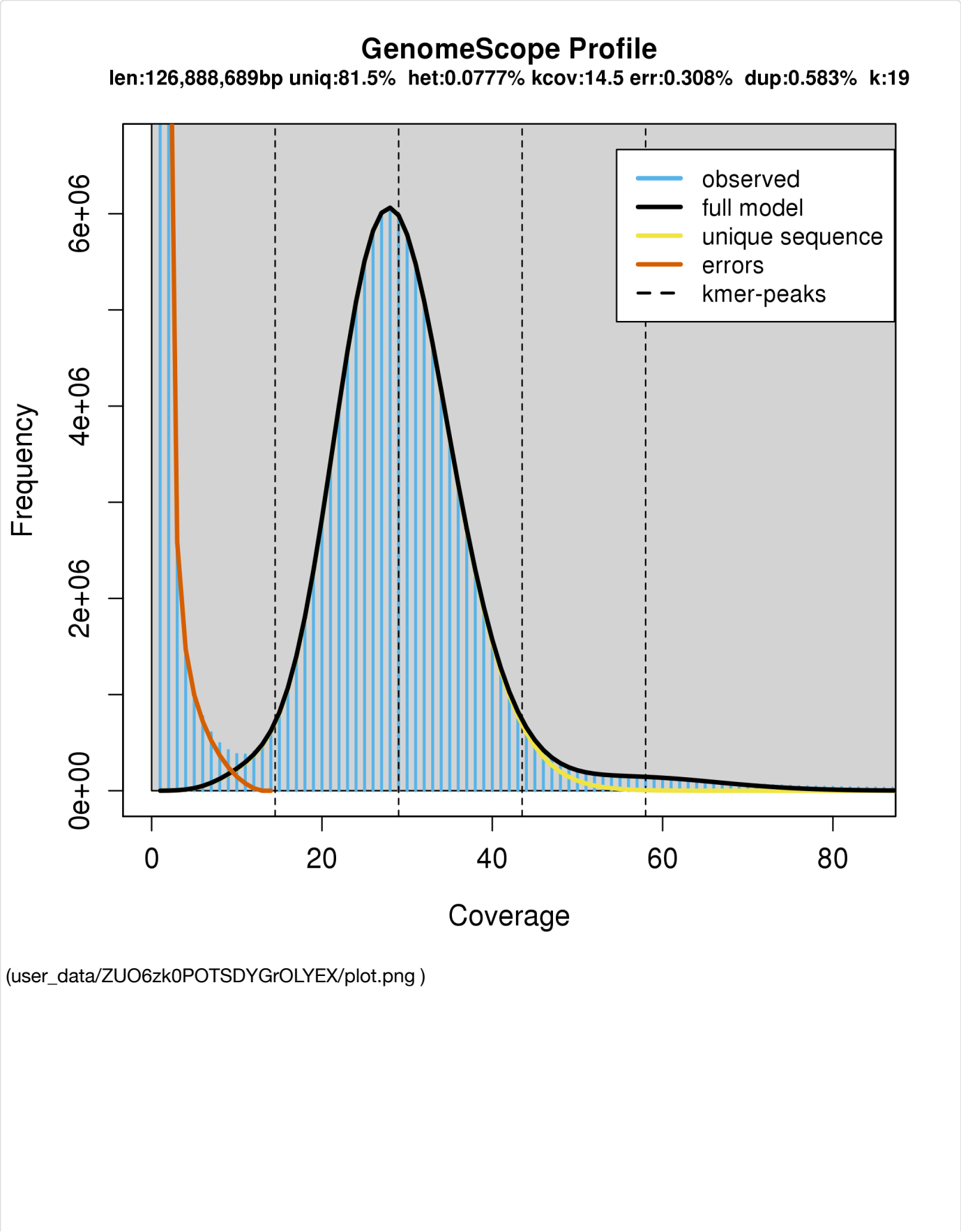
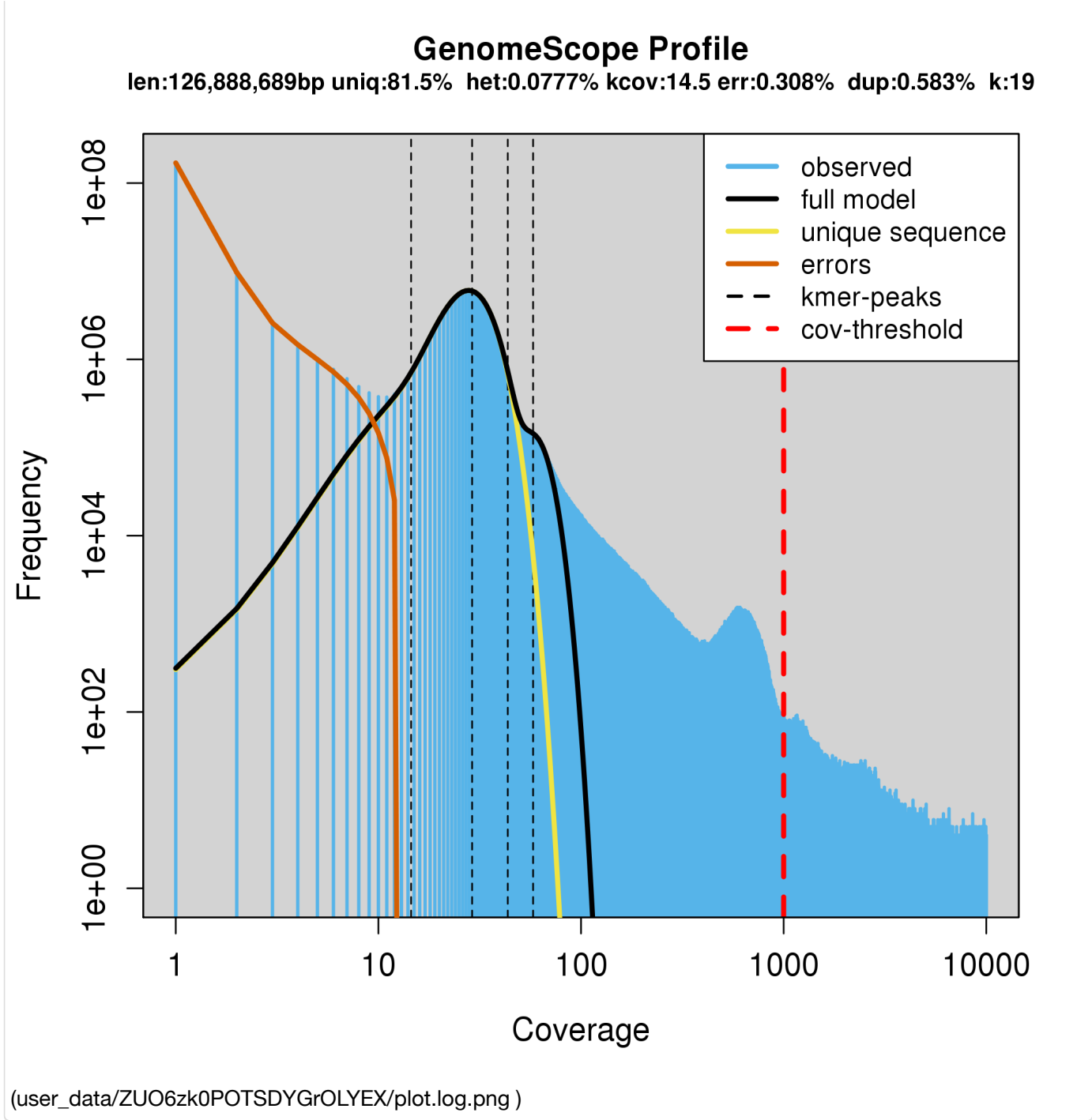


my sample





Results

GenomeScope version 1.0
k = 19

property	min	max
Heterozygosity	0.0746863%	0.080733%
Genome Haploid Length	126,841,320 bp	126,888,689 bp
Genome Repeat Length	23,505,821 bp	23,514,600 bp
Genome Unique Length	103,335,498 bp	103,374,090 bp
Model Fit	97.8553%	99.6896%
Read Error Rate	0.308184%	0.308184%

Model

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

Parameters:

	Estimate	Std. Error	t value	Pr(> t)
d	3.193e-02	2.676e-04	119.33	<2e-16 ***
r	7.771e-04	1.512e-05	51.41	<2e-16 ***
kmercov	1.450e+01	1.354e-03	10712.76	<2e-16 ***
bias	5.829e-01	1.484e-03	392.88	<2e-16 ***
length	1.068e+08	3.771e+04	2831.01	<2e-16 ***

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

Residual standard error: 4793 on 980 degrees of freedom

Number of iterations to convergence: 4

Achieved convergence tolerance: 7.227e-06

View analysis later

Return to view your results at any time:

<http://genomescope.org/analysis.php?code=ZUO6zk0POTSDYGrOLYEX>

Progress

starting

round 0 trimming to 11 trying 4peak model... converged. score: 24324456629.3571

round 1 trimming to 16 trying 4peak model... converged. score: 23120861302.3564

round 2 trimming to 21 trying 4peak model... converged. score: 59984964544.6909

round 3 trimming to 26 trying 4peak model... converged. score: 187653457766.981

done