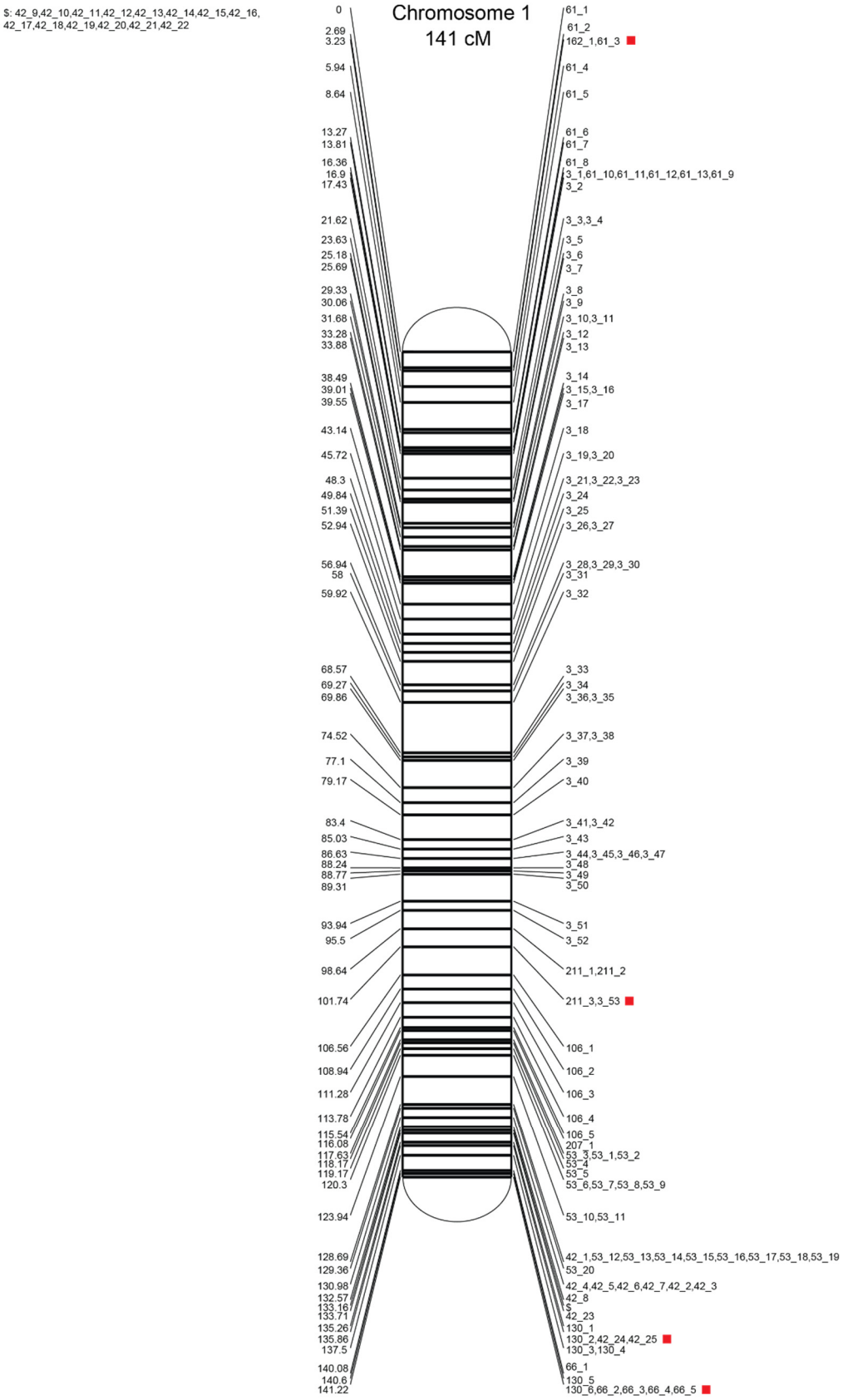
Supplementary Figure

Figure S1 The male genetic linkage map based on 1672 haplotype blocks derived from 104 single sperm genomes. The map distance for each block is on the left hand side of each linkage group, whereas the marker name is listed on the right hand side, with the number before the underscore designating the scaffold and the number after representing a randomly assigned ranking number (see supplementary data). The red squares next to marker names indicate possibly mis-assembled genomic regions in the *Daphnia arenata* reference genome. Some map positions consist of many haplotype blocks and these blocks are shown in the top left corner.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3.23
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8.64
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23.63
25.18
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42_4,42_5,42_6,42_7,42_2,42_3
42_8
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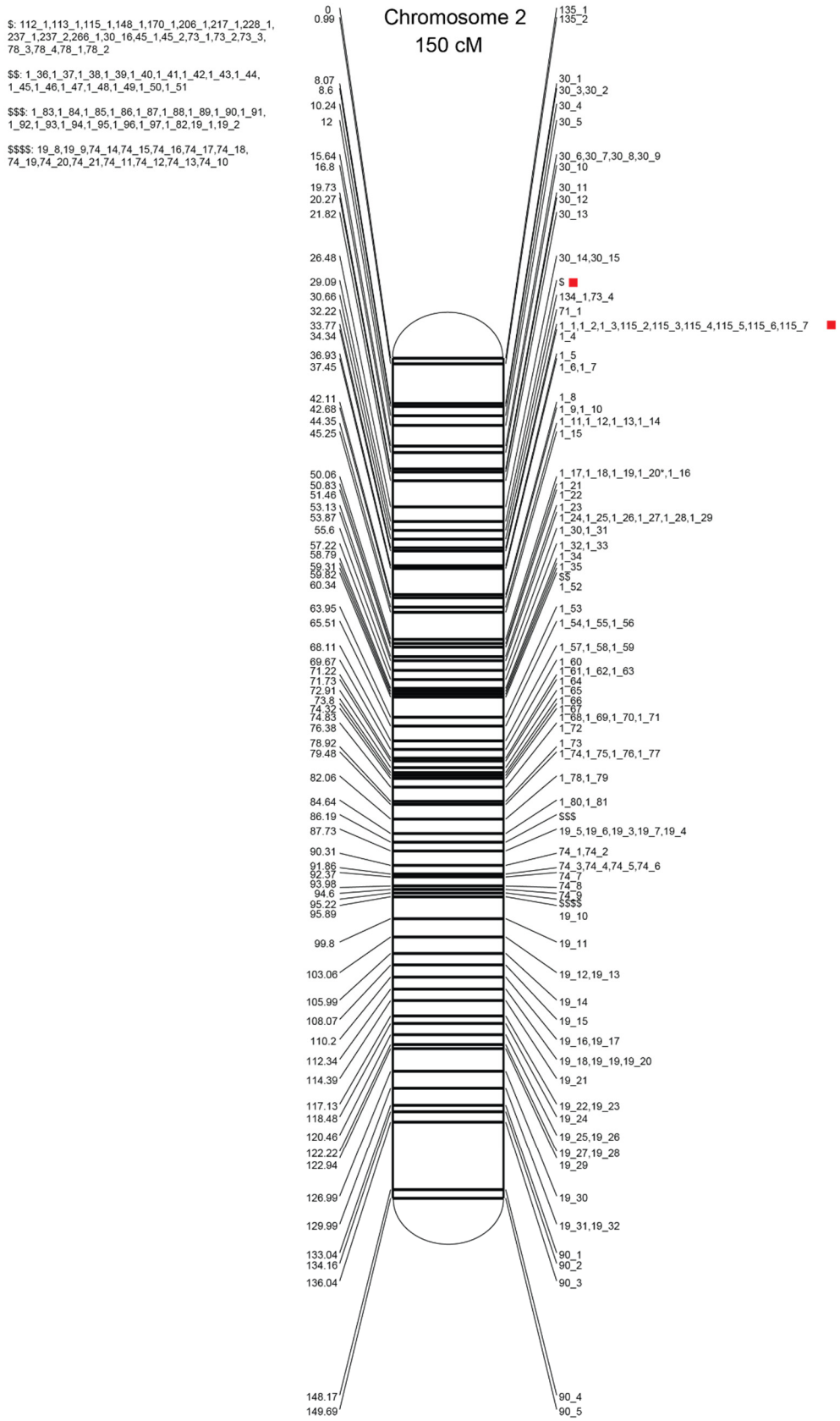
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8.6
10.24
12
15.64
16.8
19.73
20.27
21.82
26.48
29.09
30.66
32.22
33.77
34.34
36.93
37.45
42.11
42.68
44.35
45.25
50.06
50.83
51.46
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58.79
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65.51
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71.73
72.91
73.8
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74_7
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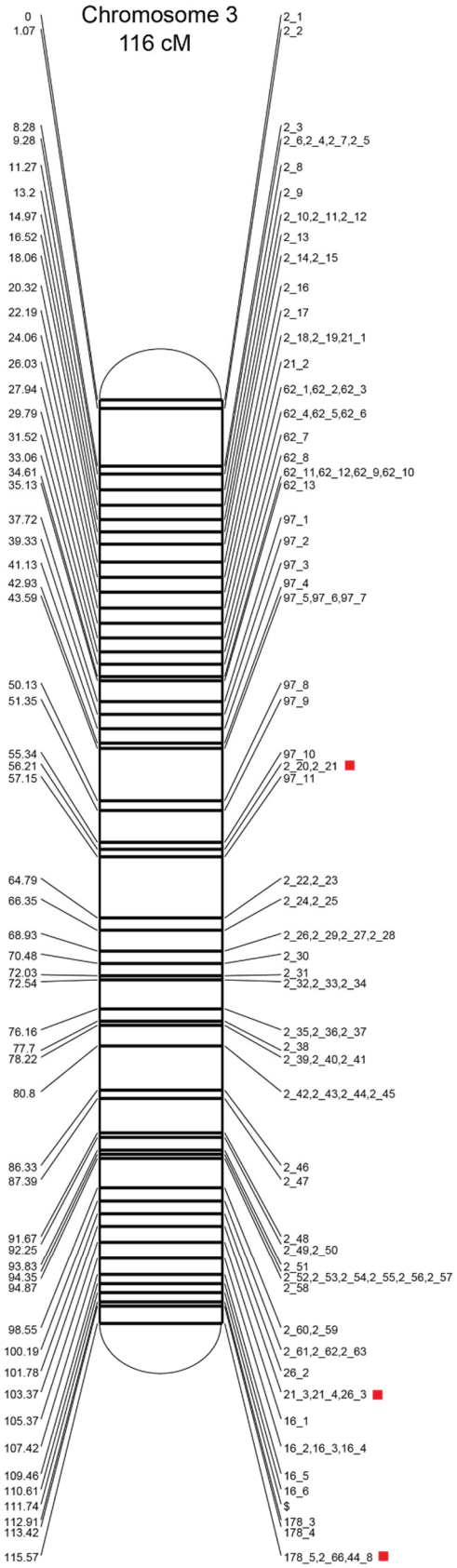

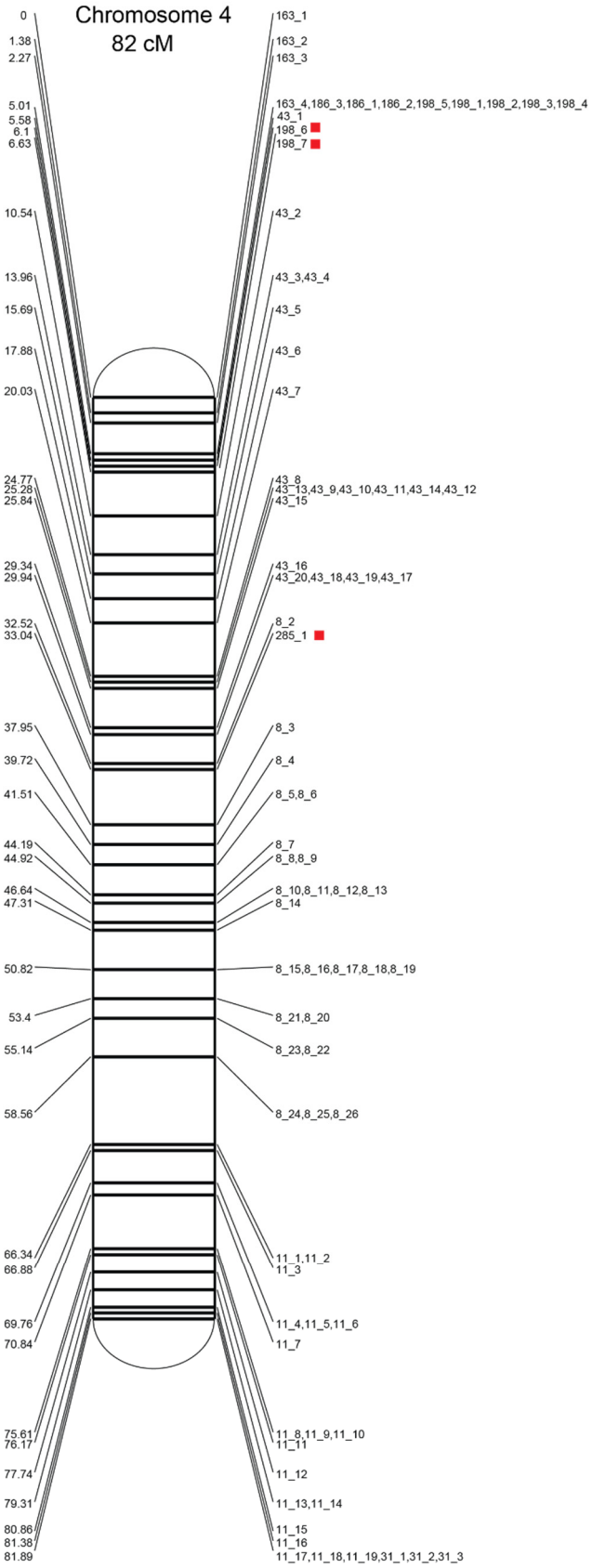
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25.28
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32.52
33.04
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38_11

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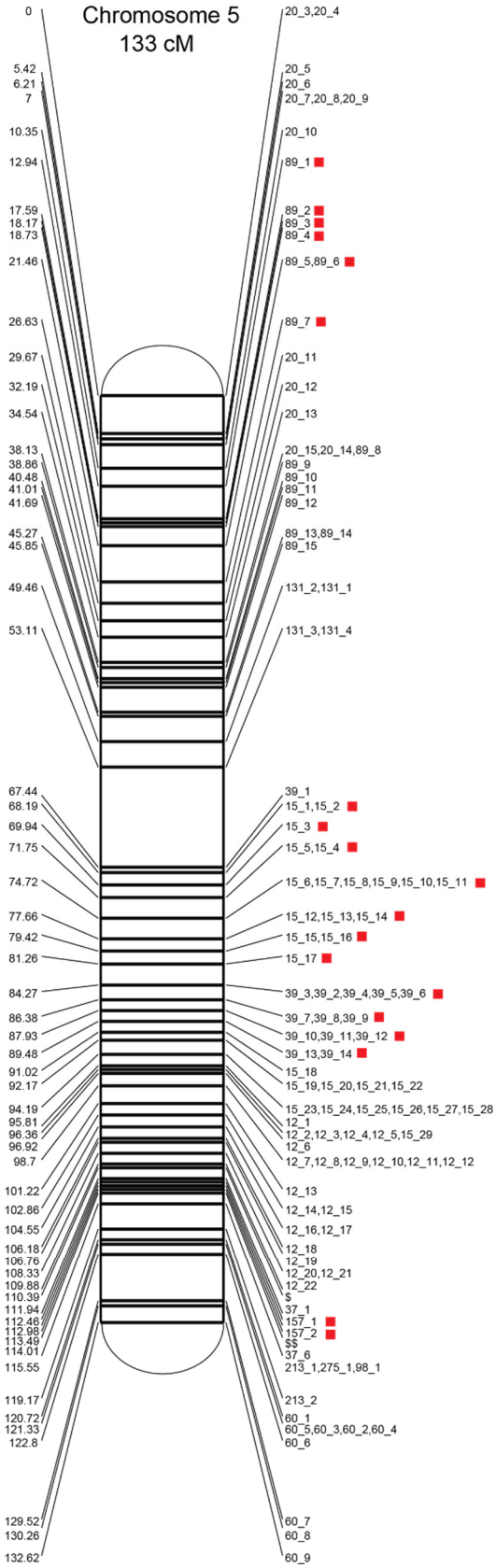

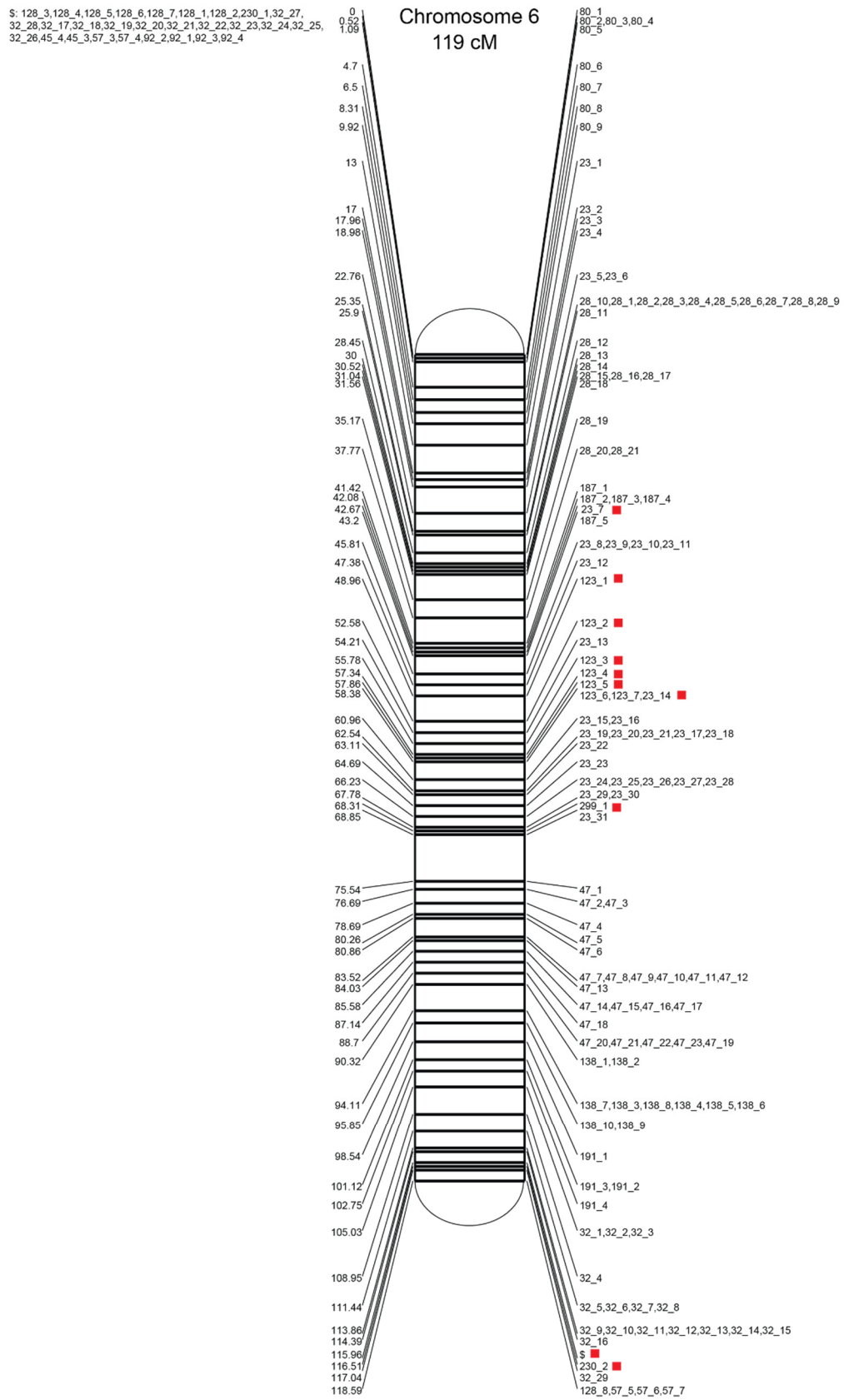
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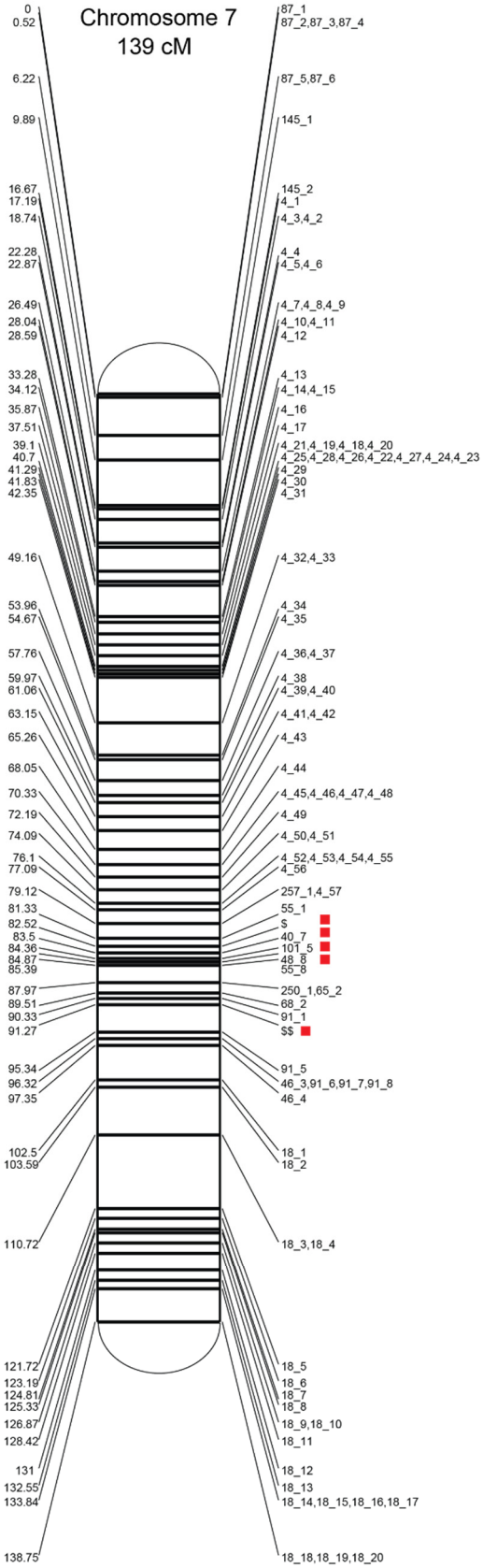

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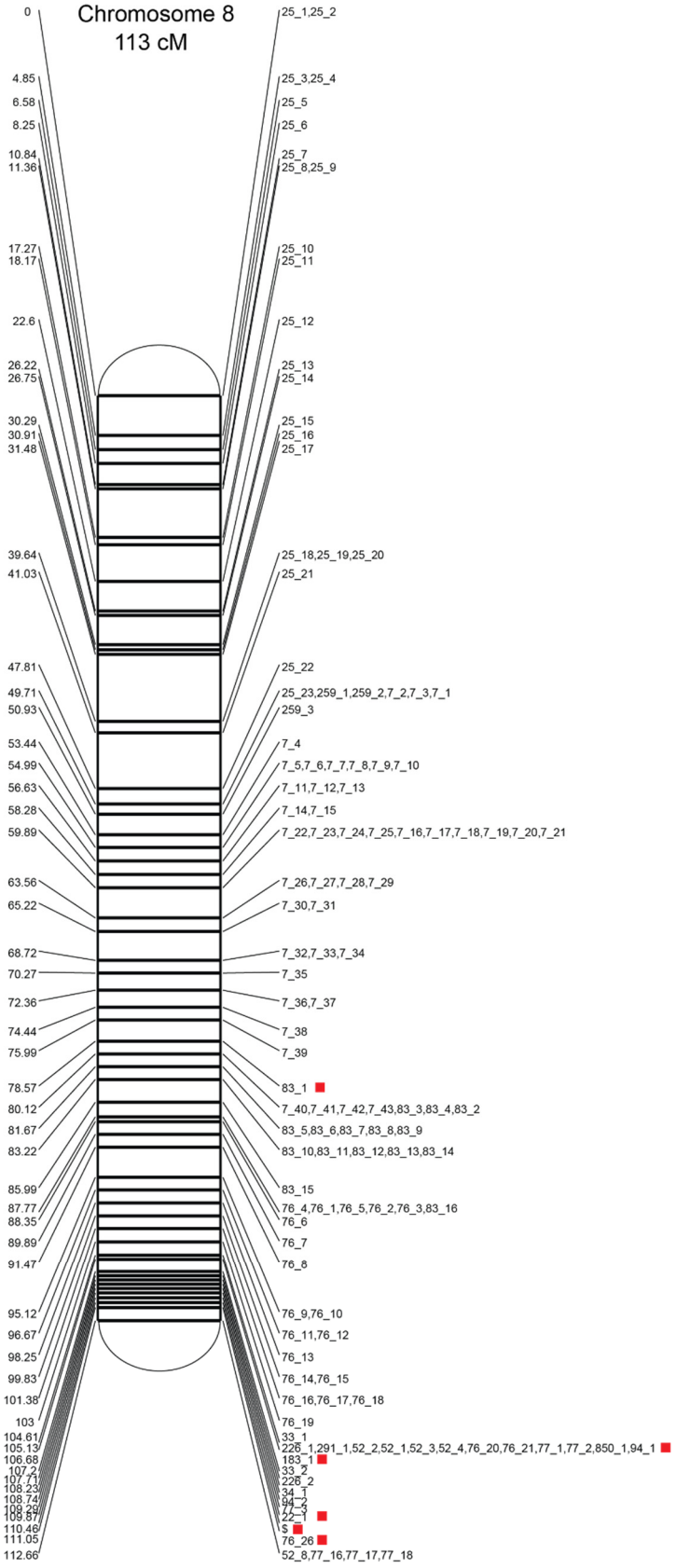

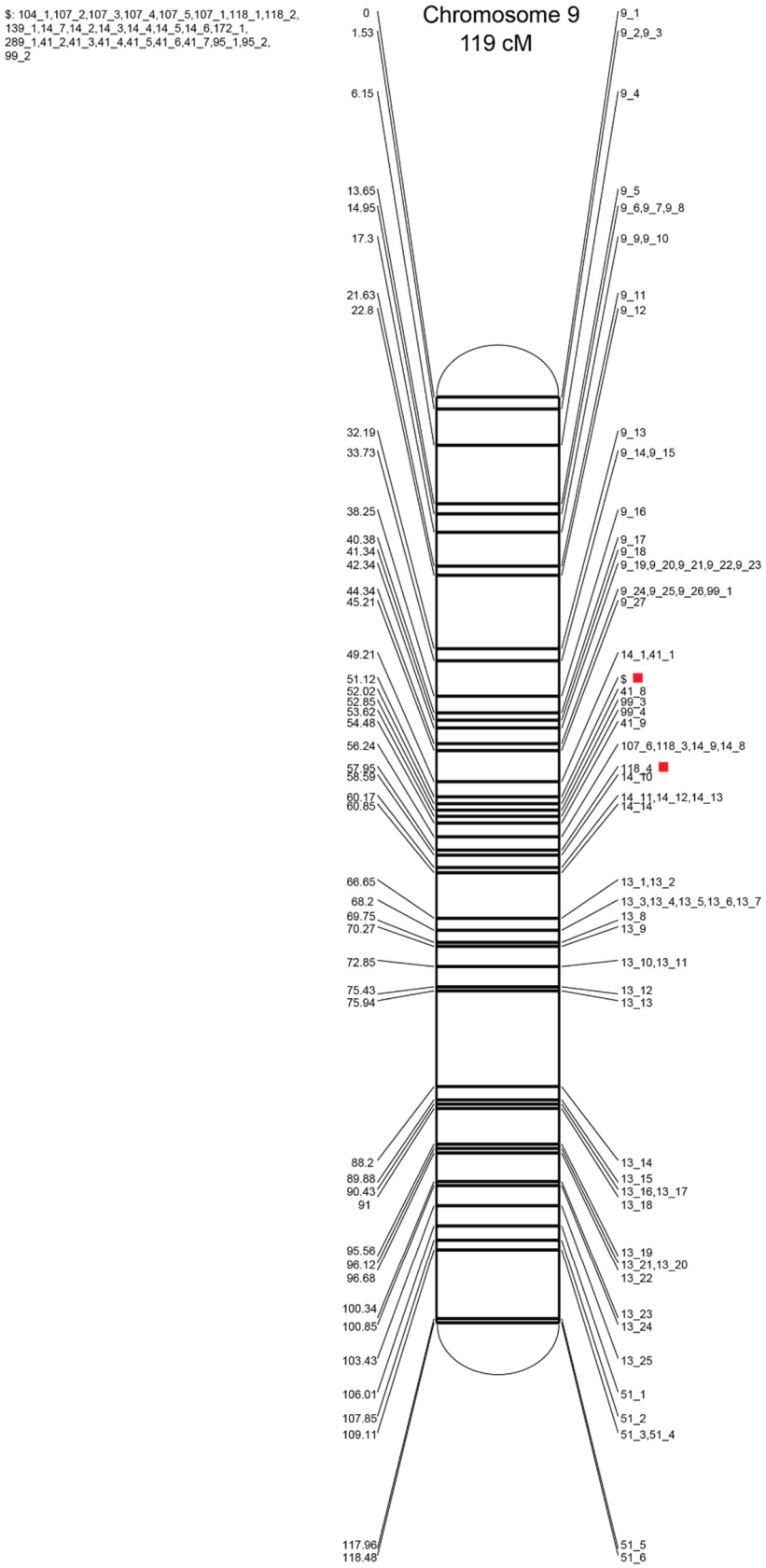
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99_2
Chromosome 9
119 cM
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6.15
13.65
14.95
17.3
21.63
22.8
32.19
33.73
38.25
40.38
41.34
42.34
44.34
45.21
49.21
51.12
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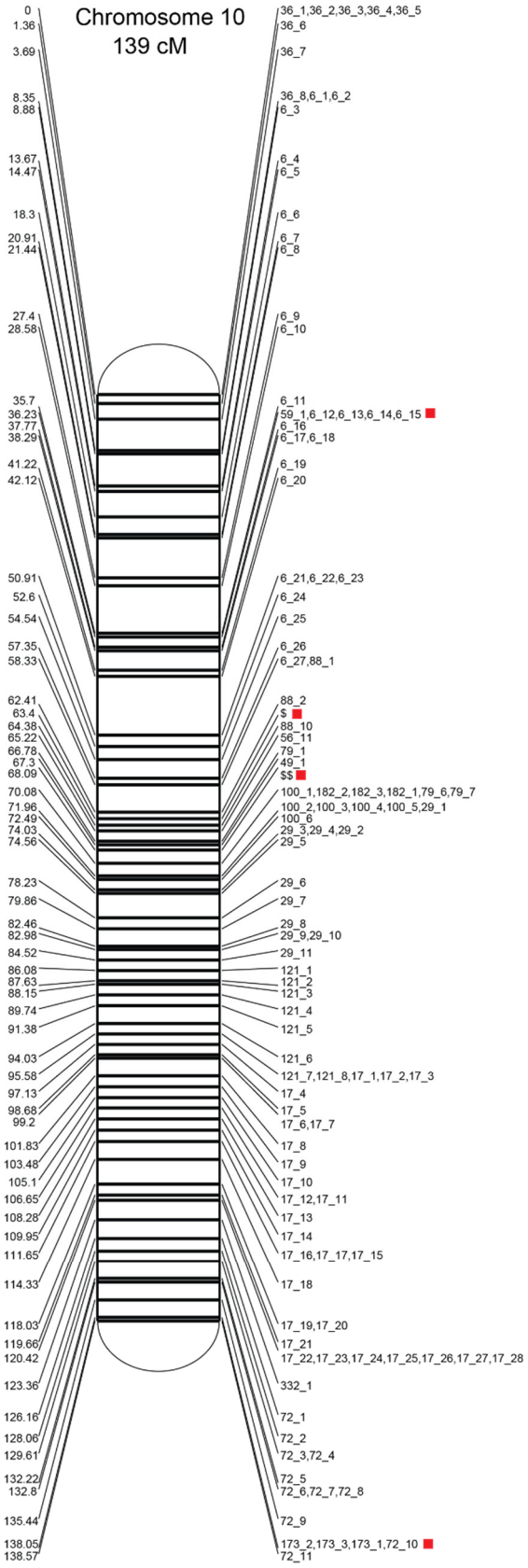

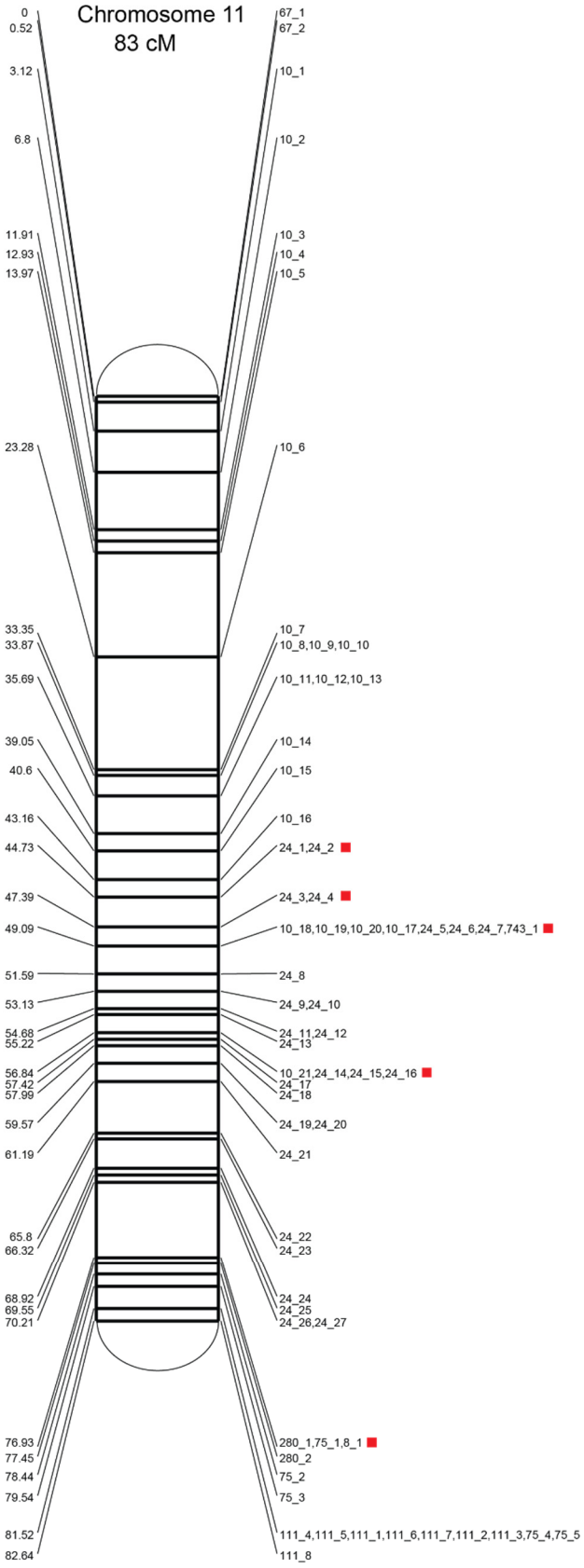
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23.28
33.35
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35.69
39.05
40.6
43.16
44.73
47.39
49.09
51.59
53.13
54.68
55.22
56.84
57.42
57.99
59.57
61.19
65.8
66.32
68.92
69.55
70.21
76.93
77.45
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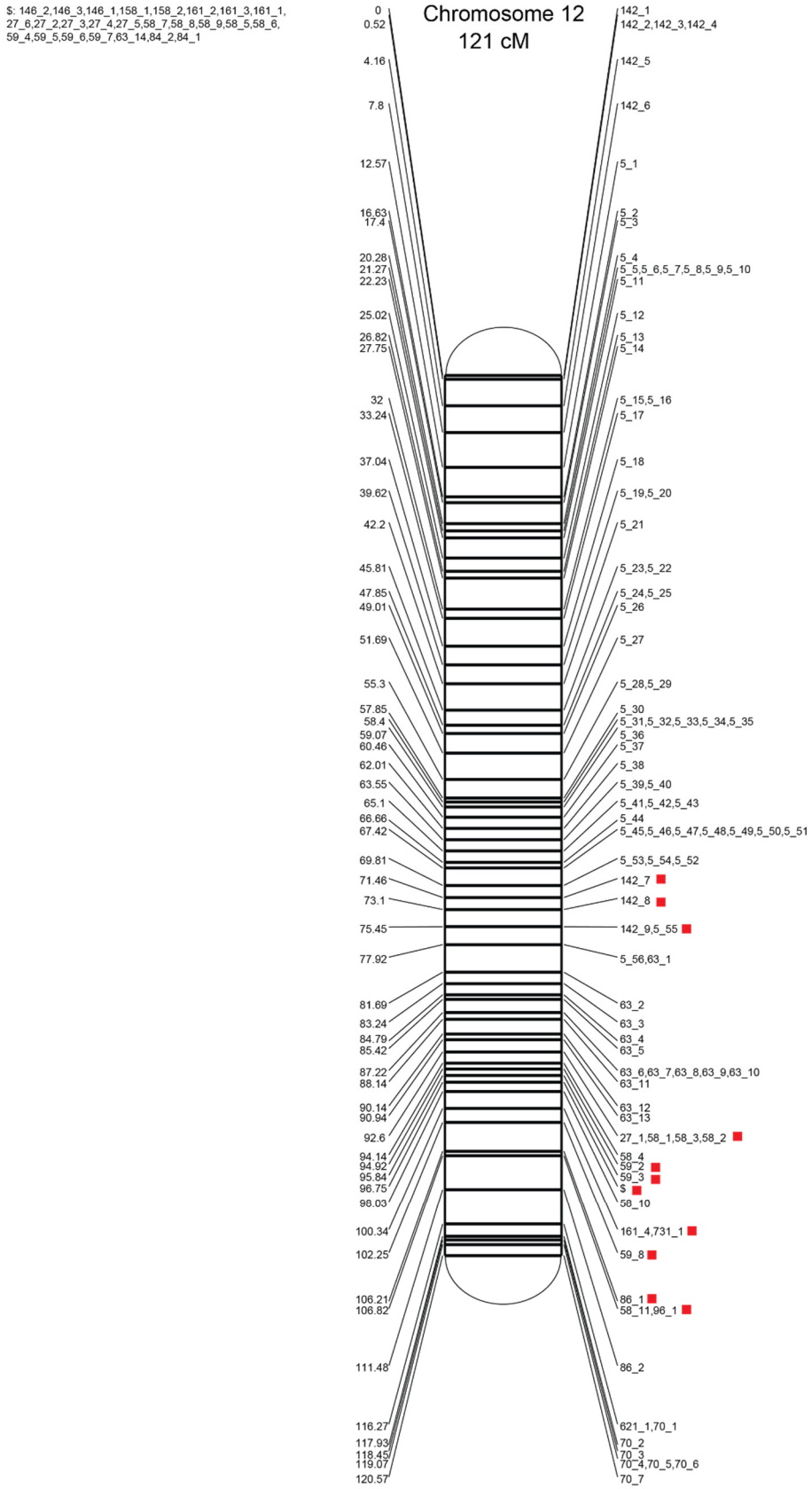
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7.8
12.57
16.63
17.4
20.28
21.27
22.23
25.02
26.82
27.75
32
33.24
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42.2
45.81
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51.69
55.3
57.85
58.4
59.07
60.46
62.01
63.55
65.1
66.66
67.42
69.81
71.46
73.1
75.45
77.92
81.69
83.24
84.79
85.42
87.22
88.14
90.14
90.94
92.6
94.14
94.92
95.84
96.75
98.03
100.34
102.25
106.21
106.82
111.48
116.27
117.93
118.45
119.07
120.57
142_1
142_2,142_3,142_4
142_5
142_6
5_1
5_2
5_3
5_4
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5_11
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5_13
5_14
5_15,5_16
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5_19,5_20
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5_44
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142_7
142_8
142_9,5_55
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63_3
63_4
63_5
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63_11
63_12
63_13
27_1,58_1,58_3,58_2
58_4
59_2
59_3
$
58_10
161_4,731_1
59_8
86_1
58_11,96_1
86_2
621_1,70_1
70_2
70_3
70_4,70_5,70_6
70_7

Files S1-S4

Available for download at www.genetics.org/lookup/suppl/doi:10.1534/genetics.115.179028/-/DC1

File S1. The raw text output file for the genetic map of *D. pulex*.

File S2. Python script phasingHaplotype.py to generate haplotype blocks and input file for MSTmap software. For usage and input data format, please see beginning of the file.

File S3. MareyMap database created by combining the genetic map data and the current *Daphnia* reference assembly.

File S4. The raw text output file for the genetic map based on sperm *de novo* assembly.

File S5

Supplementary material

Method for haplotype block reconstruction

The first step in the construction of our genetic map is to remove sites where very few of the sperm have SNP calls. When very few sperm samples were sequenced at a site, it becomes difficult to detect recombination events between a pair of sites since they may be no sperm sequenced at both sites. Once these sites are removed, the remaining polymorphic sites that are adjacent to each other in the reference assembly are clustered into blocks that show no evidence of recombination, and then these blocks are phased in order to minimize the number of recombination events. Whether a recombination event occurs between two sites can be easily checked by counting the number of haplotypes that occur at each site. If only two haplotypes occur, then there is no evidence that a recombination event occurred between these sites. Then they are joined together into a longer haplotype block. Each haplotype block is extended to include all adjacent sites for which there is evidence of only two haplotypes. When a third haplotype is detected, a new block is created and the procedure is repeated. Once all the haplotype blocks are established, they are phased to minimize the number of recombination events occurring between adjacent haplotype blocks. This can be easily accomplished since each haplotype block has only two potential phases, and we assume that each haplotype block is in the phases that gives a lower number of recombination events with the upstream block. Since haplotype blocks are constructed under the assumption that sites adjacent to each other in the reference assembly are separated by very little genetic distance, it is not expected a large number of recombination events occurring between adjacent blocks. When this does occur, we can mask the downstream haplotype block which has an excessive number of recombination events and

ignore this haplotype block for phasing purposes. Finally, the adjacent haplotype blocks that are not affected by recombination events need to be placed into the same parental or maternal phases so that the MST software, which assumes that the parental and maternal identity of markers are known, can be used to construct a genetic map.