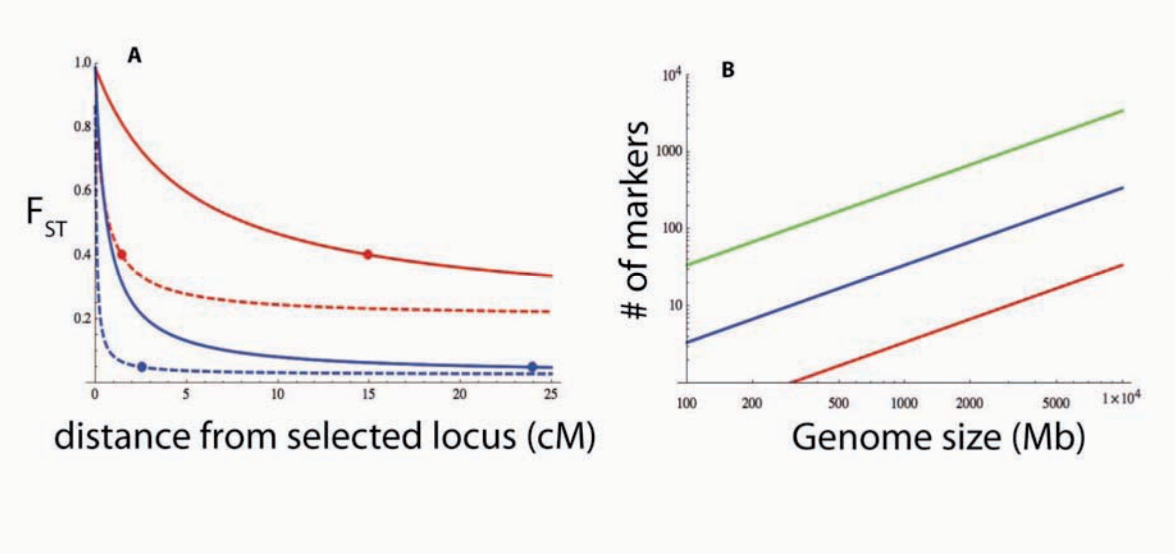

Figure S1 | **The ability to detect local adaptation depends on gametic disequilibrium between the genotyped markers and loci under selection**. **A** | F_{ST} at linked sites declines with distance from the locus under selection. Plotted are expected F_{ST} values in a symmetrical two-island model with selection on alternative alleles at a single locus, based on coalescent approximations[1], for two levels of migration (red, $Nm = 0.5$; blue, $Nm = 5.0$) and selection (solid, $s = 0.50$; dashed, $s = 0.05$). Filled circles on each curve represent the point at which F_{ST} is twice the expected background (neutral) level. **B** | Number of markers needed to reach an expectation of one marker within the region of elevated F_{ST} for the low-migration, strong-selection case in part **A**, across a range of genome sizes. This depends on the average levels of gametic disequilibrium across the genome, which are in turn determined by recombination rate (green, 10 cM/Mb; blue, 1 cM/Mb; red, 0.1 cM/Mb) and other factors. In practice, recombination rates and the scale of GD vary widely across the genome, and the power to detect F_{ST} outliers depends on sample size, expected heterozygosity, and other assumptions of the analyses.

Reference

1. Charlesworth, B., Nordborg, M. & Charlesworth, D. The effects of local selection, balanced polymorphism and background selection on equilibrium patterns of genetic diversity in subdivided populations. Genet. Res. 70, 155-174 (1997).