|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr., Marker Position, Alleles | RAFa in African Americans | Per allele  OR (95% CI)b | Heterozygotes  OR (95% CI)b | Homozygotes  OR (95% CI)b |
| 2p24, rs340623c  20,795,759,C/T | 0.17 | 1.15(1.05-1.25) | 1.17(1.04-1.31) | 1.20(0.91-1.58) |
| 2p15,rs6545977 63,154,668,G/A | 0.48 | 1.18(1.10-1.27) | 1.14(1.01-1.28) | 1.40(1.22-1.61) |
| 2q21,rs12620581c 173,037,960,A/G | 0.75 | 1.13(1.03-1.23) | 1.01(0.81-1.26) | 1.18(0.95-1.46) |
| 3q21,rs7641133  129,319,009, T/C | 0.29 | 1.16(1.08-1.25) | 1.17(1.06-1.30) | 1.33(1.11-1.58) |
| 4q24,rs7679673c  106,280,983,C/A | 0.39 | 1.08(1.01-1.16) | 1.01(0.91-1.13) | 1.19(1.03-1.39) |
| 6p21, rs1983891 41,644,405, T/C | 0.48 | 1.09(1.01-1.17) | 1.05(0.93-1.19) | 1.18(1.02-1.36) |
| 6q22,rs12202378c 117,348,714,T/C | 0.70 | 1.25(1.15-1.35) | 1.04(0.85-1.27) | 1.36(1.12-1.65) |
| 6q25,rs2076828 160,792,776,C/G | 0.56 | 1.14(1.06-1.22) | 1.18(1.03-1.35) | 1.31(1.13-1.51) |
| 7p15,rs7808935c 27,943,888,T/C | 0.70 | 1.16(1.07-1.25) | 1.30(1.07-1.58) | 1.44(1.19-1.74) |
| 8p21,rs11782388c 23,581,303,C/T | 0.70 | 1.18(1.09-1.28) | 1.26(1.04-1.53) | 1.44(1.18-1.75) |
| 10q11,rs4630243c 51,210,873,T/C | 0.76 | 1.14(1.05-1.25) | 1.00(0.80-1.24) | 1.19(0.95-1.48) |
| 11p15,rs7127900 2,190,150,A/G | 0.36 | 1.09(1.01-1.17) | 1.13(1.01-1.25) | 1.15(00.98-1.35) |
| 11q13,rs12418451c  68,691,995,A/G | 0.13 | 1.13(1.01-1.27) | 1.13(1.00-1.27) | 1.08(0.73-1.60) |
| 11q13,rs11228580c 68,758,918,C/T | 0.15 | 1.31(1.20-1.44) | 1.31(1.17-1.46) | 1.70(1.27-2.26) |
| 17q12,rs11649743  33,149,092,G/A | 0.91 | 1.15(1.01-1.31) | 0.89(0.45-1.77) | 1.04(0.53-2.06) |
| 19q13,rs8102476 43,427,453,C/T | 0.74 | 1.12(1.03-1.21) | 1.18(0.96-1.47) | 1.30(1.05-1.61) |
| 19q13,rs3760722 56,049,628,C/T | 0.72 | 1.14(1.05-1.24) | 1.06(0.86-1.30) | 1.24(1.01-1.52) |
| 22q13,rs5759167 41,830,156,G/T | 0.75 | 1.10(1.01-1.20) | 1.09(0.87-1.37) | 1.21(0.97-1.51) |
| Xp11,rs4907796 51,277,989,T/C | 0.13 | 1.25(1.12-1.39) | - | - |

**Table S7. Associations by genotype class for SNPs in known prostate cancer risk regions that were found to be nominally associated with risk in African Americans.**

aRAF, risk allele frequency. bAdjusted for age, study, the 1st 10 eigenvalues and local ancestry. cFor imputed SNPs, the probability of the number of risk alleles from MACH was converted to genotype groups (i.e. <0.5 = homozygous reference; 0.5-1.5 =heterozygous, and; >1.5=homozygous variant).