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Cross-cancer pleiotropic associations with lung cancer risk in African Americans

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Abstract

Background: Identifying genetic variants with pleiotropic associations across multiple cancers can reveal shared biologic pathways. Prior pleiotropic studies have primarily focused on European descent individuals. Yet population-specific genetic variation can occur and potential pleiotropic associations among diverse racial/ethnic populations could be missed. We examined cross-cancer pleiotropic associations with lung cancer risk in African Americans.

Methods: We conducted a pleiotropic analysis among 1,410 African American lung cancer cases and 2,843 controls. We examined 36,958 variants previously associated (or in linkage

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disequilibrium) with cancer in prior genome-wide association studies. Logistic regression analyses were conducted, adjusting for age, sex, global ancestry, study site, and smoking status.

Results: We identified three novel genomic regions significantly associated (FDR-corrected p-value < 0.10) with lung cancer risk (rs336958 on 5q14.3, rs7186207 on 16q22.2, and rs11658063 on 17q12). On chromosome 16q22.2, rs7186207 was significantly associated with reduced risk (OR=0.43, 95% CI: 0.73–0.89) and functional annotation using GTEx showed rs7186207 modifies *DHODH* gene expression. The minor allele at rs336958 on 5q14.3 was associated with increased lung cancer risk (OR=1.47, 95% CI: 1.22–1.78), while the minor allele at rs11658063 on 17q12 was associated with reduced risk (OR=0.80, 95% CI: 0.72–0.90).

Conclusion: We identified novel associations on chromosomes 5q14.3, 16q22.2, and 17q12, which contain *HNFI1B*, *DHODH*, and *HAPLN1* genes, respectively. SNPs within these regions have been previously associated with multiple cancers. This is the first study to examine cross-cancer pleiotropic associations for lung cancer in African Americans.

Impact: Our findings demonstrate novel cross-cancer pleiotropic associations with lung cancer risk in African Americans.

Keywords

Lung cancer; genetic; pleiotropy; African American

Introduction

Pleiotropy occurs when a genetic locus is associated with more than one trait (1) and has been observed across multiple phenotypes, including cancer (2–5). These shared associations suggest potential common biologic pathways. One example of pleiotropy occurs at the *TERT* gene region. Germline mutations in *TERT* are associated with telomere length (6), but have also been associated with phenotypes, such as pulmonary fibrosis (7), red blood cell count (8), and aplastic anemia (9). *TERT* mutations have also been identified across multiple cancer types (10), including breast (11), prostate (12), pancreatic (13), glioma (14), and lung (15–17). Identifying pleiotropy is a useful tool for genetic association studies to discover common biologic mechanisms, shared genetic architecture across diseases, and potentially new opportunities for therapeutic targets.

Cross-cancer pleiotropic analysis has been conducted for several cancer types (2, 3, 5, 18), including lung cancer (4, 5). Pleiotropic analysis of lung cancer has identified associations with *LSPI*, *ADAMI5/THBS3*, *CDKN2B-AS1*, and *BRCA2* genes in populations of predominantly European ancestry (4, 5). However, recent studies have shown the non-transferability of risk alleles across racial/ethnic groups (19, 20). It remains unknown whether pleiotropic associations of prior cancer variants are generalizable and associated with lung cancer among African American individuals. Furthermore, only a few studies (21) have accounted for either pleiotropy arising from variants in linkage disequilibrium or the ancestry of the discovery population. We used genome-wide genotyping data from five African American study populations to identify pleiotropic associations with lung cancer, incorporating variants in linkage disequilibrium and accounting for ancestry.

Methods

Study population

African American lung cancer cases and controls were selected from five study sites: the MD Anderson (MDA) Lung Cancer Epidemiology Study and Project CHURCH (Creating a Higher Understanding of Cancer Research & Community Health), NCI Lung Cancer Case-Control Study, the Northern California Lung Cancer Study from the University of California, San Francisco (UCSF), the Southern Community Cohort Study (SCCS), and three studies from the Karmanos Cancer Institute at Wayne State University (WSU), i.e. Family Health Study III; Women's Epidemiology of Lung Disease Study; and Exploring Health, Ancestry and Lung Epidemiology Study. A detailed description of each study has been previously reported (22). All studies were approved by the Institutional Review Board at each institution and written informed consent was obtained from all participants.

Genotyping, quality control, and imputation

Samples were previously genotyped (22) on the Illumina Human Hap 1M Duo array at the NCI Cancer Genomics Research Laboratory (CGR) in the Division of Cancer Epidemiology and Genetics (DCEG) at the National Cancer Institute. Genotyping data underwent strict quality control (Supplemental Figure 1). Briefly, single nucleotide polymorphisms (SNPs) were excluded if they were non-autosomal, had a MAF <1%, <95% genotyping efficiency, or a Hardy-Weinberg Equilibrium (HWE) p-value <1×10⁻⁶. Individuals were excluded if they had a <95% genotyping efficiency. Pairwise identity-by-descent was examined to identify related individuals; for each genetically related pair, the individual with the lowest genotyping efficiency was excluded (N=147). No individuals were excluded due to inconsistencies between reported and genetic sex, but four individuals with an "unknown" reported sex were filled in based on the calculated genetic sex. All quality control filtering was applied using PLINK (23).

Missing genotypes were imputed using IMPUTE2 (24), with pre-phasing performed using SHAPEIT (25–27). Haplotypes from the cosmopolitan 1000 Genomes phase 3 population consisting of 2,504 individuals from 26 countries were used as a reference population. SNPs imputed with low certainty were excluded based on an info score <0.4, MAF<0.01, and HWE p-value <1×10⁻⁵.

Ancestry estimation

Supervised admixture analysis was performed using ADMIXTURE software (28) to obtain global estimates of African and European ancestry for all individuals. Admixture analysis was performed on observed genotypes merged with the CEU (CEPH Utah residents with Northern and Western European ancestry) and YRI (Yoruba from Ibadan, Nigeria) HapMap reference populations (29), and pruned to a set of unlinked variants (window size = 50, step size = 10, r² > 0.1). A total of 140,591 variants remained for supervised (k=2) admixture analysis.

Selection of variants for pleiotropic analysis

All variants previously associated with any cancer type were identified from the NHGRI-EBI GWAS catalog as of April 2016. Manual review excluded studies in which the outcome was not risk (e.g. survival, prognosis, toxicity, relapse). Studies assessing interactions were also excluded. SNPs from each of the remaining studies were aggregated into a single list, hereafter referred to as “reported SNPs.”

Because genotyping arrays are designed to capture genome-wide variation using as few SNPs as possible, the majority of reported associations are rarely causal, but rather correlated (or in linkage disequilibrium, LD) with the true causal variant (30, 31). Additionally, it is established that LD patterns differ between racial/ethnic groups (32). Since the vast majority of the GWAS-reported SNPs are identified in European- or Asian-descent populations, we further expanded our list of reported SNPs based on LD structure of the 1000 Genomes (phase 3) reference population (33, 34) similar to the race/ethnicity of the population reported in the GWAS Catalog study. For example, the CHB (Han Chinese in Beijing, China) reference population was used to identify SNPs in LD with variants reported in Asian-descent populations, while the CEU (CEPH Utah Residents with Northern and Western European Ancestry) reference population was used for SNPs reported in European-descent populations. For the admixed Latino/a and African American populations we used relevant continental reference populations: CEU, CHB, YRI (Yoruba in Ibadan, Nigeria), and MXL (Mexican Ancestry from Los Angeles) for Latino/a and CEU, YRI, and ASW (Americans of African Ancestry in SW United States) for African Americans. For each reported SNP, we extracted all SNPs with a $r^2 > 0.6$ and ± 100 kb of the reported SNP in the appropriate 1000 Genomes reference population(s) using PLINK pairwise LD estimation. A final list of SNPs for analysis was generated, hereafter referred to as the “selected SNPs.”

Statistical analysis

Logistic regression was performed for each additively coded effect allele using SNPTEST to account for imputation probabilities (35). Age, sex, smoking status (current/former/never), global African ancestry, and study site were included as covariates in the logistic regression models. A Benjamini-Hochberg false discovery rate (FDR) correction was applied to p-values to account for multiple testing. Statistical significance was defined as an FDR-corrected p-value < 0.1 . Exploratory strata-specific analyses were conducted by histologic subtype, smoking status (ever/never), and sex. A meta-analysis was also conducted summarizing results from each study (adjusting for age, sex, smoking status, and global African ancestry) using a fixed effect model in METAL (36).

Results

Descriptive Characteristics

A total of 4,253 African American individuals remained following quality control, with 1,410 lung cancer cases and 2,843 controls (Table 1, Supplemental Table 1). Forty-five percent of all individuals were male and the mean age at diagnosis was 58 years. Lung cancer cases were on average five years older than controls. Among cases, 55% of participants were current smokers and 37% were former smokers, while 43% of controls

were never smokers. The median global African ancestry was similar among cases and controls (84% and 83%, respectively). The most frequent histologic cell type among cases was adenocarcinoma (45%), followed by squamous cell carcinoma (24%). Descriptive characteristics by study and case/control status are presented in Table 1.

Variant Selection

A total of 266 unique studies were extracted from the NHGRI-EBI GWAS Catalog based on the search term “neoplasm.” Forty-six studies were excluded after manual review (see Methods), resulting in 220 studies reporting associations for 959 unique SNPs (“reported SNPs”). Seventy-four percent (163 out of 220) of studies were conducted in European-descent populations, followed by 26% (57 of 220) in Asian-descent populations (Table 2). The admixed Latino/a and African American populations accounted for only 3% and 5% of prior GWAS cancer studies, respectively (Table 2). Of all reported SNPs, 629 were directly observed in the genotype data and an additional 294 were imputed. Thirty-six reported SNPs were not present in the 1000 Genomes reference populations used for LD-based selection of SNPs and were dropped from analysis. Application of the PLINK pairwise LD estimation method ($r^2 > 0.6$ and $\pm 100\text{kb}$) to all reported SNPs increased the number of SNPs from 923 to 39,010 (Table 2).

Logistic Regression Analysis

Among the 39,010 selected SNPs, 1,772 were neither observed nor imputed in our African American population and 280 SNPs failed to meet post-imputation quality control filtering, resulting in 36,958 selected SNPs for analysis. Logistic regression analysis revealed 40 SNPs that were significantly associated with lung cancer risk (Figure 1 and Table 3). The most statistically significant association was identified on chromosome 15q25.1 for rs17486278 (per allele odds ratio (OR) = 1.41, 95% confidence interval (CI): 1.26–1.57, FDR-corrected p-value = 2.32×10^{-5}), followed by chromosome 5p15 (rs2853677, OR = 1.27, 95% CI: 1.13–1.41, FDR-corrected p-value = 0.04), Table 3). Three additional SNPs, rs336958 (5q14.3), rs7186207 (16q22.2), and rs11658063 (17q12) also had significant associations with lung cancer risk. The T allele at rs336958 on 5q14.3 was associated with increased risk with an OR = 1.47 and 95% CI: 1.22–1.78 (FDR-corrected p-value = 0.06). The association on chromosome 16q22.2 consisted of four SNPs with similar effect sizes, though only one, rs7186207, surpassed a 10% FDR correction threshold (OR = 0.80, 95% CI = 0.73–0.89, FDR-corrected p-value = 0.04). On chromosome 17q12, the C allele at rs11658063 was associated with an reduced risk of lung cancer (OR = 0.80 and 95% CI: 0.72–0.90, FDR-corrected p-value = 0.10). Similar results were observed when study sites were combined using fixed effect meta-analysis (data not shown).

Exploratory Stratified Analyses

To identify histologic subtype-specific associations for lung cancer risk, we examined adenocarcinoma cases (N = 632) and squamous cell carcinoma cases (N = 337) separately. No genetic variant was significantly associated with lung cancer risk in either histological subtype (Supplemental Figure 2). On chromosome 15q25.1, stratification by sex and smoking status revealed a sex-specific association among females (rs17486278, OR = 1.51, 95% CI = 1.30–1.76, FDR-corrected p-value = 4.29×10^{-3} , Supplemental Figure 3 and

Supplemental Table 2) and among ever smokers (rs17486278, OR=1.41, 95% CI=1.26–1.58, FDR-corrected p-value= 1.42×10^{-4} , Supplemental Figure 4). One additional SNP, rs7486184 on chromosome 12q21.32 was also significantly associated with lung cancer risk among females (OR=0.74, 95% CI=0.64–0.85, FDR-corrected p-value=0.10, Supplemental Figure 3 and Supplemental Table 2). No SNPs were significant after an FDR correction in males (Supplemental Figure 3). Among ever smoking African Americans, 33 SNPs on chromosomes 5p15.33 and 16q22.2 had FDR-corrected p-values 0.10 (Supplemental Figure 4 and Supplemental Table 3). No p-values were statistically significant after FDR correction in never smokers (Supplemental Figure 4).

Discussion

The present analysis sought to identify cross-cancer pleiotropic genetic associations for lung cancer risk in African Americans. The two most significant associations were on chromosome 15q25.1 and 5p15.33, both of which have been previously associated with lung cancer in African Americans (37–39) and recently validated in a non-independent African American consortium study (22) that included cases and controls utilized in the present study. We also identified three novel associations on chromosomes 5q14.3, 16q22.2, and 17q12. Chromosome 16q22.2 was also observed among ever smokers and an additional region on 12q21.32 was specific to women. Despite not meeting our threshold for statistical significance, there was suggestive evidence for an association of 5p15.33 and 15q25.1 among never smokers. These results are consistent with prior research indicating 5p15.33 is associated with lung cancer risk among never smokers (15, 40) and contribute to the ongoing debate as to whether 15q25.1 is directly associated with lung cancer or mediated by smoking (41–45).

Excluding established risk loci 5p15.33 and 15q25.1, the most significant association was for rs7186207 on chromosome 16q22.2 (FDR-corrected p-value = 0.04). All four SNPs in this region (rs7186207, rs8051239, rs7195958, and rs3213422) had similar odds ratios and were in strong LD ($r^2 > 0.68$) with each other in both African (YRI and ASW) and European (CEU) 1000 Genomes reference populations (46). Given the high degree of correlation between variants, it is unsurprising that effect allele frequencies were similar among the four SNPs, ranging from 0.38 to 0.44. None of the four SNPs were among the reported SNPs extracted from the GWAS Catalog, but were selected because of their strong LD ($r^2 = 0.75–0.78$) with rs12597458, a variant previously associated with prostate cancer risk (12). The 16q22.2 region has been previously associated with prostate cancer (47). SNPs rs7186207, rs8051239, and rs7195958 are intergenic and located between *PKDIL3* and *DHODH* and do not appear to be located at sites with regulatory potential based on histone modification marks (Supplemental Figure 5). However, GTEx data (48) reveals rs7186207 is significantly associated with *DHODH* gene expression in lung (p-value= 2.1×10^{-7} , Figure 2) and other tissues. The remaining SNP at this locus, rs3213422, is located within the first intron of *DHODH* (Supplemental Figure 5) and encodes a missense mutation, though SIFT (49) and PolyPhen-2 (50) both predict the mutation to be tolerated/benign. Given its close proximity to the exon boundary within *DHODH*, variation at rs3213422 could also affect exon splicing and GTEx data (48) reveals rs3213422 is a splice QTL for *DHODH* in aortic artery tissue (p-value= 2.7×10^{-6}). ENCODE data reveal H3K4me3 and H3K27ac markers surrounding

rs3213422, indicative of active promoters and regulatory elements, as well as evidence for transcription factor binding (Supplemental Figure 5).

The *DHODH*, or dihydroorotate dehydrogenase, gene encodes a 43-kDa enzymatic protein localized to the inner mitochondrial membrane, where it interacts with the mitochondrial respiratory chain and acts as a rate-limiting step in *de novo* pyrimidine biosynthesis (51–53). Mutations within *DHODH* have been linked with Miller Syndrome, a recessive disorder characterized by malformations of the limbs and eyes, among other symptoms (54–57). *DHODH* has also been investigated for a role in cancer, including melanoma (58) and acute myeloid leukemia (59) and decreased expression of *DHODH* was associated with breast cancer risk (60). Several other studies have examined the utility of *DHODH* inhibitors in cancer by inducing cell cycle arrest and apoptosis in cancer cells (59, 61–66). While *DHODH* has not been previously associated with lung cancer risk, the abundance of biological evidence for its pleiotropic role in cancer gives credibility to the association.

We identified significant associations on chromosomes 5q14.3 and 17q12. Chromosome 5q14.3 SNP rs336958 is an intronic variant for *HAPLN1*, hyaluronan and proteoglycan link protein 1, which has been shown to play a role in cell adhesion and extracellular matrix structure. SNP rs336958 is in LD ($r^2=0.97$) with rs4466137 which has been associated with prostate cancer risk (67). The larger 5q14.3 region has also been associated with prostate cancer (12), breast cancer (7), and Wilms tumors (68) and allelic imbalance in this region has been associated with multiple cancers, including lung (69–71).

The most significant SNP on chromosome 17q12 is rs11658063, a variant located in the first intron of *HNF1B*. HNF1 homeobox B (*HNF1B*) encodes a transcription factor and has been shown to play a role in cell development. SNPs in the *HNF1B* gene region have been previously associated with pancreatic (72), prostate (12, 73–79), ovarian (80–82), testicular (83), and endometrial (84–86) cancers. Expression of *HNF1B* has been associated with prognosis in hepatocellular carcinoma (87) and renal cell carcinoma (88). Furthermore, methylation of *HNF1B* has been observed in prostate (89), ovarian (82, 89–91), and lung (92) cancers and may have utility as a biomarker in ovarian cancer (90, 91).

The final notable region of association was on chromosome 12q21.32, where rs7486184 was associated with lung cancer in females. The intergenic variant rs7486184 is located approximately 40kb downstream of the *KITLG* gene and is in strong LD ($r^2=0.97$) in Europeans (CEU) with reported variant rs995030 (46), which has been previously associated with testicular germ cell cancer in European-descent populations (93–95). Interestingly, rs7486184 and rs995030 may represent independent signals in African Americans since these SNPs are in weak LD in African descent populations ($r^2=0.15$ for YRI and $r^2=0.42$ for ASW) (46).

Of the SNPs previously reported to have a pleiotropic association with lung cancer (4, 5), two (rs62560775 and rs2853676) were not present in our current analysis. The remaining four SNPs (rs3817198, rs1057941, rs4072037, and rs4977756) were not significantly associated with lung cancer risk in our African American population, with ORs close to 1.0 and wide confidence intervals. However, ORs for two of the four SNPs (rs4977756 and

rs1057941) were in the same direction as previously reported (observed vs. reported ORs: 1.01 vs. 1.13 and 1.03 vs 1.04, respectively), while the observed OR for rs3817198 was in the opposite direction as previously reported (0.94 vs. 1.10). The OR for rs4072037 was not previously reported. Both previous lung cancer pleiotropy studies (4, 5) utilized predominantly European-decent populations; thus, failure to replicate could represent population-specific effects. However, the minor allele frequency of rs3817198 and rs1057941 is higher in European versus African populations (rs3817198: 30% vs. 12%, respectively; rs1057941: 44% vs. 12%, respectively), which could result in reduced statistical power to detect these associations in our African American study population. Furthermore, our failure to replicate prior pleiotropic associations could be the result of differences in study population characteristics. Namely, our study was somewhat younger (mean age at diagnosis = 58), had a higher percentage of women (55%), and a sizable percentage of never smokers (31%).

Previous pleiotropy studies have failed to consider differences in LD structure between racial/ethnic groups. Such considerations are important given recent publications noting the non-transferability of genetic risk predictions across diverse populations (19, 20). In the present analysis, a notable strength is our effort to expanded the list of reported SNPs by considering the LD structure of the racial/ethnic population of the discovery population, thus removing the assumption that the reported SNP has the same correlation structure, and therefore, tagging ability, with the causal SNP in all racial/ethnic groups. Importantly, it was through consideration of LD structure that the present study was able to identify novel lung cancer risk associations, as only two of the most significant SNPs (rs2853672 on 5p15.33 and rs1051730 on 15q25.1) were among the list of reported SNPs extracted from the GWAS catalog. The current analysis examined cancer-associated SNPs in the GWAS catalog as of April 2016. Cancer GWAS published after this date may reveal additional pleiotropic associations.

It is important to note that the present study is not independent of the study by Zanetti *et al.* as our cases and controls are a subset of the individuals in the Zanetti *et al* study (22). By restricting the analysis to SNPs with *a priori* evidence to examine cross-cancer pleiotropic associations, our study was able to identify novel lung cancer risk loci that may have been missed due to stringent multiple test corrections required in genome-wide association studies. Stratification by sex and smoking status revealed strong associations among women and ever smokers, suggesting the observed associations among all lung cancer cases and controls may be driven by these two subgroups. It remains to be determined whether the observed associations among women but not men represent a true biological phenomenon or are simply an artifact of reduced statistical power among men.

With our large sample size of African Americans and consistent results across the pooled and meta-analyses, we have identified several novel regions associated with lung cancer risk. Our findings highlight the need for a national effort dedicated to prioritizing research in diverse populations for future replication and fine mapping in African American lung cancer cases and controls to better understand the underlying mechanisms contributing to these pleiotropic signals. Functional studies should be performed to elucidate the pleiotropic effect

of these associations across cancer types and identify common biological pathways across phenotypes that may lead to therapeutic targets for lung cancer.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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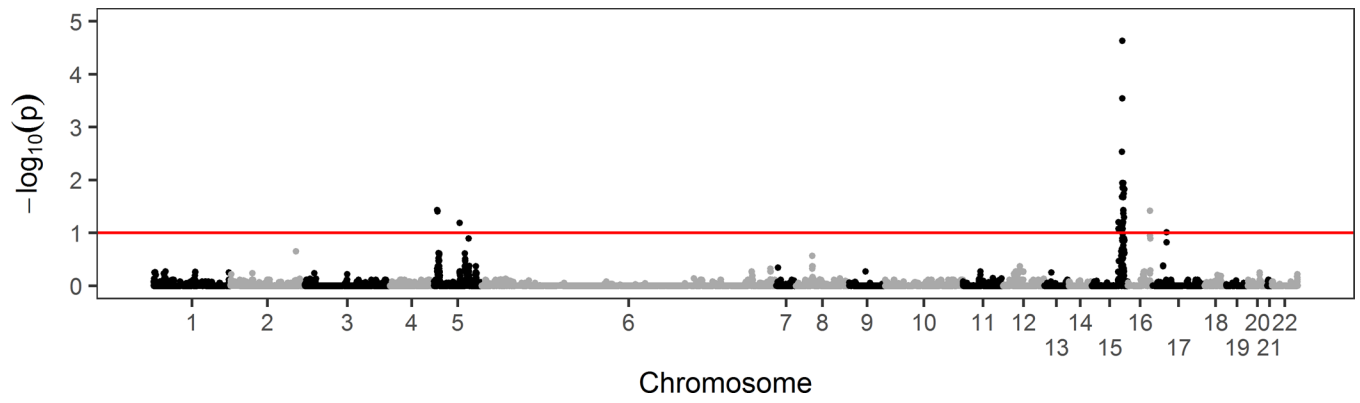


Figure 1. Manhattan plot of genetic association p-values. Logistic regression models for lung cancer risk show several novel and known genetic associations among African Americans. Red line represents 10% false discovery rate.

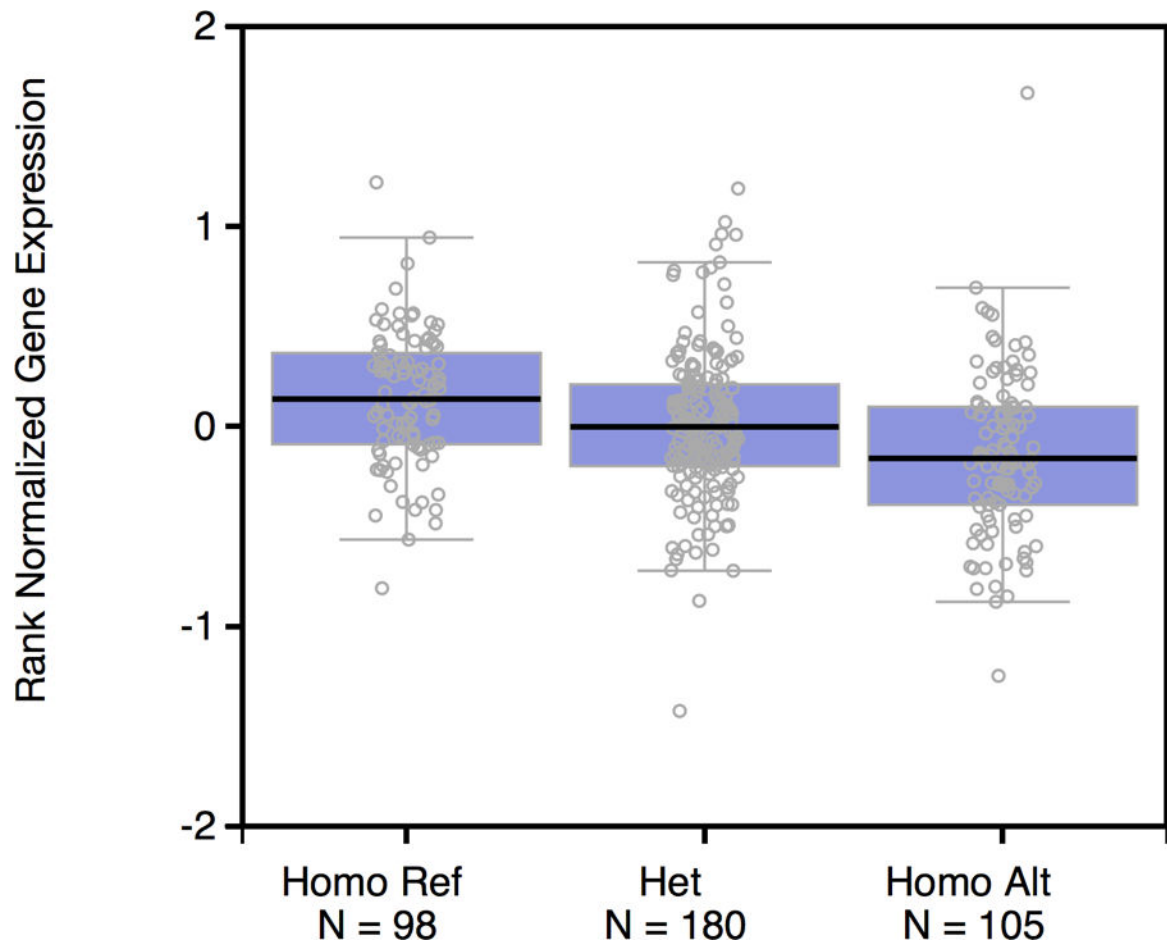


Figure 2.

Rank normalized gene expression. Single nucleotide polymorphism rs7186207 in *DHODH* is an expression quantitative trait loci (eQTL) ($p\text{-value}=2.1\times 10^{-7}$) in lung tissue. The data and figure is from the GTEx Portal (48). Homozygous reference (Homo Ref) represents TT genotype, Heterozygous (Het) represents TC genotype and Homozygous Alternative (Homo Alt) represents CC genotype.

Table 1.

Descriptive characteristics of African American lung cancer cases and controls.

Characteristic	MDA N=1374	NCI N=583	SCCS N=506	UCSF N=986	WSU N=804	Total	
						Cases N=1,410	Controls N=2,843
Status							
Cases, N (%)	373 (27.1)	208 (35.7)	168 (33.2)	325 (33.0)	336 (41.8)	1,410 (33.2)	1,410 (33.2)
Controls, N (%)	1001 (72.9)	375 (64.3)	338 (66.8)	661 (67.0)	468 (58.2)	2,843 (66.8)	2,843 (66.8)
Sex							
Male, N (%)	525 (38.2)	308 (52.8)	300 (59.3)	450 (45.6)	317 (39.4)	1,202 (42.3)	1,900 (44.7)
Female, N (%)	849 (61.8)	275 (47.2)	206 (40.7)	536 (54.4)	487 (60.6)	1,641 (57.7)	2,353 (55.3)
Mean age at diagnosis, yr (SD)	52.2 (13.5)	64.4 (9.6)	55.9 (8.9)	63.5 (11.2)	60.3 (11.3)	56.9 (13.2)	58.4 (12.6)
Smoking Status							
Current, N (%)	339 (24.8)	196 (33.7)	276 (54.8)	364 (38.1)	358 (44.6)	778 (55.3)	1,533 (36.4)
Former, N (%)	379 (27.7)	250 (43.0)	111 (22.0)	361 (37.8)	257 (32.0)	838 (29.9)	1,358 (32.3)
Never, N (%)	649 (47.5)	135 (23.2)	117 (23.2)	230 (24.1)	187 (23.3)	1,110 (7.8)	1,318 (31.3)
Median African Ancestry, % Histology	82.6	82.4	88.3	81.9	82.9	83.1	83.2
Adenocarcinoma, N (%)	173 (46.4)	97 (47.1)	47 (31.3)	145 (44.6)	170 (50.6)	632 (45.5)	632 (45.5)
Squamous Cell, N (%)	103 (27.6)	53 (25.7)	28 (18.7)	82 (25.2)	71 (21.1)	337 (24.2)	337 (24.2)
Large Cell, N (%)	2 (0.5)	5 (2.4)	11 (7.3)	4 (1.2)	12 (3.6)	34 (2.4)	34 (2.4)
Small Cell, N (%)	23 (6.2)	2 (1.0)	14 (9.3)	20 (6.0)	22 (6.8)	81 (5.8)	81 (5.8)
Other, N (%)	72 (19.3)	49 (23.8)	50 (33.3)	72 (22.2)	63 (18.8)	306 (22.0)	306 (22.0)

MDA=MD Anderson Cancer Center; NCI=National Cancer Institute; SCCS=Southern Community Cohort Study; UCSF=University of California San Francisco; WSU=Wayne State University.

Table 2.

Number of studies and variants reported in the NHGRI-EBI GWAS Catalog (as of April 2016) and the number of SNPs identified after LD-based selection.

Race/Ethnicity in GWAS Catalog	Number of Studies ^a	Number of SNPs	1000 Genomes Population Used for LD Selection	Number of SNPs after LD Selection
European	163	743	CEU	29,727
Asian	57	217	CHB	10,625
Latino	6	20	CEU, YRI, MXL, CHB	968
African American	11	49	CEU, YRI, ASW	1,490
Total	220	959		39,010

^aTotal number of studies is less than the sum of populations because 11 studies included two or more racial/ethnic populations and are counted once for each population.

Table 3.

SNPs significantly (FDR-corrected p-value < 0.10) associated with lung cancer risk among African American lung cancer cases and controls (N=4,253).

SNP	Chr.	BP	Effect/ Ref. Allele	Effect Allele Freq	Info Score	OR	95% CI	Unadjusted P-value	FDR-corrected P-value
rs17486278	15	78867482	C/A	0.3	1	1.41	(1.26–1.57)	6.27E-10	2.32×10 ⁻⁵
rs55781567	15	78857986	G/C	0.28	1	1.37	(1.23–1.53)	1.54E-08	2.84×10 ⁻⁴
rs2036527	15	78851615	A/G	0.23	1	1.36	(1.21–1.54)	2.87E-07	2.89×10 ⁻⁴
rs58365910	15	78849034	C/T	0.27	0.98	1.35	(1.2–1.51)	3.13E-07	2.89×10 ⁻⁴
rs147144681	15	78900908	T/C	0.18	1	1.36	(1.2–1.55)	2.14E-06	0.01
rs576982	15	78870803	T/C	0.29	1	0.77	(0.69–0.86)	2.74E-06	0.01
rs664172	15	78862762	A/G	0.28	1	0.76	(0.68–0.85)	2.17E-06	0.01
rs667282	15	78863472	C/T	0.29	1	0.76	(0.68–0.85)	1.91E-06	0.01
rs938682	15	78896547	A/G	0.72	1	1.3	(1.17–1.46)	2.56E-06	0.01
rs569207	15	78873119	T/C	0.28	1	0.77	(0.69–0.86)	3.71E-06	0.01
rs637137	15	78873976	A/T	0.29	1	0.77	(0.69–0.86)	4.15E-06	0.01
rs11637630	15	78899719	G/A	0.29	0.99	0.77	(0.69–0.86)	5.35E-06	0.01
rs2456020	15	78868398	T/C	0.4	1	0.79	(0.71–0.87)	5.52E-06	0.01
rs55676755	15	78898932	G/C	0.17	1	1.35	(1.19–1.54)	5.69E-06	0.01
rs7183604	15	78899213	T/C	0.28	0.99	0.77	(0.69–0.86)	4.87E-06	0.01
rs12440014	15	78926726	G/C	0.22	0.91	0.75	(0.66–0.85)	6.39E-06	0.01
rs3825845	15	78910258	T/C	0.23	1	0.76	(0.68–0.86)	8.24E-06	0.02
rs503464	15	78857896	A/T	0.27	0.98	0.77	(0.69–0.87)	1.00E-05	0.02
rs189218934	15	78903987	T/C	0.27	0.99	0.78	(0.69–0.87)	1.08E-05	0.02
rs113931022	15	78901113	T/C	0.19	1	1.32	(1.16–1.5)	2.18E-05	0.04
rs138544659	15	78900701	G/T	0.19	1	1.32	(1.16–1.49)	2.21E-05	0.04
rs112878080	15	78900647	G/A	0.19	1	1.32	(1.16–1.49)	2.21E-05	0.04
rs2853677	5	1287194	G/A	0.29	1	1.27	(1.13–1.41)	2.28E-05	0.04
rs111704647	15	78900650	T/C	0.19	1	1.31	(1.16–1.49)	2.50E-05	0.04
rs2735940	5	1296486	G/A	0.47	0.98	0.81	(0.73–0.89)	2.60E-05	0.04
rs7186207	16	72035359	T/C	0.43	1	0.80	(0.73–0.89)	2.66E-05	0.04
rs2853672	5	1292983	A/C	0.47	1	0.81	(0.73–0.89)	2.85E-05	0.04
rs56077333	15	78899003	A/C	0.19	1	1.31	(1.15–1.49)	3.24E-05	0.04
rs7170068	15	78912943	A/G	0.23	0.99	0.78	(0.69–0.88)	3.93E-05	0.05
rs1051730	15	78894339	A/G	0.12	1	1.37	(1.18–1.6)	5.00E-05	0.06
rs28491218	15	78267947	C/T	0.22	0.91	0.77	(0.68–0.87)	5.43E-05	0.06
rs951266	15	78878541	A/G	0.11	0.99	1.39	(1.18–1.63)	5.28E-05	0.06
rs12914385	15	78898723	T/C	0.2	1	1.29	(1.14–1.46)	5.69E-05	0.06
rs336958	5	82973396	T/C	0.08	1	1.47	(1.22–1.78)	5.90E-05	0.06
rs7172118	15	78862453	A/C	0.11	0.99	1.38	(1.18–1.62)	6.73E-05	0.07
rs28360704	15	78268603	T/C	0.21	0.94	0.77	(0.68–0.88)	8.70E-05	0.08
rs56390833	15	78877381	A/C	0.11	1	1.38	(1.17–1.62)	8.10E-05	0.08
rs7180002	15	78873993	T/A	0.11	1	1.38	(1.17–1.61)	8.42E-05	0.08

SNP	Chr.	BP	Effect/ Ref. Allele	Effect Allele Freq	Info Score	OR	95% CI	Unadjusted P-value	FDR-corrected P-value
rs905739	15	78845110	G/A	0.25	0.98	0.79	(0.7–0.89)	8.77E-05	0.08
rs11658063	17	36103872	C/G	0.39	0.88	0.80	(0.72–0.90)	1.04E-04	0.10
rs16969968	15	78882925	A/G	0.07	1	1.49	(1.22–1.83)	1.14E-04	0.10
rs8192482	15	78886198	T/C	0.07	1	1.49	(1.22–1.83)	1.18E-04	0.10

Effect allele = minor allele

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