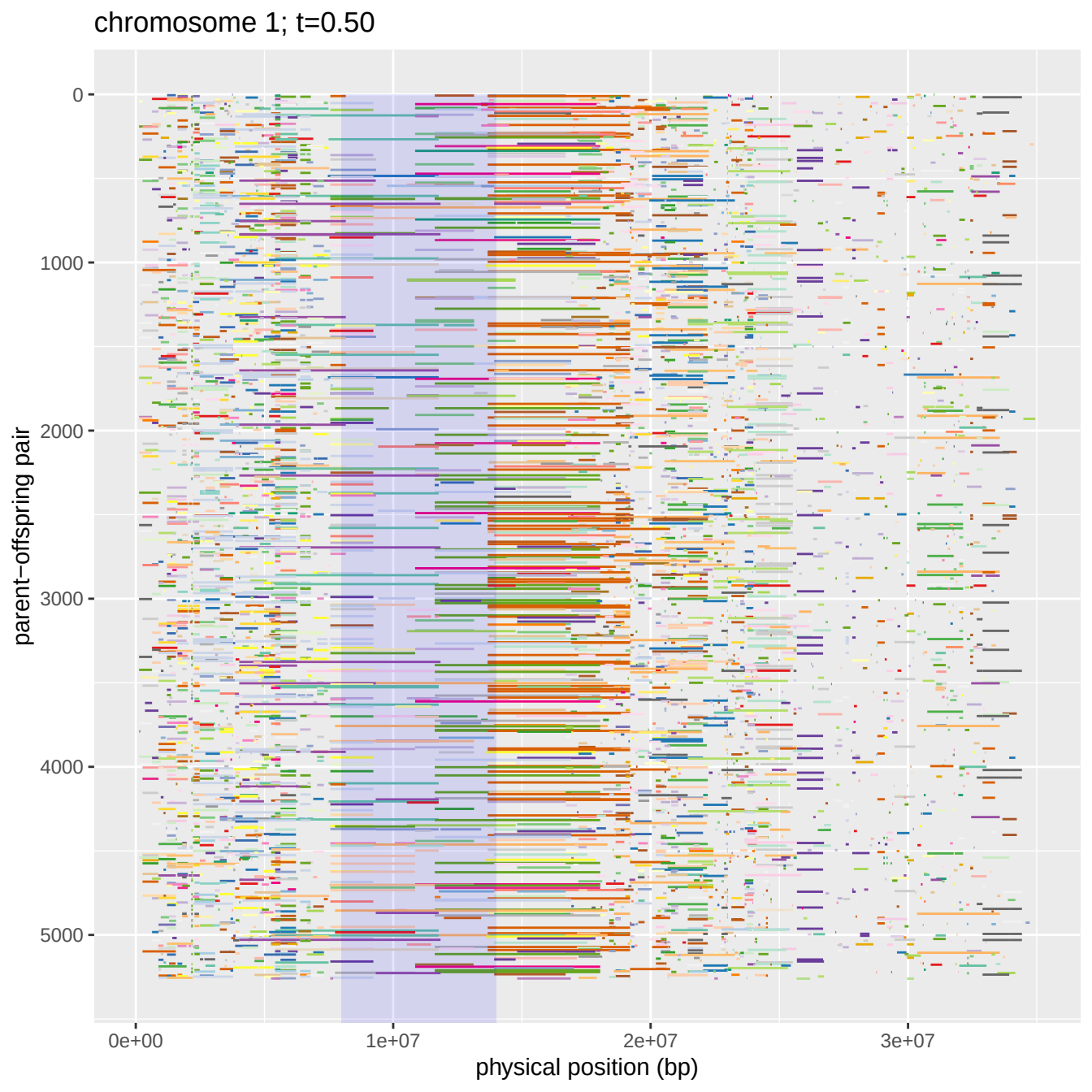
SUPPLEMENTARY INFORMATION

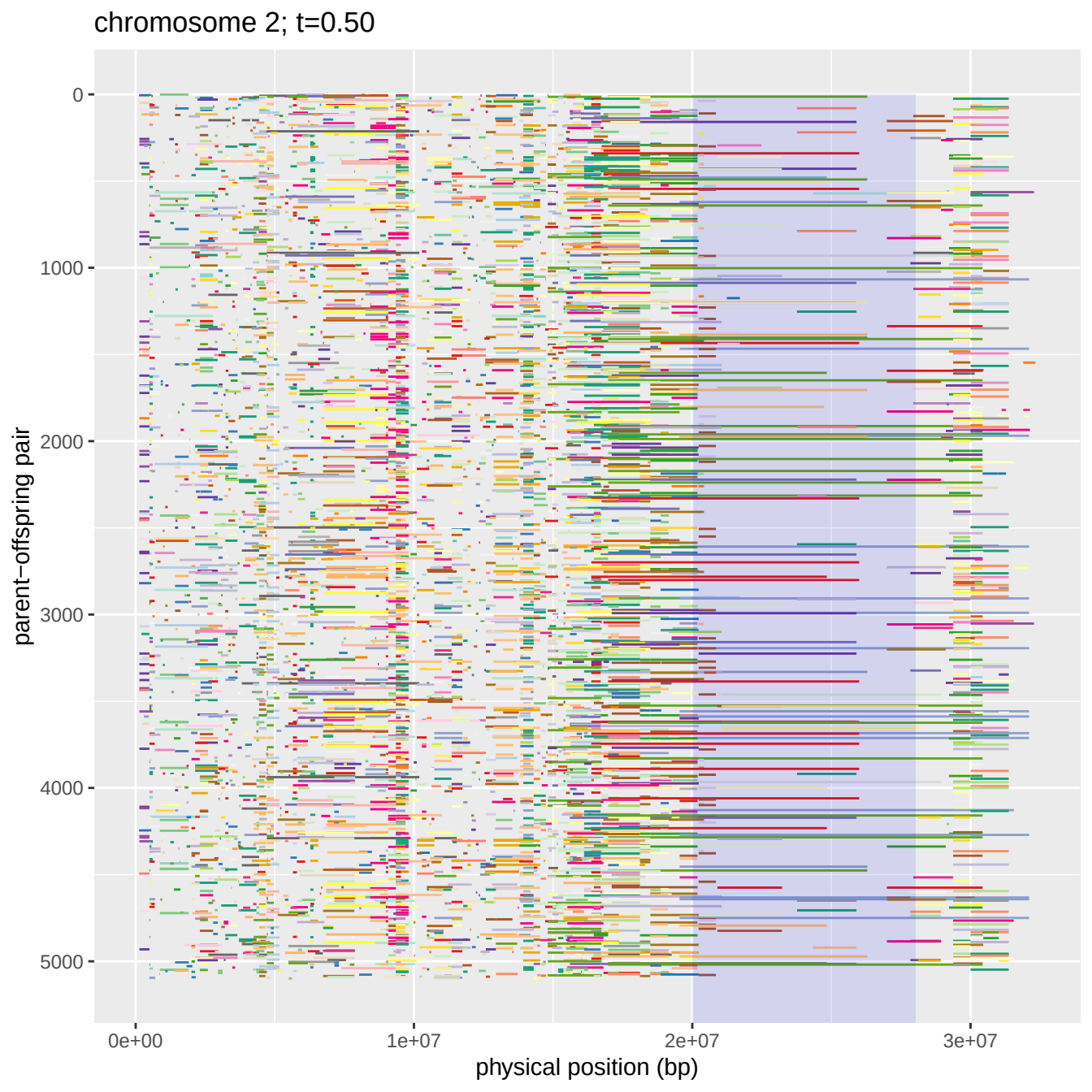
Supplementary Table 1. Number of SNPs per chromosome after filtering.

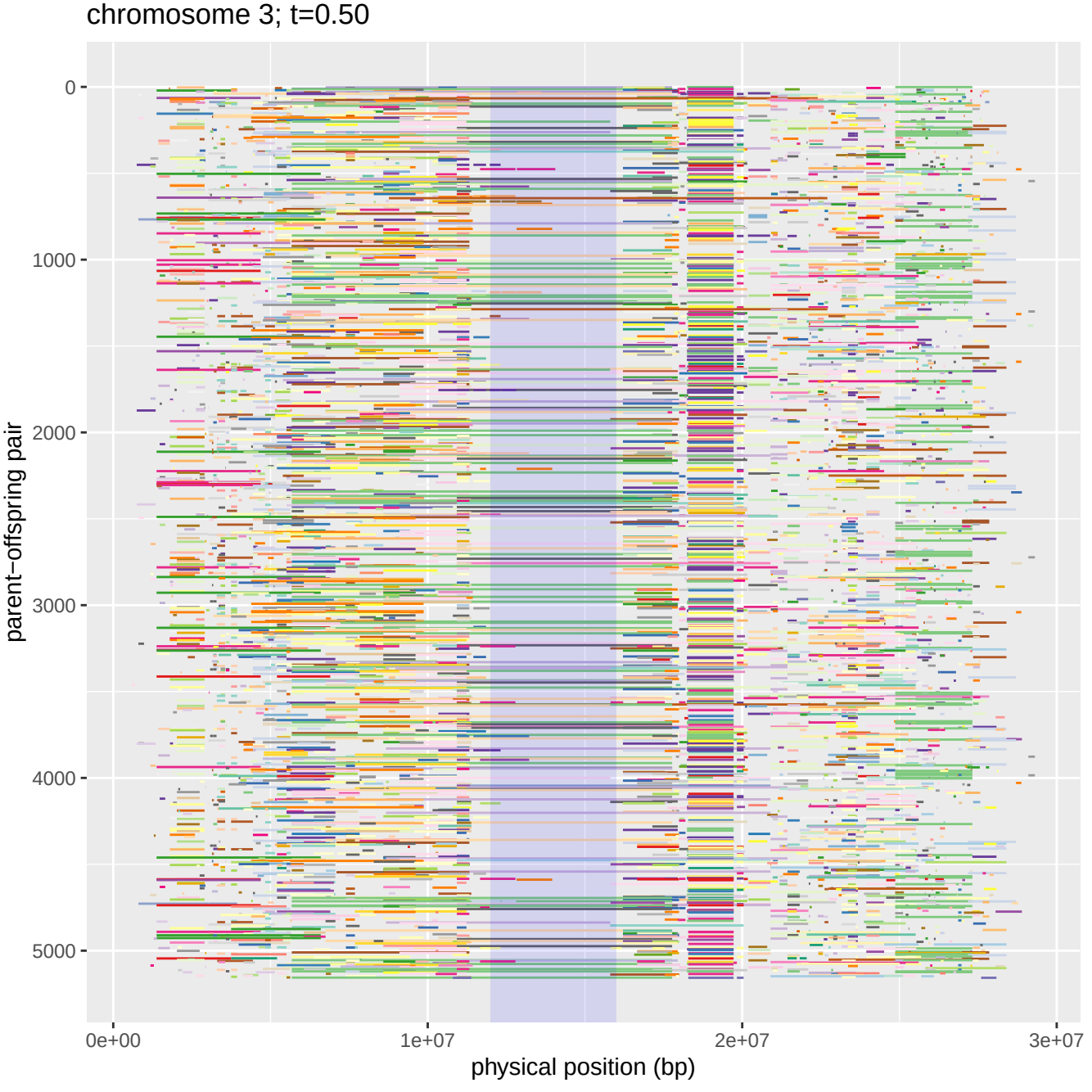
Chromosome	Number of sites before filter	Number of sites after 30% maximum-missing filter	Number of SNPs after removing monomorphic and singleton sites
1	30575	17159	3739
2	24151	14818	2265
3	22156	14493	2458
4	18271	9980	2519
5	20750	14106	1681
6	20174	12907	1609
7	12226	7163	1114
8	17991	11549	1689
9	18267	12194	1341
10	14985	8206	1573
11	18816	11267	1777
12	15906	9921	1703
13	15851	9969	2018
14	20635	11957	2939
15	20048	13239	1705
16	15447	9832	1267
17	15390	8716	2206
18	15053	9063	1524

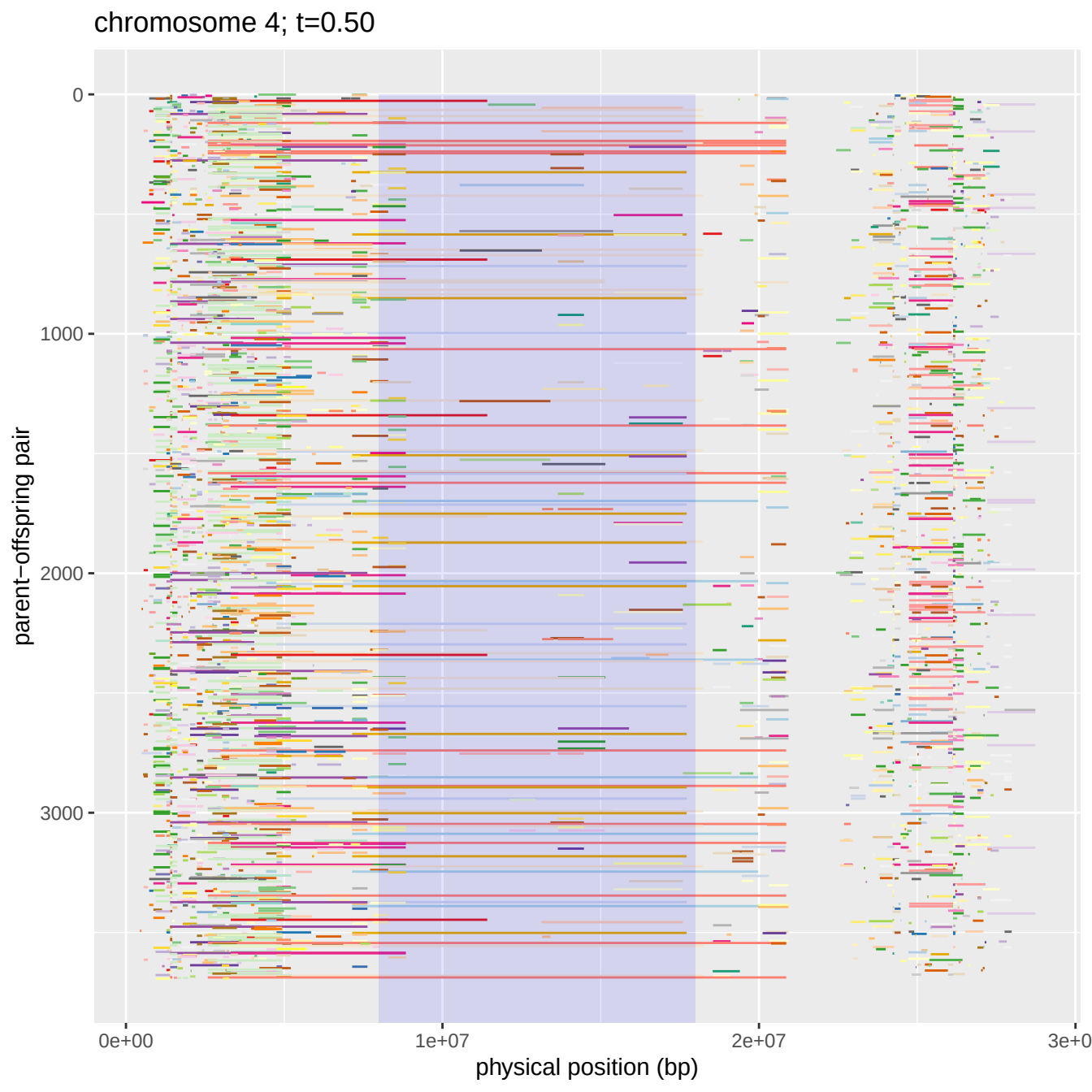
The table lists the number of sites in the dataset for each chromosome before and after applying filters to remove sites with more than 30% missingness across samples, and monomorphic and singleton sites.

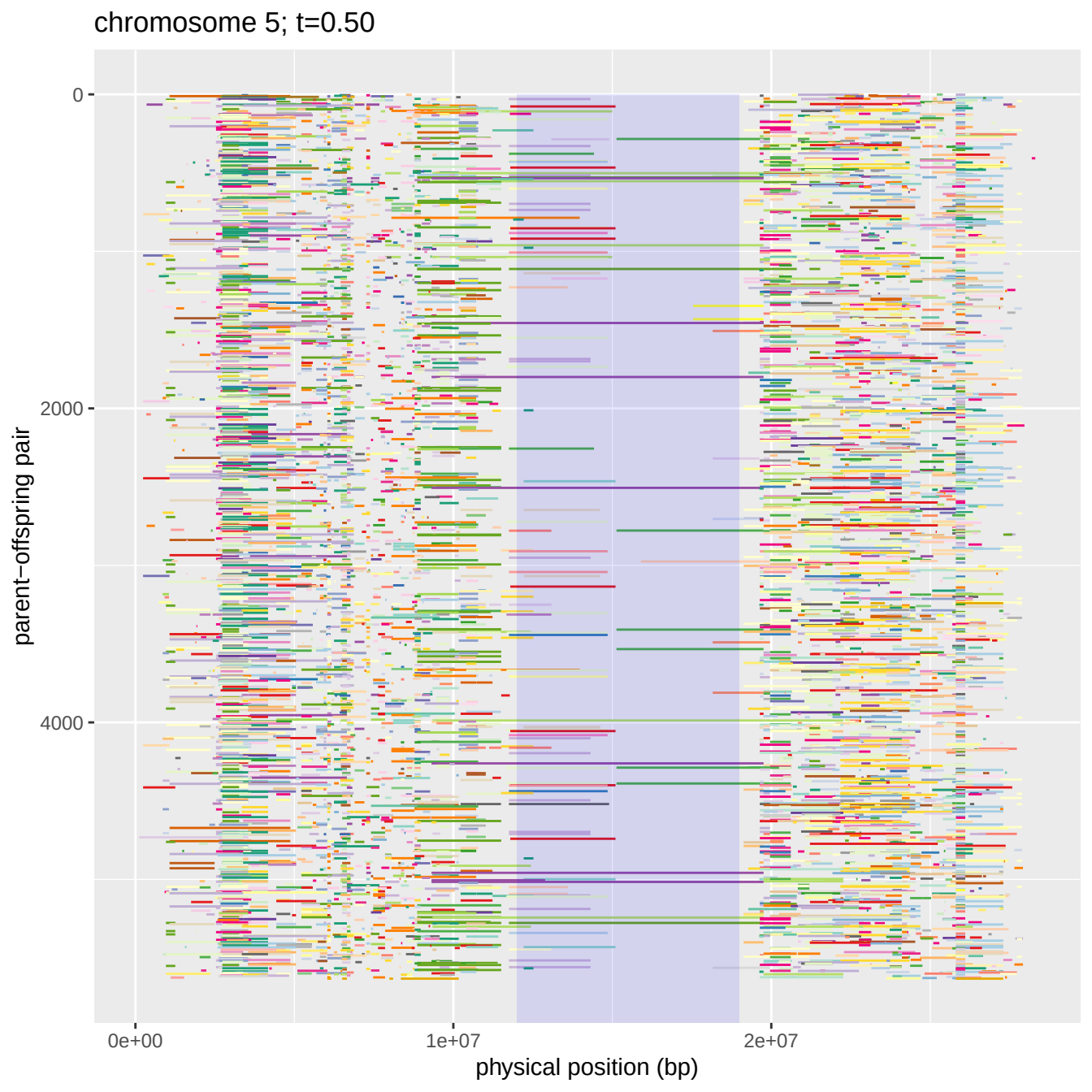
Supplementary Figure 1. **Crossover intervals inferred with SHAPEIT2-duoHMM across the 18 chromosomes.**
Each plot shows the physical position (bp) of the chromosome on the x-axis and the parent-offspring pairs on the y-axis. Horizontal lines represent intervals within which a crossover has occurred with a probability above the significance threshold t = 0.5. The lines are colored by parent such that crossover intervals detected in the same parent-offspring duo appear on the same row and in the same color. The centromere for each chromosome is shaded blue. The data were filtered to remove sites with more than 30% missingness before running SHAPEIT2-duoHMM.

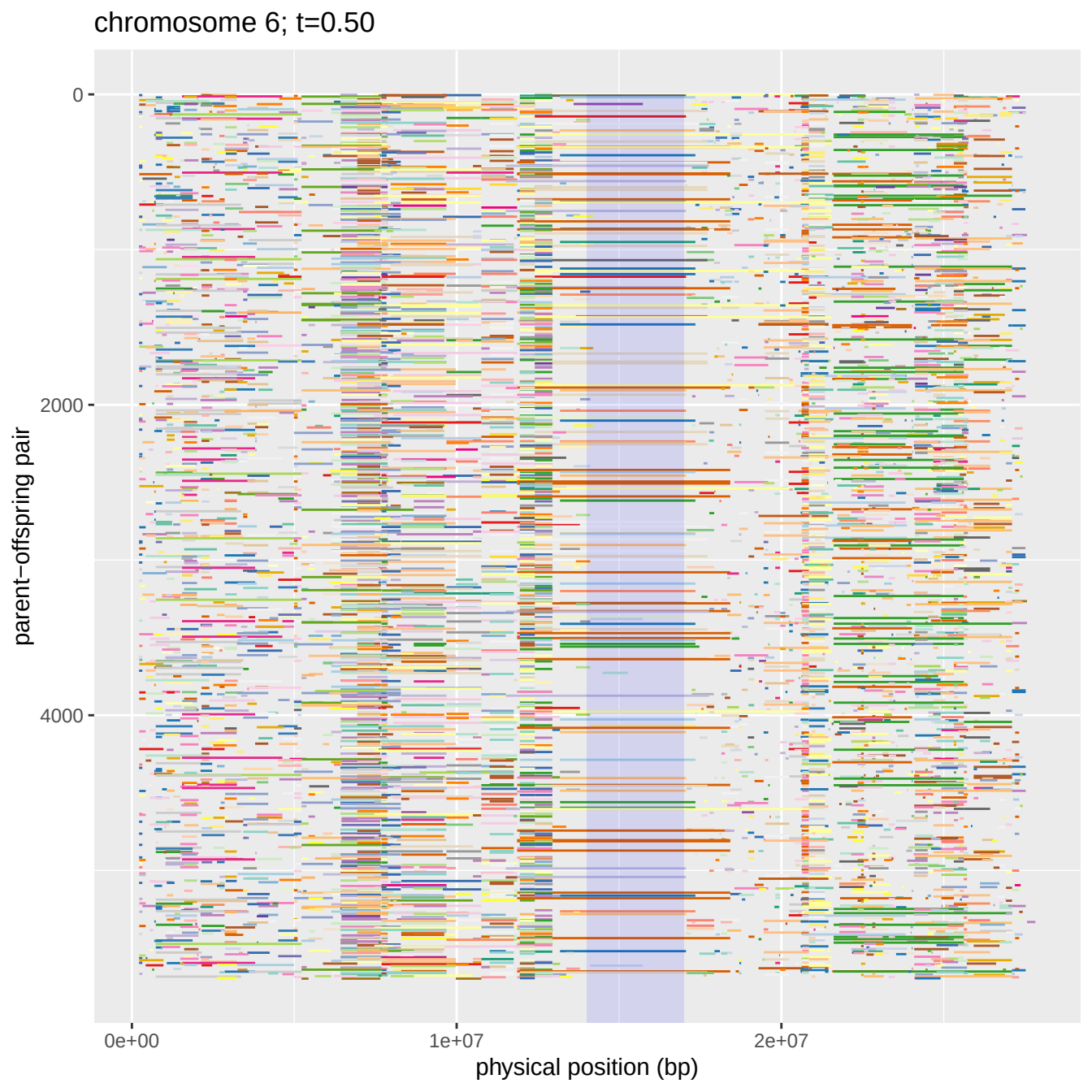

chromosome 1; t=0.50
parent−offspring pair
0
1000
2000
3000
4000
5000
0e+00
1e+07
2e+07
3e+07
physical position (bp)

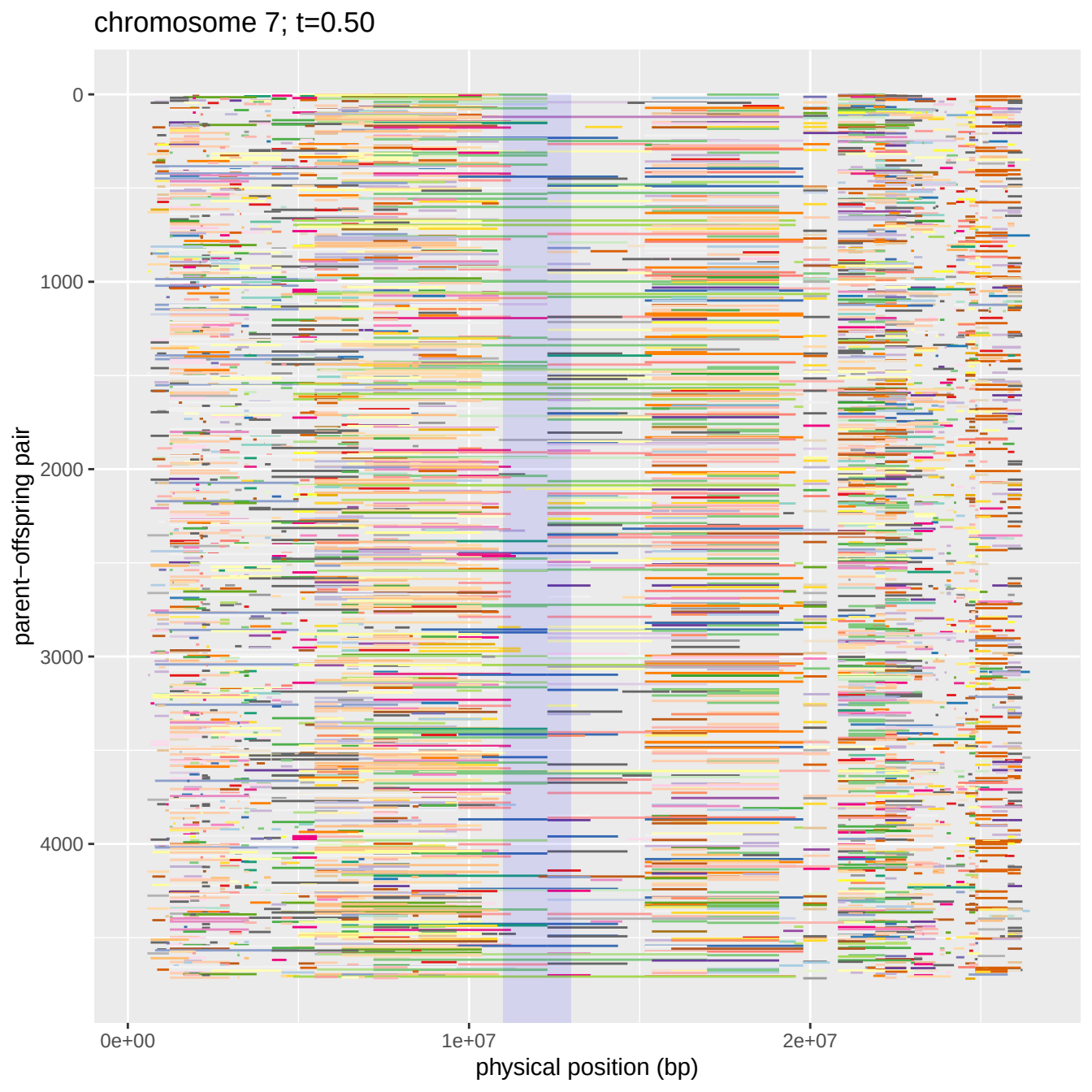

chromosome 2; t=0.50
parent−offspring pair
0
1000
2000
3000
4000
5000
0e+00
1e+07
2e+07
3e+07
physical position (bp)

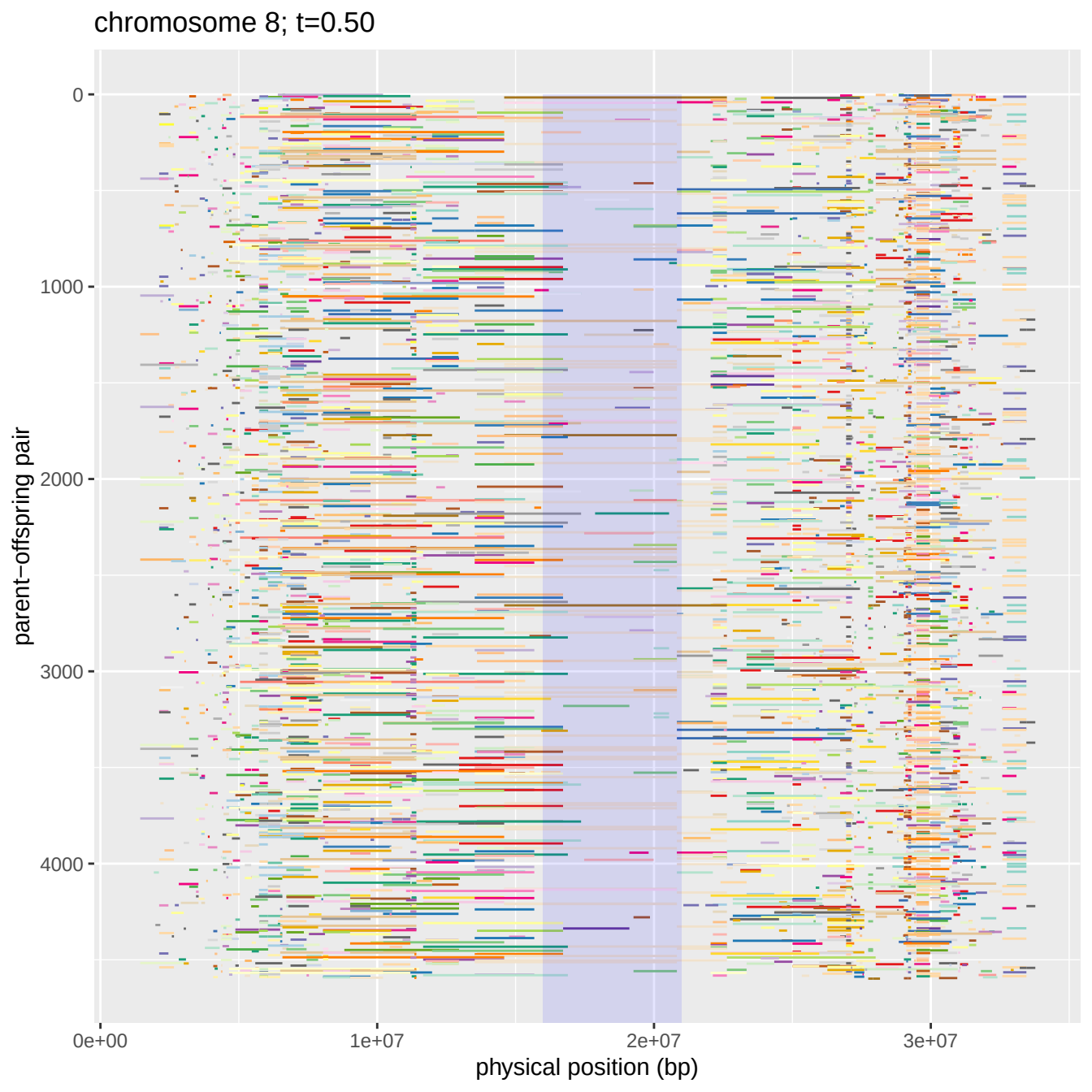

chromosome 3; t=0.50
parent−offspring pair
0
1000
2000
3000
4000
5000
0e+00
1e+07
2e+07
3e+07
physical position (bp)

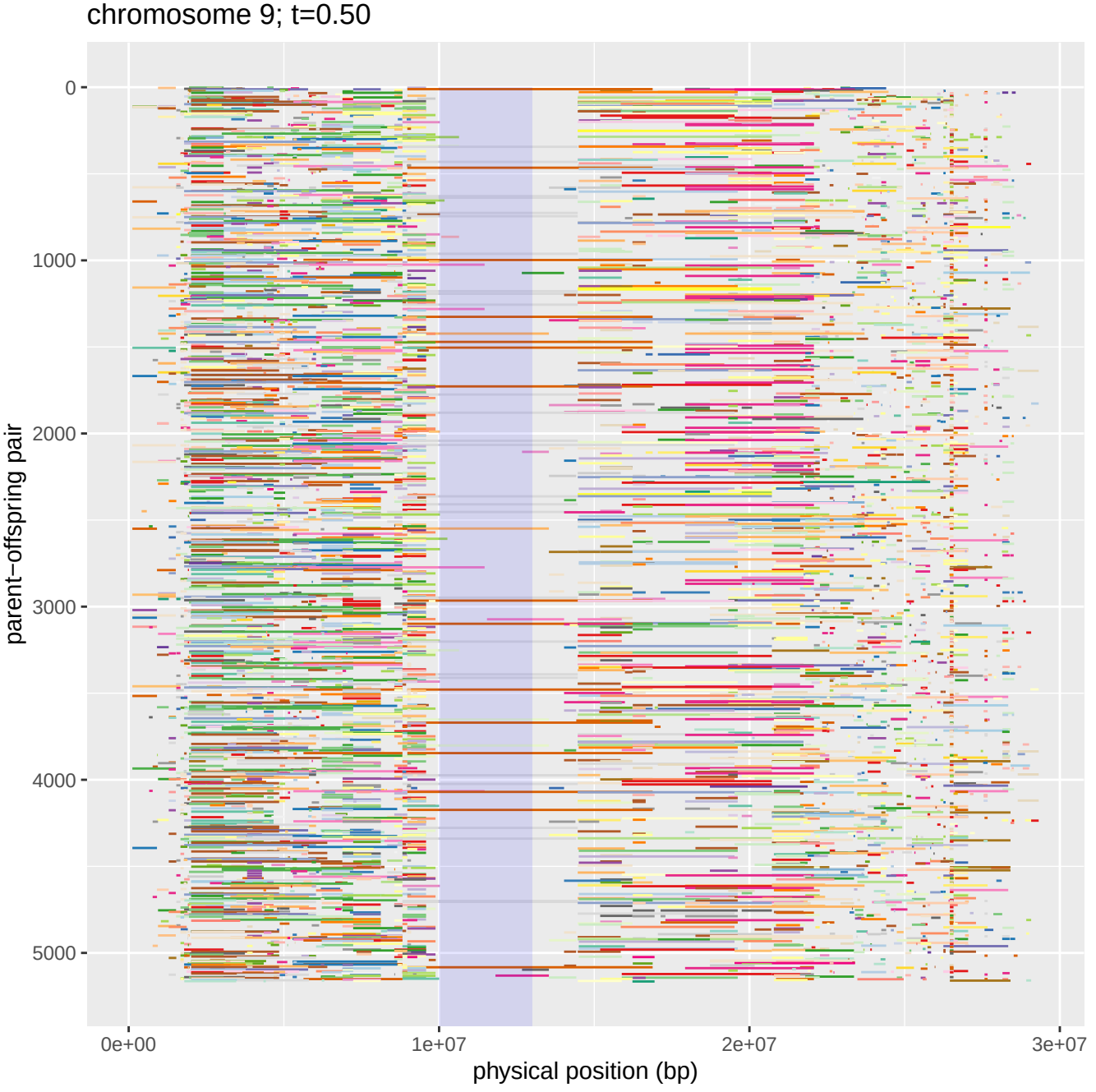

chromosome 4; t=0.50
parent−offspring pair
0
1000
2000
3000
0e+00
1e+07
2e+07
3e+0
physical position (bp)

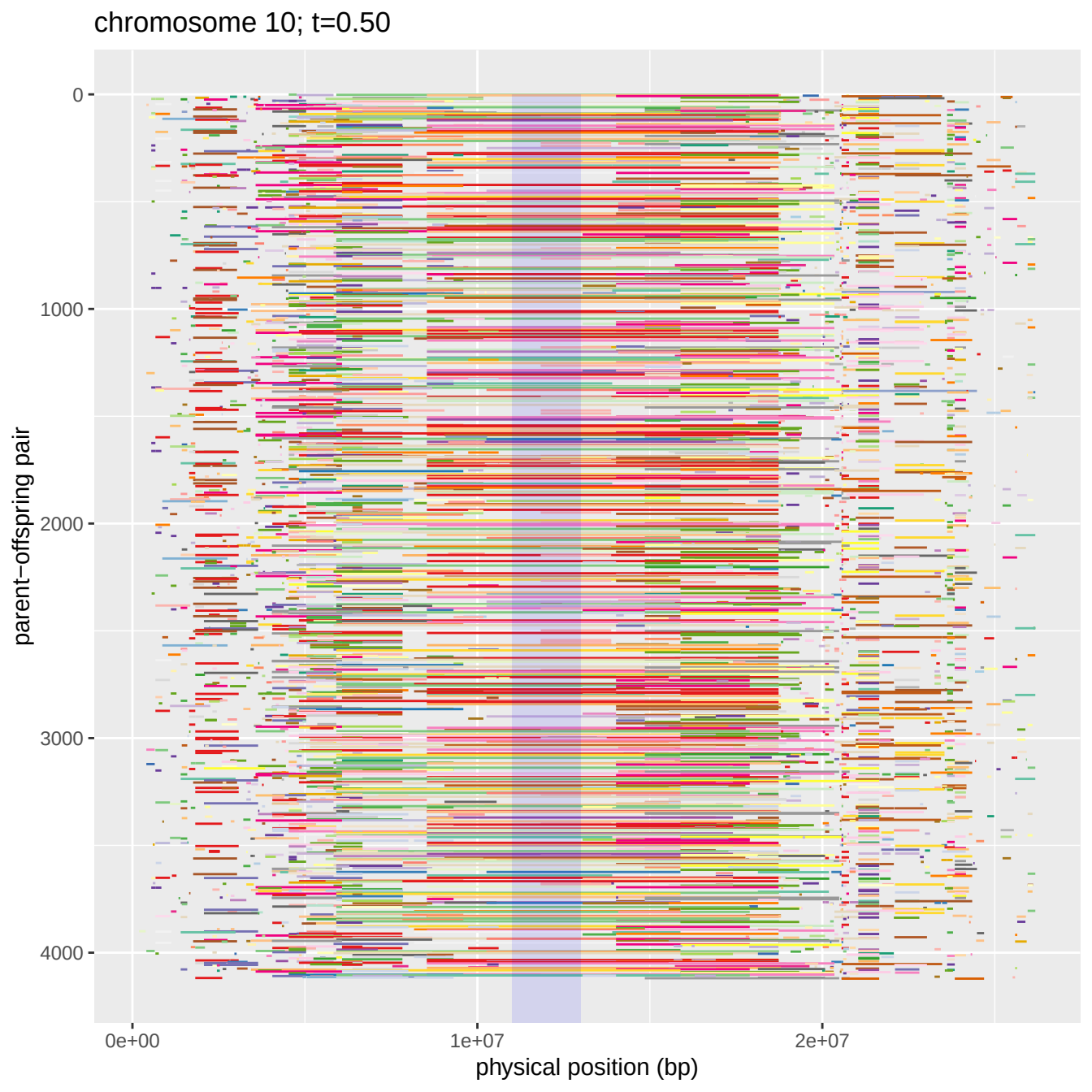

chromosome 5; t=0.50
0
2000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

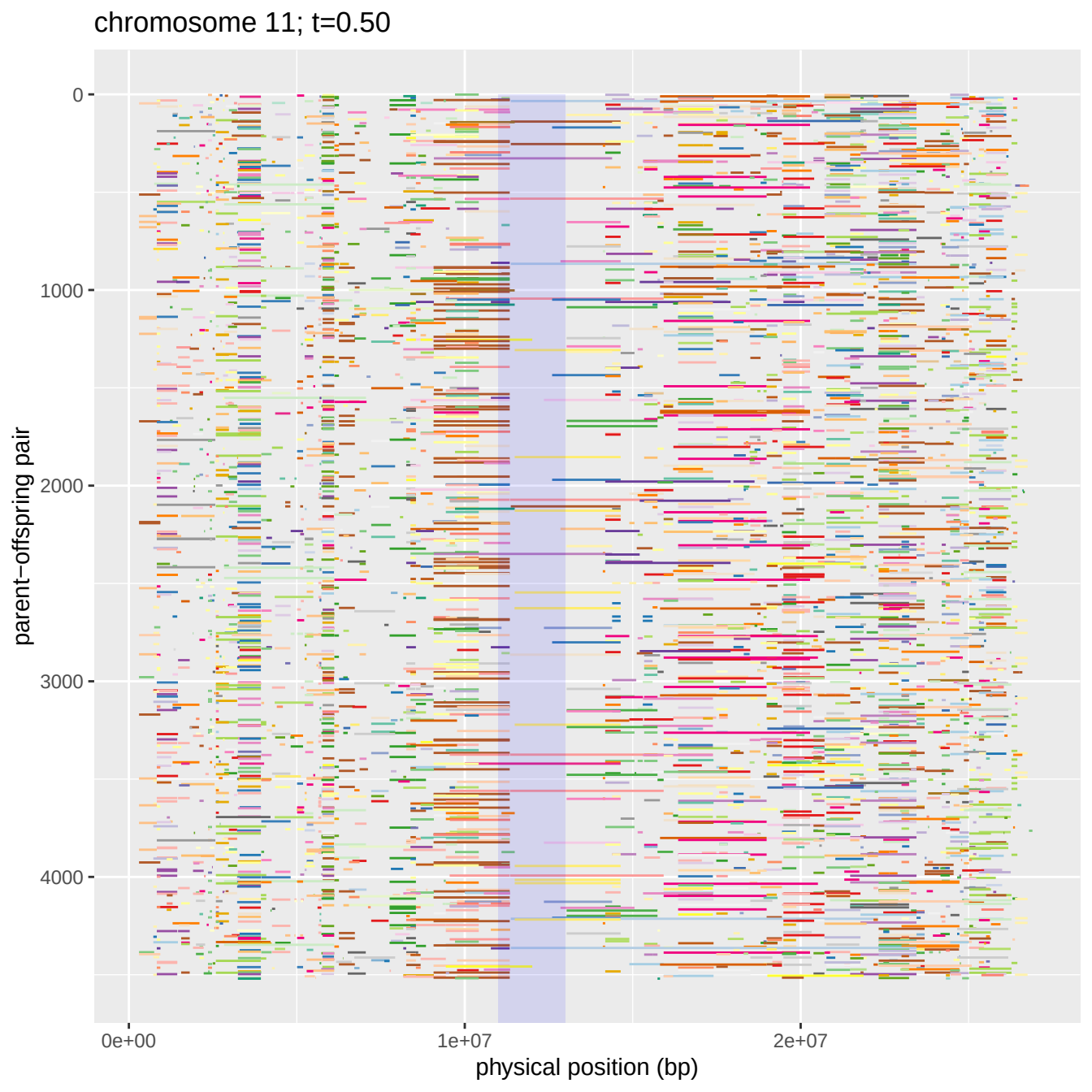

chromosome 6; t=0.50
0
2000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

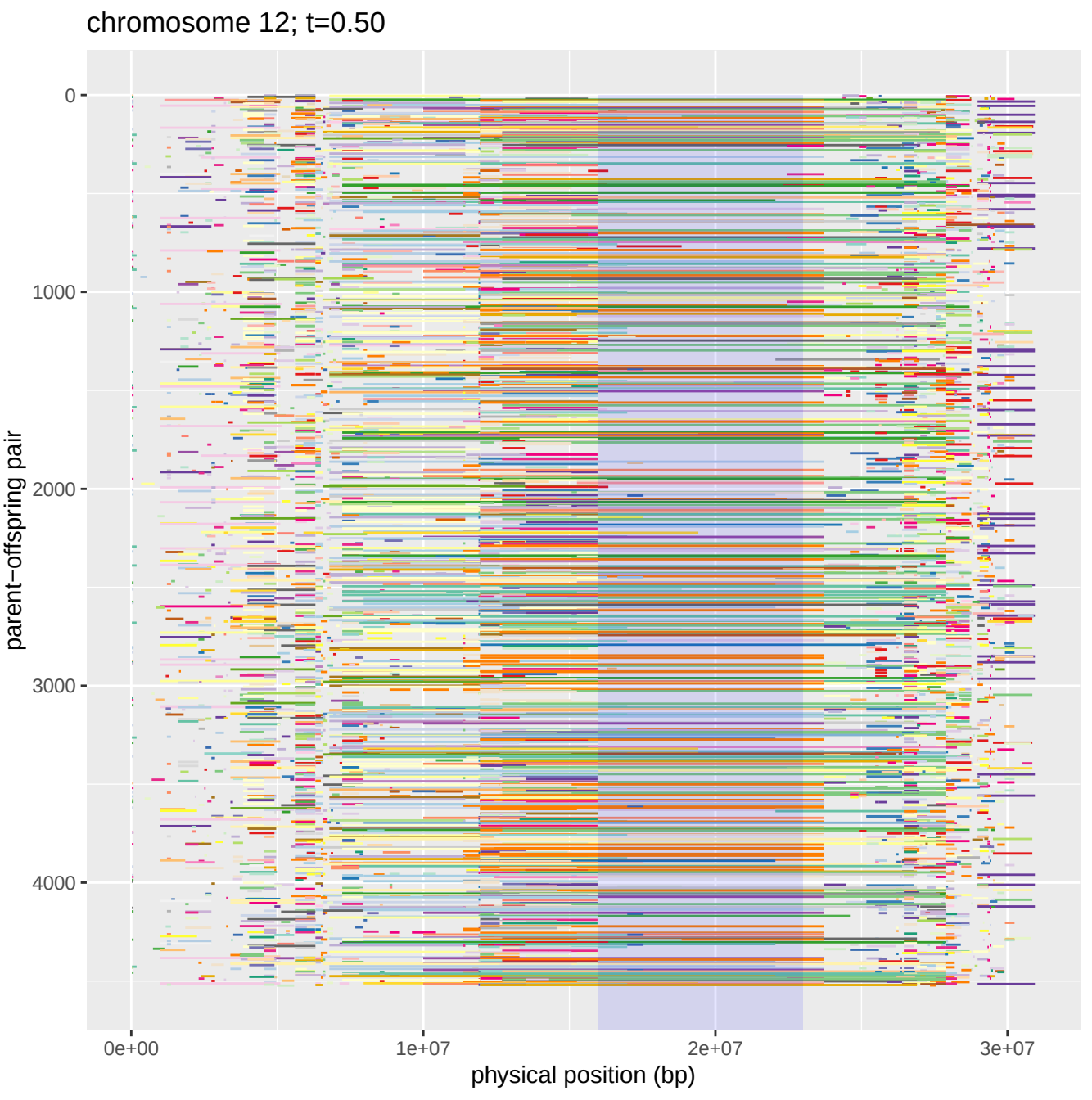

chromosome 7; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

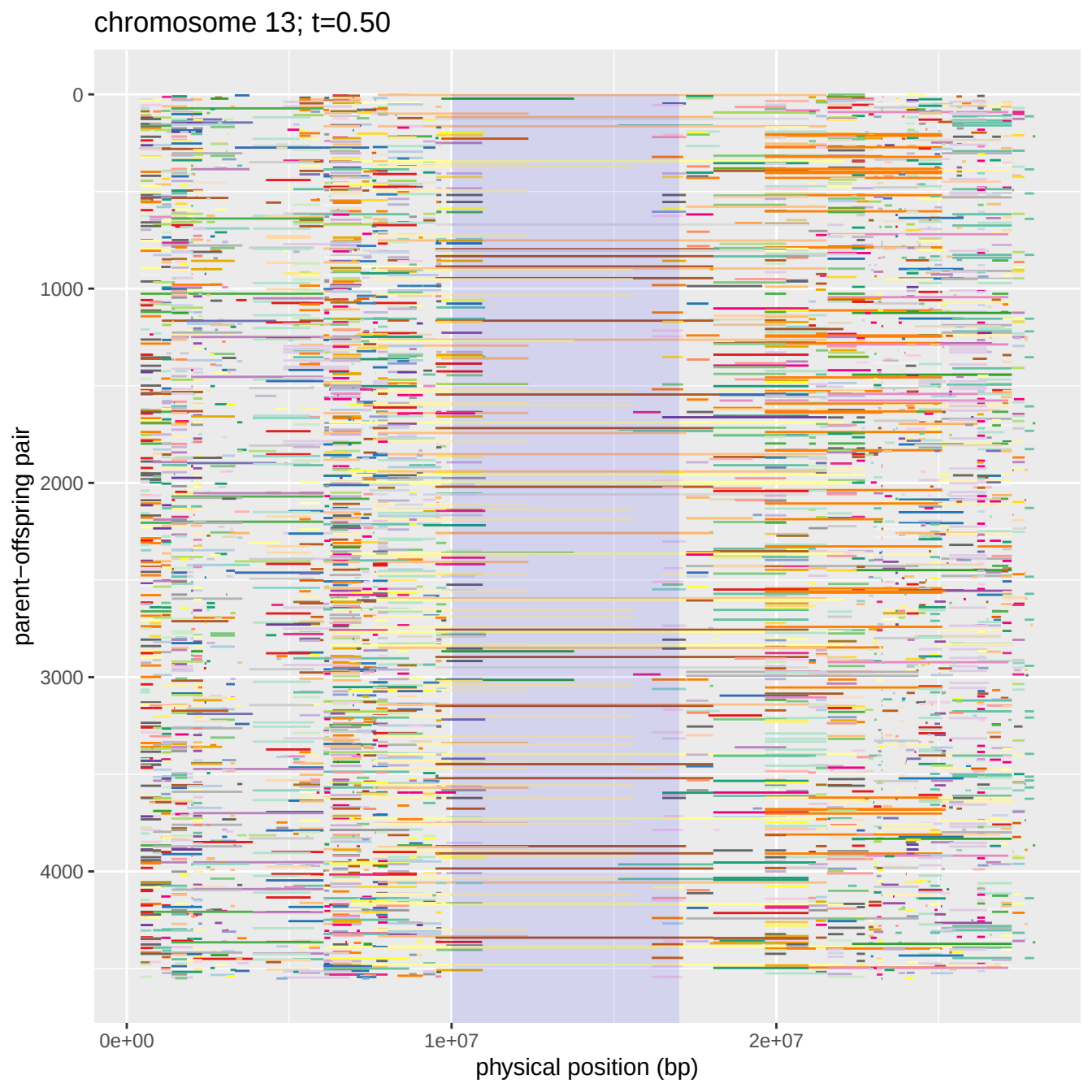

chromosome 8; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
3e+07
physical position (bp)

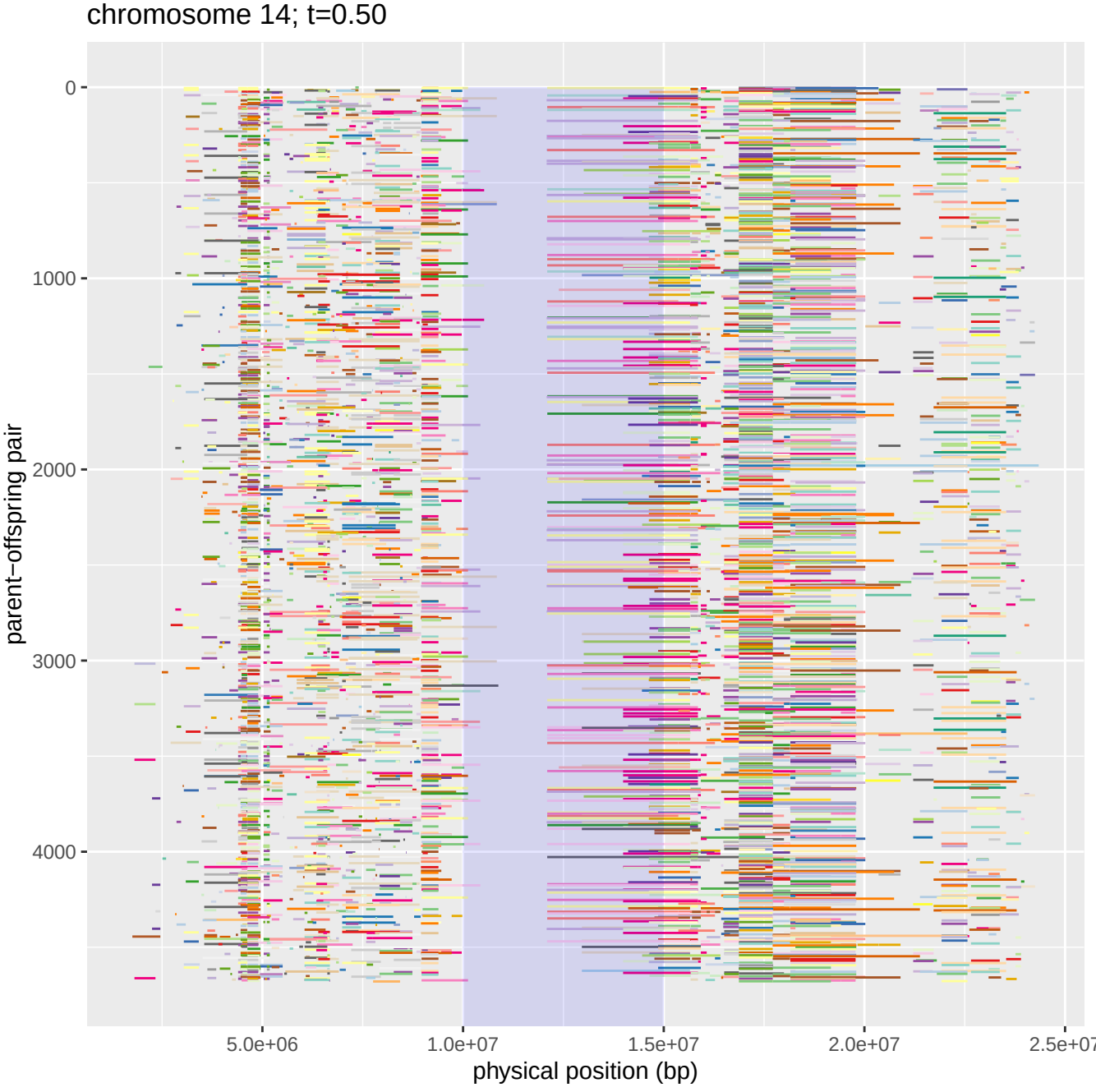

chromosome 9; t=0.50
parent−offspring pair
0
1000
2000
3000
4000
5000
0e+00
1e+07
2e+07
3e+07
physical position (bp)

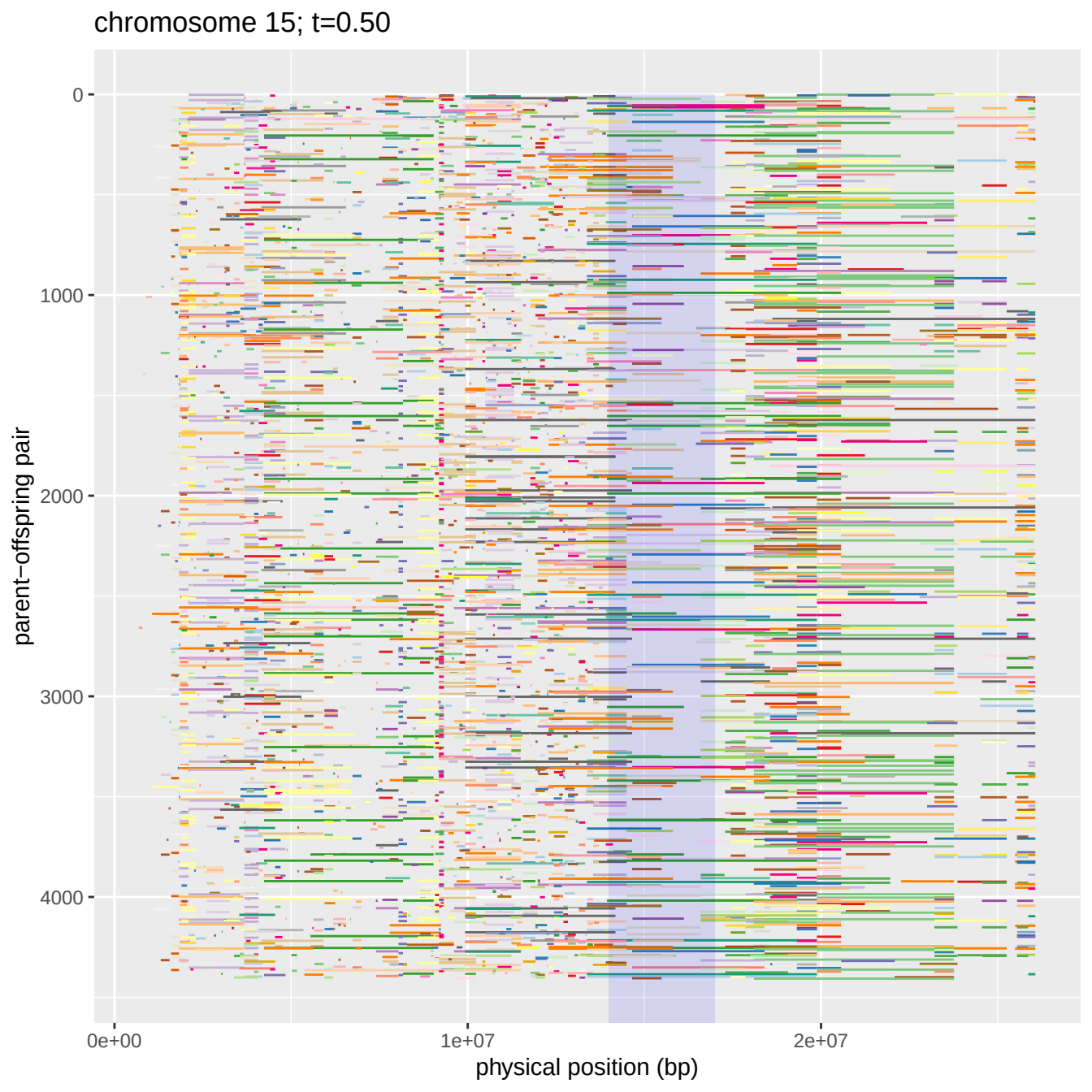

chromosome 10; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

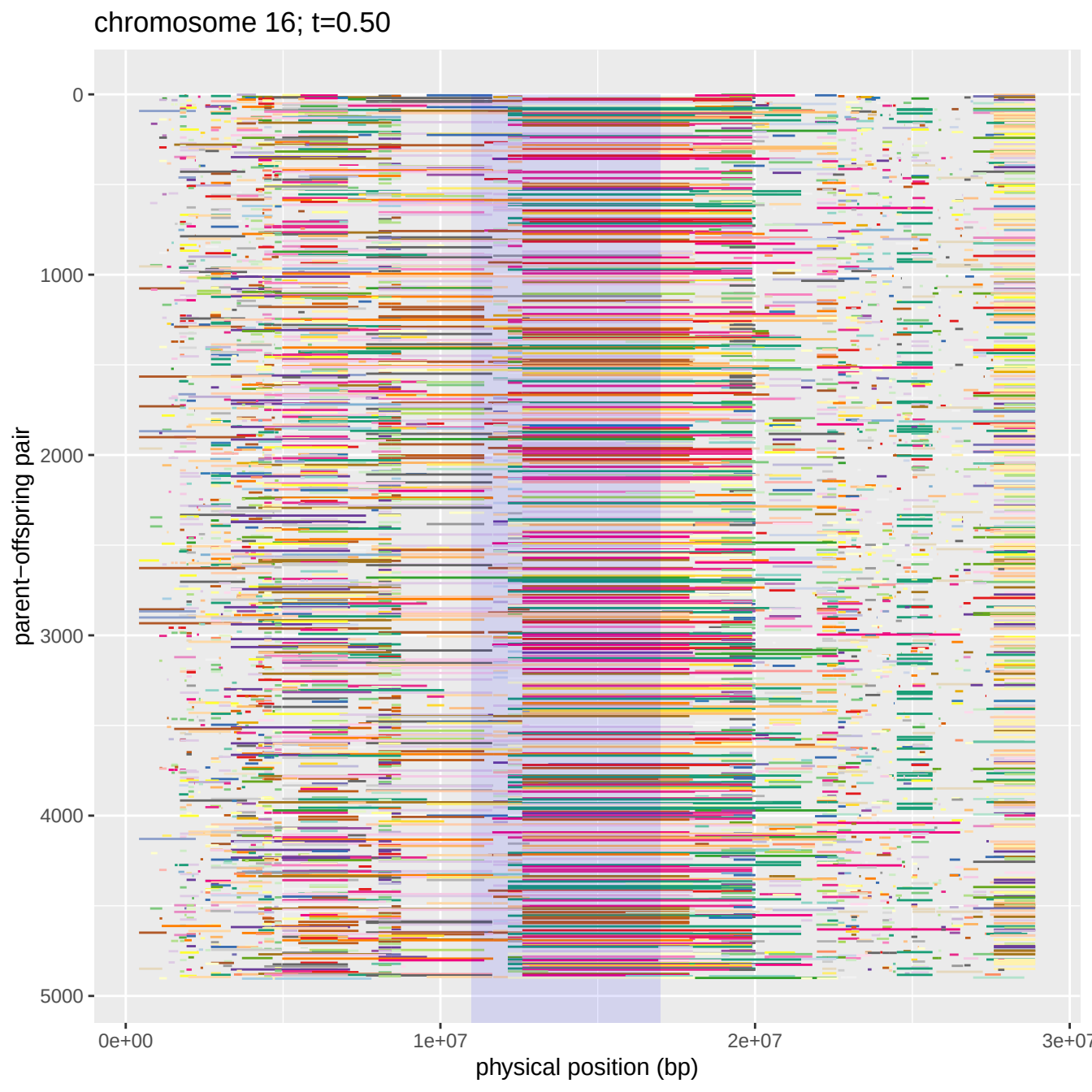

chromosome 11; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

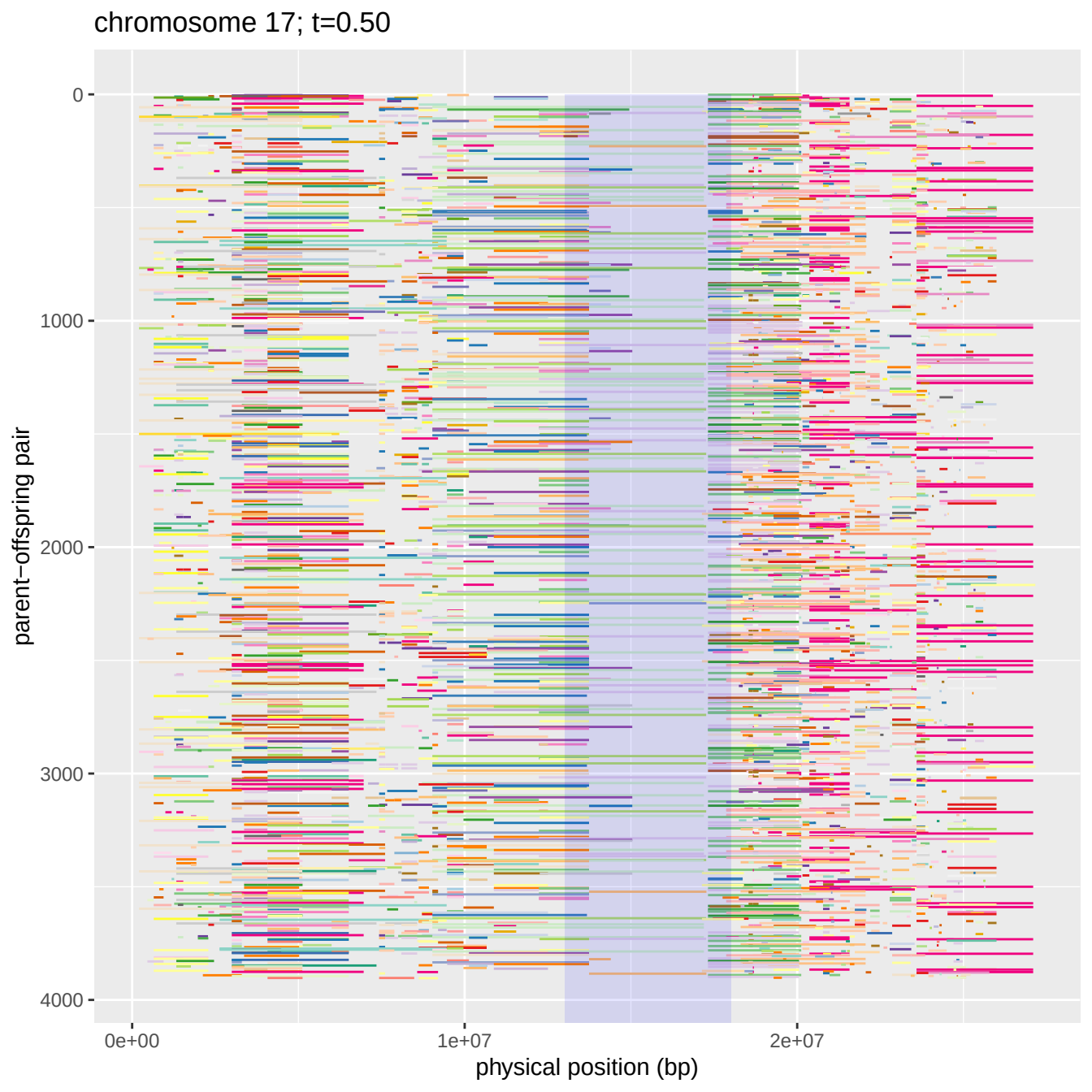

chromosome 12; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
3e+07
physical position (bp)

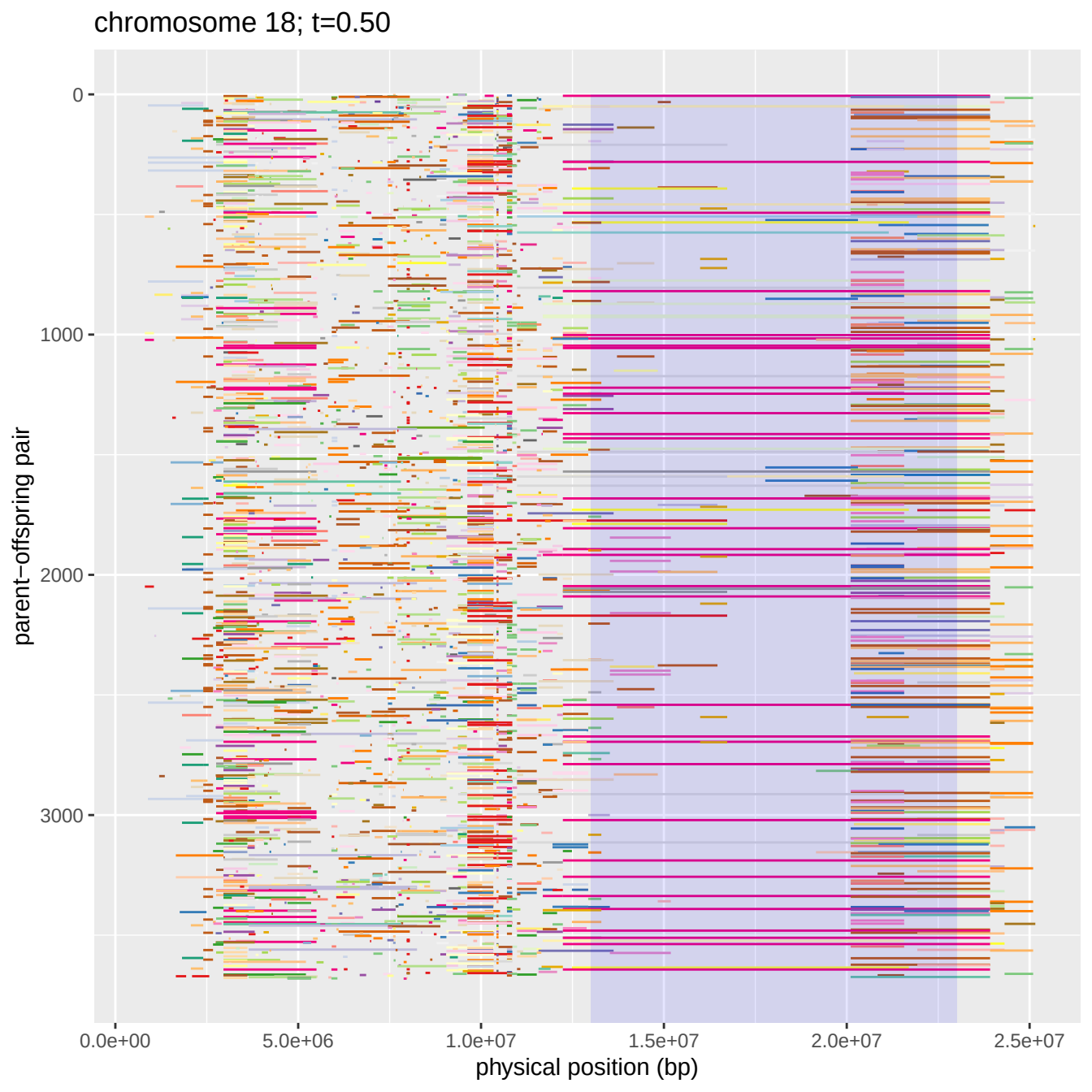

chromosome 13; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)


chromosome 14; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
5.0e+06
1.0e+07
1.5e+07
2.0e+07
2.5e+07
physical position (bp)


chromosome 15; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

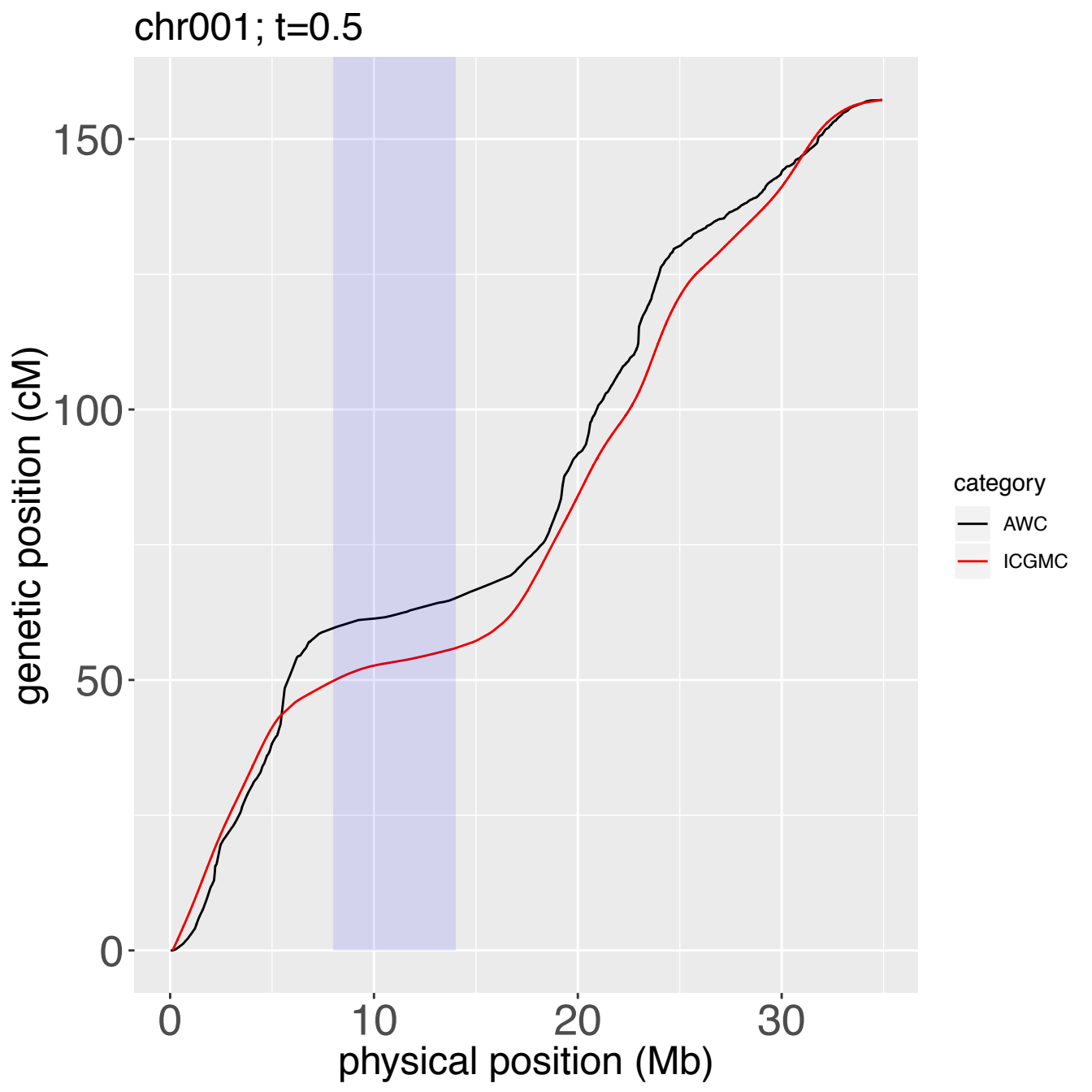

chromosome 16; t=0.50
0
1000
2000
3000
4000
5000
parent−offspring pair
0e+00
1e+07
2e+07
3e+07
physical position (bp)

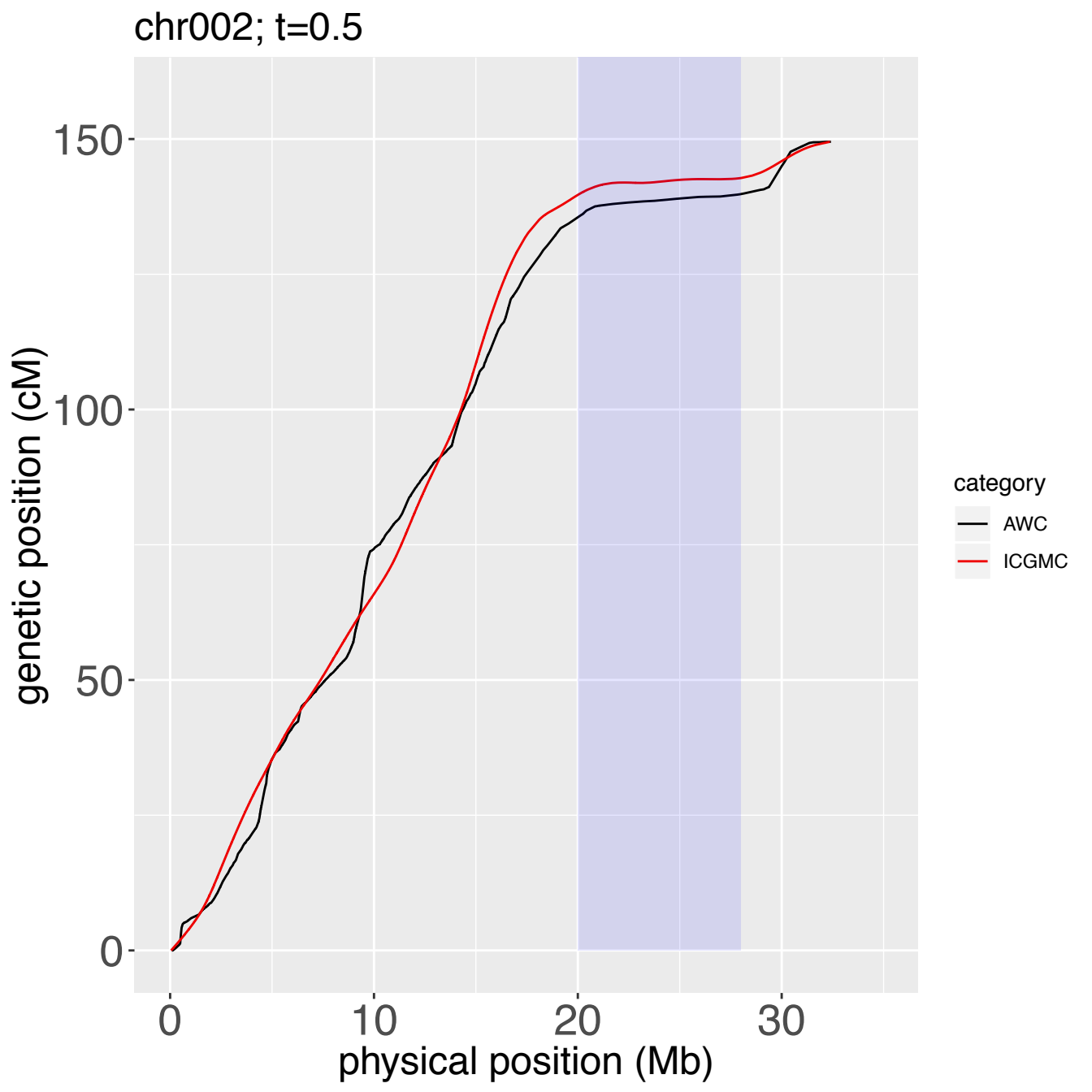

chromosome 17; t=0.50
0
1000
2000
3000
4000
parent−offspring pair
0e+00
1e+07
2e+07
physical position (bp)

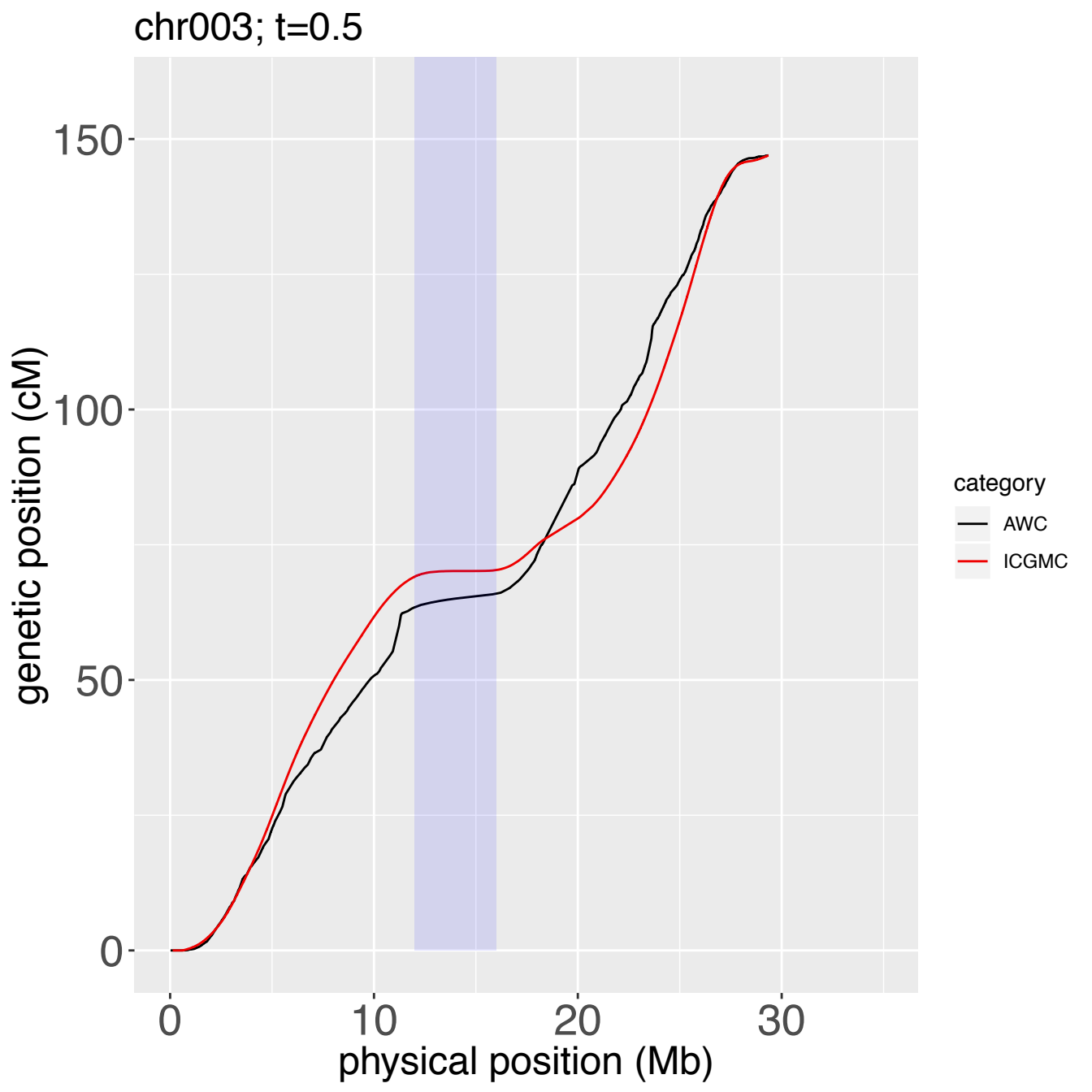

chromosome 18; t=0.50
0
1000
2000
3000
parent−offspring pair
0.0e+00
5.0e+06
1.0e+07
1.5e+07
2.0e+07
2.5e+07
physical position (bp)

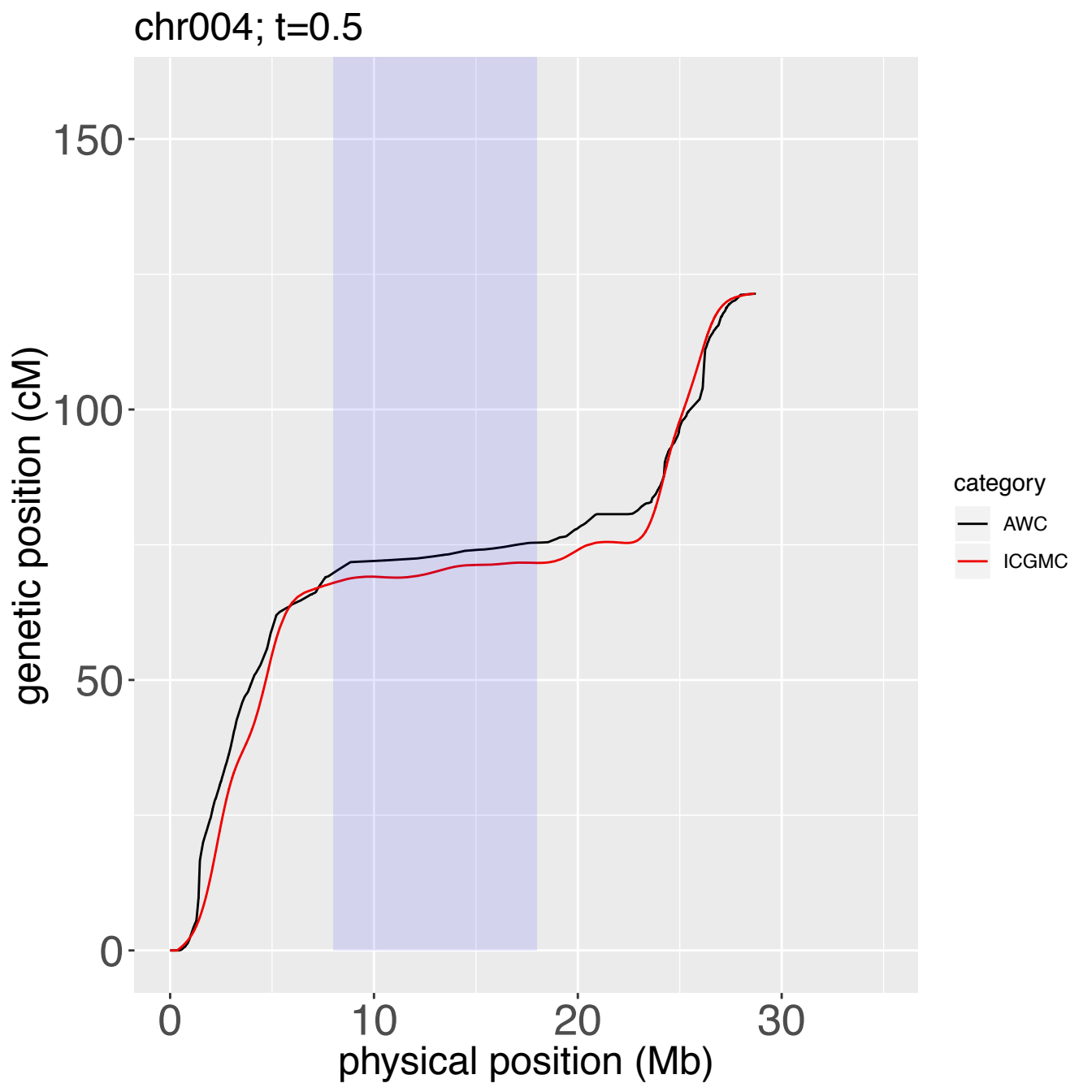
Supplementary Figure 2. Comparison of our genetic map with the previously constructed ICGMC map.

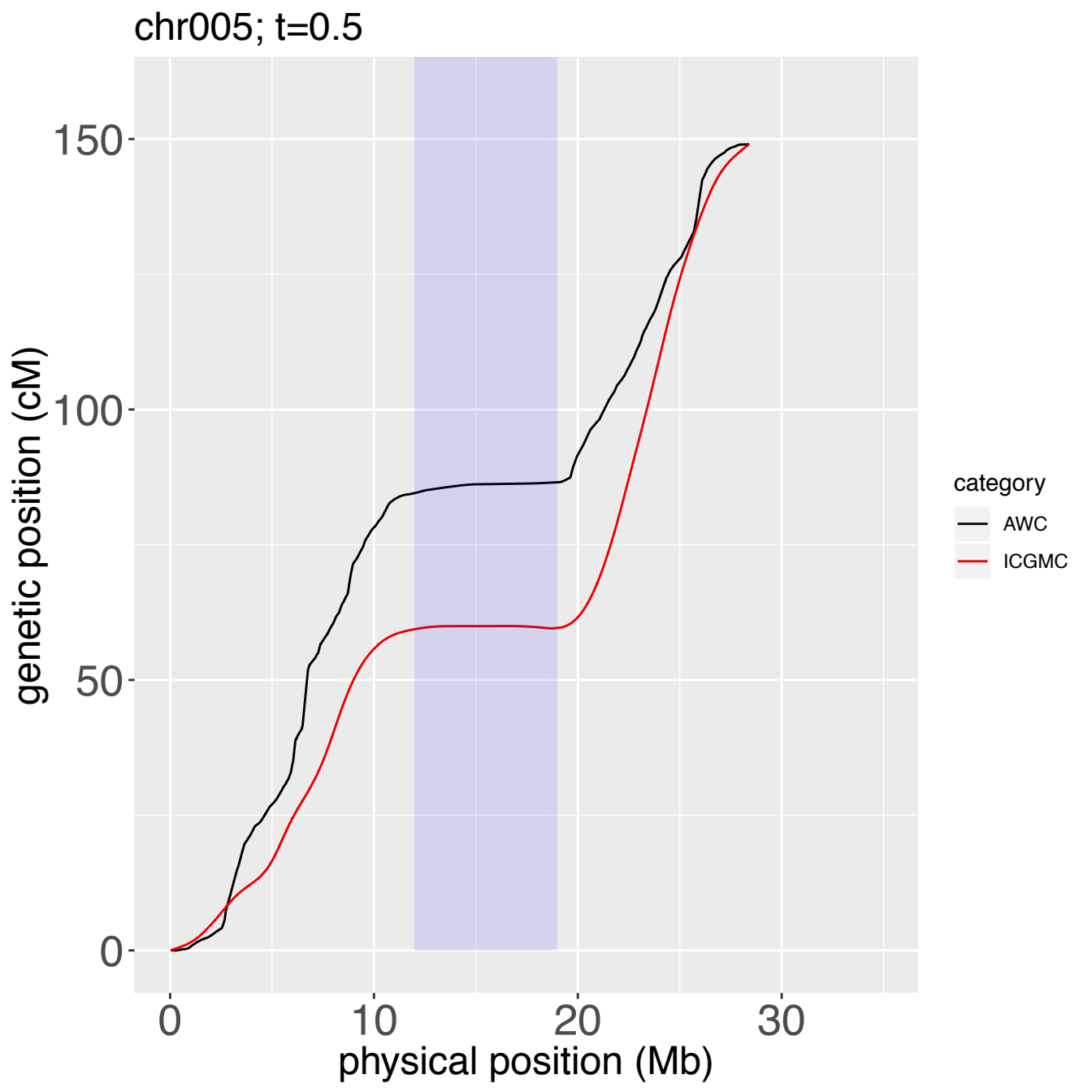
One plot for each chromosome shows the genetic position in cM of markers in our newly constructed map named AWC (black) and the ICGMC map (red) as a function of physical position in Mb. Genetic positions were calculated using the number of crossovers in intervals between SNP markers detected by SHAPEIT2-duoHMM with a significance threshold of t=0.5. The AWC map was scaled to correspond with the total genetic distance of the ICGMC map.

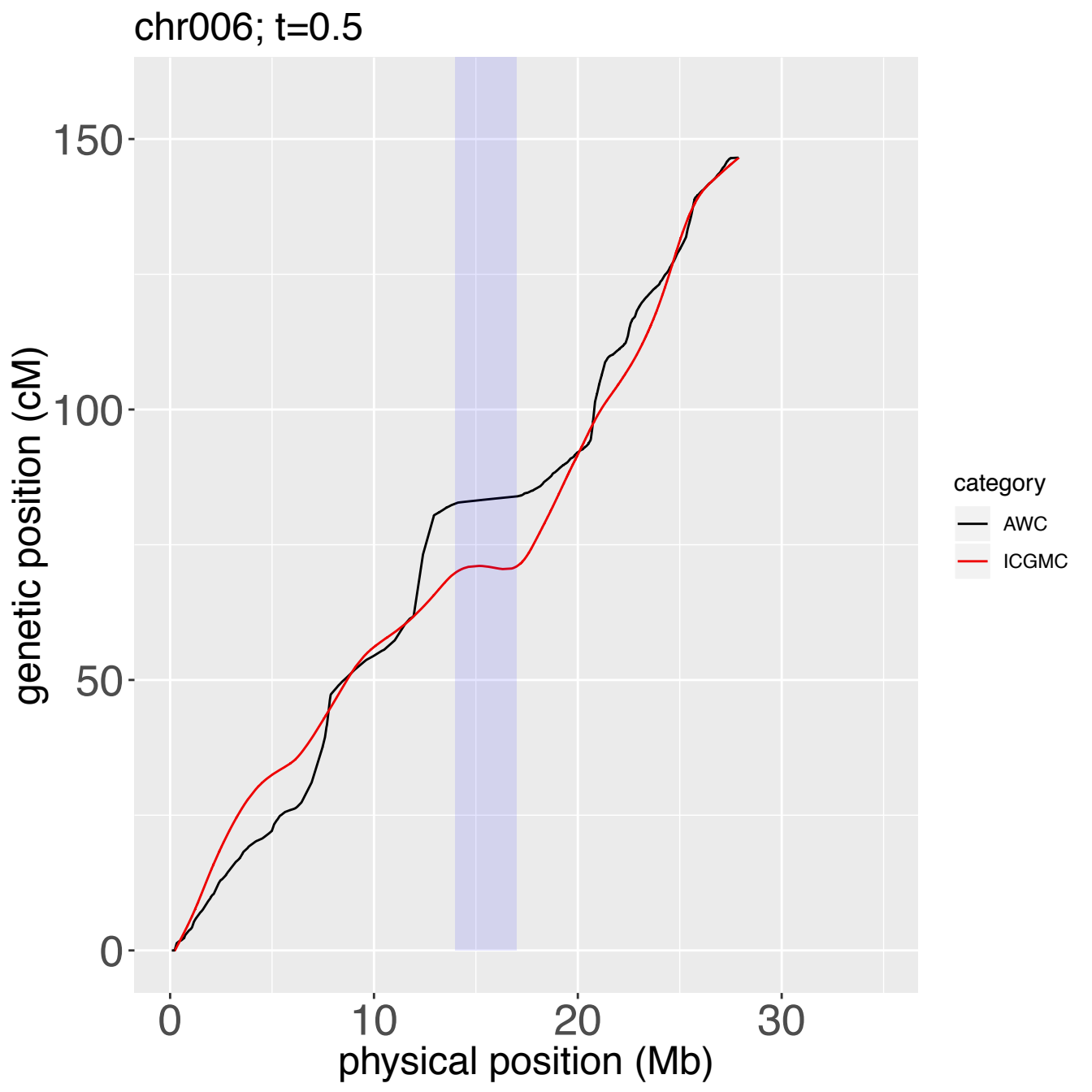

chr001; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

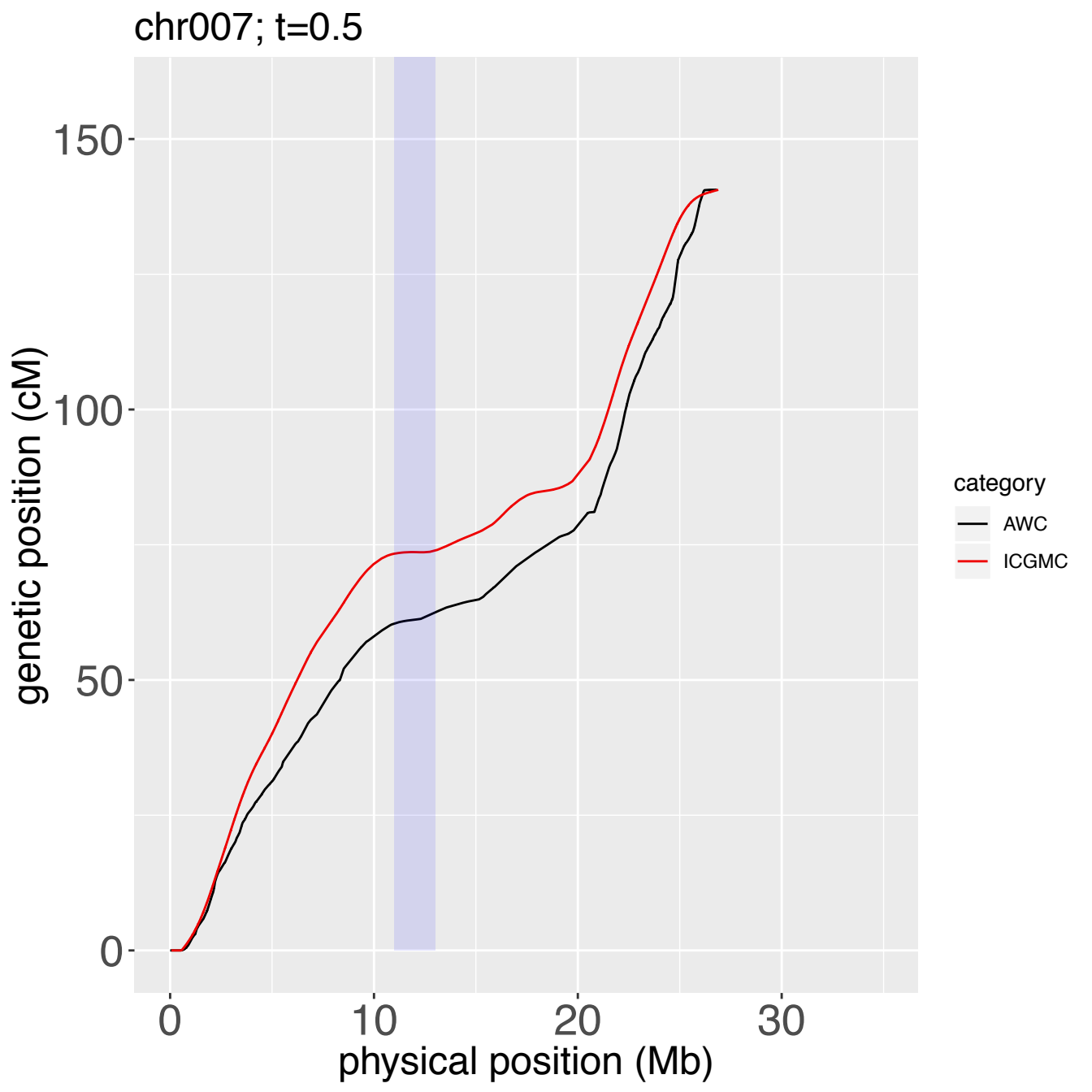

chr002; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

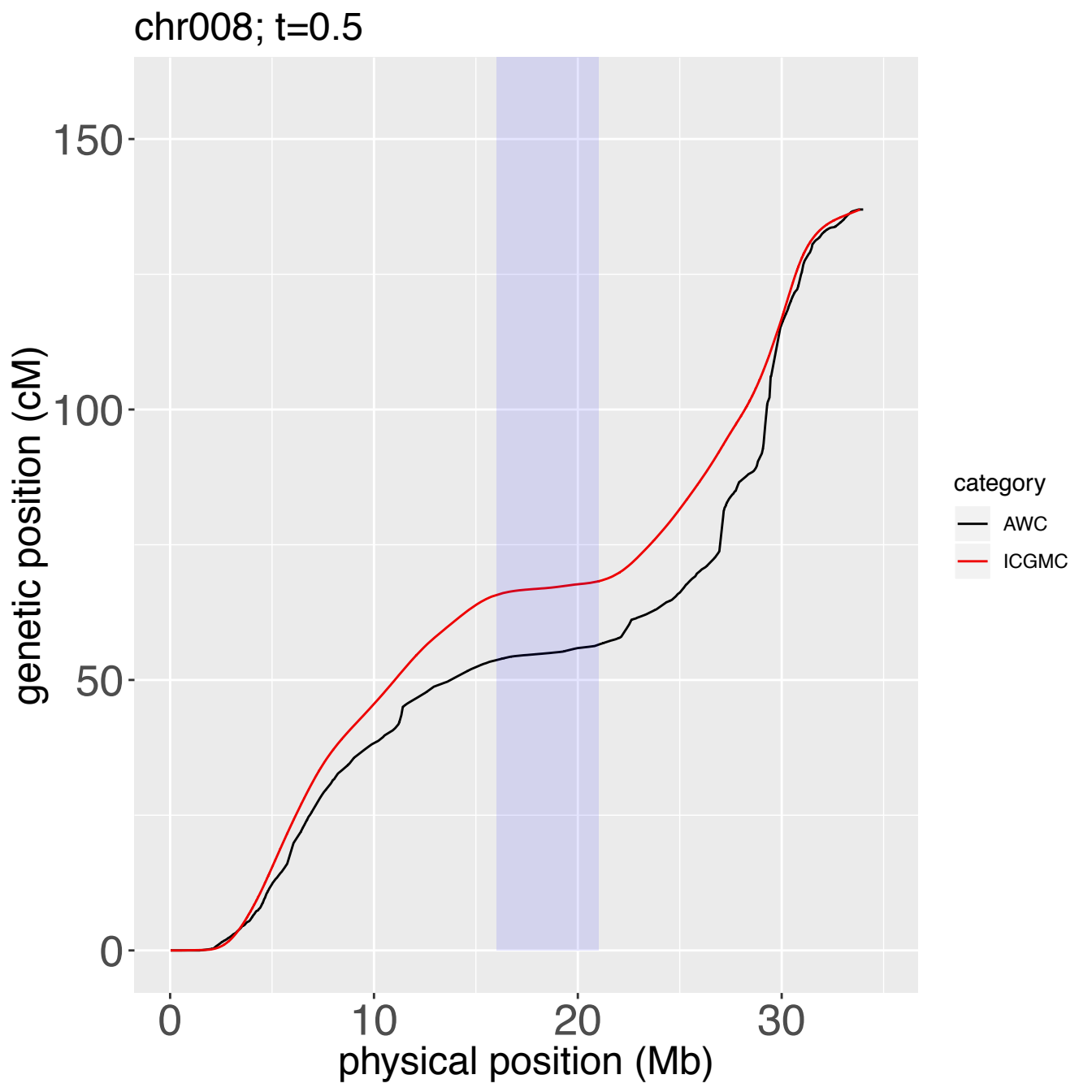

chr003; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

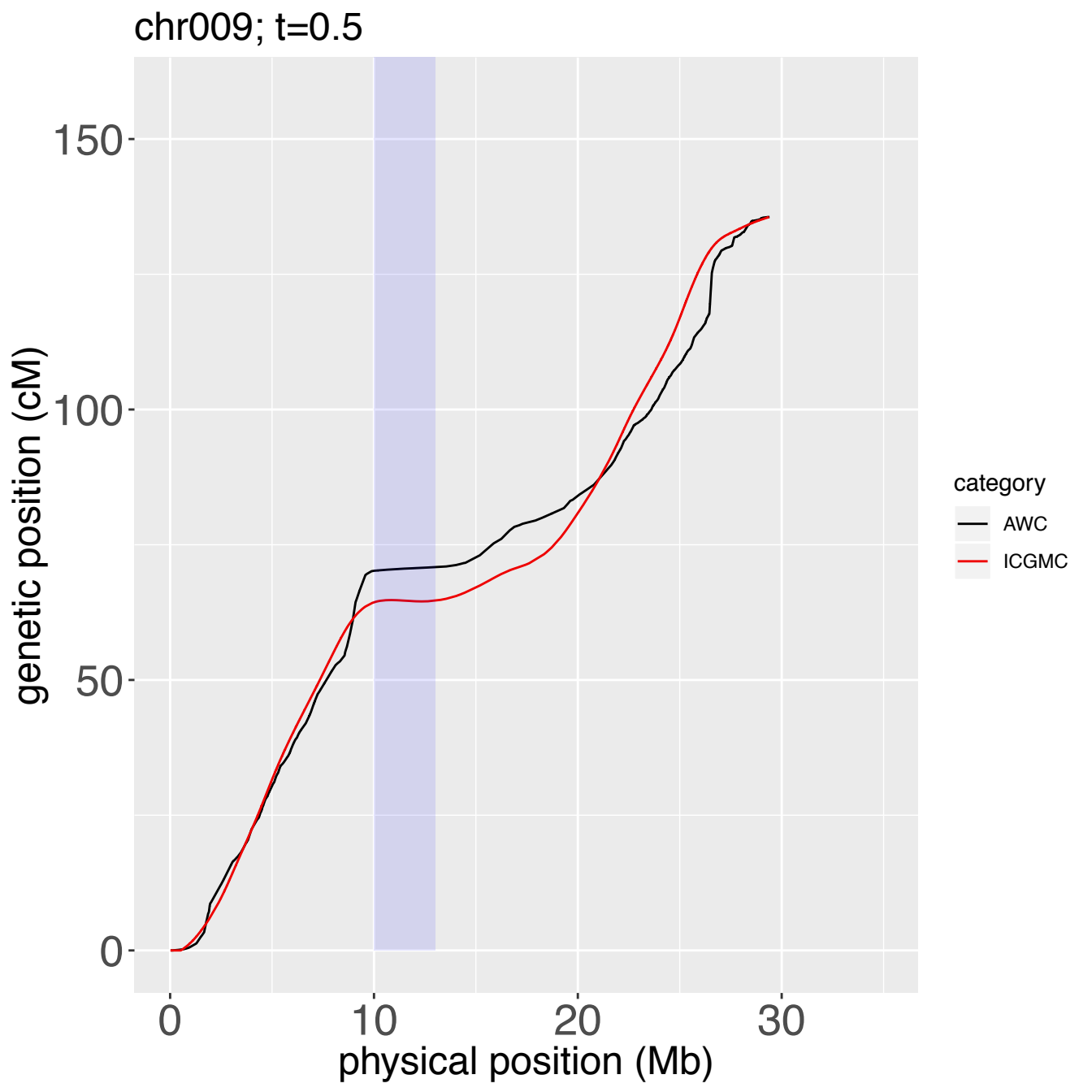

chr004; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

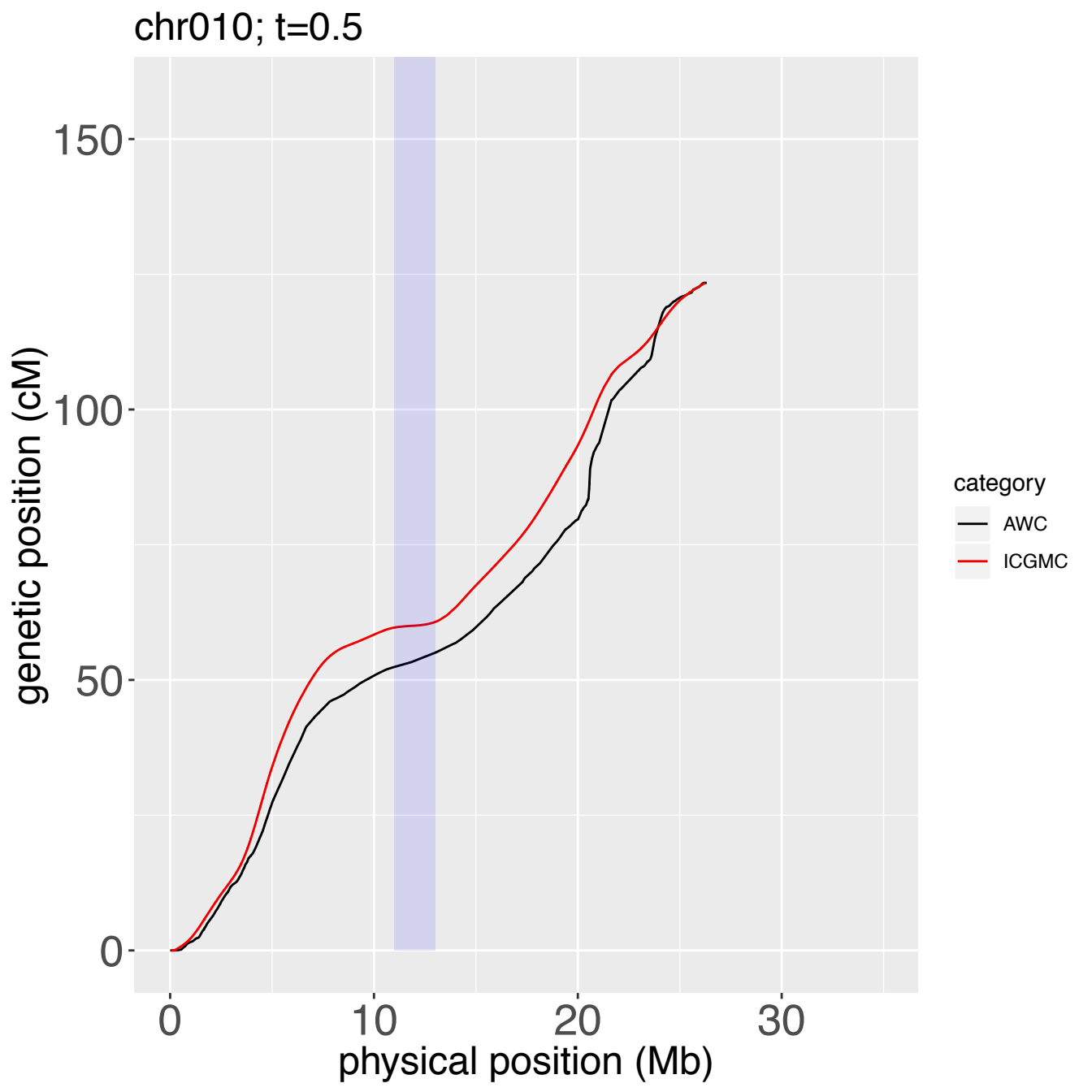

chr005; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

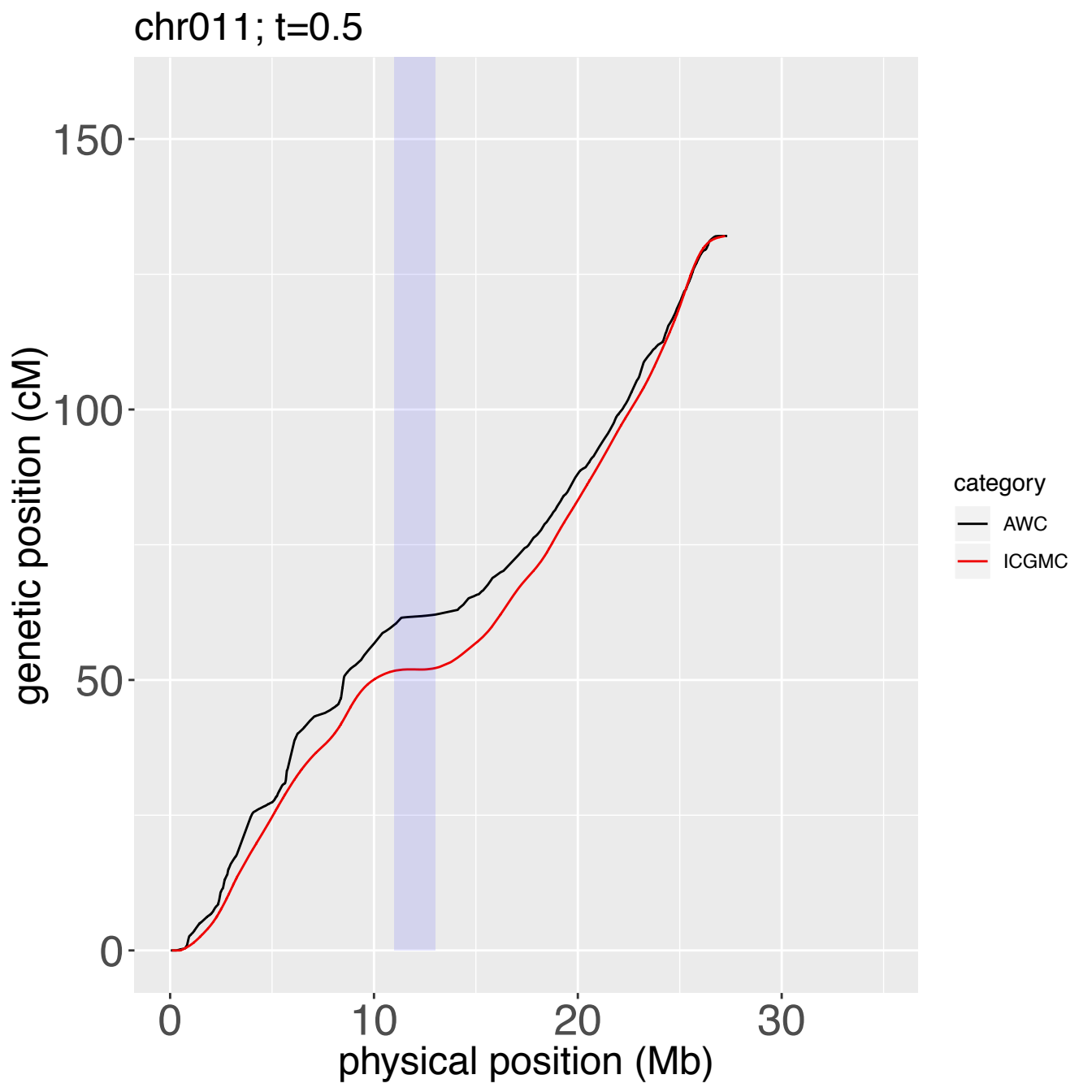

chr006; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

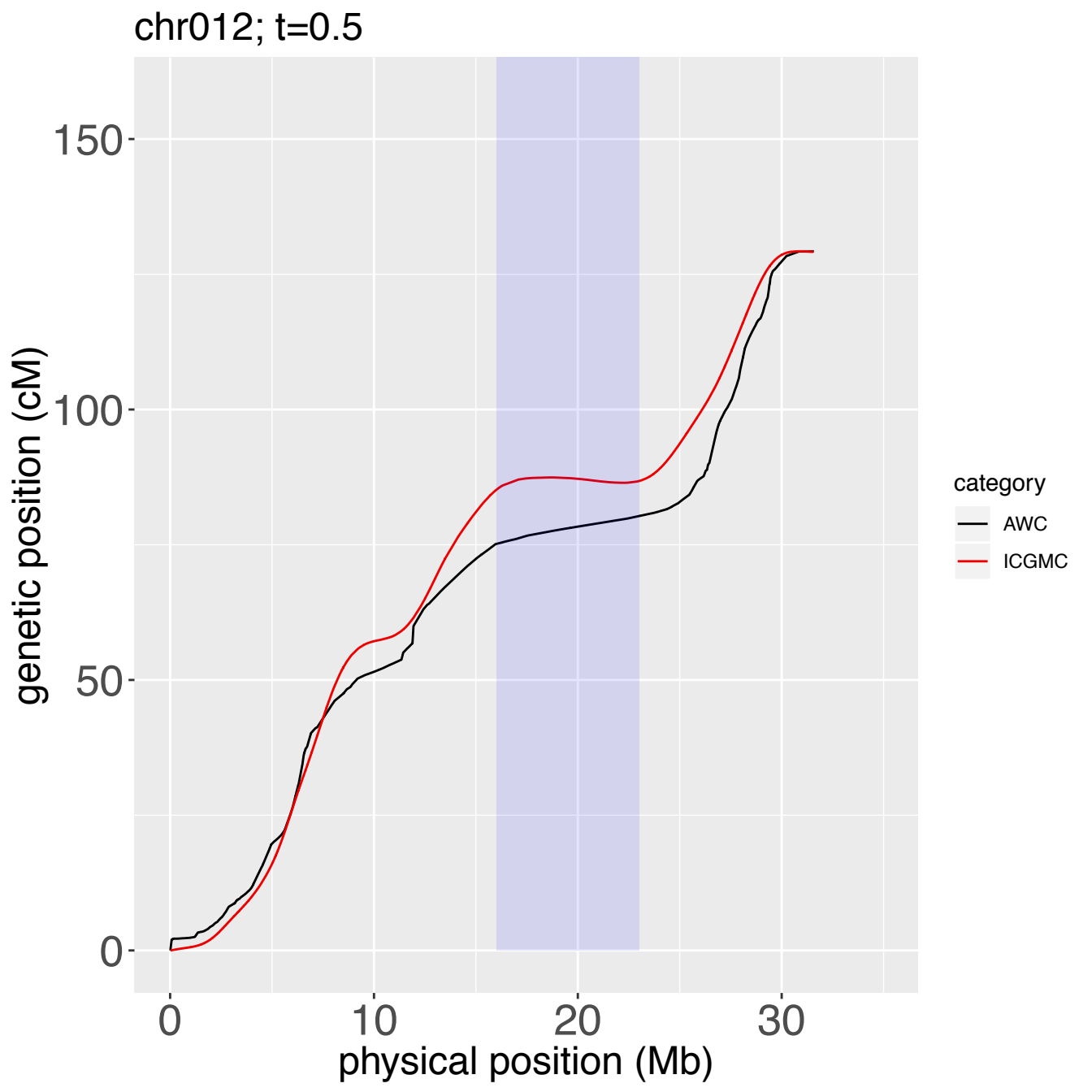

chr007; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

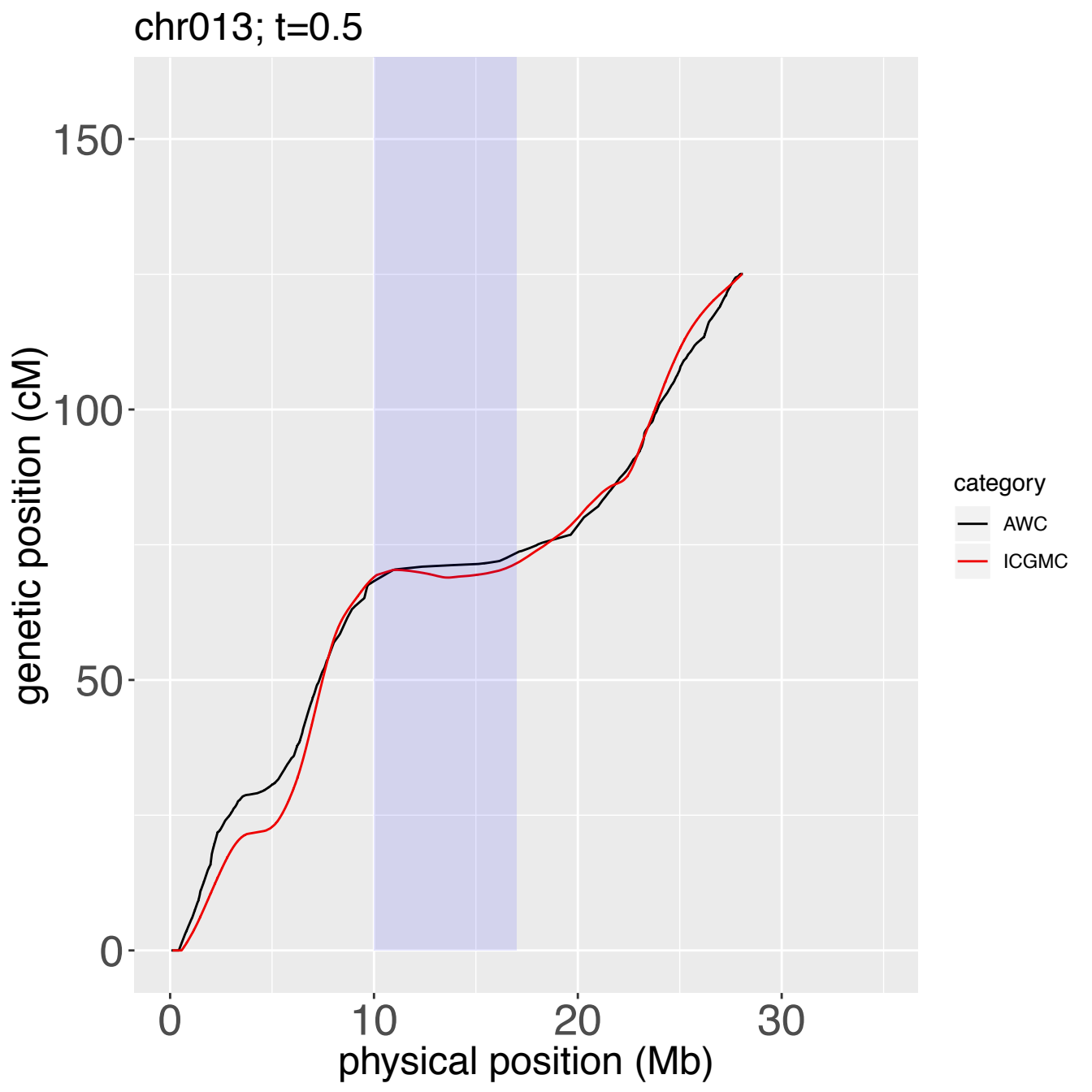

chr008; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

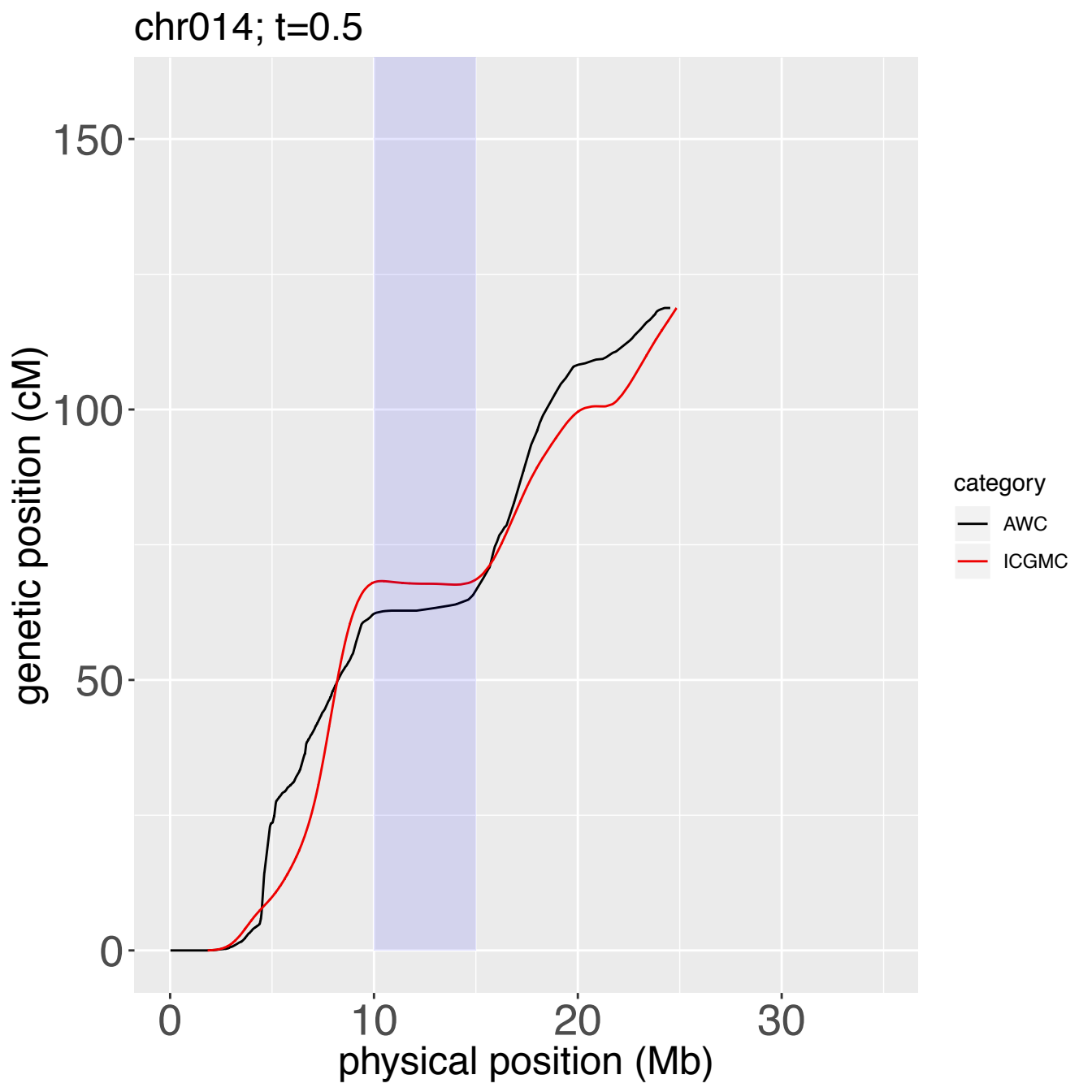

chr009; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

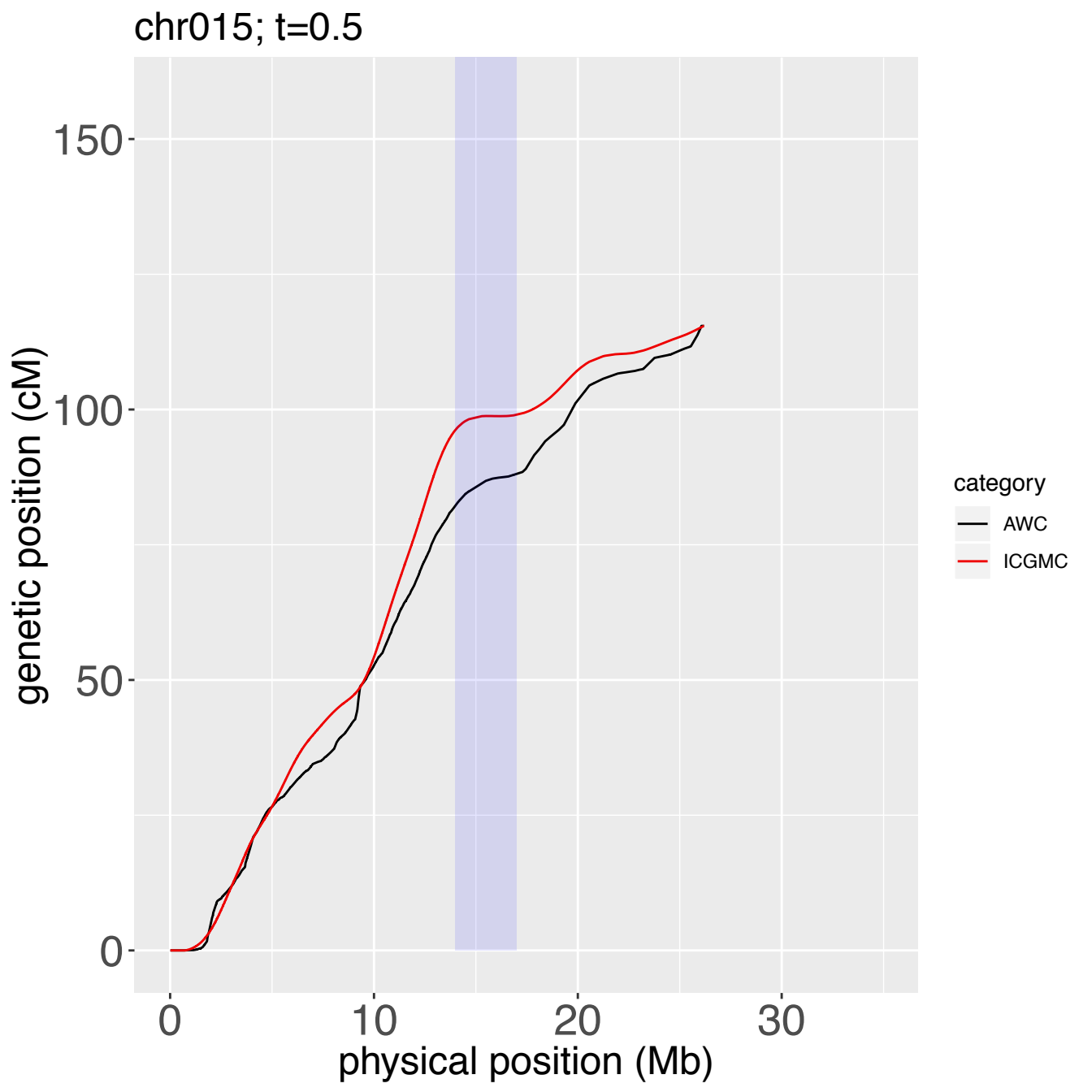

chr010; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

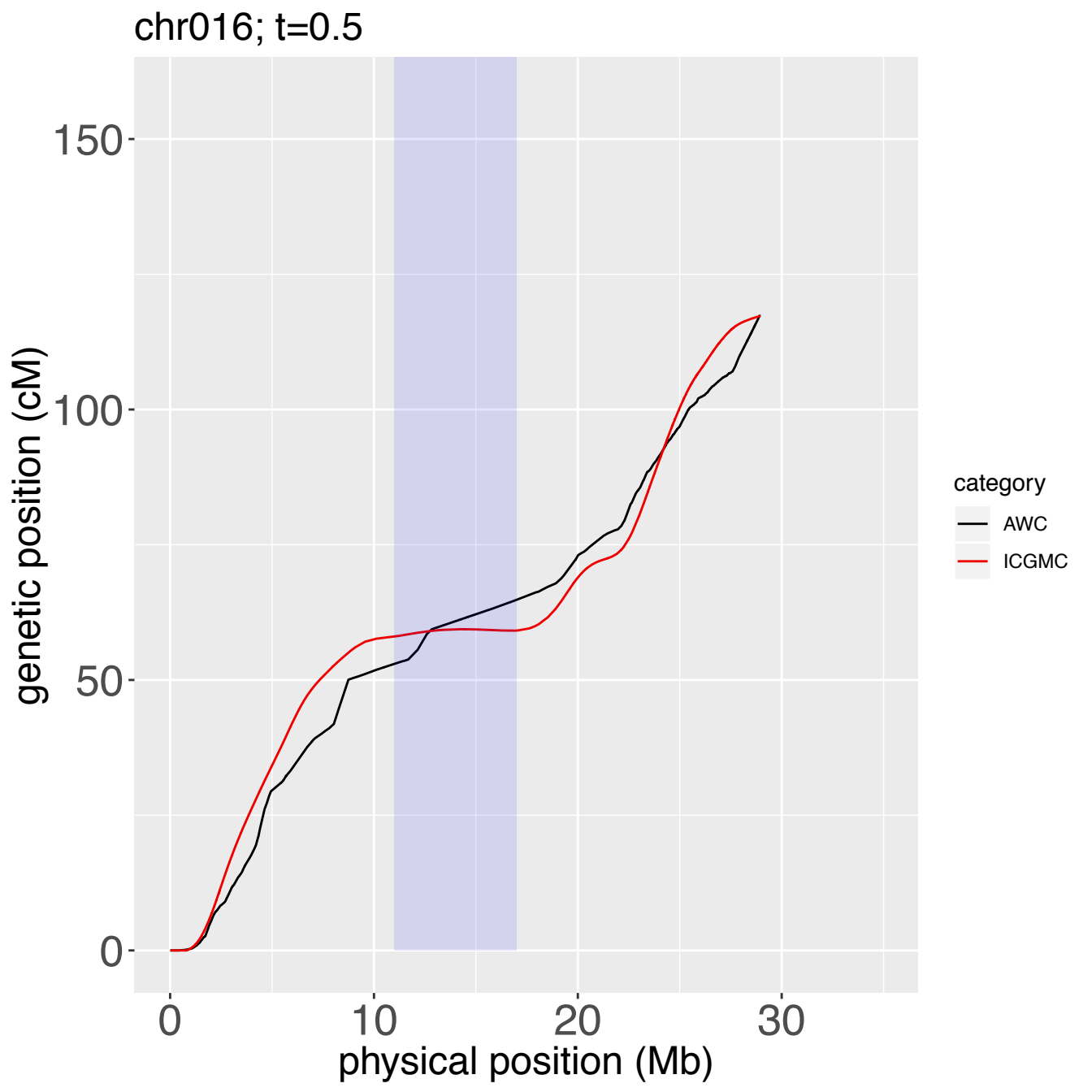

chr011; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

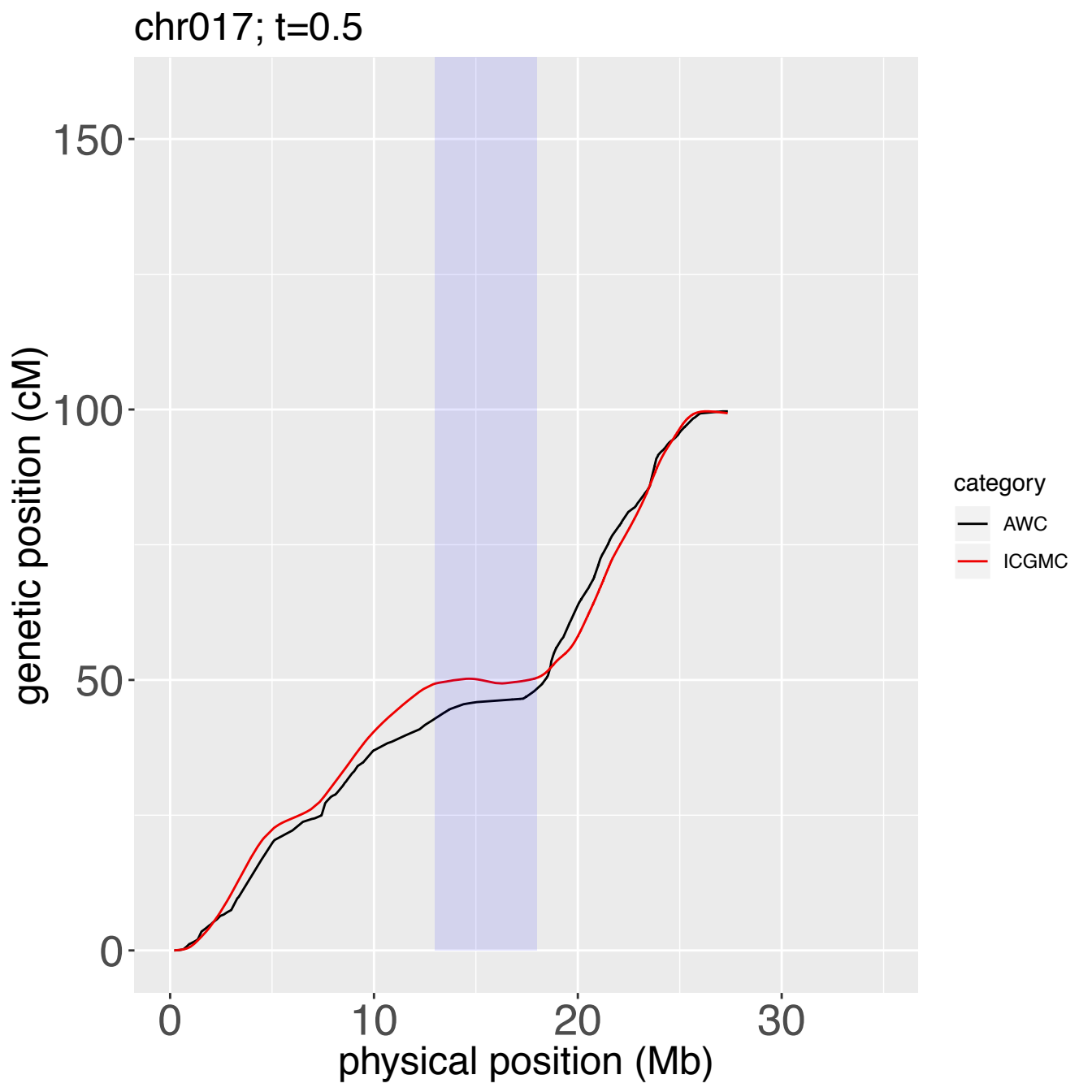

chr012; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

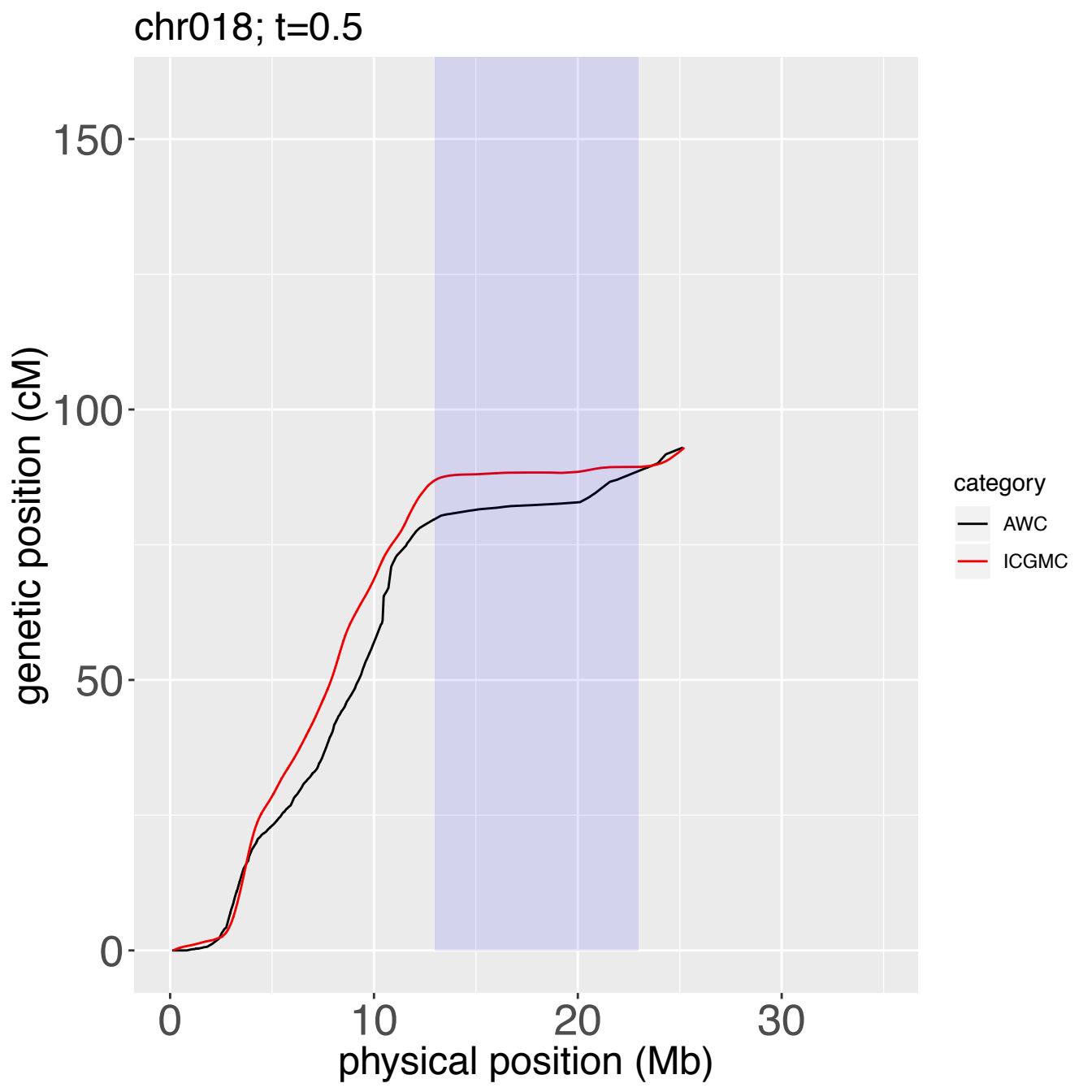

chr013; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC


chr014; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

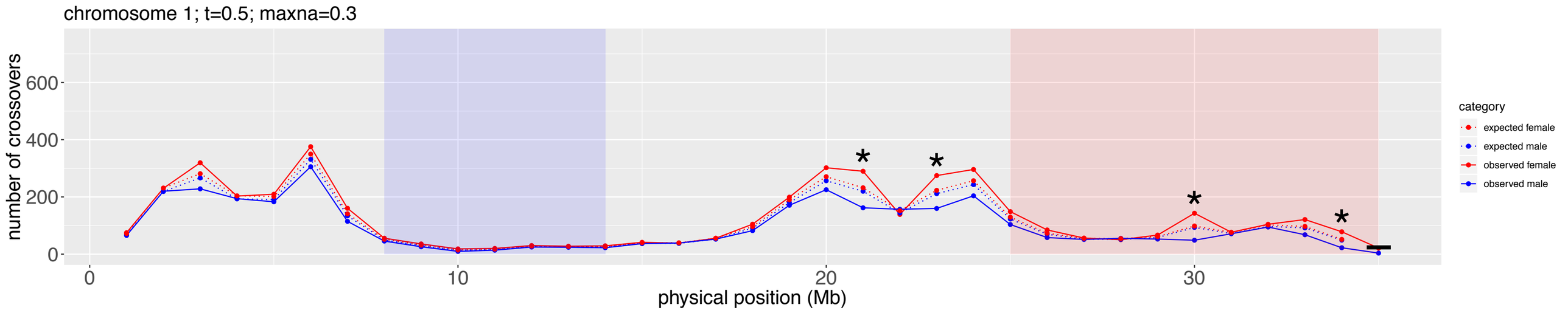

chr015; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

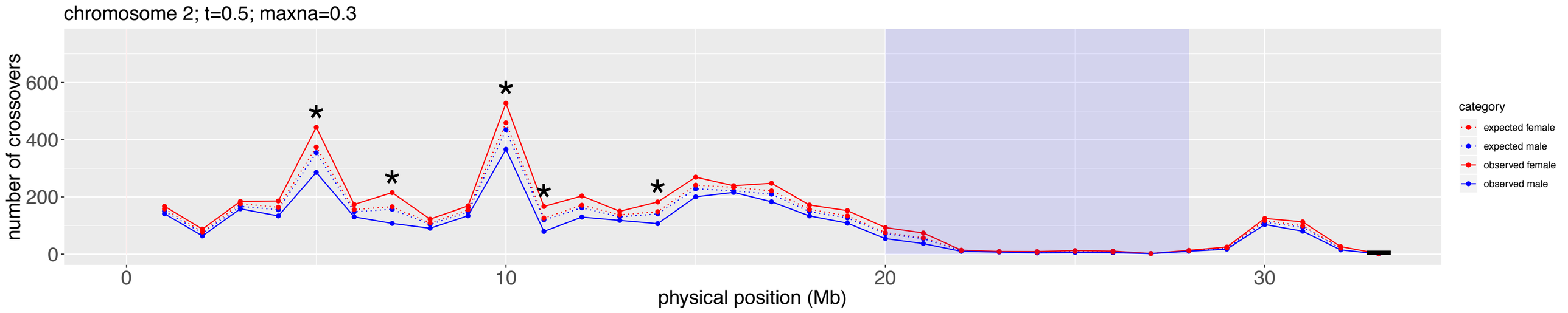

chr016; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

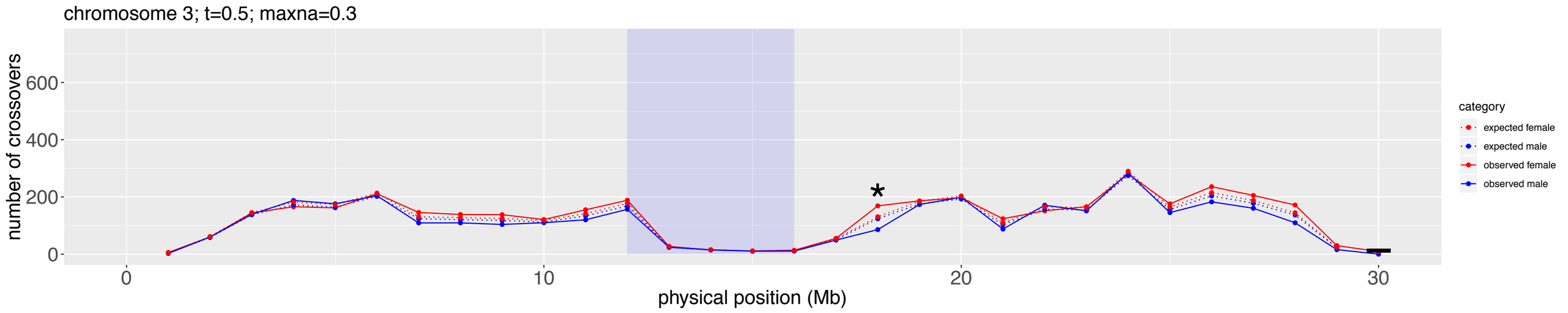

chr017; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

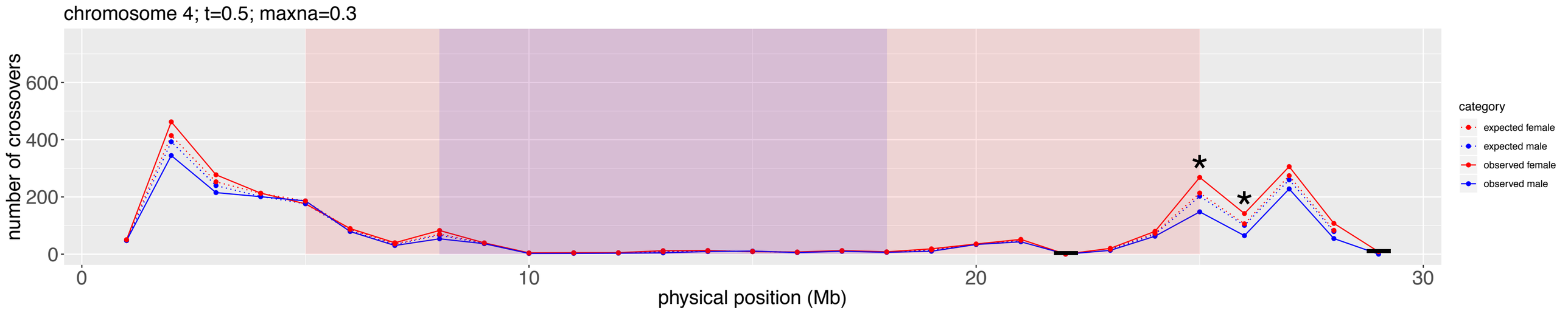

chr018; t=0.5
150
100
50
0
genetic position (cM)
0
10
20
30
physical position (Mb)
category
AWC
ICGMC

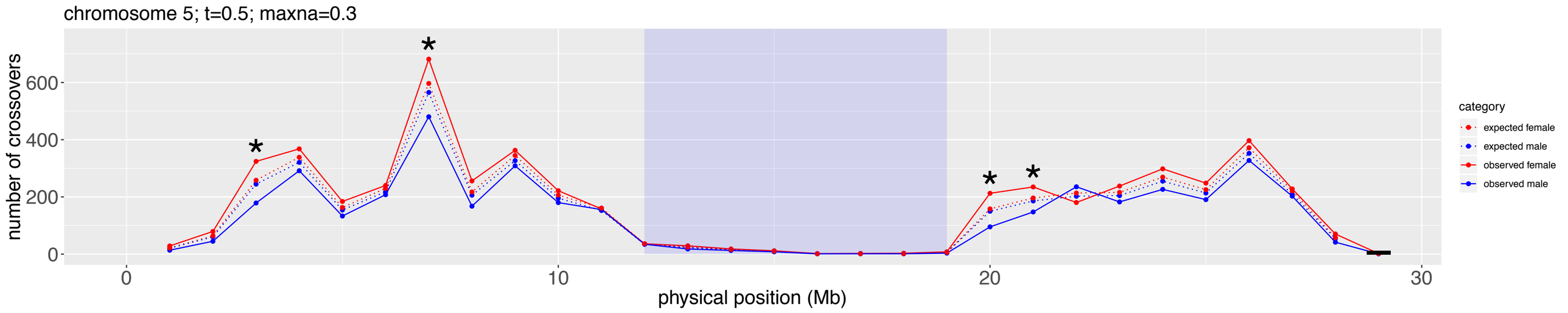
Supplementary Figure 3. Variation in crossover frequencies between male and female meioses across the 18 chromosomes.
One plot for each chromosome shows the distribution of crossovers falling within 1 Mb windows for female (red) and male (blue) meioses. Crossovers were detected by SHAPEIT2-duoHMM with a significance threshold of t=0.5. Solid lines represent observed counts and dashed lines represent expected counts under the null hypothesis of equal recombination frequency in females and males. Asterisks show windows with significantly different crossover frequency between male and female meioses indicated by a chi-square test with a Bonferonni-corrected significance threshold of α/n, where $\alpha = 0.05$ and $n = 506$. Dashes indicate windows where the chi-square test was not performed, either because the expected frequency count for one or more classes was less than five, or because the last window of the chromosome was shorter than 1 Mb. Centromeres are highlighted in blue, and *M. glaziovii* introgression regions are highlighted in red.

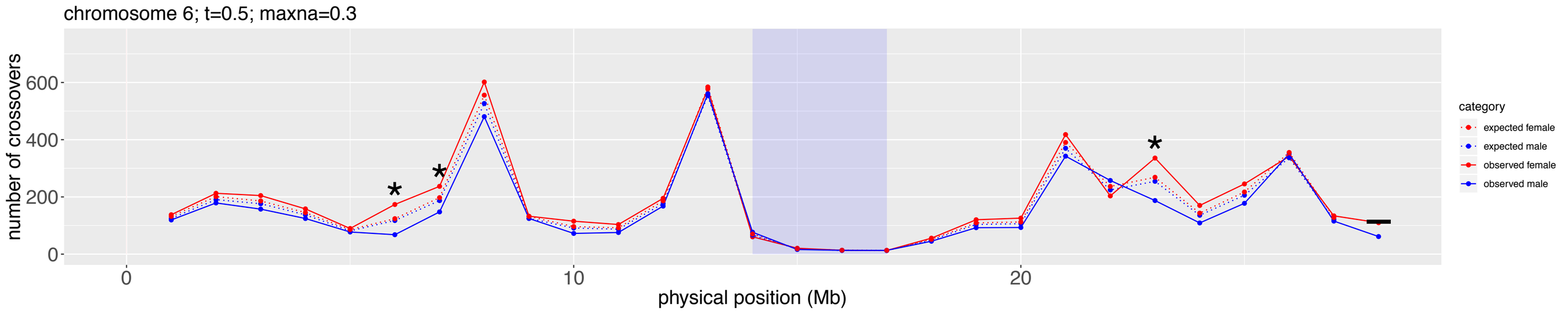

chromosome 1; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
category
expected female
expected male
observed female
observed male

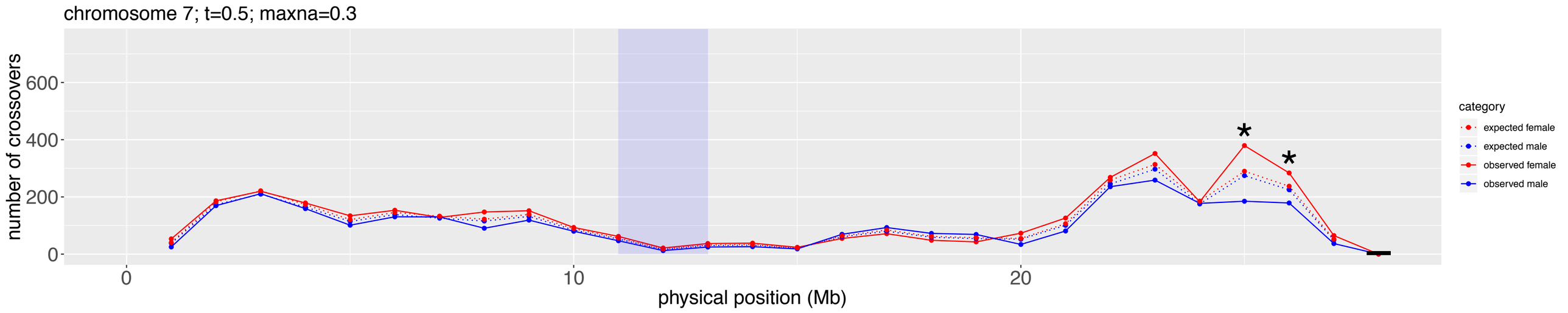

chromosome 2; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
*
*
*
*
category
expected female
expected male
observed female
observed male

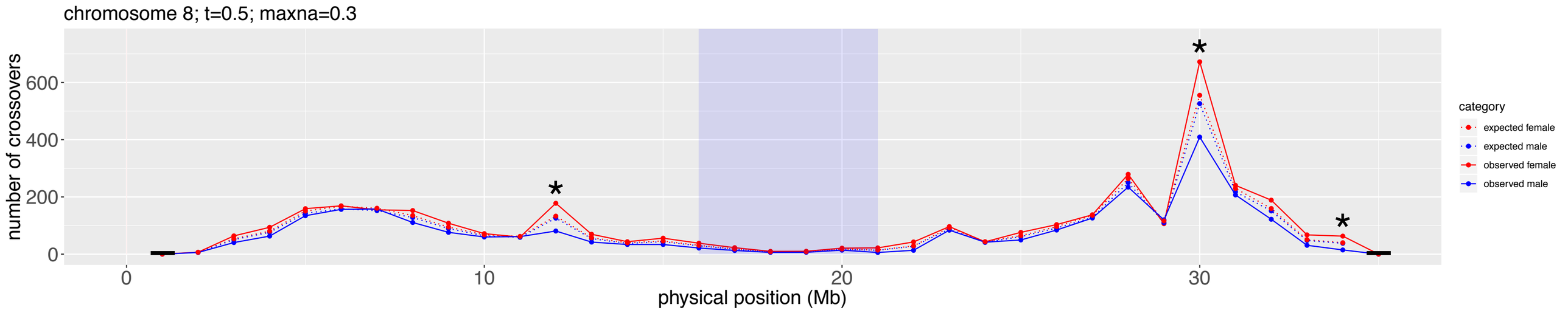

chromosome 3; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
category
expected female
expected male
observed female
observed male

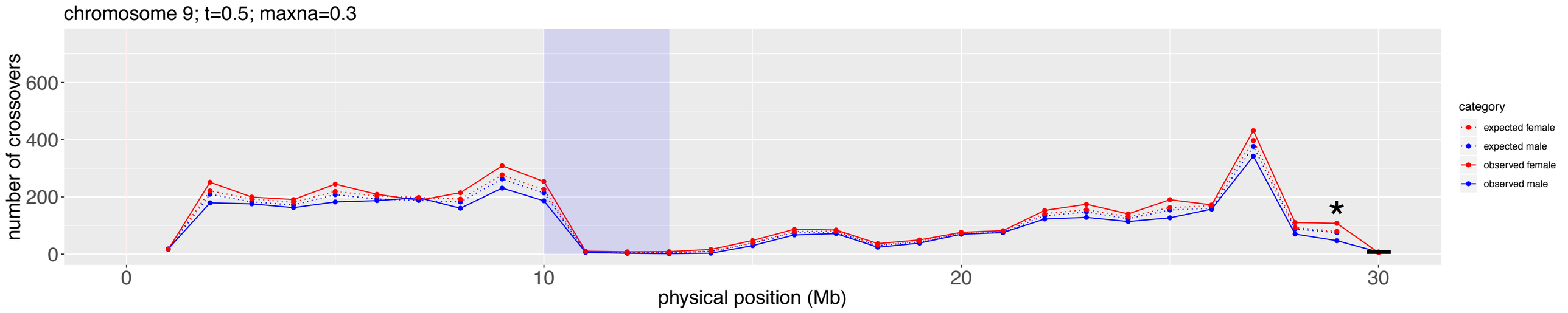

chromosome 4; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
*
category
expected female
expected male
observed female
observed male

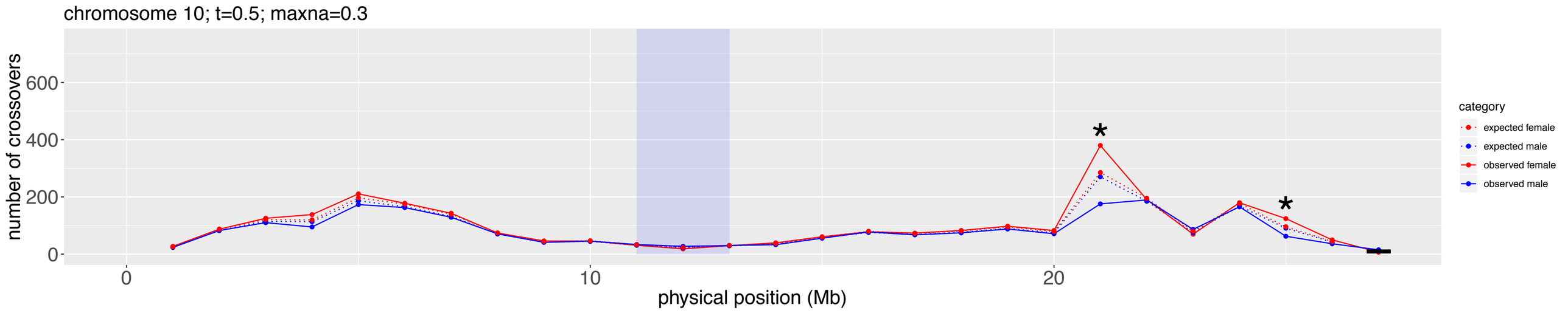

chromosome 5; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
*
*
*
category
expected female
expected male
observed female
observed male

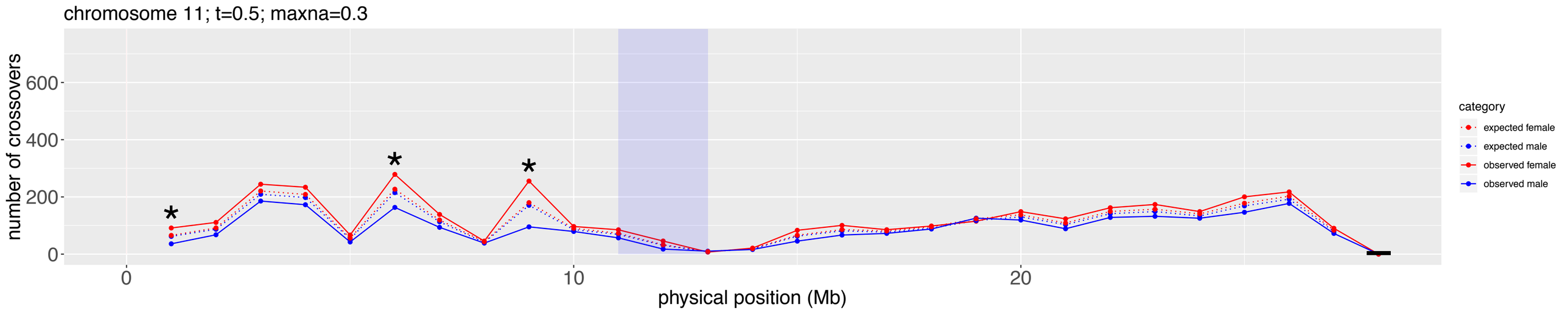

chromosome 6; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
physical position (Mb)
category
expected female
expected male
observed female
observed male

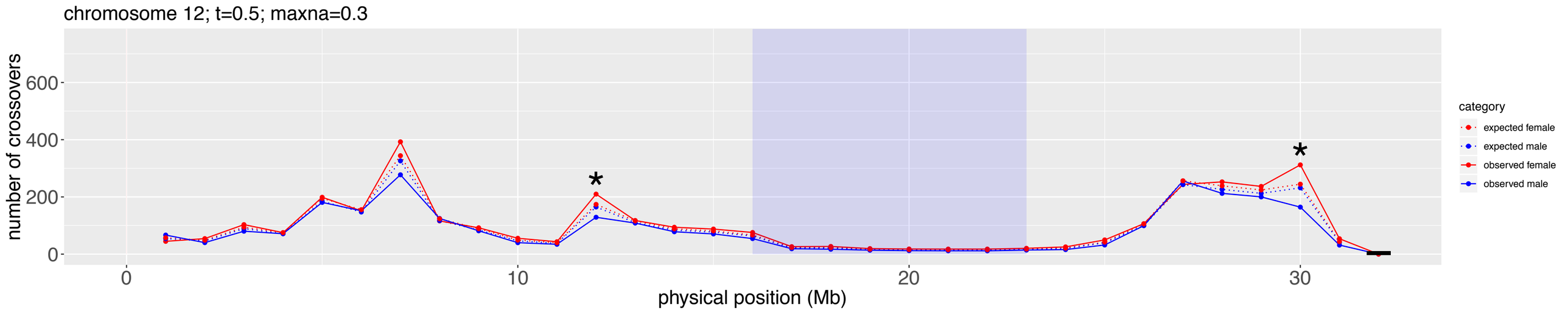

chromosome 7; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
physical position (Mb)
*
*
category
expected female
expected male
observed female
observed male

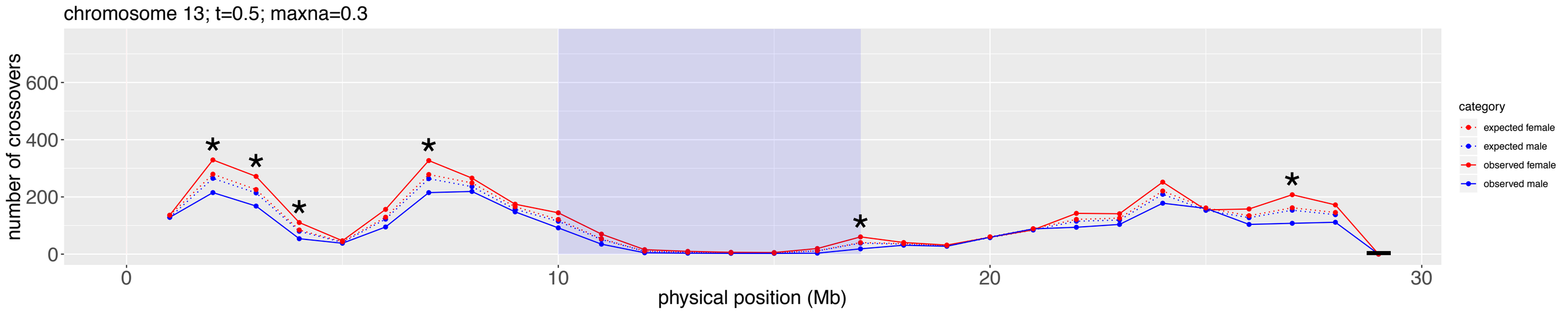

chromosome 8; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
*
*
category
expected female
expected male
observed female
observed male

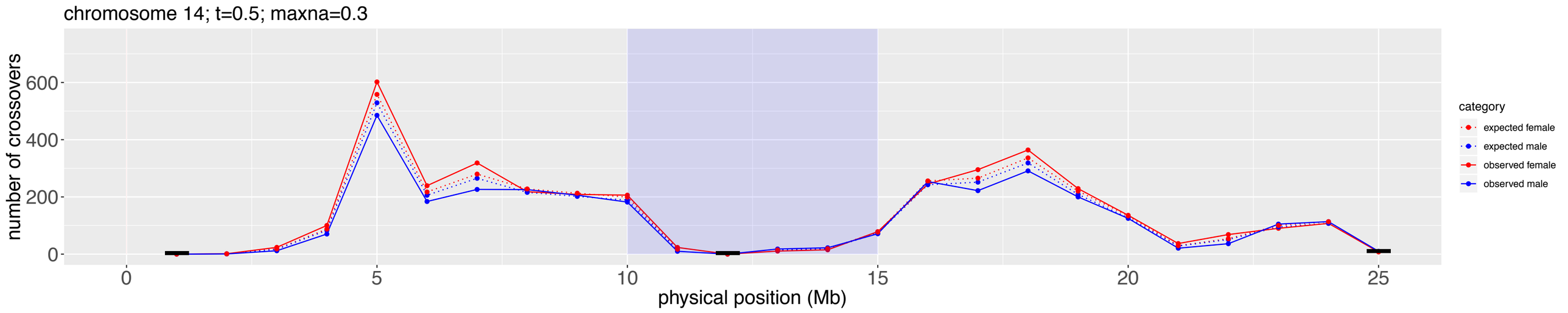

chromosome 9; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
category
expected female
expected male
observed female
observed male

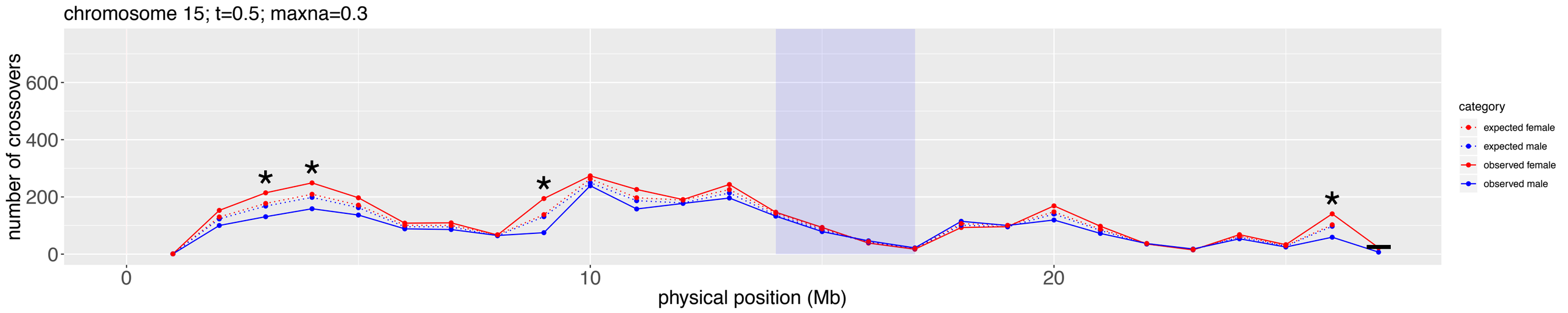

chromosome 10; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
physical position (Mb)
*
*
category
expected female
expected male
observed female
observed male

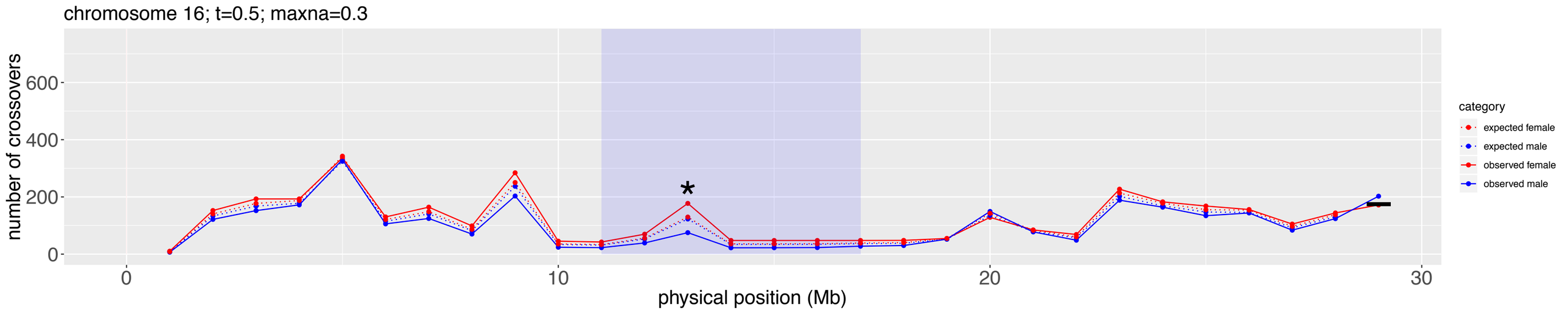

chromosome 11; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
physical position (Mb)
*
*
*
category
expected female
expected male
observed female
observed male

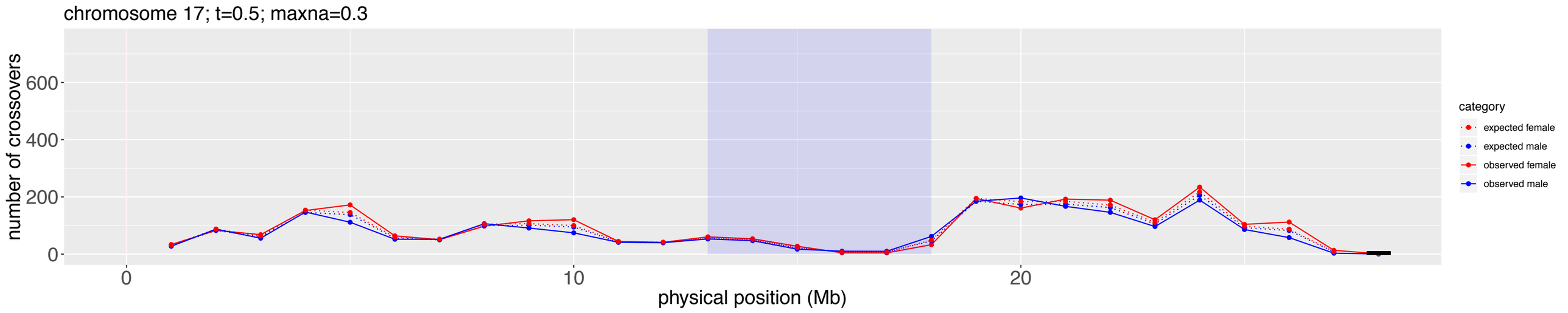

chromosome 12; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
*
category
expected female
expected male
observed female
observed male

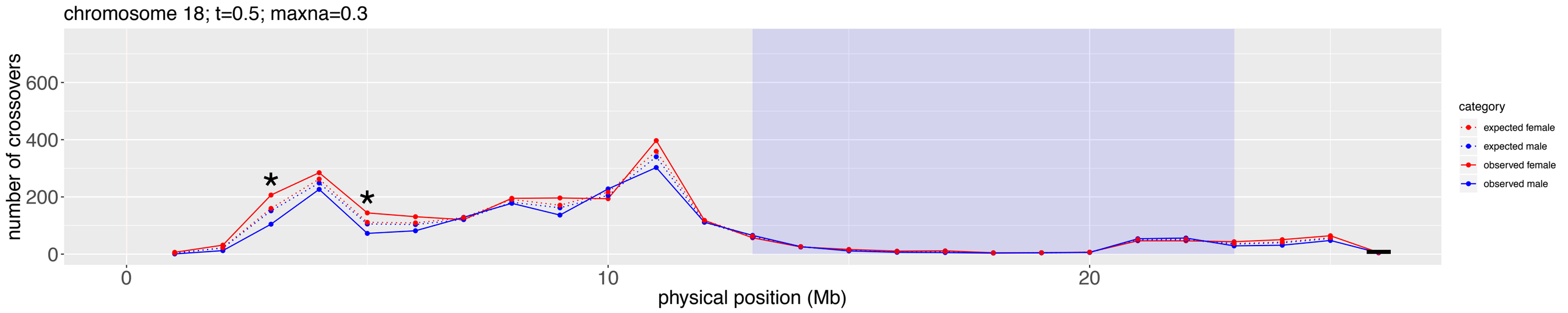

chromosome 13; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
category
expected female
expected male
observed female
observed male


chromosome 14; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
5
10
15
20
25
physical position (Mb)
category
expected female
expected male
observed female
observed male


chromosome 15; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
physical position (Mb)
category
expected female
expected male
observed female
observed male


chromosome 16; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
30
physical position (Mb)
*
category
expected female
expected male
observed female
observed male


chromosome 17; t=0.5; maxna=0.3
number of crossovers
0
200
400
600
0
10
20
physical position (Mb)
category
expected female
expected male
observed female
observed male


chromosome 18; t=0.5; maxna=0.3
number of crossovers
600
400
200
0
*
*
0
10
20
physical position (Mb)
category
expected female
expected male
observed female
observed male