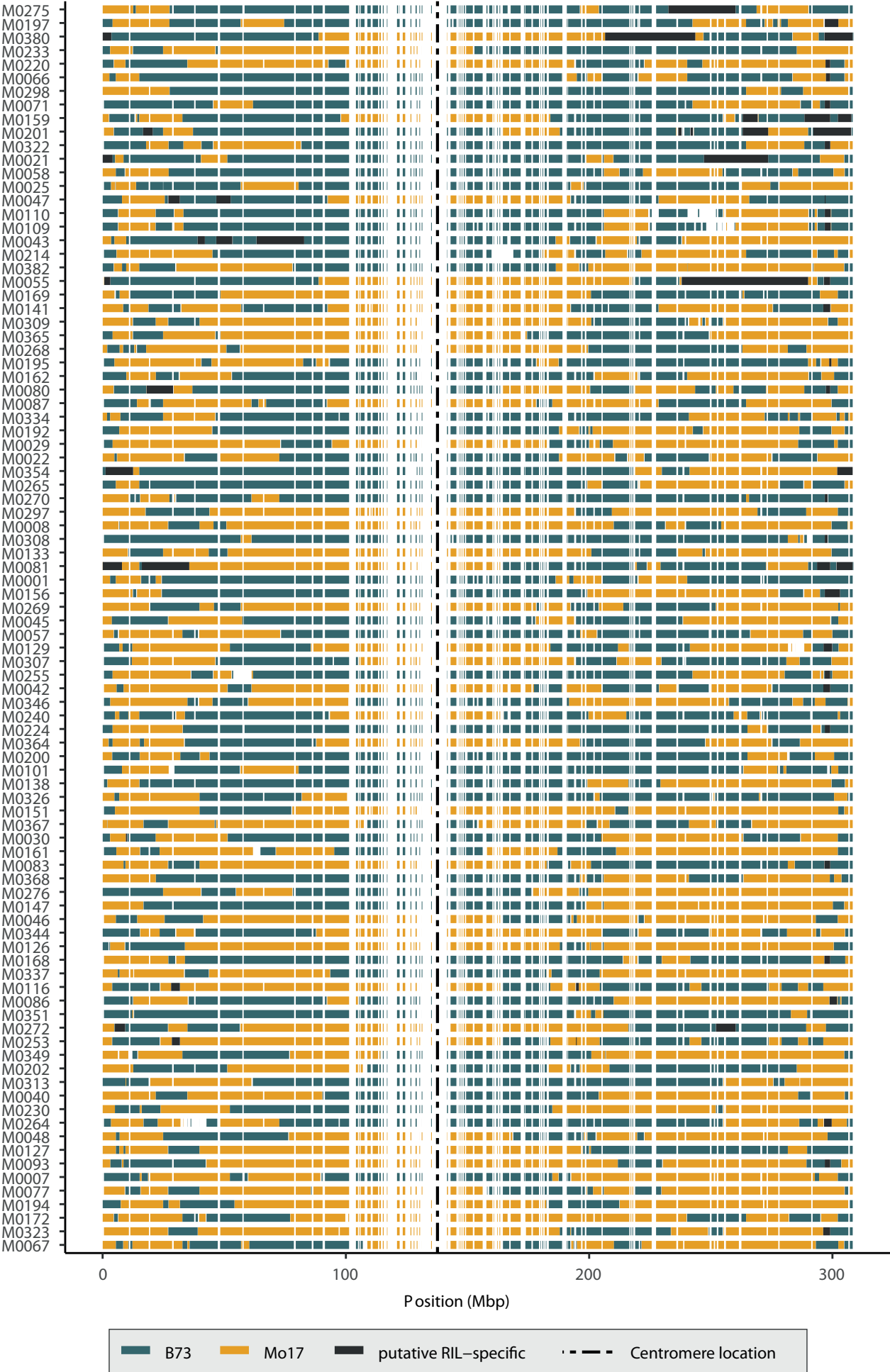
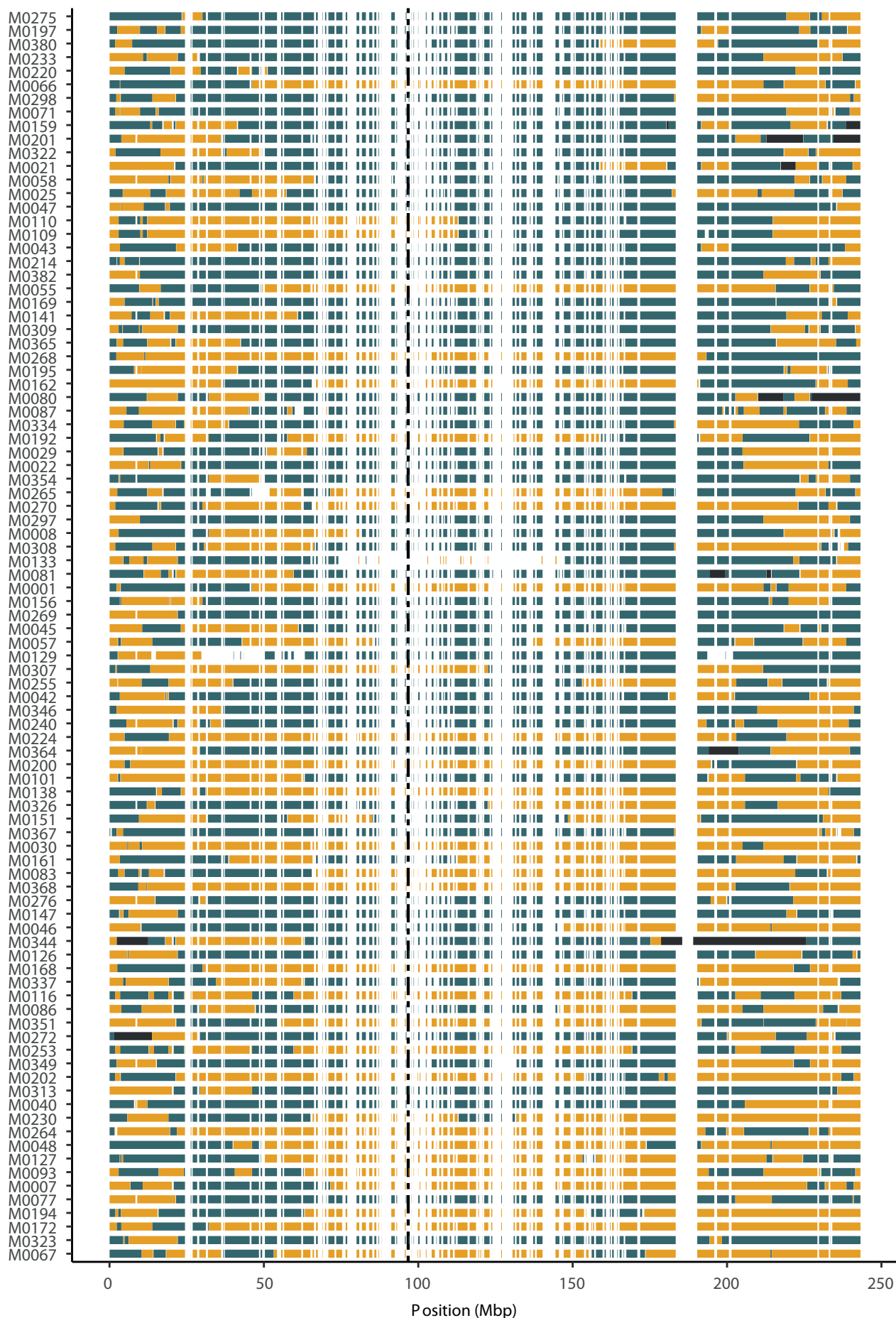


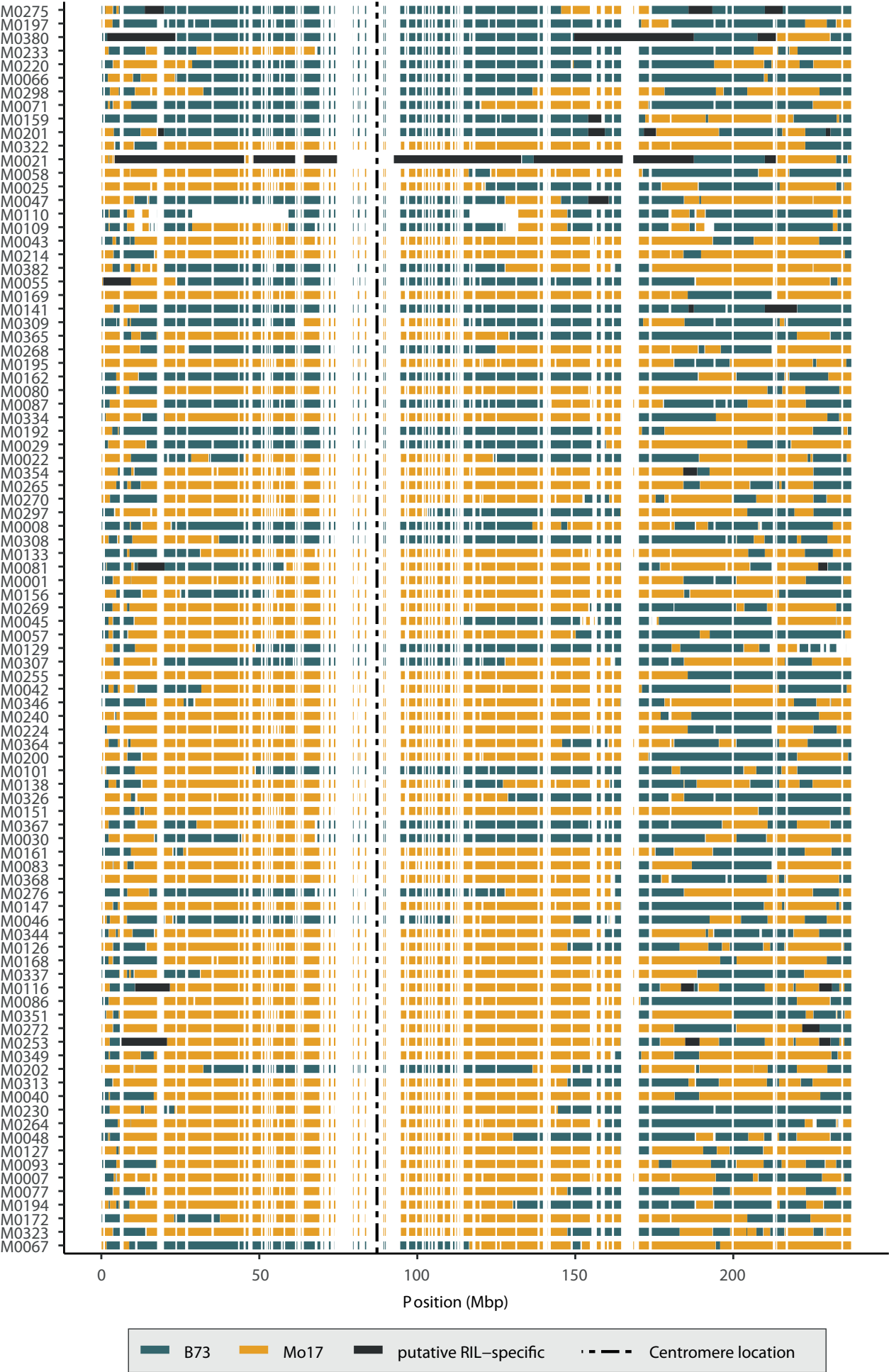
Chromosome 1



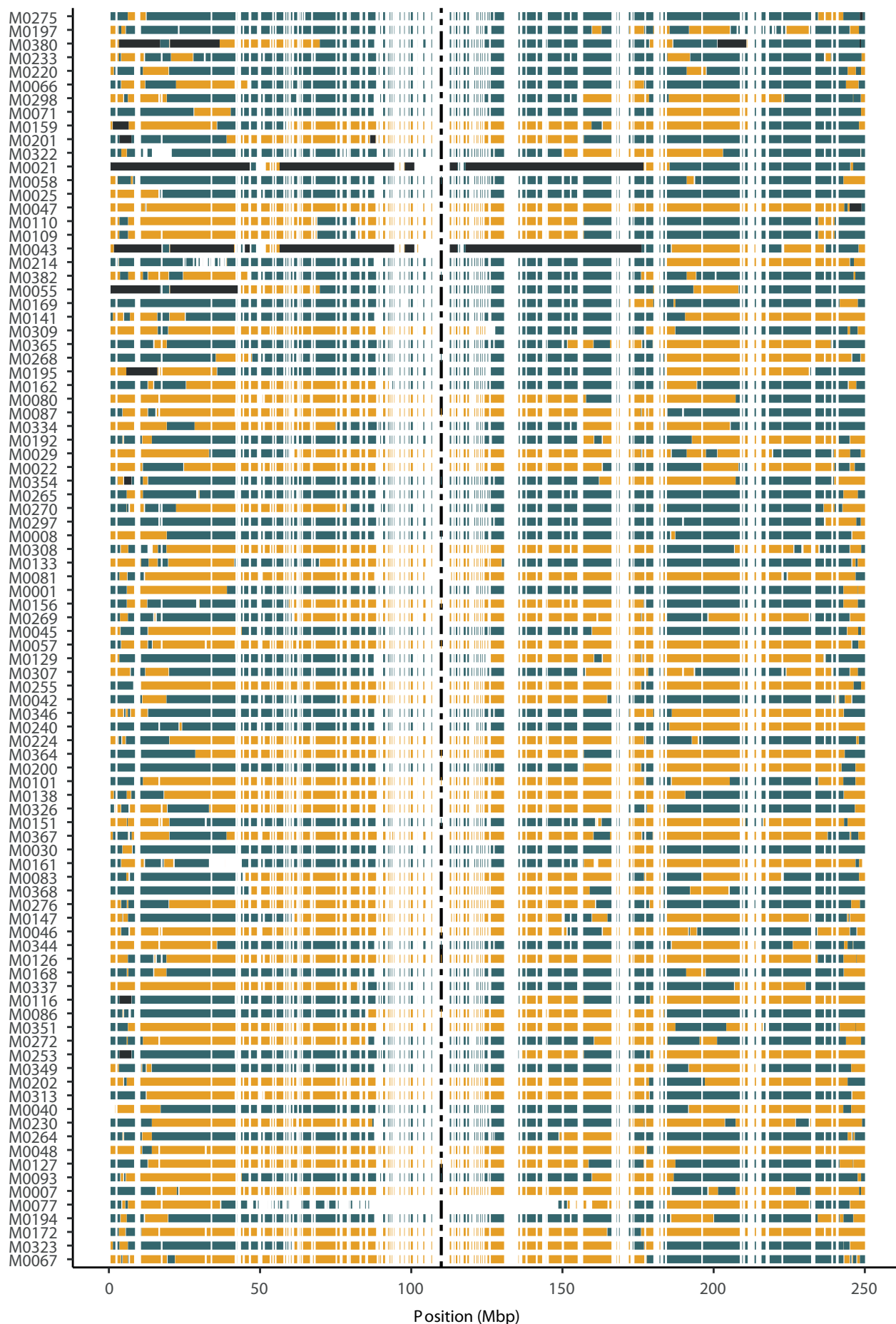
## Chromosome 2



Chromosome 3

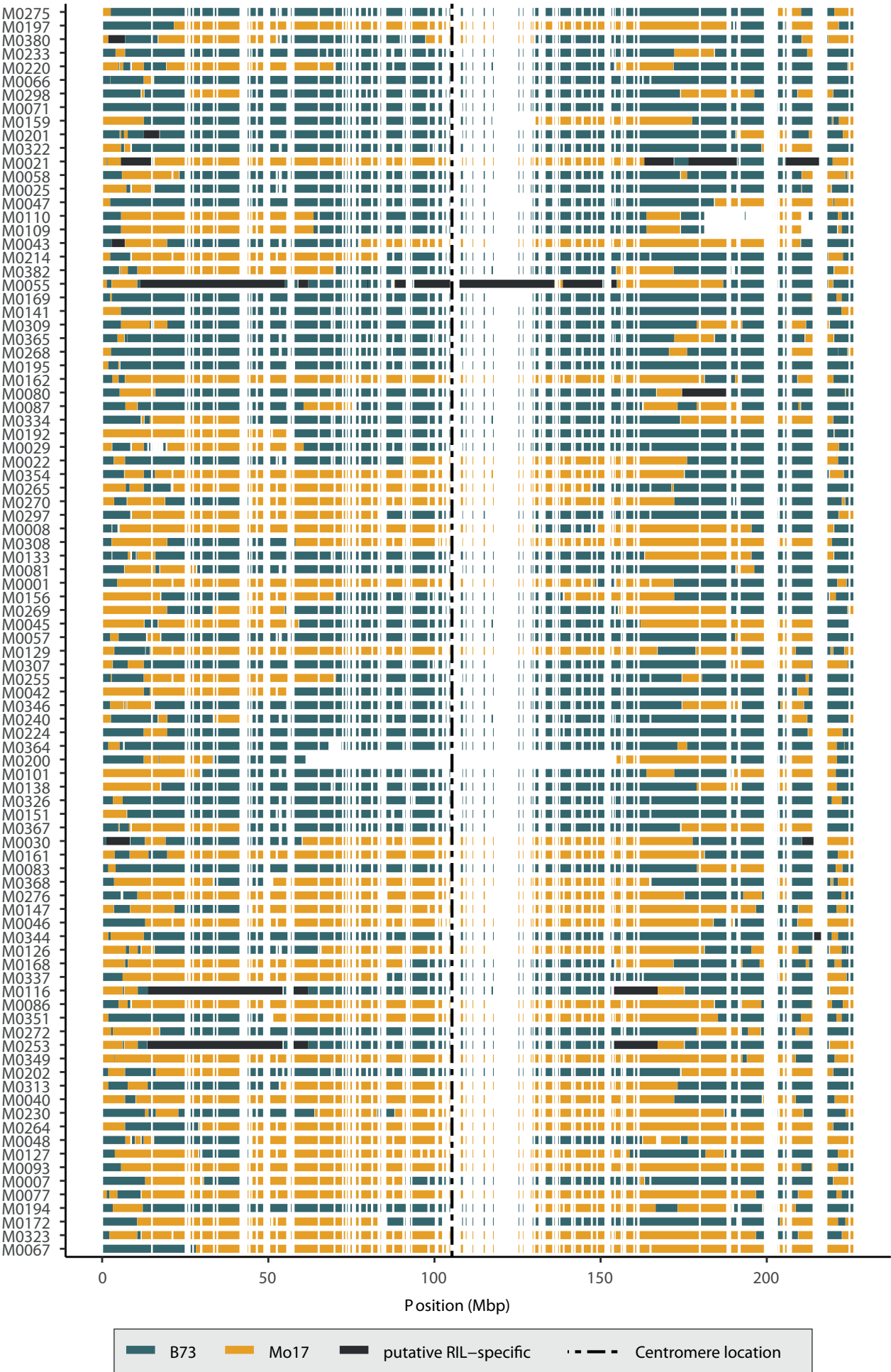


## Chromosome 4

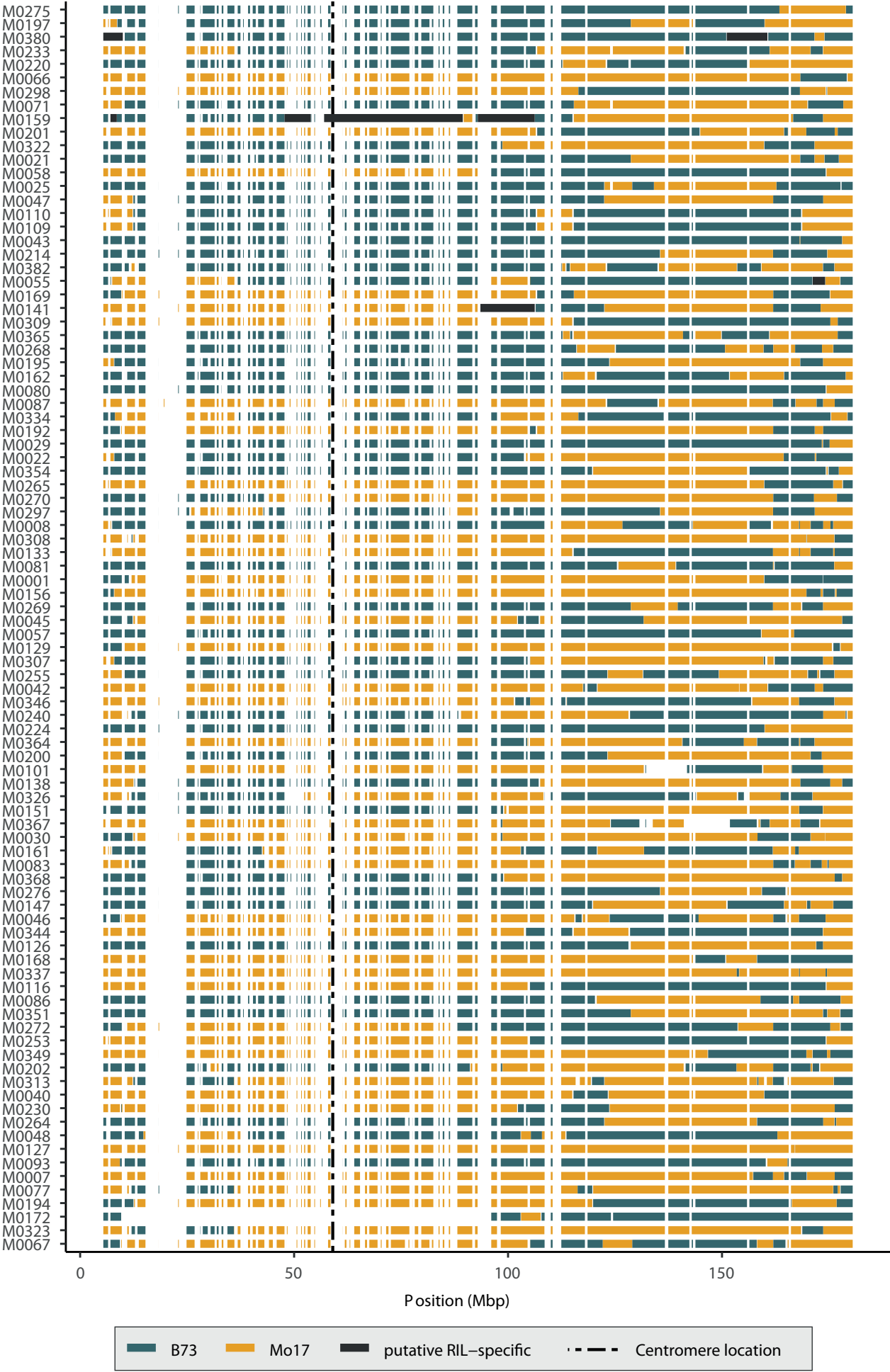




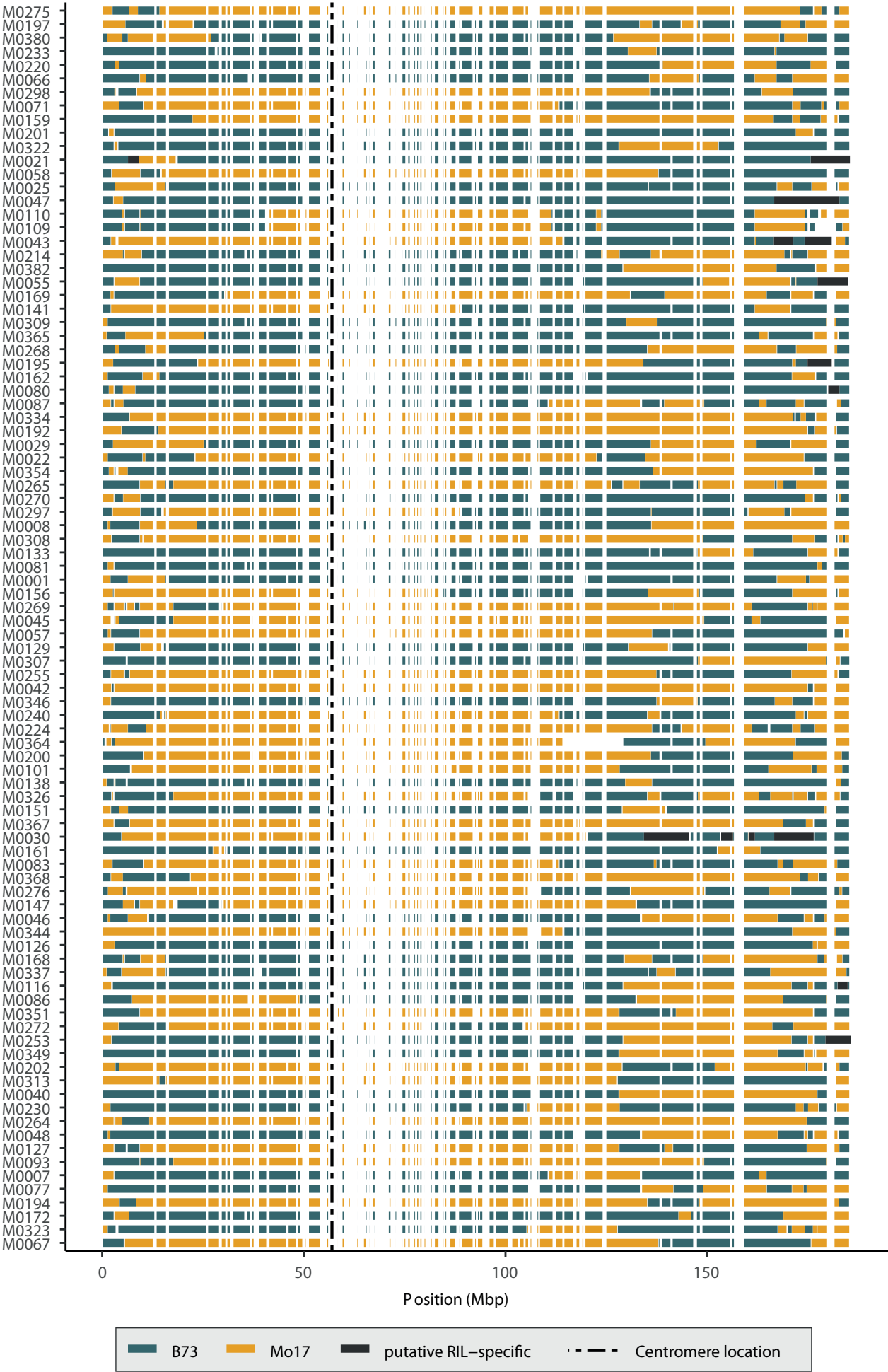
Chromosome 5



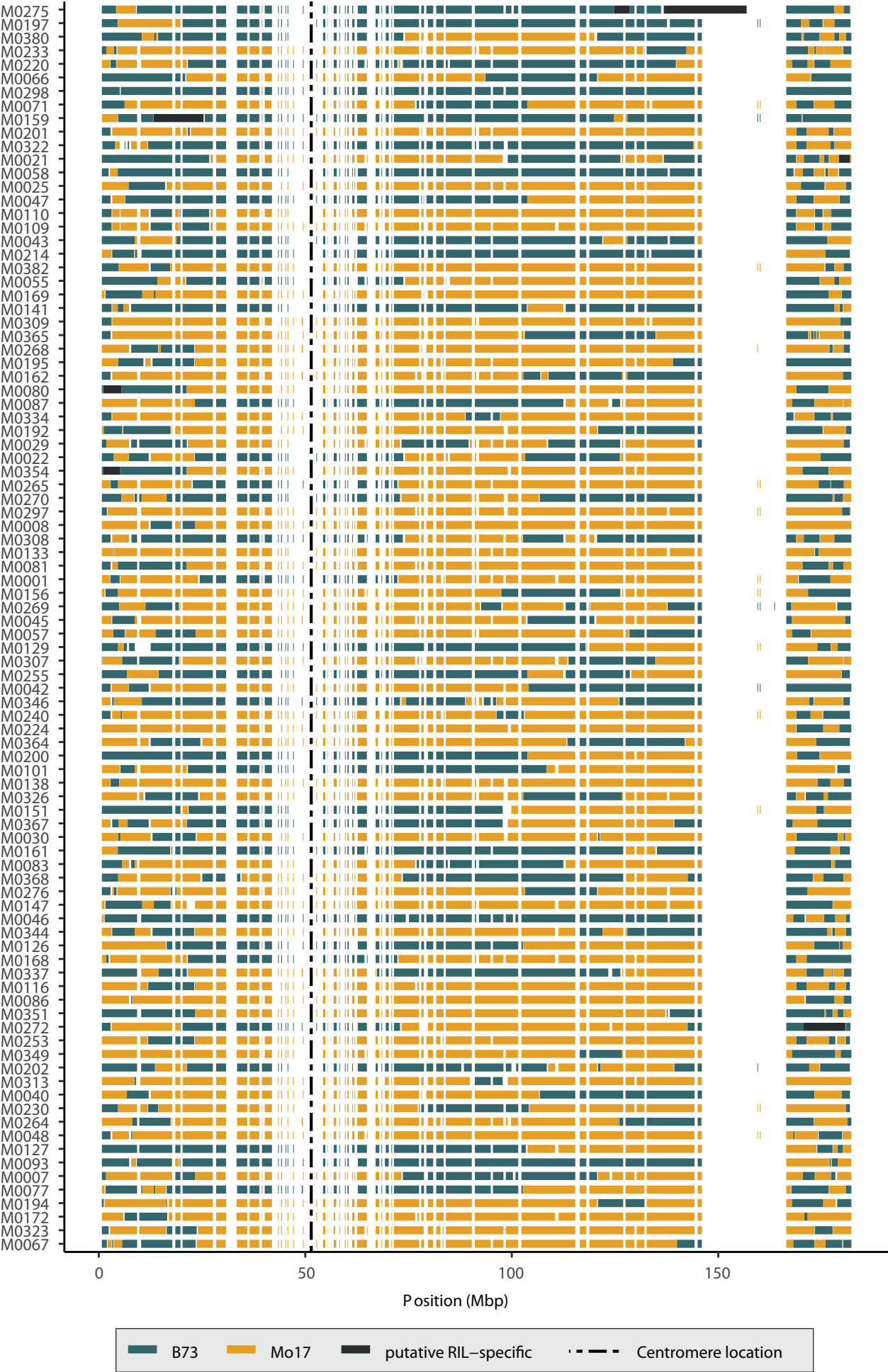
Chromosome 6



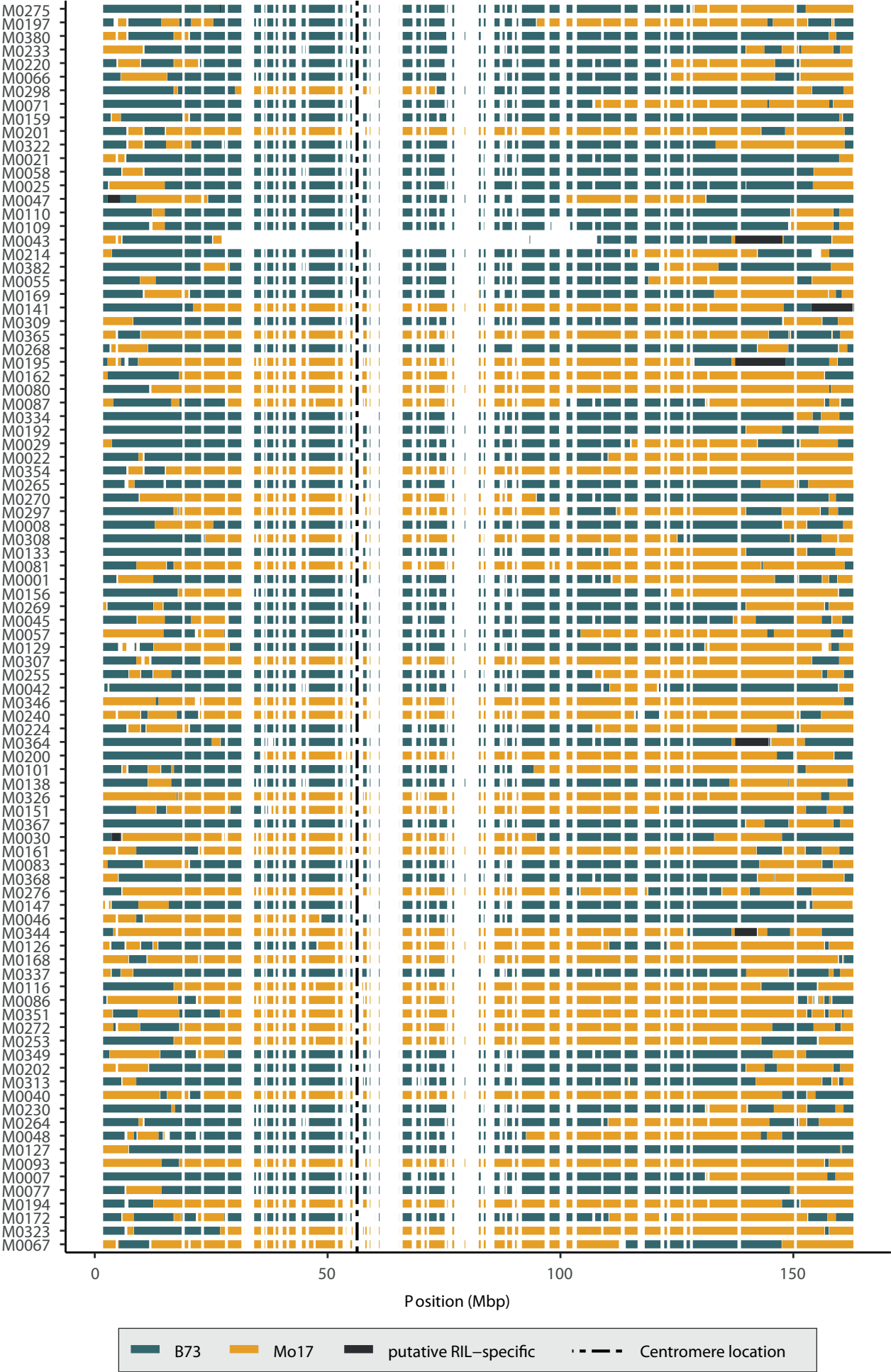
Chromosome 7



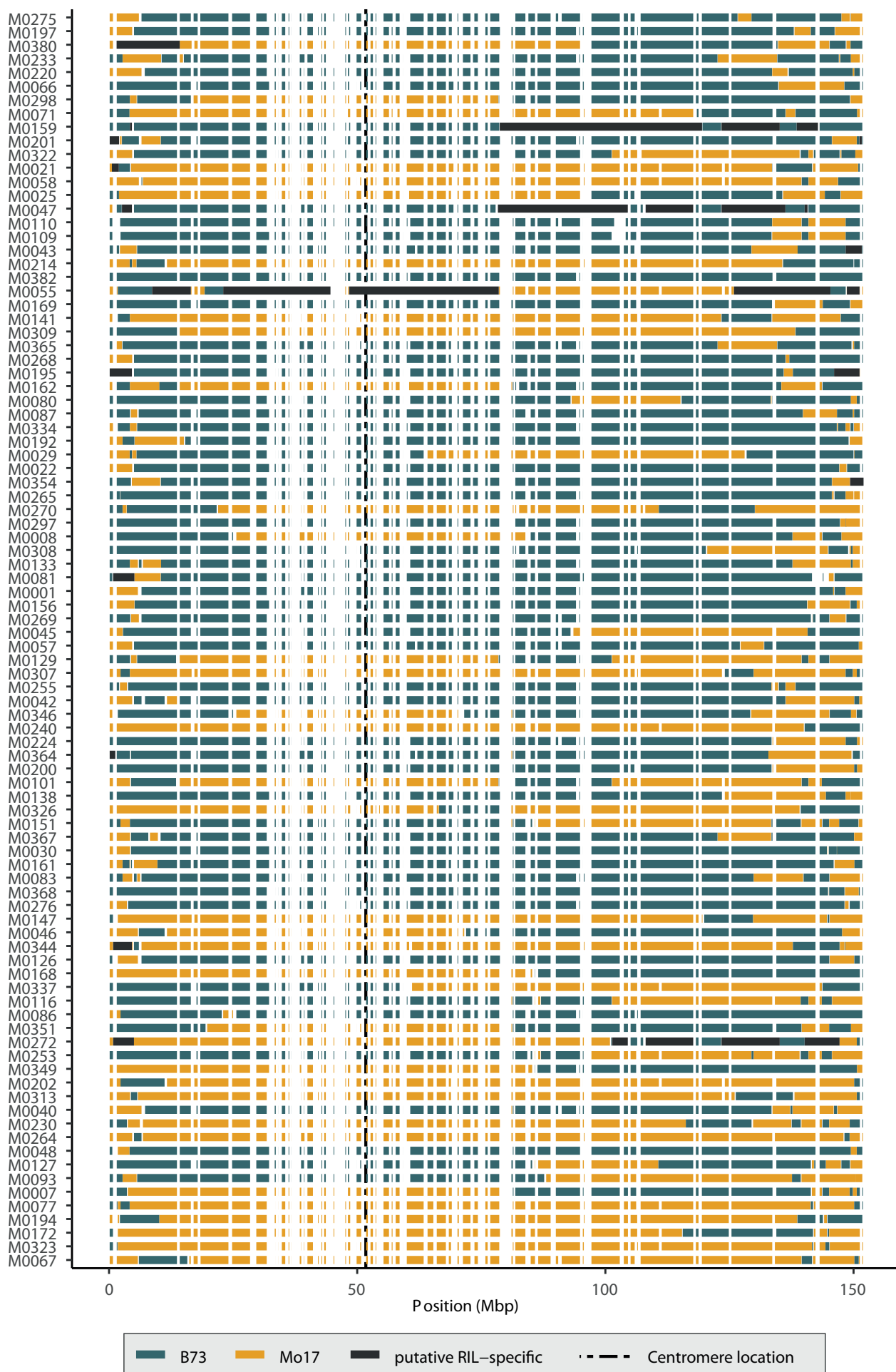
Chromosome 8



Chromosome 9

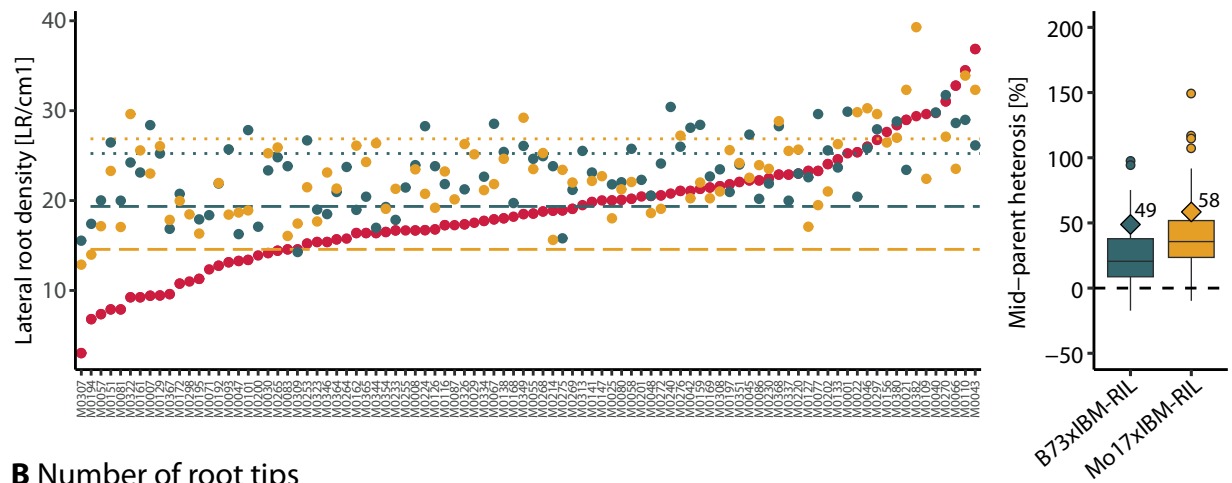


## Chromosome 10

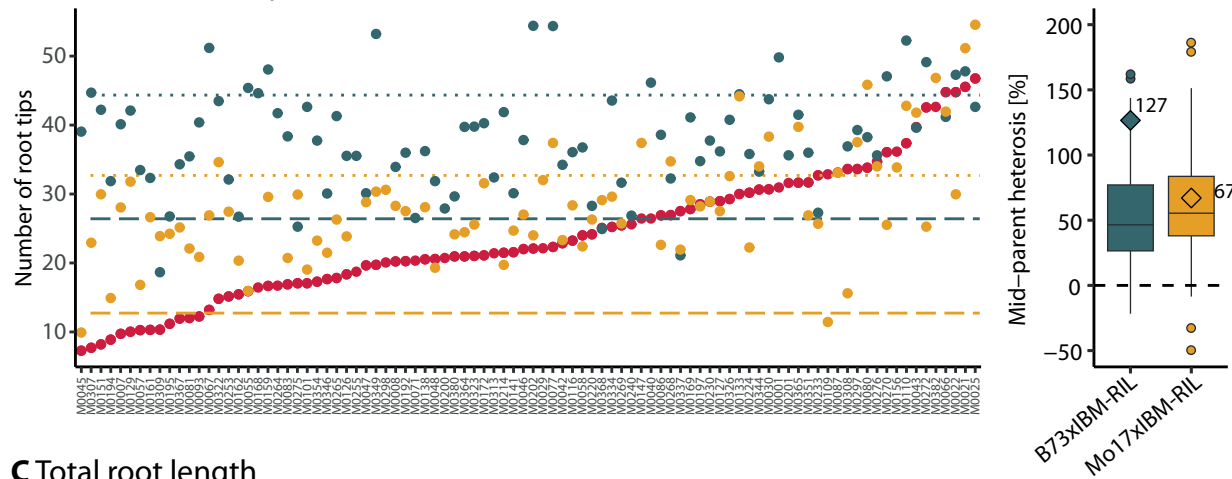


**Fig. S1:** Map of genomic regions in IBM-RILs. Each page shows the genomic regions, of all 94 IBM-RILs for one chromosome on physical scale. Regions of B73 are shown in blue, Mo17 in yellow, putative IBM-RIL specific regions, which were masked are shown in black and white spaces indicate, that no SNPs were found in this region. The centromere location is indicated by a vertical dashed line.

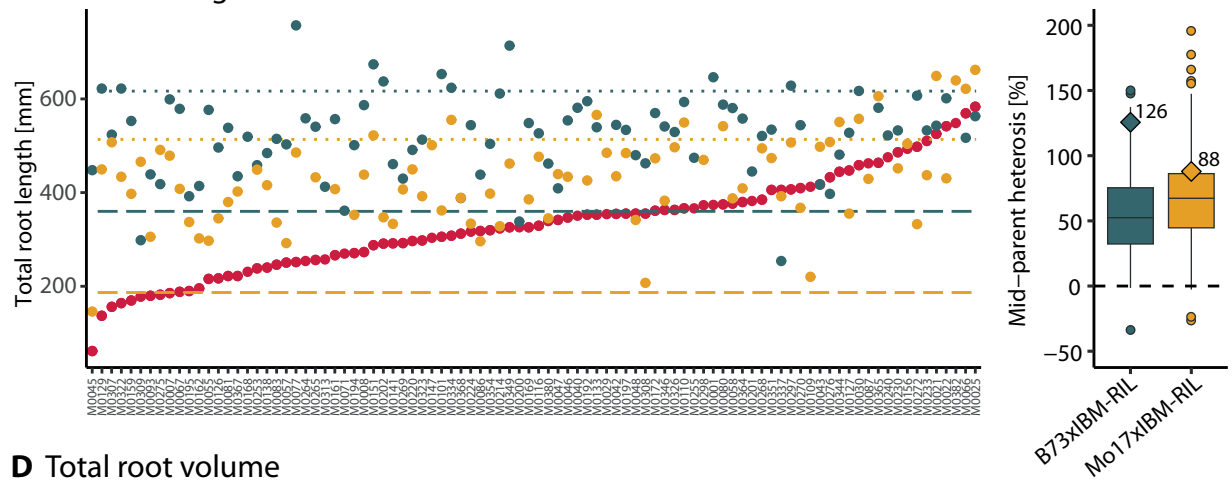
## A Lateral root density



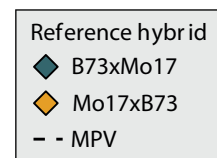
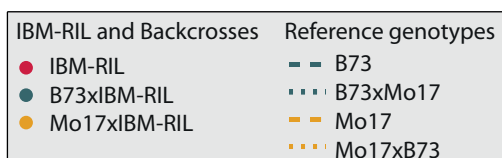
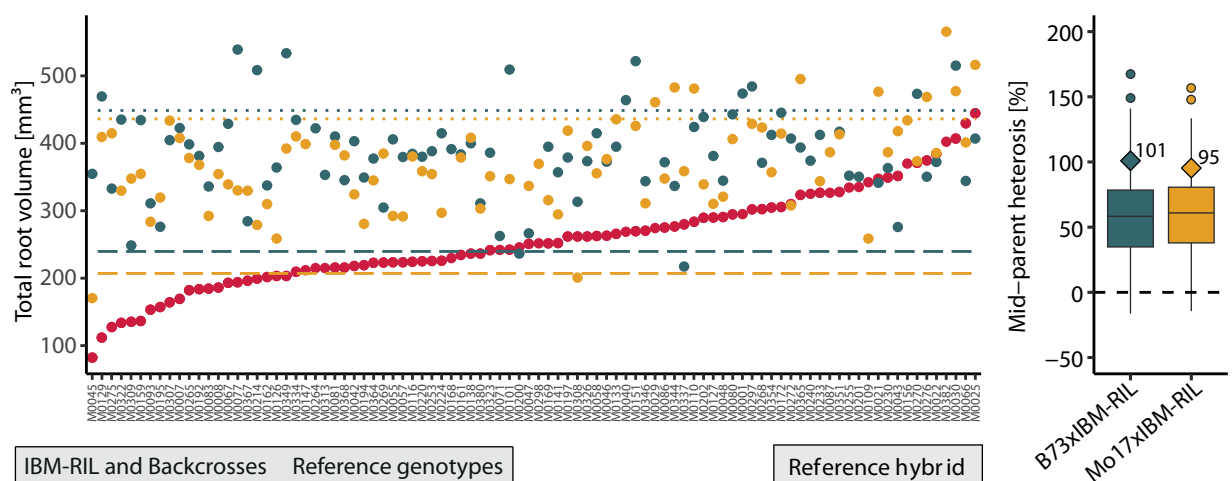
## B Number of root tips



## C Total root length

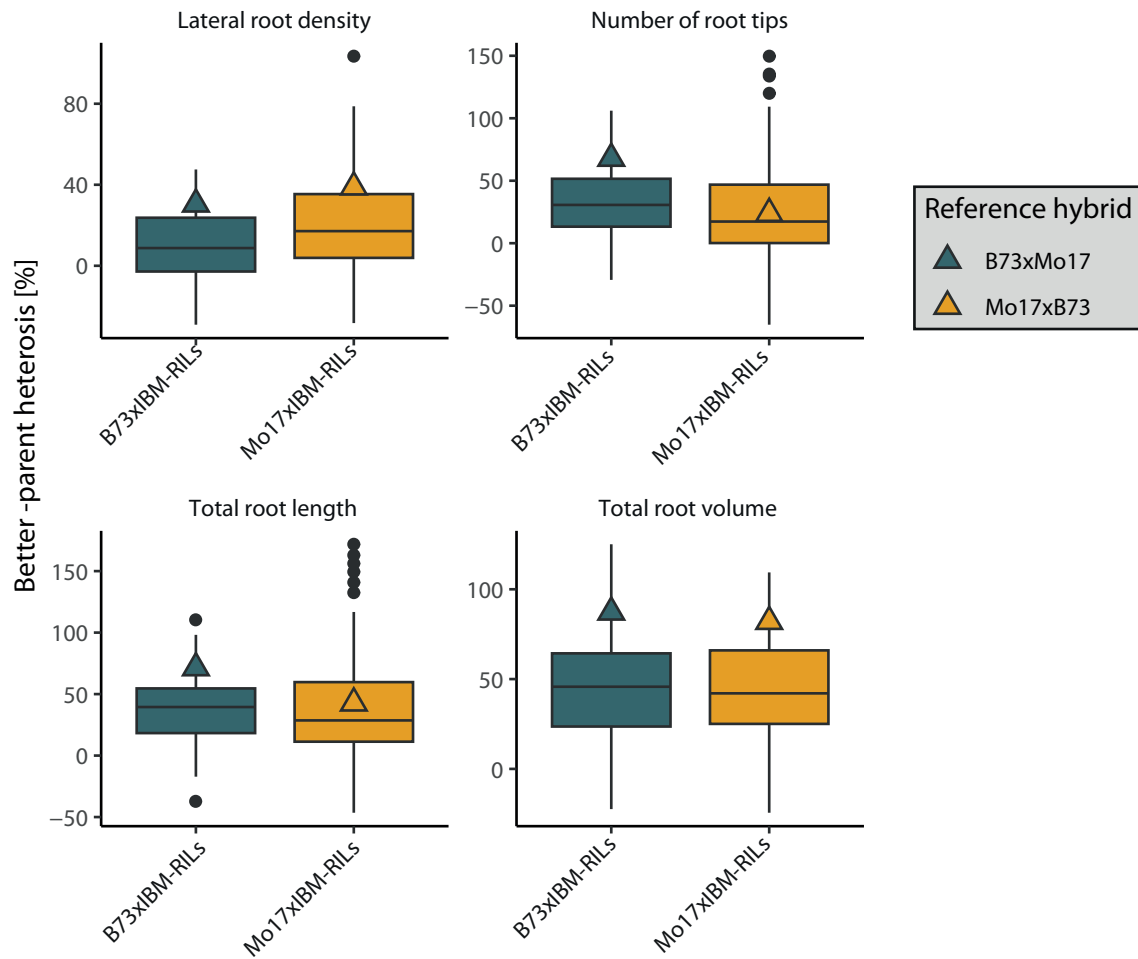


## D Total root volume



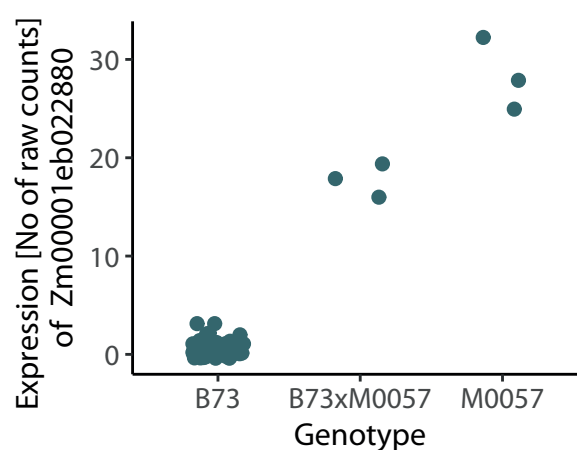
**Fig. S2:** Phenotypic values and mid-parent heterosis (MPH) of **A** lateral root density, **B** Number of root tips, **C** Total root length, **D** Total root volume. On the left panel, the estimated means for each genotype are shown. The IBM-RILs (red) and the B73xIBM-RIL (blue) and Mo17xIBM-RIL (yellow) backcross hybrids are shown as points. The reference genotypes B73 (blue) and Mo17 (yellow) are shown as dashed lines and the reciprocal reference hybrids B73xMo17 (blue) and Mo17xB73 (yellow) as dotted lines. On the right panel, the mid-parent heterosis in percent of the parental mean is shown as boxplots for B73xIBM-RILs and Mo17xIBM-RILs. The MPH for the reference hybrids B73xMo17 (blue) and Mo17xB73 (yellow) is shown as diamond shaped points and their exact values are indicated. The dashed line indicates an MPV of 0.



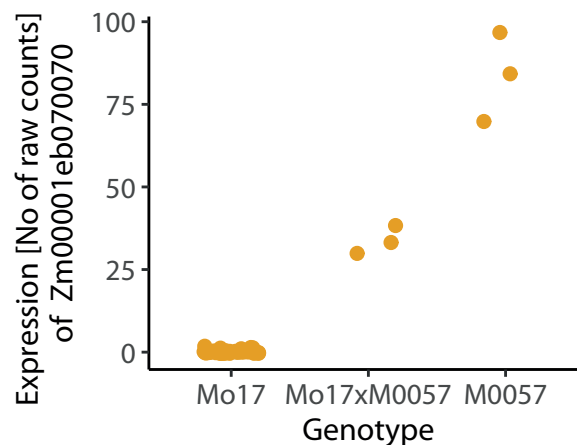


**Fig. S3:** Better-parent heterosis for different root traits. For each of the four root traits the better-parent heterosis in % of the better parent value is shown in a separate boxplot for each population. The values corresponding to the reference hybrids B73xMo17 and B73xMo17 are depicted as triangles (B73xMo17: blue, Mo17xB73: yellow).

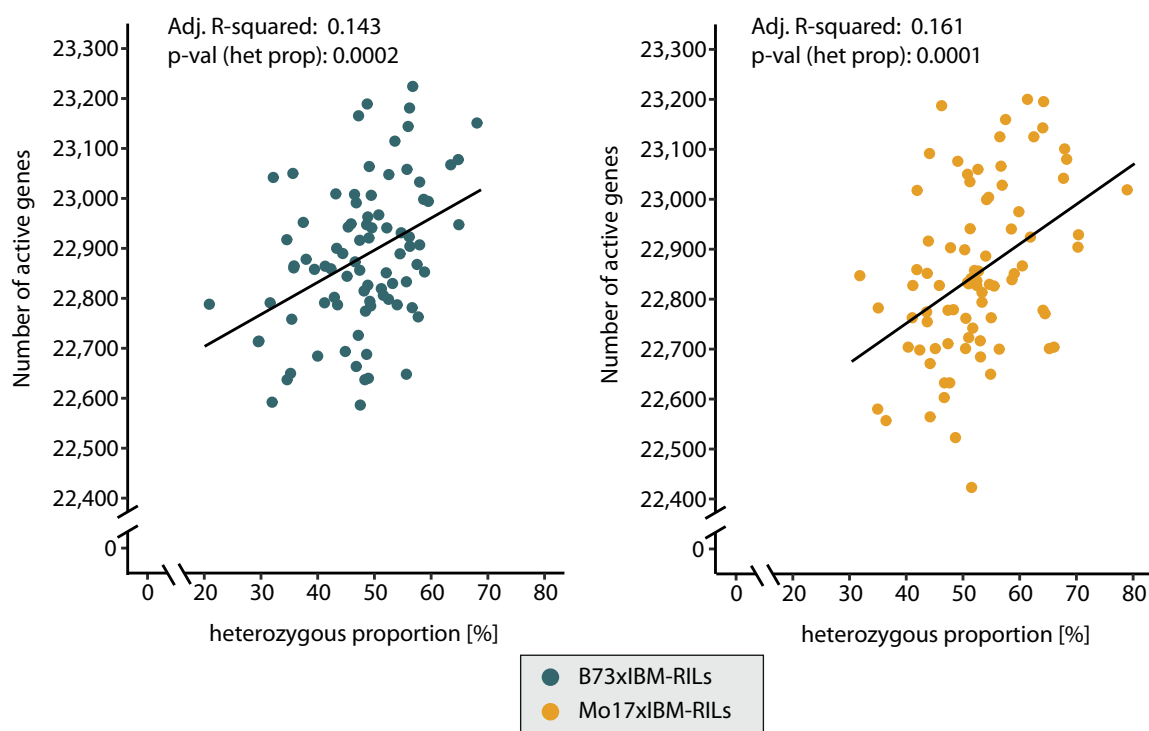
Scatter plot showing the expression of Zm00001eb120480 across three genotypes: B73, B73xM0057, and M0057. The y-axis represents 'Expression [No of raw counts] of Zm00001eb120480' ranging from 0 to 100. The x-axis represents 'Genotype'. B73 shows high expression (mostly between 50 and 100), B73xM0057 shows intermediate expression (around 30-40), and M0057 shows very low expression (near 0).



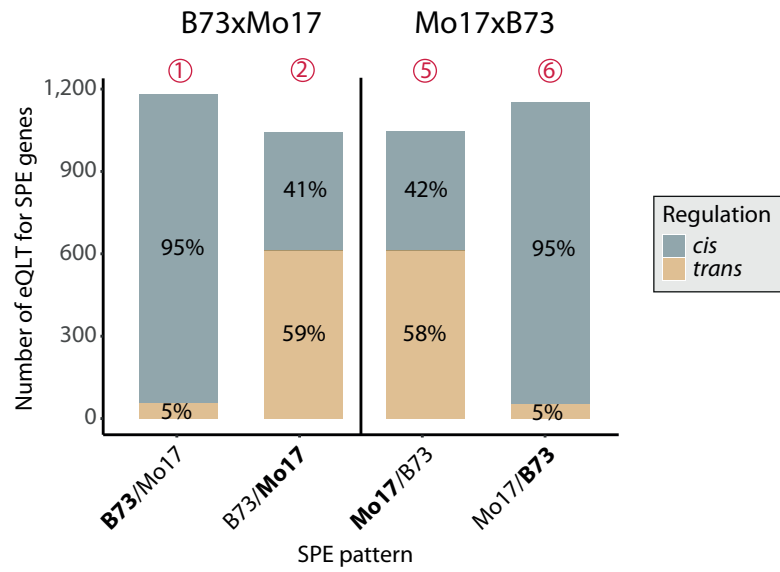
Scatter plot showing the expression of Zm00001e003570 across three genotypes: Mo17, Mo17xM0057, and M0057. The y-axis represents 'Expression [No of raw counts] of Zm00001e003570' ranging from 0 to 200. Mo17 shows high expression (approx. 120-250), Mo17xM0057 shows intermediate expression (approx. 60-100), and M0057 shows very low expression (approx. 0-10).



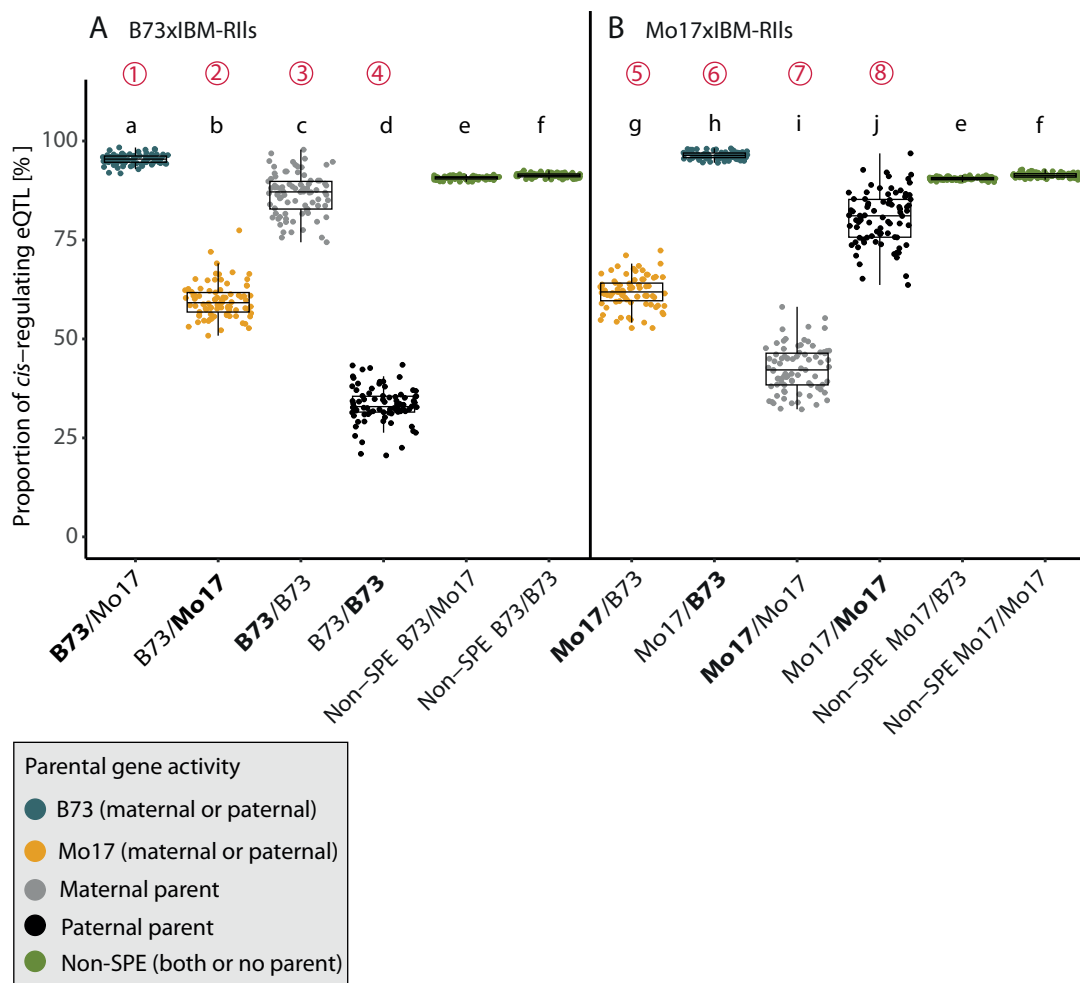
**Fig. S4:** Expression of exemplary SPE genes in of pattern 3, 4, 7, 8. The x-axis shows the respective line/genotype (parents and hybrid). The y-axis shows the number of counts aligned to the respective gene in the parents and hybrid. All example genes were located in a homozygous region.



**Fig. S5:** Correlation of heterozygosity and the total number of active genes in B73xIBM-RILs (left) and Mo17xIBM-RILs (right). The heterozygous proportion on the x-axis was calculated from the classified IBM-RIL regions. A linear regression with an intercept and the heterozygous proportion as covariate was fitted and the adjusted R-squared and p-value for the slope of the heterozygosity are indicated above the regression lines.

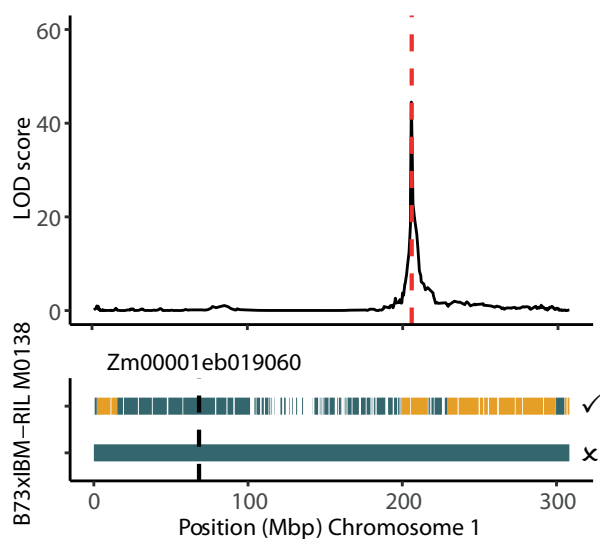


**Fig. S6:** Regulation of SPE pattern genes in fully heterozygous reference hybrids B73xMo17 (left side) and Mo17xB73 (right side). The number of *cis*-(blue) and *trans*-(yellow) acting eQTL are given as bars, with the percentages of *cis* and *trans*-acting eQTL indicated per SPE pattern. The numbers above correspond to SPE pattern as indicated in Figure 2.

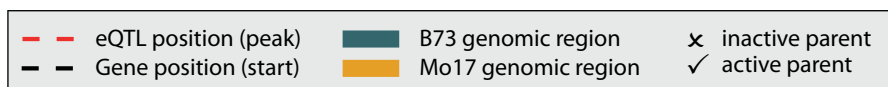
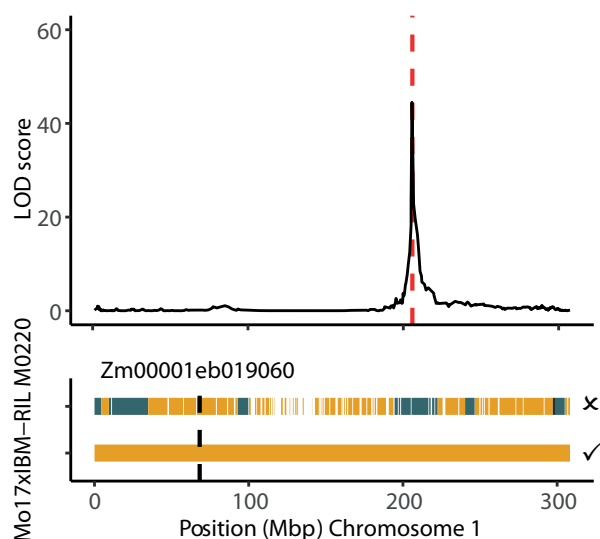


**Fig. S7:** Proportion of *cis*- and *trans*- regulation in SPE pattern genes. Boxplots display the proportion of *cis*-regulation among SPE pattern and non-SPE pattern genes in the B73xIBM-RIL (**A**) and Mo17xIBM-RIL (**B**) hybrids. Different letters indicate significantly different proportions ( $\alpha < 0.05$ ), identified with a gaussian mixed model with the hybrid as random effect, the SPE pattern and non-SPE pattern as a fixed factor and a diagonal variance component for the SPE and non-SPE pattern.

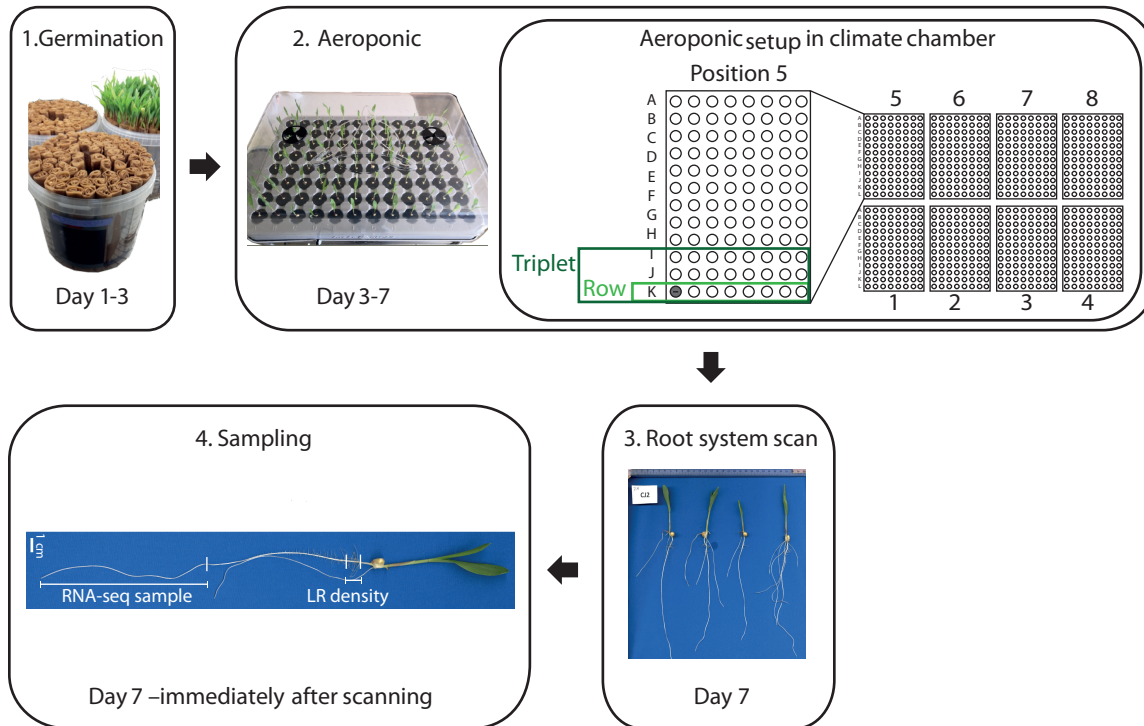
**A** ④ SPE B73/**B73** - *trans* regulation



**B** ⑦ SPE **Mo17**/Mo17 - *trans* regulation



**Fig. S8:** Examples for gene regulation pattern. **A** Homozygous SPE pattern 4 (B73/**B73**) gene in a B73xIBM-RIL, which is *trans* regulated from a heterozygous eQTL. **B** homozygous SPE pattern 7 (**Mo17**/Mo17) gene in a Mo17xIBM-RIL, which is *trans*-regulated homozygous gene from heterozygous eQTL.



**Fig. S9:** Experimental workflow incl. layout of the experimental design. Schematic depiction of the plant growing process from paper rolls until sampling of roots for RNA sequencing. The second box shows the distribution of the aeroponic systems in the climate chamber and the assignment of genotype triplets and individual genotypes within each system.