FIGURE S3.—Locus-specific ϕ_{ST} estimates for Africans and Europeans (SeattleSNPs data set). A point estimate of the genome-level ϕ_{ST} distribution (based on the median from the posterior probability distributions of α_{ST} and β_{ST}) is denoted with a solid black line. The posterior probability distributions for the outlier loci (colored lines) and 50 additional randomly chosen genetic regions (gray lines) are shown in each plot. Results from the middle five SNPs in each gene (A), the last five SNPs in each gene (B), five evenly spaced SNPs in each gene (C), and every 12th in each gene (D) are shown.