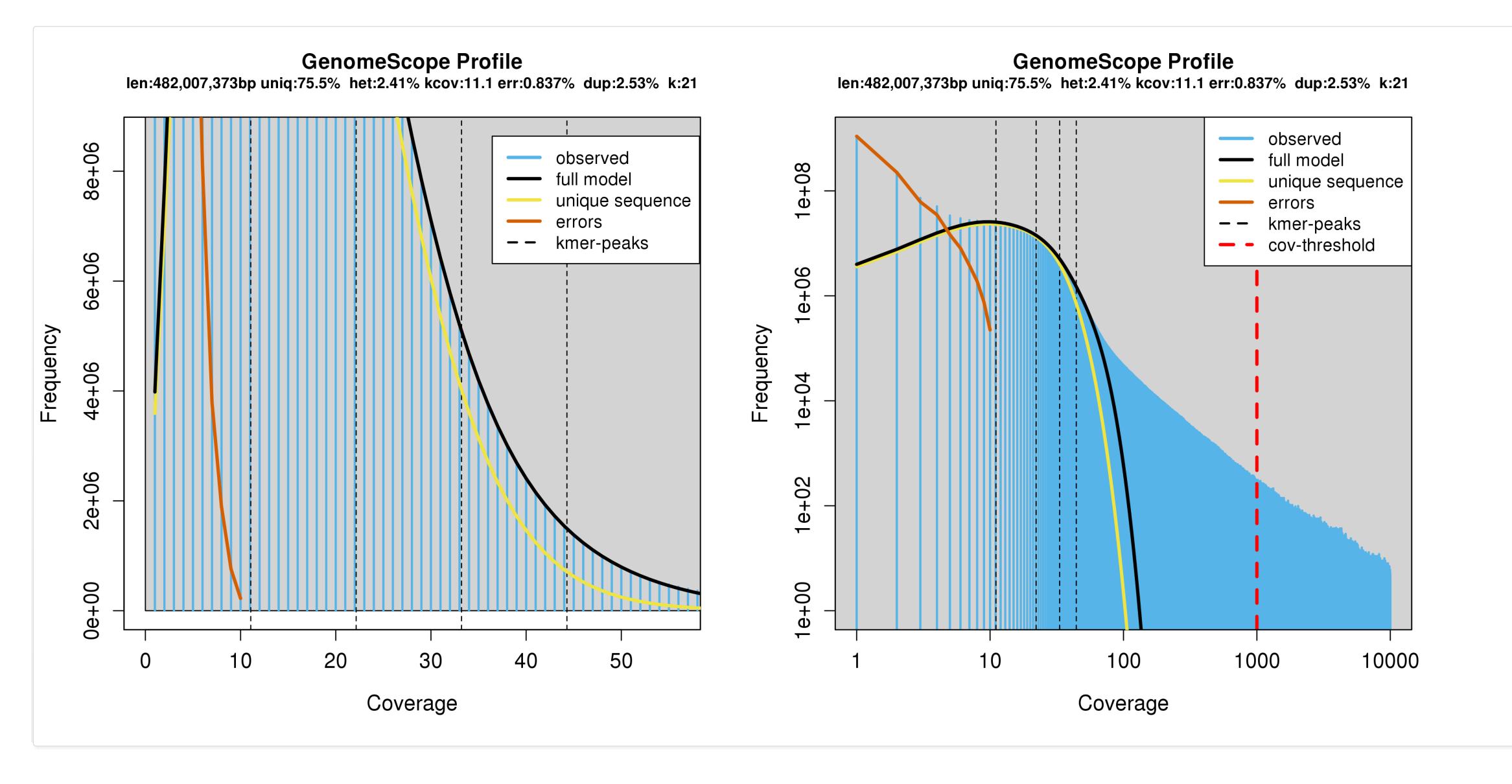
# Pbb\_fq\_fp1\_clmp\_fp2\_fqscrn\_rprd\_jfsh



# Results

GenomeScope version 1.0
k = 21

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

Read Error Rate

min 2.36469% 475,159,090 bp 116,322,298 bp 358,836,792 bp 98.2149%

0.836825%

max
2.45501%
482,007,373 bp
117,998,806 bp
364,008,567 bp
99.7399%
0.836825%

# 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:

# Parameters:

Estimate Std. Error t value Pr(>|t|)
d 9.833e-02 2.480e-03 39.65 <2e-16 \*\*\*
r 2.410e-02 2.258e-04 106.73 <2e-16 \*\*\*
kmercov 1.107e+01 3.961e-02 279.54 <2e-16 \*\*\*
bias 2.527e+00 6.101e-02 41.41 <2e-16 \*\*\*
length 3.939e+08 2.001e+06 196.81 <2e-16 \*\*\*
--Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 16500 on 981 degrees of freedom

Number of iterations to convergence: 19
Achieved convergence tolerance: 7.16e-06

# View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=tL69tlGgJn3vjkErNDIP

# Progress

# starting

round 0 trimming to 15 trying 4peak model... converged. score: 357336222930.937

round 1 trimming to 20 trying 4peak model... unconverged

round 2 trimming to 25 trying 4peak model... unconverged

round 3 trimming to 30 trying 4peak model... unconverged

done