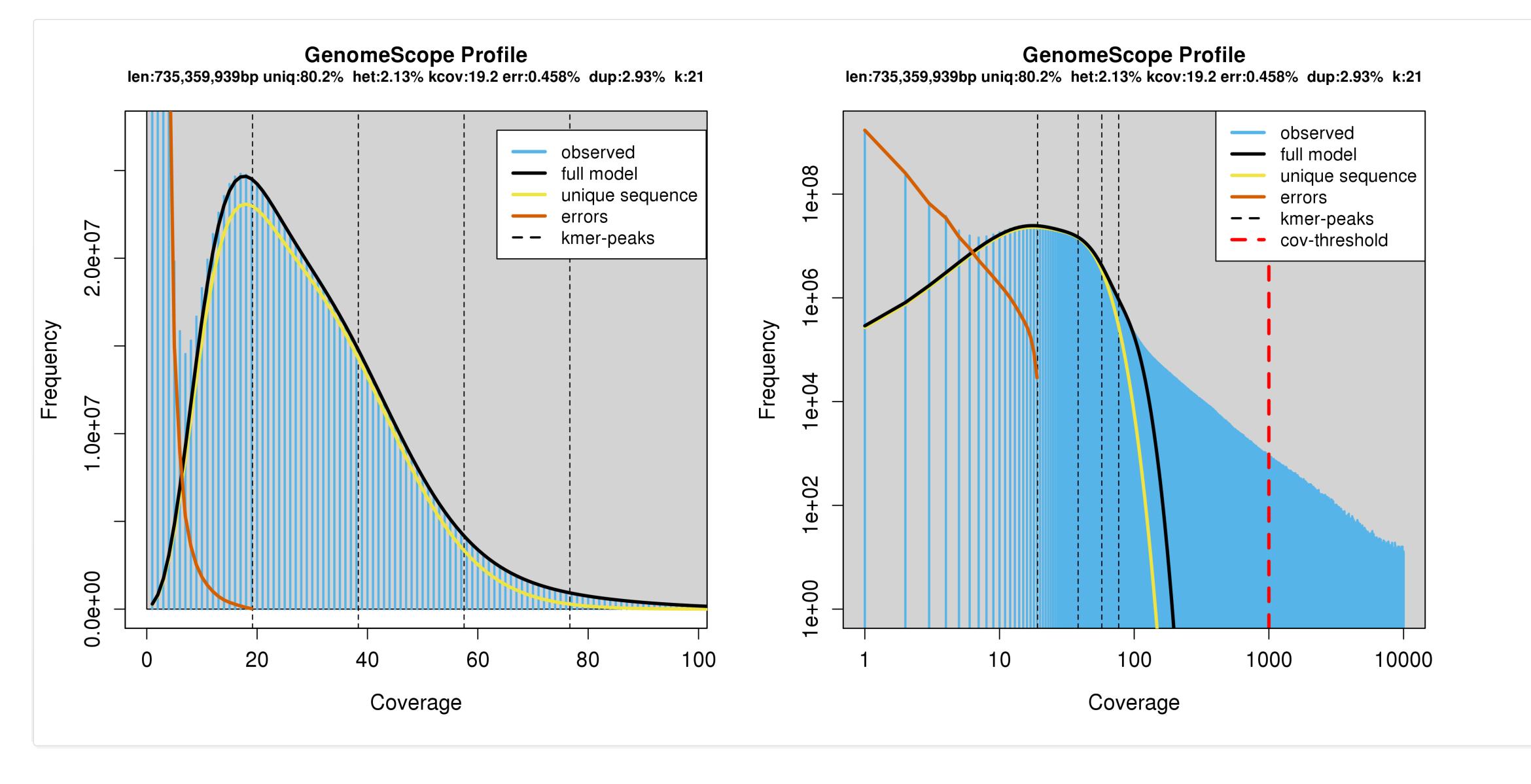
Dar_fq_fp1_clmp_fp2_fqscrn_rprd_jfsh



Results

GenomeScope version 1.0
k = 21

property
Heterozygosity
Genome Haploid Length
Genome Repeat Length
Genome Unique Length
Model Fit

Read Error Rate

min
2.12364%
733,431,964 bp
145,219,198 bp
588,212,766 bp
98.0854%
0.4579%

max
2.13738%
bp 735,359,939 bp
bp 145,600,936 bp
bp 589,759,003 bp
99.5791%
0.4579%

Model

Formula: $y \sim (((2 * (1 - d) * (1 - (1 - r)^k)) + (2 * d * (1 - (1 - r)^k)^2) + (2 * d * ((1 - r)^k) * (1 - (1 - r)^k))) * dnbinom(x, size = kmercov/bias,

mu = kmercov) * length + <math>(((1 - d) * ((1 - r)^k)) + (d * (1 - (1 - r)^k)^2)) * dnbinom(x, size = kmercov * 2/bias,

mu = kmercov * 2) * length + <math>(2 * d * ((1 - r)^k) * (1 - (1 - r)^k)) * dnbinom(x, size = kmercov * 3/bias, mu = kmercov * 3) * length + <math>(d * (1 - r)^2(2 * k)) * dnbinom(x, size = kmercov * 4/bias, mu = kmercov * 4) * length)$

Parameters:

Estimate Std. Error t value Pr(>|t|)
d 7.294e-02 7.372e-04 98.95 <2e-16 ***
r 2.131e-02 3.434e-05 620.44 <2e-16 ***
kmercov 1.917e+01 1.258e-02 1523.66 <2e-16 ***
bias 2.933e+00 1.214e-02 241.58 <2e-16 ***
length 6.288e+08 3.574e+05 1759.15 <2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 22940 on 979 degrees of freedom

Number of iterations to convergence: 8
Achieved convergence tolerance: 4.874e-06

View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=cZtfLEWKPV6ttJQSONmy

Progress

starting

round 0 trimming to 7 trying 4peak model... converged. score: 4542235072812.09 round 1 trimming to 12 trying 4peak model... converged. score: 991511295143.514

round 2 trimming to 17 trying 4peak model... converged. score: 475091065286.476

round 3 trimming to 22 trying 4peak model... converged. score: 526790683400.58

done