Features of the *Arabidopsis* recombination landscape resulting from the combined loss of sequence variation and DNA methylation

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The rate of meiotic crossing over (CO) varies considerably along chromosomes, leading to marked distortions between physical and genetic distances. The causes underlying this variation are being unraveled, and DNA sequence and chromatin states have emerged as key factors. However, the extent to which the suppression of COs within the repeat-rich pericentromeric regions of plant and mammalian chromosomes results from their high level of DNA polymorphisms and from their heterochromatic state, notably their dense DNA methylation, remains unknown. Here, we test the combined effect of removing sequence polymorphisms and repeat-associated DNA methylation on the meiotic recombination landscape of an *Arabidopsis* mapping population. To do so, we use genome-wide DNA methylation data from a large panel of isogenic epigenetic recombinant inbred lines (epiRILs) to derive a recombination map based on 126 meiotically stable, differentially methylated regions covering 81.9% of the genome. We demonstrate that the suppression of COs within pericentromeric regions of chromosomes persists in this experimental setting. Moreover, suppression is reinforced within 3-Mb regions flanking pericentromeric boundaries, and this effect appears to be compensated by increased recombination activity in chromosome arms. A direct comparison with 17 classical *Arabidopsis* crosses shows that these recombination changes place the epiRILs at the boundary of the range of natural variation but are not severe enough to transgress that boundary significantly. This level of robustness is remarkable, considering that this population represents an extreme with key recombination barriers having been forced to a minimum.

decrease in DNA methylation 1 | epigenetic inheritance | DNA methylome | epi-haplotype

Meiotic recombination is a fundamental process in genetics whereby maternally and paternally inherited homologous chromosomes exchange material, either nonreciprocally by gene conversion or reciprocally by crossing over (CO). COs are not distributed uniformly along the genome but occur more often in chromosome arms and are strongly suppressed in pericentromeric regions (1–3), partly as a result of sequence and chromatin determinants (1, 4–8). It is commonly believed that in plants and mammals high levels of DNA sequence polymorphisms as well as heterochromatic features associated with repeats, notably dense DNA methylation and transcriptional silencing, play a central role in this suppression (1, 4).

Suppression of COs by dense DNA methylation has been demonstrated experimentally in the fungus *Ascobolus* (7). Specifically, COs were reduced when the recombination interval was methylated on one homolog and were abolished almost completely when methylated on both homologs. In *Arabidopsis*, two recent mapping studies analyzed F_2 progeny derived from crosses between Columbia *ddm1* and *met1* [Col(*ddm1*),Col(*met1*)] DNA methylation mutants and wild-type Landsberg [Ler(WT)] accessions and showed that loss of DNA methylation could not alleviate the suppression of COs in pericentromeric regions of chromosomes (9, 10). However, as pointed out by the authors, this experimental design could not rule out an inhibitory effect of sequence divergence between Col and Ler on COs.

An ideal design would use crosses between isogenic individuals, with one of the crossing partners having decreased DNA methylation levels throughout the genome (9). Melamed-Bessudo and Levy (9) implemented such an approach by crossing Col(*ddm1*) mutant to Col(WT). Using two fluorescent markers spanning a 16-centimorgan (cM) interval on the arm of chromosome 3, they detected increased CO rates in F_2 plants derived from these parents relative to plants derived from a Col(WT)×Col(WT) control cross and concluded that COs in euchromatic regions can be up-regulated by loss of DNA methylation. A similar approach at a genome-wide scale and with high mapping resolution, particularly in pericentromeric regions, has not been attempted because of a lack of appropriate molecular and genetic tools. Hence, the combined effect of DNA methylation and sequence variation on COs has not been tested comprehensively in *Arabidopsis* or in any other higher eukaryote.

We previously reported the construction of a large population of epigenetic recombinant inbred lines (epiRILs) in *Arabidopsis* (11, 12), which provides a powerful experimental system to conduct such a test. These epiRILs were obtained by first crossing a fourth-generation plant homozygous for the recessive *ddm1-2* mutation with a near-isogenic WT individual. The *ddm1-2* mutation mostly affects transposable elements (TEs) and other repeats, which lose DNA methylation and become transcriptionally reactivated in a transmissible manner in many instances (11–14). However, transposition events are relatively rare (15).

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Thus, F_1 individuals can be considered homozygous throughout the genome, except at the *DDM1* locus and at the few loci affected by TE mobilization, but have chromosome pairs that differ markedly in their DNA methylation levels and transcriptional activity over TEs and other repeats (11, 16). A single F_1 *DDM1*/*ddm1* individual was backcrossed to the WT parental line, and after the progeny homozygous for the WT *DDM1* allele were selected, the epiRILs were propagated through seven rounds of selfing. In this design, more than 85% of all informative recombination events occur in the first two inbreeding generations (F_1 and backcross), with fewer informative events being contributed by each subsequent generation (17).

Previous targeted analysis indicated that many of the parental differences in DNA methylation and transcriptional activity of repeats are inherited stably in the epiRILs (11, 12). Regions with segregating DNA methylation states therefore can serve as physical markers to detect the frequency and distribution of recombination events along chromosomes even though the two homologs have nearly identical DNA sequences.

In this study we report the construction of a recombination map using genome-wide DNA methylation data from 123 epiRILs. This map was derived from 126 meiotically stable differentially methylated regions (DMRs) covering 81.9% of the total genome. Estimates of the genetic length for each chromosome revealed that global recombination rates are comparable with those of classical *Arabidopsis* crosses. On a local scale, we demonstrate that suppressed recombination activity within repeat-rich, pericentromeric regions of chromosomes is maintained robustly even after the removal of sequence polymorphisms and repeat-associated DNA methylation. Furthermore, we were able to identify 3-Mb regions flanking pericentromeric boundaries that appear to be subject to additional suppression and show that this effect is accompanied by increased recombination activity in chromosome arms. A direct comparison with 17 classical *Arabidopsis* crosses reveals that these recombination changes place the epiRILs at the boundary of the range of natural variation but appear not to be severe enough to transgress that boundary significantly.

Results

Construction of a Recombination Map Using Transgenerationally Stable DMRs. To demonstrate that transgenerationally stable DMRs can be used for the construction of a recombination map in an isogenic population, we carried out methylated DNA immunoprecipitation followed by hybridization to a whole genome DNA tiling array (MeDIP-chip) on 123 epiRILs and on the two parental lines (256 array experiments including replicates). The 123 epiRILs originally were chosen using a selective (epi)genotyping strategy for two uncorrelated complex traits, flowering time and root length. We used a three-state Hidden Markov Model (HMM) to classify tiling array signals into three underlying DNA methylation states (18): unmethylated (U), intermediate methylation (I), or methylated (M). Benchmarking of these HMM calls against whole-genome bisulphite sequencing data (~30×) for six epiRILs confirmed that both the MeDIP protocol and the analysis method performed well (*SI Appendix*, Fig. S1 and Table S1). Comparison of the two parental DNA methylomes revealed 2,611 DMRs representing clear instances of methylation loss in *ddm1* (transitions from M to U). These DMRs (median length: 1,211 bp; range: 318–24,624 bp) were distributed throughout the genome but, as expected, were more abundant in pericentromeric regions (Fig. 1*A* and *SI Appendix*, Table S2) (19).

We examined the DNA methylation state at all parental DMRs in each of the 123 epiRILs and inferred their parent of origin (i.e., epigenotypes). Segregation was not compatible with stable inheritance of *ddm1*-induced DNA hypomethylation for 1,744 (66.8%) of the parental DMRs, and in most of these cases our data pointed to fully or partially penetrant reversion to WT DNA methylation. In contrast, 867 (33.2%) of the parental DMRs segregated in the expected 3:1 Mendelian ratio (*SI Appendix*, Fig. S2 and Table S3). Stable DMRs were associated with a comparatively lower abundance of siRNAs in the WT and *ddm1* parental

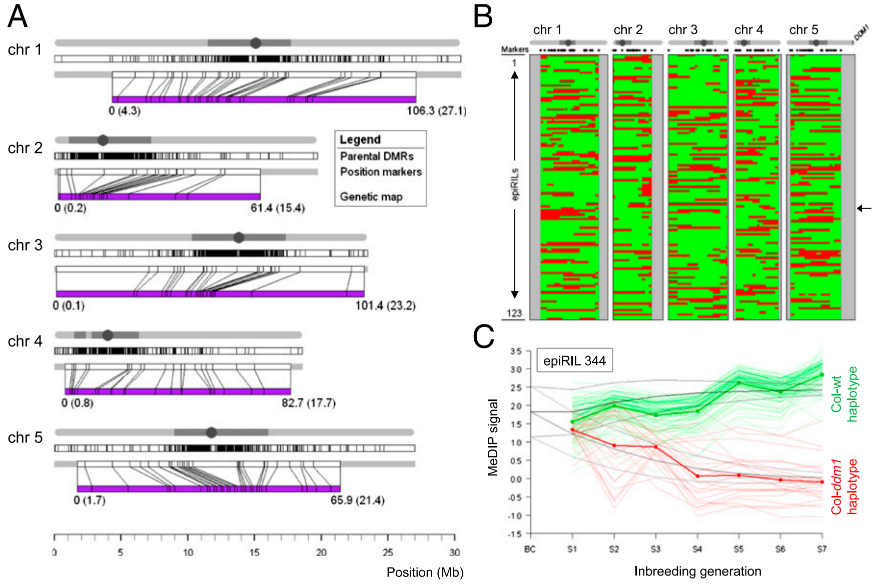

Fig. 1. Recombination map construction. (*A*) Genome-wide distribution of the 2,611 parental DMRs (*Top*) and the 126 DMRs (i.e., markers; *Middle*) retained for construction of the recombination map (purple, *Bottom*) for each of the five *Arabidopsis* chromosomes. The mapping between physical and genetic positions of markers is shown. (*B*) Inference of inherited WT (green) and ddm1 (red) haplotypes along the genome (*x*-axis) as inferred from the recombination map for each of the 123 epiRILs (*y*-axis) (*SI Appendix*, Table S5). Chromosome extremities not covered by the genetic map are indicated in gray. The genome of epiRIL 344 is indicated by an arrow. A schematic representation of each chromosome is plotted above the map with the physical location of the *DDM1* gene shown at the end of chromosome 5. (*C*) Transgenerational methylation data for epiRIL 344. Shown are the average methylation signals for the 126 markers, with regions that are predicted to become fixed for the *ddm1* haplotypes (thin red lines) and the WT haplotypes (thin green lines) after seven selfing generations. The average signals (red and green thick solid lines) are in agreement with Mendelian inbreeding theory (black solid lines).

lines (*SI Appendix*, Fig. S3). These findings are in agreement with previous analyses (11, 12) and indicated that the 867 stable DMRs are not efficient targets of siRNA-mediated DNA remethylation, even after eight rounds of meiosis. These stable DMRs therefore could serve as physical markers in an extension of the Lander–Green algorithm (20) to derive a genetic map. After application of the algorithm and removal of mainly genetically redundant markers (i.e., markers located less than 0.0001 cM apart), 126 of the original 867 markers were retained (Fig. 1 *A* and *B* and *SI Appendix*, Fig. S2 and Table S4). These 126 markers covered ∼81.9% of the total genome (74.7, 77.0, 98.4, 91.1, and 73.0% of chromosomes 1, 2, 3, 4, and 5, respectively).

Many of the 126 markers contained TE sequences, consistent with the targeted effect of *ddm1* on these and other repeats (*SI Appendix*, Fig. S4). However, in a vast majority of cases, markers included only TE relics, which likely have lost their capacity to be mobilized (*SI Appendix*, Table S6). Indeed, both comparative genomic hybridization (*SI Appendix*, Fig. S5) and preliminary whole-genome resequencing suggested that none of the 126 DMRs contain sequences that were mobilized in the parental *ddm1* line or the epiRILs (*SI Appendix*, Table S6). Consistent with this finding, pair-wise recombination fractions between the 126 markers indicated a well-behaved and robust genetic map, reminiscent of those typically seen in classical crosses involving DNA sequence markers, with high correlation among linked loci and virtually no correlations among loci in different chromosomes (*SI Appendix*, Fig. S6). Moreover, all inferred *ddm*1-inherited nonrecombinant pericentromeric haplotypes contained significantly less DNA methylation and were more actively transcribed than their WT counterparts (*SI Appendix*, Figs. S7 and S8).

To test further the transgenerational stability of the 126 markers as well as our inference of the parental epigenotypes at these marker locations, we performed genome-wide DNA methylation analysis for one selected line (epiRIL 344) for each of its seven selfing generations (7 × 2 replicates = 14 array experiments). Fixation occurred for the predicted parental epigenotype in each case, and the rate of approach toward fixation was consistent with Mendelian inbreeding theory for a backcross-derived RIL (19) (Fig. 1*C*). Taken together, these results rule out any ambiguity in the actual location or DNA methylation state of the stable DMRs used for constructing the genetic map.

Total Genetic Length in the epiRILs Does Not Diverge Significantly from the Natural Range. One approach for evaluating the epiRILs recombination map is by comparison with a Col (WT)×Col(WT)-derived reference cross. In this set-up, changes in recombination patterns can be attributed directly to DNA methylation loss. However, tracking recombination events in such a reference is experimentally challenging. It requires a system akin to the fluorescent marker reporters used by Melamed-Bessudo and Levy (9), which does not easily scale genome-wide. An alternative approach is to evaluate the epiRILs in the context of natural variation. In terms of DNA sequence and DNA methylome divergence of its founder parental lines, the epiRILs can be viewed as representing an extreme situation with key barriers to recombination having been forced to a minimum. An important question therefore is how genome-wide recombination patterns in this population compare with those seen in crosses derived from different pairs of natural accessions.

We estimated the genetic length for each of the five epiRIL chromosomes using Haldane's map function. The lengths were 106.3, 61.4, 101.4, 82.7, and 65.9 cM for chromosomes 1–5, respectively, and correlated positively with physical chromosome length (*SI Appendix*, Fig. S9). The total length of the genetic map was 417.7 cM, yielding an average marker spacing of ∼0.804 Mb (3.45 cM). These estimates are similar to those previously reported for genetic maps based on classical *Arabidopsis* crosses (21–24). The use of other map functions that account for CO interference, such as the Kosambi or Carter and Falconer functions, yielded very similar results (*SI Appendix*, Fig. S10). To perform a more direct comparison between the epiRIL map and those of classical *Arabidopsis* crosses, we reanalyzed recombination data obtained for 17 F_2 populations (24) that were derived from pairs of 18 distinct natural accessions. In total, these populations consisted of 7,045 plants (∼410 plants per cross; range: 235–462 plants), which were genotyped at 235 markers on average (range: 215–257 markers) (24). To facilitate a meaningful comparison, we constructed a consensus map using 83 markers that were shared across populations (*SI Appendix*, Fig. S11 and Table S7). Thorough testing showed that the reduction to 83 markers in the epiRIL and F_2 maps led to no significant loss of information in capturing the linkage structure along chromosomes (*SI Appendix*, Figs. S12 and S13), and the 83 markers therefore were deemed appropriate for this comparative analysis.

Estimates of the genetic length of each of the five chromosomes revealed substantial natural variation among the F_2 populations (Figs. 2*B* and 3*A*). However, the genetic lengths of the

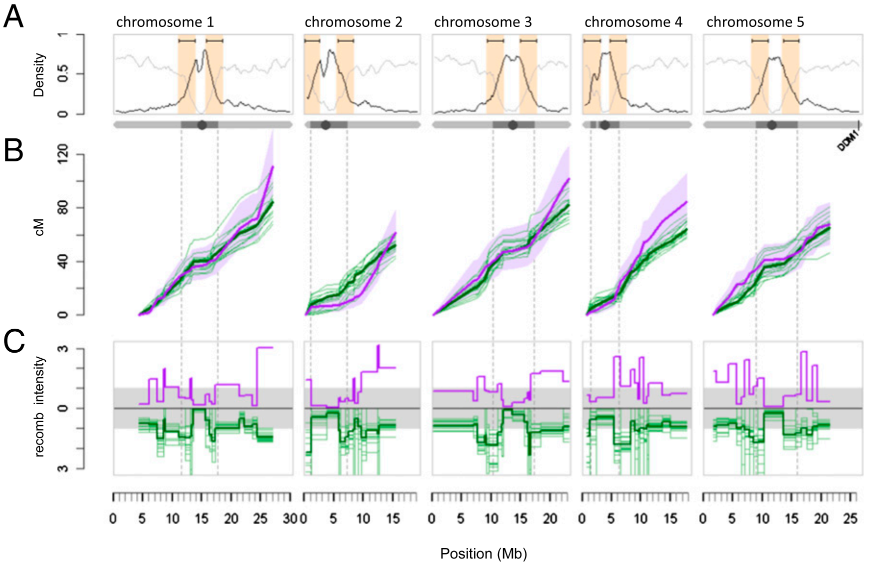

Fig. 2. Comparison of global and local recombination patterns in the epiRILs and the 17 F_2 populations (24). (*A*) Chromosome-wide gene (light gray line) and transposon (dark line) density distribution. The 3-Mb windows bracketing the intersection points between transposon- and gene-dense regions are indicated in orange. (*B*) Cumulative cM lengths of the epiRILs (thick purple line) and each of the F_2 populations (thin green lines) using the consensus map. Purple shading shows the ±95% confidence interval (CI).The thick green line denotes the average F_2 cumulative length (in cM). The dotted vertical lines define the pericentromeric regions of each chromosome. (*C*) The distribution of normalized recombination intensities (cM/Mb of a given marker interval divided by the cM/Mb chromosome average) shows suppression of recombination within pericentromeric regions and elevation at its boundaries. Color coding is as in *B*.

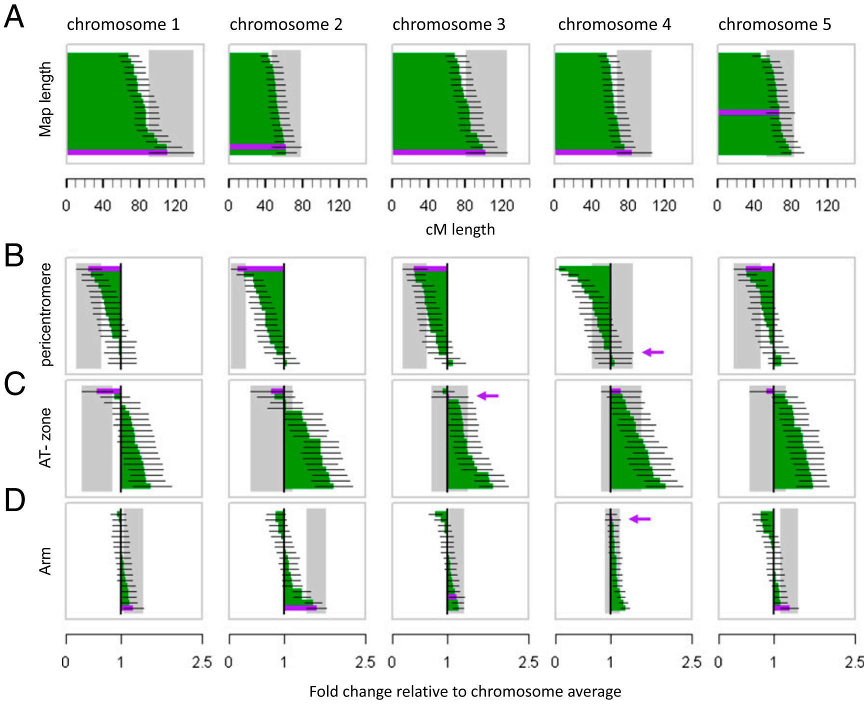

Fig. 3. Estimated genetic lengths and fold-change recombination intensities. (*A*) Estimated genetic lengths (±95% CI) of the epiRILs (purple) and each of the 17 F_2 populations (green) (24). (*B*–*D*) Fold change in recombination intensity [(cM/Mb) region/(cM/Mb) chromosome average] ±95% CI in pericentromeric regions (*B*), AT zones defined by a 3-Mb window bracketing the intersection point between transposon- and gene-dense regions at pericentromeric boundaries (*C*), and chromosome arms (*D*). Purple arrows indicate the location of the epiRILs when applicable. The values presented in each panel are ordered to highlight trends in the epiRILs recombination landscape. The identifiers of individual F_2 crosses corresponding to this ordering can be found in *SI Appendix*, Table S11.

epiRIL chromosomes did not diverge significantly from the natural range (Figs. 2*B* and 3*A*). The exception was chromosome 1, where we observed a significant increase relative to five of the F_2 crosses. Overall, therefore, our data indicate that the global recombination rate in the epiRILs is not altered drastically. Nonetheless, we noted a clear, but nonsignificant, trend toward longer genetic lengths for chromosomes 1–4 as compared with the F_2 populations (Fig. 3*A*); this trend is at least partly consistent with DNA methylation and DNA sequence polymorphisms acting as barriers to the global recombination rate in *Arabidopsis*.

Suppression of Pericentromeric Recombination Persists in the epiRILs and Shows a Trend Toward Additional Reinforcement. To explore the relationship between the epiRILs map and those of the different F_2 crosses at a subchromosomal scale, we examined in more detail the distribution of recombination intensities, expressed as cM/Mb, for each marker interval along the genome (Fig. 2*C*). All populations, including the epiRILs, had clearly suppressed recombination activity across pericentromeric regions relative to the chromosome averages (Figs. 2*C* and 3*B*). The exception to this trend was chromosome 4, for which the epiRILs showed a slight increase of recombination intensity (Fig. 3*B*). However, the presence of the heterochromatic knob on chromosome 4 in the Columbia accession, but not in other accessions, makes this result difficult to interpret (10).

Specifically, recombination intensities in pericentromeric regions of epiRIL chromosomes 1, 2, 3, and 5 were, respectively, 2.50, 6.88, 2.53, and 2.01 times lower than the chromosome average, which compares to 1.27 (range: 0.97–2.15), 1.51 (range: 0.95–3.68), 1.52 (range: 0.90–2.48), and 1.20 (range: 0.87–1.98) in the F_2 populations (Fig. 3*B* and *SI Appendix*, Table S8). This persistent suppression effect in the epiRIL agrees with the results of Melamed-Bessudo and Levy (9) and Mirouze et al. (10), who examined mapping populations derived from a Col(*ddm1*)×Ler (WT) and a Col(*met1*)×Ler(WT) cross, respectively. Hence, loss of DNA methylation appears to be insufficient to release pericentromeric suppression of recombination, even in the absence of DNA sequence polymorphisms. On the contrary, we found a clear trend toward enhanced suppression in the epiRILs: Recombination intensities in this population were consistently at the bottom of the natural range compared with the F_2 populations, even though chromosome-wide recombination rates were comparatively large. Enhanced suppressive effects also were reported by Melamed-Bessudo and Levy (9) and Mirouze et al. (10), thus highlighting an unexpected and complex relationship between DNA methylation and the suppression of recombination in pericentromeric regions of *Arabidopsis* chromosomes.

Reinforced Suppression of Recombination Extends to Pericentromeric Boundaries in the epiRILs and Appears to Be Compensated by Increased Recombination in Chromosome Arms. In contrast to core pericentromeric regions, recombination intensities in the F_2 populations increase rapidly at pericentromeric boundaries with chromosome arms (Figs. 2*C* and 3*C*). An important property of these regions is that they correspond to major transitions in genome content from TE-rich to gene-rich sequences (Fig. 2*A*) and also have been described recently as hotspots of historical recombination activity at the species level (*SI Appendix*, Fig. S14) (25). We found that nearly 40% of all detected recombination breakpoints in the F_2 populations mapped within a 3-Mb window bracketing the intersection point in these transition zones (henceforth referred to as "annotation transition zones"; AT zones), yielding local recombination intensities that were consistently above the chromosome averages (Fig. 3*C* and *SI Appendix*, Fig. S15 and Table S8).

This finding differs strongly from the situation seen in the epiRILs: AT zones accounted for only 25.31% of all detected recombinants in this population, and recombination intensities were close to the chromosome average (in chromosomes 3 and 4) or even below it (in chromosomes 1, 2, and 5) (Fig. 3*C* and *SI Appendix*, Table S8). These results suggest that the enhanced suppression of recombination seen in the epiRIL pericentromeric regions (see above) is driven at least in part by the more localized reduction of recombination within AT zones, which cover (on average) only 63.4% of the pericentromeric regions on either side of the centromeres. The two previous studies using mapping populations derived from crosses between Col (*ddm1*) and Ler(WT) (9) and between Col(*met1*)and Ler(WT) (10) were not able to delineate these local effects, most likely because of the sparsity of their genetic markers (two to three markers per pericentromeric region). Marker density in the epiRIL map, in contrast, was relatively high within AT zones and even permitted fine mapping of shared and nonshared recombination breakpoints to a resolution as low as 4 kb (*SI Appendix*, Figs. S16 and S17 and Tables S9 and S10).

Furthermore, our data indicate that suppression of recombination within AT zones in the epiRILs is accompanied by increased recombination in chromosome arms (Fig. 3*D* and *SI Appendix*, Fig. S18). This apparent compensatory effect reconciles the enhanced local suppression seen in the epiRILs with the earlier observation that chromosome-wide recombination rates are relatively large compared with the F_2 populations. This effect was most pronounced on epiRIL chromosomes 1, 2, and 5 (the chromosomes with the strongest suppression in the AT zone), with recombination intensities being 1.23, 1.6, and 1.3 times above the chromosomes' average (*SI Appendix*, Table S8). We failed to identify a similar trend in the F_2 populations (*SI Appendix*, Fig. S18 and Table S8), suggesting that this effect is a specific feature of the epiRIL recombination landscape.

Discussion

In this study we demonstrate that stable DNA methylation differences can be used as physical markers to derive genome-wide recombination patterns in a near isogenic population of epiRILs. We find that recombination suppression is maintained robustly in pericentromeric regions of the epiRILs, despite the extensive loss of sequence variation and of DNA methylation and transcriptional silencing over repeats. This observation indicates that these factors do not play a major role in the suppression of pericentromeric COs. This finding is contrary to common belief and is particularly intriguing given the interplay between recombination and transcription observed in yeast and the mouse (26, 27). Whether mechanisms exist in *Arabidopsis* that actively sequester the recombination machinery away from gene-promoter regions or other genomic elements, as in the mouse (27), remains to be determined.

Nonetheless, our results indicate that loss of DNA methylation over repeat sequences can lead to a local reinforcement of recombination suppression in pericentromeric regions and to increased recombination activity along chromosome arms. Similar results were reported by Melamed-Bessudo and Levy (9) and Mirouze et al. (10) using genetically divergent populations. Therefore we conclude that the absence of sequence polymorphisms is insufficient to counteract the enhanced suppressive effects induced by the loss of DNA methylation in pericentromeric regions. On the other hand, the lack of sequence polymorphisms still may be partly responsible for the increased recombination rates observed in chromosome extremities (9).

Melamed-Bessudo and Levy (9) demonstrated that *ddm1*-induced demethylation of only one homolog produces the same recombination changes seen when both homologs are demethylated. Our results and conclusions therefore should be generalizable to the two-homolog situation. However, it has been shown in *Ascobolus* that DNA methylation of a known recombination hotspot inhibits COs more severely when both homologs are methylated (7). Similar localized dosage effects may therefore also be present in *Arabidopsis*.

Our study and those of Melamed-Bessudo and Levy (9) and Mirouze et al. (10) have used well-characterized *ddm1* and *met1* DNA methylation mutants as a tool to perturb genome-wide methylation levels experimentally. Both *ddm1* and *met1* experience a nearly 70% reduction in DNA methylation levels genome-wide. This drastic loss probably sets an upper limit to the amount of demethylation that can be incurred in nature. Indeed, it is difficult to conceive of mechanisms that would elicit similar or more severe changes under natural settings, unless they involve spontaneous mutations in genes important for DNA methylation control, such as *ddm1* or *met1*. Interestingly, a recent analysis of *Arabidopsis* mutation accumulation lines showed that drastic alterations in the methylome of one outlier line were likely caused by a spontaneous mutation in a methyl-transferase gene (28, 29), which must have arisen during just 30 generations of selfing. This observation suggests that similar events are certainly plausible under natural conditions.

An assessment of whether strong methylation loss can elicit recombination changes at magnitudes that are sufficient to drive genome evolution in this species has been lacking. Our study is an initial step in providing such an assessment. Our analysis of the 17 F_2 populations derived from 18 natural accessions (24) allowed us to quantify the magnitude of the recombination changes observed in the epiRILs in the context of natural variation. Although we find that the epiRILs nearly always are situated at the boundary of the natural range, there is no strong evidence that local and global recombination patterns in this population markedly transgress the natural range. Indeed, in many cases, several of the F_2 populations displayed even more extreme divergence from the F_2 population average than did the epiRILs. These findings lead us to conclude that severe losses of DNA methylation along *Arabidopsis* chromosomes have no drastic implications for recombination-mediated genome evolution. This high level of robustness raises questions concerning the precise mechanisms that have shaped the recombination landscape in this species in the first place.

Of course, severe depletion of DNA methylation can drive other important events, such as large-scale structural rearrangements and polyploidization, which may impact the course of genome evolution. In addition, natural epigenetic variation, such as that associated with differential DNA methylation, can act on complex traits that are under natural selection (30), thereby changing linkage disequilibrium relations within and across chromosomes. However, understanding and documenting the impact of epigenetic variants on complex traits is challenging, mainly because of the technical difficulties in ruling out the confounding effect of DNA sequence polymorphisms (31). Because of this limitation, it has been argued that the epiRILs constitute an ideal system for the study of epigenetic inheritance in *Arabidopsis* (17, 32–34). We and others have shown recently that many adaptive phenotypes, such as plant height, flowering time, and growth rate, are highly heritable in this population (12, 35, 36). Segregating phenotypic effects also have been observed in another epiRIL population which was obtained from a cross between Col(*met*1) and Col(WT) (37).

A logical next step in the analysis of these populations is to map and characterize the epigenetic basis of these complex traits. The linkage map reported here (Fig. 1*B*) can be used in conjunction with classical quantitative trait-locus mapping methods to achieve this characterization in the *ddm*1-derived epiRILs. Ultimately, such efforts should contribute significantly to our understanding of epigenetics in adaptive evolution.

Materials and Methods

Methylome Analysis. MeDIP was carried out as previously described (18) followed by hybridization to a custom NimbleGen tiling array covering the Arabidopsis genome at 165 nt resolution (38). Including dye-swaps, we performed a total of 256 array experiments (*SI Appendix*, section 1). For each array, probe signals were classified into three underlying methylation states, methylated (M), intermediate (I), or unmethylated (U), using the HMM presented previously (*SI Appendix*, section 2) (18). These inferred methylation states were cross-validated against whole-genome bisulphite-sequencing data of six epiRILs (*SI Appendix*, section 3, Fig. S1, and Table S1).

Definition of Parental DMRs. We conducted a probe-level comparison of the HMM calls between the *ddm1* and WT parents (*SI Appendix*, section 4). Probe-level methylation calls were denoted as polymorphic when the parents differed (e.g., I in *ddm1* and M in WT) and as nonpolymorphic when they were identical (e.g., U in *ddm1* and U in WT). Neighboring probes reporting the same polymorphic state were collapsed into single regions. Hence, parental DMRs were defined as regions of at least three consecutive probes that reported the same extreme polymorphic state (i.e., transitions from M in WT to U in *ddm1* or vice versa). We found 2,611 DMRs, all of which were U in the *ddm1*. Detailed summary statistics are given in *SI Appendix*, Table S2.

Calling of Parental Origin of DMRs in the epiRILs. For any given epiRIL the parental origin of each DMR (i.e., epigenotype) was determined using an HMM-based inference method (*SI Appendix,* section 4).

Mendelian Segregation Criterion. Under the assumption that DMRs were stable for eight generations of breeding, both WT- and *ddm1*-like parental states should appear according to Mendelian segregation ratios in the epiRILs. The sampling variation around these ratios was calculated from a binomial distribution taking into account the sample size ($n = 123$), the cross design, and the 8% F_2 contamination previously reported (12). DMRs in the epiRILs showing a percentage of WT-like states between 62.7% and 83.3% (the expected value being 73%) were taken as putative transgenerationally stable markers. In total 867 parental DMRs fulfilled this criterion and were used subsequently as a starting point for map construction (*SI Appendix*, section 5, Fig. S2, and Table S3).

Extension of Lander–Green Algorithm. Derivation of a genetic map using DMRs was carried out through an extension of the Lander-Green algorithm (20), which was designed to accommodate marker and individual specific error rates. Our implementation of this algorithm is detailed in *SI Appendix,* section 6.

Transcriptome Analysis of epiRILs and *ddm1* Seedlings. Whole-genome expression profiling was performed using a custom NimbleGen tiling array (37). For experimental details, see *SI Appendix*, section 7.

Transgenerational Analysis of DMRs. MeDIP-chip was carried out for epiRIL 344 for seven generations of selfing after the backcross, following the protocol described above. At each generation, DNA from five siblings was pooled. The expected signal behavior was derived using a Markov Chain strategy, considering the Mendelian inheritance of the marker probes (*SI Appendix*, section 8).

Construction of the Consensus Map. To facilitate a meaningful comparison of the epiRILs map with those of the 17 different F_2 populations, we constructed a consensus map (*SI Appendix*, section 9 and Fig. S11) by using the epiRILs map as a reference and selecting from each of the F_2 maps the SNPs closest to the reference, allowing a maximum distance of ±1.39 Mb. The average distance from reference was ±0.17 Mb, which led to little loss of information in capturing the recombination structure along the genome (*SI Appendix*, Figs. S12 and S13). Markers deemed too distant were not included in the consensus map. This process resulted in 83 markers (*SI Appendix*, Table S7).

Recombination Intensities at Major Annotation Transitions. Fig. 2 *A* and *C* shows that the recombination intensity increases rapidly at the pericentromeric boundaries, which also coincide with major transitions in genome content from genes to transposons. To find the area where the recombination intensity is maximal, we implemented a sliding window approach (*SI Appendix*, section 10 and Fig. S15).

Note Added in Proof. During the reviewing process, Yelina et al (Yelina NE, Choi K, Chelysheva L, Macaulay M, de Snoo B, et al. (2012) Epigenetic Remodeling of Meiotic Crossover Frequency in Arabidopsis thaliana DNA Methyltransferase Mutants. PLoS Genet 8(8): e1002844. doi:10.1371/journal.pgen.1002844) reported elevated centromere-proximal COs, coincident with pericentromeric decreases and distal increases in met1 mutants. However, total numbers of CO events were found to be similar between wild type and met1. These results support the trends observed in the epiRIL population.

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1. Lichten M, de Massy B (2011) The impressionistic landscape of meiotic recombination. *Cell* 147:267–270.
2. Mézard C, Vignard J, Drouaud J, Mercier R (2007) The road to crossovers: Plants have their say. *Trends Genet* 23:91–99.
3. Muyt AD, Mercier R, Mézard C, Grelon M (2009) Meiotic recombination and crossovers in plants. *Genome Dyn* 5:14–25.
4. Edlinger B, Schlögelhofer P (2011) Have a break: Determinants of meiotic DNA double strand break (DSB) formation and processing in plants. *J Exp Bot* 62:1545–1563.
5. Chen W, Jinks-Robertson S (1999) The role of the mismatch repair machinery in regulating mitotic and meiotic recombination between diverged sequences in yeast. *Genetics* 151:1299–1313.
6. Emmanuel E, Yehuda E, Melamed-Bessudo C, Avivi-Ragolsky N, Levy AA (2006) The role of *AtMSH2* in homologous recombination in *Arabidopsis thaliana*. *EMBO Rep* 7:100–105.
7. Maloisel L, Rossignol JL (1998) Suppression of crossing-over by DNA methylation in *Ascobolus*. *Genes Dev* 12:1381–1389.
8. Shi J, et al. (2010) Widespread gene conversion in centromere cores. *PLoS Biol* 8:e1000327.
9. Melamed-Bessudo C, Levy AA (2012) Deficiency in DNA methylation increases meiotic crossover rates in euchromatic but not in heterochromatic regions in *Arabidopsis*. *Proc Natl Acad Sci USA* 109:E981–E988.
10. Mirouze M, et al. (2012) Loss of DNA methylation affects the recombination landscape in *Arabidopsis*. *Proc Natl Acad Sci USA* 109:5880–5885.
11. Teixeira FK, et al. (2009) A role for RNAi in the selective correction of DNA methylation defects. *Science* 323:1600–1604.
12. Johannes F, et al. (2009) Assessing the impact of transgenerational epigenetic variation on complex traits. *PLoS Genet* 5:e1000530.
13. Vongs A, Kakutani T, Martienssen RA, Richards EJ (1993) *Arabidopsis thaliana* DNA methylation mutants. *Science* 260:1926–1928.
14. Kakutani T, Munakata K, Richards EJ, Hirochika H (1999) Meiotically and mitotically stable inheritance of DNA hypomethylation induced by *ddm1* mutation of *Arabidopsis thaliana*. *Genetics* 151:831–838.
15. Tsukahara S, et al. (2009) Bursts of retrotransposition reproduced in *Arabidopsis*. *Nature* 461:423–426.
16. Lippman Z, et al. (2004) Role of transposable elements in heterochromatin and epigenetic control. *Nature* 430:471–476.
17. Johannes F, Colomé-Tatché M (2011) Quantitative epigenetics through epigenomic perturbation of isogenic lines. *Genetics* 188:215–227.
18. Cortijo S, Wardenaar R, Colomé-Tatché M, Johannes F, Colot V (2012) Genome-wide analysis of DNA methylation in Arabidopsis using MeDIP-chip. *Plant Epigenome: Understanding and Analysis*, eds McKeown P, Spillane C (Humana Press/Springer, New York).
19. Bernatavichute YV, Zhang X, Cokus S, Pellegrini M, Jacobsen SE (2008) Genome-wide association of histone H3 lysine nine methylation with CHG DNA methylation in *Arabidopsis thaliana*. *PLoS ONE* 3:e3156.
20. Lander ES, Green P (1987) Construction of multilocus genetic linkage maps in humans. *Proc Natl Acad Sci USA* 84:2363–2367.
21. Giraut L, et al. (2011) Genome-wide crossover distribution in *Arabidopsis thaliana* meiosis reveals sex-specific patterns along chromosomes. *PLoS Genet* 7:e1002354.
22. Drouaud J, et al. (2007) Sex-specific crossover distributions and variations in interference level along *Arabidopsis thaliana* chromosome 4. *PLoS Genet* 3:e106.
23. Drouaud J, et al. (2006) Variation in crossing-over rates across chromosome 4 of *Arabidopsis thaliana* reveals the presence of meiotic recombination "hot spots" *Genome Res* 16:106–114.
24. Salomé PA, et al. (2012) The recombination landscape in *Arabidopsis thaliana* F2 populations. *Heredity (Edinb)* 108:447–455.
25. Horton MW, et al. (2012) Genome-wide patterns of genetic variation in worldwide *Arabidopsis thaliana* accessions from the RegMap panel. *Nat Genet* 44:212–216.
26. Pan J, et al. (2011) A hierarchical combination of factors shapes the genome-wide topography of yeast meiotic recombination initiation. *Cell* 144:719–731.
27. Brick K, Smagulova F, Khil P, Camerini-Otero RD, Petukhova GV (2012) Genetic recombination is directed away from functional genomic elements in mice. *Nature* 485:642–645.
28. Schmitz RJ, et al. (2011) Transgenerational epigenetic instability is a source of novel methylation variants. *Science* 334:369–373.
29. Becker C, et al. (2011) Spontaneous epigenetic variation in the *Arabidopsis thaliana* methylome. *Nature* 480:245–249.
30. Richards EJ (2008) Population epigenetics. *Curr Opin Genet Dev* 18:221–226.
31. Johannes F, Colot V, Jansen RC (2008) Epigenome dynamics: A quantitative genetics perspective. *Nat Rev Genet* 9:883–890.
32. Richards EJ (2009) Quantitative epigenetics: DNA sequence variation need not apply. Genes Dev 15;23(14):1601–1605.
33. Weigel D (2012) Natural variation in *Arabidopsis thaliana*: From molecular genetics to ecological genomics. *Plant Physiol* 158:2–22.
34. Schmitz RJ, Ecker JR (2012) Epigenetic and epigenomic variation in *Arabidopsis thaliana*. *Trends Plant Sci* 17:149–154.
35. Roux F, et al. (2011) Genome-wide epigenetic perturbation jump-starts patterns of heritable variation found in nature. *Genetics* 188:1015–1017.
36. Latzel V, Zhang Y, Karlsson Moritz K, Fischer M, Bossdorf O (2012) Epigenetic variation in plant responses to defense hormones. *Ann Bot (Lond)*, 10.1093/aob/mcs088.
37. Reinders J, et al. (2009) Compromised stability of DNA methylation and transposon immobilization in mosaic *Arabidopsis* epigenomes. *Genes Dev* 23:939–950.
38. Roudier F, et al. (2011) Integrative epigenomic mapping defines four main chromatin states in *Arabidopsis*. *EMBO J* 30:1928–1938.

Supplementary Information Appendix:

Features of the *Arabidopsis* recombination landscape resulting from the combined loss of sequence variation and DNA methylation

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Contents

1 MeDIP protocol

The original 123 epiRILs were chosen using a selective (epi)genotyping strategy based on two uncorrelated complex traits, flowering time and root length. Phenotypically informative lines from both tails of the trait distributions were selected for DNA methylation profiling and whole genome resequencing. Extensive simulation studies indicated that local and global recombination distortion effects are negligible as a result of this selection procedure, particuarly for QTL effect sizes that are consistent with the heritability estimates obtained for these traits.

MeDIP-chip was carried out as previously described [1]. Briefly, DNA was extracted using the Qiagen MaxiPrep kit and sonicated using a Diagenode Bioruptor. Sonicated DNA (1.5μg) was denaturated at $95°$C for 10 minutes in 600μl of buffer 1 (10 mM Tris HCl pH 7.5, 500 mM NaCl, 1 mM EDTA). Immunoprecipitation was performed by adding 5μg of anti-5mC monoclonal antibody (Diagenode, cat n° MAb-006-500) to the DNA solution and by incubating the resulting mix overnight at $4°$C with gentle agitation. Forty μl of washed M280 Dynabeads (Invitrogen) were then added and the suspension was incubated at $4°$C for 4 hr with gentle agitation. The supernatant was then discarded, 300μl of buffer 1 were added to the IP pellet and the suspension was incubated 10 min at room temperature with gentle agitation. Three more washes were carried out at room temperature, using 600μl of buffer 1. The IP fraction was eluted by incubating it 1 hour at $42°$C with 300μl of buffer 2 (30mM Tris HCl pH: 8.0) and 7μl of Proteinase K (NEB, 20μg/μl). DNA from the IP fraction was recovered by phenol-chloroform extraction and ethanol precipitation. IP and INPUT (150ng) DNA were amplified using the Sigma GenomePlex Complete Whole Genome Amplification (WGA) Kit following the manufacturer's instructions. Cy3 and Cy5 labeling was performed using the Nimblegen Dual color DNA labeling kit (Roche NimbleGen) and co-hybridizations in dye-swap were performed using a custom design NimbleGen 3x720K array, as previoulsy described [2].

2 Hidden Markov Model for methylation state classification

We analyze the $\ln(IP/INPUT)$ signal using a Hidden Markov Model (HMM), as described in detail elsewhere [1]. Briefly, we view the signal as a mixture of three underlying components: the unmethylated component (U) for low signal, the intermediately methylated component (I) for middle intensity signal, and the methylated component (M) for high signal. The HMM relies on the following properties of the MeDIP-chip data: i) the probe signals are noisy proxies of an unobserved (hidden) methylated, intermediate or unmethylated state, and ii) the probe signals are spatially correlated along the genome so that neighboring probes provide similar information.

We use the $\ln(IP/INPUT)$ signal distribution of probes corresponding to introns as emission probability for the U component, in order to incorporate the biological knowledge of introns being mostly unmethylated into the estimation procedure. We approximate this distribution to an arbitrary degree using a mixture of 30 normal distributions using the EM algorithm [3]. The signal distribution for intronic sequences is not noticeably affected in *ddm1*, as expected. As emission probability for the M component we consider a normal distribution with a fixed mean at the 99^{th} percentile of the intron distribution and unknown variance. Finally, as emission probability for the I component we also consider a normal distribution with mean fixed at the mid-point between the other two means, and variance equal to the one of the M emission probability. For the analysis of the *ddm1* parent, we use instead the M and I emission probabilities of the wt-parent.

We implement the Baum-Welch algorithm [4, 5] using the above distributional constraints to find the estimates for the variances, the probe-to-probe transition probabilities, and the initial probabilities. Once these parameters are estimated we proceed to calculate the most likely chain of hidden states (U, I or M). We calculate the individually most likely single hidden probe state at each position, given the observed probe signals and the parameters of the HMM. The result of this procedure is the methylome.

3 BS-seq protocol and comparison to MeDIP

Whole genome bisulfite sequencing was carried out as previously described [6], using Illumina sequencing and read lengths of 76nt or 100nt. Reads were mapped using BS Seeker [7]. Average genome coverage was 29X for the 6 epiRILs. Conversion rates were well over 99% in each case (mean conversion rate = 99.28%), based on data obtained for unmethylated chloroplast DNA.

After the production of files with read sequences (fastq files) the read sequences were subjected to several rounds of treatment before alignment to the genome. Parts of the adapter sequence were for example also sequenced when the read length was longer than the molecule that was sequenced. These parts were removed in the first step. The adapter part was found by sliding the adapter sequence over the read sequence starting from the end of the read sequence. We allowed one mismatch for every five bases (sequencing errors). The minimum overlap was set to four bases and the last three bases were removed when the adapter sequence was not found. In the second step we removed read sequences with more than one copy (we kept one copy). These copies were likely produced during the PCR step and were thus deemed not informative. At the end before mapping we also removed read sequences that were shorter than 30bp. The reads were after these treatments aligned to the genome using BS Seeker [7]. Only reads which could be assigned to a single locus with a maximum of three mismatches were used to quantify the methylation status of individual cytosines (settings: -t N -e 73 or 98 -m 3).

In order to make the BS-seq data comparable to the MeDIP-chip data we calculated so called “BS probe signals”. These were calculated by dividing the number of methylated cytosine calls by the total number of cytosine calls in each of the windows for which the probes were designed (window length: 165 bp; signal range: $0 - 1$). By cytosine calls we mean the individual cytosine call of each read sequence.

For the comparison with the MeDIP data (comparison with HMM classification) we only selected probe windows with 35 or more cytosines, and probes with a conservation score of 95 or less. Also at least half of the cytosines should be covered by one or more reads. We applied these criteria in order to exclude misbehaving probes.

The conservation score of a probe indicates the uniqueness of the probe sequence. These scores were obtained by performing a blast search. Scores are percentage of identity with the second best hit (score range: $45 - 100$). The best hit is with the genomic location for which the probe was designed. Probes with a high conservation score are more likely to misbehave.

Figure S1 (SI Appendix) shows the distribution of BS probe signals for the different HMM classifications. This figure shows that both the MeDIP protocol and the analysis method performed well.

For a direct comparison of the HMM classification we needed to classify the BS probe signals into unmethylated, intermediate and methylated. The BS probe signals were classified by applying different sets of signal cutoffs, one cutoff for the transition from U to I and one for transition I to M. The most optimal combination of cutoffs will give the highest percentage of overlapping probe classifications. Table S1 (SI Appendix) shows the total percentage of overlapping probe classifications, and the percentages for each methylation class separately, for the most optimal cutoffs (% of HMM classification with overlap classification BS probes). This table shows that the overlap with the unmethylated and fully methylated classification is substantial ($\sim 97\%$ and $\sim 81\%$) but that there is a smaller overlap with the intermediate class ($\sim 16\%$). For the DMR analysis however, we only focus on probes that make a complete switch from methylated in wt to unmethylated in *ddm1*. For that reason the miscalls in the intermediate class are less relevant.

4 Parental DMRs and epiRILs parent of origin

We conduct a probe-level comparison of the inferred methylation states between the wt and the *ddm1* parent. Probes are classified as non-polymorphic if the methylation state is the same between parents, or as polymorphic if the methylation state between parents is different. We collapse into regions the clusters of consecutive probes (minimum of three) which are extreme polymorphisms (M-U) between the parents. There are 2611 of these regions, which we call parental DMRs. They are all hypomethylated in the *ddm1* parent (M in wt, U in *ddm1*), which is expected from the *ddm1*-induced loss of methylation reported previously [8].

For each epiRIL j we consider the collection of probes corresponding to a parental DMR i and calculate the average posterior probability from the HMM (Section 2) over these probes for the U, I and M states ($\bar{p}_{ij}(M)$, $\bar{p}_{ij}(I)$, $\bar{p}_{ij}(U)$). A region of the epiRIL is called wt-like or *ddm1*-like if the state that maximizes $\bar{p}_{ij}$ is M or U, respectively. In the case where I maximizes p_j^i we do not assign a parent of origin. Using the above, we define the measurement error associated with the parent of origin call for each DMR i and epiRIL j as

$$\epsilon_{ij} = 1 - max(\bar{p}_{ij}). \tag{1}$$

5 Mendelian ratios

Under the assumption that DMRs were stable for eight generations of breeding, both wt- and *ddm1*-like parental states should appear according to Mendelian segregation ratios in the epiRILs. The sampling variation around these ratios was calculated from a binomial distribution taking into account the sample size ($N = 123$), the cross design (backcross) and the 8% F_2 contamination previously reported [9]. This yields a confidence interval for the wt mendelian ratios of $(62.7\%, 83.3\%)$ and for the *ddm1* Mendelian ratios of $(16.7\%, 37.3\%)$.

We determine at each parental DMR the percentage of epiRILs from wt origin ($\%wt$), the percentage of epiRILs from *ddm1* origin ($\%ddm1$) and the percentage of epiRILs with intermediate methylation ($\%I$). Of course, for each DMR, $\%wt + \%ddm1 + \%I = 100\%$. We select a region as being stably inherited if the percentage of wt-like epiRILs, *ddm1*-like epiRILs and intermediate epiRILs fulfill all the following inequalities:

- $\%wt + \%I > 62.7\%$
- $\%wt < 83.3\%$
- $\%I < \%wt$
- $\%I < \%ddm1$

In this way, we select the DMRs with a low percentage of intermediate epiRILs (smaller proportion than any of the other two categories) and for which the amount of wt-like epiRILs combined with any amount of intermediate epiRILs fulfills the Mendelian criterion of inheritance. Using this definition, we find 871 regions segregating in a Mendelian fashion.

6 Lander-Green algorithm, inference of parental states and genetic length

These selected regions mentioned above are viewed as markers in a genetic map, and their observed marker states (e.g. wt or *ddm1*-like) are analogously defined as epigenotypes. Since the genomic positions of all markers are known, we need only calculate the map distance between markers, taking into account all sources of error in the parental calls. To achieve this, we develop a generalized version of the Lander-Green algorithm [10] which considers individual and marker dependent epigenotype errors. In this HMM-based algorithm the observations are the parental calls of the markers (i.e. wt-like, *ddm1*-like or I), and the hidden states are the real (unobserved) parental origins (wt-like or *ddm1*-like).

We define the probability $\Pr(c_j^i|h_j^i) = q_j^i(c_j^i, h_j^i)$ that the epigenotype c_j^i ($c_j^i = \{wt - \text{like}, \textit{ddm1} - \text{like}, I\}$) is observed at marker j in epiRIL i, given that the true epigenotype is h_j^i at that marker ($h_j^i = \{wt - \text{like}, \textit{ddm1} - \text{like}\}$). The set of probabilities q is called emission probabilities. We relate these emission probabilities to the measurement error ϵ_{ij} (Eq. 1) and to some amount of stochastic epigenetic changes, s, that could have occurred during inbreeding. These two sources of error thus quantify the quality of the parent of origin call at each DMR:

$$q_j^i(c_j^i, h_j^i) = \begin{cases} 1 - \epsilon_{ij} + s, & \text{if } c_j^i = h_j^i, \\ \epsilon_{ij} + s, & \text{if } c_j^i \neq h_j^i. \end{cases} \tag{2}$$

The variable q is a matrix of real numbers with dimension ($2 \times M$), where M is the number of markers for each epiRIL.

We also define the probability that the true epigenotype at a marker j in epiRIL i is h_j^i ($h_j^i = \{wt{-}\text{like}, \textit{ddm1}{-}\text{like}\}$) given that the observed epigenotype at that marker is c_j^i ($c_j^i = \{wt{-}\text{like}, \textit{ddm1}{-}\text{like}, I\}$). This probability can be calculated from q_j^i using the Bayes theorem:

$$p_j^i(h_j^i, c_j^i) = \Pr(h_j^i|c_j^i) = \frac{\Pr(c_j^i|h_j^i)\,\Pr(h_j^i)}{\Pr(c_j^i)},$$

where $\Pr(c_j^i|h_j^i) = q_j^i(c_j^i, h_j^i)$, $\Pr(c_j^i) = \sum_{y=\{(\text{wt},\textit{ddm1})\text{-like}\}} \Pr(c_j^i|h_j^i = y)$, and the initial probabilities $\Pr(h_j^i) = cte$ are given by the Mendelian ratios. The variable p is a matrix of real numbers with dimension ($2 \times M$) for each epiRIL.

Denote by R_j the probability of a recombinant type between locus j and $j+1$. Therefore the transition probabilities between two loci are

$$\Pr(h_{j+1}^i = y|h_j^i = z) = \begin{cases} 1 - R_j, & \text{if } y = z, \\ R_j, & \text{if } y \neq z, \end{cases}$$

where $y = z = \{\text{wt-like}, \textit{ddm1}\text{-like}\}$. The matrix of transition probabilities is:

$$T_{j,j+1} = \begin{pmatrix} t_{j,j+1}^{\text{wt-like},\text{wt-like}} & t_{j,j+1}^{\text{wt-like},\textit{ddm1}\text{-like}} \\ t_{j,j+1}^{\textit{ddm1}\text{-like},\text{wt-like}} & t_{j,j+1}^{\textit{ddm1}\text{-like},\textit{ddm1}\text{-like}} \end{pmatrix} = \begin{pmatrix} 1 - R_j & R_j \\ R_j & 1 - R_j \end{pmatrix}.$$

For each epiRIL i, we calculate the forward variable $\alpha_j^i(h)$ as

$$\begin{aligned} \alpha_1^i(h) &= p_1^i(h, c_1^i), \\ \alpha_{j+1}^i(h) &= \left[\sum_{z=\{(\text{wt},\textit{ddm1})\text{-like}\}} \alpha_j^i(z)\, t_{j,j+1}^{z,h} \right] q_{j+1}^i(c_{j+1}^i, h), \end{aligned}$$

where $h = \{\text{wt-like}, \textit{ddm1}\text{-like}\}$ and $1 \leq j \leq M_C - 1$, where M_C is the number of markers per chromosome. We also define the backward variable $\beta_j^i(h)$ as:

$$\begin{aligned} \beta_{M_C}^i(h) &= 1, \\ \beta_{j-1}^i(h) &= \sum_{z=\{(\text{wt},\textit{ddm1})\text{-like}\}} t_{j-1,j}^{h,z}\, q_j^i(c_j^i, z)\, \beta_j^i(z), \end{aligned}$$

where $h = \{\text{wt-like}, \textit{ddm1}\text{-like}\}$ and $M_C \geq j \geq 2$.

R_j is estimated iteratively using:

$$R_j = \frac{1}{N} \sum_{i=1}^{N} \frac{\Big(\alpha_j^i(y), \;\; \alpha_j^i(z)\Big) \cdot T_{j,j+1}^{*} \cdot \Big(\beta_{j+1}^i(y)\, q_{j+1}^i(c_{j+1}^i, y), \;\; \beta_{j+1}^i(z)\, q_{j+1}^i(c_{j+1}^i, z)\Big)^{tr}}{\Big(\alpha_j^i(y), \;\; \alpha_j^i(z)\Big) \cdot T_{j,j+1} \cdot \Big(\beta_{j+1}^i(y)\, q_{j+1}(c_{j+1}^i, y), \;\; \beta_{j+1}^i(z)\, q_{j+1}(c_{j+1}^i, z)\Big)^{tr}},$$

where $1 \leq j \leq M_C - 1$, $y = z = \{$wt-like,*ddm1*-like$\}$, and $T^*_{j,j+1} = ((0, R_j), (R_j, 0))$ is a 2×2 matrix. The amount of stochastic changes, s, is fixed at some value.

We use the final estimates $\hat{R}_j$ (for $j = 1, ..., M$) to calculate the likelihood of the data as

$$\log(L(\hat{R})) = \sum_{i=1}^{N} \sum_{j=1}^{M} \log\left(\Big(\alpha^i_j(y),\ \ \alpha^i_j(z)\Big) \cdot T_{j,j+1} \cdot \Big(\beta_{j+1}(y),\ \ \beta_{j+1}(z)\Big)^{tr}\right), \tag{3}$$

where again $y = z = \{$wt-like,*ddm1*-like$\}$, and N is the total number of epiRILs. The whole procedure is repeated for a series of fixed values for s and the value that maximizes the profile likelihood is taken as an estimate for the biological rate of stochasticity.

Finally, we infer parental haplotypes along the genome by selecting at each DMR the parental call that maximizes the probability of the observations given the model:

$$w^i_j = \text{argmax}(\Pr(h^i_j | c^i_j, \text{model})), \tag{4}$$

where argmax stands for the argument of the maximum. We refer to this latter inference as the epigenotype reconstruction step.

The epigenotype reconstruction step assigns unlikely epigenotypes (e.g. DMRs with initial intermediate methylation calls or DMRs with high measurement error) to the most likely wt-like or *ddm1*-like epigenotype. This process can change the Mendelian segregation ratios. We therefore reevaluate Mendelian inheritance at each DMR, such that the wt-like epigenotype percentage falls within $(\%wt < 83.3\%)$ and $(\%wt > 62.7\%)$. From the initial 871 markers, after epigenotype reconstruction 867 are selected according to this criterion. We find that among these 867 markers, only 262 map to unique genetic locations (i.e. they are more than 0.0001 cM apart from each other), the rest being genetically redundant and uninformative. We remove these redundant markers and iterate through the following steps: i) Remove markers at the same map position (distance< 0.0001cM). ii) Recalculate R_j using the Lander-Green algorithm (with constant epigenotyping error). iii) Obtain the most likely haplotype map. After 5 iterations the procedure converges to a robust map containing 184 markers. Finally, we remove problematic markers showing strong correlations across chromosomes. This final cleaning step is performed in R/qtl [11] and follows closely the relevant section on map cleaning described in Broman [12]. Our final map contains 126 robust markers.

Finally, we convert the recombination at fixation R for the epiRIL to the value of r at meiosis. We can use the result at fixation (because generation = 8 here) [13]:

$$r = \frac{2R}{3 - 4R}. \tag{5}$$

This estimator is biased [14], the modified estimator for r is given by

$$r = \frac{2R}{N(3 - 4R)^3} \left(9N - 24NR + 16R^2N - 12R + 12\right), \tag{6}$$

where $N = 123$ is the number of lines. This new estimator has a bias which is proportional to $1/N^2$.

7 Transcriptome analysis of epiRILs and *ddm1* seedlings

Whole-genome expression profiling was performed using tiling microarrays on 10 day-old seedlings grown in liquid $1/2$MS media, 16 hours of light at 22°C and 8 hours of night at $19\,^{\circ}$C. Total RNA was extracted using Rneasy Plant Minikit (Qiagen) according to the supplier's instructions. One ug of total RNA was amplified with one round of in vitro transcription 10h at 37°C using the MessageAmp II aRNA Amplification Kit (Ambion). Double stranded cDNA synthesis was then performed on 2 ug of aRNA using the SuperScript Double-Stranded cDNA Synthesis Kit (Invitrogen). Cy3 and Cy5 labeling was performed using the Nimblegen Dual color DNA labeling kit (Roche NimbleGen) according to manufacturer's instructions. Co-hybridization in dye-swap experiment was performed using the NimbleGen 3x720K array design and following manufacturer's instructions. Data acquisition was performed according to Roche Nimblegen instructions. Hybridization data was normalized using an ANOVA model, and data were averaged on the dye-swap to remove tile-specific dye biases.

8 Transgenerational data

In order to observe further evidence of the stable inheritance of methylation states, we performed measurements of the methylome of one epiRIL (line 344) for seven generations following the backcross. At each generation, the DNA of five siblings was pooled together to perform a MeDIP chip analysis, as described in Section 1. The data was normalized as described in [1].

For each of the 126 stable markers, we calculate the mean signal of all probes corresponding to that marker at every generation. We classified the markers in two different categories: wt-inherited or *ddm1*-inherited, based on the genetic map information at the last generation (Section 6).

In order to obtain a theoretical model to describe the expected behavior of the signal over generation time we calculate the expected proportions of wt/wt epigenotype, *ddm1*/*ddm1* epigenotype and wt/*ddm1* epigenotype at every generation of inbreeding following the backcross. For the wt-inherited markers, we implemented a Markov Chain with selection against the *ddm1* homozygotes at every generation. For the markers inherited from the *ddm1* parent, we implemented a Markov Chain with selection against wt/wt epigenotypes. We obtained the following results for the proportions of each of the three epigenotypes at any generation t:

$$\begin{aligned} p_{ddm1}(t) &= \left\{ \frac{1}{2^t+2}, \frac{2}{2^t+2}, 1-\frac{3}{2^t+2} \right\}; \\ p_{wt}(t) &= \left\{ 1-\frac{3}{3\times 2^t+2}, \frac{2}{3\times 2^t+2}, \frac{1}{3\times 2^t+2} \right\}, \end{aligned} \tag{7}$$

where $p_{ddm1} = \{\text{Pr}(wt/wt), \text{Pr}(wt/\textit{ddm1}), \text{Pr}(\textit{ddm1}/\textit{ddm1})\}$ are the proportions of wt/wt, wt/*ddm1* and *ddm1*/*ddm1* epigenotypes at every generation t for the probes getting fixed in a *ddm1* haplotype at generation S7, and $p_{wt} = \{\text{Pr}(wt/wt), \text{Pr}(wt/\textit{ddm1}), \text{Pr}(\textit{ddm1}/\textit{ddm1})\}$ are the proportions of wt/wt, wt/*ddm1*, and *ddm1*/*ddm1* epigenotypes at every generation t for the probes getting fixed in a wt haplotype at generation S7.

Since five plants were used at each generation to provide the DNA material for the MeDIP protocol, we needed to approximate the signal at each generation by a weighted sum over the three different epigenotypes multiplied by the mean of their signal at each generation:

$$\begin{aligned} s_{ddm1}(t) = {} & p_{ddm1}^{(1)}(t) * \mu_{wt/wt}(t) + p_{ddm1}^{(2)}(t) * \mu_{wt/ddm1}(t) \\ & + p_{ddm1}^{(3)}(t) * \mu_{ddm1/ddm1}(t); \\ s_{wt}(t) = {} & p_{wt}^{(1)}(t) * \mu_{wt/wt}(t) + p_{wt}^{(2)}(t) * \mu_{wt/ddm1}(t) + p_{wt}^{(3)}(t) * \mu_{ddm1/ddm1}(t), \end{aligned} \tag{8}$$

where $p^{(i)}$ is the component i of vector p. At every generation t we use as mean value for the signal of the *ddm1*/*ddm1* epigenotype ($\mu_{ddm1/ddm1}(t)$) the $\ln(IP/INPUT)$ signal distribution of probes corresponding to introns, and we calculate its mean by approximating this distribution to an arbitrary degree using a mixture of 30 normal distributions using the EM algorithm [3]. For the signal of the wt/wt epigenotype ($\mu_{wt/wt}(t)$), we consider the 99^{th} percentile of the intron distribution at every generation t, and for the signal of the wt/*ddm1* epigenotype ($\mu_{wt/ddm1}(t)$) we consider the middle point between $\mu_{ddm1/ddm1}(t)$ and $\mu_{wt/wt}(t)$. We can associate the methylated component with the epigenotype wt/wt and the unmethylated component with the epigenotype *ddm1*/*ddm1* because all the parental DMRs are methylated in the wt parent and unmethylated in the *ddm1* one.

9 Consensus map

We evaluated the inferred epiRILs map by comparing it to genetic maps of classical Arabidopsis experimental crosses. To this end, we re-analyzed 17 recently published F_2 populations that were derived from pairs of 18 different *Arabidopsis* natural accessions [15]. In total, 7045 plants had been genotyped (an average of 410 plants per cross, range=($235 - 462$)) at an average of 235 genome positions (range=($215 - 257$)) [15].

In order to perform a meaningful comparison of the genetic and epigenetic maps, we needed them to have similar coverage. We selected a subset of markers for each cross such that the number of markers and the bp position of those markers is the same across maps.

In particular, we chose a reference genome with markers at the position of the epigenetic markers. For each reference marker, we selected from the 17 natural accessions crosses the marker which is closest to it. For these selected markers we used the R-qtl package [11] implemented in R (http://www.r-project.org) to re-estimate the genetic map (function $est.map$ using map.function=haldane). In the cases where there was no marker close enough to the reference position, we artificially added a marker at the reference position and we used R-qtl to re-estimate the map (function $est.map$ using map.function=haldane) and to simulate the most likely genotype at that position (function $fill.geno$ with method=argmax).

In Fig. S11 (SI Appendix) we can see the representation of the consensus map in base pair positions. The mean distance from the consensus map markers is 0.17Mb and the furthest marker is at 1.39Mb from the reference marker. The main map characteristics are not affected by the use of this common map, as can be seen in Fig. S12 (SI Appendix). At the same time, the difference in recombination intensity between the accession crosses and the epiRIL at each reference marker interval ($\left(\frac{\text{cM}}{\text{Mb}}\right)_{\text{acc cross}} - \left(\frac{\text{cM}}{\text{Mb}}\right)_{\text{epiRIL}}$) is not correlated with the difference in the size of the marker interval ($\Delta\text{Mb}_{\text{acc cross}} - \Delta\text{Mb}_{\text{reference}}$), which is due to the slight mismatch of the marker positions between the reference map (i.e. the epiRIL marker positions) and the position of the accessions markers (Fig. S13 (SI Appendix)). This allows us to do a meaningful comparison of the features of the maps for each cross.

10 Recombination intensities at major annotation transitions

Figure 2A and C show how the recombination intensity increases rapidly at the pericentromeric boundaries, which also coincide with major transitions in genome content from genes to transposons. In order to find the area where the recombination intensity is maximal we implemented a sliding window approach (window size: 3 Mb, step size: 100 kb). We used the transition in genome content as a reference point. The recombination intensity of each window was calculated by dividing the percentage of recombination events within each window (% of all recombination events) by the percentage of bp covered by the same overlapping marker intervals (% of all marker intervals). This calculation was done across all sliding windows. Marker intervals with a small overlap with the window were excluded when the non-overlapping part was bigger than 1 Mb. The maximum recombination intensity of the F_2 populations was found at a distance of $+100$ kb (middle position window; in the direction of the arms; Fig. S15 (SI Appendix)).

The windows with the maximum recombination intensity (located $+100$ kb from the transition towards the arms) were further examined for the presence of shared breakpoints. In an effort to fine-map shared breakpoints within these windows, we resorted to probe-level tiling array data of specific epiRILs that were recombinant in these windows. For this analysis we only considered differentially methylated probes (M in wt and U in *ddm1*) that showed Mendelian segregation patterns in the epiRILs. To avoid misclassified probes due to cross-hybridization issues we also considered probes with a conservation score of 85 or less (high quality probes). We selected differentially methylated probes as being stably inherited if the percentage of wt-like epiRILs ($\%wt$), *ddm1*-like epiRILs ($\%ddm1$) and intermediate epiRILs ($\%I$) fulfill all the following inequalities:

- $\%wt > 62.7$
- $\%wt < 83.3$

- $\%ddm1 > \%I$

Shared breakpoints were fine-mapped by visual inspection of the probe classification (probes that fulfill the above criteria) of the recombinant epiRILs. For this purpose we only plotted probes that were M (green; wt-like) or U (red; *ddm1*-like). We considered a breakpoint as being shared if at least three epiRILs were having an overlapping breakpoint interval. The shared breakpoint interval length was calculated by taking the difference of the minimum start position and the maximum stop position of all intervals. Using the above criteria we found 12 shared breakpoints (Table S10 (SI Appendix)).

References

[1] Cortijo S, Wardenaar R, Colomé-Tatché M, Johannes F, Colot V (2012) Genome-wide analysis of dna methylation in arabidopsis using medip-chip. Methods in Molecular Biology (in press).

[2] Roudier F, Ahmed I, Bérard C, Sarazin A, Mary-Huard T, et al. (2011) Integrative epigenomic mapping defines four main chromatin states in arabidopsis. EMBO Journal 30: 1928–1938.

[3] McLachlan G, Peel D (2000) Finite Mixture Models. John Wiley and Sons, Inc.

[4] Baum L, Petrie T, Soules G, , Weiss N (1970) A maximization technique occurring in the statistical analysis of probabilistic functions of markov chains. Ann Math Stat 41: 164–171.

[5] Rabiner L (1989) A tutorial on hidden markov models and selected applications in speech recognition. Proceedings of the IEEE 77: 257–286.

[6] Cokus S, Feng S, Zhang X, Chen Z, Merriman B, et al. (2010) Shotgun bisulphite sequencing of the arabidopsis genome reveals dna methylation patterning. Nature 452: 215–219.

[7] Chen P, Cokus S, Pellegrini M (2010) Bs seeker: precise mapping for bisulfite sequencing. BMC Bioinformatics 11:203, doi 10.1186/1471-2105-11-203.

[8] Vongs A, Kakutani T, Martienssen R, Richards E (1993) *Arabidopsis thaliana* dna methylation mutants. Science 260: 1926-1928.

[9] Johannes F, Porcher E, Teixeira F, Saliba-Colombani V, Simon M, et al. (2009) Assessing the impact of transgenerational epigenetic variation on complex traits. PLoS Genetics 5: e1000530.

[10] Lander E, Green P (1987) Construction of multilocus genetic linkage maps in humans. Proceedings of the National Academy of Sciences 84: 2363–2367.

[11] Broman K, Wu H, Sen S, Churchill G (2003) R/qtl: Qtl mapping in experimental crosses. Bioinformatics 19: 889–890.

[12] Broman K (2010) Genetic map construction with r/qtl. Technical report 214.

[13] Johannes F, Colomé-Tatché M (2011) Quantitative epigenetics through epigenomic pertubation of isogenic lines. Genetics 188: 215-227.

[14] Martin O, Hospital F (2006) Two- and three-locus tests for linkage analysis using recombinant inbred lines. Genetics 173: 451–459.

[15] Salomé P, Bomblies K, Fitz J, Laitinen RAE, Warthmann N, et al. (2011) The recombination landscape in arabidopsis thaliana f2 populations. Heredity 108: 447-455.

Supplementary Information Appendix (Figures and Tables):

Features of the *Arabidopsis* recombination landscape resulting from the combined loss of sequence variation and DNA methylation

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Supplemental figure legends

Figure S1: Comparison BS-seq and MeDIP-chip (HMM classification): The distribution of the BS probe signals for the three methylation categories of the HMM classification. White, gray and dark gray box: unmethylated, intermediate and methylated probes respectively. Numbers at the top of the figure are line numbers of the epiRILs that were sequenced.

Figure S2: Segregation ratios: Segregation ratios for the 867 Mendelian DMRs (left) and the 126 Mendelian DMRs used for map construction. The green and red horizontal bars indicate the expected Mendelian ratios (73% for the wt inheritance and 27% for the *ddm1* inheritance), and the green and red areas show the ±99% CI (62.7% - 83.3% for the wt, and 16.7% - 37.3% for the *ddm1*). At the position of each DMR (x-axes) the green cross represents the percentage of wt inherited epiRILs and the red dot represents the percentage of *ddm1* inherited epiRILs.

Figure S3: Small RNA abundance: Hit-normalized density (reads per kb per 1 million reads) of 24nt small RNA (sRNA) corresponding to stable and reversible DMRs in the wt and *ddm1* parental lines. Isolation was performed as described in Pfeffer et al. (Curr. Protoc. Mol. Biol 2005). Wt and *ddm1* sRNA libraries were prepared and sequenced by Fasteris (Switzerland) using Illumina Hi-Seq 2000 technology and 200 μg of total RNA extracted from whole seedlings. Sequence reads were matched against the *Arabidopsis thaliana* genome (TAIR8) using MUMmer v3.0 software (Kurtz et al., Genome Biol. 2004). Only sRNA reads with perfect match over their entire length (15-30nt) were analyzed further (79402397 and 63798837 reads for wt and *ddm1*, respectively). The number of 24-nt reads matching the DMRs is expressed as a normalized density, as describe in Teixeira et. al. (Science 2009). A full description of the sRNA sequence data will be presented elsewhere.

Figure S4: Sequence annotation of DMRs and markers: Percentage of DMRs or markers that contain (parts of) genes, transposable elements (TE) or intergenic regions for the categories: Non-Mendelian DMRs (A), Mendelian DMRs (B) and Markers (C).

Figure S5: CGH analysis: A comparison of the $\log_2$ input signals of all wt (WT.R1, WT.R2 and WT.R3) and ddm1 (DDM1.R1 and DDM1.R2) replicates used for the detection of DMRs. For each gene, transposable element and non-Mendelian DMR (S5-1), Mendelian DMR (S5-2) or marker (S5-3) the average input signal was calculated. The signal distributions were quantile normalization. Transposable element signals and gene signals are indicated with dark gray and gray respectively. DMRs or markers are indicated with red. Numbers in the figure correspond to correlation coefficients of transposable elements (dark gray), genes (gray) and DMRs or markers (red).

Figure S6: Recombination fractions: Recombination fractions for each pair of markers along the genome. Red corresponds to small recombination fractions, blue corresponds to a large recombination fractions. This image was generated using the R-qtl package implemented in R.

Figure S7: Methylation levels of inherited non-recombinant pericentromeric regions: Percentage of unmethylated probes for the epiRILs with a non-recombinant pericentromere. Red: *ddm1*-inherited pericentromere; green: wt-inherited pericentromere.

Figure S8: Transcriptome analysis: Shown is the expression difference between wild type and epiRIL 98, epiRIL 202 and *ddm1* across the genome for probes that are hypo methylated between the parents (M in wt and U in *ddm1*). The top part of the figure shows the location of the centromere (the dot), the pericentromere (dark grey surrounding the centromere) and the chromosomal arms (gray). The part that is not covered by the genetic map is indicated with light gray. The inference of inherited wt and *ddm1* haplotypes along the genome is indicated with green and red respectively. Results show that expression is higher compared to wt in *ddm1* inherited regions and comparable to wt in wt inherited regions. These observations indicate that the transcriptomal changes induced by *ddm1* are inherited in the epiRILs.

Figure S9: Correlation between physical length and genetic length: The physical length of each of the five Arabidopsis chromosomes in Mb and their genetic length in cM are positively correlated. In the inset, the table shows the numerical values for the physical and genetic lengths for each chromosome.

Figure S10: Use of different map functions: Map increase between each pair of markers (ΔcM) for the epiRIL recombination map, calculated using different map functions: Morgan’s map function (black), Haldane’s map function (blue), Kosambi’s map function (red) and Carter and Falconer’s map function (orange). Changes in map lengths are modest, and do not alter any of the conclusions concerning local recombination changes observed in the epiRILs (see main text).

Figure S11: Consensus map: For each chromosome, the markers for the epiRIL (top) and the 17 different accession crosses are represented in light gray circles. The markers selected for the consensus map are represented with solid colored dots, and the light colored vertical lines show the position of the reference marker. If one cross between accessions had no marker closer enough to the reference marker, one extra marker was added (colored cross). The color code is a guide to the eye.

Figure S12: Change in genetic length: The genetic length (cM) versus the marker position (Mb) for the 17 accession crosses (top) and the epiRIL (bottom) is shown, both for the consensus map (in red) and the original map for each accession cross and the epiRIL (black). No major deviations from the original map are observed when the consensus map is utilized.

Figure S13: Correlation between Δ(bp) and Δ(cM/Mb): Correlation plot between the difference in inter-marker length for the epiRIL map compared to the accession crosses map ($\Delta(\text{bp})=\Delta(\text{bp})_{\text{accession cross}} - \Delta(\text{bp})_{\text{epiRIL}}$), and the difference in recombination activity at that marker interval ($\Delta(\text{cM/Mb})= \Delta(\text{cM/Mb})_{\text{accession cross}} - \Delta(\text{cM/Mb})_{\text{epiRIL}}$). The fraction of variance explained by the model is $R^2=0.000274$.

Figure S14: Location of historical recombination hotspots: Shown are the locations of hotspots detected by Horton et al. (Nat. Genet. 2012). Top: gene (gray line) and transposon (black line) density along the chromosomes. Middle: location of the centromere (dot), the pericentromere (dark grey) and the chromosomal arms (light gray). Bottom: location of the hotspots. The hotspot density of all detected hotspots is indicated in gray. This hotspot density is determined with the use of a sliding window approach (window size: 1 Mb; step size: 200 kb). The blue lines indicate hotspots that were identified in at least eight of the nine regional samples (Horton et al., Nat. Genet. 2012).

Figure S15: Recombination intensity around major annotation transitions: Shown is the recombination intensity of 3 Mb windows at different distances from the major annotation transitions. The recombination intensity is calculated across all sliding windows at the same distance from the transitions. The maximum recombination intensity of the F2 populations was found at a distance of + 100 kb (in the direction of the arms).

Figure S16: Gene density and Recombination rates along pericentromeric regions: Gene density is shown along the pericentromeric regions of all five chromosomes in successive 105kb windows (red dots; the heterochromatic knob on chr4 is also shown) and for the 67 breakpoint point intervals that have been narrowed down to less than 500 kb (blue crosses). The proportion of COs contributed by each interval to the total number of COs for that chromosome is indicated by vertical purple bars.

Figure S17: Fine mapping shared recombination breakpoints within AT-zones in the epiRILs: Shown are three examples of shared recombination breakpoints that map within AT-zones, that is, within 3 Mb of the inflection points between transposon and gene density at pericentromeric boundaries (grey rectangle). For each example, we plot all the tiling array probes that were M in wt and U in *ddm1* and which showed Mendelian segregation patterns in the epiRILs. Shared breakpoints are shown by an arrow and could be fine-mapped within 158 kb, 93 kb and 68 kb on chromosomes 2, 3 and 4 respectively.

Figure S18: Regression plot of fold change recombination intensity: A comparison of recombination intensity fold changes (cM/Mb of a given region divided by cM/Mb chromosome average; see Figure 3 in the main text) between AT-zones and chromosome arms. There is a negative relationship between AT-zones and chromosome arms in the epiRILs and (on average) a positive relationship in the F2 populations. This indicates that the recombination suppression in AT-zones is compensated by increased recombination in chromosome arms in the epiRILs, and that this effect is a specific feature of this population.

Supplemental table legends

Table S1: Correspondence between HMM and BS-seq: Overlap between HMM and BS-seq (in %) for all probes, and for probes that are classified as U, I or M by HMM for the epiRILs that were sequenced.

Table S2: Parental DMRs: The chromosome and position (start bp and stop bp) for the 2611 parental DMRs are given.

Table S3: DMRs with Mendelian segregation: The chromosome and position (start bp and stop bp) are given for the 867 parental DMRs that show Mendelian segregation

Table S4: Markers: The chromosome, position (start bp and stop bp) and genetic position (cM) are given for the 126 non-redundant markers.

Table S5: epiRIL line numbers: epiRIL numbers in Figure 1B and their corresponding line numbers.

Table S6: Analysis of transposable elements (TEs) which are located within or overlap with markers: Column 1 (marker_id) provides identifiers for the markers used for map construction which overlap with TEs. Column 8 (mobilization) denotes potential mobility of TEs (highlighted in gray) located within or overlapping markers based on bioinformatic analysis (Buisine et al., Genomics 2008). Column 10 (evidence sequencing) provides information about the actual mobility of TEs based on preliminary re-sequencing data. The remaining columns contain information about the ID of the TE (TE_id), the family (TE_family), the clade (TE_clade), the order (TE_order), the class (TE_class) and if the TE encodes its own transposase protein (autonomy). See also legend at the bottom of the table.

Table S7: Consensus map: For each of the 83 markers of the consensus map, the chromosome and position (bp start and bp stop) corresponding to the epiRIL markers are given, and the position and name of the retained SNPs for each of the 17 natural accession crosses are shown.

Table S8: Fold change recombination intensities: Recombination intensity (cM/Mb) of pericentromeric regions, AT - zones and chromosome arms compared to chromosome average. For the F_2 populations the median value is shown with its range. (A): fold-increase relative to chromosome average (intensity region / intensity chromosome average). (B): fold-decrease relative to chromosome average (intensity chromosome average / intensity region).

Table S9: Fine-mapping individual recombination breakpoints: Name refers to the left DMR that was used initially to identify each breakpoint interval within pericentromeric regions. Intervals were narrowed down first by considering all of the parental DMRs included in these intervals and that fulfill the Mendelian segregation criterion. Some intervals could be further narrowed down by considering individual probes outside of DMRs and for which parental DNA methylation states (M in wild type and U in *ddm1*) segregate in Mendelian fashion. Column F indicates the number of epiRILs with breakpoints in the corresponding interval and column G the proportion of breakpoints contributed by this interval to the total number of recombinants for that chromosome.

Table S10: Fine-mapping of shared recombination breakpoints: Location and length of shared breakpoint intervals, and the number of epiRILs with a shared breakpoint interval.

Table S11: Genetic lengths and fold change recombination intensity: Estimated genetic lengths (A), and fold change in recombination intensity (FC) of pericentromeric regions (B), AT–zones (C) and chromosome arms (D). FC = intensity of region / intensity chromosome average. Lower and upper bounds are given by 95% confidence intervals. These tables show the ordering of the 17 F_2 crosses (Salomé et al, Heredity 2012) shown in Figure 3 of the main text. These crosses are: P2:Lov-5×Sha, P3:Bur-0×Bay-0, P6:Van-0×Bor-4, P7:NFA-8×Van-0, P8:Est-1×RRS7, P9:Tsu-1×RRS10, P10:Bur-0×Cvi-0, P12:Est-1×Br-0, P15:Br-0×C24, P17:Cvi-0×RRS7, P19:Bay-0×Lov-5, P20:Bor-4×NFA-8, P35:Tamm-2×Col-0, P66: Fei-0×Col-0, P129:C24×RRS10, P145:Sha×Fei-0, P169:Ts-1×Tsu-1.

Figure S1

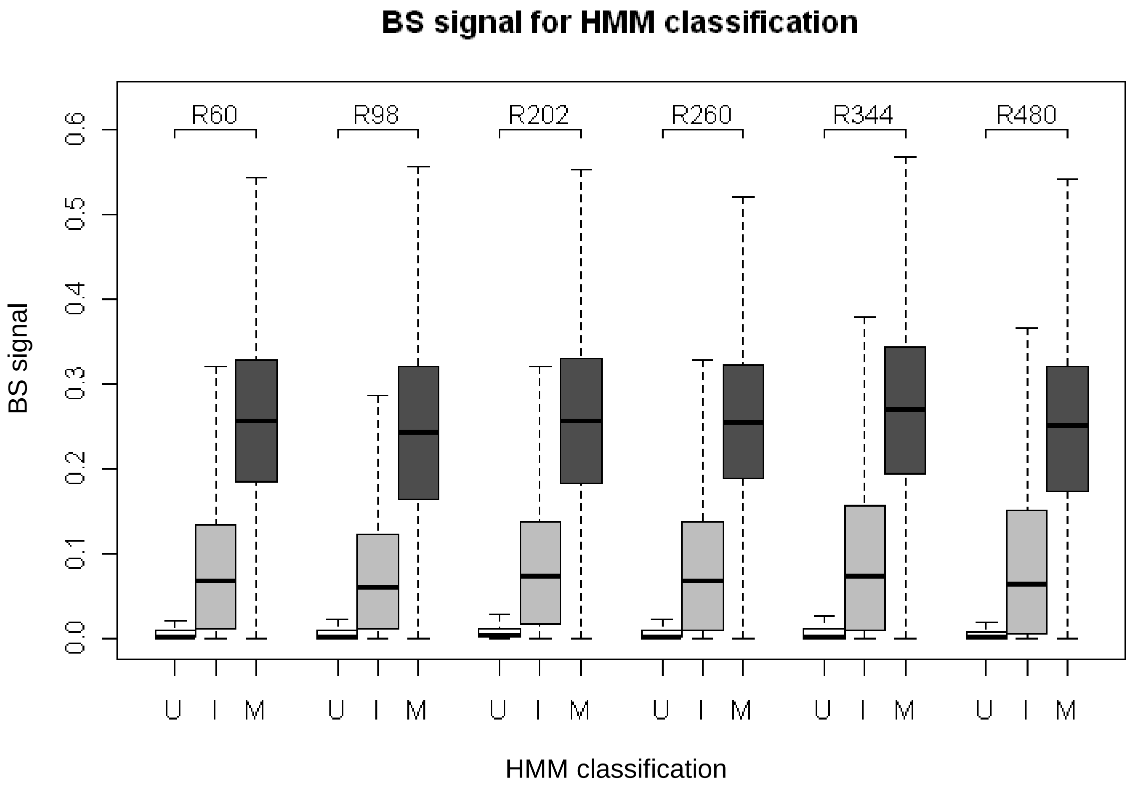
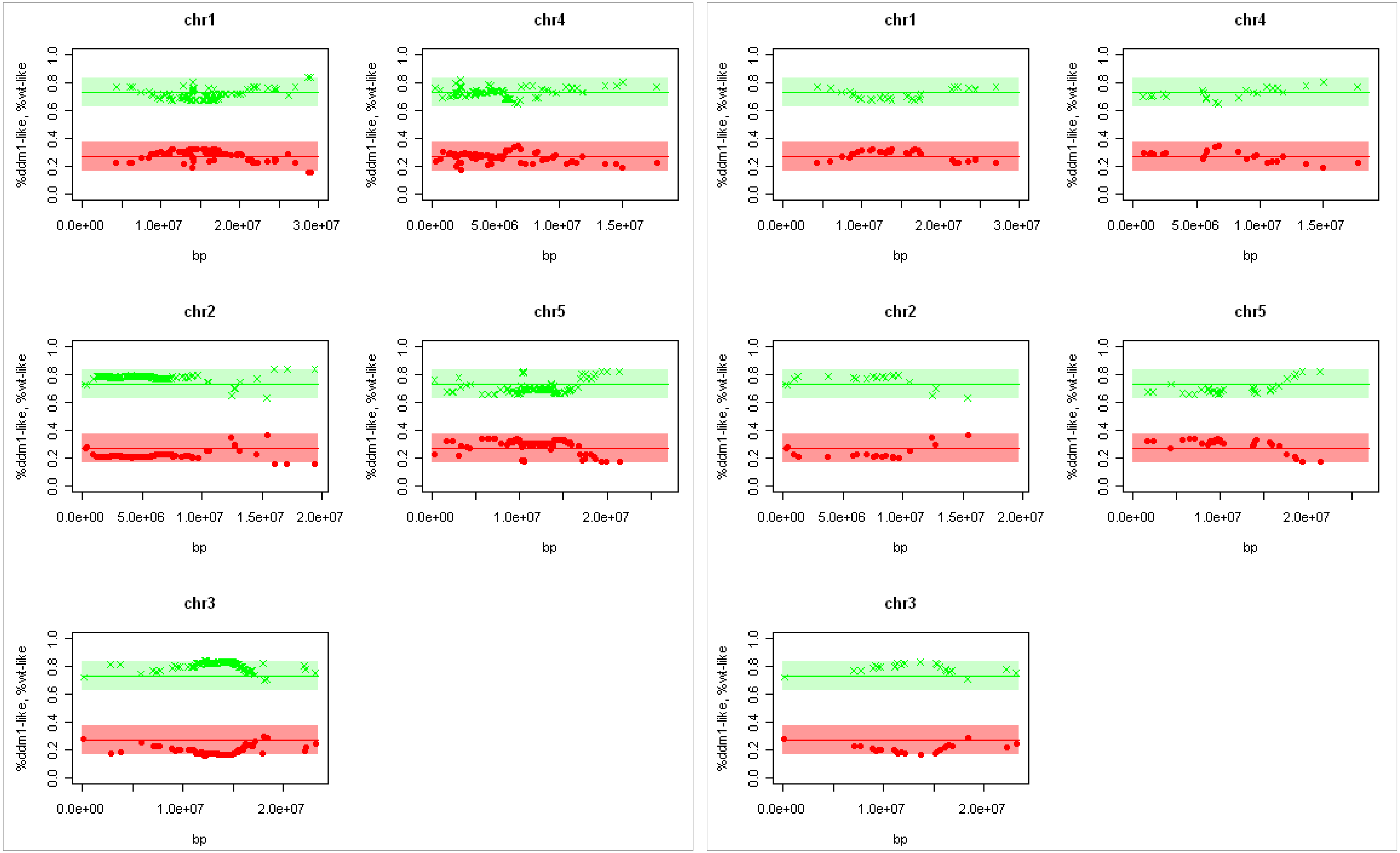

BS signal for HMM classification
BS signal
0.0
0.1
0.2
0.3
0.4
0.5
0.6
R60
R98
R202
R260
R344
R480
U
I
M
HMM classification

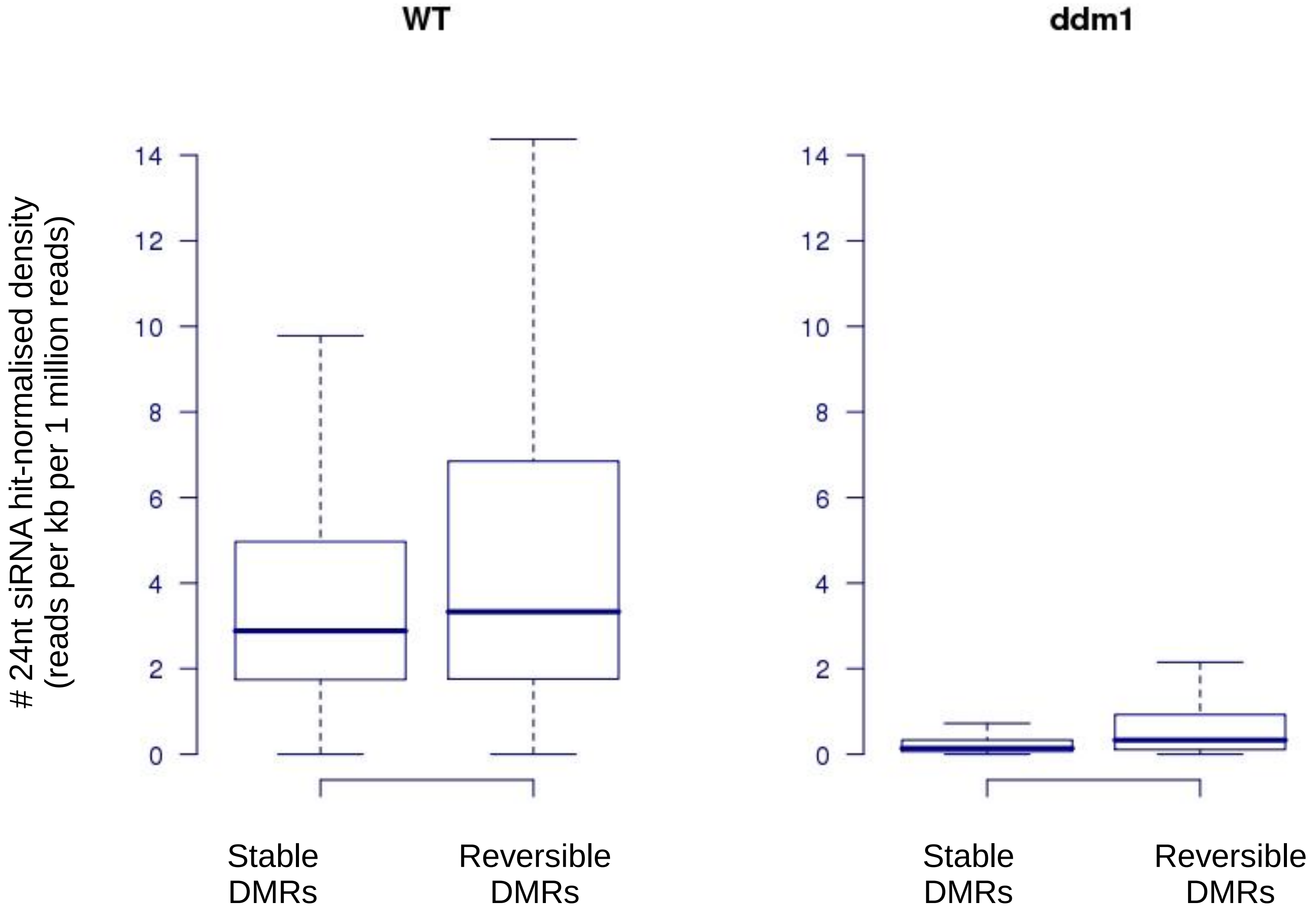
Figure S2



867 Mendelian DMRs

126 Mendelian DMRs
used for map construction

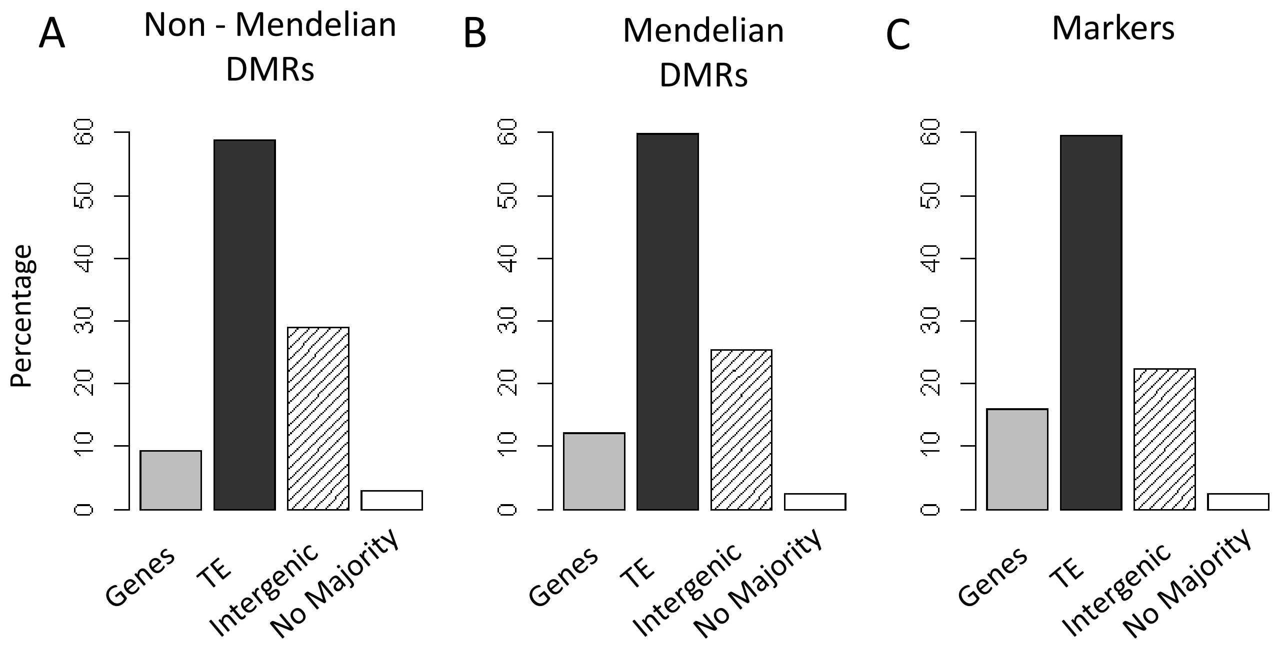
Figure S3



Wilcoxon rank test
p-value = 0.0003155

Wilcoxon rank test
p-value < 2.2e-16

Figure S4



#	163	1025	503	53
%	9.3	58.8	28.8	3.0

105	519	221	22
12.1	59.9	25.5	2.5

20	75	28	3
15.9	59.5	22.2	2.4

Figure S5-1

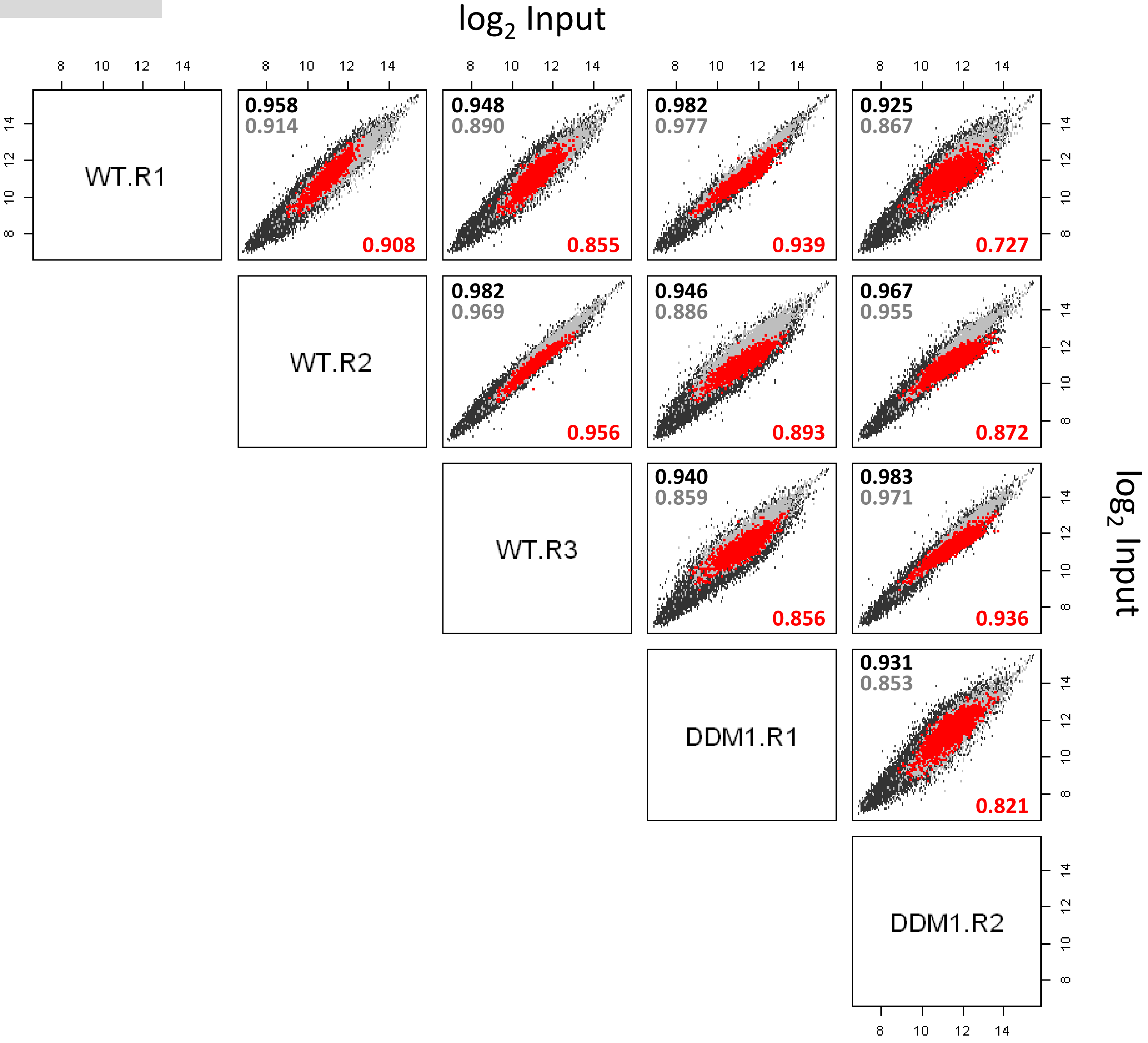

log2 Input
WT.R1
WT.R2
WT.R3
DDM1.R1
DDM1.R2
8
10
12
14
0.958
0.914
0.908
0.948
0.890
0.855
0.982
0.977
0.939
0.925
0.867
0.727
0.982
0.969
0.956
0.946
0.886
0.893
0.967
0.955
0.872
0.940
0.859
0.856
0.983
0.971
0.936
0.931
0.853
0.821
log2 Input

Figure S5-2

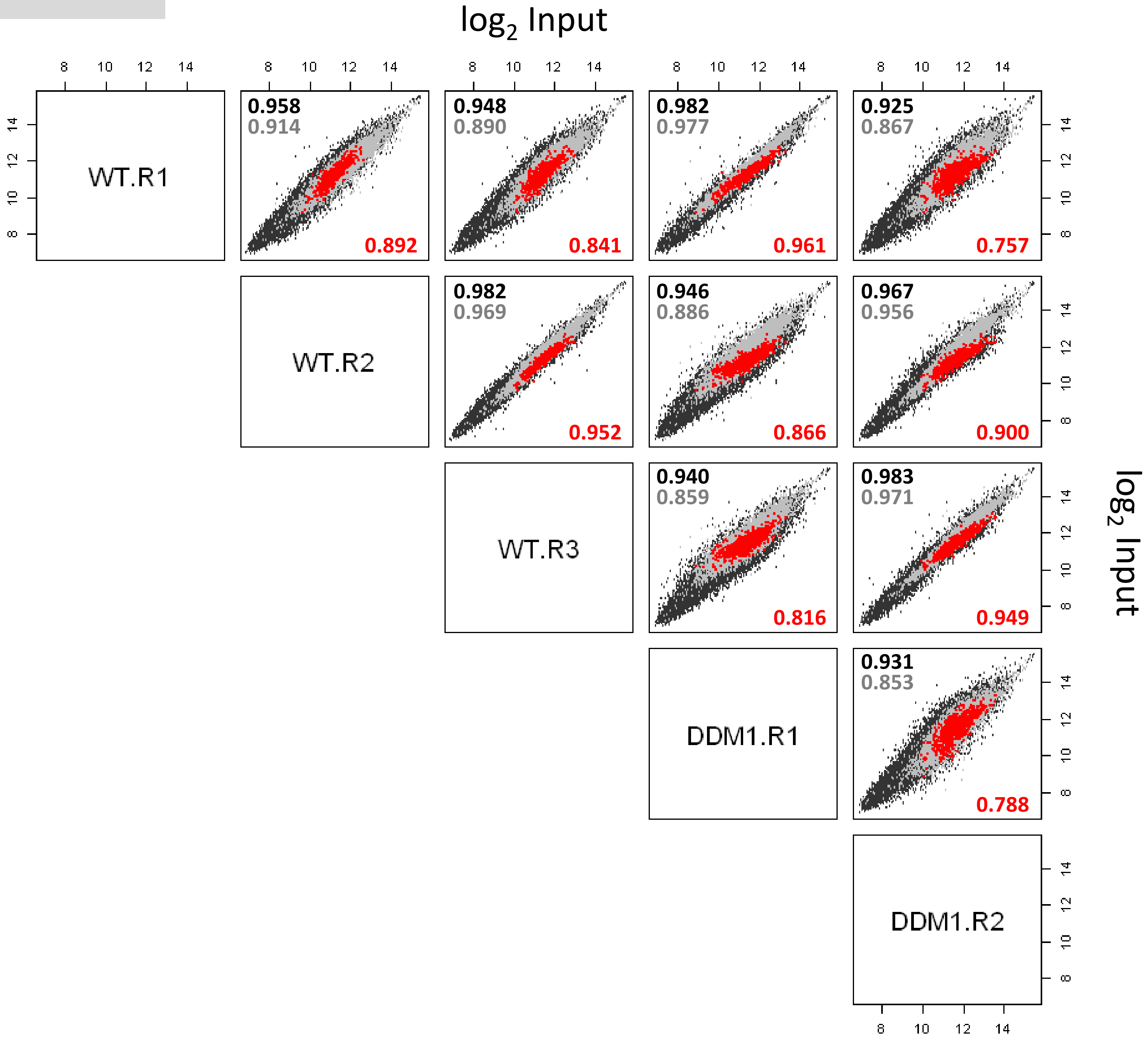

log$_2$ Input
8 10 12 14
WT.R1
WT.R2
WT.R3
DDM1.R1
DDM1.R2
0.958
0.914
0.892
0.948
0.890
0.841
0.982
0.977
0.961
0.925
0.867
0.757
0.982
0.969
0.952
0.946
0.886
0.866
0.967
0.956
0.900
0.940
0.859
0.816
0.983
0.971
0.949
0.931
0.853
0.788
log$_2$ Input

Figure S5-3

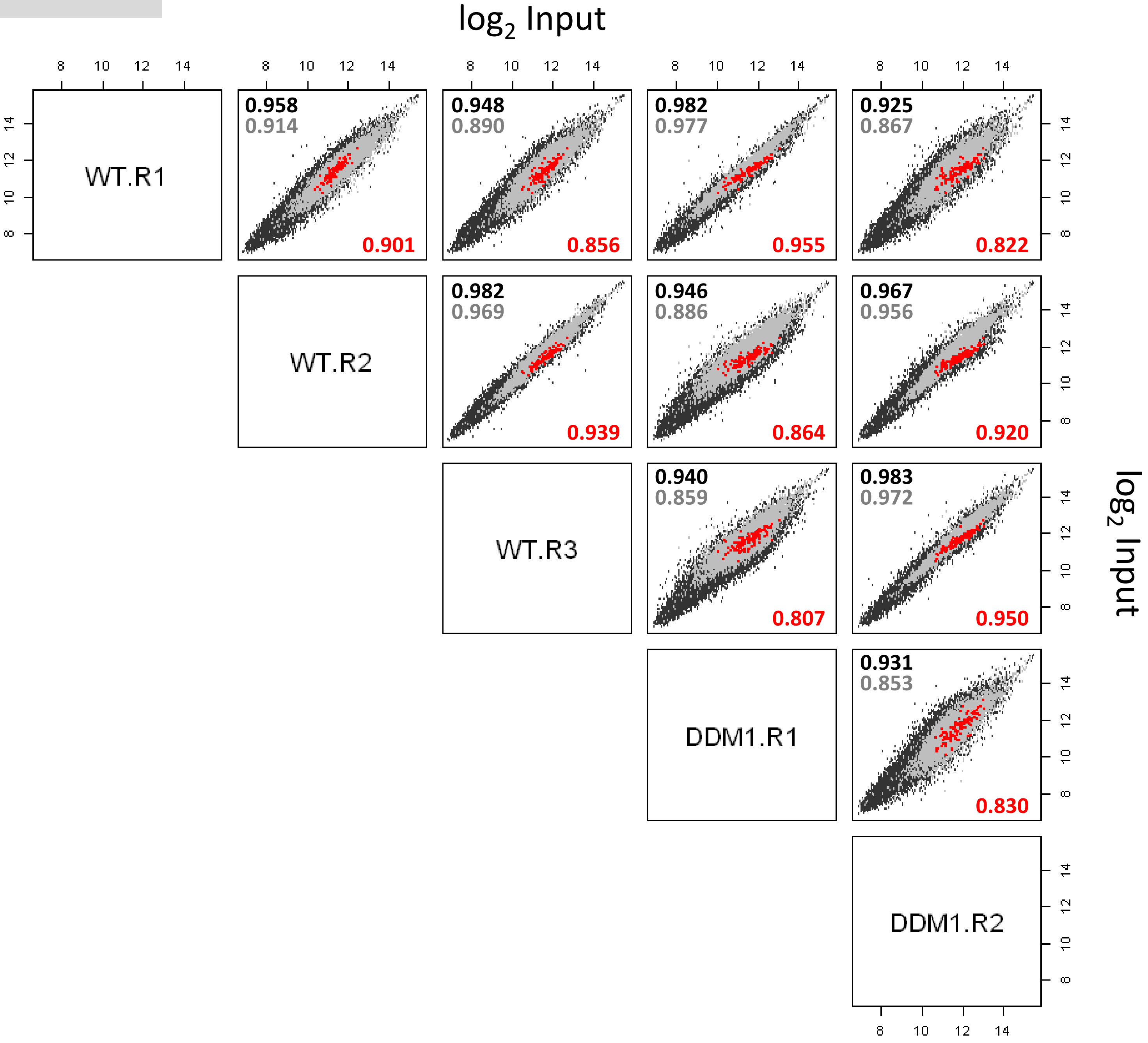

$\log_2$ Input
$\log_2$ Input
8
10
12
14
WT.R1
WT.R2
WT.R3
DDM1.R1
DDM1.R2
0.958
0.914
0.901
0.948
0.890
0.856
0.982
0.977
0.955
0.925
0.867
0.822
0.982
0.969
0.939
0.946
0.886
0.864
0.967
0.956
0.920
0.940
0.859
0.807
0.983
0.972
0.950
0.931
0.853
0.830

Figure S6

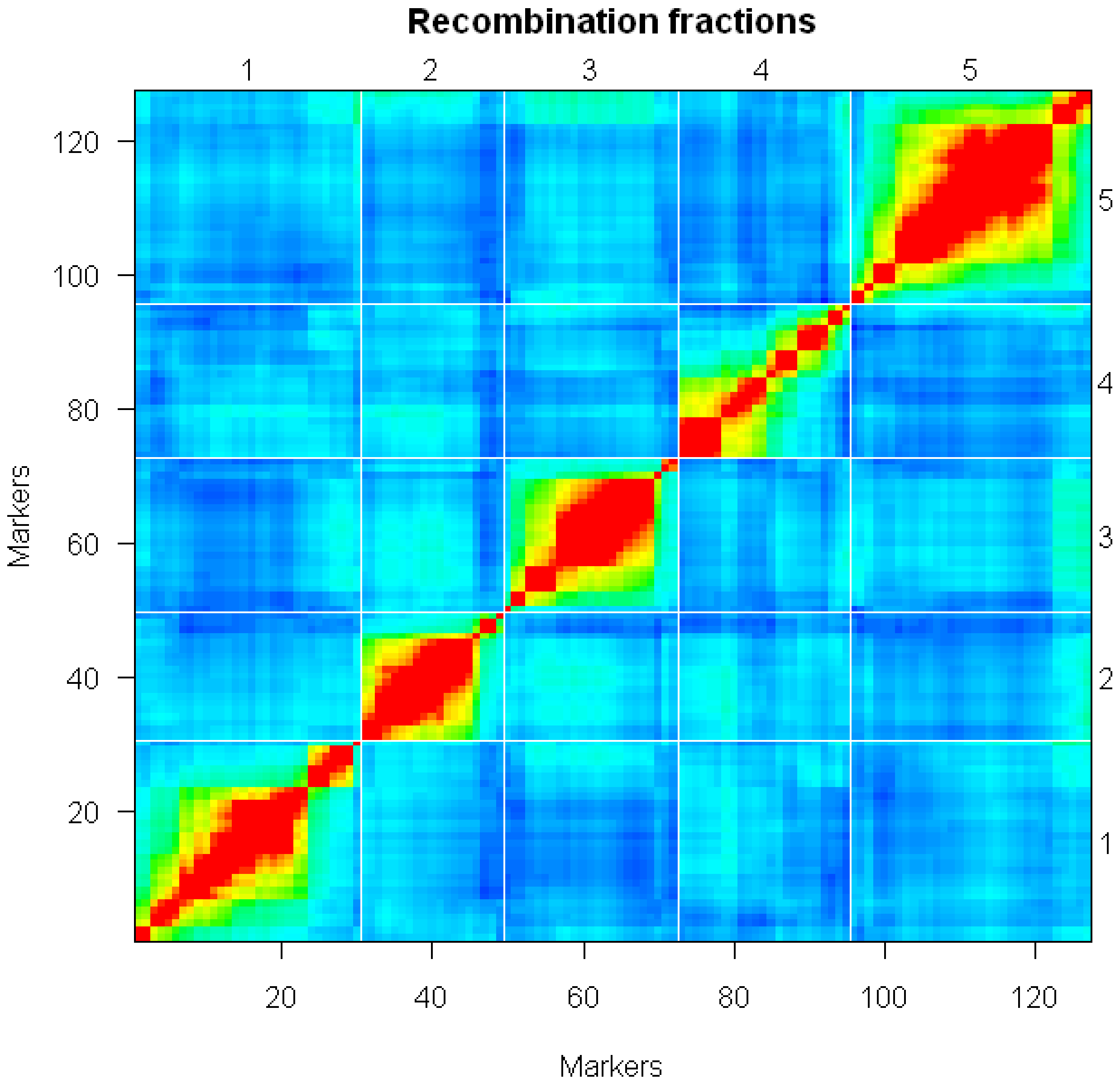

Recombination fractions
1
2
3
4
5
120
100
80
60
40
20
Markers
5
4
3
2
1
20
40
60
80
100
120
Markers

Figure S7

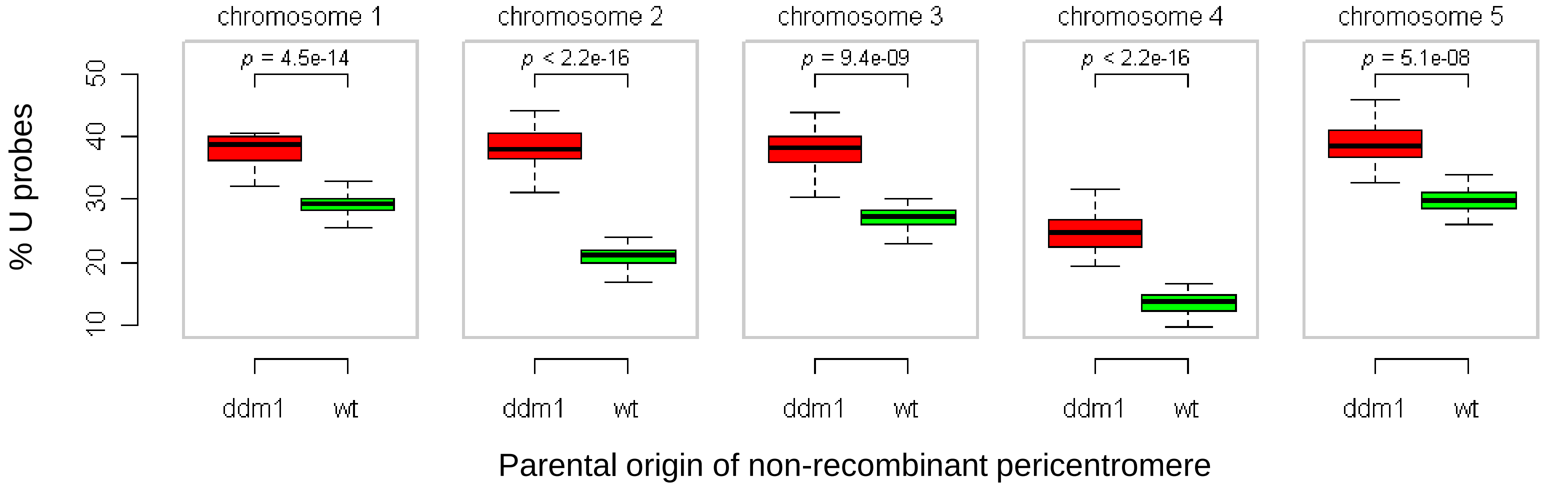

chromosome 1
p = 4.5e-14
chromosome 2
p < 2.2e-16
chromosome 3
p = 9.4e-09
chromosome 4
p < 2.2e-16
chromosome 5
p = 5.1e-08
% U probes
10
20
30
40
50
ddm1
wt
ddm1
wt
ddm1
wt
ddm1
wt
ddm1
wt
Parental origin of non-recombinant pericentromere

Figure S8-1

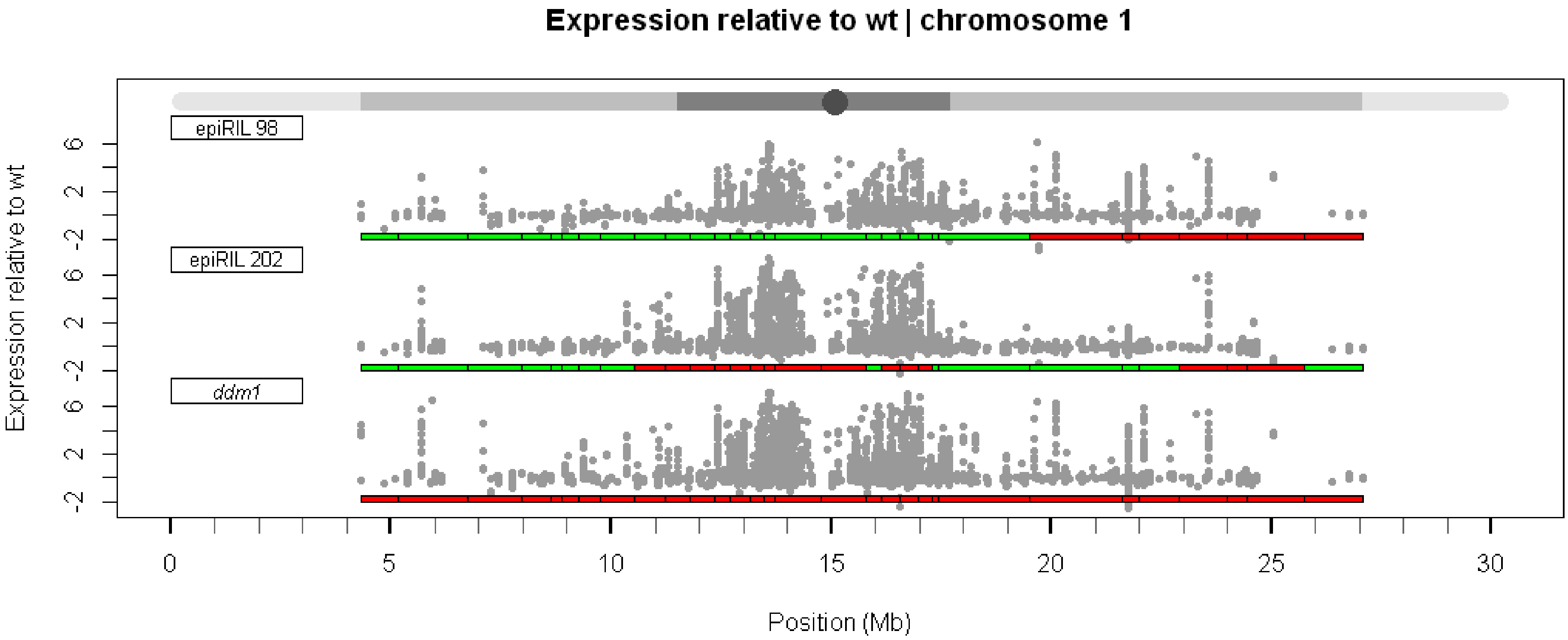

Expression relative to wt | chromosome 1
epiRIL 98
epiRIL 202
ddm1
Expression relative to wt
-2
2
6
0
5
10
15
20
25
30
Position (Mb)

Figure S8-2

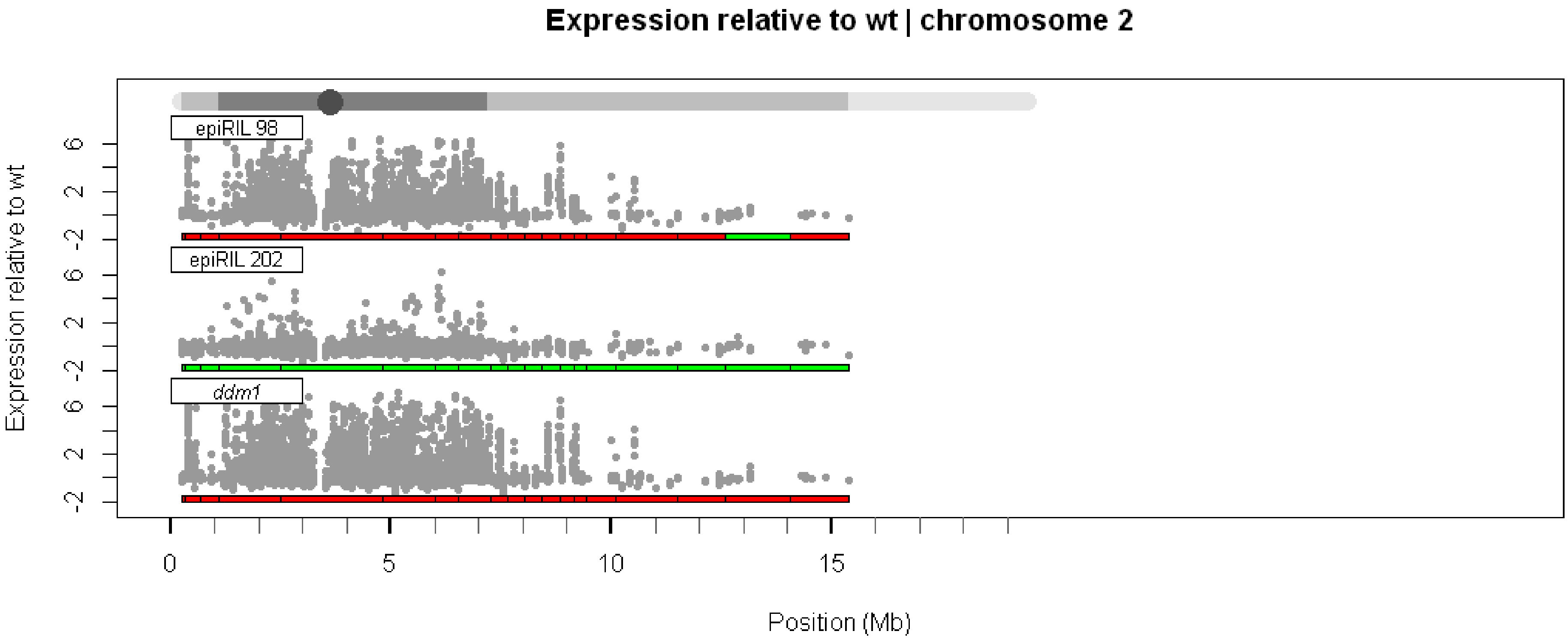

Expression relative to wt | chromosome 2
epiRIL 98
epiRIL 202
ddm1
Expression relative to wt
6
2
-2
6
2
-2
6
2
-2
0
5
10
15
Position (Mb)

Figure S8-3

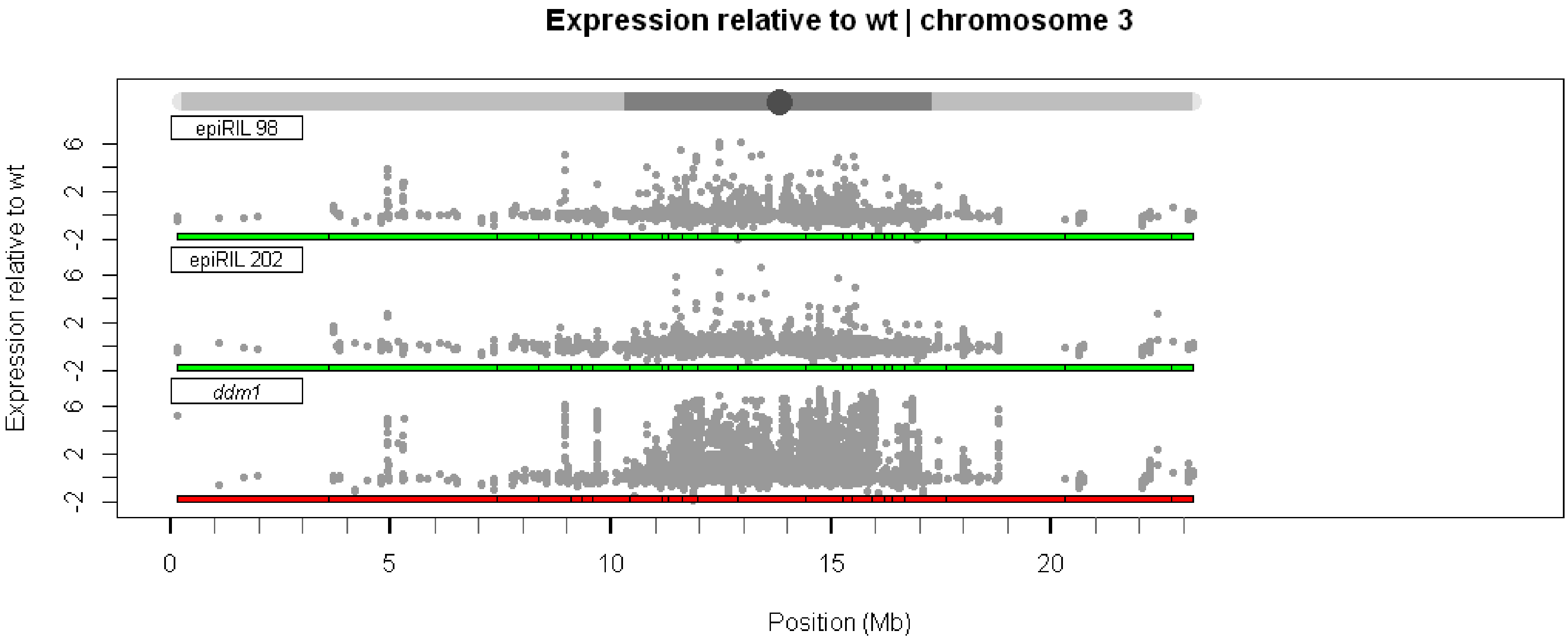

Expression relative to wt | chromosome 3
epiRIL 98
epiRIL 202
ddm1
Expression relative to wt
6
2
-2
0
5
10
15
20
Position (Mb)

Figure S8-4

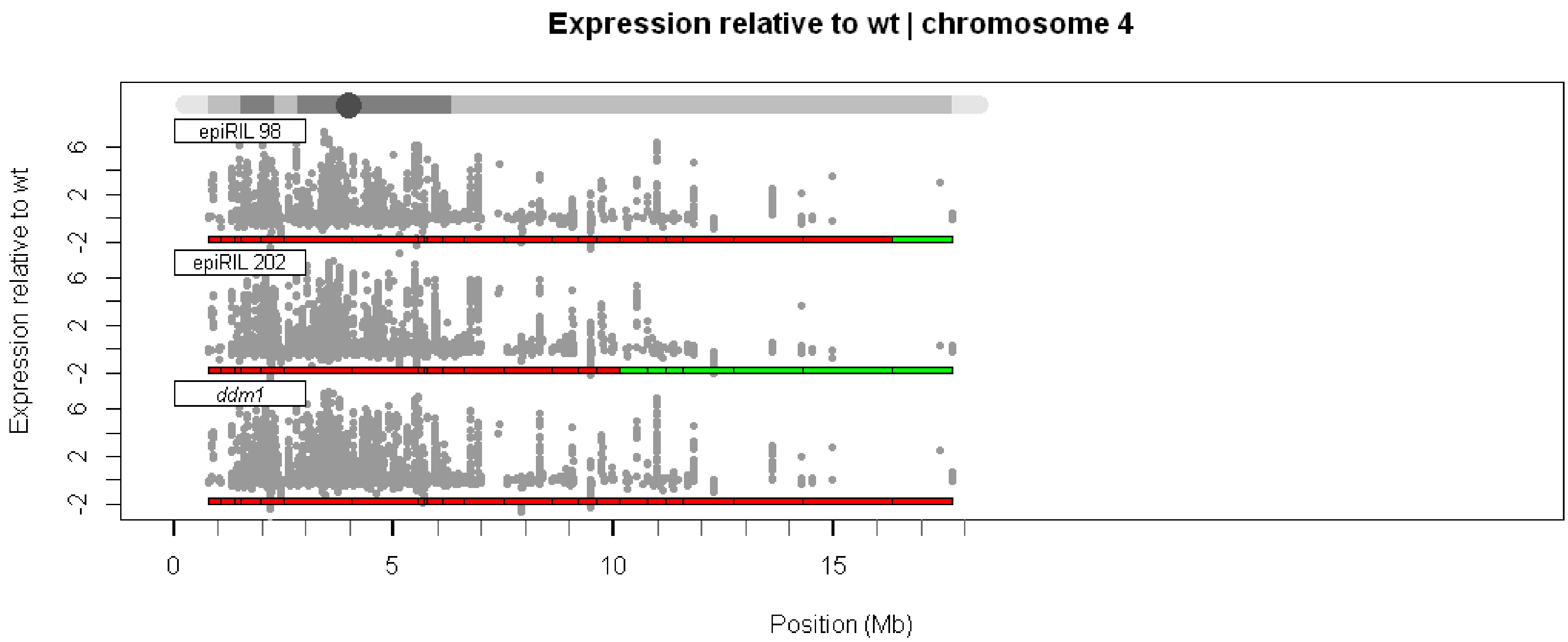

Expression relative to wt | chromosome 4
epiRIL 98
epiRIL 202
ddm1
Expression relative to wt
6
2
-2
6
2
-2
6
2
-2
0
5
10
15
Position (Mb)

Figure S8-5

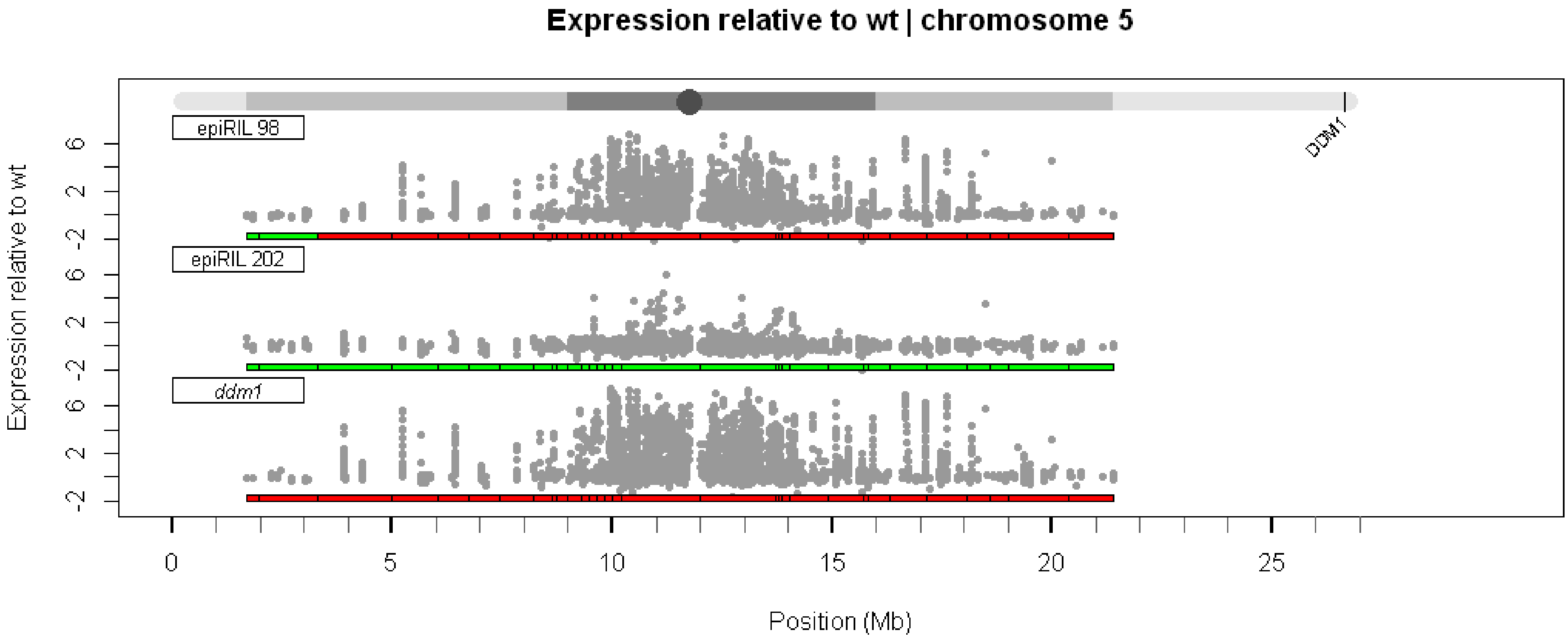
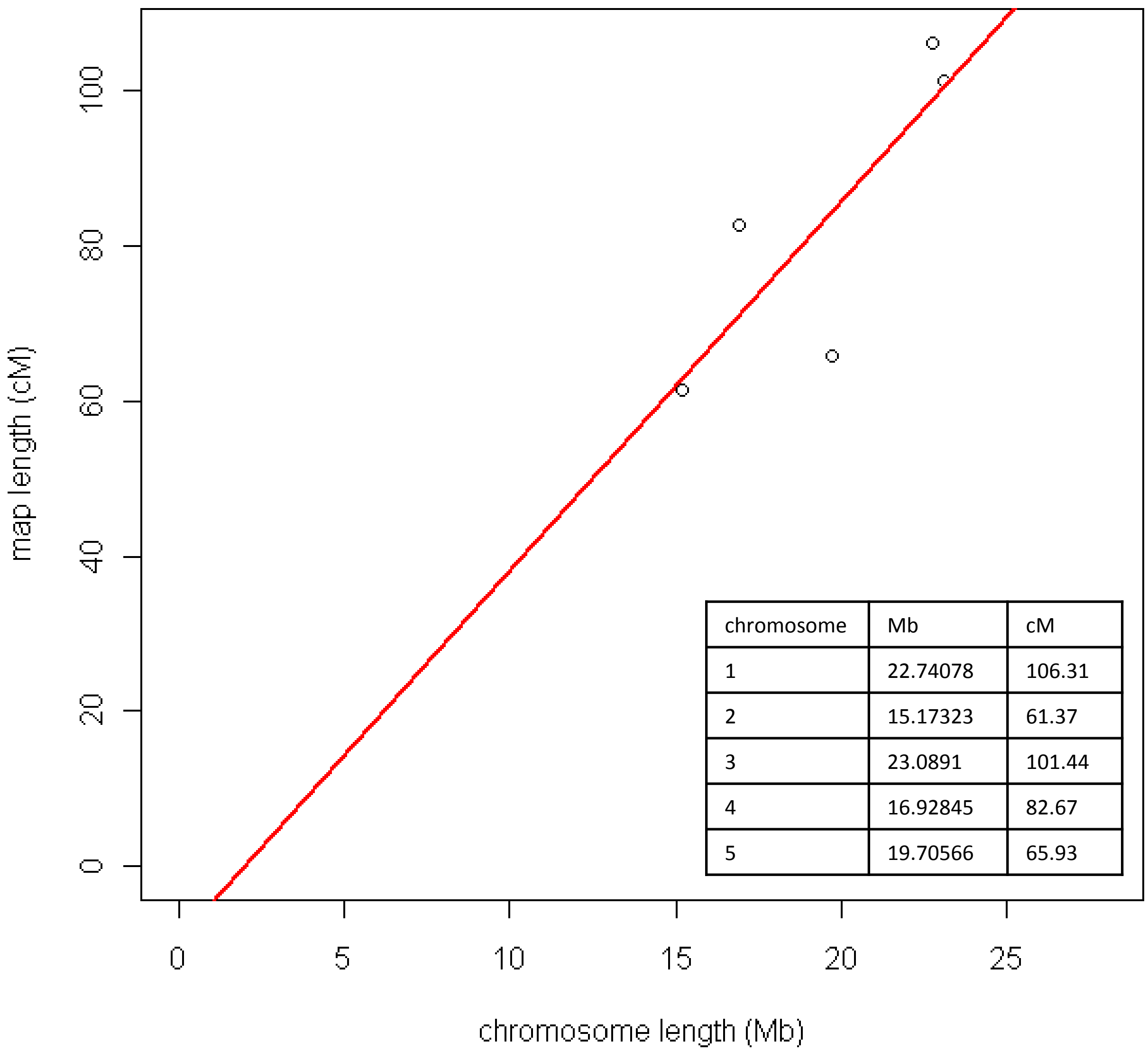

Expression relative to wt | chromosome 5
DDM1
epiRIL 98
epiRIL 202
ddm1
Expression relative to wt
6
2
-2
6
2
-2
6
2
-2
0
5
10
15
20
25
Position (Mb)

Figure S9



chromosome	Mb	cM
1	22.74078	106.31
2	15.17323	61.37
3	23.0891	101.44
4	16.92845	82.67
5	19.70566	65.93

Figure S10

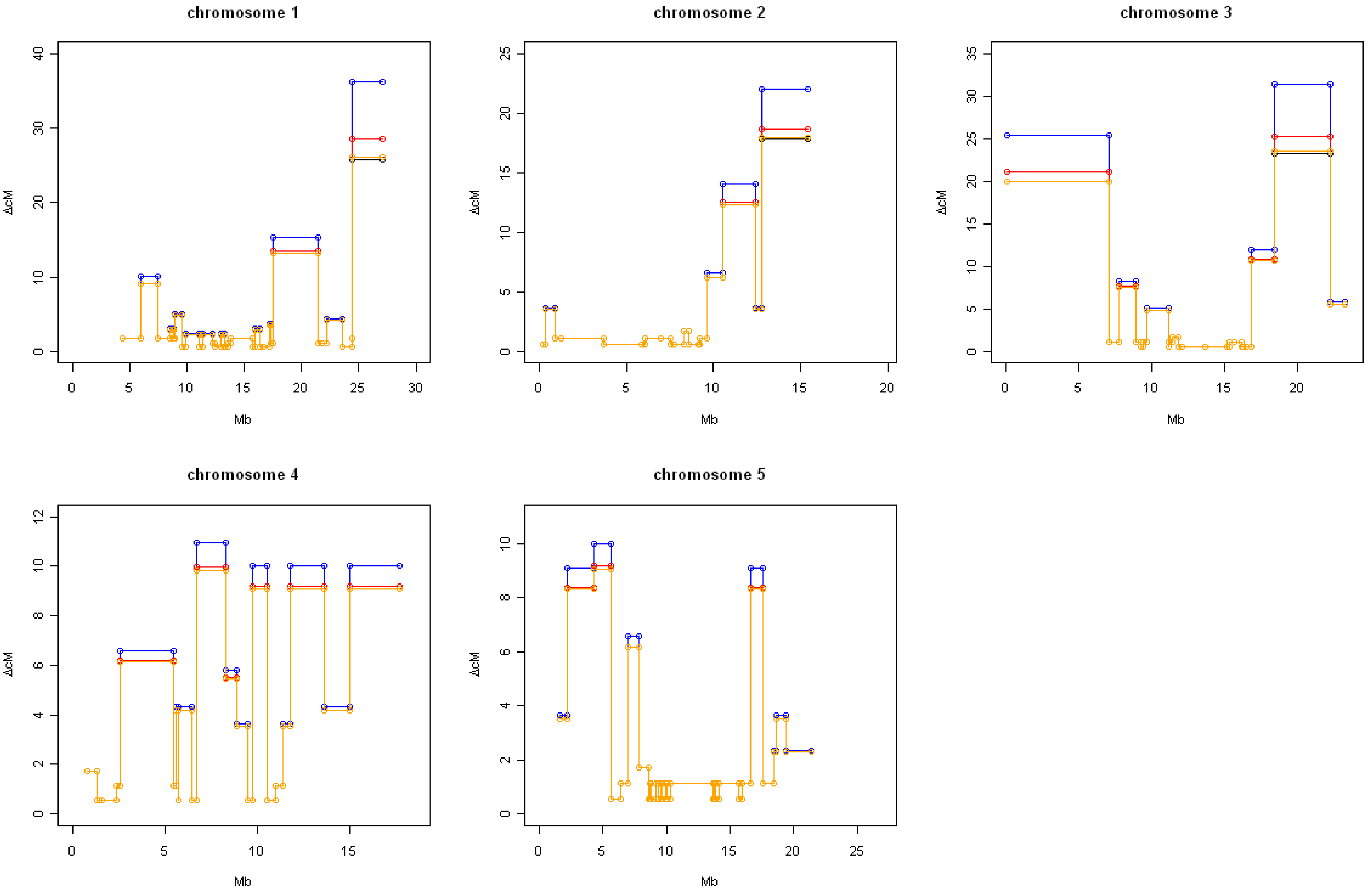

chromosome 1
0
10
20
30
40
ΔcM
0
5
10
15
20
25
30
Mb
chromosome 2
0
5
10
15
20
25
ΔcM
0
5
10
15
20
Mb
chromosome 3
0
5
10
15
20
25
30
35
ΔcM
0
5
10
15
20
Mb
chromosome 4
0
2
4
6
8
10
12
ΔcM
0
5
10
15
Mb
chromosome 5
0
2
4
6
8
10
ΔcM
0
5
10
15
20
25
Mb

Figure S11

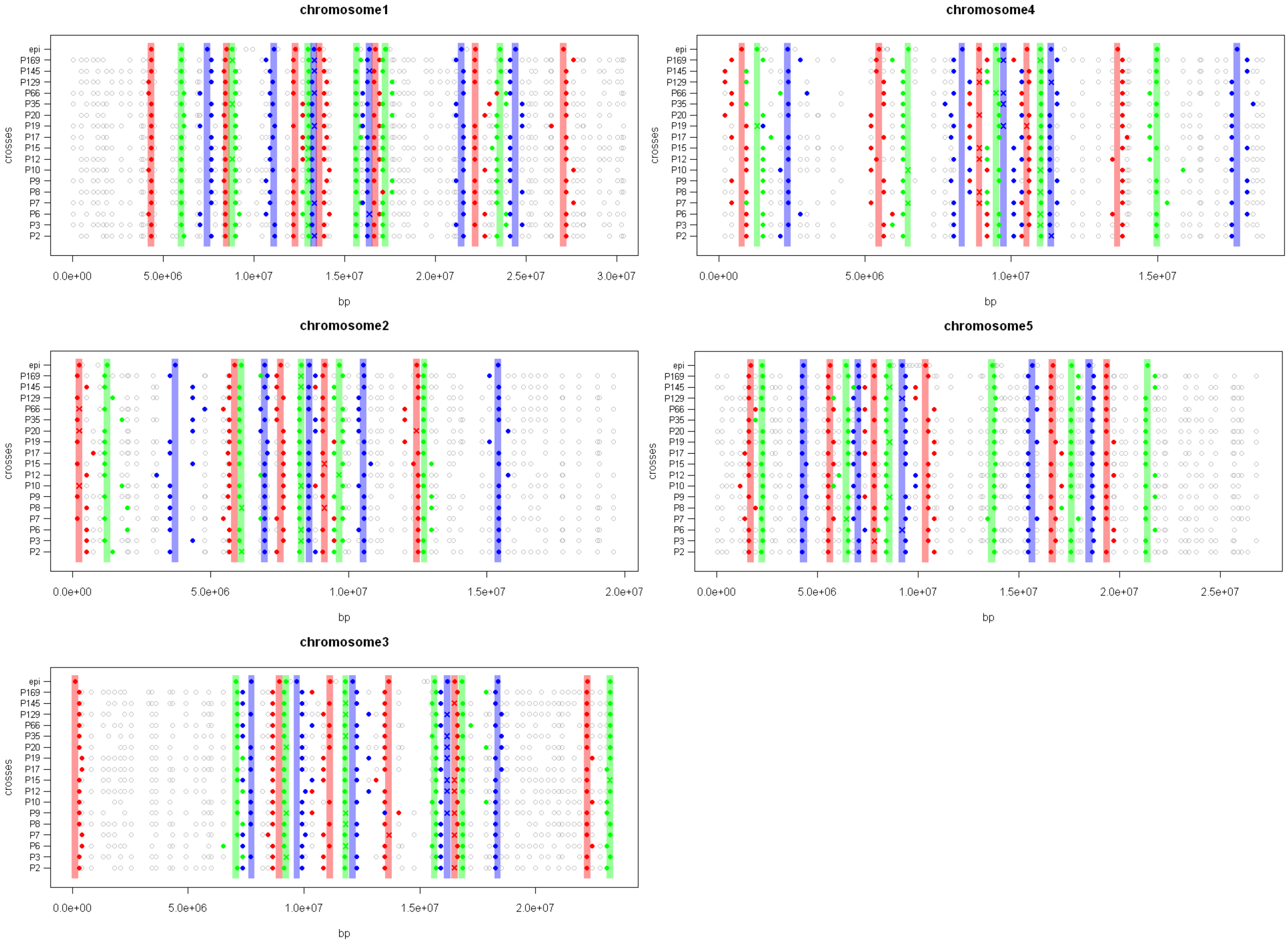

chromosome1
chromosome4
chromosome2
chromosome5
chromosome3
crosses
epi
P169
P145
P129
P66
P35
P20
P19
P17
P15
P12
P10
P9
P8
P7
P6
P3
P2
bp
0.0e+00
5.0e+06
1.0e+07
1.5e+07
2.0e+07
2.5e+07
3.0e+07

Figure S12

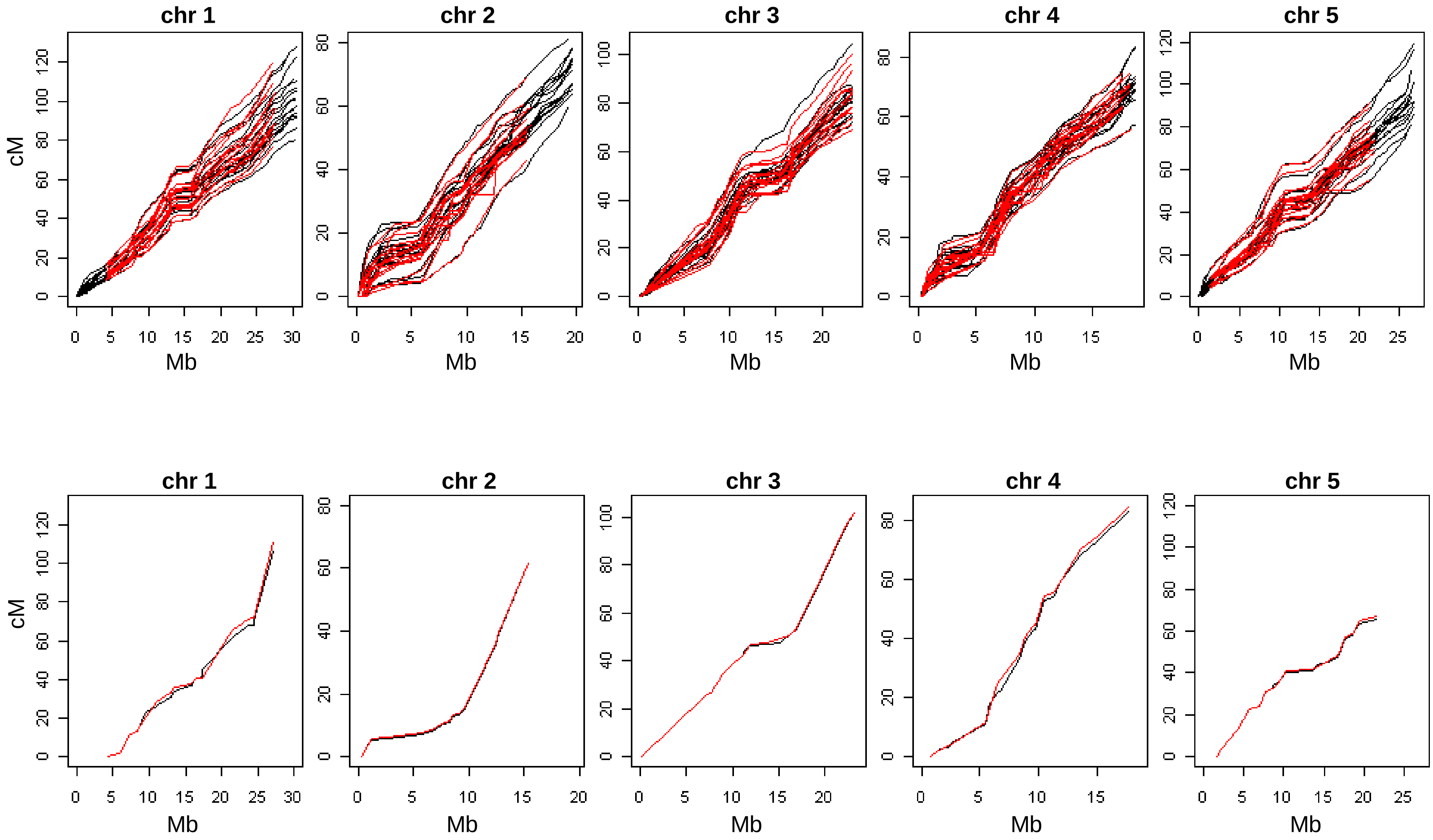

chr 1
chr 2
chr 3
chr 4
chr 5
cM
Mb
0
20
40
60
80
100
120
0
5
10
15
20
25
30
chr 1
chr 2
chr 3
chr 4
chr 5
cM
Mb

Figure S13

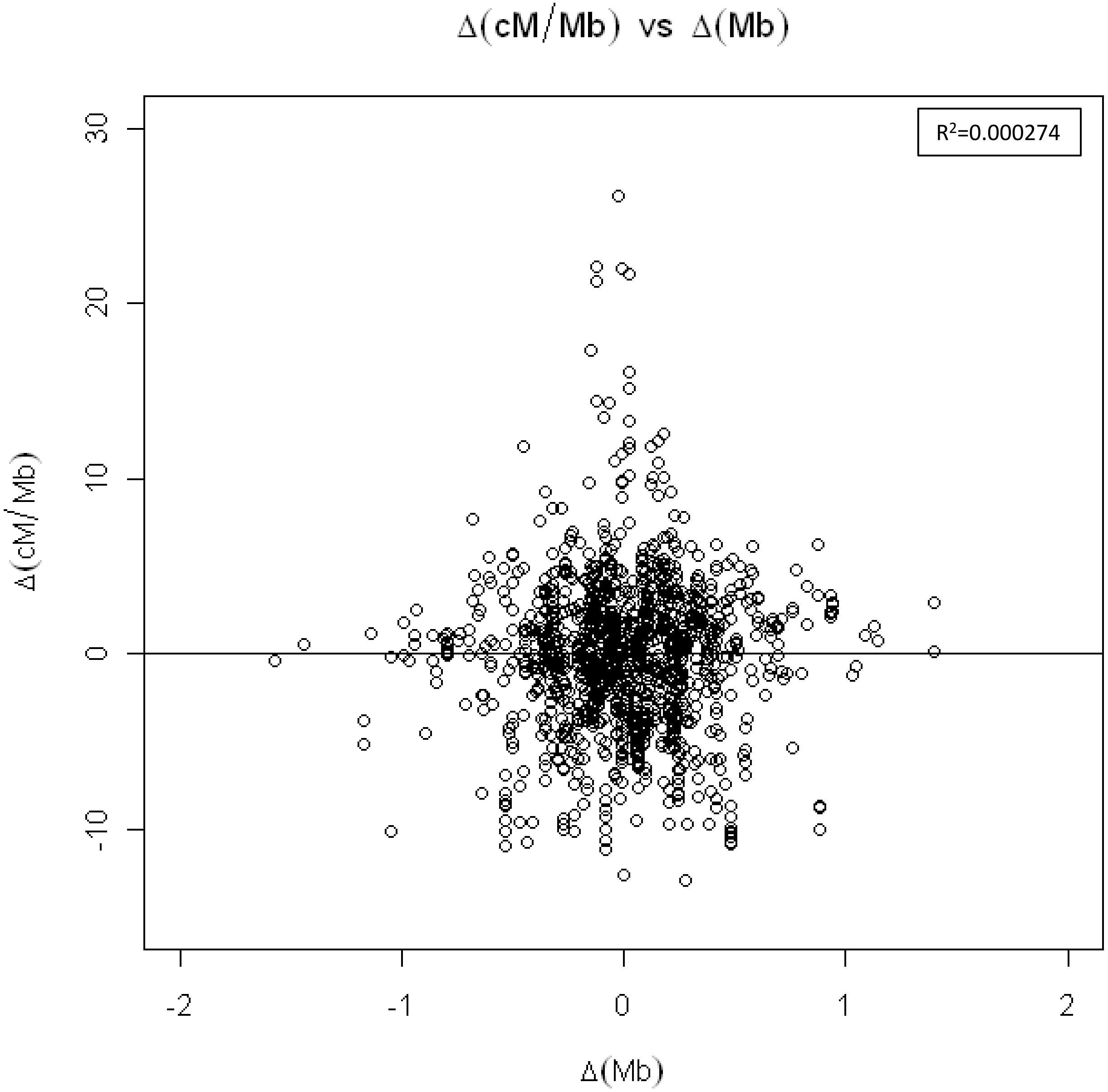


Figure S14-1

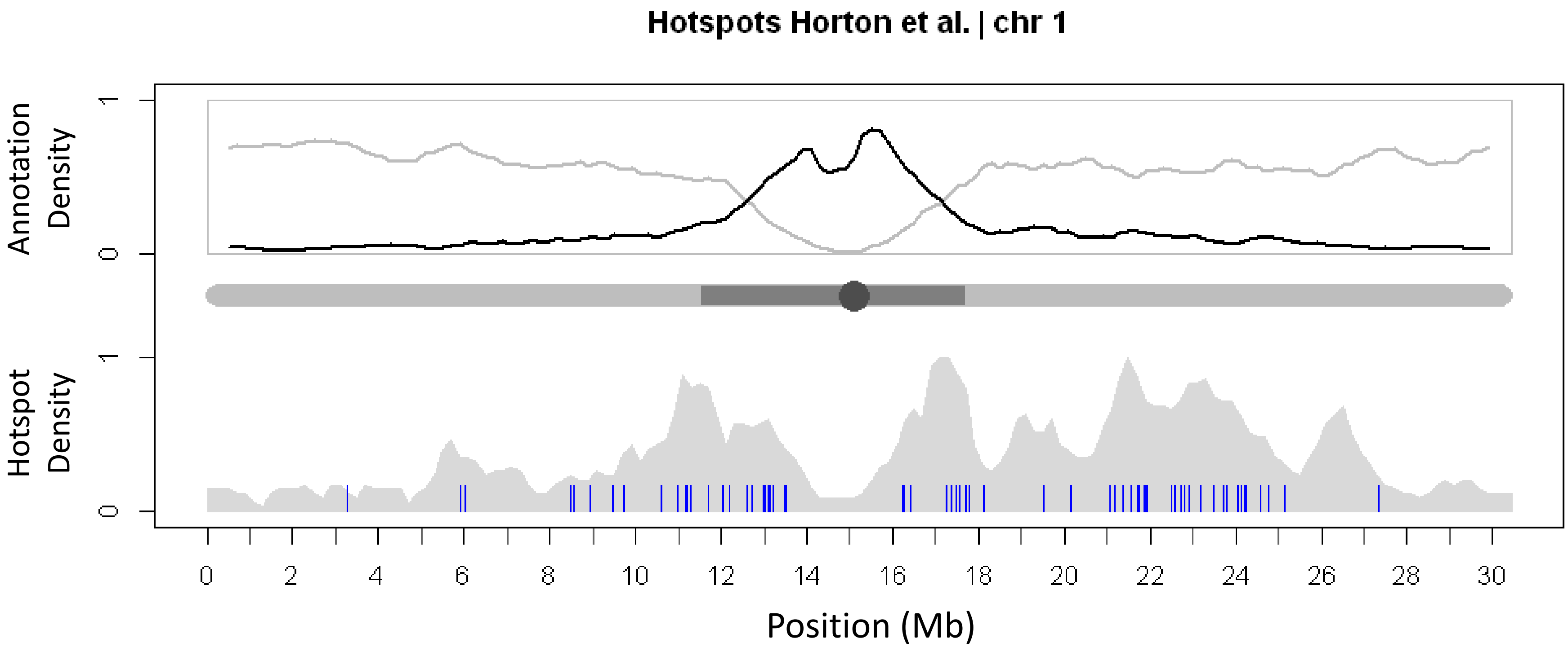

Hotspots Horton et al. | chr 1
Annotation Density
1
0
Hotspot Density
1
0
0
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
Position (Mb)

Figure S14-2

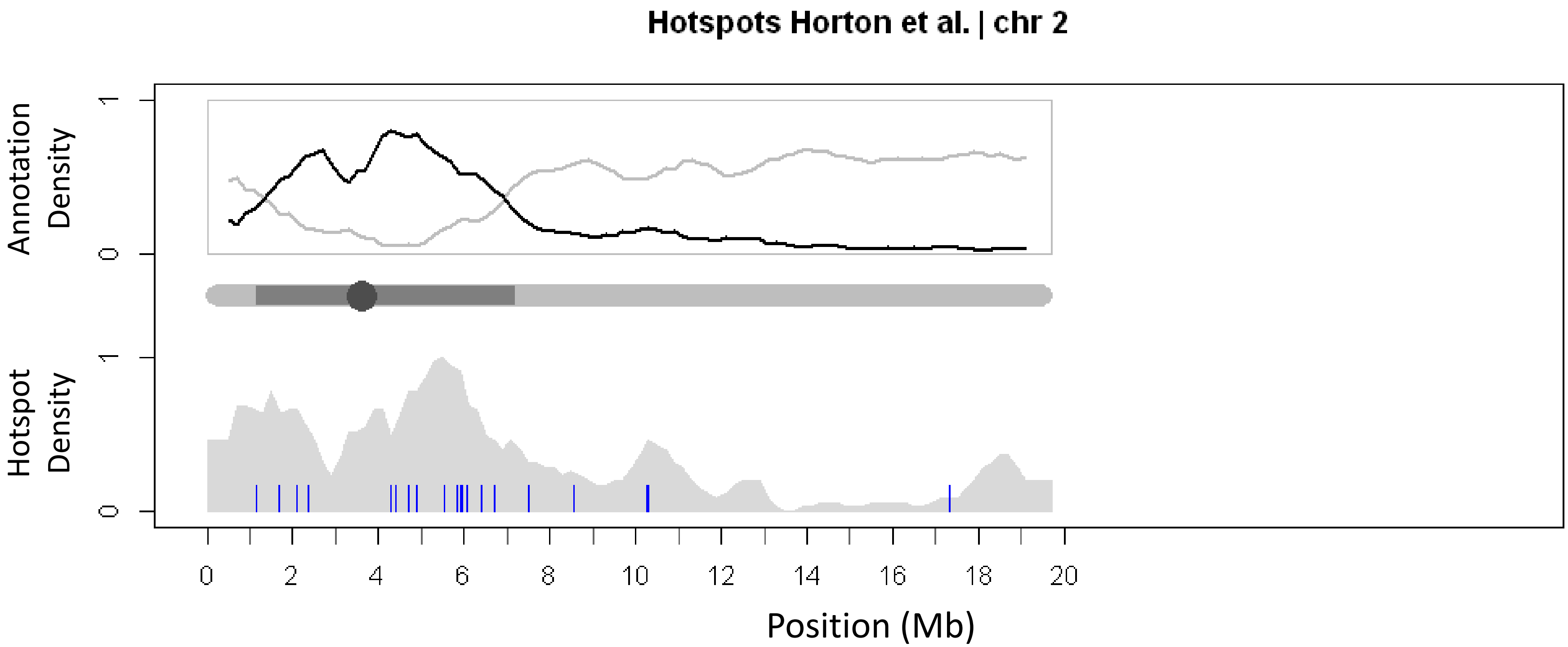

Hotspots Horton et al. | chr 2
Annotation Density
1
0
Hotspot Density
1
0
0
2
4
6
8
10
12
14
16
18
20
Position (Mb)

Figure S14-3

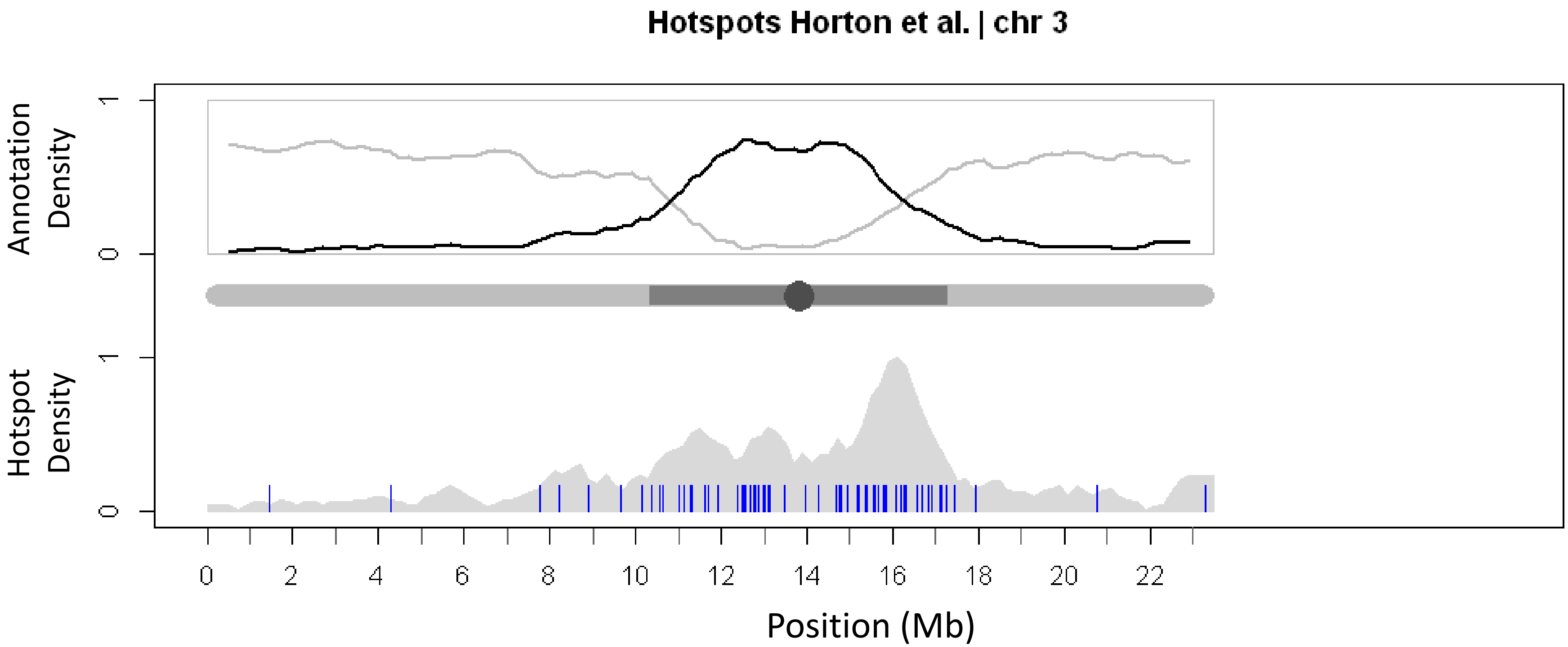

Hotspots Horton et al. | chr 3
Annotation Density
1
0
Hotspot Density
1
0
0
2
4
6
8
10
12
14
16
18
20
22
Position (Mb)

Figure S14-4

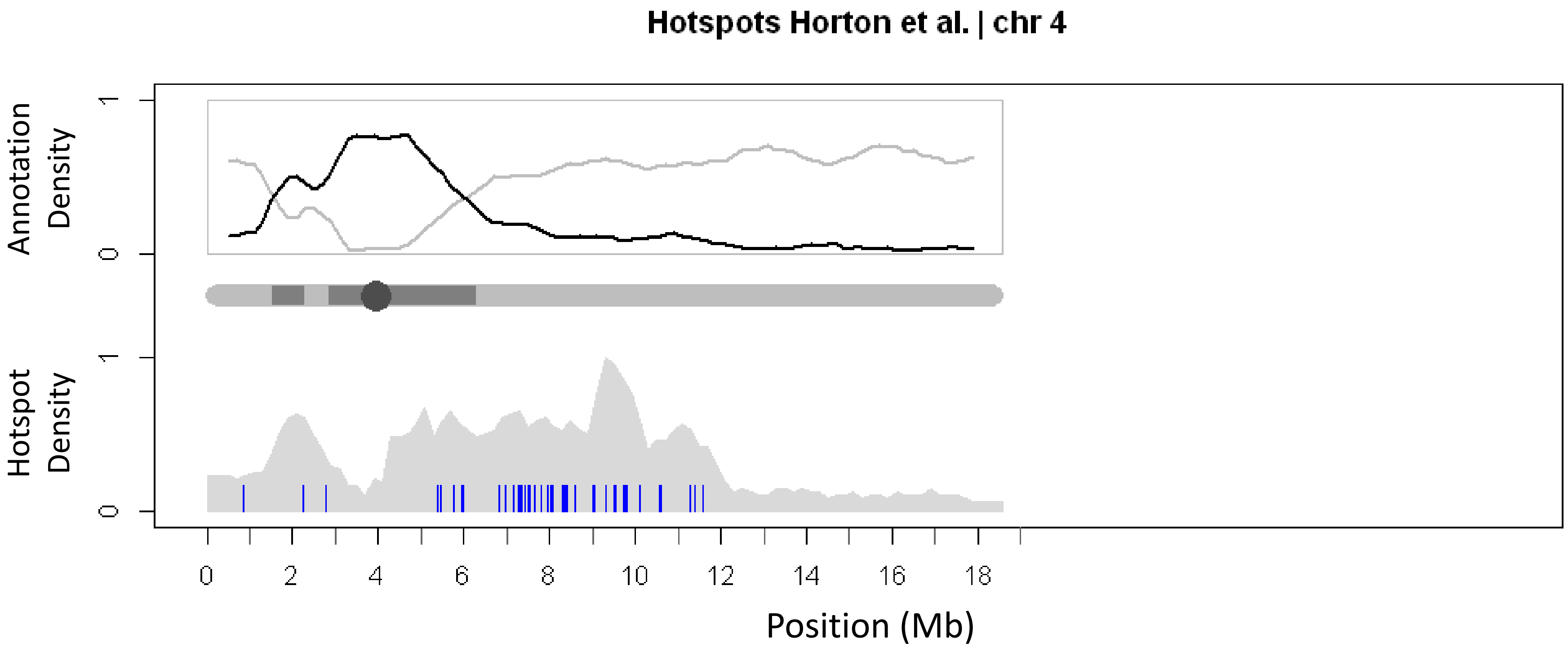

Hotspots Horton et al. | chr 4
Annotation Density
Hotspot Density
1
0
1
0
0
2
4
6
8
10
12
14
16
18
Position (Mb)

Figure S14-5

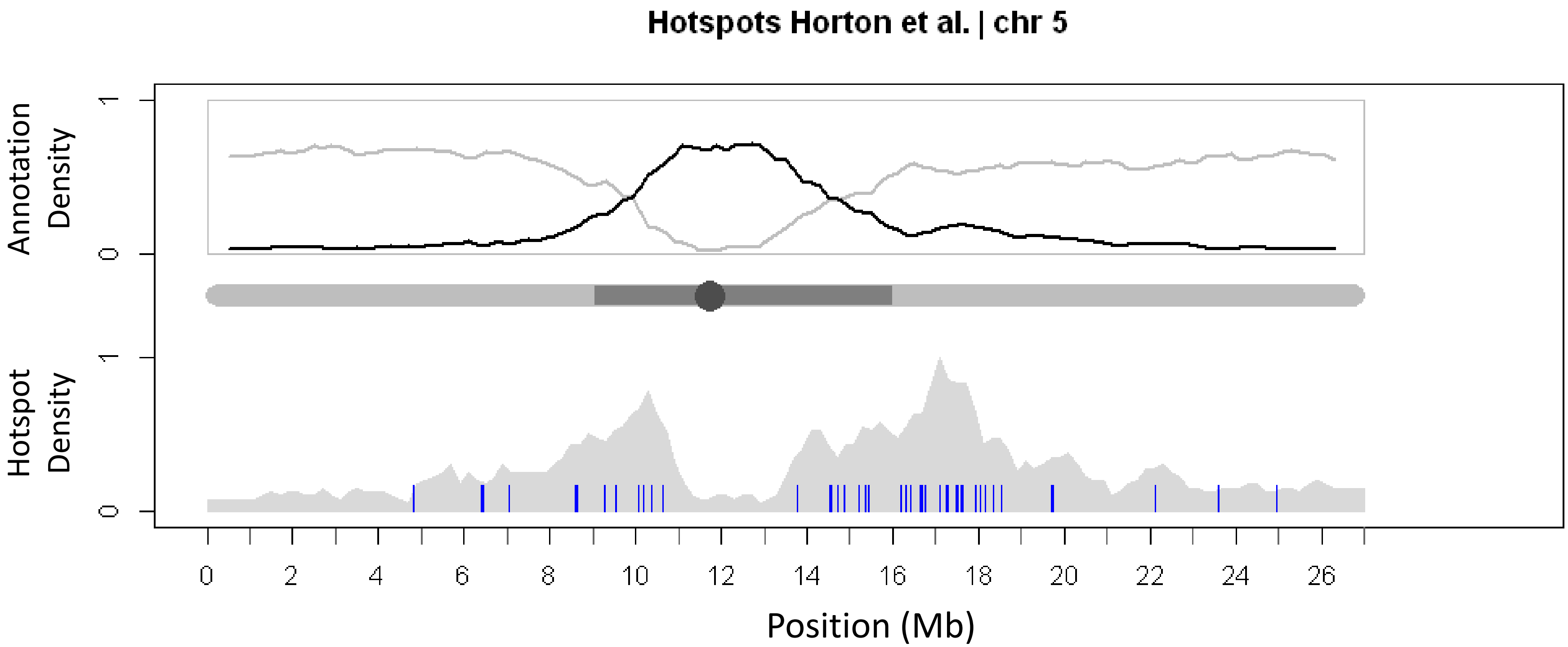
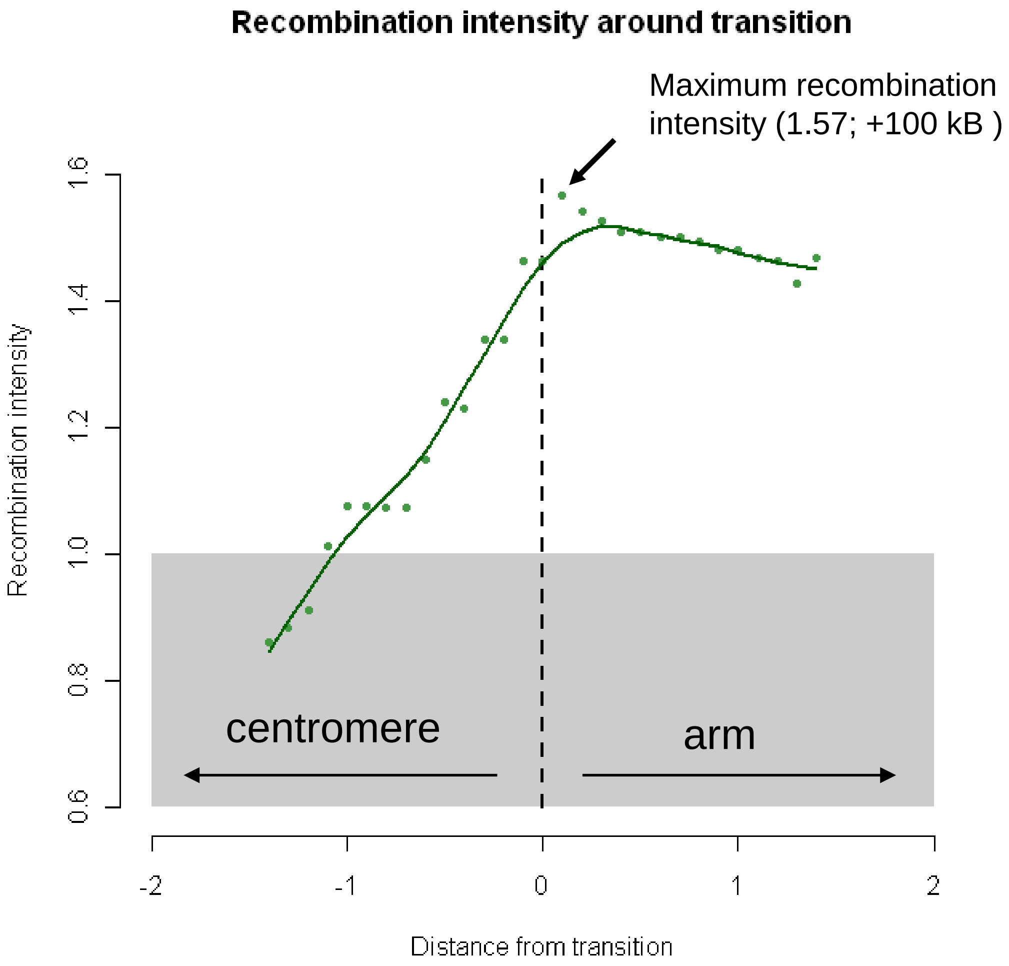

Hotspots Horton et al. | chr 5
Annotation Density
1
0
Hotspot Density
1
0
0
2
4
6
8
10
12
14
16
18
20
22
24
26
Position (Mb)

Figure S15



Maximum recombination intensity (1.57; +100 kB)

Figure S16

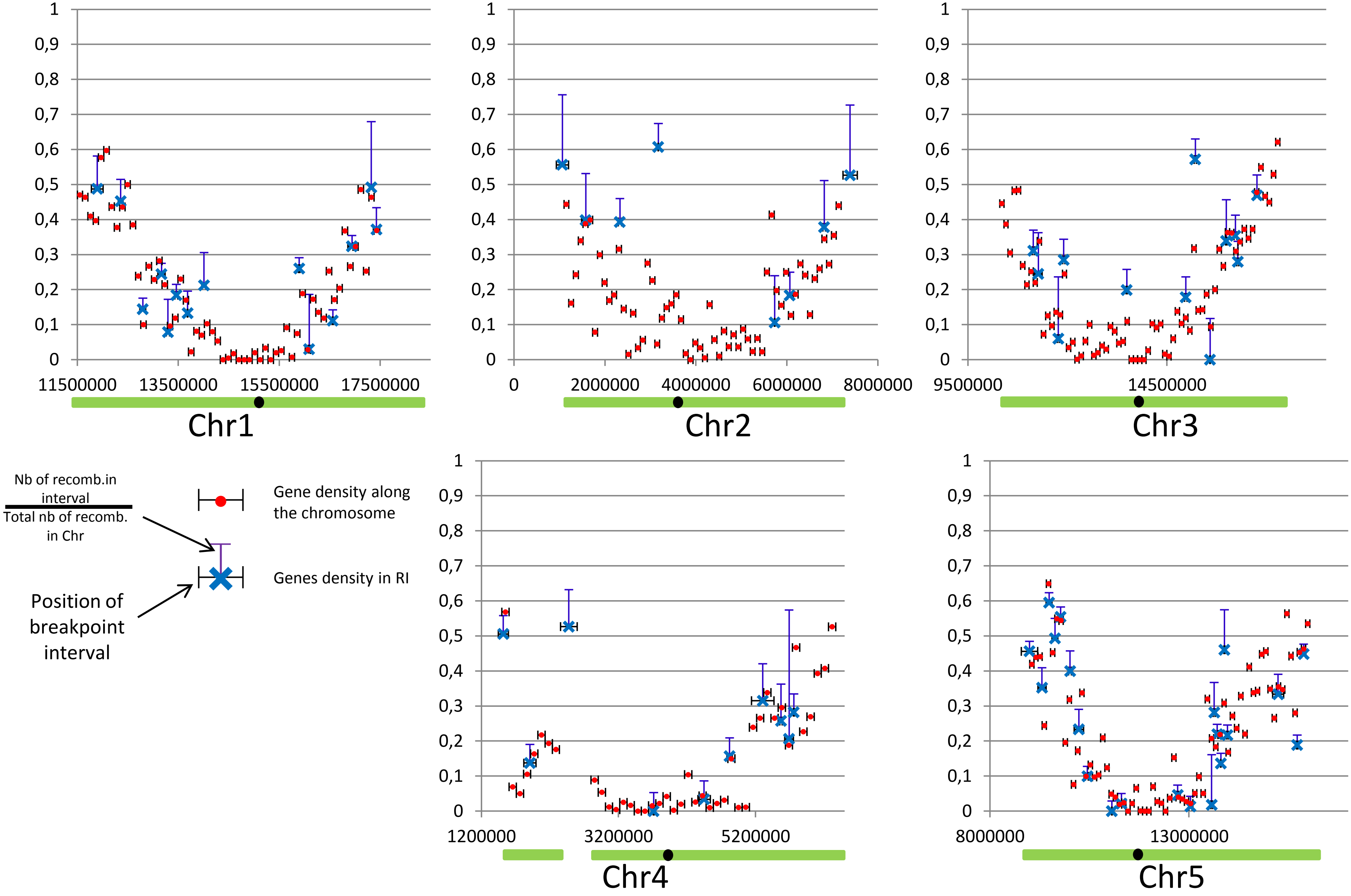

1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
11500000
13500000
15500000
17500000
Chr1
0
2000000
4000000
6000000
8000000
Chr2
9500000
14500000
Chr3
1200000
3200000
5200000
Chr4
8000000
13000000
Chr5
Nb of recomb.in interval
Total nb of recomb. in Chr
Gene density along the chromosome
Genes density in RI
Position of breakpoint interval

Figure S17

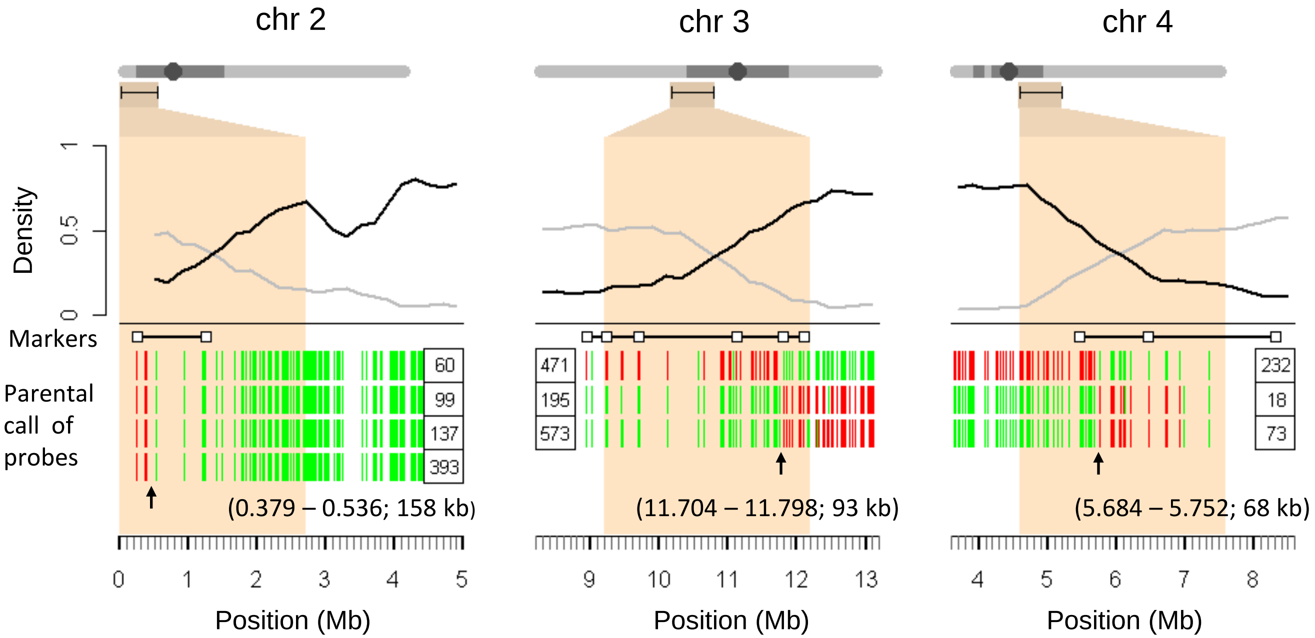

chr 2
chr 3
chr 4
Density
0
0.5
1
Markers
Parental call of probes
60
99
137
393
471
195
573
232
18
73
(0.379 – 0.536; 158 kb)
(11.704 – 11.798; 93 kb)
(5.684 – 5.752; 68 kb)
0
1
2
3
4
5
9
10
11
12
13
4
5
6
7
8
Position (Mb)
Position (Mb)
Position (Mb)

Figure S18

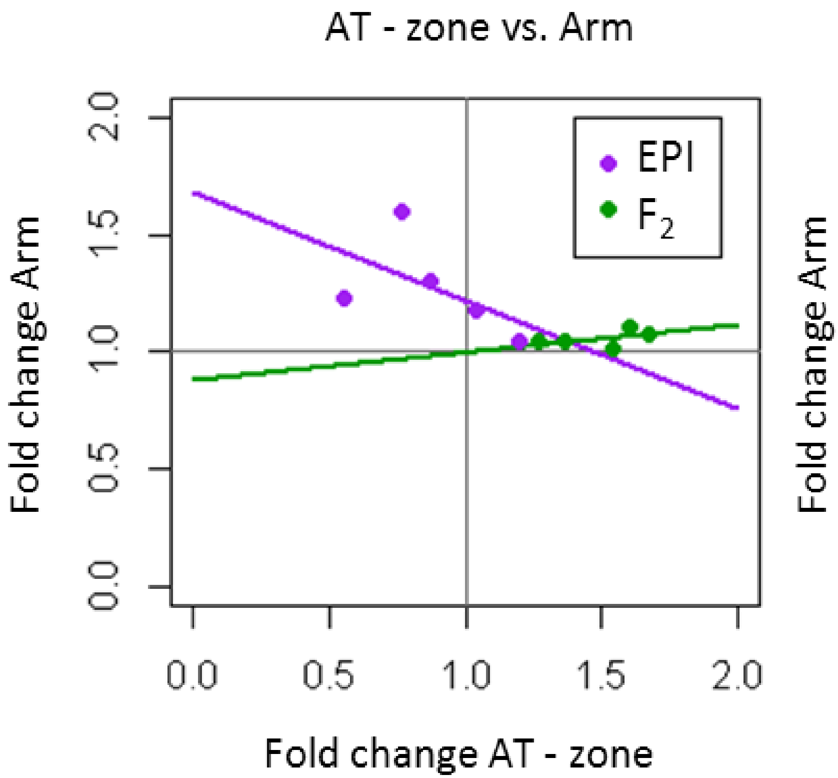

AT - zone vs. Arm
EPI
F_2
Fold change Arm
0.0
0.5
1.0
1.5
2.0
Fold change AT - zone
Fold change Arm

Table S1

	R60	R98	R202	R260	R344	R480
% Overlap	87.97	87.20	86.56	86.66	86.06	81.00
% U probes	98.23	97.77	97.53	97.79	98.15	95.37
% I probes	9.37	16.34	19.07	12.45	9.91	28.11
% M probes	83.91	78.53	80.83	86.14	81.21	73.30

Table S2

dmr_id	chromosome	start_bp	stop_bp
DMR-1	1	525857	526242
DMR-2	1	4145856	4146121
DMR-3	1	4330606	4332076
DMR-4	1	5098227	5098853
DMR-5	1	5353427	5354443
DMR-6	1	5691687	5695344
DMR-7	1	5893659	5893999
DMR-8	1	5913461	5915811
DMR-9	1	6010663	6013983
DMR-10	1	6156483	6158964
DMR-11	1	6302732	6303012
DMR-12	1	7073762	7074092
DMR-13	1	7254722	7257249
DMR-14	1	7430002	7432267
DMR-15	1	7745823	7748073
DMR-16	1	8159758	8160748
DMR-17	1	8453446	8453821
DMR-18	1	8456761	8459067
DMR-19	1	8461252	8461915
DMR-20	1	8490901	8491751
DMR-21	1	8779330	8780036
DMR-22	1	8801988	8802650
DMR-23	1	8816171	8816837
DMR-24	1	8830699	8831320
DMR-25	1	8931514	8932319
DMR-26	1	9004728	9015770
DMR-27	1	9018095	9018740
DMR-28	1	9370023	9373488
DMR-29	1	9464911	9465256
DMR-30	1	9574179	9575333
DMR-31	1	9585538	9585888
DMR-32	1	9676596	9681110
DMR-33	1	9682045	9691308
DMR-34	1	9928550	9929215
DMR-35	1	10007603	10007973
DMR-36	1	10152819	10153458
DMR-37	1	10154128	10156602
DMR-38	1	10357405	10358870
DMR-39	1	10545345	10545839
DMR-40	1	10591542	10592022
DMR-41	1	10602467	10602964
DMR-42	1	10745827	10746132
DMR-43	1	10930125	10930458

DMR-44	1	11044649	11045616
DMR-45	1	11047114	11051415
DMR-46	1	11089513	11090028
DMR-47	1	11096911	11100708
DMR-48	1	11102419	11102716
DMR-49	1	11148121	11152847
DMR-50	1	11155054	11155344
DMR-51	1	11301045	11301528
DMR-52	1	11302214	11303059
DMR-53	1	11305681	11306466
DMR-54	1	11309661	11310311
DMR-55	1	11322798	11324178
DMR-56	1	11366246	11367244
DMR-57	1	11502846	11503351
DMR-58	1	11511756	11512571
DMR-59	1	11517887	11518652
DMR-60	1	11519343	11519828
DMR-61	1	11752127	11754934
DMR-62	1	11789416	11794100
DMR-63	1	11984511	11984824
DMR-64	1	11992096	11992401
DMR-65	1	12018333	12019768
DMR-66	1	12037760	12038430
DMR-67	1	12176188	12176848
DMR-68	1	12222214	12223049
DMR-69	1	12273252	12276332
DMR-70	1	12315004	12316774
DMR-71	1	12403422	12409842
DMR-72	1	12477035	12477365
DMR-73	1	12568561	12569061
DMR-74	1	12570419	12571041
DMR-75	1	12591046	12591497
DMR-76	1	12627186	12628276
DMR-77	1	12631300	12632109
DMR-78	1	12665781	12666246
DMR-79	1	12667939	12671224
DMR-80	1	12674514	12675189
DMR-81	1	12691357	12691647
DMR-82	1	12698951	12699226
DMR-83	1	12699935	12701714
DMR-84	1	12711641	12722880
DMR-85	1	12724010	12728956
DMR-86	1	12741147	12741472
DMR-87	1	12753406	12760337
DMR-88	1	12856990	12862085
DMR-89	1	12886199	12886839
DMR-90	1	12922989	12923311

DMR-91	1	12953326	12953821
DMR-92	1	12987529	12987854
DMR-93	1	12997426	13001226
DMR-94	1	13003181	13008641
DMR-95	1	13018502	13019187
DMR-96	1	13021477	13023341
DMR-97	1	13098250	13102655
DMR-98	1	13139284	13140168
DMR-99	1	13181421	13183006
DMR-100	1	13183871	13186306
DMR-101	1	13238644	13239154
DMR-102	1	13239811	13242134
DMR-103	1	13243578	13244443
DMR-104	1	13245769	13246224
DMR-105	1	13264736	13265031
DMR-106	1	13292792	13293122
DMR-107	1	13303473	13304498
DMR-108	1	13311395	13313565
DMR-109	1	13329072	13340087
DMR-110	1	13340457	13340972
DMR-111	1	13348682	13349007
DMR-112	1	13354819	13355104
DMR-113	1	13372768	13377246
DMR-114	1	13377891	13380727
DMR-115	1	13382192	13386947
DMR-116	1	13391912	13397522
DMR-117	1	13406151	13407751
DMR-118	1	13410597	13416544
DMR-119	1	13419144	13422650
DMR-120	1	13427752	13429697
DMR-121	1	13433353	13434184
DMR-122	1	13435634	13436504
DMR-123	1	13441785	13444705
DMR-124	1	13447666	13448656
DMR-125	1	13483008	13484797
DMR-126	1	13486951	13488601
DMR-127	1	13491291	13491906
DMR-128	1	13499704	13500341
DMR-129	1	13502344	13502970
DMR-130	1	13505971	13507291
DMR-131	1	13546183	13546503
DMR-132	1	13561188	13566504
DMR-133	1	13574775	13575380
DMR-134	1	13575905	13578212
DMR-135	1	13609050	13611740
DMR-136	1	13614690	13616505
DMR-137	1	13618483	13621742

DMR-138	1	13628014	13629692
DMR-139	1	13680349	13682839
DMR-140	1	13690605	13696354
DMR-141	1	13711542	13711832
DMR-142	1	13715007	13715657
DMR-143	1	13719771	13720576
DMR-144	1	13723276	13726066
DMR-145	1	13730541	13731347
DMR-146	1	13736274	13736584
DMR-147	1	13745340	13746177
DMR-148	1	13752141	13752791
DMR-149	1	13755266	13756219
DMR-150	1	13762371	13762816
DMR-151	1	13767461	13767792
DMR-152	1	13779346	13779696
DMR-153	1	13780371	13780806
DMR-154	1	13814841	13815321
DMR-155	1	13815957	13817799
DMR-156	1	13819638	13820442
DMR-157	1	13826895	13828486
DMR-158	1	13833771	13837234
DMR-159	1	13844188	13848140
DMR-160	1	13849806	13850281
DMR-161	1	13859059	13859839
DMR-162	1	13872096	13873549
DMR-163	1	13874905	13878010
DMR-164	1	13879195	13879640
DMR-165	1	13924397	13925524
DMR-166	1	13927386	13927651
DMR-167	1	13931632	13932637
DMR-168	1	13937767	13938707
DMR-169	1	13949477	13950282
DMR-170	1	13956862	13960687
DMR-171	1	13964788	13965280
DMR-172	1	13969593	13972424
DMR-173	1	13976502	13977367
DMR-174	1	13983607	13984268
DMR-175	1	13984918	13985273
DMR-176	1	13986093	13986393
DMR-177	1	13988207	13989704
DMR-178	1	13990239	13990519
DMR-179	1	13997825	13998275
DMR-180	1	14000766	14001618
DMR-181	1	14021704	14022069
DMR-182	1	14037747	14039365
DMR-183	1	14039913	14040404
DMR-184	1	14041565	14044311

DMR-185	1	14050129	14050964
DMR-186	1	14052579	14054259
DMR-187	1	14055047	14061305
DMR-188	1	14063657	14066620
DMR-189	1	14066965	14070057
DMR-190	1	14077334	14077690
DMR-191	1	14083297	14084617
DMR-192	1	14099117	14099611
DMR-193	1	14103543	14104753
DMR-194	1	14112958	14119383
DMR-195	1	14131943	14137208
DMR-196	1	14139558	14141023
DMR-197	1	14146506	14147761
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DMR-199	1	14190383	14191339
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DMR-2580	5	18122622	18123624
DMR-2581	5	18161903	18163873

DMR-2582	5	18210722	18211277
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DMR-2584	5	18488790	18489135
DMR-2585	5	18507760	18512393
DMR-2586	5	18667661	18667936
DMR-2587	5	18949985	18956210
DMR-2588	5	19375838	19376828
DMR-2589	5	19378317	19379292
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DMR-2591	5	19510945	19511770
DMR-2592	5	19514719	19515047
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DMR-2595	5	20544046	20544482
DMR-2596	5	20611856	20612171
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DMR-2599	5	20677340	20677995
DMR-2600	5	21391149	21392149
DMR-2601	5	21848807	21854609
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DMR-2603	5	22020306	22022116
DMR-2604	5	22022901	22024096
DMR-2605	5	22630468	22635399
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Table S3

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MM9	1	8830699	8831320
MM10	1	8931514	8932319
MM11	1	9574179	9575333
MM12	1	9928550	9929215
MM13	1	10357405	10358870
MM14	1	10545345	10545839
MM15	1	11044649	11045616
MM16	1	11047114	11051415
MM17	1	11096911	11100708
MM18	1	11102419	11102716
MM19	1	11309661	11310311
MM20	1	11322798	11324178
MM21	1	11502846	11503351
MM22	1	11511756	11512571
MM23	1	11517887	11518652
MM24	1	11519343	11519828
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MM26	1	12315004	12316774
MM27	1	12403422	12409842
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MM35	1	13021477	13023341
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MM37	1	13239811	13242134
MM38	1	13264736	13265031
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MM41	1	13391912	13397522
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MM43	1	13419144	13422650

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MM46	1	13491291	13491906
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MM67	1	14041565	14044311
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MM71	1	14131943	14137208
MM72	1	14146506	14147761
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MM89	1	15815259	15817608
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MM95	1	16077497	16079431
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MM97	1	16174849	16176279
MM98	1	16179459	16183728
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MM102	1	16378251	16379910
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MM117	1	16848979	16849677
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MM123	1	17258838	17264340
MM124	1	17265653	17266923
MM125	1	17284412	17285075
MM126	1	17363118	17368434
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MM129	1	17536099	17536719
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MM148	1	21459776	21460452
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MM572	4	2136479	2143881
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MM731	5	9929045	9929765
MM732	5	9949501	9953791
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MM747	5	10381174	10383134
MM748	5	10398185	10400340

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MM755	5	10547800	10554452
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MM779	5	11521513	11522958
MM780	5	11523473	11525597
MM781	5	11527937	11528397
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MM783	5	11592613	11593588
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MM787	5	11670167	11672138
MM788	5	11673627	11676125
MM789	5	12114819	12115809
MM790	5	12205600	12206406
MM791	5	12207061	12208388
MM792	5	12209678	12211177
MM793	5	12213679	12214479
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MM799	5	12458552	12459337
MM800	5	12527671	12529631
MM801	5	12531155	12532310
MM802	5	12624492	12625157
MM803	5	12672331	12675961
MM804	5	12693478	12695123
MM805	5	12738226	12745781
MM806	5	12747461	12749075
MM807	5	12753573	12755493
MM808	5	12801876	12806521
MM809	5	12983219	12984218
MM810	5	12996743	13006353
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MM812	5	13082244	13082714
MM813	5	13131903	13134333
MM814	5	13271156	13277603
MM815	5	13354624	13354939
MM816	5	13364736	13369487
MM817	5	13382842	13383212
MM818	5	13510531	13511584
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MM820	5	13549016	13549637
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MM822	5	13609582	13610201
MM823	5	13656931	13661362
MM824	5	13666130	13666998
MM825	5	13753476	13758196
MM826	5	13797308	13803111
MM827	5	13805059	13806068
MM828	5	13806603	13806933
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MM831	5	13878051	13878481
MM832	5	13901149	13908033
MM833	5	13929365	13930310
MM834	5	13946515	13949105
MM835	5	13985794	13986619
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MM837	5	14130621	14135451
MM838	5	14297458	14297785
MM839	5	14564932	14566037
MM840	5	14574666	14575466
MM841	5	14592988	14595078
MM842	5	15092886	15099318

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MM848	5	15700805	15707179
MM849	5	15736222	15737247
MM850	5	15739215	15739555
MM851	5	15819093	15819918
MM852	5	15823391	15823866
MM853	5	15937735	15939668
MM854	5	16674280	16675285
MM855	5	16925220	16927520
MM856	5	17105759	17113165
MM857	5	17459022	17459667
MM858	5	17460152	17462942
MM859	5	17613965	17620413
MM860	5	17621236	17623160
MM861	5	18161903	18163873
MM862	5	18488790	18489135
MM863	5	18667661	18667936
MM864	5	19375838	19376828
MM865	5	19378317	19379292
MM866	5	19982222	19983047
MM867	5	21391149	21392149

Table S4

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MM7	1	8801988	8802650	16,44647406
MM10	1	8931514	8932319	18,17569552
MM11	1	9574179	9575333	23,22803886
MM12	1	9928550	9929215	23,78509645
MM17	1	11096911	11100708	26,13156496
MM20	1	11322798	11324178	26,68862279
MM25	1	12273252	12276332	29,03509124
MM27	1	12403422	12409842	30,16821303
MM33	1	13003181	13008641	30,72527098
MM39	1	13329072	13340087	33,07173949
MM52	1	13618483	13621742	33,62837936
MM58	1	13833771	13837234	34,76092688
MM87	1	15689530	15690065	36,49000221
MM91	1	15911298	15911993	37,04689724
MM101	1	16372020	16377961	40,03276696
MM114	1	16718975	16720795	40,58982491
MM123	1	17258838	17264340	41,14688279
MM126	1	17363118	17368434	44,7961642
MM128	1	17523013	17526003	45,92928462
MM147	1	21457161	21459296	61,19827022
MM150	1	21750810	21758234	62,33139088
MM157	1	22234806	22236246	63,46451242
MM158	1	23570478	23572928	67,8020507
MM159	1	24432541	24433101	68,35910841
MM160	1	24459659	24460449	70,08832178
MM163	1	27070457	27071391	106,3130768
MM166	2	245700	249332	0
MM167	2	373127	378679	0,557051032
MM168	2	930664	930979	4,206332442
MM171	2	1251574	1252848	5,339454041
MM240	2	3730709	3734122	6,472575946
MM330	2	5859874	5864604	7,029634072
MM335	2	6116421	6119529	7,586692197
MM357	2	6961080	6965815	8,719814102
MM371	2	7544676	7545673	9,852936007
MM372	2	7784246	7791011	10,40999413
MM373	2	8278256	8281520	10,9670522
MM374	2	8568345	8571152	12,69627436
MM378	2	9129123	9130835	13,25333242

MM379	2	9194501	9198421	13,81039055
MM380	2	9659660	9659972	14,94351194
MM382	2	10540595	10541195	21,51183147
MM383	2	12456566	12461464	35,62247261
MM385	2	12743505	12743777	39,27171782
MM388	2	15418592	15418927	61,37189962
MM392	3	129256	129877	0
MM396	3	7061219	7061849	25,45450367
MM398	3	7738889	7739204	26,58762309
MM399	3	8937125	8938547	34,7998638
MM400	3	9228167	9232640	35,93298506
MM402	3	9436406	9439321	36,49004313
MM405	3	9693424	9699210	37,62316466
MM414	3	11117372	11121888	42,67550807
MM415	3	11172354	11176989	43,23256577
MM418	3	11393148	11396743	44,36568761
MM427	3	11797070	11799048	46,09490971
MM432	3	12096151	12098525	46,65196778
MM466	3	13667971	13671251	47,20902596
MM495	3	15186655	15188455	47,76608414
MM499	3	15318785	15325698	48,32314227
MM515	3	15632482	15638053	49,45626417
MM527	3	16184523	16191125	50,58938608
MM529	3	16257166	16260312	51,1464442
MM531	3	16508925	16509440	51,70350239
MM537	3	16821132	16825096	52,26055959
MM544	3	18370976	18371431	64,21989515
MM546	3	22243503	22246468	95,64195903
MM547	3	23215509	23218355	101,4372846
MM550	4	788271	788751	0
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MM553	4	1592613	1594726	2,843331184
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MM654	4	5468765	5470776	11,10178238
MM661	4	5588246	5589431	12,23486366
MM665	4	5751470	5752399	16,57240194
MM666	4	5766434	5769097	17,1294594
MM678	4	6467386	6472846	21,46699775
MM679	4	6723446	6729234	22,02400587
MM686	4	8313708	8319324	32,98211535
MM689	4	8906581	8907231	38,77739831
MM691	4	9483934	9485359	42,42664598
MM693	4	9734038	9737673	42,98370303
MM694	4	10527354	10529034	52,98573323
MM695	4	10992797	10997912	53,54279052

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MM699	4	11820310	11824620	58,32518253
MM701	4	13624419	13631859	68,32719735
MM703	4	14987455	14988333	72,66473374
MM704	4	17712926	17716726	82,66675312
MM706	5	1686487	1686997	0
MM707	5	2262159	2262544	3,649261727
MM712	5	4320753	4323348	12,73687297
MM713	5	5635294	5635620	22,73888351
MM715	5	6433688	6438813	23,29594081
MM716	5	7027577	7028347	24,4290622
MM718	5	7823819	7824639	30,99738813
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MM721	5	8666296	8667301	33,28366771
MM722	5	8788121	8788791	34,41678967
MM724	5	9206569	9207339	34,97384774
MM725	5	9412161	9414631	36,1069697
MM726	5	9561317	9563131	36,66402777
MM728	5	9712277	9712777	37,79714973
MM731	5	9929045	9929765	38,3542078
MM734	5	10049721	10056270	39,48732977
MM744	5	10351503	10356268	40,04438789
MM823	5	13656931	13661362	41,17750986
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MM827	5	13805059	13806068	42,29162611
MM832	5	13901149	13908033	43,42474808
MM837	5	14130621	14135451	43,98180614
MM845	5	15663492	15668447	45,11492811
MM849	5	15736222	15737247	45,67198623
MM853	5	15937735	15939668	46,22904436
MM854	5	16674280	16675285	47,36216554
MM859	5	17613965	17620413	56,44976439
MM862	5	18488790	18489135	57,58285581
MM863	5	18667661	18667936	59,92932394
MM865	5	19378317	19379292	63,57860502
MM867	5	21391149	21392149	65,92506578

Table S5

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103	492
104	493
105	494
106	495
107	497
108	500
109	503
110	506
111	508
112	523
113	538
114	539
115	556
116	558
117	559
118	561
119	567
120	570
121	572
122	573
123	579

Table S6

marker_id	TE_id	TE_family	TE_clade	TE_order	TE_class	autonomy	mobilization	mobilization_comment	evidence sequencing
MM1	AT1TE14085	ATMU4	undefined	MuDr	DNA	auto	defective	TIR, no continuous ORF	
MM2	AT1TE19430	ATCOPIA64	undefined	copia	LTR	auto	defective	no RT	
MM5	AT1TE27405	ATLINEIII	L1	LINE	Non-LTR	auto	defective	short	
MM11	AT1TE30845	HELITRON1	undefined	undefined	Helitron	auto	defective	short, no ORFs	
MM12	AT1TE32015	ATCOPIA64	undefined	copia	LTR	auto	defective	no RT	
MM17	AT1TE35855	ATLINE2	L1	LINE	Non-LTR	auto	defective	short	
MM17	AT1TE35860	ATLINEIII	L1	LINE	Non-LTR	auto	defective	short	
MM25	AT1TE39880	ATCOPIA35	undefined	copia	LTR	auto	defective	short, defective LTRs, no RT	
MM27	AT1TE40340	ATLANTYS1	Tat-like	gypsy	LTR	auto	defective	short	
MM27	AT1TE40345	TAT1_ATH	Tat-like	gypsy	LTR	auto	defective	short	
MM27	AT1TE40355	ATCOPIA60	undefined	copia	LTR	auto	defective	no RT	
MM33	AT1TE42395	ATGP3	Chromovirus	gypsy	LTR	auto	potentially mobile	LTRs, pol protein seems complete	NO
MM33	AT1TE42400	ATGP3	Chromovirus	gypsy	LTR	auto	defective	short	
MM39	AT1TE43585	ATCOPIA84	undefined	copia	LTR	auto	defective	no RT	
MM39	AT1TE43605	ATGP3	Chromovirus	gypsy	LTR	auto	defective	defective LTRs	
MM52	AT1TE44600	TA11	L1	LINE	Non-LTR	auto	defective	short	
MM52	AT1TE44605	TA11	L1	LINE	Non-LTR	auto	defective	no RT	
MM58	AT1TE45360	ATCOPIA94	undefined	copia	LTR	auto	defective	short	
MM58	AT1TE45365	ATCOPIA75	undefined	copia	LTR	auto	defective	short	
MM87	AT1TE51665	ATENSPM3	undefined	En-Spm	DNA	auto	defective	short, no TIR	
MM87	AT1TE51670	ATENSPM7	undefined	En-Spm	DNA	auto	defective	short, TIR	
MM91	AT1TE52380	VANDAL12	undefined	MuDr	DNA	auto	defective	short, no TIR	
MM91	AT1TE52385	VANDAL9	undefined	MuDr	DNA	auto	defective	no TIR	
MM101	AT1TE53960	ATLANTYS2	Tat-like	gypsy	LTR	auto	defective	short	
MM101	AT1TE53970	ATCOPIA69	undefined	copia	LTR	auto	defective	no RT	
MM101	AT1TE53975	ATLANTYS2	Tat-like	gypsy	LTR	auto	defective	defective LTRs	
MM123	AT1TE57215	ATLANTYS1	Tat-like	gypsy	LTR	auto	defective	short	
MM123	AT1TE57220	ATLANTYS1	Tat-like	gypsy	LTR	auto	defective	defective LTRs	
MM123	AT1TE57225	ATLANTYS1	Tat-like	gypsy	LTR	auto	defective	short	
MM126	AT1TE57530	ATCOPIA49	undefined	copia	LTR	auto	defective	no RT	
MM128	AT1TE58075	ATCOPIA38A	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO

MM147	AT1TE70805	ATLINE1_1	L1	LINE	Non-LTR	auto	defective	RT, TSD, frameshifts	
MM150	AT1TE71770	ATHATN3	undefined	HAT	DNA	auto	defective	short, TIR	
MM150	AT1TE71775	ATCOPIA8B	undefined	copia	LTR	auto	defective	no RT	
MM150	AT1TE71780	ATCOPIA67	undefined	copia	LTR	auto	defective	short	
MM150	AT1TE71790	VANDAL1N1	undefined	MuDr	DNA	non-auto	defective	no TIR	
MM157	AT1TE73425	ATLINEIII	L1	LINE	Non-LTR	auto	defective	short	
MM159	AT1TE80250	ATCOPIA49	undefined	copia	LTR	auto	defective	short	
MM166	AT2TE01000	ATLINEIII	L1	LINE	Non-LTR	auto	defective	no RT	
MM167	AT2TE01550	ATLINE1_5	L1	LINE	Non-LTR	auto	defective	short	
MM167	AT2TE01555	ATLINE1_4	L1	LINE	Non-LTR	auto	defective	short	
MM167	AT2TE01560	TA11	L1	LINE	Non-LTR	auto	defective	short	
MM240	AT2TE16160	ATLINE2	L1	LINE	Non-LTR	auto	defective	no RT	
MM240	AT2TE16165	ATENSPM10	undefined	En-Spm	DNA	auto	defective	short, no TIR	
MM330	AT2TE23855	ATCOPIA13	undefined	copia	LTR	auto	defective	RT, defective LTRs, but intact ORF	
MM335	AT2TE24860	ATHILA8A	Errantivirus	gypsy	LTR	auto	defective	defective LTRs	
MM357	AT2TE28325	ATCOPIA38B	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM371	AT2TE30990	RathE3_cons	undefined	SINE	Non-LTR	non-auto	not defined		
MM372	AT2TE32120	TA11	L1	LINE	Non-LTR	auto	defective	RT, ORF1 too short or fragmented, no TSD	
MM373	AT2TE34410	ATLINEIII	L1	LINE	Non-LTR	auto	defective	no RT	
MM374	AT2TE35840	ATCOPIA69	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM378	AT2TE38575	ATCOPIA74	undefined	copia	LTR	auto	defective	no RT	
MM379	AT2TE38900	ATCOPIA76	undefined	copia	LTR	auto	defective	RT, defective LTRs	
MM382	AT2TE45205	BRODYAGA1	undefined	MuDr	DNA	non-auto	not defined	TIR	
MM383	AT2TE54360	ATLINEIII	L1	LINE	Non-LTR	auto	potentially mobile	RT, 2 ORFs, no frameshifts, no TSD	NO
MM383	AT2TE54365	ATLINE2	L1	LINE	Non-LTR	auto	defective	short	
MM400	AT3TE38565	ATCOPIA65	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM400	AT3TE38575	ATCOPIA45	undefined	copia	LTR	auto	defective	short	
MM402	AT3TE39395	ATLINE2	L1	LINE	Non-LTR	auto	defective	no RT	
MM405	AT3TE40420	ATCOPIA82	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM405	AT3TE40425	ATLINE1_3A	L1	LINE	Non-LTR	auto	defective	short	
MM414	AT3TE46245	ATCOPIA19	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM415	AT3TE46480	TA11	L1	LINE	Non-LTR	auto	defective	short	
MM415	AT3TE46490	ATLINE1_5	L1	LINE	Non-LTR	auto	defective	short	
MM415	AT3TE46495	ATLINE1_5	L1	LINE	Non-LTR	auto	defective	short	
MM418	AT3TE47500	ATGP3	Chromovirus	gypsy	LTR	auto	defective	defective LTRs	
MM418	AT3TE47505	ATCOPIA37	undefined	copia	LTR	auto	defective	short	

MM418	AT3TE47515	ATCOPIA37	undefined	copia	LTR	auto	defective	short	
MM427	AT3TE49090	ATMU5	undefined	MuDr	DNA	auto	defective	TIR, no continuous ORF	
MM432	AT3TE50320	ATHATN3	undefined	HAT	DNA	auto	defective	short, no TIR	
MM466	AT3TE55430	ATCOPIA65	undefined	copia	LTR	auto	defective	no RT	
MM495	AT3TE61685	ATLINE1_2	L1	LINE	Non-LTR	auto	defective	RT, no ORF1	
MM499	AT3TE62220	ATLINEIII	L1	LINE	Non-LTR	auto	defective	no RT	
MM499	AT3TE62225	ATHILA5	Errantivirus	gypsy	LTR	auto	defective	short	
MM499	AT3TE62230	ATCOPIA95	undefined	copia	LTR	auto	defective	short	
MM515	AT3TE63165	ATCOPIA16	undefined	copia	LTR	auto	defective	no RT	
MM527	AT3TE65525	ATLINEIII	L1	LINE	Non-LTR	auto	defective	no RT	
MM529	AT3TE65835	TA11	L1	LINE	Non-LTR	auto	defective	RT, ORF1 too short or fragmented, no TSD	
MM529	AT3TE65840	ATLINE1_4	L1	LINE	Non-LTR	auto	defective	short	
MM537	AT3TE68090	ATCOPIA81	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM546	AT3TE90530	ATCOPIA23	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM547	AT3TE94580	ATLINEIII	L1	LINE	Non-LTR	auto	potentially mobile	RT, 2 ORFs, no frameshifts, no TSD	NO
MM551	AT4TE06710	ATCOPIA2	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM553	AT4TE08110	AT9TSD1	undefined	MuDr	DNA	non-auto	not defined	TIR	
MM586	AT4TE10975	TA11	L1	LINE	Non-LTR	auto	defective	short	
MM586	AT4TE10980	TA11	L1	LINE	Non-LTR	auto	defective	no RT	
MM587	AT4TE12170	ATLINE1_3A	L1	LINE	Non-LTR	auto	defective	short	
MM587	AT4TE12175	ATCOPIA69	undefined	copia	LTR	auto	defective	no RT	
MM678	AT4TE27640	ATCOPIA50	undefined	copia	LTR	auto	defective	no RT	
MM679	AT4TE28870	ATCOPIA17	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM686	AT4TE36845	ATCOPIA17	undefined	copia	LTR	auto	defective	no RT	
MM686	AT4TE36850	ATCOPIA17	undefined	copia	LTR	auto	defective	short	
MM689	AT4TE39815	ATLINE1_2	L1	LINE	Non-LTR	auto	potentially mobile	RT, 2 ORFs, no frameshifts, no TSD	NO
MM691	AT4TE42860	ATCOPIA4	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM693	AT4TE44080	ATCOPIA1	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM695	AT4TE50435	ATCOPIA47	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM698	AT4TE52315	ATCOPIA10	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM698	AT4TE52320	ATLINE2	L1	LINE	Non-LTR	auto	defective	short	
MM699	AT4TE54700	ATGP3	Chromovirus	gypsy	LTR	auto	defective	LTRs, pol protein incomplete	
MM701	AT4TE64170	ATCOPIA8A	undefined	copia	LTR	auto	defective	short	
MM701	AT4TE64175	ATCOPIA8A	undefined	copia	LTR	auto	defective	short	
MM701	AT4TE64180	ATCOPIA8B	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM703	AT4TE71195	VANDAL6	undefined	MuDr	DNA	auto	defective	TIR, ORF too short	

MM704	AT4TE85580	ATCOPIA45	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM706	AT5TE06100	ATREP4	undefined	undefined	Helitron	non-auto	not defined	short, no ORFs	
MM715	AT5TE23285	ATCOPIA90	undefined	copia	LTR	auto	defective	no RT	
MM716	AT5TE25460	VANDAL20	undefined	MuDr	DNA	auto	defective	TIR, no continuous ORF	
MM719	AT5TE31020	ATLINE1_6	L1	LINE	Non-LTR	auto	potentially mobile	RT, 2 ORFs, no frameshifts, no TSD	NO
MM725	AT5TE34170	ATLINE1_6	L1	LINE	Non-LTR	auto	defective	short	
MM725	AT5TE34175	ATLINE1_6	L1	LINE	Non-LTR	auto	defective	short	
MM726	AT5TE34730	VANDAL8	undefined	MuDr	DNA	auto	defective	TIR, no continuous ORF	
MM728	AT5TE35265	ATMU5	undefined	MuDr	DNA	auto	defective	no TIR, no continuous ORF	
MM731	AT5TE36160	ATLINE2	L1	LINE	Non-LTR	auto	defective	short	
MM734	AT5TE36610	ATREP3	undefined	undefined	Helitron	non-auto	not defined	short, no ORFs	
MM734	AT5TE36615	ATLINE1_6	L1	LINE	Non-LTR	auto	defective	short	
MM734	AT5TE36620	ATLINE1_6	L1	LINE	Non-LTR	auto	defective	no RT	
MM744	AT5TE37800	TA11	L1	LINE	Non-LTR	auto	defective	RT, TSD, frameshifts	
MM823	AT5TE48535	TA11	L1	LINE	Non-LTR	auto	defective	short	
MM823	AT5TE48540	ATLINE1_5	L1	LINE	Non-LTR	auto	defective	short	
MM825	AT5TE48930	ATCOPIA24	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM832	AT5TE49480	ATLINEIII	L1	LINE	Non-LTR	auto	defective	short	
MM832	AT5TE49485	ATLINEIII	L1	LINE	Non-LTR	auto	defective	short	
MM832	AT5TE49490	ATLINEIII	L1	LINE	Non-LTR	auto	defective	short	
MM832	AT5TE49495	ATLINEIII	L1	LINE	Non-LTR	auto	defective	RT, ORF1 too short or fragmented, no TSD	
MM837	AT5TE50380	ATCOPIA91	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM845	AT5TE56585	ATCOPIA25	undefined	copia	LTR	auto	potentially mobile	RT, LTRs, ORF>340aa	NO
MM849	AT5TE56780	ATLINEIII	L1	LINE	Non-LTR	auto	defective	RT, ORF1 too short or fragmented, no TSD	
MM859	AT5TE63610	ENDOVIR1	Errantivirus	gypsy	LTR	auto	potentially mobile	LTRs, pol protein seems complete	NO
MM865	AT5TE69650	ATLINE2	L1	LINE	Non-LTR	auto	defective	short	

Abbreviations:

TIR	Terminal Inverted Repeat
ORF	Open Reading Frame
RT	Reverse Transcriptase
LTR	Long Terminal Repeats
TSD	Target Site Duplications

Table S7

Marker_id_epiRIL	chromosome	epiRIL_start_bp	epiRIL_stop_bp	Marker_id_P2	Marker_id_P3
MM1	1	4330606	4332076	1-4359800	1-4359800
MM2	1	6010663	6013983	1-6149751	1-6001538
MM4	1	7430002	7432267	1-7644962	1-7047756
MM5	1	8490901	8491751	1-8439006	1-8439006
MM7	1	8801988	8802650	1-8993233	1-8993233
MM17	1	11096911	11100708	1-11139723	1-11139723
MM25	1	12273252	12276332	1-12179065	1-12179065
MM33	1	13003181	13008641	1-13038240	1-13005911
MM39	1	13329072	13340087	1-13334580	1-13207971
MM52	1	13618483	13621742	1-13859051	1-13859051
MM87	1	15689530	15690065	1-15630635	1-15630635
MM101	1	16372020	16377961	1-16279095	1-16279095
MM114	1	16718975	16720795	1-16645134	1-16645134
MM123	1	17258838	17264340	1-17102334	1-17102334
MM147	1	21457161	21459296	1-21559246	1-21167712
MM157	1	22234806	22236246	1-22743028	1-22200580
MM158	1	23570478	23572928	1-23381914	1-23906908
MM159	1	24432541	24433101	1-24114746	1-24810967
MM163	1	27070457	27071391	1-27230162	1-27230162
MM166	2	245700	249332	2-498807	2-498807
MM171	2	1251574	1252848	2-1447413	2-1172482
MM240	2	3730709	3734122	2-3520754	2-4344527
MM330	2	5859874	5864604	2-5682223	2-5682223
MM335	2	6116421	6119529	2-6117975	2-6044749
MM357	2	6961080	6965815	2-6970449	2-6970449
MM371	2	7544676	7545673	2-7400522	2-7633698
MM373	2	8278256	8281520	2-8225326	2-8279888
MM374	2	8568345	8571152	2-8796903	2-8561080
MM378	2	9129123	9130835	2-9057864	2-9461465
MM380	2	9659660	9659972	2-9461465	2-9792570
MM382	2	10540595	10541195	2-10556376	2-10556376
MM383	2	12456566	12461464	2-12520610	2-12520610
MM385	2	12743505	12743777	2-12717797	2-12717797
MM388	2	15418592	15418927	2-15445245	2-15445245
MM392	3	129256	129877	3-290174	3-290174
MM396	3	7061219	7061849	3-7123630	3-7359421
MM398	3	7738889	7739204	3-7359421	3-7702216
MM399	3	8937125	8938547	3-8633204	3-8633204
MM400	3	9228167	9232640	3-9136628	3-9230404
MM405	3	9693424	9699210	3-9924267	3-9924267
MM414	3	11117372	11121888	3-10847881	3-10847881
MM427	3	11797070	11799048	3-11748521	3-11748521
MM432	3	12096151	12098525	3-12276692	3-12276692

MM466	3	13667971	13671251	3-13495418	3-13495379
MM515	3	15632482	15638053	3-15712057	3-15712057
MM527	3	16184523	16191125	3-15913994	3-15913994
MM531	3	16508925	16509440	3-16509183	3-16629399
MM537	3	16821132	16825096	3-16848354	3-16848354
MM544	3	18370976	18371431	3-18258898	3-18258898
MM546	3	22243503	22246468	3-22221736	3-22221736
MM547	3	23215509	23218355	3-23088778	3-23211977
MM550	4	788271	788751	4-945976	4-945976
MM551	4	1312610	1315610	4-1512987	4-1512987
MM586	4	2356046	2357721	4-2103325	4-2383725
MM654	4	5468765	5470776	4-5643991	4-5643991
MM678	4	6467386	6472846	4-6293204	4-5931550
MM686	4	8313708	8319324	4-8034821	4-8034821
MM689	4	8906581	8907231	4-9167906	4-9167906
MM691	4	9483934	9485359	4-9575956	4-9575956
MM693	4	9734038	9737673	4-10089916	4-10346818
MM694	4	10527354	10529034	4-10346818	4-10607774
MM695	4	10992797	10997912	4-11017270	4-10995355
MM698	4	11363449	11369169	4-11366309	4-11320394
MM701	4	13624419	13631859	4-13788227	4-13788227
MM703	4	14987455	14988333	4-14957828	4-14957828
MM704	4	17712926	17716726	4-17538469	4-17538469
MM706	5	1686487	1686997	5-1603469	5-1603469
MM707	5	2262159	2262544	5-2229415	5-2287470
MM712	5	4320753	4323348	5-4233682	5-4233682
MM713	5	5635294	5635620	5-5535964	5-5535964
MM715	5	6433688	6438813	5-6519202	5-6519202
MM716	5	7027577	7028347	5-7047330	5-7047330
MM718	5	7823819	7824639	5-7813295	5-7824229
MM719	5	8574747	8577717	5-8427379	5-8427379
MM724	5	9206569	9207339	5-9358168	5-9358168
MM744	5	10351503	10356268	5-10782718	5-10488859
MM823	5	13656931	13661362	5-13784419	5-13784419
MM845	5	15663492	15668447	5-15466566	5-15466566
MM854	5	16674280	16675285	5-16583743	5-16816665
MM859	5	17613965	17620413	5-17591339	5-17591339
MM862	5	18488790	18489135	5-18638175	5-18707445
MM865	5	19378317	19379292	5-19320777	5-19697188
MM867	5	21391149	21392149	5-21294493	5-21294493

Marker_id_P6	Marker_id_P7	Marker_id_P8	Marker_id_P9	Marker_id_P10	Marker_id_P12
1-4200550	1-4359800	1-4359800	1-4359800	1-4200550	1-4359800
1-6001538	1-6001538	1-6001538	1-6001538	1-6001538	1-6001538
1-7047756	1-7644962	1-7644962	1-7644962	1-7644962	1-7644962
1-8439006	1-8439006	1-8439006	1-8350582	1-8439006	1-8439006
1-9205325	1-8993233	1-9001217	1-8993233	1-8993233	1-8802319
1-10653718	1-10903254	1-10903254	1-10653718	1-11026901	1-10903254
1-12179065	1-12179065	1-12179065	1-12179065	1-12179065	1-12686038
1-12686038	1-13038240	1-12686038	1-13005911	1-13038240	1-13005911
1-13207971	1-13334580	1-13207971	1-13207971	1-13207971	1-13207971
1-14158183	1-13859051	1-13859051	1-14001934	1-14158183	1-13859051
1-15630635	1-15897174	1-15630635	1-15630635	1-15630635	1-15630635
1-16374991	1-15985718	1-16279095	1-16279095	1-16279095	1-16279095
1-16913975	1-16645134	1-17102334	1-16645134	1-16645134	1-16913975
1-17102334	1-17102334	1-17605952	1-17605952	1-17102334	1-17102334
1-21559246	1-21559246	1-21559246	1-21167712	1-21559246	1-21559246
1-22743028	1-22200580	1-22200580	1-22200580	1-22743028	1-22200580
1-23906908	1-23381914	1-23381914	1-23381914	1-23381914	1-23381914
1-24114746	1-24114746	1-24810967	1-24114746	1-24114746	1-24114746
1-27230162	1-27634939	1-27230162	1-27230162	1-27634939	1-27230162
2-498807	2-176156	2-498807	2-176156	2-247516	2-498807
2-1986922	2-1172482	2-1986922	2-1172482	2-1788467	2-1172482
2-3520754	2-3520754	2-3520754	2-3520754	2-3520754	2-3042043
2-5682223	2-5469974	2-5682223	2-5627965	2-5682223	2-5682223
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1-14001934	1-13859051	1-13859051
1-15630635	1-15630635	1-15897174
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1-17605952	1-17102334	1-17102334
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3-18532958	3-18258898	3-18258898
3-22221736	3-22221736	3-22221736
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5-19320777	5-19320777	5-19320777
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Table S8

A- Fold-increase relative to chromosome average

	1	2	3	4	5	
Peri	0.40 0.79 (0.46 - 1.03)	0.15 0.66 (0.27 - 1.06)	0.40 0.66 (0.40 - 1.11)	1.03 0.72 (0.07 - 1.07)	0.50 0.83 (0.50 - 1.15)	epiRILs F_2s
AT zone	0.55 1.27 (0.89 - 1.55)	0.76 1.67 (0.84 - 1.92)	1.04 1.37 (0.93 - 1.85)	1.19 1.60 (1.23 - 2.01)	0.87 1.54 (1.22 - 1.73)	epiRILs F_2s
Arms	1.23 1.04 (0.94 - 1.16)	1.60 1.08 (0.85 - 1.54)	1.18 1.04 (0.78 - 1.21)	1.05 1.11 (1.02 - 1.28)	1.30 1.01 (0.76 - 1.12)	epiRILs F_2s

B- Fold-decrease relative to chromosome average

	1	2	3	4	5	
Peri	2.50 1.27 (0.97 - 2.15)	6.88 1.51 (0.95 - 3.68)	2.53 1.52 (0.90 - 2.48)	0.97 1.39 (0.93 - 14.01)	2.01 1.20 (0.87 - 1.98)	epiRILs F_2s
AT zone	1.80 0.79 (0.64 - 1.13)	1.31 0.60 (0.52 - 1.19)	0.96 0.73 (0.54 - 1.08)	0.84 0.62 (0.50 - 0.81)	1.15 0.65 (0.58 - 0.82)	epiRILs F_2s
Arms	0.81 0.96 (0.86 - 1.06)	0.62 0.93 (0.65 - 1.18)	0.85 0.96 (0.83 - 1.28)	0.95 0.90 (0.78 - 0.98)	0.77 0.99 (0.89 – 1.32)	epiRILs F_2s

Table S9

Interval Name	Chromosome	Start	Stop	Length	#Recombinant epiRILs	Breakpoints Proportions
MM24	Chr1	11519877	11754109	234232	3	0,09375
MM26	Chr1	12315004	12403422	88419	2	0,0625
MM29	Chr1	12741147	12856990	115844	1	0,03125
MM36	Chr1	13098250	13239811	141562	1	0,03125
MM38	Chr1	13264736	13329072	64337	3	0,09375
MM45	Chr1	13433353	13491291	57939	1	0,03125
MM53	Chr1	13680349	13690605	10257	2	0,0625
MM62	Chr1	13969593	14052579	82987	3	0,09375
MM90	Chr1	15881127	15911298	30172	1	0,03125
MM95	Chr1	16077497	16109836	32340	5	0,15625
MM107	Chr1	16554298	16567689	13392	1	0,03125
MM119	Chr1	16858275	17025691	167417	1	0,03125
MM125	Chr1	17284412	17363118	78707	6	0,1875
MM126	Chr1	17363118	17491702	128585	2	0,0625
MM168	Chr2	930664	1198126	267463	3	0,2
MM176	Chr2	1490016	1665553	175538	2	0,13333333
MM198	Chr2	2293691	2365305	71615	1	0,06666667
MM230	Chr2	3171525	3175617	4093	1	0,06666667
MM326	Chr2	5725548	5737238	11691	2	0,13333333
MM333	Chr2	6016231	6112653	96423	1	0,06666667
MM353	Chr2	6790136	6849039	58904	2	0,13333333
MM365	Chr2	7231001	7544676	313676	3	0,2
MM414	Chr3	11117372	11172354	54983	1	0,05882353
MM415	Chr3	11172354	11366256	193903	2	0,11764706
MM426	Chr3	11745751	11797070	51320	3	0,17647059
MM428	Chr3	11880839	11935156	54318	1	0,05882353
MM464	Chr3	13475436	13506800	31365	1	0,05882353
MM490	Chr3	14942954	15004668	61715	1	0,05882353
MM495	Chr3	15186655	15240769	54115	1	0,05882353
MM509	Chr3	15581951	15586908	4958	2	0,11764706
MM524	Chr3	15973325	16008020	34696	2	0,11764706
MM527	Chr3	16184523	16256031	71509	1	0,05882353
MM529	Chr3	16257166	16304478	47313	1	0,05882353
MM536	Chr3	16702155	16821132	118978	1	0,05882353
MM552	Chr4	1447714	1592613	144900	1	0,05263158
MM557	Chr4	1820123	1996722	176600	1	0,05263158
MM586	Chr4	2356046	2596832	240787	2	0,10526316
MM615	Chr4	3707081	3719963	12883	1	0,05263158
MM629	Chr4	4358332	4539542	181211	1	0,05263158
MM644	Chr4	4782418	4861117	78700	1	0,05263158
MM651	Chr4	5141956	5468765	326810	2	0,10526316
MM660	Chr4	5555107	5588246	33140	2	0,10526316

MM664	Chr4	5627718	5751470	123753	7	0,36842105
MM665	Chr4	5751470	5766434	14965	1	0,05263158
MM722	Chr5	8788121	9203261	415141	1	0,02857143
MM724	Chr5	9206569	9412161	205593	2	0,05714286
MM725	Chr5	9412161	9561317	149157	1	0,02857143
MM726	Chr5	9561317	9707999	146683	2	0,05714286
MM728	Chr5	9712277	9840810	128534	1	0,02857143
MM733	Chr5	9980031	10049721	69691	2	0,05714286
MM739	Chr5	10116048	10351503	235456	2	0,05714286
MM748	Chr5	10398185	10497167	98983	1	0,02857143
MM771	Chr5	11055838	11068088	12251	1	0,02857143
MM774	Chr5	11198254	11408293	210040	1	0,02857143
MM804	Chr5	12693478	12738226	44749	1	0,02857143
MM810	Chr5	12996743	13078281	81539	1	0,02857143
MM820	Chr5	13549016	13592209	43194	5	0,14285714
MM822	Chr5	13609582	13656931	47350	3	0,08571429
MM824	Chr5	13666130	13753476	87347	1	0,02857143
MM826	Chr5	13797308	13805059	7752	1	0,02857143
MM831	Chr5	13878051	13901149	23099	4	0,11428571
MM834	Chr5	13946515	13985794	39280	1	0,02857143
MM843	Chr5	15101170	15376021	274852	2	0,05714286
MM848	Chr5	15700805	15736222	35418	1	0,02857143
MM852	Chr5	15823391	15937735	114345	1	0,02857143

Table S10

Window*	Start marker interval	Stop marker interval	# Recombinations	# Recombinant epiRILs	# epiRILs with shared breakpoint	% epiRILs with shared breakpoint	Start shared Breakpoint interval	Stop shared Breakpoint interval	Length shared Breakpoint interval
Chr 1 B	11,100,758	13,618,482	13	12	3	25.0	11,518,537	12,273,391	754,855
					3	25.0	13,101,452	13,241,436	139,985
Chr 1 A	15,690,116	17,258,837	6	6	0	0.0	-	-	-
Chr 2 B	249,383	1,251,573	9	9	4	44.4	378,733	536,423	157,691
Chr 2 A	5,864,654	8,568,344	10	10	3	33.3	8,281,415	8,568,344	286,930
Chr 3 B	8,938,604	12,096,150	20	19	5	26.3	9,710,200	10,112,728	402,529
					3	15.8	11,704,365	11,797,504	93,140
Chr 3 A	15,638,113	18,370,975	21	21	3	14.3	16,973,828	17,989,636	1,015,809
					4	19.0	17,995,327	18,370,975	375,649
Chr 4 B	788,808	2,356,045	6	6	0	0.0	-	-	-
Chr 4 A	5,470,842	8,313,707	31	26	3	11.5	5,683,645	5,751,920	68,276
					3	11.5	6,919,334	6,977,247	57,914
					4	15.4	6,977,575	8,313,907	1,336,333
Chr 5 B	7,824,697	10,351,502	16	16	3	18.8	8,667,186	9,206,733	539,548
Chr 5 A	13,661,415	16,674279	11	11	0	0.0	-	-	-

* B = window **B**efore centromere
A = window **A**fter centromere

Table S11-A

chr 1				chr 2				chr 3				chr 4				chr 5			
cross	cM	low	up	cross	cM	low	up	cross	cM	low	up	cross	cM	low	up	cross	cM	low	up
P129	67.5	57.9	79.1	P3	42.2	34.5	51.4	P35	68.9	57.8	80.3	P35	57.1	47.5	67.0	P8	46.7	37.8	56.2
P9	70.2	59.1	81.9	P66	44.3	35.8	53.3	P9	71.0	59.9	83.3	P12	58.8	49.6	69.8	P129	57.3	47.6	67.1
P35	73.5	63.3	85.8	P10	47.8	39.8	57.9	P129	73.6	63.1	85.7	P9	60.3	50.7	71.0	P169	58.9	49.1	68.8
P12	73.8	63.8	85.5	P169	48.8	40.7	58.8	P169	73.8	62.4	85.5	P19	61.0	51.6	73.1	P9	60.7	51.5	71.7
P169	76.7	64.7	89.0	P129	49.5	40.6	59.0	P10	75.6	64.5	87.8	P10	61.5	51.5	75.2	P35	62.3	52.8	71.7
P3	77.8	65.8	89.8	P9	50.4	41.7	60.7	P15	75.9	64.3	88.0	P3	62.9	52.9	74.9	P7	63.2	53.6	74.0
P8	78.0	66.5	90.3	P8	50.4	42.1	60.7	P2	77.9	67.3	90.8	P8	63.1	52.9	73.5	P145	63.8	54.6	75.5
P15	81.8	69.6	95.1	P15	51.6	42.9	60.9	P66	78.2	66.3	91.9	P129	63.4	53.8	75.2	P12	64.5	54.7	75.8
P145	84.4	72.4	97.2	P35	52.0	43.3	62.5	P8	82.0	69.7	95.9	P7	64.0	54.0	76.2	P19	64.9	55.4	76.5
P66	86.4	74.9	100.5	P20	52.5	43.0	62.4	P145	84.1	72.9	97.0	P66	64.8	54.1	75.6	P2	66.7	56.7	77.3
P6	86.7	74.7	99.8	P6	53.5	44.4	64.7	P12	84.3	71.8	98.7	P15	65.0	54.5	77.9	EPI	67.3	52.7	83.6
P19	86.9	74.9	100.9	P145	54.8	45.0	65.4	P3	84.7	73.3	98.4	P2	67.4	57.5	80.3	P17	67.5	57.5	79.6
P10	87.1	75.1	100.2	P7	55.6	46.4	66.3	P7	85.4	72.5	100.1	P17	69.3	58.8	81.1	P6	68.9	58.5	80.4
P7	89.3	76.9	103.7	P2	57.8	48.7	68.7	P17	85.9	74.6	100.5	P6	69.7	58.7	82.4	P15	69.2	58.9	80.8
P17	96.0	82.9	110.1	P12	58.8	48.2	70.5	P19	93.0	79.9	108.6	P169	70.5	59.9	82.5	P10	70.8	60.0	82.2
P20	99.0	86.5	113.5	P19	59.6	49.3	70.9	P6	95.0	80.5	111.4	P145	72.3	61.6	84.9	P66	73.9	63.0	86.8
P2	109.2	95.9	126.0	EPI	61.7	46.9	78.7	P20	99.5	85.8	114.6	P20	75.5	64.9	87.3	P3	77.4	67.3	89.2
EPI	110.7	89.8	138.5	P17	61.9	52.0	73.2	EPI	101.7	80.5	125.9	EPI	84.6	68.3	105.2	P20	80.5	68.8	93.5

Table S11-B

chr 1				chr 2				chr 3				chr 4				chr 5			
cross	FC	low	up	cross	FC	low	up	cross	FC	low	up	cross	FC	low	up	cross	FC	low	up
EPI	0.40	0.19	0.64	EPI	0.15	0.03	0.31	EPI	0.40	0.18	0.63	P7	0.07	0.00	0.17	EPI	0.50	0.27	0.77
P6	0.46	0.29	0.67	P3	0.27	0.13	0.44	P7	0.40	0.25	0.59	P10	0.24	0.1	0.41	P20	0.50	0.34	0.67
P35	0.52	0.29	0.77	P7	0.43	0.28	0.61	P6	0.42	0.26	0.59	P20	0.40	0.22	0.61	P8	0.59	0.35	0.83
P7	0.59	0.38	0.81	P129	0.46	0.29	0.65	P145	0.54	0.35	0.75	P2	0.48	0.28	0.70	P3	0.68	0.49	0.88
P169	0.65	0.43	0.91	P20	0.49	0.31	0.69	P8	0.58	0.39	0.78	P15	0.53	0.31	0.79	P2	0.75	0.52	0.97
P15	0.67	0.45	0.93	P2	0.55	0.37	0.75	P19	0.59	0.40	0.77	P3	0.61	0.36	0.88	P9	0.77	0.56	1.00
P12	0.70	0.45	0.99	P8	0.55	0.35	0.77	P20	0.59	0.42	0.78	P8	0.68	0.44	0.96	P15	0.77	0.57	1.00
P145	0.72	0.49	0.96	P6	0.60	0.38	0.82	P2	0.63	0.44	0.86	P129	0.68	0.42	0.95	P169	0.78	0.53	1.03
P3	0.73	0.49	1.02	P145	0.66	0.46	0.86	P15	0.65	0.46	0.88	P169	0.72	0.45	1.01	P145	0.83	0.61	1.07
P20	0.79	0.57	1.02	P15	0.66	0.45	0.87	P129	0.66	0.46	0.88	P19	0.76	0.53	1.03	P12	0.83	0.60	1.09
P8	0.81	0.58	1.06	P19	0.67	0.49	0.87	P3	0.69	0.50	0.90	P145	0.77	0.53	1.04	P66	0.86	0.66	1.07
P17	0.84	0.60	1.12	P10	0.69	0.46	0.92	P66	0.69	0.49	0.93	P35	0.81	0.52	1.12	P7	0.91	0.66	1.15
P2	0.86	0.62	1.09	P169	0.73	0.51	0.95	P169	0.80	0.59	1.00	P6	0.85	0.58	1.15	P129	0.92	0.67	1.19
P129	0.98	0.71	1.28	P35	0.74	0.52	0.98	P35	0.80	0.55	1.07	P9	0.89	0.61	1.20	P17	0.95	0.71	1.17
P19	0.98	0.76	1.25	P9	0.84	0.62	1.07	P9	0.83	0.61	1.09	P12	0.89	0.60	1.20	P35	0.99	0.75	1.26
P9	0.98	0.70	1.27	P66	0.87	0.65	1.11	P12	0.86	0.64	1.09	EPI	1.03	0.66	1.42	P19	1.04	0.80	1.29
P66	1.02	0.79	1.28	P17	1.00	0.80	1.21	P17	0.99	0.77	1.23	P66	1.03	0.72	1.39	P6	1.15	0.91	1.39
P10	1.03	0.77	1.29	P12	1.06	0.83	1.29	P10	1.11	0.90	1.34	P17	1.07	0.78	1.38	P10	1.15	0.91	1.43

Table S11-C

chr 1				chr 2				chr 3				chr 4				chr 5			
cross	FC	low	up	cross	FC	low	up	cross	FC	low	up	cross	FC	low	up	cross	FC	low	up
EPI	0.55	0.29	0.86	EPI	0.76	0.39	1.16	P6	0.93	0.74	1.13	EPI	1.19	0.83	1.57	EPI	0.87	0.56	1.23
P6	0.89	0.64	1.16	P3	0.84	0.51	1.19	EPI	1.04	0.71	1.39	P6	1.23	0.93	1.53	P17	1.22	0.97	1.44
P35	1.01	0.71	1.35	P10	1.04	0.75	1.33	P20	1.21	0.99	1.46	P17	1.29	0.99	1.62	P15	1.27	1.01	1.55
P20	1.10	0.85	1.35	P66	1.04	0.71	1.35	P7	1.26	0.99	1.51	P66	1.30	1.01	1.59	P66	1.35	1.10	1.59
P169	1.15	0.85	1.50	P17	1.34	1.01	1.71	P9	1.26	1.04	1.52	P3	1.37	1.04	1.72	P7	1.37	1.09	1.65
P8	1.19	0.90	1.50	P20	1.36	1.03	1.69	P19	1.29	1.07	1.55	P169	1.43	1.17	1.72	P2	1.38	1.12	1.63
P3	1.21	0.86	1.55	P129	1.41	1.08	1.76	P169	1.29	1.02	1.57	P12	1.47	1.13	1.83	P20	1.38	1.16	1.64
P129	1.25	0.96	1.58	P15	1.44	1.11	1.82	P129	1.30	1.07	1.55	P8	1.48	1.18	1.80	P129	1.50	1.18	1.83
P15	1.27	0.96	1.61	P8	1.47	1.17	1.78	P3	1.32	1.06	1.56	P20	1.52	1.26	1.80	P169	1.54	1.22	1.82
P7	1.27	0.94	1.62	P2	1.67	1.37	2.00	P17	1.37	1.12	1.61	P129	1.60	1.31	1.88	P6	1.54	1.26	1.83
P145	1.31	1.00	1.64	P6	1.67	1.36	2.00	P15	1.38	1.11	1.65	P35	1.64	1.26	2.03	P8	1.56	1.23	1.90
P2	1.34	1.02	1.67	P12	1.67	1.32	2.04	P12	1.38	1.14	1.63	P145	1.69	1.41	1.98	P145	1.60	1.30	1.93
P17	1.38	1.06	1.71	P145	1.70	1.34	2.07	P2	1.48	1.18	1.77	P19	1.71	1.32	2.13	P35	1.60	1.31	1.91
P12	1.41	1.07	1.76	P35	1.71	1.40	1.99	P8	1.51	1.22	1.80	P2	1.73	1.35	2.10	P9	1.64	1.37	1.92
P9	1.44	1.14	1.77	P19	1.78	1.43	2.10	P66	1.55	1.27	1.83	P9	1.79	1.42	2.17	P3	1.67	1.42	1.93
P66	1.46	1.17	1.77	P7	1.83	1.51	2.15	P145	1.76	1.50	2.03	P15	1.80	1.49	2.11	P10	1.69	1.41	1.97
P10	1.47	1.15	1.81	P169	1.85	1.51	2.20	P35	1.78	1.51	2.06	P7	1.92	1.63	2.22	P19	1.72	1.46	1.97
P19	1.55	1.23	1.93	P9	1.92	1.58	2.26	P10	1.85	1.58	2.12	P10	2.01	1.65	2.33	P12	1.73	1.42	2.02

Table S11-D

chr 1				chr 2				chr 3				chr 4				chr 5			
cross	FC	low	up	cross	FC	low	up	cross	FC	low	up	cross	FC	low	up	cross	FC	low	up
P15	0.94	0.81	1.09	P35	0.85	0.68	1.02	P10	0.78	0.66	0.90	P17	1.02	0.92	1.11	P19	0.76	0.62	0.90
P2	0.97	0.85	1.10	P9	0.86	0.66	1.04	P35	0.89	0.77	1.01	EPI	1.05	0.91	1.18	P10	0.76	0.63	0.90
P17	0.98	0.85	1.11	P12	0.90	0.74	1.07	P145	0.95	0.84	1.06	P8	1.06	0.95	1.15	P9	0.80	0.67	0.94
P19	0.99	0.85	1.12	P19	0.91	0.73	1.09	P17	0.96	0.84	1.07	P145	1.06	0.96	1.15	P145	0.81	0.68	0.95
P9	0.99	0.84	1.14	P169	0.95	0.77	1.13	P129	0.99	0.87	1.11	P66	1.06	0.97	1.14	P35	0.93	0.78	1.07
P12	1.01	0.86	1.15	P17	0.99	0.84	1.14	P2	1.00	0.89	1.12	P2	1.07	0.97	1.17	P12	0.95	0.81	1.09
P129	1.02	0.86	1.15	P7	1.00	0.83	1.17	P8	1.00	0.89	1.12	P9	1.08	0.97	1.16	P169	0.97	0.83	1.11
P145	1.02	0.89	1.16	P6	1.04	0.87	1.22	P9	1.02	0.89	1.13	P12	1.08	0.98	1.18	P6	1.00	0.86	1.13
P10	1.04	0.91	1.17	P15	1.08	0.91	1.27	P66	1.04	0.94	1.14	P35	1.11	1.00	1.21	P7	1.01	0.86	1.16
P8	1.06	0.92	1.20	P2	1.09	0.91	1.24	P3	1.06	0.95	1.17	P15	1.11	1.02	1.20	P66	1.02	0.88	1.15
P66	1.06	0.93	1.19	P8	1.10	0.94	1.26	P12	1.06	0.95	1.16	P169	1.11	1.03	1.19	P129	1.02	0.87	1.17
P7	1.07	0.94	1.22	P145	1.13	0.98	1.30	P15	1.08	0.98	1.18	P19	1.11	1.00	1.21	P8	1.04	0.88	1.20
P169	1.09	0.94	1.22	P66	1.14	0.97	1.31	P169	1.10	0.98	1.21	P6	1.13	1.04	1.20	P2	1.05	0.93	1.18
P3	1.13	0.99	1.26	P129	1.15	0.97	1.33	P19	1.12	1.01	1.21	P3	1.13	1.04	1.21	P15	1.10	0.97	1.22
P35	1.15	1.01	1.28	P10	1.33	1.16	1.49	P20	1.14	1.03	1.24	P129	1.17	1.08	1.27	P20	1.11	0.99	1.23
P20	1.15	1.04	1.27	P20	1.34	1.17	1.49	EPI	1.18	1.04	1.31	P20	1.20	1.13	1.27	P17	1.12	0.99	1.25
P6	1.16	1.02	1.29	P3	1.54	1.38	1.69	P6	1.20	1.10	1.29	P10	1.25	1.17	1.32	P3	1.12	0.99	1.24
EPI	1.23	1.05	1.41	EPI	1.60	1.42	1.77	P7	1.21	1.11	1.30	P7	1.28	1.19	1.36	EPI	1.30	1.14	1.45