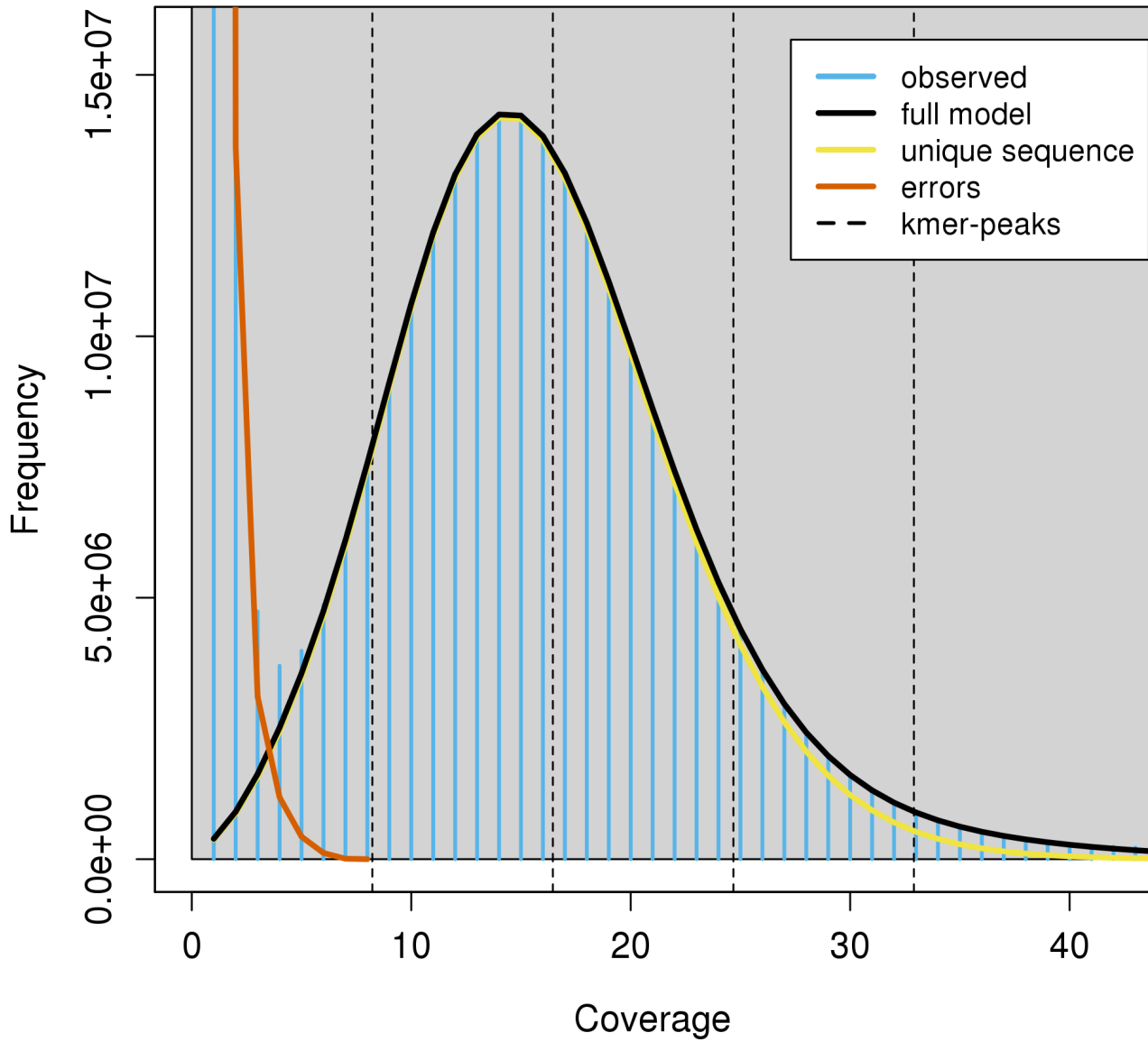


KG_A.japonica

GenomeScope Profile

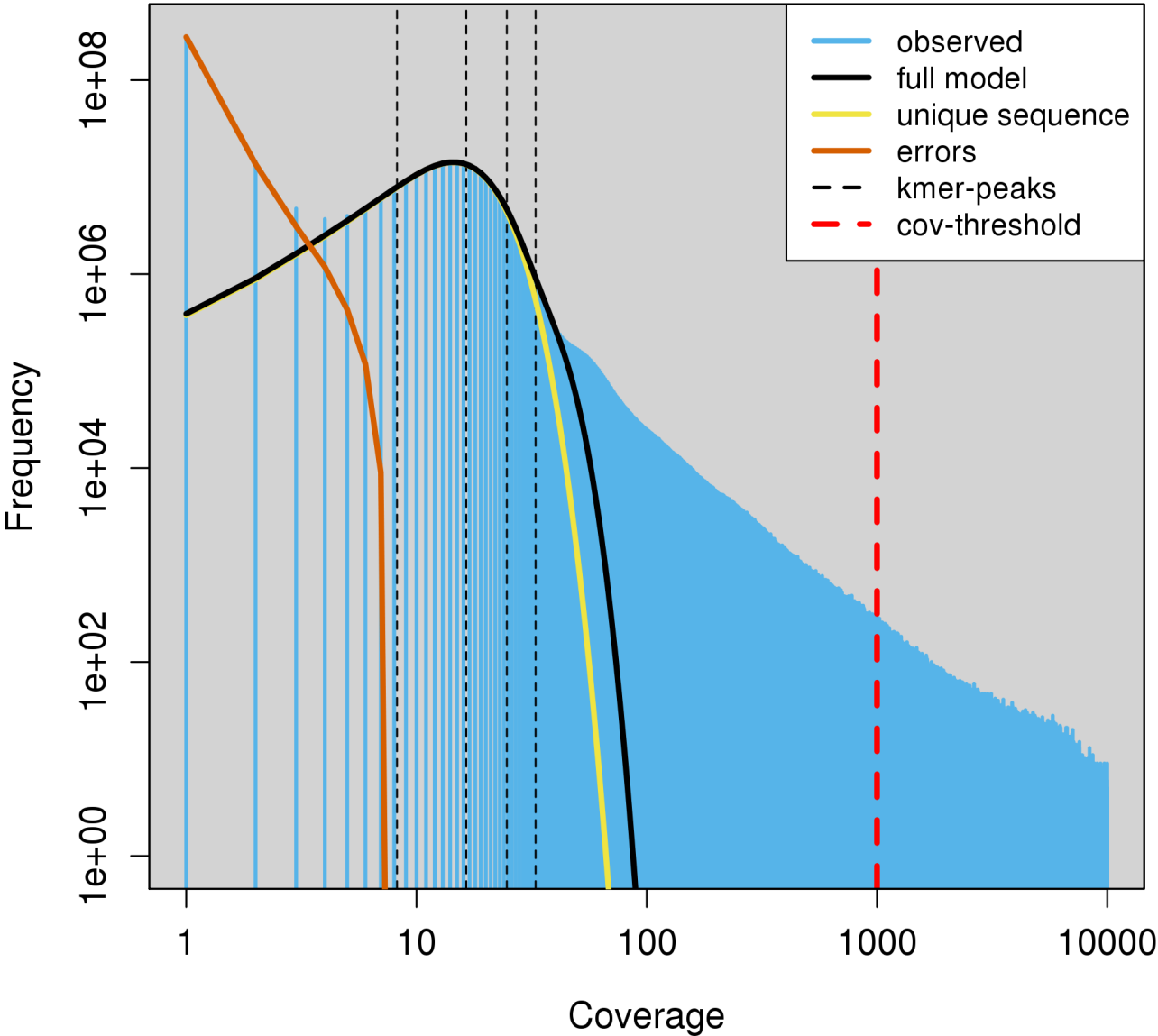
len:271,604,874bp uniq:76.3% het:0.184% kcov:8.23 err:0.225% dup:1.11% k:31



(user_data/NVnqzbpVctKlccSRKrfu/plot.png)

GenomeScope Profile

len:271,604,874bp uniq:76.3% het:0.184% kcov:8.23 err:0.225% dup:1.11% k:31



(user_data/NVnqzbpVctKlccSRKrfu/plot.log.png)

Results

GenomeScope version 1.0		
k = 31		
property	min	max
Heterozygosity	0.172201%	0.19504%
Genome Haploid Length	270,814,072 bp	271,604,874 bp
Genome Repeat Length	64,283,476 bp	64,471,190 bp
Genome Unique Length	206,530,595 bp	207,133,684 bp
Model Fit	96.8744%	99.7354%
Read Error Rate	0.225189%	0.225189%

Model

```

Formula: y ~ (((2 * (1 - d) * (1 - (1 - r)^k)) + (2 * d *
r)^k)^2) +
(2 * d * ((1 - r)^k) * (1 - (1 - r)^k))) * dnbinom(x,
kmercov/bias,
mu = kmercov) * length + (((1 - d) * ((1 - r)^k)) + ((
1 - (1 - r)^k)^2)) * dnbinom(x, size = kmercov * 2/b
mu = kmercov * 2) * length + (2 * d * ((1 - r)^k) * (
(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	3.811e-02	9.290e-04	41.02	<2e-16 ***
r	1.836e-03	5.710e-05	32.16	<2e-16 ***
kmercov	8.226e+00	5.996e-03	1371.82	<2e-16 ***
bias	1.108e+00	9.741e-03	113.71	<2e-16 ***
length	2.150e+08	1.865e+05	1152.63	<2e-16 ***

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

Residual standard error: 19340 on 987 degrees of freedom

Number of iterations to convergence: 8
Achieved convergence tolerance: 2.091e-06

View analysis later

Return to view your results at any time:

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

Progress

starting

round 0 trimming to 4 trying 4peak model... converged. score: 613904454840.962

round 1 trimming to 9 trying 4peak model... converged. score: 369460990887.007

round 2 trimming to 14 trying 4peak model... converged. score: 10270343929066.8

round 3 trimming to 19 trying 4peak model... unconverged

done