

Next-generation sequencing-based identification of EGFR and NOTCH2 complementary mutations in non-small cell lung cancer

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Abstract. Although targeted therapy has emerged as an effective treatment strategy for non-small cell lung cancer (NSCLC), some patients cannot benefit from such therapy due to the limited number of therapeutic targets. The present study aimed to identify mutated genes associated with clinicopathological characteristics and prognosis and to screen for mutations that are not concurrent with applicable drug target sites in patients with NSCLC. Tumor tissue and blood samples were obtained from 97 patients with NSCLC. A lung cancer-specific panel of 55 genes was established and analyzed using next-generation sequencing (NGS). The results obtained from the clinical cohort were compared with the NSCLC dataset from The Cancer Genome Atlas (TCGA). Subsequently, 25 driver genes were identified by taking the intersection of the 55 lung-cancer-specific genes with three databases, namely, the Catalog of Somatic Mutations in Cancer database, the Network of Cancer Genes database and Vogelstein's list. Functional annotation and protein-protein interaction analysis were conducted on these 25 driver genes. The χ^2 test and logistic regression were used to evaluate the association between mutations in the 25 driver genes and the clinicopathological characteristics of 97 patients, and phosphatase and tensin homolog (PTEN) and kirsten rat sarcoma viral oncogene homolog (KRAS) were associated with stage at diagnosis and sex, respectively, while epidermal growth factor receptor (EGFR) was associated with sex, stage at diagnosis, metastasis, CEA and CYFRA21-1. Moreover, the association between the 25 driver gene mutations and overall survival were examined using Cox regression analysis. Age and Notch homolog 2 (NOTCH2) mutations were independent prognostic

factors in TCGA dataset. The correlations between statistically significant mutations in EGFR, KRAS, PTEN and NOTCH2 were further examined, both in the clinical data and TCGA dataset. There was a negative correlation between EGFR and NOTCH2 mutations (correlation coefficient, -0.078; $P=0.027$). Thus, the present study highlights the importance of NOTCH2 mutations and might provide novel therapeutic options for patients with NSCLC who do not harbor EGFR mutations.

Introduction

According to the 2018 Global Cancer Statistics, lung cancer has the highest morbidity and mortality among all malignant diseases (1). Although the incidence of lung cancer is similar in China and the USA, the mortality of lung cancer in China is 1.4 times greater than that in the USA, and the number of deaths has been gradually increasing every year (2). The clinical management of lung cancer has improved with the in-depth understanding of its molecular pathogenesis. Targeted therapies have achieved significant improvement in patient outcomes and quality of life compared with radiotherapy and chemotherapy (3), especially in patients with epidermal growth factor receptor (EGFR) mutations (4,5). Different from the general applicability of radiotherapy and chemotherapy, targeted therapy is primarily based on the presence or absence of certain genes and mutations, which are mainly identified using sequencing technologies (6,7).

Next-generation sequencing (NGS) is an innovative sequencing technology involving 'massively parallel' sequencing. It has higher sensitivity and is more cost-effective and less time-consuming compared with the single-gene mutation and/or partial exon variation analysis, such as PCR-based analysis, Sanger sequencing or pyrosequencing (8). As targeted anticancer medications have been included in health insurance in China, NGS and targeted therapy drugs are becoming more widely applied in clinical medicine. Activating mutations in EGFR are the prevalent targetable mutations in lung adenocarcinoma. Currently, first-, second- and third-generation Food and Drug Administration (FDA)-approved tyrosine kinase inhibitors (TKIs) are in use (9,10). For example, in the treatment of advanced anaplastic lymphoma kinase (ALK)-positive non-small cell lung cancer (NSCLC), lorlatinib is a potent,

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brain-penetrant, third-generation ALK/repressor of silencing 1 TKI with robust clinical activity (11).

Therapeutic strategies only focus on mutation sites that can be targeted by drugs recommended by The American Society of Clinical Oncology (12) or The Chinese Society of Clinical Oncology (13) guidelines. When no such mutations have been identified, targeted therapy would be considered not applicable. Moreover, immunotherapy is also not generally accepted, owing to high costs, and therefore chemotherapy becomes the only viable option (14). However, in clinical practice, the vast majority of patients may eventually give up chemotherapy, due to severe side effects or chemoresistance, failure to prolong survival and even death (15). Thus, it is still of great importance to further identify genetic mutations that are closely related to the poor prognosis and clinicopathological characteristics of patients with lung cancer, thus promoting research and development of new drugs with target mutation sites that are complementary to currently applied targets.

The aim of the present study was to identify mutations that were not concurrent with applicable drug target sites. A lung cancer-specific panel of 55 genes was established by multigenic screening in order to analyze gene mutations in 97 patients with NSCLC. Moreover, these 55 genes were further analyzed using a mutation dataset of NSCLC obtained from The Cancer Genome Atlas (TCGA) database. By comparing to the Catalog of Somatic Mutations in Cancer (COSMIC) database, Network of Cancer Genes (NCG) database and Vogelstein's list (16), 25 driver genes, in which acquired mutations or expressed aberrantly are causally linked to cancer progression, were identified out of the 55 genes and subjected to functional annotation and protein-protein interaction (PPI) analysis. Subsequently, the associations between mutations in the 25 driver genes and clinicopathological characteristics of 97 patients were examined. Using TCGA, the association between the mutations in the 25 driver genes and overall survival of 701 patients was analyzed. Furthermore, the relationships between genes of clinical significance, including EGFR, kirsten rat sarcoma viral oncogene homolog (KRAS) and phosphatase and tensin homolog (PTEN) and Notch homolog 2 (NOTCH2), were analyzed in TCGA data and in the clinical data obtained from the patients. The findings of the present study may promote the development of new drugs targeting these mutations and provide new therapeutic options for patients lacking suitable drug target sites.

Materials and methods

Patients and samples. A total of 97 patients with NSCLC admitted in The Affiliated Hospital of Chengde Medical University (Hebei, China) from November 2018 to July 2020 were enrolled in the current study. The present study was approved by the Research Ethics Review Committee of Chengde Medical University (Hebei, China; approval no. 2017003) and written informed consent was provided by all patients prior to the study start. The inclusion criteria were: i) Patients had a clear clinical diagnosis of NSCLC; ii) detailed clinical data were recorded accurately and completely, including the patient's sex, age, smoking history, histological type, clinical stage at diagnosis, T classification, N classification, M classification, the levels of tumor markers [carcinoembryonic antigen (CEA), neuron-specific enolase (NSE), cytokeratin 19 fragment 21-1

(CYFRA21-1), squamous-cell carcinoma antigen (SCC) and cancer antigen 125 (CA125)]; clinical staging was based on the American Joint Committee on Cancer (AJCC) Classification (8th edition) (17); and iii) patients with available samples, including formalin-fixed and paraffin-embedded (FFPE) tissues and blood. The patient data (97 patients) used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

The tumor tissues were collected and fixed in 4% formalin at 4°C for 30 min, dehydrated and embedded in paraffin. Sample sections were cut to 5- μ m thickness. Blood samples (5 ml) were collected in ethylene diamine tetra-acetic acid anticoagulant tubes and gently inverted 8-10 times. All the patients had no history of blood transfusion within 4 weeks and fasted for 8-12 h prior to blood sample collection. None of the blood samples used for NGS had signs of hemolysis, lipid turbidity or jaundice.

A TCGA dataset (Nat Genet 2016) (18) containing data from 1,144 lung cancer patient samples were downloaded from cBioPortal database (v3.0.2; <http://www.cbioportal.org/>). For survival analysis, 701 patients among the 1,144 samples in the TCGA dataset who met the inclusion criteria were included in the present study. The inclusion criteria were: i) Patients had a clear clinical diagnosis of NSCLC; ii) detailed clinical data were recorded accurately and completely, including the patient's sex, age, smoking history, histologic type, clinical stage at diagnosis, T classification, N classification, M classification, overall survival status and time; and iii) the mutations status of the 25 driver genes was described.

In addition, the intersection of the mutated genes of patients with NSCLC and the mutations in TCGA dataset were analyzed using Venn software (<http://www.bioinformatics.com.cn/static/others/jvenn/index.html>).

Design and general performance of the lung cancer-specific 55-gene NGS panel. A lung cancer-specific 55-gene NGS panel was established. The inclusion criteria for the gene panel were: i) Genes from FDA-approved and/or National Comprehensive Cancer Network-recommended drugs for the treatment of NSCLC; ii) genes annotated by databases, such as Clinical Knowledgebase (<https://ckb.jax.org/>; updated in October 2017), Oncology Knowledge Base (OncoKB; <http://oncokb.org/>; updated in December 2019;), cBioPortal, My Cancer Genome database (<https://www.mycancergenome.org/>; updated in April 2019) and Clinical Trials (<https://clinicaltrials.gov/>; updated in June 2018); and iii) genes involved in clinical studies that have been previously reported in detail.

Genomic DNA was extracted from blood samples using the QIAamp DNA Blood Mini kit (cat. no. 51106; Qiagen GmbH) and from FFPE tissues using the GeneRead DNA FFPE kit (cat. no. 180134; Qiagen GmbH). Concentration of extracted Genomic DNA (gDNA) was measured using a Qubit 3.0 fluorometer (Thermo Fisher Scientific, Inc.) and purity was measured by a spectrophotometer. DNA had a concentration of at least 50 ng/ μ l with an OD 260/280 between 1.8-2.0. DNA integrity was assessed using 1% agarose gel electrophoresis.

The gDNA was fragmented randomly by Covaris to generate gDNA fragments with a maximum of 250 bp and then subjected to three enzymatic steps: End-repair, A-tailing and adapter ligation. DNA libraries were purified with Agencourt

AMPure XP beads (Beckman Coulter, Inc.), and PCR was performed. A TrueSeq DNA library preparation kit (Illumina, Inc.) was used to prepare the sequencing library according to the manufacturer's protocol. Target sequences were enriched using commercial hybridization probes (Nimblegen, Roche, <https://www.roche.com>) designed for human DNA regions of our interest. The panel included the following 55 genes: SLC19A1, ERCC1, TP53, ABCB1, XRCC1, DHFR, PAPD7, MTHFR, CDA, XPC, RRM1, ESR2, GGH, EGFR, SLC29A1, GSTP1, NT5C2, PTEN, DYNC2H1, DCK, SOD2, UGT1A1, CMPK1, RB1, CDC5L, KRAS, PIK3CA, CTNNB1, TERT, BRAF, ERBB2, NOTCH2, ALK, RET, PDGFRA, FBXW7, FGFR3, MET, MUC4, NOS3, ROS1, KIT, CD3EAP, ERBB4, MTOR, NRAS, APC, NF1, SMAD4, SMO, STK11, TPMT, VHL, KDM6A and TYMS. The hybridization product was subsequently purified, amplified and qualified. Finally, sequencing was performed on the Illumina next500 platform (Illumina, Inc.). Raw data in FASTQ format were processed to remove reads containing adapters, reads containing ploy-N, and low-quality reads. All variants had >99% confidence, as well as an average sequencing depth of over 500X. Structural variations were annotated using the Refseq release 96 (<http://www.ncbi.nlm.nih.gov/refseq/>) and Gencode gene annotation library (<https://www.gencodegenes.org/>). Waterfall plots and Circos plots were generated using R software (v 3.6.1; <https://www.R-project.org>).

Identification of driver gene. Three databases were used to identify driver genes, including the COSMIC database, NCG database, and Vogelstein's list. The COSMIC database is the largest and most comprehensive resource for exploring the impact of somatic mutations in human cancer in the world, which contains 576 genes. The NCG database is a manually curated repository of 2,372 genes whose somatic modifications have known (711 genes) or predicted (1,661 genes) cancer driver roles (19), and 125 mutated driver genes were identified in Vogelstein's study with a total of 294,881 mutations being reported (16). The intersection of the common mutant genes both in clinical and TCGA data and the specific genes in the three databases were analyzed using Venn software (v2.0; <http://www.bioinformatics.com.cn/static/others/jvenn/index.html>).

Actionable target analysis. The analysis of actionable mutations was carried out using the Pharmacogenomics Knowledgebase (PharmGKB; <http://www.pharmgkb.org/>) for single nucleotide polymorphisms (SNPs) and OncoKB for single nucleotide variants (SNVs). The variants-drug relationships were compiled by combining the mutation data and the two annotation databases. The SNPs were evaluated using the PharmGKB database to identify potentially actionable variants that could reflect the efficacy and toxic side effects of chemotherapeutic drugs. The SNV variant sites, which may guide targeted therapy, were annotated using the OncoKB database, which is a comprehensive precision oncology database that offers evidence-based drug information on FDA-approved therapies and other investigational agents. The final list was filtered based on previously published preclinical data and clinical trials in cancer.

Function annotation analysis. Gene Ontology (GO) annotation and Kyoto Encyclopedia of Genes and Genomes (KEGG)

pathway enrichment analysis were performed using the DAVID v6.8 online tool (<https://david-d.ncicrf.gov/>). GO functional categories included biological process, cellular component and molecular function. Statistically significant terms were determined using a two-sided $P < 0.05$.

Pathogenicity prediction. Variant deleteriousness was predicted using the Polymorphism Phenotyping version 2 (Polyphen-2) database (v2.2.2; <http://genetics.bwh.harvard.edu/pph2/>) (20) and the MutationTaster web-based tool (v2; <http://www.mutationtaster.org/>) (21). The Polyphen-2 score and the MutationTaster score were calculated. Specifically, the effects of SNVs and SNPs were evaluated using the Polyphen-2 database and classified into three categories (probably damaging, possibly damaging and benign), based on their predicted effect on protein function. The insertions and deletions (indels) were analyzed by the MutationTaster tool, which categorizes mutations into one of four possible types: i) Disease-causing (probably deleterious); ii) disease-causing automatic (known to be deleterious); iii) polymorphism (probably harmless); and iv) polymorphism automatic (known to be harmless).

PPI network construction and mutual exclusivity analysis. The PPI network was analyzed using the STRING online tool (v11.0; <https://string-db.org/>). The list of official gene names was imported into STRING and the species was set to *Homo sapiens*. The medium confidence was set to 0.400. The MCODE plug-in in Cytoscape (v3.6.2, www.cytoscape.org) was used to screen for PPI network modules with the following parameters: i) Degree cutoff, 2; ii) node score cutoff, 0.2; iii) k-core, 2; and iv) max depth, 100. The hub genes were defined by the maximal clique centrality (MCC) algorithm in the cytoHubba plug-in in Cytoscape. Mutual exclusivity analysis was performed on driver genes using the mutual exclusivity tool in the cBioPortal database.

Statistical analysis. Statistical analysis was performed using SPSS software (version 19; SPPS, Inc.). All metric and normally distributed data are presented as mean \pm standard deviation, non-normally distributed data as median (25-75th percentile), and n (%) for categorical data. Scatter plots were plotted using GraphPad Prism 8.0 (GraphPad Prism Software Inc.).

The clinicopathological characteristics from the patients with NSCLC (with or without mutations) were compared using the χ^2 or Fisher's exact test if the expected cell value was < 5 . The factors with two-sided $P < 0.1$ were considered potentially significant. Furthermore, logistic regression was used to evaluate the correlations between these factors. Logistic, ordered logistic and multinomial logistic regression analysis were used for binary, ordered and unordered categorical outcome variable analysis, respectively. If the two-sided P-value of the parallelism test was < 0.05 in the ordered logistic regression, multinomial logistic regression was used. Two-sided $P < 0.05$ was considered to indicate a statistically significant difference.

For survival analysis, 701 patients among the 1,144 samples in the TCGA dataset who met the inclusion criteria were included in this study. Univariate Cox regression analysis was used to screen for significant variables (two-sided $P < 0.05$).

for multivariate Cox analysis. The Kaplan-Meier method and log-rank test were used to generate and analyze the survival curves.

Following the integration of 97 patient data and 701 TCGA data, the correlations among EGFR, PTEN, KRAS and NOTCH2 mutations were assessed using Kendall's τ -b correlation test. $P < 0.05$ was considered to indicate a statistically significant difference. Correlation coefficient (CC) values range from +1 to -1, with positive value representing positive correlation and negative value representing negative correlation and 0 value representing no correlation.

Results

Clinicopathological characteristics of the patients with NSCLC. The clinicopathological characteristics of the 97 patients are presented in Table I. A total of 46 (47.4%) patients were males and 51 (52.6%) were females. The patient age ranged from 28-75 years, with a median age of 59 years. Patients aged >60 years accounted for 42.3% (41/97) of the cohort, whereas those aged ≤ 60 years old represented 57.7% (56/97). Moreover, 21 (21.6%) patients had smoking history, while 76 (78.4%) patients had never smoked. For the histological type, 80 (82.5%) patients had adenocarcinoma, 12 (12.4%) patients had squamous cell carcinoma and 5 patients (5.1%) had other NSCLC types. According to the AJCC clinical staging criteria, 10 (10.3%) patients had stage I or II, 12 (12.4%) had stage III and 75 (77.3%) had stage IV. In terms of TNM classification, 11 (11.3%) patients were of T1 classification, 45 (46.4%) were of T2 classification, 21 (21.7%) were of T3 classification and 20 (20.6%) were of T4 classification. In addition, 16 (16.5%) patients had N0 classification, 10 (10.3%) had N1 classification, 43 (44.3%) had N2 classification and 28 (28.9%) had N3 classification. A total of 23 (23.7%) patients were of M0 classification and 74 (76.3%) were of M1 classification. Moreover, 66 (68.0%), 49 (50.5%), 67 (69.1%), 8 (8.2%), and 52 (53.6%) patients exhibited increased CEA, NSE, CYFRA21-1, SCC, and CA-125, respectively.

Mutational analysis. A lung cancer-specific 55-gene panel was established and analyzed using NGS. All 97 patients harbored gene mutations and the mutational profile of 55 genes was summarized in Fig. 1A. The most frequent gene mutations were found in SLC19A1 (100%), ERCC1 (94%), ABCB1 (92%), TP53 (90%) and XRCC1 (90%). Overall, five types of mutations were observed, namely SNVs, SNPs, indels, copy number variants (CNVs) and fusions. SNVs mostly occurred in the EGFR, PTEN, RB1 and KRAS genes, which were either confirmed or potential molecular targets, while the common mutation types of SLC19A1 and ERCC1 genes were identified as SNPs, which could reflect chemotherapeutic drug efficacy and toxic side effects. Some genes, such as TP53 and EGFR, displayed both SNVs and SNPs. The other three mutation types were less observed in this study. Indels occurred in 13 genes in total. Only EGFR harbored a CNV and ALK harbored a fusion.

The chromosomal locations of the 55 genes were then examined (Fig. 1B). Chromosomes 1 and 7 were enriched in most of the genes (12 in total) followed by chromosomes 3, 4 and 6. Among the 55 genes, SLC19A1, which had the highest frequency of the SNPs, was located on chromosome 21 and

Table I. Clinicopathological characteristics of patients with non-small cell lung cancer.

Clinicopathological characteristics	n (%)
Total	97 (100.0)
Sex	
Male	46 (47.4)
Female	51 (52.6)
Age, years	
≤ 60	56 (57.7)
> 60	41 (42.3)
Smoking history	
Never smoker	76 (78.4)
Current/Former	21 (21.6)
Histological type	
Adenocarcinoma	80 (82.5)
Squamous cell carcinoma	12 (12.4)
Other	5 (5.1)
Stage at diagnosis	
I/II	10 (10.3)
III	12 (12.4)
IV	75 (77.3)
T classification	
T1	11 (11.3)
T2	45 (46.4)
T3	21 (21.7)
T4	20 (20.6)
N classification	
N0	16 (16.5)
N1	10 (10.3)
N2	43 (44.3)
N3	28 (28.9)
M classification	
M0	23 (23.7)
M1	74 (76.3)
CEA, ng/ml	
≤ 5	31 (32.0)
> 5	66 (68.0)
NSE, ng/ml	
≤ 16.3	48 (49.5)
> 16.3	49 (50.5)
CYFRA21-1, ng/ml	
≤ 3.3	30 (30.9)
> 3.3	67 (69.1)
SCC antigen, ng/ml	
≤ 2.7	89 (91.8)
> 2.7	8 (8.2)
CA125, U/ml	
≤ 35	45 (46.4)
> 35	52 (53.6)

CEA, carcinoembryonic antigen; NSE, neuron-specific enolase; CYFRA21-1, cytokeratin 19 fragment 21-1; SCC, squamous cell carcinoma; CA125, cancer antigen 125.

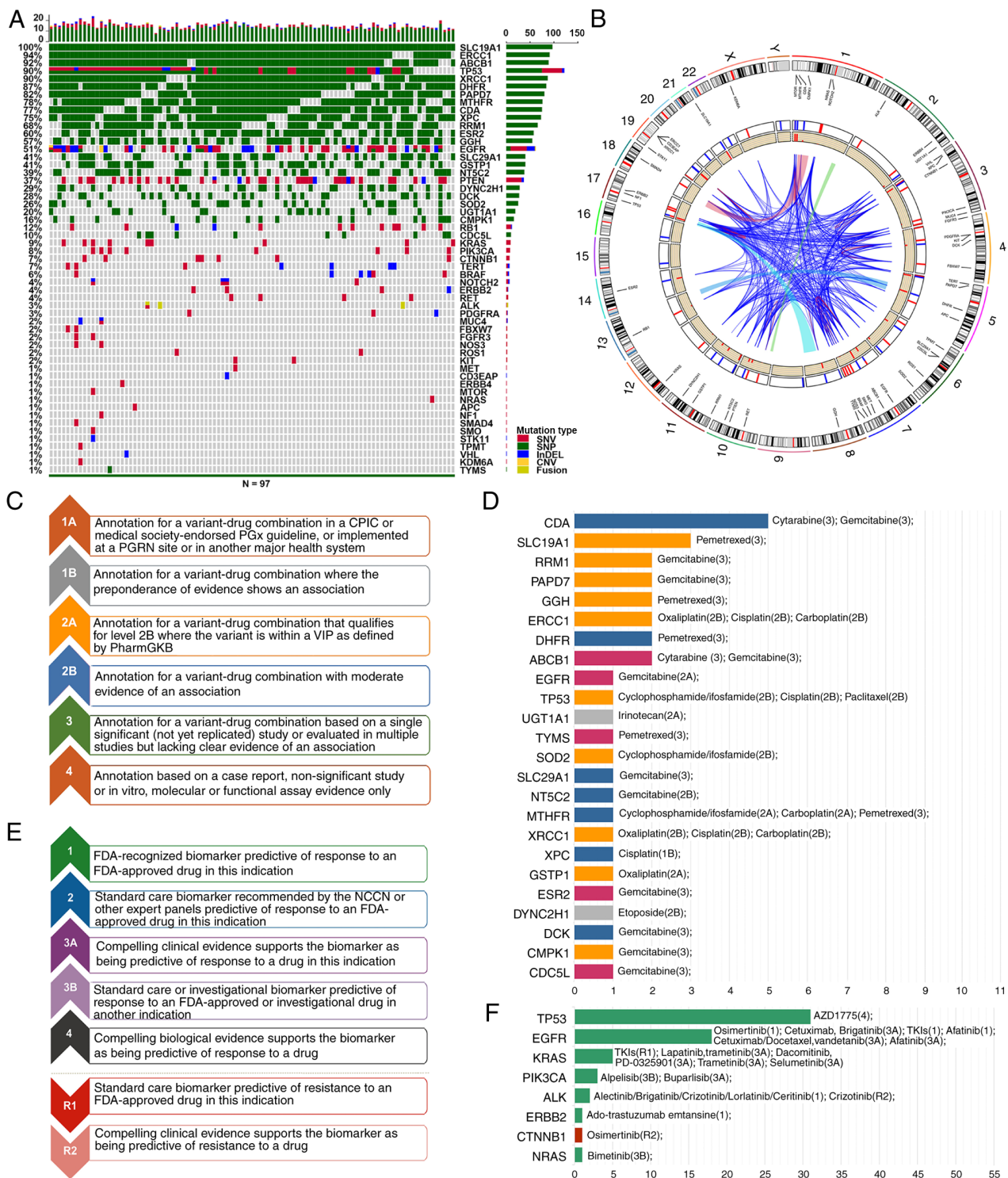


Figure 1. Mutational analysis of 55 lung cancer-specific genes in 97 patients with NSCLC. (A) Waterfall plot of mutational landscape. The 55 mutated genes identified using NGS were ranked by mutant frequency. Each row represents a gene and each column represents a patient. (B) Circos view of the 55 mutant genes on chromosomes. Starting from the outside, the first circle indicates the distribution of the 55 genes across the human genome indicated by lines. The second circle represents two therapeutic modalities: Chemotherapy (blue) and targeted therapy (red). The third circle represents the gene mutation rates. The lines in the center area represent interconnections among 55 genes. (C-F) Actionable analysis of 55 gene mutations. (C) Evidence levels of the PharmGKB database. (D) Number of SNPs and drug annotation information. Each horizontal bar represents a gene. The x-axis indicates the number of mutations. The mutation sites were annotated using the PharmGKB database, and the corresponding chemotherapeutic drugs and their evidence levels are shown. The color of columns represents the drug efficacy and the toxic side effects. Yellow represents better drug efficacy and purple represents worse drug efficacy. Gray represents lower toxic side effects and blue represents higher toxic side effects. (E) Evidence levels of the OncoKB database. (F) Number of SNVs and drug annotation information. Each horizontal bar represents a gene. The x-axis indicates the number of mutations. The mutation sites were annotated using the OncoKB database, and the corresponding targeted drugs and their evidence levels are shown. The color of columns represents drug susceptibility. Green represents sensitivity to annotated drugs and red represents resistance to annotated drugs. FDA, Food and Drug Association; NSCLC, non-small cell lung cancer; NGS, next-generation sequencing; PharmGKB, Pharmacogenomics Knowledgebase; SNP, single nucleotide polymorphism; OncoKB, Oncology Knowledge Base; SNV, single nucleotide variants; CNV, copy number variants; CPIC, Clinical Pharmacogenetics Implementation Consortium; PGx, pharmacogenomics; PGRN, Pharmacogenomics Research Network; VIP, Very Important Pharmacogene, FDA, Food and Drug Administration; NCCN, National Comprehensive Cancer Network.

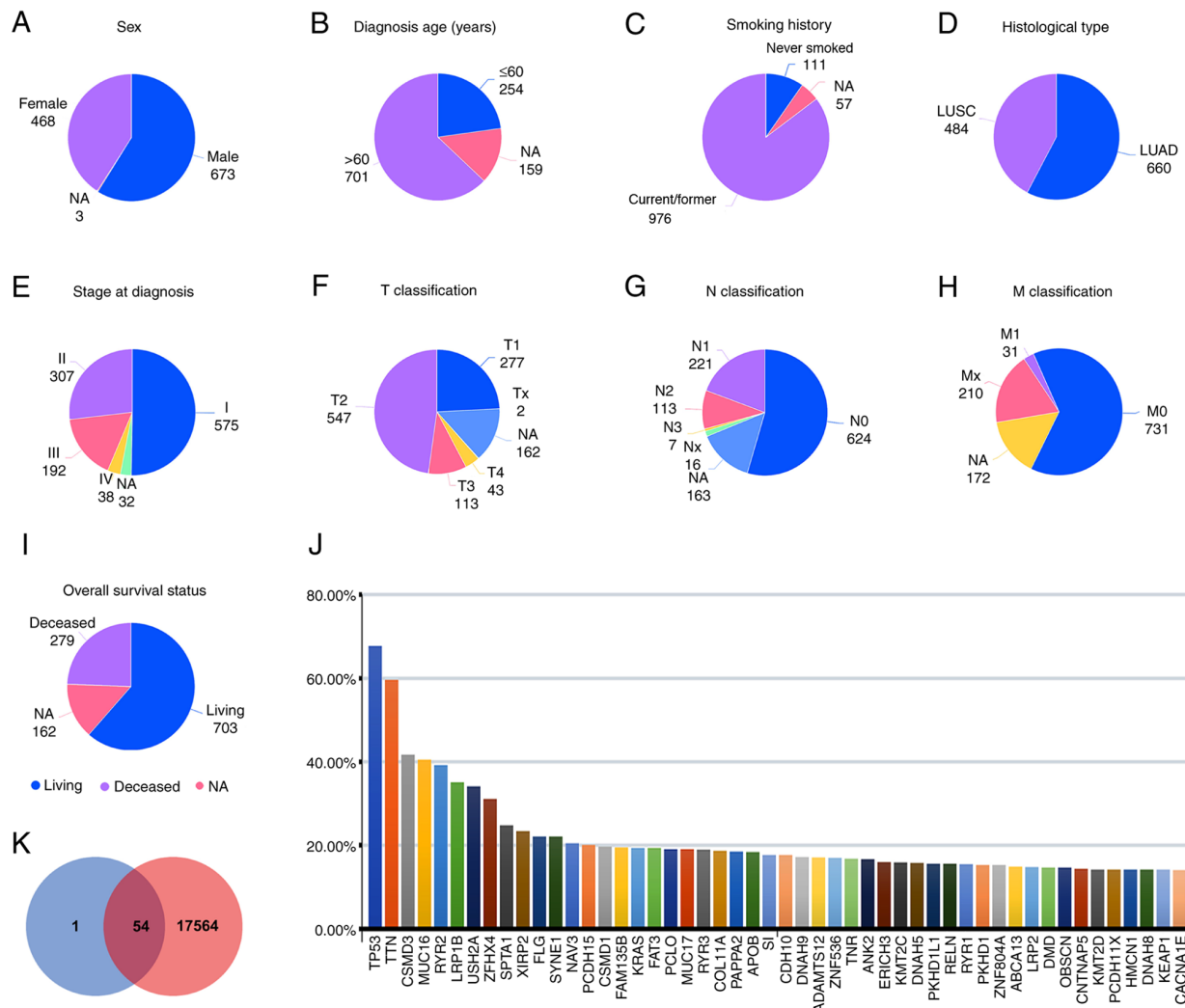


Figure 2. Comparison with the TCGA database. Distribution of clinicopathological characteristics including (A) sex, (B) diagnosis age, (C) smoking history, (D) histologic type, (E) stage at diagnosis, (F) T classification, (G) N classification, (H) M classification and (I) overall survival status. (J) Top 50 genes with the highest mutation frequencies. (K) Venn diagram of genes shared in the clinical data and TCGA dataset. The lung cancer-specific 55-gene NGS panel is shown in blue and the mutational profile of the TCGA dataset is shown in red. TCGA, The Cancer Genome Atlas; NGS, next-generation sequencing; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; NA, not available.

EGFR, which had the highest SNV frequencies, was mapped to chromosome 7 (Fig. 1B; outer circle).

Moreover, 33 genes were therapeutic targets and 24 genes could reflect efficacy and toxic side effects of chemotherapeutic drugs. Among them, EGFR and TP53 could be used to indicate the applicability of both targeted therapy and chemotherapeutic drugs (Fig. 1B; middle circle). Mutation rates were consistent with the results shown in Fig. 1A (Fig. 1B; innermost circle). Additionally, a total of 386 interactions among 54 genes constituting a gene-gene network was identified. Only one gene, CDC5L, did not interact with any other gene.

To evaluate the actionable mutations that could guide treatment decisions, the annotated information in PharmGKB and OncoKB databases was added to the lung cancer-specific 55-gene panel. A total of 24 SNPs that could reflect the efficacy and the toxic side effects of chemotherapeutic drugs were identified using the PharmGKB database (Fig. 1C and D). Among them, 7 genes (CDA, DHFR, SLC29A1, NT5C2, MTHFR, XPC and DCK) were associated with highly toxic side effects, while UTG1A1 and DYNC2H1 indicated low

toxic side effects. A total of 10 gene mutations (SLC19A1, RRM1, PAPD7, GGH, ERCC1, TP53, SOD2, XRCC1, GSTP1 and CMPK1) were associated with good drug efficacy. Among them, the p.Pro72Arg mutation in TP53 suggested that cisplatin, cyclophosphamide and ifosfamide, might show better efficacy and lower toxic side effects. ABCB1, EGFR, TYMS, ESR2 and CDC5L were associated with poor drug efficacy.

In addition, the OncoKB database was used to annotate confirmed or potential target genes (Fig. 1E). Altogether, 8 genes were identified as the targets of FDA-approved or other evidence-supported drugs (Fig. 1F). Only one actionable mutation in CTNNB1 indicated resistance to osimertinib, suggesting that osimertinib should not be recommended for patients with CTNNB1 mutations. The mutations in the remaining genes reflected sensitivity to the corresponding targeted therapy drugs. Although TP53 had the most targeted sites, only the drug AZD1775 was annotated as the lowest supporting level (level 4, Fig. 1F). Moreover, EGFR had up to 18 actionable mutations targeted

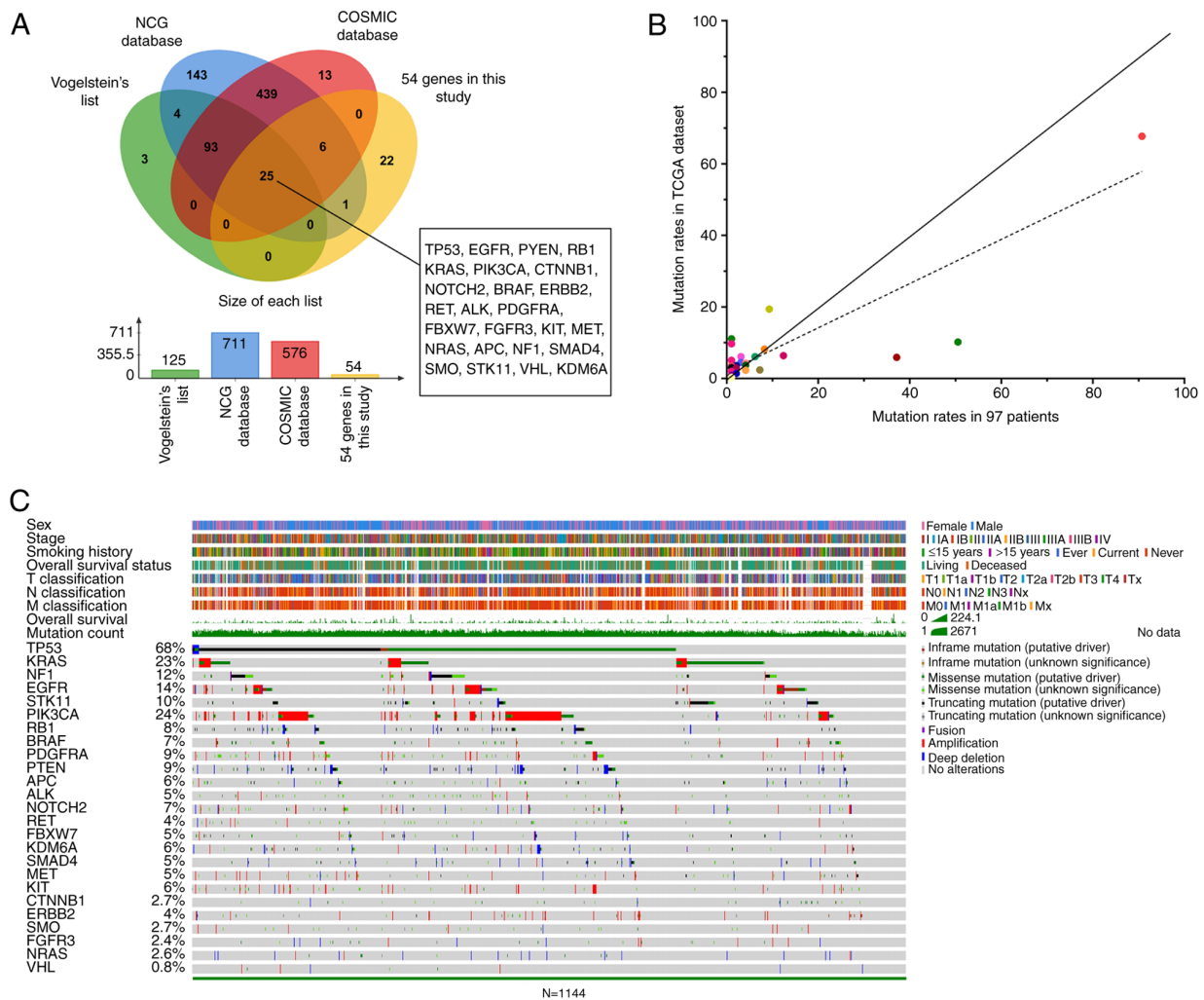


Figure 3. Identification of 25 driver genes. (A) Venn diagram of 25 driver genes identified by taking the intersection of 55 genes and three databases of the COSMIC database, NCG database and Vogelstein's list. The bar chart represents the number of genes in each database. (B) OncoPrint map of the mutational status of 25 driver genes in TCGA dataset (n=1,144). Each row represents a gene and each column represents a patient. Summary rows of each case at the top were clinicopathological characteristics (sex, stage, smoking history, overall survival status, T classification, N classification, M classification, overall survival). (C) Mutation rates of 25 driver genes were compared between 97 patients (abscissa) and the TCGA dataset (ordinate). The fitting curve is represented by a dashed line, whereas the ideal curve is shown as a solid, diagonal line. COSMIC, Catalog of Somatic Mutations in Cancer; NCG, Network of Cancer Genes; TCGA, The Cancer Genome Atlas.

by osimertinib, cetuximab, brigatinib, afatinib, cetuximab and vandetanib (Fig. 1F).

Comparison with TCGA database. In order to evaluate the universality of the lung cancer-specific 55-gene panel in patients with NSCLC, the mutational status of the clinical cohort was compared with TCGA NSCLC cohort (18). The clinical characteristics of 1,144 patients were obtained, including sex, diagnosis age, smoking history, histologic types, clinical stage, T classification, N classification, M classification and overall survival status (Fig. 2A-I). Overall, each sample had ≥ 1 mutation and the 1,144 samples harbored a total of 17,618 mutations. The top 50-ranked genes are plotted in Fig. 2J according to the mutation rate. Mutation frequency was highest for TP53 (67.70%), followed by TTN (59.60%), CSMD3 (41.70%), MUC16 (40.50 %) and RYR2 (39.20%). In addition, the intersection of the 55 mutated genes of lung cancer-specific panel and the 17,618 mutations in TCGA dataset were analyzed (Fig. 2K). Notably, of the 55 genes,

54 genes presented mutations in both two cohorts, and only UGT1A1 was not included in the mutation profile of the TCGA dataset.

Identification of driver genes. The COSMIC database, NCG database and Vogelstein's list, which contained 576 genes, 711 known genes and 125 mutated driver genes, respectively, were used to identify driver genes. After analyzing the intersection of these three databases and the above 54 genes, 25 driver genes were screened: TP53, EGFR, PTEN, RB1, KRAS, PIK3CA, CTNNB1, NOTCH2, BRAF, ERBB2, RET, ALK, PDGFRA, FBXW7, FGFR3, KIT, MET, NRAS, APC, NF1, SMAD4, SMO, STK11, VHL and KDM6A (Fig. 3A). The 25 driver genes were then uploaded to the cBioPortal database. The mutation count, mutation rates and genetic alterations of 25 driver genes, as well as sex, smoking history and other clinical characteristics of 1,144 patients with NSCLC are shown in Fig. 3C. The five most frequently mutated genes were TP53 (68%), KRAS (23%), EGFR (14%), NF1 (12%) and

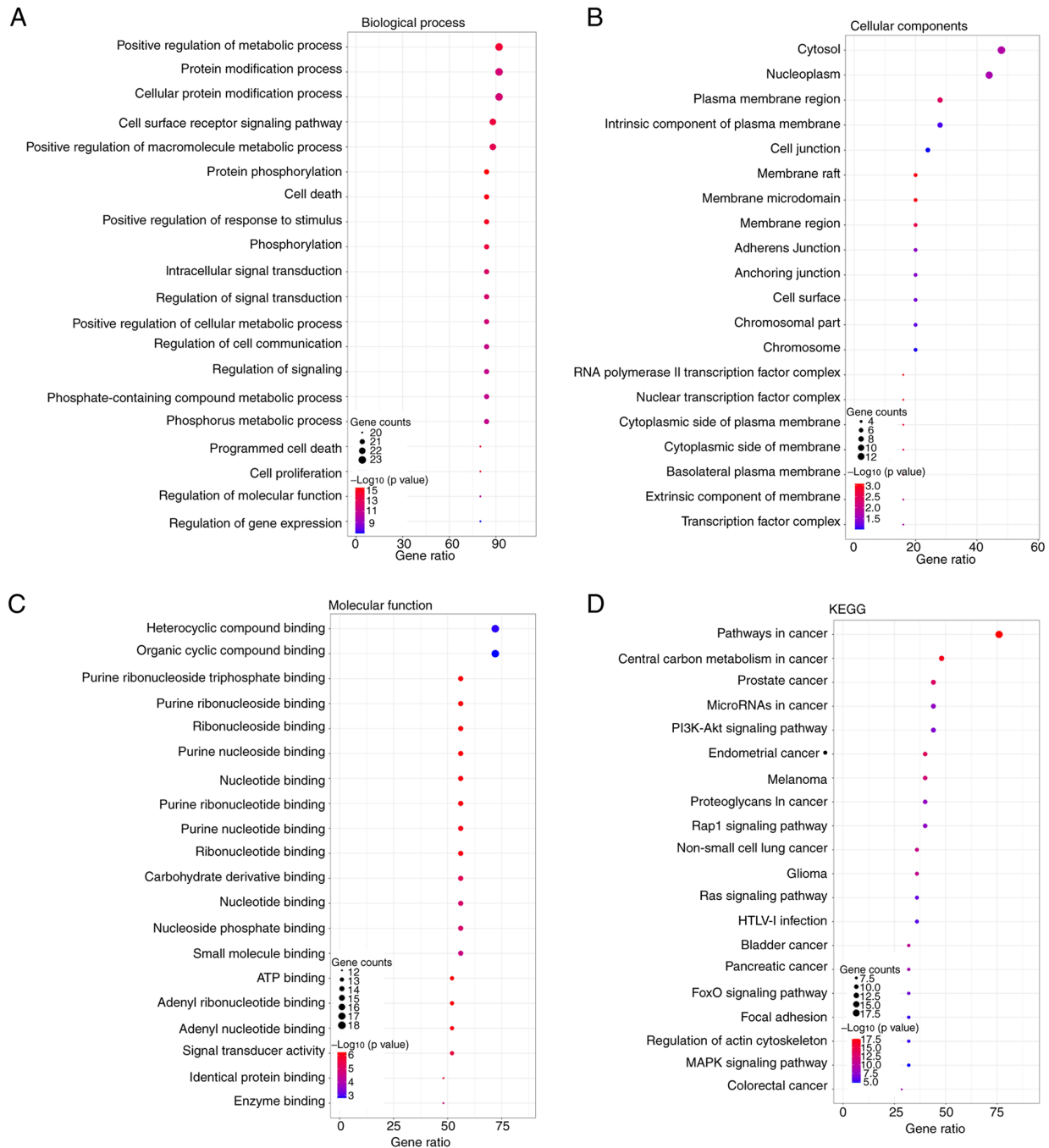


Figure 4. GO functional and KEGG pathway analyses of 25 driver genes. (A) Top 20 significantly enriched biological process. (B) Top 20 significantly enriched cell component. (C) Top 20 significantly enriched molecular function. (D) Top 20 significantly enriched KEGG pathway. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

STK11 (10%). To validate the consistency of the 25 driver genes mutations in 97 patients and TCGA dataset, scatter plots were generated based on the mutation rates of the two cohorts (Fig. 3B). Most points were close to the diagonal line, suggesting that the mutation rates of the 25 driver genes in the clinical cohort were highly similar to those of TCGA results. These findings demonstrate the strong reliability of the 25 driver genes, which may be used for the subsequent studies.

Function annotation and PPI network analysis of 25 driver genes. To annotate the 25 driver genes, GO and KEGG pathway analyses were performed. The biological process

category contained 977 terms, of which the major terms were 'positive regulation of metabolic process', 'protein modification process' and 'cellular protein modification process' (Fig. 4A). The top enriched terms for cellular component (Fig. 4B) and molecular function (Fig. 4C) were 'cytosol' and 'heterocyclic compound binding', respectively. In the KEGG pathway analysis, a number of pathways related to Oncology were observed, including 'pathways in cancer', 'central carbon metabolism in cancer', 'prostate cancer' and 'microRNAs in cancer' (Fig. 4D).

Furthermore, the deleteriousness of the 25 driver genes was predicted using the Polyphen-2 and MutationTaster

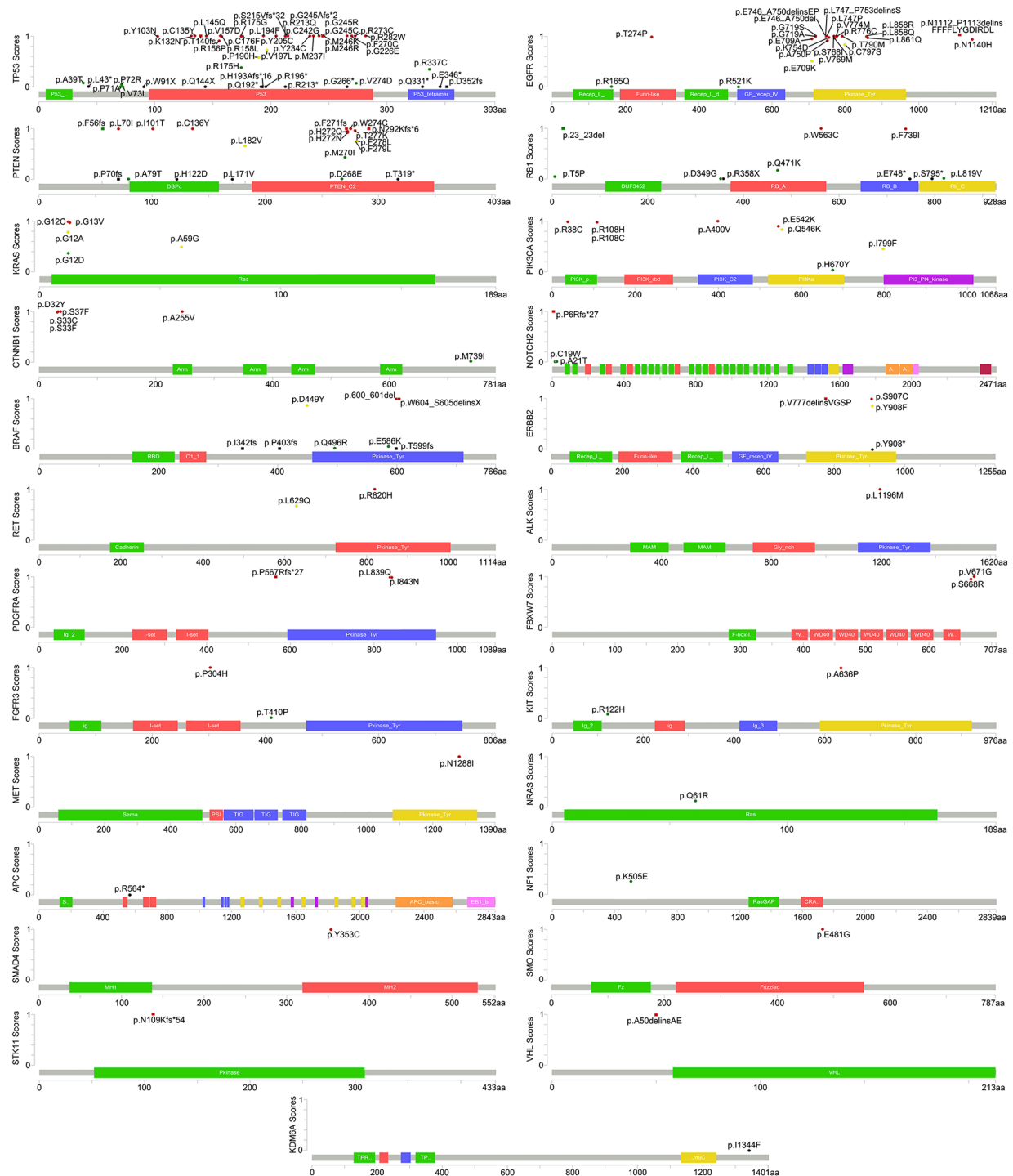
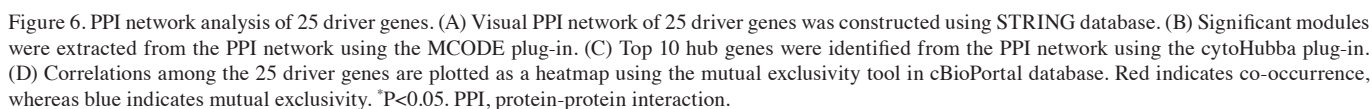


Figure 5. Mutation positions in the 25 driver genes and variant effect of each position. Mutations identified in the Polyphen-2 database are represented by circles, whereas those identified using the MutationTaster tool are shown as squares. In Polyphen-2 (circles), red represents 'probably damaging', yellow represents 'possibly damaging', and green represents 'benign' mutations. In MutationTaster (squares), red represents disease-causing mutations, whereas green represents polymorphisms. Failed predictions are shown in black. The predicted scores are indicated in the y-axis.

tools, and the Polyphen-2 score and the MutationTaster score were calculated (Fig. 5). The greatest number of mutation positions was noted in TP53, which was 46. Among them, 26 variant sites were strongly predicted to be 'probably damaging' or 'disease causing', 2 variant sites were considered to be 'possibly damaging', 7 variant sites were predicted to be 'benign' or 'polymorphism' and the remaining 11 variant sites failed the deleteriousness

prediction because the mutation positions were not clearly indicated.

Additionally, in order to explore the potential relationships between the 25 driver genes, a PPI network was constructed. As shown in Fig. 6A, there were 25 nodes and 181 edges in the PPI network. One significant module had 18 nodes linked via 131 edges with score of 15.412 (Fig. 6B). In this module, PTEN was identified as the seed gene. The top 10 hub genes



Associations between gene mutations and clinicopathological characteristics. The relationships between the 25 driver genes and 13 clinicopathological characteristics were examined in 97 patients with NSCLC. The results indicated that the mutations of 13 genes (EGFR, PTEN, KRAS, PIK3CA, BRAF, ERBB2, RET, ALK, FBXW7, KIT, MET, NRAS and APC) were associated with all of these clinicopathological characteristics ($P < 0.1$; Table SI), except smoking history ($P > 0.1$).

Survival analysis. Univariate and multivariate Cox regression analysis were carried out on 25 driver genes (Fig. 7A) and 8 clinicopathological characteristics (Fig. 7B) for the

Table II. Logistic regression analysis of driver genes and clinicopathological characteristics.

A, EGFR mutation			
Clinical characteristics	P-value	OR	95% CI
Sex	0.004	3.428	1.484-7.916
Stage at diagnosis ^a	0.036	0.148	0.025-0.885
Metastasis	0.007	5.149	1.557-17.023
CEA	0.036	3.161	1.078-9.264
CYFRA21-1	0.018	3.289	1.227-8.812
B, PTEN mutation			
Clinical characteristics	P-value	OR	95% CI
Sex	-	-	-
Stage at diagnosis ^b	0.032	0.066	0.006-0.791
Metastasis	-	-	-
CEA	-	-	-
CYFRA21-1	-	-	-
C, KRAS mutation			
Clinical characteristics	P-value	OR	95% CI
Sex	0.020	0.078	0.009-0.672
Stage at diagnosis	-	-	-
Metastasis	-	-	-
CEA	-	-	-
CYFRA21-1	-	-	-

^a, Stage IV, ^b, Stage III, the reference category is Stage I/II; OR, odd ratio; CI, confidence interval. CEA, carcinoembryonic antigen; CYFRA21-1, cytokeratin 19 fragment 21-1.

survival of 701 patients with NSCLC from TCGA. Univariate Cox regression analysis demonstrated that EGFR mutations (P=0.015), NOTCH2 mutations (P=0.008), age (P=0.037), clinical stage at diagnosis (P<0.001), T classification (P=0.009) and N classification (P<0.001) were significantly associated with overall survival in patients with NSCLC. These significant factors were further analyzed using multivariate Cox regression analysis (Fig. 7C). The results showed that NOTCH2 mutations (P=0.011) and age (P=0.031) were independent factors for overall survival. Compared with the wild-type group, patients with NOTCH2 mutations had a lower risk of death [hazard ratio (HR), 0.429; 95% CI, 0.224-0.821; P=0.011]. Moreover, patients with NSCLC aged >60 years had a significantly shorter survival time than patients aged ≤60 years (HR, 1.47; 95% CI, 1.03-2.08; P=0.031). Kaplan-Meier survival curves were generated according to NOTCH2 mutation status (P=0.006; Fig. 7D) or age (P=0.036; Fig. 7E), suggesting that NOTCH2 mutation and age may represent predictive indicators of overall survival in patients with NSCLC.

Correlation analysis of the genes with clinical significance. Based on the results of logistic regression and multivariate Cox regression analysis, four genes of clinical significance (EGFR, KRAS, PTEN and NOTCH2) were subjected to correlation analysis in 798 patients, consisting of 97 patients from the clinical cohort and 701 patients from TCGA. As indicated by Kendall's τ -b correlation test, there was a negative correlation between EGFR and NOTCH2 mutations (correlation coefficient, -0.078; P=0.027) and a positive correlation between EGFR mutation and KRAS mutation (correlation coefficient, 0.136; P<0.001) (Fig. 8). However, the correlations between other gene pairs were not statistically significant.

The negative correlation between EGFR and NOTCH2 mutations was consistent with the predicted results of the mutual exclusivity analysis in the cBioPortal database (log₂ odds ratio, -1.398; P=0.017). However, a correlation between EGFR and KRAS mutations was not observed in cBioPortal (P=0.215).

Discussion

NGS technology is now widely available, making it possible to test multiple genes simultaneously. Several genomic studies based on NGS technology have been performed to broadly assess the molecular profile of the tumor (22,23). Guibert *et al* (22) performed plasma NGS using enhanced tagged amplicon sequencing of hotspots and coding regions from 36 genes and demonstrated the ability of amplicon-based plasma NGS to detect a full range of targetable genotypes in NSCLC, including fusion genes, with high accuracy. Craig *et al* (23) demonstrated that a panel of 11 lung cancer-specific driver genes used in competitive multiplex PCR amplicon NGS library preparation for Standardized Nucleic Acid Quantification for Sequencing could measure mutations in the 0.05-1.00% variant allele frequency range and enable the identification of an airway epithelial cell somatic mutation 'field of injury' associated with lung cancer risk. In the present study, a lung cancer-specific panel of 55 genes was established in order to examine driver gene mutations. To the best of the authors' knowledge, such a panel is considered relatively large in NGS studies of NSCLC. Moreover, in the 55-gene panel, the mutational status of 54 genes was largely consistent with TCGA data, except that UGT1A1 mutation was not observed in TCGA cohorts. Although previous studies have reported that UGT1A1 polymorphisms are associated with irinotecan-induced toxicity and treatment outcome in lung cancer (24,25), UGT1A1 was excluded from the present study, because the SNP frequency of UGT1A1 ranked third from the bottom in the SNP-containing 97 patient gene list and UGT1A1 mutations were absent from TCGA.

Of the 54 aforementioned 54 genes, 25 driver genes were identified by taking the intersection of three databases, including the COSMIC database, the NCG database and Vogelstein's list, which are commonly used to identify driver genes. Choi *et al* (26) performed whole-exome sequencing of a *Pseudomyxoma peritonei* case secondary to an ovarian mucinous tumor whose genome harbored 28 somatic non-silent mutations. Of these, eight putative driver gene mutations were further identified using COSMIC database. In the present study, the aforementioned databases were combined to

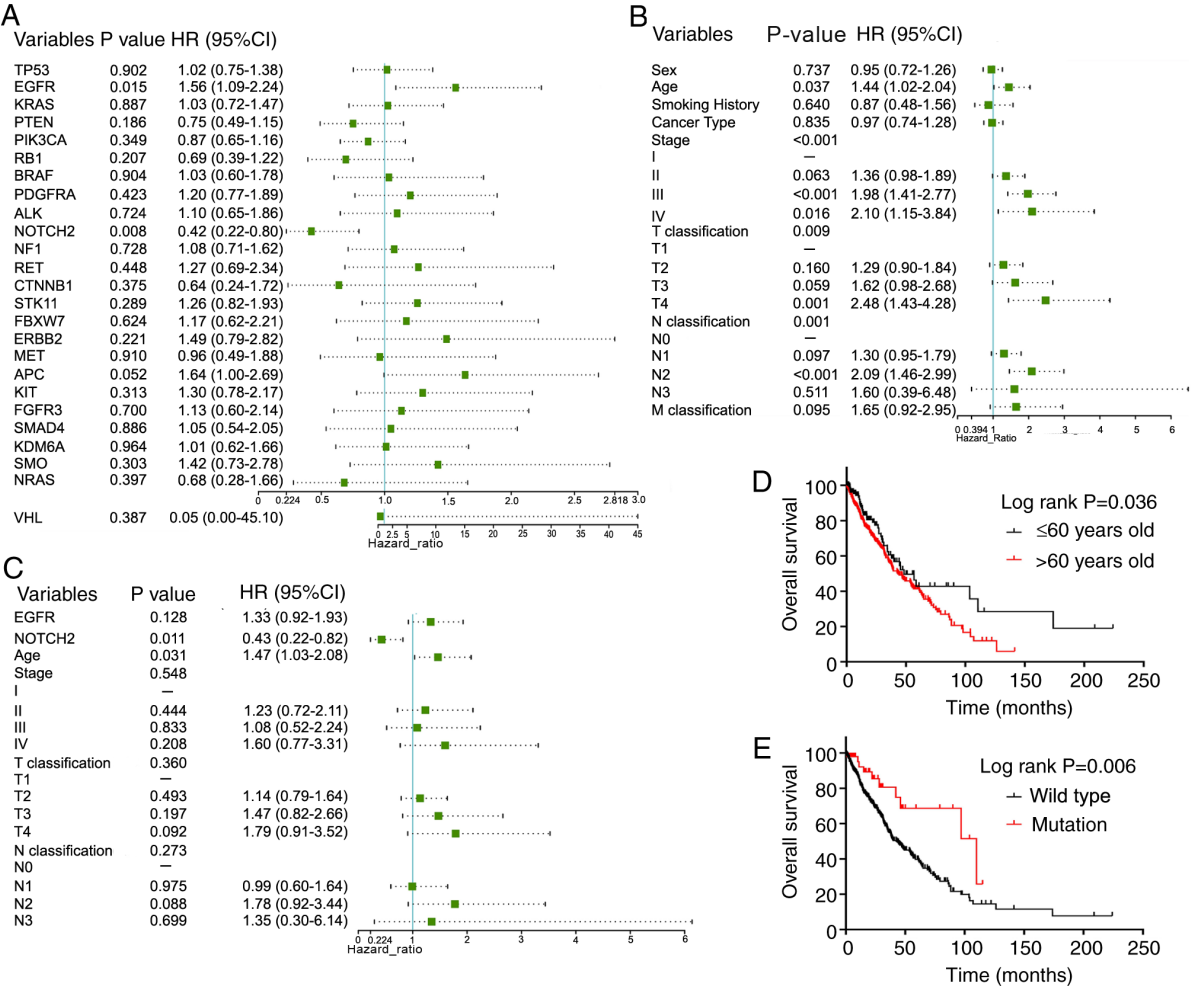


Figure 7. Survival analysis of 25 driver genes and clinical pathological characteristics in 701 patients with NSCLC from TCGA. (A) Univariate Cox regression analysis of 25 driver genes. (B) Univariate Cox regression analysis of 8 clinical pathological characteristics. (C) Multivariate Cox regression analysis of statistically significant driver genes (EGFR and NOTCH2) and clinicopathological characteristics (age, stage, T classification and N classification). (D) Overall survival according to age group. (E) Overall survival according to NOTCH2 mutation status. NSCLC, non-small cell lung cancer. TCGA, The Cancer Genome Atlas; EGFR, epidermal growth factor receptor; CI, confidence interval; HR, hazard ratio.

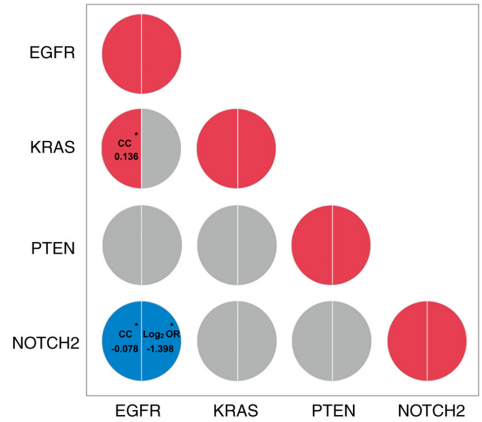


Figure 8. Correlation analysis of the genes with clinical significance. The correlations among EGFR, KRAS, PTEN and NOTCH2 mutations in 798 patients (97 patients from the clinical cohort and 701 from TCGA) are indicated on the left semi-circles, while the results from cBioPortal database were shown on the right semi-circles. Red represents a positive correlation, blue represents a negative correlation, grey represents a no correlation. Statistically significant CC and log₂ ORs are displayed. *P<0.05. EGFR, epidermal growth factor receptor; KRAS, kirsten rat sarcoma viral oncogene homolog; PTEN, phosphatase and tensin homolog; CC, correlation coefficient; OR, odds ratio.

improve screening accuracy. Moreover, the co-occurrence of mutations in the 25 driver genes was compared in 97 patients from a clinical cohort and TCGA samples in order to validate their reliability in different cohorts. Ample evidence has shown that mutations of the 25 driver genes, which were identified in the present study, could promote oncogenic transformation and all of them have been detected as diagnostic NGS to facilitate precision therapeutic approaches in lung cancer (27-30). Among them, EGFR mutations are one of the best-characterized, which have been implicated in pathogenesis of NSCLC (31). Centeno *et al* (32) demonstrated that increased autophosphorylation in the p.Arg776Gly mutation in EGFR might be associated with a proliferative advantage, suggesting that germline mutations in EGFR may contribute to oncogenesis.

The other gene that has been studied extensively is TP53. It has been reported that nondisruptive mutations in TP53 negatively affect responsiveness to crizotinib and are associated with shorter progression-free survival in ALK-rearranged patients with NSCLC (33). Notably, the present study indicated that TP53 was the most frequently mutated driver gene in the TCGA dataset. Halvorsen *et al* (34) suggested that TP53 point mutations

were found in ~47.2% of the NSCLC samples, with the highest mutation frequency (65%) in squamous cell carcinoma. Despite the high frequency of mutant TP53 in tumor cells, the development and clinical application of TP53 targeting drugs have been unsuccessful to date. In the present study, TP53 had the greatest number of mutation sites at 46. Only the p.Pro72Arg mutation suggested that the chemotherapeutic agents, cisplatin, cyclophosphamide and ifosfamide, might show better efficacy and lower toxic side effects. All the remaining mutation sites were subjected to targeted drug AZD1775, a WEE1 kinase inhibitor that has been evaluated in phase-I clinical trials since 2016 (35). Unexpectedly, TP53 mutations were not associated with clinicopathological characteristics or poor prognosis in the current study. These might be one of the reasons why TP53-targeted drug has not been applied in clinic.

Subsequently, the associations of 25 driver genes with clinicopathological characteristics were assessed using logistic regression analysis, which indicated three driver genes were significantly associated with certain clinical factors. Indeed, EGFR and KRAS mutations were associated with sex. Carriers of EGFR mutations showed sex skewing, in accordance with the findings by Minamimoto *et al* (36) that females were more likely to harbor EGFR mutations. The report that estrogen receptor α expression correlated with EGFR mutation in lung adenocarcinomas might indicate the reasons for sex difference (37). The mutation rate of KRAS in male patients is reported to be remarkably high (38), and similar results were also observed in the present study. Carey *et al* (39) reported that expression of Ras or its effector-loop mutants reduced the androgen levels required for the growth of LNCaP prostate cancer cells, whereas high androgen level in males increased tumorigenicity.

Furthermore, the present study identified other distinct clinical characteristics between the EGFR mutant and wild-type groups. Patients with EGFR mutations were more likely to have the features of metastatic and stage-IV than patients with nonmutated tumors. The results were in line with other studies. For example, patients with NSCLC with EGFR mutation have a higher incidence of brain metastasis, compared to EGFR wild type (40). Zhang *et al* (41) demonstrated that the migration and invasiveness of A549 lung cancer cells were promoted by enhancing the EGFR and ERK signaling pathway following filamin A expression silencing, which could also explain the relationship between EGFR mutation and metastasis. Additionally, the present findings indicated that EGFR mutation was linked to higher CEA and CYFRA21-1 levels. CEA is a secreted glycoprotein biomarker, the levels of which can reflect tumor growth, recurrence and metastasis (41). A previous study has reported a positive correlation between serum CEA levels and EGFR mutation rates in patients with NSCLC; specifically, the EGFR mutation-positive rate increased with increasing CEA levels within a certain range (42). CYFRA21-1 is cytokeratin 19 (CK 19) fragment, a member of type OI epithelial cytokeratins, which can contribute to the mechanical integrity of the cell and participate in cell division, motility and cell-to-cell contact (43). It has been confirmed that activating EGFR mutations were correlated with increased CK 19 expression in human lung cancer (44).

Cox regression analysis demonstrated that age and NOTCH2 mutation were independent prognostic factors for overall survival of patients with NSCLC in the present study.

Molinier *et al* (45) confirmed that patients with lung adenocarcinoma aged >70 years experienced shorter survival. NOTCH2 is a member of the NOTCH family of receptors (46). The current study identified NOTCH2 mutation as an independent prognostic factor in NSCLC. Several studies have reported high-frequency mutations of NOTCH2 in lung cancer patients, further highlighting the importance of this molecule (47,48). Chen *et al* (49) indicated that NOTCH2 expression was higher in patients with lung adenocarcinoma than other histology types of NSCLC, which was accompanied by high recurrence rates. It has also been reported that NOTCH2 can suppress apoptosis of H69AR small cell lung carcinoma cells (50) and that concomitant upregulation of NOTCH2 and SIX1 contributed to preinvasive-to-invasive adenocarcinoma progression by inducing epithelial-mesenchymal transition and nuclear atypia (51).

The aforementioned findings imply that NOTCH2 could promote tumor progression and affect the prognosis of patients. However, the role of NOTCH2 in cancer is both complex and paradoxical. Other reports have shown that NOTCH2 deletion could result in markedly increased carcinogenesis and increased MAPK activity, which may ultimately lead to death in Kras^{G12D}-driven endogenous NSCLC model mice, due to high tumor burden (52). This contradiction is likely due to the crosstalk between the NOTCH signaling pathway and other pathways, such as the PTEN pathway and MAPK pathway. For instance, delta-like ligand 4, a vascular ligand of NOTCH1-4, upregulates PTEN expression by activating NOTCH1 in NSCLC cells (53). NOTCH2 significantly increases phosphorylated ERK1 and ERK2 levels in DMS53 small cell lung cancer cells, leading to activation of the MAPK pathway (54).

A key finding of the present study was that NOTCH2 and EGFR mutations were mutually exclusive. It has been demonstrated that EGFR mutations enabled the constitutive activation of the downstream MAPK signaling pathway (55), which was also considered as the downstream of NOTCH. Therefore, the NOTCH and EGFR signaling pathways might influence each other, resulting in active and complex crosstalk, rather than independent function, during NSCLC progression. Understanding these interactions will greatly broaden our knowledge about NSCLC diseases, thus promoting the development of treatment options and personalized approaches. For patients with EGFR mutations, EGFR TKIs are the treatment of choice (56); however, a large proportion of patients (40-60%) does not present EGFR mutations (57). According to the results of mutual exclusivity analysis, the patients with wild-type EGFR tended to present NOTCH2 mutations, highlighting the importance of NOTCH2 mutational status and suggesting that the patients without EGFR mutation might benefit from NOTCH pathway inhibitors, such as γ -secretase inhibitors (58).

In summary, the present study demonstrated the ability of NGS to detect a wide range of mutation types in NSCLC and affirmed the value of some underappreciated mutations in tumor progression. These results may help provide additional therapeutic possibilities for patients with NSCLC. However, further studies are warranted to elucidate the underlying mechanisms or develop new drugs.

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Availability of data and materials

The patient data used and/or analyzed during the current study are available from the corresponding author on reasonable request. TCGA dataset analyzed for this study can be found in the cBioPortal database (http://www.cbioportal.org/study/summary?id=nsclc_tcga_broad_2016).

Authors' contributions

LeL and LN designed the study, analyzed the data and wrote and revised the manuscript. CD and LiL contributed to sample collection, quality control and NGS analysis. NG, YX and XL performed experiments on tumor tissue and blood and collected and analyzed patient data. LC, QX and LZ acquired and analyzed the public database data, recruited the patients and supervised the study. All authors have read and approved the final manuscript. LeL and LN confirmed the authenticity of the data shown in the present manuscript.

Ethics approval and consent to participate

This study was approved by the Research Ethics Review Committee of Chengde Medical University (Hebei, China; approval no. 2017003). All participants provided written informed consent.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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