

Construction of reference chromosome-scale pseudomolecules for potato: Integrating the potato genome with genetic and physical maps

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Footnotes:

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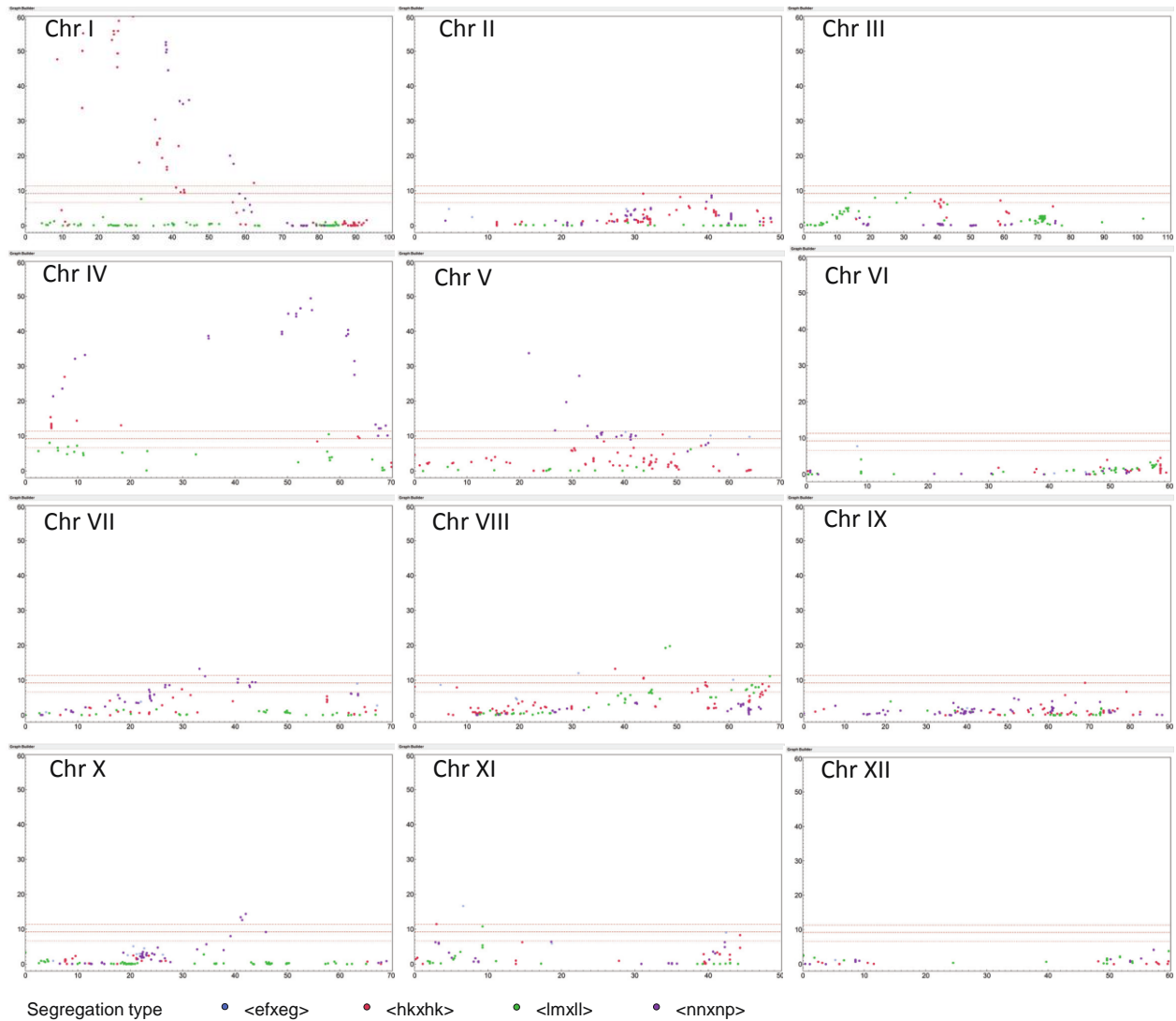
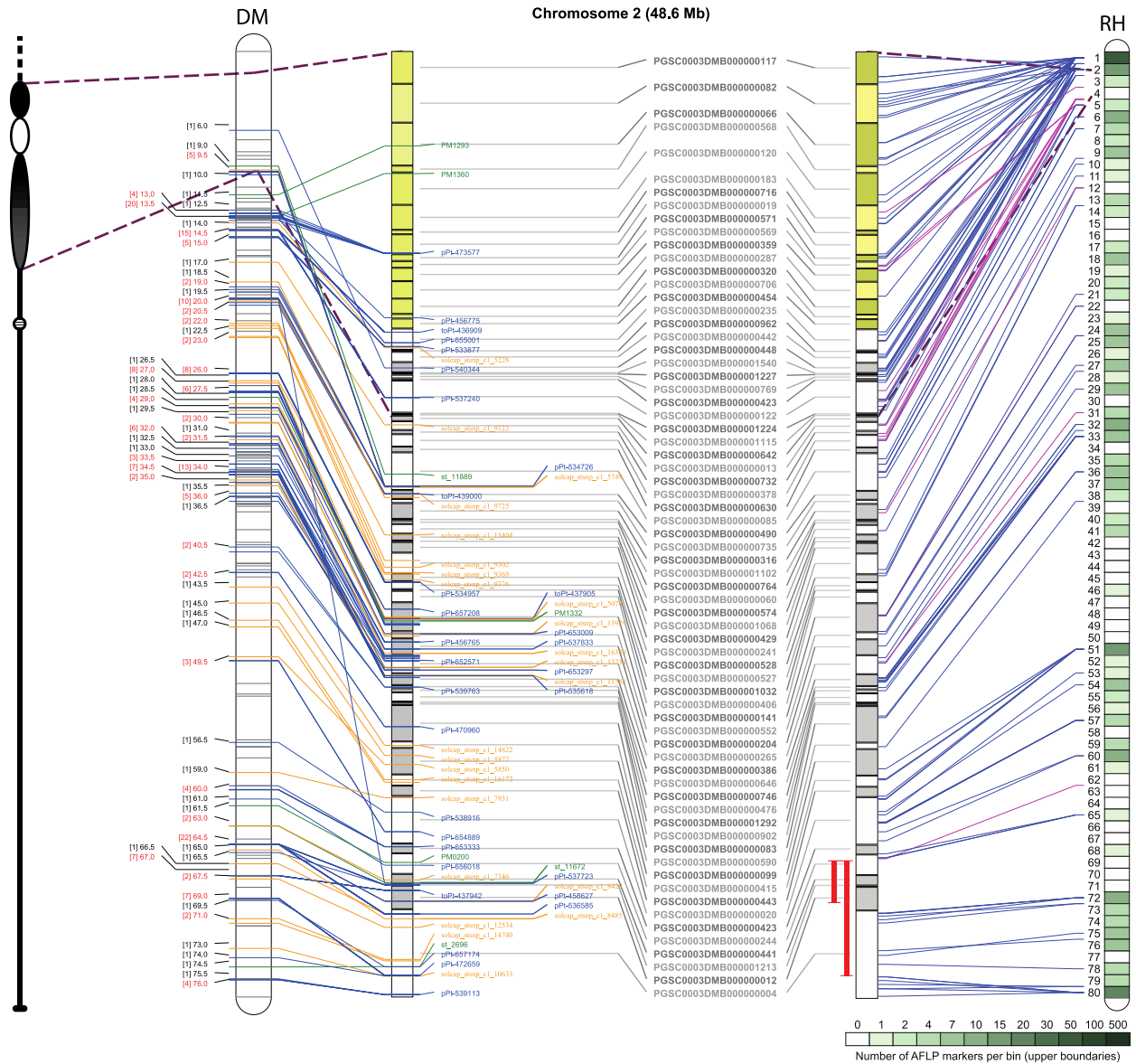
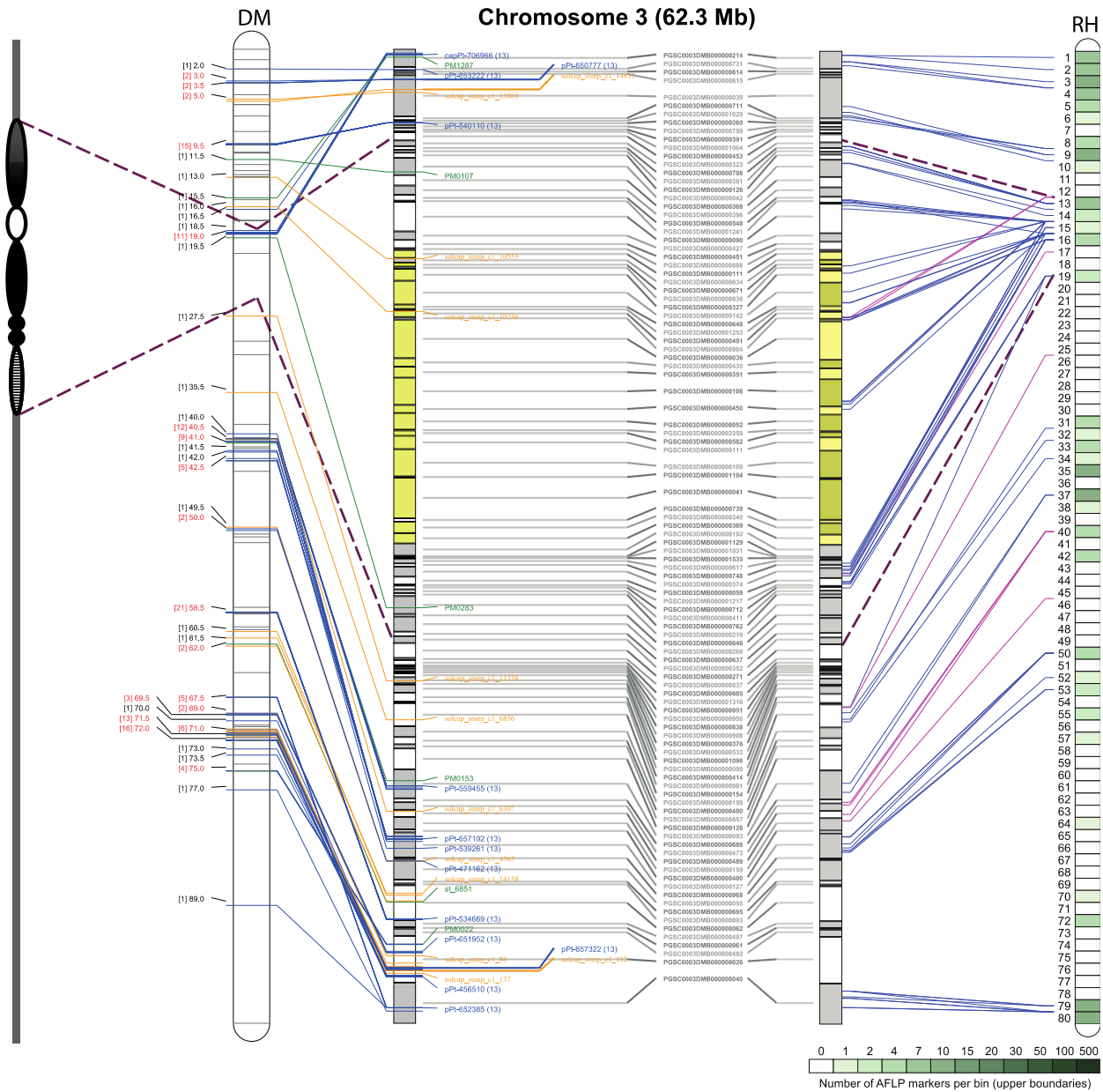
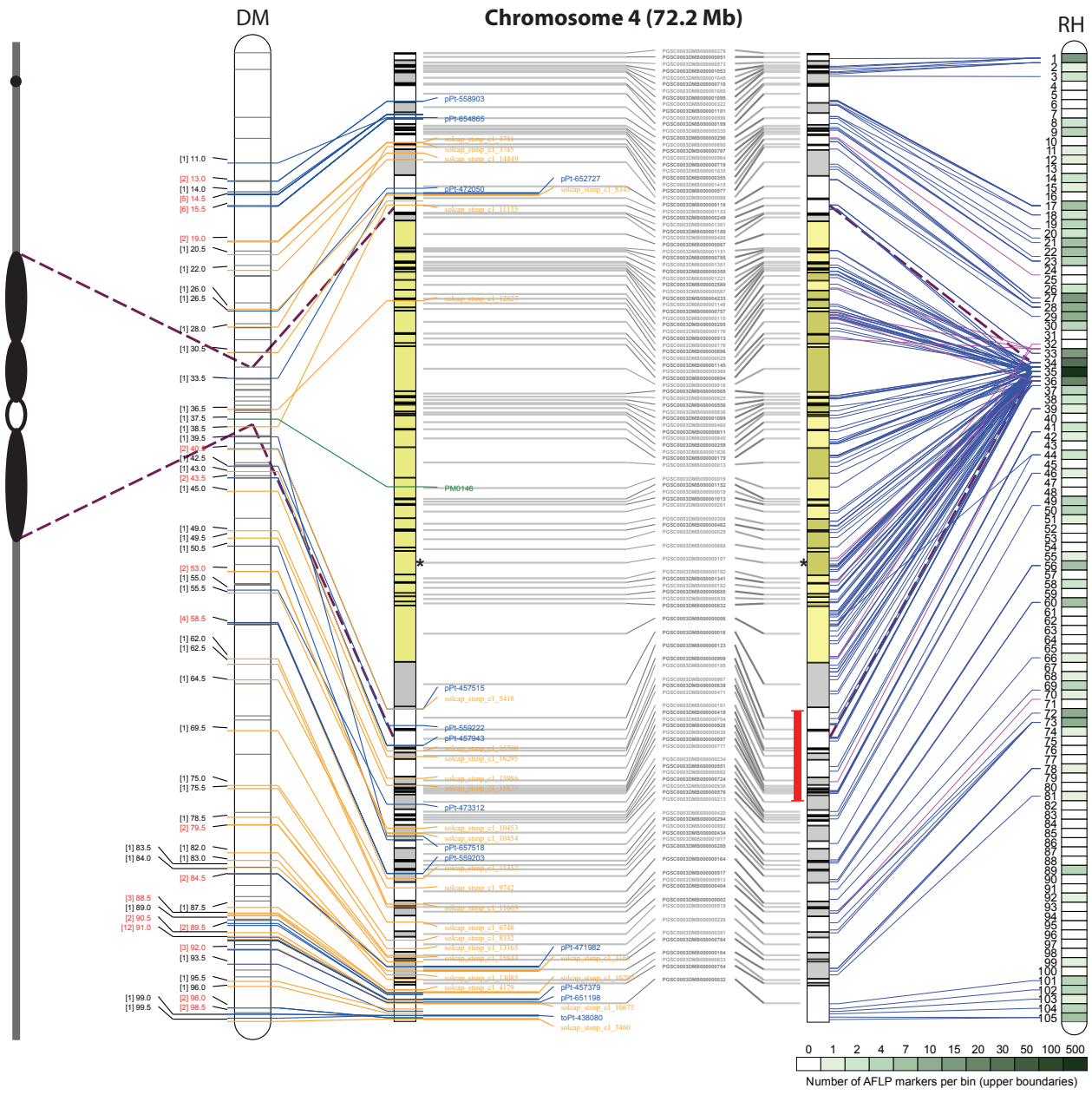
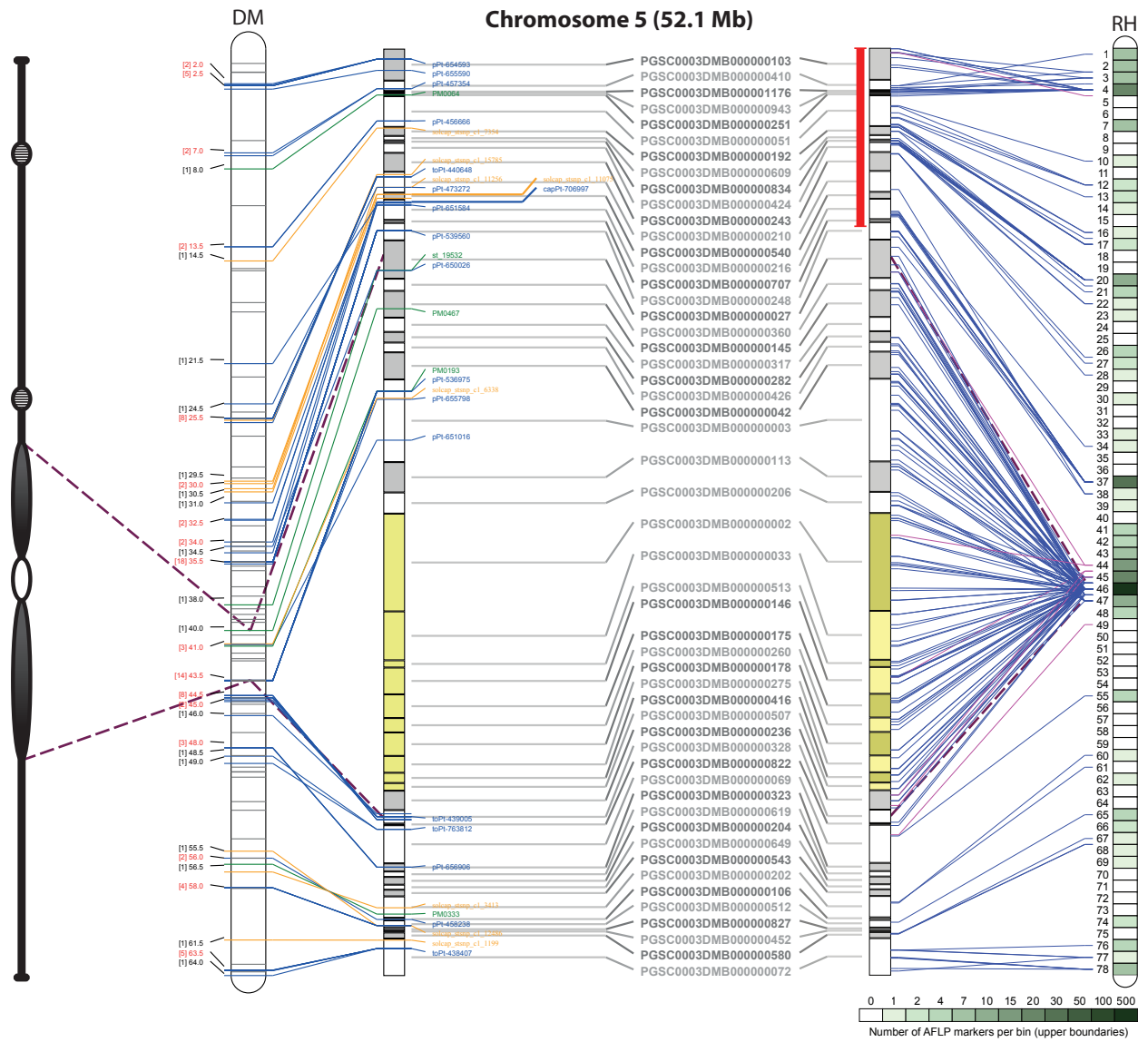


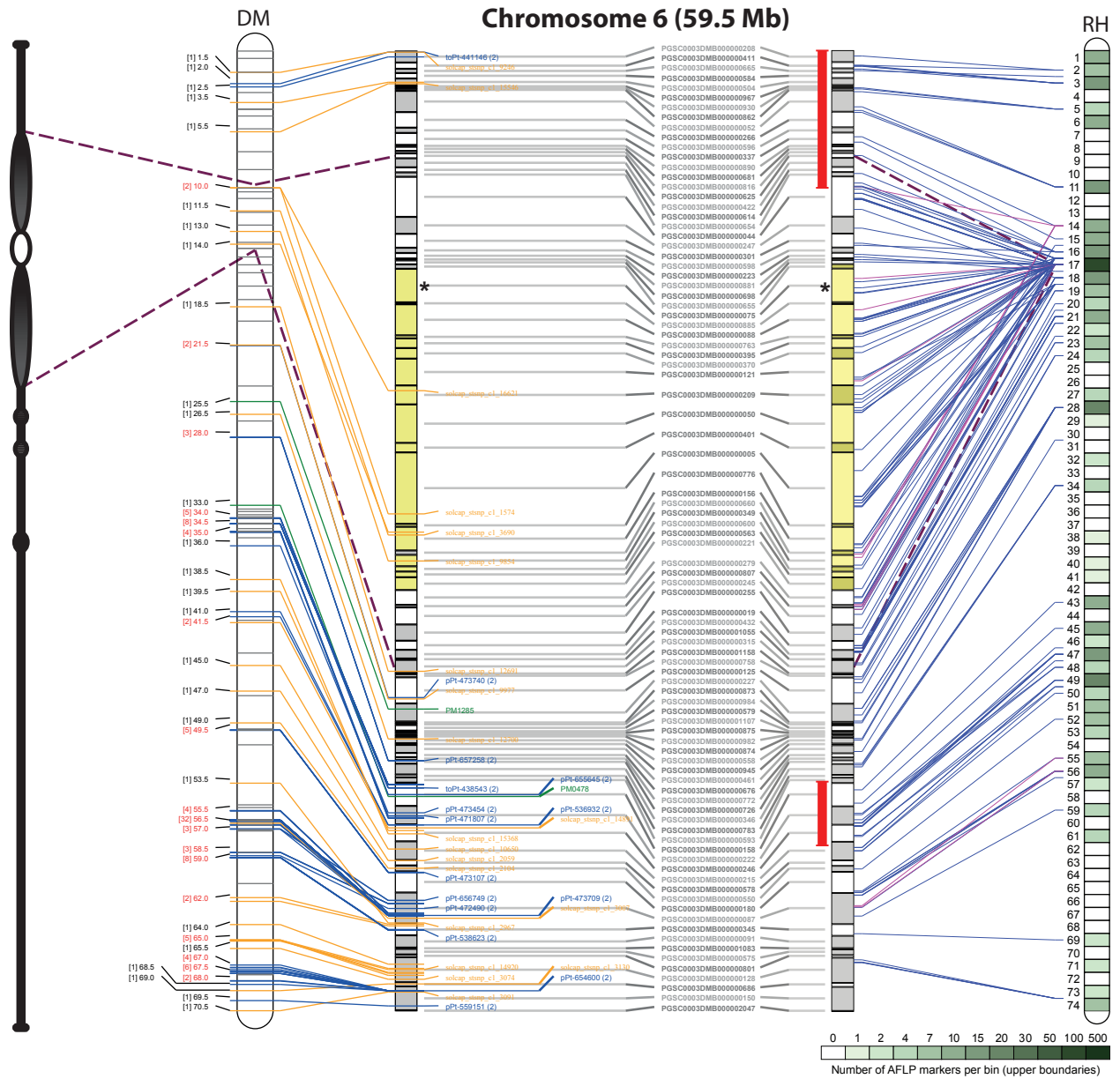
Figure S1 Genome-wide patterns of marker segregation distortion in DMDD population for 1830 STS markers from different segregation categories plotted as a function of Chi-square value (y-axis) against marker physical position (x-axis) on each of the 12 potato chromosomes. Dotted, dashed and dotted-dashed lines represent Chi-square significance values at $p = 0.01$ for marker segregation categories with two, three and four genotypic classes, respectively.

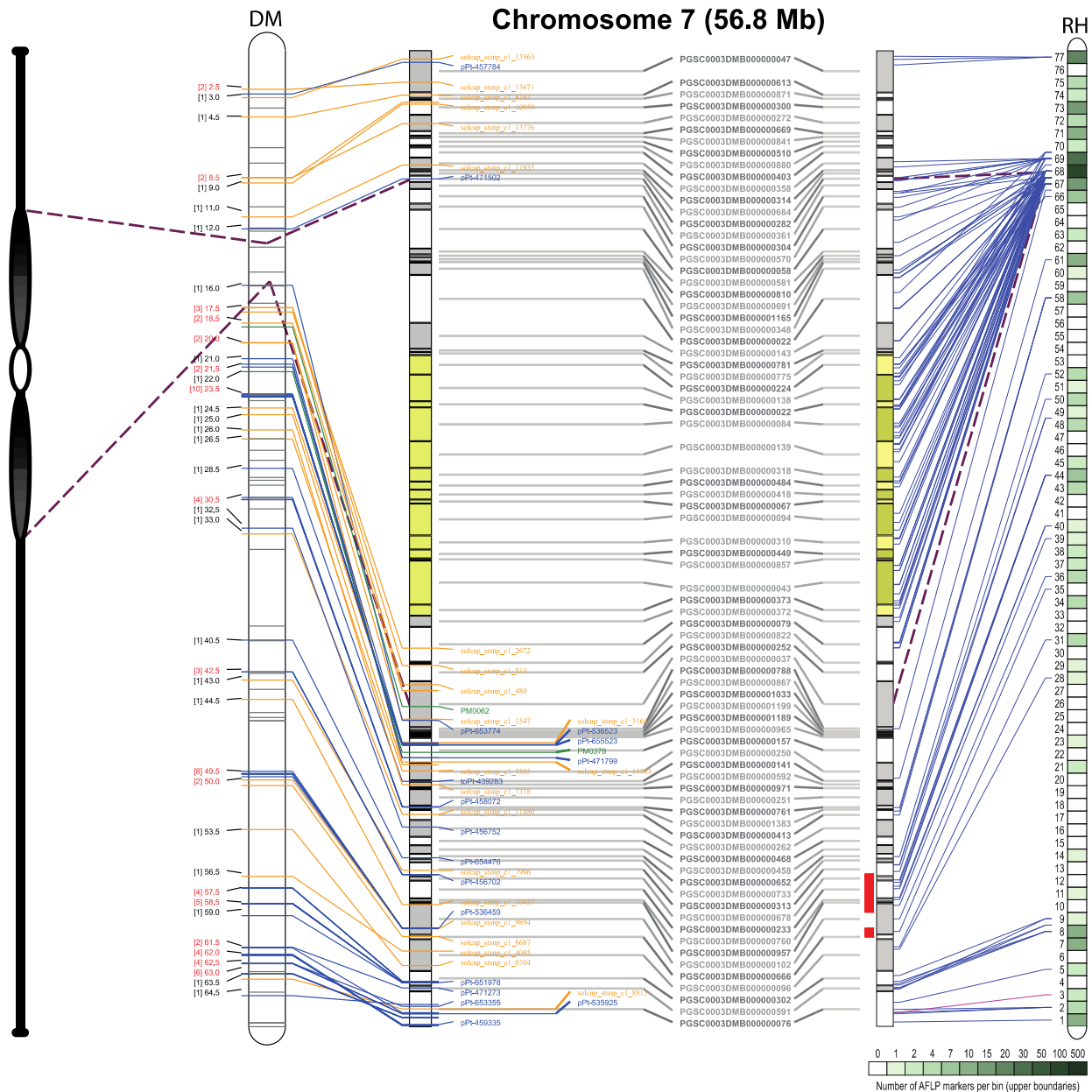


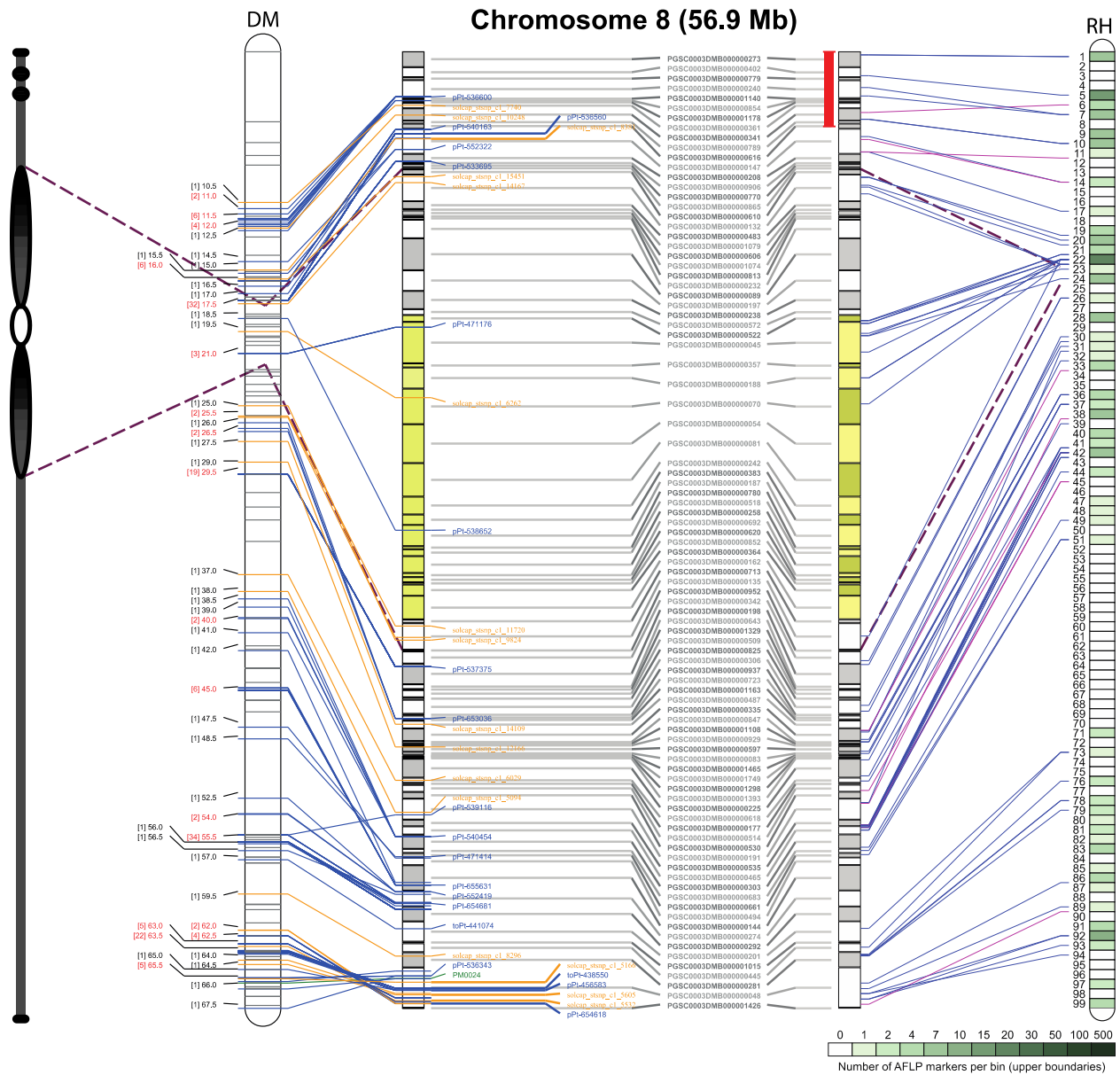


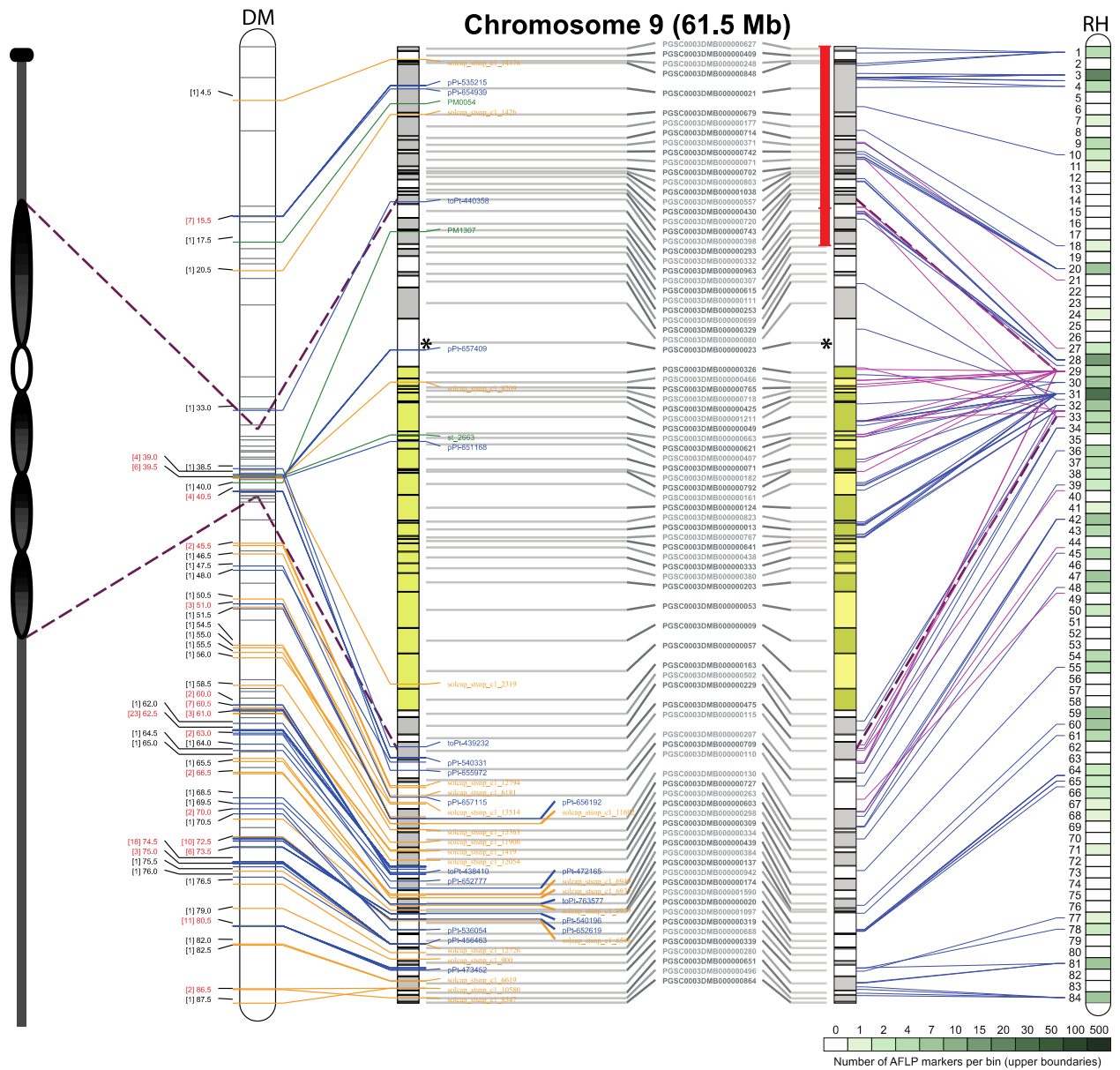


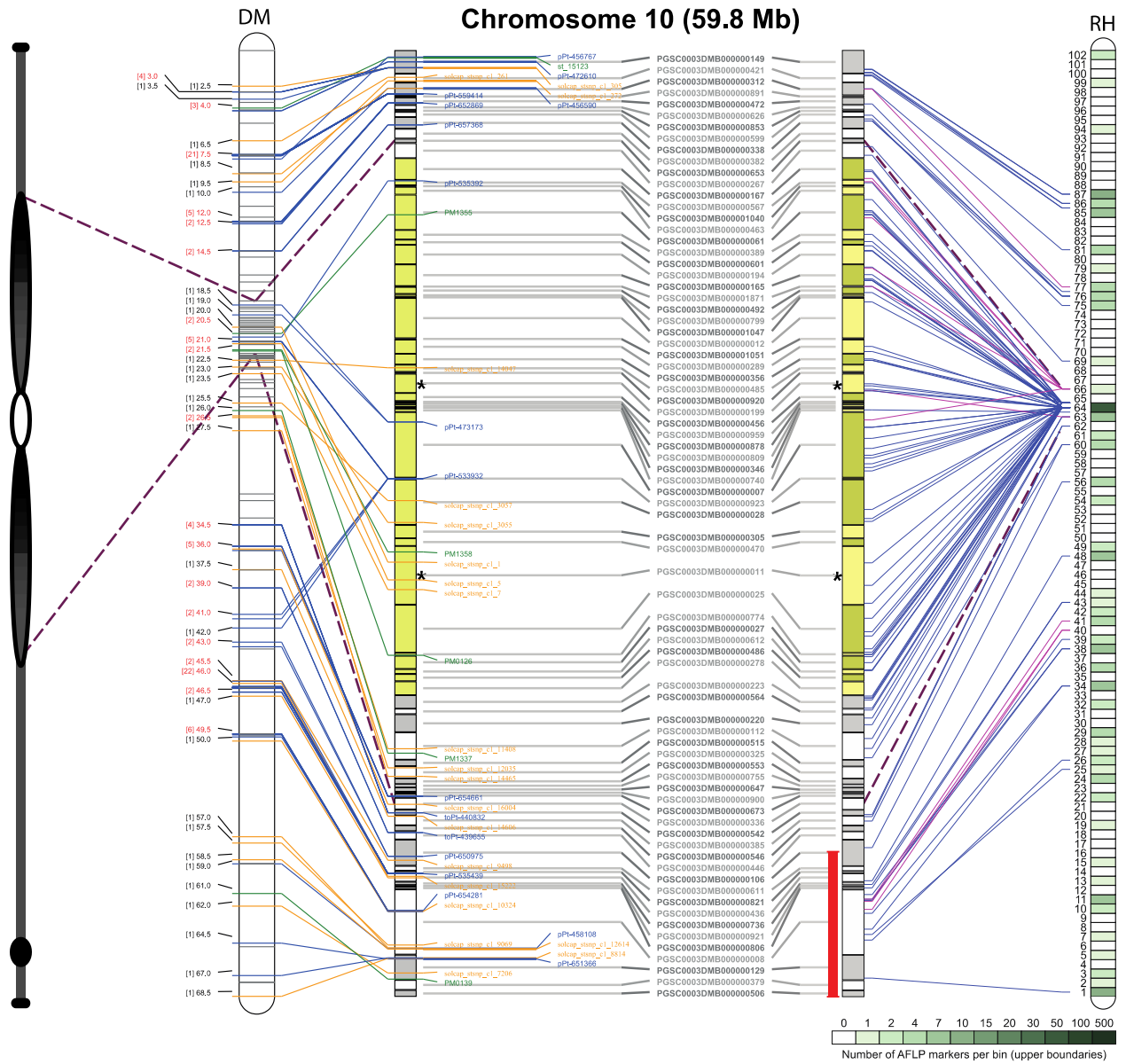


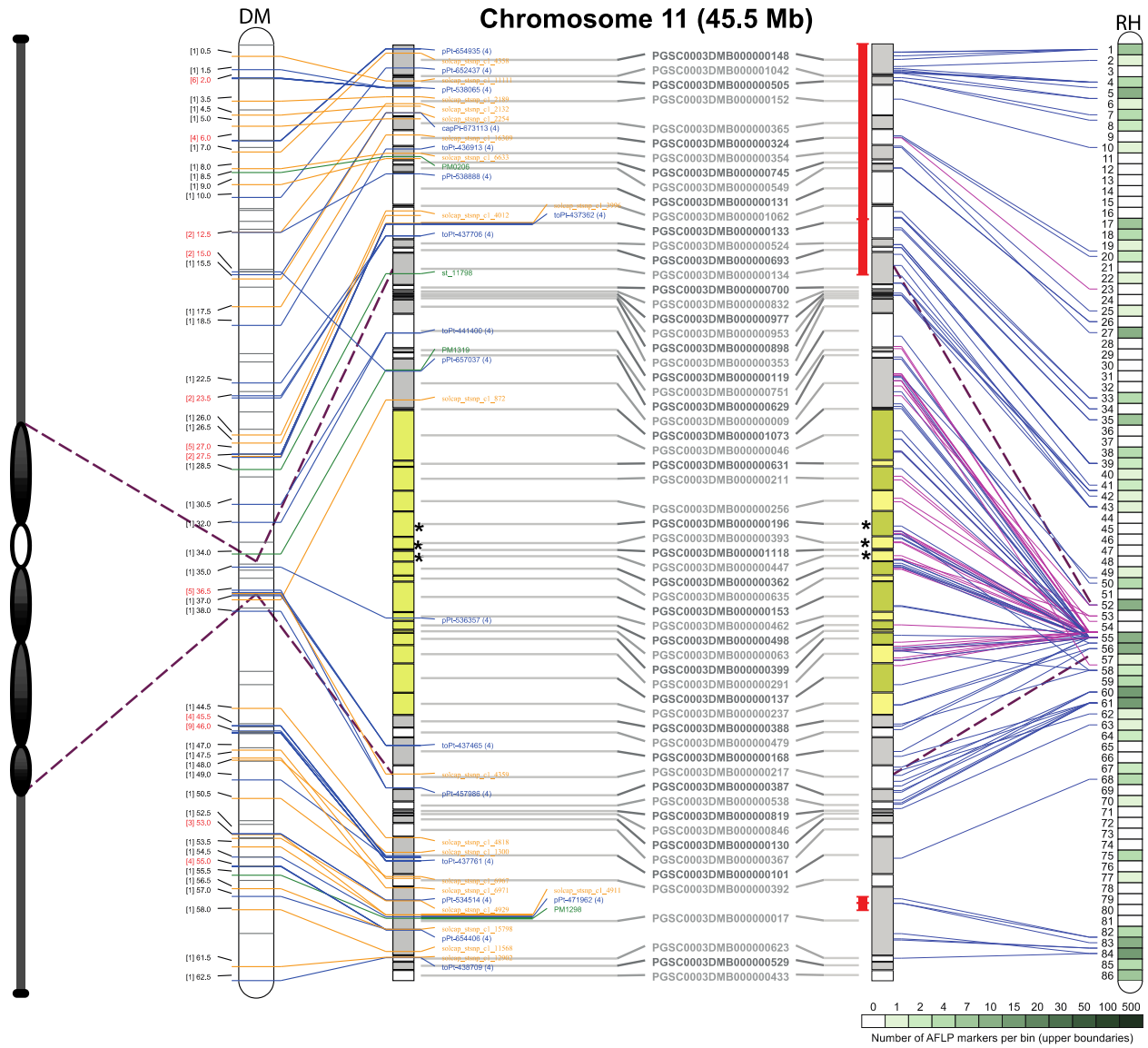












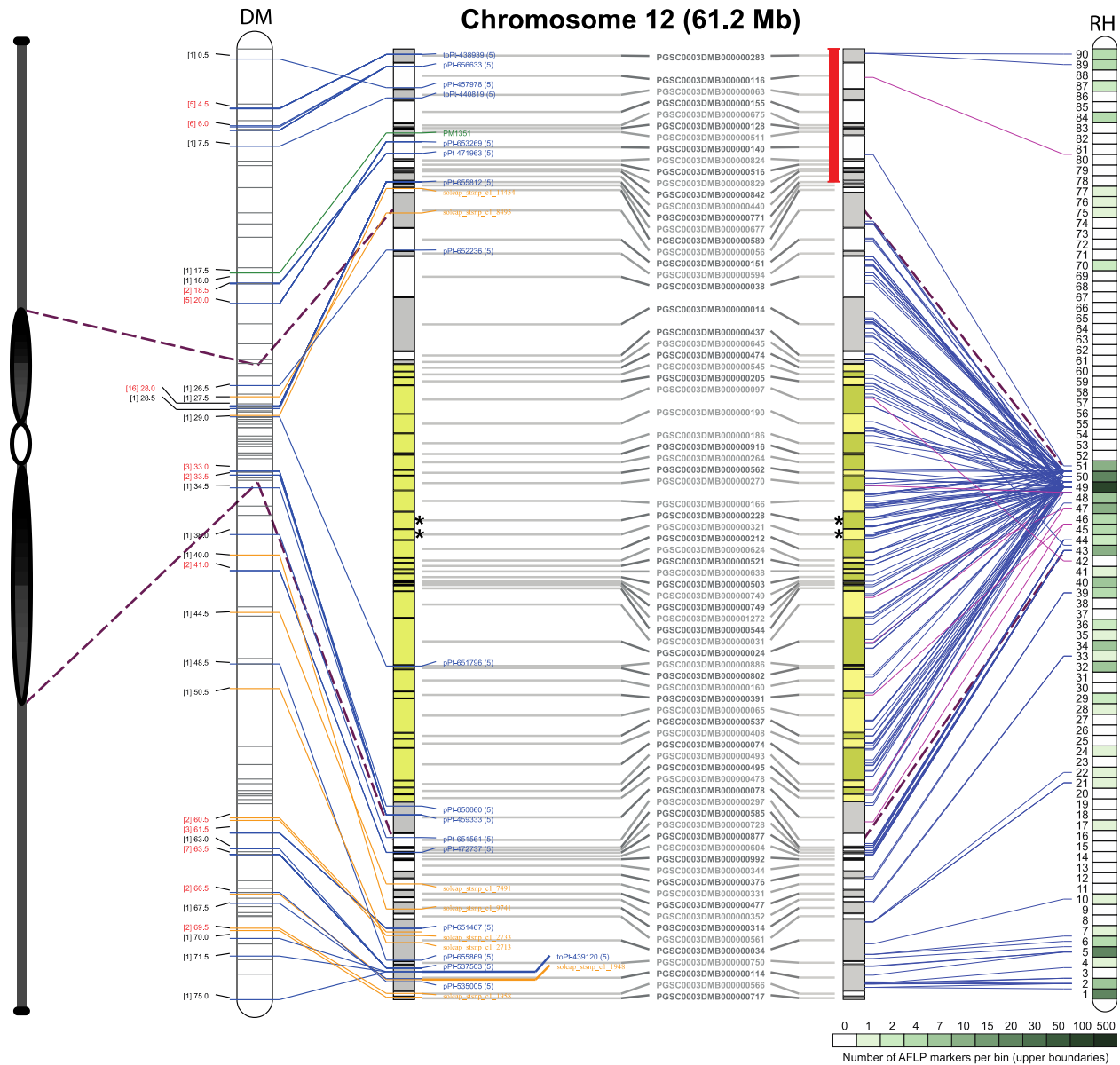


Figure S2 Illustration of the chromosome 2 - 12 pseudomolecules (PMs) integrated with the DM and RH genetic maps. STS and AFLP markers anchor sequence locations in the chromosome PMs to the DMDD and RH genetic maps, respectively. The AFLP marker positions in the PM were identified through sequence tag alignment of BAC clones from the RH WGP physical map. Superscaffolds comprising the PM are shown as alternating grey and white rectangular blocks. The layout of the PM for each of the genetic maps is shown separately but is identical with superscaffold IDs depicted in the middle. The pachytene idiogram is adapted from the potato reference genome publication (Potato Genome Sequencing Consortium 2011). The putative centromere region and pericentromeric/heterochromatic boundaries are demarcated by asterisks and dashed lines, respectively. Each DMDD marker type is colour coded: blue = DArTs, yellow = SNPs, green = SSRs. Blue and magenta lines emerging from the RH genetic map represent AFLP anchors and the intensity of green color corresponds to the AFLP marker density per bin as reported by Van Os *et al.* (2006). Magenta lines represent AFLP markers with a relatively inaccurate mapping position on the RH genetic map, covering an interval of 5 or more bins. Regions in the central heterochromatin where superscaffold order and orientation are not completely resolved are indicated in yellow. Inversions with the tomato sequence are indicated with red interval bars.

Tables S1-S9

Available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.007153/-/DC1>

Table S1 Details of (A) Simple sequence repeat (SSR), (B) Single nucleotide polymorphism (SNP) and (C) Amplified fragment length polymorphism (AFLP) markers employed in DMDD genotyping.

Table S2 Location of sequence-tagged site (STS) markers employed in DMDD genotyping on the DM version 3 superscaffolds and DM version 4.03 pseudomolecules. STS markers include DArTs, SSRs and SNPs.

Table S3 Revised annotation details for the Infinium 8.3k Potato Array SNPs (Felcher *et al.* 2012) on DM version 4.03 pseudomolecules.

Table S4 Genetic and physical locations of STS markers (DArTs, SSRs and SNPs) mapped in DMDD and anchored in DM version 4.03 pseudomolecules.

Table S5 Paracentric inversions between potato and tomato chromosomes detected by dot plot alignments between the chromosome pseudomolecules V4.03 of potato line DM and V2.40 of tomato cv. 'Heinz 1706'.

Table S6 Summary of six BAC pools sequence assembly data comprising 82 DM BAC clones used for validating link peak-based orientation strategy for chromosome 4.

Table S7 BAC pool assembly and validation details for chromosome 4 pseudomolecule version 4.03.

Table S8 Centromere localisation in DM V3 sequence assembly.

Table S9 Accessioned Golden Path (AGP) for the reference DM chromosome-scale pseudomolecules version 4.03. File also includes revised annotation details for potato genes and repeat regions (Potato Genome Sequencing Consortium 2011) and a list of chimeric superscaffolds.