

Figure 1. Distribution of the total number of genotyped individuals (left panel) and the total number of informative individuals (right panel) for each *minK* value and in the full-ped configurations in the simulation study.

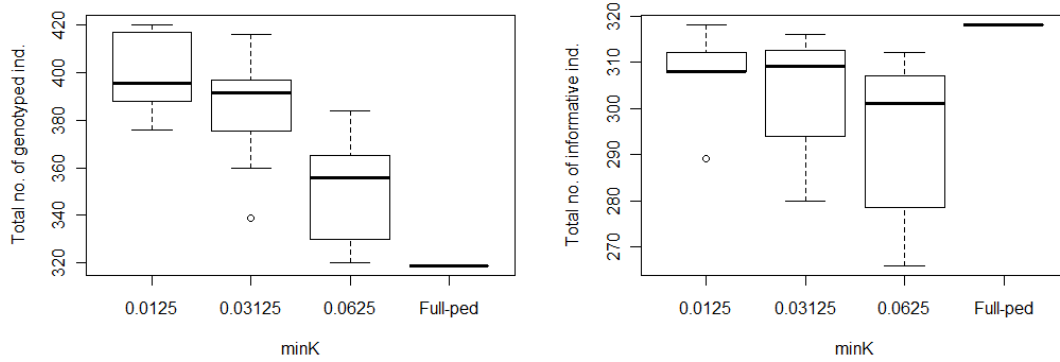


Figure 2. Ratio between the power of the MS over the power of the full-ped analysis according to the proportion of variance explained by the QTL (h_{QTL}^2) by significance level α and summary statistic.

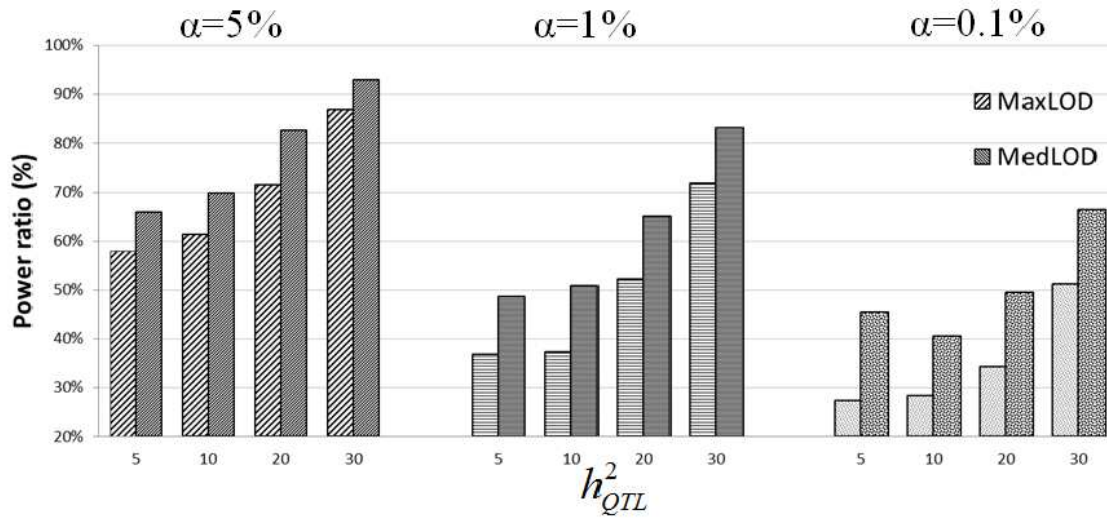


Figure 3. Distribution of the total number of genotyped individuals (left panel) and the total number of informative individuals (right panel) for each *minK* value and in the full-ped configurations in the real case scenario.

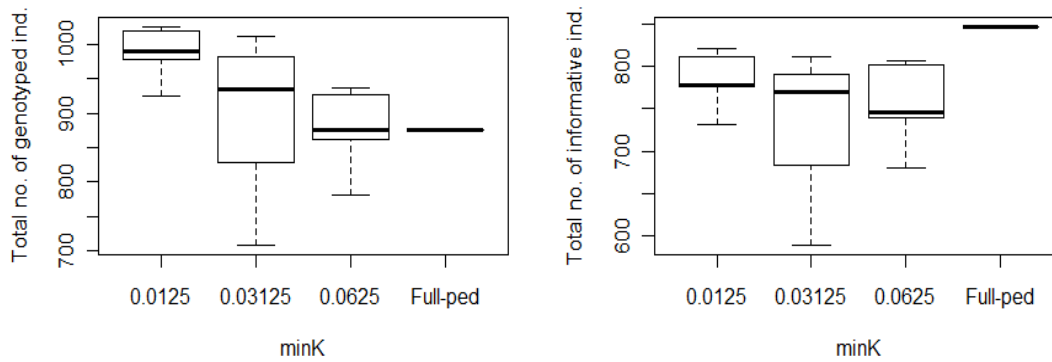


Figure 4. Distribution of heritability (%) for each *minK* value in the real case scenario.

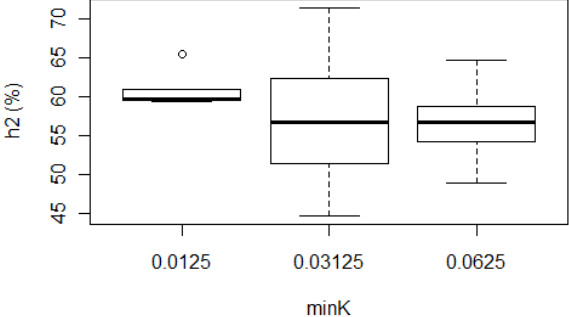


Figure 5. Distribution of heritability (%) according to the quantile distribution of the number of individuals (A), the number of informative individuals (B), the number of genotyped individuals (C) and the number of phenotyped individuals (D) in the real case scenario.

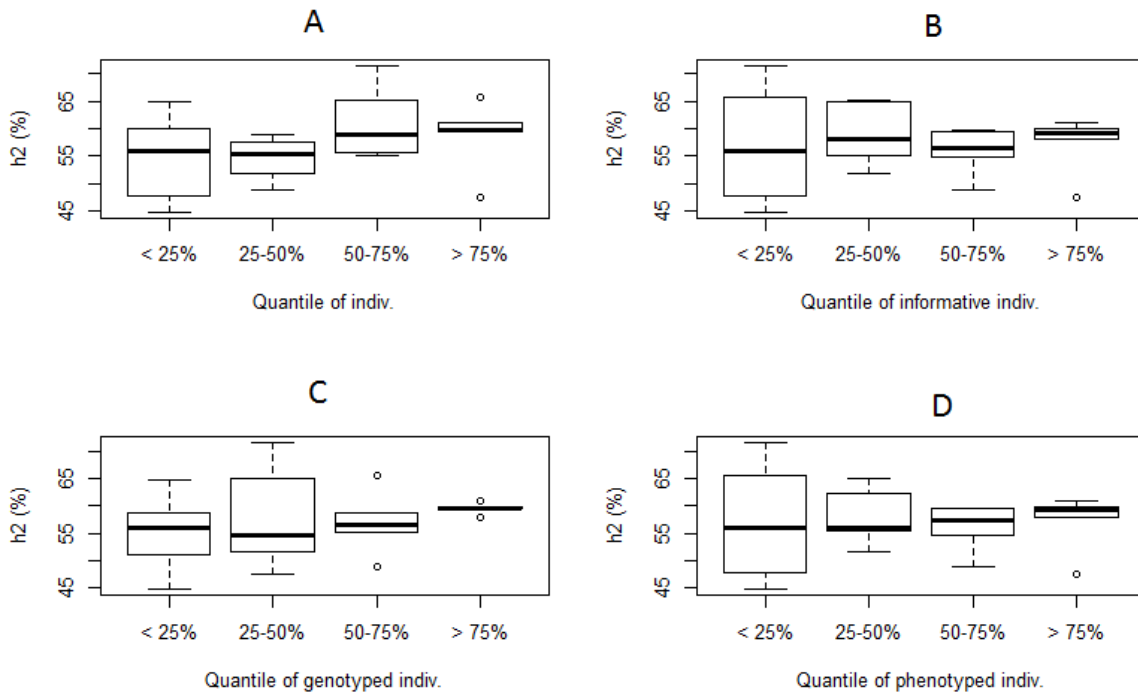


Figure 6. MS analysis on chromosome 22. LOD-score distribution of each pedigree configuration based on STR (left panels) and SNP (right panels) arrays. The STR and SNP positions are shown on the top and bottom horizontal axes, respectively. In each of the panels, scans from the pedigrees obtained with a *minK* of 0.0125, 0.03125, and 0.0625, are highlighted in blue, red, and green, respectively. Vertical dotted lines indicate the reference 1-LOD region from [18].

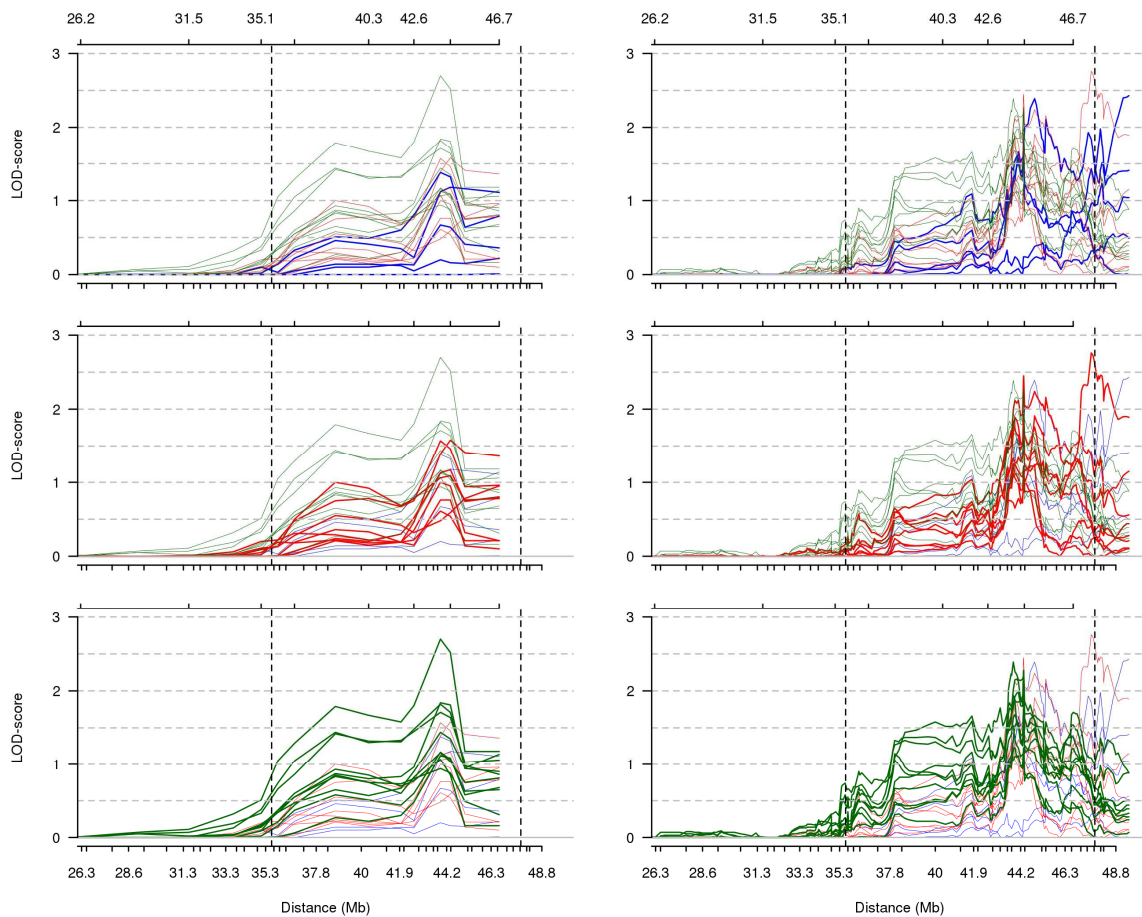


Table 1. Characteristics of the pedigree before splitting.

	Pedigree used for simulation	Pedigree used in the real-case scenario
Relative pairs		
Parent/Offspring	908	3,126
Sib/Sib	491	1,417
Grandparents	1,174	3,506
Avuncular	1,403	3,511
Half sib	5	32
Cousin	1,670	3,640
Loops	43	110
Individuals characteristics		
Male	294	1,116
Female	304	1,103
Founder	144	656
Non-founder	454	1,563
Total	598	2,219

Table 2. Asymptotic and empirical significance LOD-score thresholds at $\alpha = 5\%$, 1% , and 0.1% in the full-ped, in each pedigree configuration, and for the summary statistics used in the MS approach.

Threshold		5.00%	1.00%	0.10%
Full-ped		0.567	1.124	2.068
MS	Ped. conf. no. 1	0.551	1.077	1.868
	Ped. conf. no. 2	0.546	1.084	1.85
	Ped. conf. no. 3	0.554	1.065	1.875
	Ped. conf. no. 4	0.557	1.091	1.858
	Ped. conf. no. 5	0.554	1.081	1.874
	Ped. conf. no. 6	0.543	1.063	1.843
	Ped. conf. no. 7	0.551	1.067	1.776
	Ped. conf. no. 8	0.556	1.074	1.827
	Ped. conf. no. 9	0.559	1.097	1.797
	Ped. conf. no. 10	0.556	1.082	1.876
	Ped. conf. no. 11	0.565	1.102	1.89
	Ped. conf. no. 12	0.556	1.1	1.778
	Ped. conf. no. 13	0.559	1.093	1.892
	Ped. conf. no. 14	0.552	1.085	1.799
	Ped. conf. no. 15	0.558	1.1	1.916
	Ped. conf. no. 16	0.547	1.07	1.81
	Ped. conf. no. 17	0.566	1.109	2.012
	Ped. conf. no. 18	0.547	1.055	1.797
	Ped. conf. no. 19	0.562	1.134	1.878
	Ped. conf. no. 20	0.567	1.129	1.945
	Ped. conf. no. 21	0.574	1.096	1.836
	Ped. conf. no. 22	0.571	1.099	1.919
	Ped. conf. no. 23	0.567	1.116	1.879
	Ped. conf. no. 24	0.563	1.104	1.876
	Ped. conf. no. 25	0.562	1.112	1.937
	Ped. conf. no. 26	0.558	1.101	1.901
	Ped. conf. no. 27	0.564	1.123	1.864
	Ped. conf. no. 28	0.565	1.1	1.875
	Ped. conf. no. 29	0.565	1.102	1.854
	Ped. conf. no. 30	0.555	1.093	1.963
		<i>MaxLOD</i>	1.443	2.072
	<i>MedLOD</i>	0.338	0.669	1.209

*Empirical thresholds based on 45 000 replicates under the hypothesis of no linkage. The asymptotic thresholds derived from a mixture of Chi-squares with 0 and 1 degrees of freedom were 0.588, 1.175 and 2.074 at $\alpha = 5\%$, 1% and 0.1% respectively.