

Supporting information – SNP filtering and identification of family structure

Initial data filtering

The genotype VCF file for all 1997 samples was filtered with `vcftools` (Danecek et al. 2011), retaining only contain single nucleotide polymorphisms (SNPs) within the extended probe regions (120 ± 100 bp) that had a minor allele frequency (MAF) > 0.4 , < 20 % missing data and a quality score > 20 . Samples with $> 20\%$ heterozygous calls or a combined rate of heterozygous calls and missing data $> 40\%$ were filtered out due to likely contamination of diploid tissue from the DNA extraction or due to low quality sequencing. A final filtration step was set so that only SNPs heterozygous in the maternal genotype *Z4006* were kept for the PCA analysis. This resulted in a data set containing 1,559 samples and 14,794 SNPs that we used for analysis of family structure.

PCA and hierarchical clustering analysis

All 1,559 samples were used in a principal component analysis (PCA) to evaluate the relationship among samples. The reference allele was coded as “0” while the alternative allele was coded as “1”, and all missing data were re-coded to the average value for that marker (i.e. the allele frequency of the alternate allele). The first PCA two axes combined explained 17% of the variation among individuals (10% and 7 % for PC1 and PC2, respectively) while the remaining axes individually explained 0.6-1%. The samples grouped into a number of distinct clusters which all were oriented differently along the PC1-PC2 axes. The PCA analysis thus indicate that our data are more heterogeneous than what would be expected among offspring after meiosis from a single maternal tree. This therefore indicates that our samples are likely coming from more than one maternal tree (*i.e.*, ramets from different genotypes).

We ran a hierarchical clustering analysis with the R function `hclust` using the “ward.D2” clustering algorithm (R Core Team 2013), to evaluate the number of unique clusters in the data by cutting the tree at branch level three and four (Figure S1). Two of the clusters were identical for the different branch levels, whereas the last cluster we obtained when cutting at branch level three got subdivided into two separate clusters when cutting at branch level four (Figure S2A and B). To evaluate how the amount of missing data per sample affects the clustering, the fraction of missing data was used to colorize each sample in the PCA. Samples positioned close to the center have higher levels of missing data than samples further away from the center (Figure S2C).

Since high levels of missing data have impacts on the clustering of samples, we decided to utilize all available information for reconstructing a trustworthy family structure in the data that could be used in the creation of the genetic map. We therefore used strict cutoffs to divide our samples into clusters representing putatively different maternal families: Cluster 1 (321 samples) - $PC2 > 5$; Cluster 2 (279 samples) – $PC1 > 0$ and $PC2 < -5$; and Cluster 3 (858 samples) - $PC1 < -2$. Samples with high levels of missing data (in the center of the PCA) as well as all samples belonging to cluster 4 (too few individuals to create an independent genetic map) were removed from further analysis (Figure S2D). To confirm that these clusters represent single segregating families, PCAs were conducted on the individuals from the clusters separately. For all three clusters, all axes explained roughly the same

amount of variation and all the samples grouped into a single cloud without any detectable outliers (Figure S3).

Filtering the data for each family cluster separately

The unfiltered VCF file was divided into three separate VCF files, each containing samples with $< 10\%$ heterozygous calls and which belong to a specific cluster identified through the PCA and hierarchical clustering approach. The VCF files were then filtered with `vcftools` (Danecek et al. 2011) and `R` (R Core Team 2013) to only contain biallelic SNPs within the extended probe regions (120 ± 100 bp) and that have $< 20\%$ missing data (all heterozygous calls treated as missing) and a $MAF > 0.4$ (see informative markers at <https://doi.org/10.5281/zenodo.1209841>).

For each unique probe in the three data sets, only the most balanced marker (highest MAF and lowest amount of missing data) was kept for map creation and named with an ID based on scaffold and probe position (hereafter called probe-marker). This resulted in 9,073 probe-markers from 7,101 scaffolds for Cluster 1 (314 samples), 11,648 probe-markers from 8,738 scaffolds for Cluster 2 (270 samples), and 19,006 probe-markers from 13,301 scaffolds for Cluster 3 (842 samples). The three datasets combined covers a total of 21,056 unique probe-markers from 14,336 scaffolds that can be anchored to the genetic maps.

Figure S1. Cluster dendrogram based on genetic distances between samples. Horizontal lines indicate cluster memberships when cutting the tree at three or four branches.

Figure S2. Sample distribution along PC1 and PC2 from the principle component analysis (PCA). A) Samples are colored according to cluster membership when the corresponding dendrogram (Figure 1) is cut at the three-branch level. B) Samples are colored according to cluster membership when the corresponding dendrogram (Figure S1) is cut at the four-branch level. C) Samples colored according the per-sample fraction of missing data. Darker color indicate higher fractions of called markers. D) Sample memberships in clusters used for map creation.

Figure S3: PCA analysis of the three clusters separately. The first two axes (PC1 and PC2) explain 3.3-3.9% of the variations in each of the clusters and all samples group into a single cloud without any outliers.

Figure S4: Test of segregation distortion for probe-markers in the three clusters. Markers are ordered according to p-value and plotted against their corresponding $-\log_{10}$ p-value. Orange horizontal line indicates the Bonferroni threshold with an alpha of 0.05. Black markers show no segregation distortion while red markers show signs of segregation distortion. A) Probe-markers in cluster 1. B) Probe-markers in cluster 2. C) Probe-markers in cluster 3. ~2 % of the cluster 3 probe-markers show signs of segregation distortion.

Figure S5: Heatmap showing the number of shared scaffolds between the three components map LGs. Number of shared scaffolds (> 0) is stated in each pairwise comparison.

Figure S6: Heatmaps of LOD scores (upper triangular) and recombination fraction (lower triangular) for each LG in the three component maps. The maps are ordered according to consensus LG belonging (A-L for LGI-LGXII, respectively) and original LG name is stated for each of the three component LGs (LG1-12 for cluster 1, cluster 2 and cluster 3, respectively).

Figure S7: Comparison of the three component maps (grey) and the consensus map (black) for each LG (A-L for LGI-XII, respectively). Left side of each figure shows how the position of each probe-marker in the component maps (blue – cluster 1, red – cluster 2 and green – cluster 3) correlates to the position in the consensus map. The total size of each map is labeled on top of each map. Right side shows the order correlation between the three component maps and the consensus map with Kendall's τ labeled for each map comparison.

Figure S8: Order correlation (calculated with Kendall's τ) between all three components maps as well as against the consensus map (A-L for LGI-XII, respectively). Lower triangular shows the marker orders while upper triangular shows the correlation coefficient. Probe-markers showing segregation distortion in cluster 3 are colorized in turquoise while all other probe-markers are colorized in black

Figure S9: Physical position (in bp) versus genetic position (in cM) for all probe-markers in component maps as well as the consensus maps that are located on

scaffolds showing signs of splits within LGs. All gene-models positioned on the scaffold are visualized as horizontal bars in the bottom on the figure (with thick bars representing exons and thin bars representing introns). Grey vertical bars indicate gap positions in the assembly (N:s). Scaffold names and the maximum distance (cM) between probe-markers are represented in the title of each figure

Figure S10: Physical position (in bp) versus LG (1-12) for all probe-markers in the consensus maps that are located on scaffolds showing signs of splits between LGs. All gene-models positioned on the scaffold are visualized as horizontal bars in the bottom on the figure (with thick bars representing exons and thin bars representing introns). Grey vertical bars indicate gap positions in the assembly (N:s). Scaffold names are represented in the title of each figure.

Figure S1

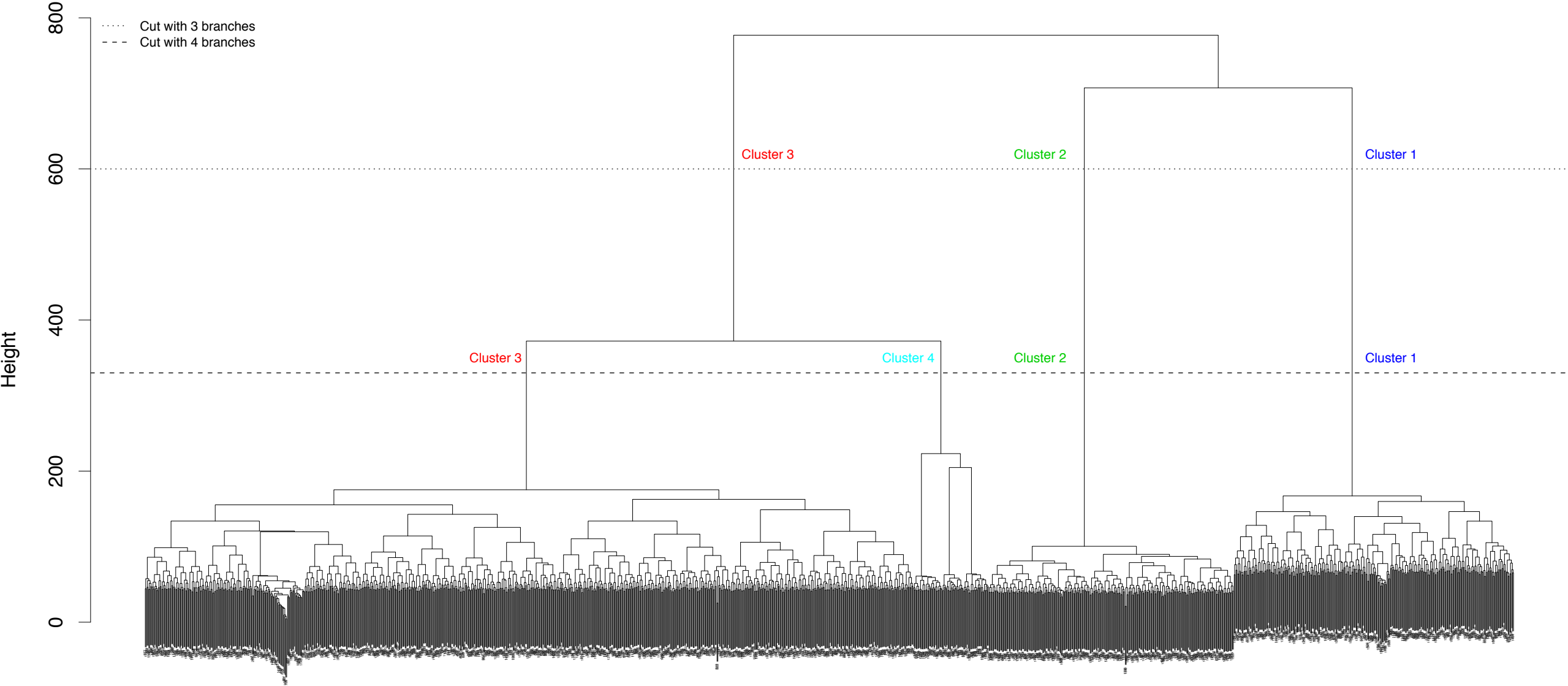
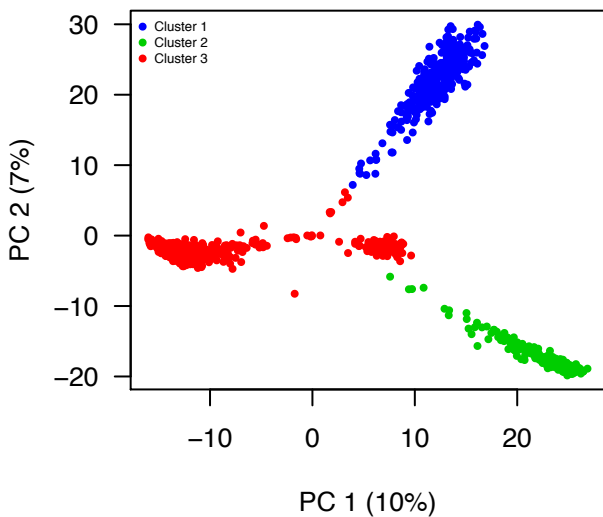
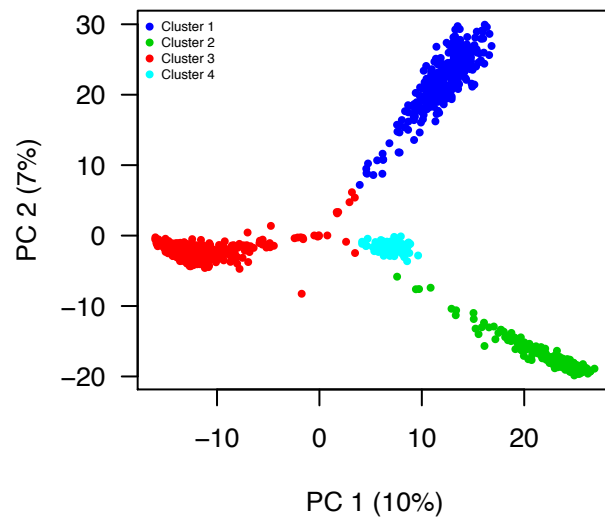


Figure S2

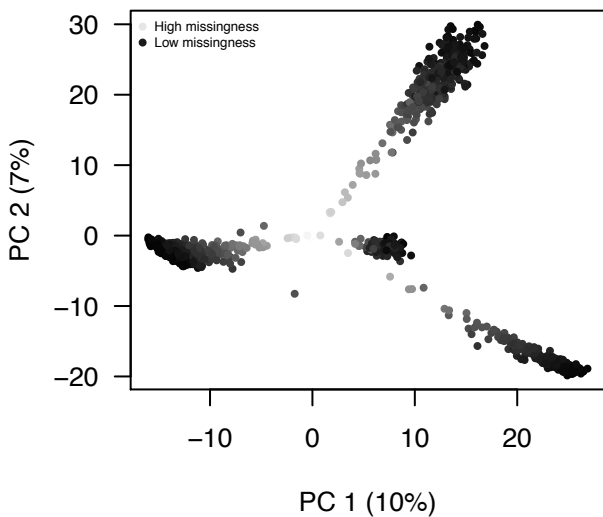
A



B



C



D

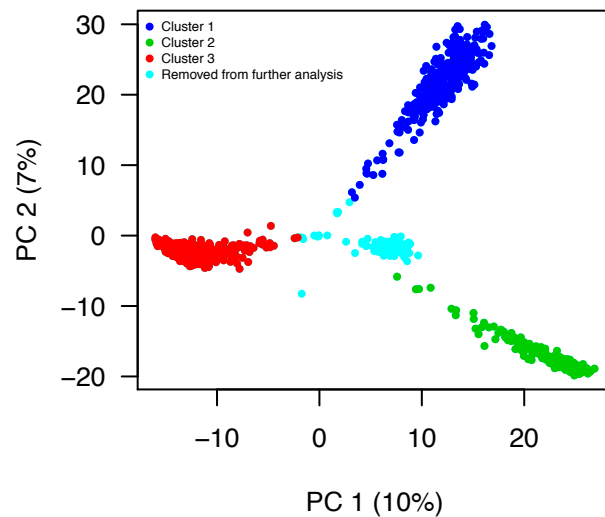


Figure S3

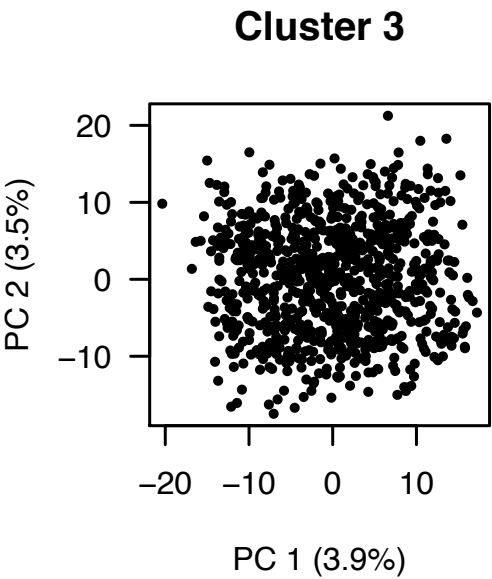
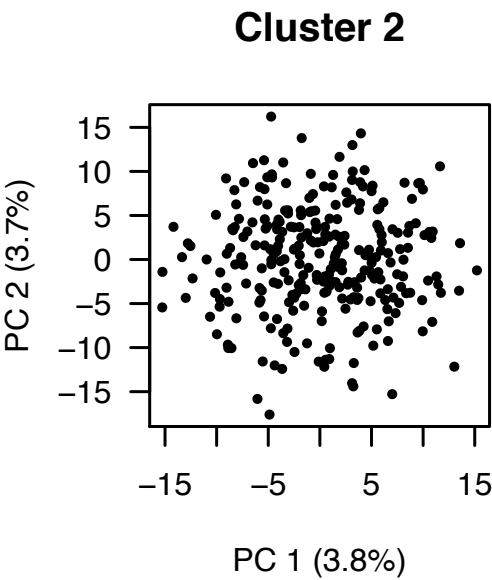
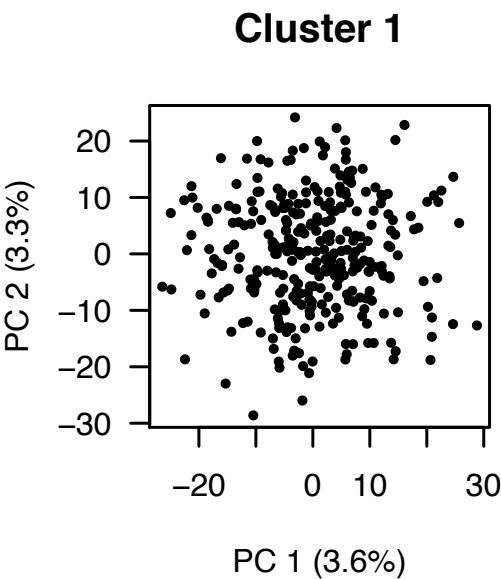
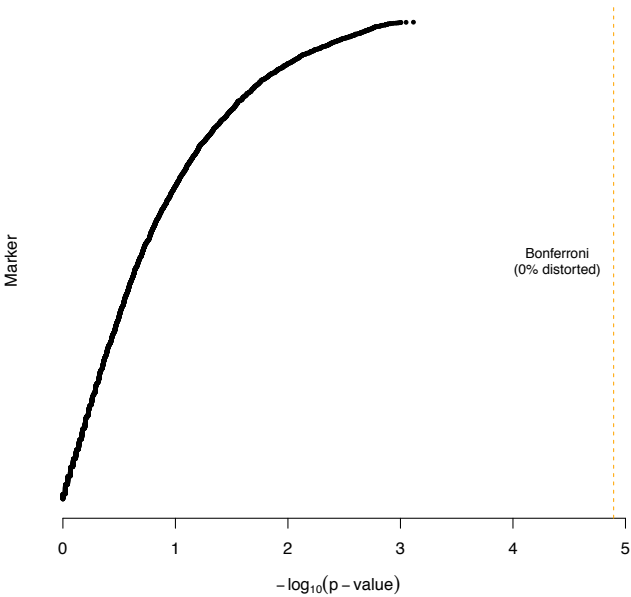
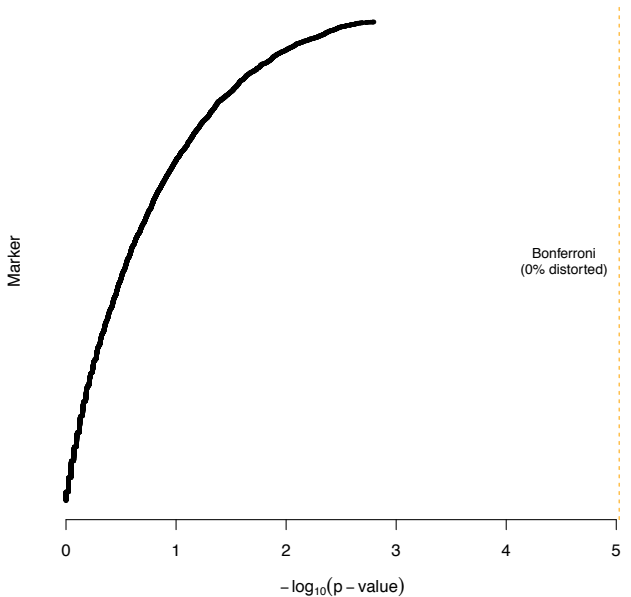


Figure S4

A) Cluster 1



B) Cluster 2



C) Cluster 3

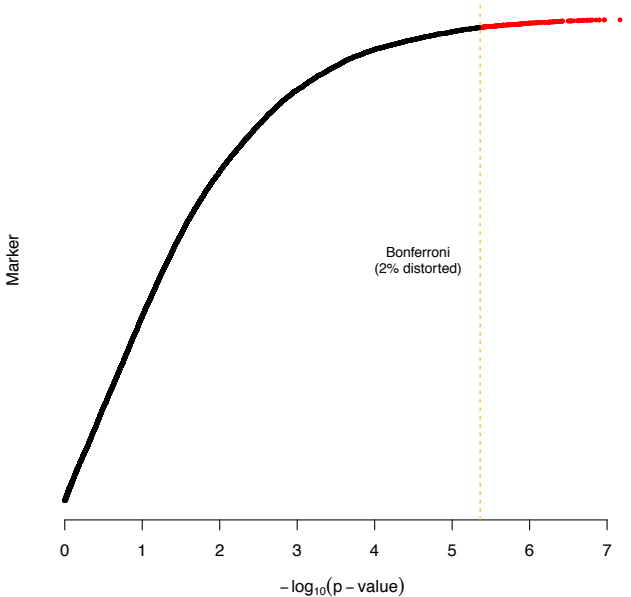


Figure S5

Shared scaffolds between Cluster LGs

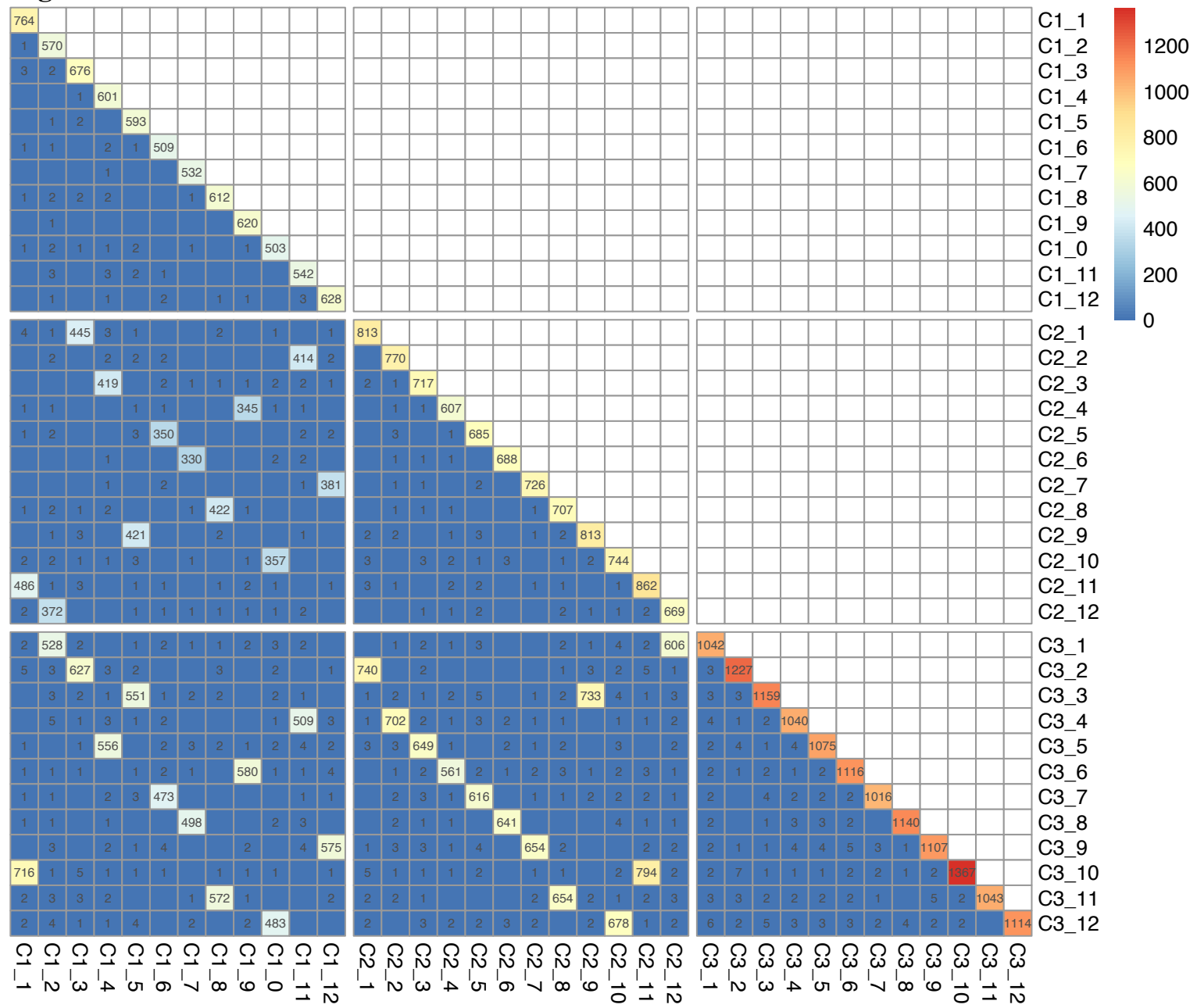
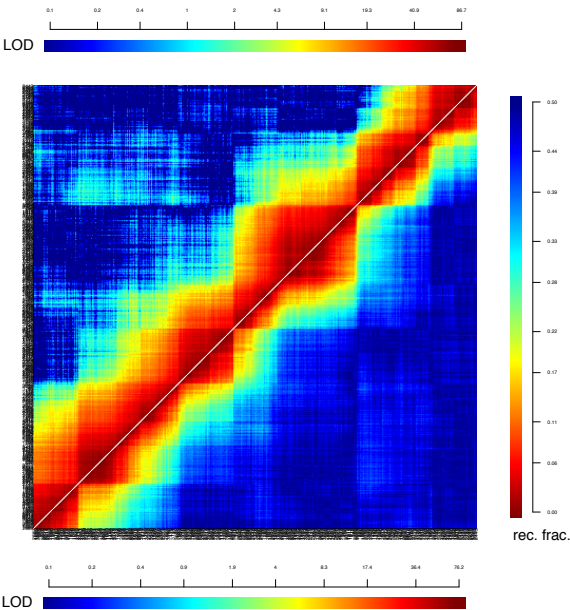


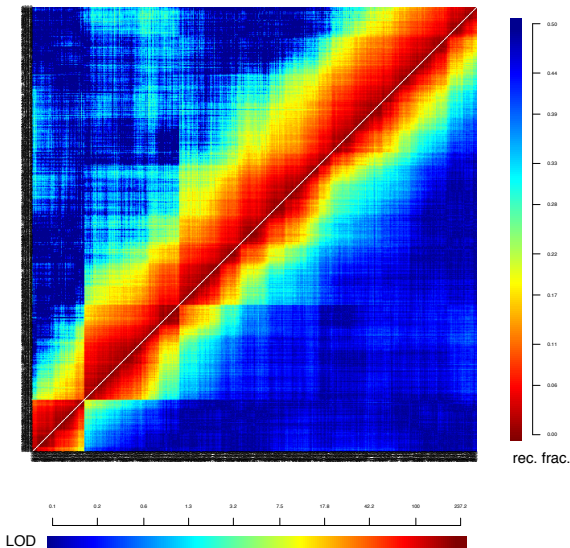
Figure S6

A) Consensus LG I

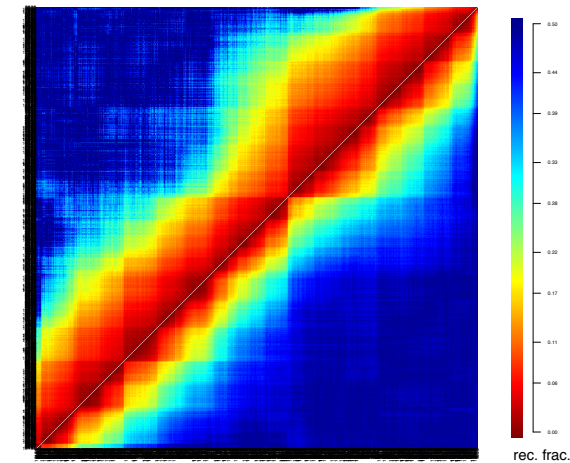
C1: LG 1



C2: LG 11

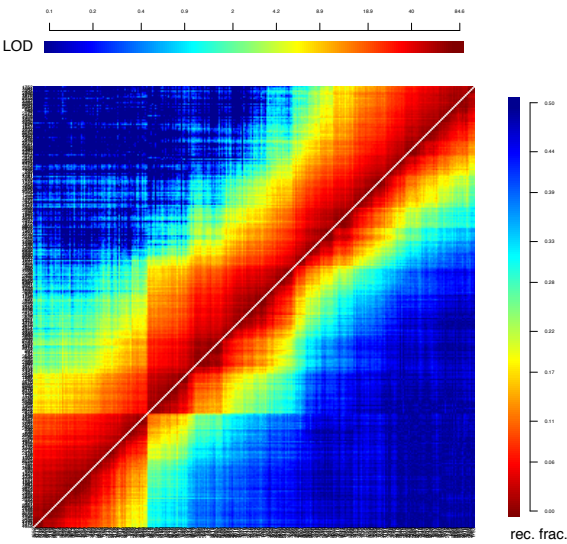


C3: LG 10

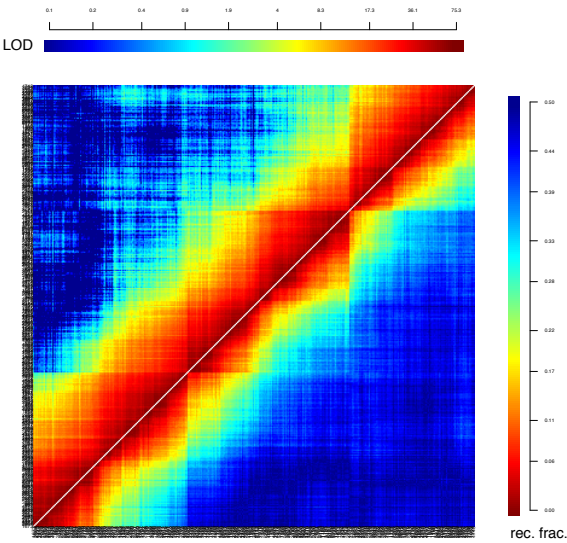


B) Consensus LG II

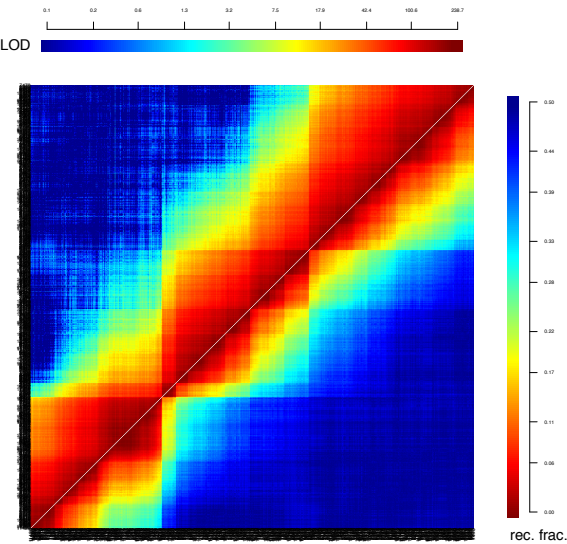
C1: LG 2



C2: LG 12

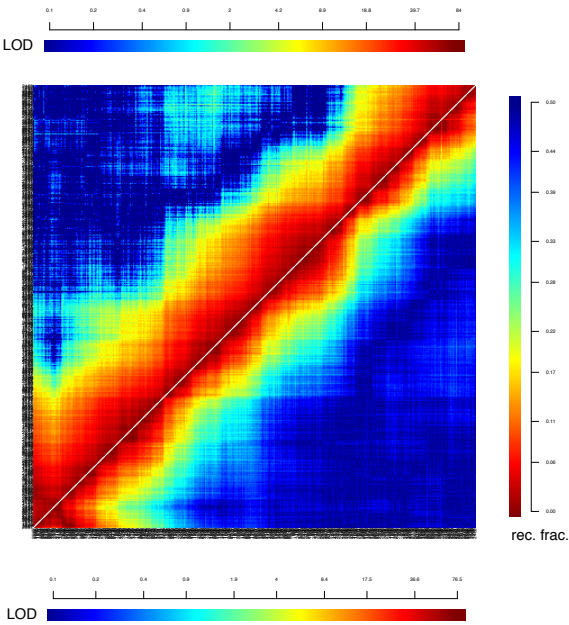


C3: LG 1

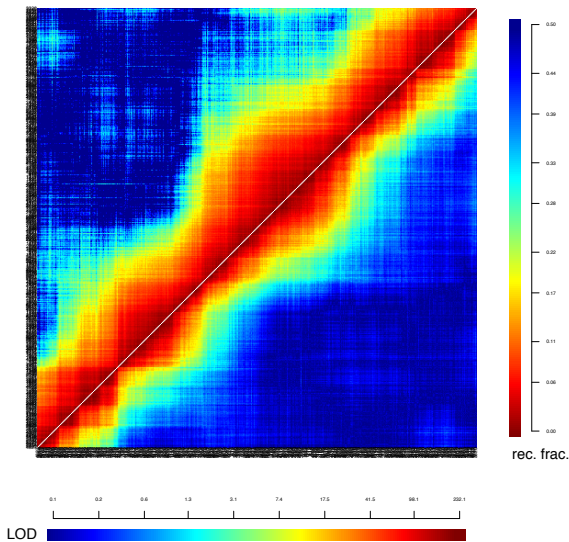


C) Consensus LG III

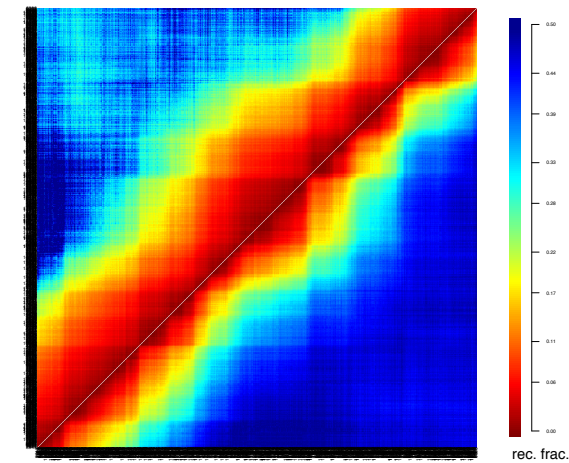
C1: LG 3



C2: LG 1

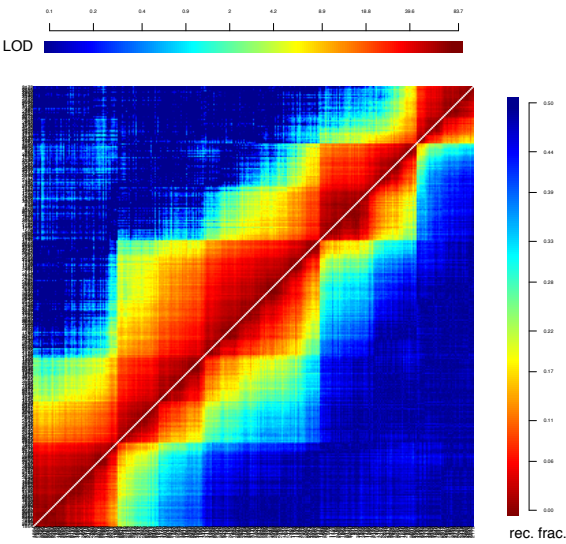


C3: LG 2

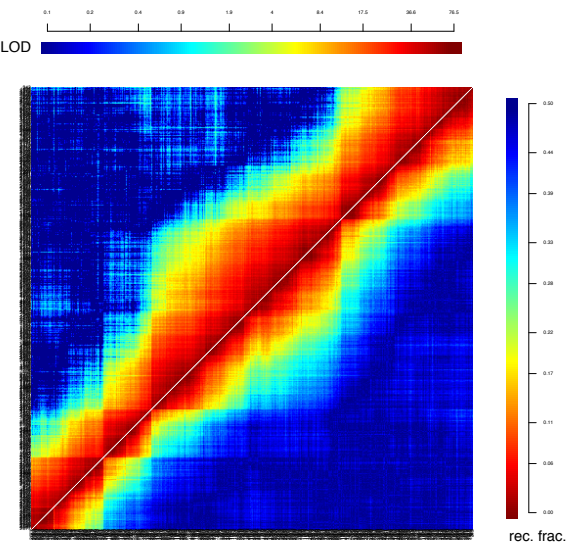


D) Consensus LG IV

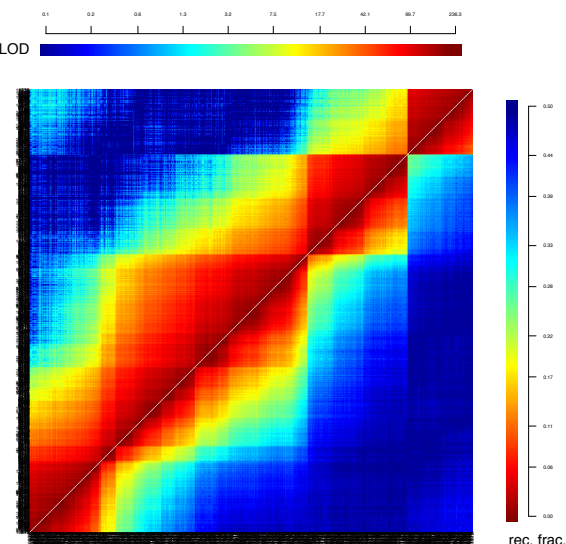
C1: LG 4



C2: LG 3

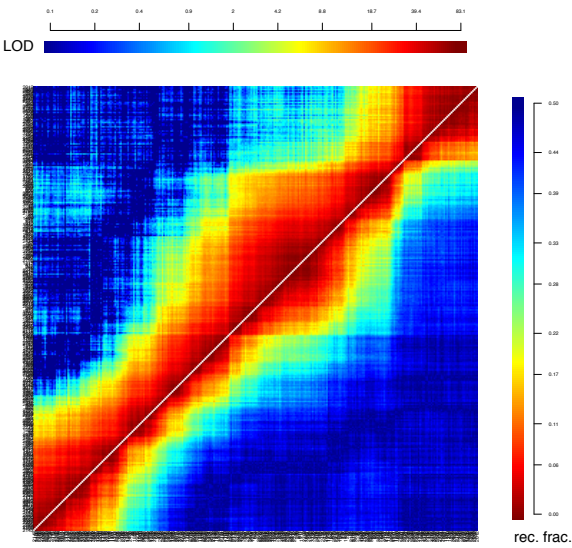


C3: LG 5

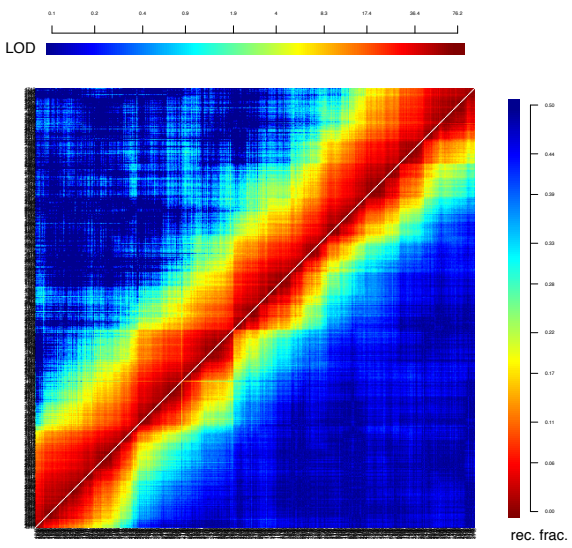


E) Consensus LG V

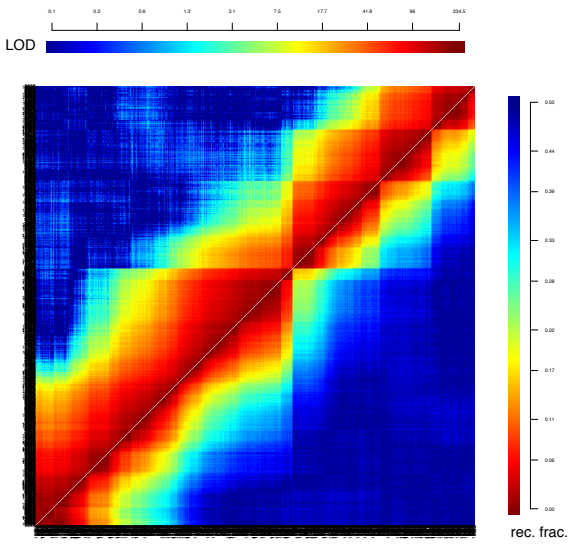
C1: LG 5



C2: LG 9

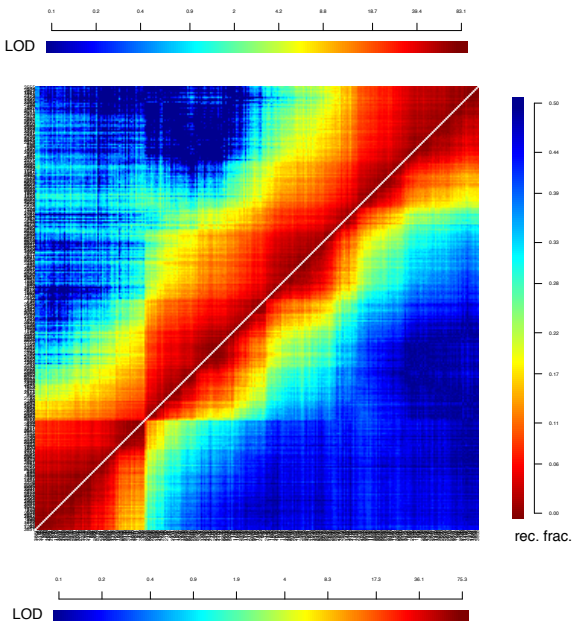


C3: LG 3

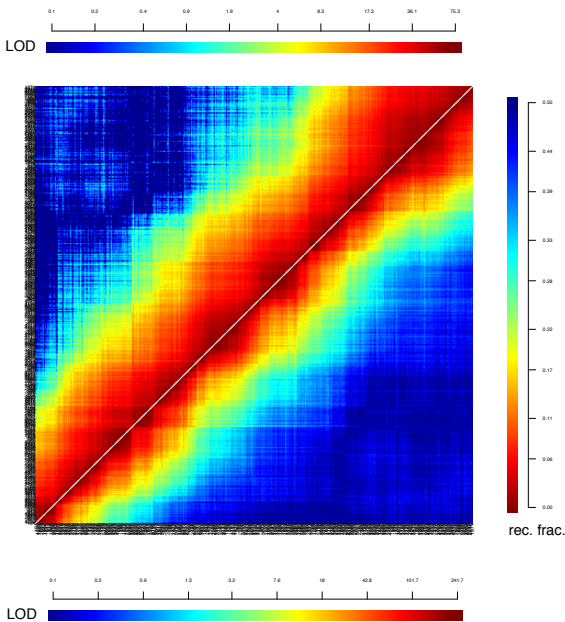


F) Consensus LG VI

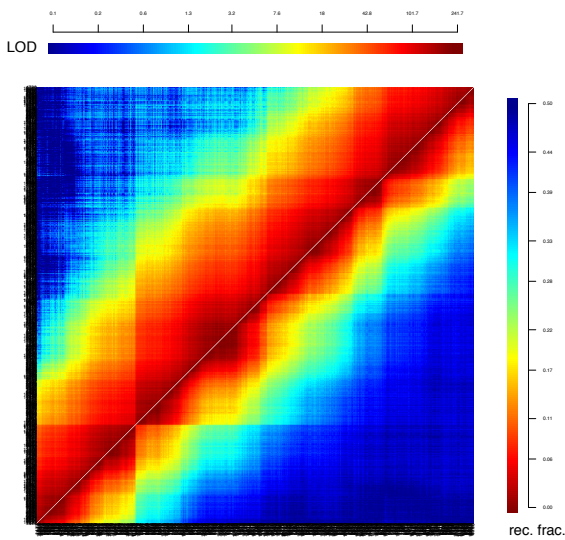
C1: LG 6



C2: LG 5

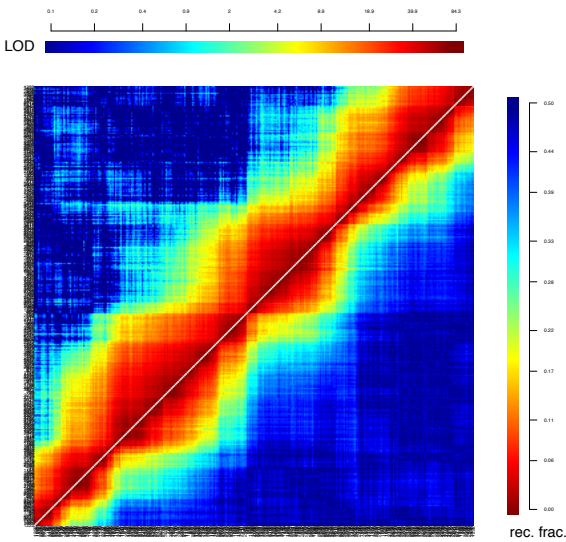


C3: LG 7

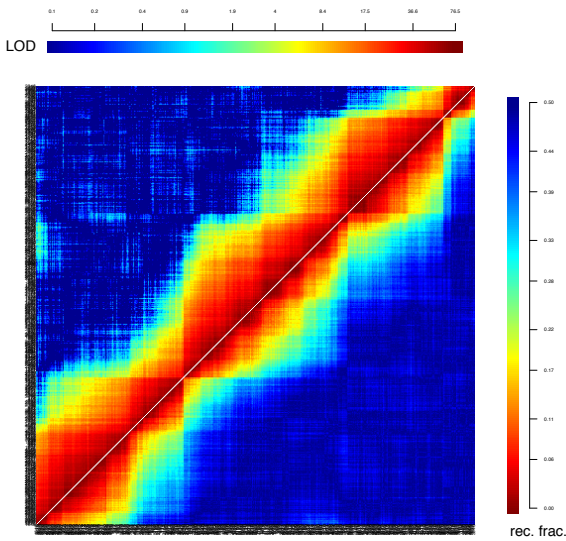


G) Consensus LG VII

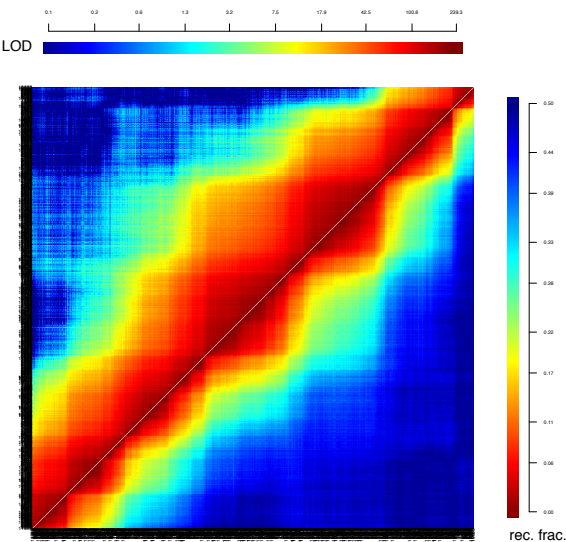
C1: LG 7



C2: LG 6

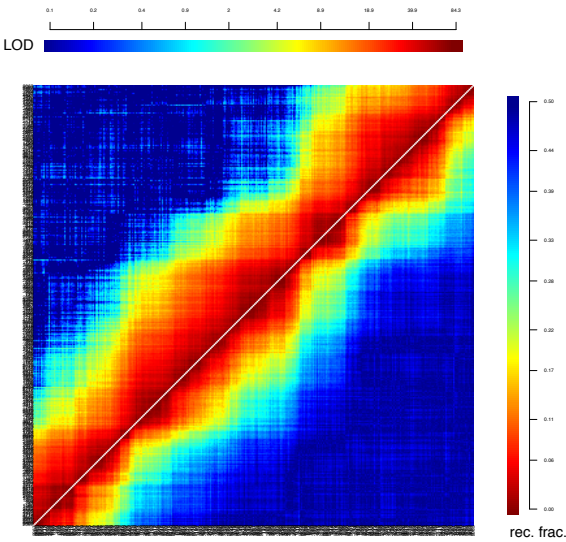


C3: LG 8

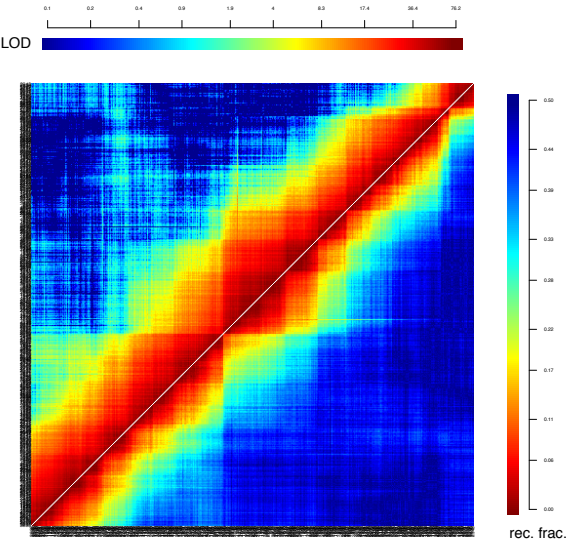


H) Consensus LG VIII

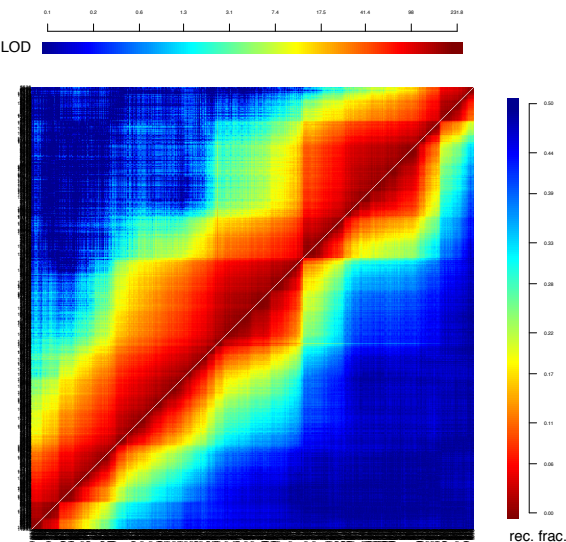
C1: LG 8



C2: LG 8

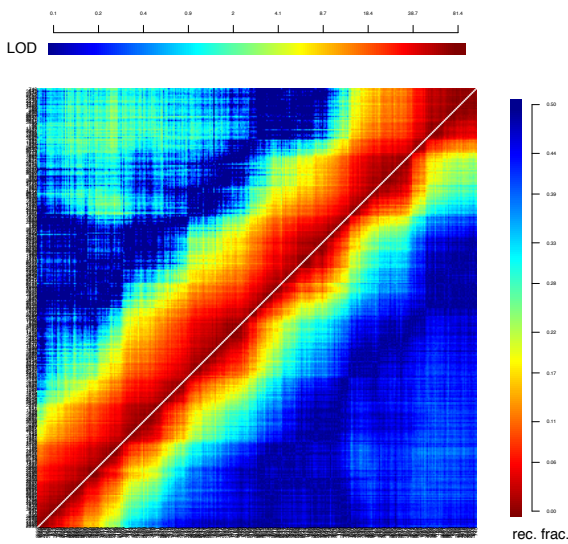


C3: LG 11

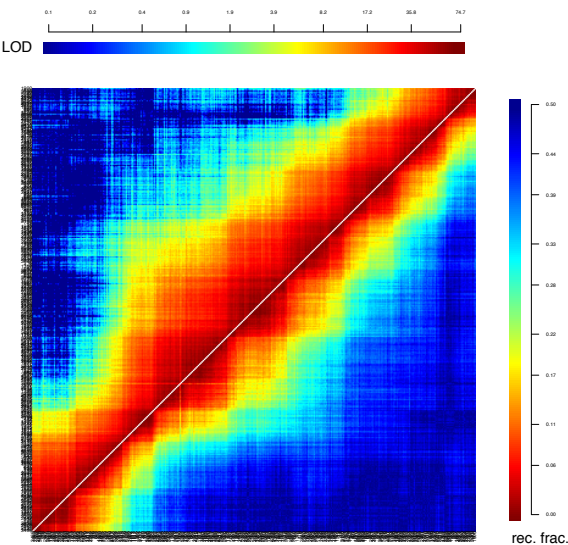


I) Consensus LG IX

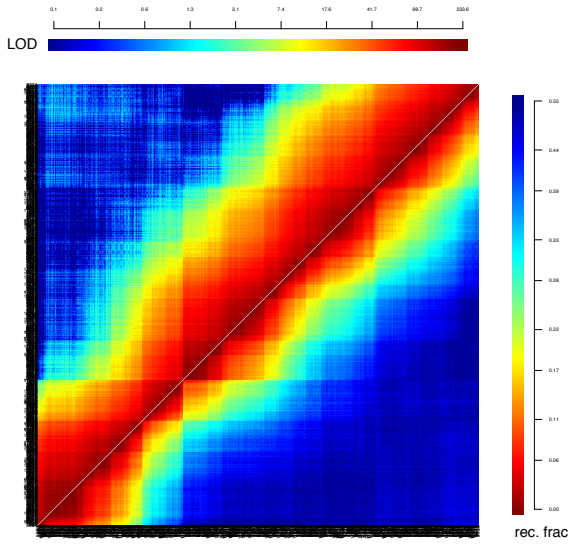
C1: LG 9



C2: LG 4

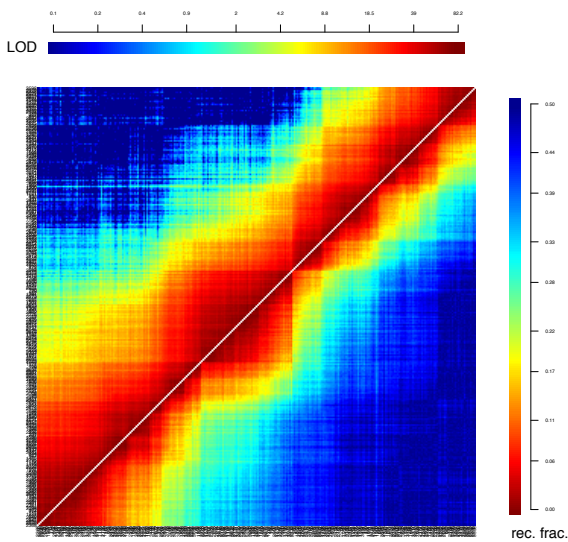


C3: LG 6

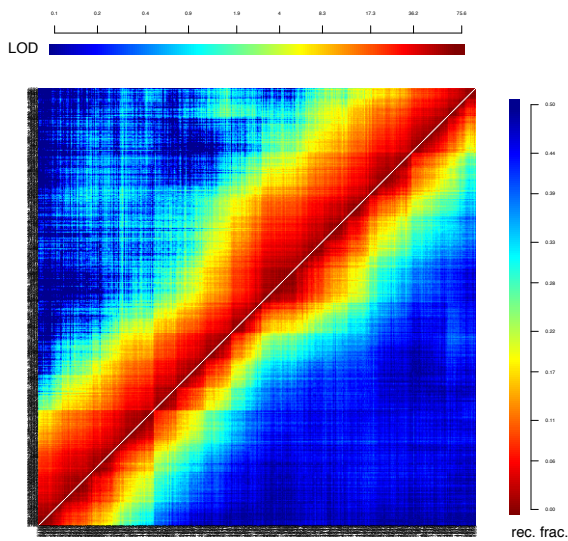


J) Consensus LG X

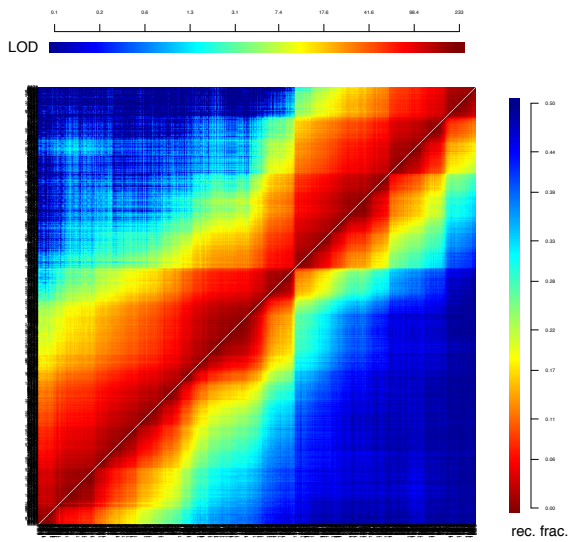
C1: LG 10



C2: LG 10

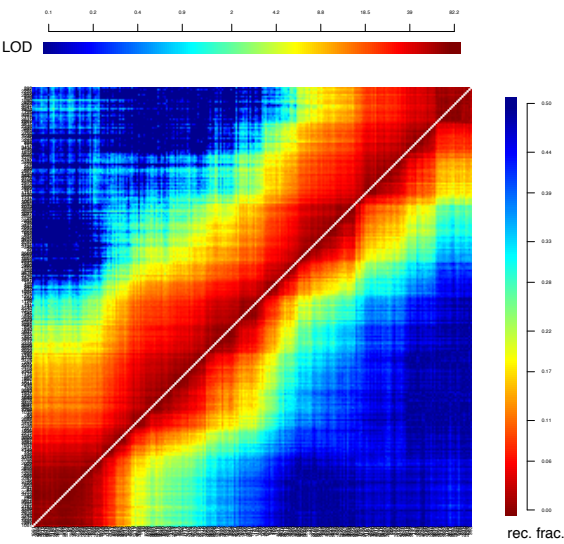


C3: LG 12

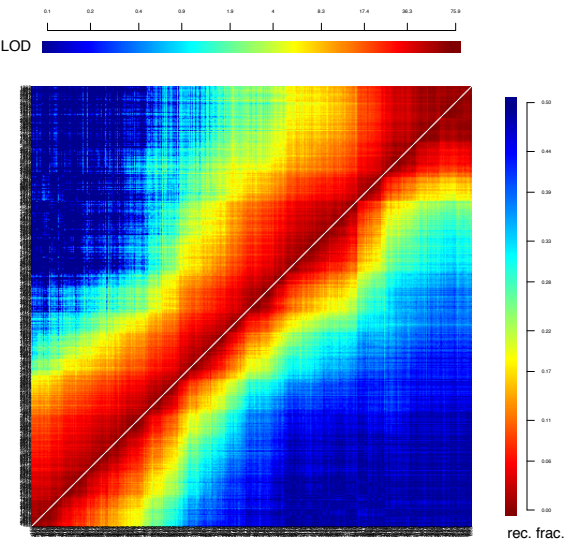


K) Consensus LG XI

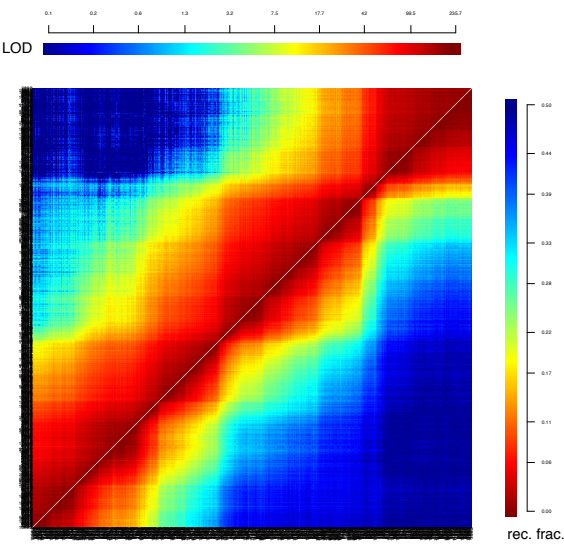
C1: LG 11



C2: LG 2

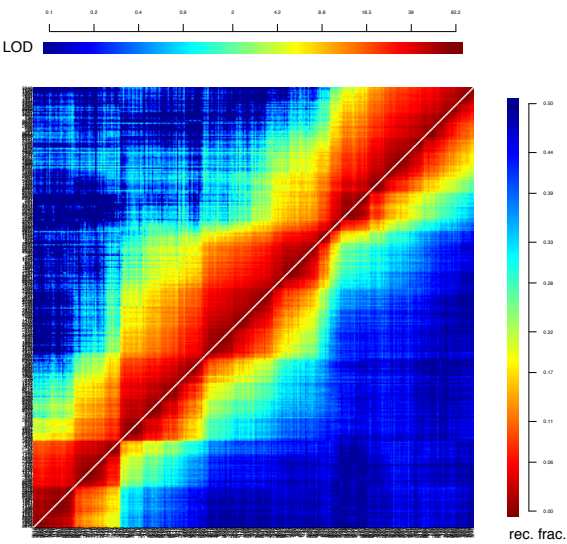


C3: LG 4

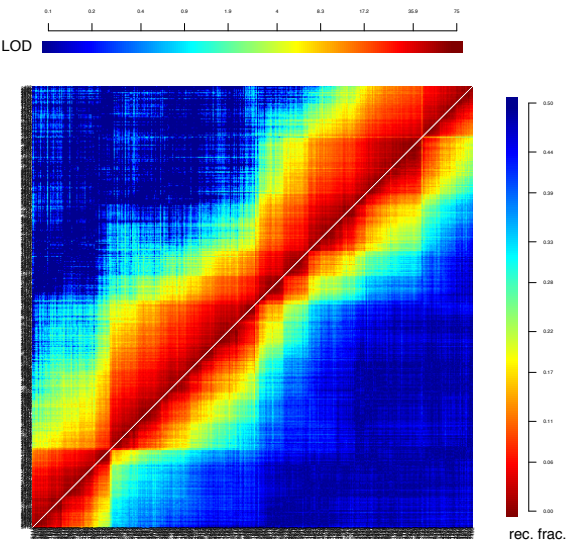


L) Consensus LG XII

C1: LG 12



C2: LG 7



C3: LG 9

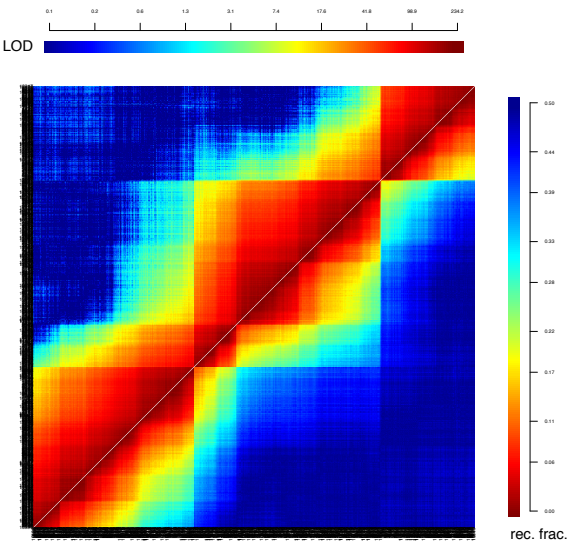
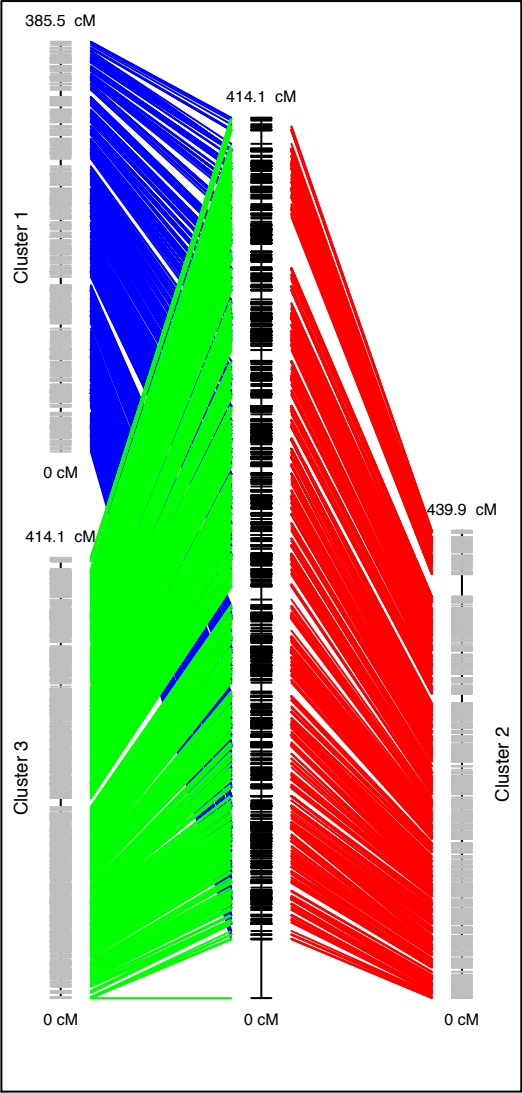


Figure S7
A)

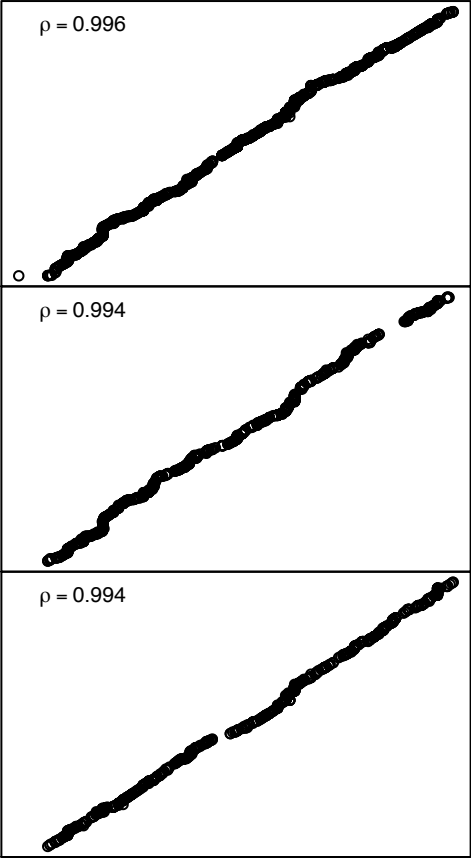


LG I

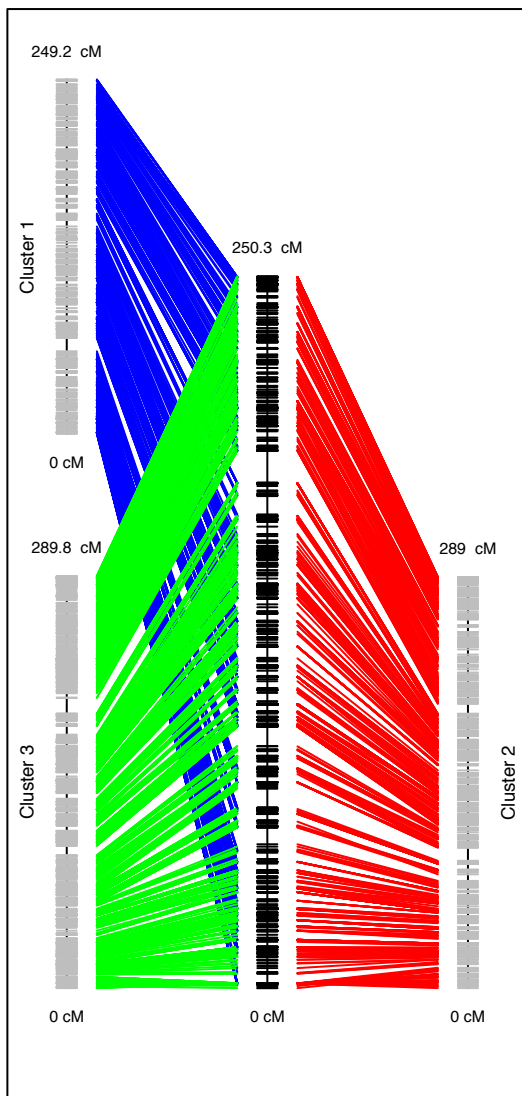
Cluster 3

Cluster 2

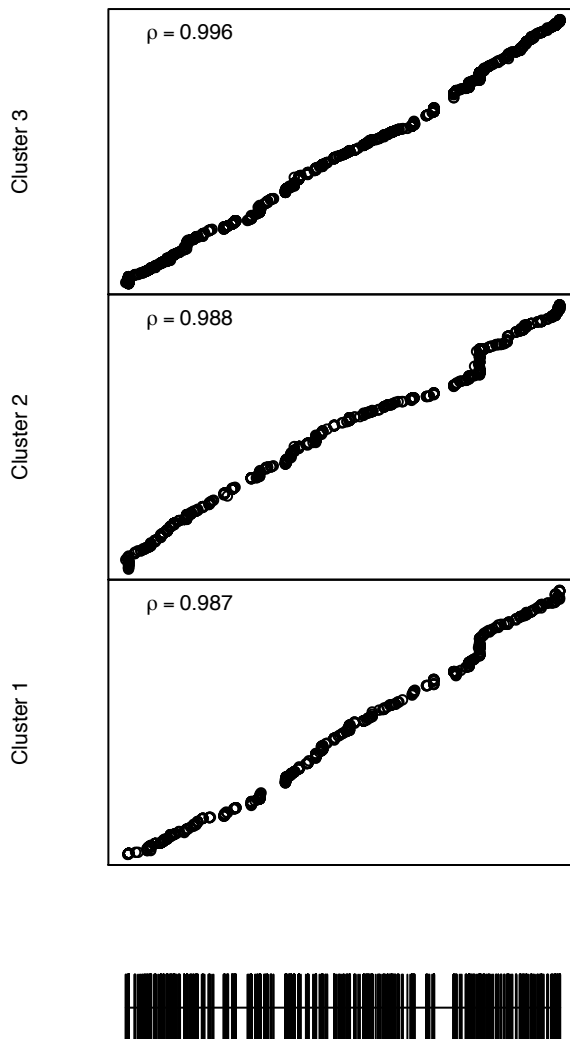
Cluster 1



B)

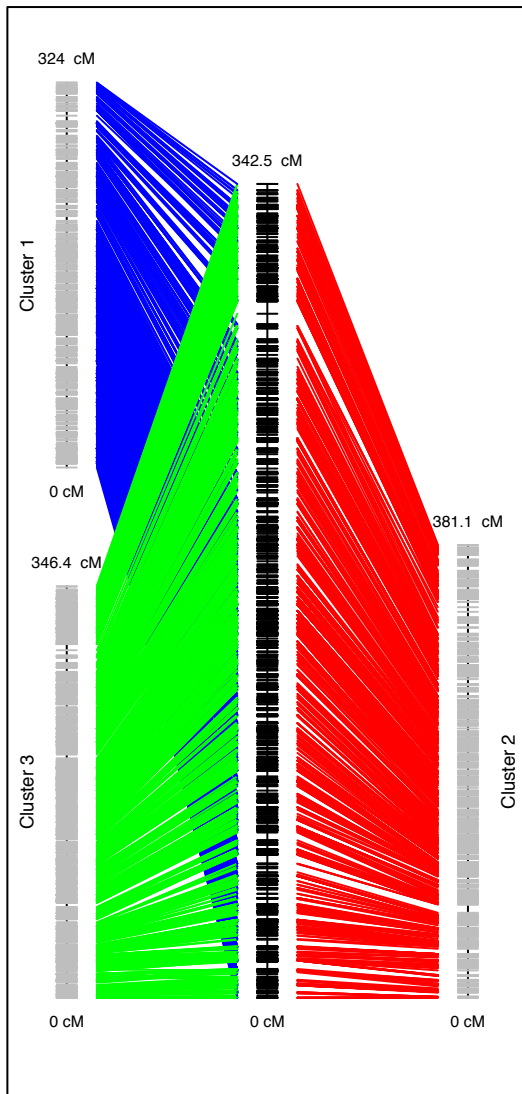


LG II



C)

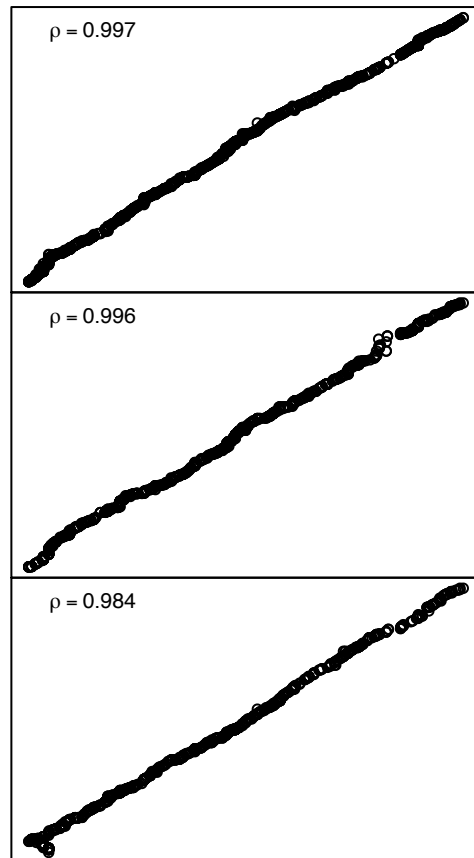
LG III



Cluster 3

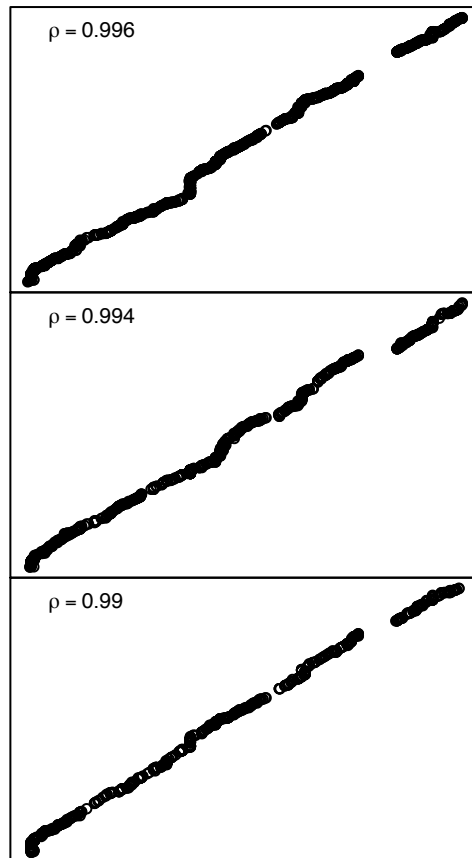
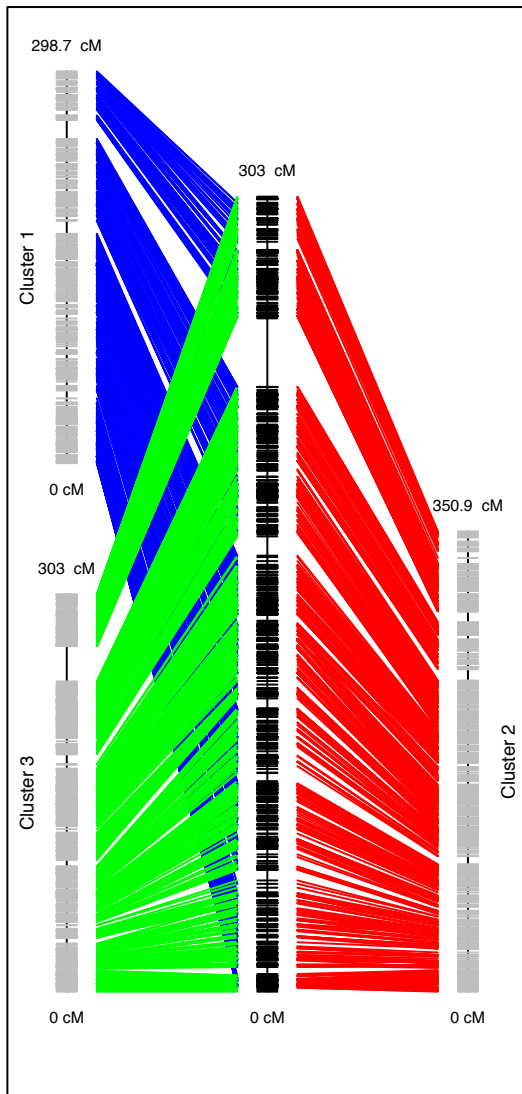
Cluster 2

Cluster 1



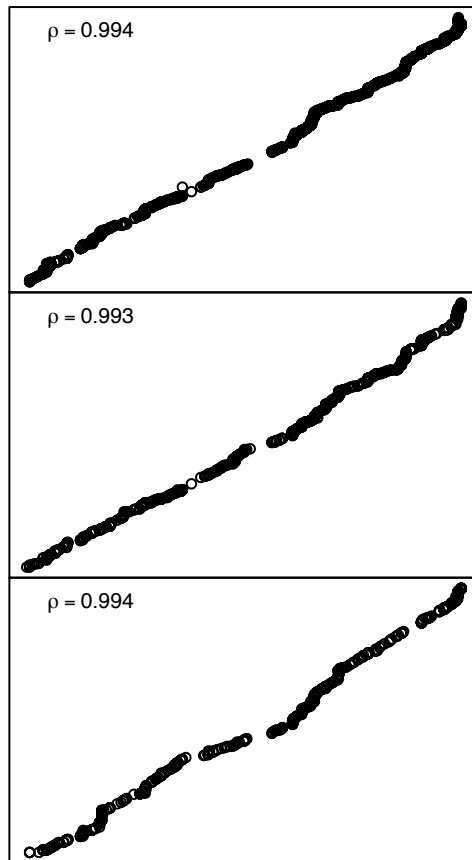
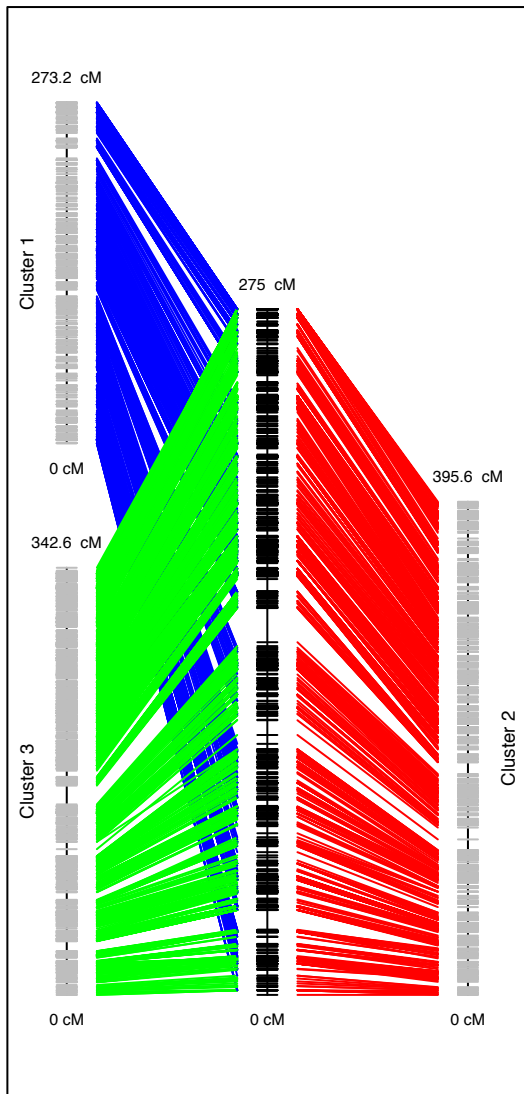
D)

LG IV



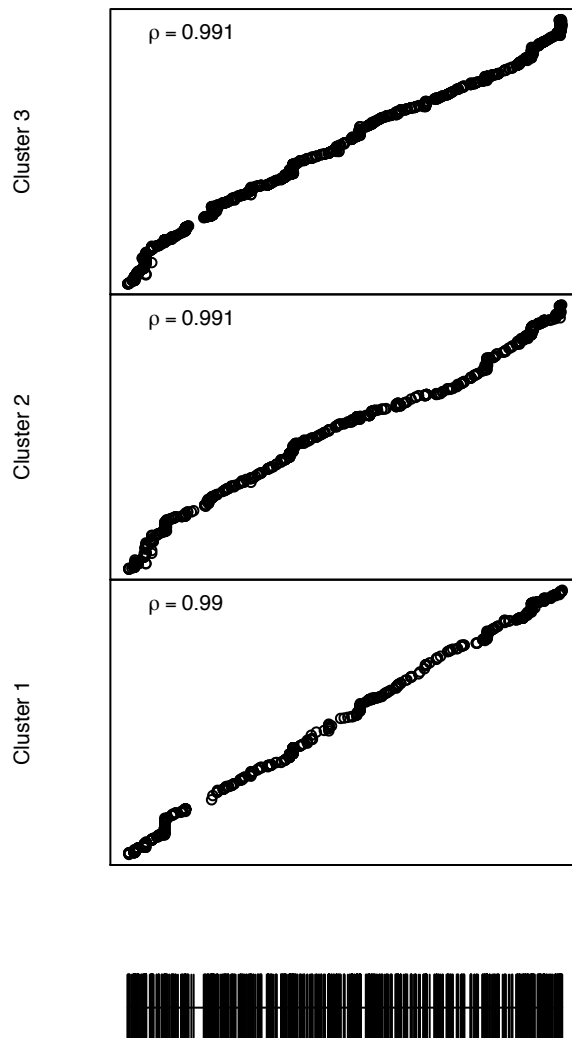
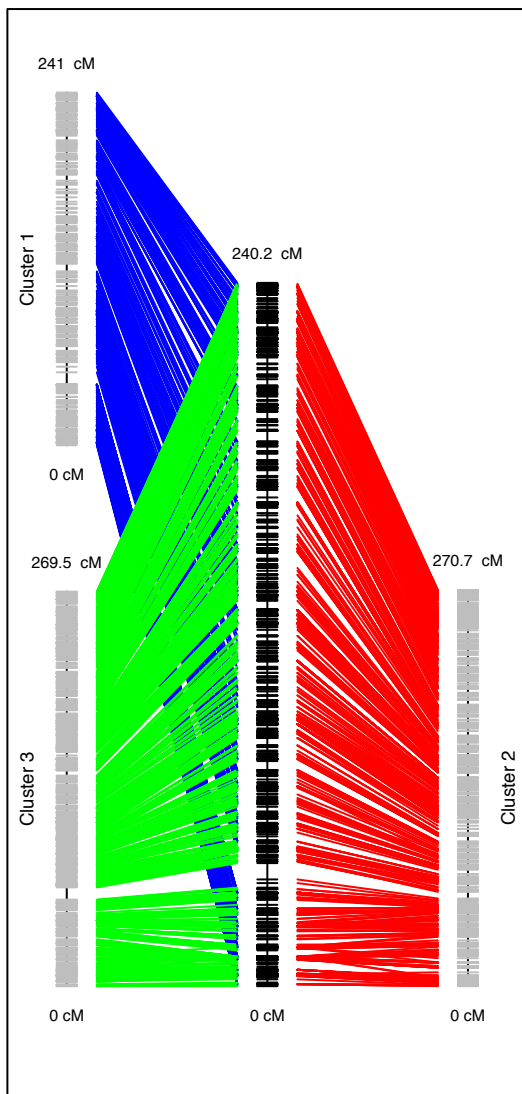
E)

LG V



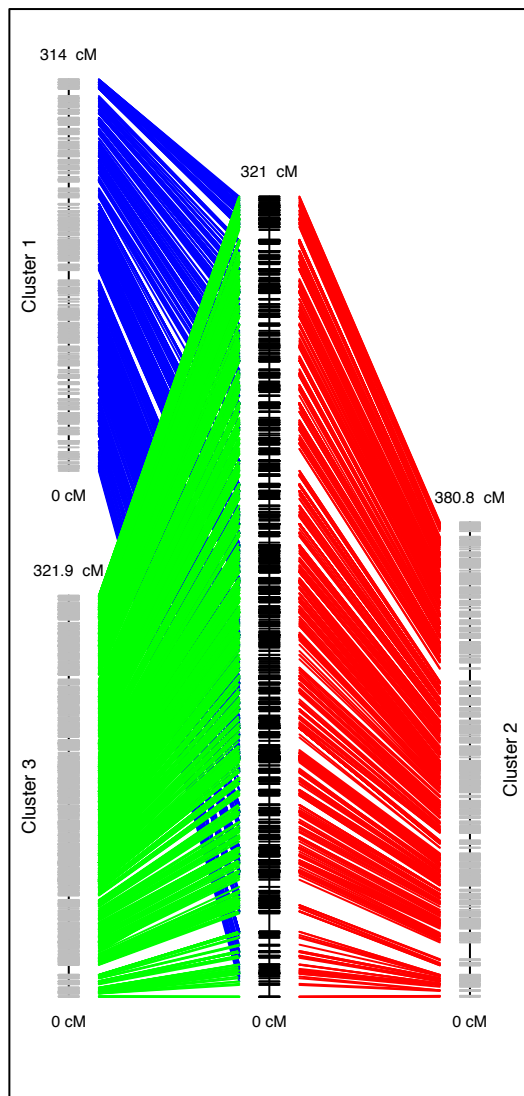
F)

LG VI



G)

LG VII



Cluster 3

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Cluster 2

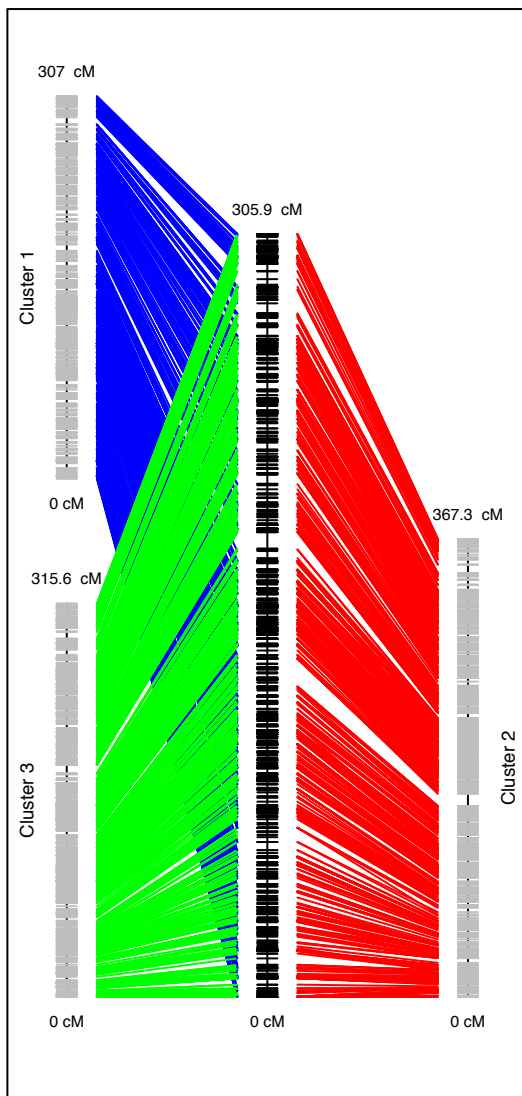
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Cluster 1

 $\rho = 0.994$ 

H)

LG VIII



Cluster 3

$\rho = 0.998$

Cluster 2

$\rho = 0.993$

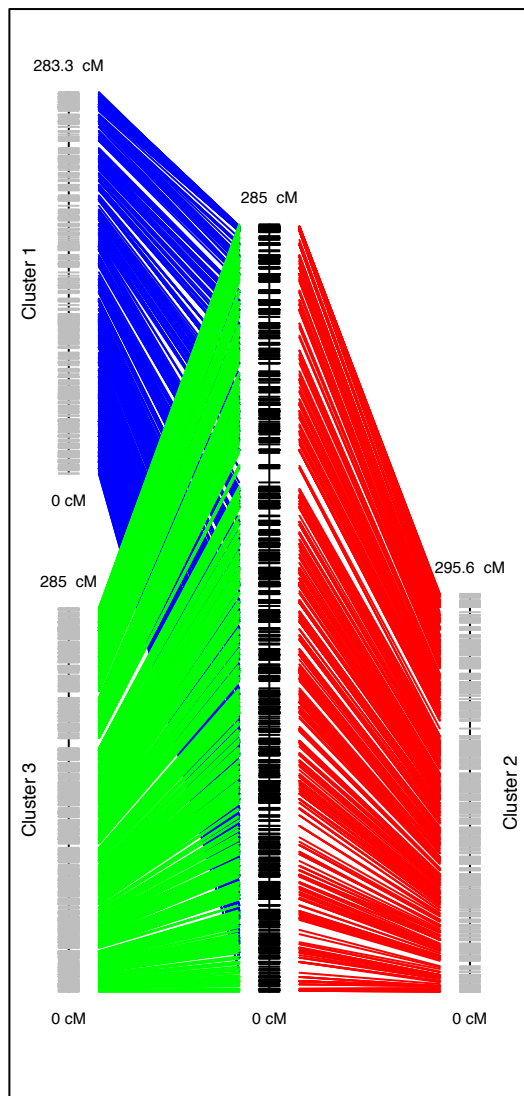
Cluster 1

$\rho = 0.994$



I)

LG IX



Cluster 3

$$\rho = 0.996$$

Cluster 2

$$\rho = 0.99$$

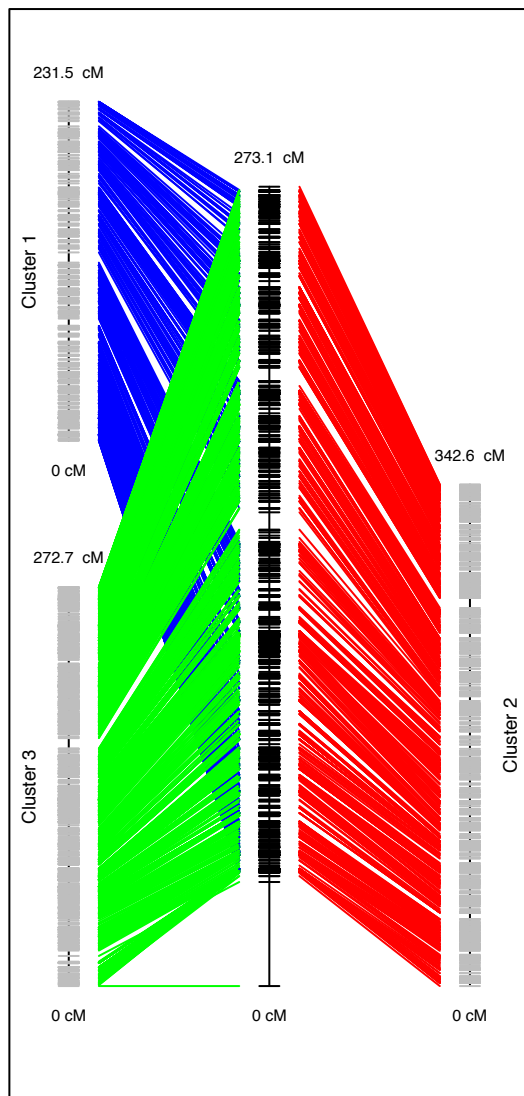
Cluster 1

$$\rho = 0.993$$



J)

LG X



Cluster 3

 $\rho = 0.997$

o

Cluster 2

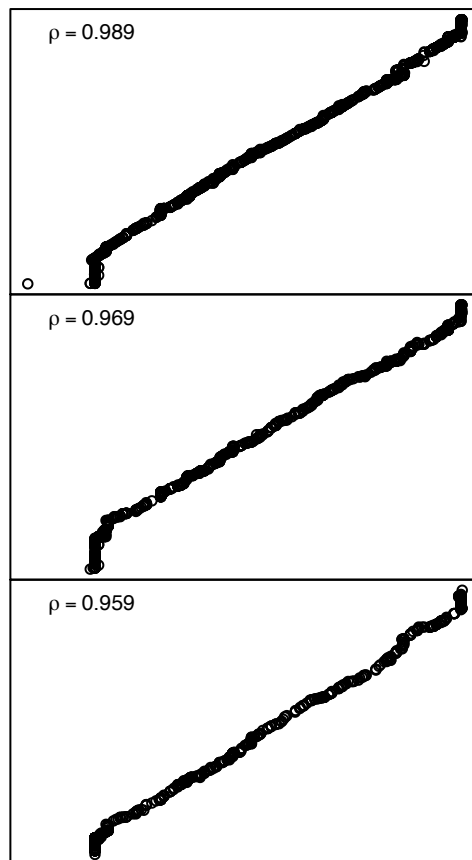
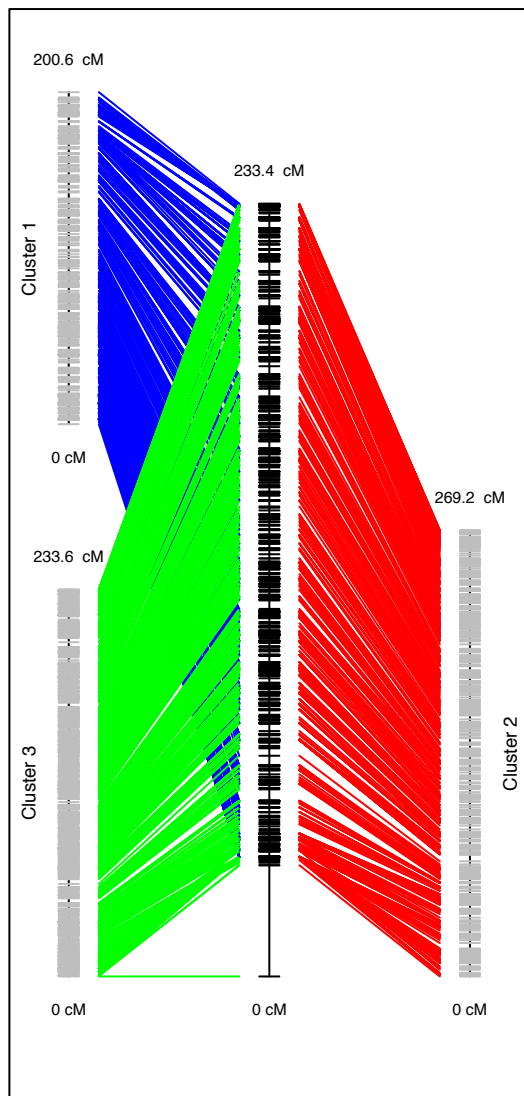
 $\rho = 0.994$

Cluster 1

 $\rho = 0.994$ 

K)

LG XI



L)

LG XII

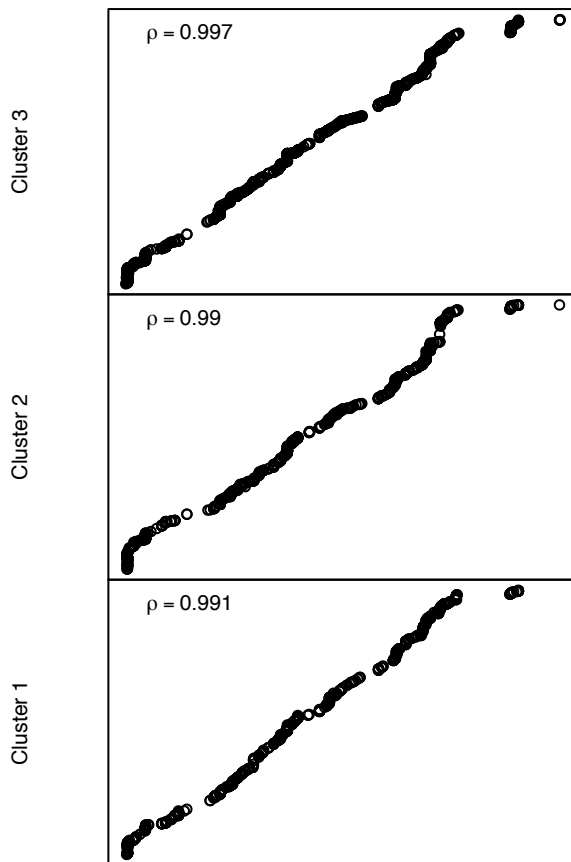
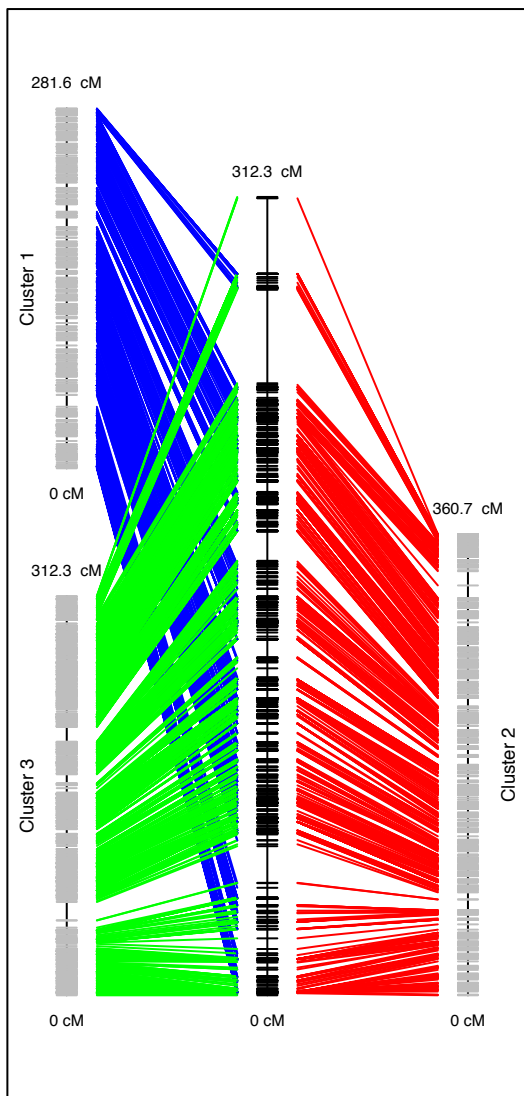


Figure S8

A)

LG I

Consensus

0.994

0.994

0.996

Cluster 1

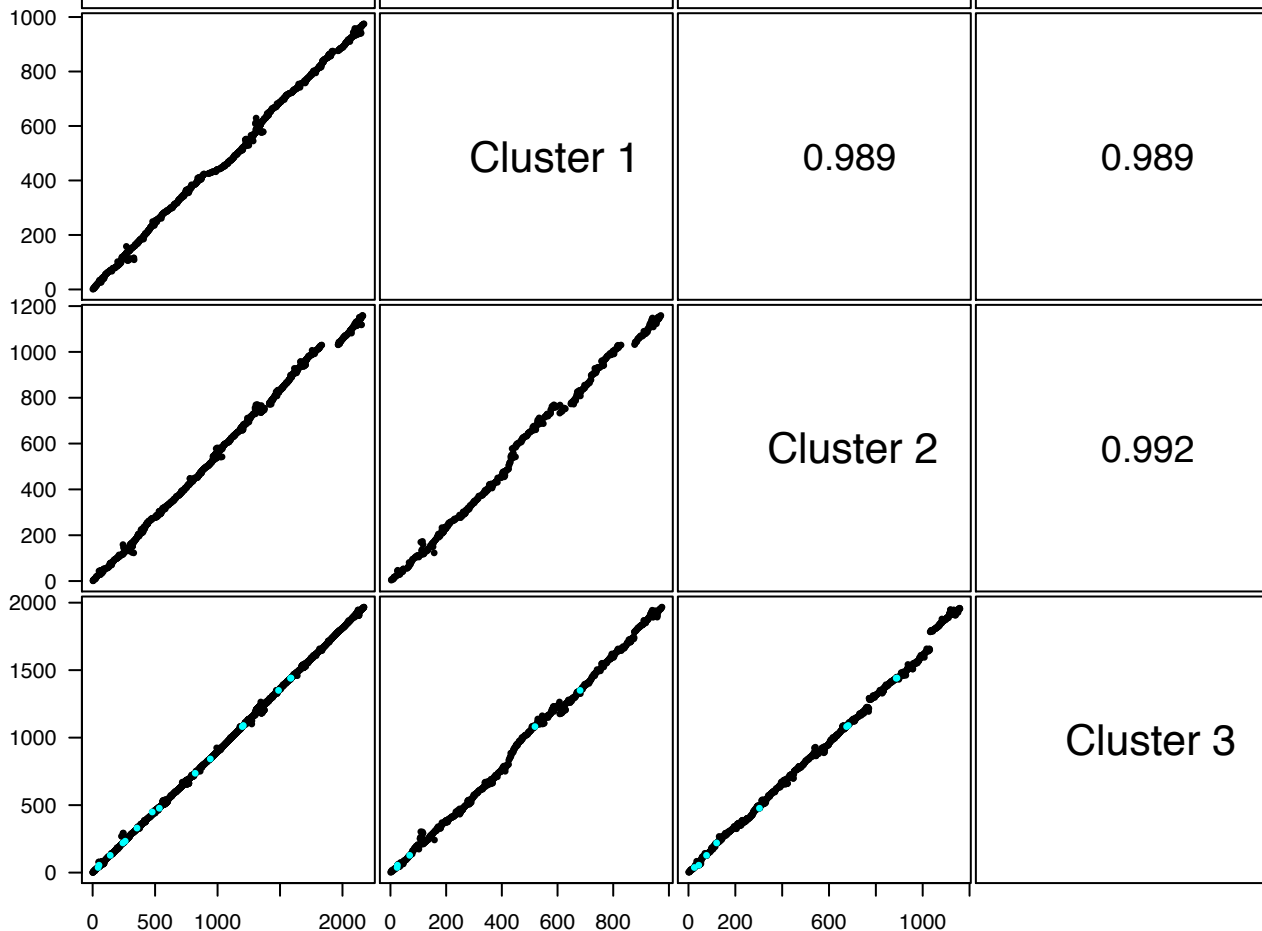
0.989

0.989

Cluster 2

0.992

Cluster 3



B)

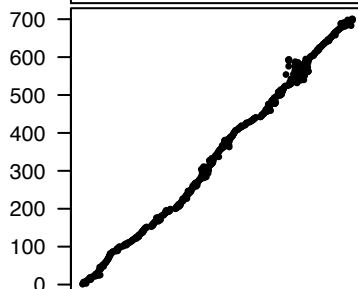
LG II

Consensus

0.987

0.988

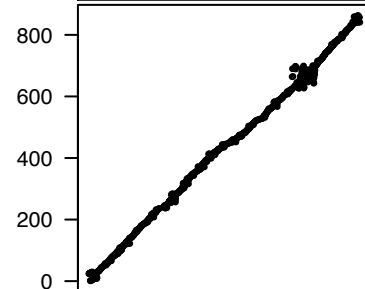
0.996



Cluster 1

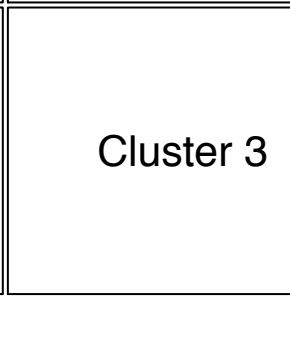
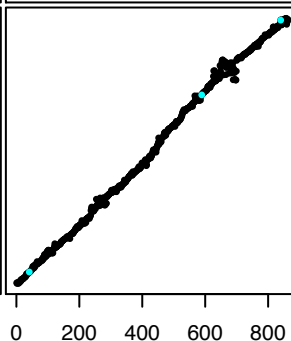
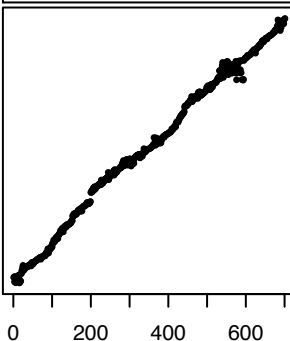
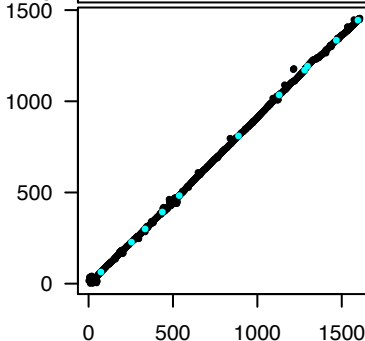
0.988

0.985



Cluster 2

0.988



Cluster 3

c)

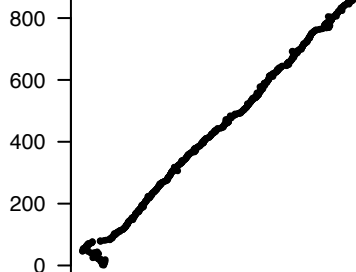
LG III

Consensus

0.984

0.996

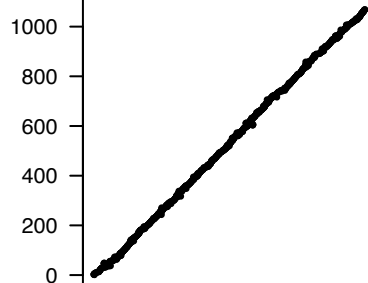
0.997



Cluster 1

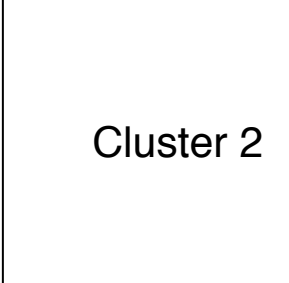
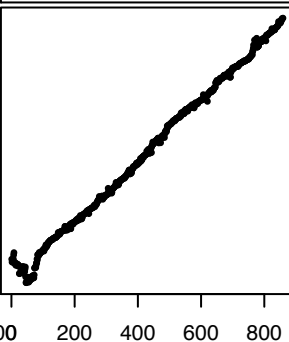
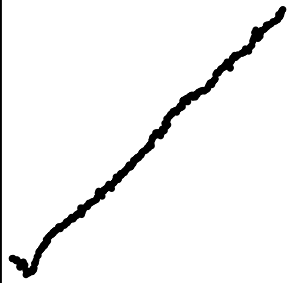
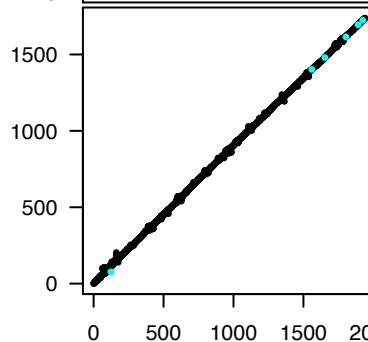
0.982

0.981



Cluster 2

0.993



Cluster 3

D)

LG IV

Consensus

0.99

0.994

0.996

Cluster 1

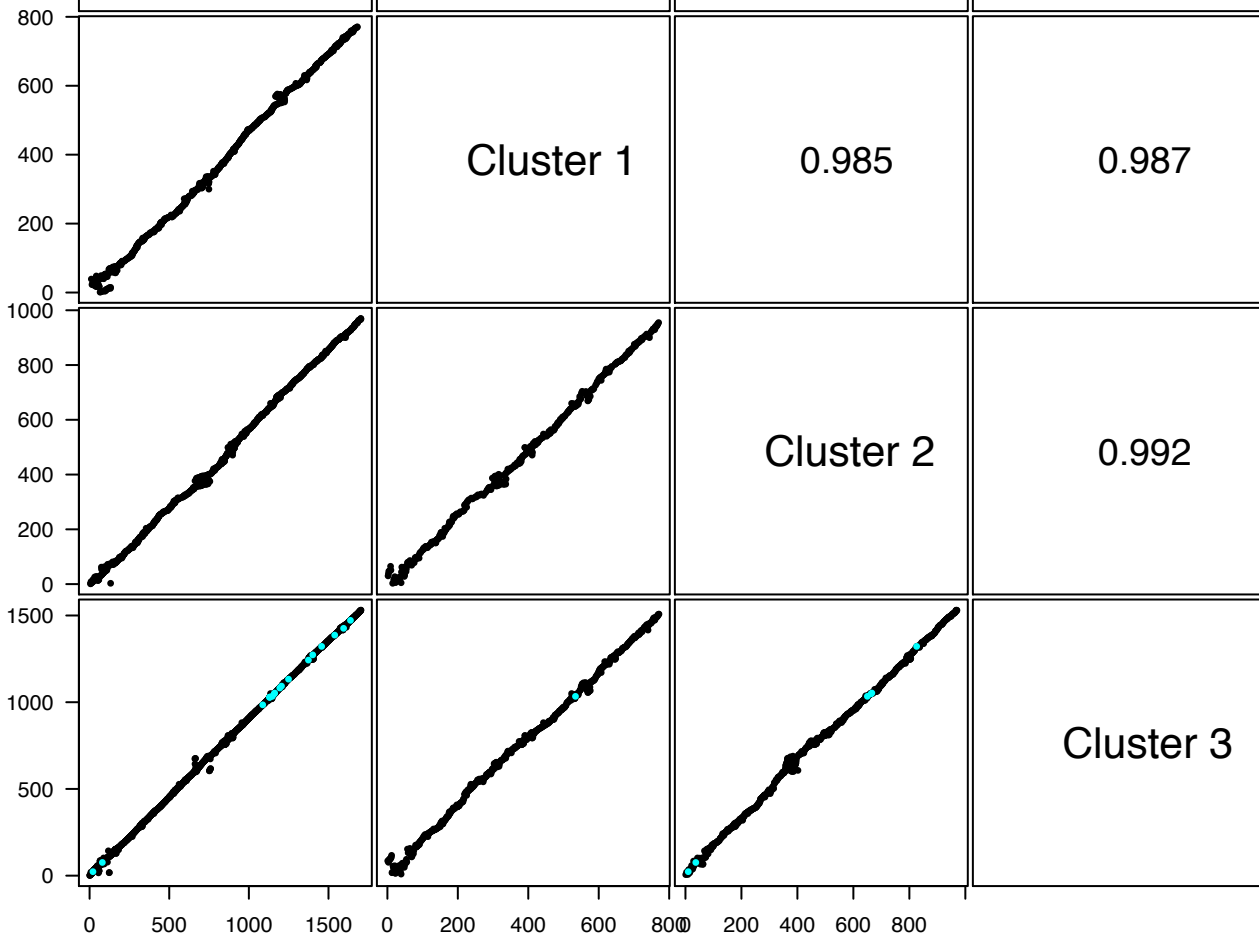
0.985

0.987

Cluster 2

0.992

Cluster 3



E)

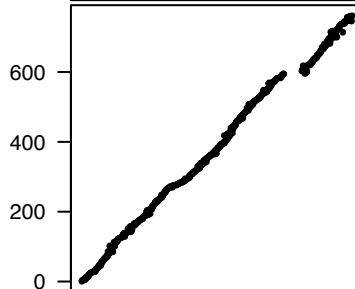
LG V

Consensus

0.994

0.993

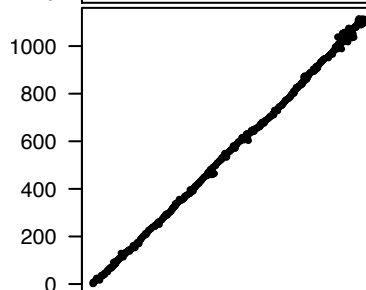
0.994



Cluster 1

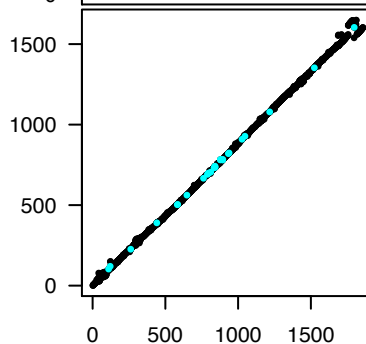
0.99

0.989



Cluster 2

0.987



Cluster 3

F)

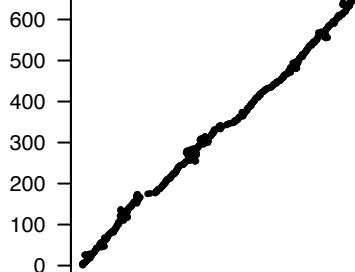
LG VI

Consensus

0.99

0.991

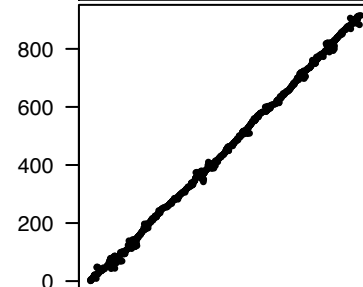
0.991



Cluster 1

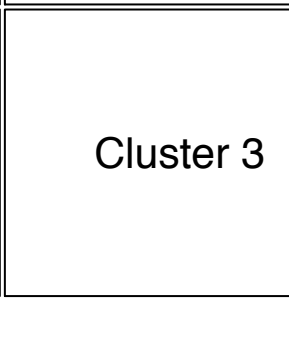
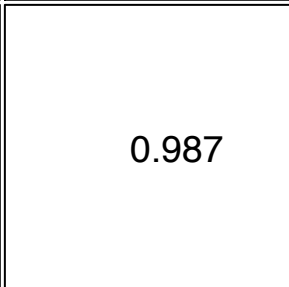
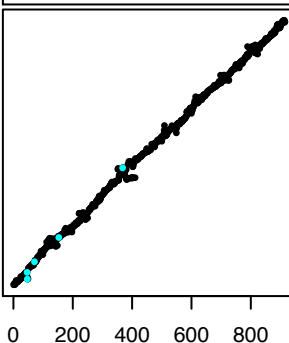
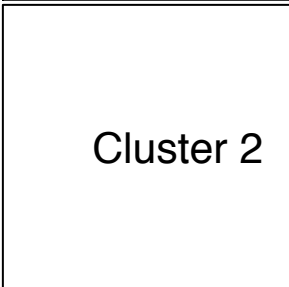
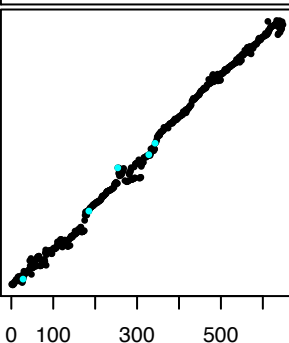
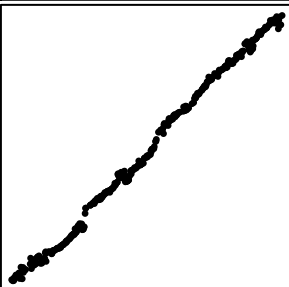
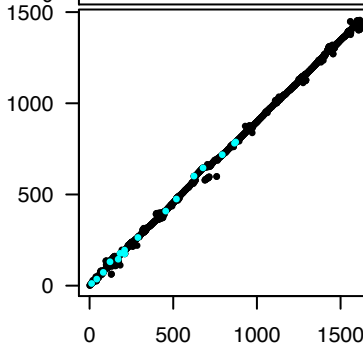
0.981

0.982



Cluster 2

0.987



Cluster 3

G)

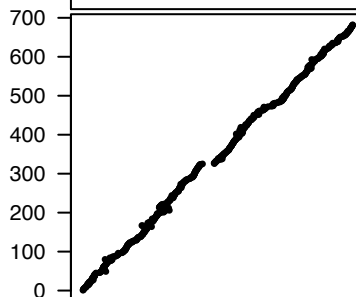
LG VII

Consensus

0.994

0.995

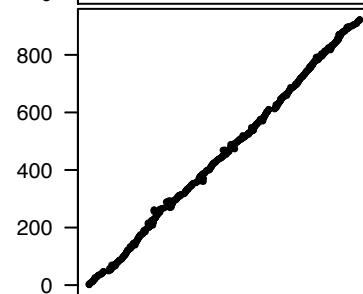
0.998



Cluster 1

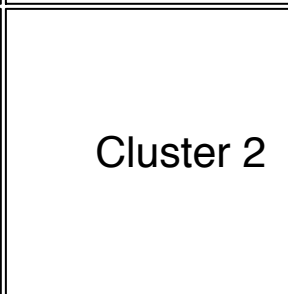
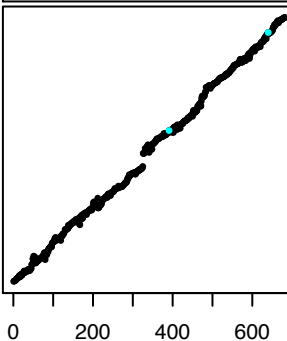
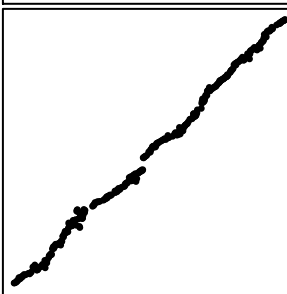
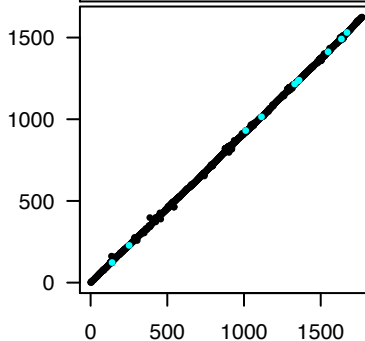
0.988

0.992



Cluster 2

0.992



Cluster 3

H)

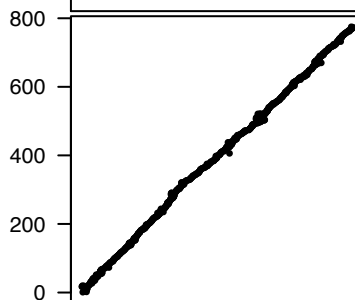
LG VIII

Consensus

0.994

0.993

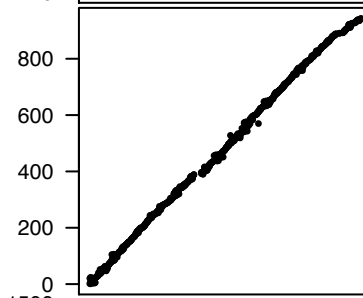
0.998



Cluster 1

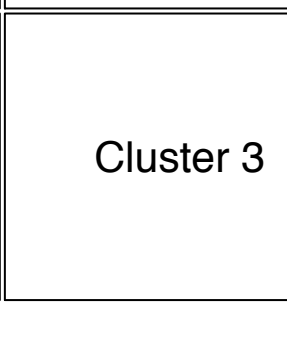
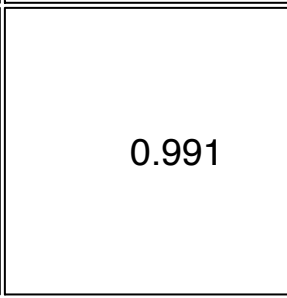
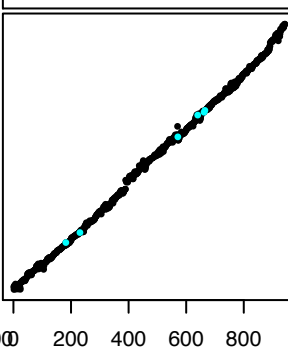
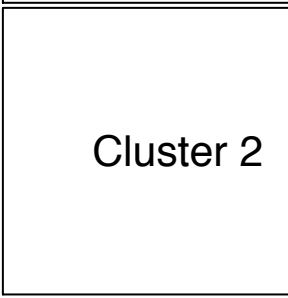
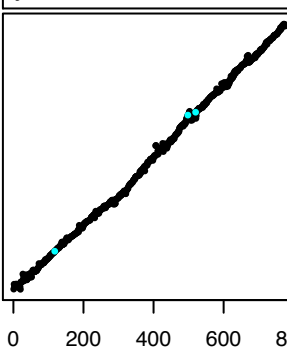
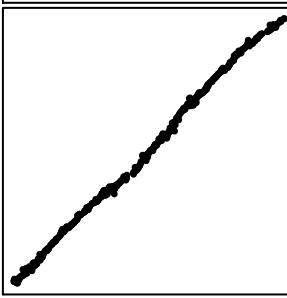
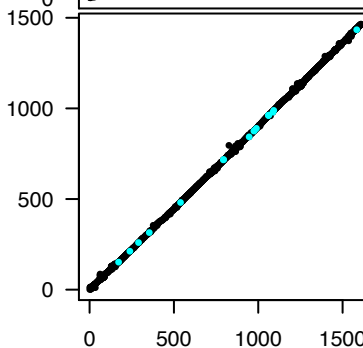
0.989

0.992



Cluster 2

0.991



Cluster 3

I)

LG IX

Consensus

0.993

0.99

0.996

Cluster 1

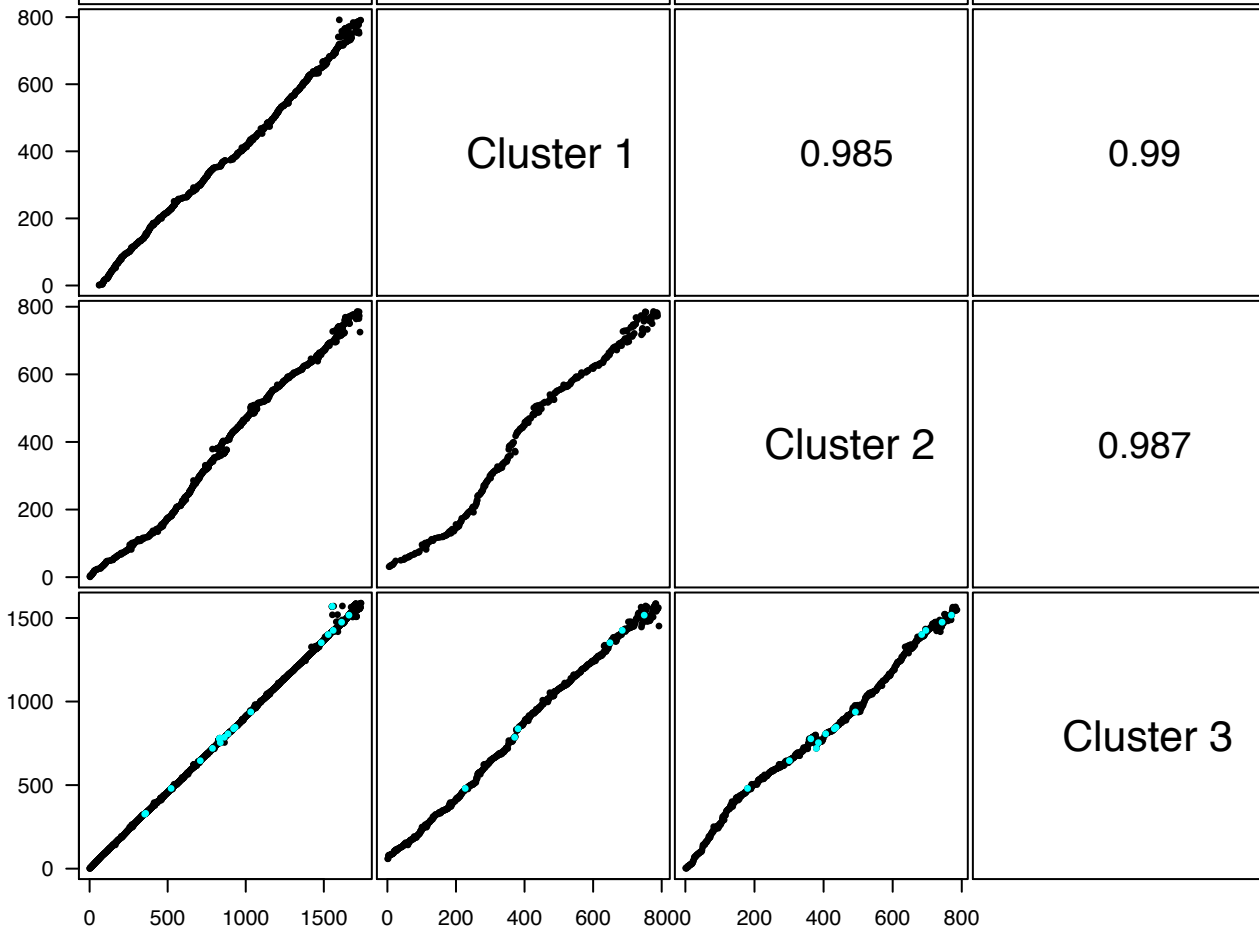
0.985

0.99

Cluster 2

0.987

Cluster 3



J)

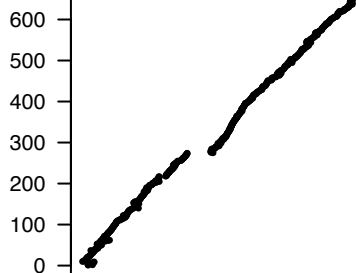
LG X

Consensus

0.994

0.994

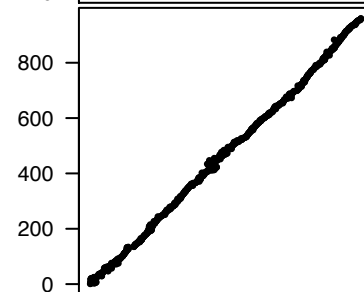
0.997



Cluster 1

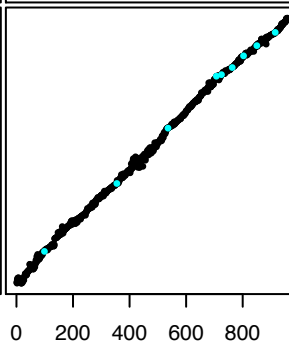
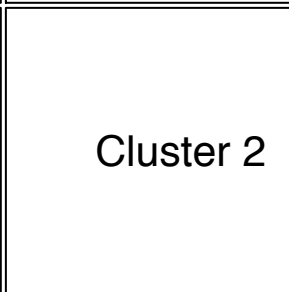
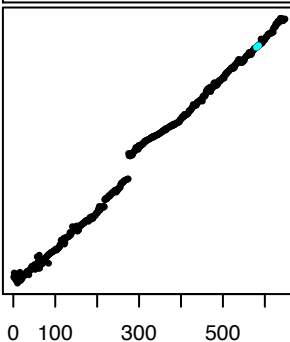
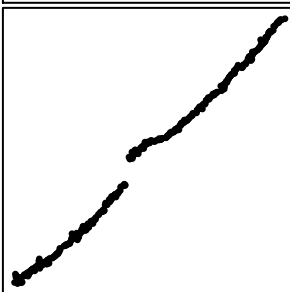
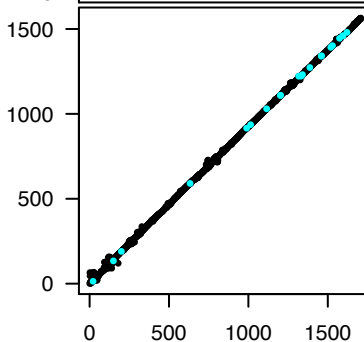
0.989

0.992



Cluster 2

0.991



Cluster 3

K)

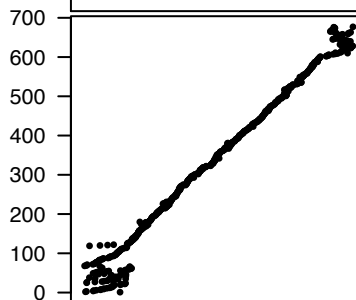
LG XI

Consensus

0.959

0.969

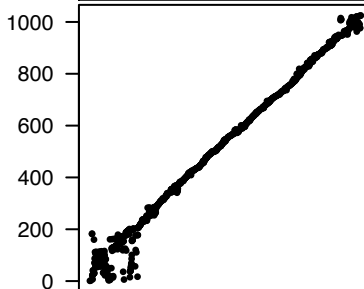
0.989



Cluster 1

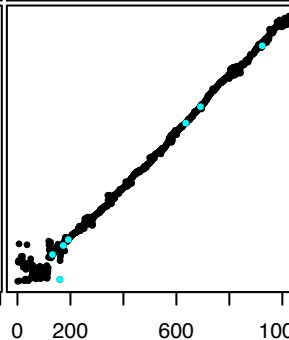
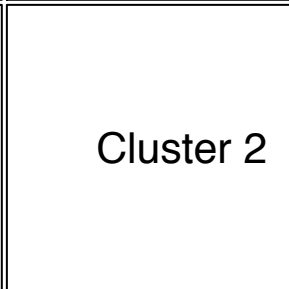
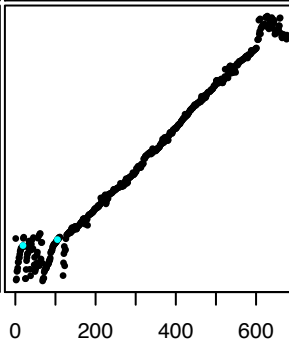
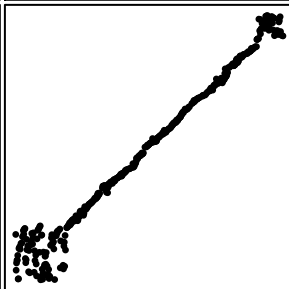
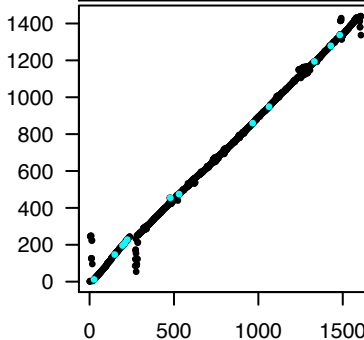
0.942

0.954



Cluster 2

0.972



Cluster 3

L)

LG XII

Consensus

0.991

0.99

0.997

Cluster 1

0.989

0.99

Cluster 2

0.992

Cluster 3

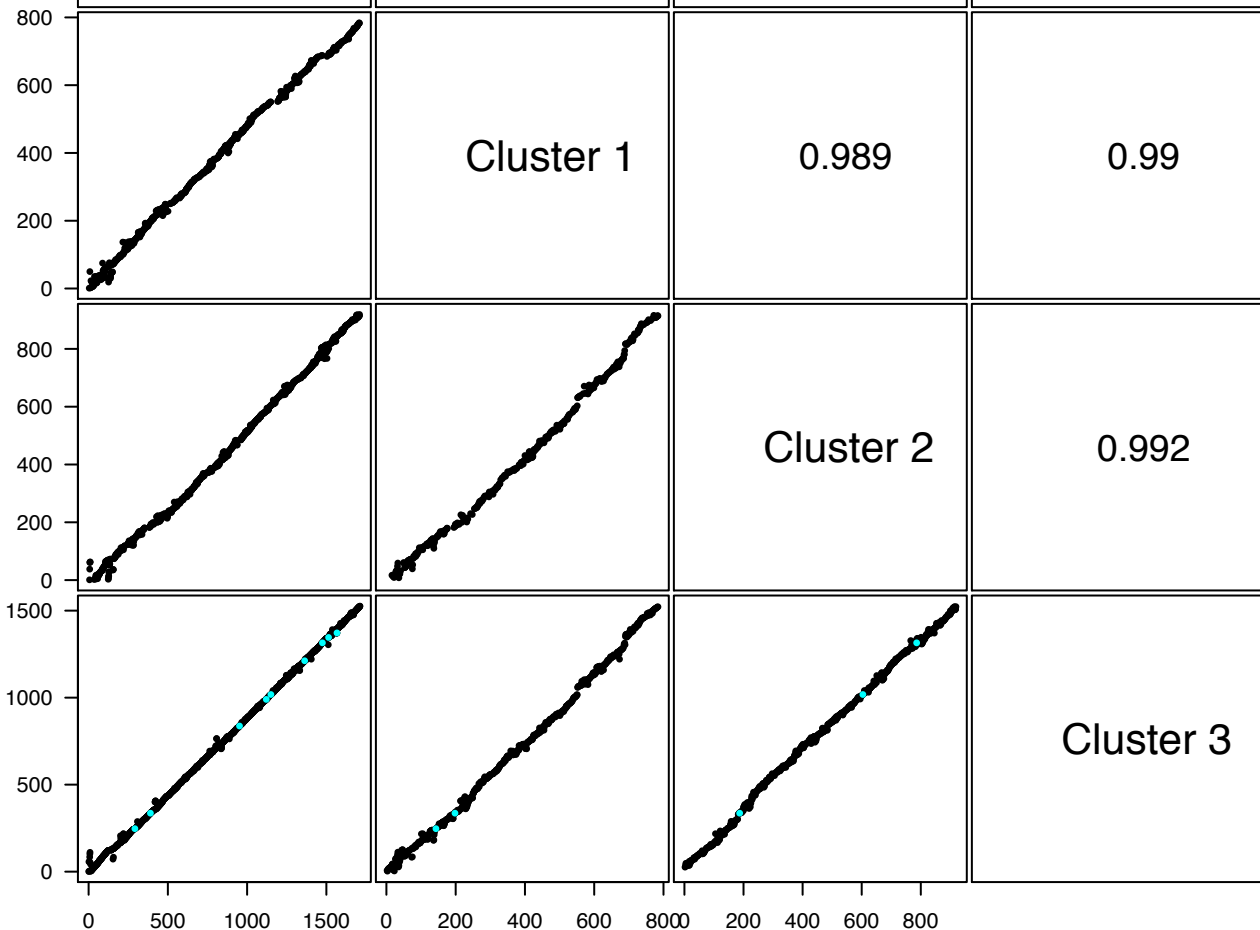
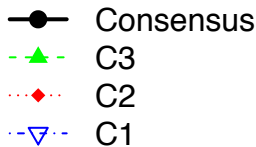
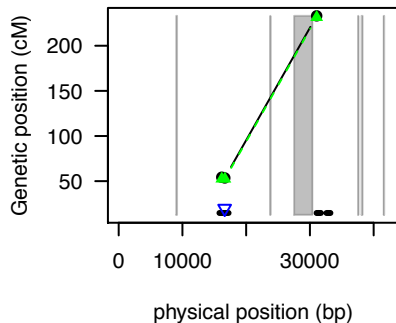


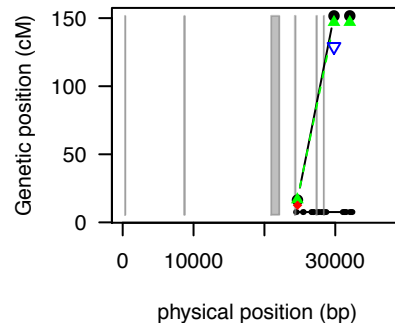
Figure S9



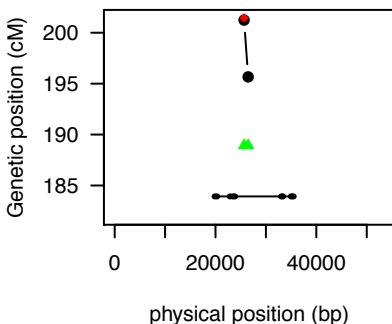
MA_3254: 179.5 cM



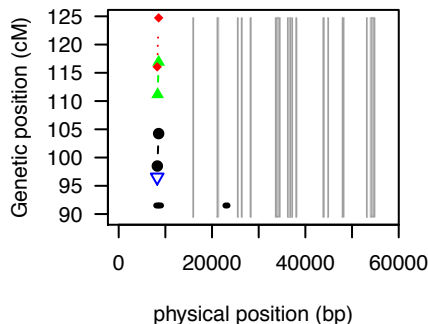
MA_6685: 135.3 cM



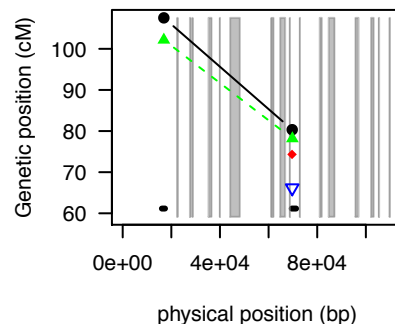
MA_9458: 5.6 cM



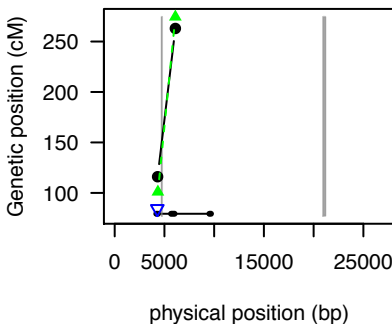
MA_13639: 5.7 cM



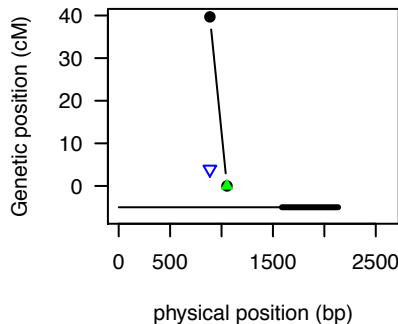
MA_19420: 27.2 cM



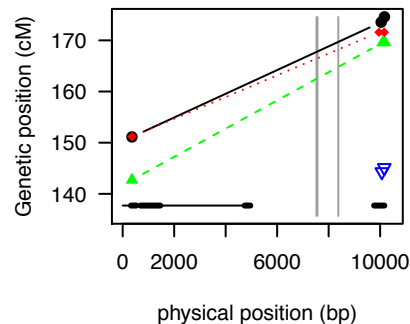
MA_102666: 146.9 cM



MA_281725: 39.7 cM



MA_478788: 23.5 cM



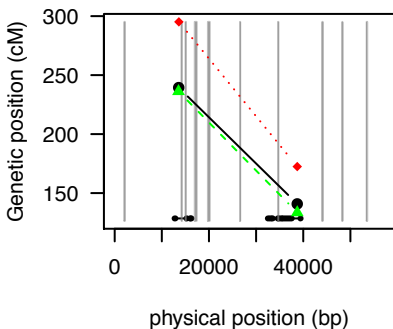
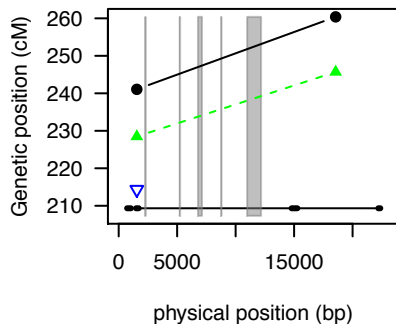
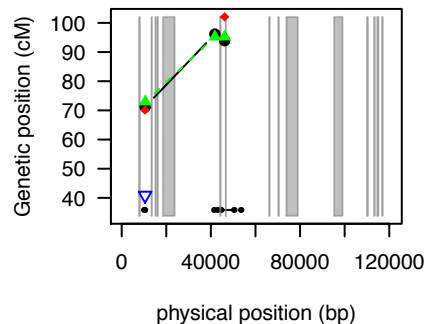
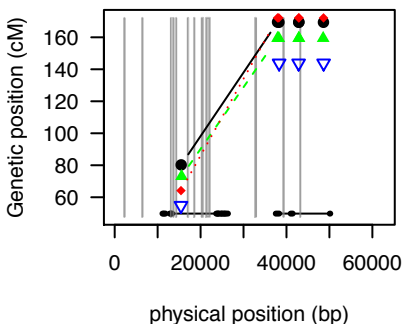
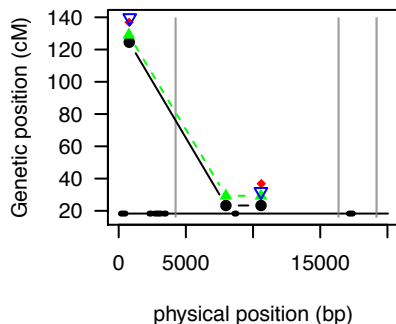
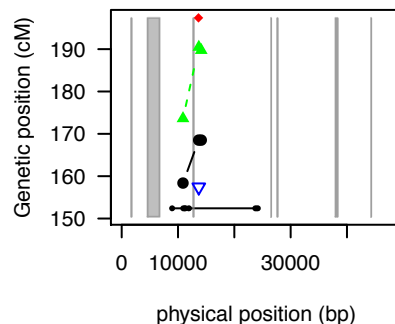
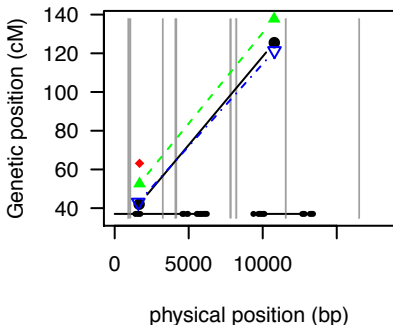
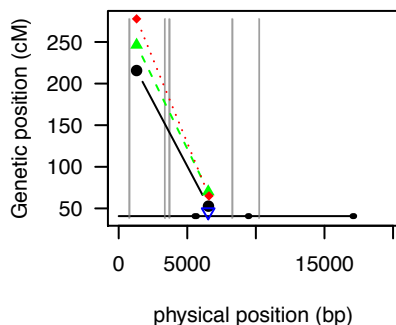
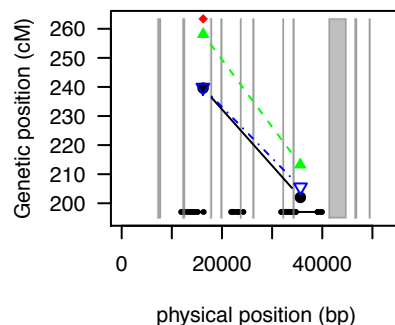
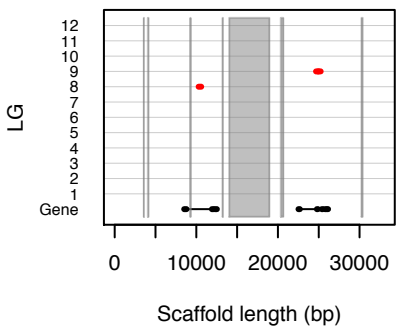
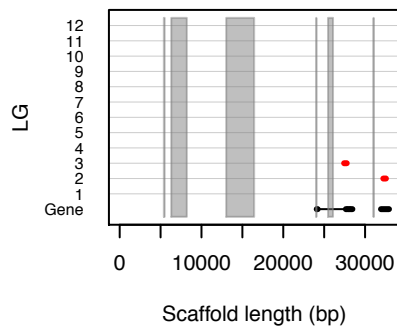
MA_10433250: 98.5 cM**MA_10435318: 19.3 cM****MA_10435645: 25 cM****MA_10435921: 89.3 cM****MA_10436779: 101.2 cM****MA_10436848: 10.1 cM****MA_10437069: 83.5 cM****MA_10437161: 163 cM****MA_10437163: 37.6 cM**

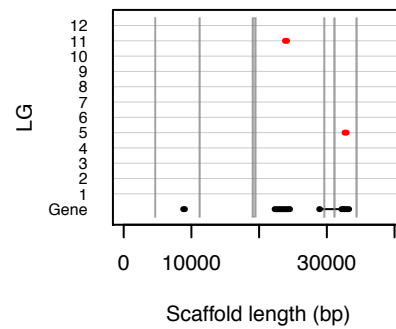
Figure S10 **MA_10096**



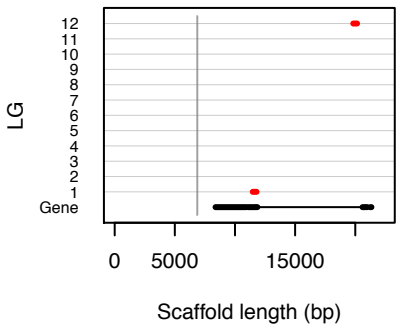
MA_10425884



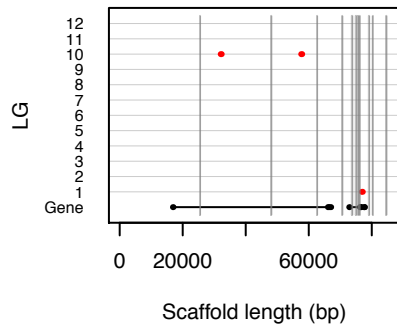
MA_10426261



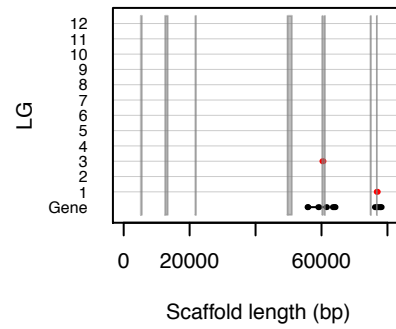
MA_10426430



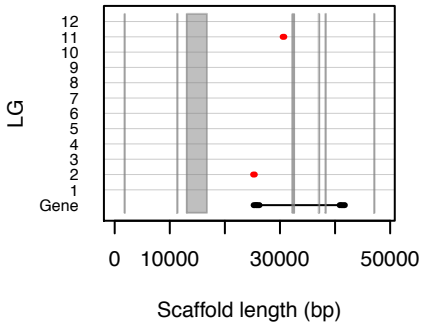
MA_10426627



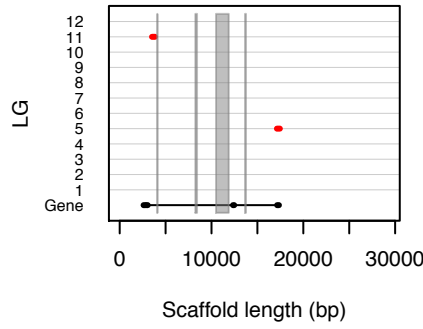
MA_10426701



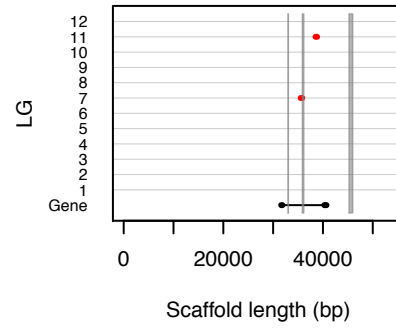
MA_10426933



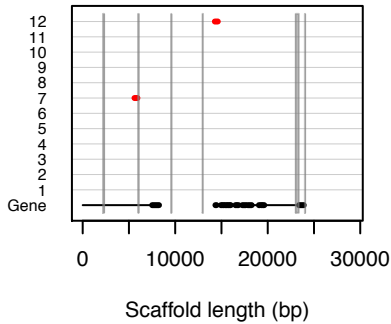
MA_10427077



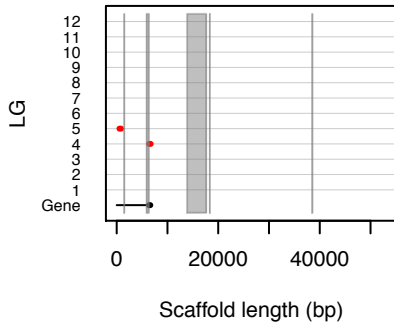
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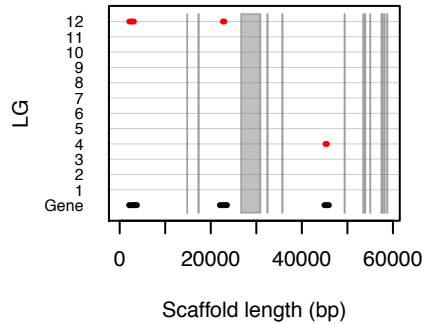
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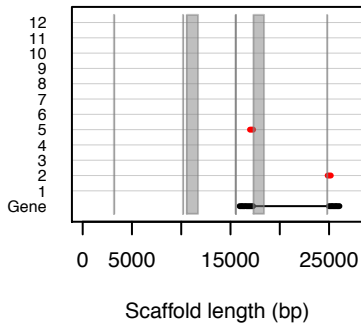
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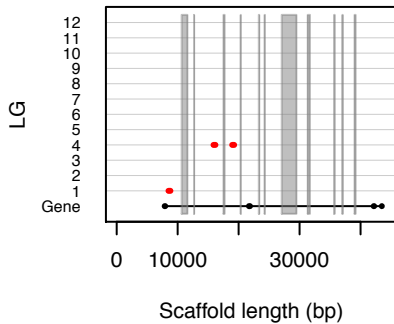
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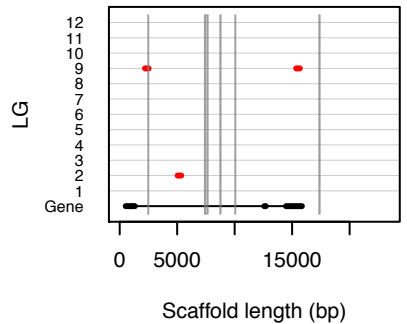
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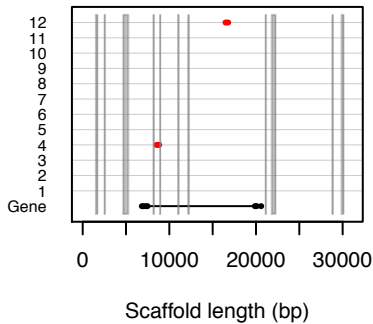
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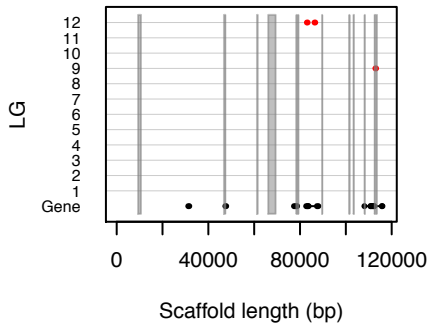
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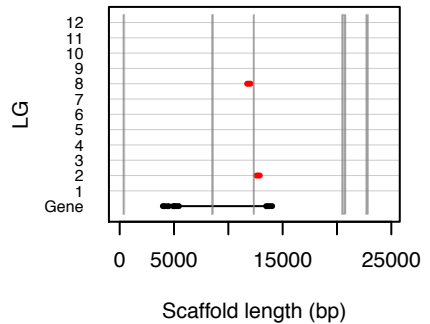
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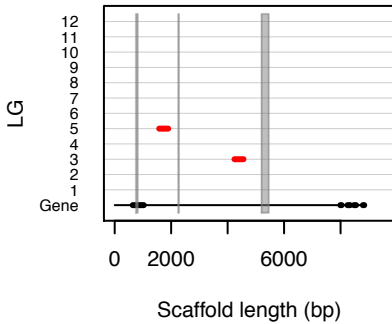
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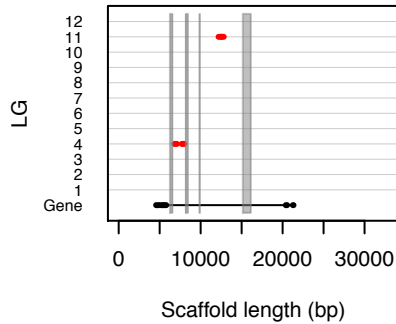
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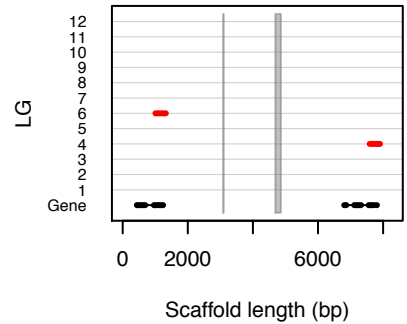
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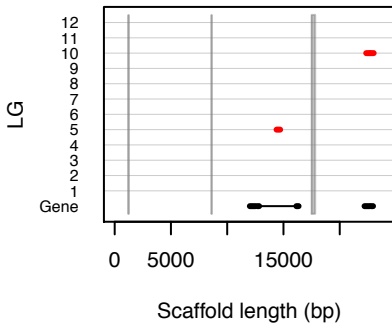
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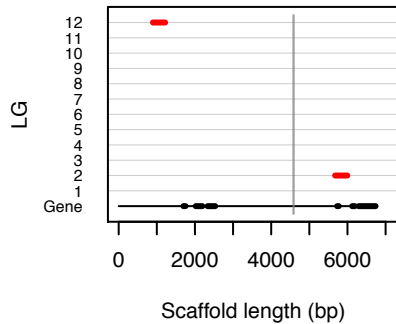
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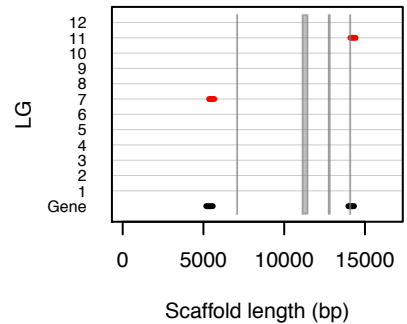
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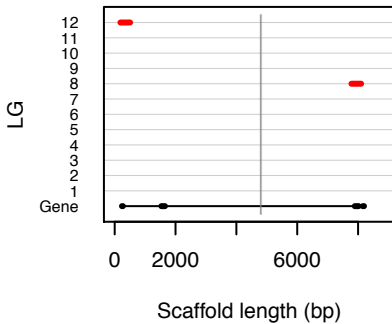
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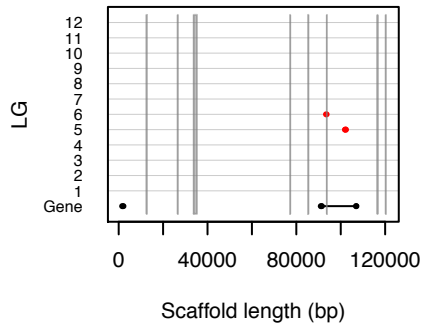
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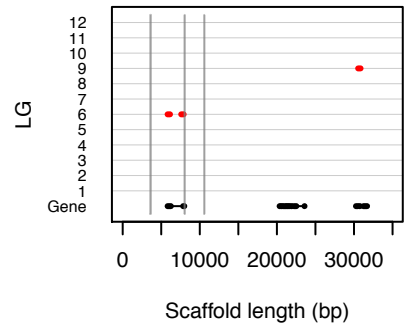
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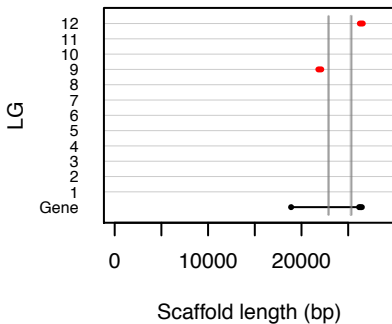
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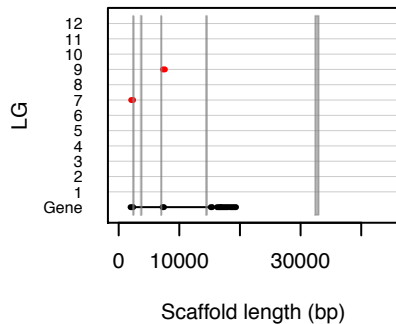
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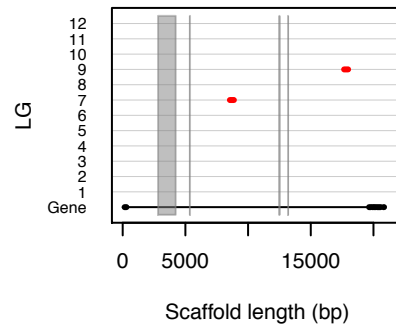
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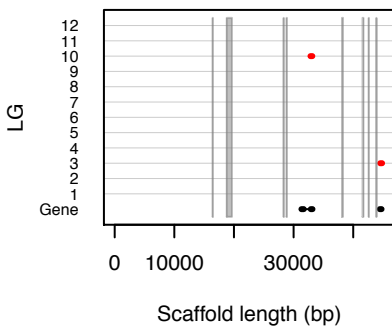
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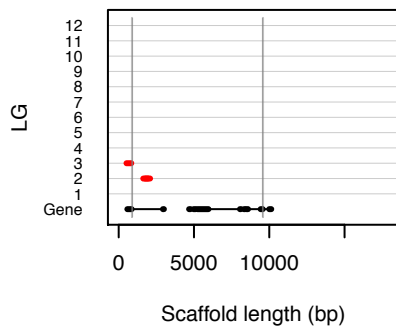
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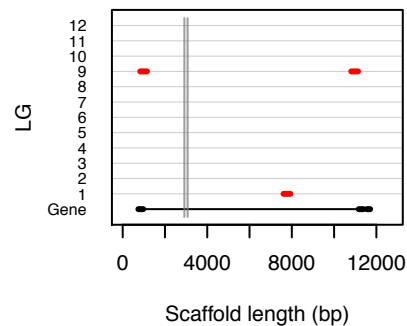
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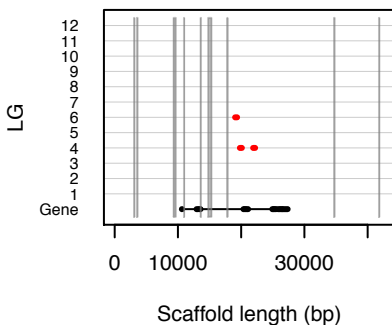
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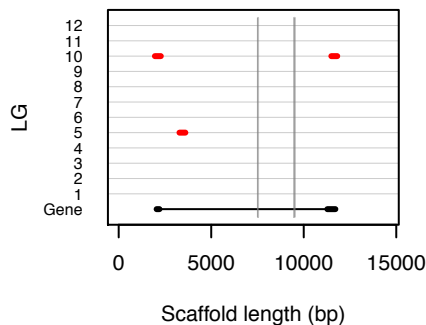
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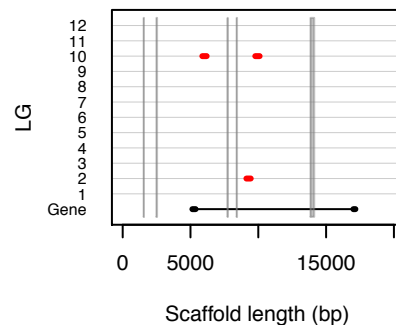
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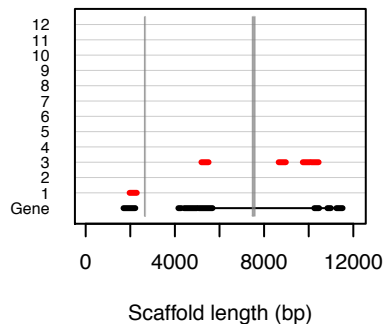
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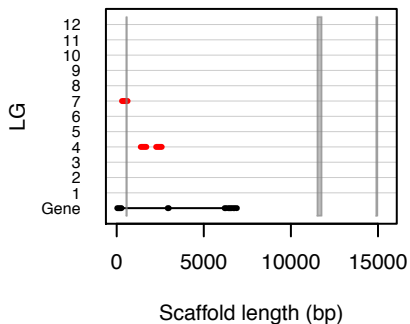
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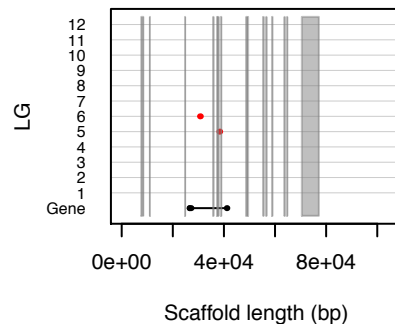
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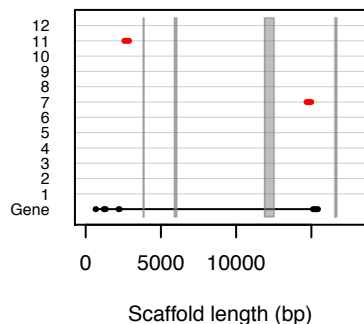
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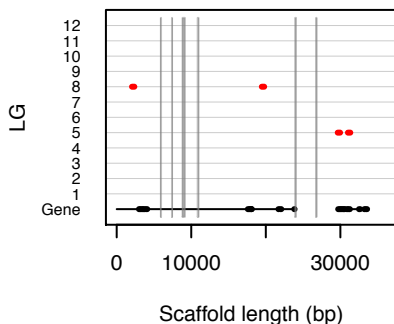
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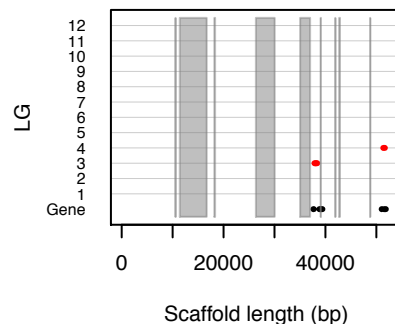
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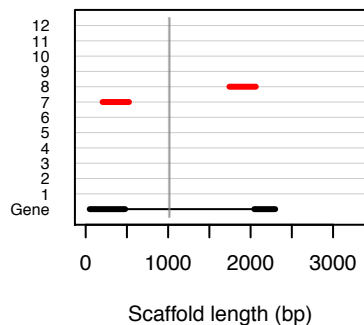
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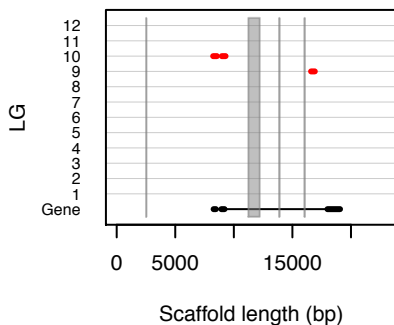
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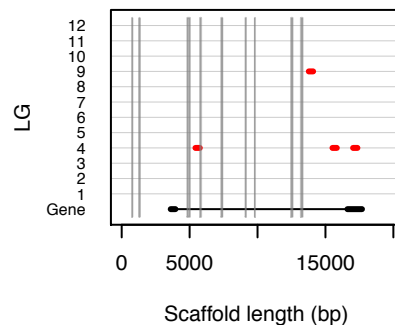
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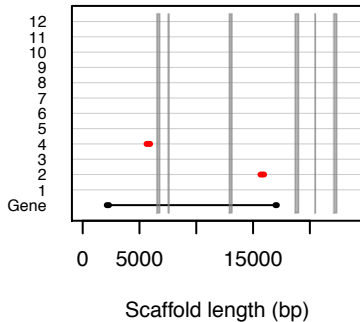
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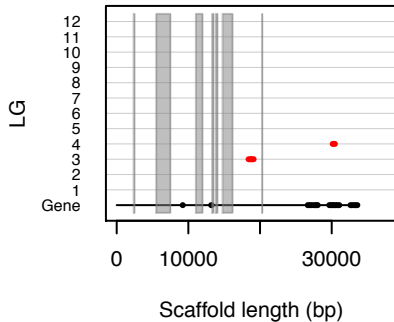
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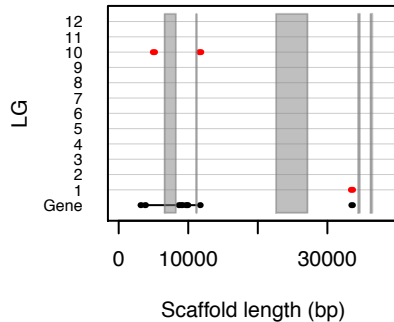
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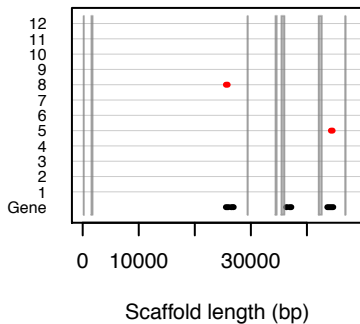
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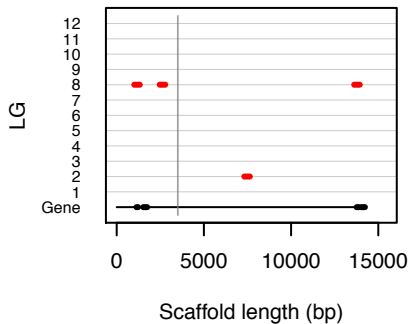
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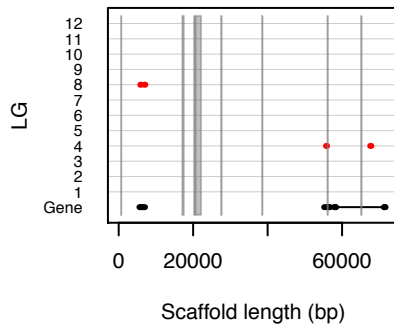
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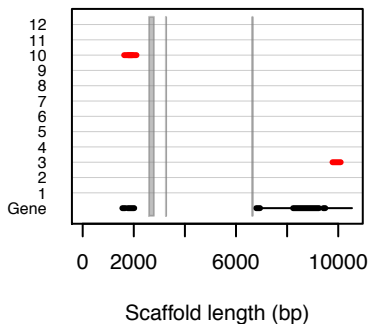
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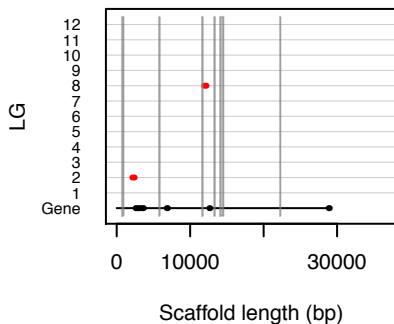
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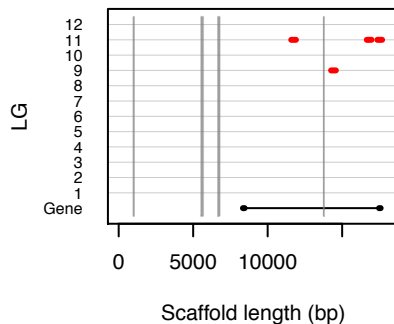
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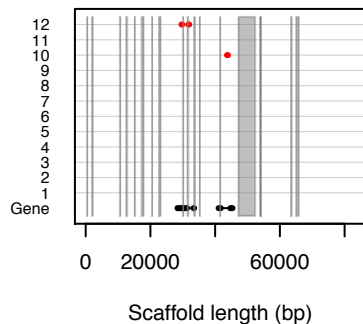
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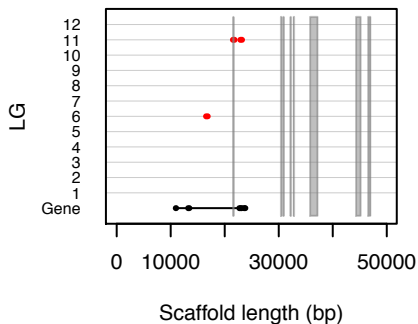
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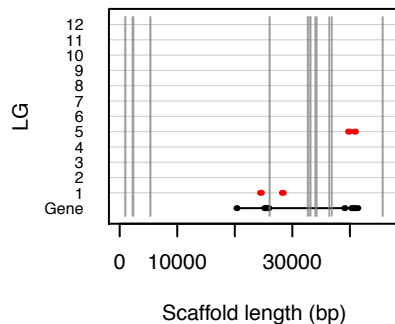
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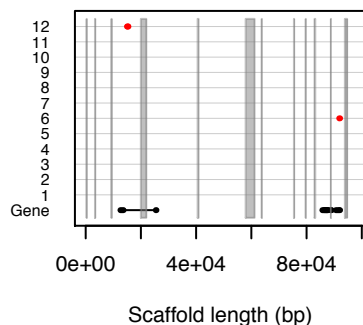
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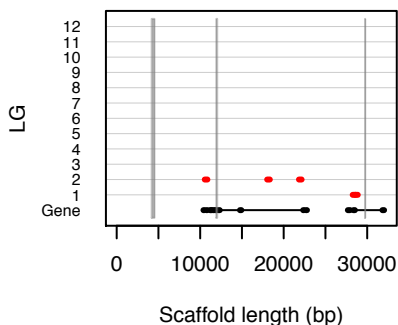
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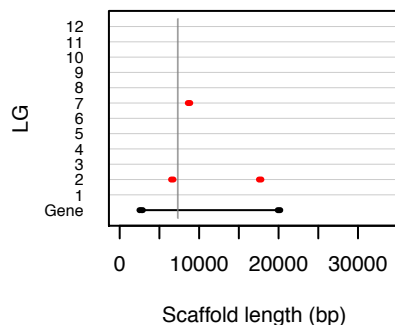
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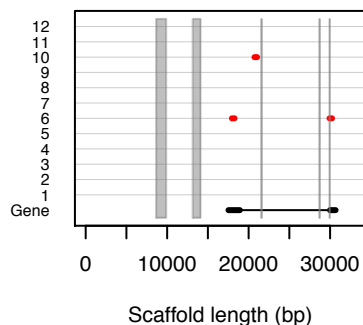
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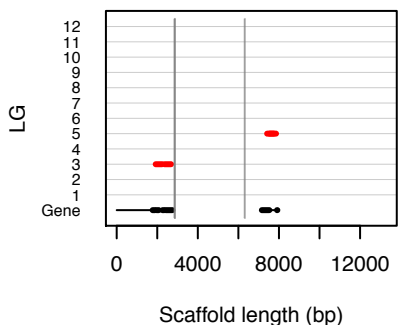
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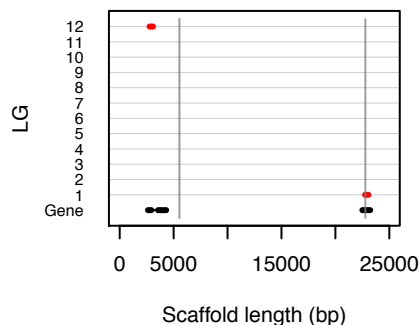
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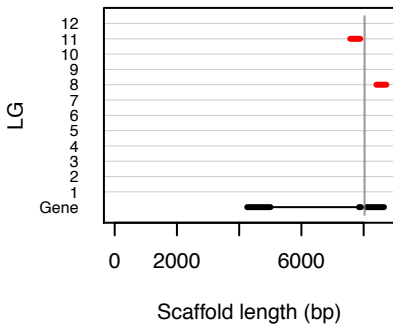
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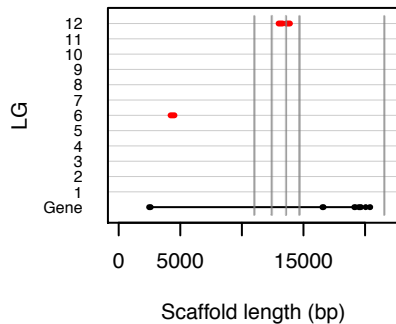
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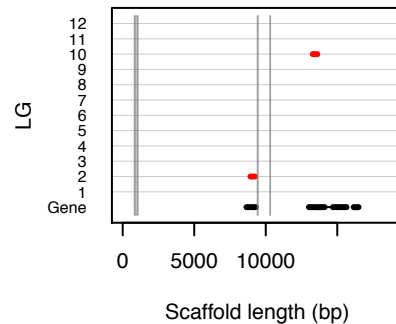
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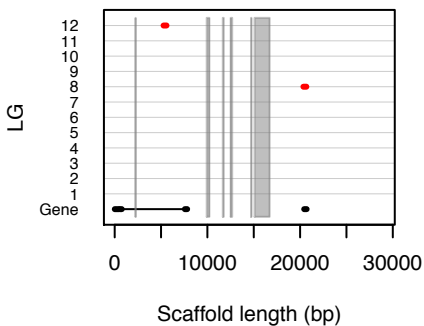
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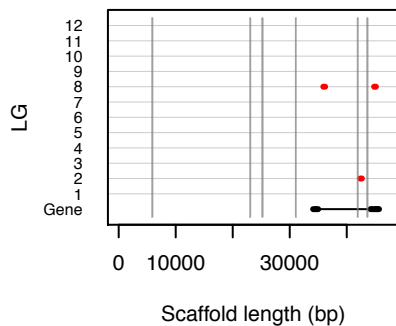
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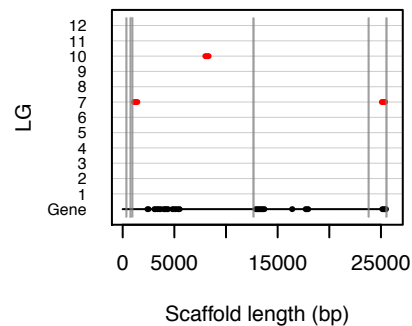
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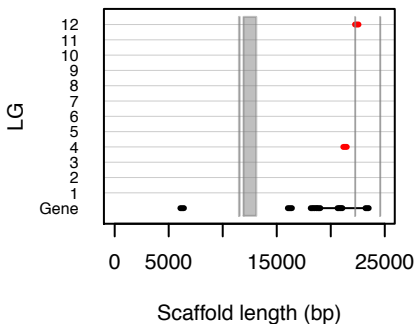
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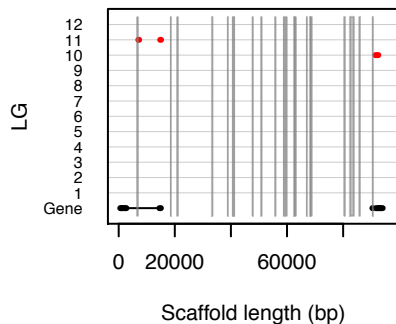
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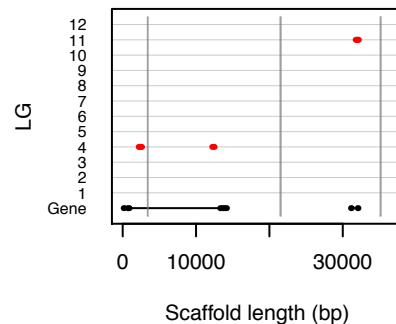
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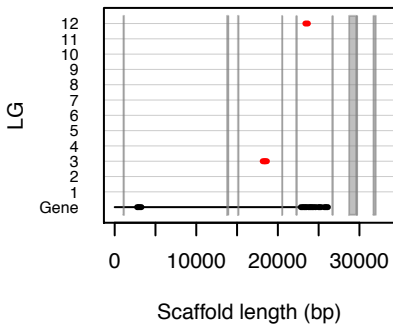
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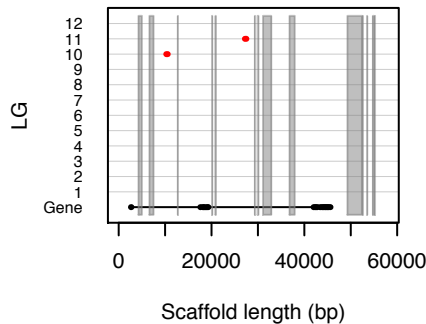
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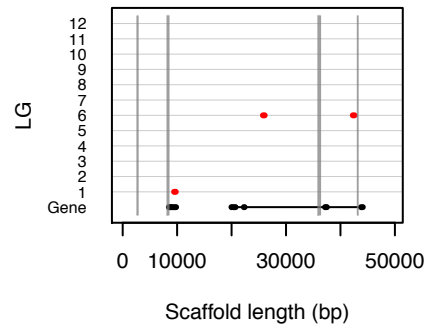
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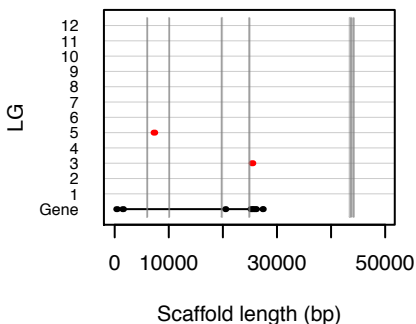
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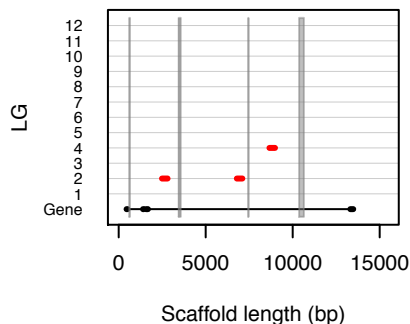
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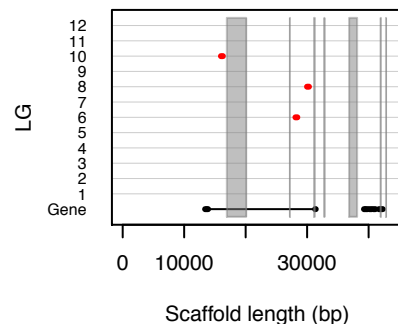
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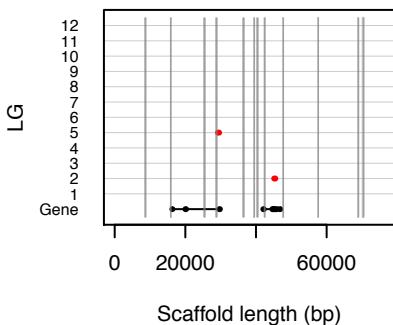
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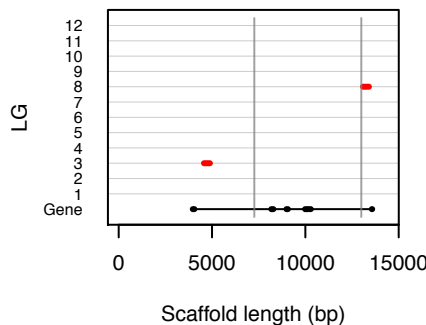
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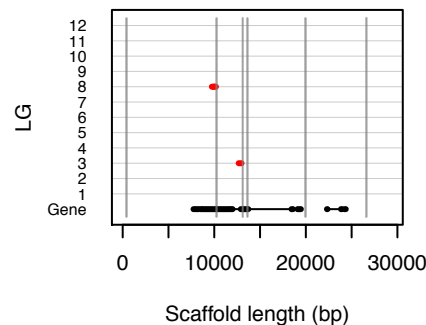
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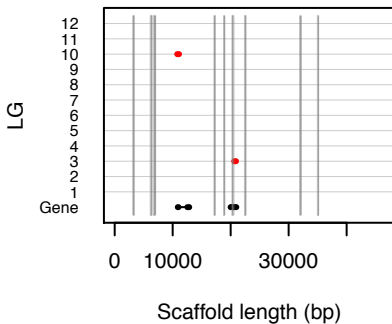
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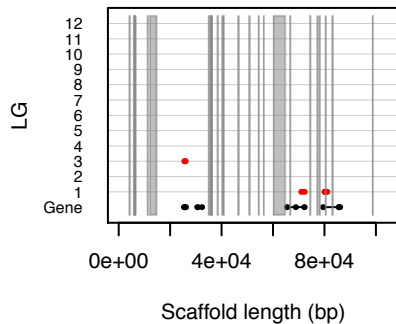
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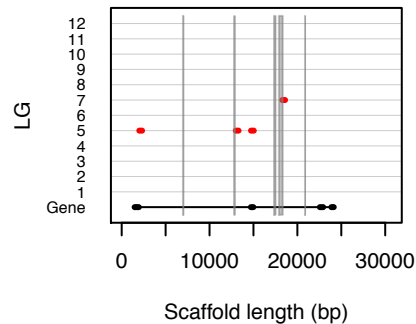
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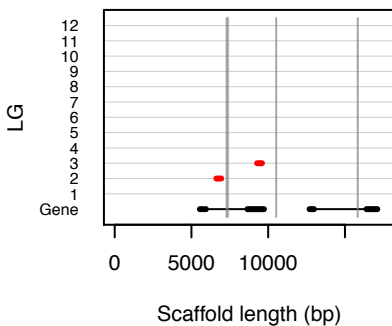
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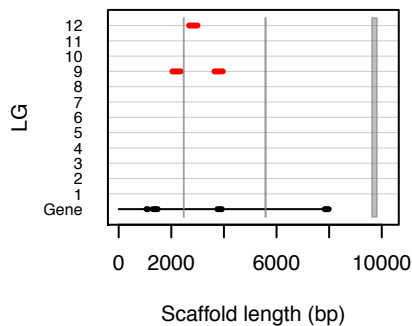
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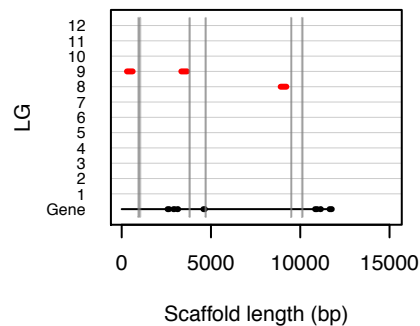
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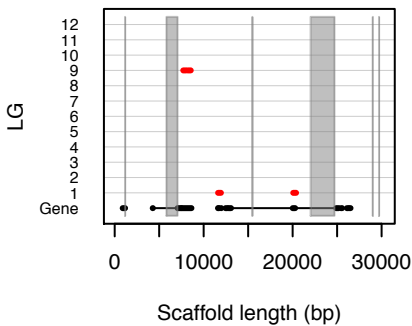
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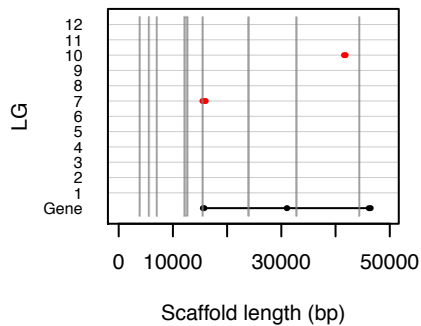
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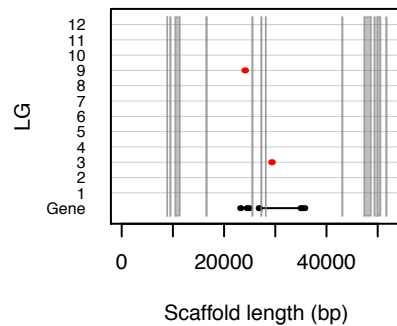
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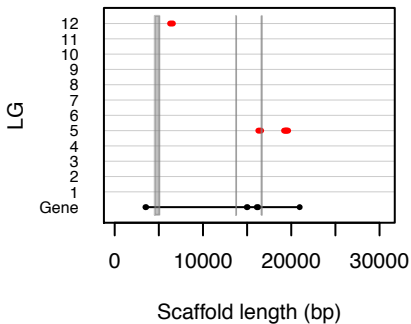
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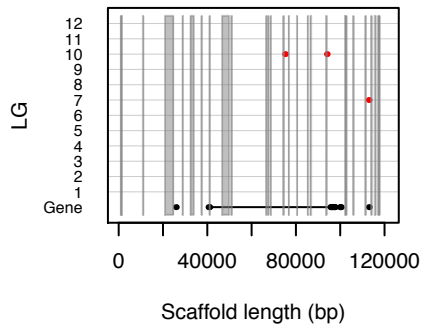
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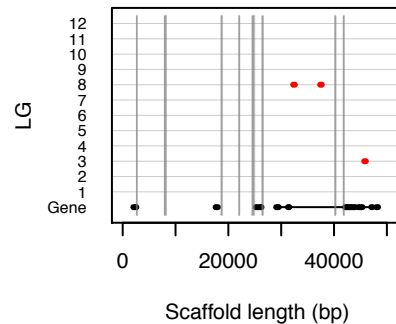
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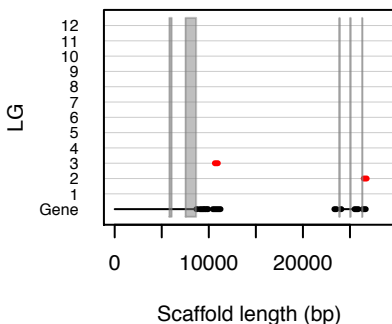
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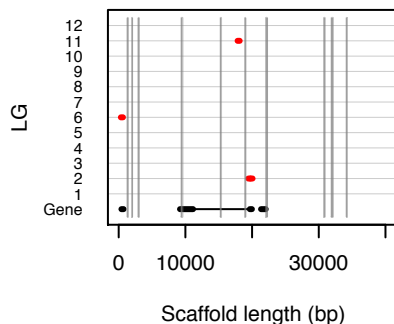
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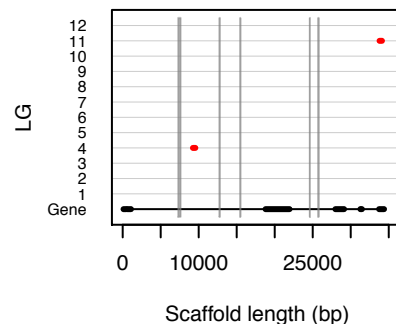
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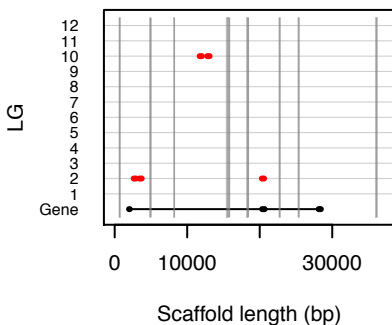
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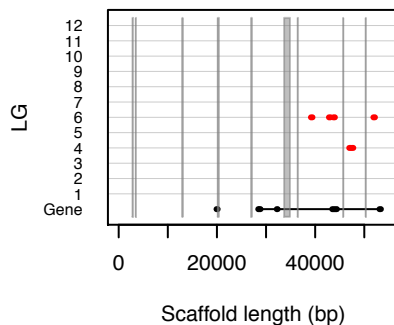
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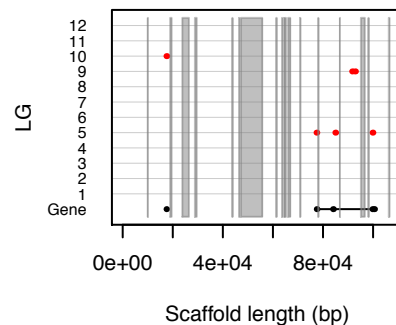
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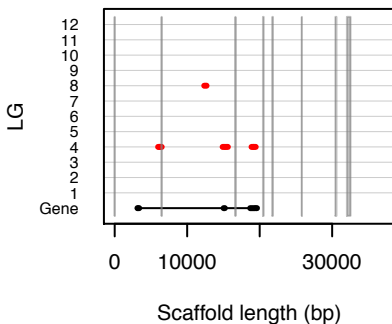
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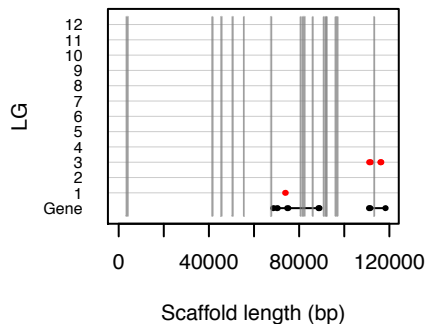
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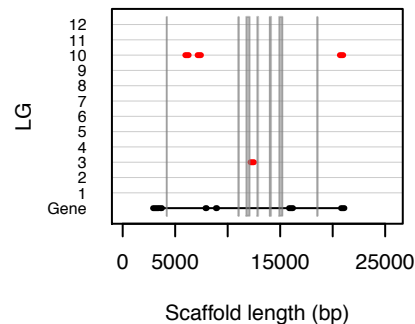
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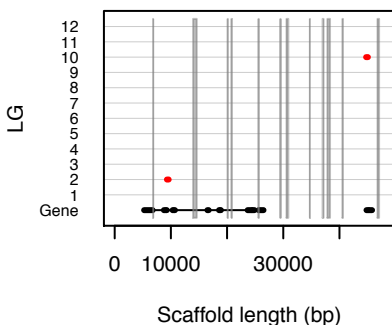
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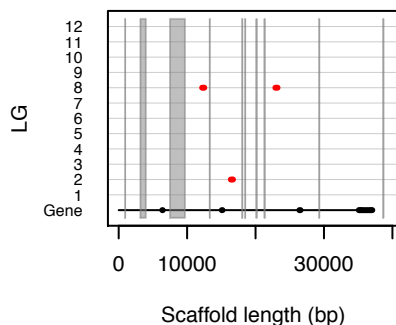
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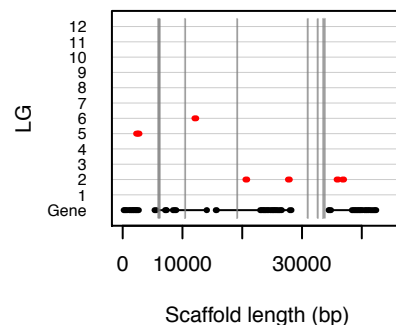
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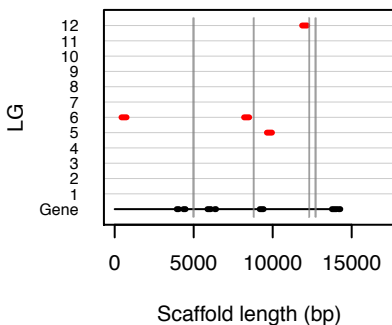
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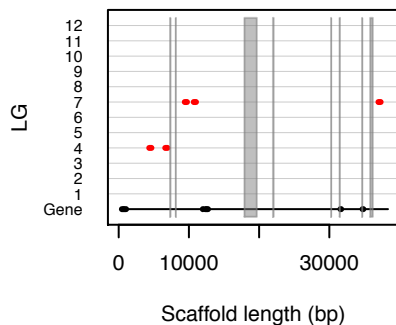
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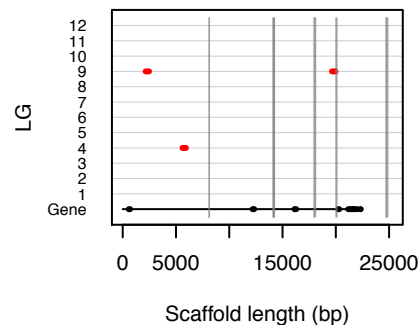
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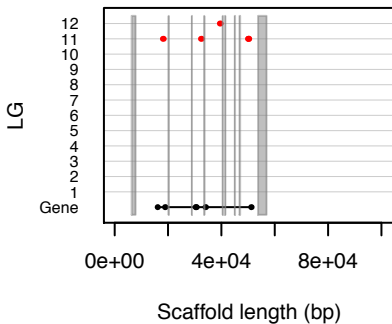
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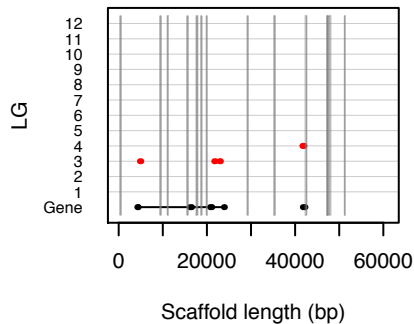
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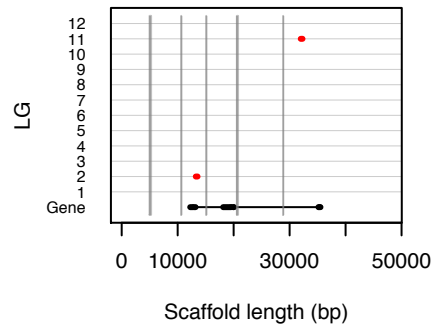
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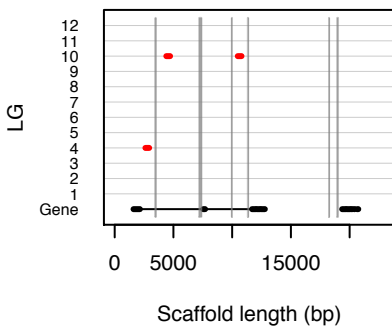
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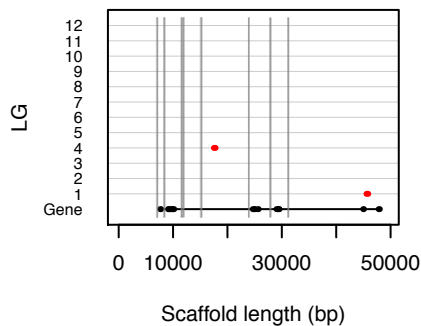
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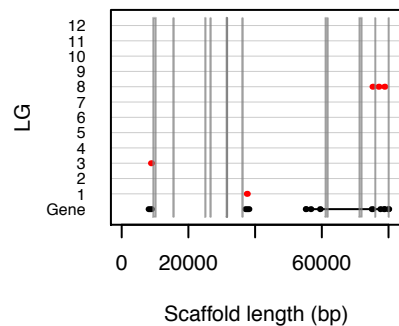
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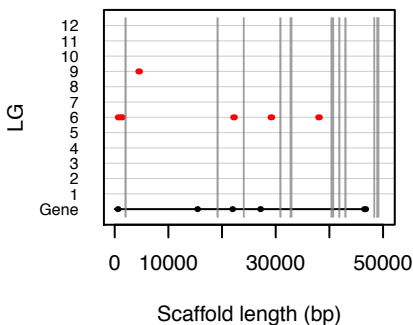
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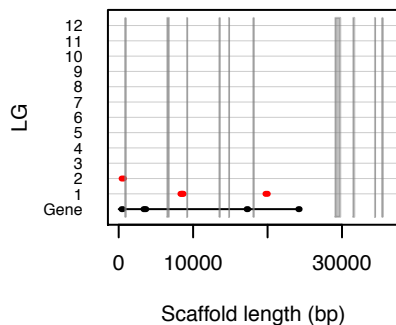
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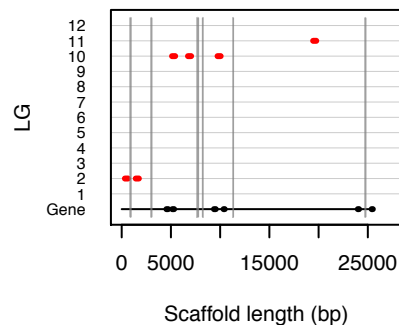
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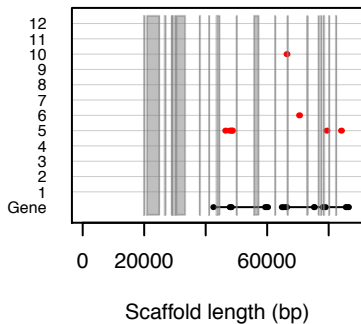
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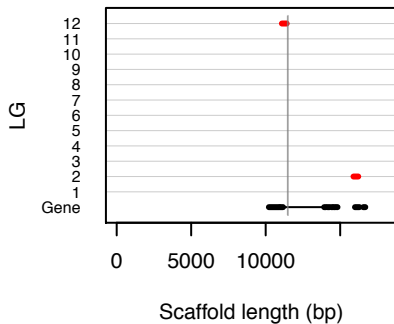
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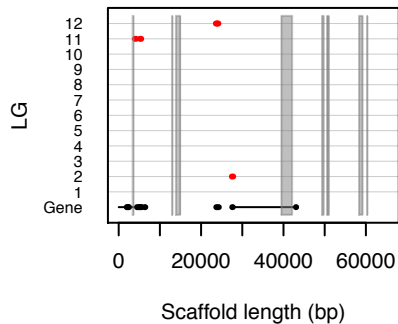
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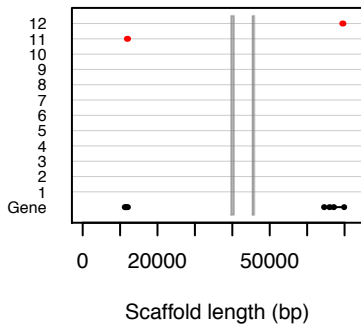
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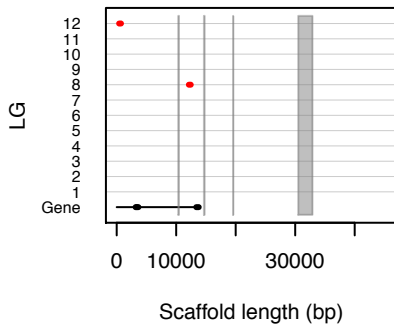
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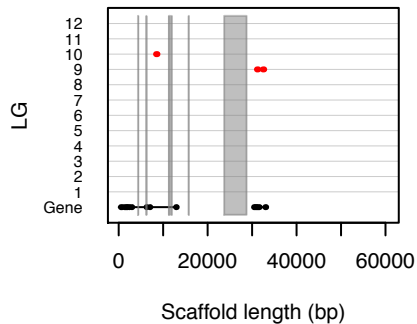
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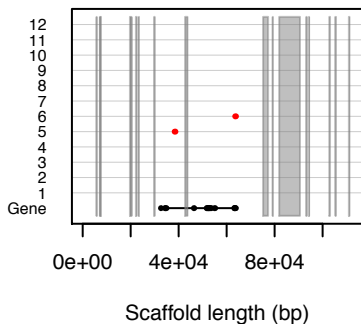
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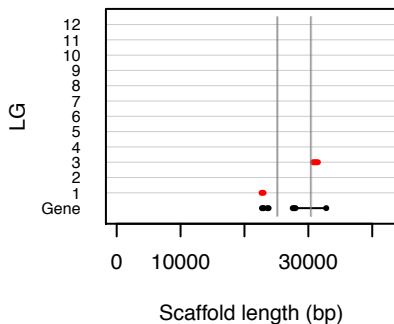
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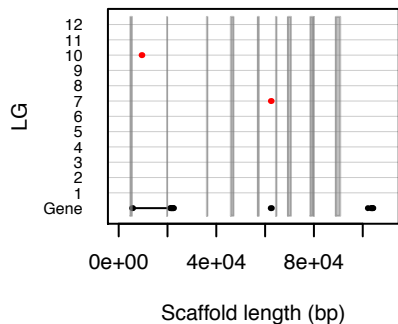
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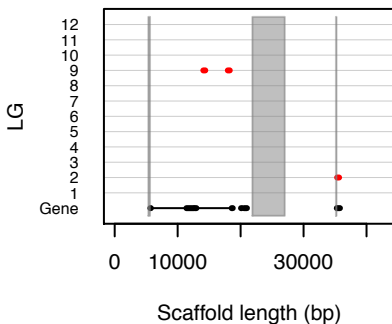
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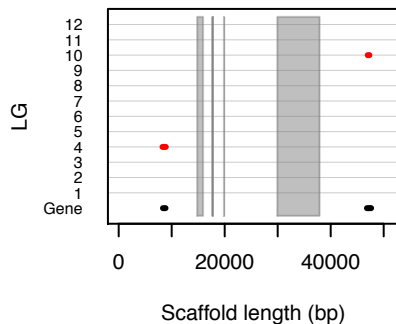
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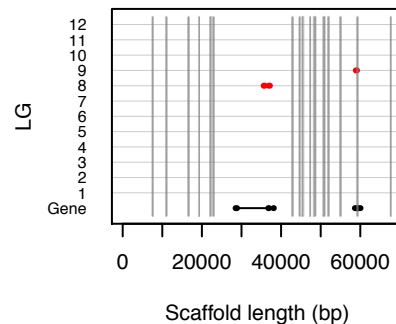
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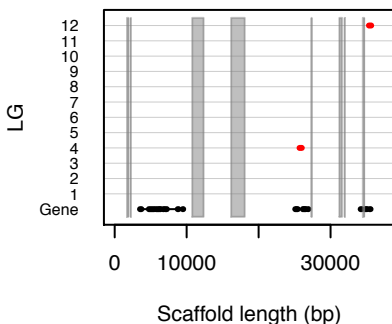
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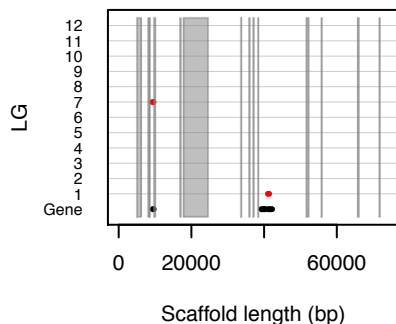
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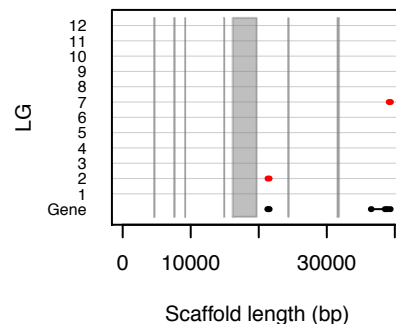
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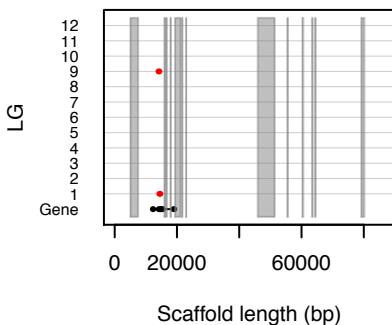
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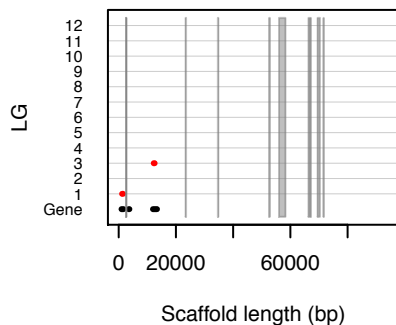
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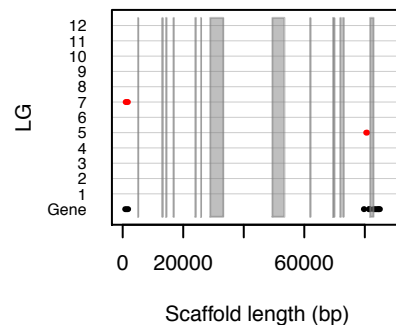
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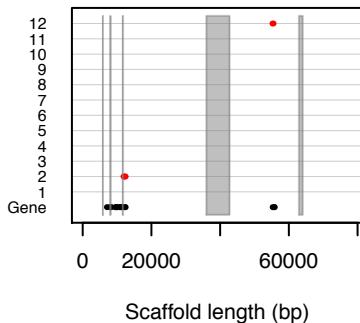
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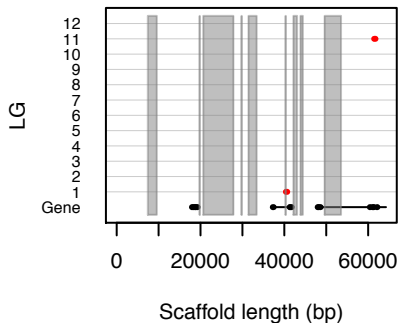
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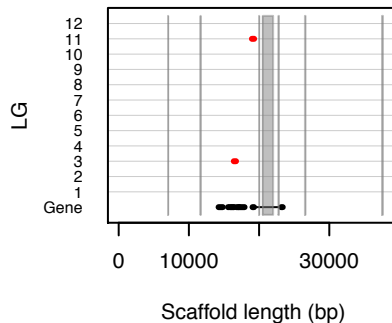
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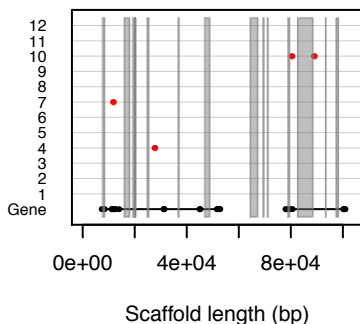
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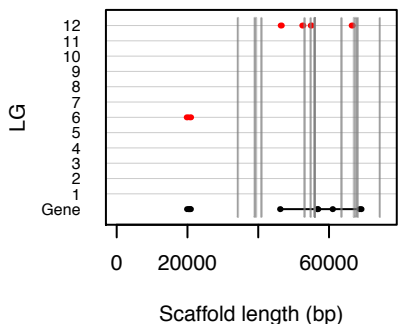
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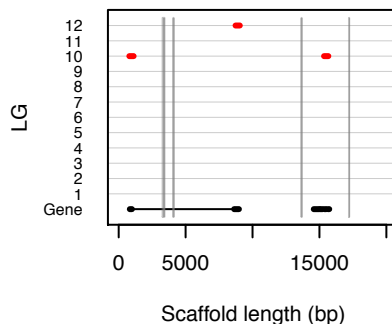
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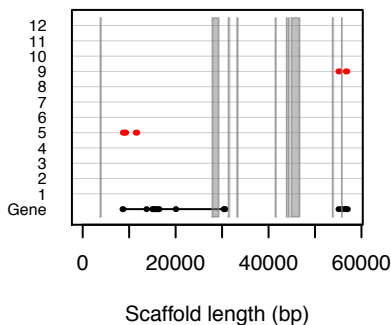
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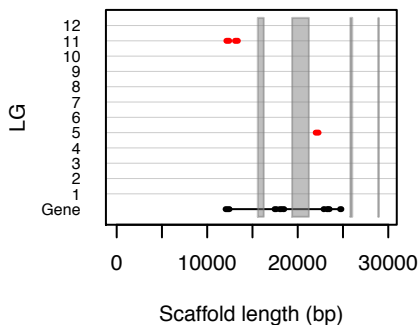
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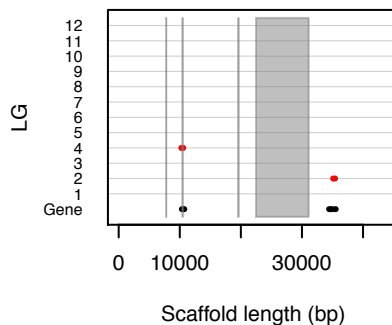
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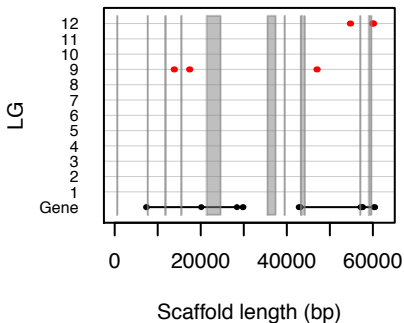
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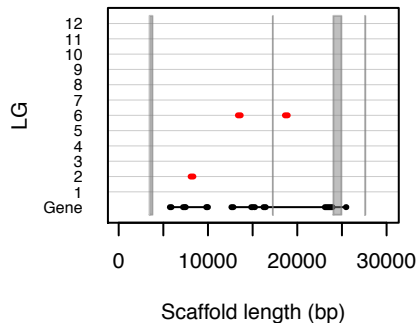
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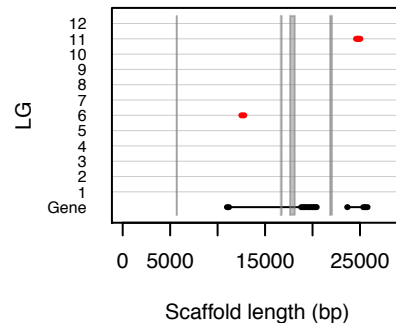
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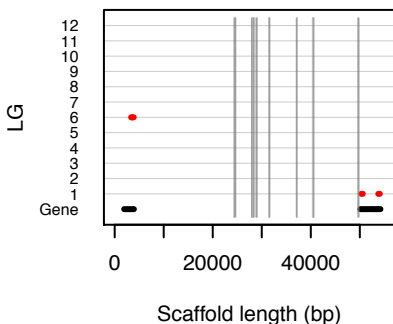
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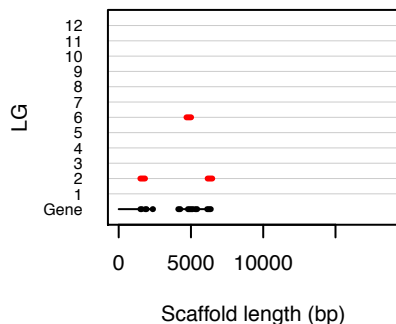
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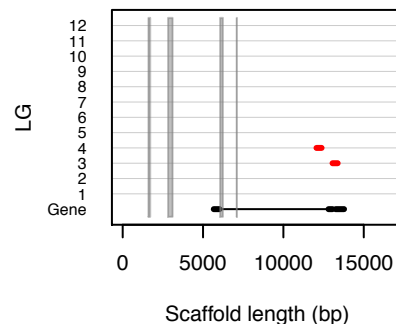
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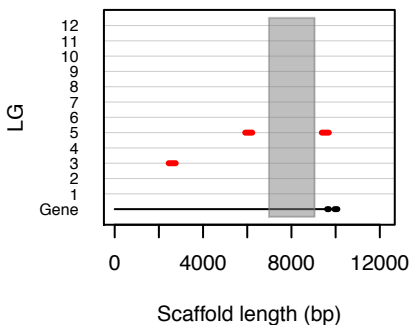
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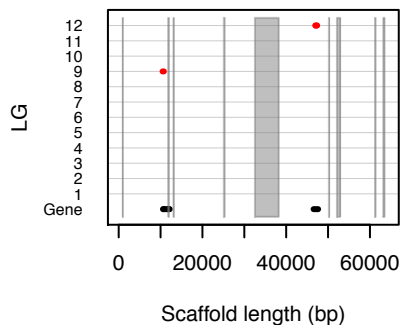
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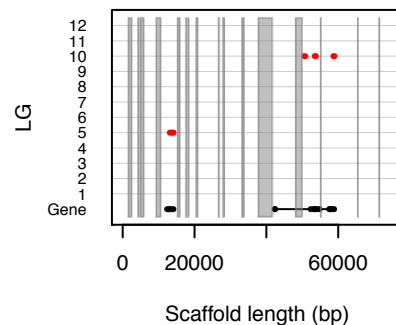
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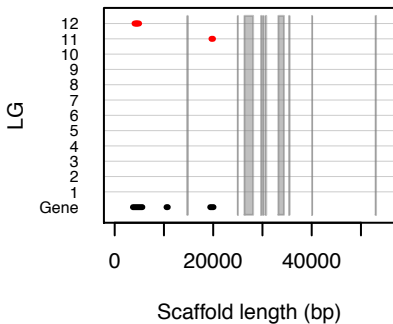
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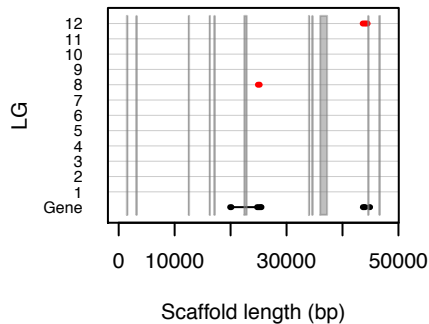
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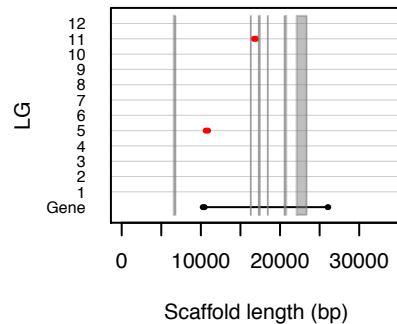
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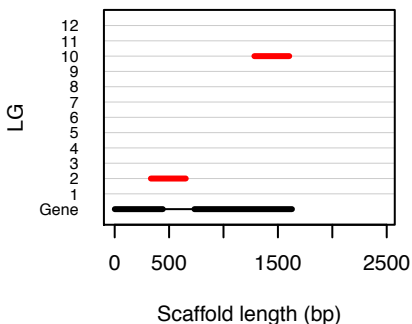
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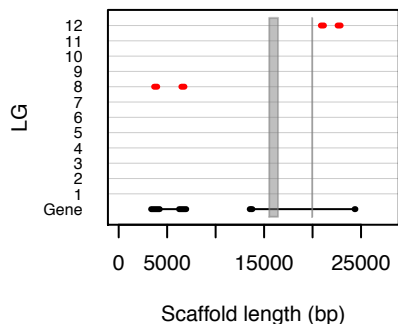
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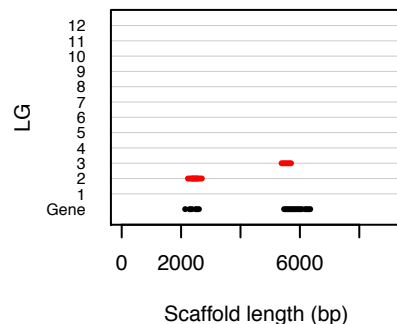
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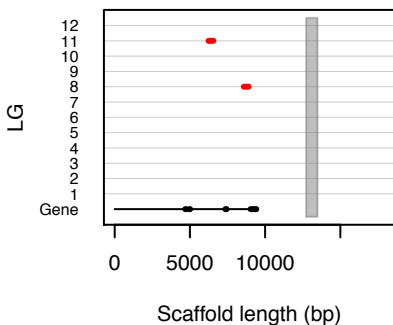
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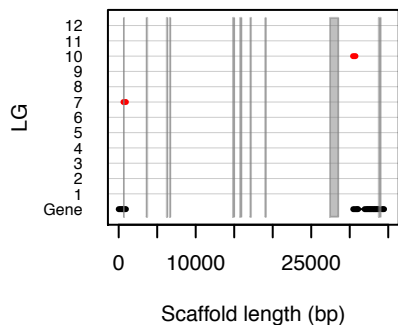
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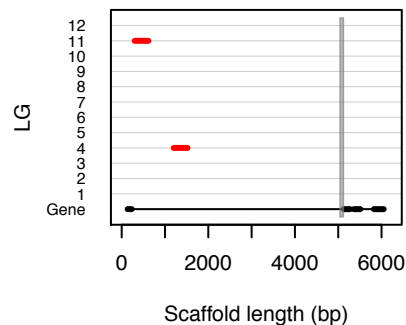
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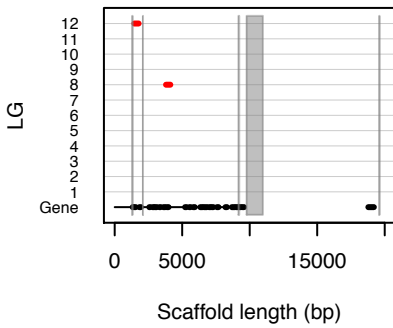
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MA_842474



MA_87238



MA_96038

