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Susceptibility loci of *CNOT6* in the general mRNA degradation pathway and lung cancer risk - a re-analysis of eight GWASs

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Conflict of interest:

The authors disclose no potential conflicts of interest.

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Abstract

Purpose—mRNA degradation is an important regulatory step for controlling gene expression and cell functions. Genetic abnormalities of the genes involved in mRNA degradation were found to be associated with cancer risks. Therefore, we systematically investigated the roles of genetic variants of genes in the general mRNA degradation pathway in lung cancer risk.

Experimental design—Meta-analyses were conducted in six lung cancer genome-wide association studies (GWASs) from the Transdisciplinary Research in Cancer of the Lung and additional two GWASs from Harvard University and deCODE in the International Lung Cancer Consortium. Expression quantitative trait loci analysis (eQTL) was used for *in silico* functional validation of the identified significant susceptibility loci.

Results—This pathway-based analysis included 4,603 single nucleotide polymorphisms (SNP) in 68 genes in 14,463 lung cancer cases and 44,188 controls, of which 20 SNPs were found to be associated with lung cancer risk with a false discovery rate threshold of <0.05. Among the 11 newly identified SNPs in *CNOT6*, which were in high linkage disequilibrium, the rs2453176 with a RegulomDB score “1f” was chosen as the tag SNP for further analysis. We found that the rs2453176 T allele was significantly associated with lung cancer risk (odds ratio=1.11, 95% confidence interval=1.04–1.18, $P=0.001$) in the eight GWASs. In the eQTL analysis, we found that levels of *CNOT6* mRNA expression were significantly correlated with the rs2453176 T allele, which provided additional biological basis for the observed positive association.

Conclusion—The *CNOT6* rs2453176 SNP may be a new functional susceptible locus for lung cancer risk.

Keywords

lung cancer risk; pathway analysis; molecular epidemiology

Introduction

Lung cancer is one of the most frequently diagnosed cancers with about 1.8 million new lung cancer cases reported in 2012 worldwide, accounting for about 13% of total cancer diagnoses [1]. In the United States, 224,390 new lung cancer cases are estimated to occur in 2016 [2]. In addition to other factors, such as occupational and environmental carcinogens, cigarette smoking is the major risk factor for lung cancer [3,4], but not all smokers develop

lung cancer, which suggests that genetic predisposition play an essential role in the lung carcinogenesis [5].

In recent years, some genome-wide association studies (GWASs) of lung cancer have been conducted, and a number of genetic variants, i.e., single nucleotide polymorphisms (SNPs), have been found to be associated with lung cancer risk. For example, the significant susceptibility loci associated with lung cancer risk include 5p15.3 (rs401681, rs4975616 and rs472010 in *CLPTMIL* and rs2736100 in *TERT*) [6–11], 6p21.3 (rs3117582 in *BAG6* or *APOM* and rs2395185 in *HLA-DRB5* or *HLA-DRB9*) [6,8,9,11], 6q22.1 (rs9387478 in *RAP1BP3* or *DCBLD1*) [11] and 15q25.1 (rs8034191 in *HYKK* and rs1051730 in *CHRNA3*) [6,8,9,12–15]. Among these SNPs, rs1051370, rs3117582 and rs2731600 were found to be specifically associated with risk of lung adenocarcinoma (AD) [9], whereas rs12296850 (mapped to 12q23.1) in *SLC17A8* or *NR1H4* was found to be a susceptibility locus for risk of squamous cell carcinoma (SC) [16]. Interestingly, the vast majority of the SNPs identified by GWASs are in introns or intergenic regions, and their functional evidence is limited. In the present study, we employed the pathway-based strategy that dramatically decreases the number of SNPs to be analyzed and thus significantly reduced multiple testing with the aim to identify possible lung cancer risk-associated functional SNPs that may have not been revealed by previous lung cancer GWASs.

The degradation of mRNA is an important regulatory step for controlling gene expression and cell functions [17,18]. The general cytoplasmic mRNA decay pathway usually begins with the deadenylation, which removes the poly(A) tail Ccr4-Not complex [19], followed by degradation of mRNA proceeding in two directions of 5'-3' or 3'-5'. The 5'-3' mRNA degradation initiates with decapping N⁷-methylguanosine (m⁷G) cap mainly by DCP1/DCP2 proteins and subsequently degraded by the exoribonuclease Xrn1, while the 3'-5' mRNA degradation is mainly catalyzed by 10–12 subunit exosome [20].

Some studies suggest that genetic abnormalities of genes involved in the general mRNA degradation pathway may be associated with lung cancer. For example, various genetic variants in *LSM2-LSM8*, which encode cofactors for mRNA decapping, were recently found in lung cancer cell lines [21]. Therefore, we hypothesize that genetic variants of the general mRNA degradation pathway are associated with lung cancer risk. To test the hypothesis, we conducted the comprehensive meta-analysis of the eight published lung cancer GWASs from the ILCCO (International Lung Cancer Consortium)-TRICL (Transdisciplinary Research in Cancer of the Lung) consortia, focusing on the SNPs of the genes in the general mRNA degradation pathway.

Materials and Methods

Study populations

The first part of the study populations came from the TRICL consortium, which included 12,160 lung cancer cases and 16,838 controls (all Europeans) of six previously published GWASs from: the MD Anderson Cancer Center (MDACC), the Institute of Cancer Research (ICR), the National Cancer Institute (NCI), the International Agency for Research on Cancer (IARC), Toronto study from Samuel Lunenfeld Research Institute study (Toronto), and the

German Lung Cancer Study (GLC) [22]. The second part of the study populations included GWASs of European ancestry from Harvard Lung Cancer Study (984 cases and 970 controls) [23] and Icelandic Lung Cancer Study (deCODE) (1,319 cases and 26,380 controls) [15] of the ILCCO. Written informed consents were achieved for all participants, and the present study was approved by each institutional review board of the participating institutions.

GWAS genotyping and imputation

Genotyping in the eight GWASs was performed by Illumina HumanHap 317, 317+240S, 370Duo, 550, 610 or 1M arrays. The imputation was conducted by IMPUTE2 v2.1.1 or MaCH v1.0 software using the reference panel from the 1000 Genomes Project (phase I integrated release 3, March 2012). Standard quality control on samples was performed on all scans in the analysis, excluding any participants with low call rate (< 90%), extremely high or low heterozygosity ($P < 1.0 \times 10^{-4}$), non-European (with the HapMap phase II CEU, JPT/CHB and YRI populations as a reference) and imputed SNPs with an information score < 0.40 in IMPUTE2 or $r^2 < 0.30$ in MaCH.

Gene and SNP selection

Genes in the general mRNA degradation pathway were identified from the Molecular Signatures Database [24] and the literature [19]. Overall, 75 genes located on autosomal chromosomes were selected. Among them, seven genes were pseudogenes or duplicates or withdrawn from updated NCBI. After removal of these genes, genotypes of 68 genes were abstracted from the GWAS datasets (detailed in Supplementary Table S1). The final meta-analysis contained 4,603 SNPs with the following standards: genotyping rate 90%, minor allele frequency 5%, and Hardy Weinberg Equilibrium exact P value 10^{-5} . The overall workflow is shown in Figure 1.

In silico functional validation

Two *in silico* tools, SNPinfo (<http://snpinfo.niehs.nih.gov/snpinfo/snpfunc.htm>) [25], RegulomeDB (<http://regulomedb.org/>) [26], were used to predict potential functions. Expression quantitative trait loci (eQTL) analysis was performed by using the expression data of lymphoblastoid cell lines from 373 Europeans available in the 1000 Genomes Project (<http://www.1000genomes.org/category/frequently-asked-questions/gene-expression>) [27] and The Cancer Genome Atlas (TCGA) (<https://tcga-data.nci.nih.gov/tcga/>) [28].

Statistical analysis

Logistic regression model was used to calculate the odds ratios (ORs) and their 95% confidence intervals (CIs) in an additive genetic model with PLINK (v1.06) software. A meta-analysis with the inverse variance method was employed on the 4,603 SNPs with Stata software (v12, State College, Texas, US). Cochran's Q statistic was applied to test for heterogeneity and the I^2 statistic for the proportion of the total variation in the meta-analysis [29]. The fixed-effects model was used when there was no heterogeneity among GWASs (Q-test $P > 0.100$ and $I^2 < 50\%$); otherwise, the random-effects model was used. Multiple testing correction was conducted with false discovery rate (FDR) with a threshold < 0.050

[30]. A linear regression model was also performed to evaluate the correlation between SNPs and mRNA expression levels of the corresponding genes. A paired t-test was used to compare the mRNA expression levels of genes in the lung cancer and normal adjacent tissue from the TCGA database. LocusZoom (<http://locuszoom.sph.umich.edu/locuszoom/>) was applied to construct regional association plots using Europeans from the 1000 Genomes Project as the reference (phase I integrated release 3, March 2012) [31]. Haploview v4.2 was used to generate the Manhattan plot and LD plots [32]. All analyses were conducted with SAS (version 9.4; SAS Institute, Cary, NC, USA) except for those specified otherwise.

Results

Associations of the SNPs with lung cancer risk

We first performed a meta-analysis in the TRICL database consisted of six previously published GWAS datasets with 12,160 cases and 16,838 controls. The basic information of these six studies is presented in Supplemental Table S2. A total of 4,603 SNPs in the pathway were extracted, of which 318 SNPs were associated with lung cancer risk at $P < 0.05$ in the additive model and 20 SNPs on *LSM2SKIV2L* and *CNOT6* remained significantly associated with lung cancer risk with $FDR < 0.05$ after multiple testing corrections (Figure 2A and Table 1). Among these SNPs, we excluded those of *LSM2* and *SKIV2L*, because they were mapped to and in high LD with previously GWAS-reported locus at 6p21.33 [6,8]. As a result, 11 SNPs of *CNOT6* located at 5q35.3 were left for further analysis. In the LD analysis, these 11 SNPs shared moderate to high LD ($r^2 \geq 0.60$, Figure 2B and 2C). We finally chose rs2453176 as the tag SNP, because it was significantly associated with lung cancer risk (OR = 1.13, 95% CI = 1.06–1.19, $P = 4.33 \times 10^{-5}$) (Table 1) and potentially functional according to function prediction and its imputation quality was the best among the 11 SNPs (Table 2). We used the forest plot to illustrate the association between rs2453176 and lung cancer risk in the six GWASs (Figure 3), and the rs2453176 T allele was associated with an increased lung cancer risk in five GWASs, except for the GLC GWAS.

We expanded our analysis to include additional two independent lung cancer GWASs (Supplemental Table S2). The deCODE GWAS validated our result of the *CNOT6* rs2453176 tag SNP (OR = 1.14, 95% CI = 1.01–1.28, $P = 0.032$), while the GWAS from Harvard University displayed the same trend as the GLC GWAS (OR = 0.85, 95% CI = 0.68–1.05, $P = 0.133$) (Figure 3 and Table 3).

As we combined all the data from the eight GWASs, the functional *CNOT6* rs2453176 tag SNP was found to be significantly associated with an increased risk of lung cancer (OR = 1.11, 95% CI = 1.04–1.18, $P = 0.001$) after the FDR correction (Figure 3 and Table 3).

Stratified analyses by lung cancer histology

Since lung cancer has different histological types that could have distinct biological behaviors, we performed AD and SC subgroup analysis and found that the rs2453176 T allele was associated with a borderline increased risk in AD (OR = 1.13, 95% CI = 1.00–1.27, $P = 0.050$, Table 3), but it was significantly associated with SC risk (OR = 1.12, 95%

CI = 1.03–1.22, $P = 0.006$, Table 3). Because smoking is a major risk factor for lung cancer, we further stratified the data into smokers and non-smokers and found that the rs2453176 T allele was associated with a significantly increased risk in smokers (OR = 1.09, 95% CI = 1.02–1.17, $P = 0.011$, Table 4), while the allele was not statistically significant in non-smokers (OR = 1.10, 95% CI = 0.89–1.36, $P = 0.363$, Table 4). Homogeneity tests suggested that there was no heterogeneity between strata either in subgroups of histologic types or smoking status (Table 3 and Table 4, all $P > 0.05$).

Functional validation by eQTL analysis

Because the *CNOT6* rs2453176 SNP was predicted with a score of "1f", suggesting the most confident functional annotation by regulomeDB [26], we further explored the underlying molecular mechanism by performing the eQTL analysis. With mRNA expression data of lymphoblastoid cell lines from 373 Europeans available from the 1000 Genomes Project, We found that expected mRNA expression levels of *CNOT6* were significantly decreased with an increased number of the rs2453176 T allele in both the additive ($P = 0.008$) (Figure 4A) and dominant ($P = 0.007$) (Figure 4B) models but not the recessive model (Figure 4C). We also used the 105 normal adjacent tissue samples in the TCGA to further explore the correlation between the rs2453176 genotypes and their corresponding mRNA expression levels, but we did not observe a statistical significance ($P > 0.05$) (Supplemental Figure S1A-S1C). We also compared the mRNA expression level of *CNOT6* in the 107 paired samples and did not find a statistically significant difference ($P > 0.05$) (Supplemental Figure S1D).

Discussion

In the present study, we found that a novel potentially functional susceptibility locus rs2453176 C>T of *CNOT6* in the general mRNA degradation pathway was associated with an increased lung cancer risk in 14,463 cases and 44,188 controls. This association was further supported by a significant correlation between a decreased mRNA expression level and an increasing number of the A allele in the eQTL analysis.

Gene expression disorder is one of cancer hallmarks, and instability of mRNA may result in altered transcript/protein levels of oncogenes and tumor repressor genes [33]. The degradation of mRNA is a key step in controlling the expression of genes related to cell proliferation. For example, the CCR4-Not complex consists of highly conserved exoribonucleases and adaptor proteins that hydrolyze and shorten the poly(A) tail, which starts the initial and the rate-limiting step of mRNA degradation [19]. Located at 5q35.3, *CNOT6* encodes a protein that has a 3'-5' RNase activity and acts as a catalytic subunit of the CCR4-Not deadenylation complex [34]. Although it remains unclear how the catalytic subunit works during the deadenylation process, some studies reported that its expression level was associated with carcinogenesis or prognosis. For example, one study of lung cancer found that the *CNOT6* overexpression in lung SC predicted a significantly less metastasis [33]. Another study of acute leukemia discovered that *CNOT6* had a significantly lower expression in patients than in controls [35]. These two studies suggest that high

expression levels of *CNOT6* may promote the degradation of mRNA of some oncogenes and the suppression of cell proliferation in carcinogenesis.

In the present study, we identified that the *CNOT6* rs2453176 T allele was associated with an increased risk of lung cancer, which was supported by the association of *CNOT6* rs2453176 T allele with a decreased mRNA expression level in lymphoblastoid cell lines from 373 Europeans. This finding is consistent with the role of *CNOT6* in lung cancer prognosis as previously described [33]. The ENCODE project data from University of California Santa Cruz show that the *CNOT6* rs2453176 locus is located at the DNase I hypersensitive region (Supplemental Figure S2). Usually such an area has a loose chromatin structure and renders it a region with a high affinity for transcription factors (TFs). As a result, some TFs, including MAFK and MAFF, bond to this region in many cell types (Supplemental Figure S2). For example, MAFK and MAFF were found to form heterodimers with a series of TFs and suppressed gene transcriptions [36,37]. Based on these, we speculate that the rs2453176 T allele may have a relatively high affinity with MAFK or MAFF and thus leads to the decreased mRNA expression of *CNOT6*. It is likely that a reduced quantity of *CNOT6* may not be optimal in the mRNA degradation of some aberrant genes, which may in turn increases lung cancer risk, but these speculations need to be further investigated.

In the stratification analysis, rs2453176 was associated with lung cancer risk in both AD and SC subtypes, which is not surprising, because smoking has been established as a predominant risk factor for developing lung cancer, regardless histologic types [38]. Genetic susceptibility to smoking-related lung cancer risk may determine smoking behavior and tobacco metabolism [39]. Indeed, we found that the rs2453176 T allele was associated with a higher risk of lung cancer in smokers than in non-smokers. One study reported that smoking would enhance the activity of the GATA family [40], and another study reported that nicotine would increase the expression of EP300 and promote the lung cancer growth [41]. From the Supplemental Figure S2, GATA1, GATA2 and EP300 are the TFs that bind to the rs2453176 locus, possibly explaining why carriers of the rs2453176 T allele may have an increased risk of lung cancer in smokers than non-smokers.

There are some limitations in the present study. First, we employed the gene set enrichment analysis with a collection of annotated gene sets to define the general mRNA degradation pathway to be investigated, but we may have missed some newly discovered genes in the pathway. However, we searched the literatures and added genes as many as possible. Second, due to the data limitation, we had no access to family history and others factors that may have an impact on lung cancer risk. Third, we used the eQTL analyses from lymphoblastoid cell lines and normal adjacent tissue in TCGA database to validate the risk association. Although the results from the cell lines support our identified association, they may only reflect the baseline or genetically determined expression levels without exposure to smoking. The gene expressions in the normal adjacent lung tissues may be in some degree different from the normal lung tissue and did not support the association.

Overall, the present study of eight published GWASs identified a novel *CNOT6* rs2453176 SNP in the general mRNA degradation pathway to be significantly associated with lung

cancer risk in European populations, and the risk was more evident in smokers than in non-smokers. Although we used the publically available gene expression database from blood to confirm the biological significance of the variant, further functional evaluations in normal lung tissue are warranted to validate our findings.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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TRICL

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deCODE

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Abbreviations

AD	Adenocarcinoma
CI	confidence interval
eQTL	expression quantitative trait loci
FDR	false discovery rate
GWAS	genome-wide association study
ILCCO	International Lung Cancer Consortium
LD	linkage disequilibrium
OR	odds ratio
SC	squamous cell carcinoma
SNP	single nucleotide polymorphisms
TCGA	The Cancer Genome Atlas
TRICL	Transdisciplinary Research in Cancer of the Lung

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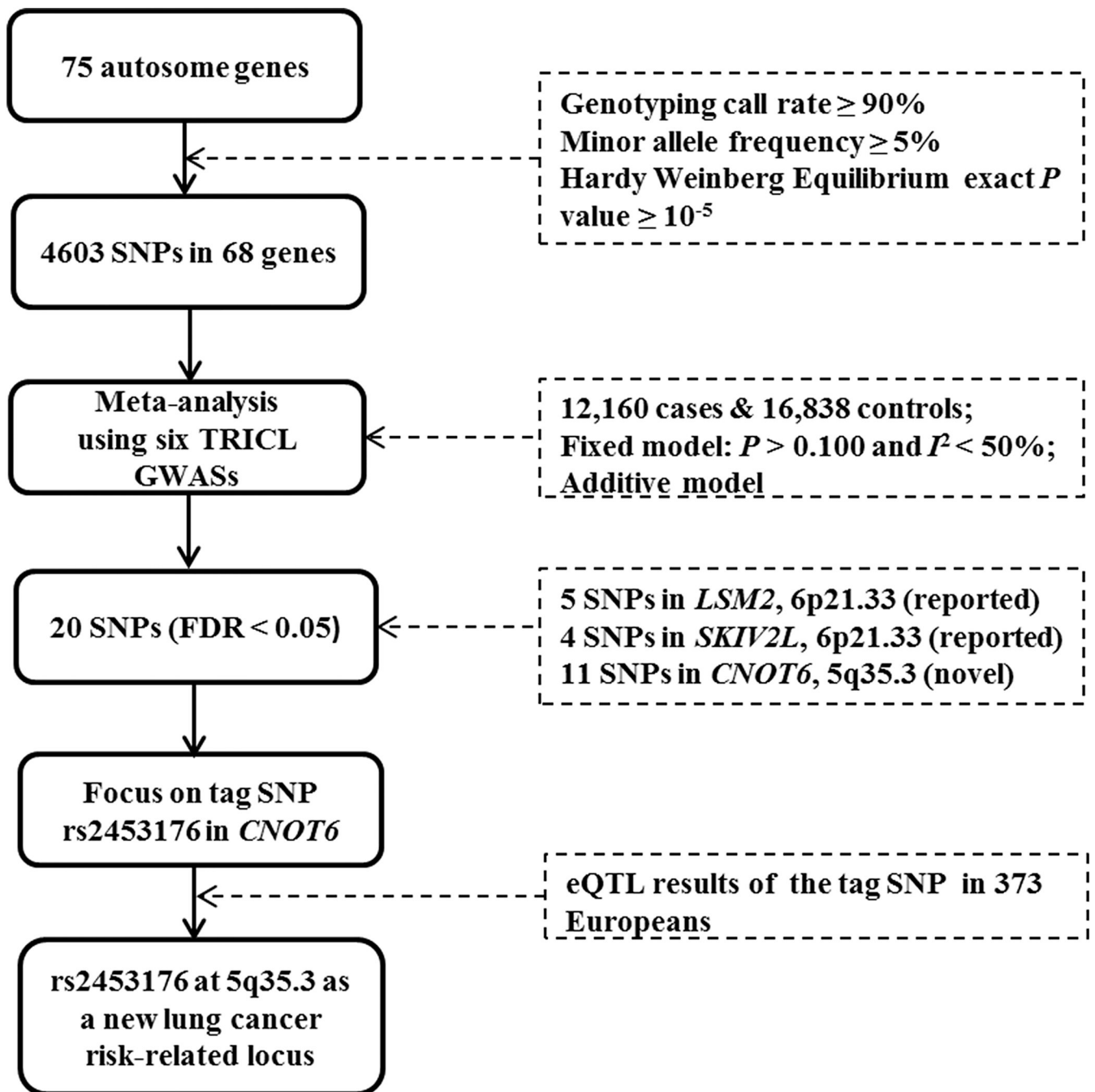


Figure 1. Study workflow

SNP: single nucleotide polymorphism; FDR: false discovery rate; TRICL: Transdisciplinary Research in Cancer of the Lung; GWAS: genome-wide association study; eQTL: expression quantitative trait loci.

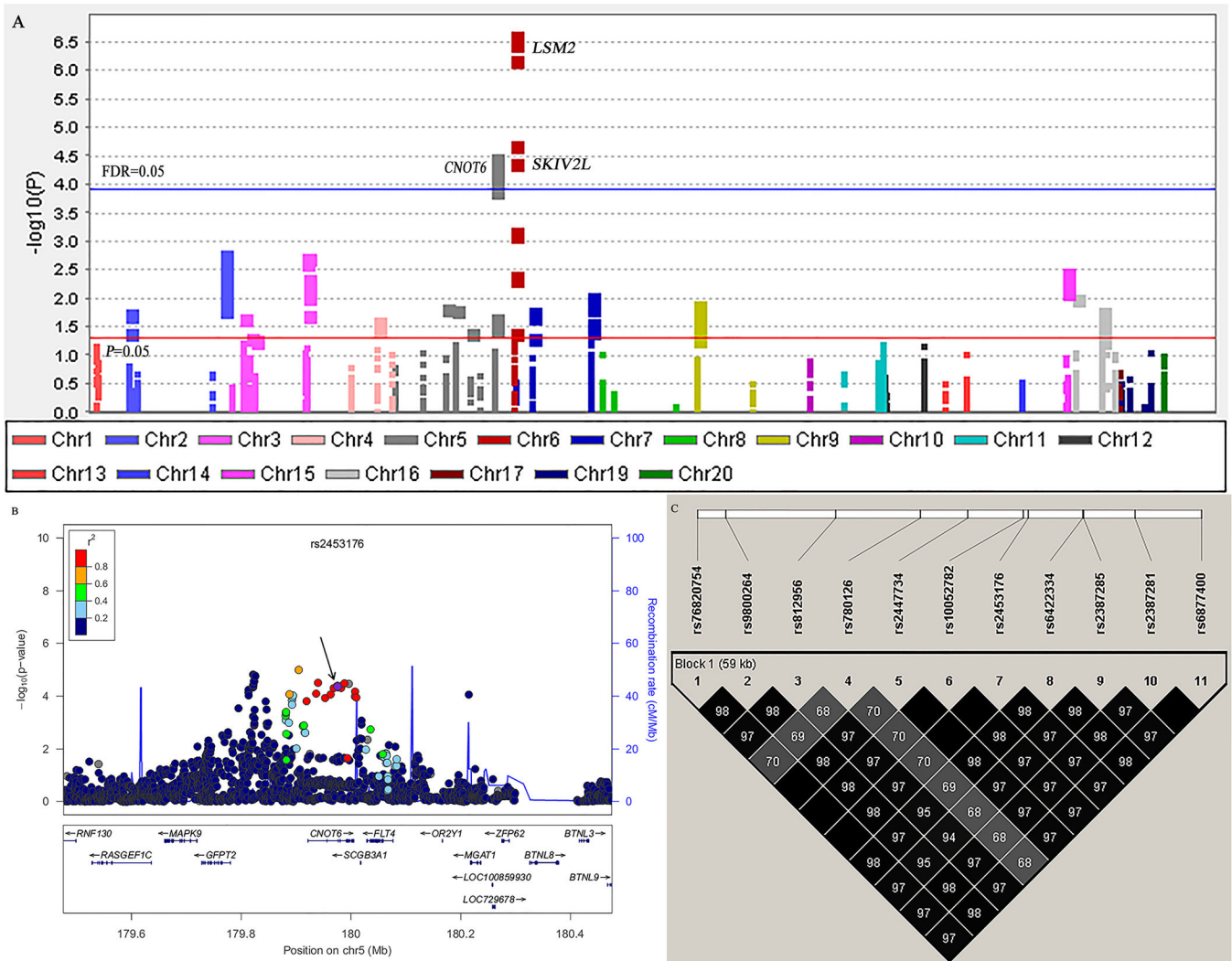


Figure 2. Screening of SNPs in the general mRNA degradation pathway

A, Manhattan Plot of genome-wide association results from the general mRNA degradation pathway in TRICL. The x-axis shows SNPs' positions on each chromosome. The y-axis shows the association P values with lung cancer risk (as $-\log_{10} P$ values). The FDR threshold of 0.05 was shown by a horizontal blue line. The P value of 0.05 was shown by a horizontal red line. **B**, Regional association plot for SNP rs2453176 in 500 kb up- and downstream region. The left-hand y-axis shows P values of the SNPs, which are transformed as $-\log_{10}(P)$ against chromosomal base pair positions. The right-hand y-axis shows the recombination rate estimated from HapMap Data Rel 22/phase II European population; **C**, The linkage disequilibrium plots of 11 SNPs in *CNOT6*. The value within each diamond represents the pairwise correlation between SNPs (measured as r^2) defined by the upper left and the upper right sides of the diamond.

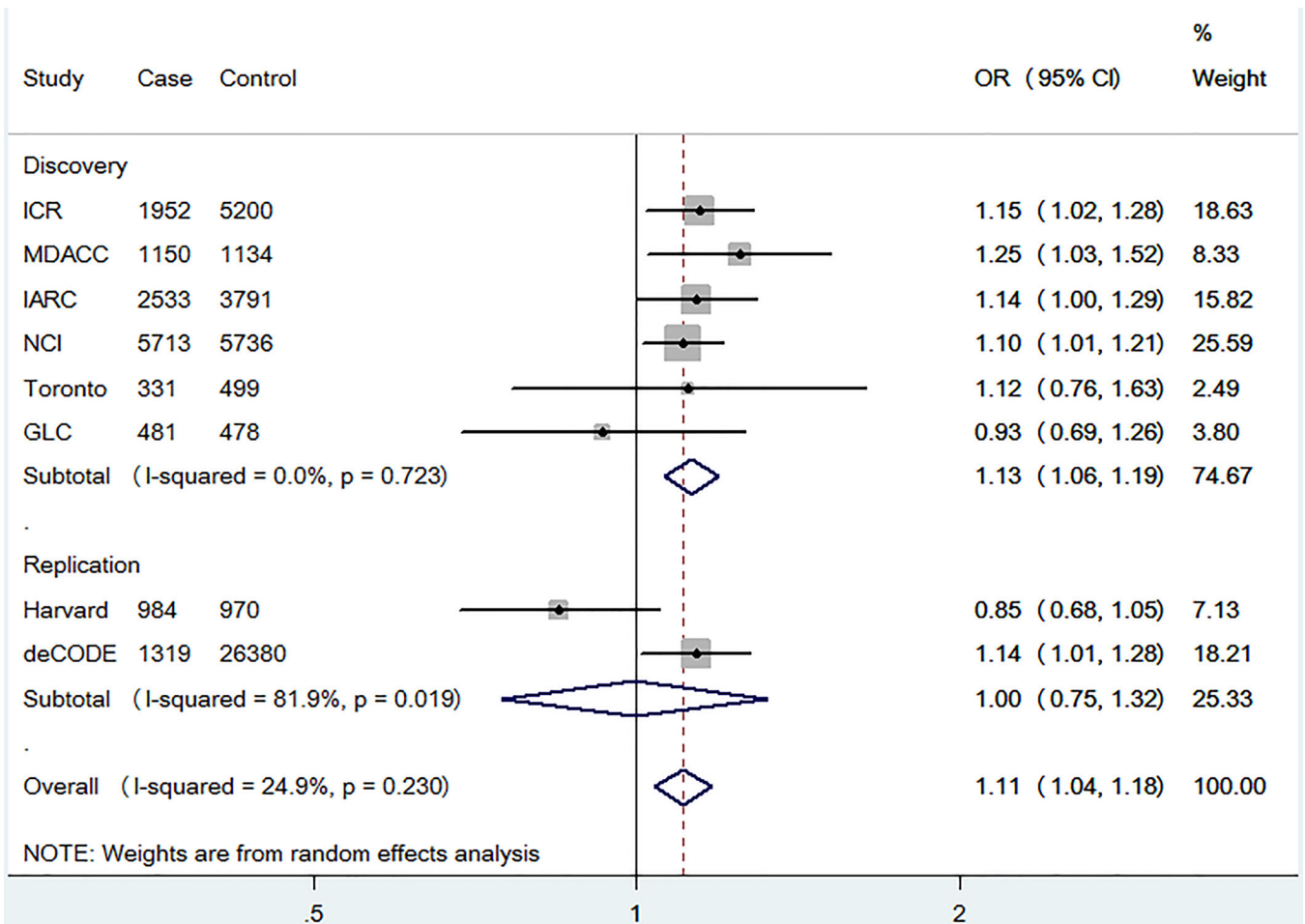


Figure 3. Forest plots for associations between *CNOT6* rs2453176 and lung cancer risk for all participants ($P = 0.0013$).

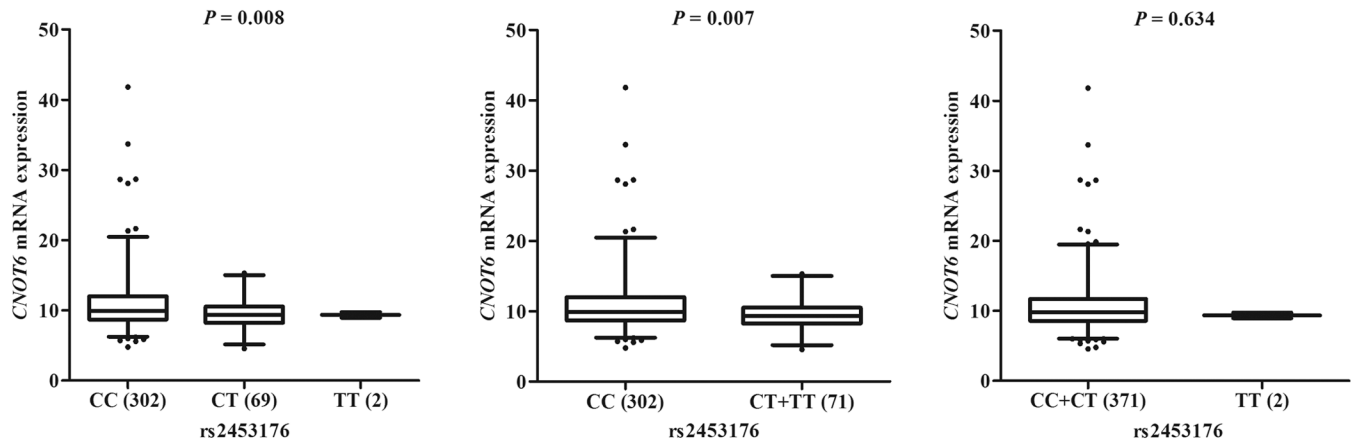


Figure 4. The eQTL analysis of *CNOT6* mRNA expression for rs2453176 with lymphoblastoid cell data of 373 Europeans from 1000 Genomes Project

A. additive model, $P = 0.008$; B. dominant model, $P = 0.007$; C. recessive model, $P = 0.634$.

Table 1

Associations between SNPs in the general mRNA degradation pathway and lung cancer risk with FDR < 0.050 in TRICL GWASs

SNP	Gene	Chr.	Position (hg19)	Allele ^a	EAF	Q ^b	r ²	Effect ^c	OR (95% CI)	P	FDR
rs115834633	<i>LSM2</i>	6	31765984	G/A	0.11	0.200	30.79	+++++	1.20 (1.14–1.27)	3.92E-11	<.0001
rs114312980	<i>LSM2</i>	6	31768799	A/C	0.11	0.230	26.77	+++++	1.20 (1.14–1.27)	4.39E-11	<.0001
rs115801685	<i>LSM2</i>	6	31772093	C/A	0.11	0.220	27.36	+++++	1.20 (1.14–1.27)	4.54E-11	<.0001
rs115489726	<i>LSM2</i>	6	31766660	C/T	0.11	0.240	25.69	+++++	1.20 (1.14–1.27)	8.76E-11	<.0001
rs114637560	<i>LSM2</i>	6	31765864	T/A	0.15	0.260	22.42	+++++	1.14 (1.08–1.20)	3.04E-07	0.0003
rs114984862	<i>SKIV2L</i>	6	31936668	C/T	0.27	0.290	18.64	+++++	1.09 (1.05–1.13)	1.87E-05	0.013
rs9800264	<i>CNOT6</i>	5	179940091	G/A	0.10	0.750	0.00	+++++	1.13 (1.07–1.19)	3.12E-05	0.013
rs2387281	<i>CNOT6</i>	5	179988283	T/C	0.10	0.743	0.00	+++++	1.13 (1.07–1.19)	3.28E-05	0.013
rs6877400	<i>CNOT6</i>	5	179996111	T/C	0.10	0.747	0.00	+++++	1.13 (1.07–1.19)	3.41E-05	0.013
rs116188106	<i>SKIV2L</i>	6	31927342	G/A	0.27	0.298	17.82	+++++	1.09 (1.04–1.13)	3.70E-05	0.013
rs114011334	<i>SKIV2L</i>	6	31928799	C/T	0.27	0.297	17.92	+++++	1.09 (1.04–1.13)	3.77E-05	0.013
rs115002281	<i>SKIV2L</i>	6	31929014	C/A	0.27	0.297	17.95	+++++	1.08 (1.04–1.13)	3.79E-05	0.013
rs10052782	<i>CNOT6</i>	5	179975104	C/T	0.10	0.723	0.00	+++++	1.13 (1.06–1.19)	4.09E-05	0.013
rs64222334	<i>CNOT6</i>	5	179982151	C/T	0.10	0.734	0.00	+++++	1.13 (1.06–1.19)	4.14E-05	0.013
rs2453176	<i>CNOT6</i>	5	179975792	C/T	0.10	0.723	0.00	+++++	1.13 (1.06–1.19)	4.33E-05	0.013
rs2387285	<i>CNOT6</i>	5	179982278	A/G	0.10	0.700	0.00	+++++	1.12 (1.06–1.19)	4.92E-05	0.014
rs2447734	<i>CNOT6</i>	5	179968674	G/C	0.10	0.720	0.00	+++++	1.12 (1.06–1.19)	4.97E-05	0.014
rs76820754	<i>CNOT6</i>	5	179936737	G/A	0.10	0.735	0.00	+++++	1.12 (1.06–1.19)	8.06E-05	0.021
rs780126	<i>CNOT6</i>	5	179963034	C/T	0.13	0.758	0.00	+++++	1.12 (1.06–1.18)	8.67E-05	0.021
rs812956	<i>CNOT6</i>	5	179953048	G/C	0.10	0.653	0.00	+++++	1.12 (1.06–1.18)	1.18E-04	0.027

SNP: single nucleotide polymorphism; FDR: false discovery rate; TRICL: Transdisciplinary Research in Cancer of the Lung; GWAS: genome-wide association study; Chr.: chromosome; EAF: effect allele frequency; OR: odds ratio; CI: confidence interval;

^aReference allele/effect allele;

^bFixed effect models were used when no heterogeneity was found between studies (Q-test $P > 0.100$ and $I^2 < 50.0\%$); otherwise, random effect models were used;

^c“+” means a positive association, and “-” means a negative association.

Linkage disequilibrium between the 11 SNPs of *CNOT6* in European populations included in the 1000 Genomes Project and imputation quality scores

Table 2

SNP	Position (hg19)	D'	r ²	Function prediction			Imputation quality						
				SNPinfo ^d	Regulome DB ^b	Info ICR	Rsq MDACC	Rsq IARC	Info NCI	Info Toronto	Rsq GLC		
rs2453176	179975792			--	1f	1.000	0.999	1.000	1.000	1.000	1.000	1.000	1.000
rs780126	179963034	1.00	0.71	--	--	0.874	0.751	0.703	0.859	0.857	0.784		
rs2387281	179988283	1.00	0.97	--	--	0.998	0.972	0.969	0.996	0.990	0.967		
rs6877400	179996111	1.00	0.97	Splicing site	5	0.998	0.964	0.965	0.996	0.990	0.953		
rs2387285	179982278	1.00	0.97	--	4	0.990	0.966	0.923	0.988	0.981	0.964		
rs812956	179953048	1.00	0.97	--	6	0.991	0.961	0.962	0.988	0.978	0.976		
rs9800264	179940091	1.00	0.99	--	--	0.999	0.970	0.977	0.998	0.993	1.000		
rs6422334	179982151	1.00	0.99	--	5	0.999	0.982	0.976	0.997	0.994	0.979		
rs10052782	179975104	1.00	1.00	--	6	1.000	0.998	1.000	1.000	1.000	1.000		
rs76820754	179936737	1.00	1.00	--	6	1.000	0.970	0.971	0.999	0.998	0.999		
rs2447734	179968674	1.00	1.00	--	--	1.000	0.994	0.999	0.999	0.997	0.999		

SNP: single nucleotide polymorphism;

Imputation quality: Rsq: MaCH r-squared; Info: IMPUTE2 information score;

^a <https://snpinfo.niehs.nih.gov/snpinfo/snpfunc.htm>;

^b <http://regulomedb.org/>.

Table 3

Associations between of *CNOT6* rs2453176 (C>T) and lung cancer risk stratified by histologic types in all eight lung cancer GWASs from ILCCO-TRICL

Study	Overall				AD				SC			
	Case	Control	OR (95% CI)	P	Case	Control	OR (95% CI)	P	Case	Control	OR (95% CI)	P
ICR	1952	5200	1.15 (1.02–1.28)	0.020	465	5200	1.38 (1.12–1.70)	0.002	611	5200	1.14 (0.95–1.38)	0.158
MDACC	1150	1134	1.25 (1.03–1.52)	0.027	619	1134	1.06 (0.92–1.47)	0.206	306	1134	1.45 (1.08–1.94)	0.013
IARC	2533	3791	1.14 (1.00–1.29)	0.053	517	2824	1.13 (0.90–1.42)	0.301	911	2968	1.18 (0.98–1.41)	0.081
NCI	5713	5736	1.10 (1.01–1.21)	0.025	1841	5736	1.17 (1.03–1.33)	0.016	1447	5736	1.04 (0.91–1.20)	0.543
Toronto	331	499	1.12 (0.76–1.63)	0.057	90	499	1.48 (0.83–2.64)	0.186	50	499	1.00 (0.44–2.25)	0.998
GLC	481	478	0.93 (0.69–1.26)	0.064	186	478	1.25 (0.86–1.83)	0.240	97	478	0.90 (0.52–1.54)	0.695
Discovery combined	12160	16838	1.13 (1.06–1.19)	4.33E-05	3818	15871	1.21 (1.11–1.32)	2.04E-05	3424	16015	1.13 (1.03–1.23)	0.009
Harvard	984	970	0.85 (0.68–1.05)	0.133	597	970	0.79 (0.62–1.01)	0.130	216	970	1.08 (0.75–1.56)	0.678
deCODE	1319	26380	1.14 (1.01–1.28)	0.032	547	26380	1.02 (0.85–1.21)	0.858	259	26380	1.11 (0.86–1.43)	0.436
Replication combined	2303	27350	1.00 (0.75–1.32)	0.098	1144	27350	0.91 (0.71–1.16)	0.449	475	27350	1.10 (0.89–1.36)	0.381
Overall	14463	44188	1.11 (1.04–1.18)	0.001	4862	43221	1.13 (1.00–1.27)	0.050	3897	43365	1.12 (1.03–1.22)	0.006

GWAS: genome-wide association study; ILCCO: International Lung Cancer Consortium; TRICL: Transdisciplinary Research in Cancer of the Lung; AD, adenocarcinoma; SC, squamous cell carcinoma; OR: odds ratio; CI: confidence interval

Homogeneity tests suggest that there is no heterogeneity between the subgroups of AD and SC in each GWAS and overall result ($P > 0.05$).

Associations between of *CNOT6* rs2453176 (C>T) and lung cancer risk stratified by smoking status in six lung cancer GWASs from ILCCO-TRICL Consortium

Table 4

Study	Smoker				Non-smoker			
	Case	Control	OR (95% CI)	P	Case	Control	OR (95% CI)	P
MDACC	1150	1134	1.25 (1.03–1.52)	0.027				
IARC	2367	2508	1.12 (0.97–1.29)	0.131	159	1253	1.40 (0.94–2.09)	0.096
NCI	5342	4336	1.10 (1.00–1.22)	0.058	350	1379	0.99 (0.72–1.37)	0.972
Toronto	236	272	1.14 (0.70–1.86)	0.606	95	217	1.13 (0.61–2.11)	0.702
GLC	433	258	1.00 (0.67–1.49)	0.995	35	220	1.64 (0.71–3.82)	0.250
Harvard	892	809	0.87 (0.70–1.09)	0.221	92	161	0.71 (0.38–1.33)	0.288
Overall	10420	9317	1.09 (1.02–1.17)	0.011	731	3230	1.10 (0.89–1.36)	0.363

GWAS: genome-wide association study; ILCCO: International Lung Cancer Consortium; TRICL: Transdisciplinary Research in Cancer of the Lung; OR: odds ratio; CI: confidence interval. Homogeneity tests suggest there is no heterogeneity between the subgroups of smoker and non-smoker in each GWAS and overall result ($P > 0.05$).