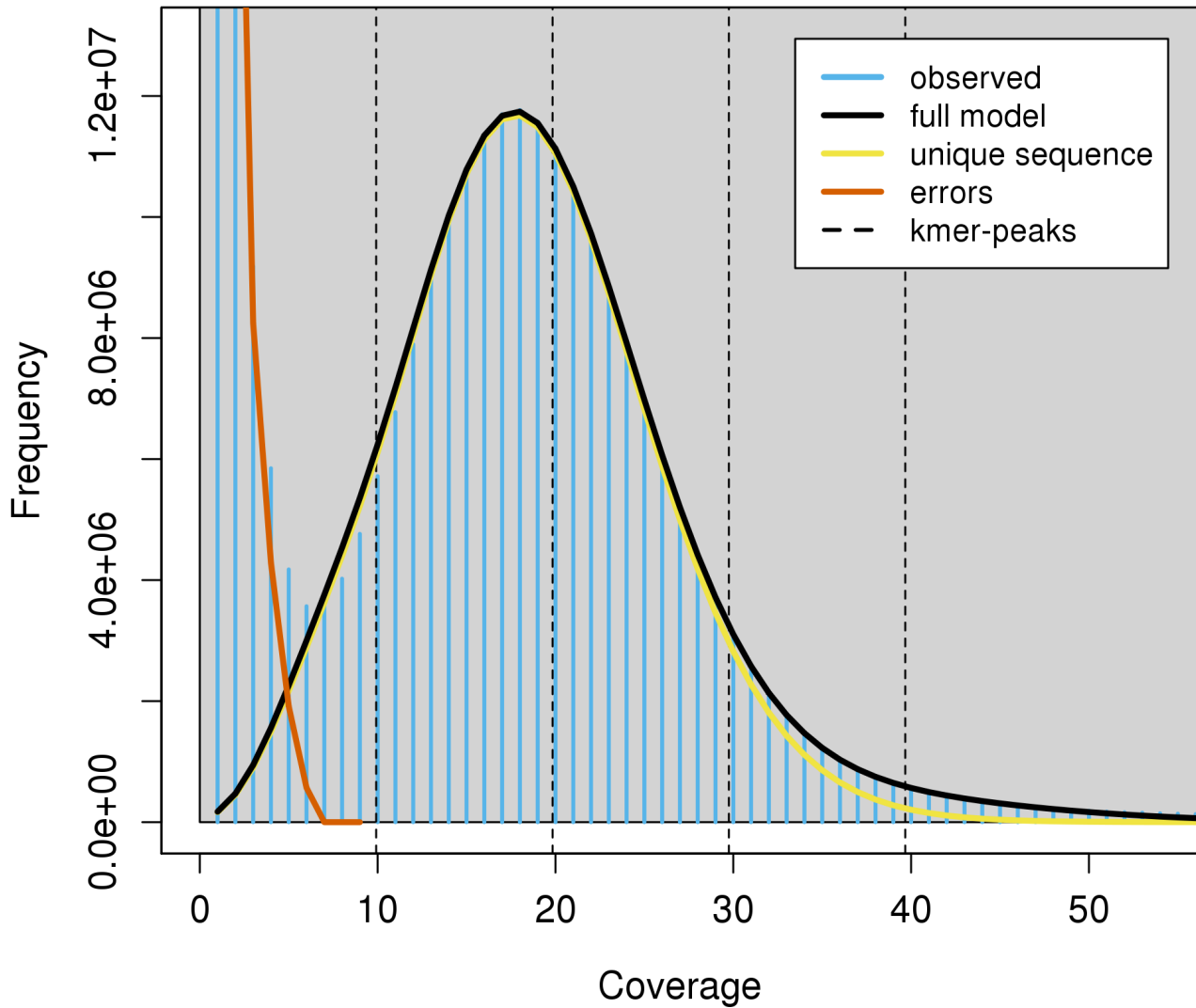


AM_Ajaponica_kmer21

GenomeScope Profile

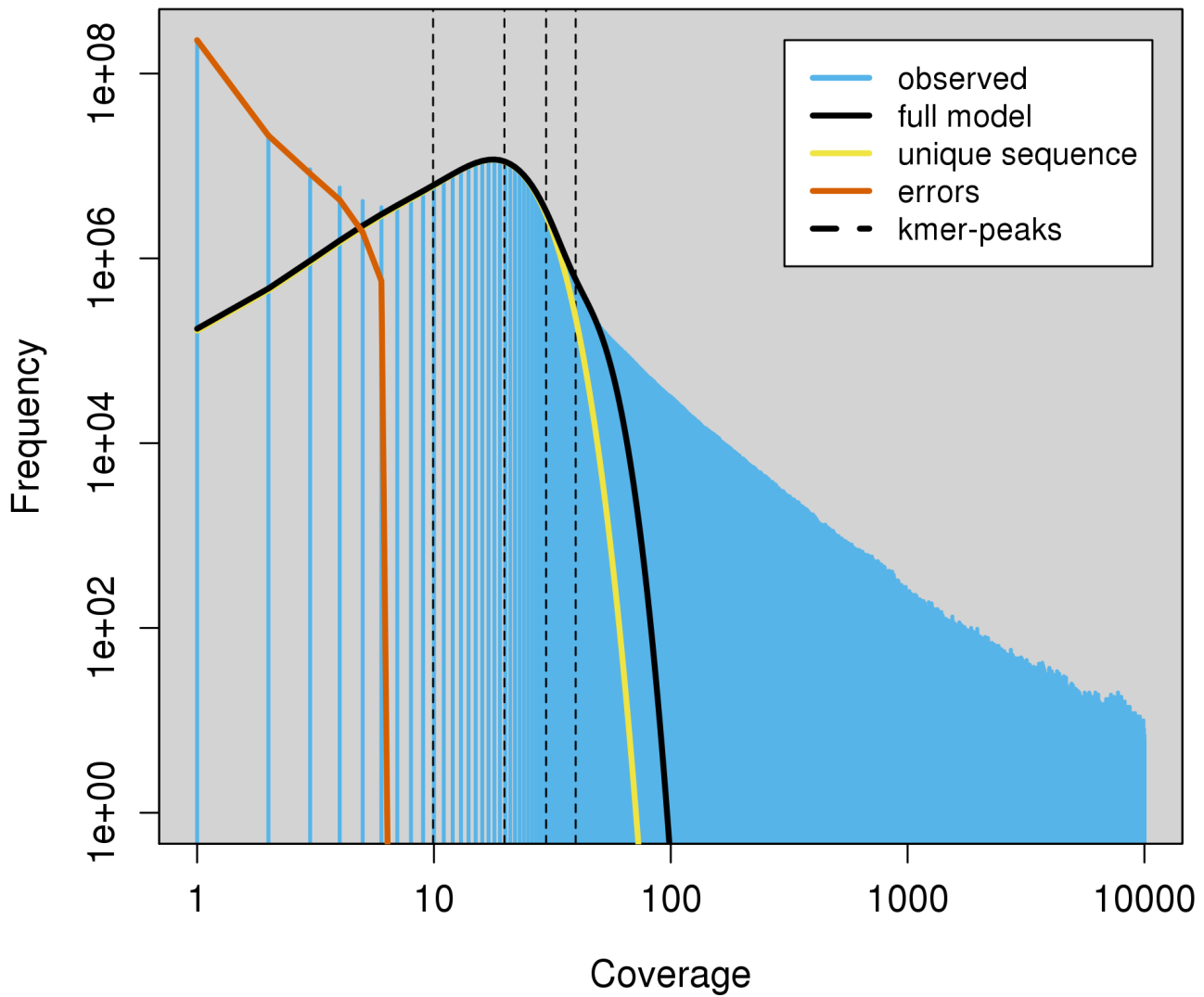
len:284,109,951bp uniq:67%
aa:99.6% ab:0.401%
kcov:9.92 err:0.27% dup:1.03 k:21 p:2



(user_data/ULemk0pi0OnvGbcEFuv/linear_plot.png)

GenomeScope Profile

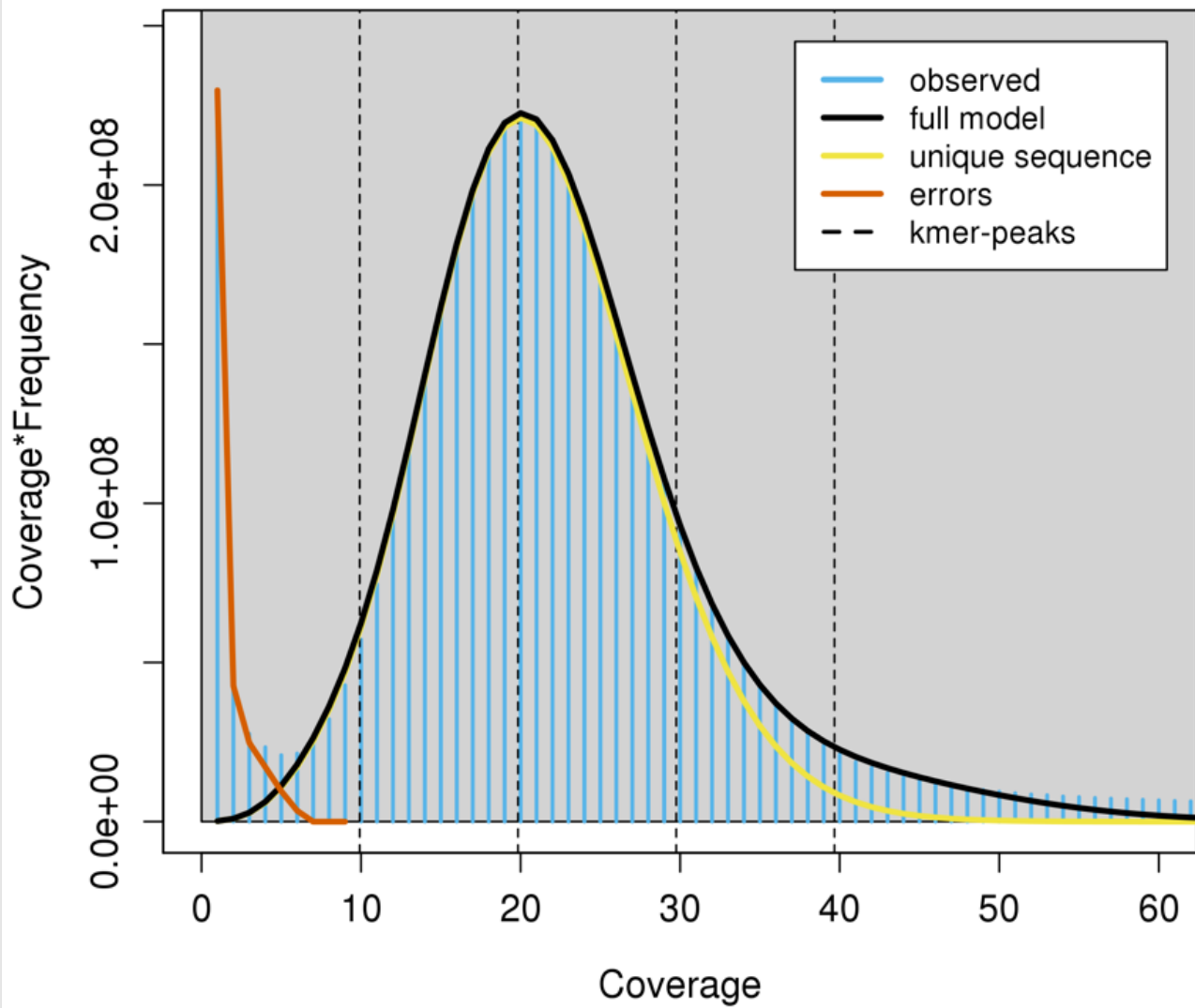
len:284,109,951bp uniq:67%
aa:99.6% ab:0.401%
kcov:9.92 err:0.27% dup:1.03 k:21 p:2



(user_data/ULemyk0pi0OnvGbcEFuv/log_plot.png)

GenomeScope Profile

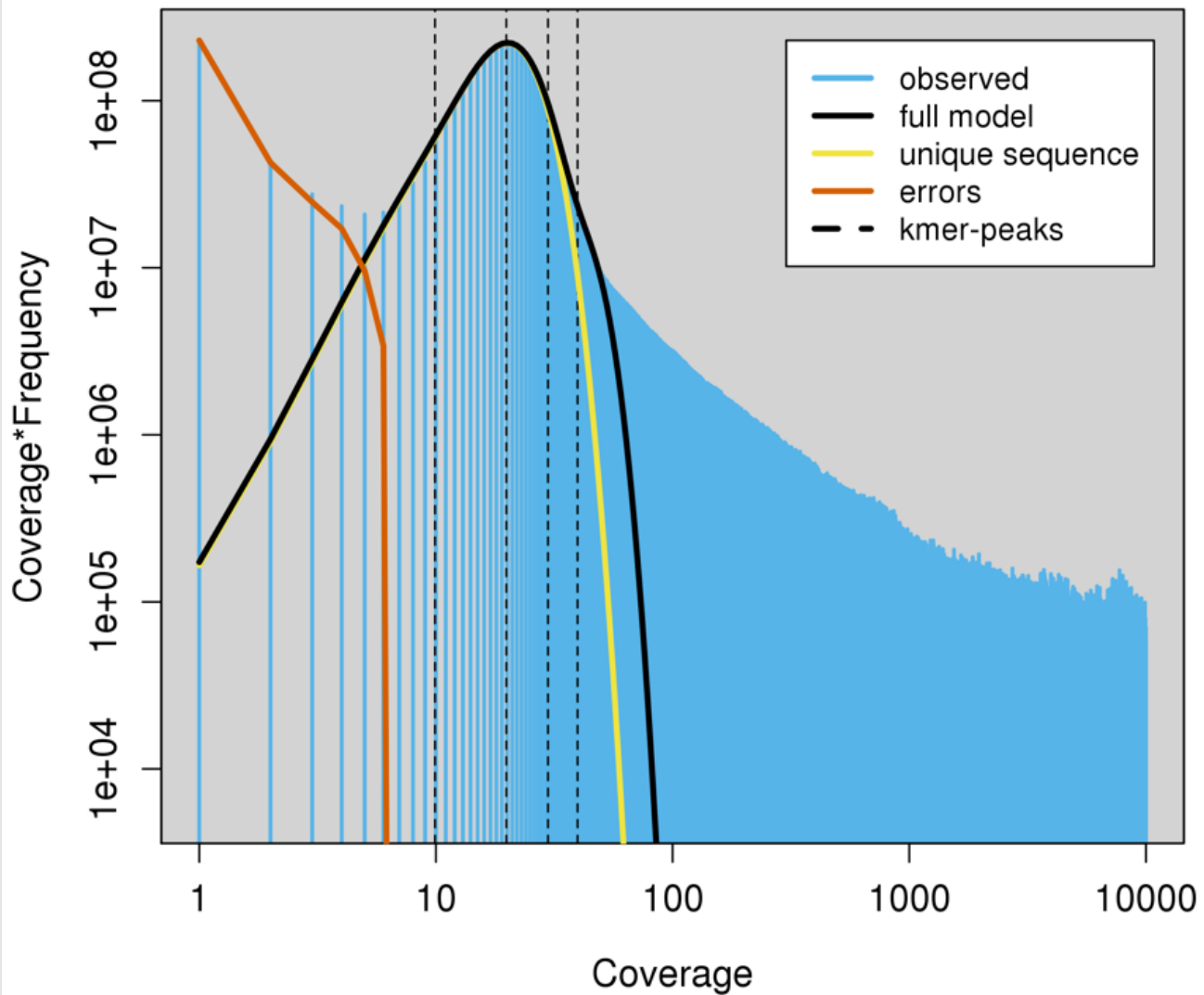
len:284,109,951bp uniq:67%
aa:99.6% ab:0.401%
kcov:9.92 err:0.27% dup:1.03 k:21 p:2



(user_data/ULemk0pi0OnvGbcEFuv/transformed_linear_plot.png)

GenomeScope Profile

len:284,109,951bp uniq:67%
aa:99.6% ab:0.401%
kcov:9.92 err:0.27% dup:1.03 k:21 p:2



(user_data/ULemyk0pi0OnvGbcEFuv/transformed_log_plot.png)

Results

Model

GenomeScope version 2.0
input file = user_uploads/ULemyk0pi0OnvGbcEFuv
output directory = user_data/ULemyk0pi0OnvGbcEFuv
p = 2
k = 21

property	min	max
Homozygous (aa)	99.4539%	99.7447%
Heterozygous (ab)	0.255329%	0.546144%
Genome Haploid Length	280,087,408 bp	284,109,951 bp
Genome Repeat Length	92,534,753 bp	93,863,713 bp
Genome Unique Length	187,552,656 bp	190,246,239 bp
Model Fit	71.6194%	98.8866%
Read Error Rate	0.270286%	0.270286%

Formula: y_transform ~ x^transform_exp * length * predict.kmercov, bias, x)

Parameters:

	Estimate	Std. Error	t value	Pr(> t)
d	4.539e-02	1.321e-03	34.369	< 2e-16 ***
r1	4.007e-03	7.270e-04	5.512	4.01e-08 ***
kmercov	9.918e+00	3.536e-02	280.518	< 2e-16 ***
bias	1.030e+00	2.842e-02	36.228	< 2e-16 ***
length	1.979e+08	6.682e+05	296.130	< 2e-16 ***

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

Residual standard error: 897800 on 1995 degrees of freedom

Number of iterations to convergence: 7
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=ULemyk0pi0OnvGbcEFuv>

Progress

starting

round 0 trimming to 5 trying 2p peak model... converged. score: 1675139648879292

round 1 trimming to 10 trying 2p peak model... converged. score: 1654904031313456

round 2 trimming to 15 trying 2p peak model... converged. score: 1762391908864047

round 3 trimming to 20 trying 2p peak model... converged. score: 1504433504963350

done