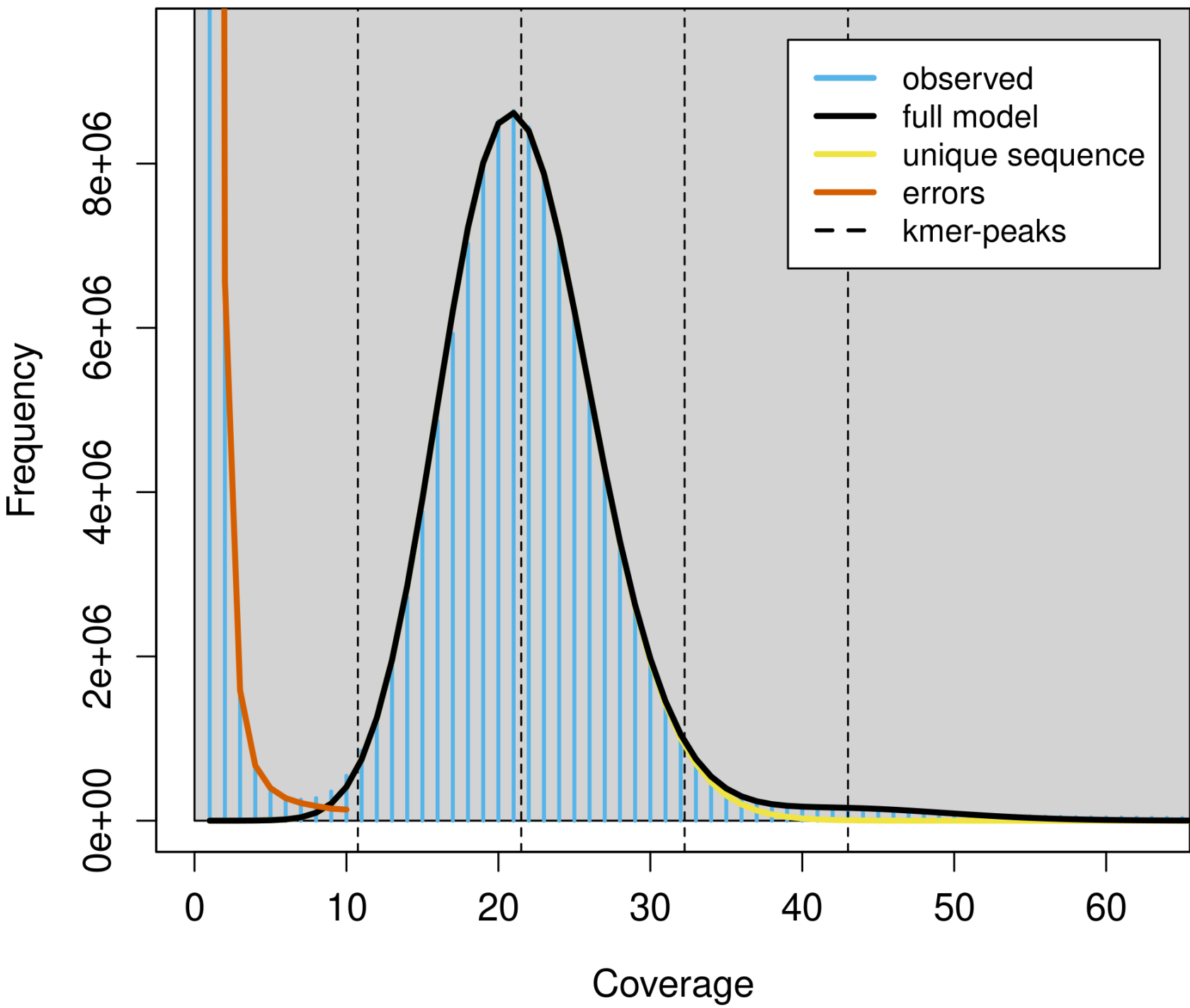


my sample

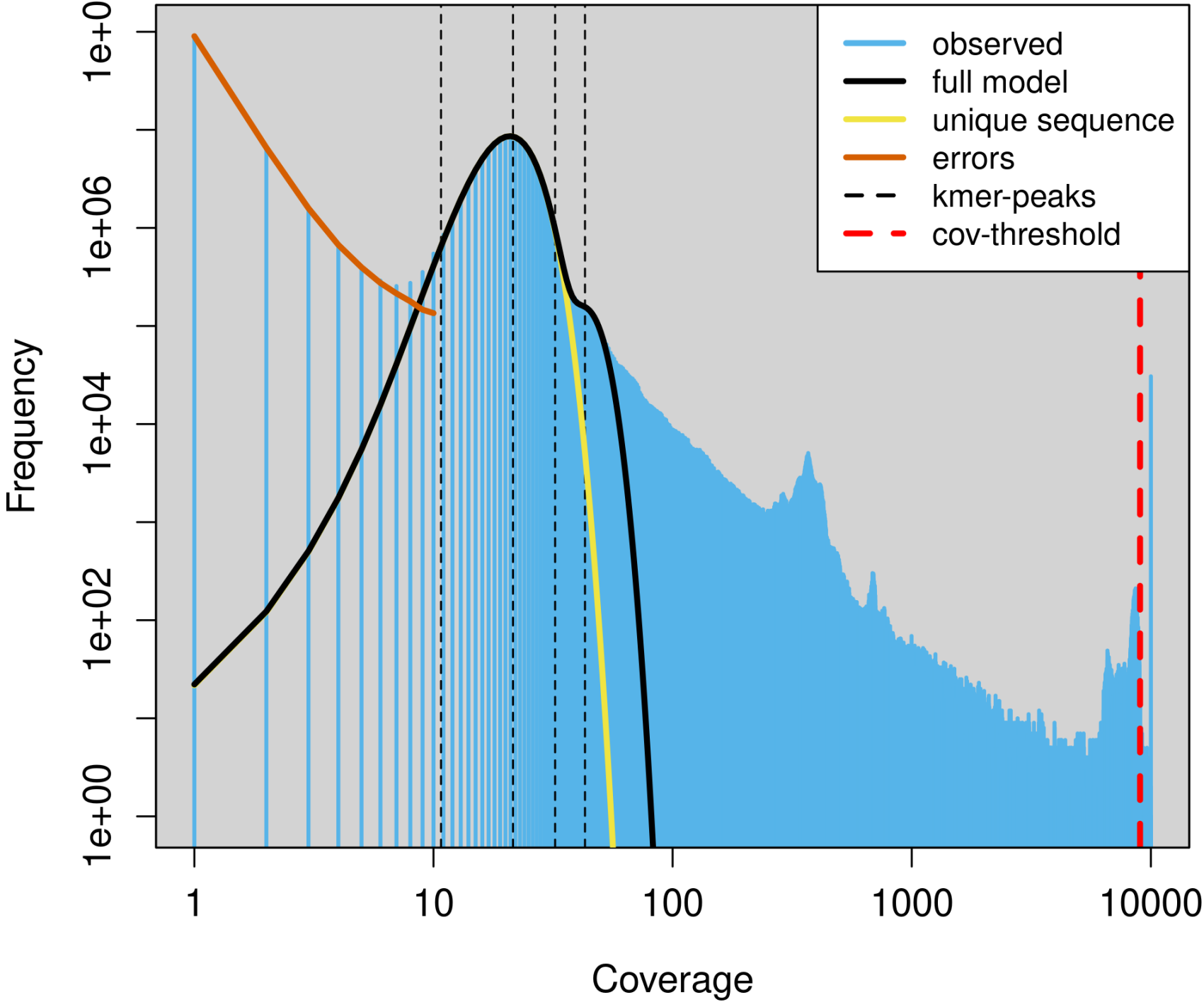
GenomeScope Profile

len:173,058,040bp uniq:61.8%
aa:100% ab:0.001%
kcov:10.8 err:0.151% dup:0.141 k:21 p:2



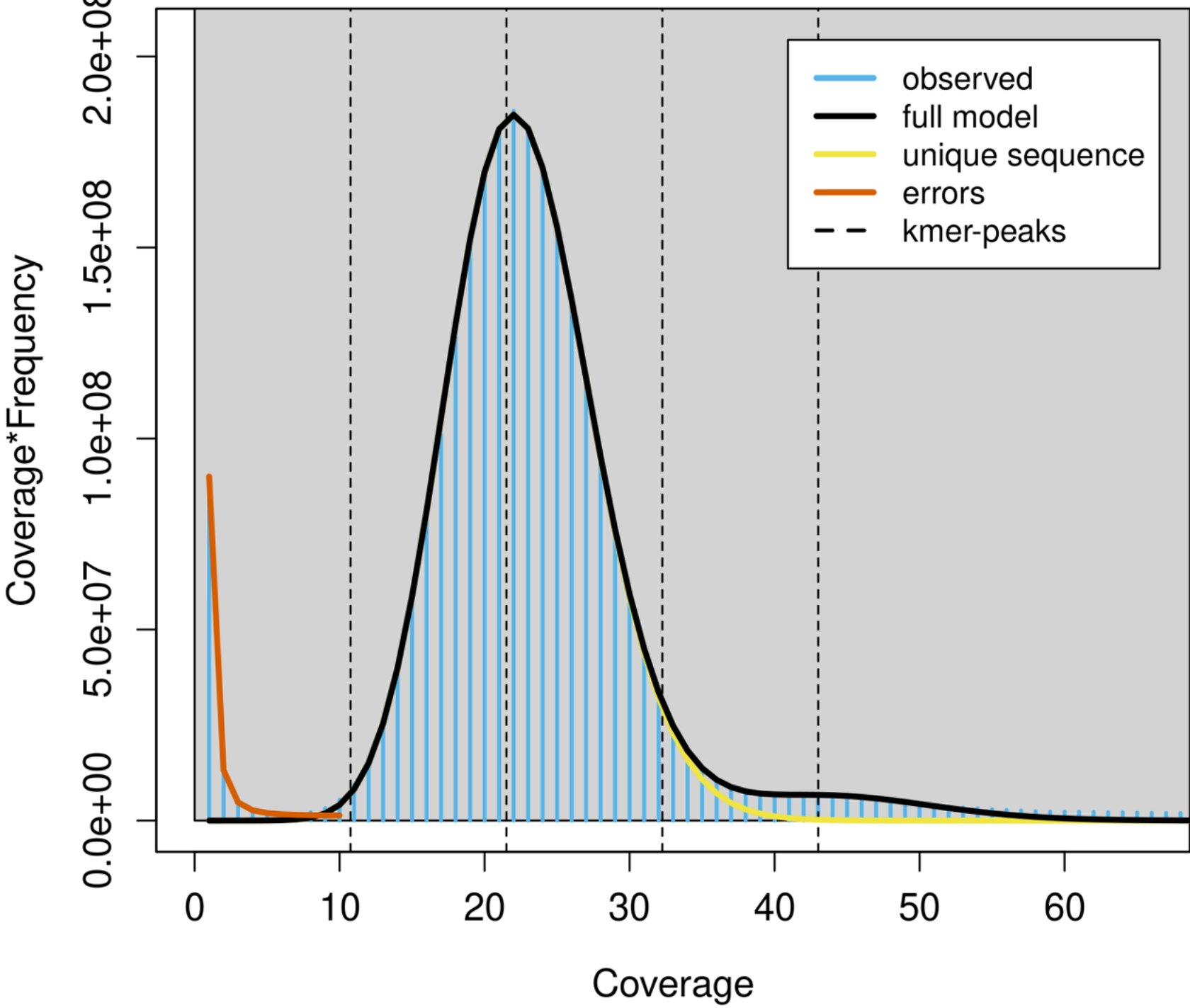
GenomeScope Profile

len:173,058,040bp uniq:61.8%
aa:100% ab:0.001%
kcov:10.8 err:0.151% dup:0.141 k:21 p:2



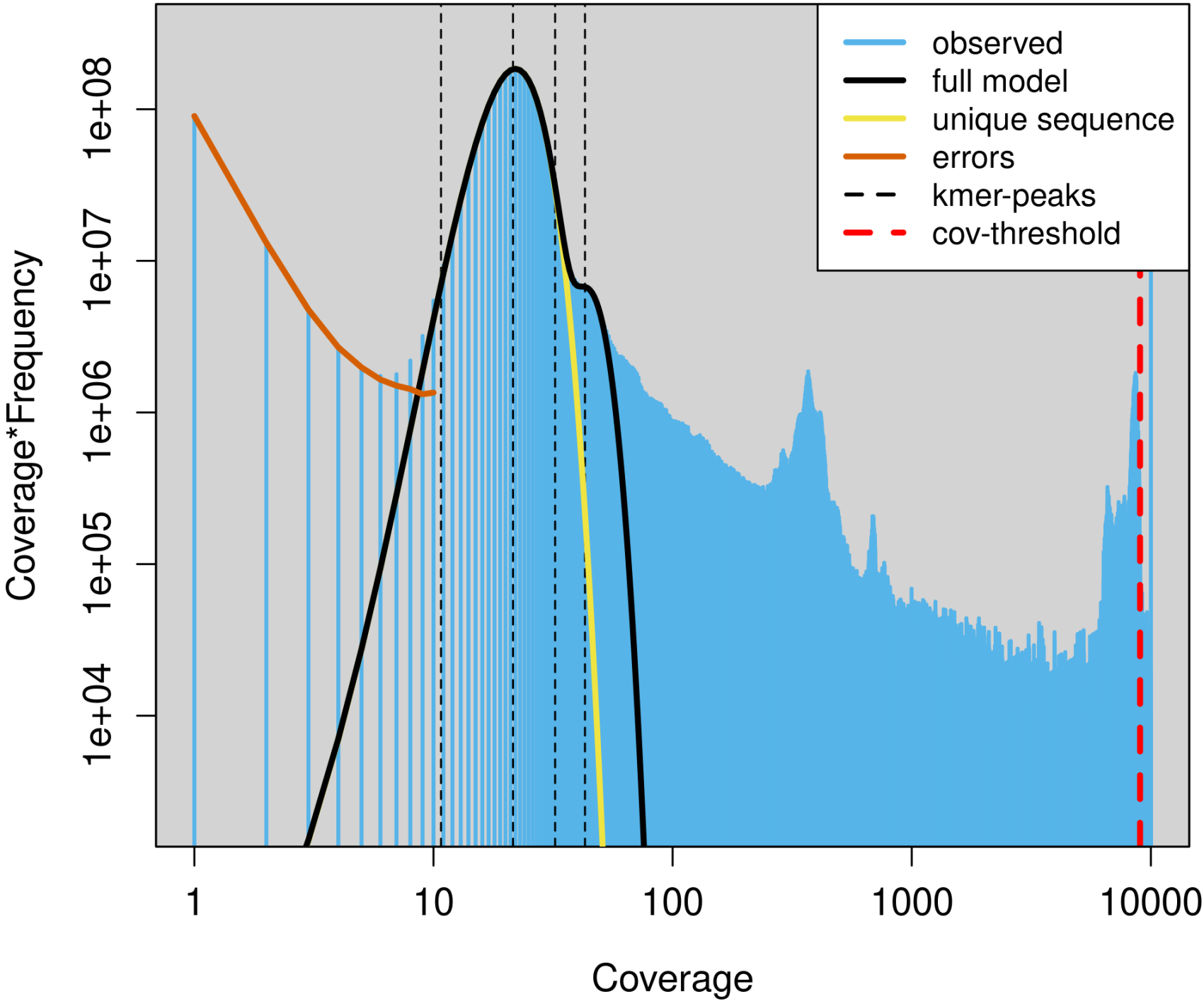
GenomeScope Profile

len:173,058,040bp uniq:61.8%
aa:100% ab:0.001%
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GenomeScope Profile

len:173,058,040bp uniq:61.8%
aa:100% ab:0.001%
kcov:10.8 err:0.151% dup:0.141 k:21 p:2



Results

GenomeScope version 2.0
input file = user_uploads/PCG7En92mHfZ3fQh18UD
output directory = user_data/PCG7En92mHfZ3fQh18UD
p = 2
k = 21

property	min	max
Homozygous (aa)	99.4862%	100%
Heterozygous (ab)	0%	0.51377%
Genome Haploid Length	171,801,248 bp	173,058,040 bp
Genome Repeat Length	65,627,383 bp	66,107,473 bp
Genome Unique Length	106,173,865 bp	106,950,568 bp
Model Fit	63.3386%	98.3903%
Read Error Rate	0.151391%	0.151391%

Model

Formula: $y_{transform} \sim x_{transform_exp} * length * predict2_0(r1, k, d, kmercov, bias, x)$

Parameters:

	Estimate	Std. Error	t value	Pr(> t)
d	2.440e-02	9.223e-04	26.460	< 2e-16 ***
r1	1.000e-05	2.564e-03	0.004	0.997
kmercov	1.075e+01	1.959e-02	548.793	< 2e-16 ***
bias	1.407e-01	1.704e-02	8.257	2.69e-16 ***
length	1.092e+08	4.767e+06	22.912	< 2e-16 ***

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

Residual standard error: 389800 on 1995 degrees of freedom

Number of iterations to convergence: 21
Achieved convergence tolerance: 1.49e-08

View analysis later

Return to view your results at any time:

<http://genomescope.org/genomescope2.0/analysis.php?code=PCG7En92mHfZ3fQh18UD>

Progress

starting

round 0 trimming to 6 trying 2p peak model... converged. score: 1059894422140061

round 1 trimming to 11 trying 2p peak model... converged. score: 1059644166951790

round 2 trimming to 16 trying 2p peak model... converged. score: 1066037748404818

round 3 trimming to 21 trying 2p peak model... converged. score: 1100692509086466

done