# Summary of QTL mapping population

## 1 Summary

Cross type F2 intercross

Number of individuals 150

Number of phenotypes 1 Percent phenotyped 100

Number of chromosomes 7

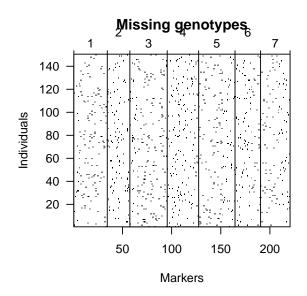
Autosomes 1 2 3 4 5 6 7

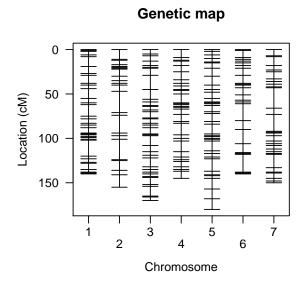
Total markers 220

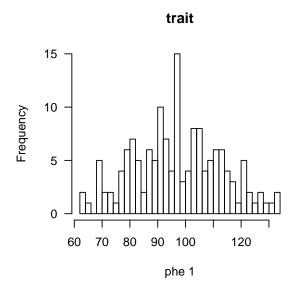
Number of markers 34 23 38 32 37 26 30

Percent genotyped 97

Genotypes(%) AA:25.2 AB:49.7 BB:25.1 not BB:0.0 not AA:0.0

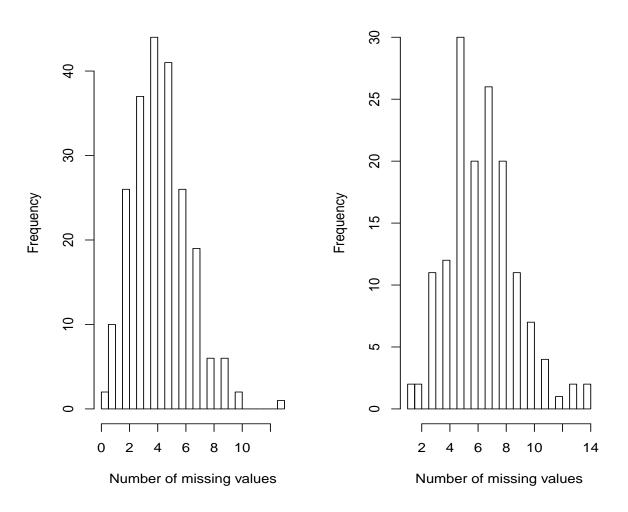






#### Missing values per marker

#### Missing values per individual

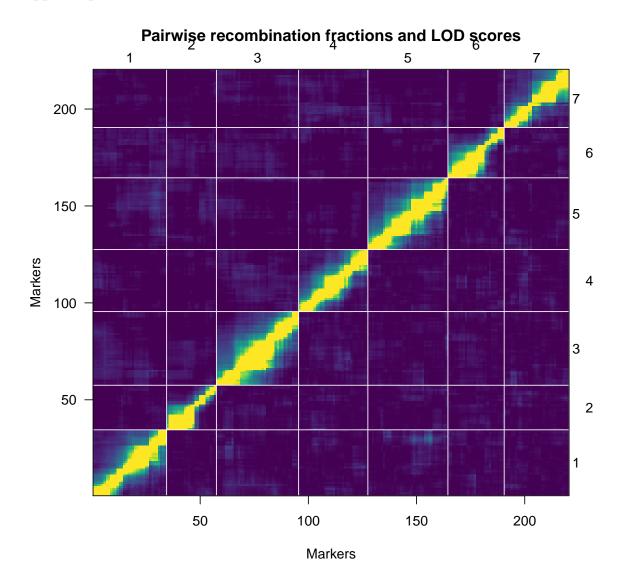


### 2 Segregation distortion

Markers that show evidence of segregation distortion.

## 3 Marker recombinations

Recombination frequencies No apparent problems.



Number of recombinations per chromosome per individual Mean number of recombinations per chromosome per individual: 2.67

Table 1: Individuals with highest number of recombinations per chromosome

	1	2	3	4	5	6	7	mean
44	5	4	4	4	6	3	5	4.43
13	7	4	2	4	5	5	2	4.14
22	1	7	4	4	3	4	5	4.00
150	2	4	5	4	5	5	3	4.00
59	3	3	9	3	2	4	3	3.86
134	2	4	4	6	5	2	4	3.86
39	3	4	4	3	5	4	3	3.71
45	4	4	6	2	5	3	2	3.71
46	4	5	5	3	3	1	5	3.71
68	5	2	3	4	4	3	5	3.71
125	7	3	2	5	6	1	2	3.71
128	4	4	3	3	5	2	5	3.71
61	5	4	4	4	2	3	3	3.57
84	4	5	3	3	4	3	3	3.57
137	2	2	5	5	2	4	5	3.57