

Supplemental figures

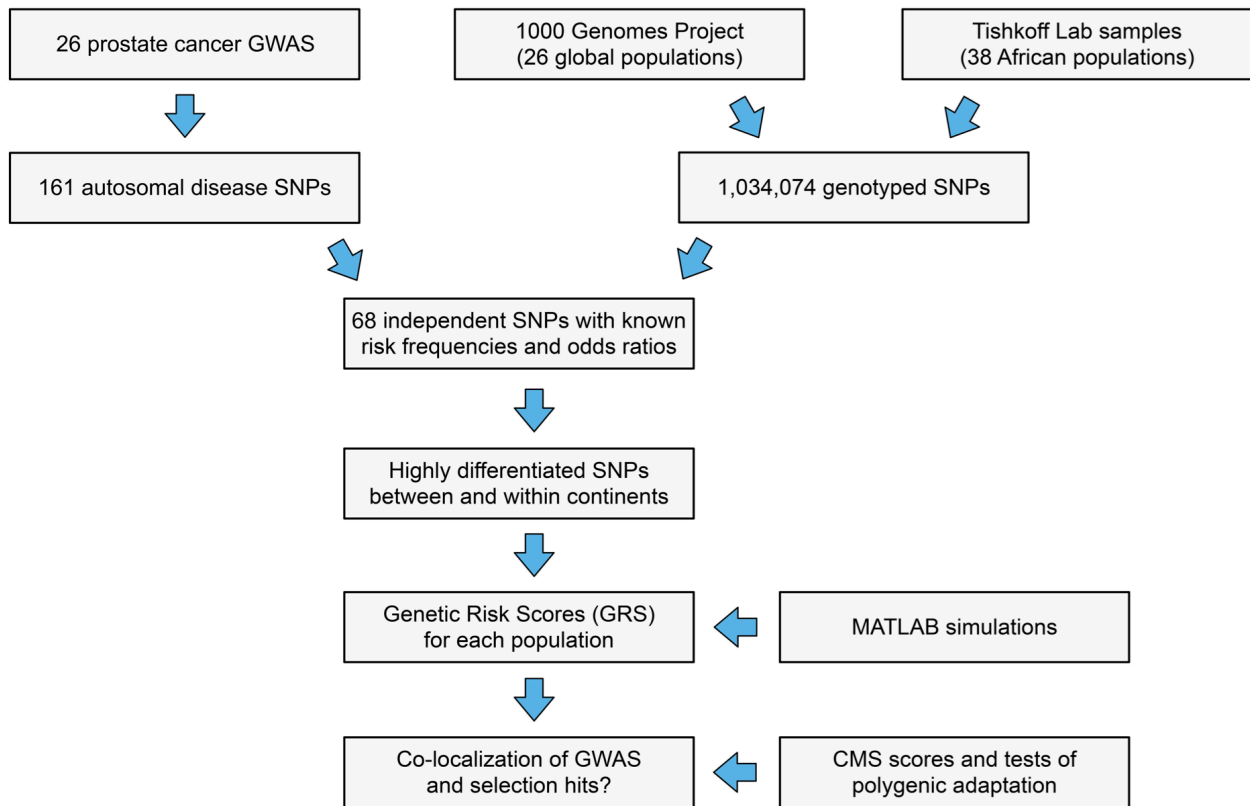


Figure S1. Bioinformatics pipeline.

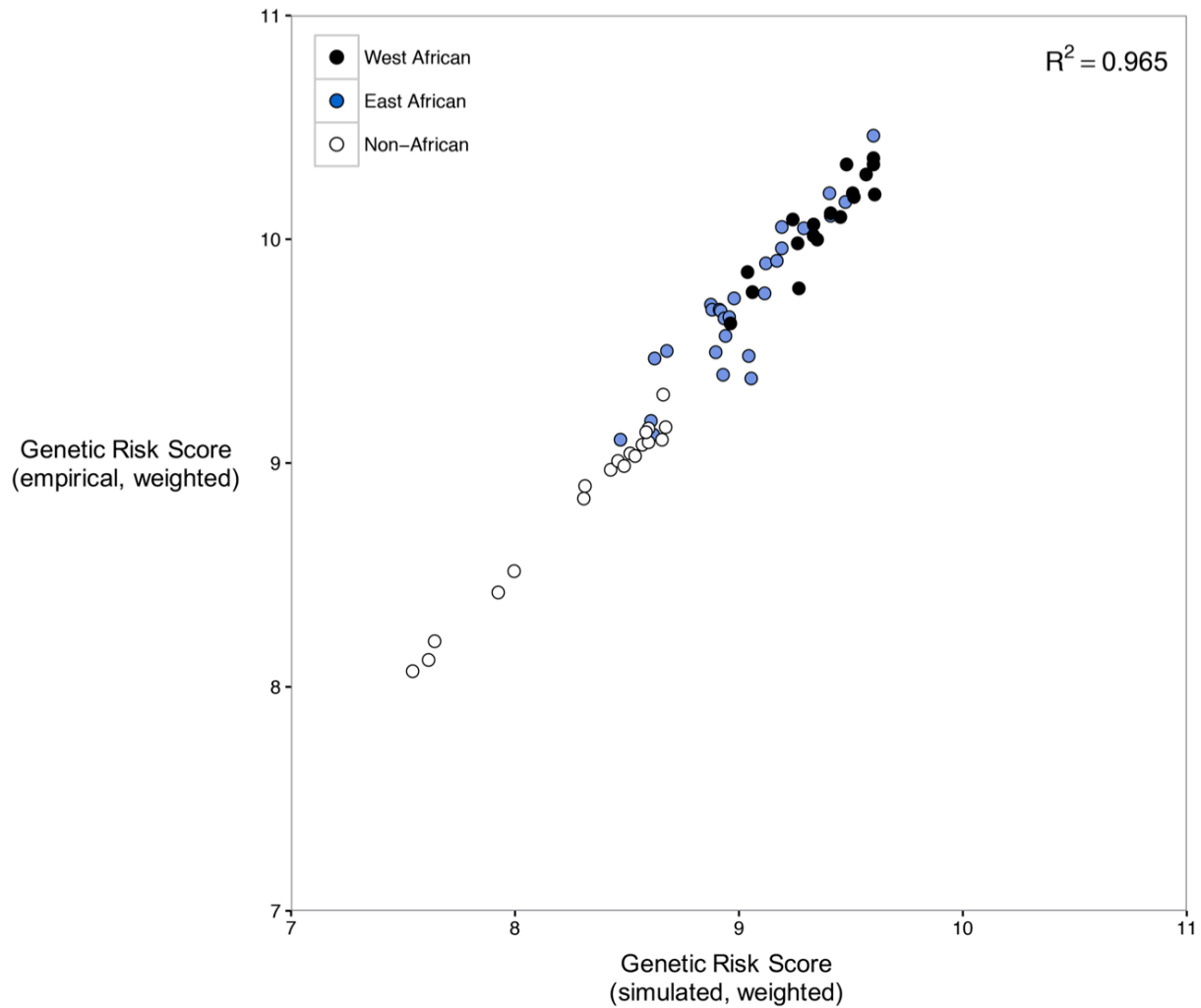


Figure S2. Empirical vs. simulated genetic risk scores for each population (median GRS shown). Empirical estimates of CaP risk use the actual genotypes of individuals in the Tishkoff Lab and 1000 Genomes Project datasets (between 9 and 113 individuals per population). Simulated genomes assume that CaP susceptibility loci are independent (one million individuals simulated per population). GRS statistics were weighted using ORs from GWAS study populations.

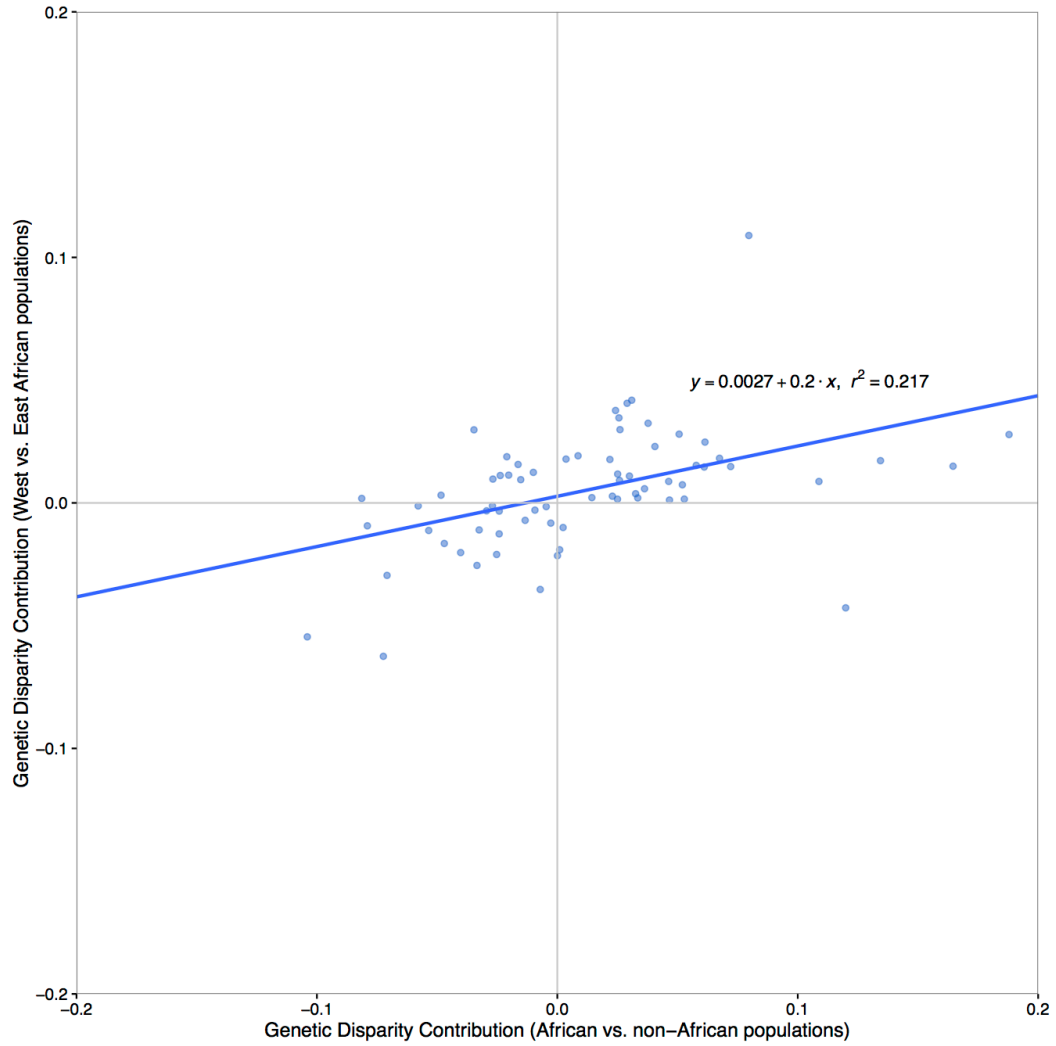


Figure S3. Many SNPs contribute to differences in risk on both a continental and subcontinental scale. GDC statistics that compare African and non-African populations are plotted vs. GDC statistics that compare West and East African populations.

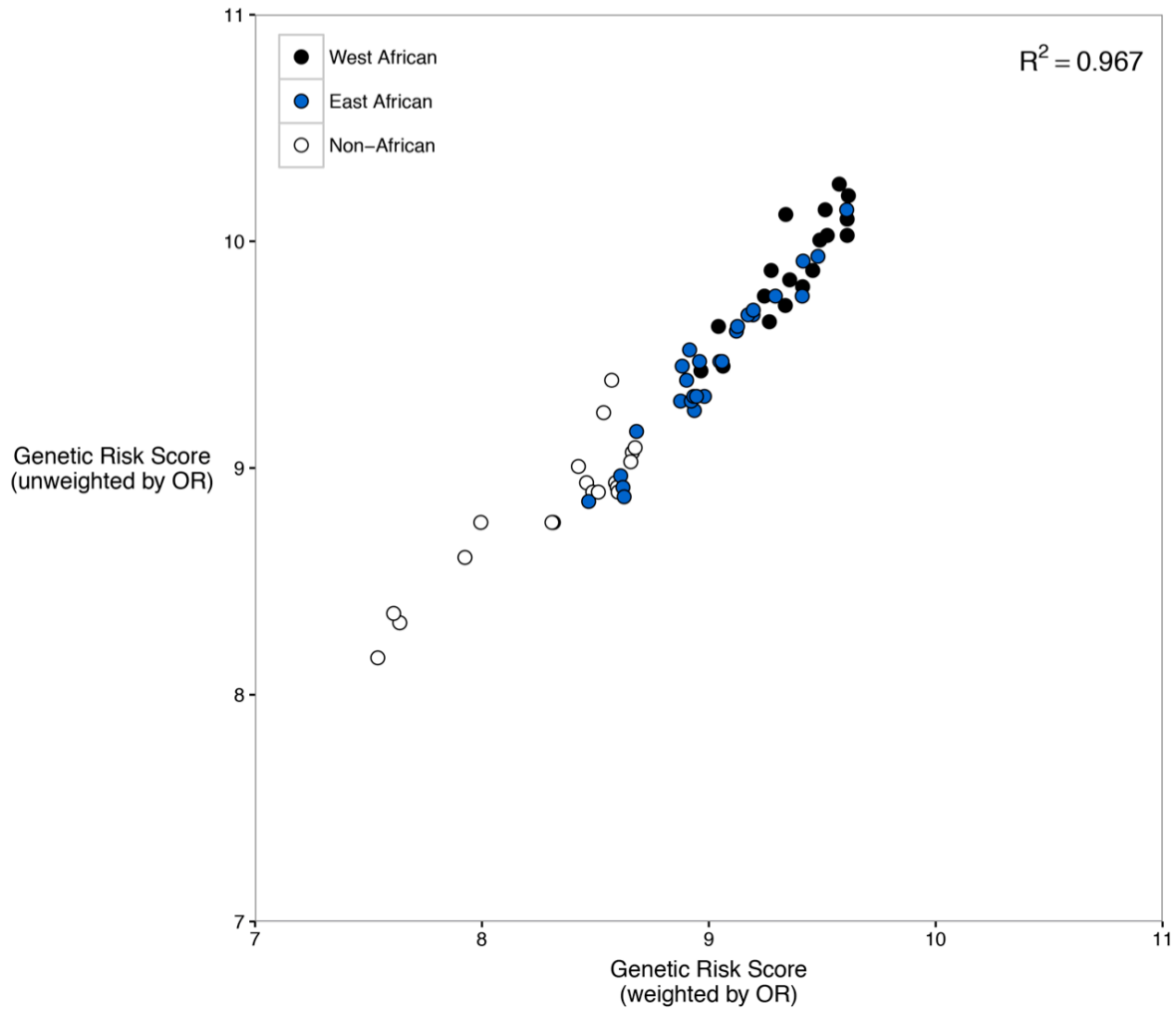


Figure S4. Unweighted vs. weighted genetic risk scores for each population (median GRS shown). Unweighted GRS statistics were calculated using an OR of 1.167 for each SNP, i.e. the mean OR of CaP risk alleles. Weighted GRS statistics were calculated using ORs from GWAS study populations. One million simulated individuals per population.

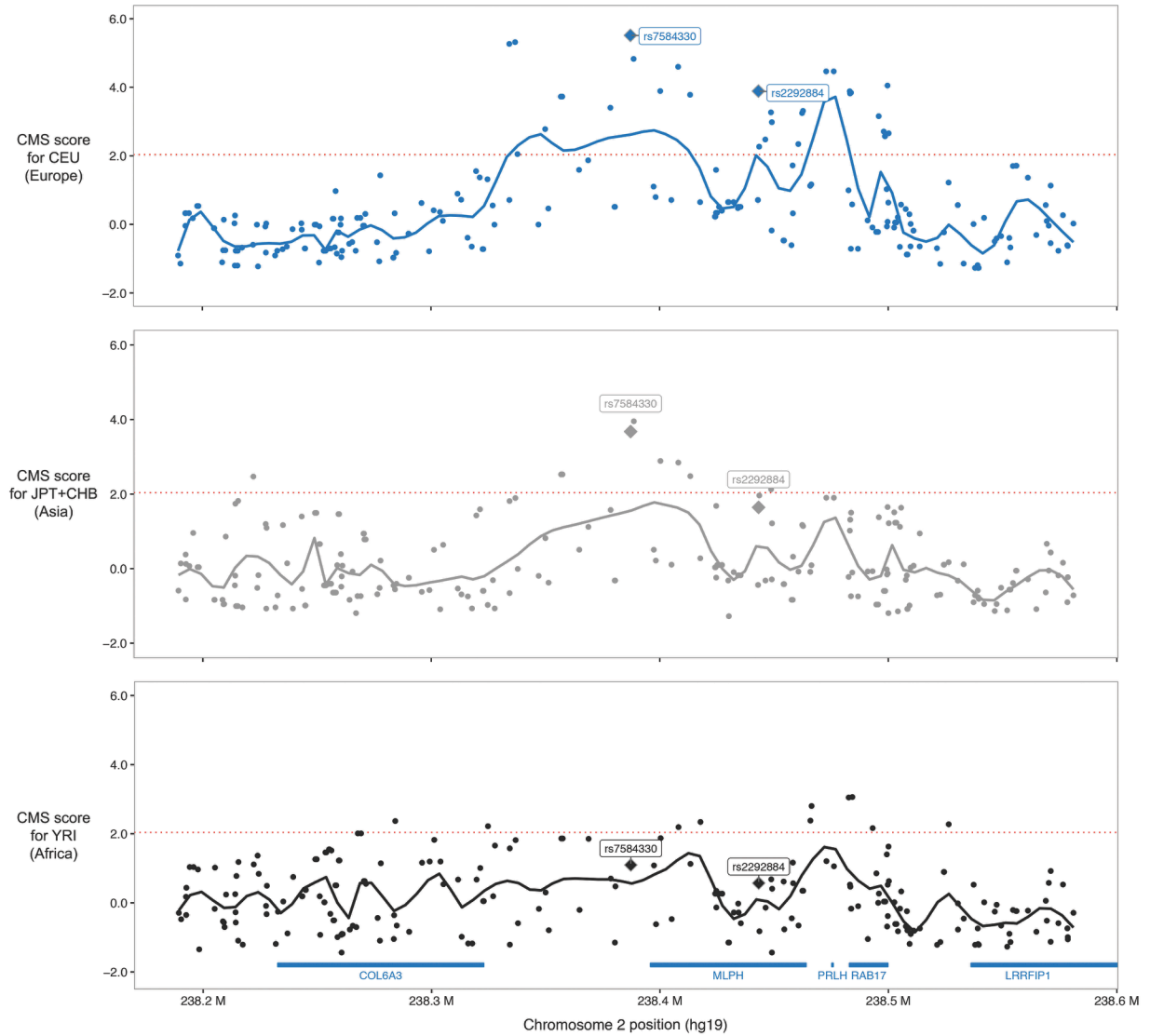


Figure S5. Scans of selection in the 2q37 region. Diamonds denote CaP SNPs, including SNPs excluded from our set of 68 independent SNPs because of linkage. One CaP susceptibility locus in the 2q37 region (rs7584330) was included in our list of 68 independent SNPs. Circles denote SNPs on the Illumina1M-Duo array and solid lines are moving averages. A dashed red line indicates the genome-wide 95th percentile of CMS scores for individual SNPs. The 2q37 region has strong signatures of local adaptation in European genomes, weak signatures of local adaptation in Asian genomes, and no signatures of local adaptation in African genomes.

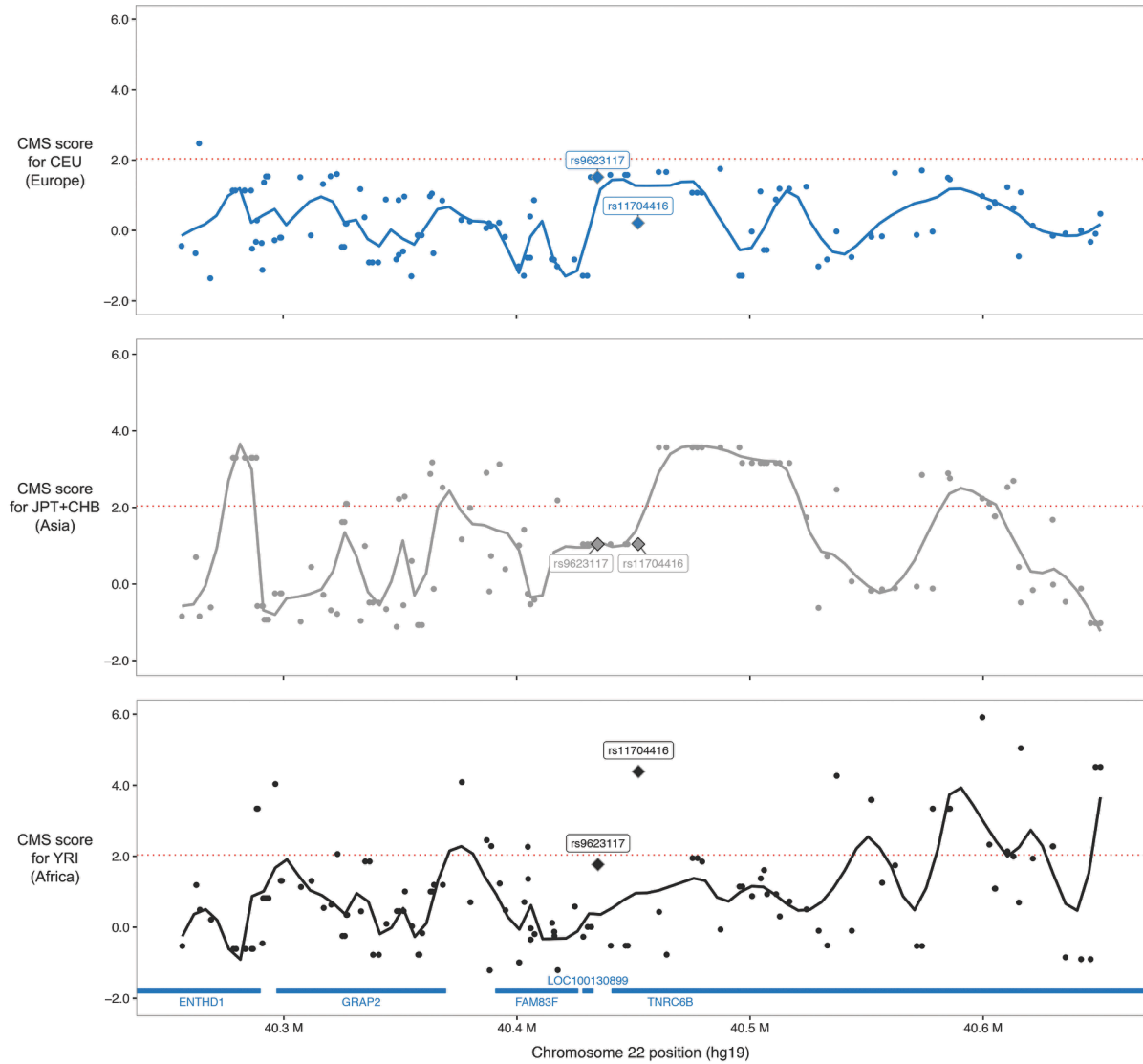


Figure S6. Scans of selection in the 22q13 region. Diamonds denote CaP SNPs, including SNPs excluded from our set of 68 independent SNPs because of linkage. One CaP susceptibility locus in the 22q13 region (rs9623117) was included in our list of 68 independent SNPs. Circles denote SNPs on the Illumina1M-Duo array and solid lines are moving averages. A dashed red line indicates the genome-wide 95th percentile of CMS scores for individual SNPs. The 22q13 region has moderate signatures of local adaptation in Asian and African genomes, and no signatures of local adaptation in European genomes.

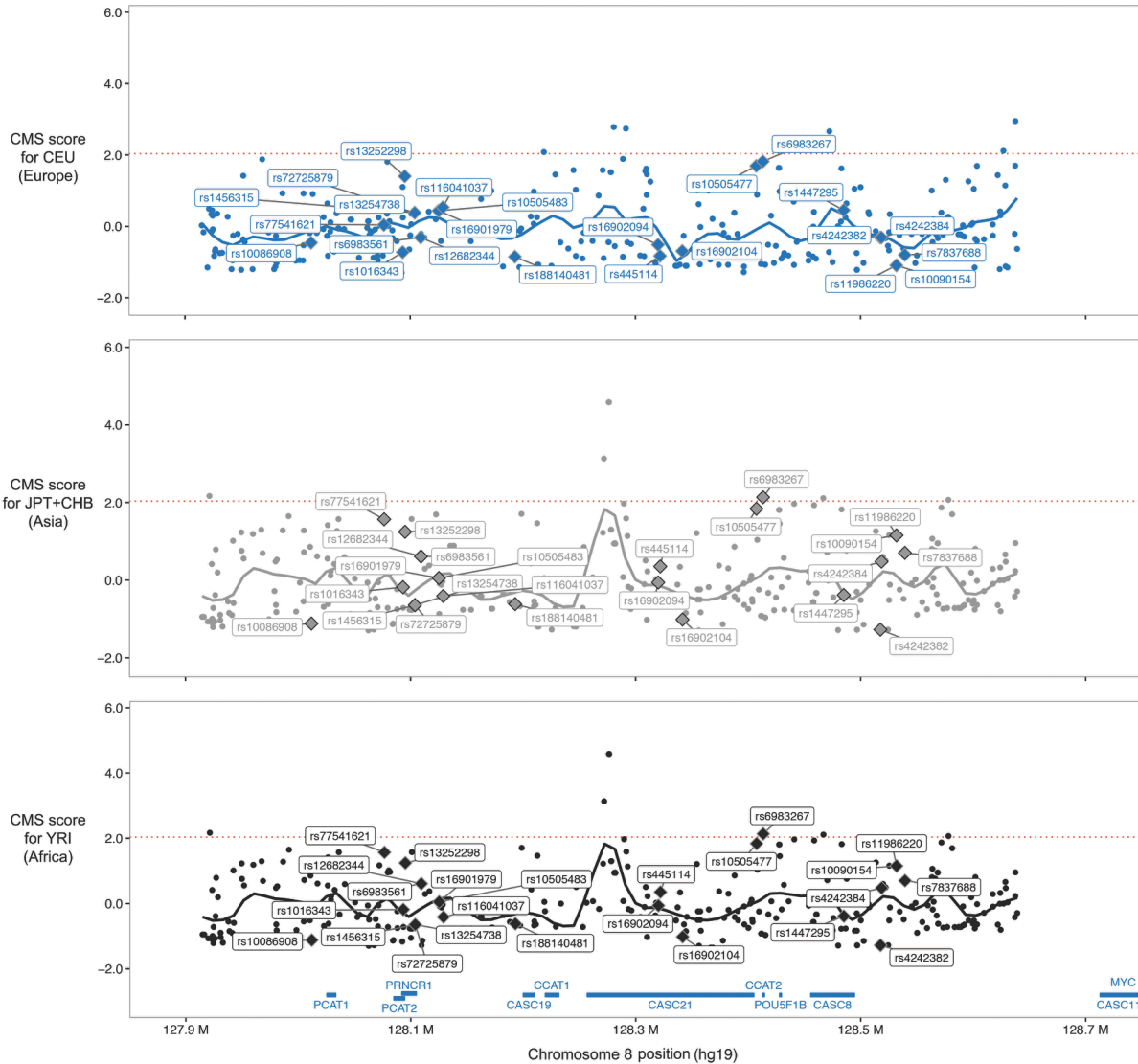


Figure S7. Scans of selection in the 8q24 region. Diamonds denote CaP SNPs, including SNPs excluded from our set of 68 independent SNPs because of linkage. Three CaP susceptibility loci in the 8q24 region (rs6983267, rs4242382, and rs1016343) were included in our list of 68 independent SNPs. Circles denote SNPs on the Illumina1M-Duo array and solid lines are moving averages. A dashed red line indicates the genome-wide 95th percentile of CMS scores for individual SNPs. There is no indication of recent adaptation in the 8q24 region for European, Asian, or African populations.