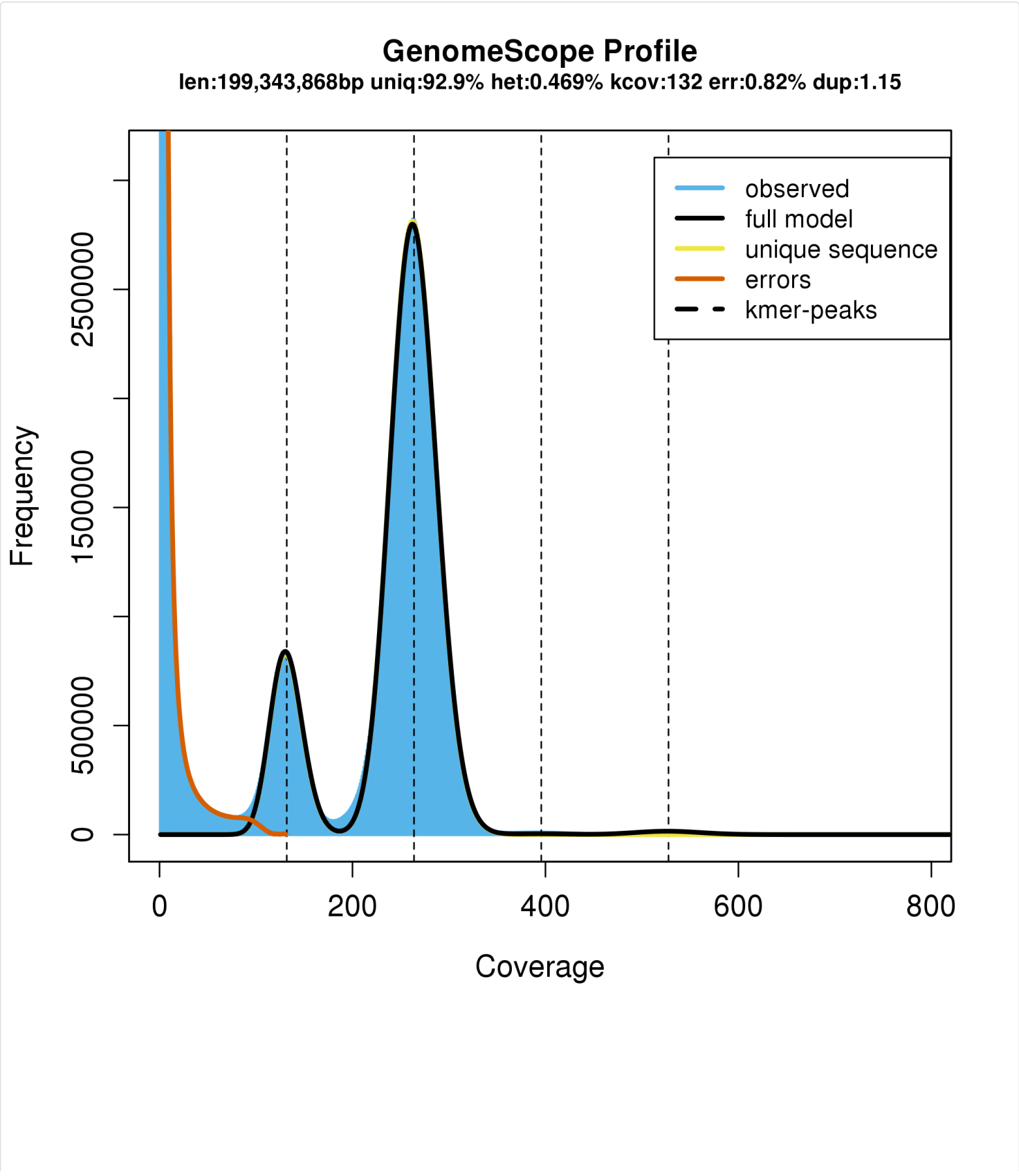
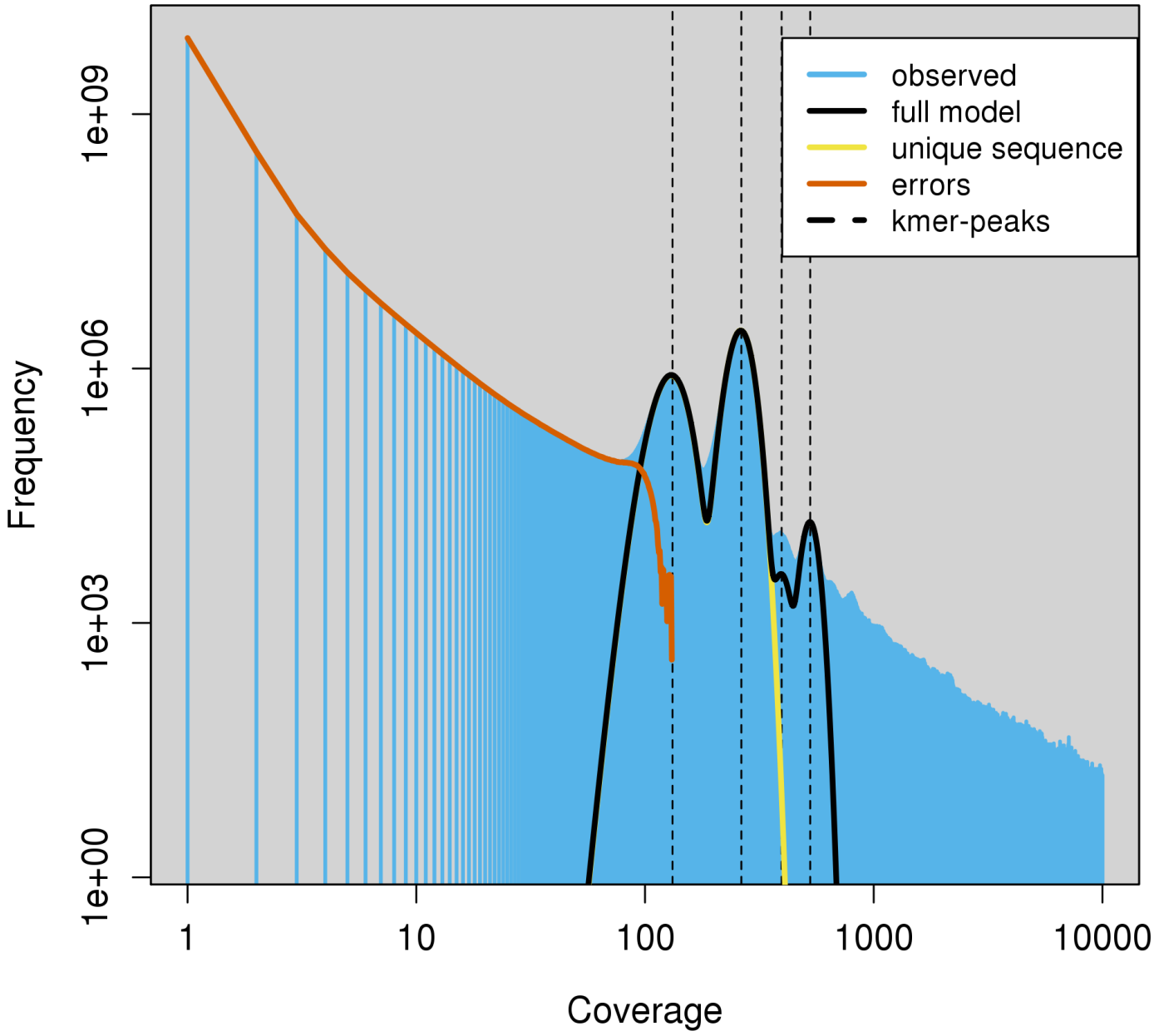

GenomeScope Profile
len:199,343,868bp uniq:92.9% het:0.469% kcov:132 err:0.82% dup:1.15
observed
full model
unique sequence
errors
kmer-peaks
Frequency
0
500000
1500000
2500000
0
200
400
600
800
Coverage

GenomeScope Profile

len:199,343,868bp uniq:92.9% het:0.469% kcov:132 err:0.82% dup:1.15



Results

Model

```
k = 21

property                  min              max
Heterozygosity            0.468619%        0.479918%
Genome Haploid Length     199,195,451 bp   199,343,868 bp
Genome Repeat Length      14,161,640 bp    14,172,191 bp
Genome Unique Length      185,033,812 bp   185,171,677 bp
Model Fit                 95.4213%         96.0784%
Read Error Rate           0.820201%        0.820201%
```

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

Parameters:
         Estimate Std. Error  t value Pr(>|t|)
d       8.513e-03  1.812e-03    4.697 2.68e-06 ***
r       4.743e-03  2.825e-05  167.893  < 2e-16 ***
kmercov 1.319e+02  2.457e-02 5370.534  < 2e-16 ***
bias    1.169e+00  8.721e-03  134.108  < 2e-16 ***
length  1.884e+08  7.342e+05  256.567  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '

Residual standard error: 26720 on 9981 degrees of freedom

Number of iterations to convergence: 6
Achieved convergence tolerance: 3.148e-06
```

View analysis later

Return to view your results at any time:

http://qb.cshl.edu/genomescope/analysis.php?code=TRpKdSHytjlB1vBGsPne

Progress

starting

round 0 trimming to 15 trying 4peak model... converged. score: 294195068059.79

round 1 trimming to 20 trying 4peak model... converged. score: 294195072722.062

round 2 trimming to 25 trying 4peak model... converged. score: 294195074109.985

round 3 trimming to 30 trying 4peak model... converged. score: 294195073399.253

done