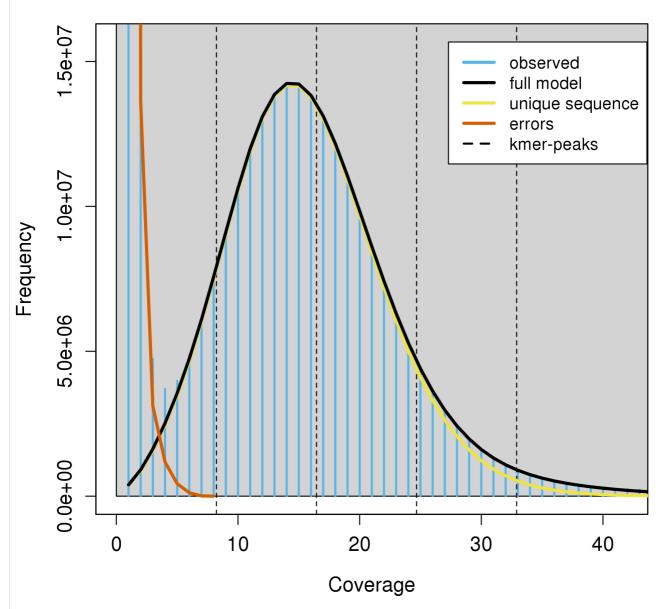
KG_A.japonica_km31

GenomeScope Profile

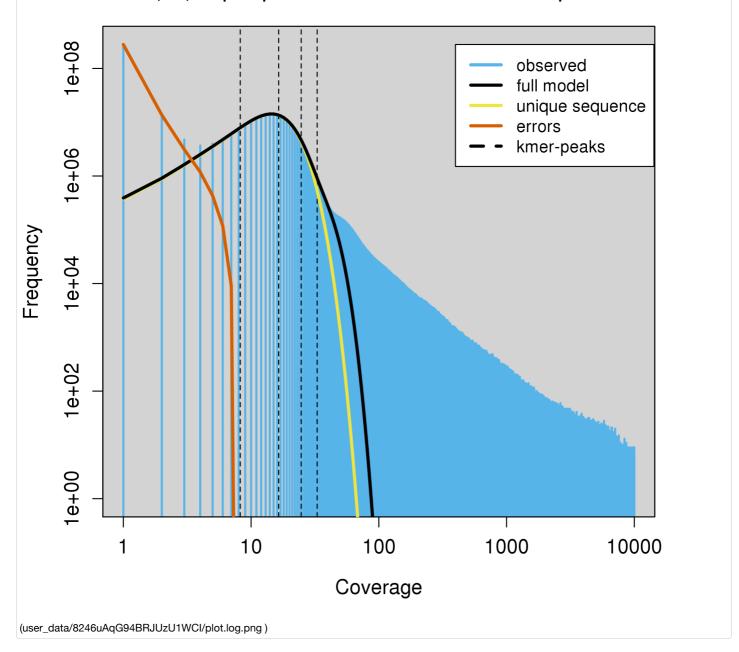
len:313,461,456bp uniq:66% het:0.184% kcov:8.23 err:0.196% dup:1.11% k:31



(user_data/8246uAqG94BRJUzU1WCI/plot.png)

GenomeScope Profile

len:313,461,456bp uniq:66% het:0.184% kcov:8.23 err:0.196% dup:1.11% k:31





GenomeScope version 1.0

k = 31

property
Heterozygosity
Genome Haploid Length
Genome Repeat Length
Genome Unique Length
Model Fit
Read Error Rate

min 0.180016% 313,173,088 bp 106,436,530 bp 206,736,559 bp 96.7638% 0.195742%

max 0.187225% 313,461,456 bp 106,534,536 bp 206,926,921 bp 99.7354% 0.195742%

Model

```
Formula: y \sim (((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 - r)^k))
                  (1 - (1 - r)^k)^2) * dnbinom(x, size = kmercov * 2/b mu = kmercov * 2) * length + (2 * d * ((1 - r)^k) * (
                  \begin{array}{lll} & \text{find} & -\text{kine Fcov} & 2) & \text{Fength} + \left(2 & \text{d.s.} \left((1-1) & \text{k}\right)\right) & \\ & \left(1-r\right)^{k}\right) & \text{dnbinom}(x, \text{size} = \text{kmercov} & 3/\text{bias}, \text{mu} : \\ & 3) & \text{length} + \left(d & \left(1-r\right)^{k}\right) & \text{dnbinom}(x, \text{size} \\ & 4/\text{bias}, \text{mu} = \text{kmercov} & 4\right) & \text{length}) \end{array}
Parameters:
                                        Estimate Std. Error t value Pr(>|t|)
d 3.811e-02 2.932e-04 130.0 r 1.836e-03 1.802e-05 101.9 kmercov 8.226e+00 1.893e-03 4346.1 bias 1.108e+00 3.075e-03 360.3
                                                                                                                                                                                     <2e-16 ***
                                                                                                                                                                                    <2e-16 ***
                                                                                                                                                                                  <2e-16 ***
                                                                                                                                                                                    <2e-16 ***
length 2.150e+08 5.888e+04 3651.7 <2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
Residual standard error: 6104 on 9907 degrees of freedom
Number of iterations to convergence: 8
Achieved convergence tolerance: 2.691e-06
```

View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=8246uAqG94BRJUzU1WCI

Progress

starting

round 0 trimming to 4 trying 4peak model... converged. score: 613926278506.121 round 1 trimming to 9 trying 4peak model... converged. score: 369481626357.766 round 2 trimming to 14 trying 4peak model... converged. score: 10270676965048.9 round 3 trimming to 19 trying 4peak model... unconverged done