Supplementary Information Appendix:

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

Maria Colomé-Tatché[1†], Sandra Cortijo[2†], René Wardenaar[1], Lionel Morgado[1] Benoit Lahouze[2], Alexis Sarazin[2], Mathilde Etcheverry[2], Antoine Martin[2], Suhua Feng[3], Evelyne Duvernois-Berthet[2], Karine Labadie[4], Patrick Wincker[4], Steven E. Jacobsen[3], Ritsert C. Jansen[1], Vincent Colot[2*] and Frank Johannes[1*]

[1]Groningen Bioinformatics Centre, University of Groningen, Nijenborgh 7, 9747 AG Groningen, The Netherlands. [2]Institut de Biologie de l'École Normale Supérieure (IBENS), CNRS UMR8197-INSERM U1024, 46 rue d'Ulm, 75230 Paris cedex 05, France. [3]Howard Hughes Medical Institute, Department of Molecular, Cell, and Developmental Biology, University of California, Los Angeles, CA 90095-1606, USA. [4]Genoscope, Institut de Génomique, CEA, 2 rue Gaston Crémieux, Evry, F-91057, France.

[†]Equal contributions

[*]To whom correspondence should be addressed; E-mail: f.johannes@rug.nl, colot@biologie.ens.fr

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^i_j 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:

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

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:

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

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

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

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 $19\,°$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 $p_{ddm1} = \{\Pr(wt/wt), \Pr(wt/ddm1), \Pr(ddm1/ddm1)\}$ 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 $p_{wt} = \{\Pr(wt/wt), \Pr(wt/ddm1), \Pr(ddm1/ddm1)\}$ 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:

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

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)).

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Supplementary Information Appendix (Figures and Tables):

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

Maria Colomé-Tatché[1†], Sandra Cortijo[2†], René Wardenaar[1], Lionel Morgado[1], Benoit Lahouze[2], Alexis Sarazin[2], Mathilde Etcheverry[2], Antoine Martin[2], Suhua Feng[3], Evelyne Duvernois-Berthet[2], Karine Labadie[4], Patrick Wincker[4], Steven E. Jacobsen[3], Ritsert C. Jansen[1], Vincent Colot[2*] and Frank Johannes[1*]

[1]Groningen Bioinformatics Centre, University of Groningen, Nijenborgh 7, 9747 AG Groningen, The Netherlands. [2]Institut de Biologie de l'École Normale Supérieure (IBENS), CNRS UMR8197-INSERM U1024, 46 rue d'Ulm, 75230 Paris cedex 05, France. [3]Howard Hughes Medical Institute, Department of Molecular, Cell, and Developmental Biology, University of California, Los Angeles, CA 90095-1606, USA. [4]Genoscope, Institut de Génomique, CEA, 2 rue Gaston Crémieux, Evry, F-91057, France.

[†]Equal contributions

[*]To whom correspondence should be addressed; E-mail: f.johannes@rug.nl, colot@biologie.ens.fr

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

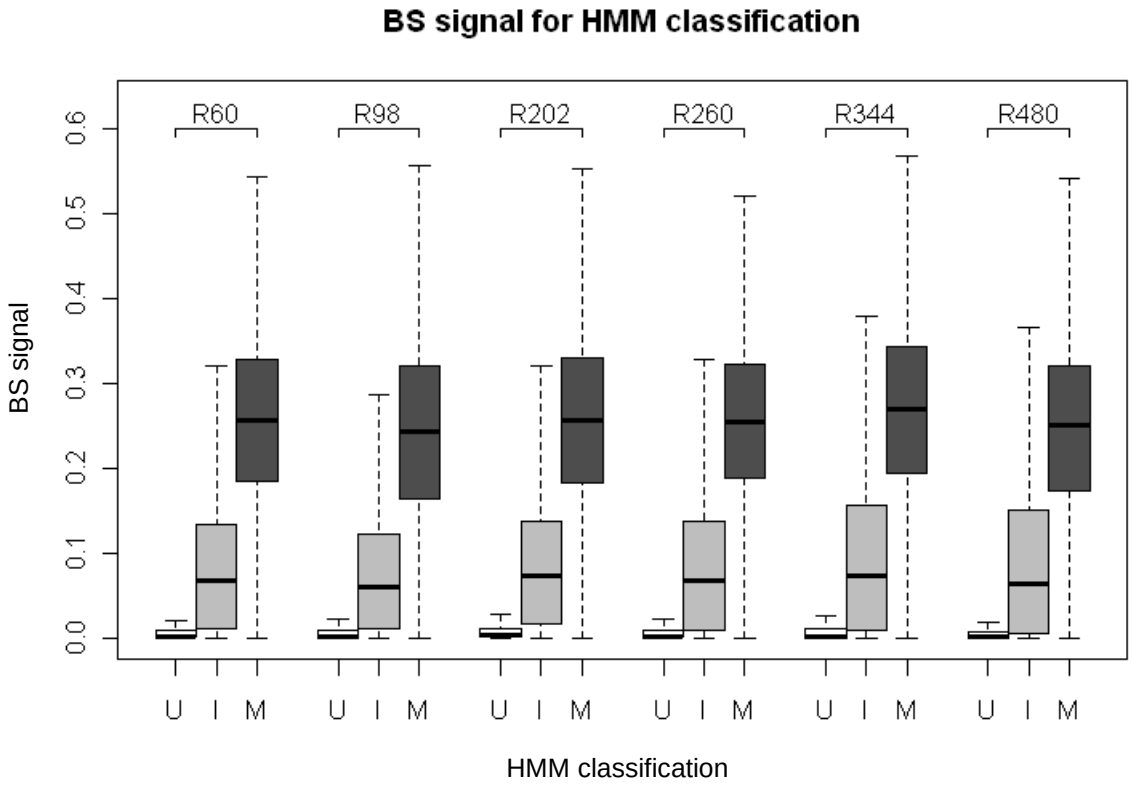
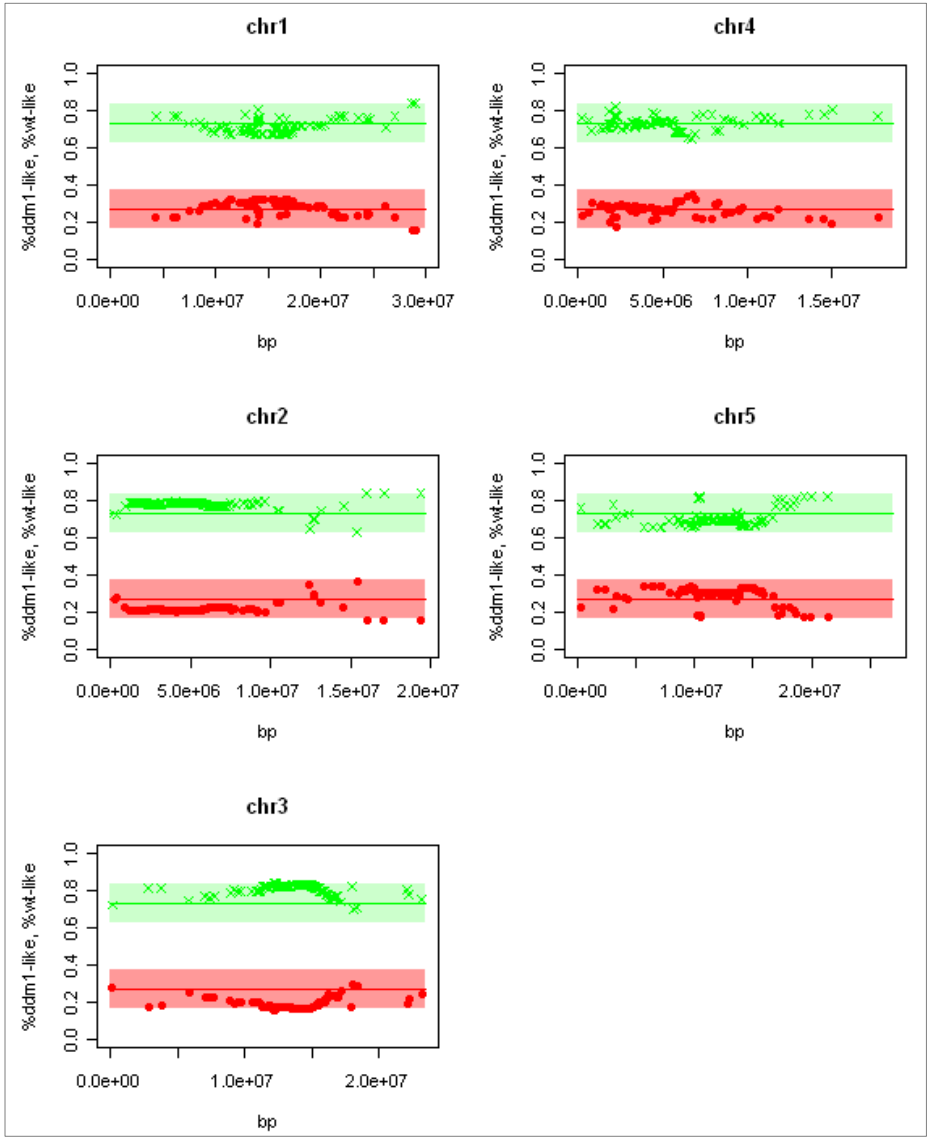

BS signal for HMM classification
R60
R98
R202
R260
R344
R480
BS signal
0.0
0.1
0.2
0.3
0.4
0.5
0.6
U I M U I M U I M U I M U I M U I M
HMM classification

Figure S2

867 Mendelian DMRs



126 Mendelian DMRs
used for map construction

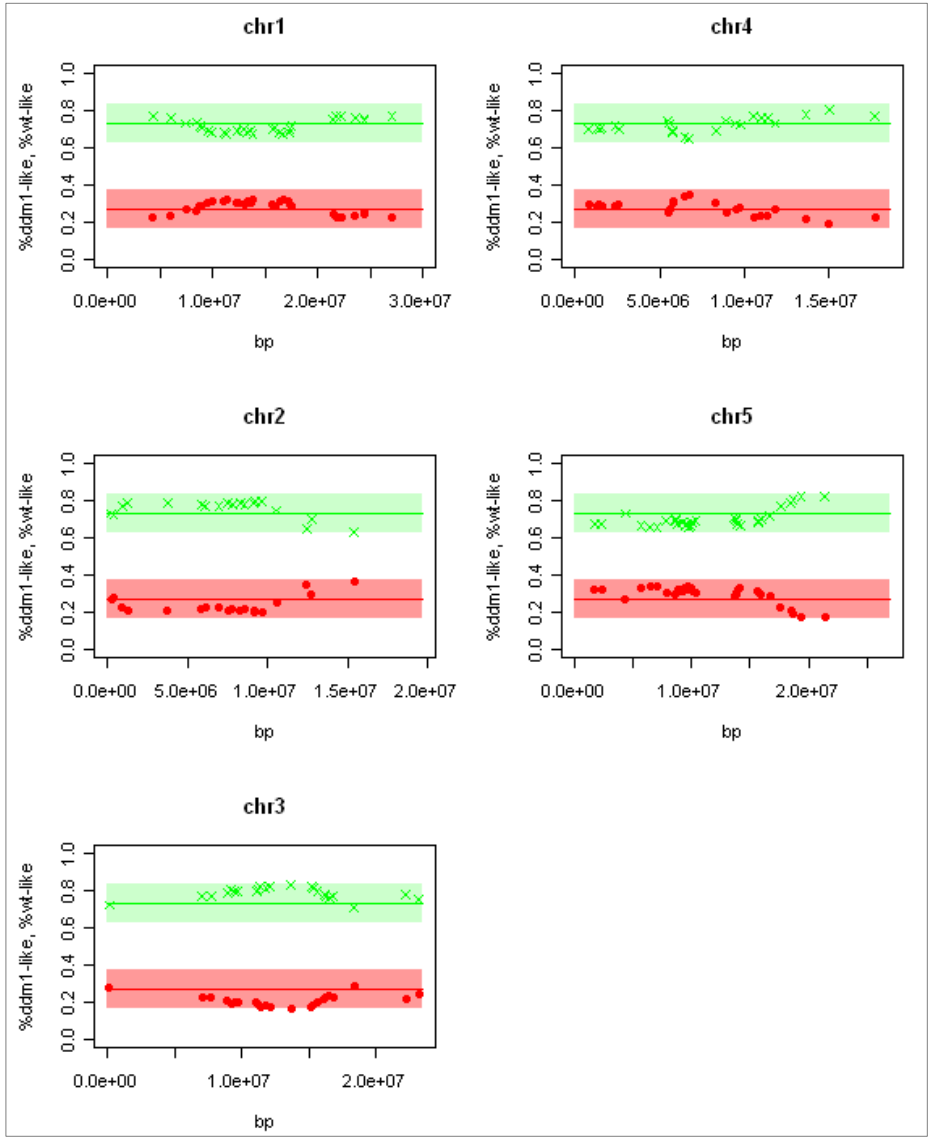
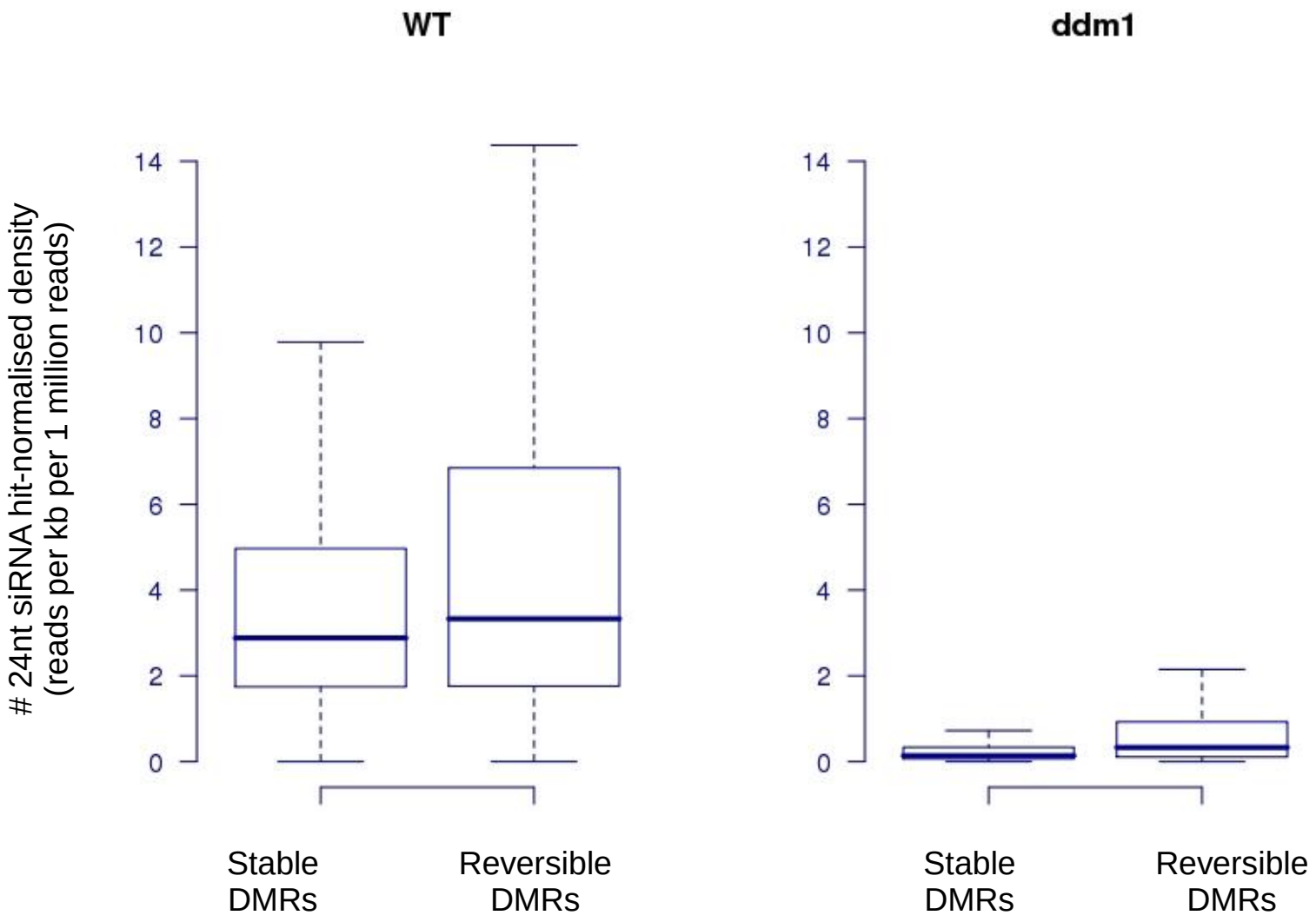


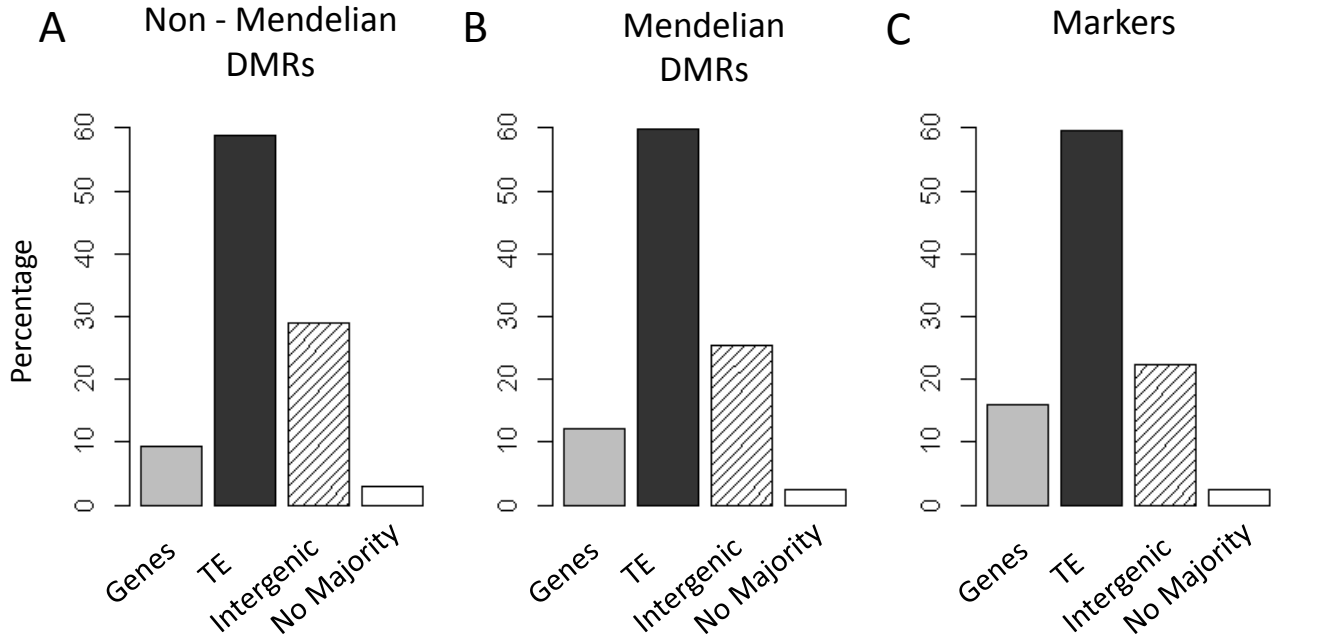
Figure S3



Wilcoxon rank test
p-value = 0.0003155

Wilcoxon rank test
p-value < 2.2e-16

Figure S4

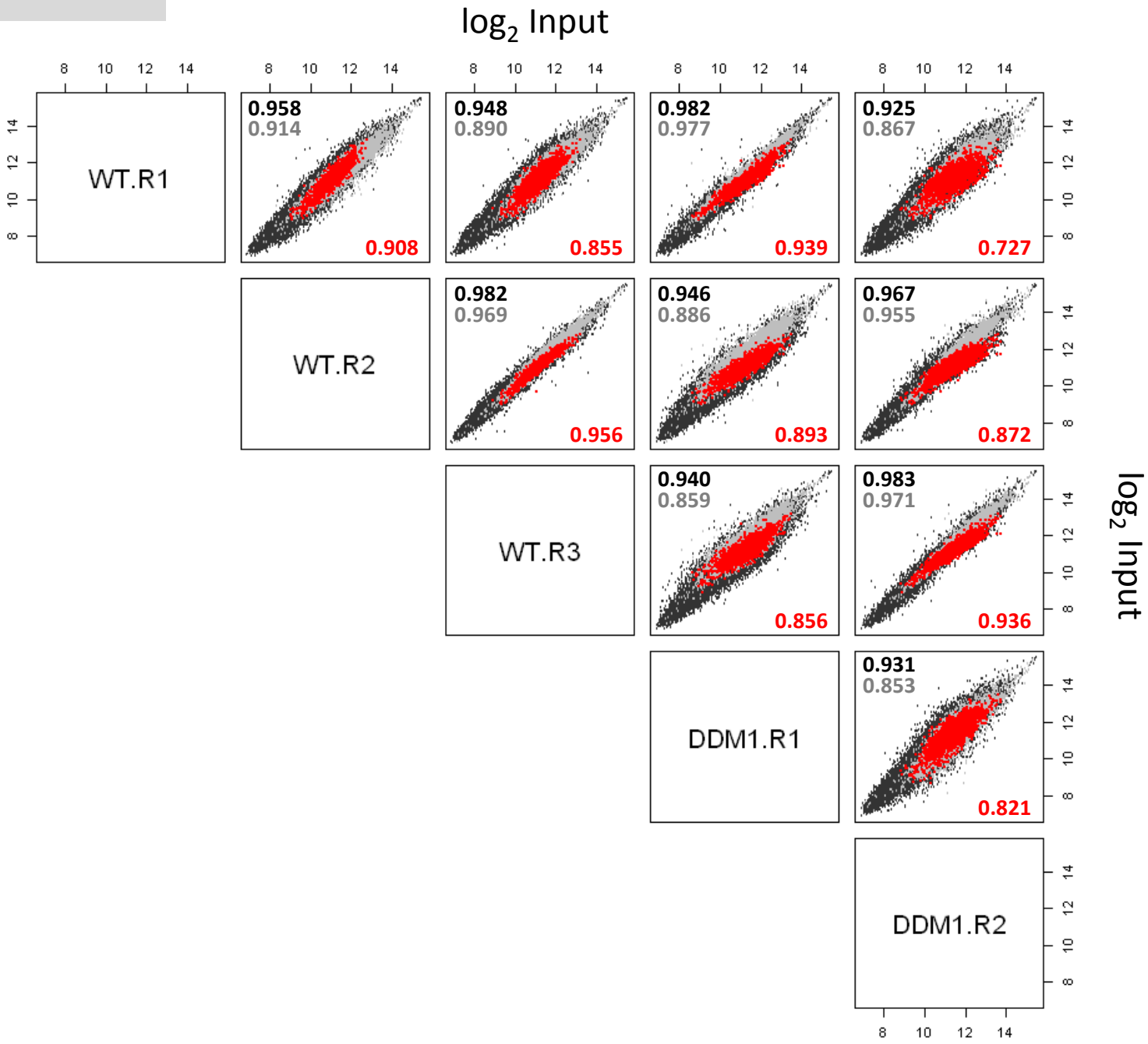


#	163	1025	503	53
%	9.3	58.8	28.8	3.0

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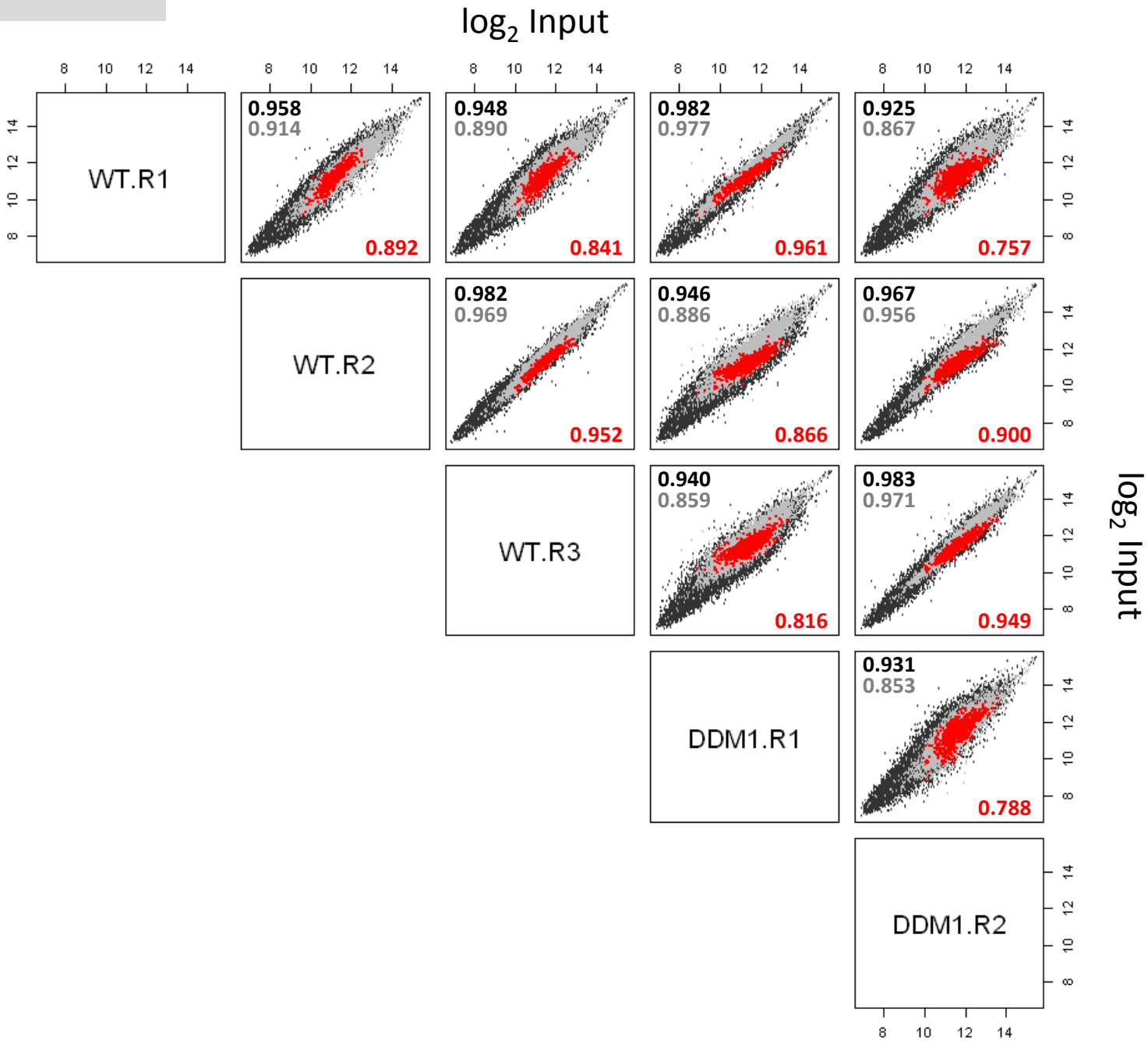
0.914
0.908
0.948
0.890
0.855
0.982
0.977
0.939
0.925
0.867
0.727
0.982
0.969
0.956
0.946
0.886
0.893
0.967
0.955
0.872
0.940
0.859
0.856
0.983
0.971
0.936
0.931
0.853
0.821
8
10
12
14
log2 Input

Figure S5-2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WT.R1
WT.R2
WT.R3
DDM1.R1
DDM1.R2
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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
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0.949
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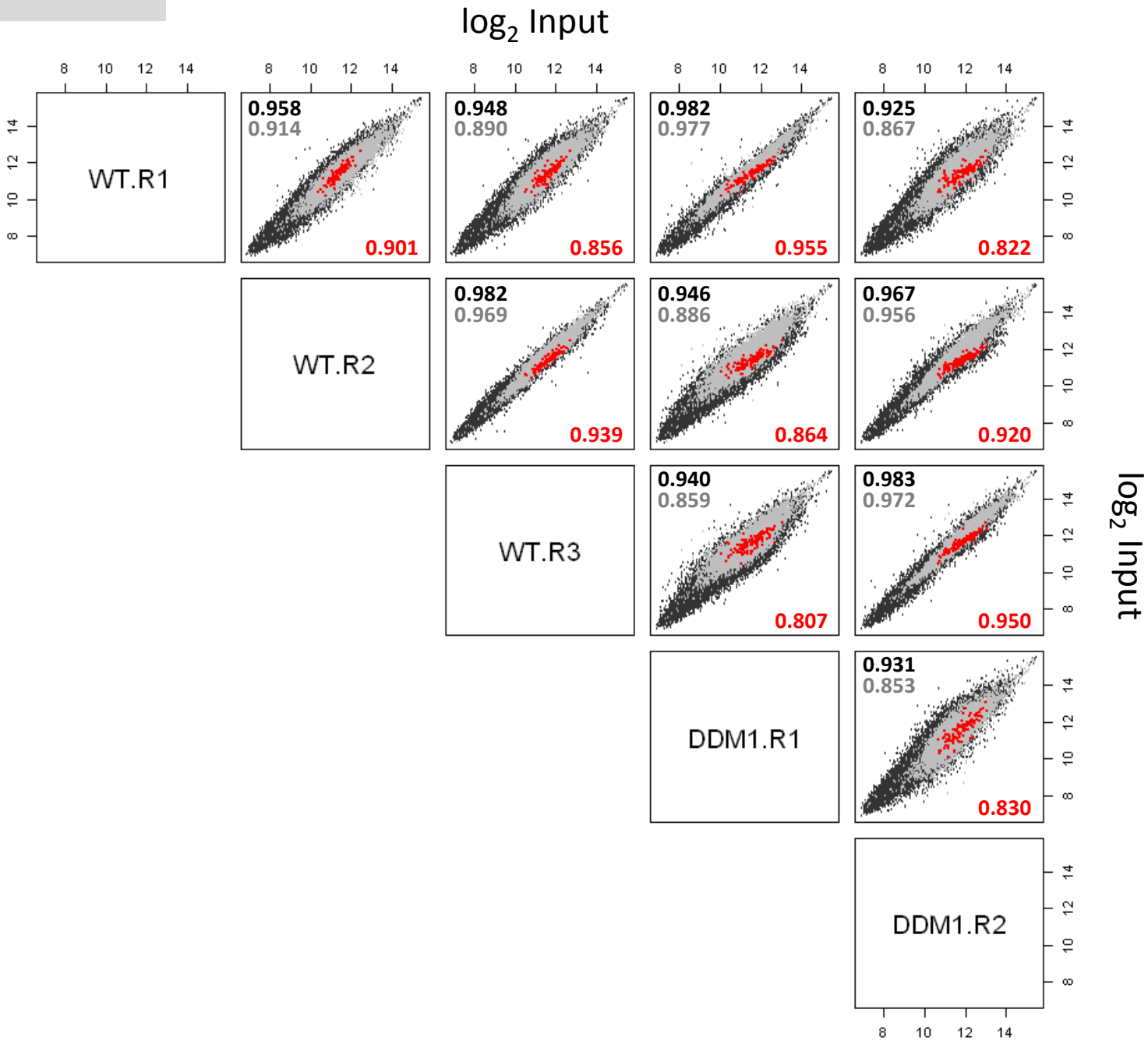
0.853
0.788
8
10
12
14
log2 Input

Figure S5-3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WT.R1
WT.R2
WT.R3
DDM1.R1
DDM1.R2
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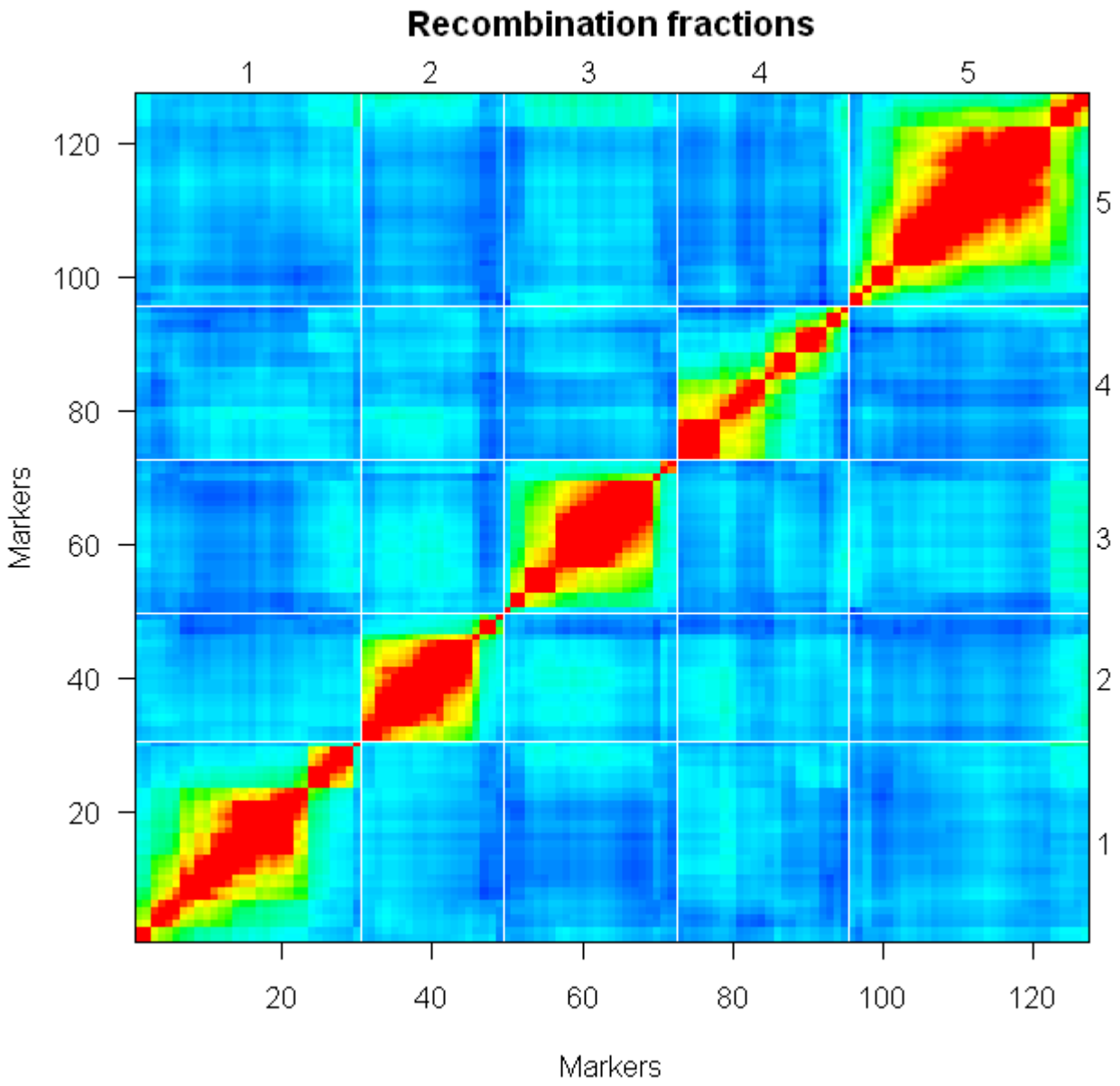
0.914
0.901
0.948
0.890
0.856
0.982
0.977
0.955
0.925
0.867
0.822
0.982
0.969
0.939
0.946
0.886
0.864
0.967
0.956
0.920
0.940
0.859
0.807
0.983
0.972
0.950
0.931
0.853
0.830
8
10
12
14
log2 Input

Figure S6


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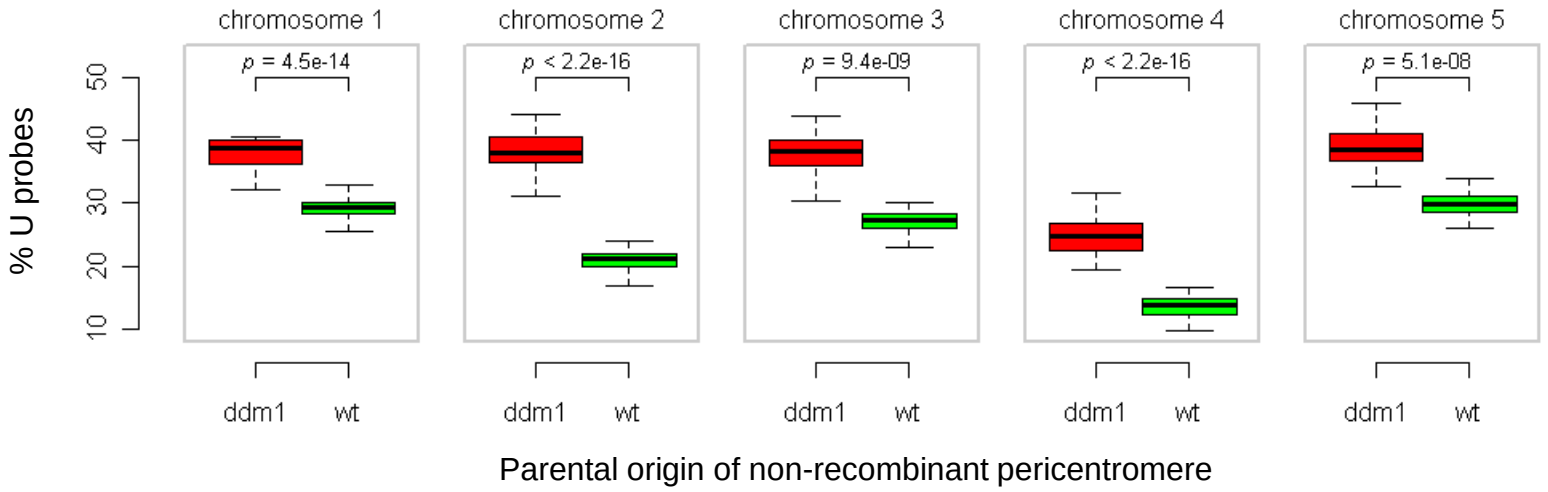
100
80
60
40
20
Markers
20
40
60
80
100
120
Markers

Figure S7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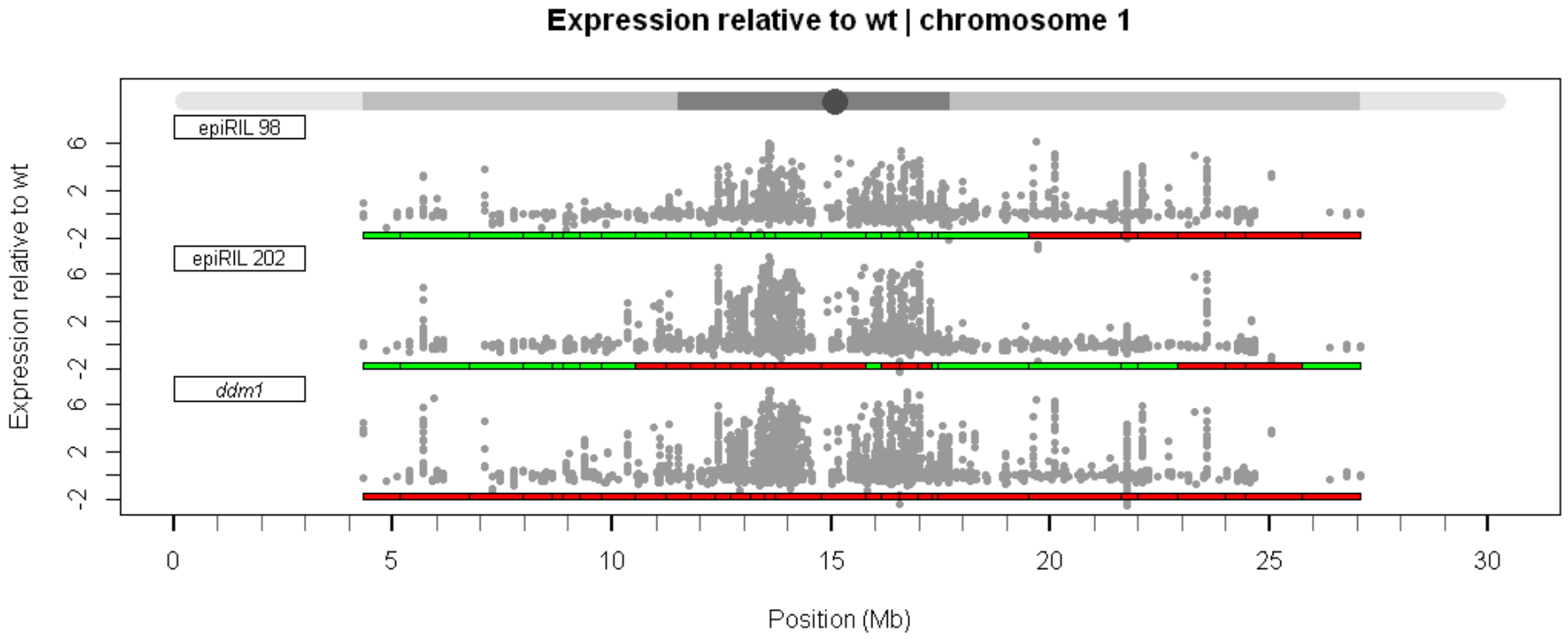
chromosome 2
chromosome 3
chromosome 4
chromosome 5
p = 4.5e-14
p < 2.2e-16
p = 9.4e-09
p < 2.2e-16
p = 5.1e-08
% U probes
10
20
30
40
50
ddm1
wt
Parental origin of non-recombinant pericentromere

Figure S8-1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epiRIL 202
ddm1
Expression relative to wt
Position (Mb)
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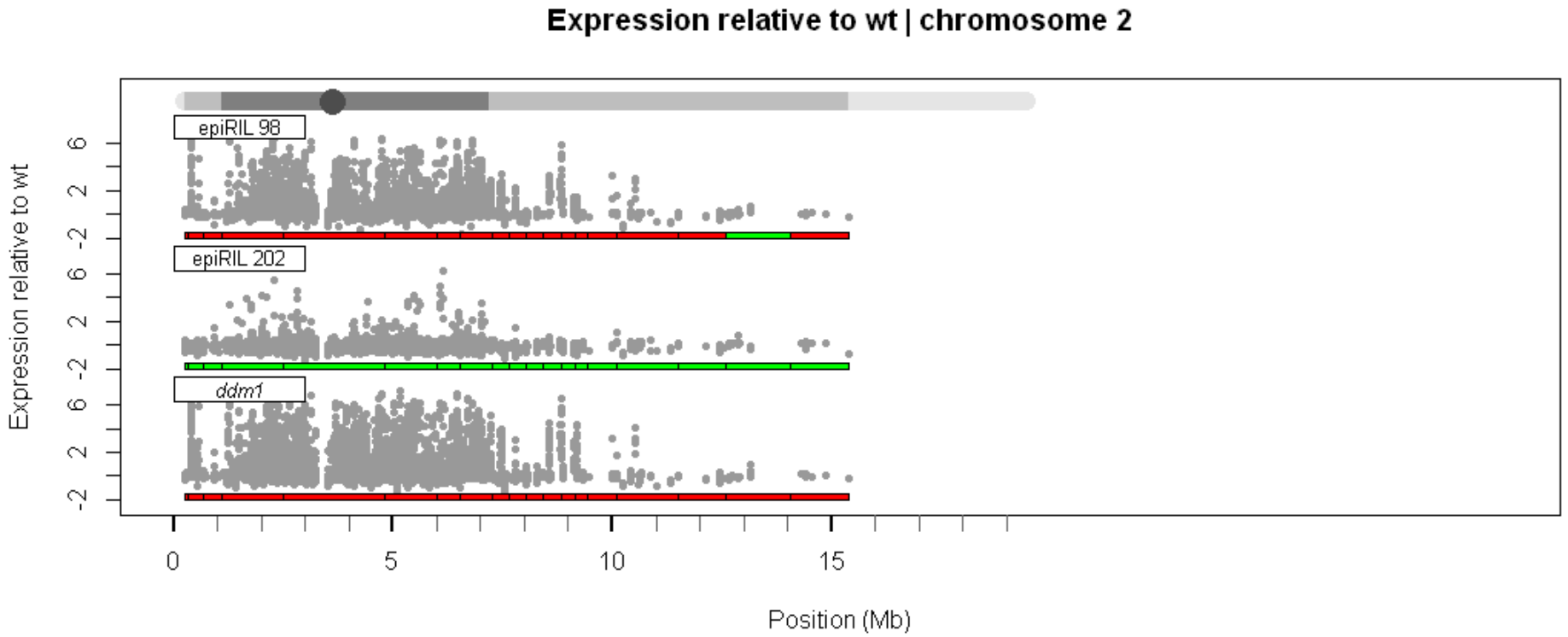
5
10
15
20
25
30

Figure S8-2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epiRIL 202
ddm1
Expression relative to wt
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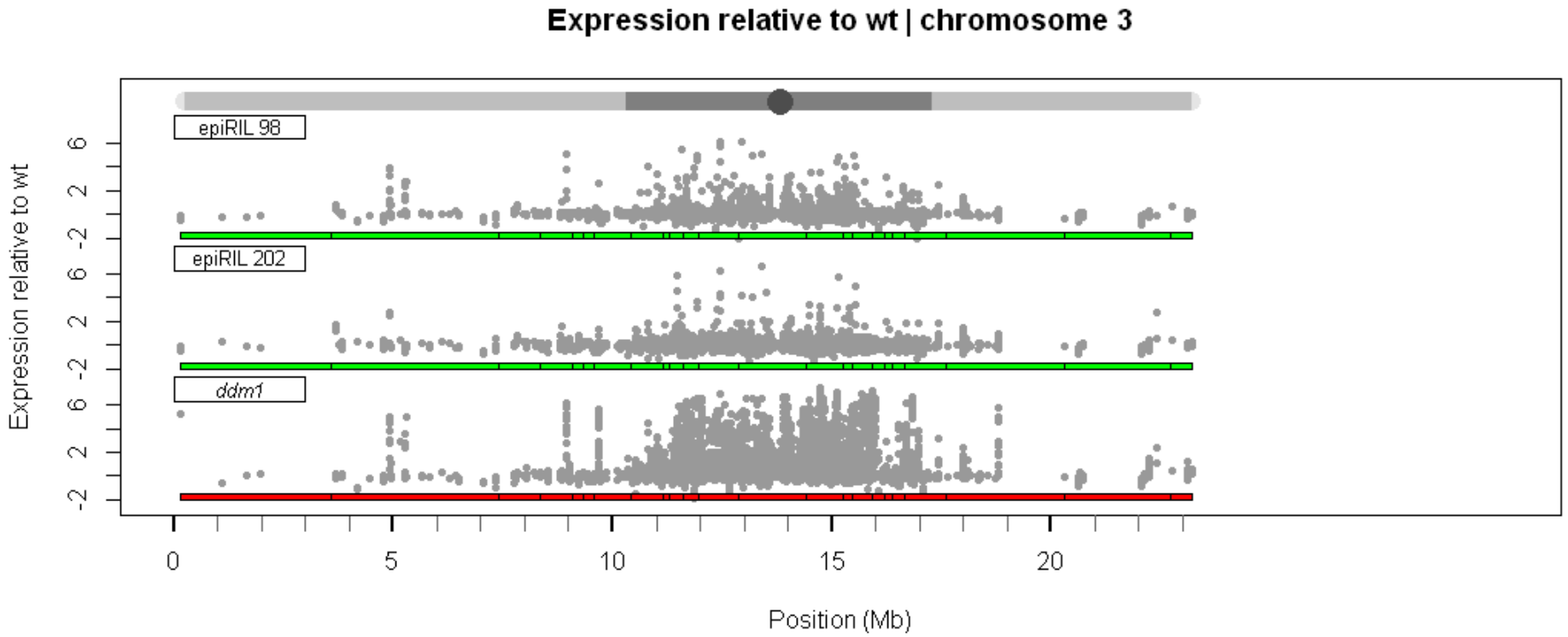
0
5
10
15
Position (Mb)

Figure S8-3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epiRIL 98
epiRIL 202
ddm1
Expression relative to wt
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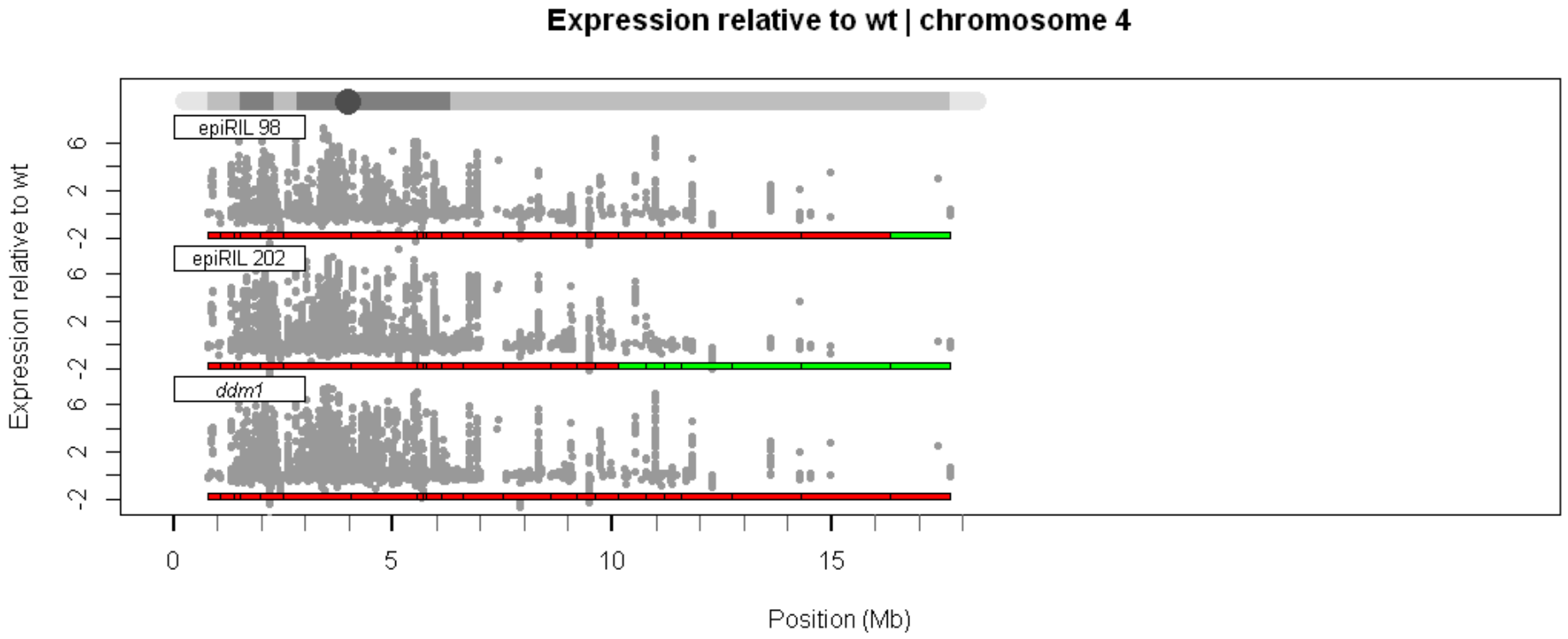
0
5
10
15
20
Position (Mb)

Figure S8-4


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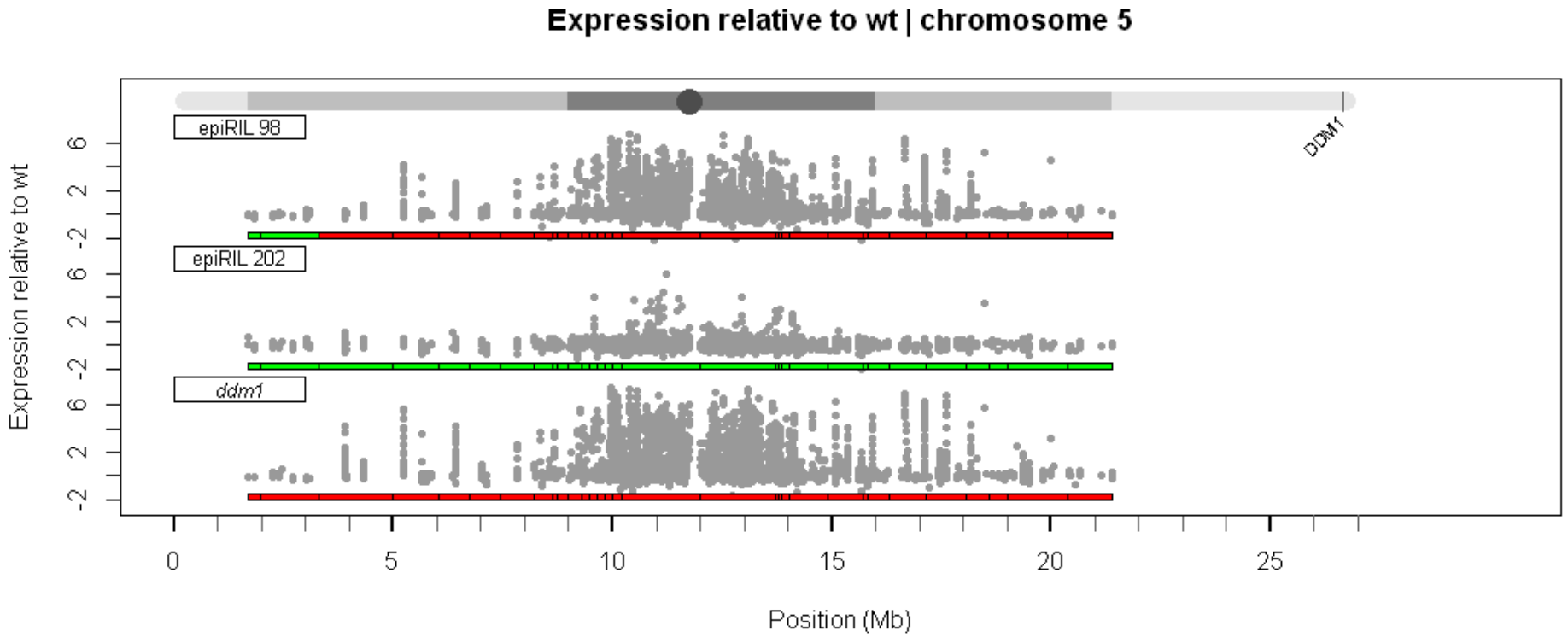
-2
6
2
-2
6
2
-2
0
5
10
15
Position (Mb)

Figure S8-5


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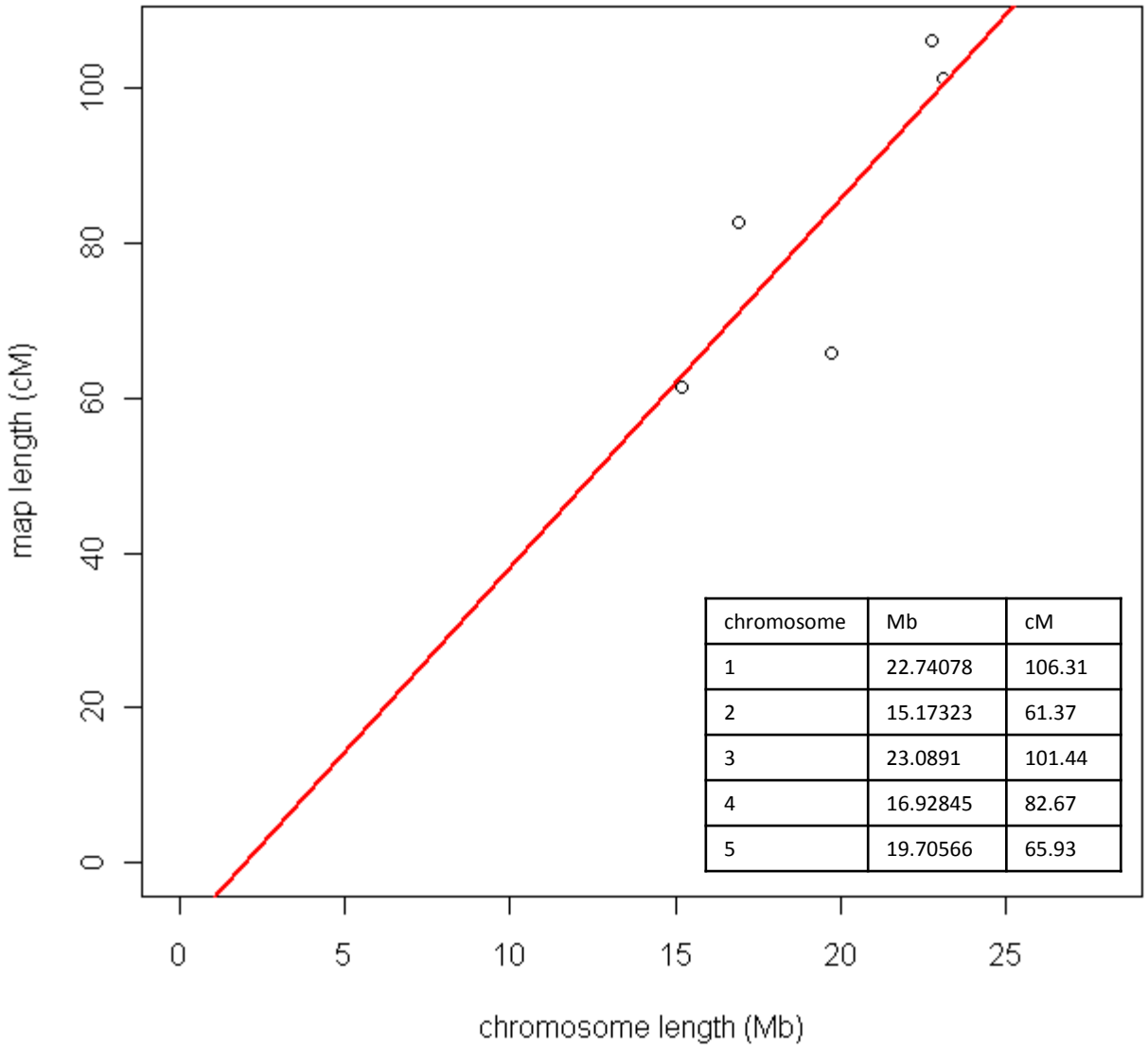
2
6
-2
2
6
-2
2
6
0
5
10
15
20
25
Position (Mb)

Figure S9



chromosome	Mb	cM
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Figure S10

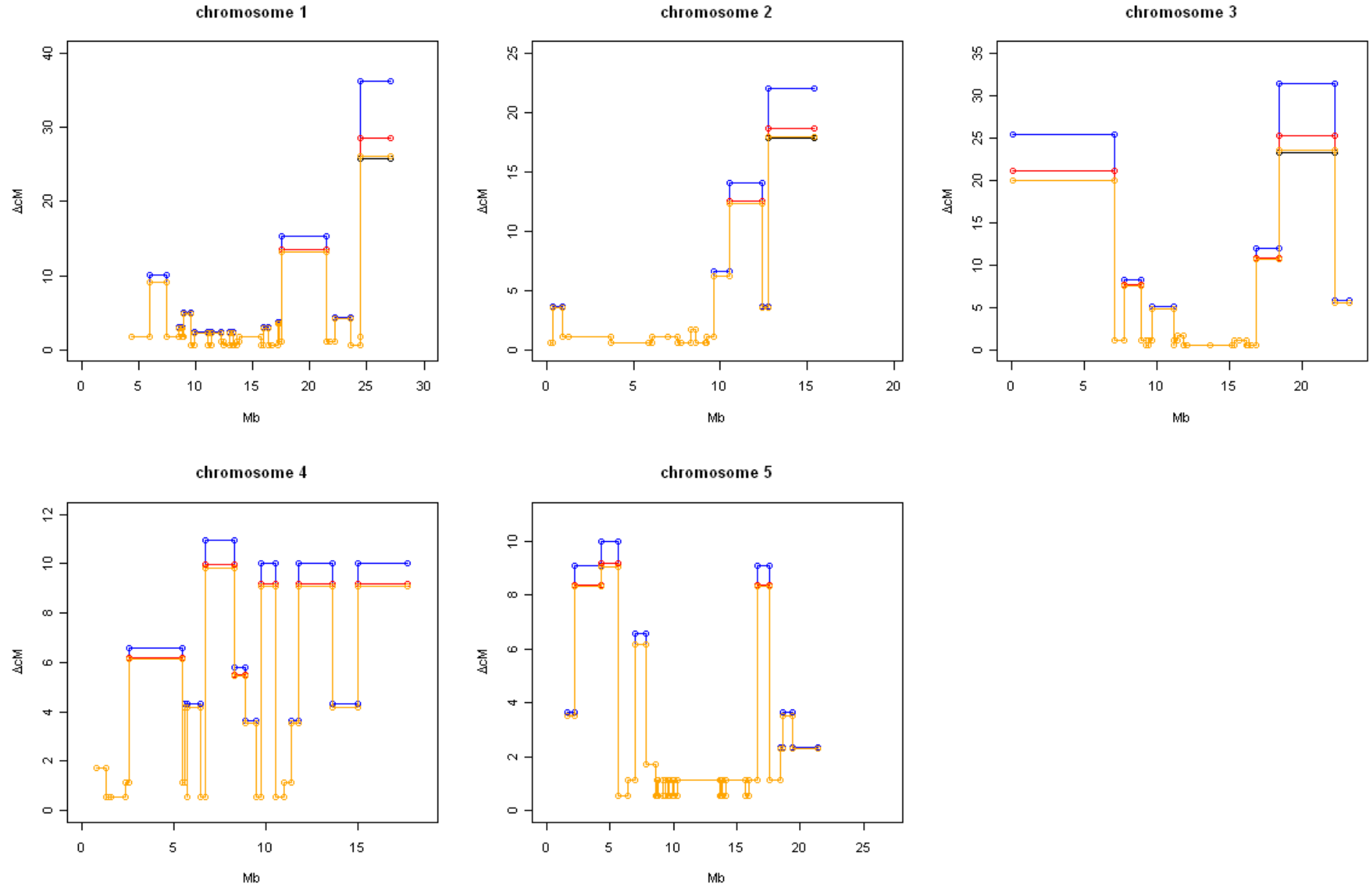
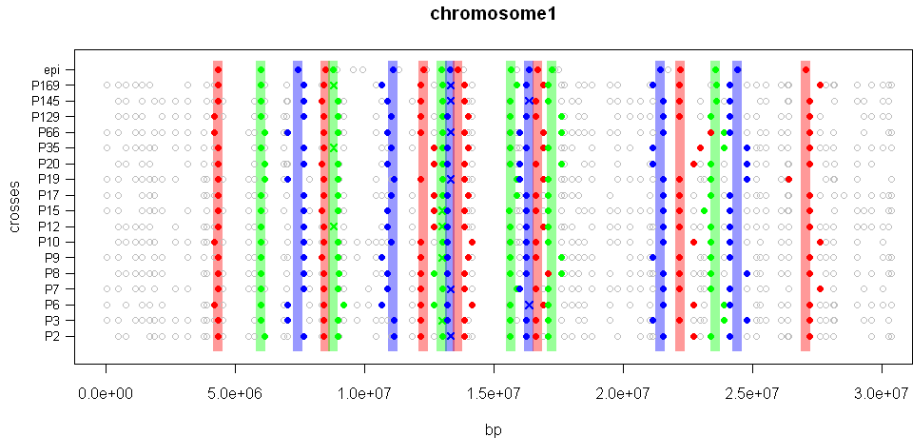
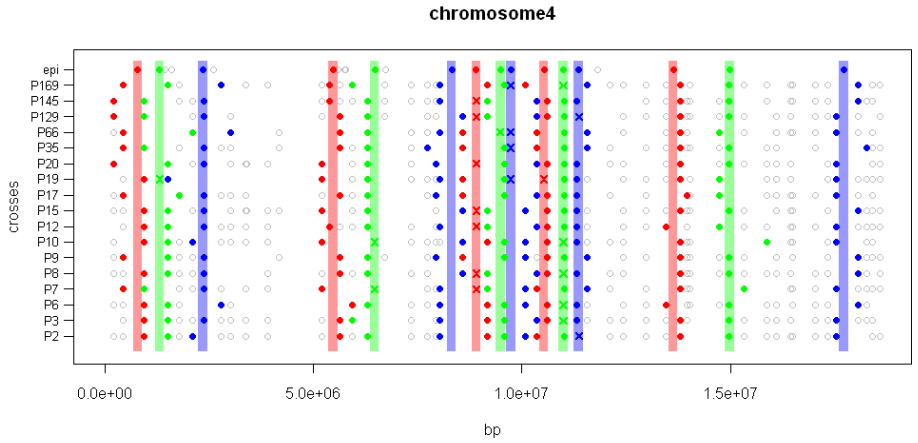
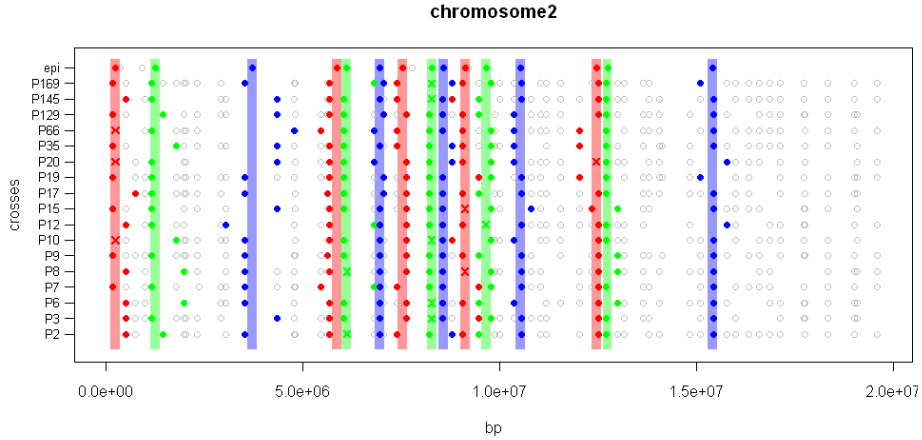
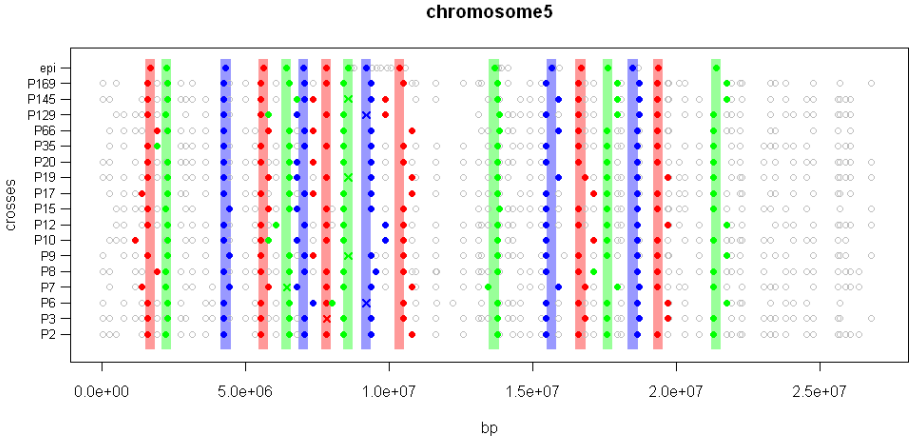

chromosome 1
chromosome 2
chromosome 3
chromosome 4
chromosome 5
ΔcM
Mb

Figure S11


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


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


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


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

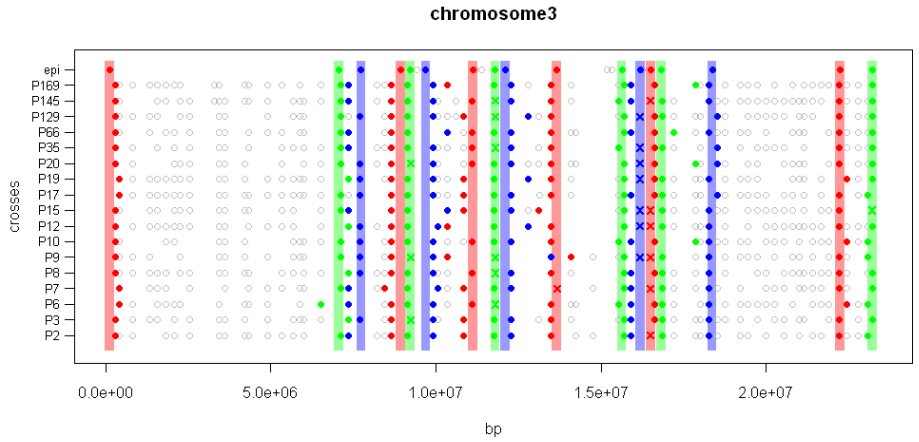

chromosome3
crosses
epi
P169
P145
P129
P66
P35
P20
P19
P17
P15
P12
P10
P9
P8
P7
P6
P3
P2
0.0e+00
5.0e+06
1.0e+07
1.5e+07
2.0e+07
bp

Figure S12

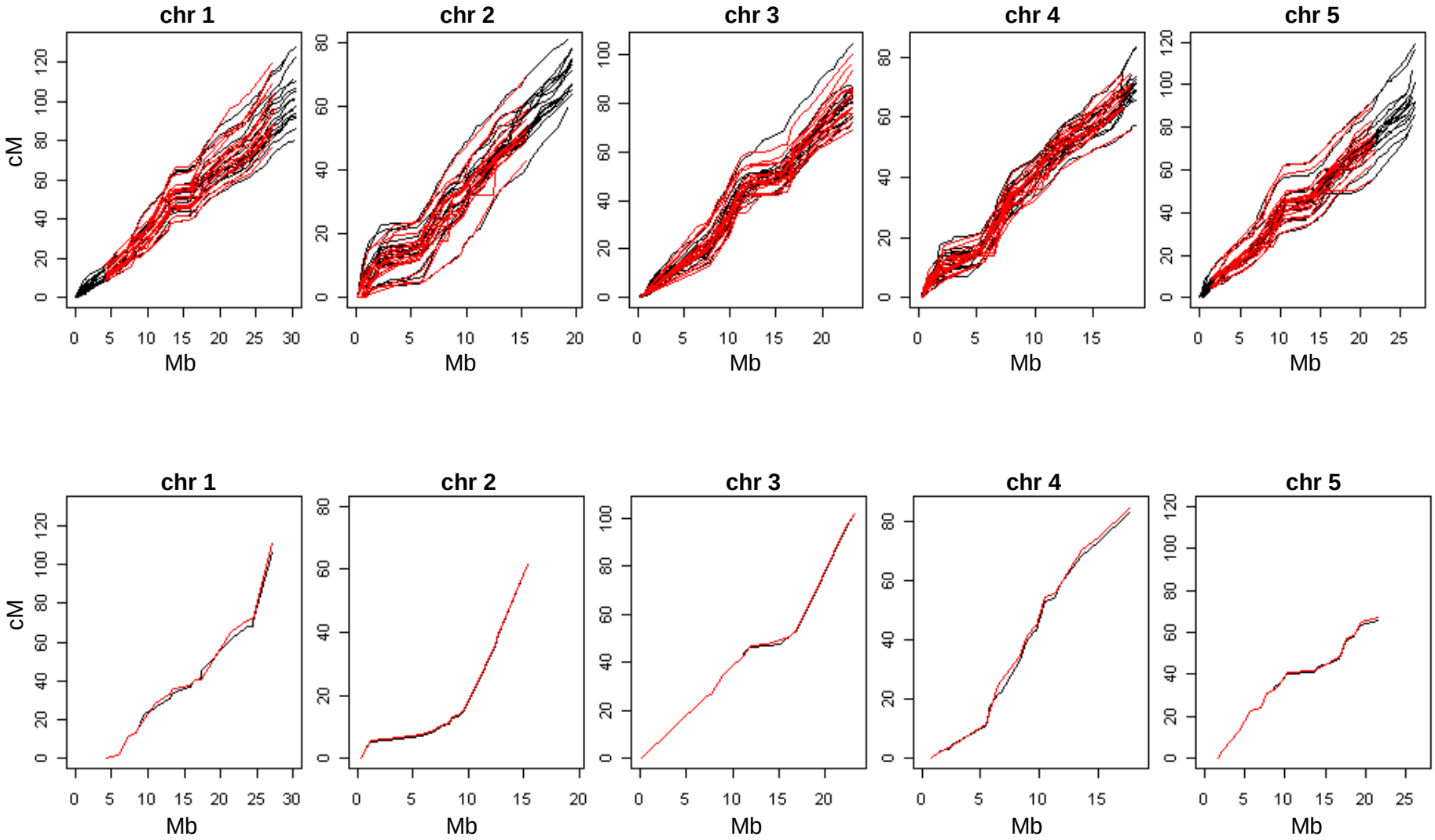


Figure S13

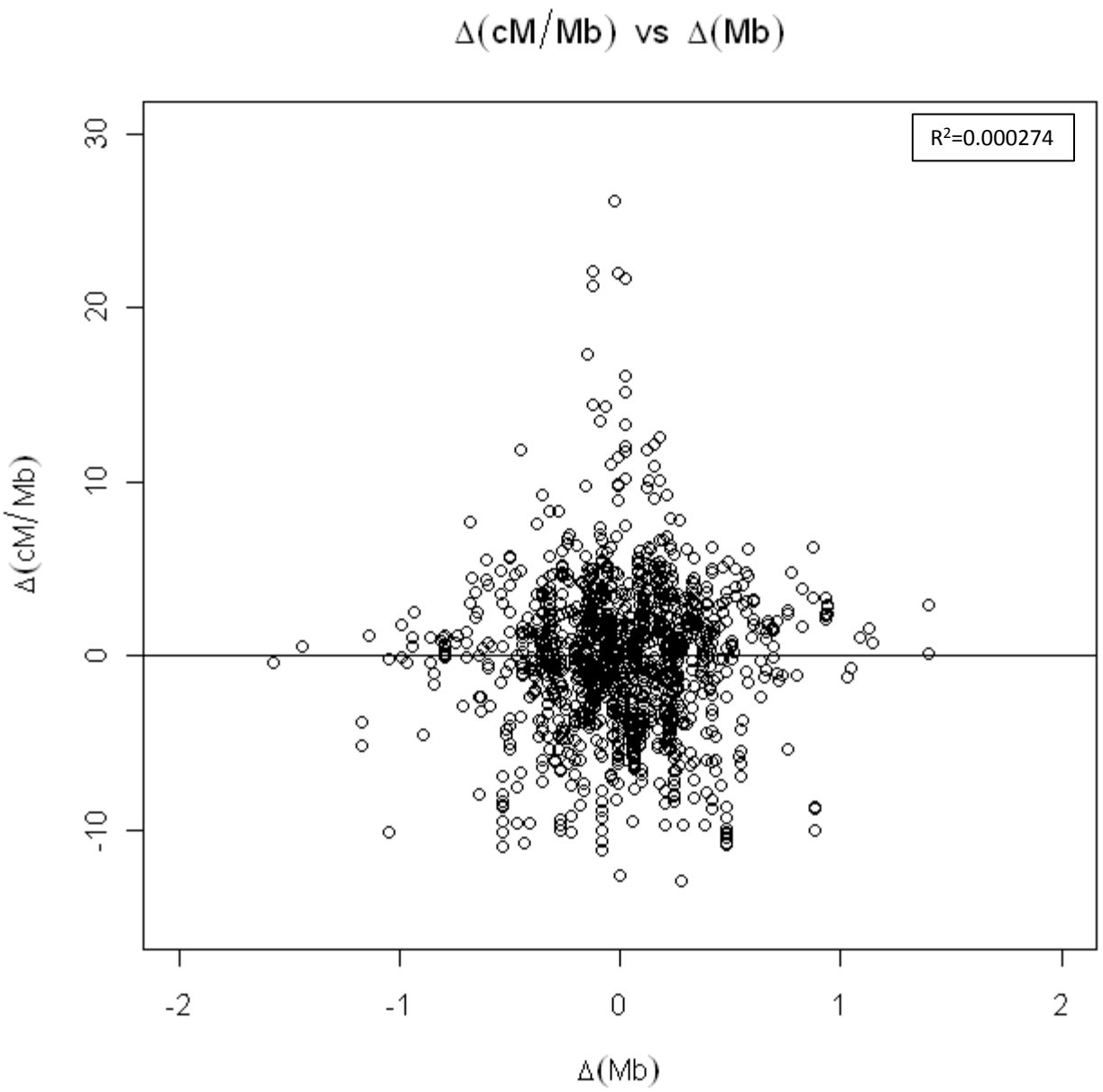


Figure S14-1

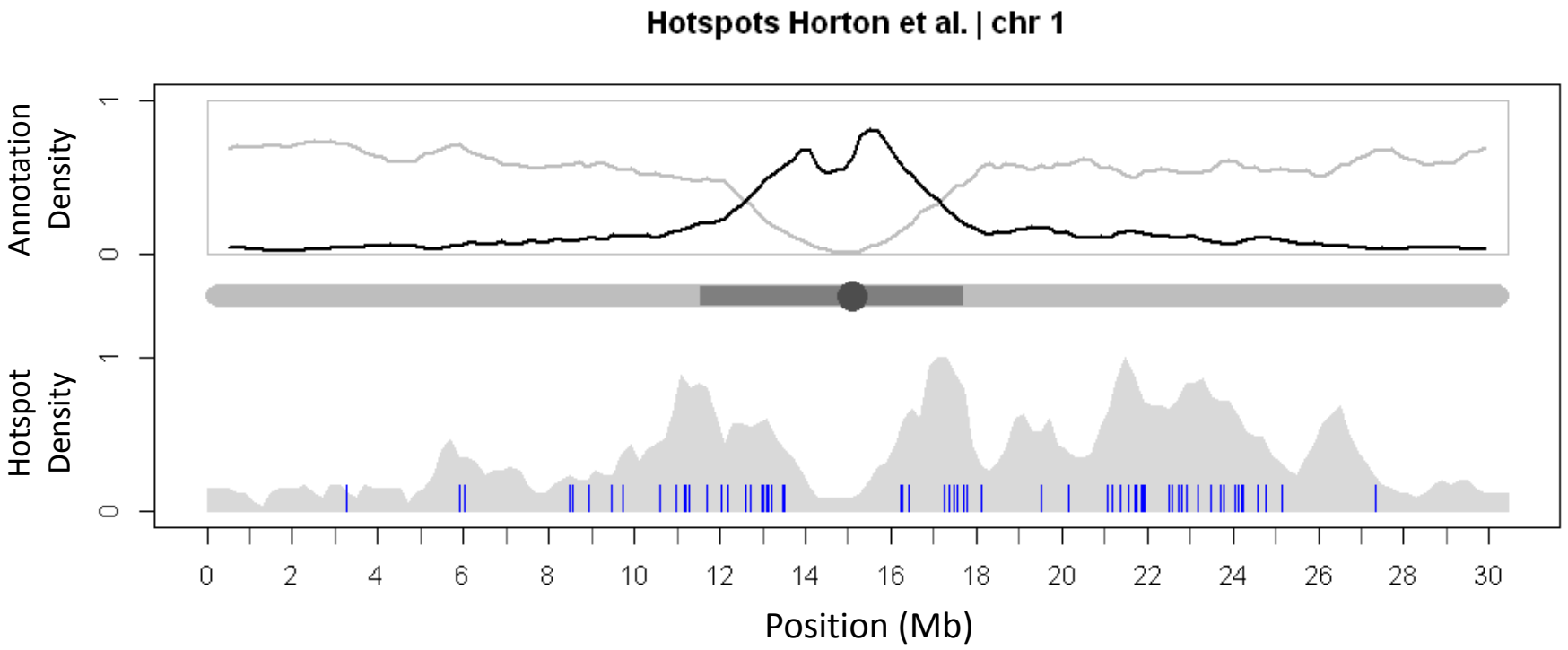

Hotspots Horton et al. | chr 1
Annotation Density
Hotspot Density
0
1
0
1
0
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
Position (Mb)

Figure S14-2

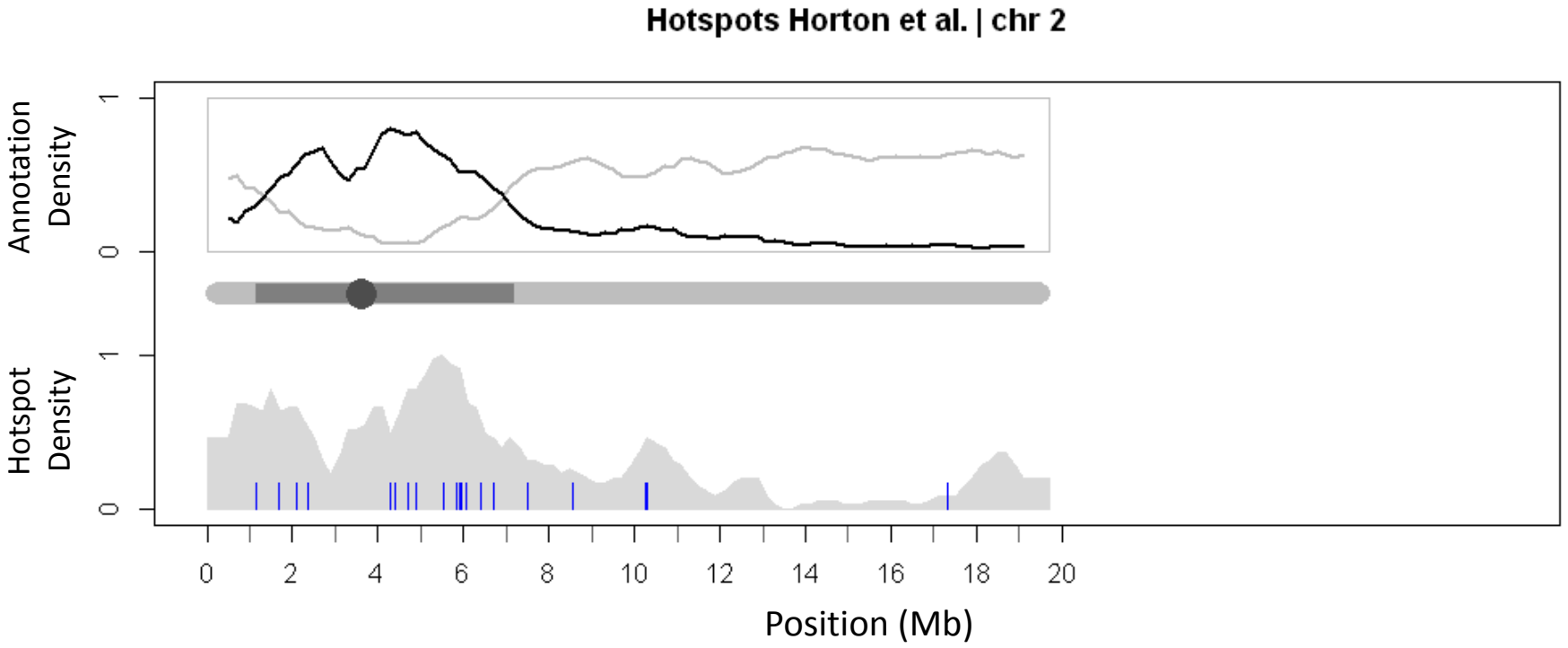

Hotspots Horton et al. | chr 2
Annotation Density
Hotspot Density
0
1
0
1
0
2
4
6
8
10
12
14
16
18
20
Position (Mb)

Figure S14-3

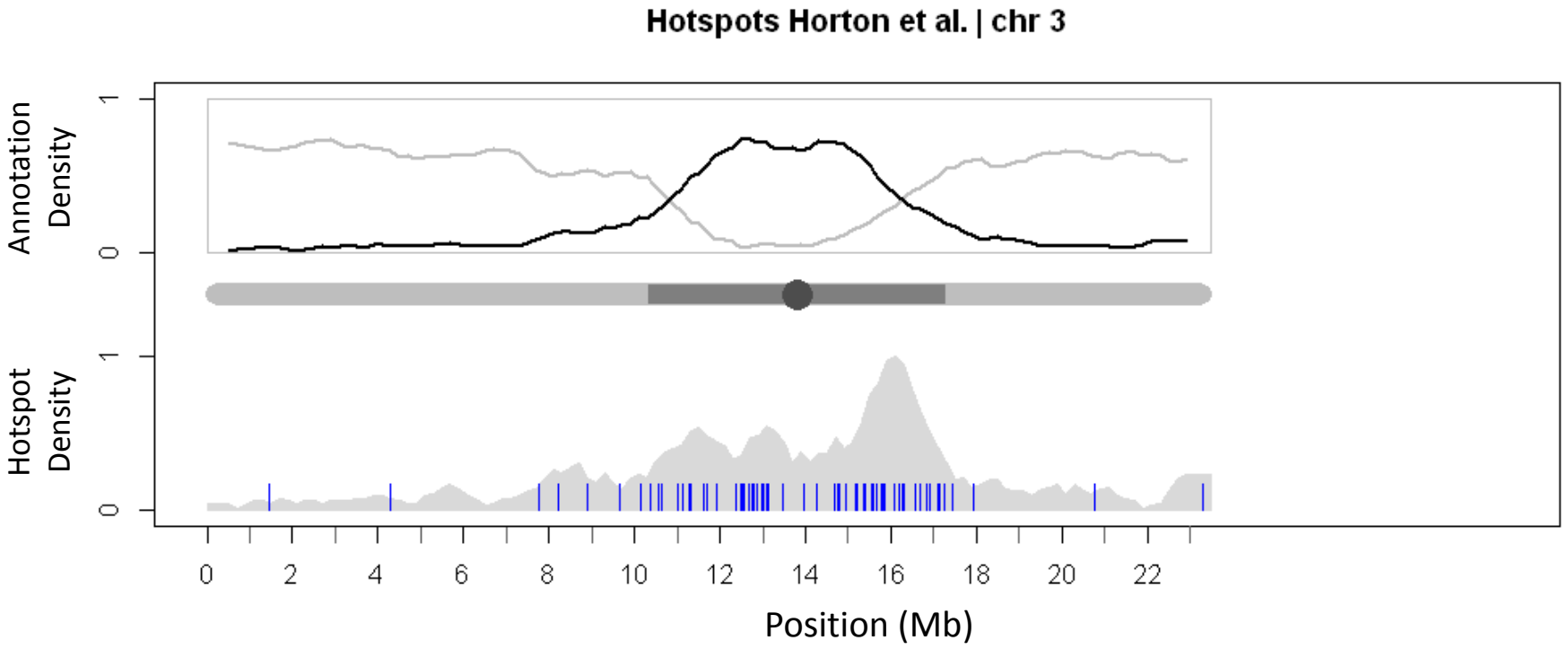

Hotspots Horton et al. | chr 3
Annotation Density
Hotspot Density
0
1
0
1
0
2
4
6
8
10
12
14
16
18
20
22
Position (Mb)

Figure S14-4

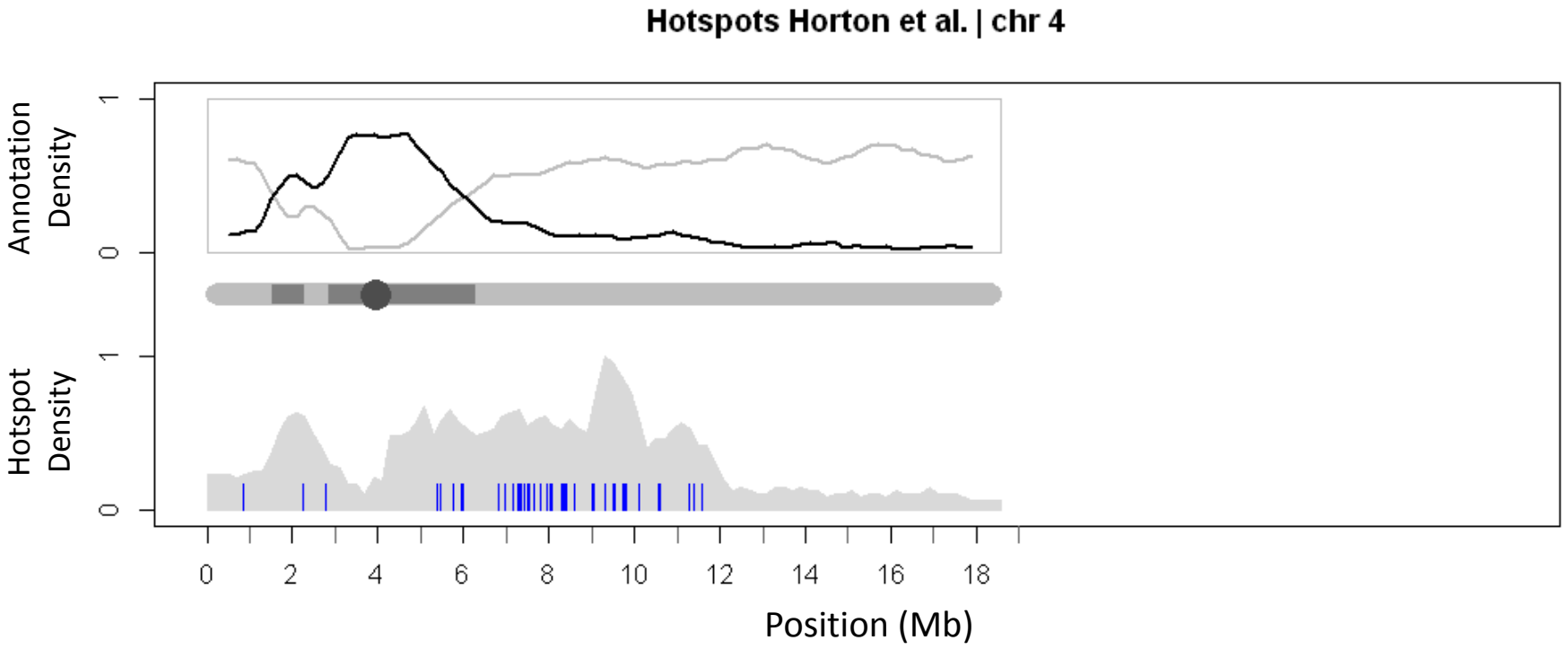

Hotspots Horton et al. | chr 4
Annotation Density
Hotspot Density
0
1
0
1
0
2
4
6
8
10
12
14
16
18
Position (Mb)

Figure S14-5

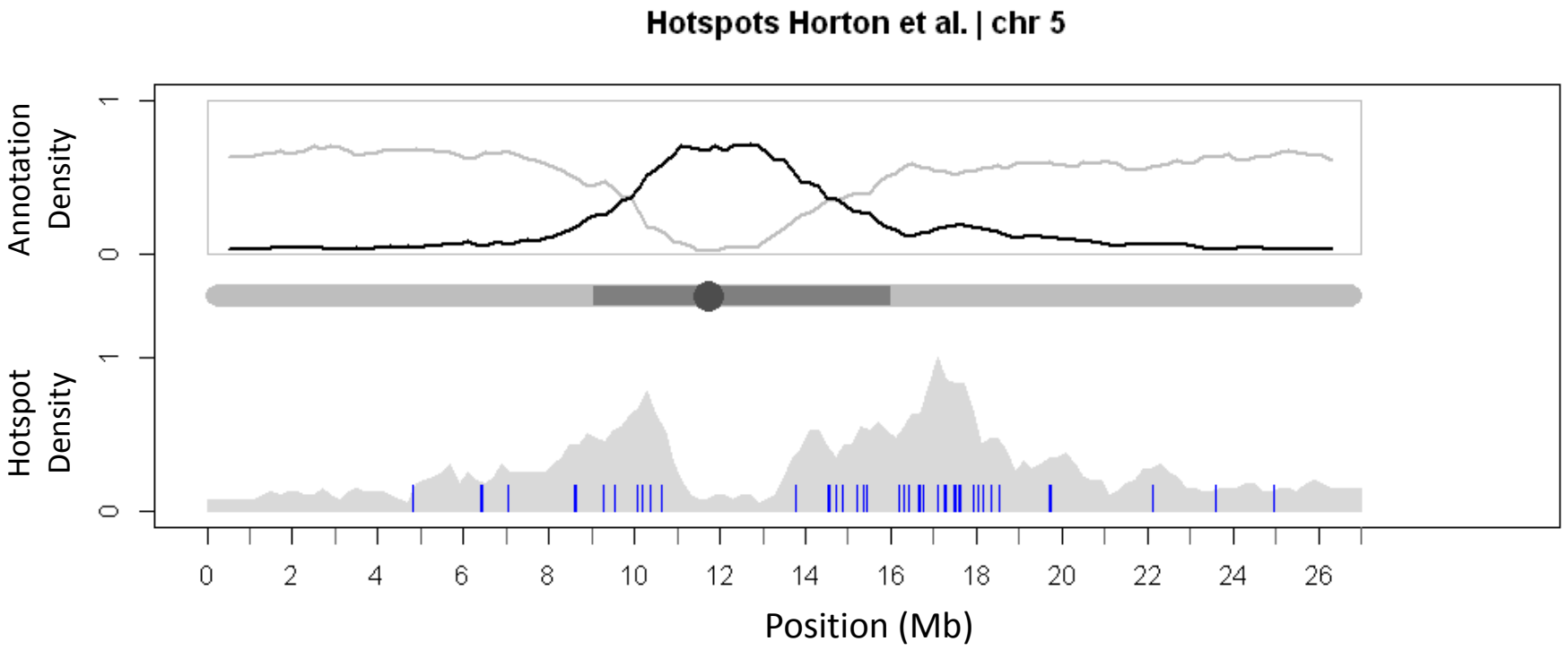

Hotspots Horton et al. | chr 5
Annotation Density
Hotspot Density
0
1
0
1
0
2
4
6
8
10
12
14
16
18
20
22
24
26
Position (Mb)

Figure S15

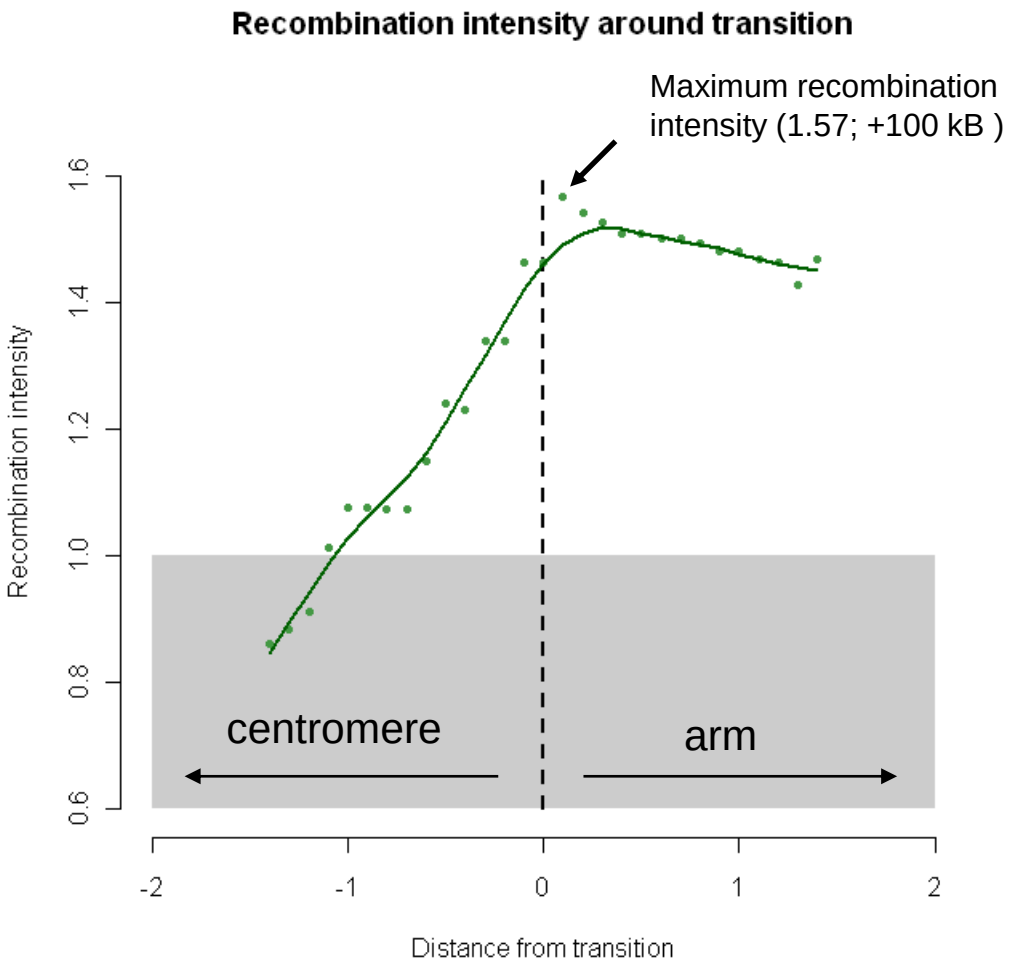
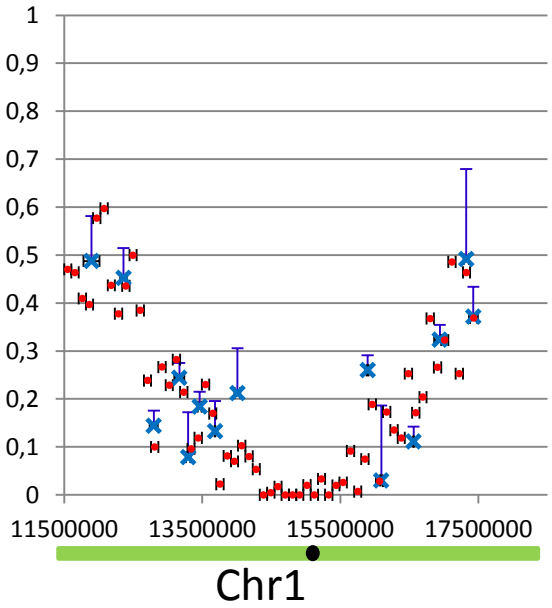
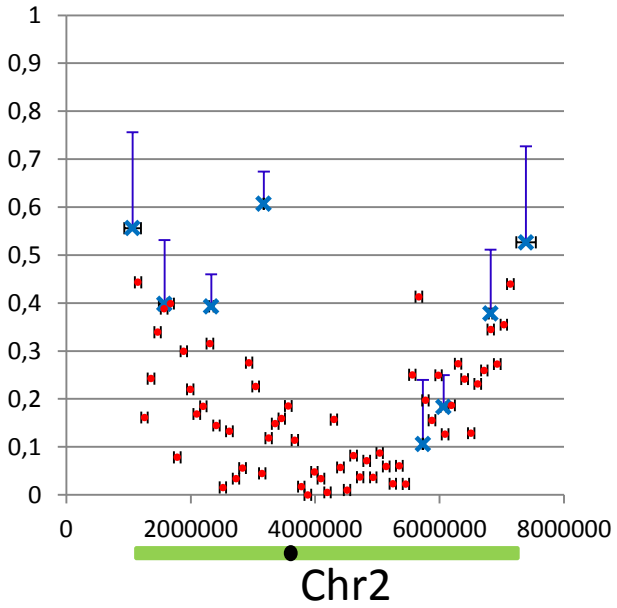
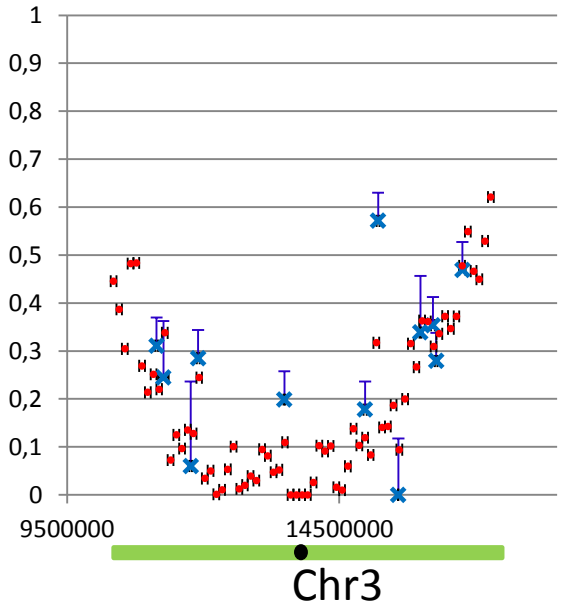
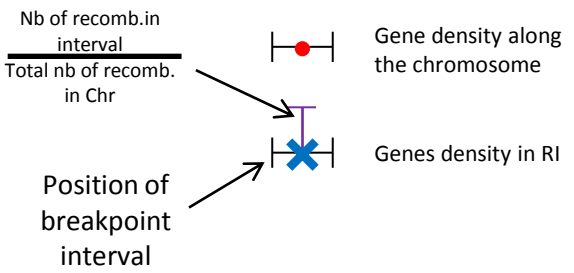

Recombination intensity around transition
Maximum recombination intensity (1.57; +100 kB)
Recombination intensity
0.6
0.8
1.0
1.2
1.4
1.6
centromere
arm
-2
-1
0
1
2
Distance from transition

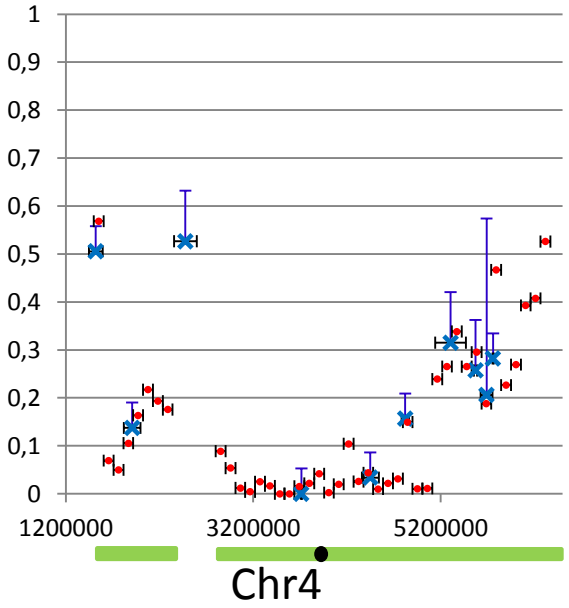
Figure S16


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


1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
0
2000000
4000000
6000000
8000000
Chr2


1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
9500000
14500000
Chr3


Nb of recomb.in interval
Total nb of recomb. in Chr
Gene density along the chromosome
Genes density in RI
Position of breakpoint interval


1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
1200000
3200000
5200000
Chr4

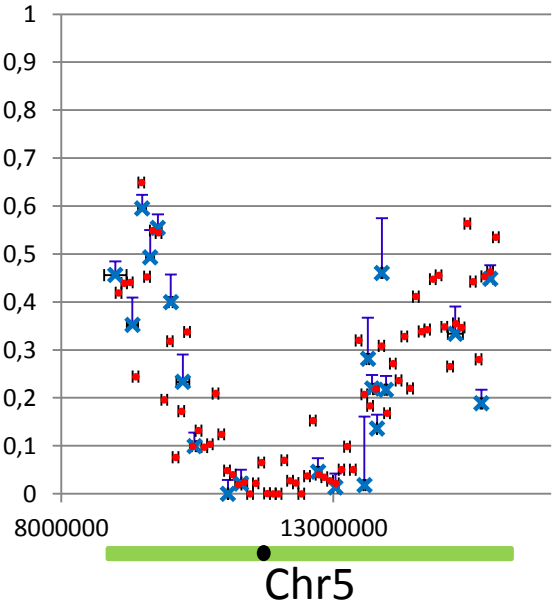

1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
8000000
13000000
Chr5

Figure S17

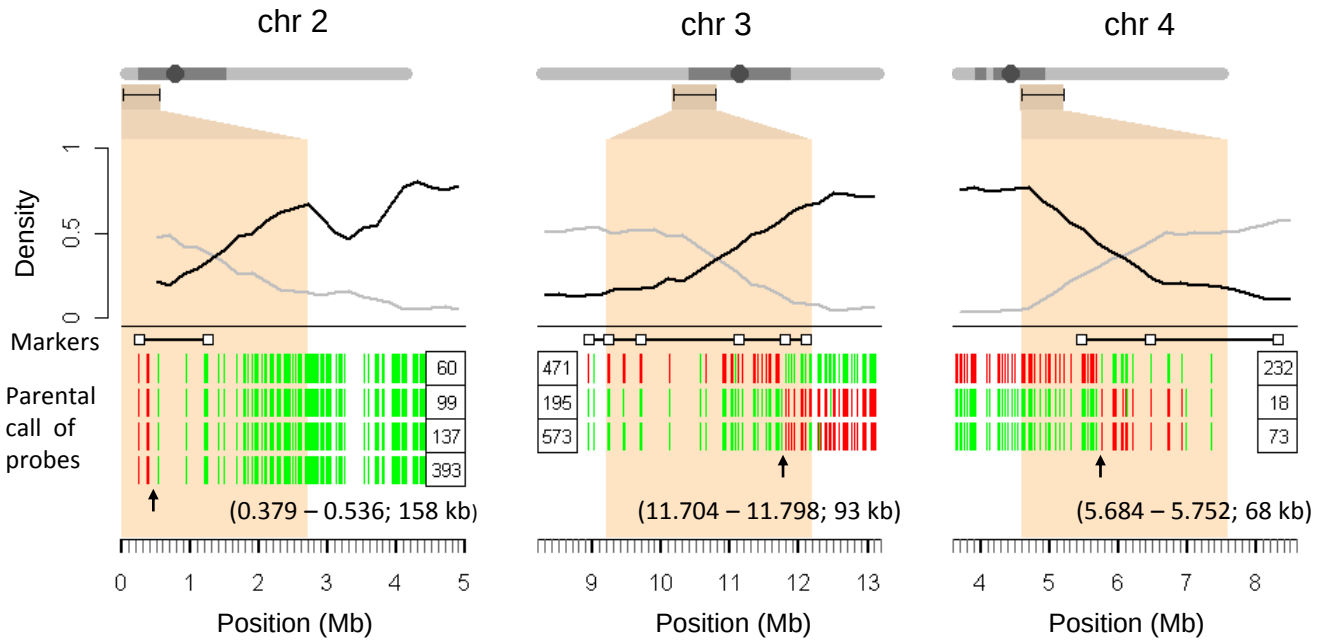

chr 2
chr 3
chr 4
Density
1
0.5
0
Markers
Parental call of probes
60
99
137
393
471
195
573
232
18
73
(0.379 – 0.536; 158 kb)
(11.704 – 11.798; 93 kb)
(5.684 – 5.752; 68 kb)
0 1 2 3 4 5
9 10 11 12 13
4 5 6 7 8
Position (Mb)
Position (Mb)
Position (Mb)

Figure S18

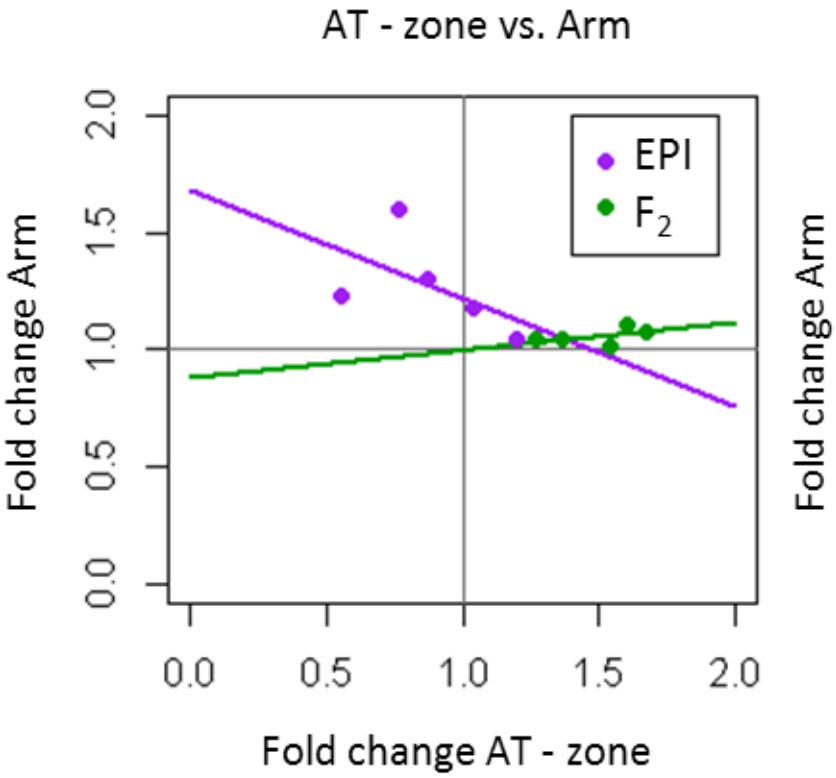

AT - zone vs. Arm
EPI
F_2
Fold change Arm
Fold change Arm
Fold change AT - zone
0.0
0.5
1.0
1.5
2.0

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
DMR-198	1	14189208	14189839
DMR-199	1	14190383	14191339
DMR-200	1	14197654	14198638
DMR-201	1	14220243	14222676
DMR-202	1	14302730	14306046
DMR-203	1	14326954	14327284
DMR-204	1	14335079	14335886
DMR-205	1	14347579	14349784
DMR-206	1	14353688	14355518
DMR-207	1	14362323	14362593
DMR-208	1	14372715	14374834
DMR-209	1	14393152	14394827
DMR-210	1	14399266	14401046
DMR-211	1	14407851	14408131
DMR-212	1	14418868	14420507
DMR-213	1	14449277	14449602
DMR-214	1	14460170	14462150
DMR-215	1	14464620	14465570
DMR-216	1	14472698	14473024
DMR-217	1	14513578	14514098
DMR-218	1	14541178	14545088
DMR-219	1	14819493	14820677
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DMR-221	1	14848035	14849200
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DMR-2601	5	21848807	21854609
DMR-2602	5	21951441	21951806
DMR-2603	5	22020306	22022116
DMR-2604	5	22022901	22024096
DMR-2605	5	22630468	22635399
DMR-2606	5	23152000	23157256
DMR-2607	5	24035420	24035780
DMR-2608	5	24036886	24039514
DMR-2609	5	24363110	24363575
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Table S3

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MM8	1	8816171	8816837
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
MM28	1	12665781	12666246
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MM30	1	12856990	12862085
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MM35	1	13021477	13023341
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MM37	1	13239811	13242134
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MM39	1	13329072	13340087
MM40	1	13340457	13340972
MM41	1	13391912	13397522
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MM43	1	13419144	13422650

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MM45	1	13433353	13434184
MM46	1	13491291	13491906
MM47	1	13499704	13500341
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MM67	1	14041565	14044311
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MM86	1	15628145	15632000
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MM95	1	16077497	16079431
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MM97	1	16174849	16176279
MM98	1	16179459	16183728
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MM123	1	17258838	17264340
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MM148	1	21459776	21460452
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MM547	3	23215509	23218355
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MM549	4	633119	636937
MM550	4	788271	788751
MM551	4	1312610	1315610
MM552	4	1447714	1448102
MM553	4	1592613	1594726
MM554	4	1647079	1650360
MM555	4	1789984	1791244
MM556	4	1792739	1794717
MM557	4	1820123	1823150
MM558	4	1836482	1837117
MM559	4	1846186	1847676
MM560	4	1848556	1850185

MM561	4	1856114	1856584
MM562	4	1857244	1859444
MM563	4	1922637	1924607
MM564	4	1961217	1961702
MM565	4	1968459	1973961
MM566	4	1976874	1979234
MM567	4	1987439	1993922
MM568	4	1996722	1997328
MM569	4	2046033	2048209
MM570	4	2064710	2069637
MM571	4	2107230	2110519
MM572	4	2136479	2143881
MM573	4	2171105	2175733
MM574	4	2176043	2177404
MM575	4	2178034	2179053
MM576	4	2188113	2203742
MM577	4	2205950	2208691
MM578	4	2212028	2214798
MM579	4	2250134	2252125
MM580	4	2254091	2256545
MM581	4	2263009	2264516
MM582	4	2279834	2288764
MM583	4	2302576	2308022
MM584	4	2309384	2310726
MM585	4	2355263	2355598
MM586	4	2356046	2357721
MM587	4	2596832	2603097
MM588	4	2899556	2904543
MM589	4	2982274	2983224
MM590	4	2983754	2985514
MM591	4	3129448	3130223
MM592	4	3138800	3145420
MM593	4	3292909	3299374
MM594	4	3301512	3308118
MM595	4	3330408	3331687
MM596	4	3360614	3361429
MM597	4	3364190	3366030
MM598	4	3367340	3369655
MM599	4	3370683	3371328
MM600	4	3405807	3408122
MM601	4	3417186	3418862
MM602	4	3422432	3423107
MM603	4	3423627	3427223
MM604	4	3448202	3451852
MM605	4	3476097	3480542
MM606	4	3503945	3505655
MM607	4	3522800	3524570

MM608	4	3525396	3527433
MM609	4	3533867	3536281
MM610	4	3640781	3647018
MM611	4	3647858	3649143
MM612	4	3652663	3653605
MM613	4	3683359	3683960
MM614	4	3685475	3689756
MM615	4	3707081	3715518
MM616	4	3719963	3722449
MM617	4	3726918	3727888
MM618	4	3754128	3756927
MM619	4	3795890	3797500
MM620	4	3880354	3883009
MM621	4	3883829	3885754
MM622	4	3913026	3913536
MM623	4	3920752	3921447
MM624	4	3921727	3922552
MM625	4	4250264	4252431
MM626	4	4267401	4268226
MM627	4	4319094	4320859
MM628	4	4345663	4346146
MM629	4	4358332	4359964
MM630	4	4394491	4400778
MM631	4	4539542	4540007
MM632	4	4590672	4594634
MM633	4	4606661	4608185
MM634	4	4611100	4612759
MM635	4	4613461	4614391
MM636	4	4623691	4627766
MM637	4	4628919	4633706
MM638	4	4704695	4705510
MM639	4	4711416	4716693
MM640	4	4718724	4720694
MM641	4	4730724	4732878
MM642	4	4733238	4735513
MM643	4	4742818	4746454
MM644	4	4782418	4788161
MM645	4	4861117	4862429
MM646	4	4864243	4866216
MM647	4	4951544	4954674
MM648	4	5004468	5007767
MM649	4	5077279	5078214
MM650	4	5124451	5125409
MM651	4	5141956	5142391
MM652	4	5207957	5210103
MM653	4	5303817	5308932
MM654	4	5468765	5470776

MM655	4	5479496	5480971
MM656	4	5481345	5483015
MM657	4	5484117	5486134
MM658	4	5494070	5494833
MM659	4	5507085	5512217
MM660	4	5555107	5556550
MM661	4	5588246	5589431
MM662	4	5590701	5596682
MM663	4	5623225	5625700
MM664	4	5627718	5630511
MM665	4	5751470	5752399
MM666	4	5766434	5769097
MM667	4	5862018	5864623
MM668	4	5879330	5881930
MM669	4	5905577	5908182
MM670	4	5913994	5916774
MM671	4	5937095	5938217
MM672	4	5939694	5943984
MM673	4	5965792	5971022
MM674	4	6035420	6036060
MM675	4	6059158	6061610
MM676	4	6112787	6114123
MM677	4	6125997	6130122
MM678	4	6467386	6472846
MM679	4	6723446	6729234
MM680	4	6916150	6919455
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MM683	4	7890527	7891464
MM684	4	8109456	8110246
MM685	4	8148075	8150547
MM686	4	8313708	8319324
MM687	4	8327940	8329535
MM688	4	8620148	8623068
MM689	4	8906581	8907231
MM690	4	9068914	9078668
MM691	4	9483934	9485359
MM692	4	9486574	9490039
MM693	4	9734038	9737673
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MM695	4	10992797	10997912
MM696	4	11039328	11040489
MM697	4	11045990	11046270
MM698	4	11363449	11369169
MM699	4	11820310	11824620
MM700	4	11825565	11826547
MM701	4	13624419	13631859

MM702	4	14531237	14532254
MM703	4	14987455	14988333
MM704	4	17712926	17716726
MM705	5	250204	250970
MM706	5	1686487	1686997
MM707	5	2262159	2262544
MM708	5	2374188	2375393
MM709	5	3005869	3007624
MM710	5	3249529	3249844
MM711	5	3944883	3945355
MM712	5	4320753	4323348
MM713	5	5635294	5635620
MM714	5	6407124	6407784
MM715	5	6433688	6438813
MM716	5	7027577	7028347
MM717	5	7118301	7118816
MM718	5	7823819	7824639
MM719	5	8574747	8577717
MM720	5	8622629	8624390
MM721	5	8666296	8667301
MM722	5	8788121	8788791
MM723	5	9203261	9203876
MM724	5	9206569	9207339
MM725	5	9412161	9414631
MM726	5	9561317	9563131
MM727	5	9707999	9708274
MM728	5	9712277	9712777
MM729	5	9840810	9843947
MM730	5	9925635	9926240
MM731	5	9929045	9929765
MM732	5	9949501	9953791
MM733	5	9980031	9982666
MM734	5	10049721	10056270
MM735	5	10059908	10060603
MM736	5	10061223	10063868
MM737	5	10100538	10102484
MM738	5	10104439	10106449
MM739	5	10116048	10116333
MM740	5	10167992	10173112
MM741	5	10182490	10183203
MM742	5	10216019	10219279
MM743	5	10235840	10236459
MM744	5	10351503	10356268
MM745	5	10359252	10361017
MM746	5	10379549	10380204
MM747	5	10381174	10383134
MM748	5	10398185	10400340

MM749	5	10406614	10416616
MM750	5	10446350	10448004
MM751	5	10470245	10473768
MM752	5	10476219	10477066
MM753	5	10497167	10504586
MM754	5	10510858	10514670
MM755	5	10547800	10554452
MM756	5	10574704	10578175
MM757	5	10774381	10775334
MM758	5	10793374	10795838
MM759	5	10802058	10802926
MM760	5	10805387	10806029
MM761	5	10808554	10813619
MM762	5	10838571	10839853
MM763	5	10848777	10851102
MM764	5	10884071	10887425
MM765	5	10888060	10888390
MM766	5	10889685	10892155
MM767	5	10894129	10895614
MM768	5	11038835	11040815
MM769	5	11043845	11045147
MM770	5	11046447	11050769
MM771	5	11055838	11056338
MM772	5	11068088	11068878
MM773	5	11069378	11070905
MM774	5	11198254	11202694
MM775	5	11408293	11412746
MM776	5	11425654	11428787
MM777	5	11452669	11453159
MM778	5	11467885	11469206
MM779	5	11521513	11522958
MM780	5	11523473	11525597
MM781	5	11527937	11528397
MM782	5	11582073	11583358
MM783	5	11592613	11593588
MM784	5	11609462	11612587
MM785	5	11623639	11625794
MM786	5	11647518	11652328
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
MM794	5	12239264	12240049
MM795	5	12267973	12268453

MM796	5	12372248	12372748
MM797	5	12374678	12378188
MM798	5	12455244	12455524
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
MM811	5	13078281	13079386
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
MM819	5	13545206	13548491
MM820	5	13549016	13549637
MM821	5	13592209	13593709
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
MM829	5	13814680	13817763
MM830	5	13838944	13840924
MM831	5	13878051	13878481
MM832	5	13901149	13908033
MM833	5	13929365	13930310
MM834	5	13946515	13949105
MM835	5	13985794	13986619
MM836	5	14100634	14107050
MM837	5	14130621	14135451
MM838	5	14297458	14297785
MM839	5	14564932	14566037
MM840	5	14574666	14575466
MM841	5	14592988	14595078
MM842	5	15092886	15099318

MM843	5	15101170	15102675
MM844	5	15376021	15377701
MM845	5	15663492	15668447
MM846	5	15670446	15671106
MM847	5	15687245	15693500
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

marker	chr	start_bp	stop_bp	cM
MM1	1	4330606	4332076	0
MM2	1	6010663	6013983	1,729195471
MM4	1	7430002	7432267	11,73119575
MM5	1	8490901	8491751	13,46041678
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
MM551	4	1312610	1315610	1,729214934
MM552	4	1447714	1448102	2,286273001
MM553	4	1592613	1594726	2,843331184
MM586	4	2356046	2357721	3,40038931
MM587	4	2596832	2603097	4,533510704
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

MM698	4	11363449	11369169	54,67591218
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
MM719	5	8574747	8577717	32,7266097
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
MM825	5	13753476	13758196	41,73456799
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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19	73
20	92
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22	94
23	95
24	98
25	99

NUMBER	ID
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28	112
29	114
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32	137
33	144
34	147
35	148
36	150
37	159
38	164
39	166
40	169
41	170
42	172
43	183
44	193
45	195
46	202
47	208
48	215
49	216
50	218

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64	277
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66	305
67	315
68	323
69	326
70	333
71	340
72	344
73	350
74	356
75	361

NUMBER	ID
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77	363
78	366
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86	408
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94	454
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97	467
98	471
99	473
100	477

NUMBER	ID
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103	492
104	493
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118	561
119	567
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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
2-6044749	2-6809099	2-6117975	2-6044749	2-6044749	2-6809099
2-6970449	2-6970449	2-6970449	2-6970449	2-6970449	2-6970449
2-7633698	2-7400522	2-7633698	2-7633698	2-7633698	2-7633698
2-8279888	2-8225326	2-8225326	2-8225326	2-8279888	2-8225326
2-8561080	2-8561080	2-8561080	2-8561080	2-8561080	2-8561080
2-9057864	2-9461465	2-9129979	2-9057864	2-8796903	2-9057864
2-9461465	2-9792570	2-9792570	2-9461465	2-9792570	2-9659816
2-10365194	2-10556376	2-10556376	2-10556376	2-10365194	2-10556376
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1-13207971	1-13334580	1-13334580
1-14001934	1-13859051	1-13859051
1-15630635	1-15630635	1-15897174
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1-16645134	1-16645134	1-16913975
1-17605952	1-17102334	1-17102334
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3-16629399	3-16509183	3-16629399
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3-18532958	3-18258898	3-18258898
3-22221736	3-22221736	3-22221736
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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