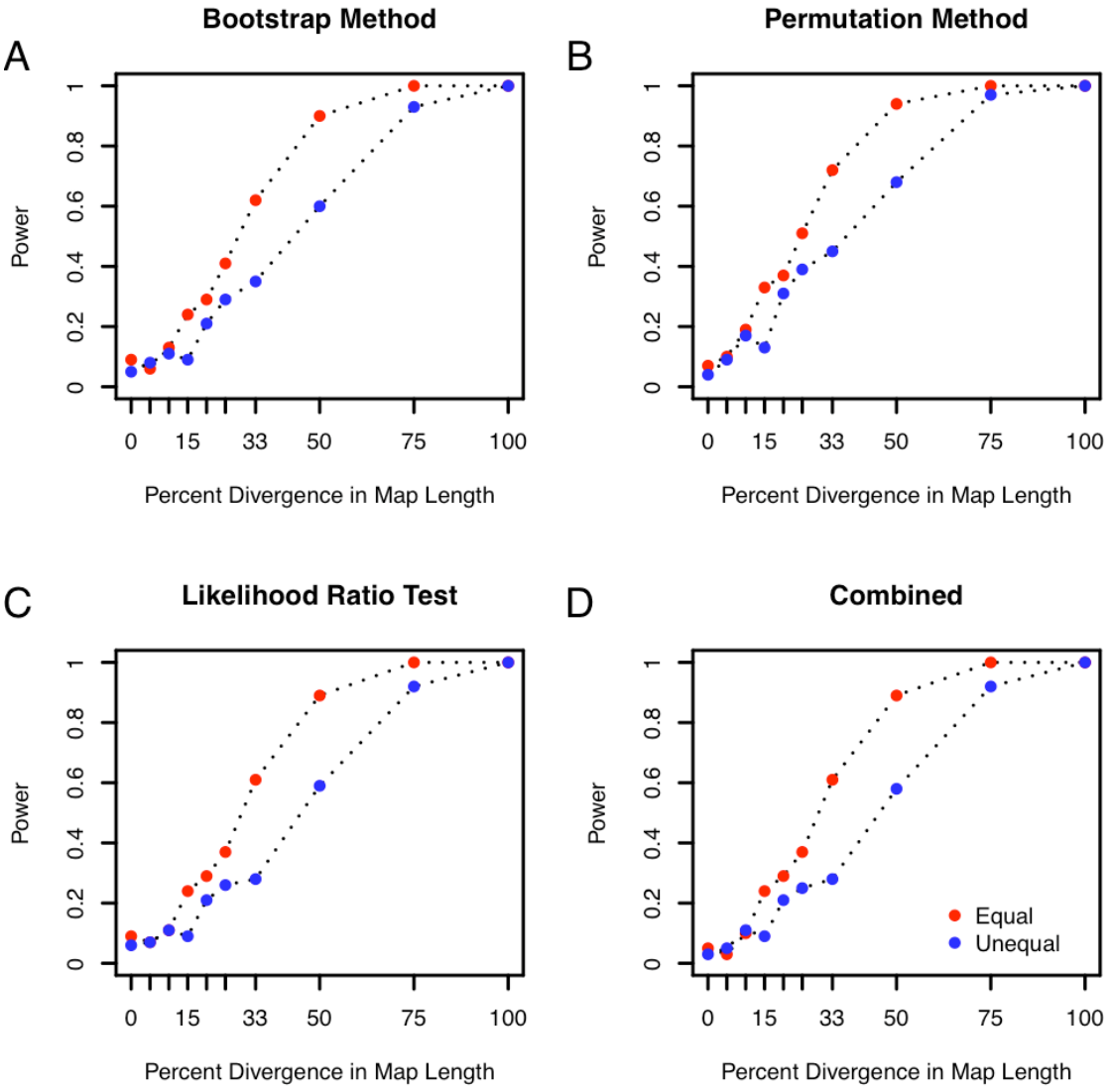
Supplementary Figure 1. Power to detect significant map length differences for sub-chromosomal intervals. We simulated 100 intervals in n = 575 individuals assuming a sex-averaged map length of 10cM and no crossover interference. We simulated a second set of 100 intervals in n = 575 individuals assuming a sex-averaged map length of (10cM $\times p$) + 10cM, where p represents the proportional difference in map length and was initially set to 0. We tested for significant differences between the first and second dataset using the bootstrap, permutation, and likelihood ratio methods as described in **Methods**. An identical simulation procedure was repeated for varying values of p: 0.05, 0.10, 0.15, 0.20, 0.25, 0.33, 0.50, 0.75, 1.00. The fraction of the 100 simulation replicates that yielded significant test results (i.e., statistical power) at each p is presented for the bootstrap test (red points, **A**), the permutation test (red points, **B**), and the likelihood ratio test (red points, **C**). The power to detect significant differences in map length using concordance among the three tests is shown in (red points, **D**). An identical set of simulations was conducted with variable sample size between the two maps (n = 400 for one map and n = 200 for the second; blue points **A-D**). As expected, unequal sample sizes have the effect of reducing power.

Supplementary Figure 2. Power to detect significant whole-chromosome map length differences between two crosses. We simulated 100 chromosomes comprised of 8 intervals each 10 sex-averaged cM in length in n = 575 individuals under a simplified model of no crossover interference. A second set of chromosomes was simulated assuming a map length in each interval of (10cM $\times$ *p)* + 10cM, where *p* was initially set to 0. Under this simulation protocol, the expected difference in chromosome map length between the two simulation sets is (8 intervals $\times$ 10cM $\times$ *p*). We tested for significant differences in whole-chromosome map length between the two simulation sets using the bootstrap, permutation, and likelihood ratio methods as described in the main text. An identical simulation procedure was repeated for additional values of *p*: 0.05, 0.10, 0.15, 0.20, 0.25, 0.33, 0.50, 0.75, 1.00. The fraction of the 100 simulation replicates that yielded significant test results (i.e., statistical power) at each *p* is presented for the bootstrap test (red points, **A**), the permutation test (red points, **B**), and the likelihood ratio test (red points, **C**). The power to detect significant differences in map length using three-way agreement among the permutation, bootstrap, and LRT approaches is given by the red points in (**D**). An identical set of simulations was conducted with variable sample size between the two maps (n = 400 for one map and n = 200 for the second; blue points **A-D**).

Supplementary Figure 1.



Supplementary Figure 2.