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 approximations1, 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