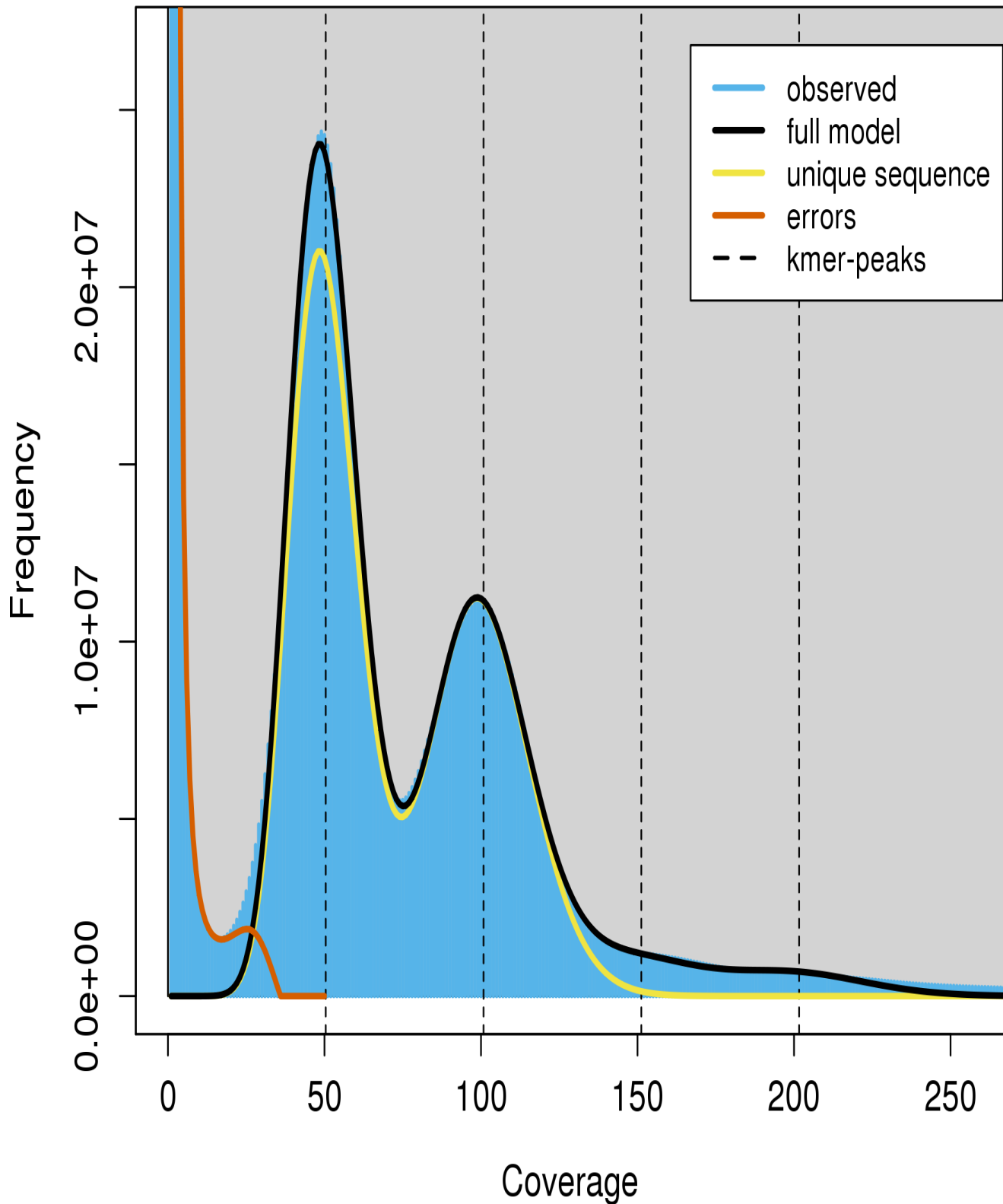


Dreissena rostriformis trimmomatic-trimmed PE reads (1P and 2P)

GenomeScope Profile

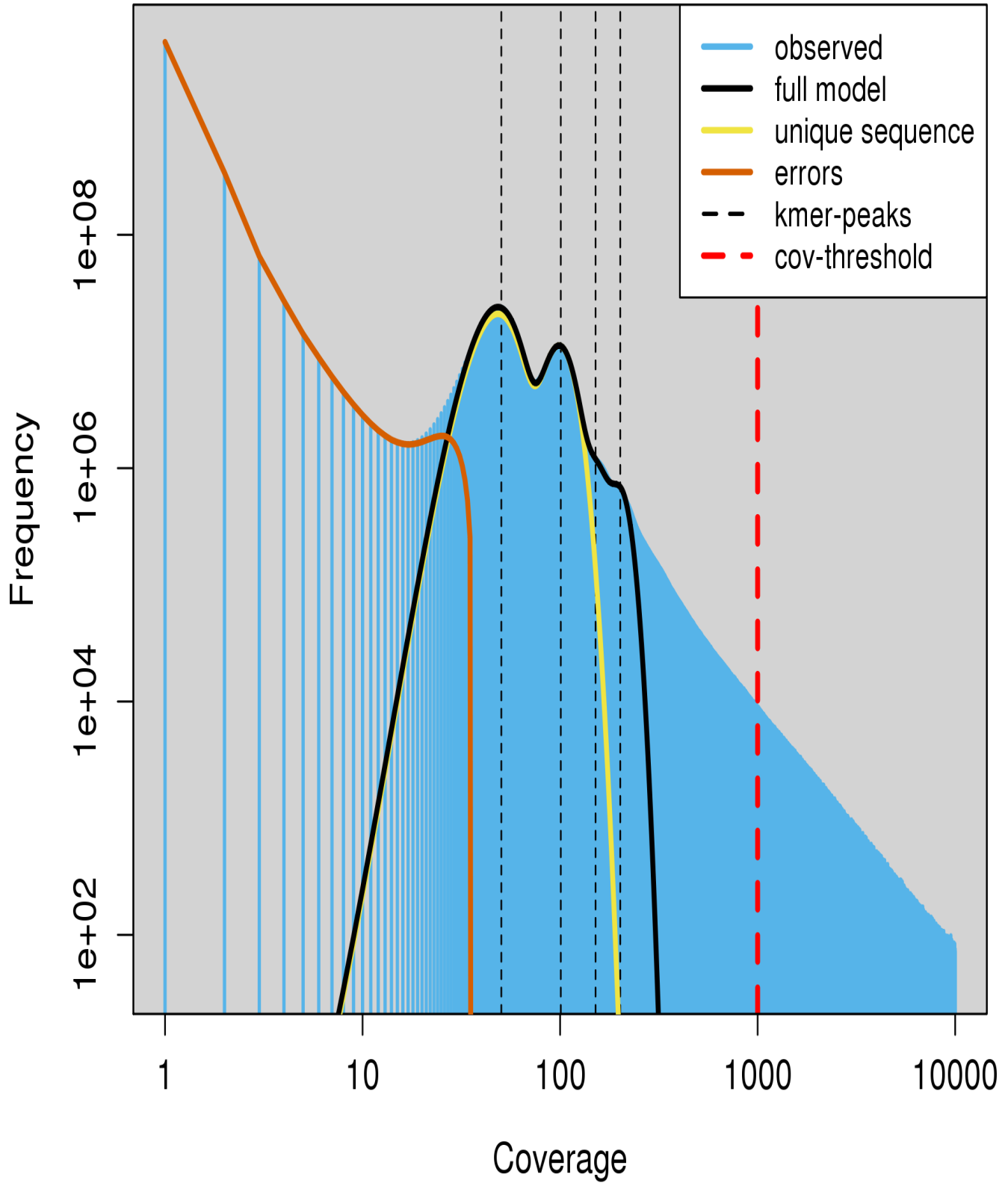
len:1,081,038,339bp uniq:67.5% het:2.45% kcov:50.4 err:0.278% dup:1.46% k:21



(user_data/19ScrqZLdCOI8Kd3Y4e/plot.png)

GenomeScope Profile

len:1,081,038,339bp uniq:67.5% het:2.45% kcov:50.4 err:0.278% dup:1.46% k:21



(user_data/19ScrqZLdCOI18Kd3Y4e/plot.log.png)

Results

GenomeScope version 1.0

k = 21

| property | min | max |
|-----------------------|------------------|------------------|
| Heterozygosity | 2.44195% | 2.46651% |
| Genome Haploid Length | 1,079,384,847 bp | 1,081,038,339 bp |
| Genome Repeat Length | 350,997,522 bp | 351,535,209 bp |
| Genome Unique Length | 728,387,325 bp | 729,503,130 bp |
| Model Fit | 94.1321% | 97.1487% |
| Read Error Rate | 0.277706% | 0.277706% |

Model

Formula: $y \sim (((2 * (1 - d) * (1 - (1 - r)^k)) + (2 * d * (1 - (1 - r)^k)^2) + (2 * d * ((1 - r)^k) * (1 - (1 - r)^k))) * \text{dnbinom}(x, \text{size} = \text{kmercov}/\text{bias}, \text{mu} = \text{kmercov}) * \text{length} + (((1 - d) * ((1 - r)^k) + (d * (1 - (1 - r)^k)^2)) * \text{dnbinom}(x, \text{size} = \text{kmercov} * 2/\text{bias}, \text{mu} = \text{kmercov} * 2) * \text{length} + (2 * d * ((1 - r)^k) * (1 - (1 - r)^k)) * \text{dnbinom}(x, \text{size} = \text{kmercov} * 3/\text{bias}, \text{mu} = \text{kmercov} * 3) * \text{length} + (d * (1 - r)^{(2 * k)}) * \text{dnbinom}(x, \text{size} = \text{kmercov} * 4/\text{bias}, \text{mu} = \text{kmercov} * 4) * \text{length})$

Parameters:

| | Estimate | Std. Error | t value | Pr(> t) | |
|---------|-----------|------------|---------|----------|-----|
| d | 1.258e-01 | 2.137e-03 | 58.87 | <2e-16 | *** |
| r | 2.454e-02 | 6.139e-05 | 399.79 | <2e-16 | *** |
| kmercov | 5.040e+01 | 1.929e-02 | 2613.16 | <2e-16 | *** |
| bias | 1.456e+00 | 7.547e-03 | 192.88 | <2e-16 | *** |
| length | 8.145e+08 | 1.450e+06 | 561.72 | <2e-16 | *** |

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

Residual standard error: 141100 on 966 degrees of freedom

Number of iterations to convergence: 6

Achieved convergence tolerance: 2.944e-06

[View analysis later](#)

Return to view your results at any time:

<http://genomescope.org/analysis.php?code=19ScrqZLdCOI8Kd3Y4e>

Progress

starting

round 0 trimming to 15 trying 4peak model... converged. score: 17514640674697.4

round 1 trimming to 20 trying 4peak model... converged. score: 17311387539608.2

round 2 trimming to 25 trying 4peak model... converged. score: 16098427644466.7

round 3 trimming to 30 trying 4peak model... converged. score: 13388484217665

done