GenomeScope Profile

len:447,271,428bp uniq:62.2%
aa:98.8% ab:1.2%
kcov:40 err:0.234% dup:0.48 k:21 p:2

(user_data/mgblRVJABhwmhm7NHQLp/linear_plot.png)

GenomeScope Profile

len:447,271,428bp uniq:62.2%
aa:98.8% ab:1.2%
kcov:40 err:0.234% dup:0.48 k:21 p:2
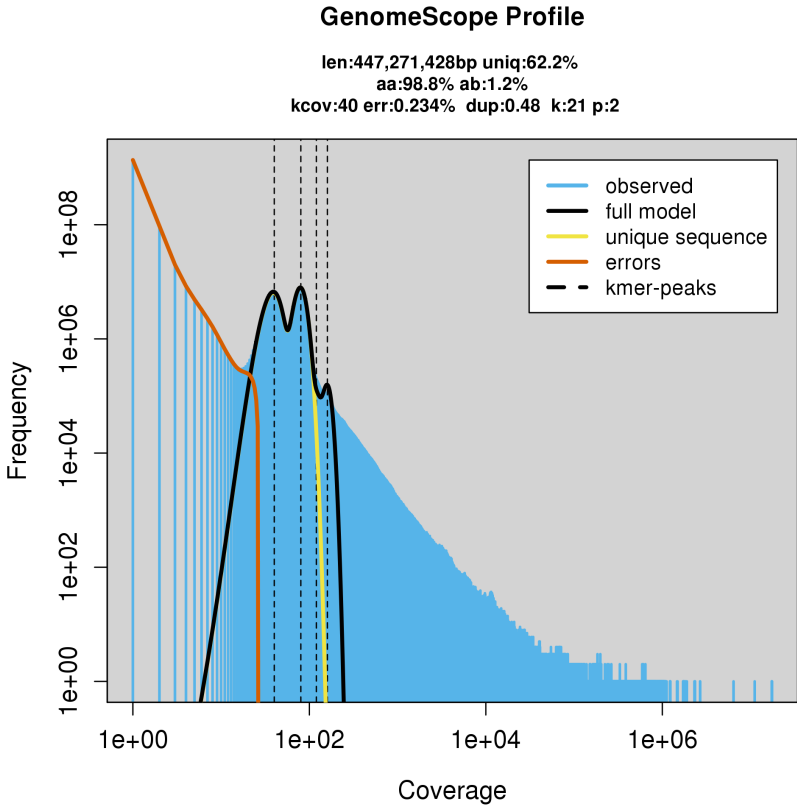
(user_data/mgblRVJABhwmhm7NHQLp/log_plot.png)

GenomeScope Profile

len:447,271,428bp uniq:62.2%
aa:98.8% ab:1.2%
kcov:40 err:0.234% dup:0.48 k:21 p:2
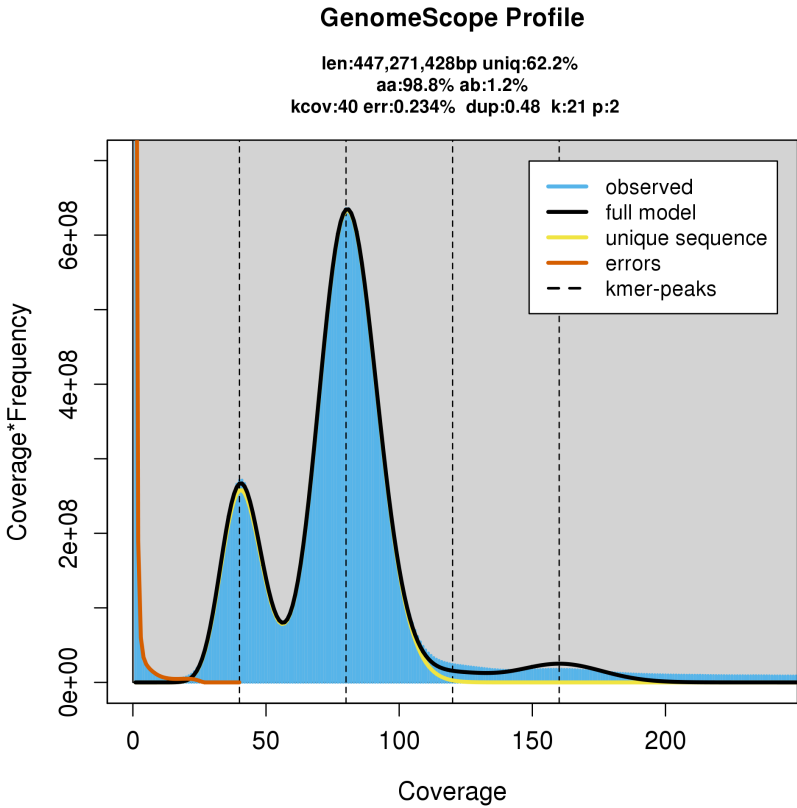

(user_data/mgblRVJABhwmhm7NHQLp/transformed_linear_plot.png)

GenomeScope Profile

len:447,271,428bp uniq:62.2%
aa:98.8% ab:1.2%
kcov:40 err:0.234% dup:0.48 k:21 p:2
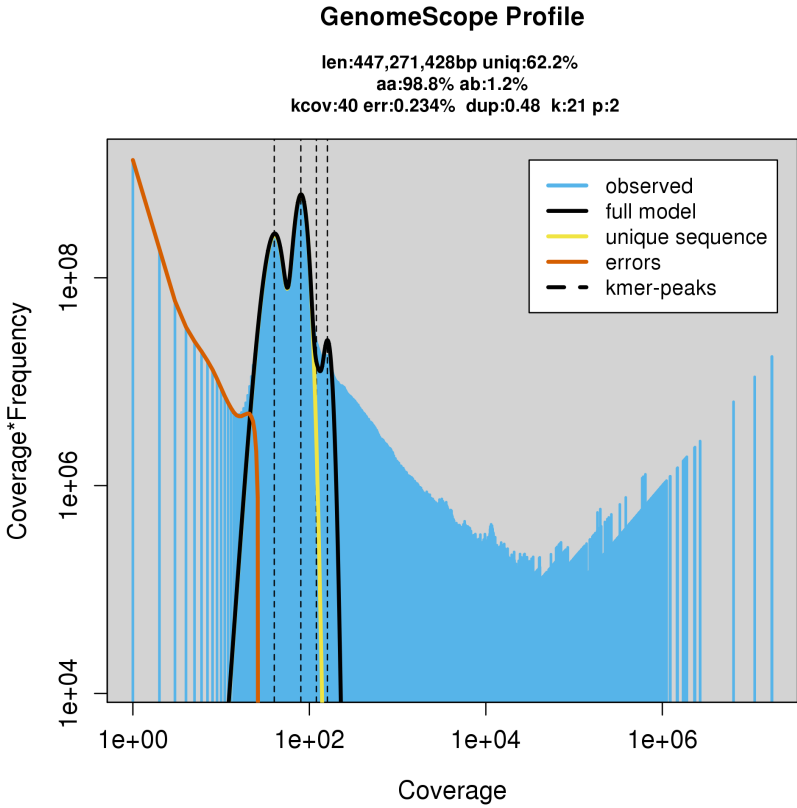
(user_data/mgblRVJABhwmhm7NHQLp/transformed_log_plot.png)

Results

```
GenomeScope version 2.0
input file = user_uploads/mgblRVJABhwmhm7NHQLp
output directory = user_data/mgblRVJABhwmhm7NHQLp
p = 2
k = 21

property                        min              max
Homozygous (aa)                 98.7942%         98.8095%
Heterozygous (ab)               1.19051%         1.20584%
Genome Haploid Length           446,862,409 bp   447,271,428 bp
Genome Repeat Length            168,786,884 bp   168,941,377 bp
Genome Unique Length            278,075,525 bp   278,330,051 bp
Model Fit                       65.0376%         96.9746%
Read Error Rate                 0.234341%        0.234341%
```

Model

```
Formula: y_transform ~ x^transform_exp * length * predict2_0(r1, k, d,
    kmercov, bias, x)

Parameters:
          Estimate Std. Error t value Pr(>|t|)
d        3.451e-02  7.377e-04   46.79   <2e-16 ***
r1       1.198e-02  3.832e-05  312.65   <2e-16 ***
kmercov 4.002e+01  9.154e-03 4372.10   <2e-16 ***
bias     4.802e-01  4.369e-03  109.91   <2e-16 ***
length  2.881e+08  4.142e+05  695.71   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3301000 on 1995 degrees of freedom

Number of iterations to convergence: 5
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=mgblRVJABhwmhm7NHQLp

Progress

starting

round 0 trimming to 15 trying 2p peak model... converged. score: 25495889625800224

round 1 trimming to 20 trying 2p peak model... converged. score: 25495816345774840

round 2 trimming to 25 trying 2p peak model... converged. score: 25495491329747476

round 3 trimming to 30 trying 2p peak model... converged. score: 25495909870729340

done