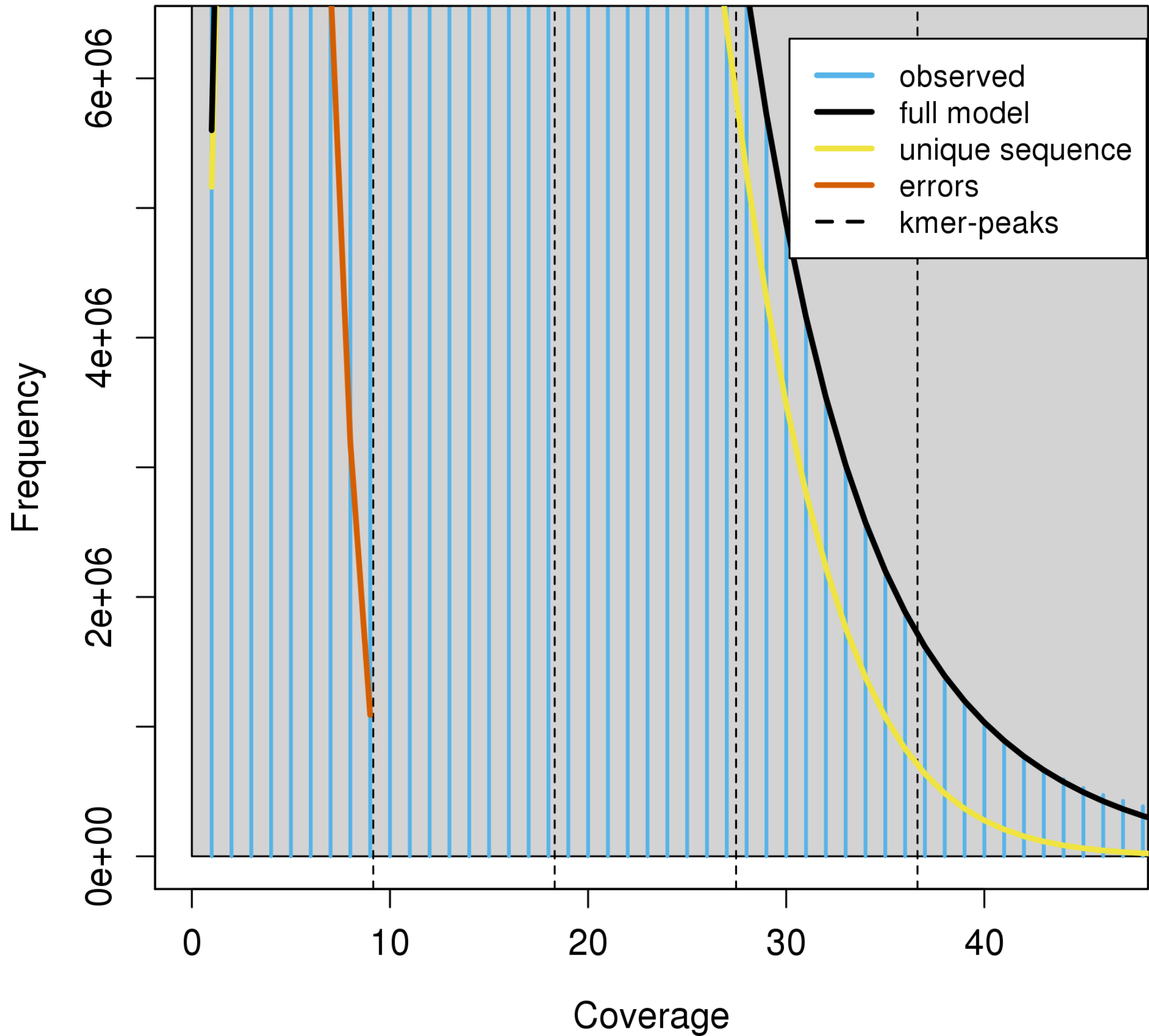


Psq_fq_fp1_clmp_fp2_fqscrn_rprd_jfsh

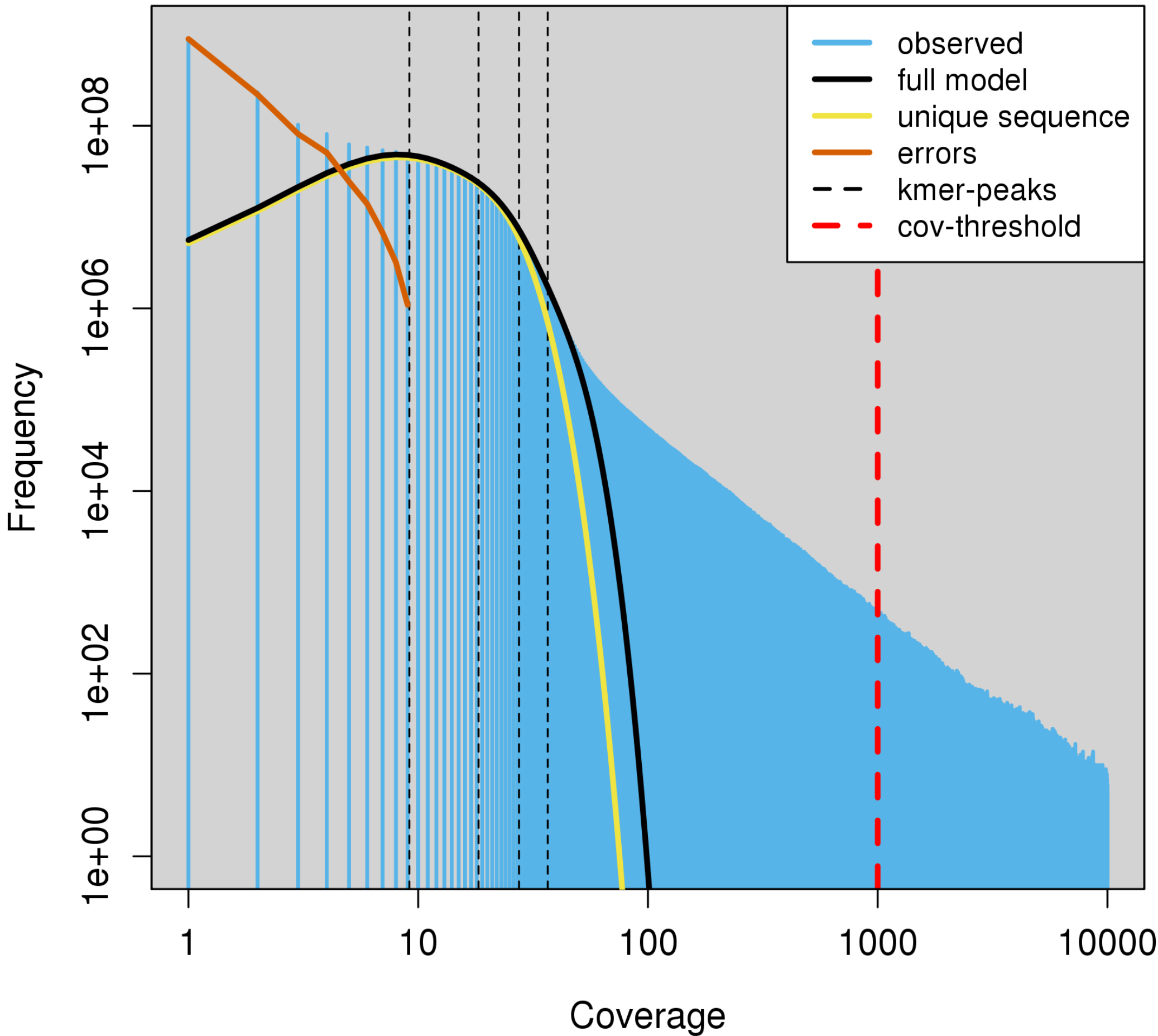
GenomeScope Profile

len:653,788,079bp uniq:76.8% het:2.78% kcov:9.16 err:0.759% dup:1.34% k:21



GenomeScope Profile

len:653,788,079bp uniq:76.8% het:2.78% kcov:9.16 err:0.759% dup:1.34% k:21



Results

GenomeScope version 1.0		
k = 21		
property	min	max
Heterozygosity	2.72749%	2.84147%
Genome Haploid Length	645,720,680 bp	653,788,079 bp
Genome Repeat Length	150,122,287 bp	151,997,861 bp
Genome Unique Length	495,598,393 bp	501,790,219 bp
Model Fit	97.8671%	99.5152%
Read Error Rate	0.759302%	0.759302%

Model

```
Formula: y ~ (((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 + (((1 - d) * ((1 - r)^k)) + (d * (1 - (1 - r)^k)^2)) * dnbinom(x, size = kmercov * 2/bias, mu = kmercov * 2) * length + (2 * d * ((1 - r)^k) * (1 - (1 - r)^k)) * dnbinom(x, size = kmercov * 3/bias, mu = kmercov * 3) * length + (d * (1 - r)^(2 * k)) * dnbinom(x, size = kmercov * 4/bias, mu = kmercov * 4) * length)

Parameters:
      Estimate Std. Error t value Pr(>|t|)
d      7.820e-02  1.783e-03  43.85  <2e-16 ***
r      2.784e-02  2.849e-04  97.72  <2e-16 ***
kmercov 9.156e+00  2.842e-02  322.16  <2e-16 ***
bias    1.339e+00  3.458e-02   38.72  <2e-16 ***
length  5.319e+08  1.735e+06   306.65  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 23860 on 981 degrees of freedom

Number of iterations to convergence: 13
Achieved convergence tolerance: 6.314e-06
```

[View analysis later](#)

Return to view your results at any time:

<http://genomescope.org/analysis.php?code=yGwdxslfXlkOeltsW66k>

Progress

starting

round 0 trimming to 15 trying 4peak model... converged. score: 1976490395910.62

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