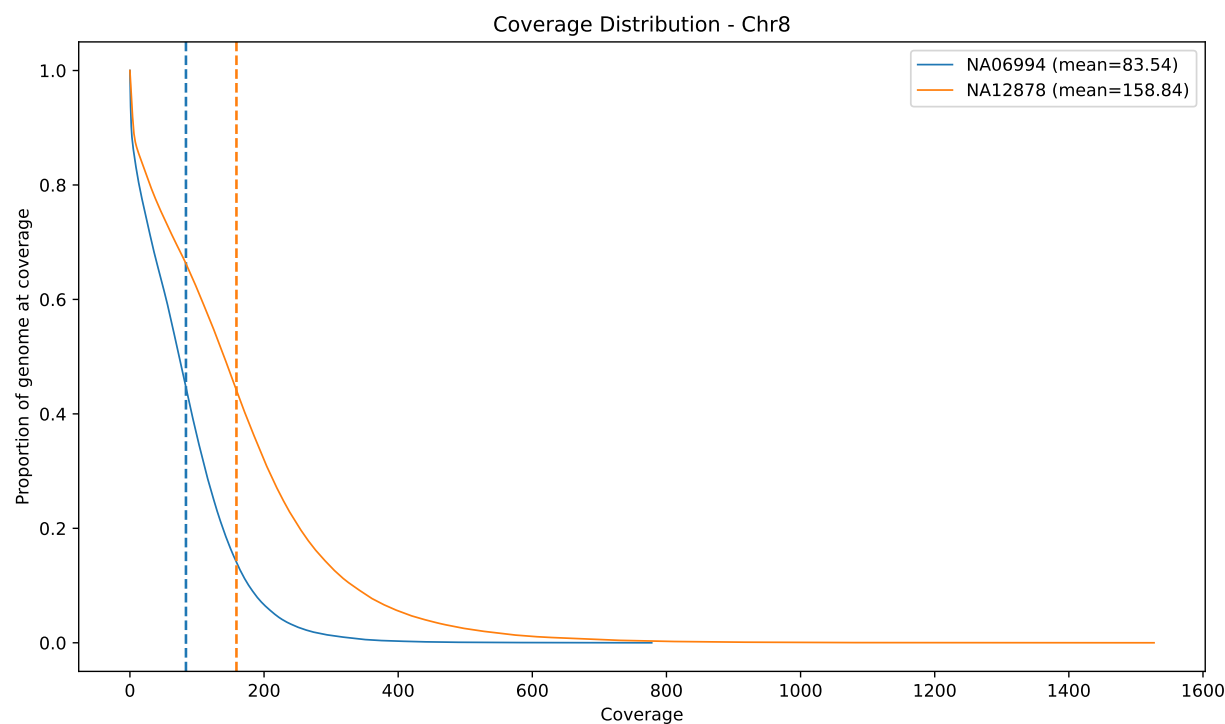


Figure: Genome Coverage for sample Chr8_coverage

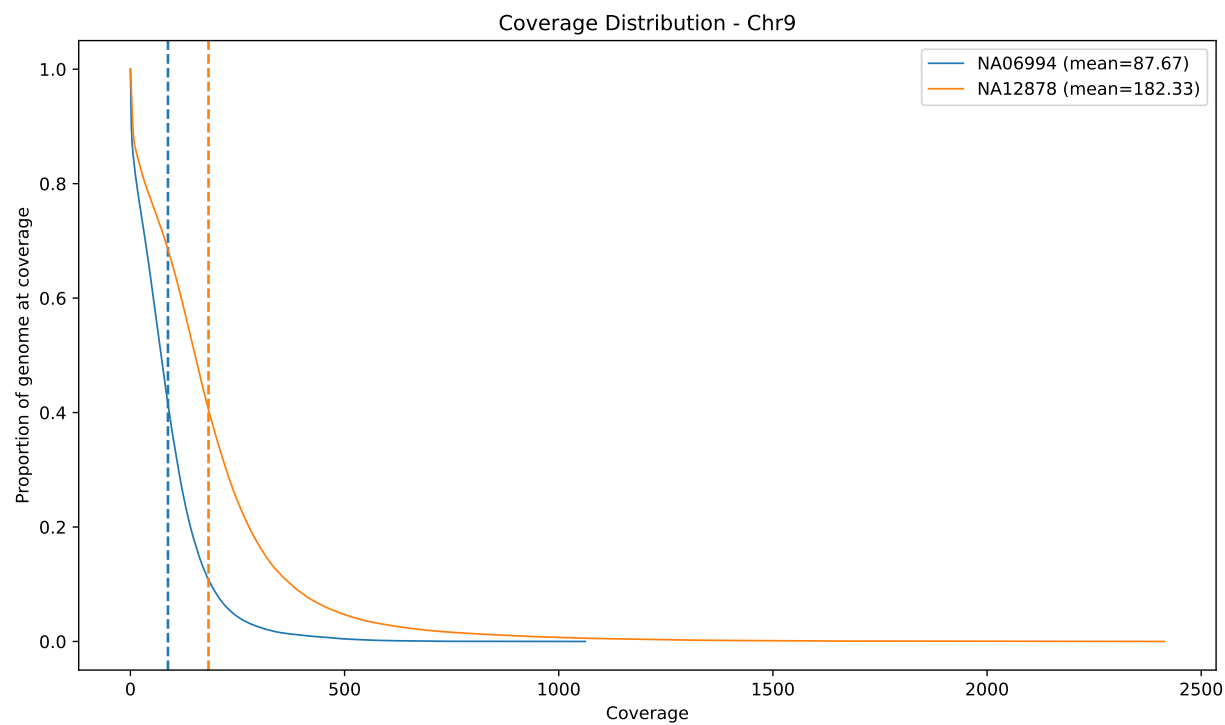


Figure: Genome Coverage for sample Chr9_coverage

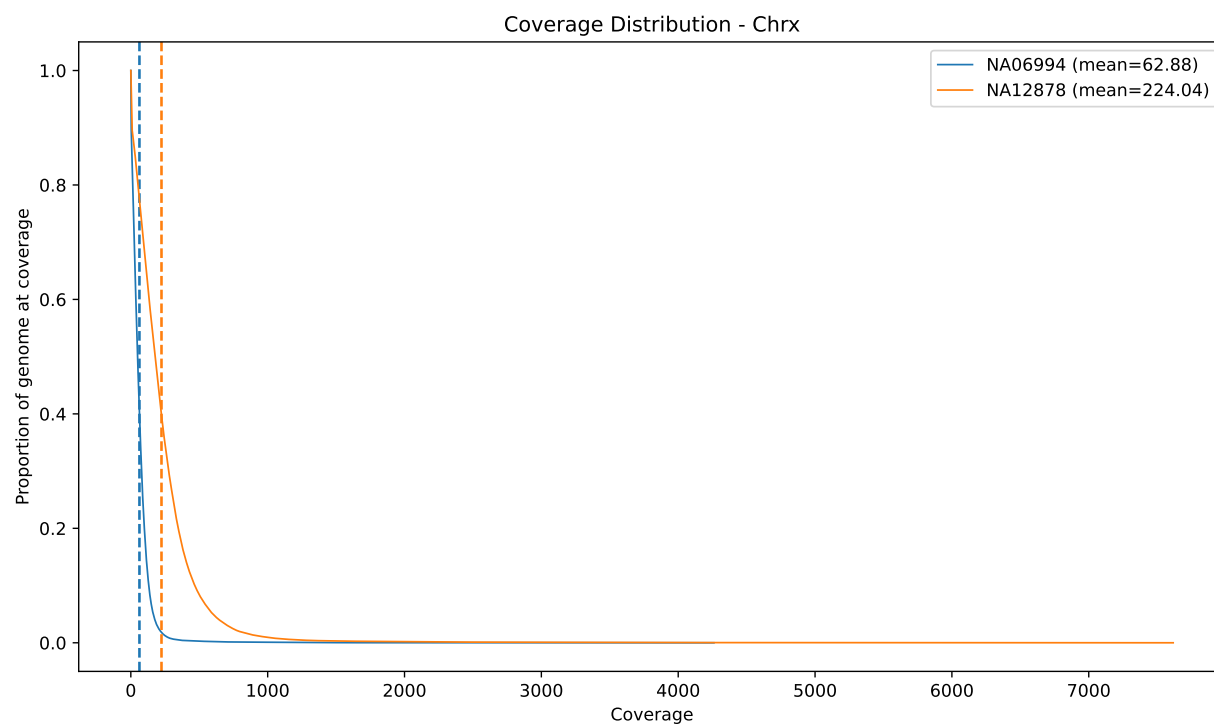


Figure: Genome Coverage for sample ChrX_coverage

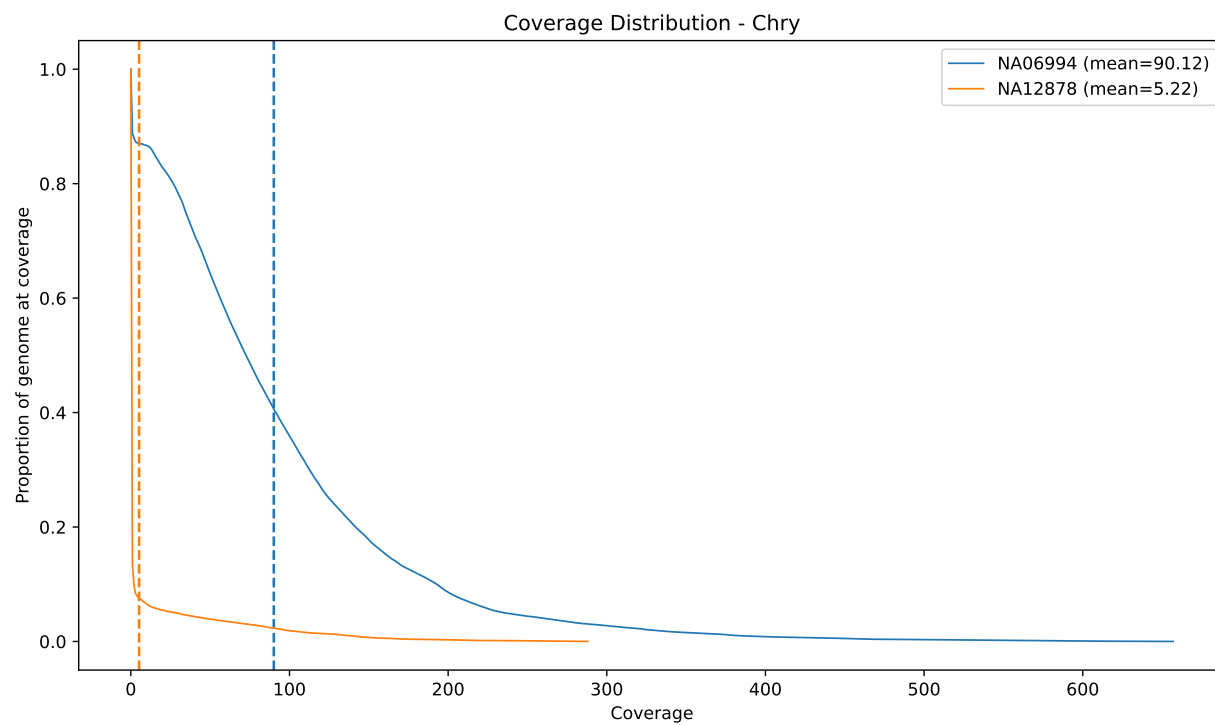


Figure: Genome Coverage for sample Chry_coverage

1.4 Genome Contamination

This section provides an analysis of contamination levels of exogenous DNA or non-human organisms in the samples. The results are derived from Kraken reports, which classify the taxonomic composition of the samples based on their genomic data.

1.4.1 Sample: NA06994_Contamination

- **Contamination:** 0.14%

Interpretation: Sample quality is high.

1.4.2 Sample: NA12878_Contamination

- **Contamination:** 0.25%

Interpretation: Sample quality is high.

1.5 Genome Contamination Plots

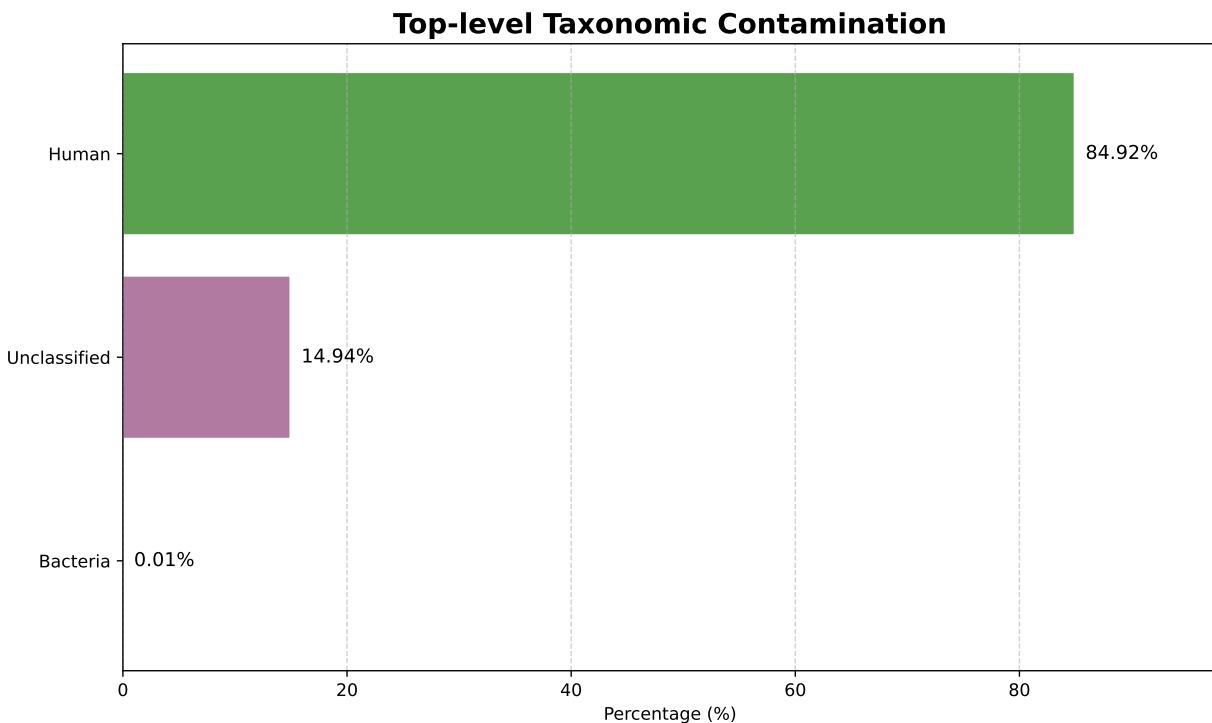


Figure: Genome Contamination Plots for sample NA06994_Contamination

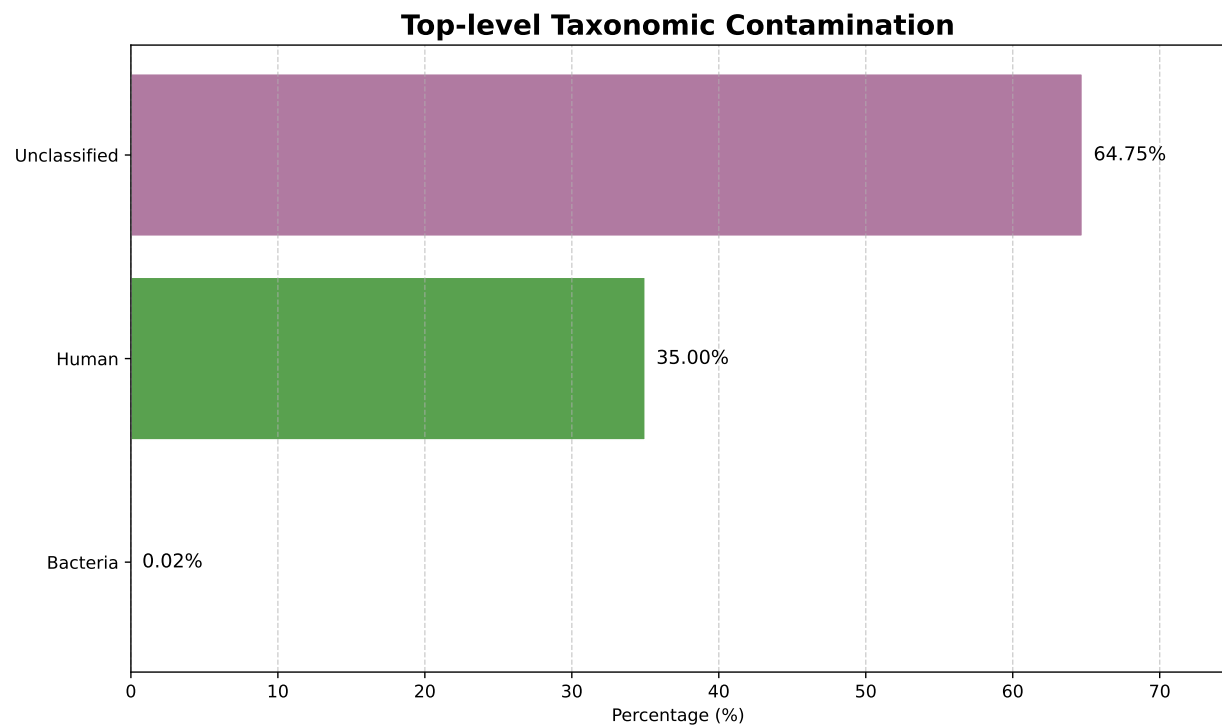


Figure: Genome Contamination Plots for sample NA12878_Contamination