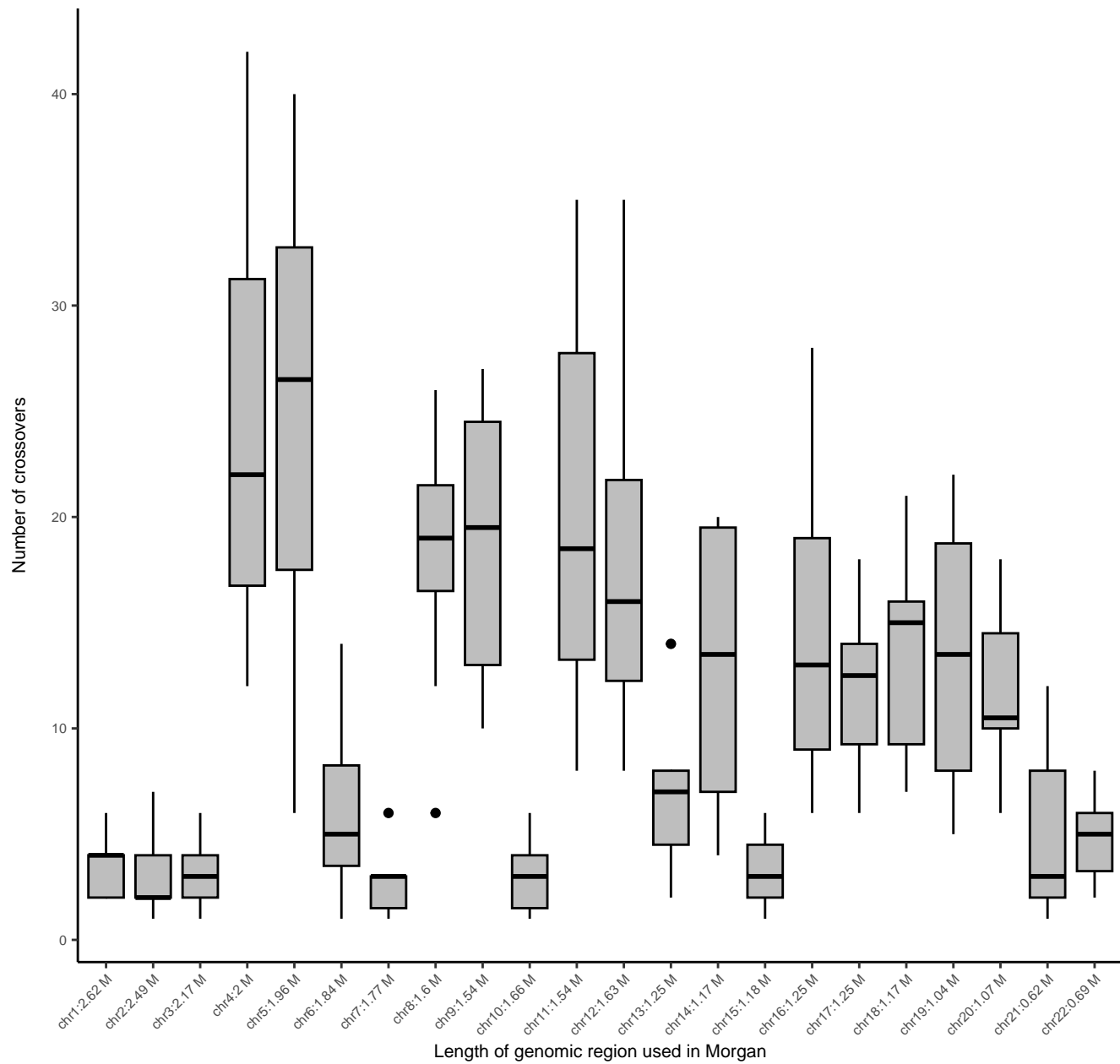
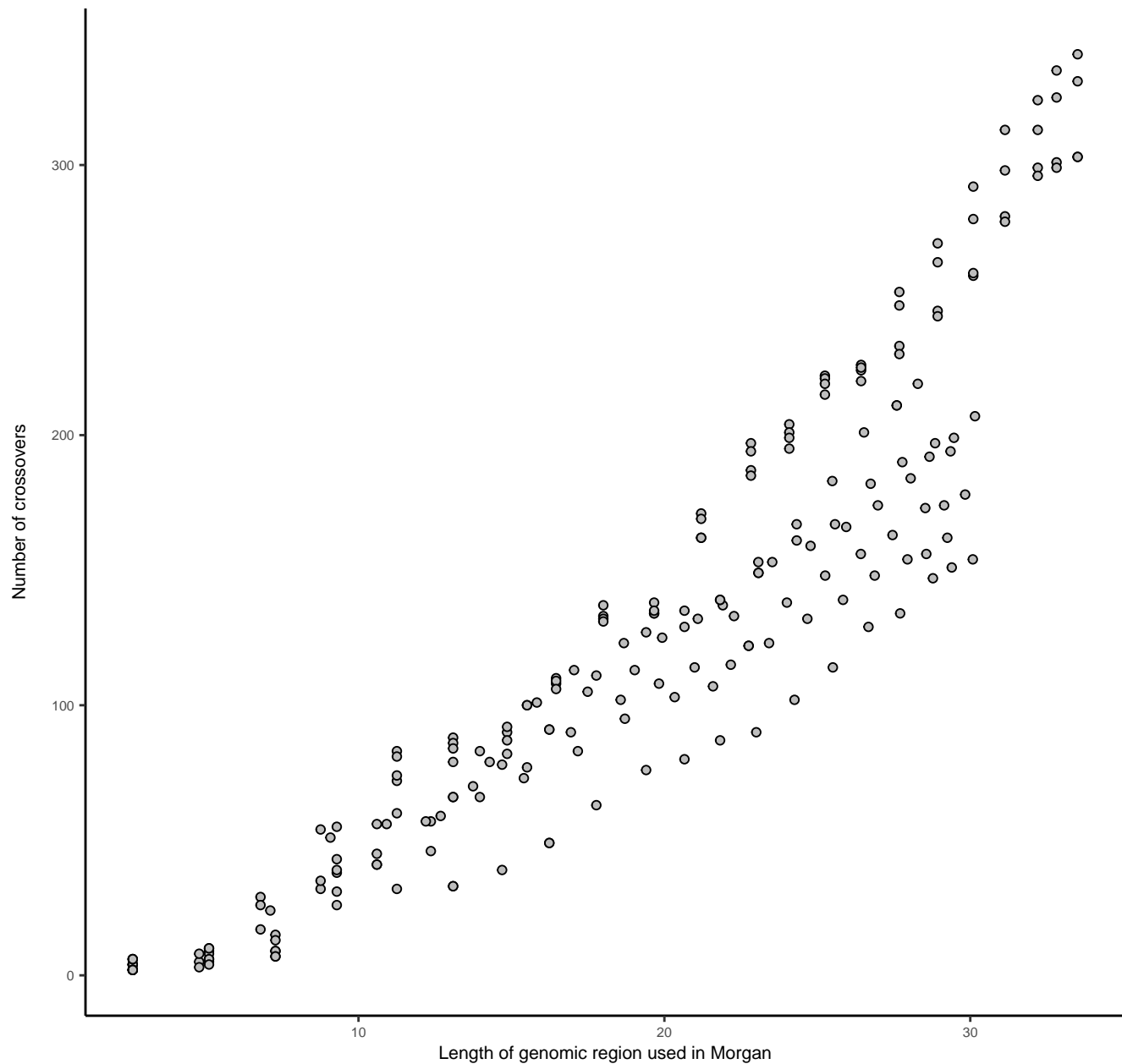


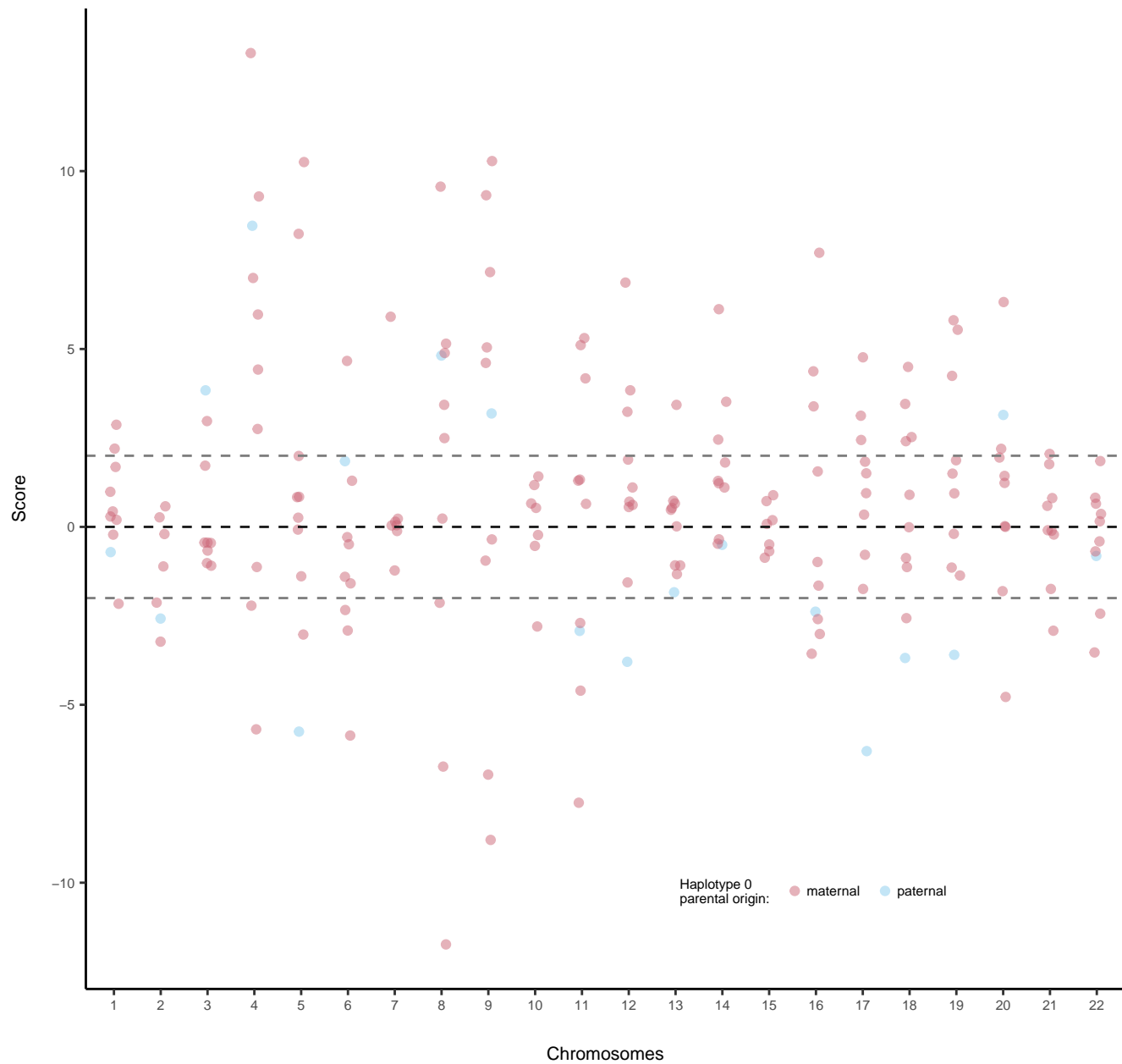
a. Crossover inference  
– intra-chromosomal phased data



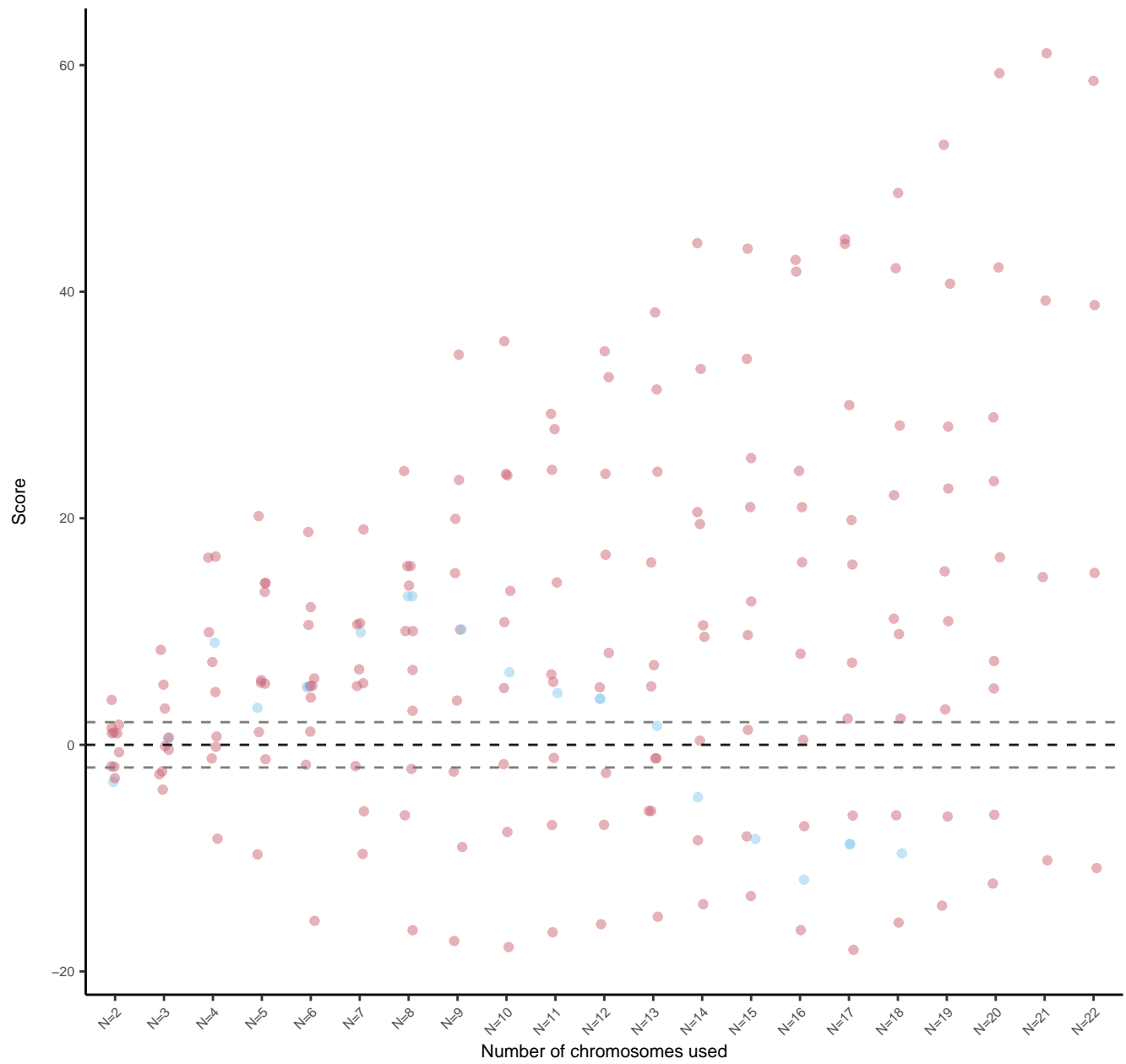
b. Crossover inference  
– inter-chromosomal phased data



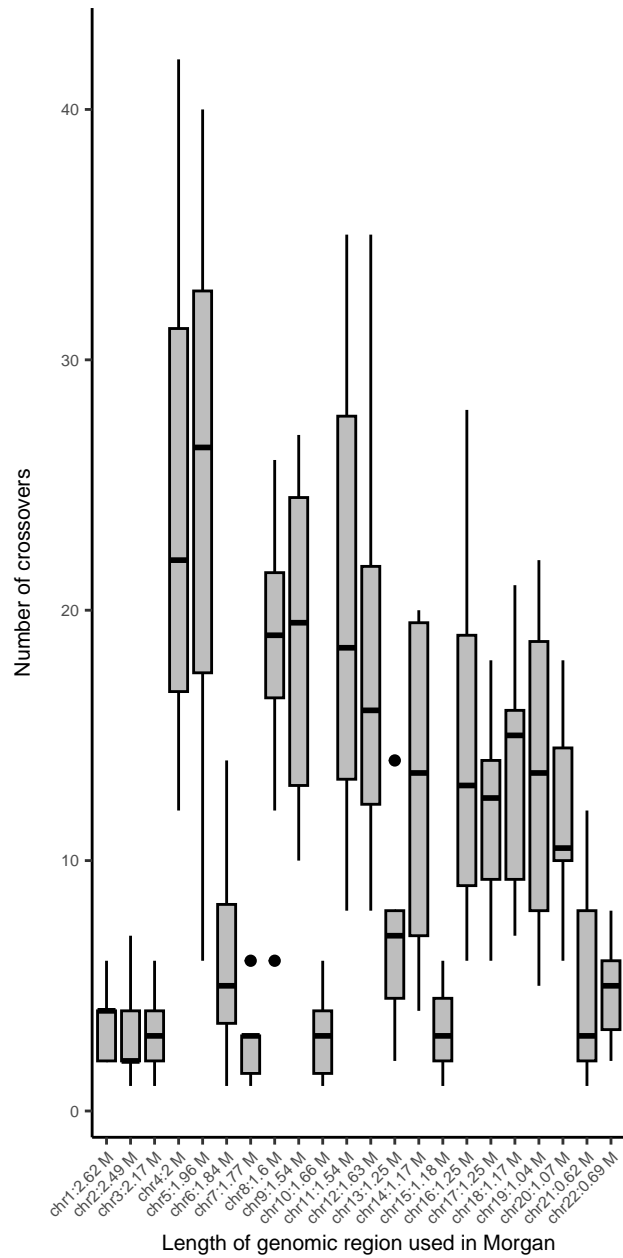
c. Sibling score  
– intra-chromosomal phased data



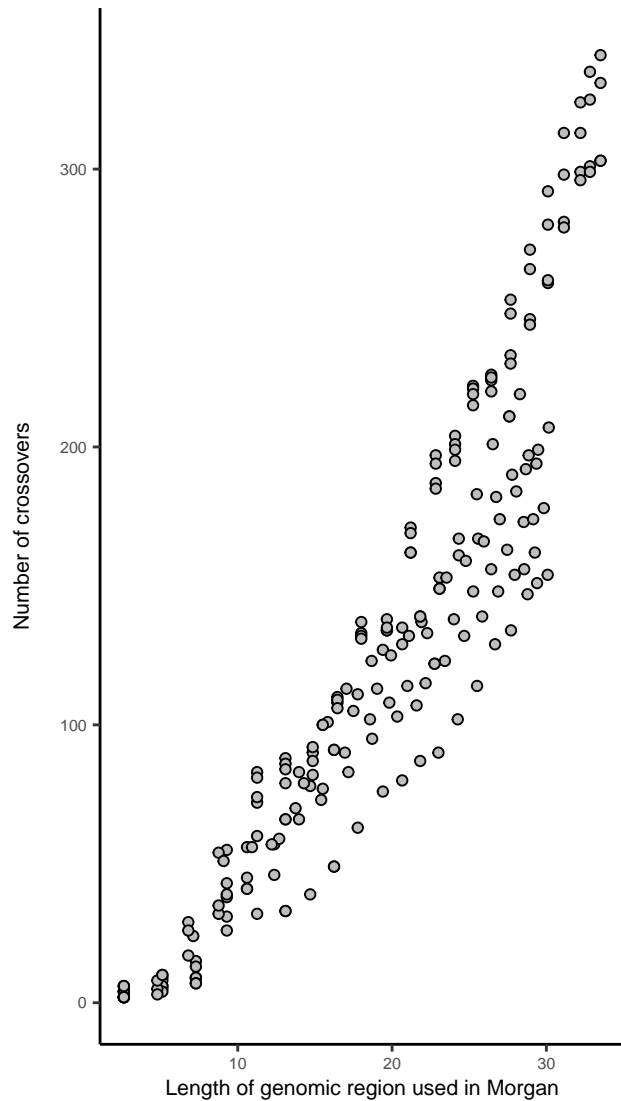
d. Sibling score  
– inter-chromosomal phased data



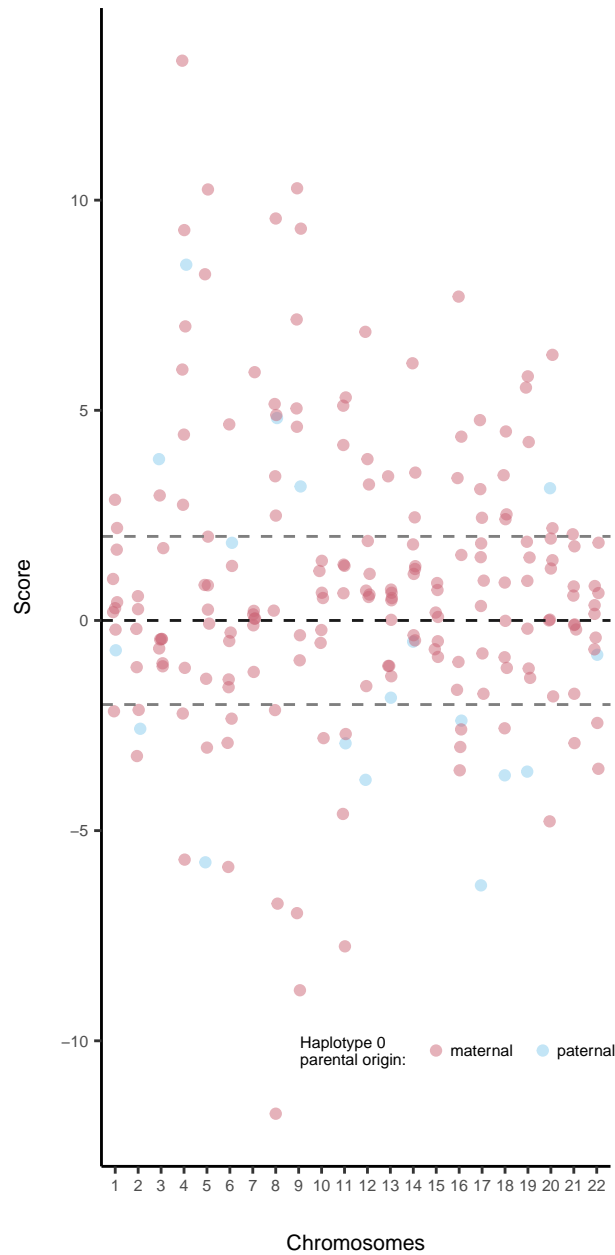
a. Crossover inference  
– intra-chromosomal phased data



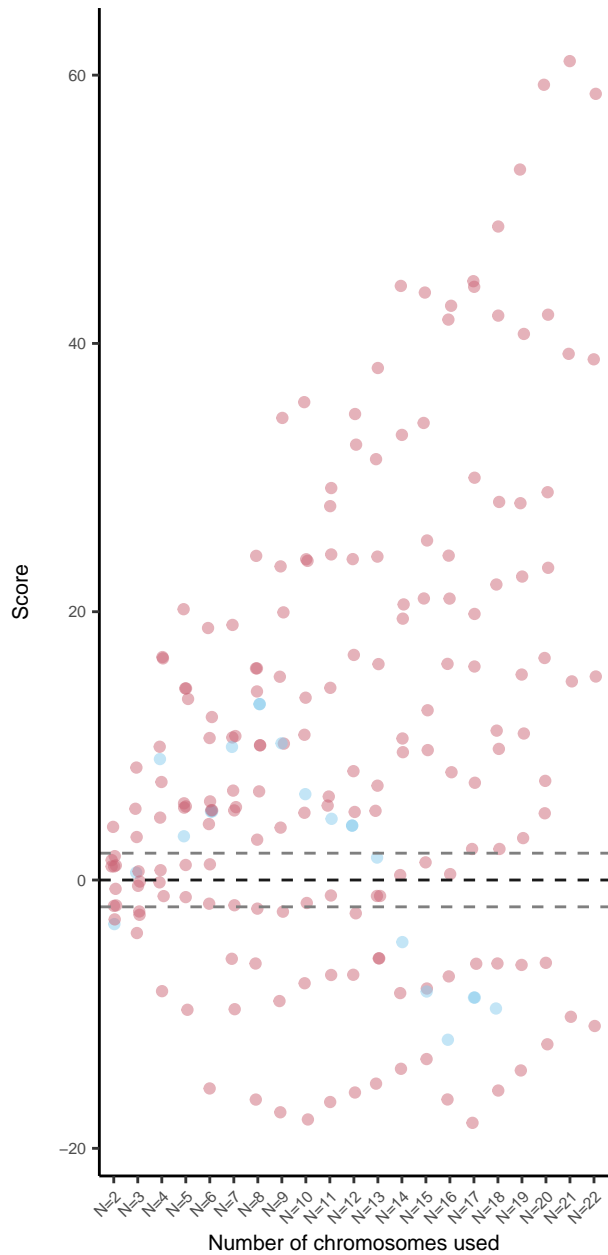
b. Crossover inference  
– inter-chromosomal phased data



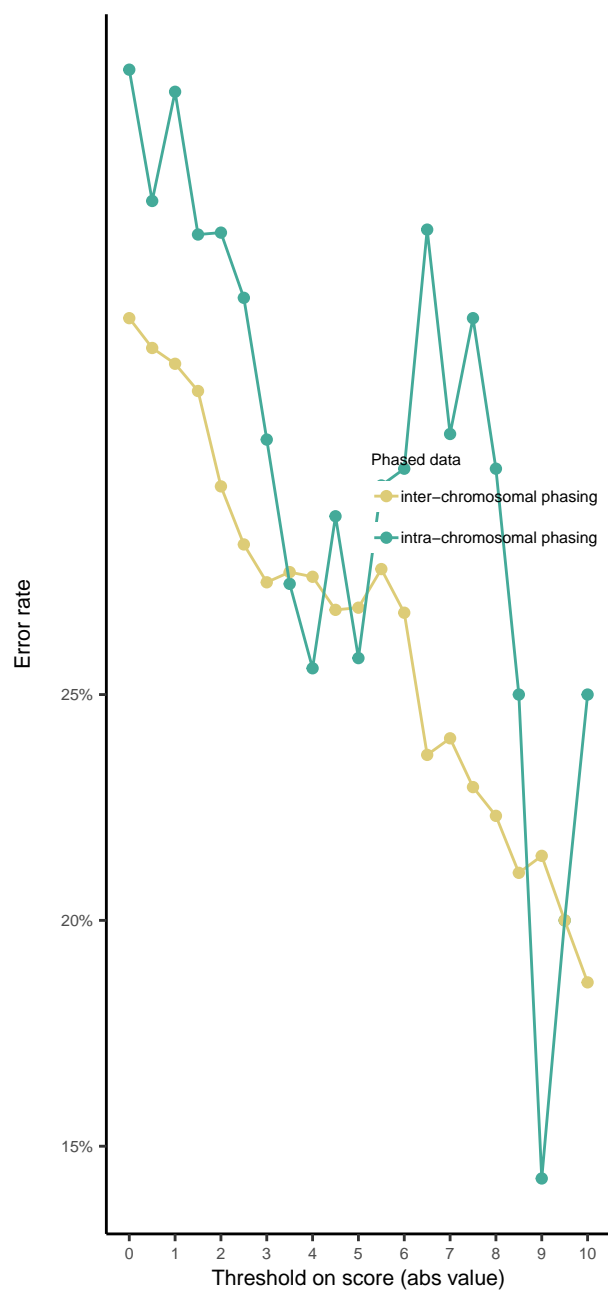
c. Sibling score  
– intra-chromosomal phased data



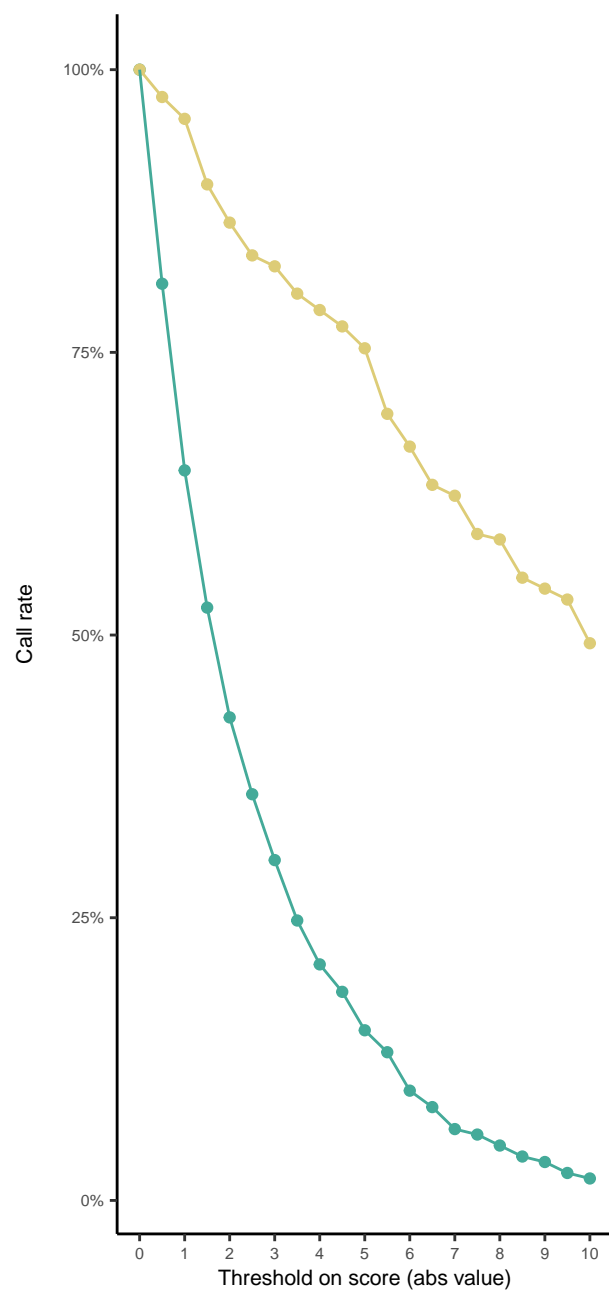
d. Sibling score  
– inter-chromosomal phased data

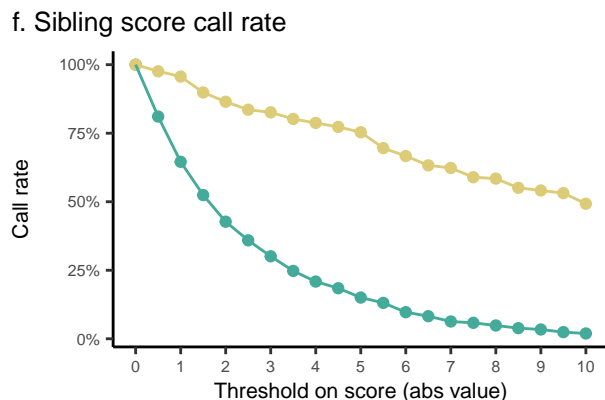
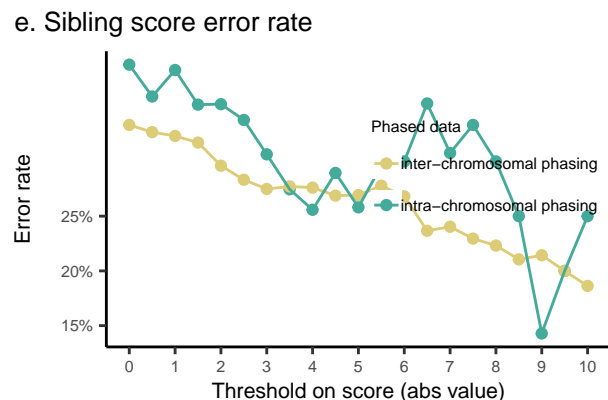
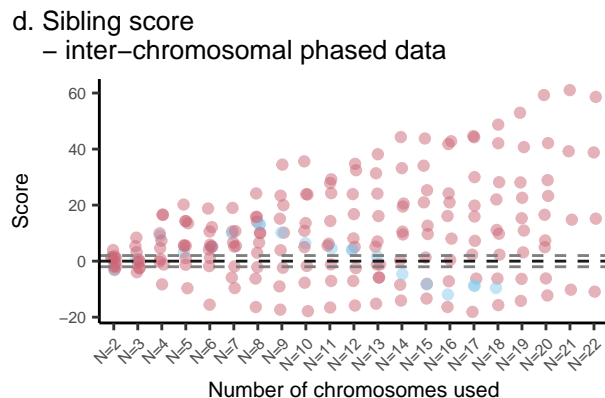
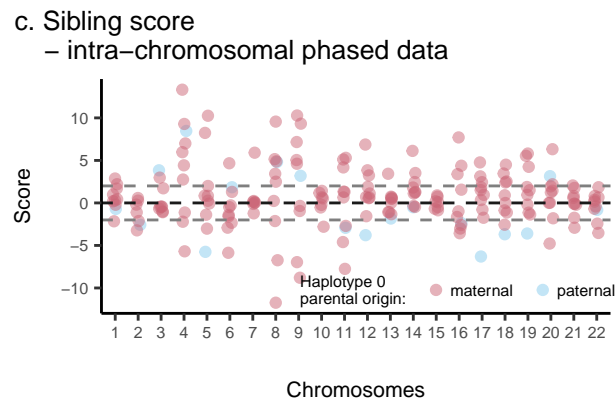
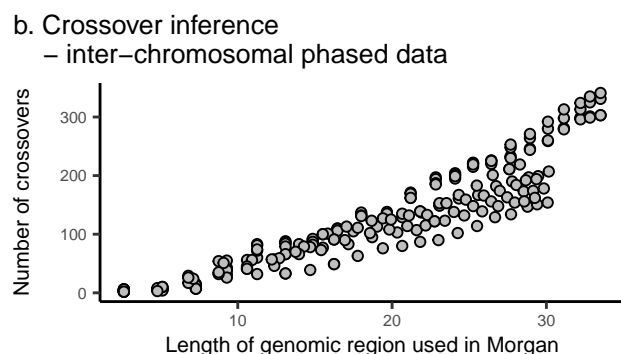
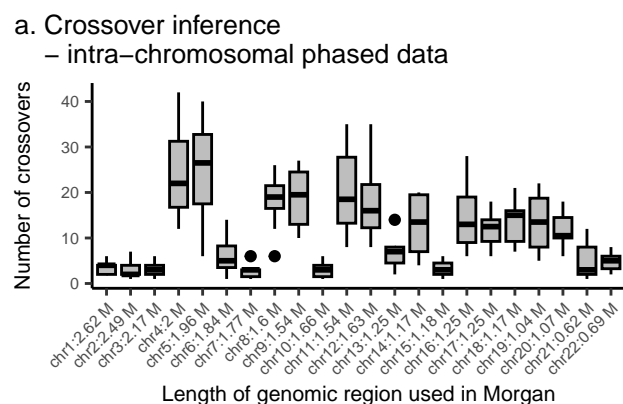


e. Sibling score error rate



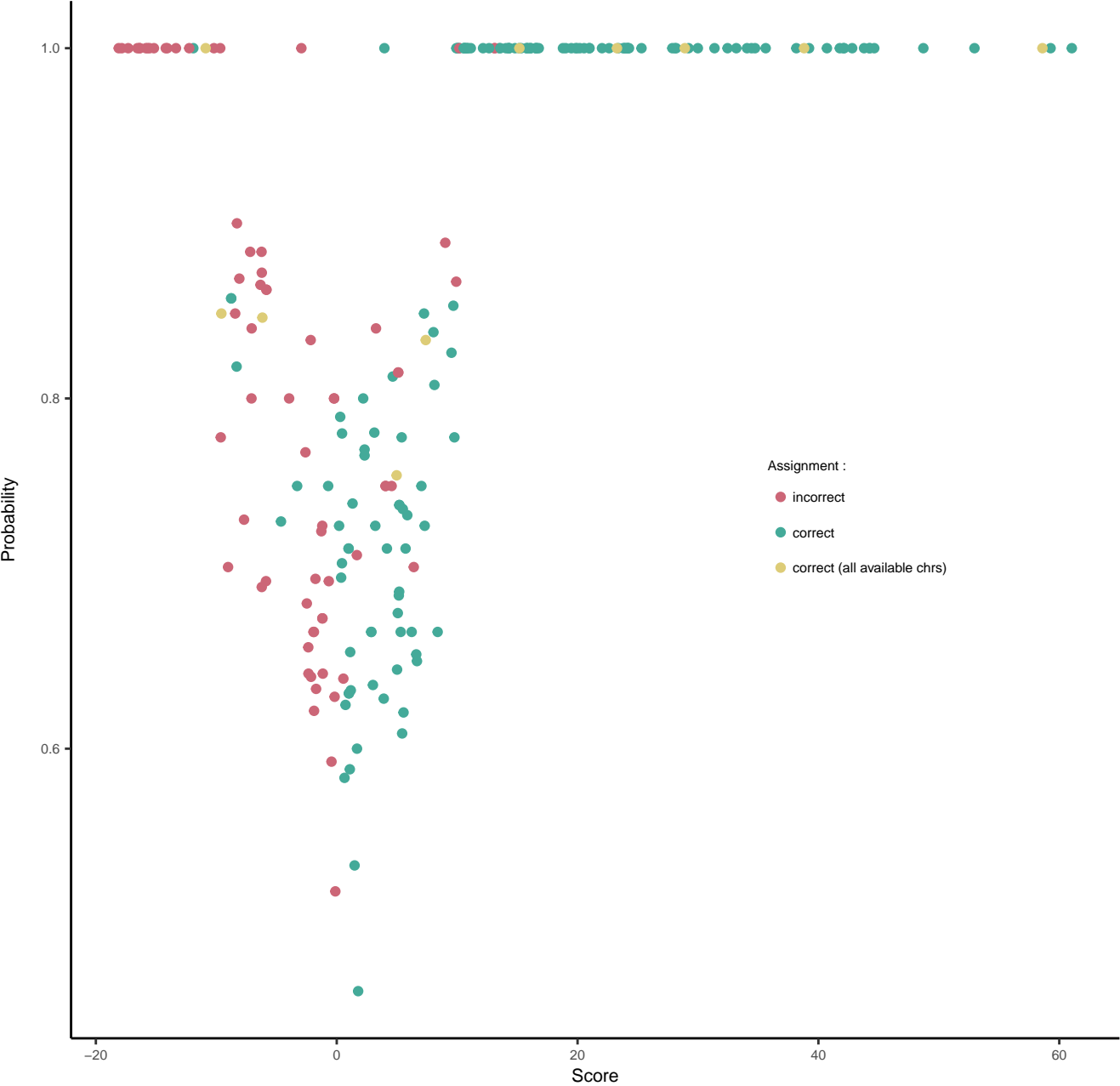
f. Sibling score call rate



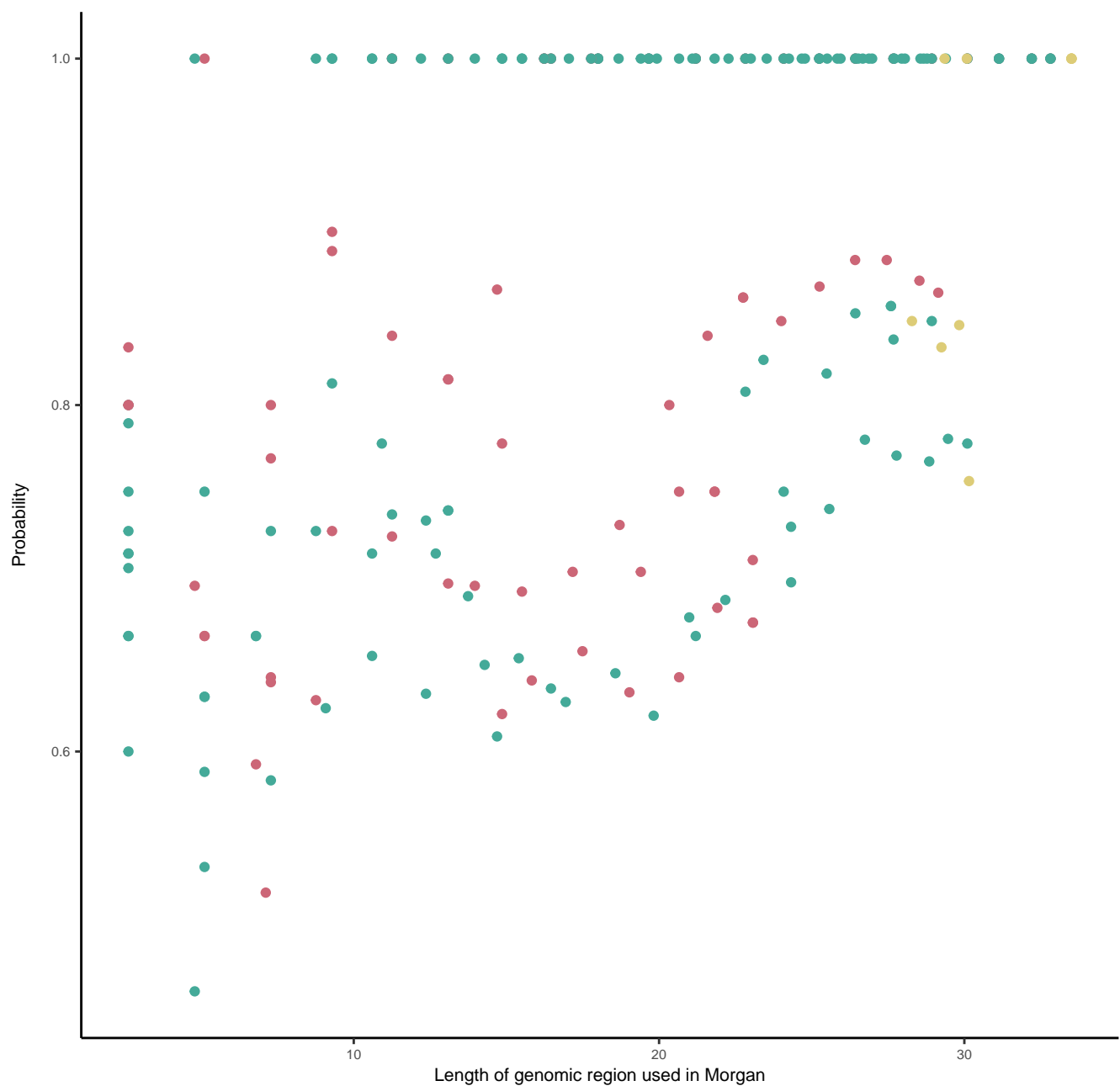




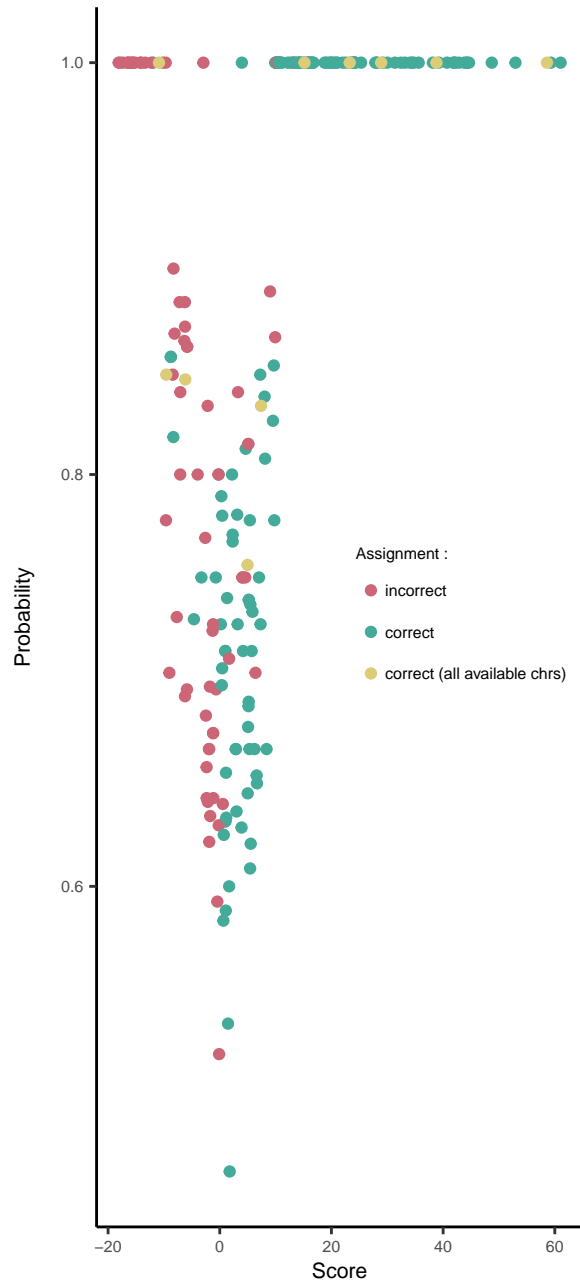
a. Probabilities vs. sib-score – validation cohort



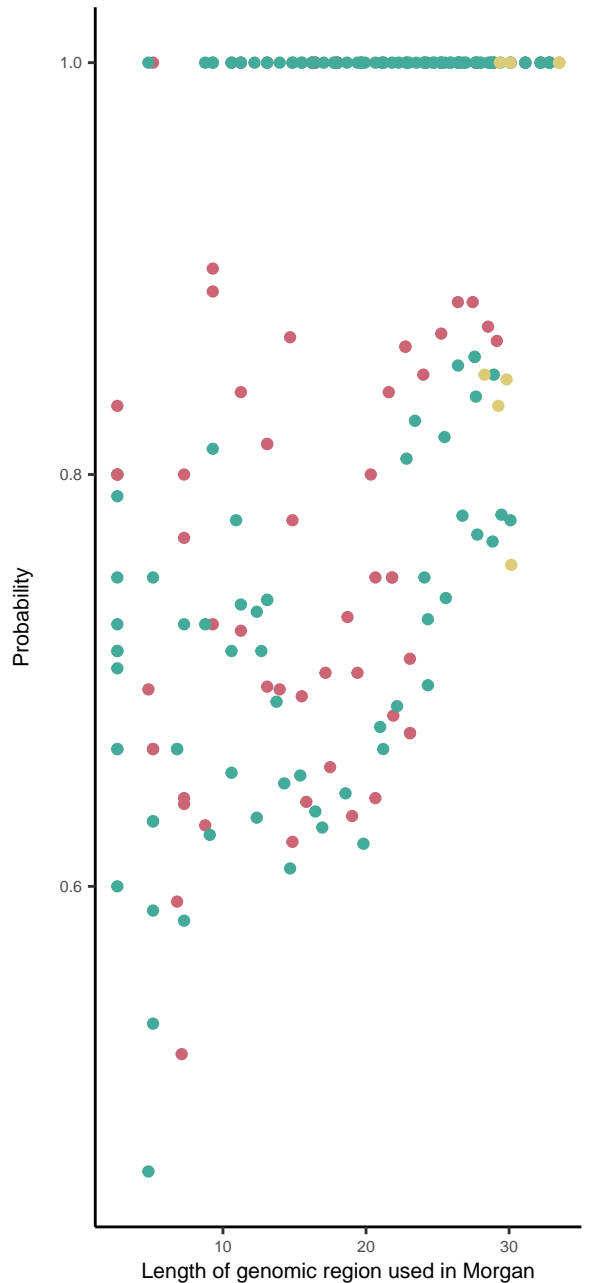
b. Probabilities vs. Morgan length – validation cohort



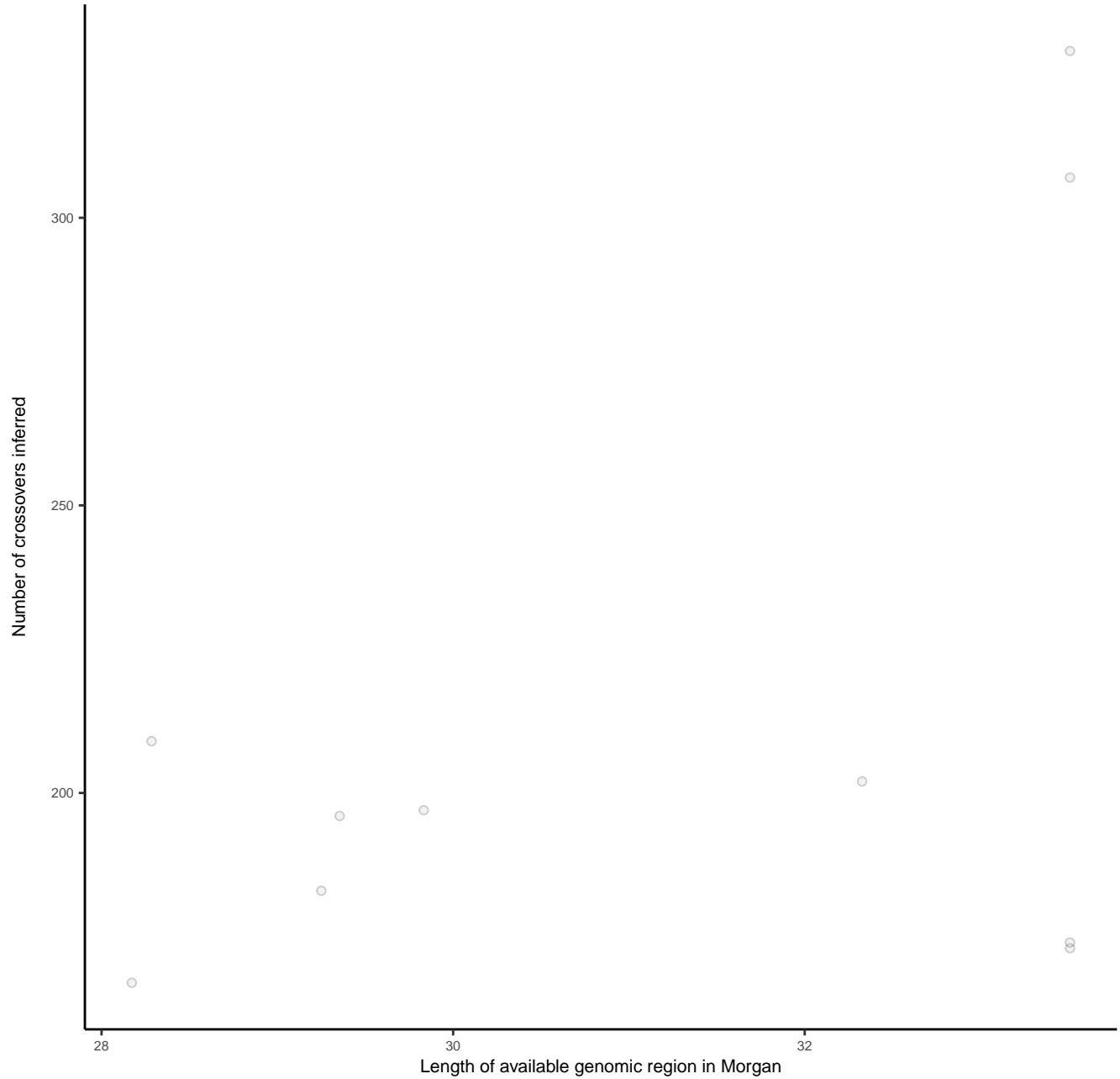
a. Probabilities vs. sib-score – validation cohort



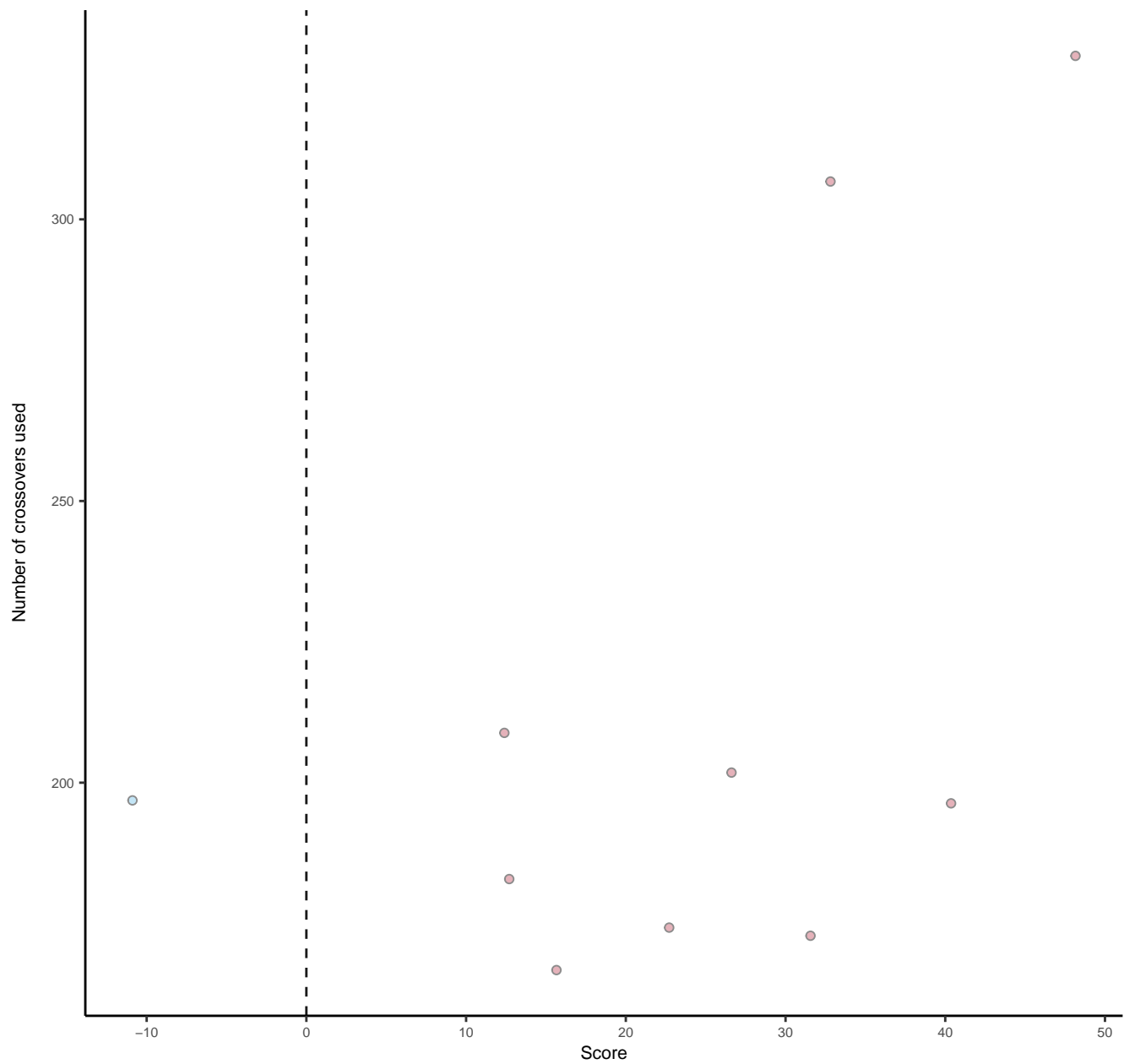
b. Probabilities vs. Morgan length – validation cohort



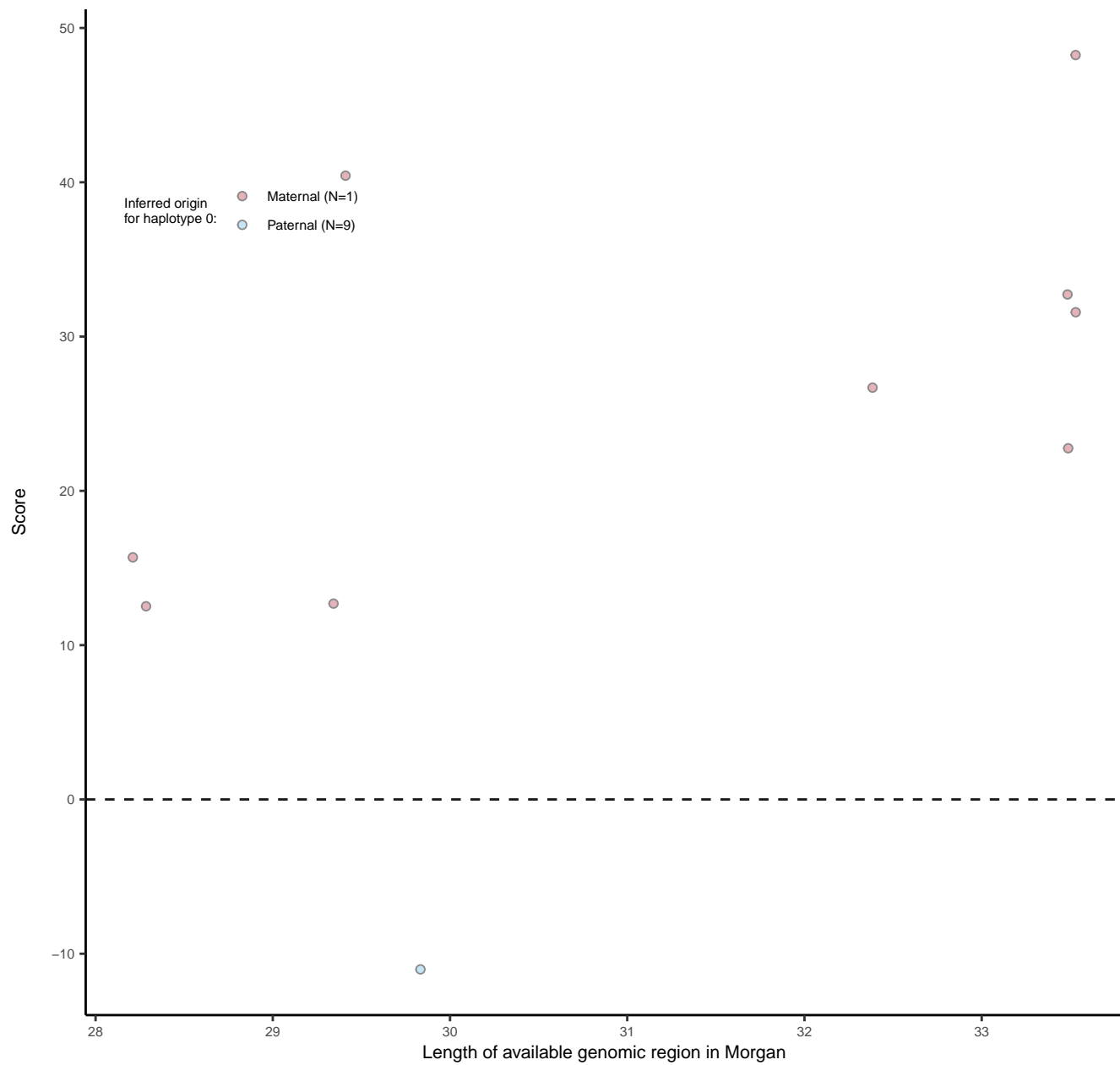
c. Crossovers inference for N=26,635 individuals



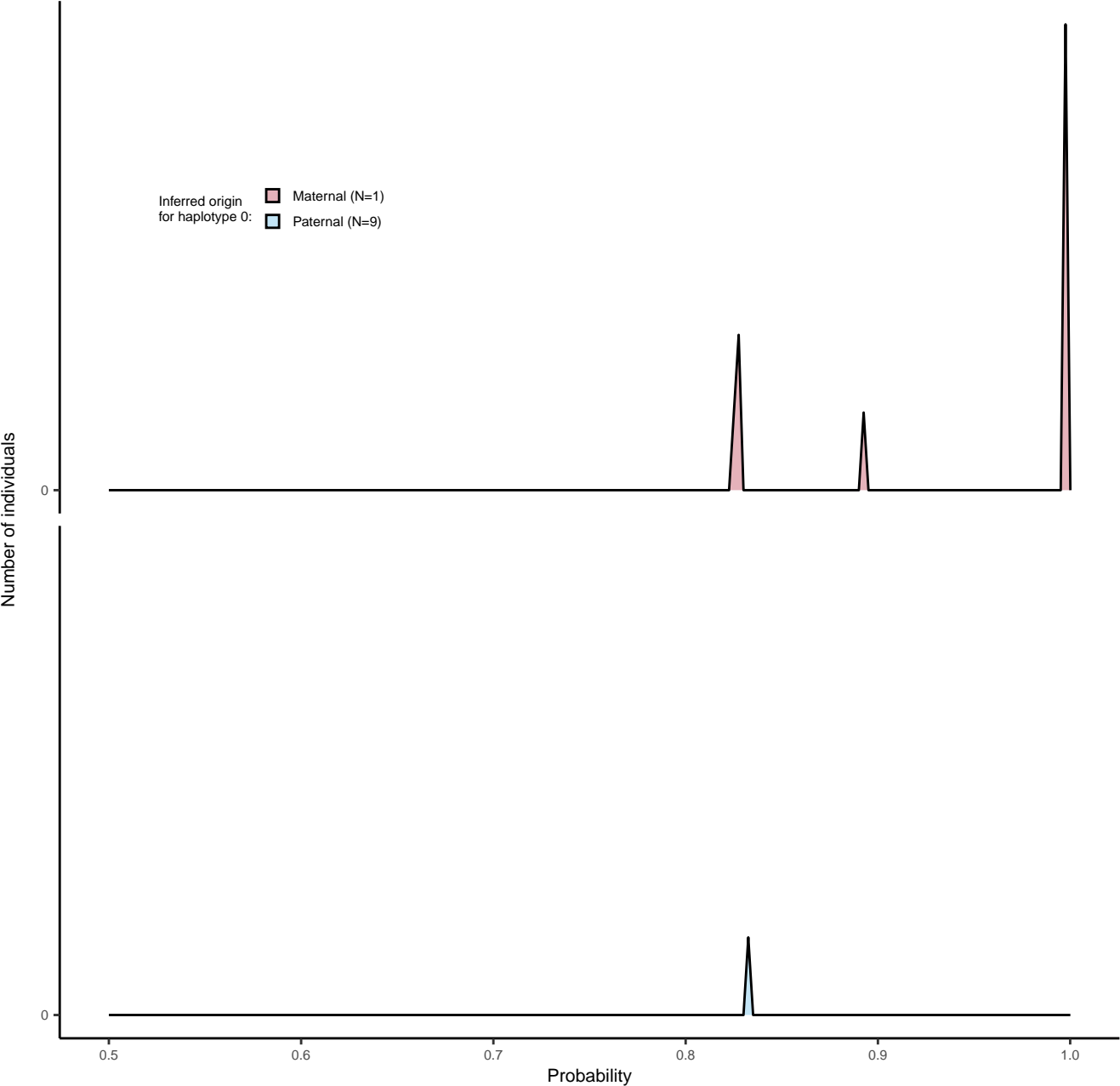
d. Inter-chromosomal sibling score for N=10 individuals



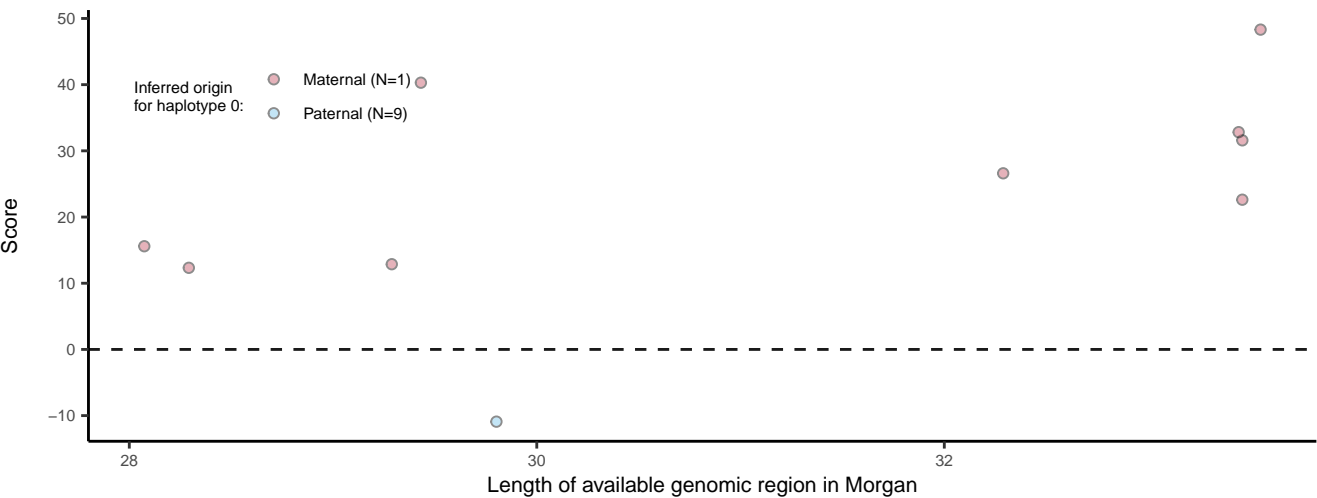
c. Inter-chromosomal sibling score for N=10 individuals



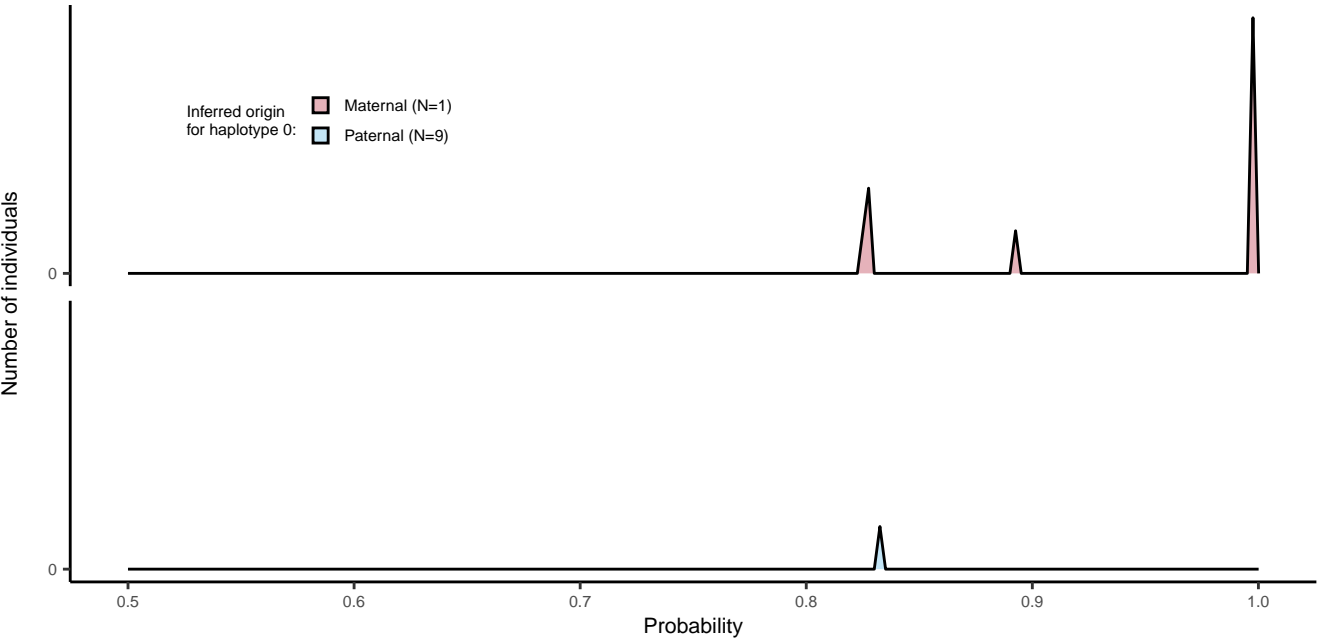
d. Haplotypes' parent-of-origin probabilities for N=10 individuals



c. Inter-chromosomal sibling score for N=10 individuals

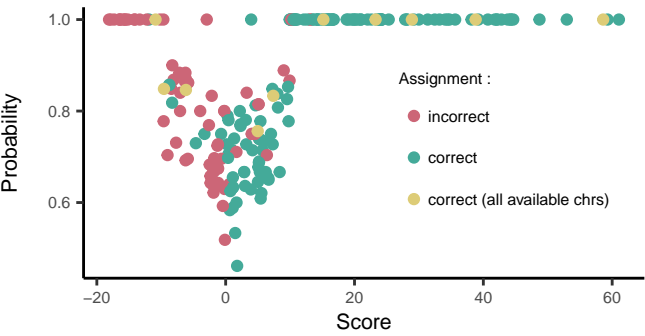


d. Haplotypes' parent-of-origin probabilities for N=10 individuals

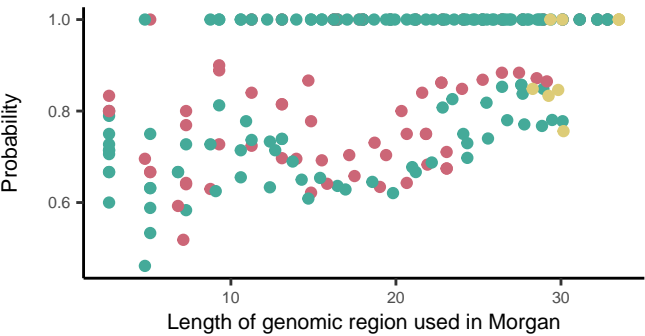




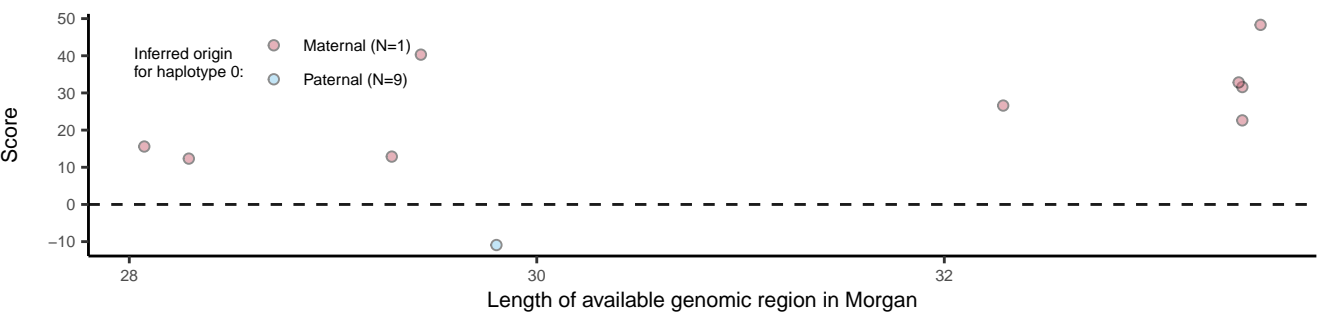
a. Probabilities vs. sib-score – validation cohort



b. Probabilities vs. Morgan length – validation cohort



c. Inter-chromosomal sibling score for N=10 individuals



d. Haplotypes' parent-of-origin probabilities for N=10 individuals

