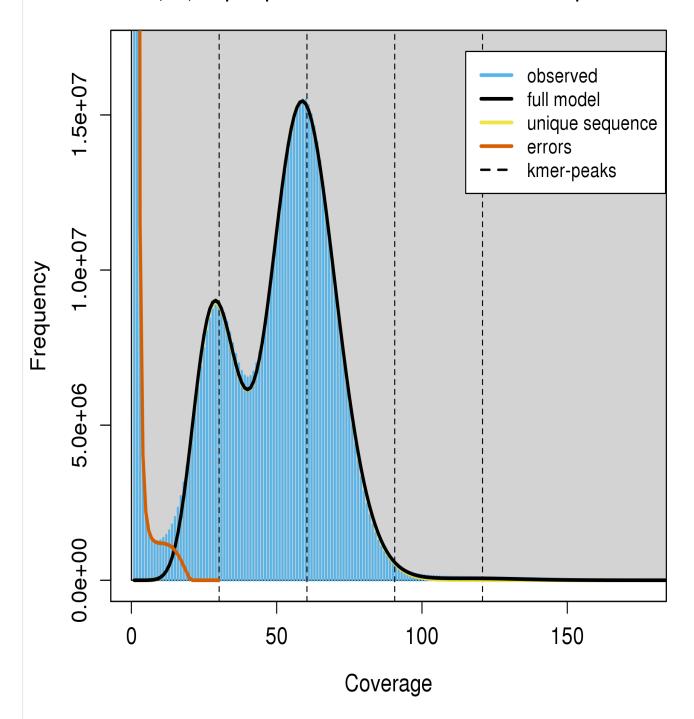
Goy_ssl_decontam

1 of 5

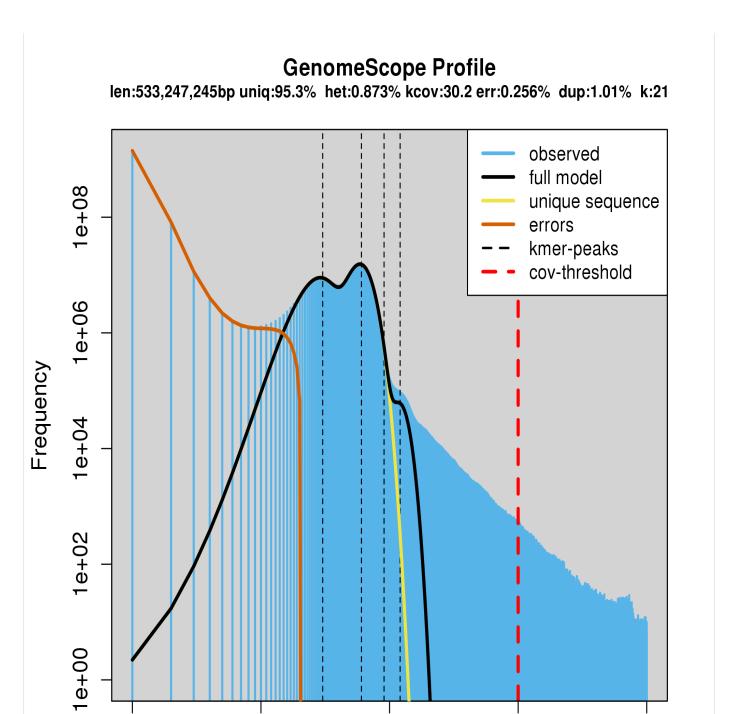
GenomeScope Profile

len:533,247,245bp uniq:95.3% het:0.873% kcov:30.2 err:0.256% dup:1.01% k:21



 $(user_data/GtcmGEsUFzCZjnuqRQE9/plot.png\)$

2 of 5 9/15/2021, 1:57 PM



(user_data/GtcmGEsUFzCZjnuqRQE9/plot.log.png)

10

Results

3 of 5 9/15/2021, 1:57 PM

100

Coverage

1000

10000

```
GenomeScope version 1.0
k = 21
                                     min
property
                                                             max
                                      0.869466%
                                                            0.877487%
Heterozygosity
                                   0.869466% 0.877487% 532,667,711 bp 533,247,245 bp 25,218,558 bp 25,245,996 bp 507,449,153 bp 508,001,249 bp
Genome Haploid Length
Genome Repeat Length
Genome Unique Length
Model Fit
                                     96.5314%
                                                            97.1227%
Read Error Rate
                                      0.256321%
                                                           0.256321%
```

Model

```
Formula: y \sim (((2 * (1 - d) * (1 - (1 - r)^k)) + (2 * d * (1 - (1 - r)^k))))
r)^k)^2 +
    (2 * d * ((1 - r)^k) * (1 - (1 - r)^k))) * dnbinom(x, size =
kmercov/bias,
   mu = kmercov) * length + (((1 - d) * ((1 - r)^k)) + (d * d)
    (1 - (1 - r)^k)^2) * dnbinom(x, size = kmercov * 2/bias,
    mu = kmercov * 2) * length + (2 * d * ((1 - r)^k) * (1 - r)^k) * (1 - r)^k
    (1 - r)^k)) * dnbinom(x, size = kmercov * 3/bias, mu = kmercov *
    3) * length + (d * (1 - r)^{(2 * k)}) * dnbinom(x, size = kmercov *
    4/bias, mu = kmercov * 4) * length)
Parameters:
        Estimate Std. Error t value Pr(>|t|)
        6.395e-03 1.138e-03 5.621 2.48e-08 ***
      8.735e-03 2.005e-05 435.591 < 2e-16 ***
kmercov 3.021e+01 8.212e-03 3678.529 < 2e-16 ***
bias 1.011e+00 4.719e-03 214.170 < 2e-16 ***
length 5.109e+08 6.196e+05 824.513 < 2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 64290 on 977 degrees of freedom
Number of iterations to convergence: 6
Achieved convergence tolerance: 5.616e-06
```

View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=GtcmGEsUFzCZjnuqRQE9

Progress

starting

4 of 5 9/15/2021, 1:57 PM

round 0 trimming to 9 trying 4peak model... converged. score: 4270712947814.61 round 1 trimming to 14 trying 4peak model... converged. score: 4129845800509.25 round 2 trimming to 19 trying 4peak model... converged. score: 3963096418457.89 round 3 trimming to 24 trying 4peak model... converged. score: 3985218647758.91 done

5 of 5 9/15/2021, 1:57 PM