Online Resource 2

Article title: “Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat”

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UC1110/PI610750 genetic map

The genetic map for the UC1110/PI610750 mapping population can be found on the following pages. This map, featuring a total of 1,494 probes mapped to 558 loci, is presented as a series of ideograms, with one ideogram (i.e. one chromosome) per page. Please note that the 21 chromosomes are not drawn to scale relative to one other; rather, each has been scaled to fit the page in an attempt to provide maximum resolution. For a searchable spreadsheet of all markers and their mapped positions, please see Online Resource 3.

Markers are mapped with a minimum confidence of LOD 3, unless otherwise indicated: Dashed vertical bars linking neighboring loci indicate a LOD ≥ 2, and solid vertical bars indicate a LOD ≥ 1.5. For example, the presented order of **gwm6** and **gwm538** on Chromosome 4B has a LOD between 1.5 and 2. Markers which could not be ordered with a LOD of at least 1.5 were assigned to the same locus (see note 2 below).

Some additional notes relating to format:

1. At any given locus, markers separated by a comma (,) are perfectly linked in this population.
2. At any given locus, markers or groups of markers separated by a double colon (::) are not perfectly linked in this population but could not be ordered with a LOD score greater than 1.5.
3. Italicized, square brackets surrounding an italicized marker name (*e.g.* ***[barc287]***) indicate that the marker, due to missing data, maps to two or more neighboring loci with equal probability.
4. Non-DArT markers are shown in bold, and curly brackets ({ }) are used to indicate traits associated with a given probe (*e.g.* on chromosome 1A, the probe **umn19** is associated with the high molecular weight glutenin gene **{Glu-A1}**).
5. Map units are Kosambi centimorgans.

Stripe rust QTL information

To the left of the ideograms for chromosomes 2A, 2B, 3B, and 5A can be found summary stripe rust resistance QTL information. For each season (2007-2010) and each phenotypic dataset (reaction type and disease severity), a vertical bar is shown which spans the region where the QTL LOD score (CIM analysis) exceeds the threshold LOD score of 3.3. Solid bars correspond to reaction type, following the 11-point scale described in Online Resource 1, and diagonally dashed bars correspond to disease severity (% flag leaf area affected at early-milk to hard-dough stage). Overlaying each bar is a number which represents the magnitude and location of the peak LOD score.

> For example, the peak LOD score for disease severity for the 2B QTL in 2009 was 7.5. This peak value occurred slightly proximal of marker **wmc474**.

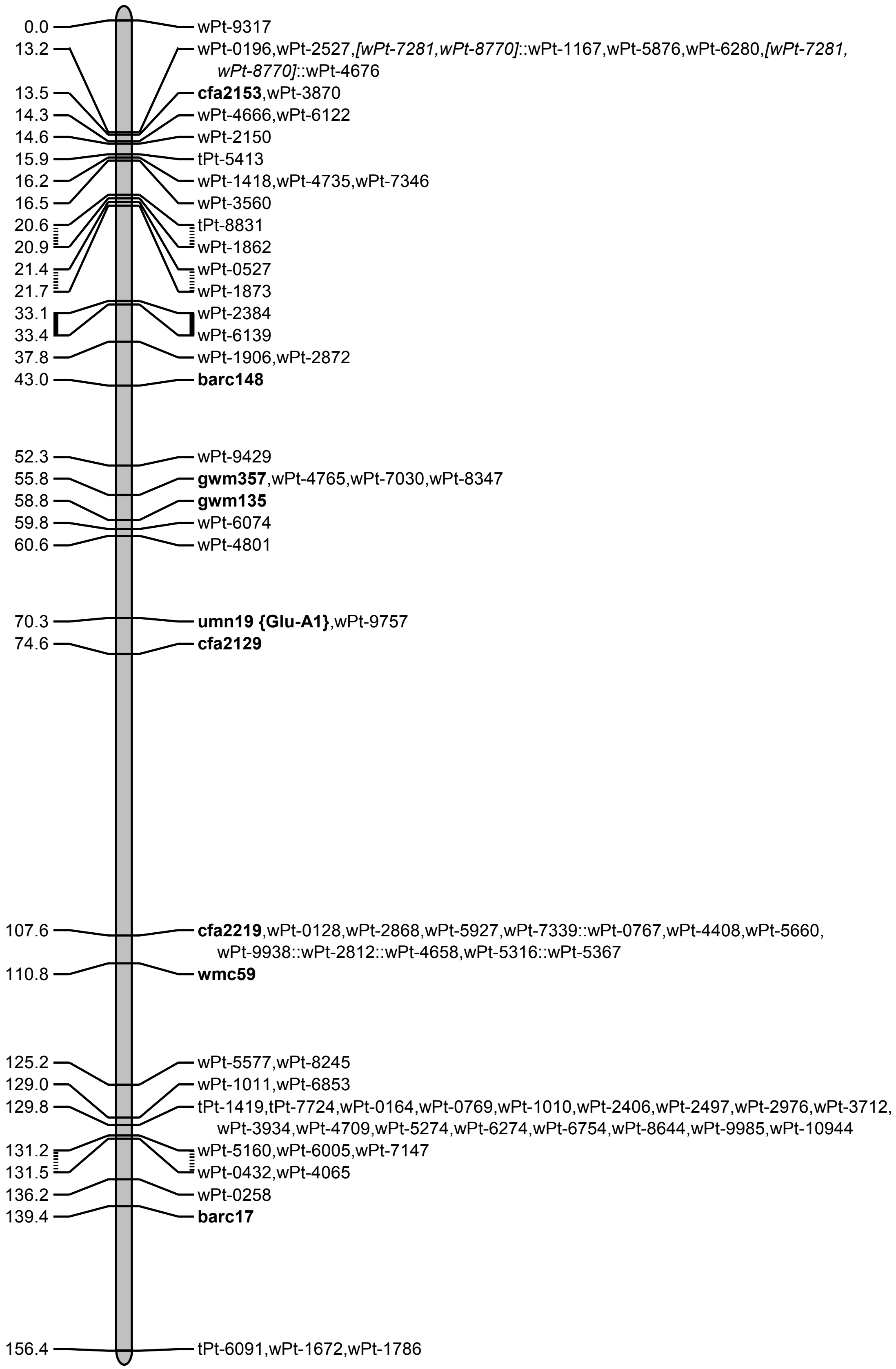
Orange shading of the chromosomes themselves indicates the extent of the putative QTL regions. For the 2A QTL, boundaries are based solely on drops in LOD values in both phenotypic scales over multiple seasons. For the 3B, 5A, and 2B QTL, boundaries are more certain as they are based on actual recombination events (see the Results section of the text). Final notes:

1. No disease severity data was collected in 2007.
2. The 2A QTL lacks bars for 2007 and 2008 because the LOD scores that year did not exceed the threshold value of 3.3 (see Figure 1).
3. The percent variation explained by each QTL is based on a simplified ANOVA model which includes only the first-order effects (i.e. no interactions) of the peak markers of the four QTL regions. Years and blocks within year were included as class variables.

Chromosome 1A | 84 probes mapped to 33 loci; total length 156.4 cM

YR QTL

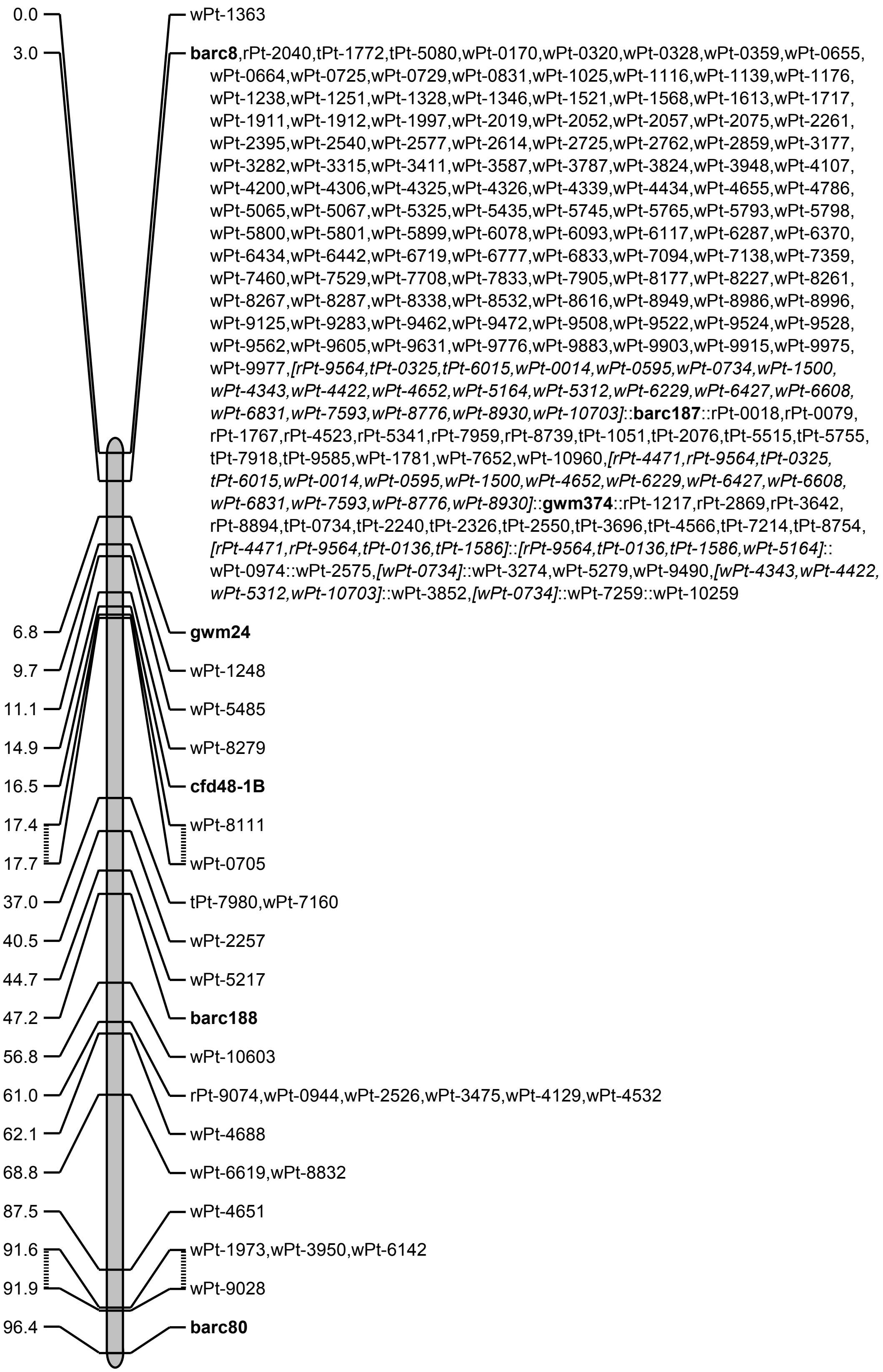
(none)



Chromosome 1B | 204 probes mapped to 21 loci; total length 96.4 cM

YR QTL

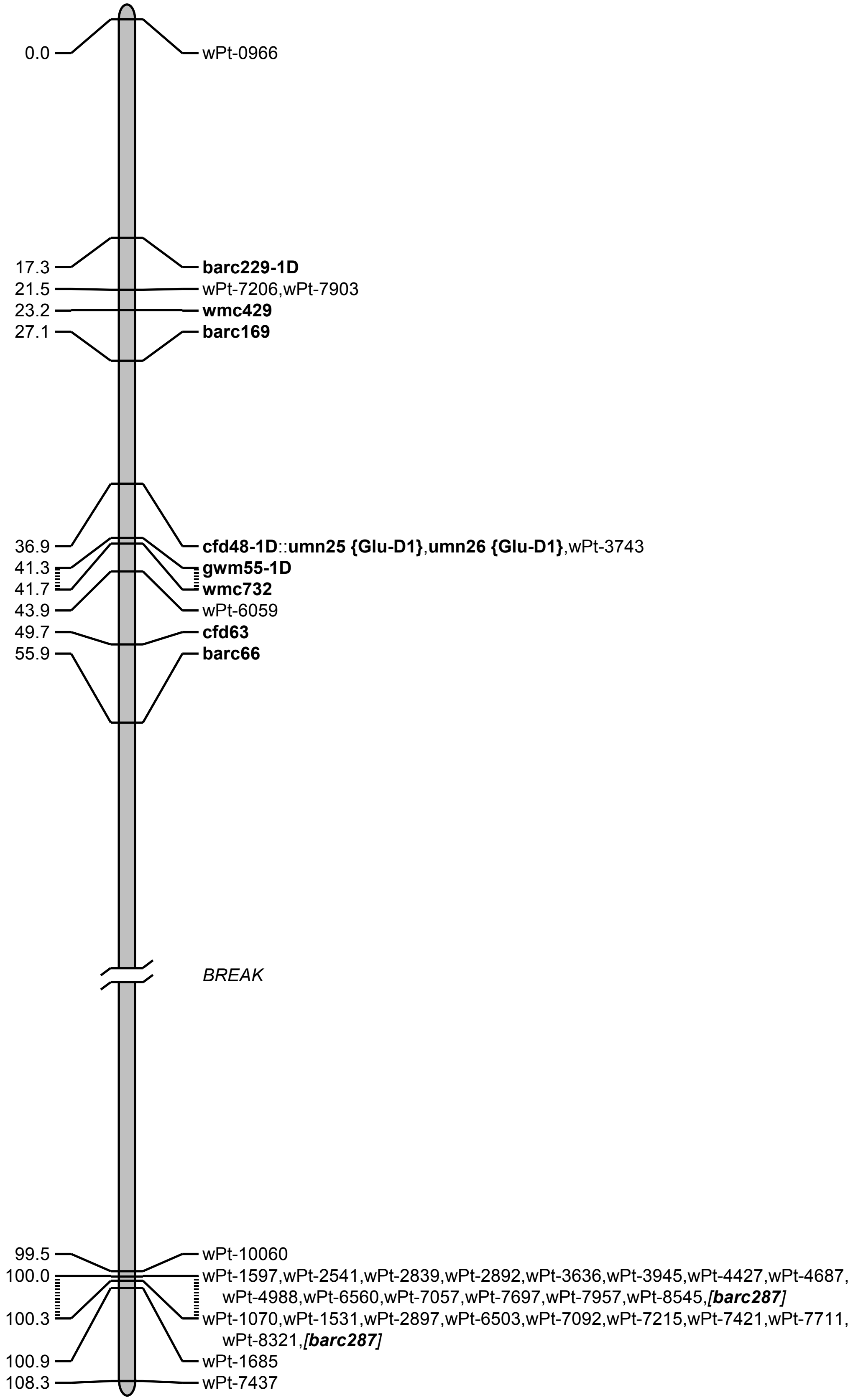
(none)



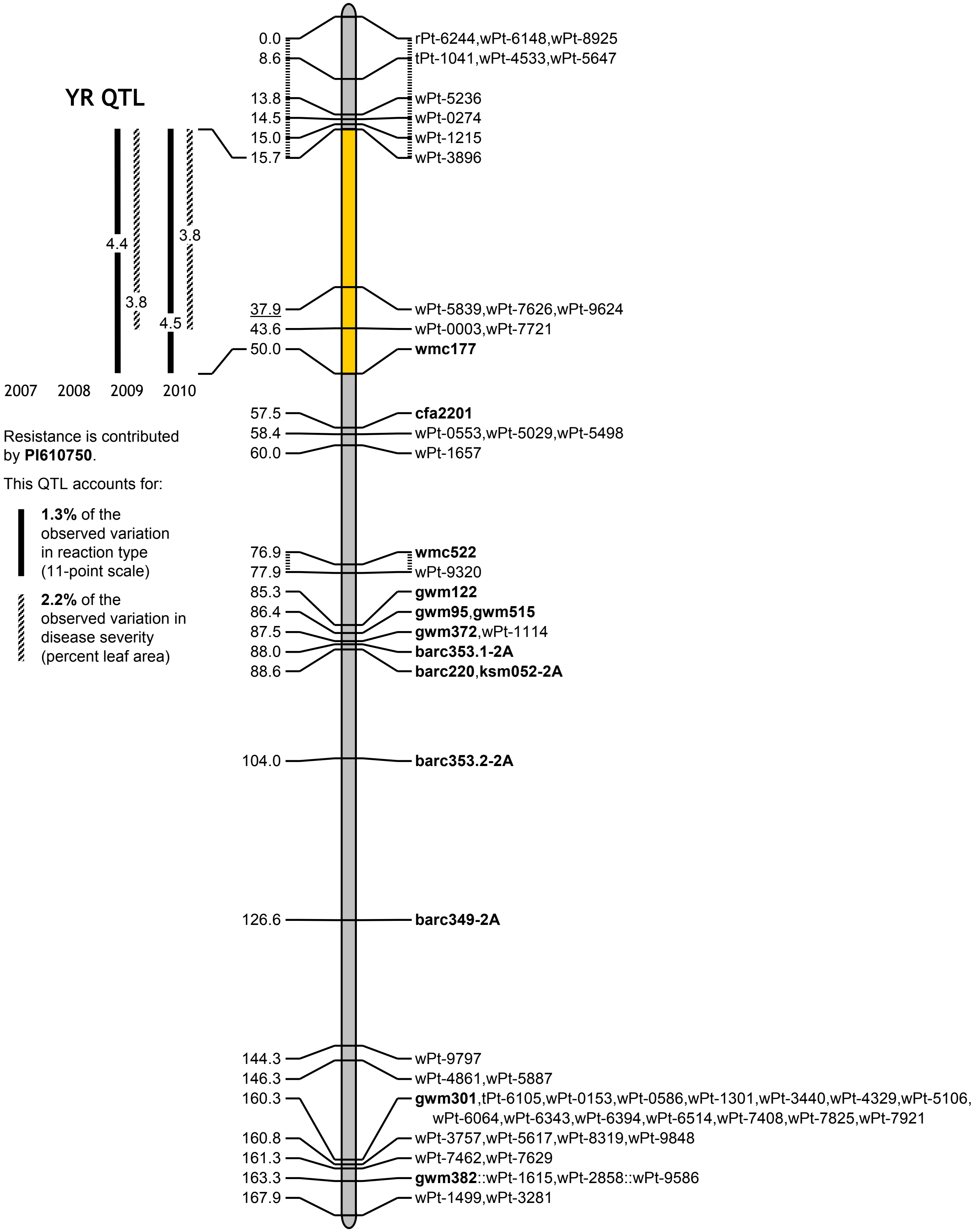
Chromosome 1D | 42 probes mapped to 16 loci; total length 108.3 cM

YR QTL

(none)



Chromosome 2A | 63 probes mapped to 28 loci; total length 167.9 cM

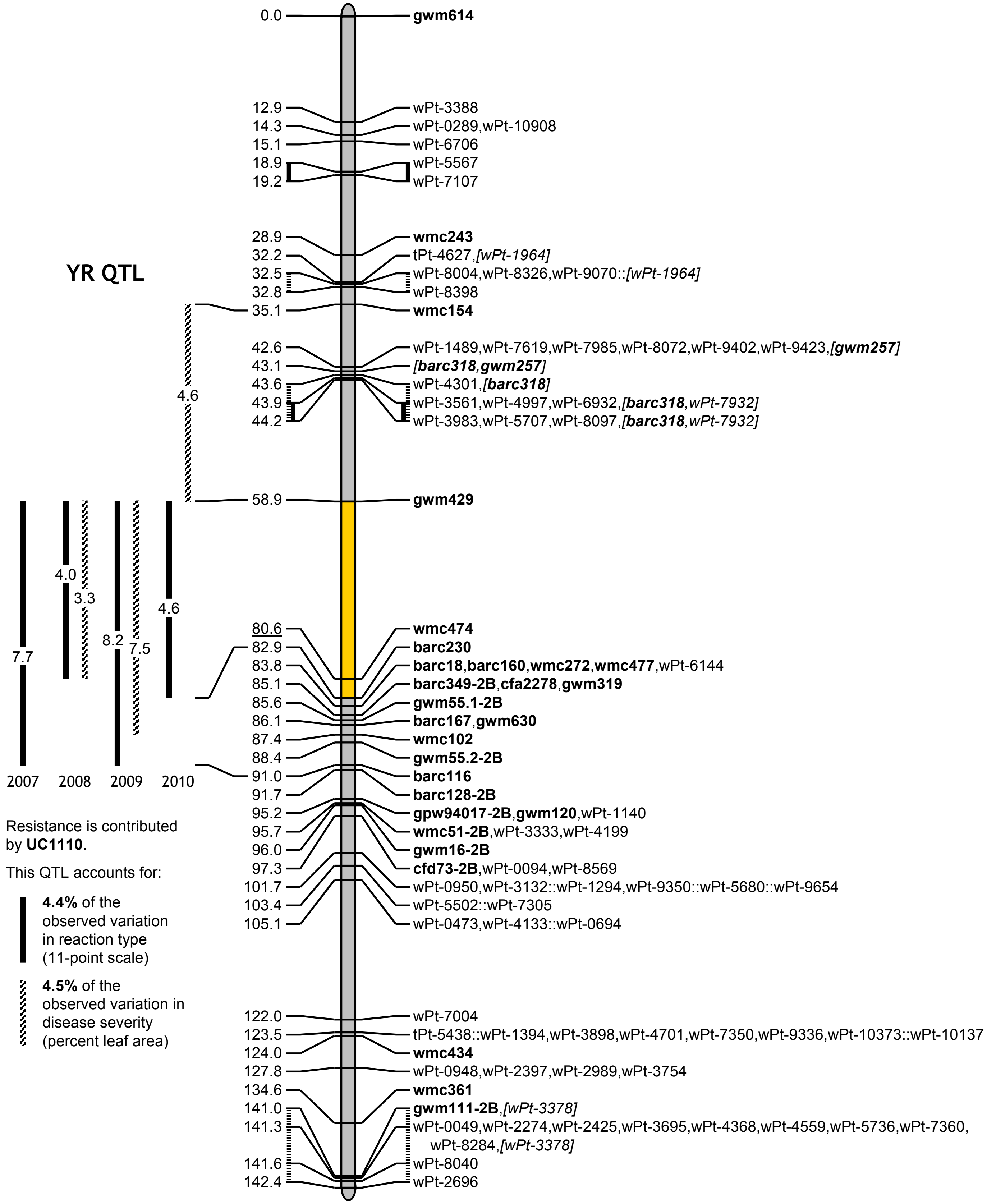


Resistance is contributed by **PI610750**.

This QTL accounts for:

- ▮ **1.3%** of the observed variation in reaction type (11-point scale)
- ▨ **2.2%** of the observed variation in disease severity (percent leaf area)

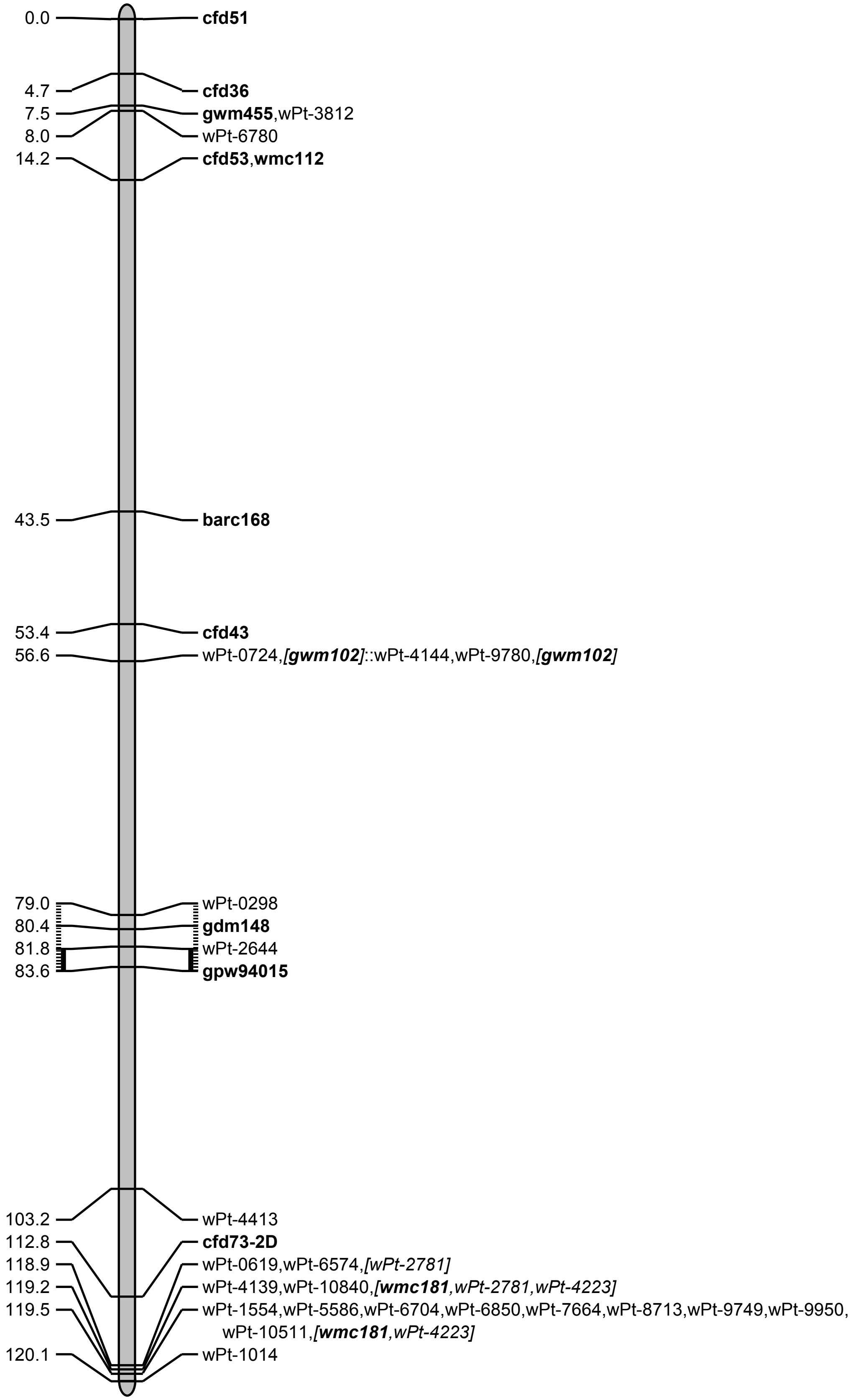
Chromosome 2B | 98 probes mapped to 43 loci; total length 142.4 cM



Chromosome 2D | 36 probes mapped to 18 loci; total length 120.1 cM

YR QTL

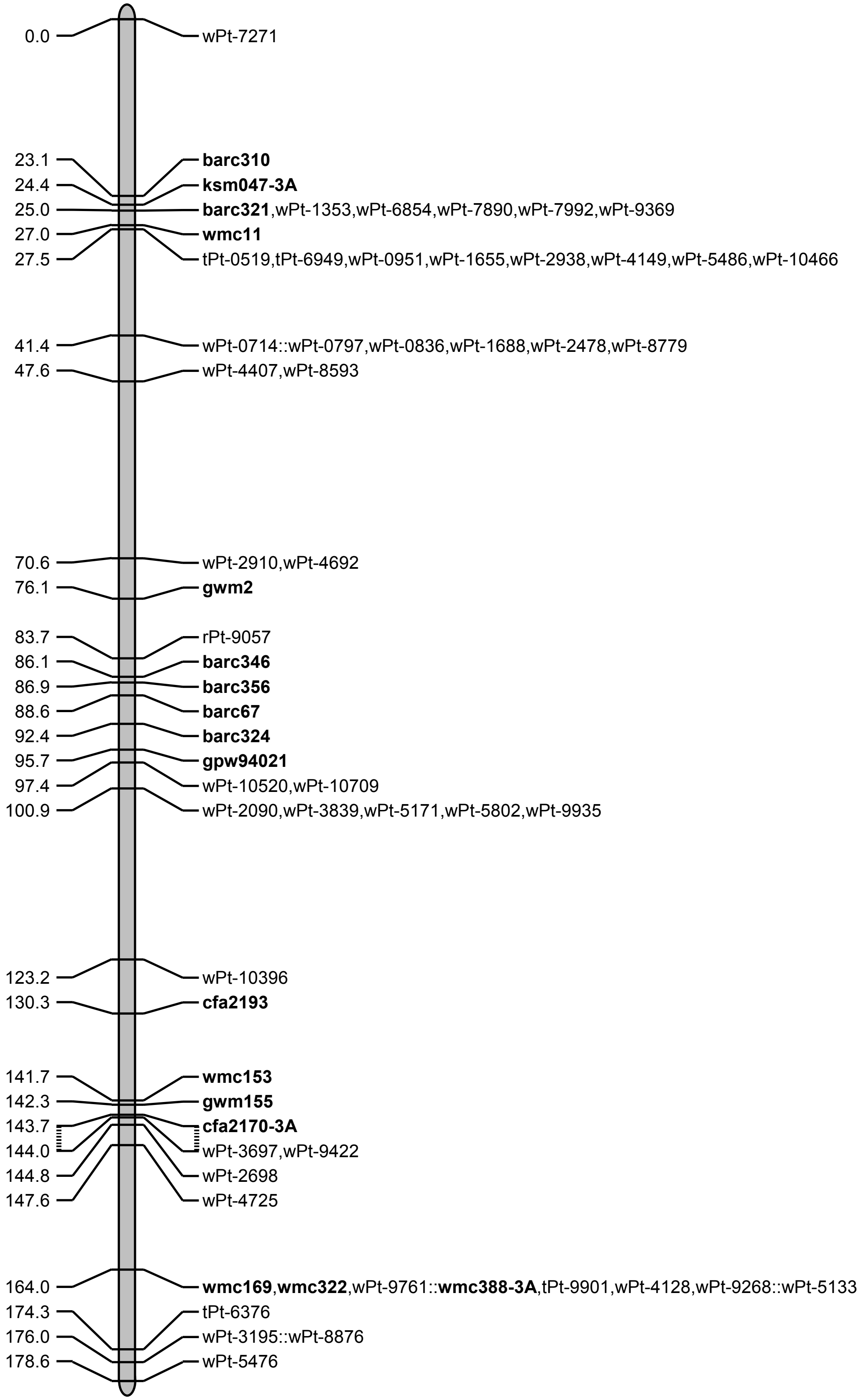
(none)



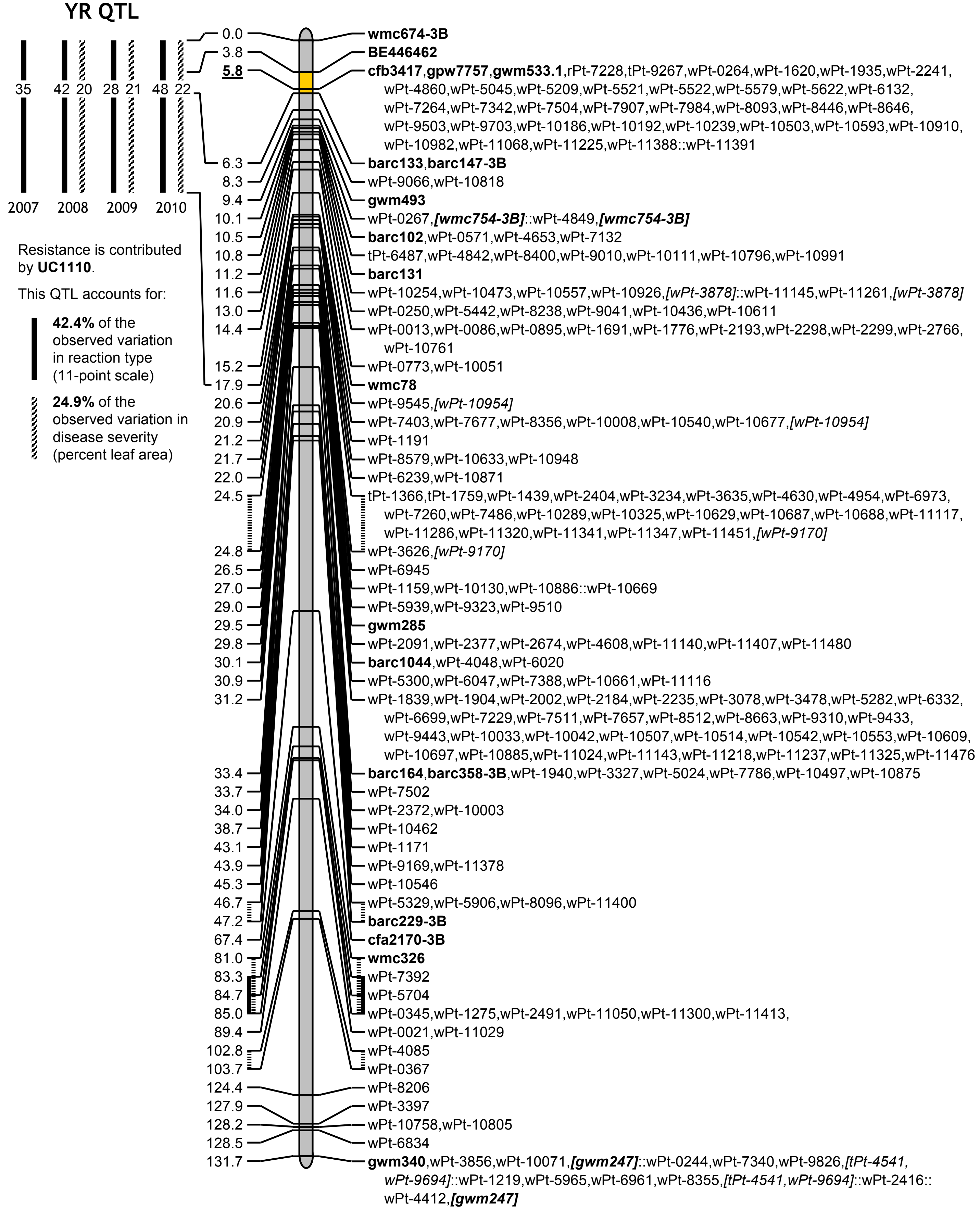
Chromosome 3A | 63 probes mapped to 30 loci; total length 178.6 cM

YR QTL

(none)



Chromosome 3B | 236 probes mapped to 52 loci; total length 131.7 cM



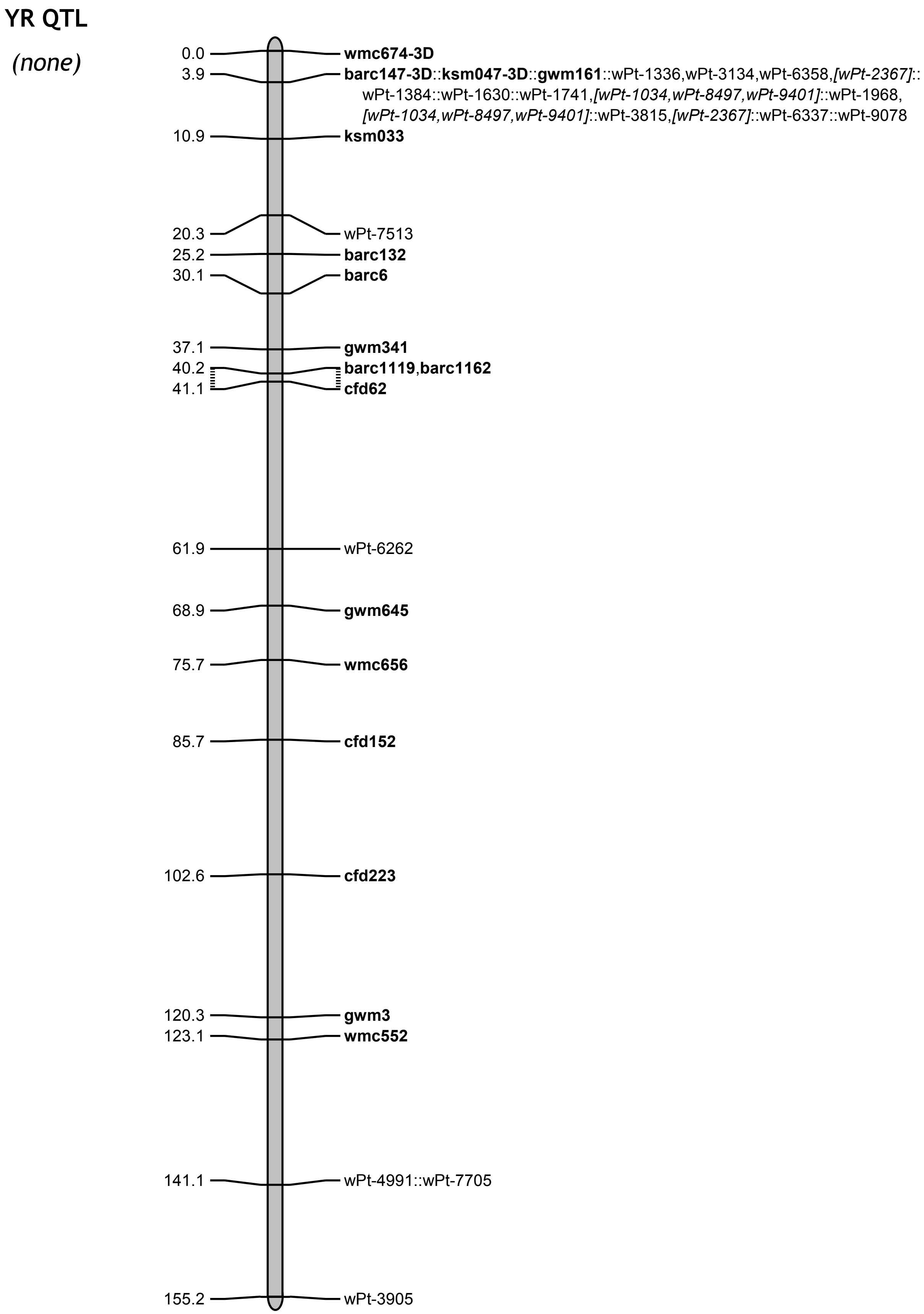
Resistance is contributed by **UC1110**.

This QTL accounts for:

42.4% of the observed variation in reaction type (11-point scale)

24.9% of the observed variation in disease severity (percent leaf area)

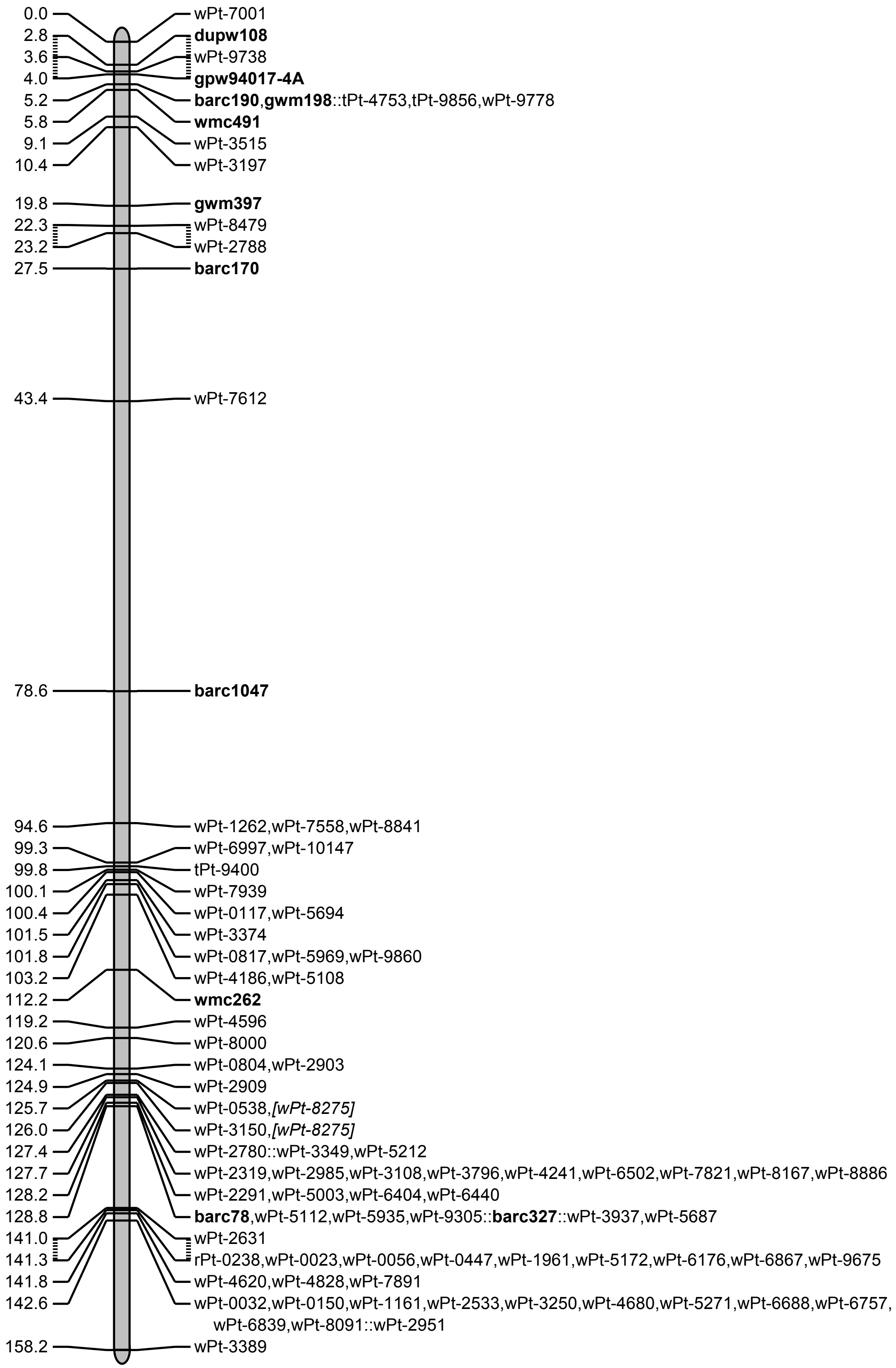
Chromosome 3D | 36 probes mapped to 18 loci; total length 155.2 cM



Chromosome 4A | 91 probes mapped to 38 loci; total length 158.2 cM

YR QTL

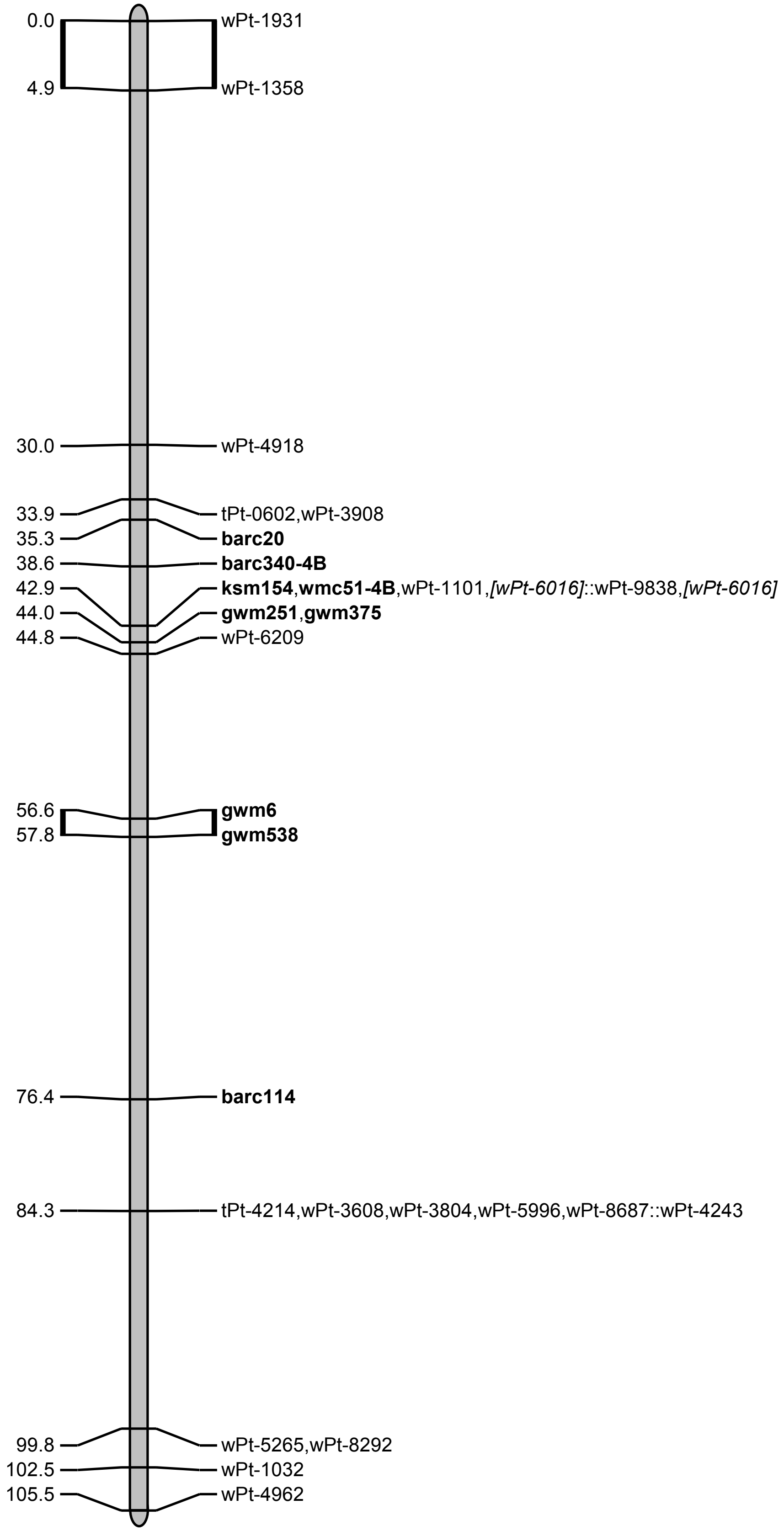
(none)



Chromosome 4B | 28 probes mapped to 16 loci; total length 105.5 cM

YR QTL

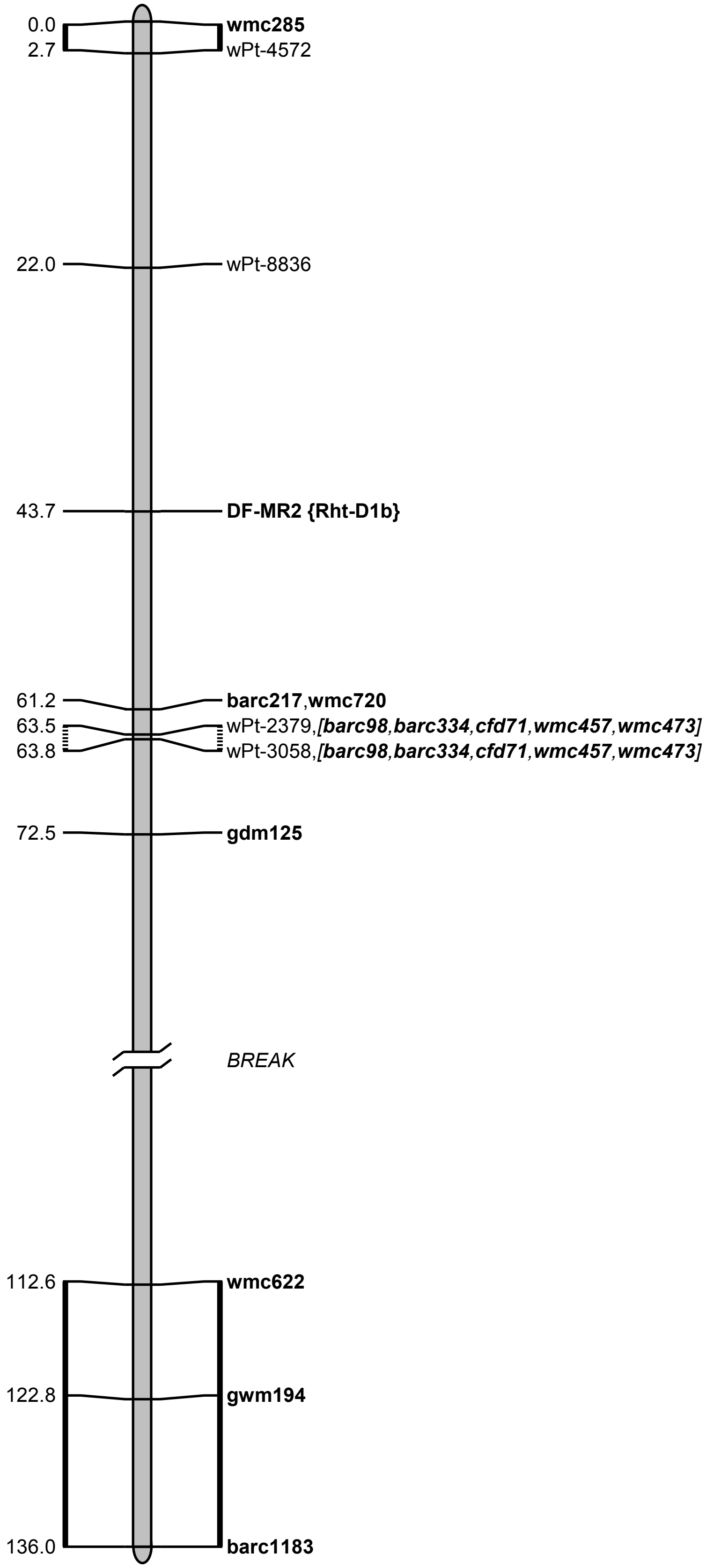
(none)



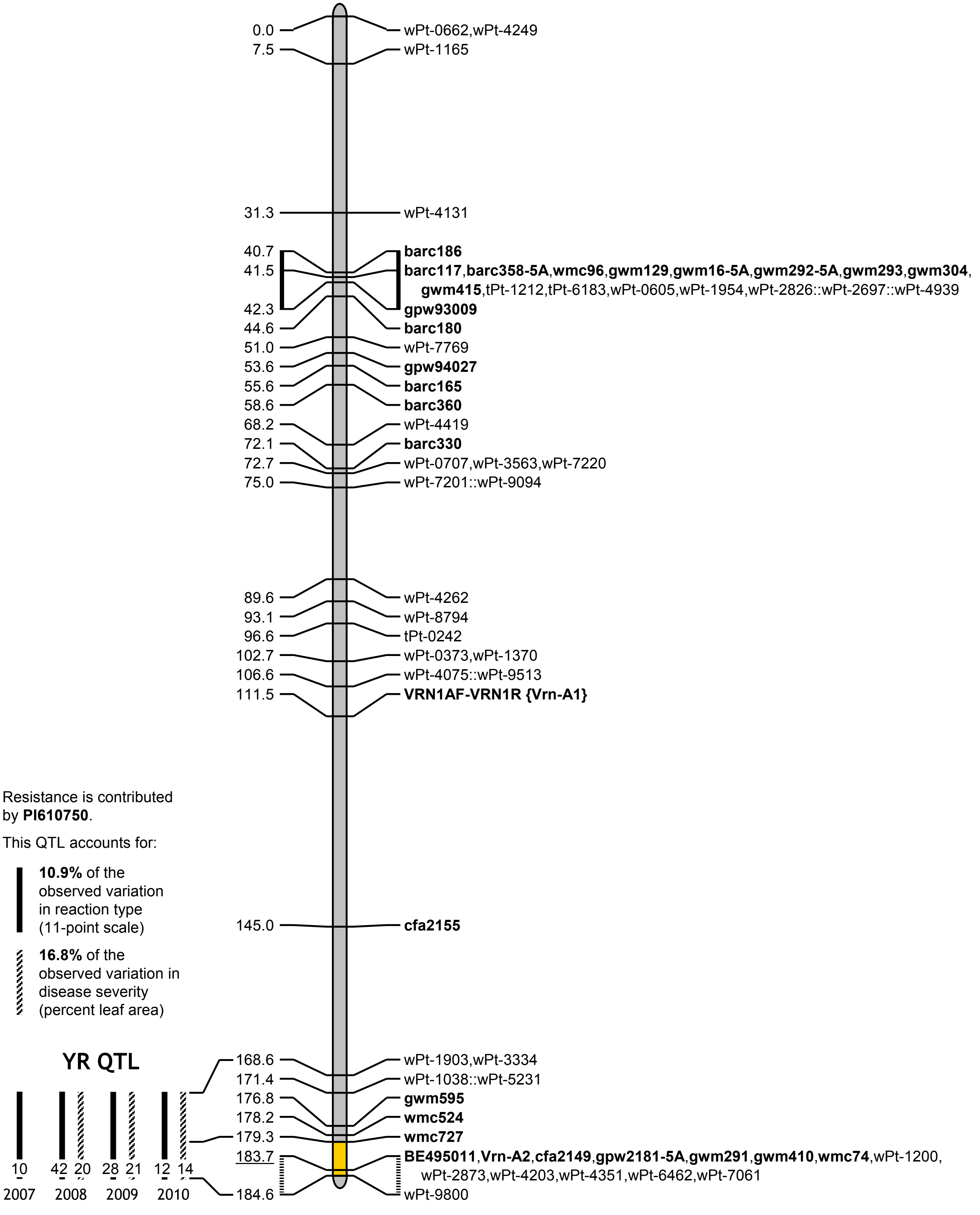
Chromosome 4D | 17 probes mapped to 11 loci; total length 136.0 cM

YR QTL

(none)



Chromosome 5A | 64 probes mapped to 29 loci; total length 184.6 cM



Resistance is contributed by **PI610750**.

This QTL accounts for:

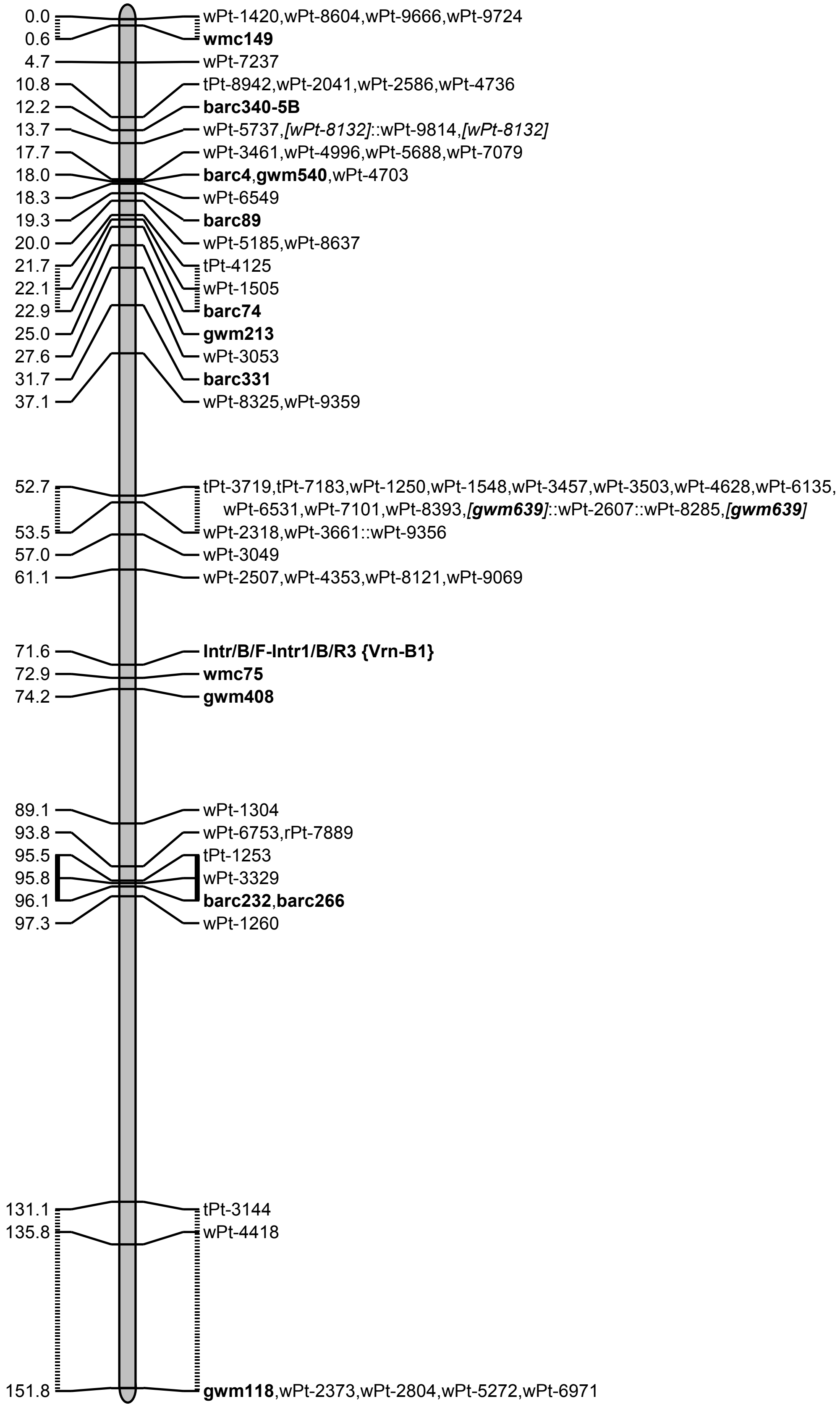
10.9% of the observed variation in reaction type (11-point scale)

16.8% of the observed variation in disease severity (percent leaf area)

Chromosome 5B | 73 probes mapped to 34 loci; total length 151.8 cM

YR QTL

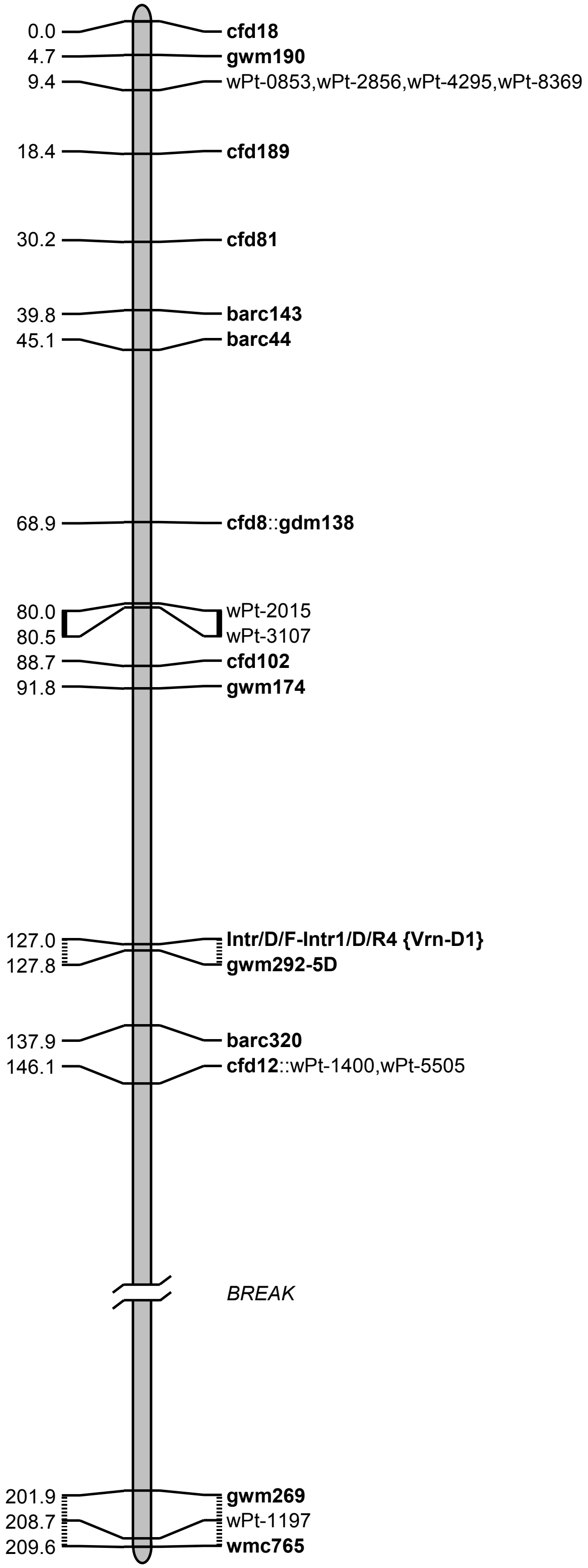
(none)



Chromosome 5D | 25 probes mapped to 19 loci; total length 209.6 cM

YR QTL

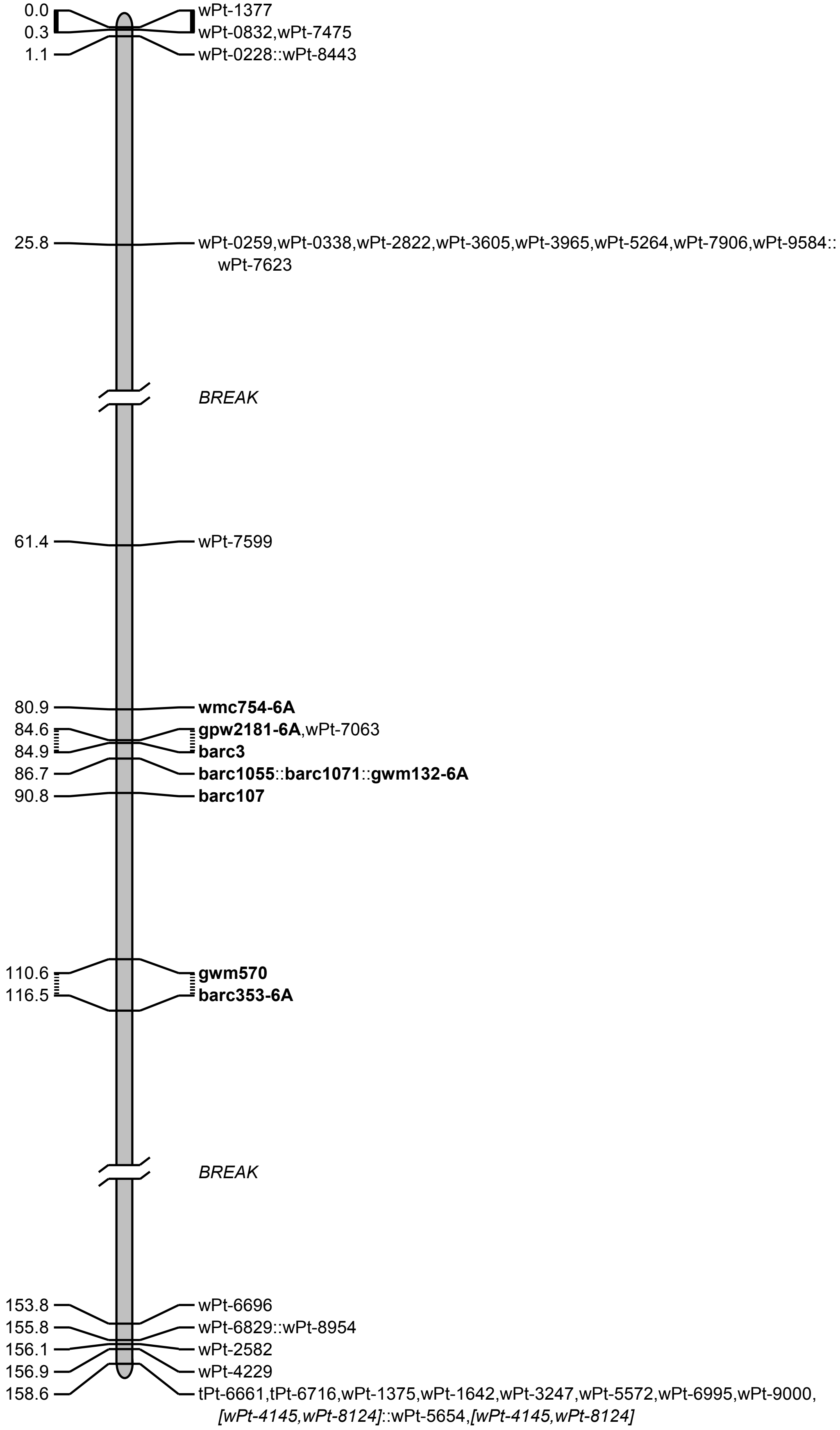
(none)



Chromosome 6A | 41 probes mapped to 17 loci; total length 158.6 cM

YR QTL

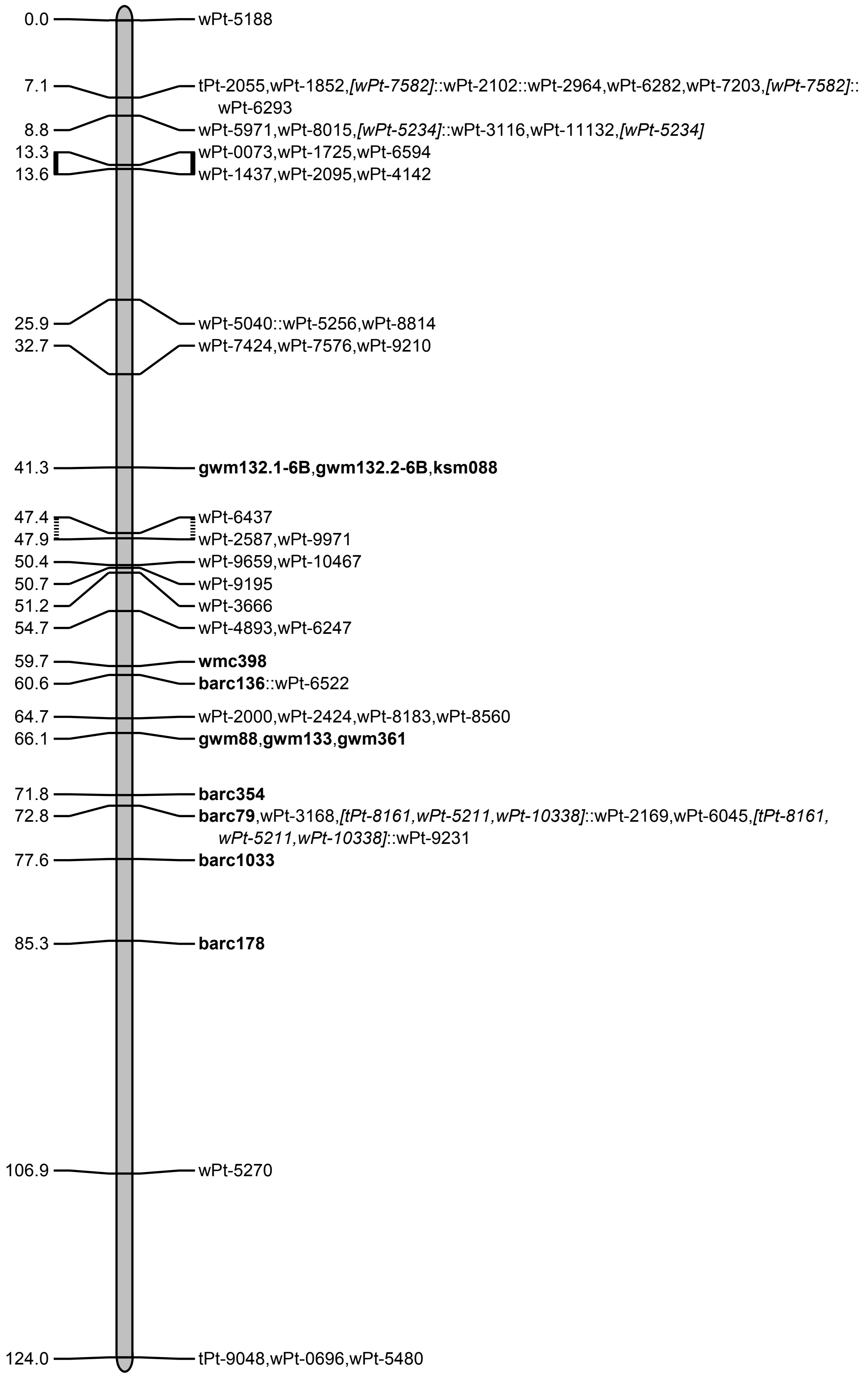
(none)



Chromosome 6B | 63 probes mapped to 24 loci; total length 124.0 cM

YR QTL

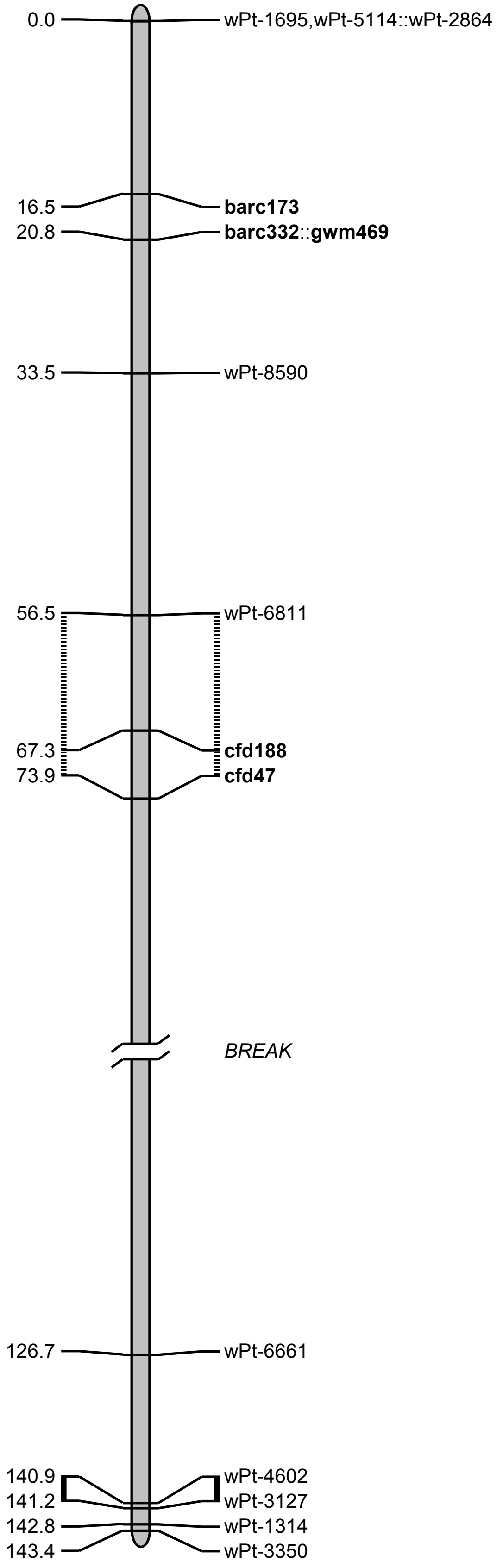
(none)



Chromosome 6D | 15 probes mapped to 12 loci; total length 143.4 cM

YR QTL

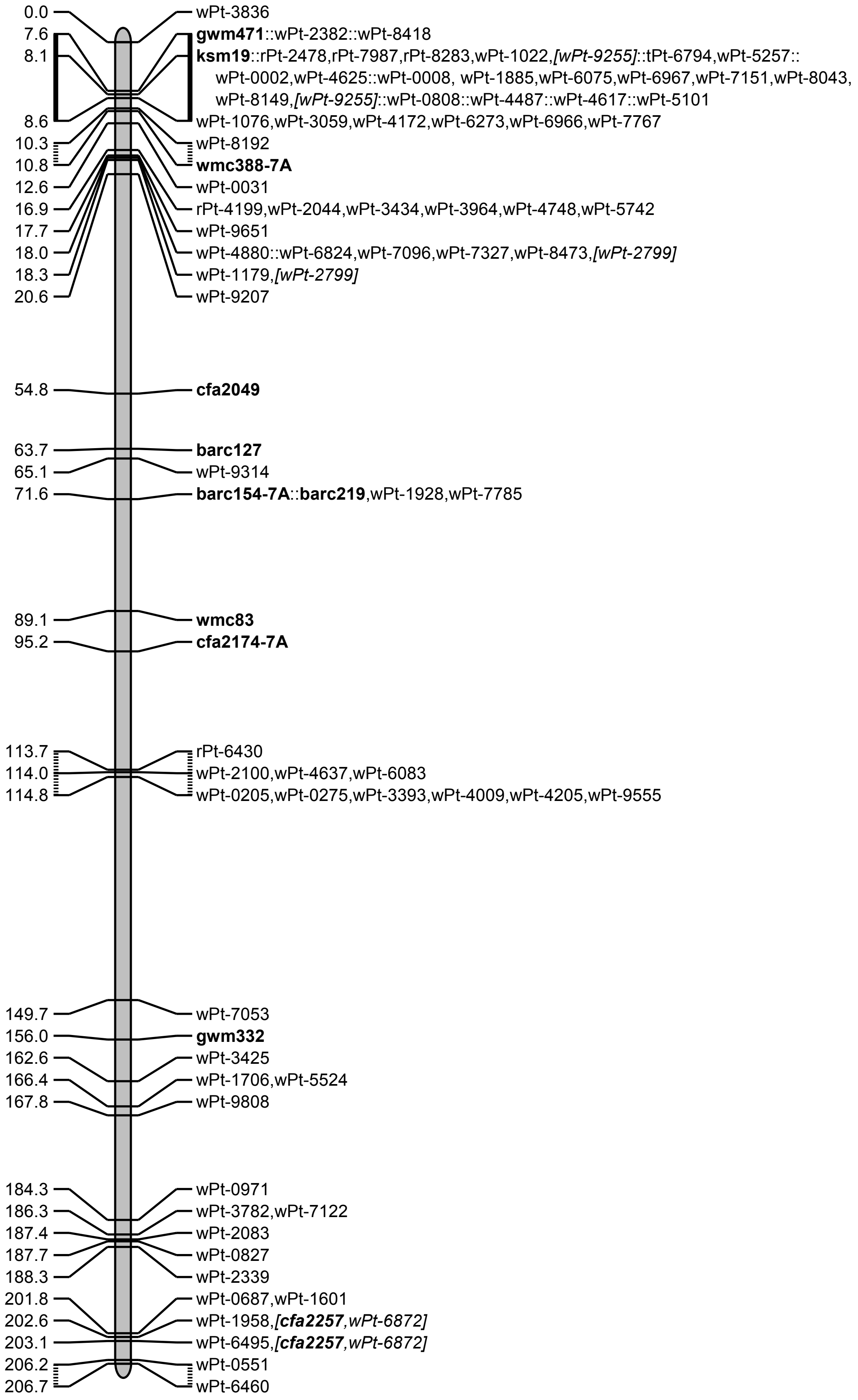
(none)



Chromosome 7A | 88 probes mapped to 36 loci; total length 206.7 cM

YR QTL

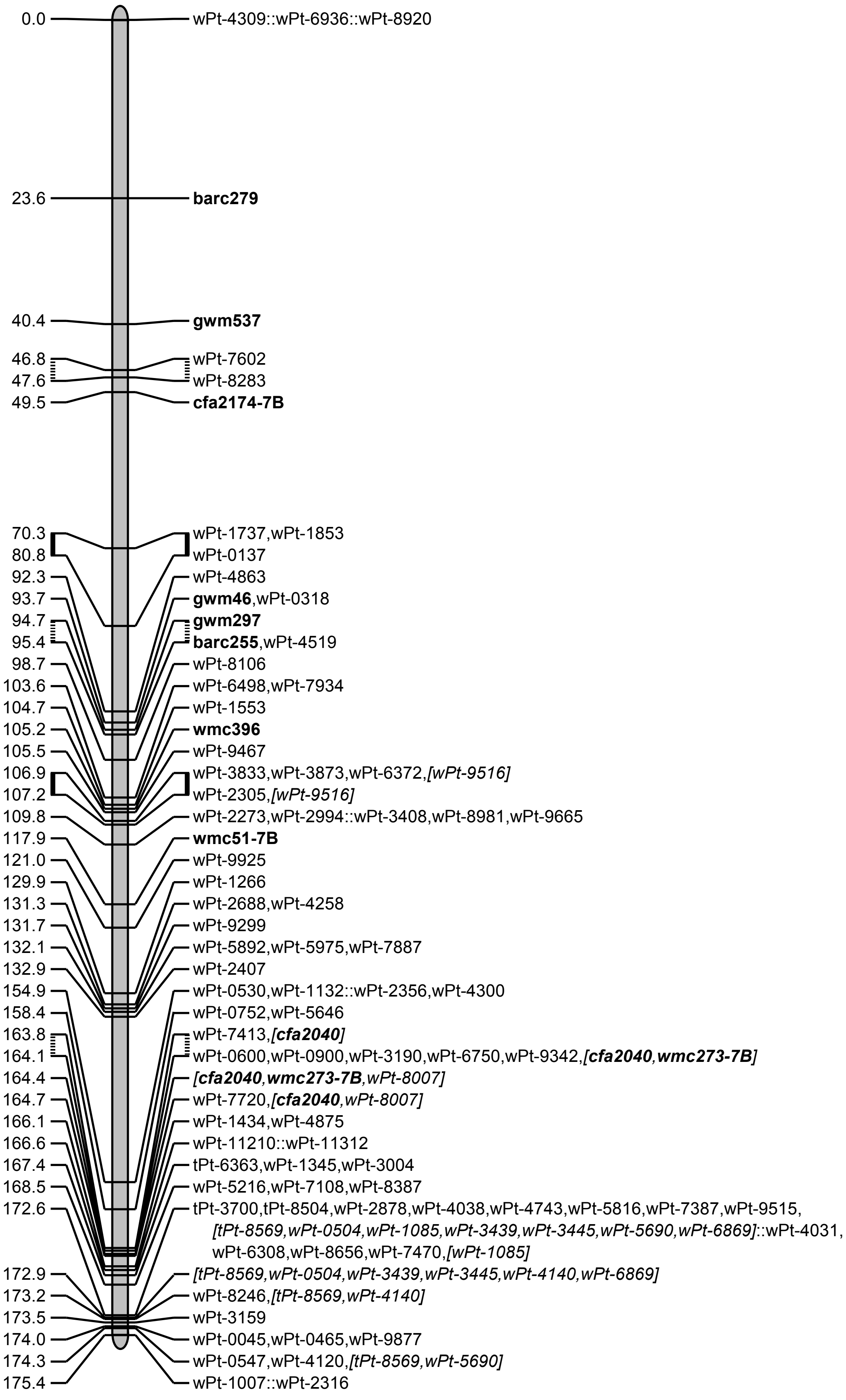
(none)



Chromosome 7B | 98 probes mapped to 44 loci; total length 175.4 cM

YR QTL

(none)



Chromosome 7D | 29 probes mapped to 19 loci; total length 146.0 cM

YR QTL

(none)