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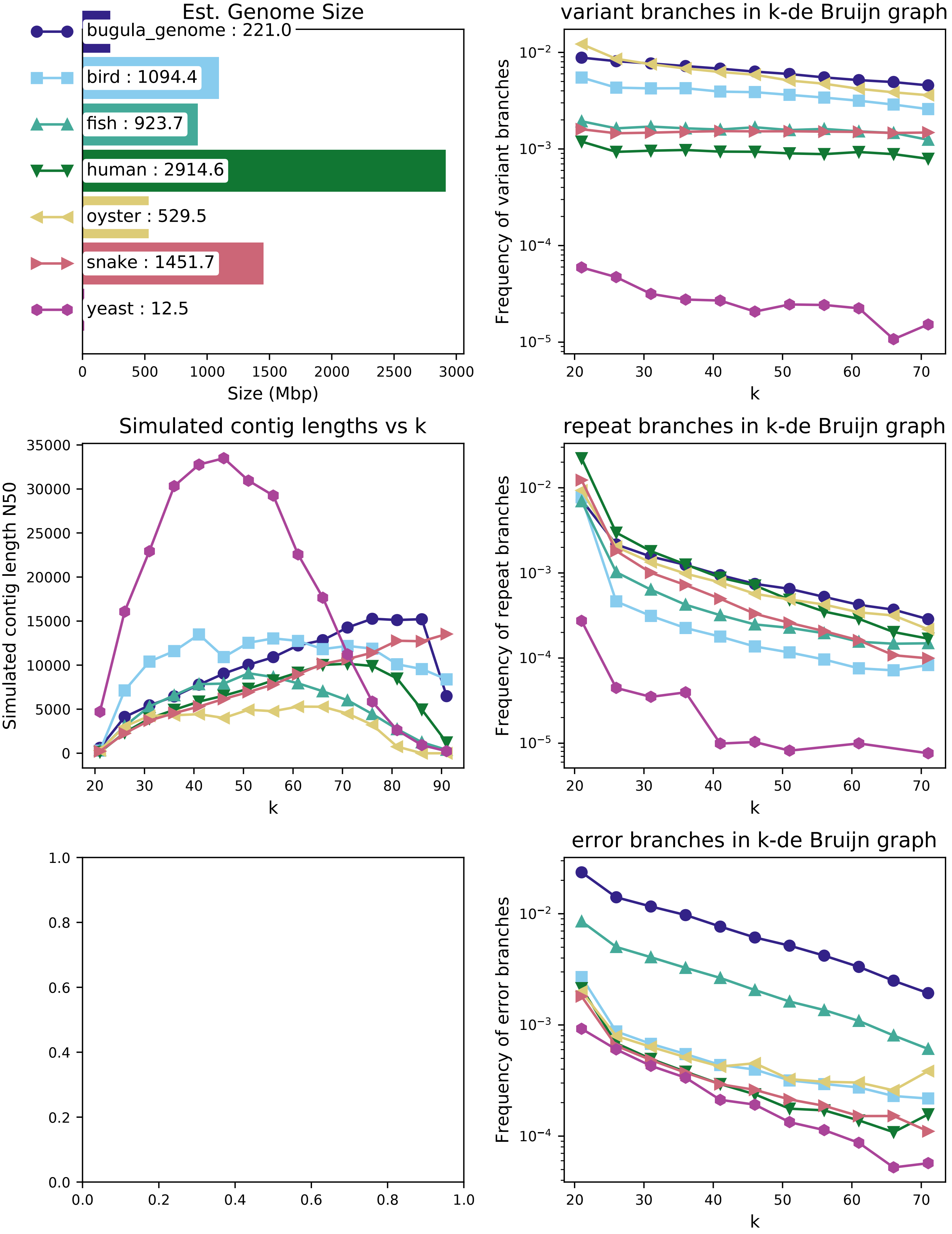
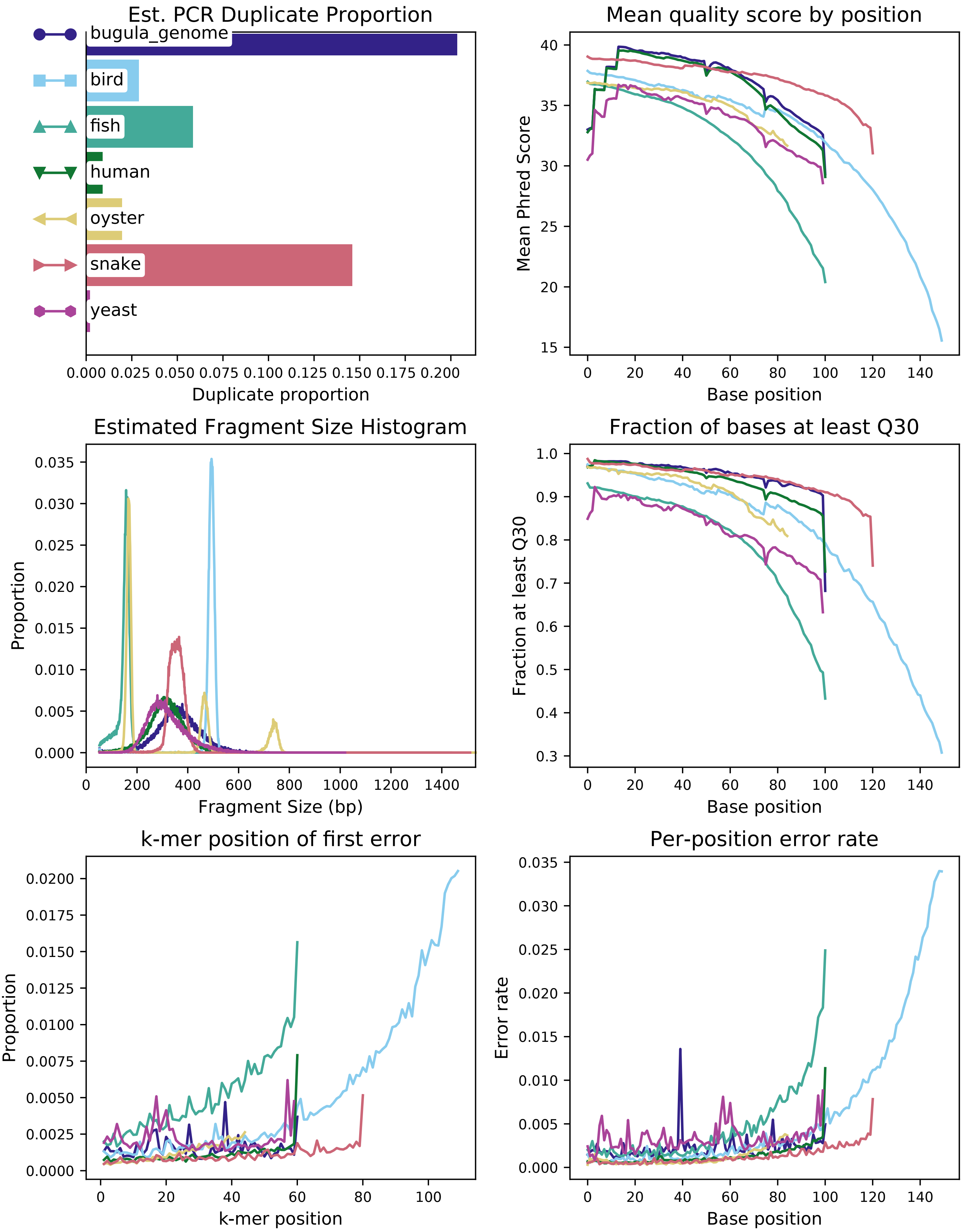
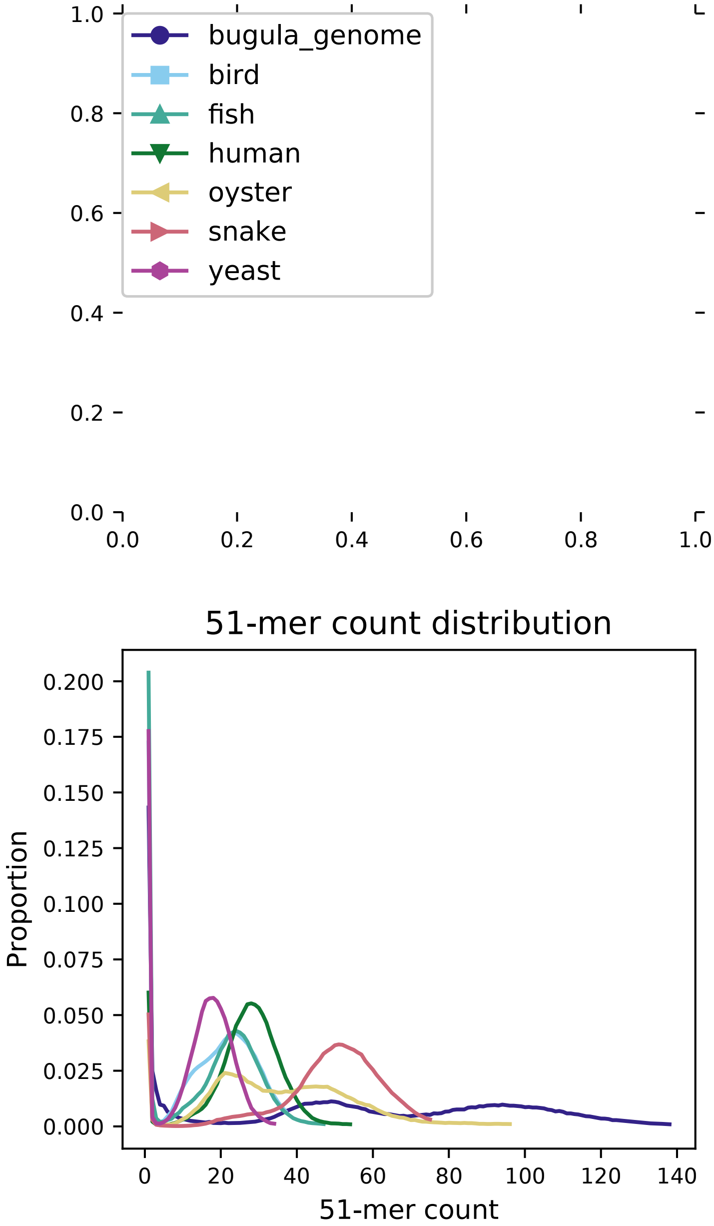
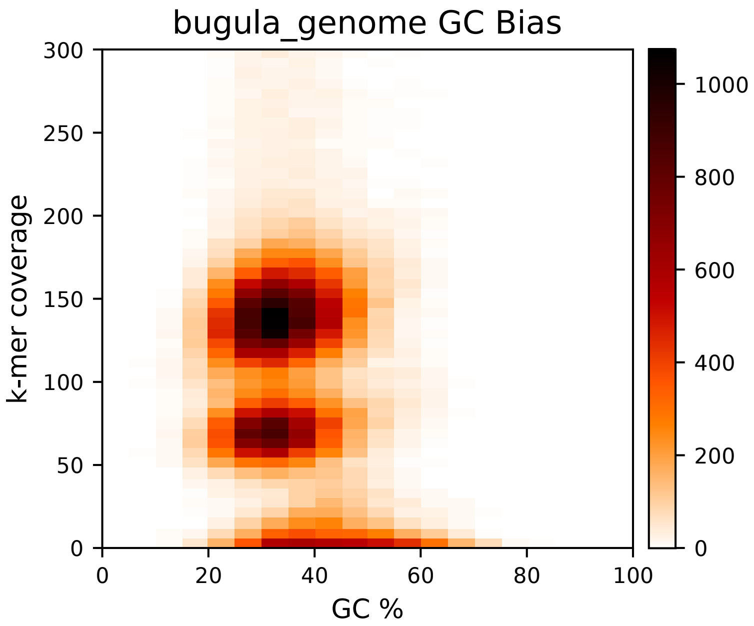
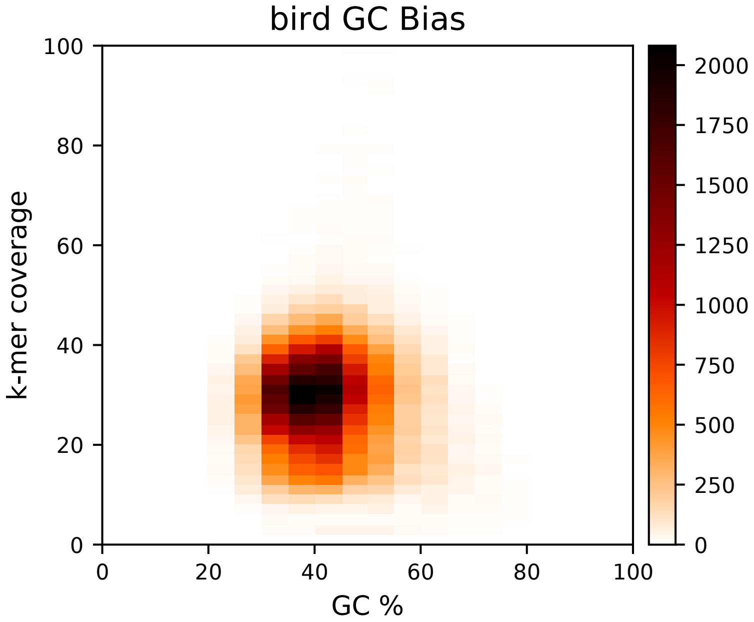
Supplemental Data 1. SGA Preqc Results.

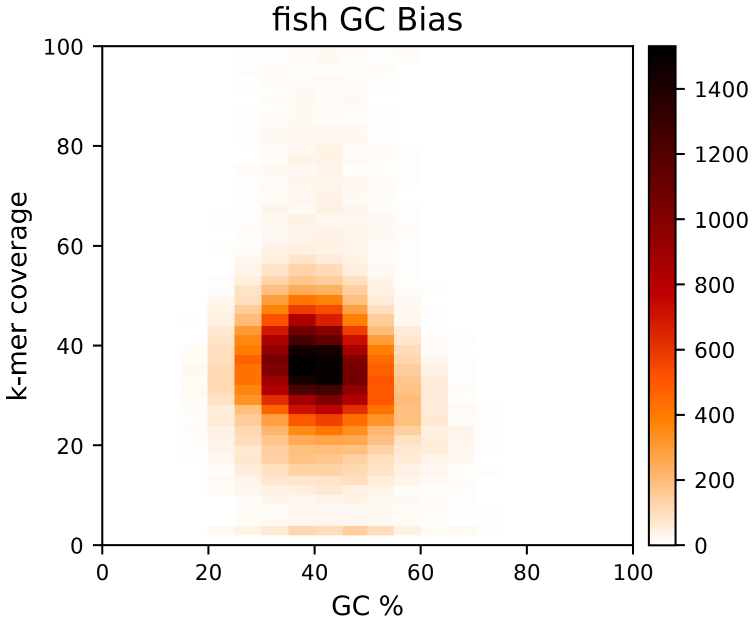


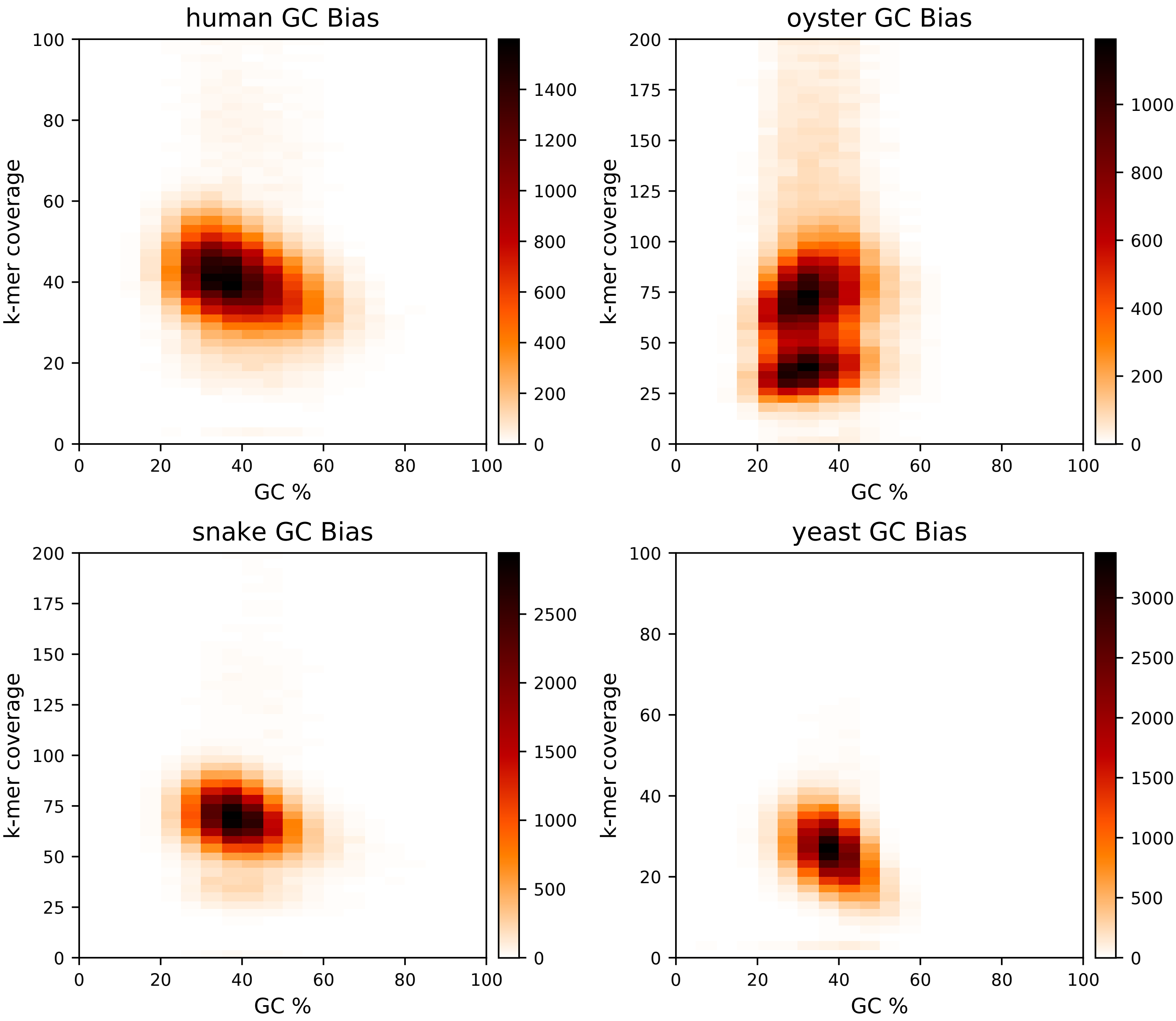

Est. PCR Duplicate Proportion
bugula_genome
bird
fish
human
oyster
snake
yeast
0.000 0.025 0.050 0.075 0.100 0.125 0.150 0.175 0.200
Duplicate proportion
Mean quality score by position
Mean Phred Score
40
35
30
25
20
15
0 20 40 60 80 100 120 140
Base position
Estimated Fragment Size Histogram
Proportion
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0 200 400 600 800 1000 1200 1400
Fragment Size (bp)
Fraction of bases at least Q30
Fraction at least Q30
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0 20 40 60 80 100 120 140
Base position
k-mer position of first error
Proportion
0.0200
0.0175
0.0150
0.0125
0.0100
0.0075
0.0050
0.0025
0.0000
0 20 40 60 80 100
k-mer position
Per-position error rate
Error rate
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0 20 40 60 80 100 120 140
Base position


1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
bugula_genome
bird
fish
human
oyster
snake
yeast
51-mer count distribution
Proportion
0.200
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0
20
40
60
80
100
120
140
51-mer count


bugula_genome GC Bias
k-mer coverage
300
250
200
150
100
50
0
0
20
40
60
80
100
GC %
1000
800
600
400
200
0


bird GC Bias
k-mer coverage
100
80
60
40
20
0
0
20
40
60
80
100
GC %
2000
1750
1500
1250
1000
750
500
250
0


fish GC Bias
k-mer coverage
100
80
60
40
20
0
0
20
40
60
80
100
GC %
1400
1200
1000
800
600
400
200
0


human GC Bias
k-mer coverage
0
20
40
60
80
100
GC %
0
20
40
60
80
100
0
200
400
600
800
1000
1200
1400
oyster GC Bias
k-mer coverage
0
25
50
75
100
125
150
175
200
GC %
0
20
40
60
80
100
0
200
400
600
800
1000
snake GC Bias
k-mer coverage
0
25
50
75
100
125
150
175
200
GC %
0
20
40
60
80
100
0
500
1000
1500
2000
2500
yeast GC Bias
k-mer coverage
0
20
40
60
80
100
GC %
0
20
40
60
80
100
0
500
1000
1500
2000
2500
3000

Supplemental Table 1. Repeat content of the *B.neritina* genome

```
==================================================
sequences:          3547
total length:  214693723 bp  (214693723 bp excl N/X-runs)
GC level:         34.72 %
bases masked:   55542846 bp ( 25.87 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
Retroelements        27447     18300120 bp    8.52 %
   SINEs:               46         2112 bp    0.00 %
   Penelope           2397       785481 bp    0.37 %
   LINEs:            14371      4770421 bp    2.22 %
    CRE/SLACS            0            0 bp    0.00 %
     L2/CR1/Rex       3895      1796007 bp    0.84 %
     R1/LOA/Jockey       0            0 bp    0.00 %
     R2/R4/NeSL        793       382779 bp    0.18 %
     RTE/Bov-B        2100      1154705 bp    0.54 %
     L1/CIN4          5186       651449 bp    0.30 %
   LTR elements:     13030     13527587 bp    6.30 %
     BEL/Pao          1006       758652 bp    0.35 %
     Ty1/Copia         336       311928 bp    0.15 %
     Gypsy/DIRS1      9542     12168188 bp    5.67 %
       Retroviral      329        83829 bp    0.04 %

DNA transposons      28516      7942958 bp    3.70 %
   hobo-Activator     2880       662976 bp    0.31 %
   Tc1-IS630-Pogo     1570       565921 bp    0.26 %
   En-Spm                0            0 bp    0.00 %
   MuDR-IS905            0            0 bp    0.00 %
   PiggyBac              0            0 bp    0.00 %
   Tourist/Harbinger     0            0 bp    0.00 %
   Other (Mirage,       58        27429 bp    0.01 %
    P-element, Transib)

Rolling-circles          0            0 bp    0.00 %
Unclassified:        84448     21541525 bp   10.03 %
Total interspersed repeats:    47784603 bp   22.26 %
Small RNA:           11631      1882093 bp    0.88 %
Satellites:              0            0 bp    0.00 %
Simple repeats:      68160      5532140 bp    2.58 %
Low complexity:       6521       344010 bp    0.16 %
==================================================
```

```
* most repeats fragmented by insertions or deletions
  have been counted as one element.
  Runs of >=20 X/Ns in query were excluded in % calcs.
  RepeatMasker Combined Database: Dfam_3.1
```