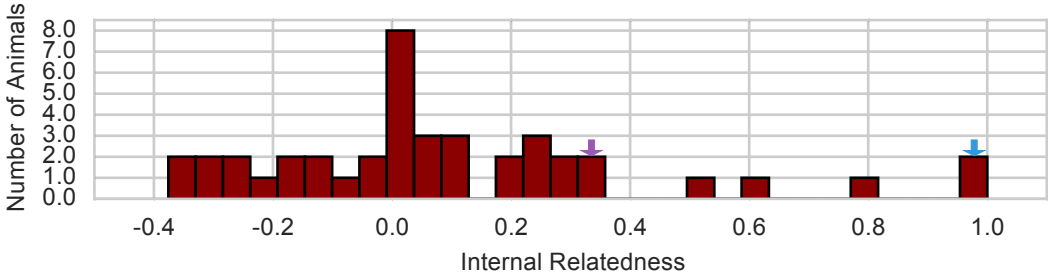
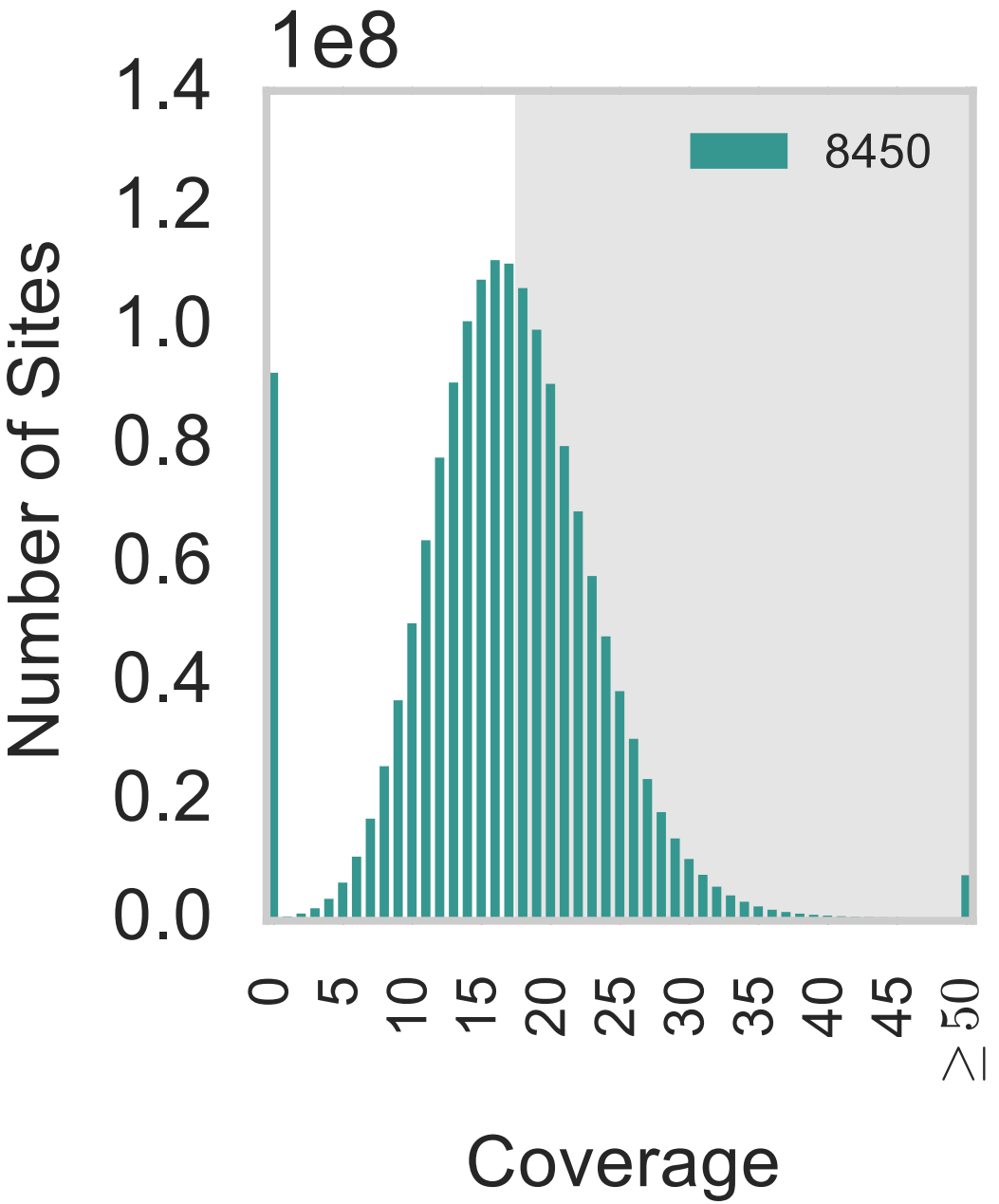
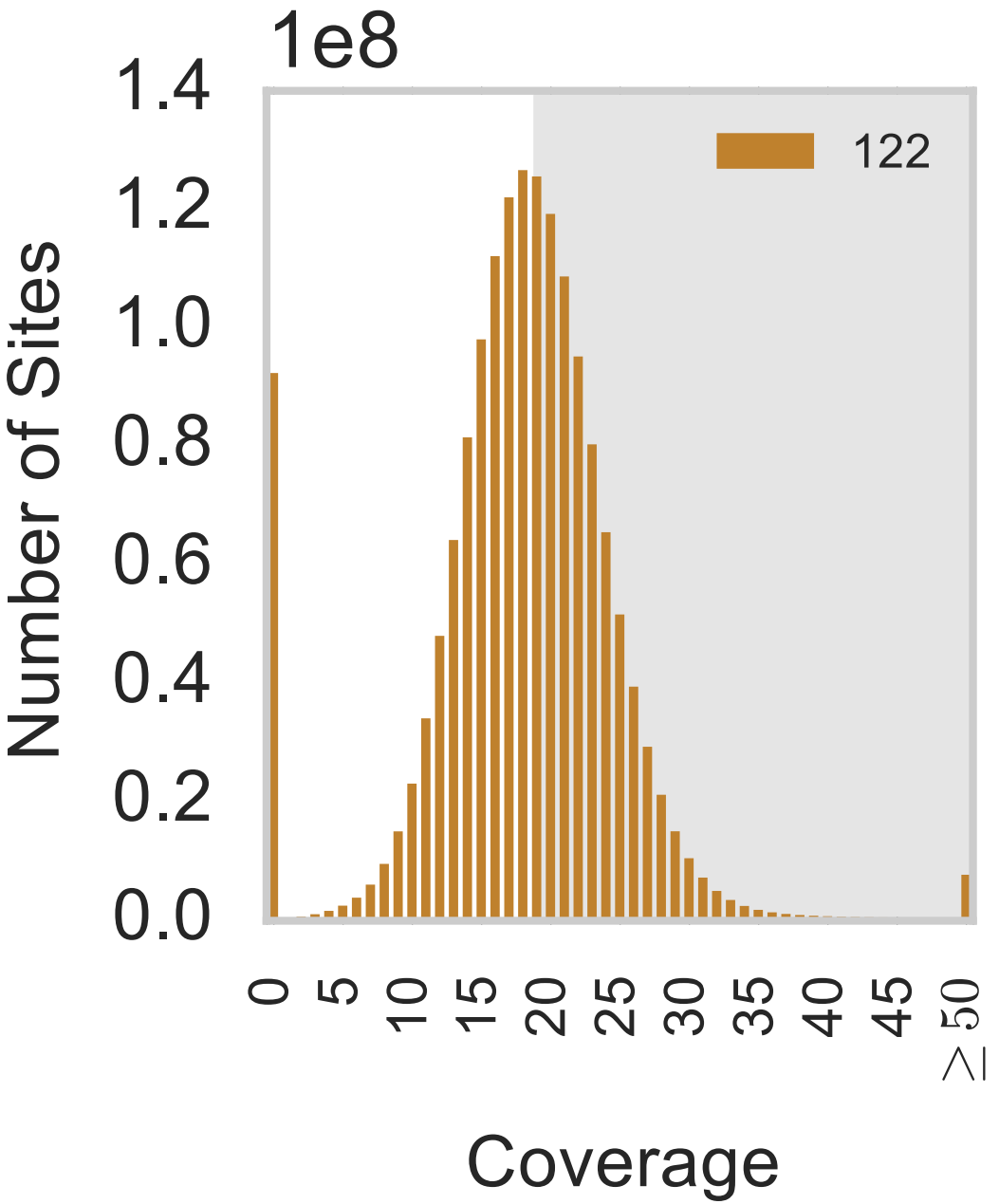
ID#	animal	Ai5013		Cvanu7		Cvanu24		D106	
4272	male ino	299	333	303		202	214	272	314
302	male gul	205	248	323	334	200		243	248
122	female mar	214	257	328	352	200		295	299
8449	offspring 1		257	328		200		295	
8450	offspring 2		257	328		200			299

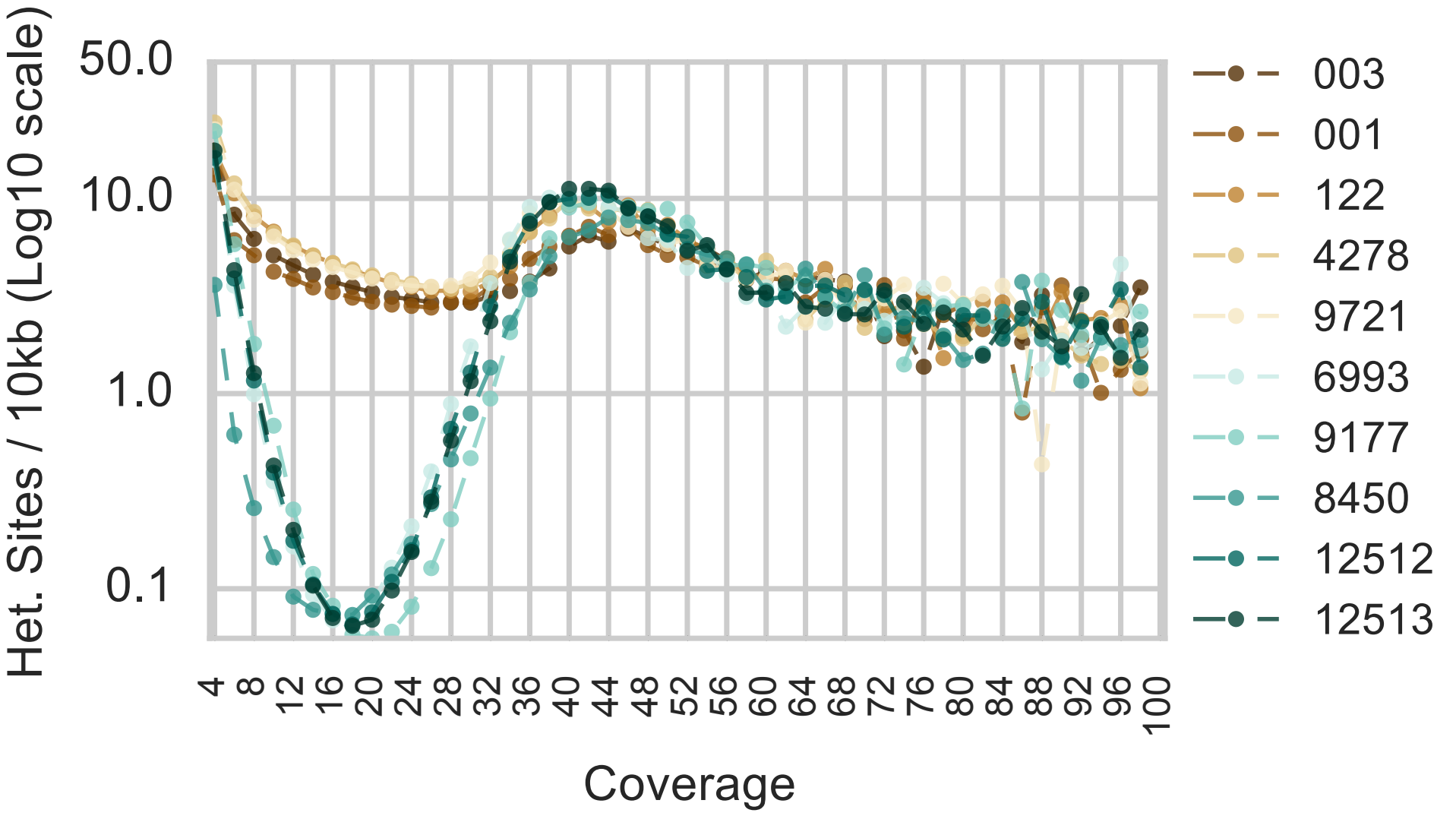
ID#	animal	D111		MS1		MS7		MS8	
4272	male ino	292	336	293	306	265		116	
302	male gul	246	281	231		318		116	119
122	female mar	150		217		244	283	113	114
8449	offspring 1	150		217			282		114
8450	offspring 2	150		217		244			114

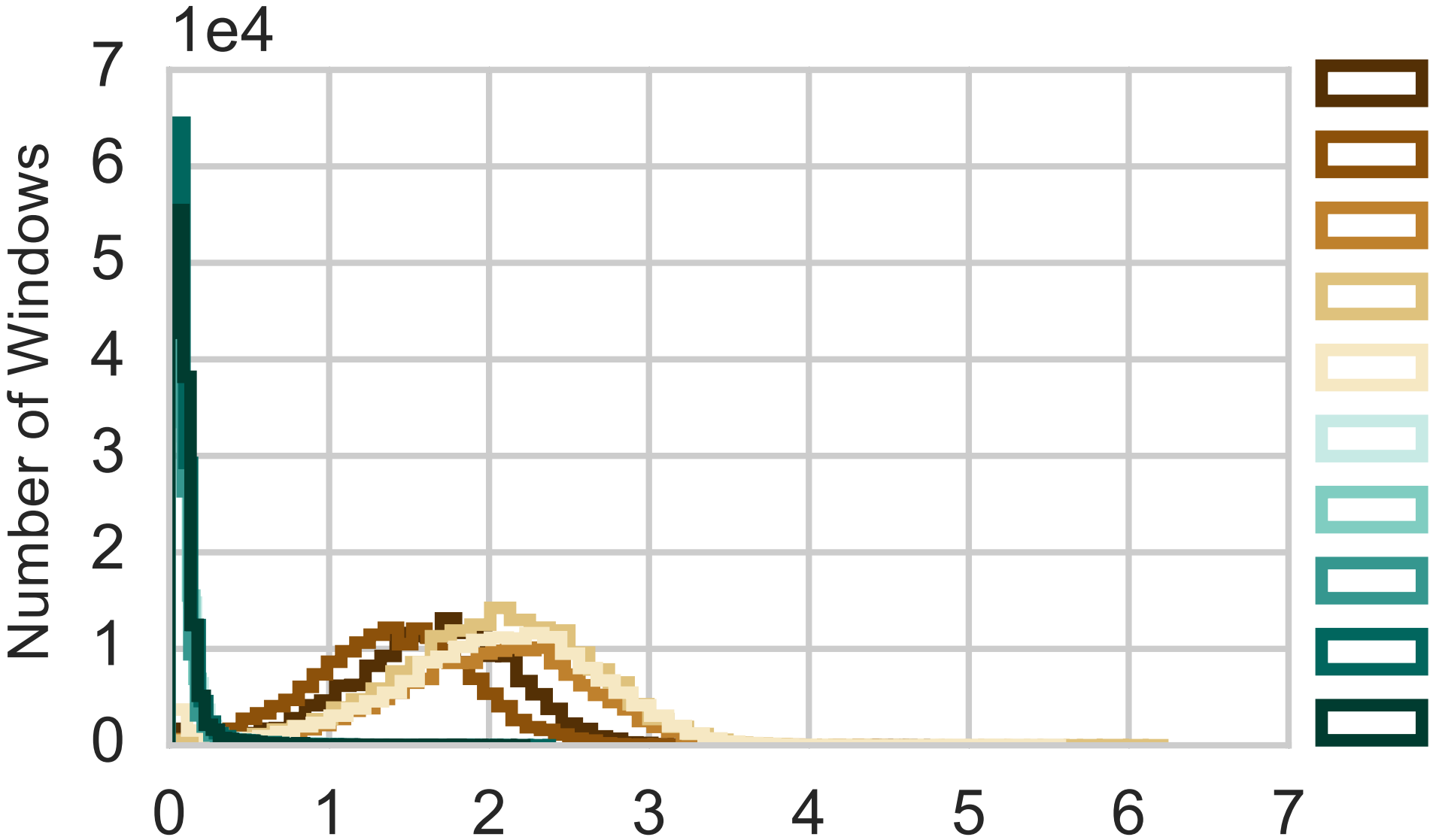
B

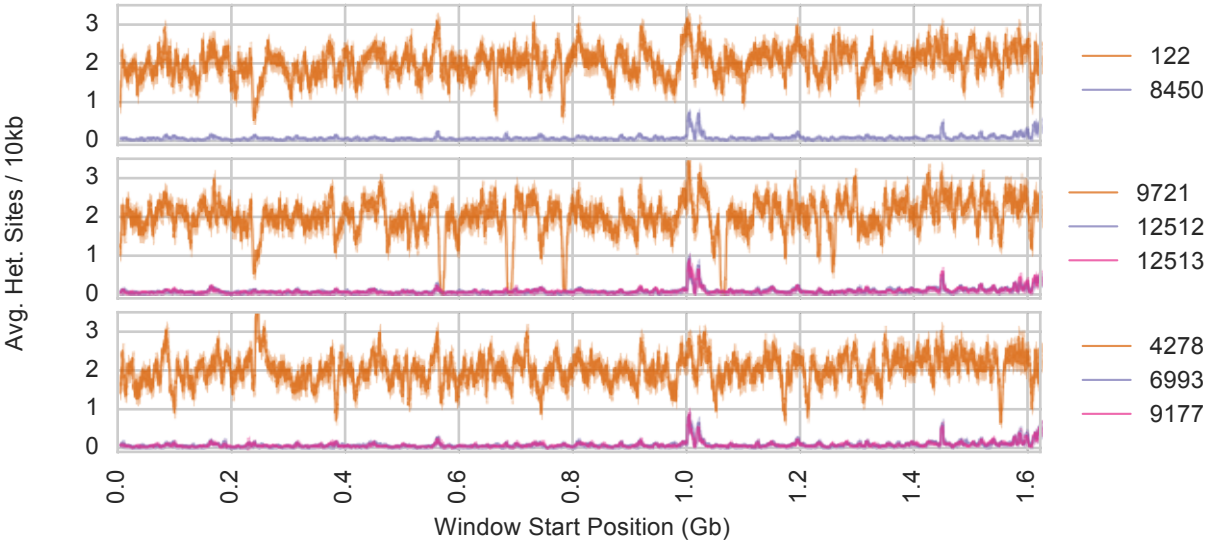

Number of Animals
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
Internal Relatedness

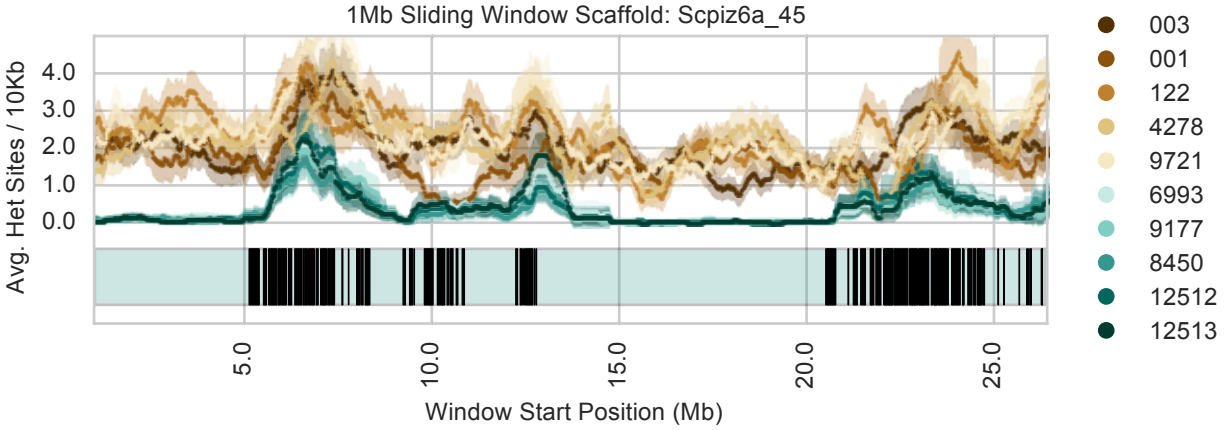

1e8
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Number of Sites
8450
0
5
10
15
20
25
30
35
40
45
50
Coverage

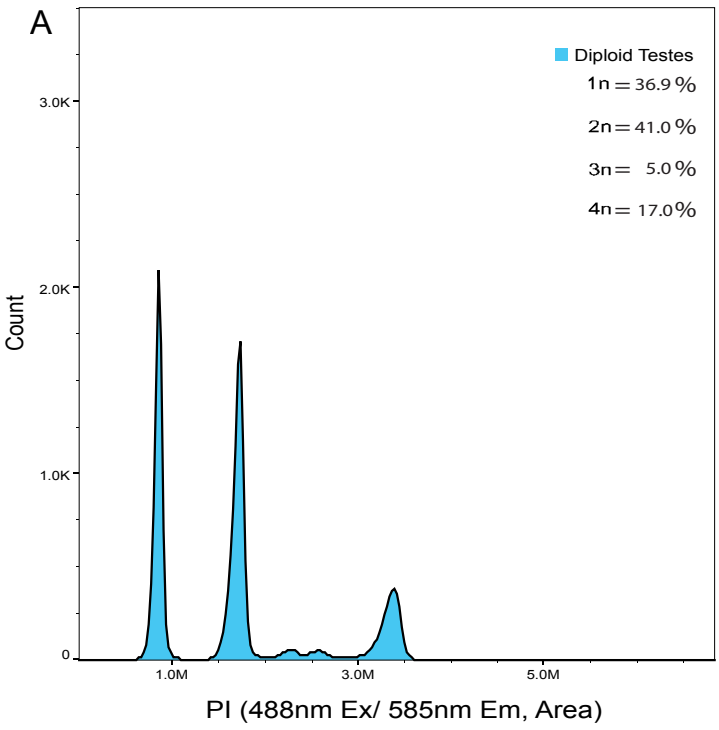

1e8
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Number of Sites
122
0
5
10
15
20
25
30
35
40
45
50
Coverage

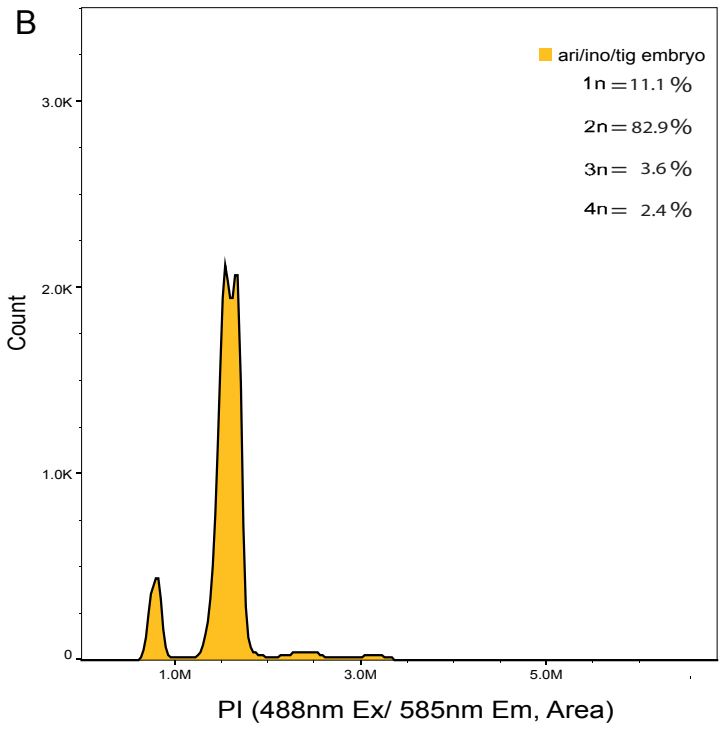

Het. Sites / 10kb (Log10 scale)
50.0
10.0
1.0
0.1
4
8
12
16
20
24
28
32
36
40
44
48
52
56
60
64
68
72
76
80
84
88
92
96
100
Coverage
003
001
122
4278
9721
6993
9177
8450
12512
12513

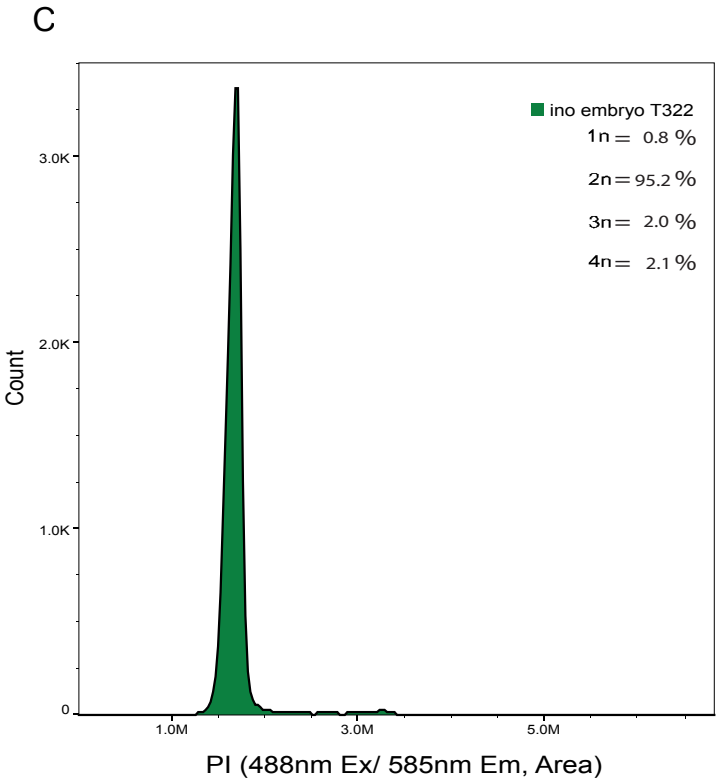

1e4
7
6
5
4
3
2
1
0
Number of Windows
0
1
2
3
4
5
6
7

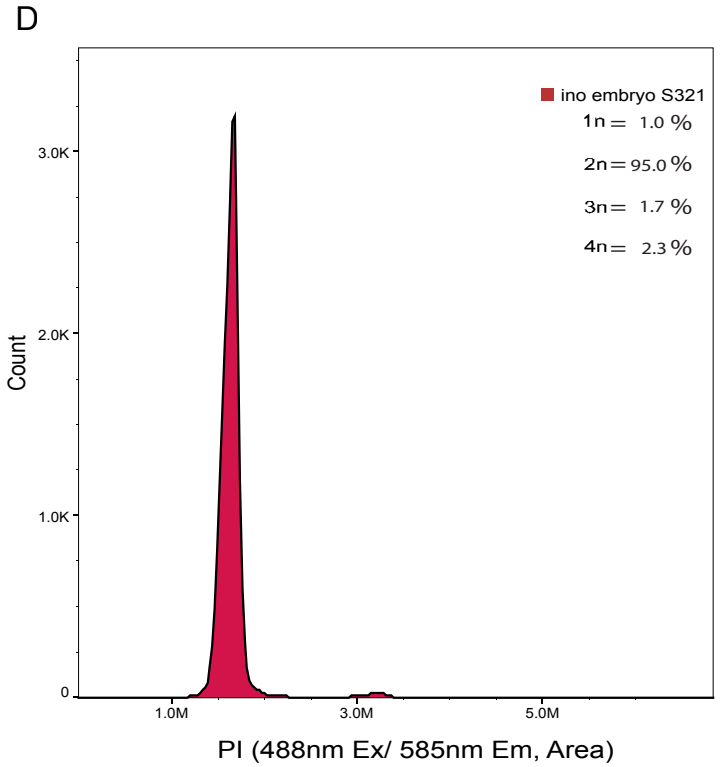

Avg. Het. Sites / 10kb
3
2
1
0
122
8450
9721
12512
12513
4278
6993
9177
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
Window Start Position (Gb)

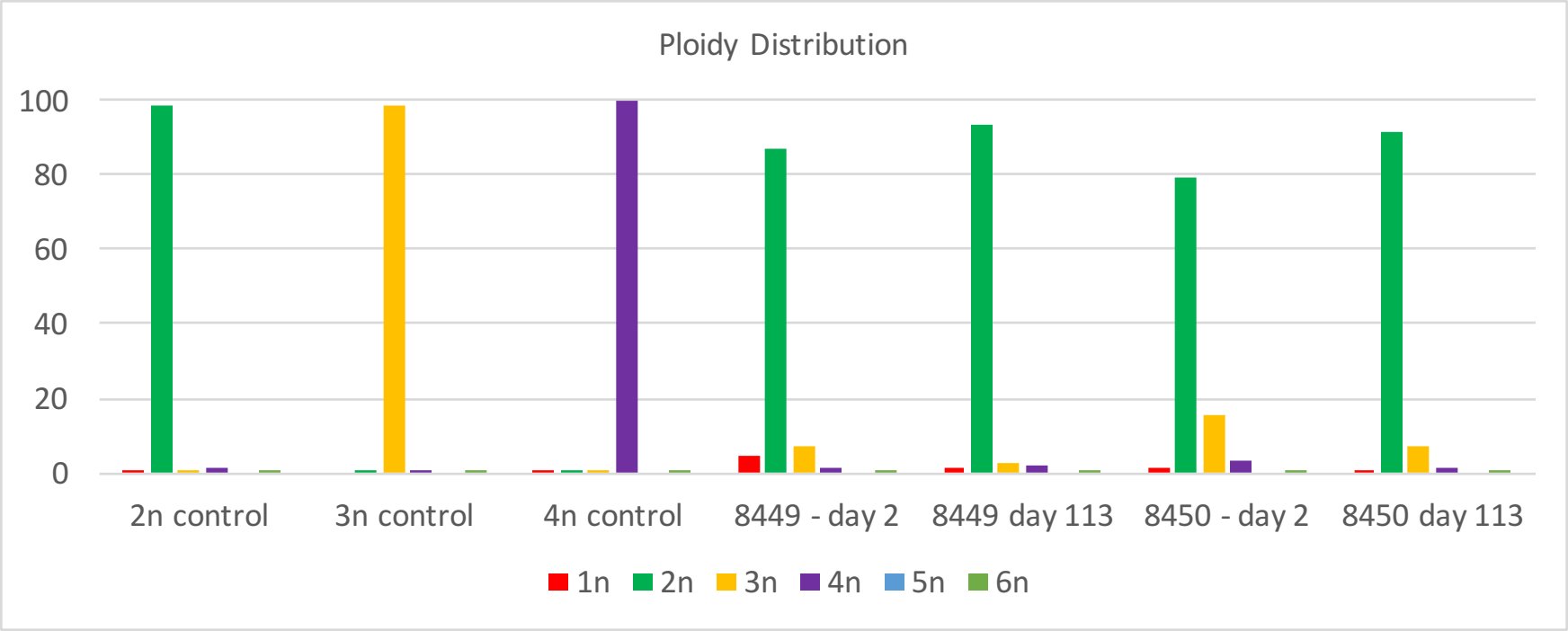

1Mb Sliding Window Scaffold: Scpiz6a_45
Avg. Het Sites / 10Kb
4.0
3.0
2.0
1.0
0.0
5.0
10.0
15.0
20.0
25.0
Window Start Position (Mb)
003
001
122
4278
9721
6993
9177
8450
12512
12513

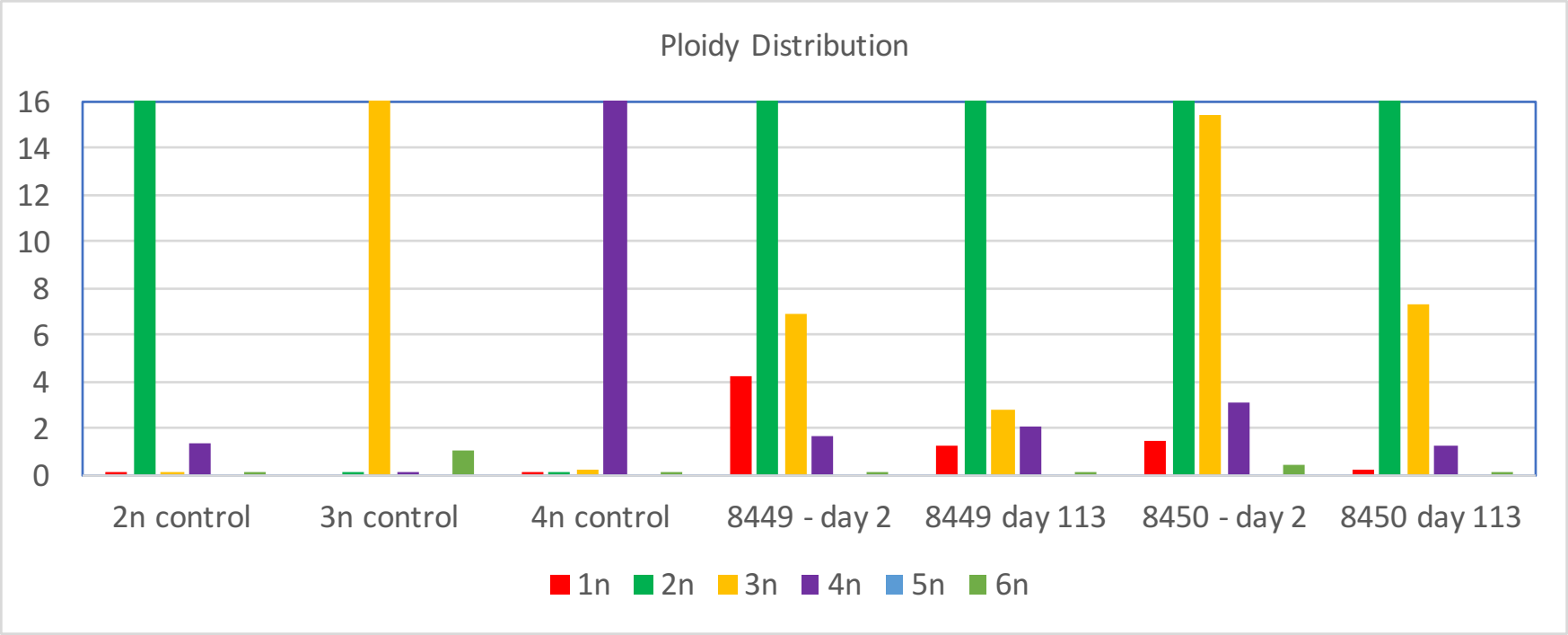

A
Diploid Testes
1n = 36.9 %
2n = 41.0 %
3n = 5.0 %
4n = 17.0 %
Count
3.0K
2.0K
1.0K
0
1.0M
3.0M
5.0M
PI (488nm Ex/ 585nm Em, Area)

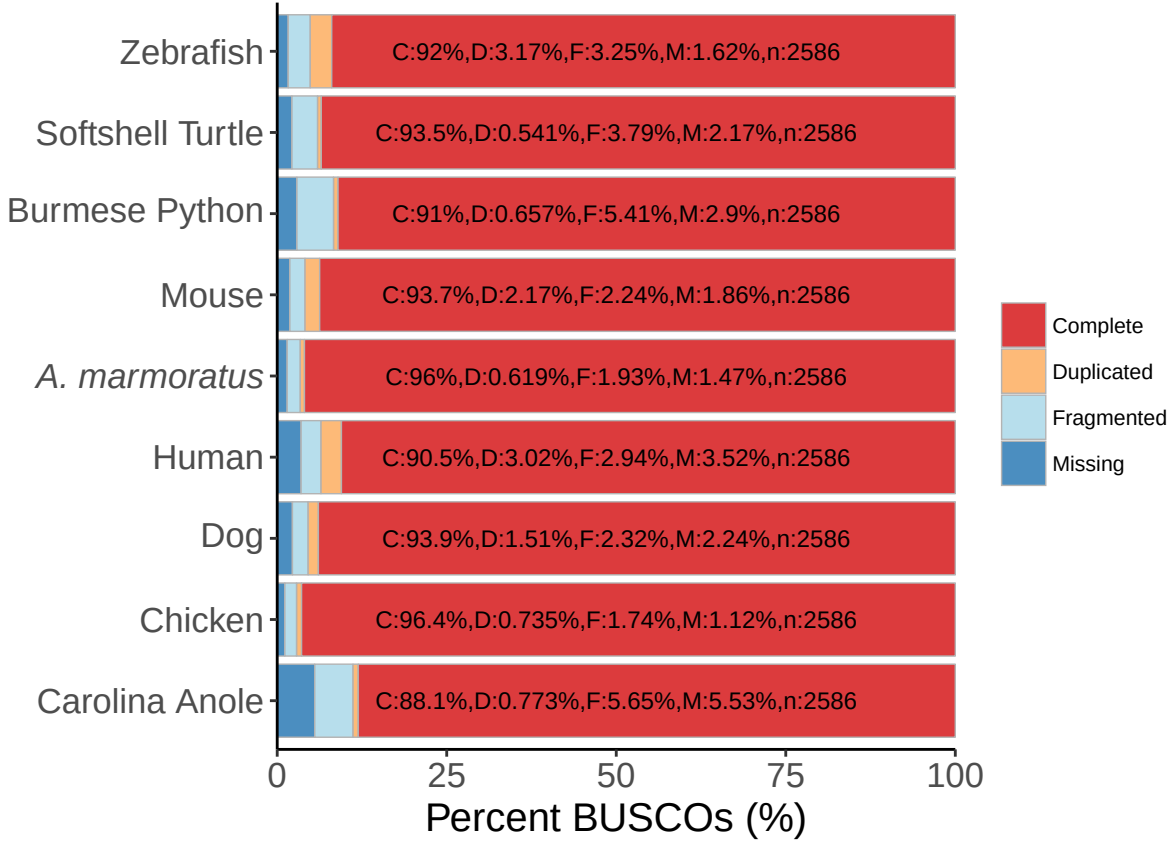

B
ari/ino/tig embryo
1n = 11.1 %
2n = 82.9 %
3n = 3.6 %
4n = 2.4 %
Count
3.0K
2.0K
1.0K
0
1.0M
3.0M
5.0M
PI (488nm Ex/ 585nm Em, Area)

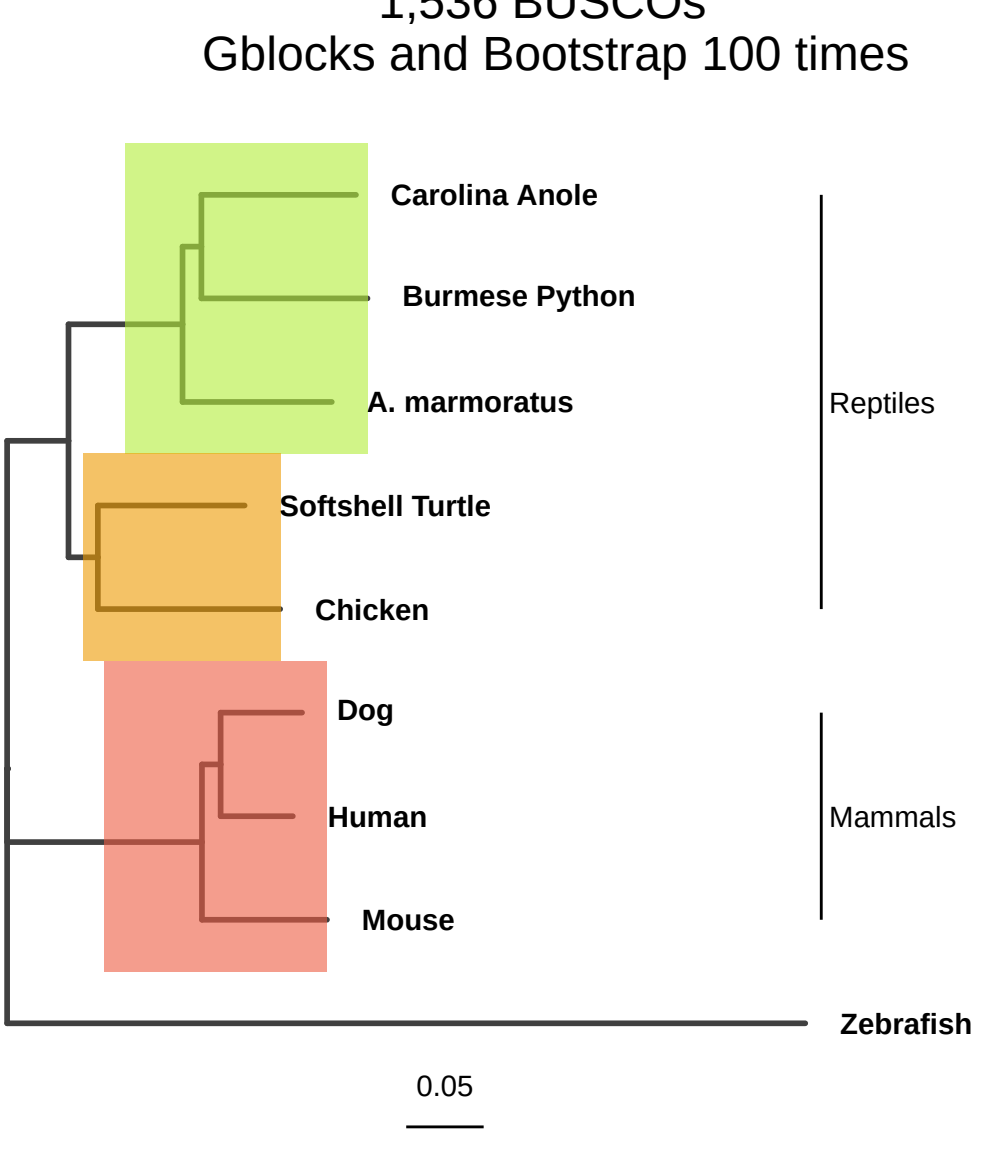

C
ino embryo T322
1n = 0.8 %
2n = 95.2 %
3n = 2.0 %
4n = 2.1 %
Count
3.0K
2.0K
1.0K
0
1.0M
3.0M
5.0M
PI (488nm Ex/ 585nm Em, Area)

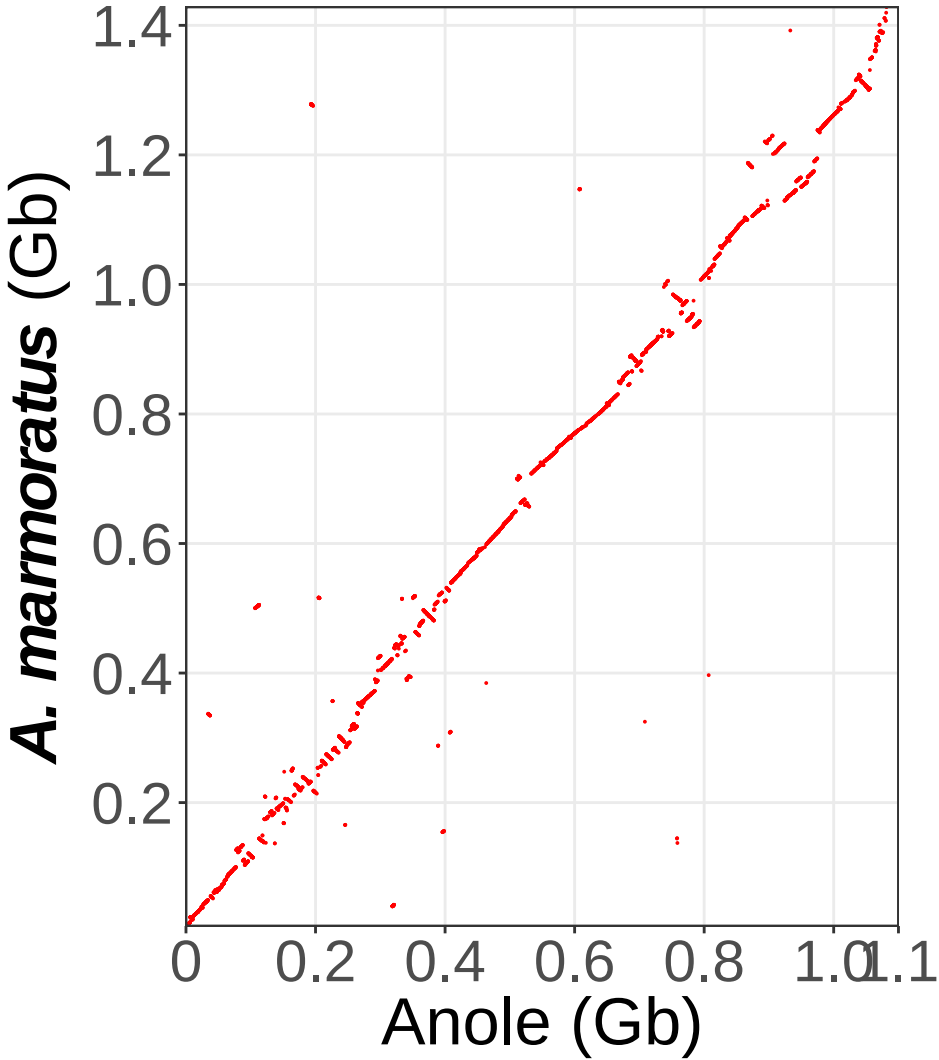

D
ino embryo S321
1n = 1.0 %
2n = 95.0 %
3n = 1.7 %
4n = 2.3 %
Count
3.0K
2.0K
1.0K
0
1.0M
3.0M
5.0M
PI (488nm Ex/ 585nm Em, Area)

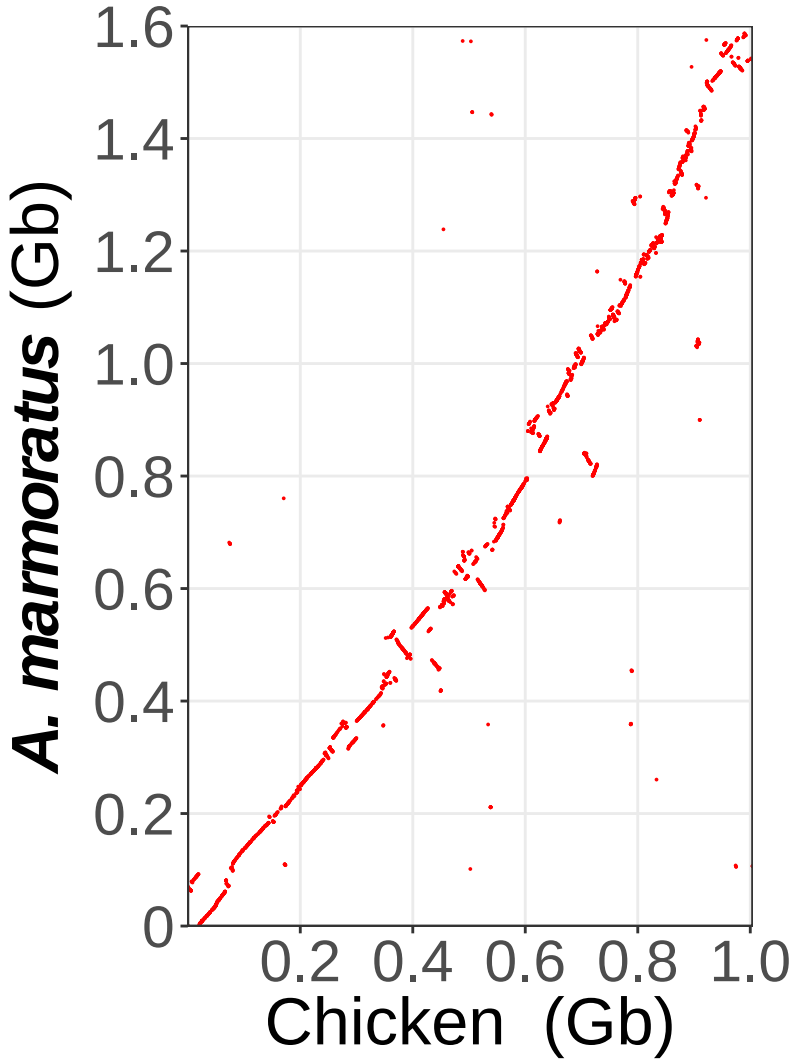

Ploidy Distribution
100
80
60
40
20
0
2n control
3n control
4n control
8449 - day 2
8449 day 113
8450 - day 2
8450 day 113
1n
2n
3n
4n
5n
6n

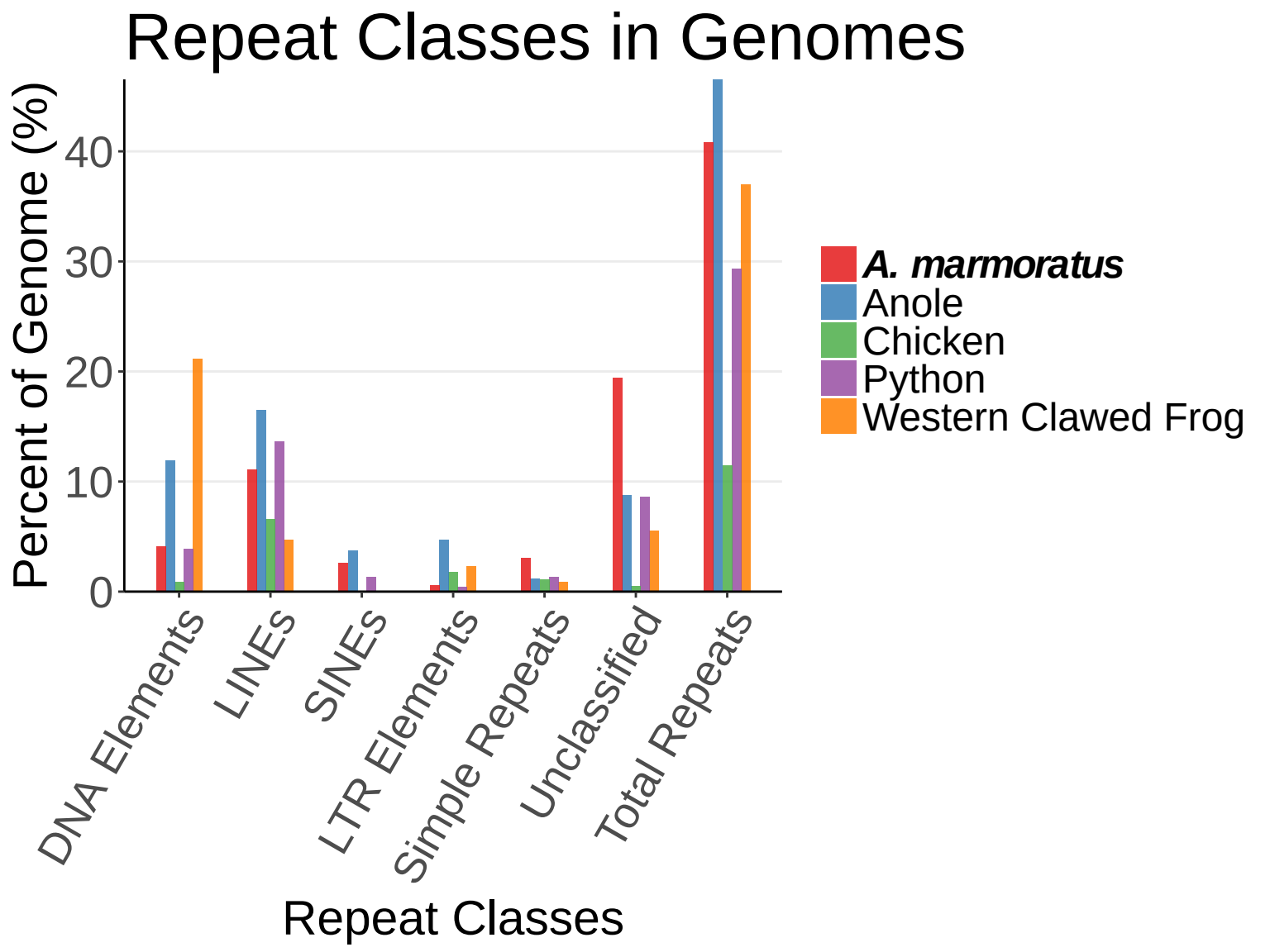

Ploidy Distribution
16
14
12
10
8
6
4
2
0
2n control
3n control
4n control
8449 - day 2
8449 day 113
8450 - day 2
8450 day 113
1n
2n
3n
4n
5n
6n

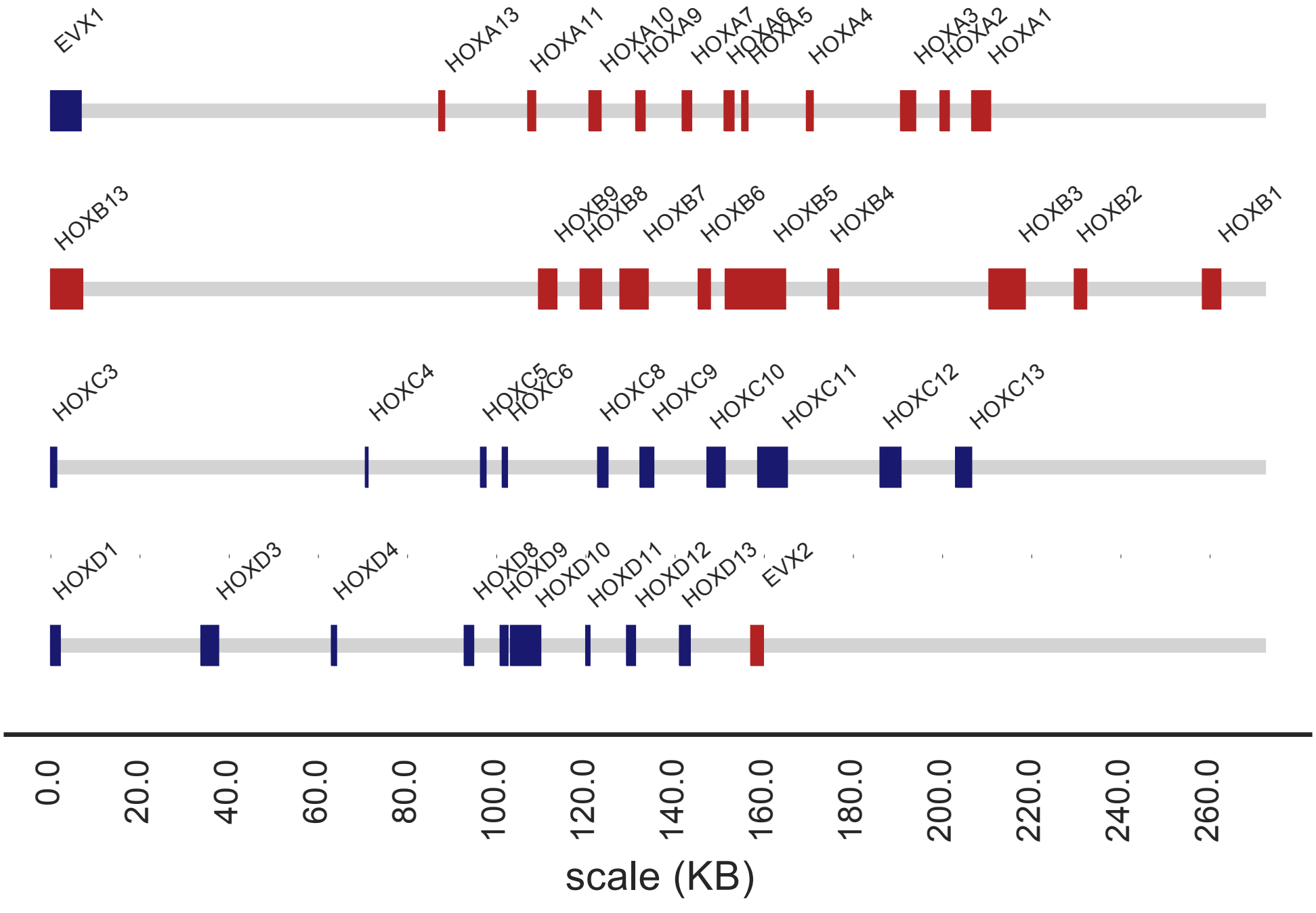

Zebrafish
Softshell Turtle
Burmese Python
Mouse
A. marmoratus
Human
Dog
Chicken
Carolina Anole
C:92%,D:3.17%,F:3.25%,M:1.62%,n:2586
C:93.5%,D:0.541%,F:3.79%,M:2.17%,n:2586
C:91%,D:0.657%,F:5.41%,M:2.9%,n:2586
C:93.7%,D:2.17%,F:2.24%,M:1.86%,n:2586
C:96%,D:0.619%,F:1.93%,M:1.47%,n:2586
C:90.5%,D:3.02%,F:2.94%,M:3.52%,n:2586
C:93.9%,D:1.51%,F:2.32%,M:2.24%,n:2586
C:96.4%,D:0.735%,F:1.74%,M:1.12%,n:2586
C:88.1%,D:0.773%,F:5.65%,M:5.53%,n:2586
0
25
50
75
100
Percent BUSCOs (%)
Complete
Duplicated
Fragmented
Missing

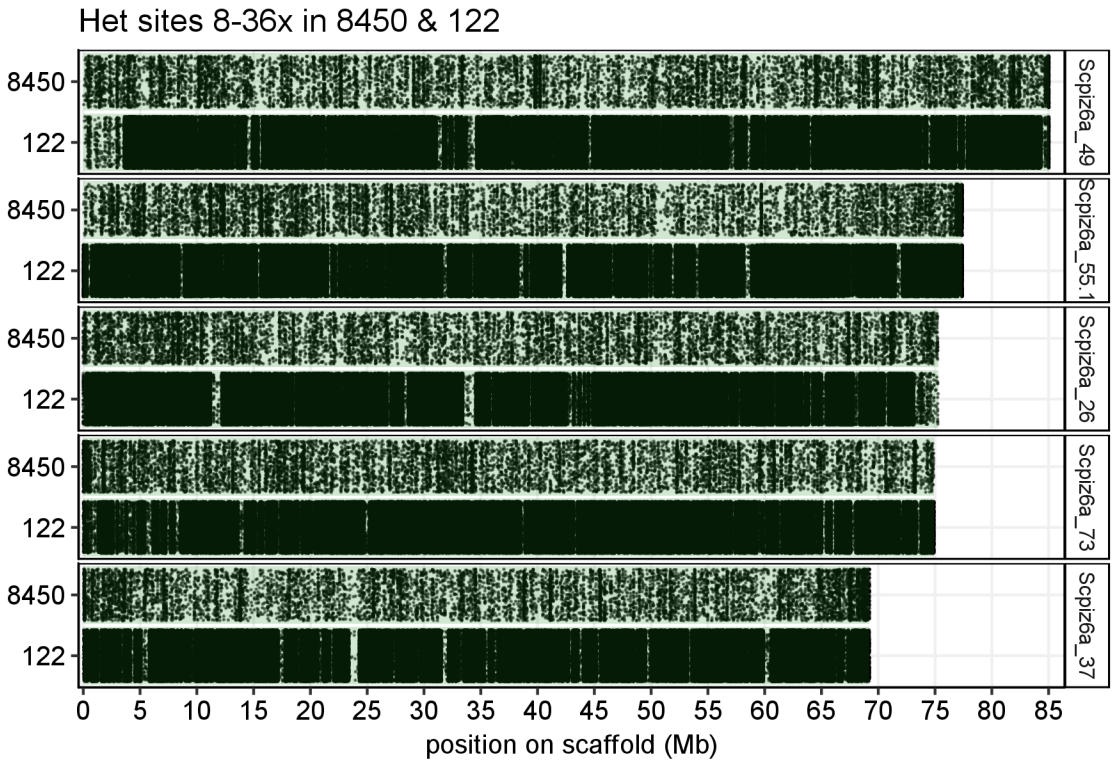

1,536 BUSCOs
Gblocks and Bootstrap 100 times
Carolina Anole
Burmese Python
A. marmoratus
Softshell Turtle
Chicken
Dog
Human
Mouse
Zebrafish
Reptiles
Mammals
0.05

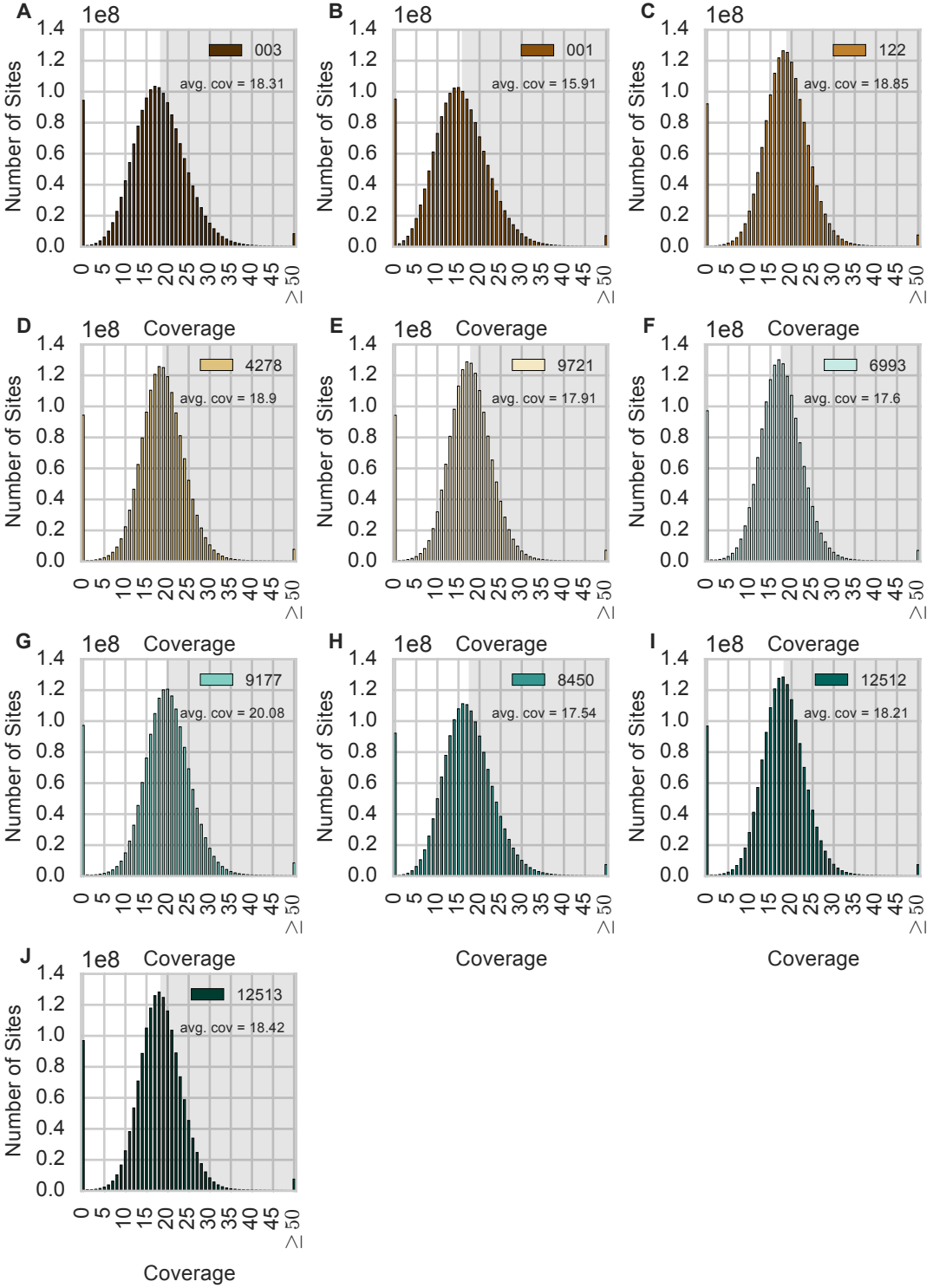

1.4
1.2
1.0
0.8
0.6
0.4
0.2
A. marmoratus (Gb)
0
0.2
0.4
0.6
0.8
1.0
1.1
Anole (Gb)

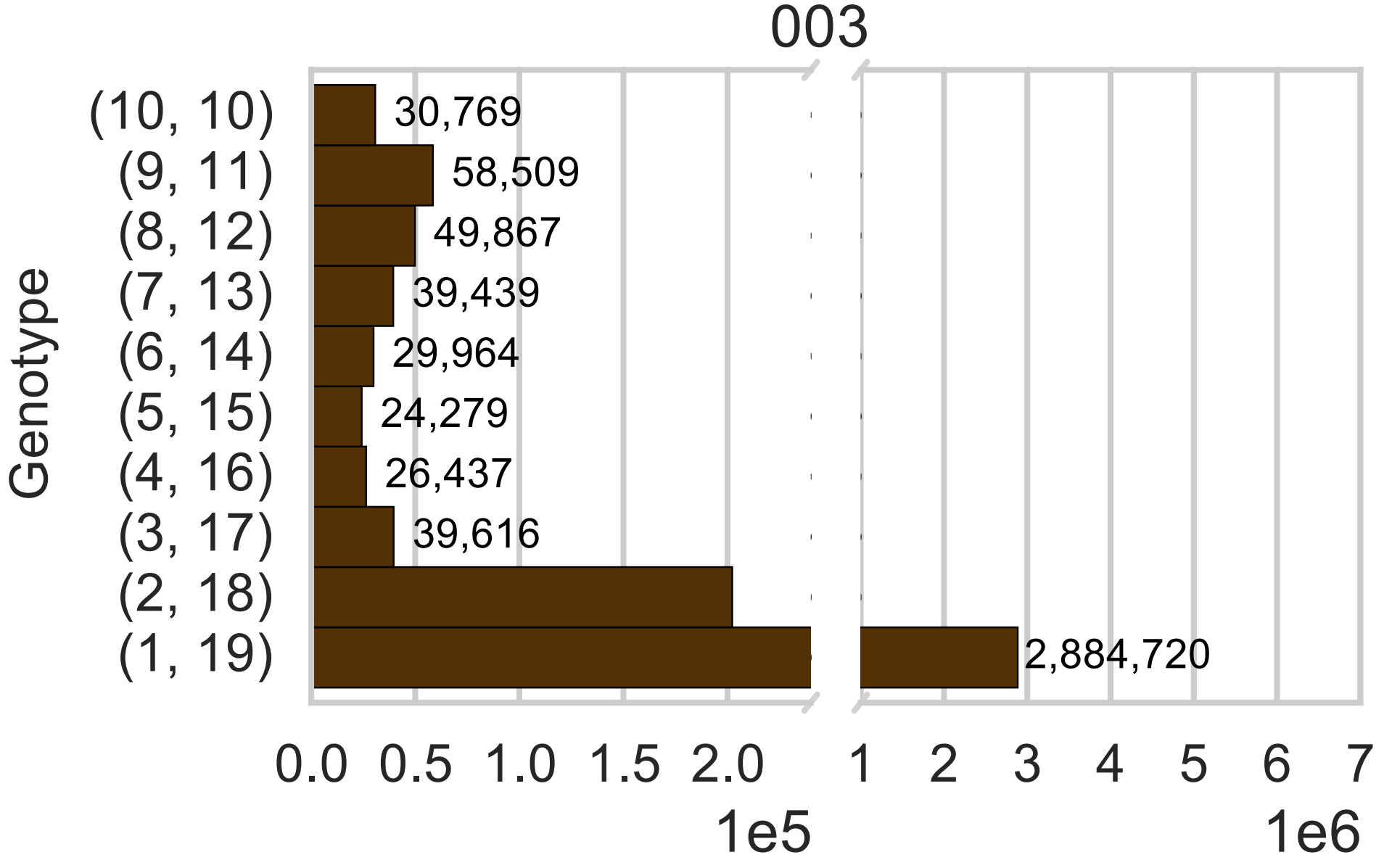

A. marmoratus (Gb)
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
0.2
0.4
0.6
0.8
1.0
Chicken (Gb)

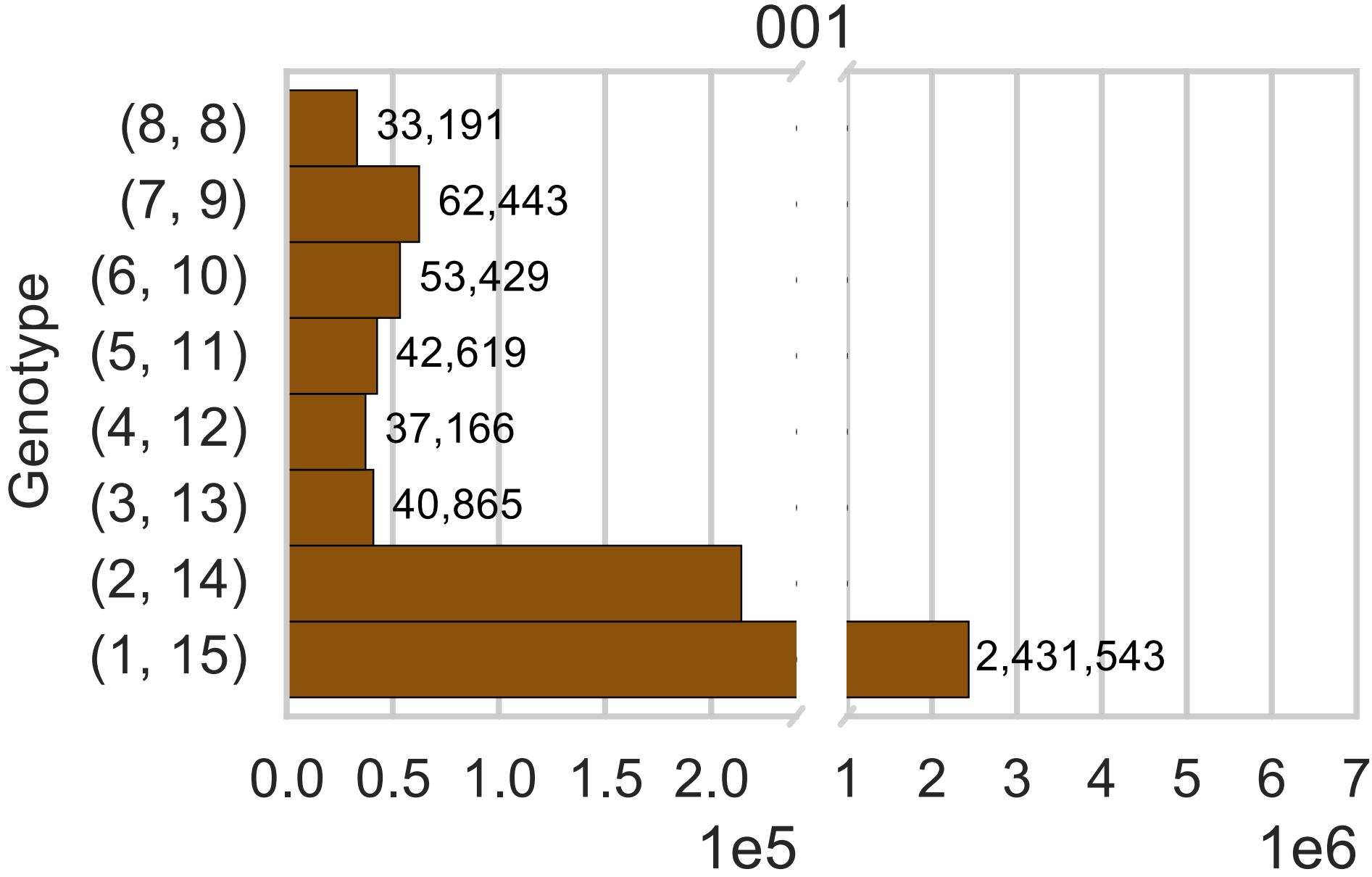

Repeat Classes in Genomes
Percent of Genome (%)
0
10
20
30
40
DNA Elements
LINEs
SINEs
LTR Elements
Simple Repeats
Unclassified
Total Repeats
Repeat Classes
A. marmoratus
Anole
Chicken
Python
Western Clawed Frog

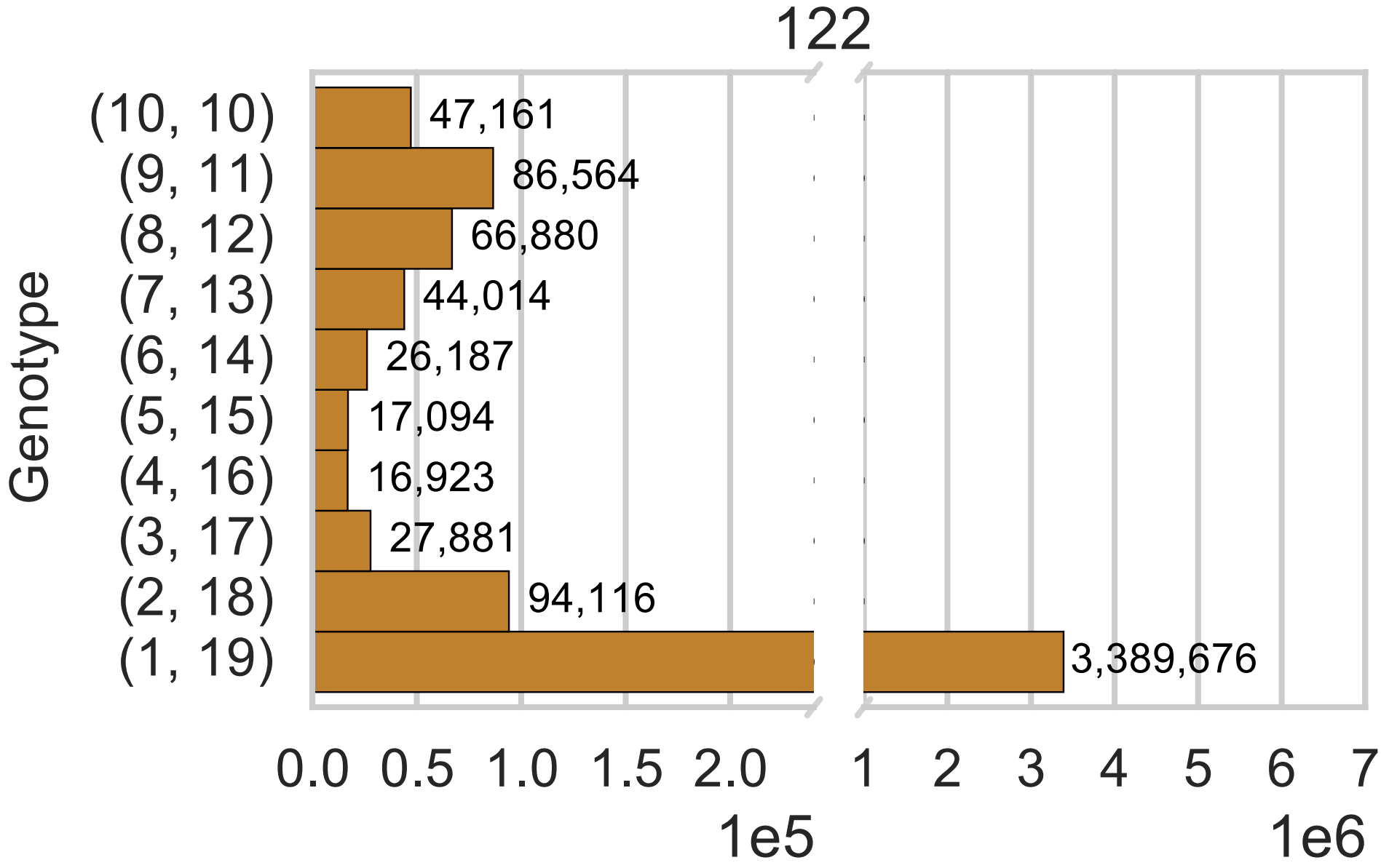

EVX1
HOXA13
HOXA11
HOXA10
HOXA9
HOXA7
HOXA6
HOXA5
HOXA4
HOXA3
HOXA2
HOXA1
HOXB13
HOXB9
HOXB8
HOXB7
HOXB6
HOXB5
HOXB4
HOXB3
HOXB2
HOXB1
HOXC3
HOXC4
HOXC5
HOXC6
HOXC8
HOXC9
HOXC10
HOXC11
HOXC12
HOXC13
HOXD1
HOXD3
HOXD4
HOXD8
HOXD9
HOXD10
HOXD11
HOXD12
HOXD13
EVX2
0.0
20.0
40.0
60.0
80.0
100.0
120.0
140.0
160.0
180.0
200.0
220.0
240.0
260.0
scale (KB)

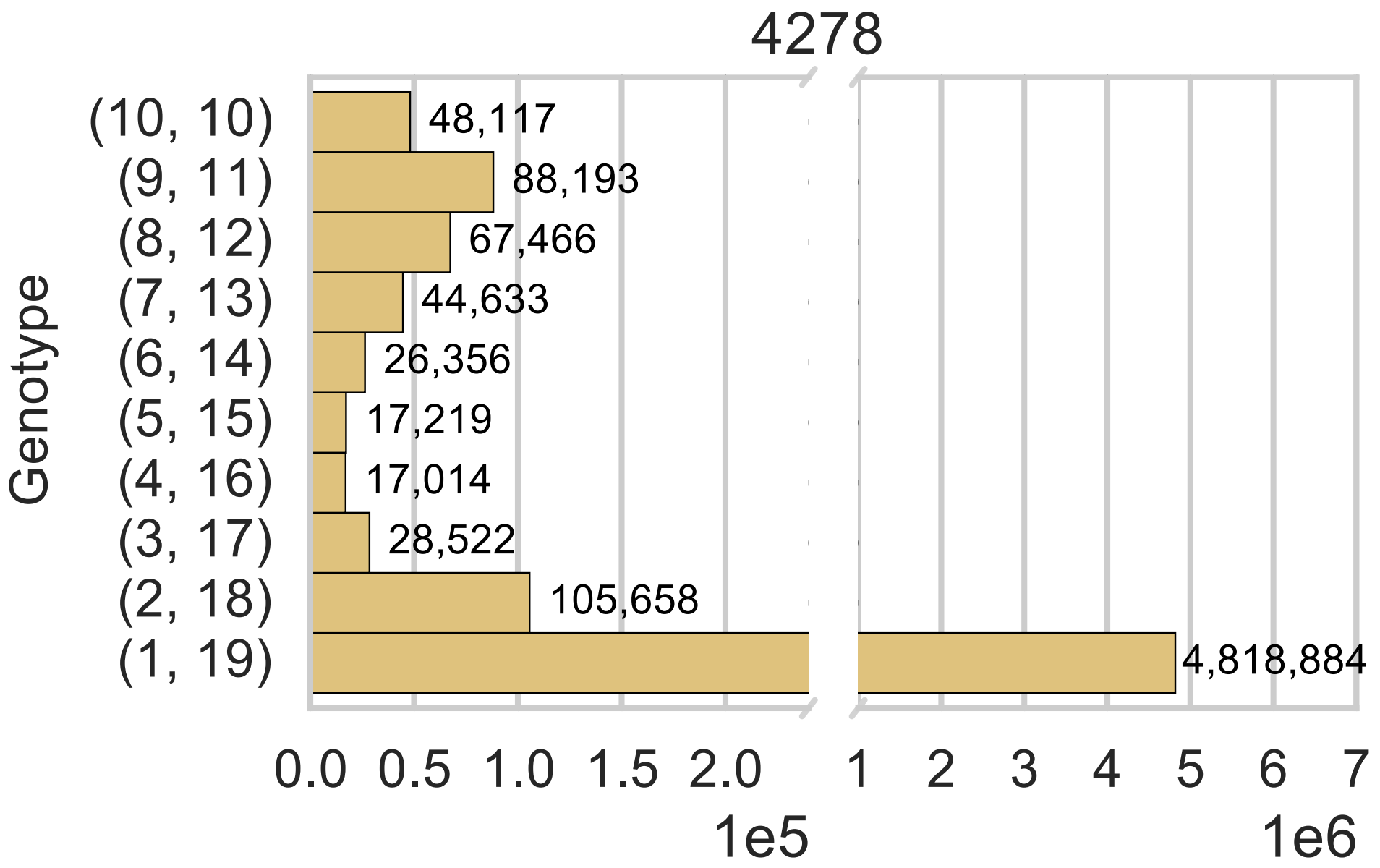

Het sites 8-36x in 8450 & 122
8450
122
Scpiz6a_49
Scpiz6a_55.1
Scpiz6a_26
Scpiz6a_73
Scpiz6a_37
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
position on scaffold (Mb)

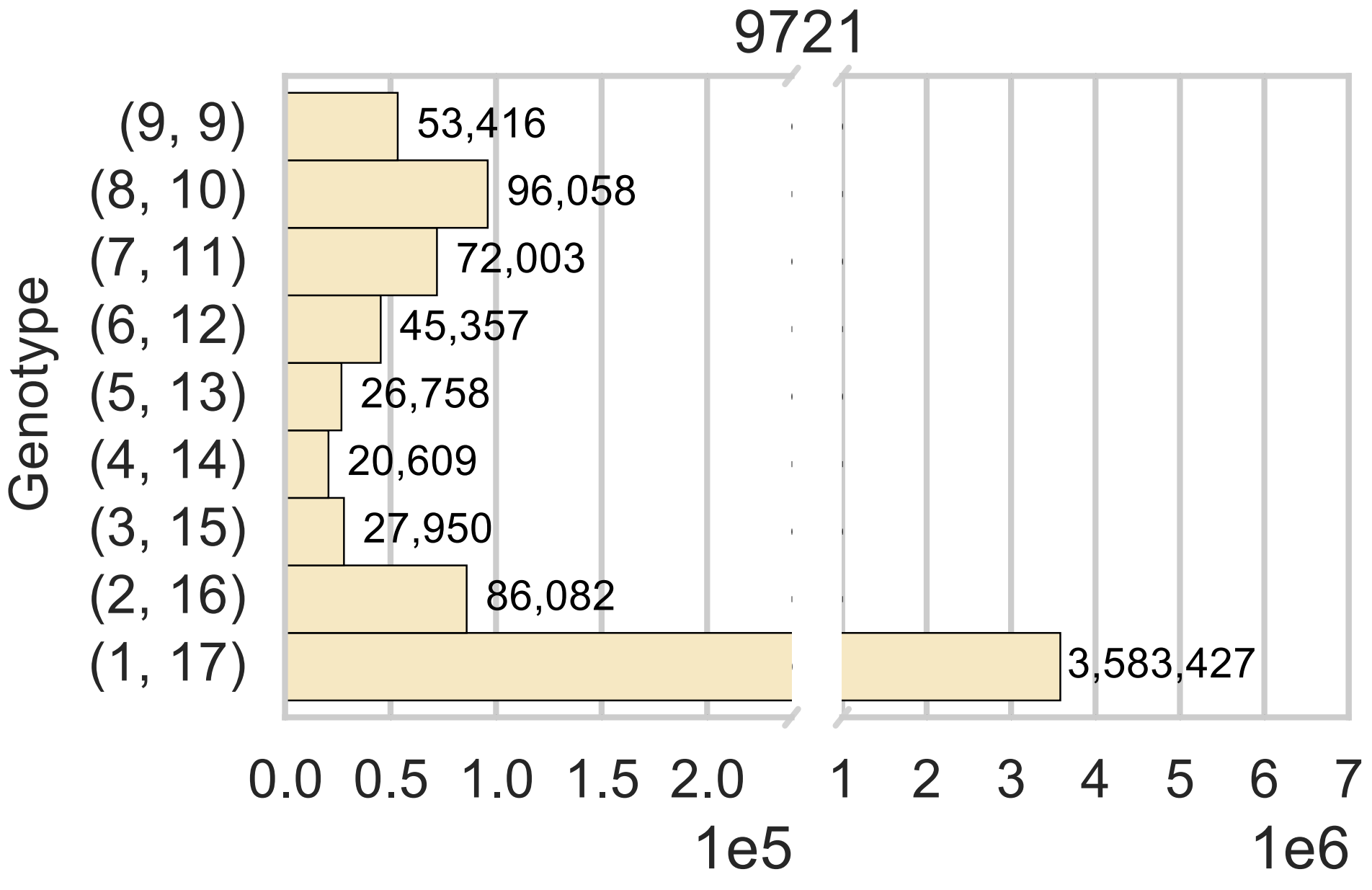

A
1e8
003
avg. cov = 18.31
B
1e8
001
avg. cov = 15.91
C
1e8
122
avg. cov = 18.85
D
1e8
Coverage
4278
avg. cov = 18.9
E
1e8
Coverage
9721
avg. cov = 17.91
F
1e8
Coverage
6993
avg. cov = 17.6
G
1e8
Coverage
9177
avg. cov = 20.08
H
1e8
Coverage
8450
avg. cov = 17.54
I
1e8
Coverage
12512
avg. cov = 18.21
J
1e8
Coverage
12513
avg. cov = 18.42
Number of Sites
Coverage
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
5
10
15
20
25
30
35
40
45
50
>|

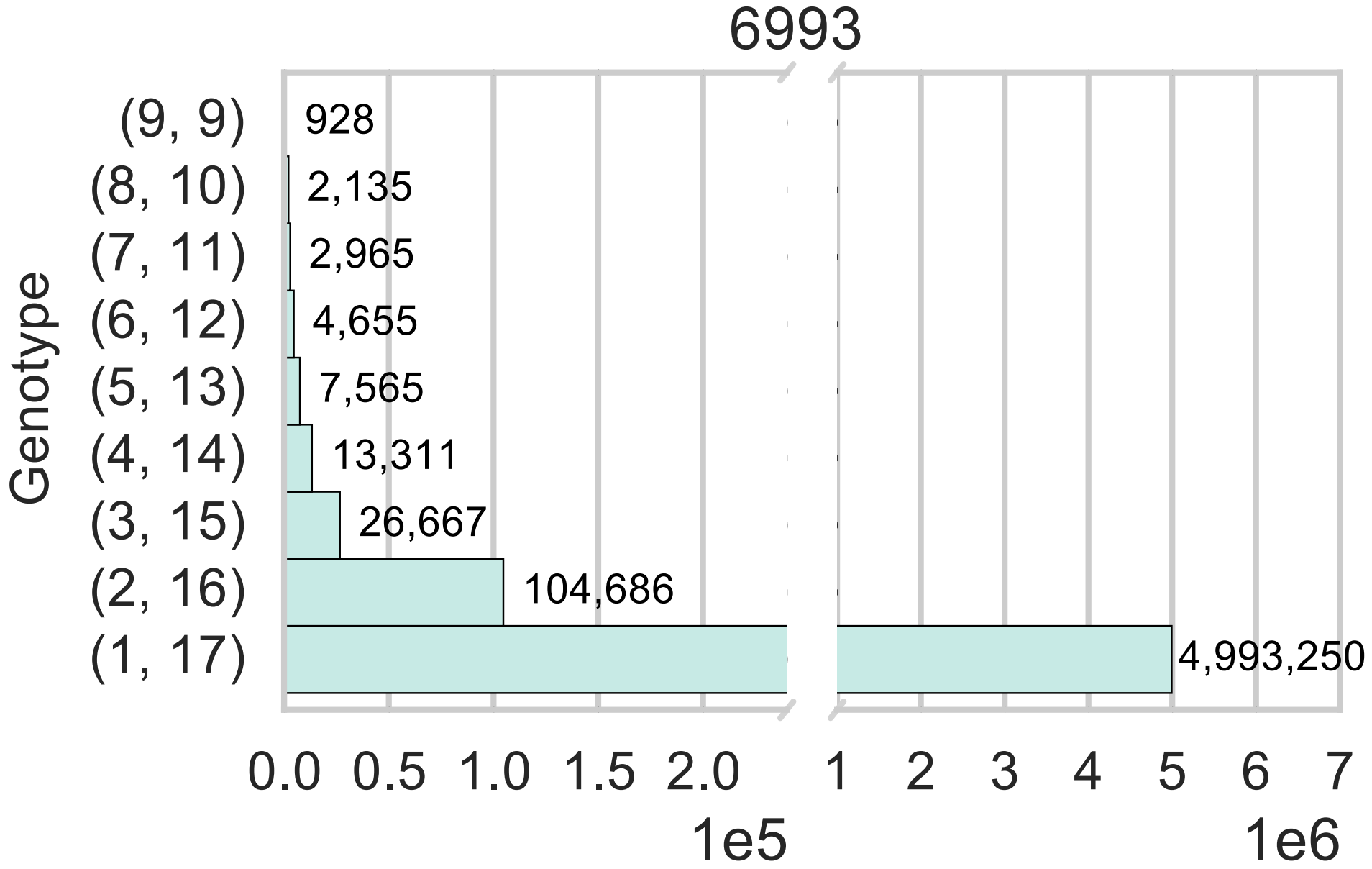

003
Genotype
(10, 10)
(9, 11)
(8, 12)
(7, 13)
(6, 14)
(5, 15)
(4, 16)
(3, 17)
(2, 18)
(1, 19)
30,769
58,509
49,867
39,439
29,964
24,279
26,437
39,616
2,884,720
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6

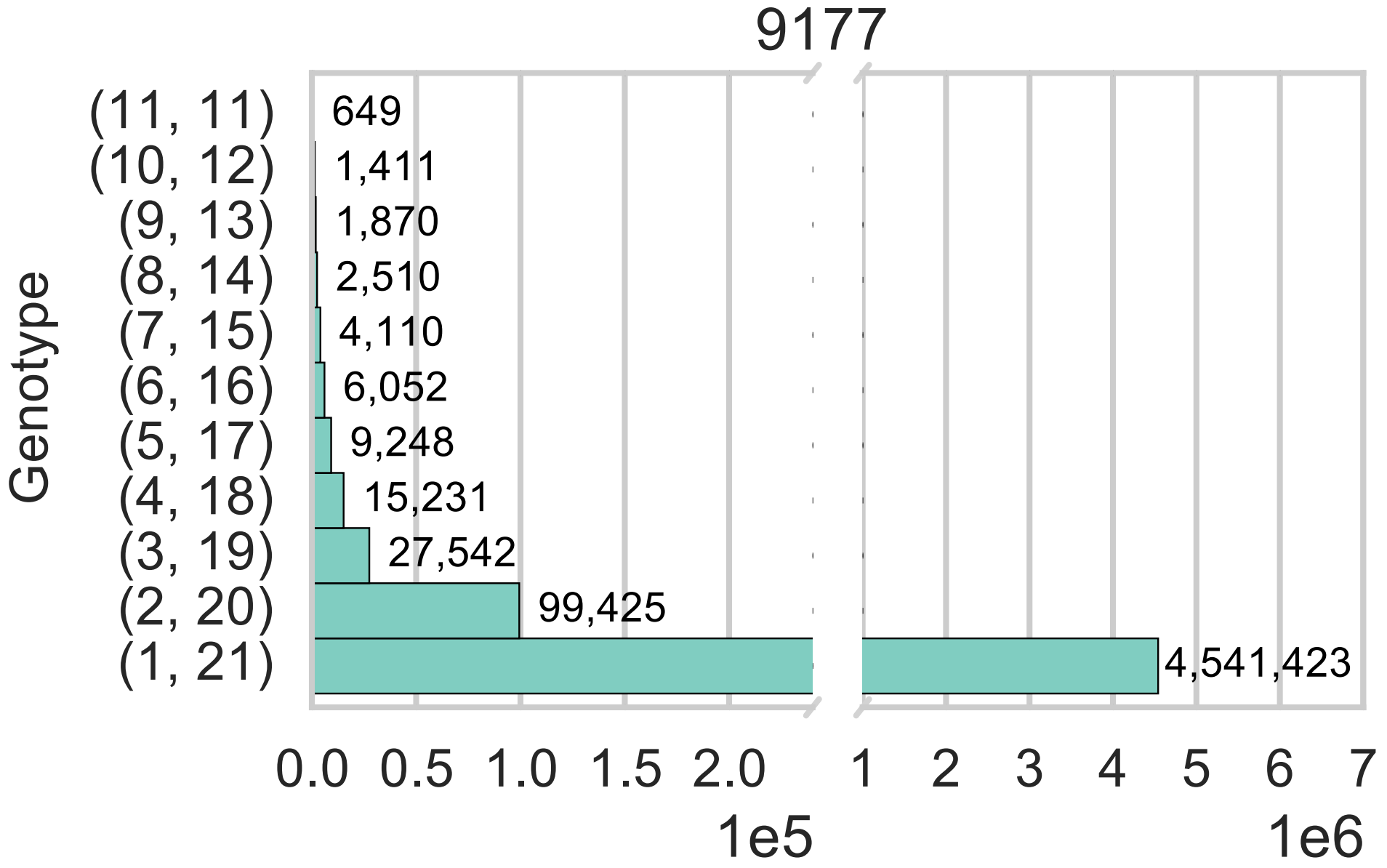

001
Genotype
(8, 8)
(7, 9)
(6, 10)
(5, 11)
(4, 12)
(3, 13)
(2, 14)
(1, 15)
33,191
62,443
53,429
42,619
37,166
40,865
2,431,543
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6

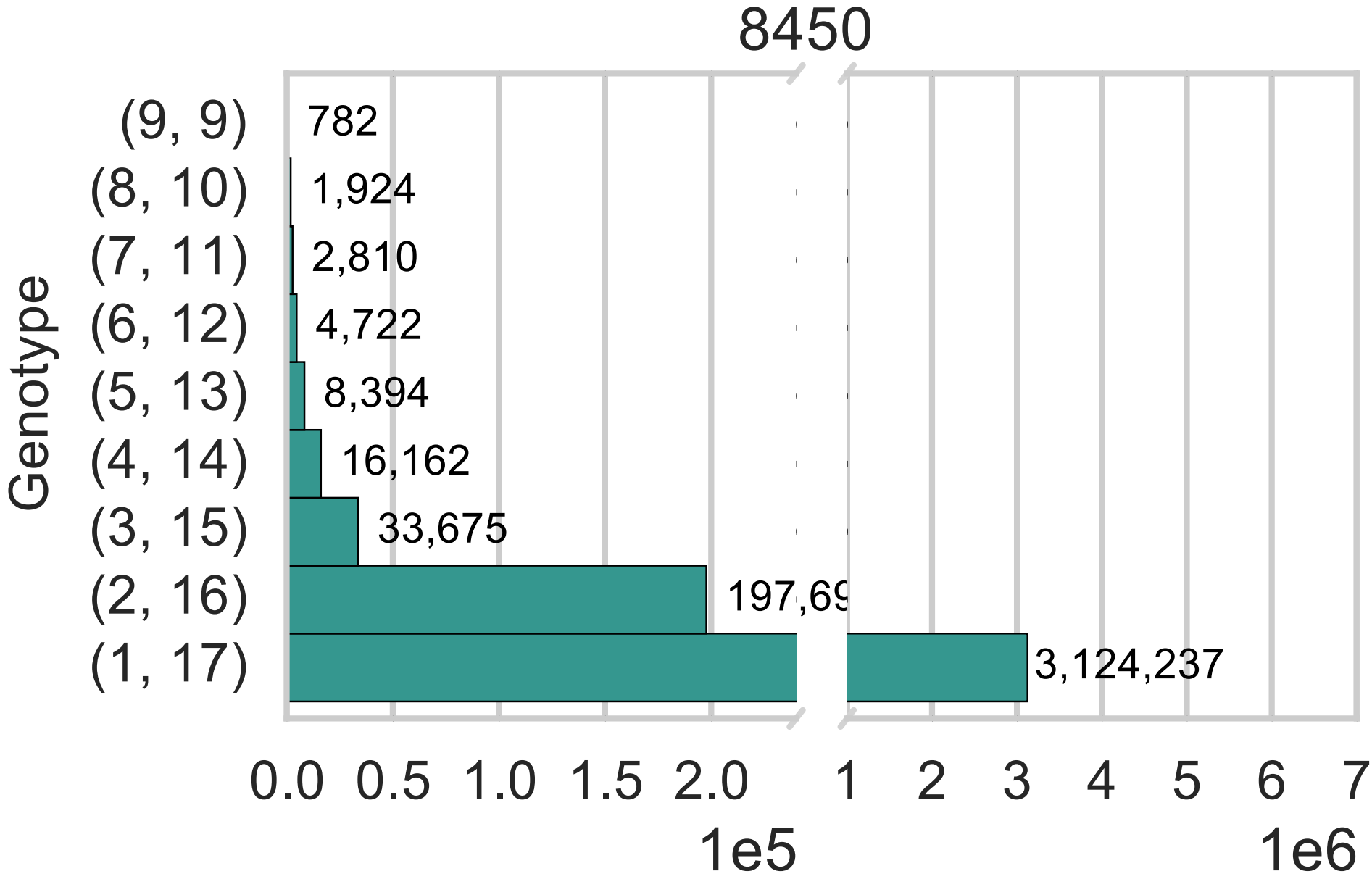

122
Genotype
(10, 10)
(9, 11)
(8, 12)
(7, 13)
(6, 14)
(5, 15)
(4, 16)
(3, 17)
(2, 18)
(1, 19)
47,161
86,564
66,880
44,014
26,187
17,094
16,923
27,881
94,116
3,389,676
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6

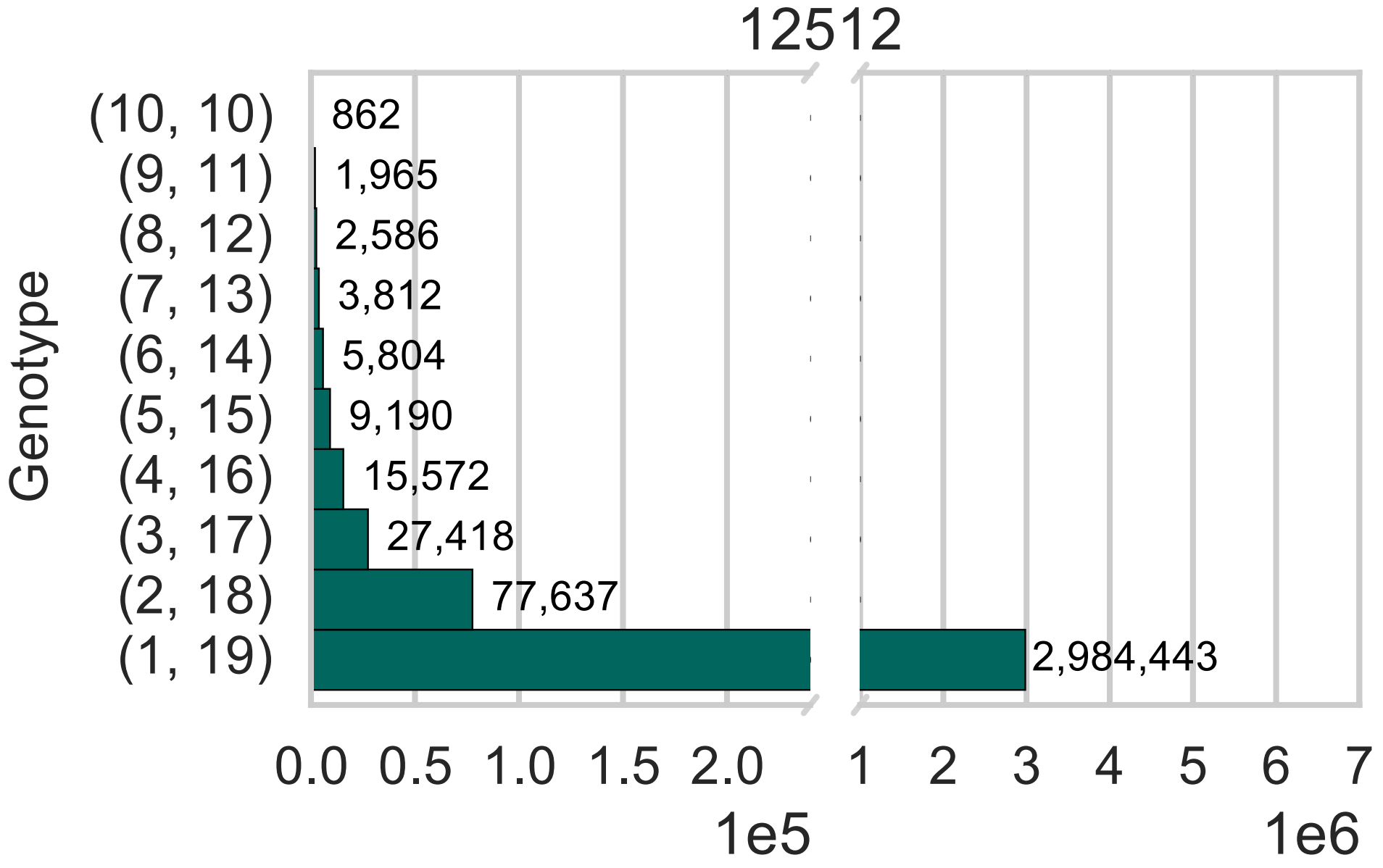

4278
Genotype
(10, 10)
(9, 11)
(8, 12)
(7, 13)
(6, 14)
(5, 15)
(4, 16)
(3, 17)
(2, 18)
(1, 19)
48,117
88,193
67,466
44,633
26,356
17,219
17,014
28,522
105,658
4,818,884
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6


9721
Genotype
(9, 9)
(8, 10)
(7, 11)
(6, 12)
(5, 13)
(4, 14)
(3, 15)
(2, 16)
(1, 17)
53,416
96,058
72,003
45,357
26,758
20,609
27,950
86,082
3,583,427
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6


6993
Genotype
(9, 9)
(8, 10)
(7, 11)
(6, 12)
(5, 13)
(4, 14)
(3, 15)
(2, 16)
(1, 17)
928
2,135
2,965
4,655
7,565
13,311
26,667
104,686
4,993,250
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6


9177
Genotype
(11, 11)
(10, 12)
(9, 13)
(8, 14)
(7, 15)
(6, 16)
(5, 17)
(4, 18)
(3, 19)
(2, 20)
(1, 21)
649
1,411
1,870
2,510
4,110
6,052
9,248
15,231
27,542
99,425
4,541,423
0.0
0.5
1.0
1.5
2.0
1e5
1
2
3
4
5
6
7
1e6


8450
Genotype
(9, 9)
(8, 10)
(7, 11)
(6, 12)
(5, 13)
(4, 14)
(3, 15)
(2, 16)
(1, 17)
782
1,924
2,810
4,722
8,394
16,162
33,675
197,69
3,124,237
0.0
0.5
1.0
1.5
2.0
1
2
3
4
5
6
7
1e5
1e6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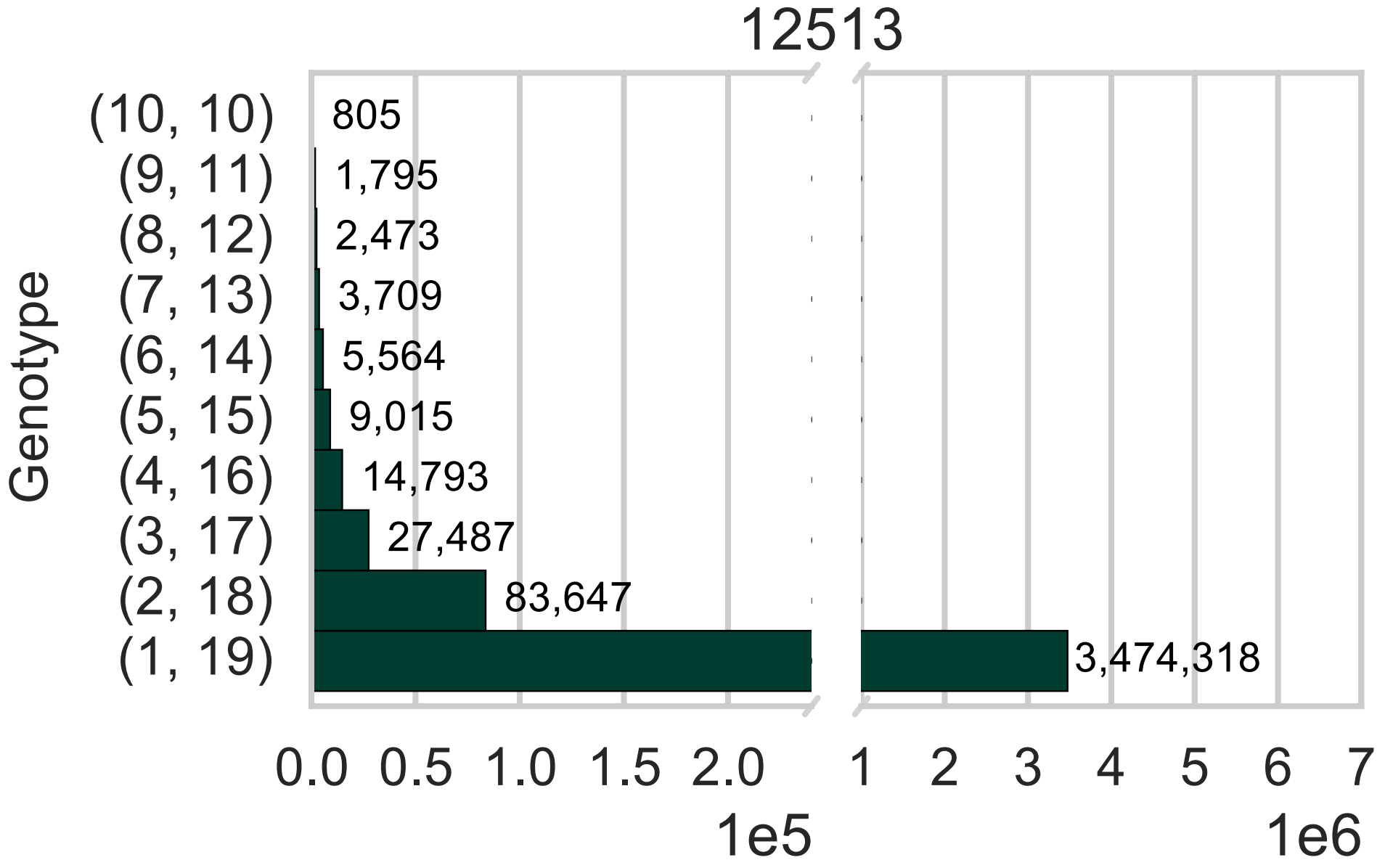
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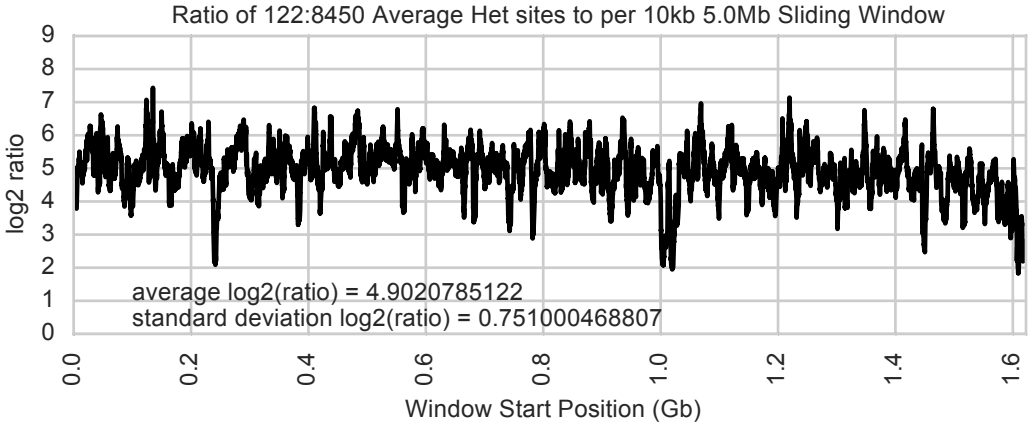
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log2 ratio
9
8
7
6
5
4
3
2
1
0
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standard deviation log2(ratio) = 0.751000468807
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
Window Start Position (Gb)