

Supplementary Table 1

	Female map	Male map
Linkage Groups	19	19
Markers (unique)	14596	13996
Markers per Mb	69.3	68.3
N50 Scaffolds	1961	1911
Scaffolds	4184	4011
Scaffolds with 1 marker	1320	1294
Scaffolds with 2 markers	969	855
Scaffolds with 3 markers	502	525
Scaffolds with >=4 markers	1393	1337
Total bases	210,660,926 (54,6%)	205,055,562 (53,1%)

Supplementary Table 2

	Map based	LD based
Min.	1.605	1.969
1st Quantile	12.685	10.039
Median	16.022	13.958
Mean	15.570	16.100
3rd Quantile	18.692	18.375
Max.	26.911	231.801

Figure S1. Comparison between the physical chromosomes of *P. trichocarpa* and the probe-marker position (in cM) of the *P. tremula* consensus LGs. LG – chromosome comparisons with more than 150 markers-pairs were considered as homologous and all LGs were therefore renamed to the homologous chromosome name in *P. trichocarpa*.

Figure S2. Circos plot of the consensus map. A) Marker distribution over the 19 chromosomes (Chr 1- Chr 19). Each black vertical line represents a marker (19,519 in total) in the map and is displayed according to the marker positions in cM. Track B-C visualizes multi marker scaffolds, where each line is a pairwise position comparison of probe-markers from the same scaffold. B) Position comparisons of probe-markers from the same scaffold that are located on the same chromosome. Grey lines indicate probe-markers that are located < 20 cM from each other and red lines indicate probe-markers ≥ 20 cM apart. C) Position comparisons of probe-markers from the same scaffold that are mapping to different chromosomes. Orange lines indicated probe-markers from the same scaffold split over 2 chromosomes, while dark blue lines indicated probe-markers split over 3 chromosomes.

Figure S3. Physical position (in bp) versus genetic position (in cM) for all probe-markers in the parental maps that are located on scaffolds showing signs of splits within a chromosome (maximum distance between probe markers from the same scaffold > 20 cM). Red dots indicate position in the female map while blue dots indicate position in the male map. Grey dots indicate probe-markers positioned on other chromosomes (these splits are further investigated in Figure S2). All gene-models positioned on the scaffold are visualized as horizontal black bars in the bottom on the figure. Green vertical bars indicate gap positions in the assembly (N:s). Blue or red vertical lines represent the assembly gap or artificial gap, respectively, that the scaffold was split at before creation of physical chromosomes with Allmaps. Scaffold names and chromosome belonging are represented in the title of each plot.

Figure S4. Physical position (in bp) versus chromosome grouping (1-19) for all probe-markers in the consensus map that are located on scaffolds showing signs of splits between chromosomes. All gene-models positioned on the scaffold are visualized as horizontal black bars in the bottom on the figure. Green vertical bars indicate gap positions in the assembly (N:s). Blue or red vertical lines represent the assembly gap or artificial gap, respectively, that the scaffold was split at before creation of physical chromosomes with Allmaps. Scaffold name is represented in the title of each plot.

Figure S5. Scaffolds showing the breakpoint splits within gene-models. The genomic positions of gene-models (exons plus introns) are represented with thin black lines, where gene models on the plus strand are represented above gene models on the minus strand. Exons from gene-models on the plus strand are represented with red boxes while exons from gene-models on the minus strand are represented with green boxes. Breakpoint decisions are represented with blue vertical lines. Scaffold name is represented in the title of each plot.

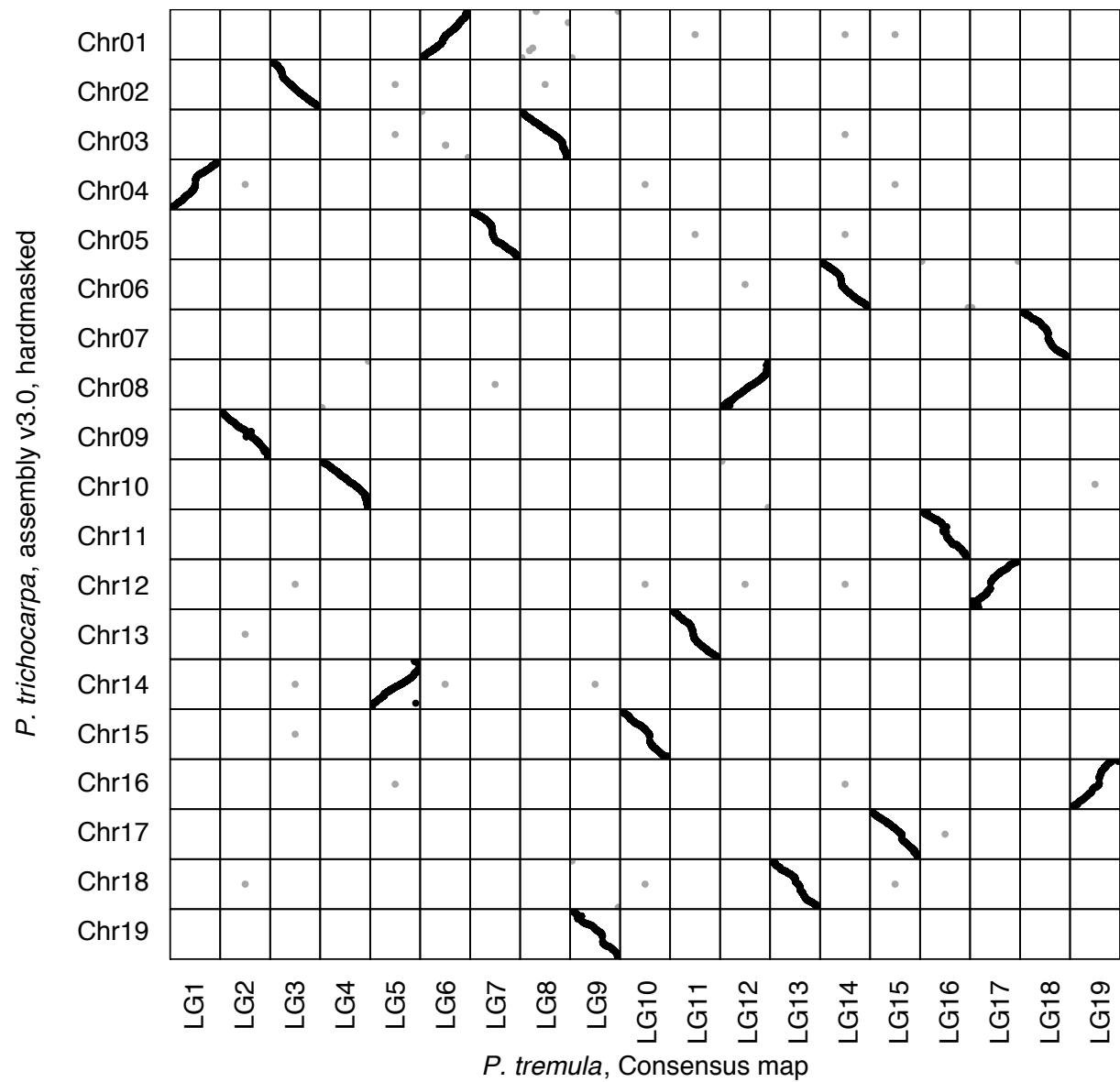
Figure S6. Genetic maps and resulting physical map created by Allmaps. For each of the 19 chromosomes, the left panel shows the marker distribution (in cM) for the genetic maps and the anchored genomic region (in Mb) for the physical map, while the right panel is showing the correspondence between the physical (x-axis) and recombination-based (y-axis) position of markers. The female map is depicted in green and the male map is depicted in orange.

Figure S7. Summary statistics for genetic linkage map based (purple) and sequenced based (orange) estimates of recombination rate (cM/Mb) in windows of 1 Mb. Red dots correspond to the average recombination rate over all windows and grey dots are outliers.

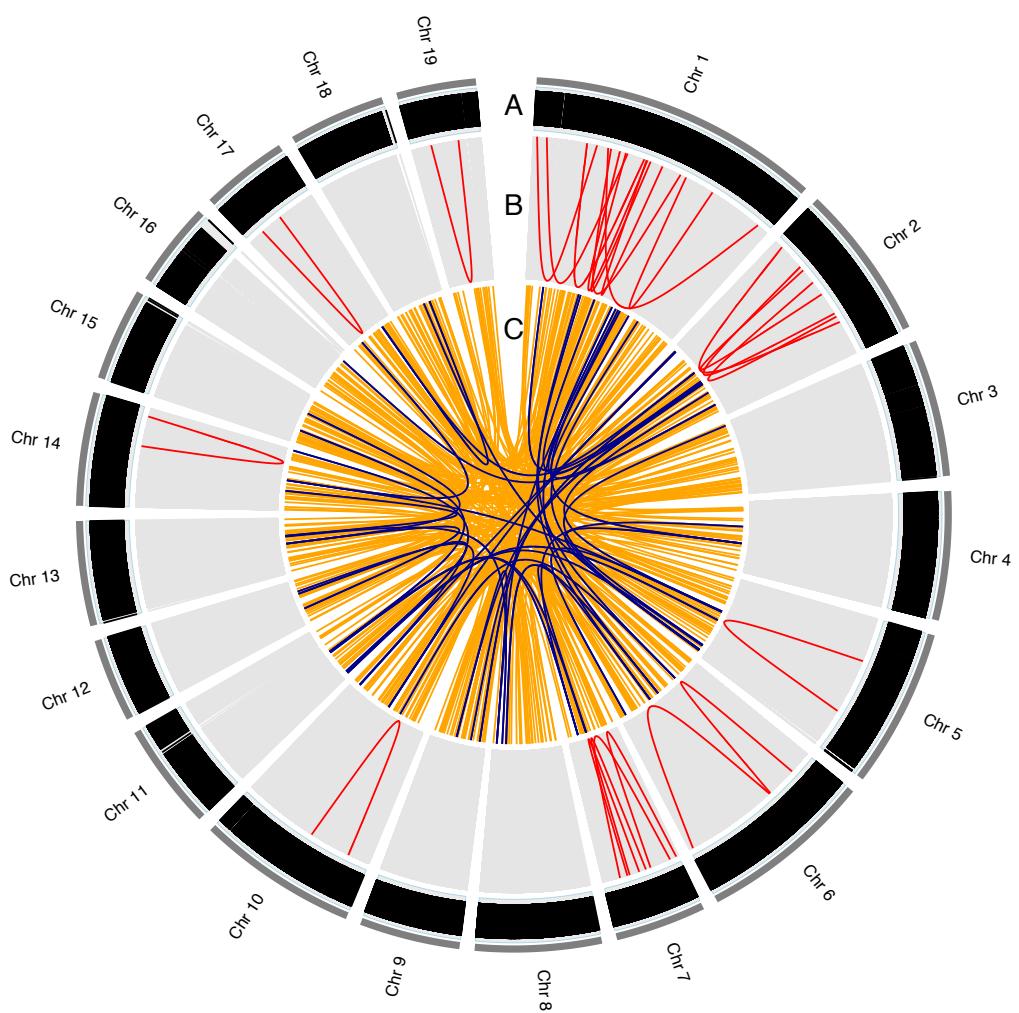
Figure S8. Manhattan plots for all genomic features.

Figure S9. Correlation between LD-based and map-based recombination rate

Supplementary Figure 1



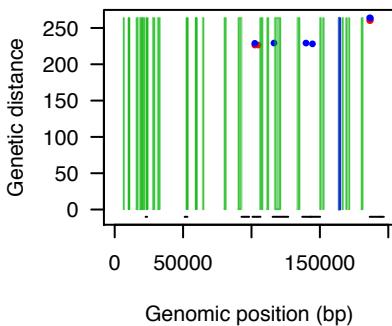
Supplementary Figure 2



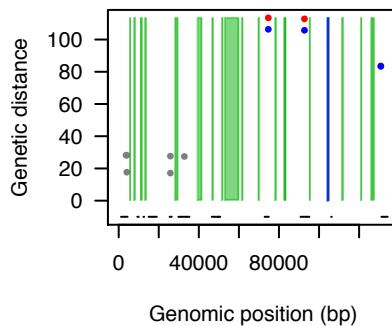
Supplementary Figure 3

- Female probe–marker
- Male probe–marker
- Probe–marker on other Chr
- Gene
- Assembly gaps
- Split gap
- Artificial gap

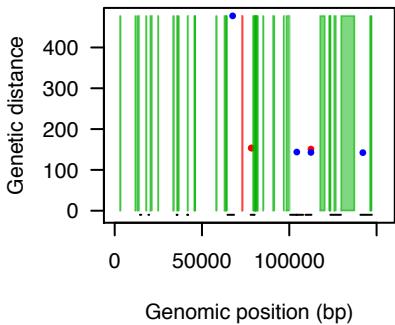
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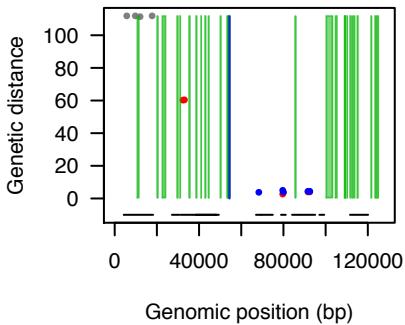
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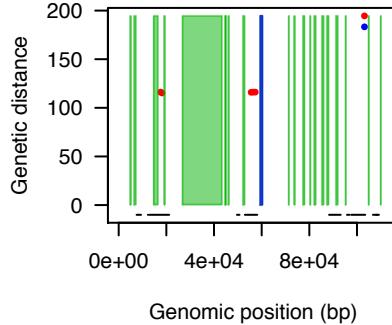
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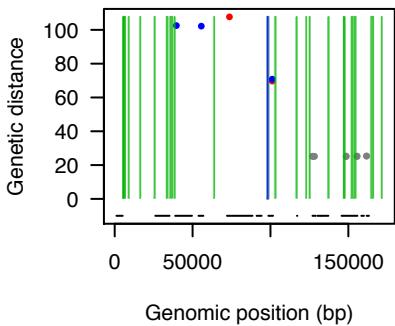
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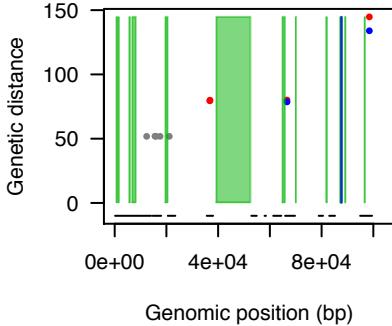
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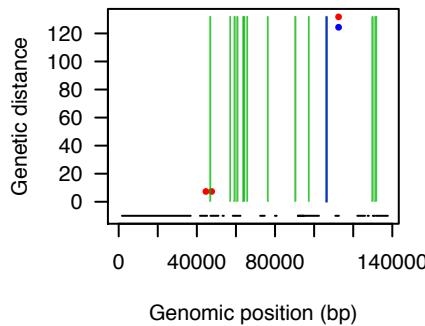
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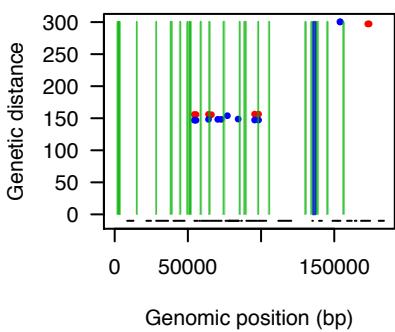
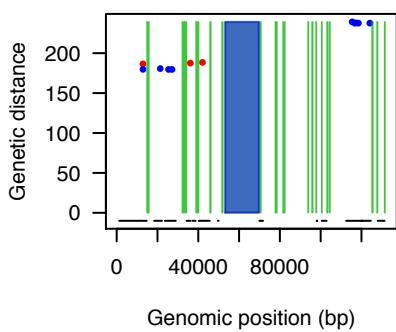
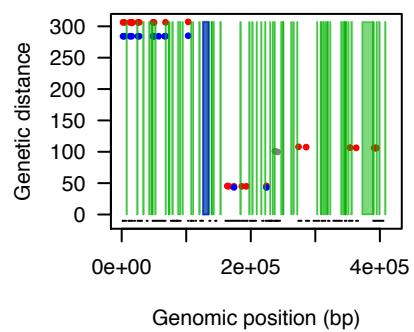
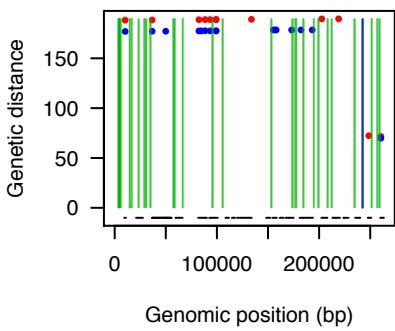
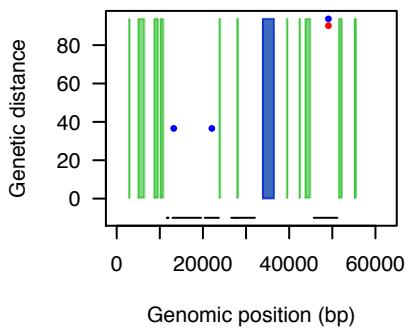
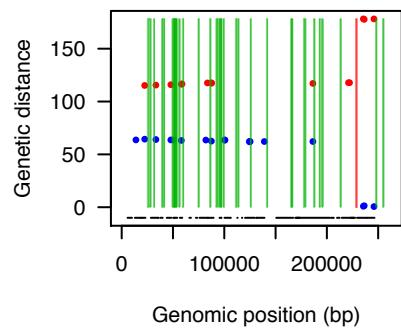
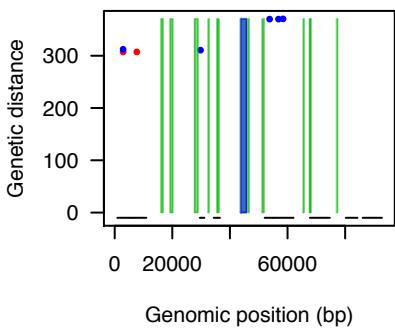
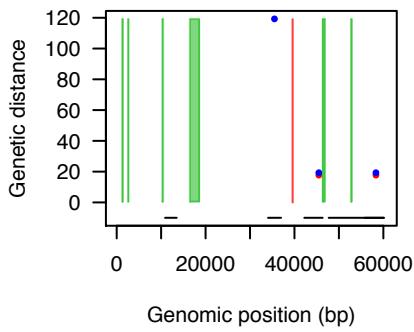
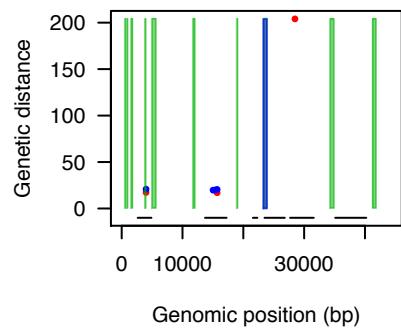


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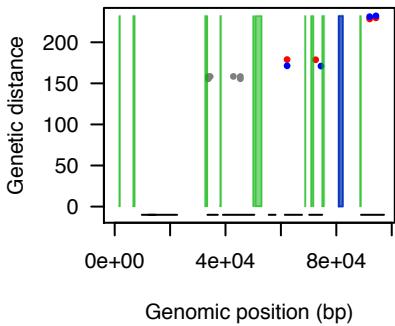


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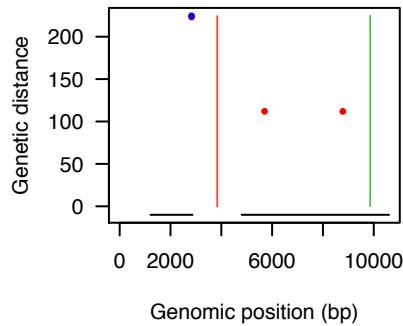


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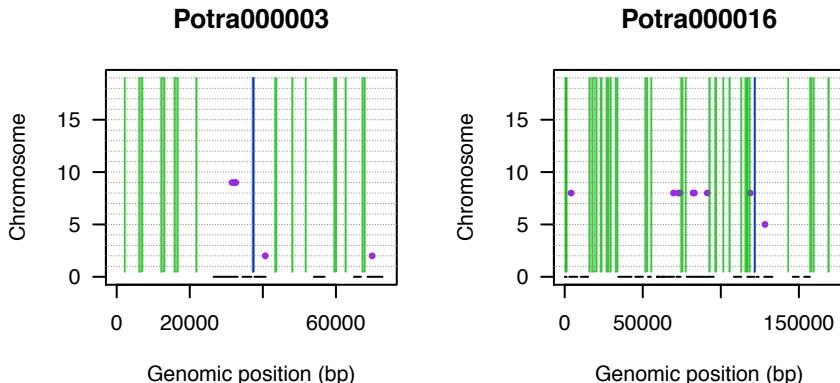
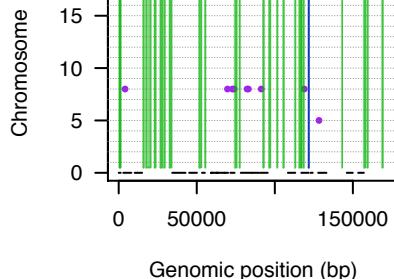
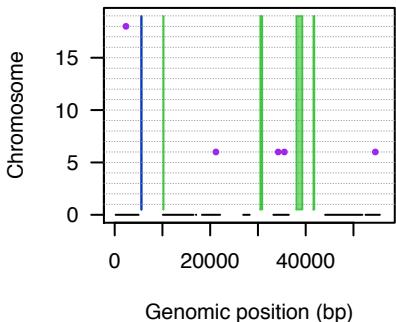
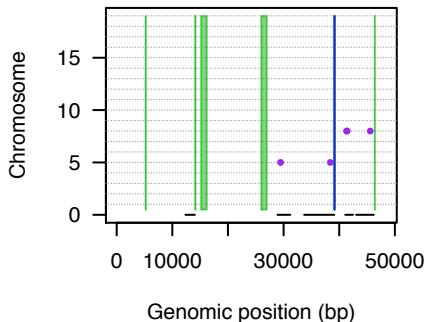
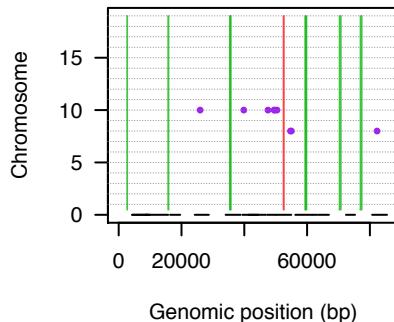
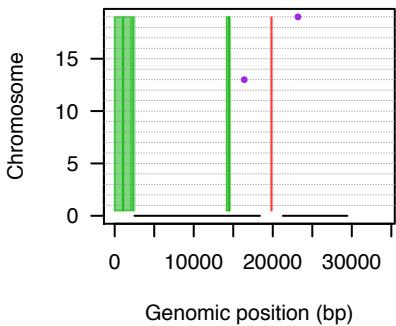
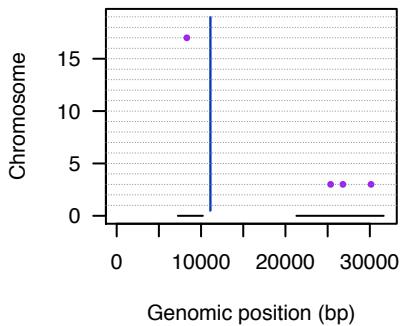
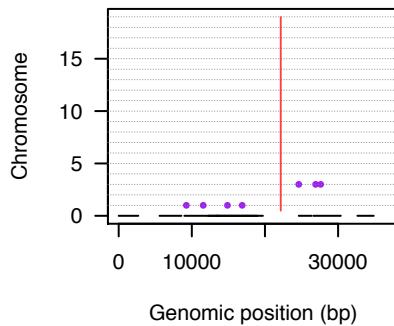
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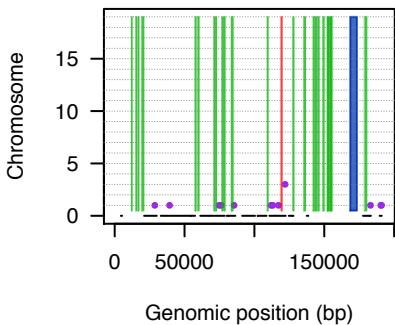
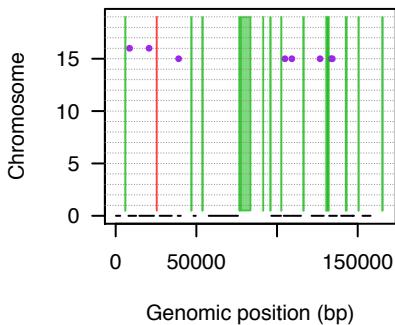
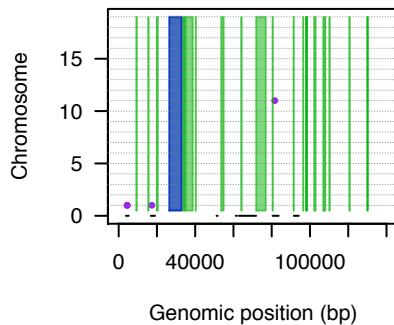
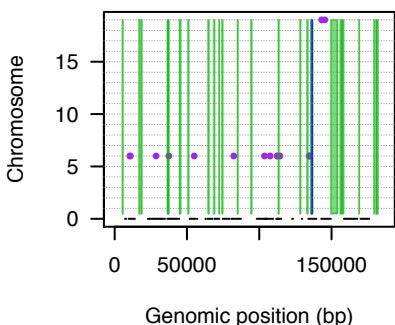
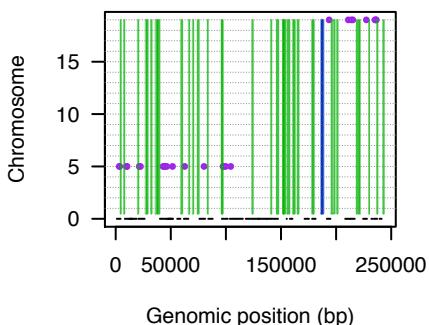
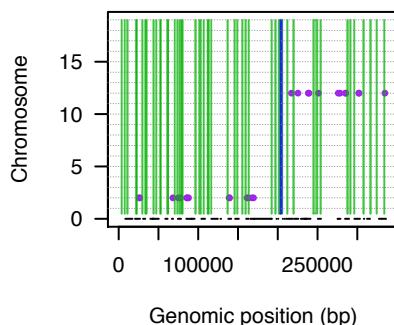
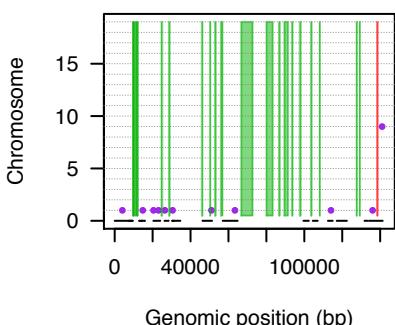
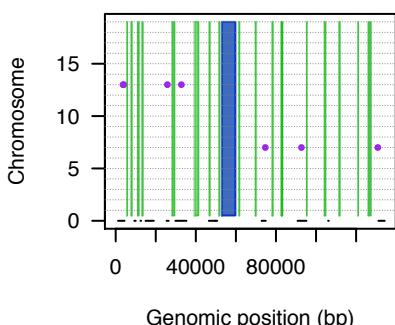
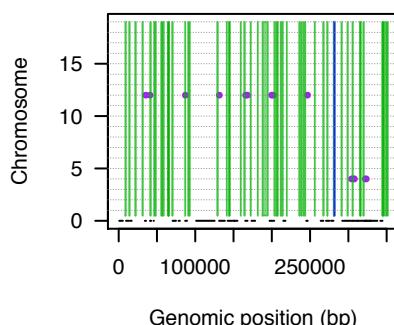


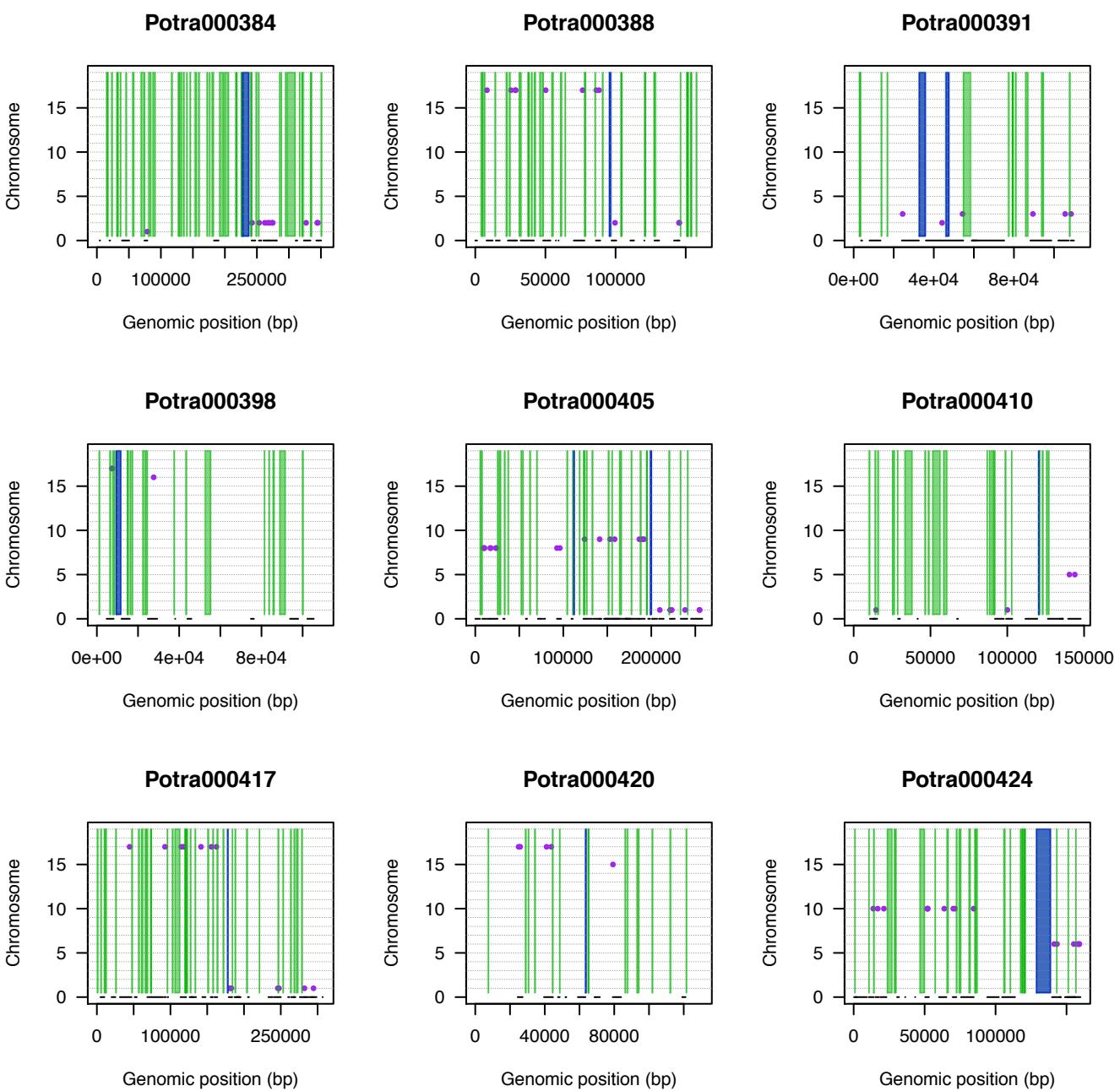
Supplementary Figure 4

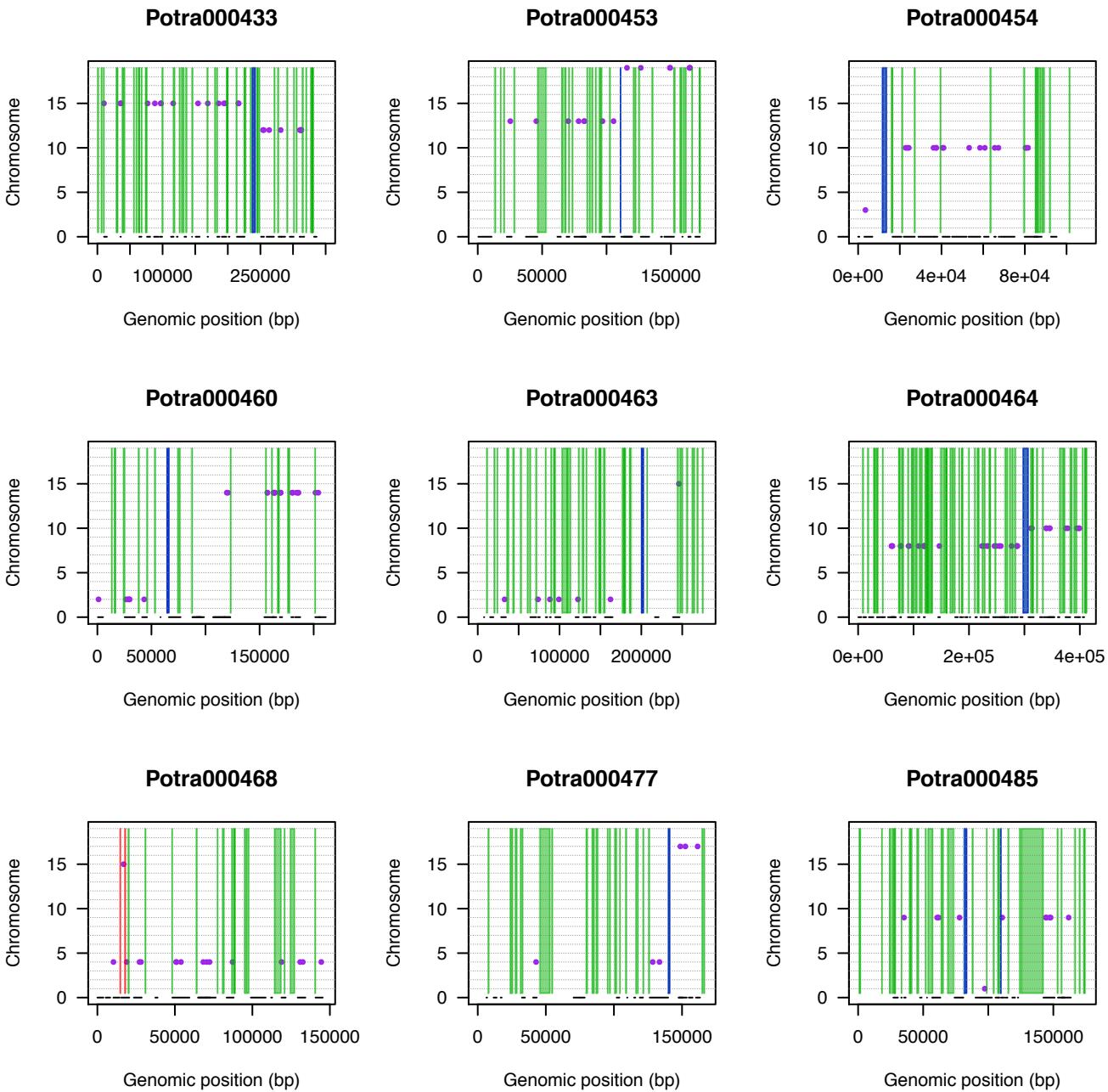
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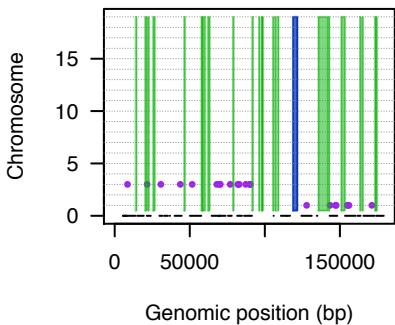
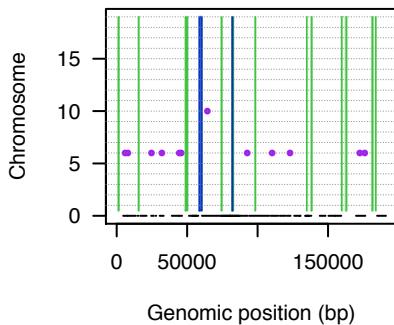
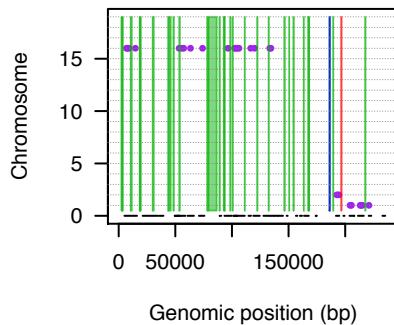
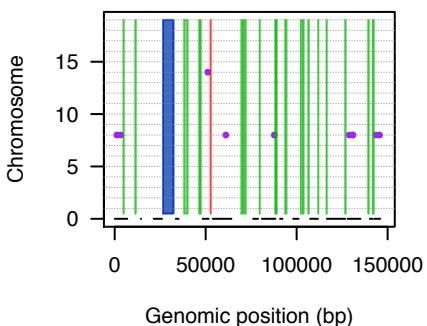
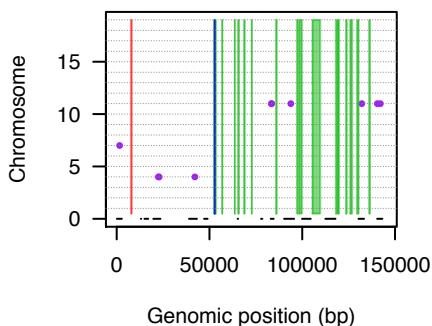
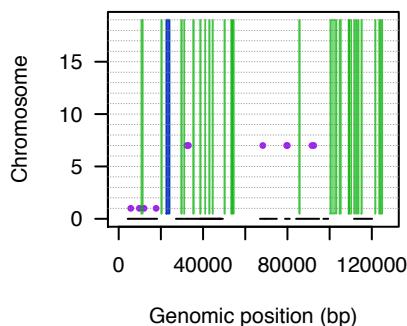
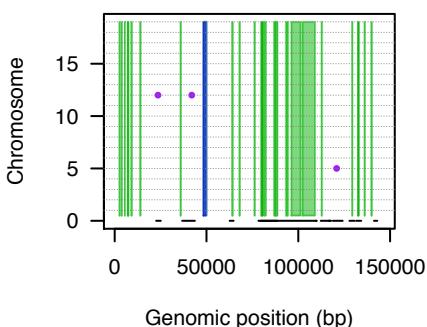
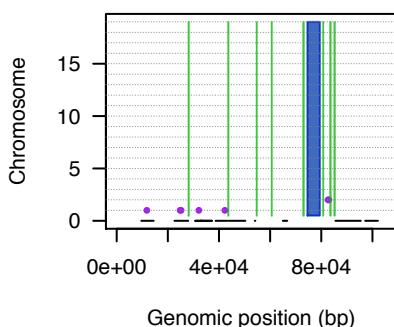
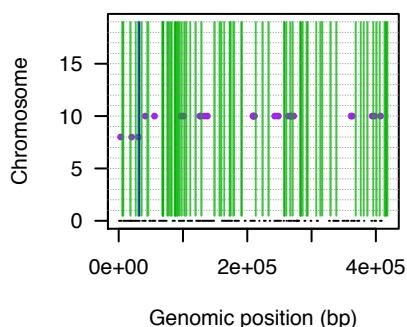
- Probe-marker
- Gene
- Assembly gaps
- Gap split
- Artificial split

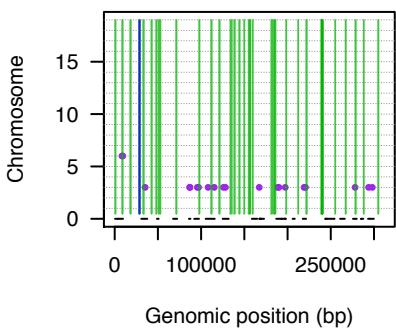
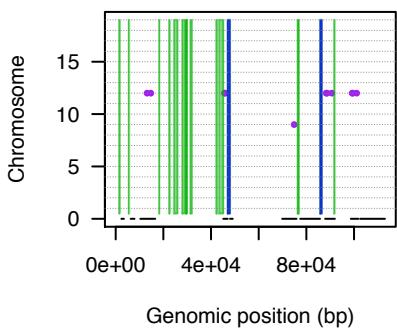
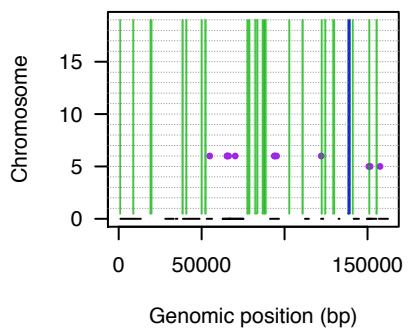
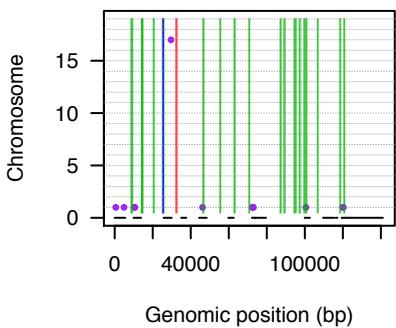
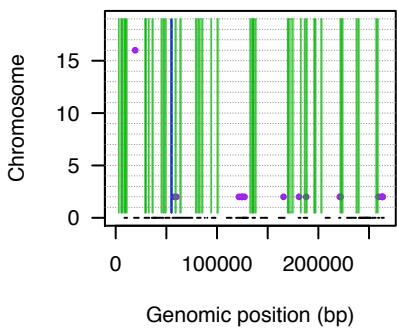
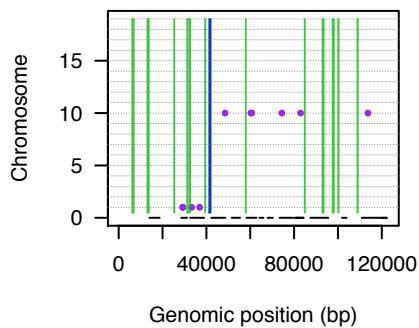
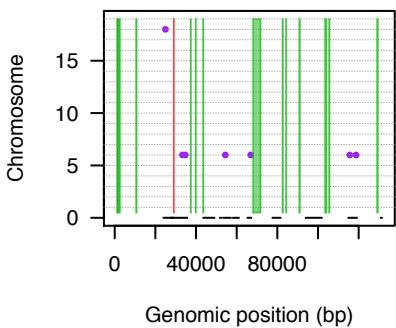
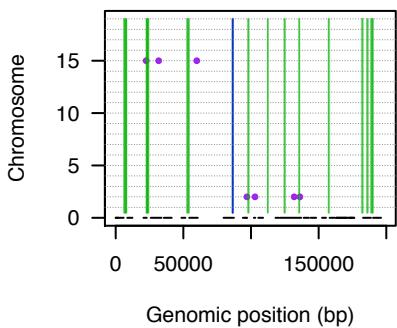
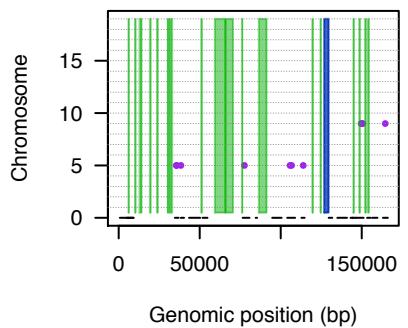
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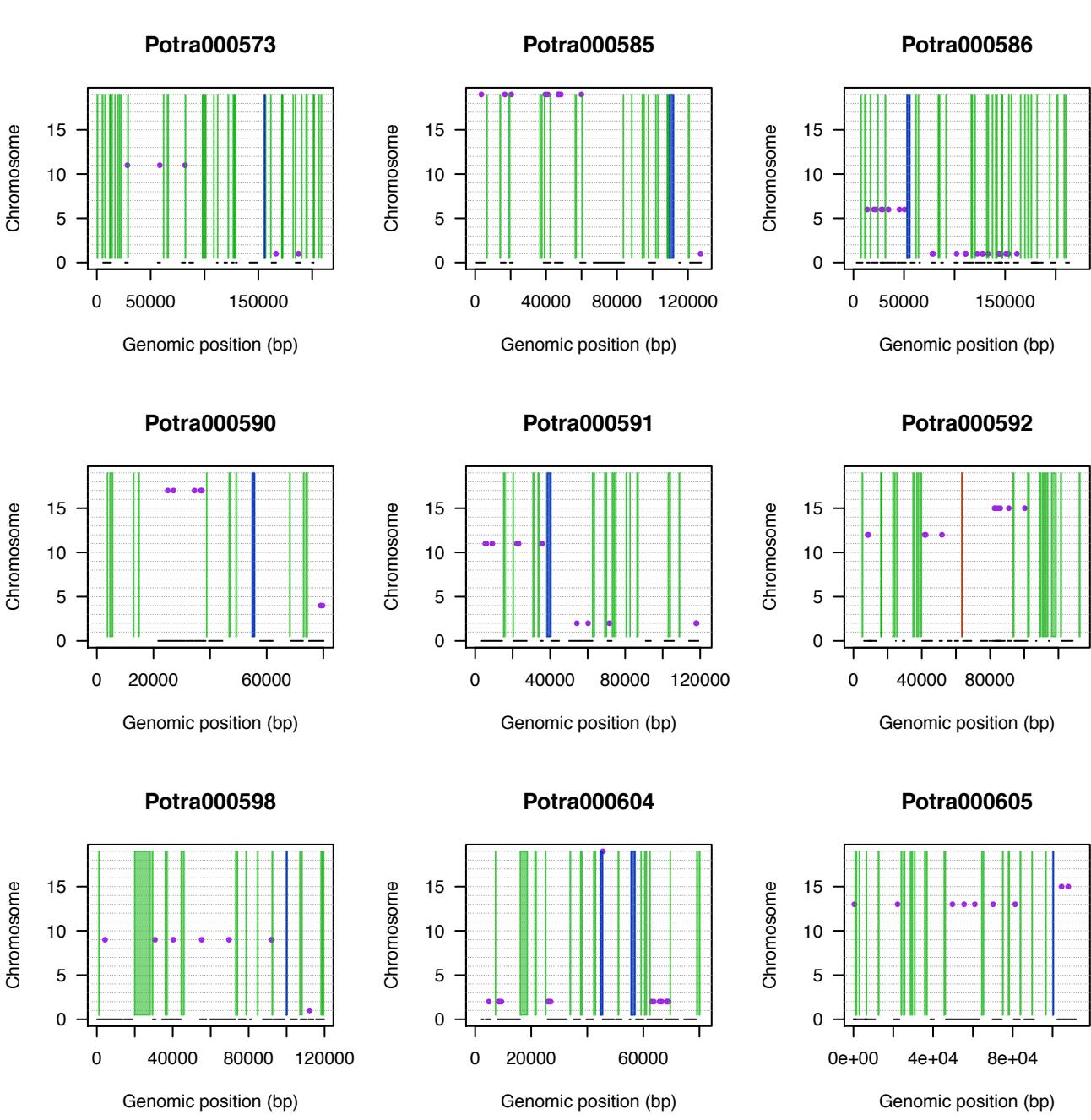
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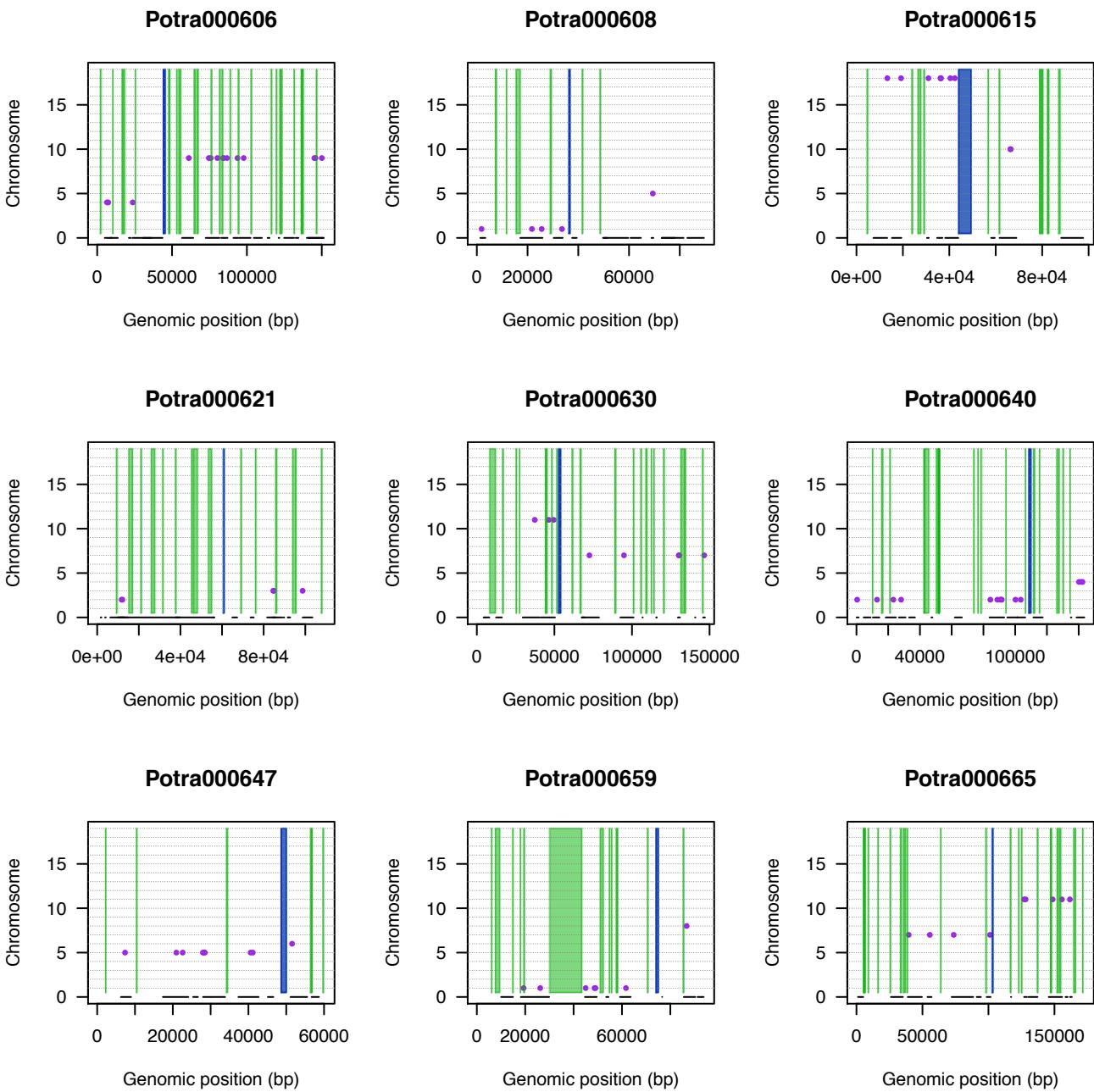


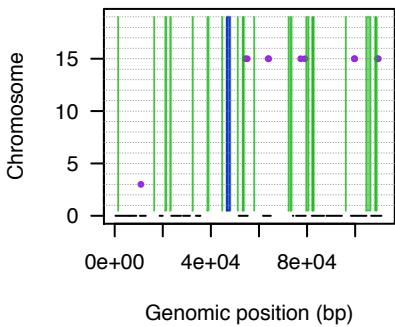
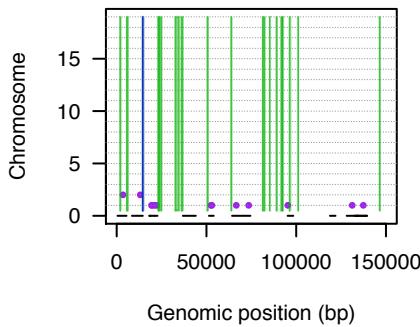
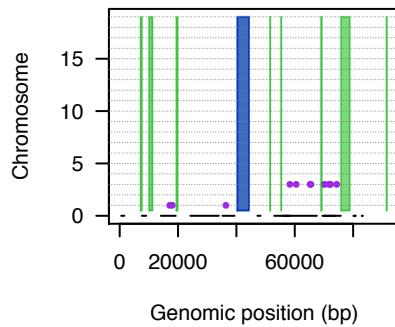
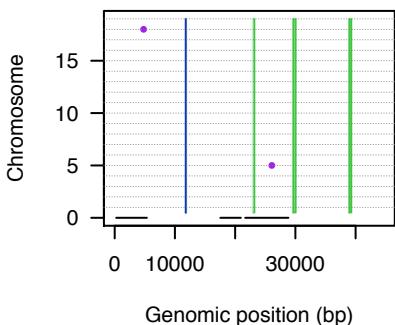
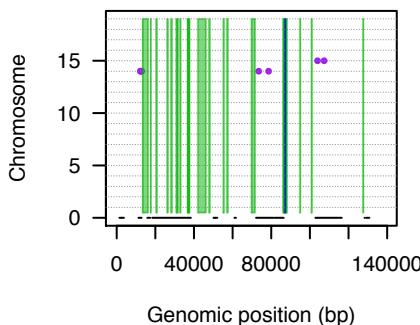
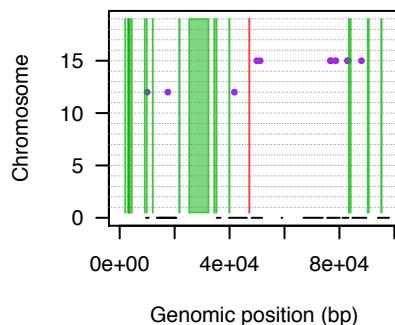
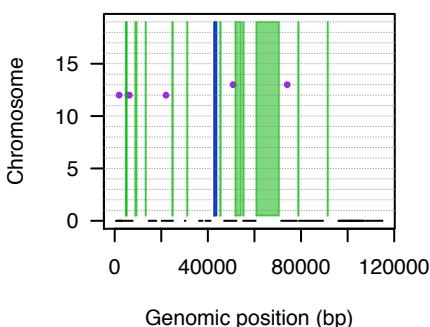
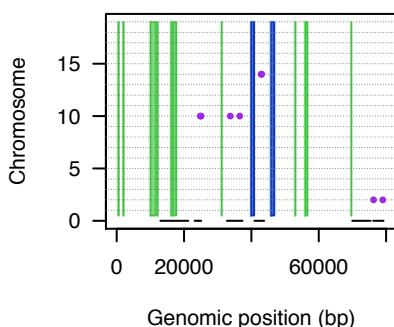
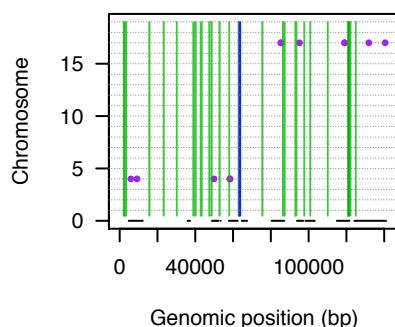


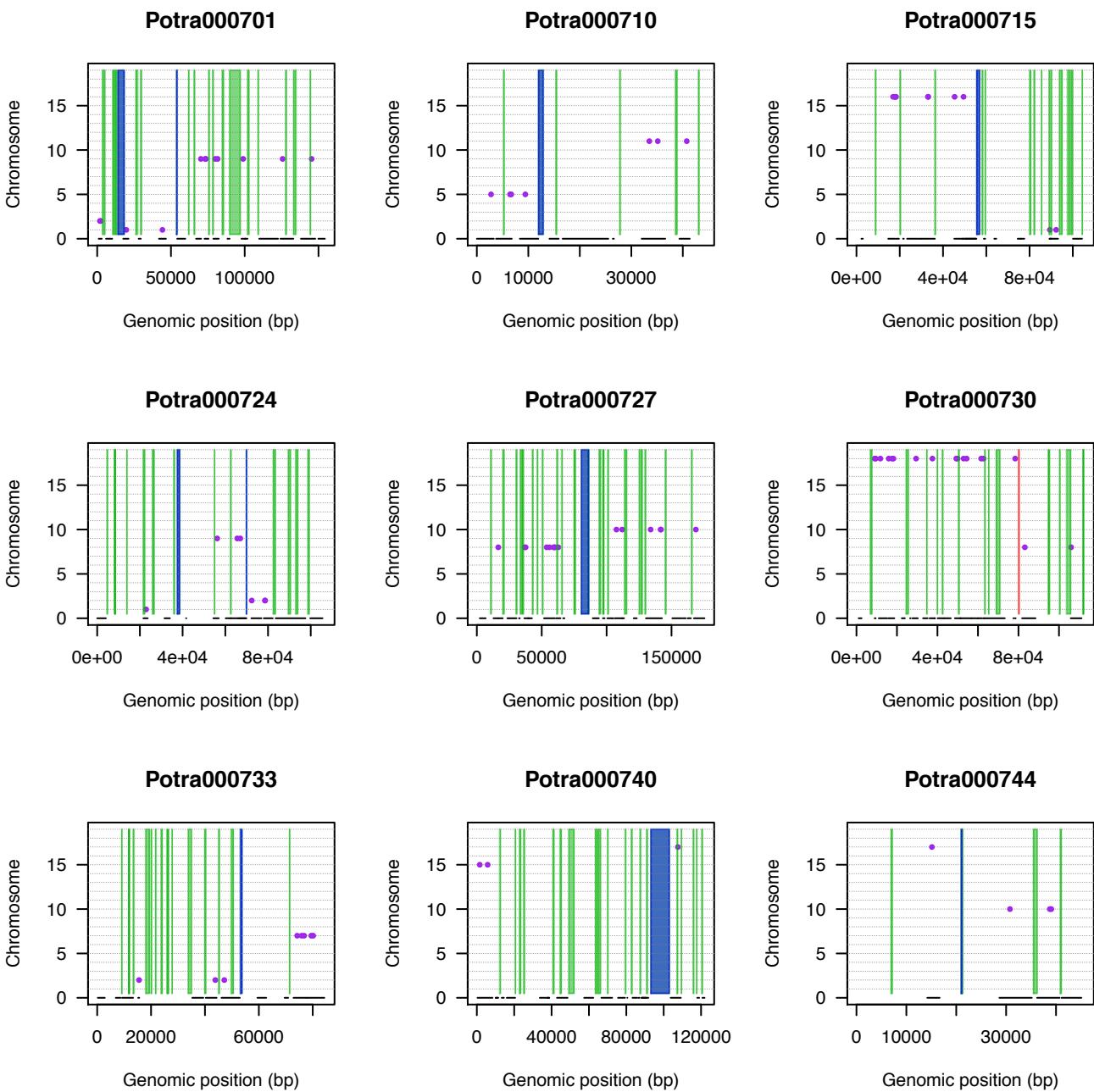
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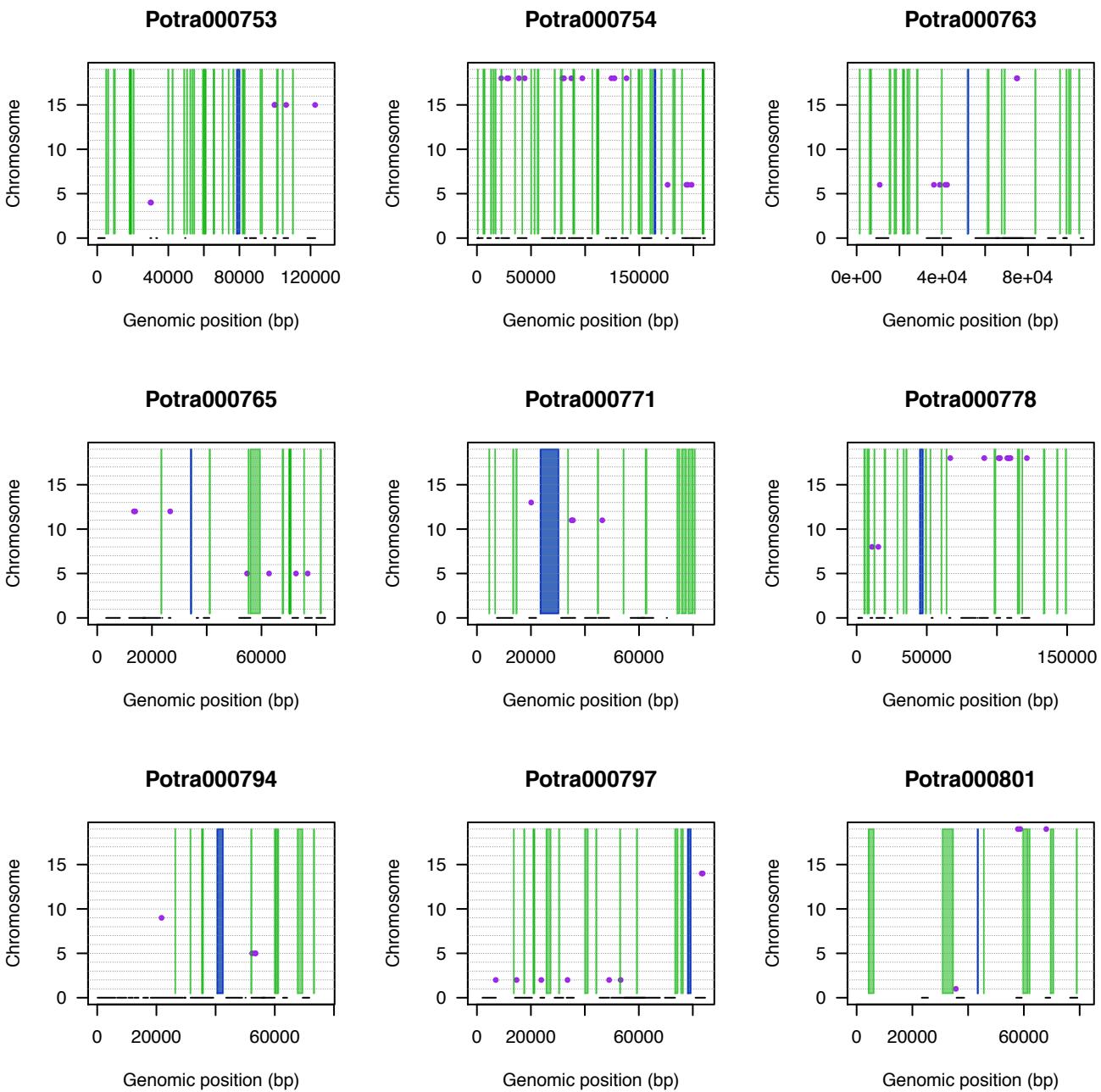
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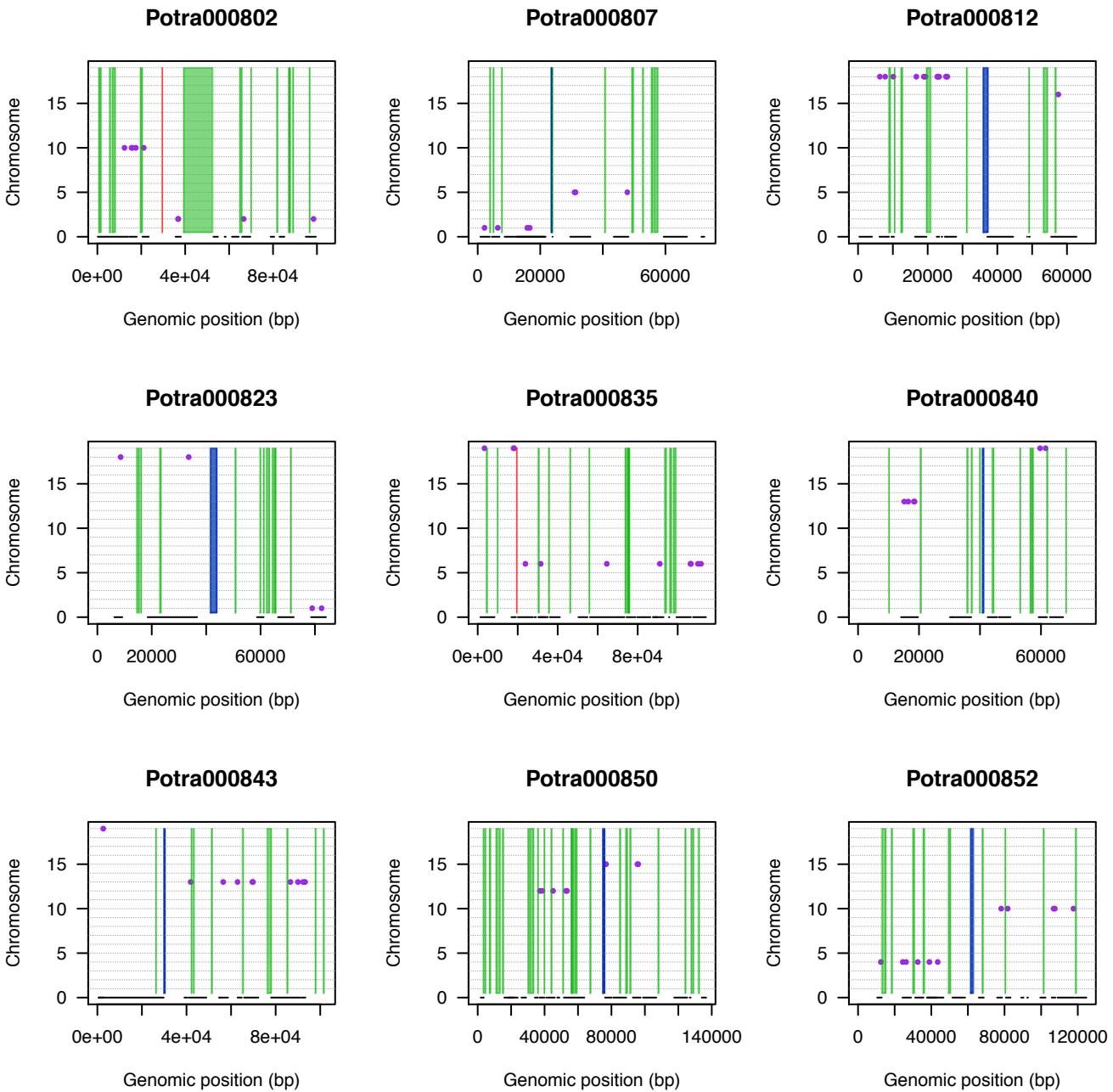


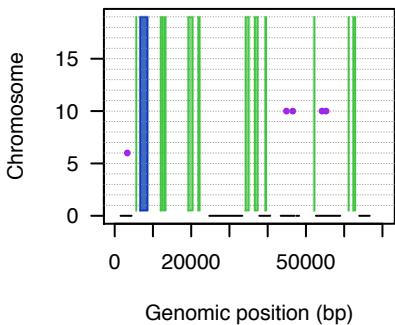
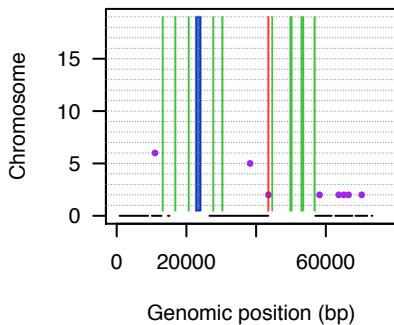
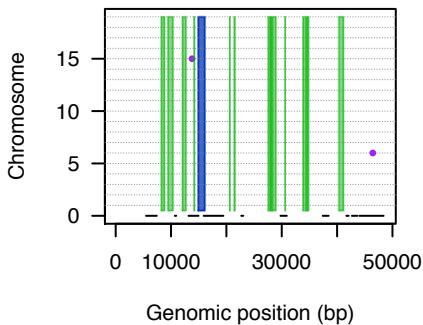
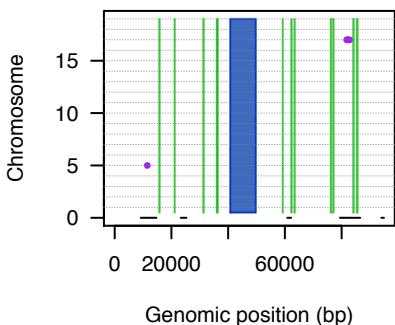
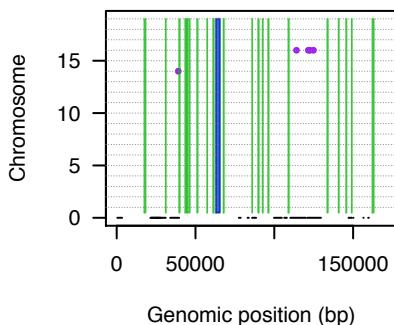
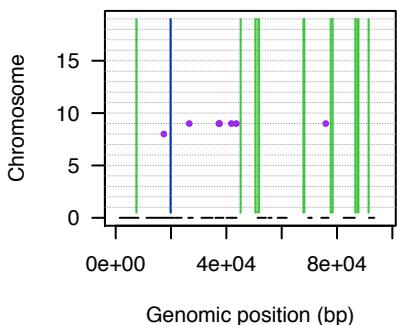
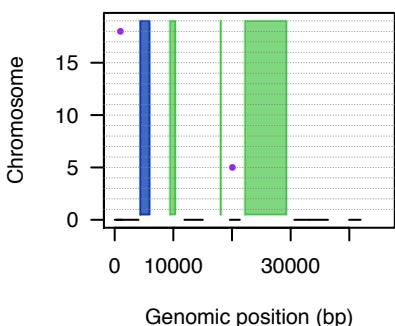
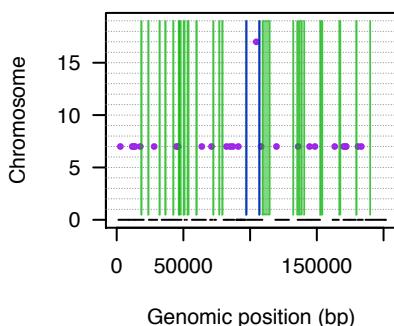
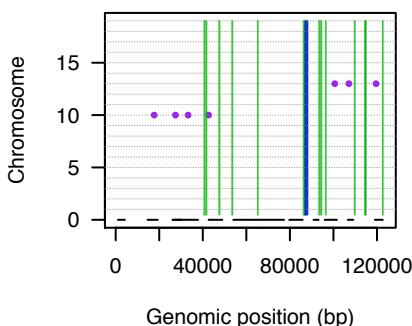


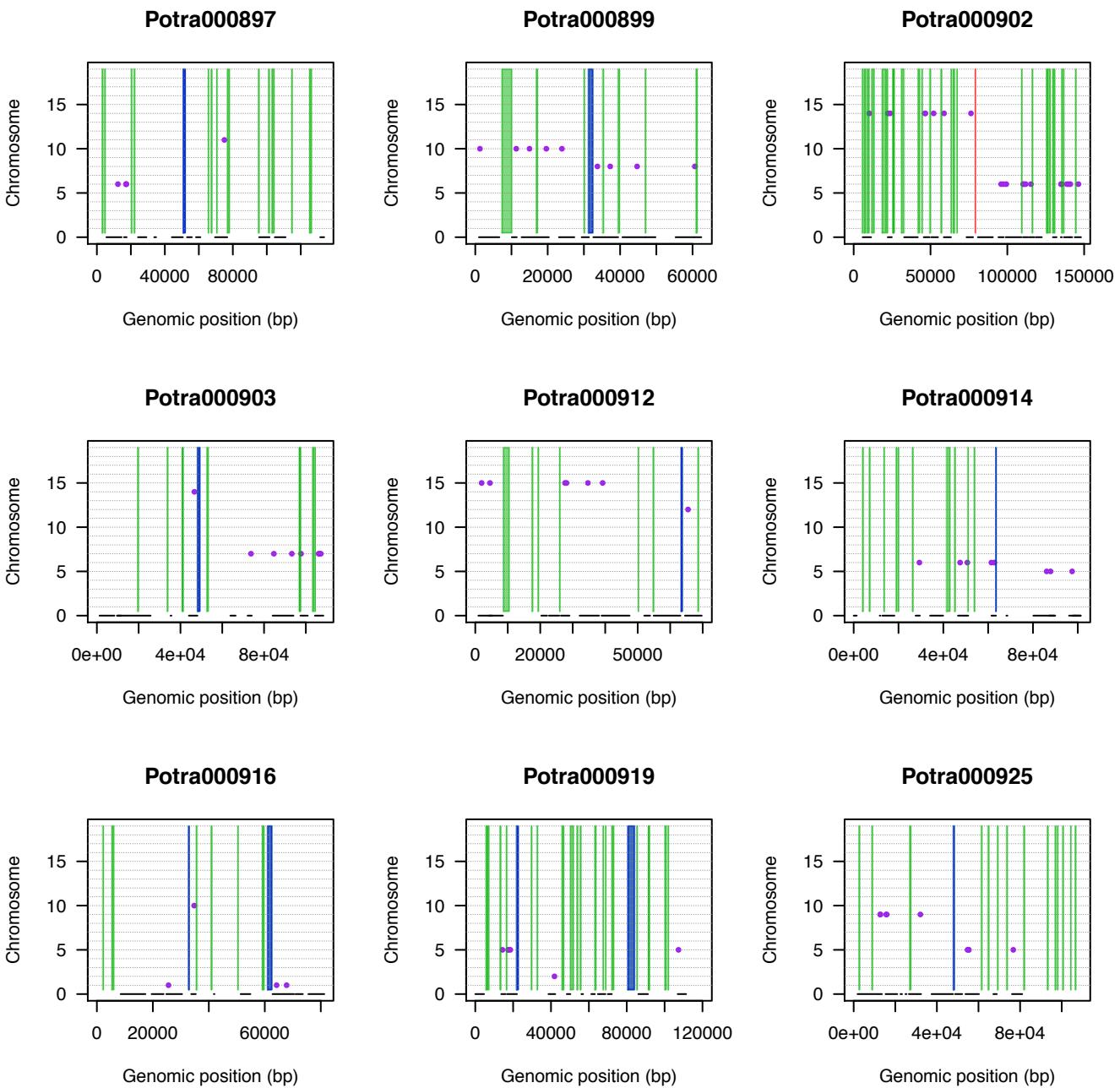
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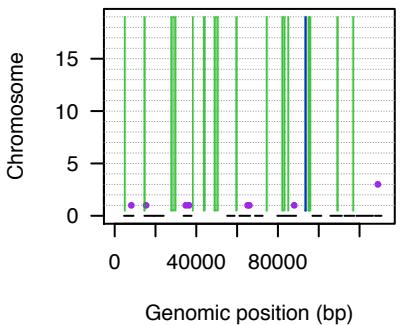
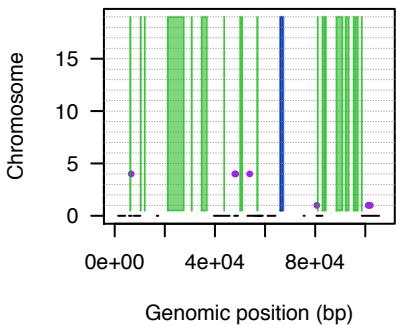
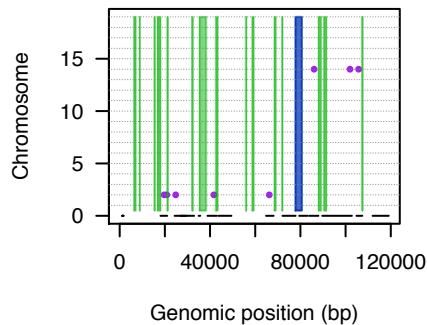
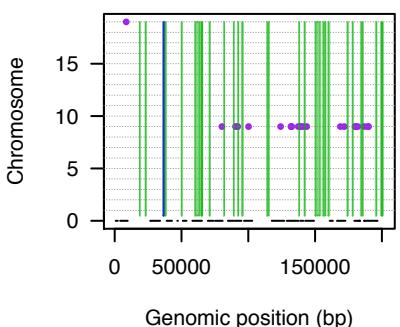
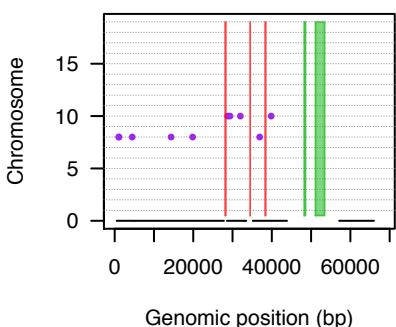
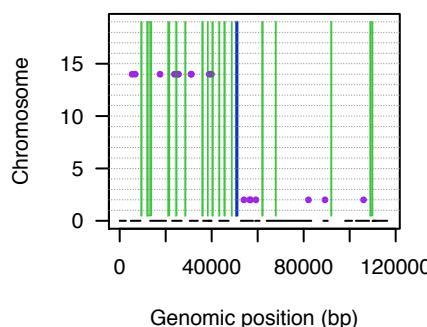
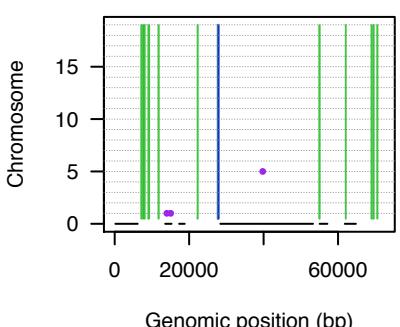
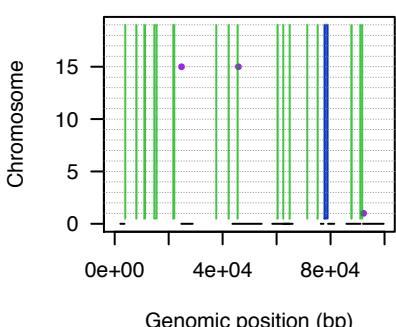
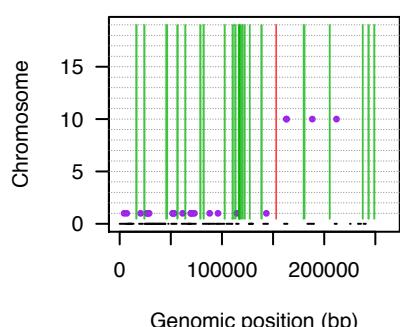


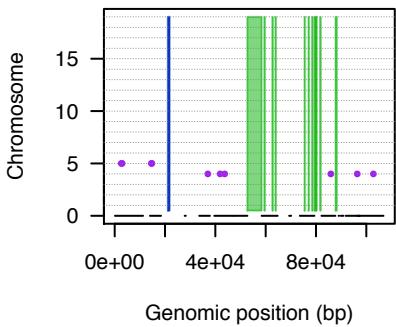
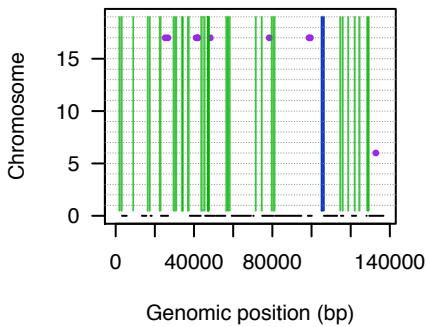
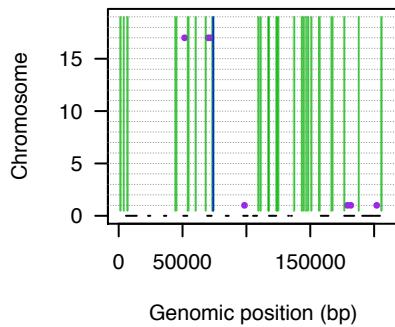
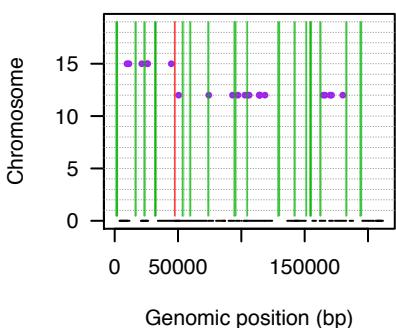
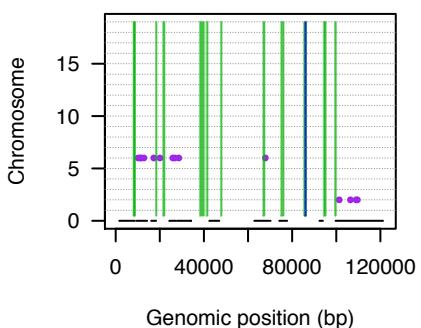
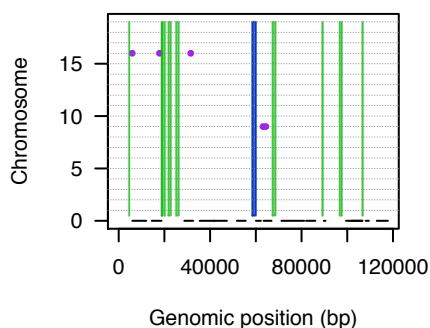
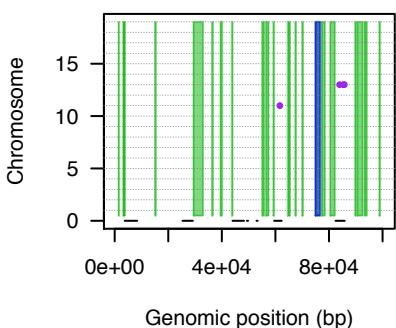
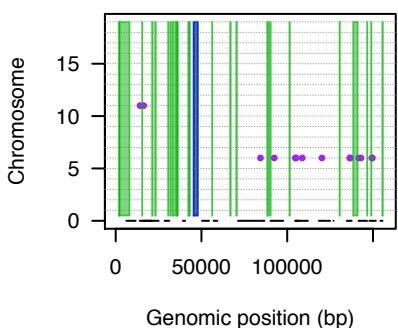
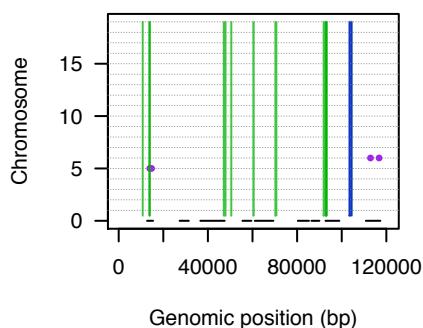


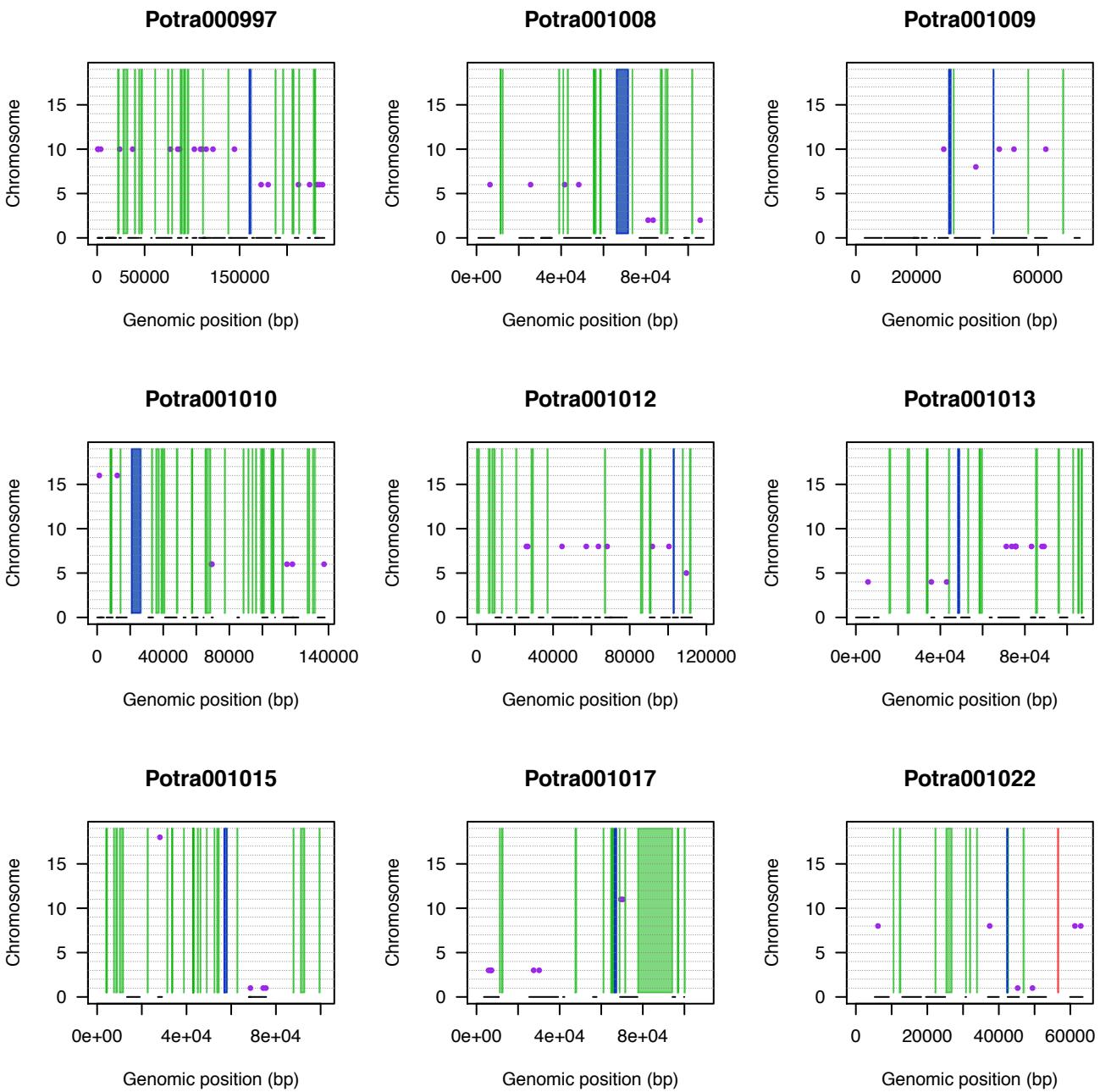


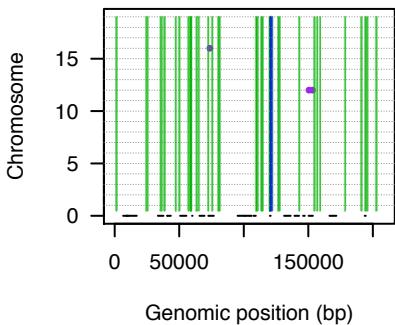
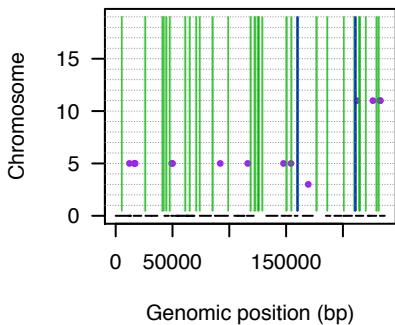
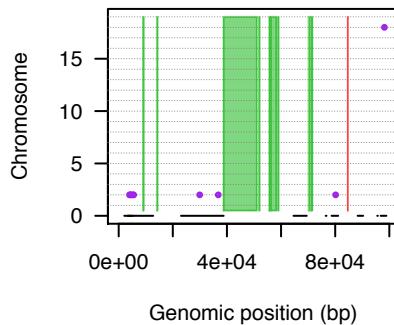
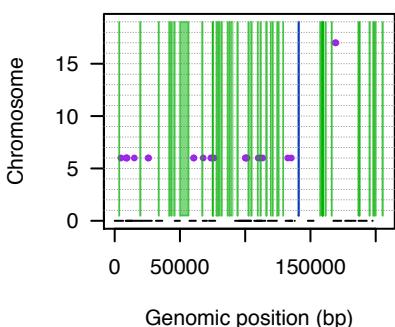
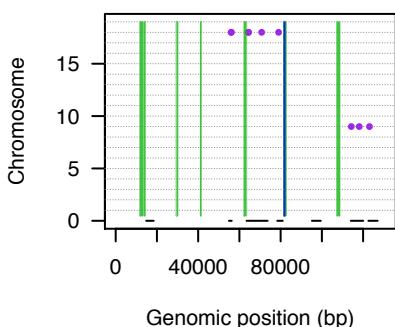
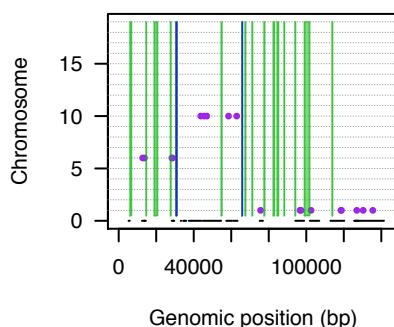
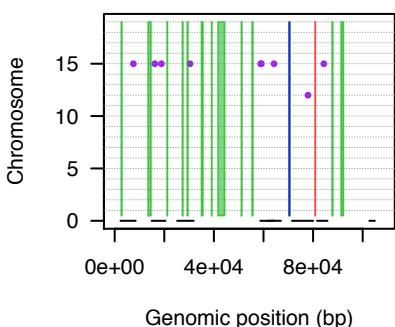
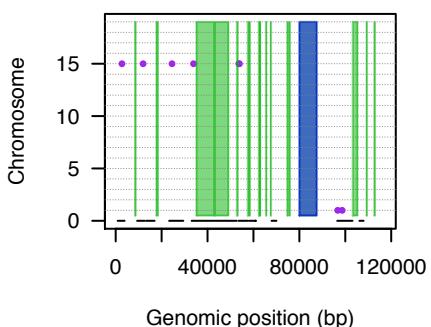
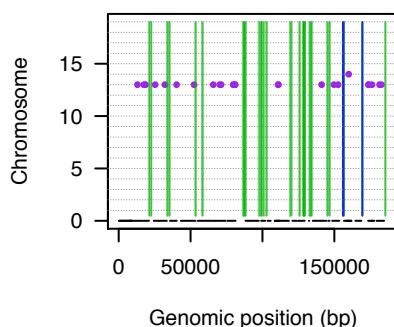
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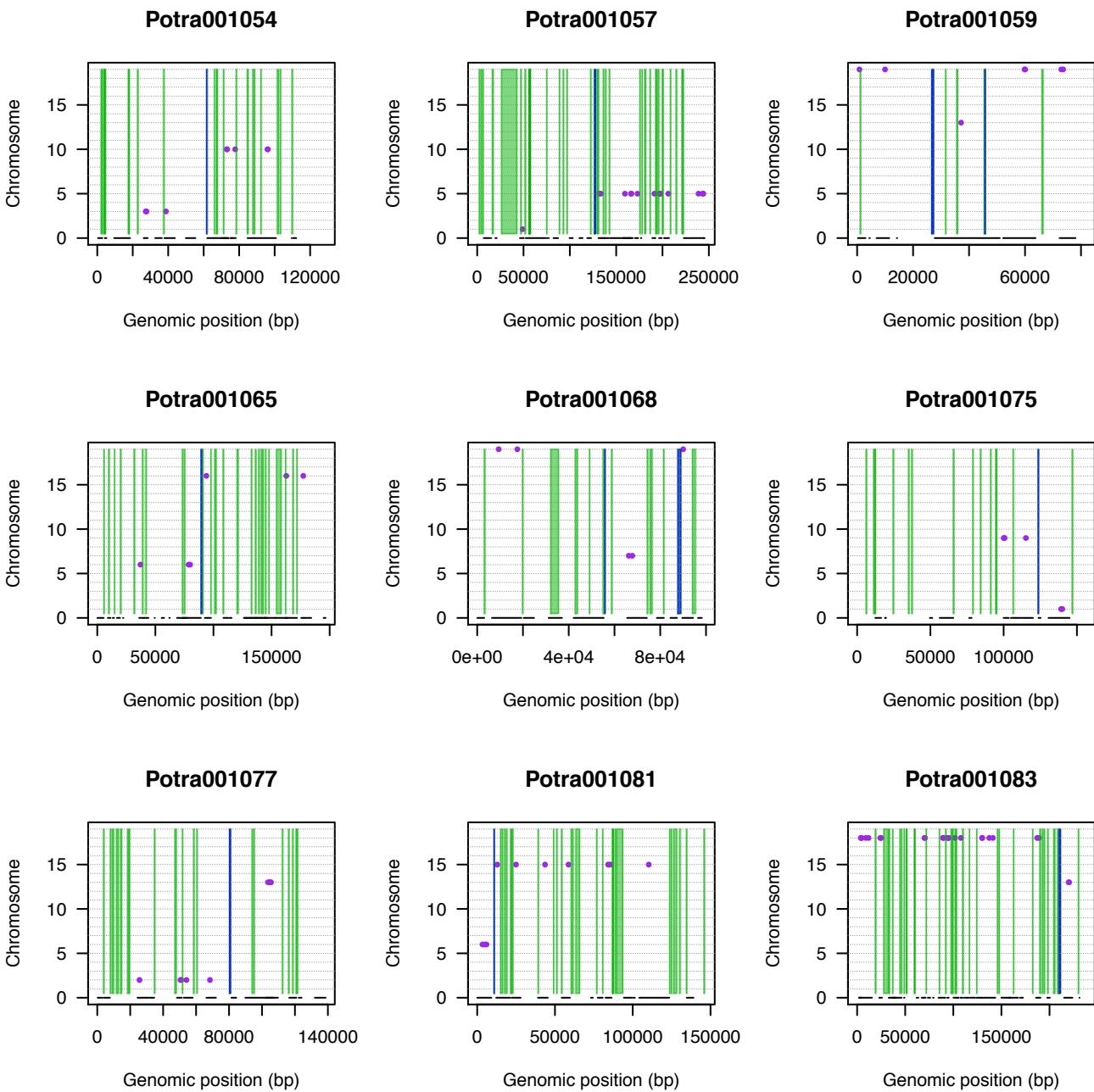


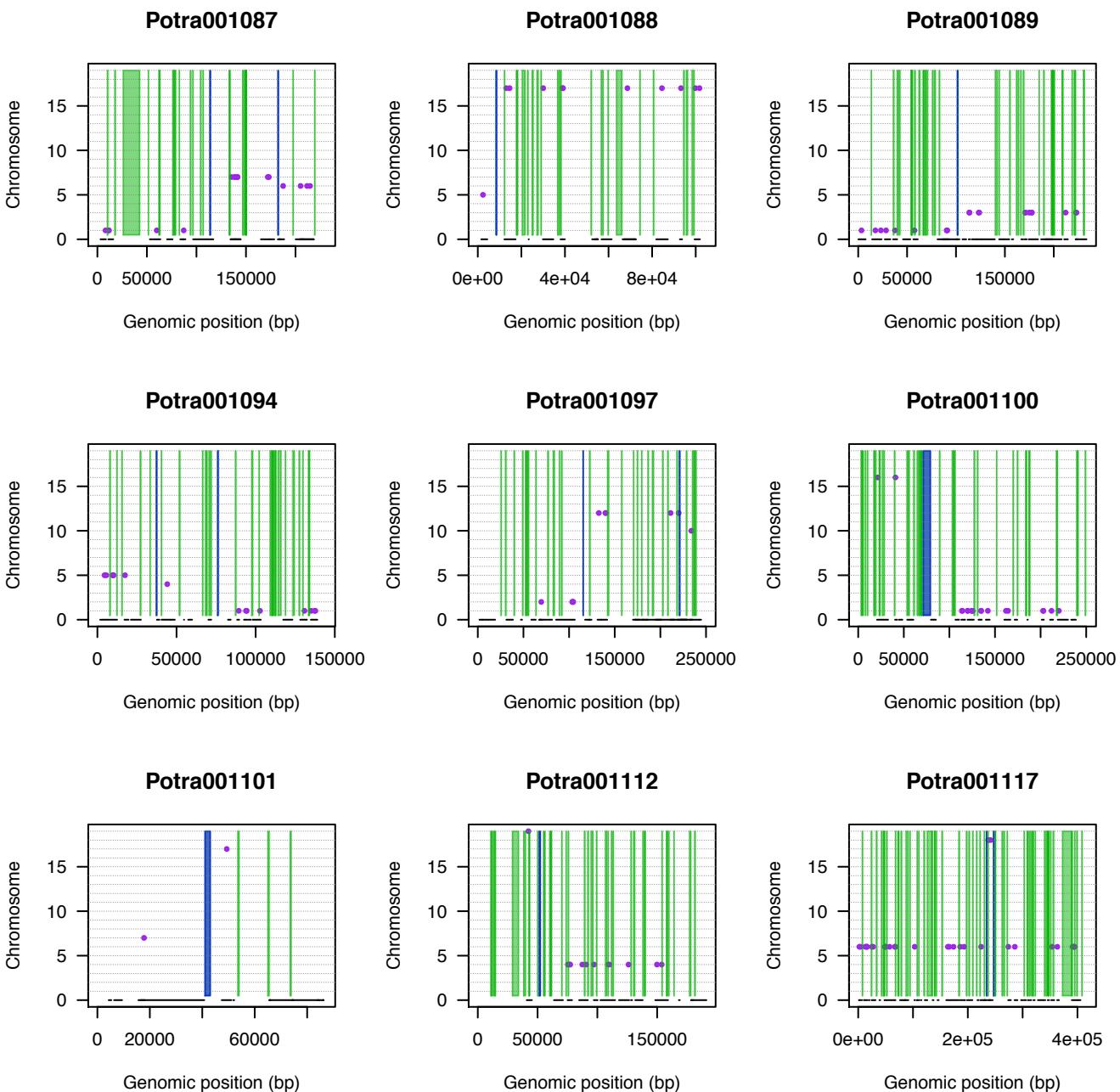
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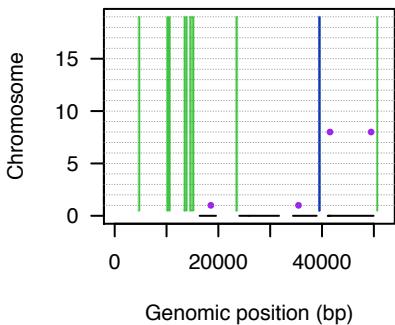
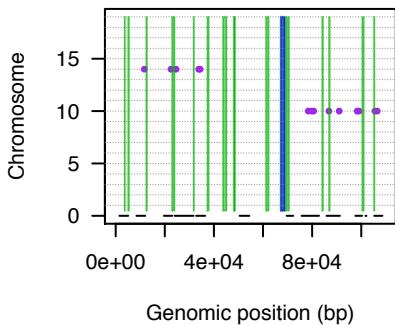
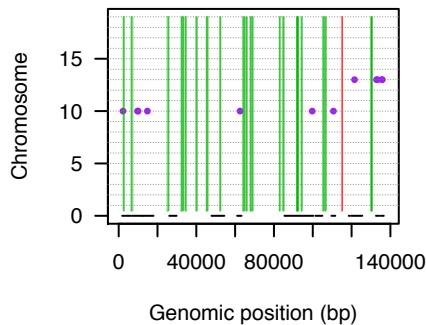
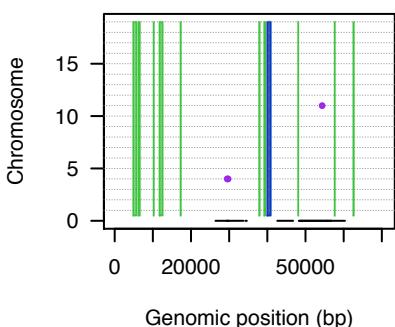
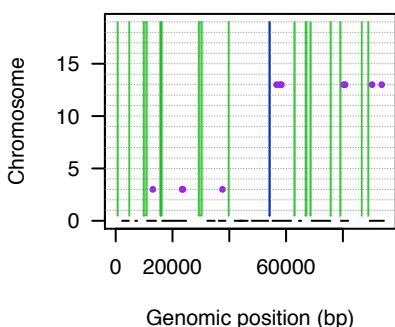
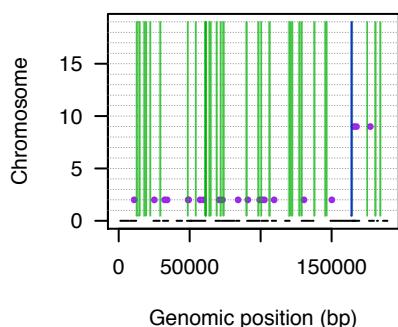
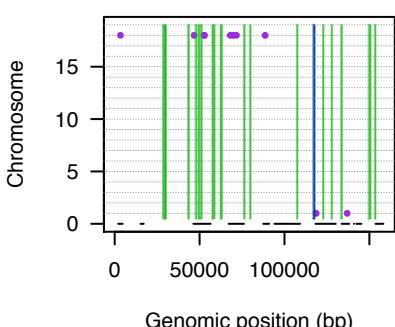
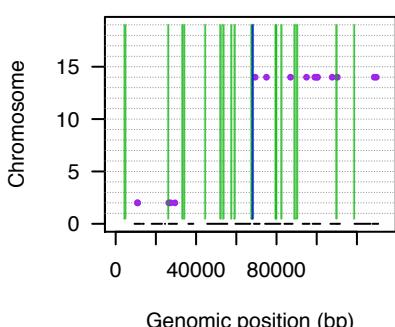
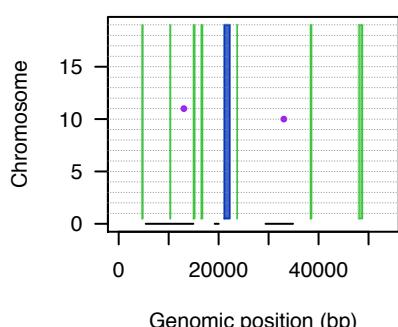
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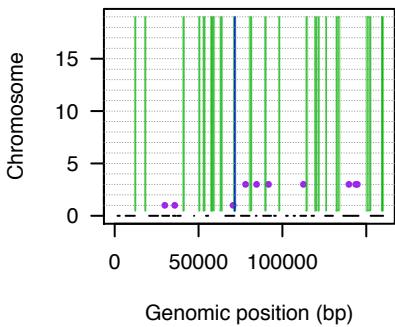
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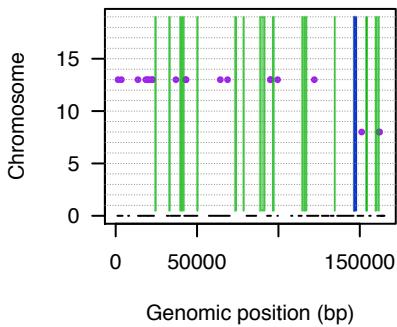


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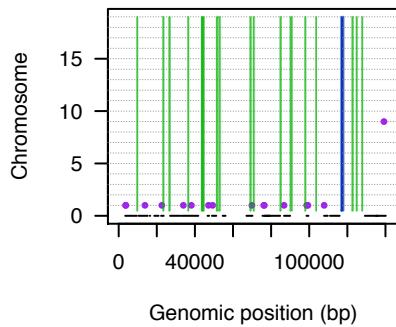
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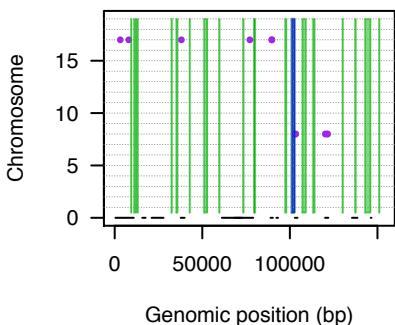
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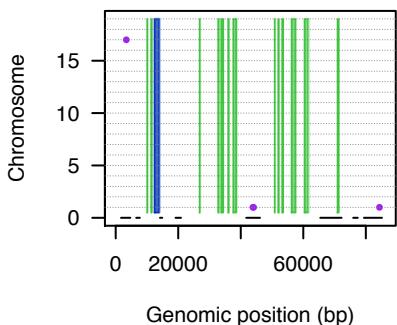
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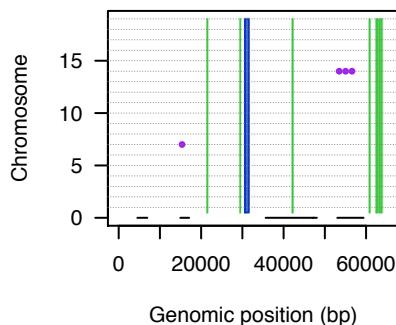
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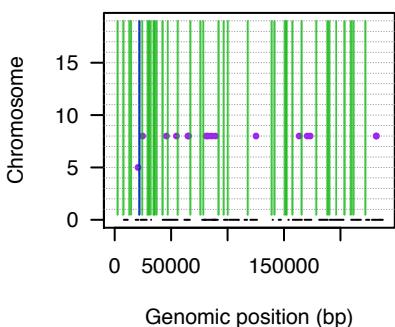
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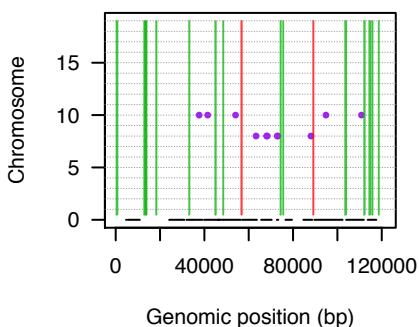
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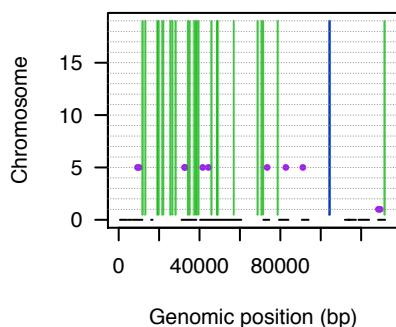
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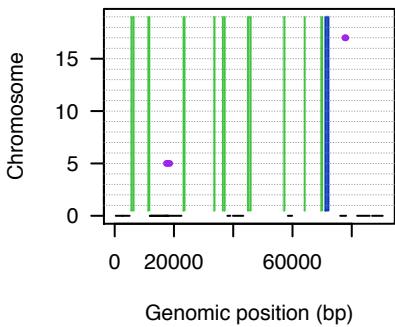
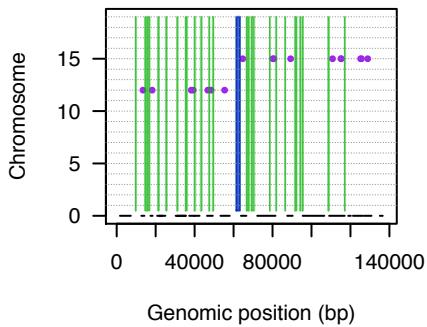
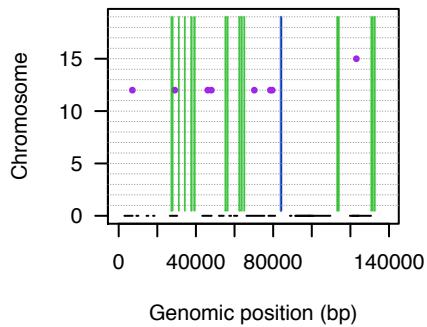
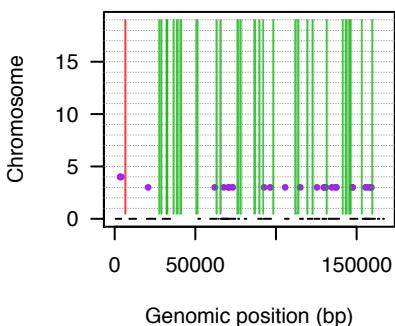
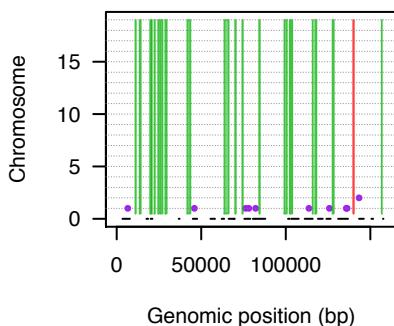
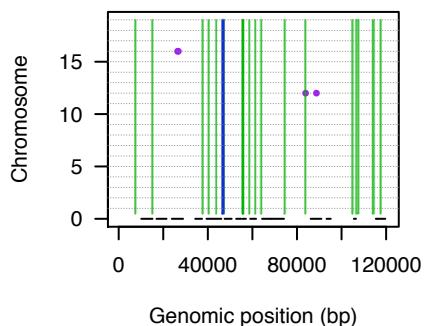
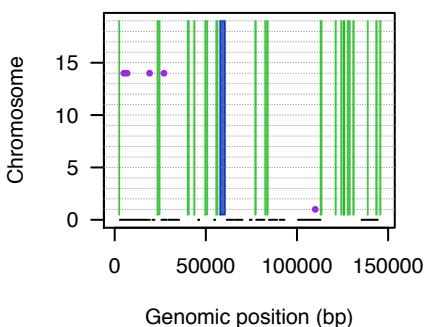
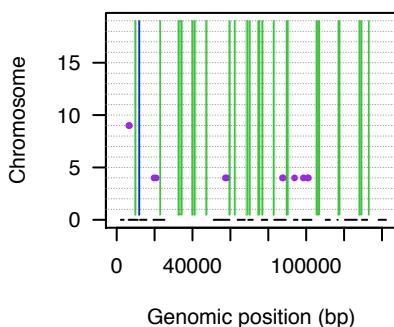
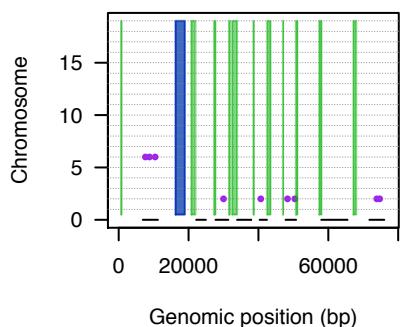


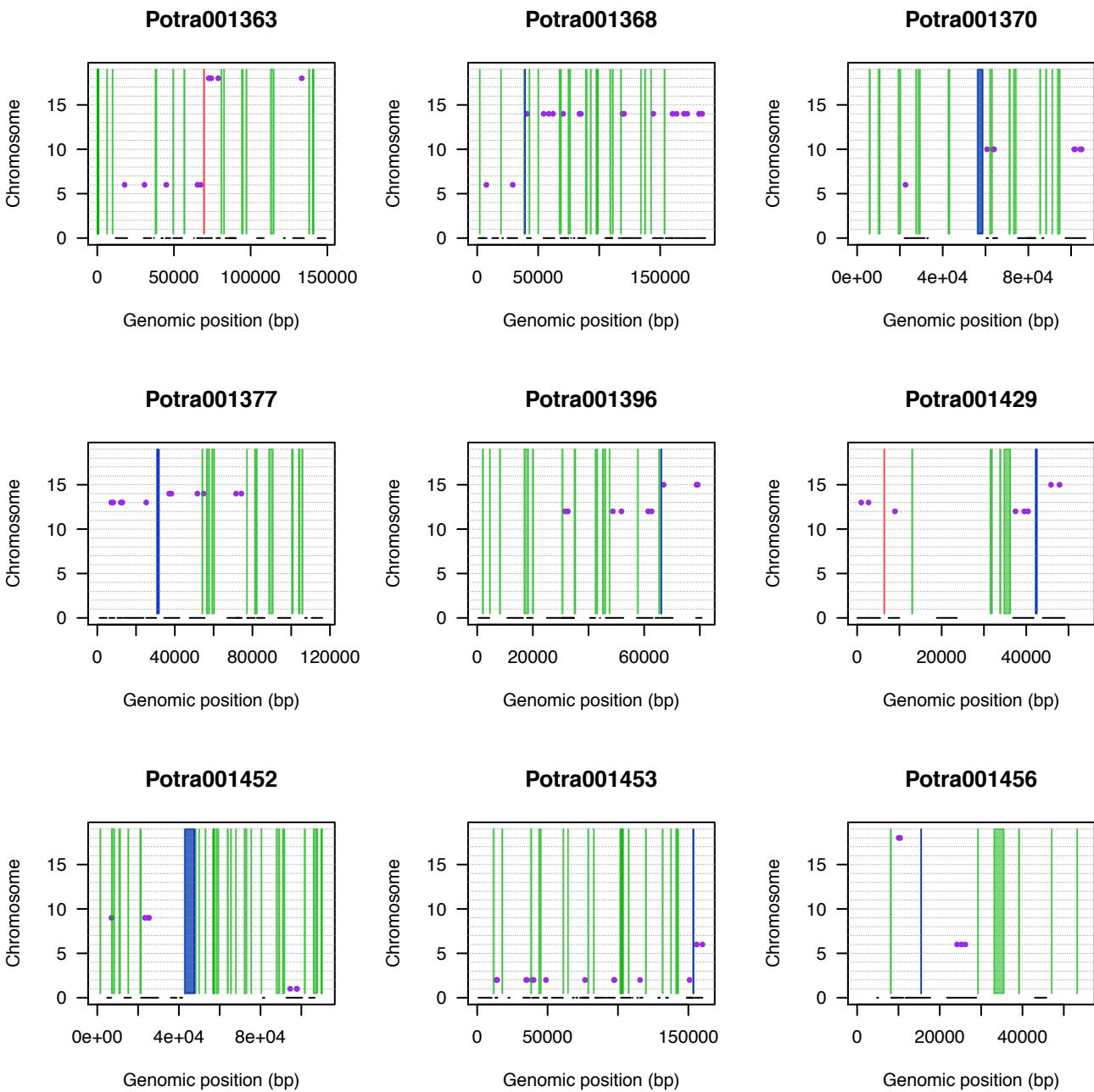
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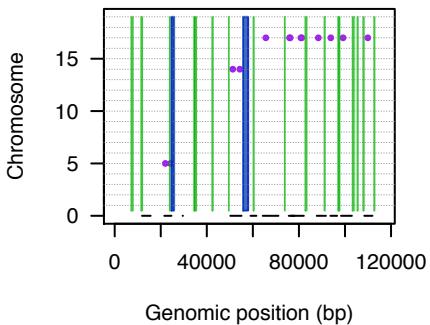
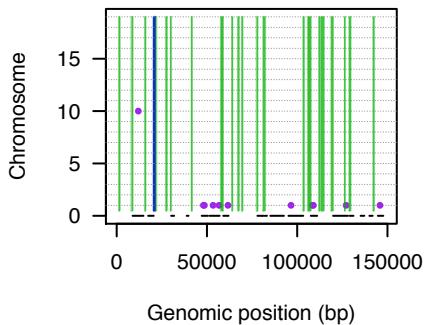
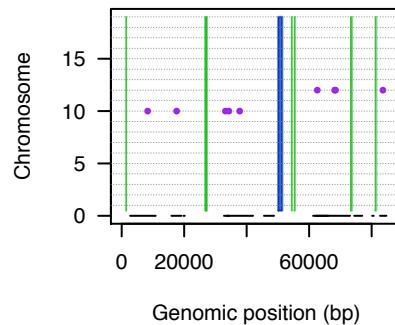
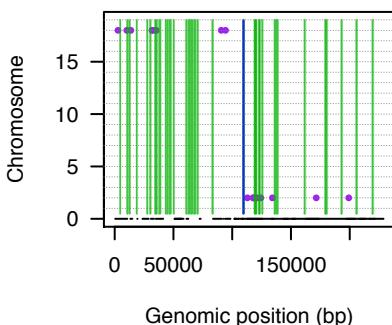
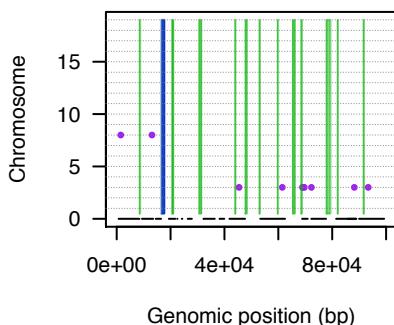
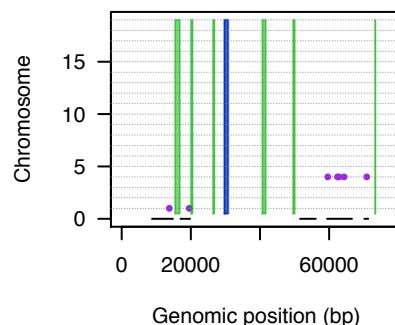
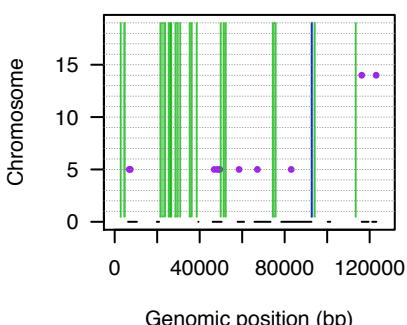
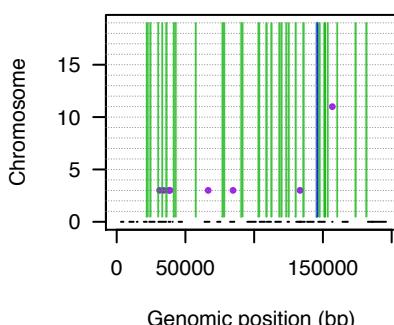
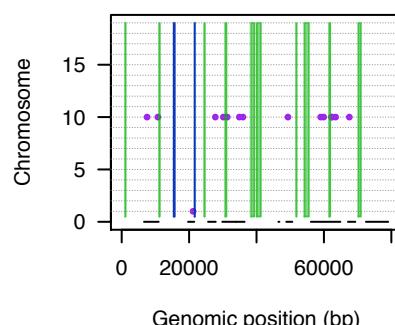


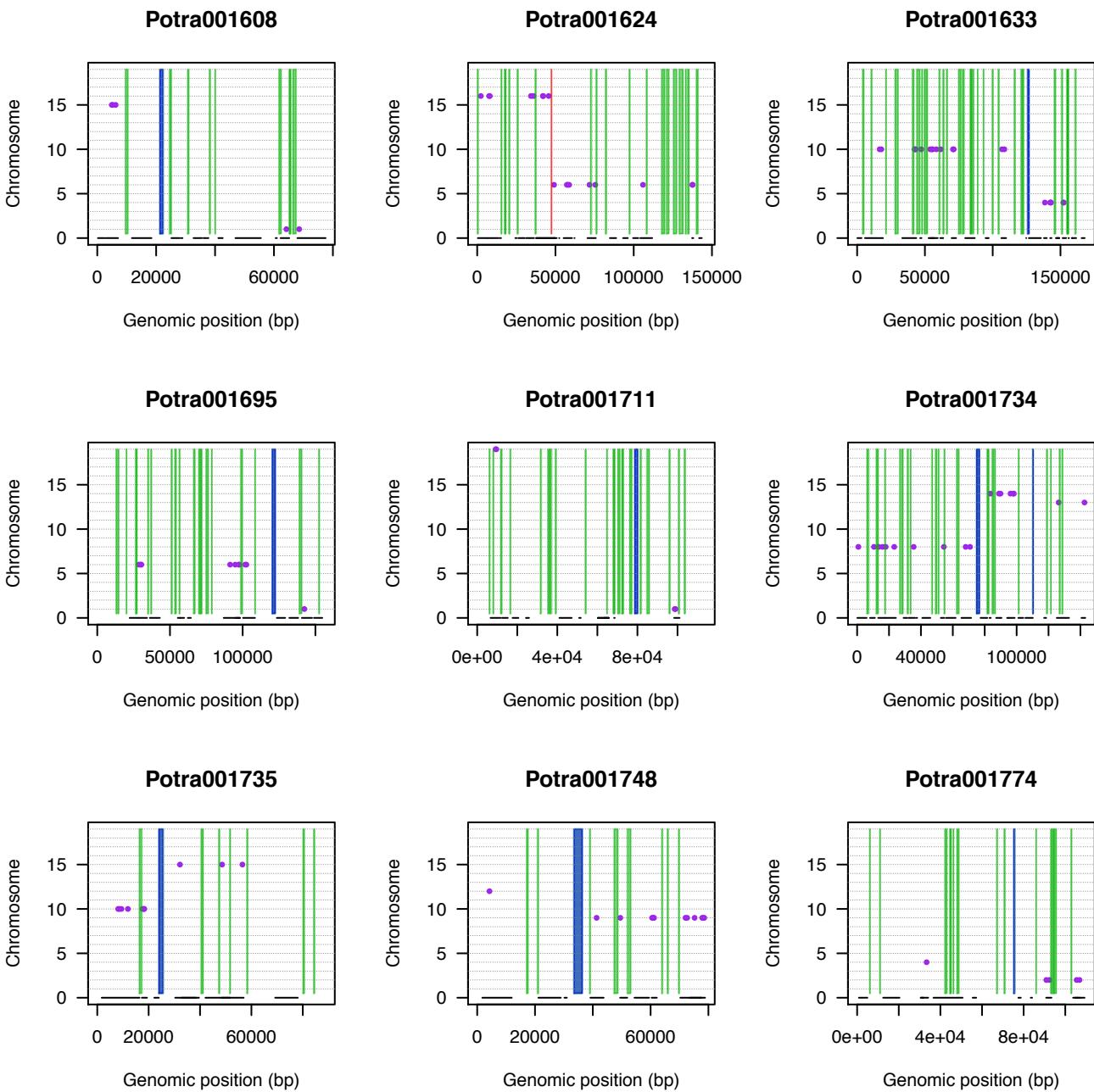
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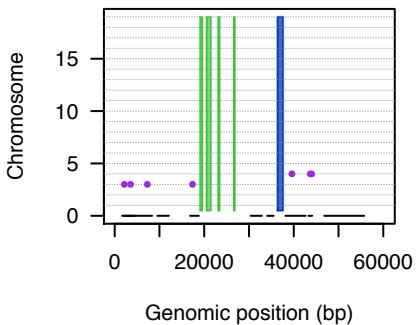
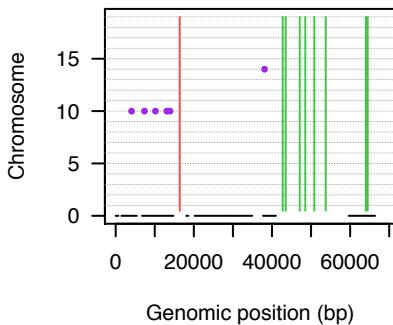
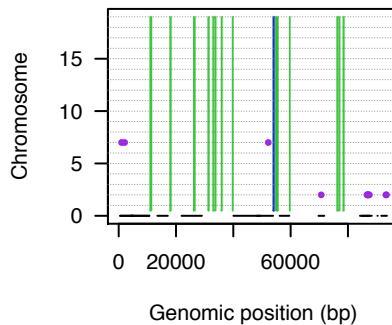
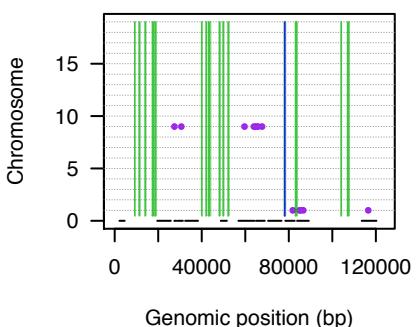
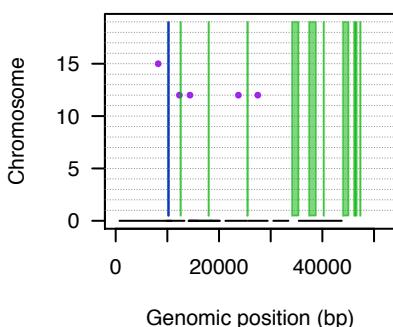
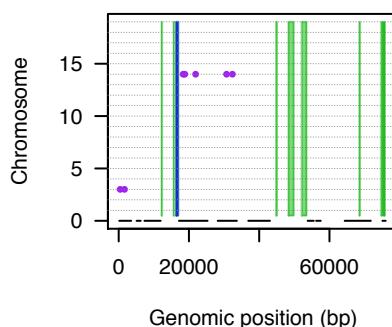
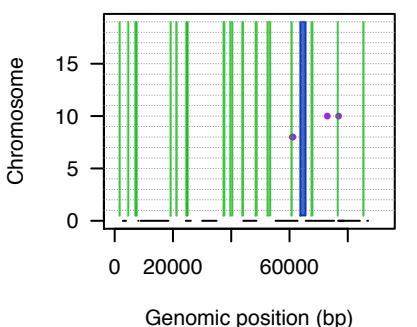
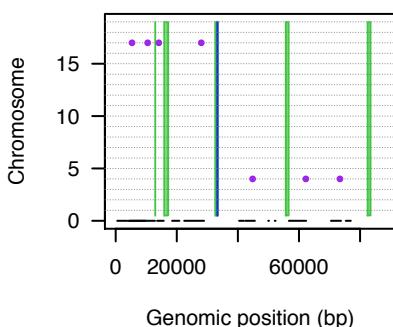
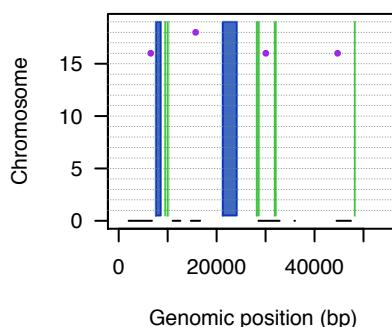


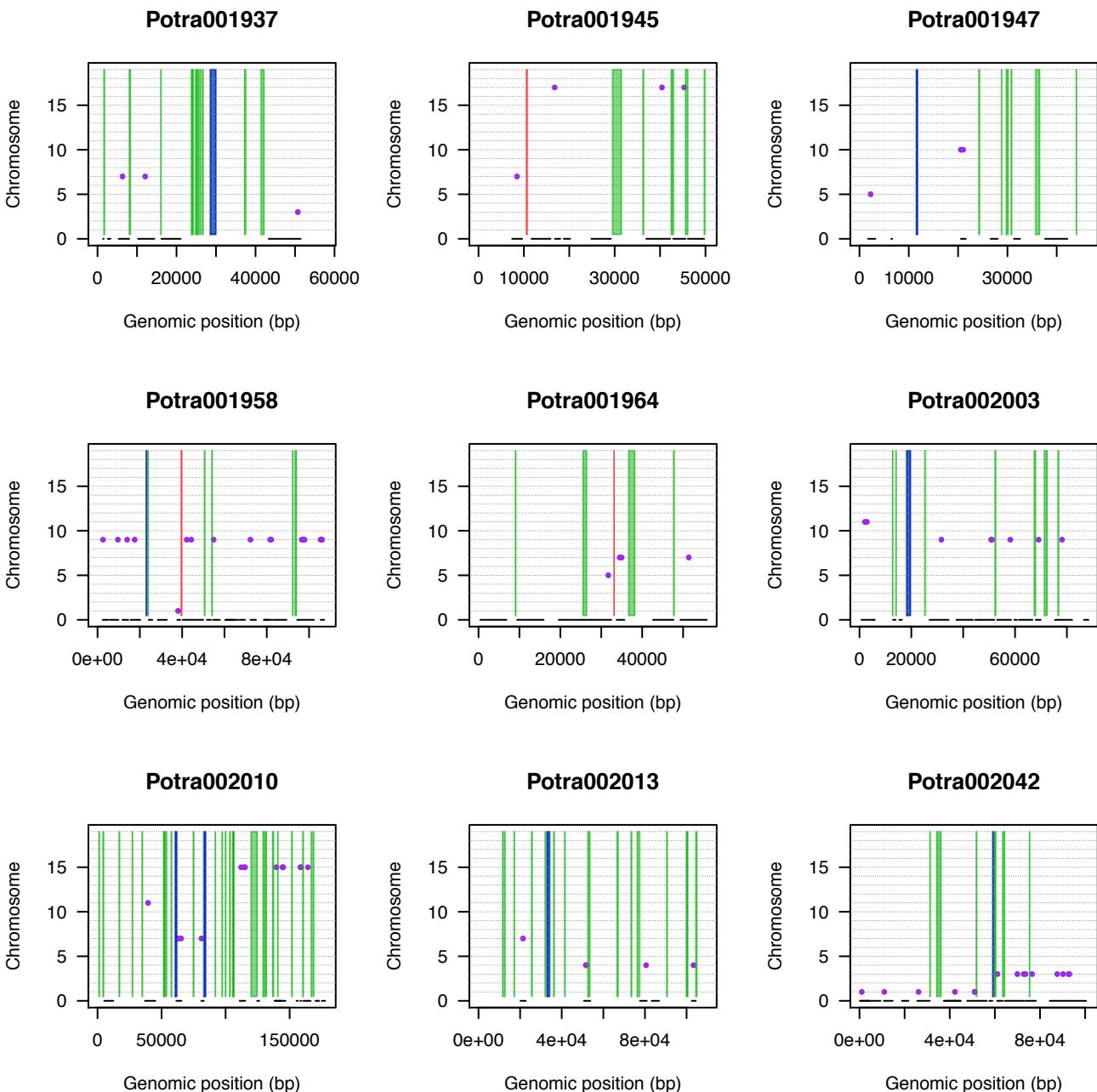
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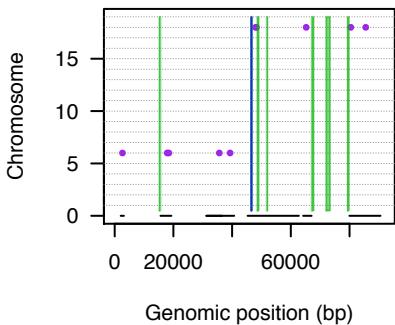
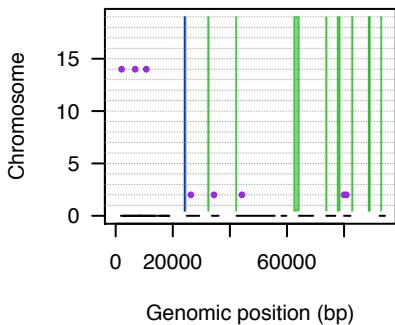
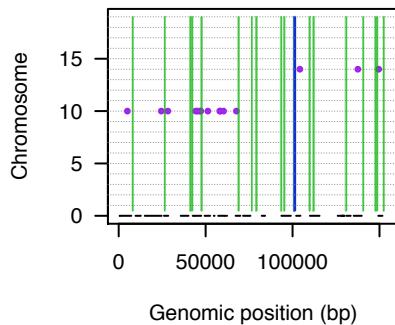
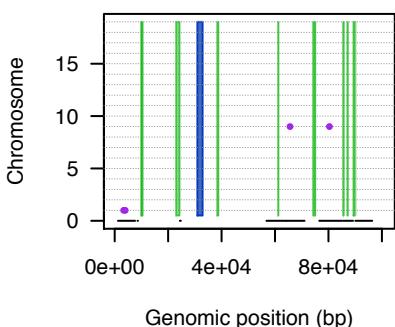
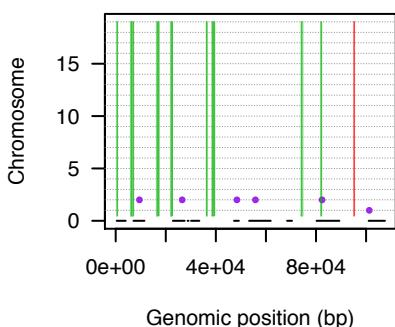
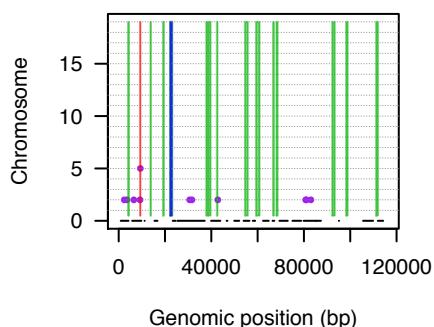
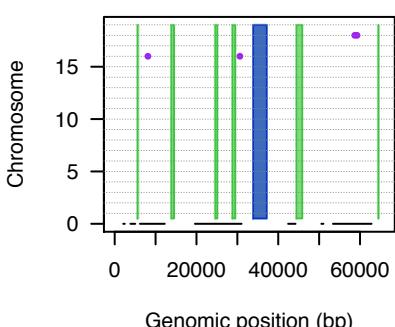
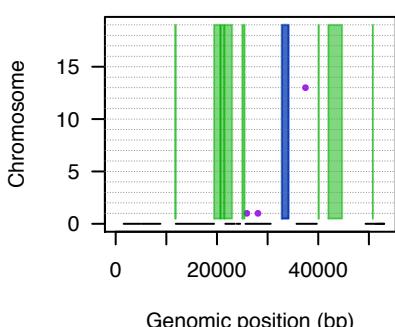
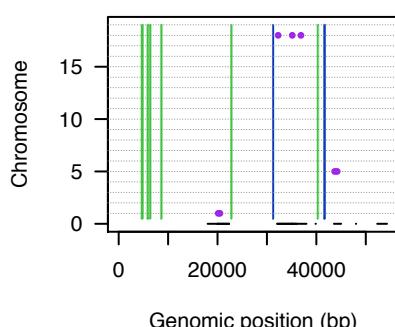


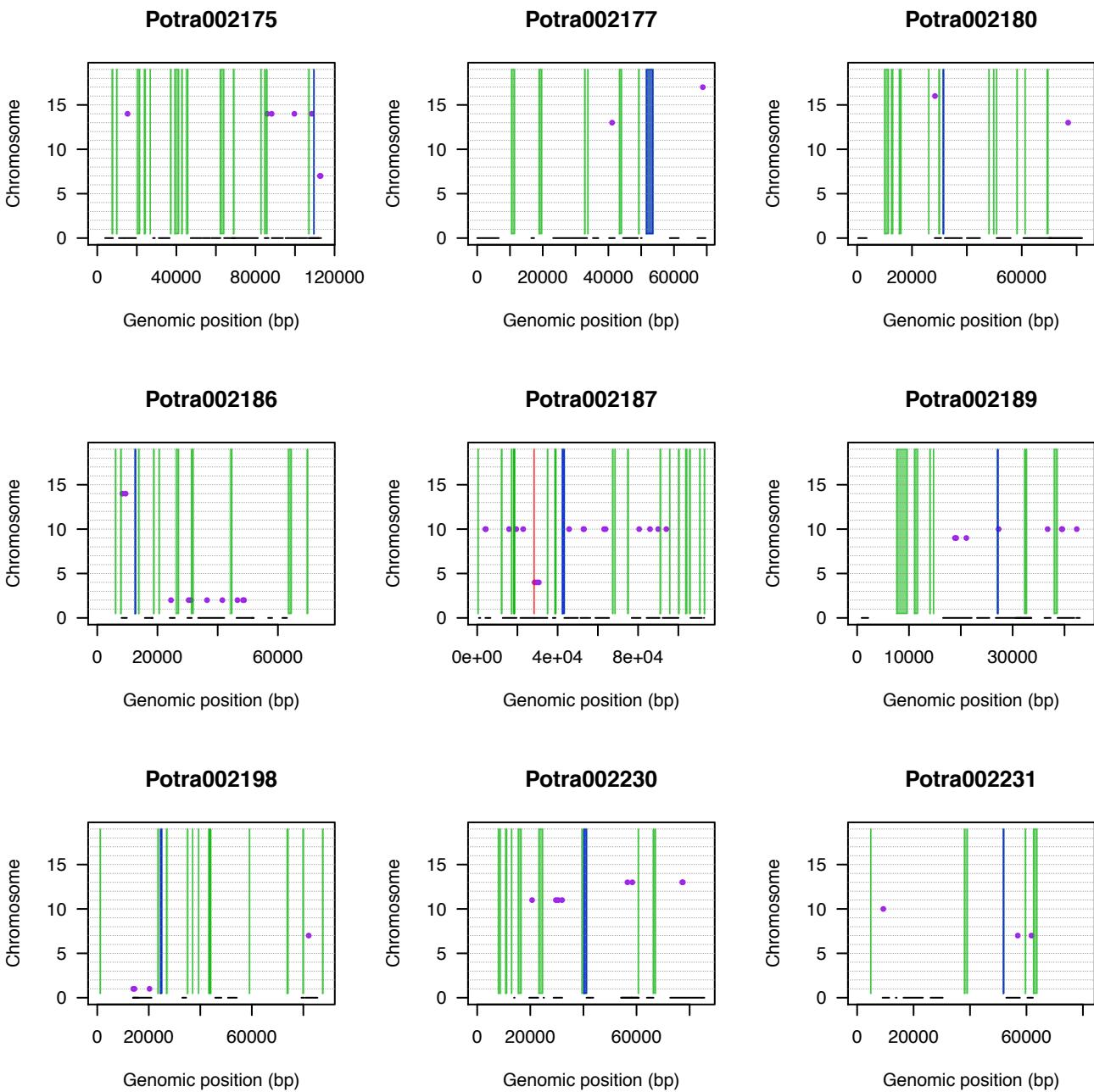
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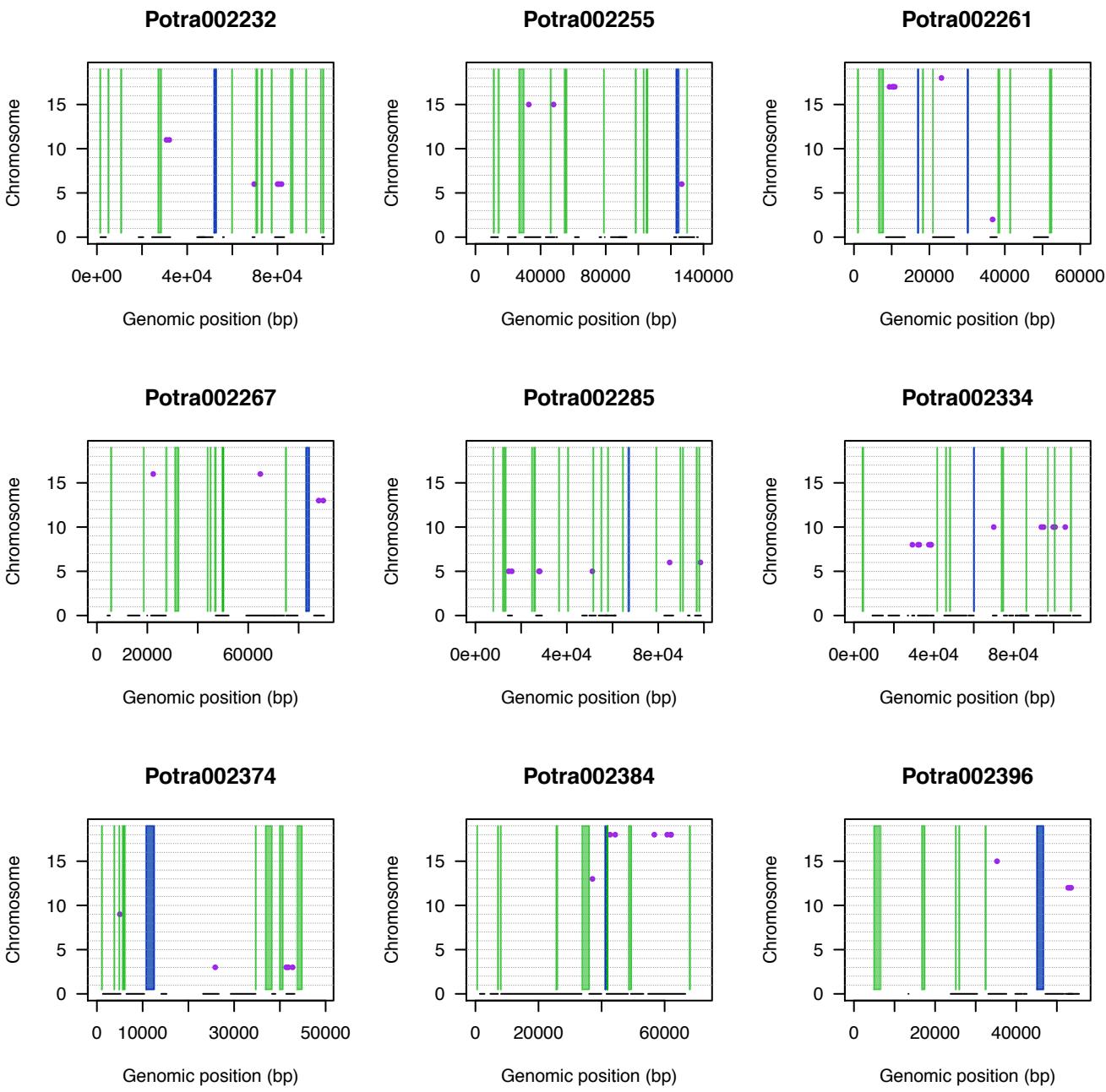


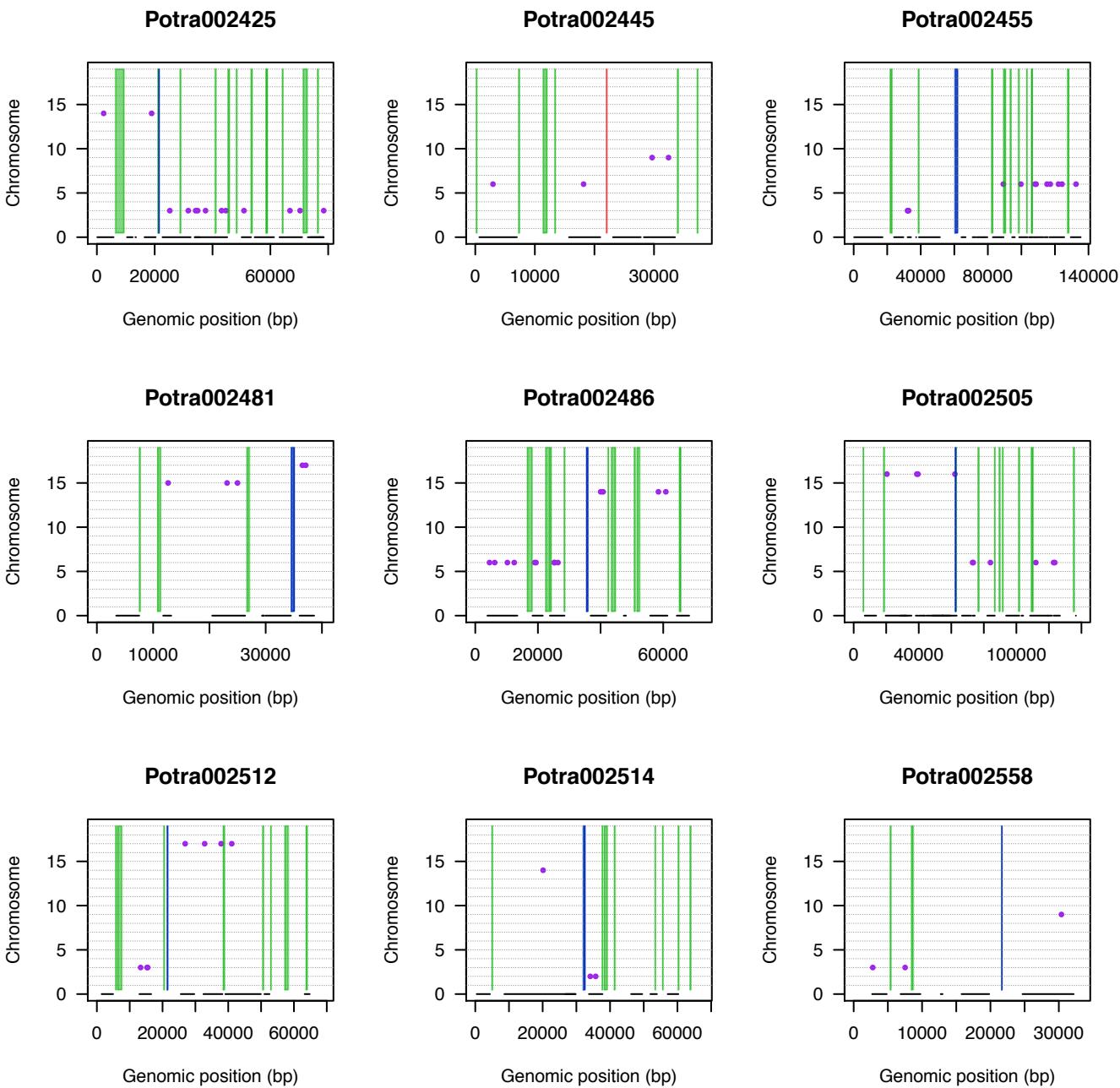
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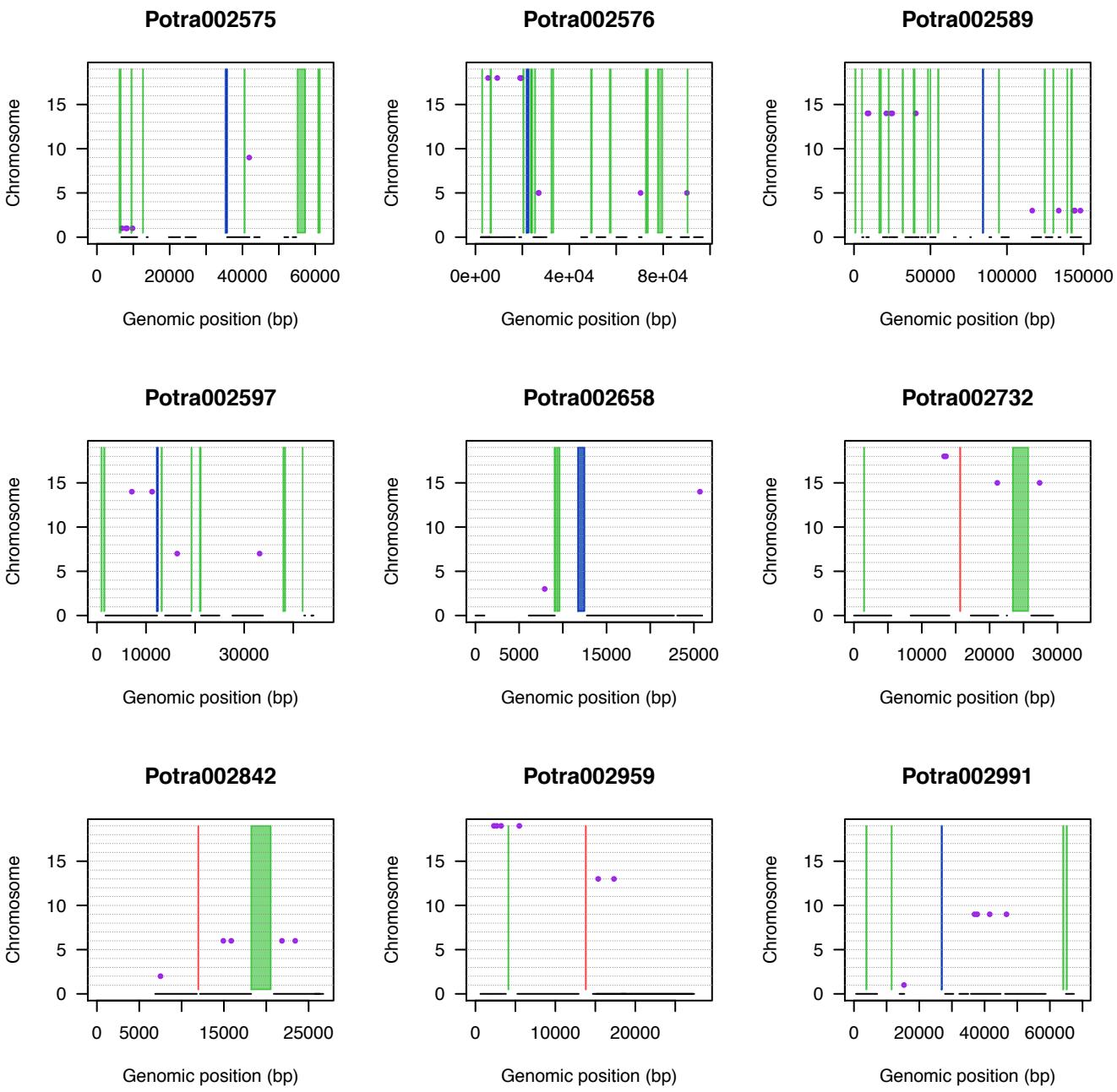


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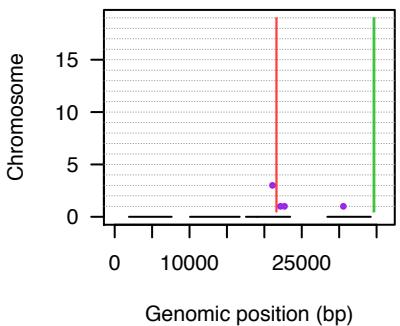




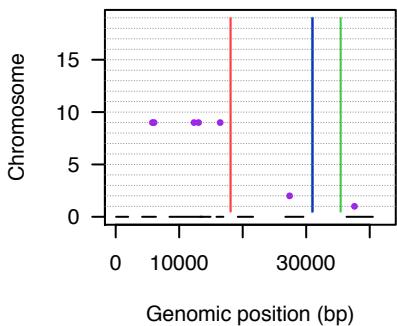




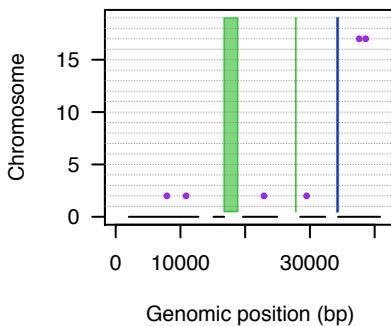
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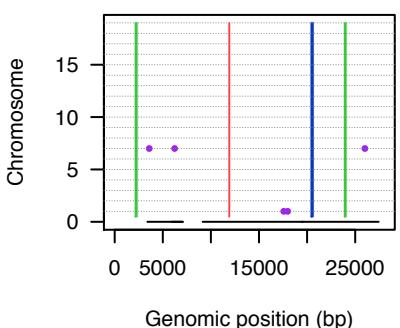
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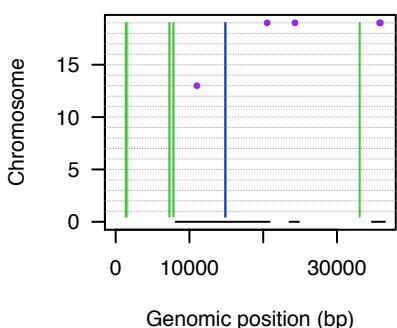
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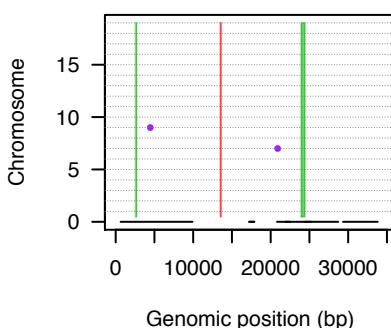
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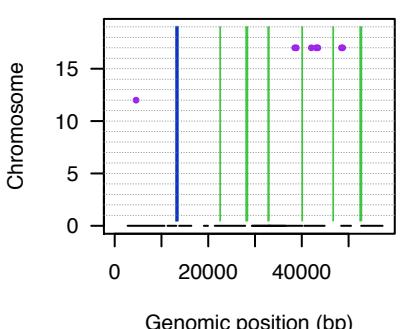
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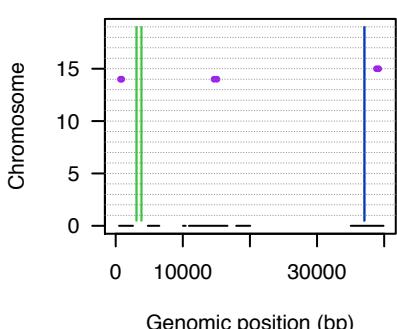
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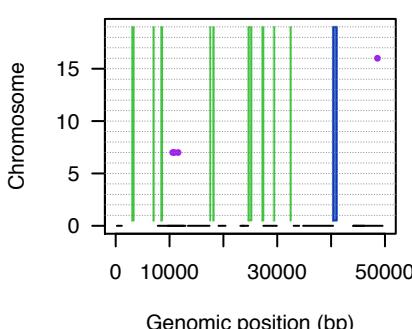
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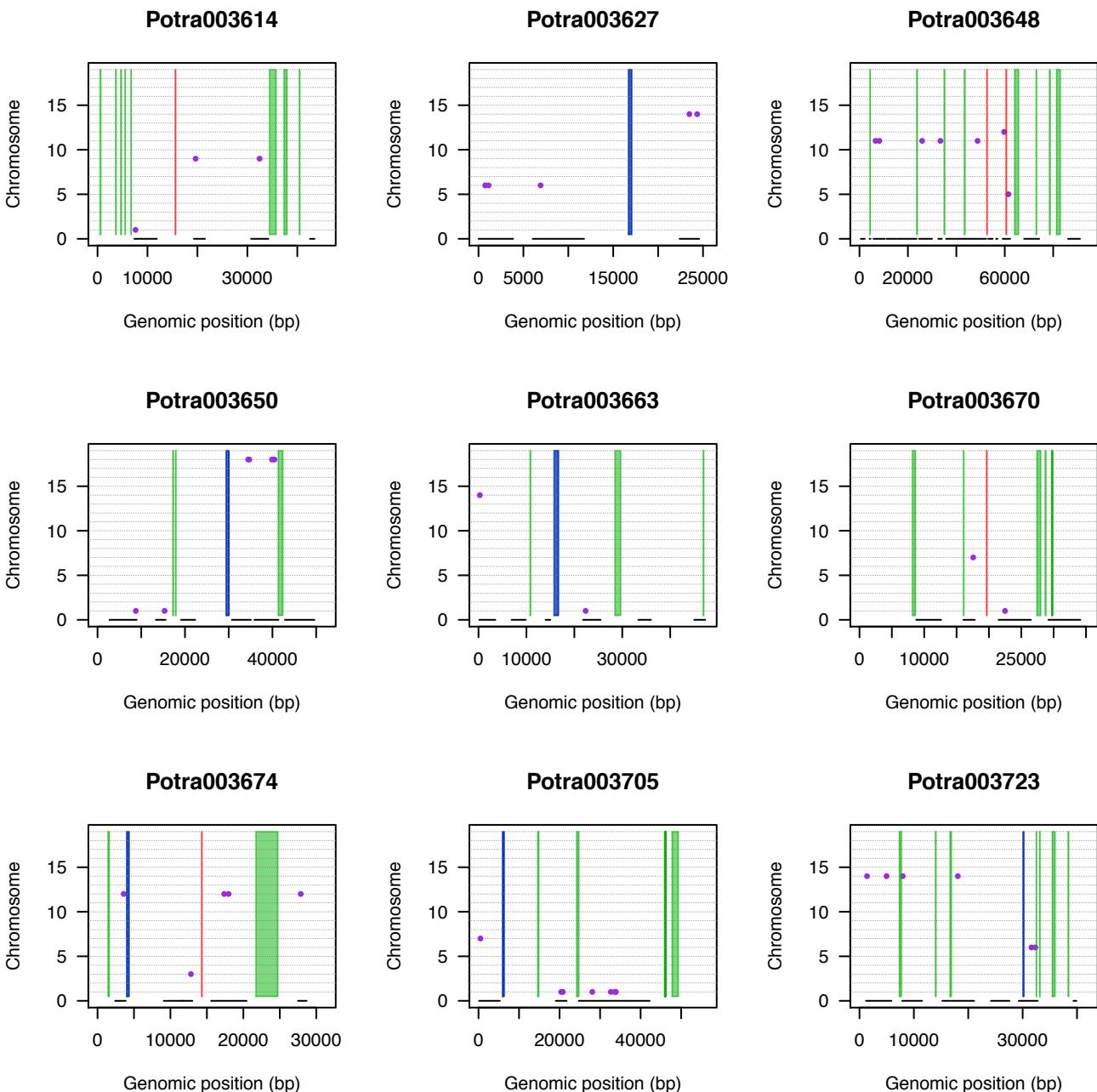


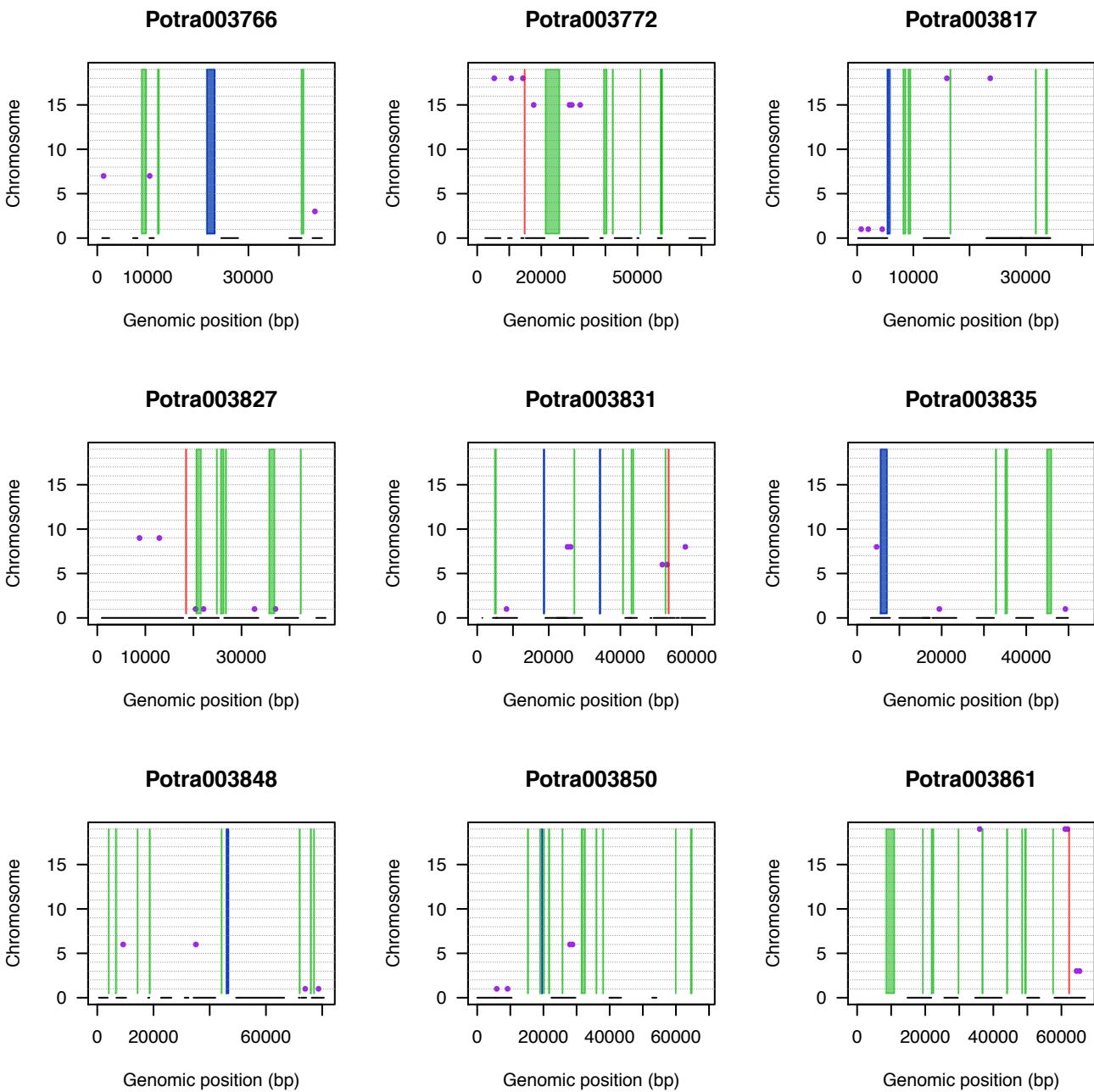
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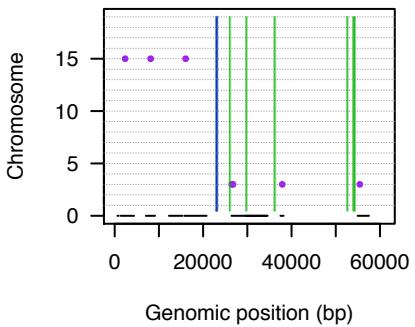
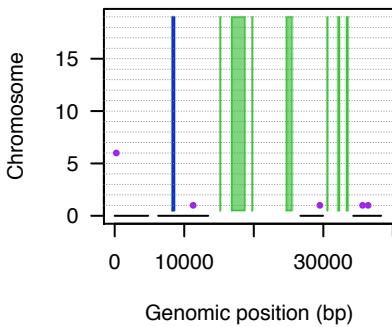
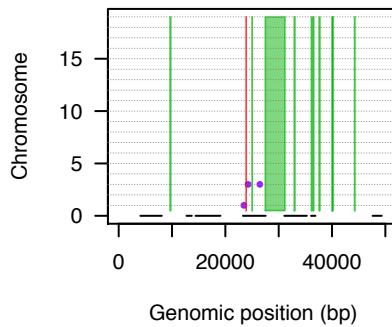
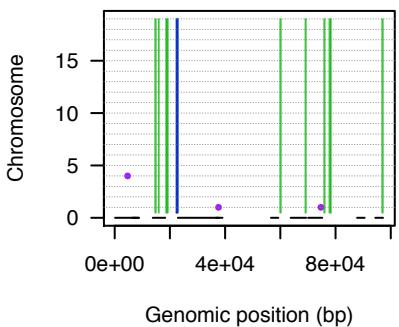
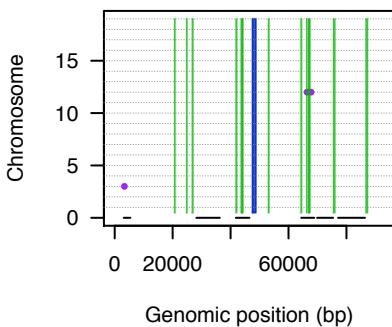
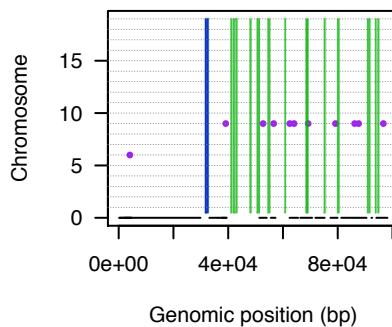
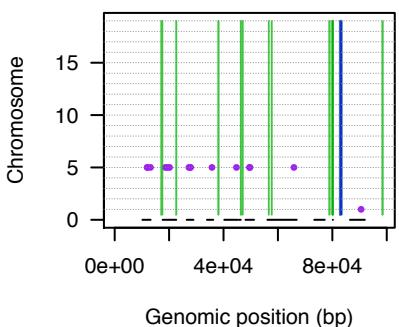
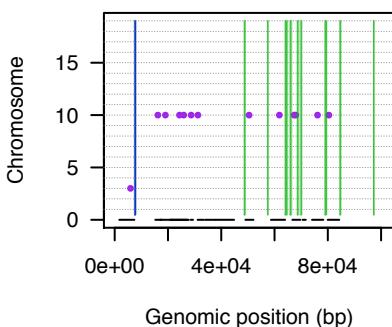
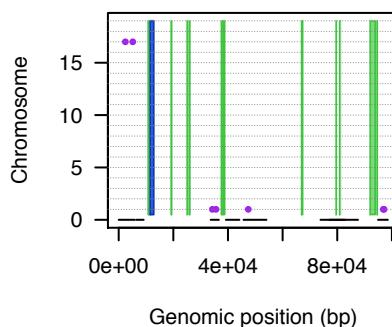


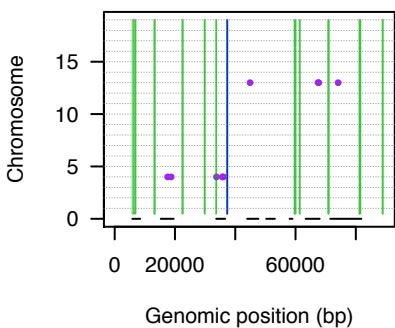
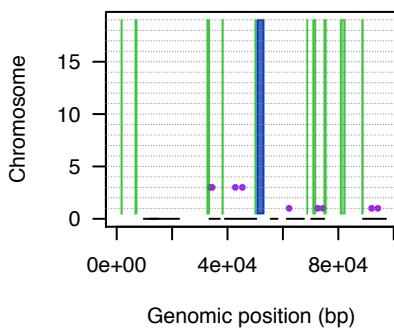
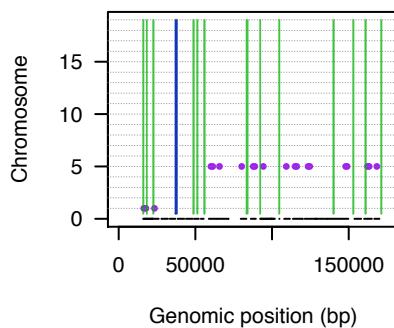
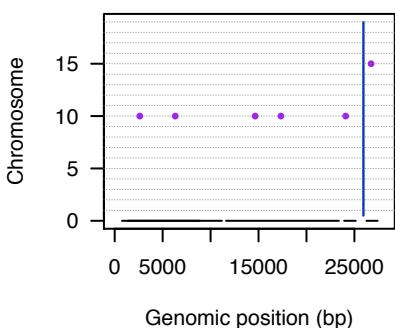
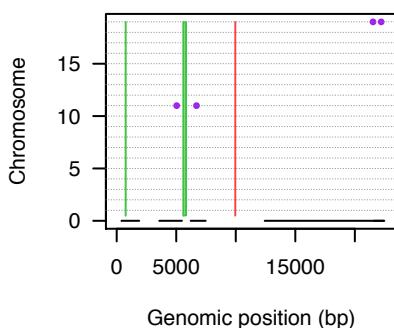
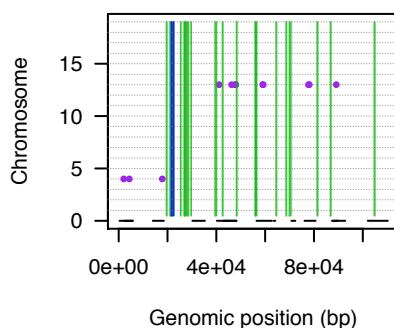
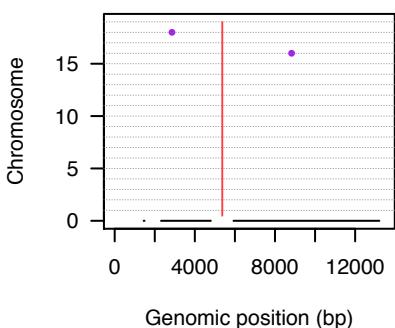
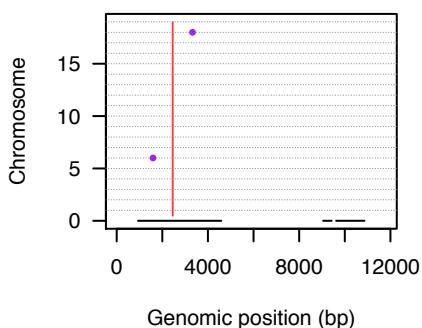
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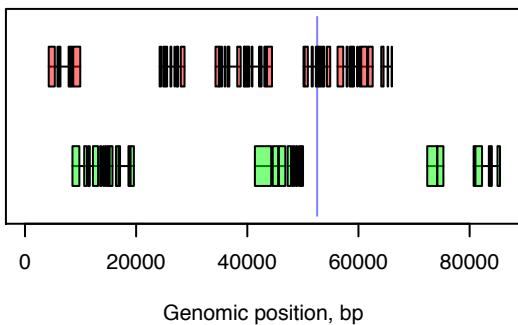


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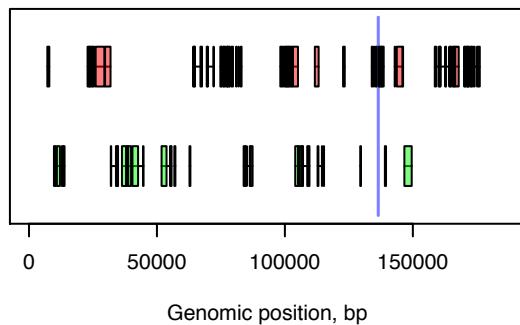
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Supplementary Figure 5

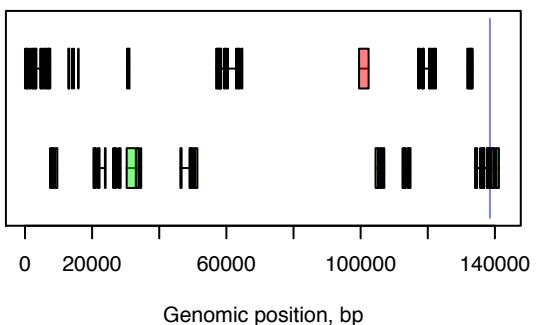
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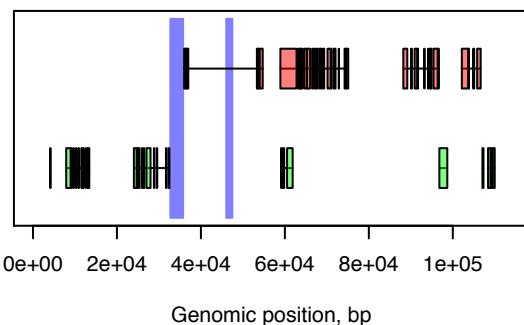
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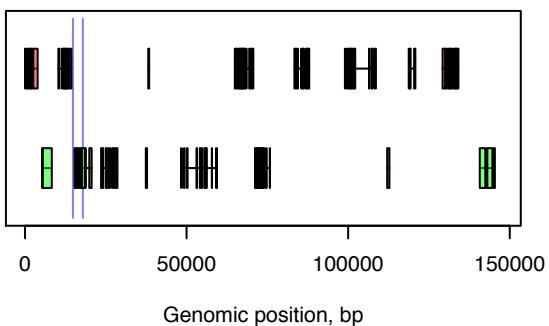
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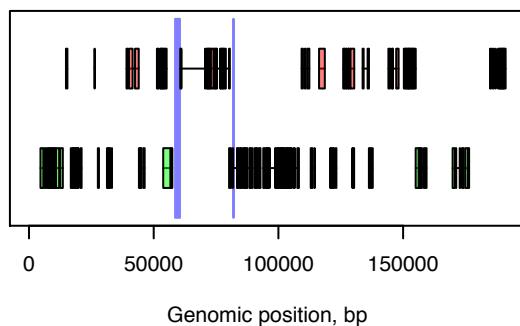
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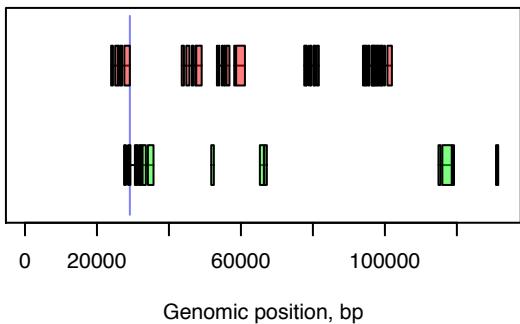
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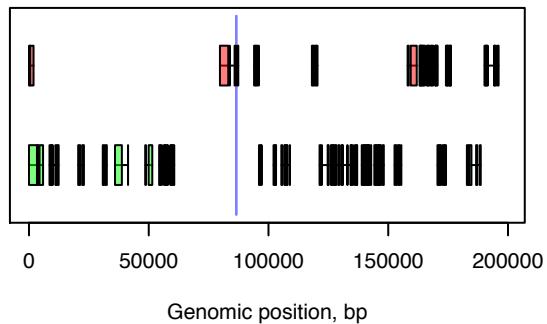
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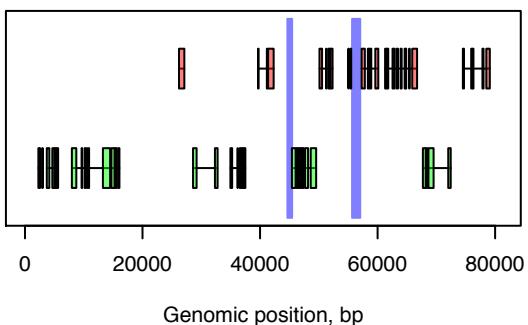
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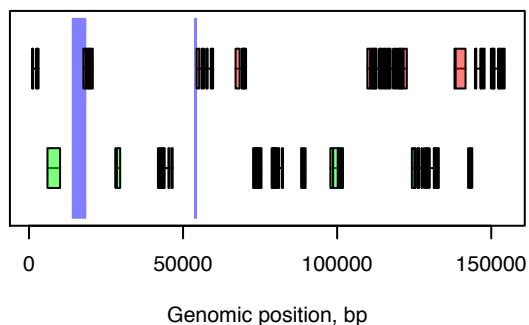
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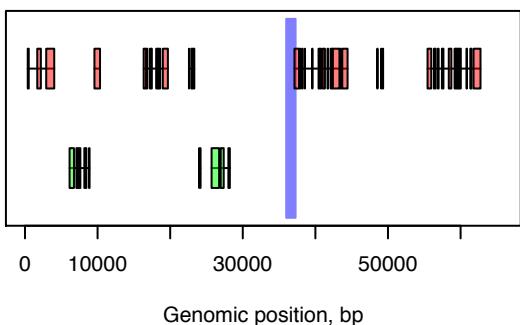
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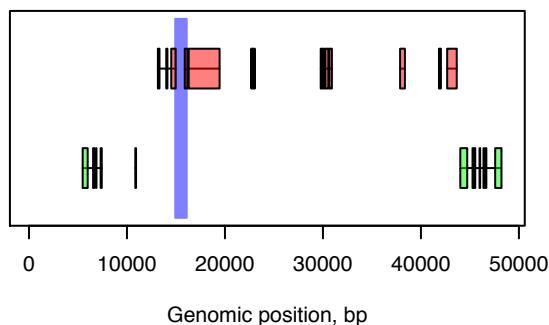
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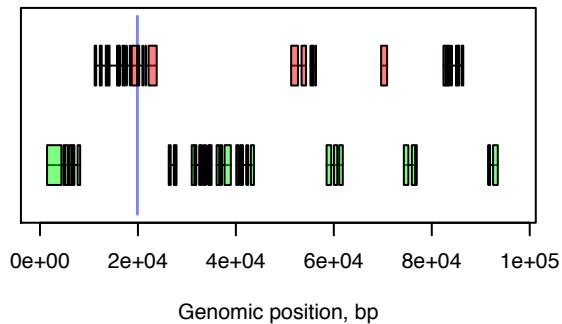
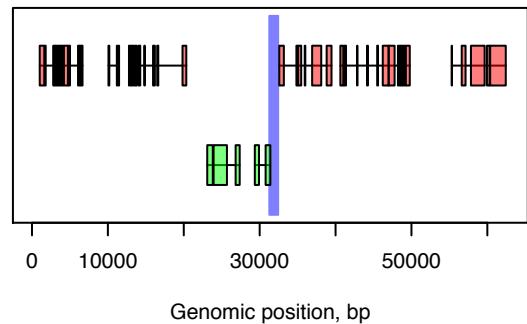
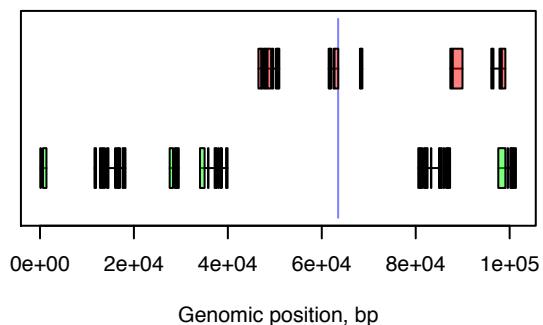
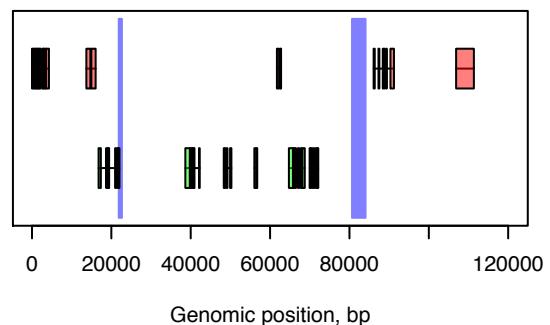
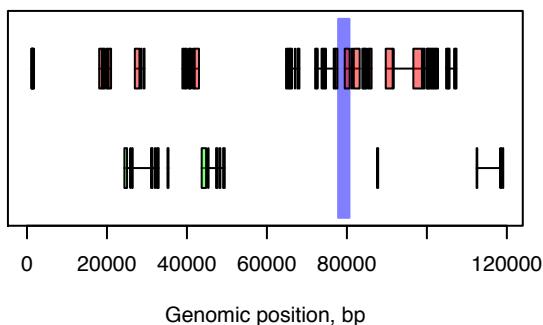
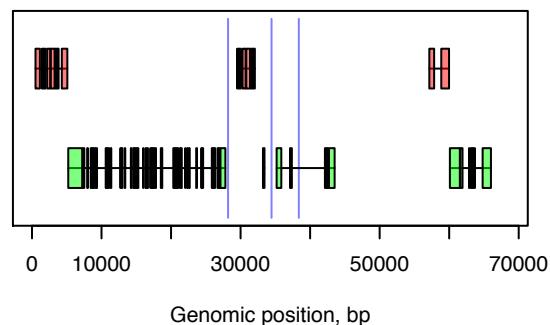


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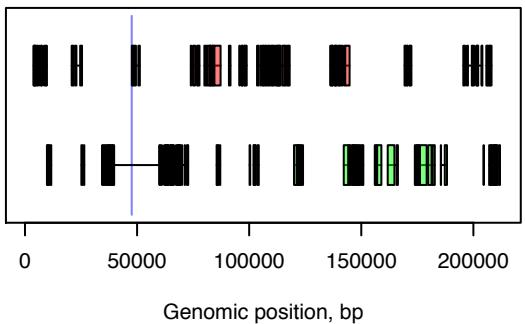


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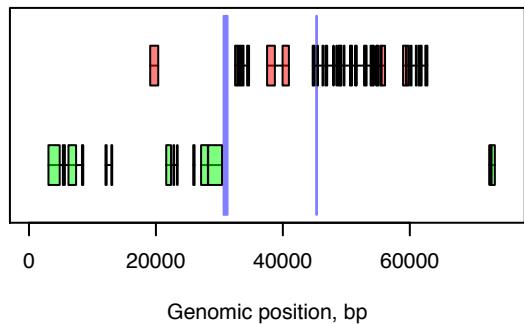


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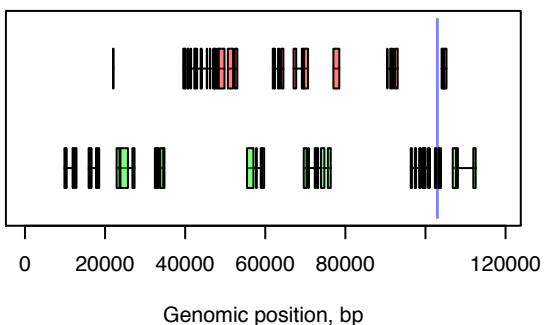
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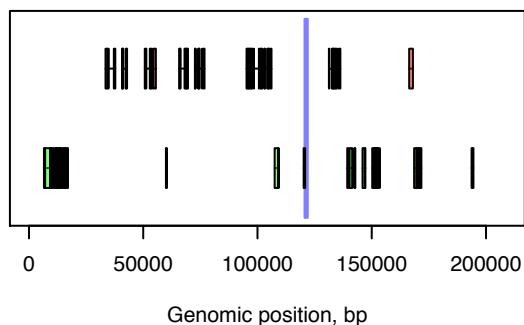
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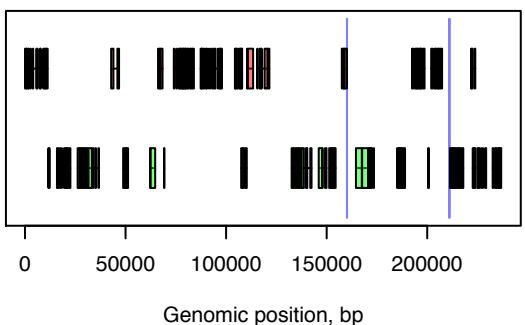
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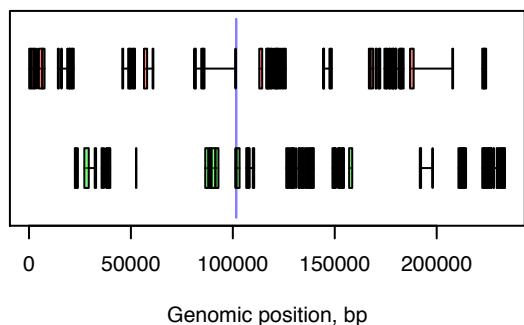
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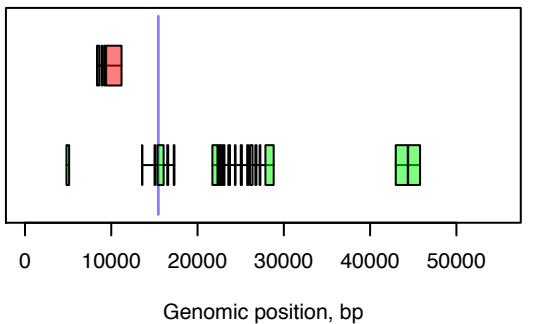
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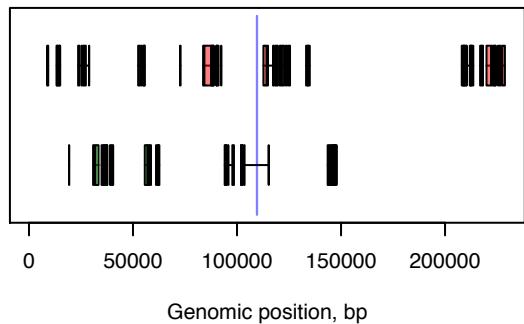
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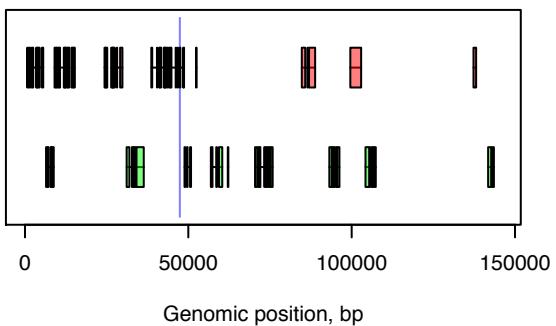
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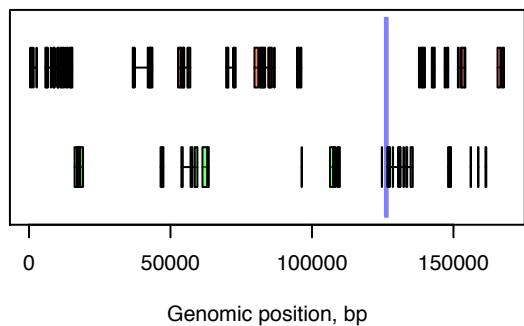
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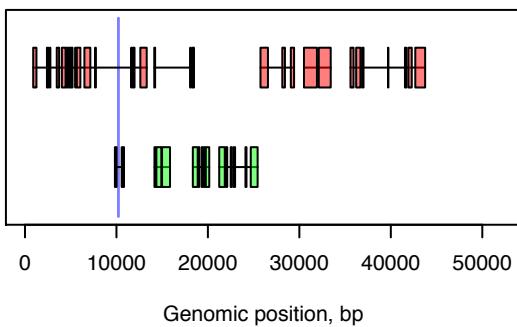
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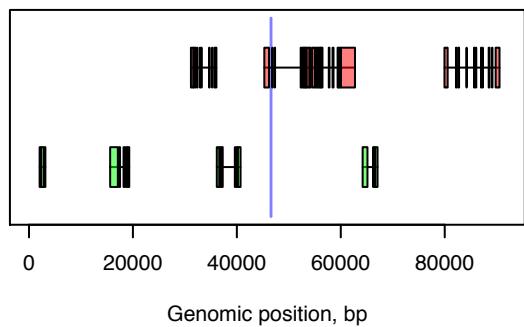
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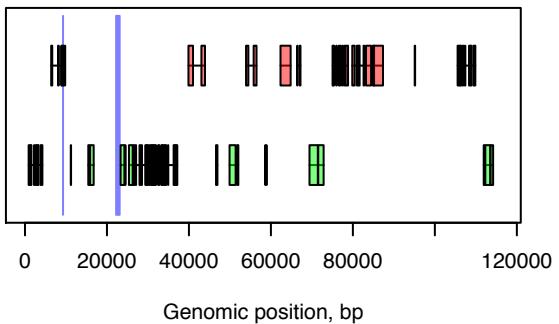
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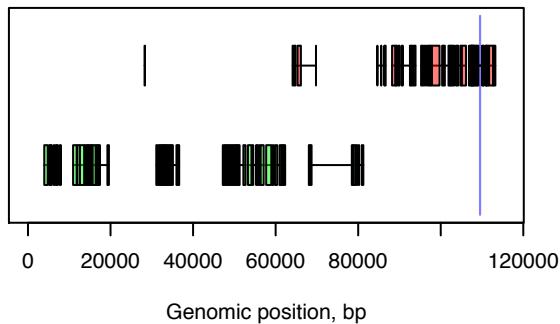
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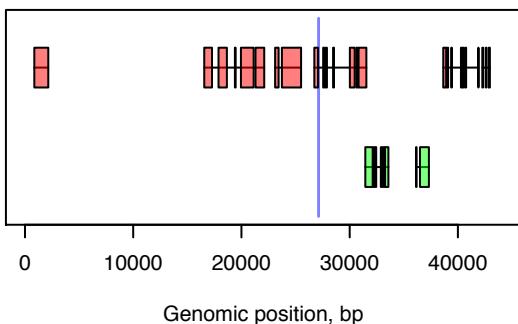
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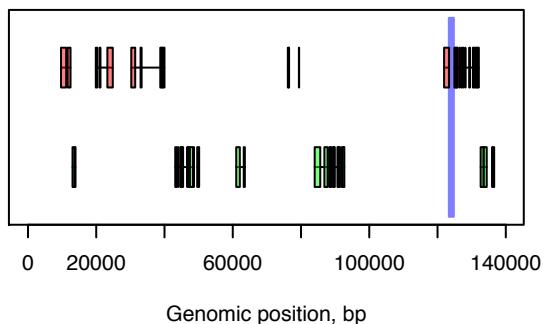
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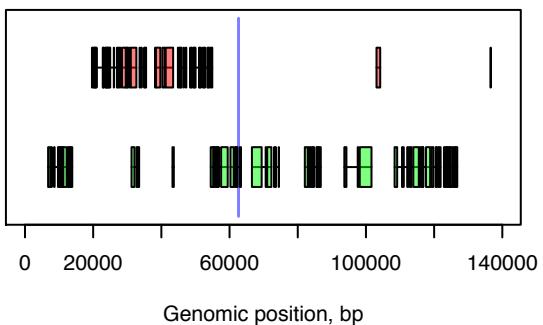
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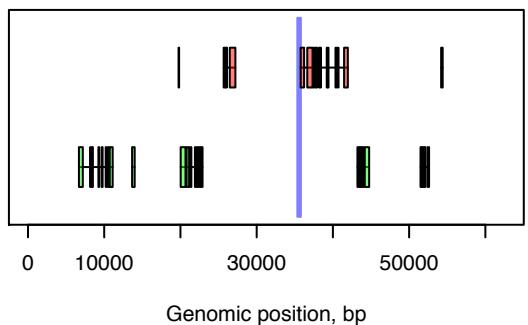
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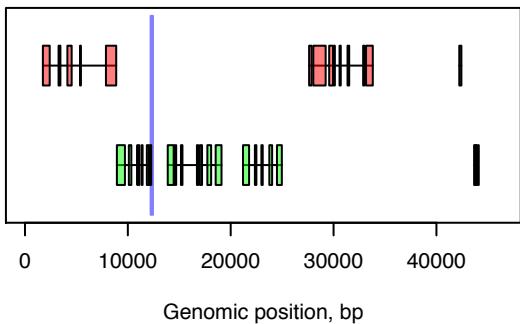
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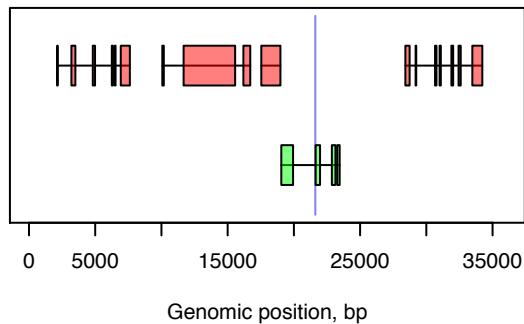
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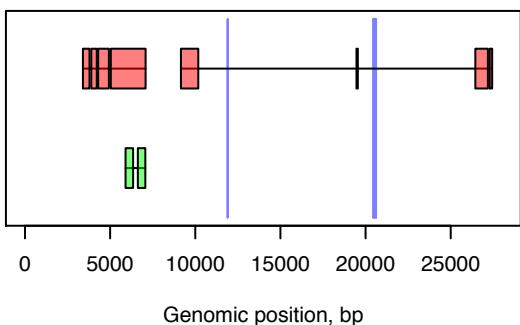
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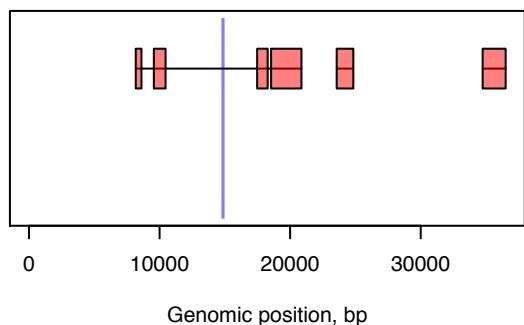
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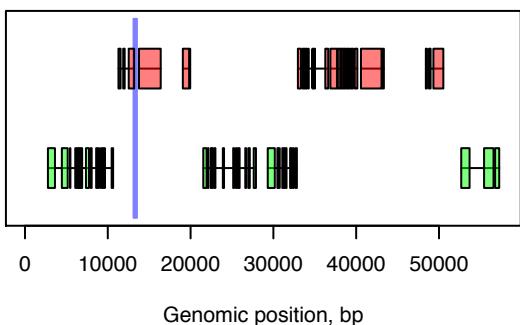
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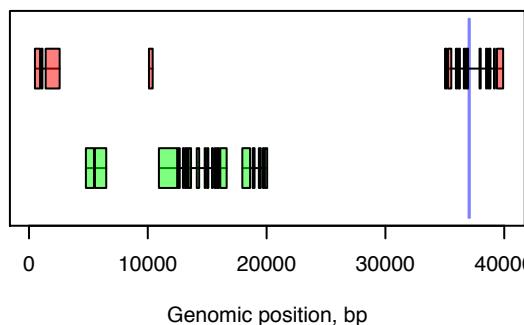
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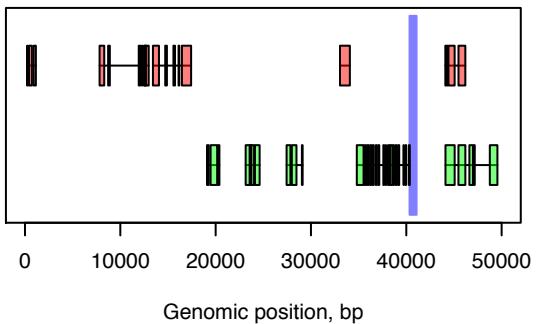
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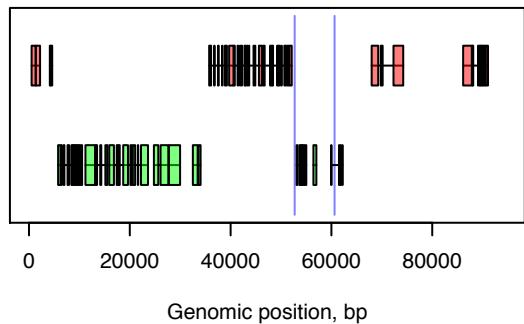
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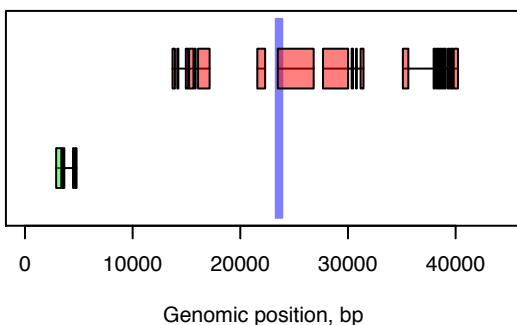
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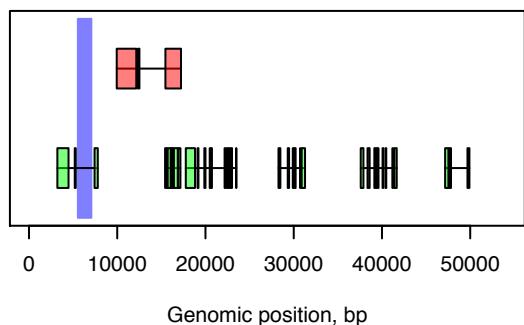
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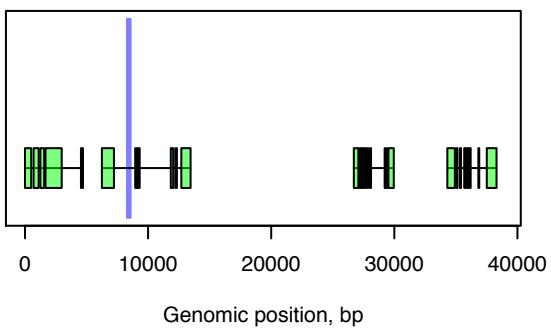
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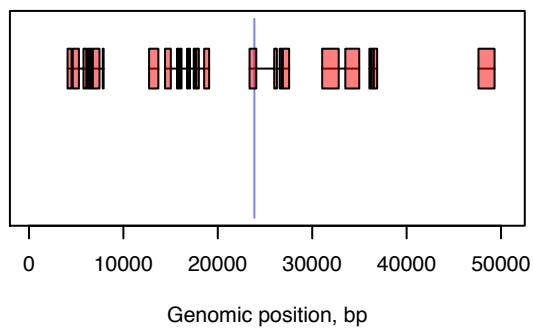
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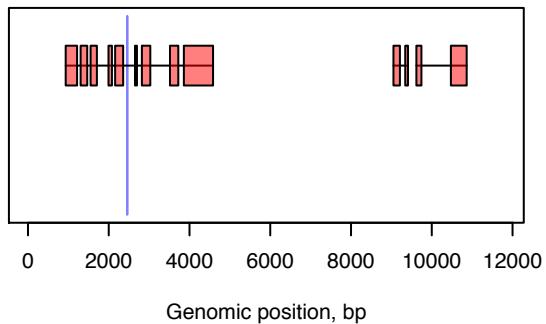
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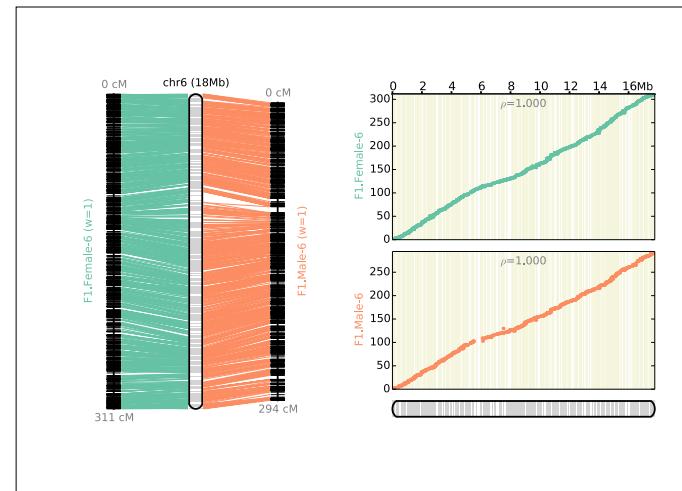
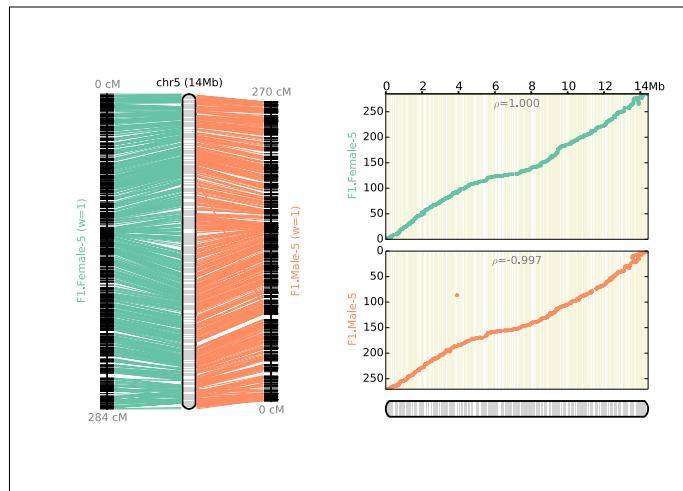
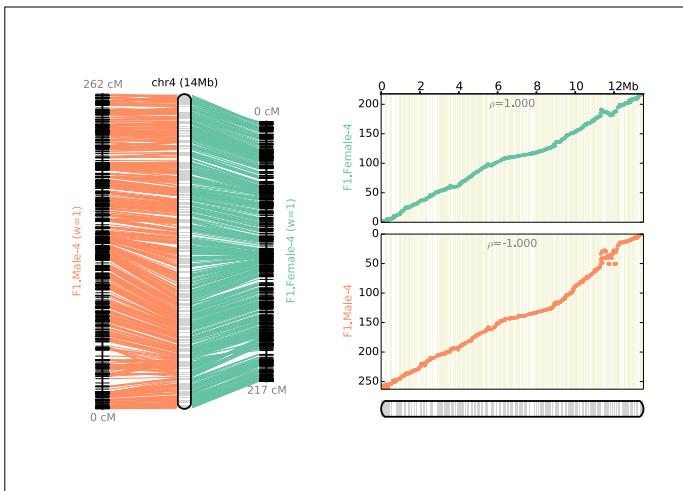
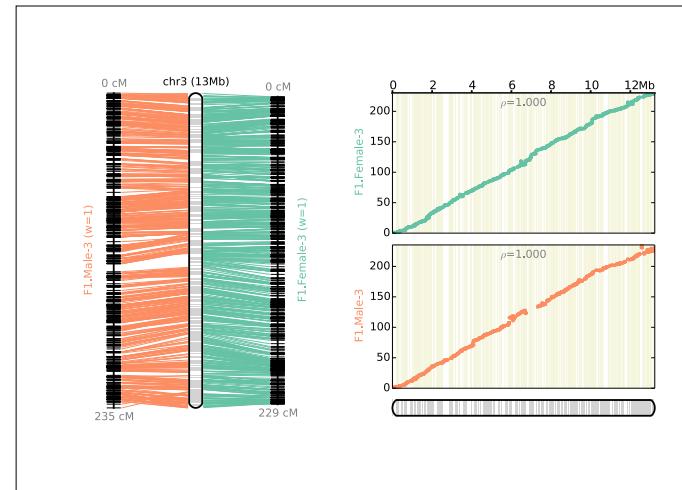
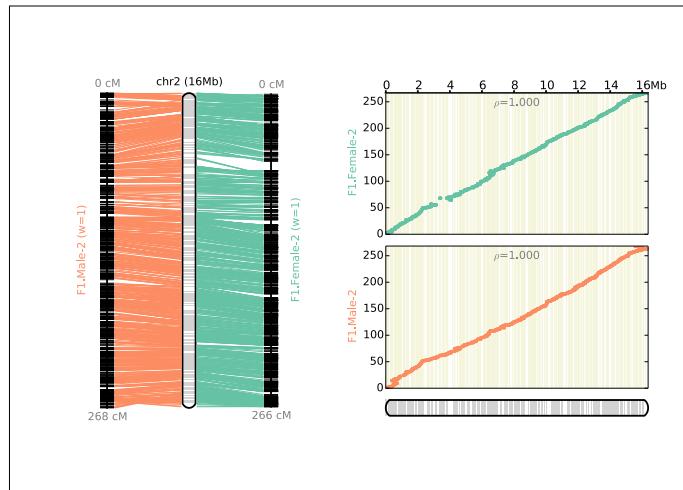
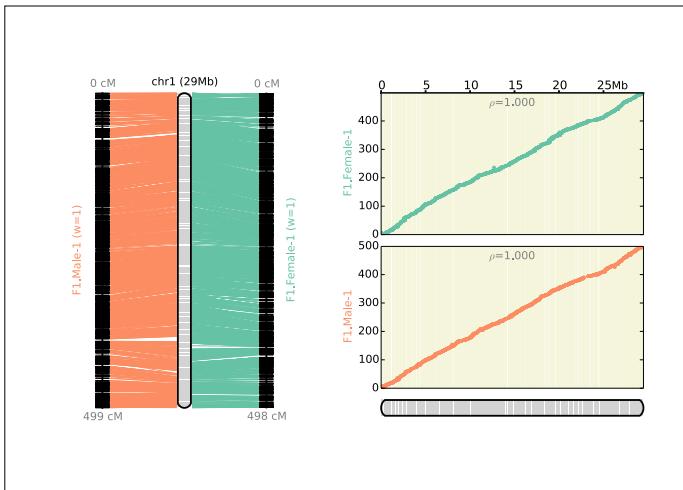
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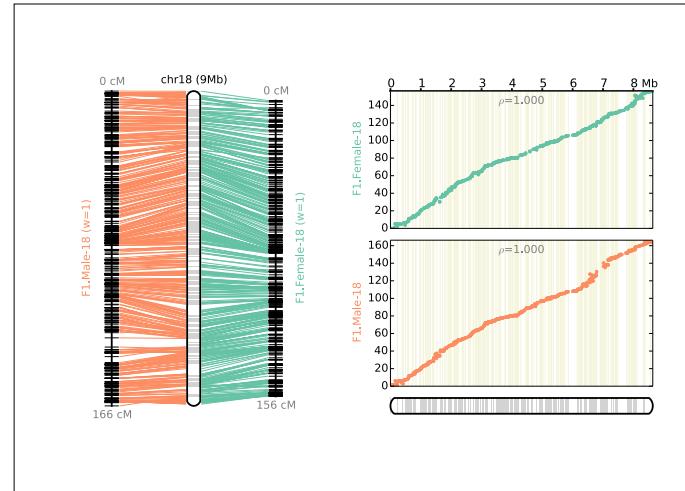
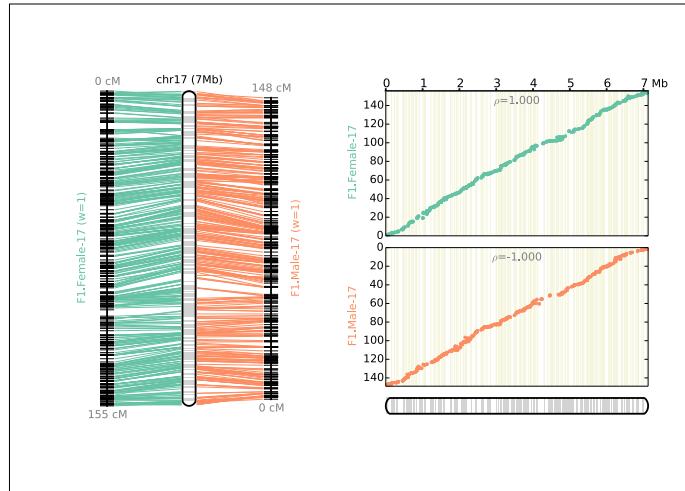
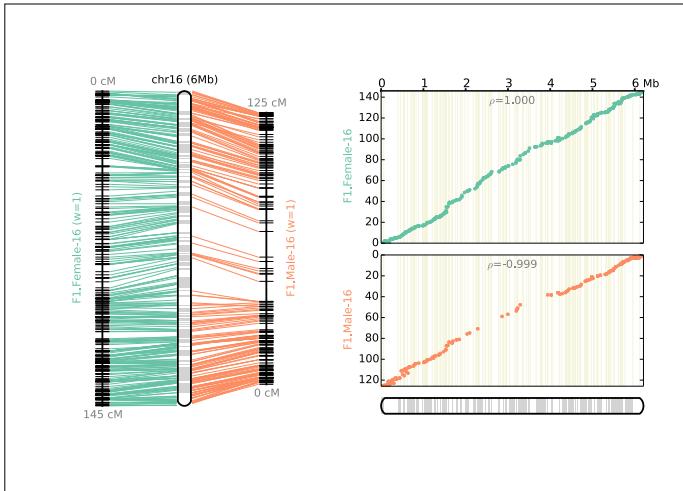
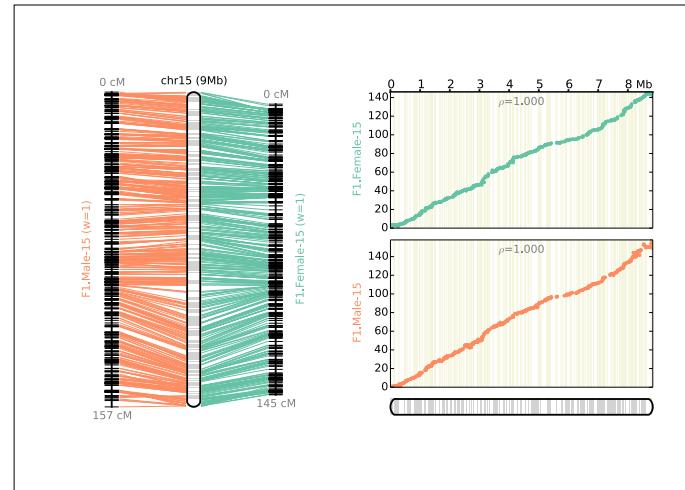
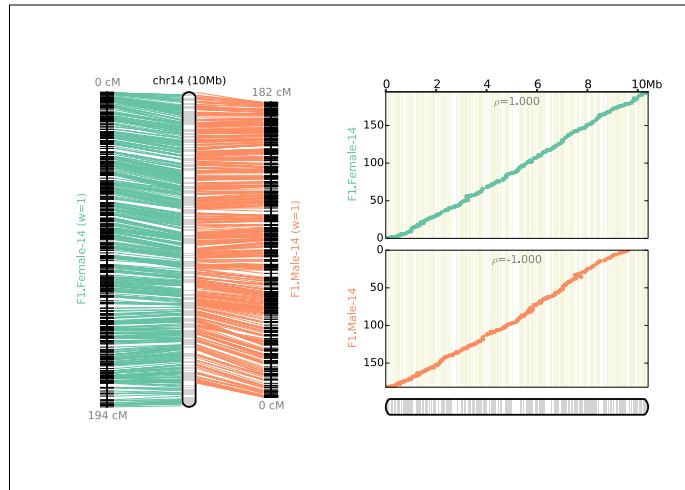
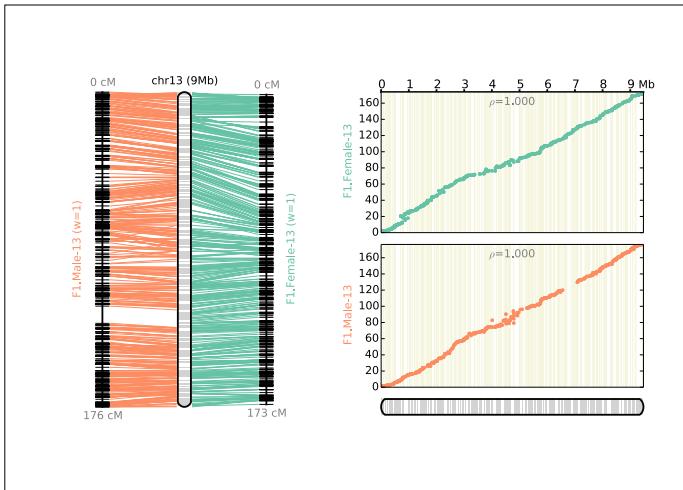
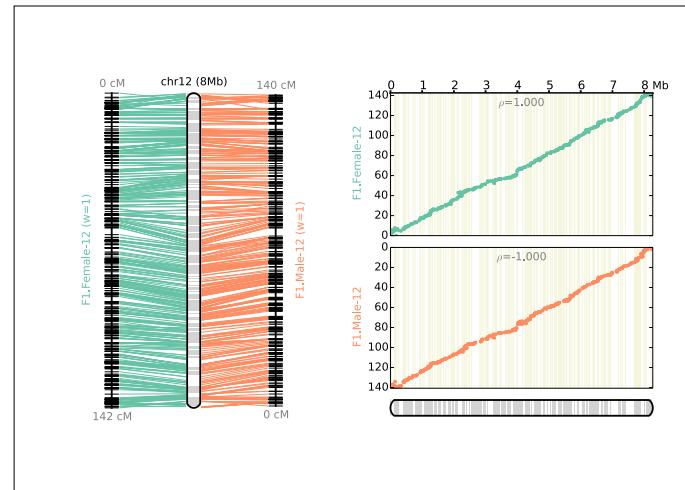
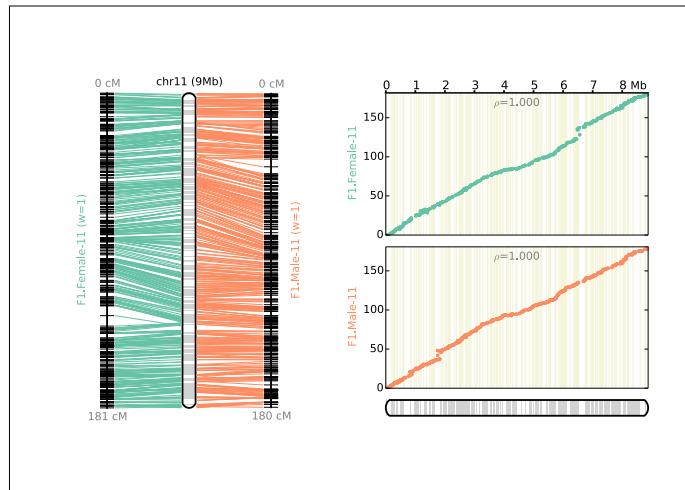
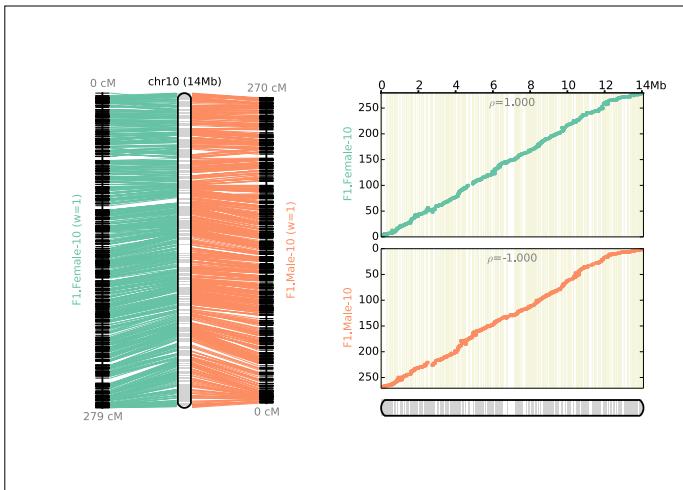


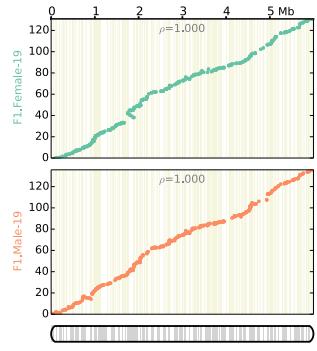
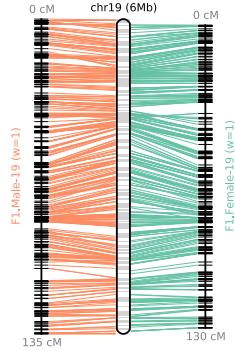
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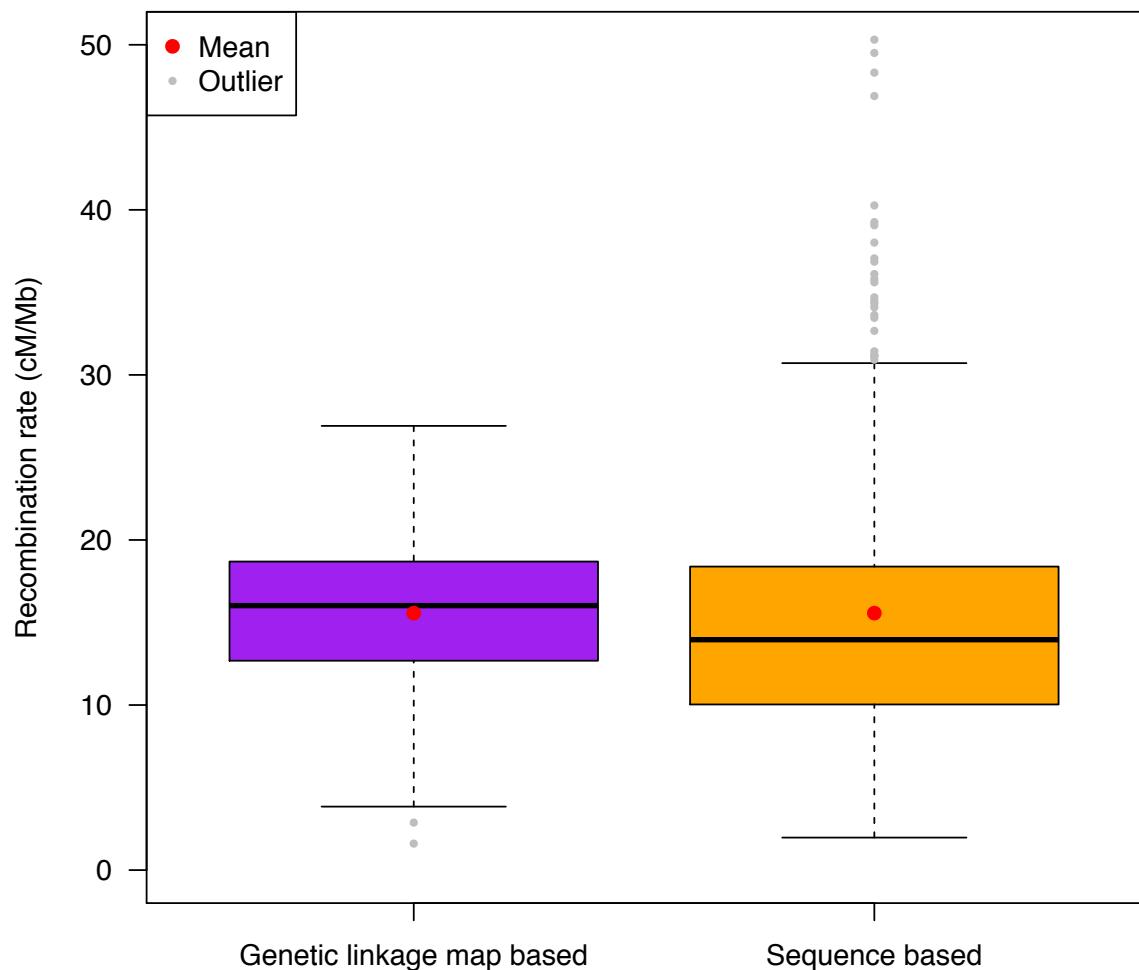
Supplementary Figure 6



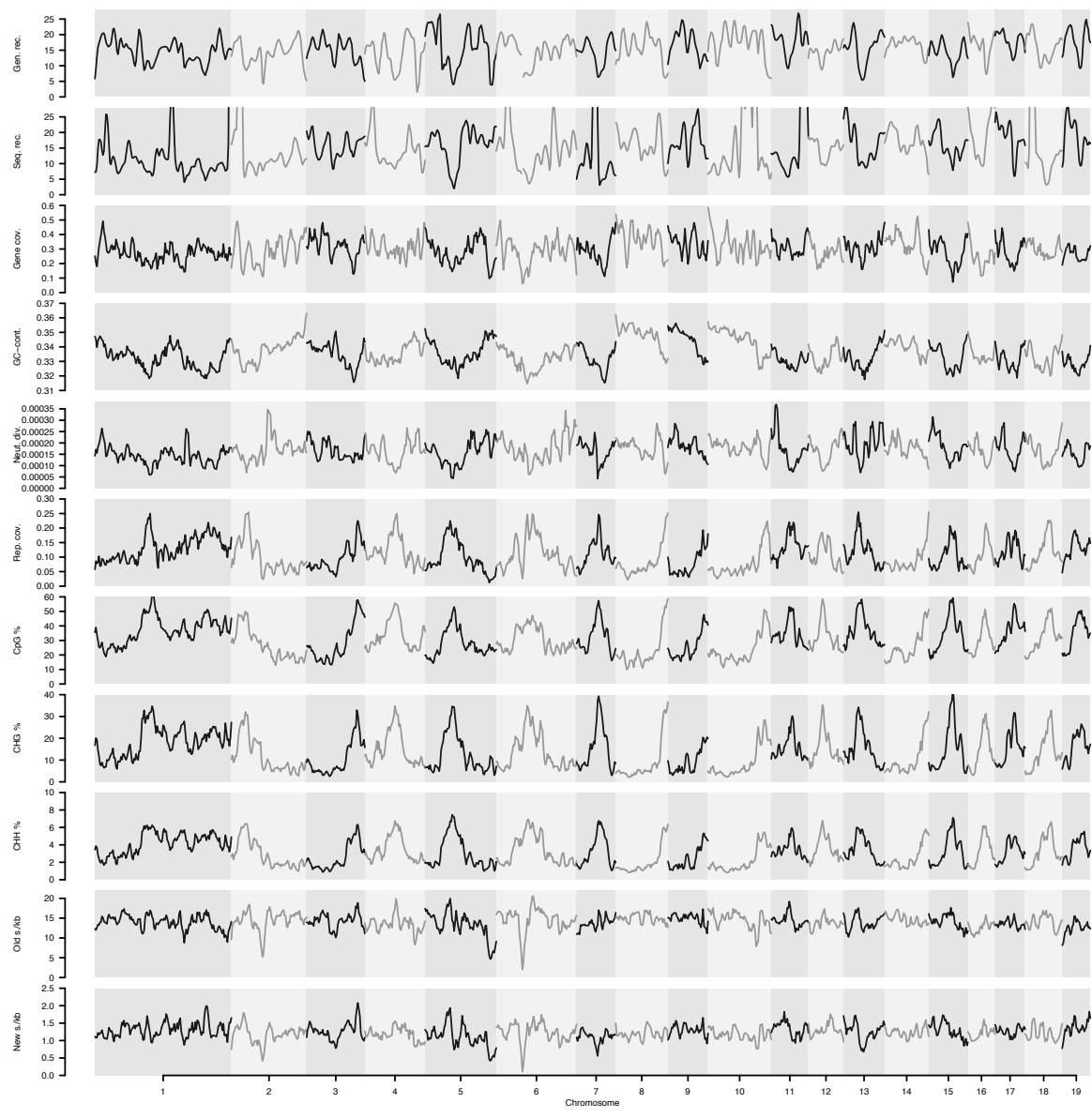




Supplementary Figure 7



Supplementary Figure 8



Supplementary Figure 9

