

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.

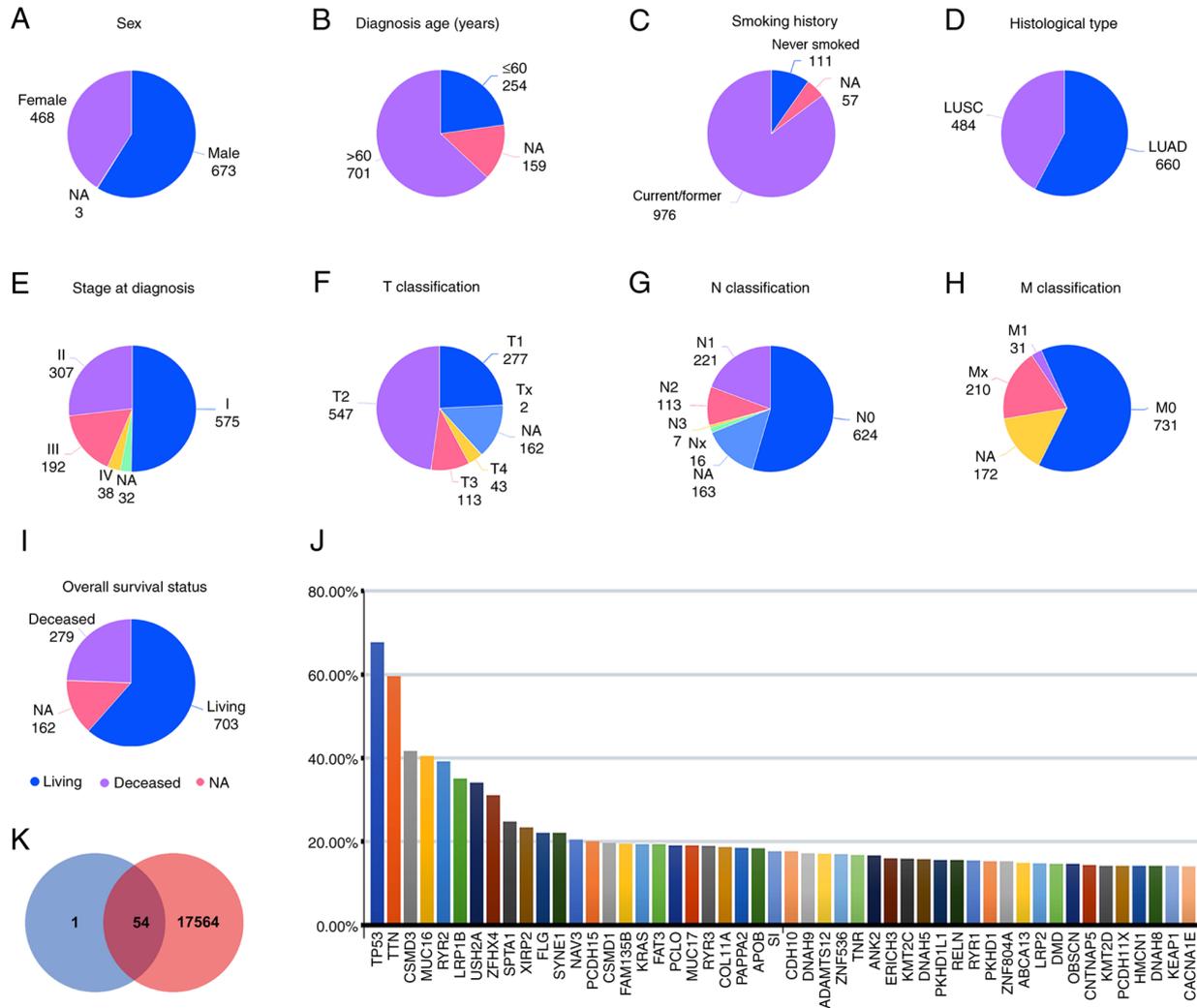


Figure 2. Comparison with the TCGA database. Distribution of clinicopathological characteristics including (A) sex, (B) diagnosis age, (C) smoking history, (D) histologic type, (E) stage at diagnosis, (F) T classification, (G) N classification, (H) M classification and (I) overall survival status. (J) 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; inner-most 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 were 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 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

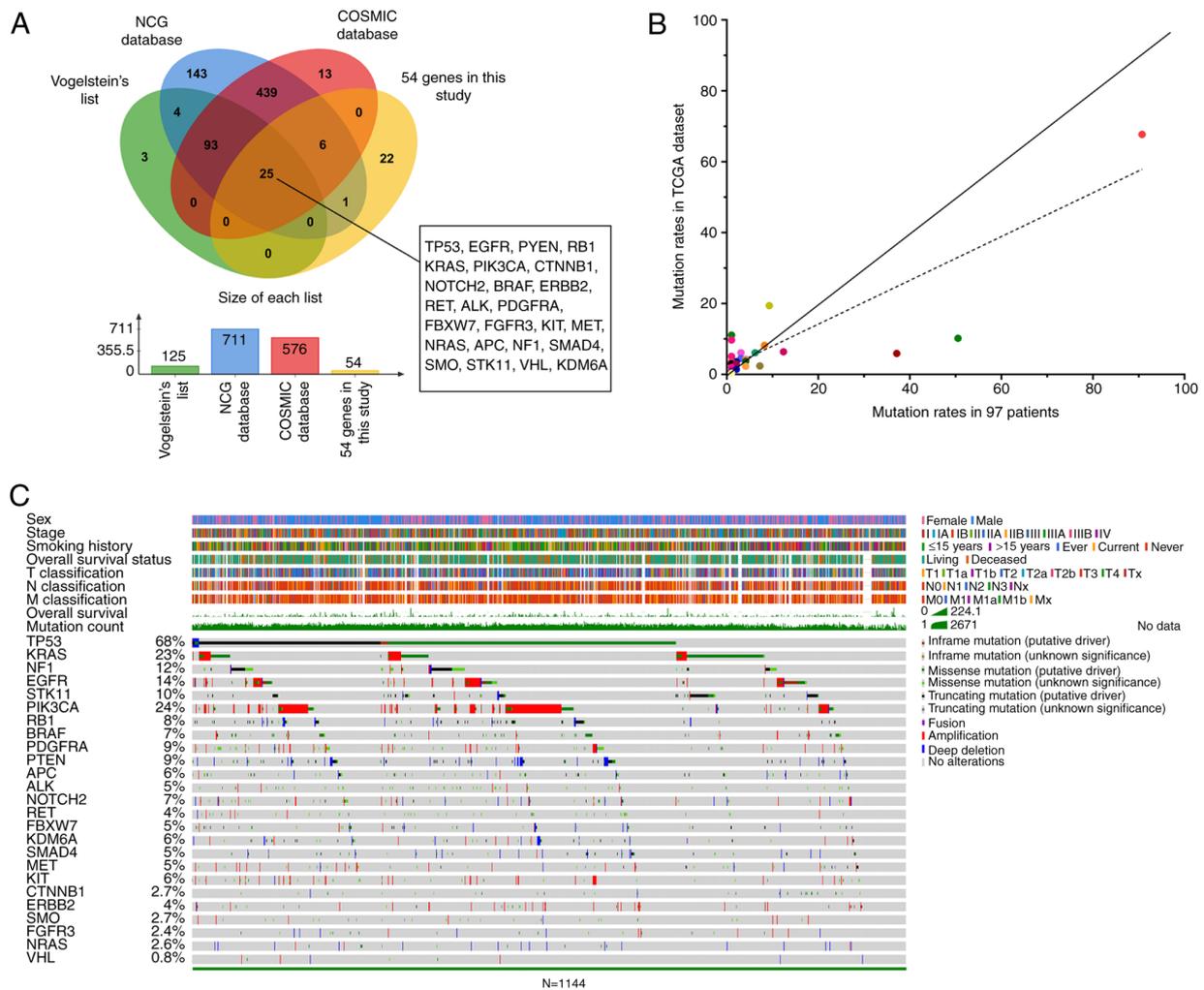


Figure 3. Identification of 25 driver genes. (A) Venn diagram of 25 driver genes identified by taking the intersection of 55 genes and three databases of the COSMIC database, NCG database and Vogelstein's list. The bar chart represents the number of genes in each database. (B) OncoPrint map of the mutational 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, CTNNA1, 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

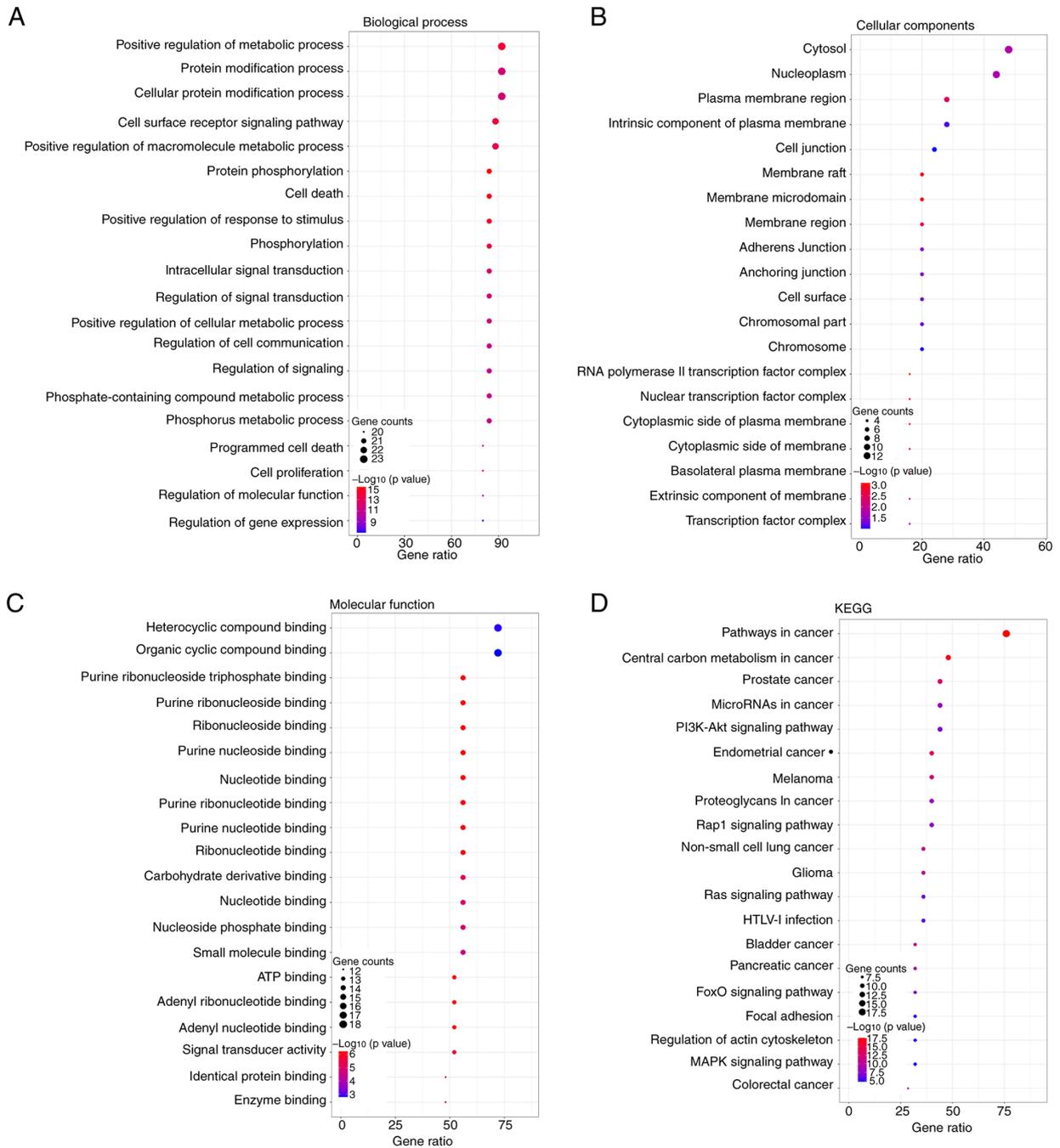


Figure 4. GO functional and KEGG pathway analyses of 25 driver genes. (A) Top 20 significantly enriched biological process. (B) Top 20 significantly enriched cell component. (C) Top 20 significantly enriched molecular function. (D) Top 20 significantly enriched KEGG pathway. GO, Gene Ontology; KEGG,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

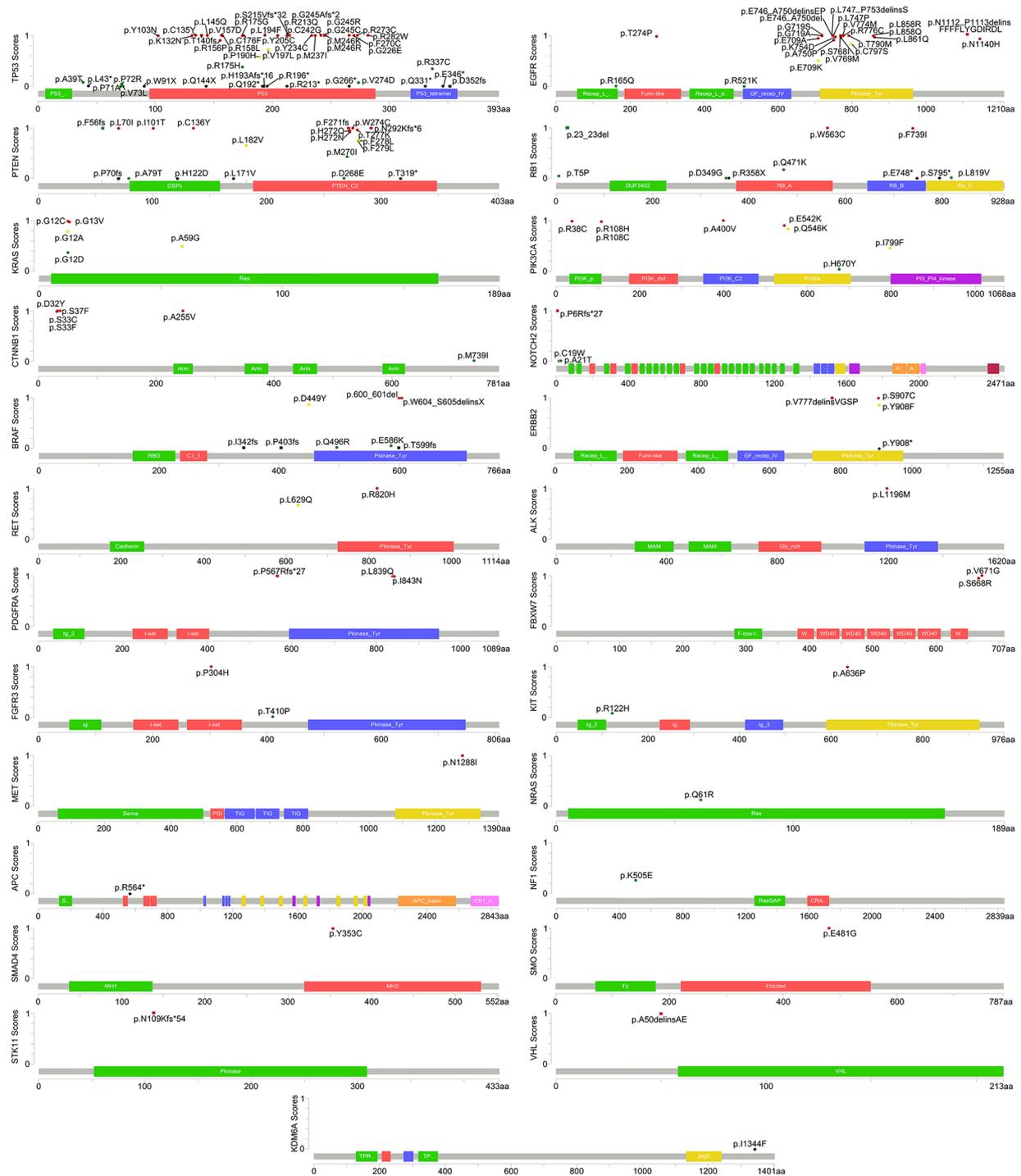


Figure 5. Mutation positions in the 25 driver genes and predicted effect of each position. Mutations identified in the Polyphen-2 database are represented by circles, whereas those identified using the MutationTaster tool are shown as squares. In Polyphen-2 (circles), red represents 'probably damaging', 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

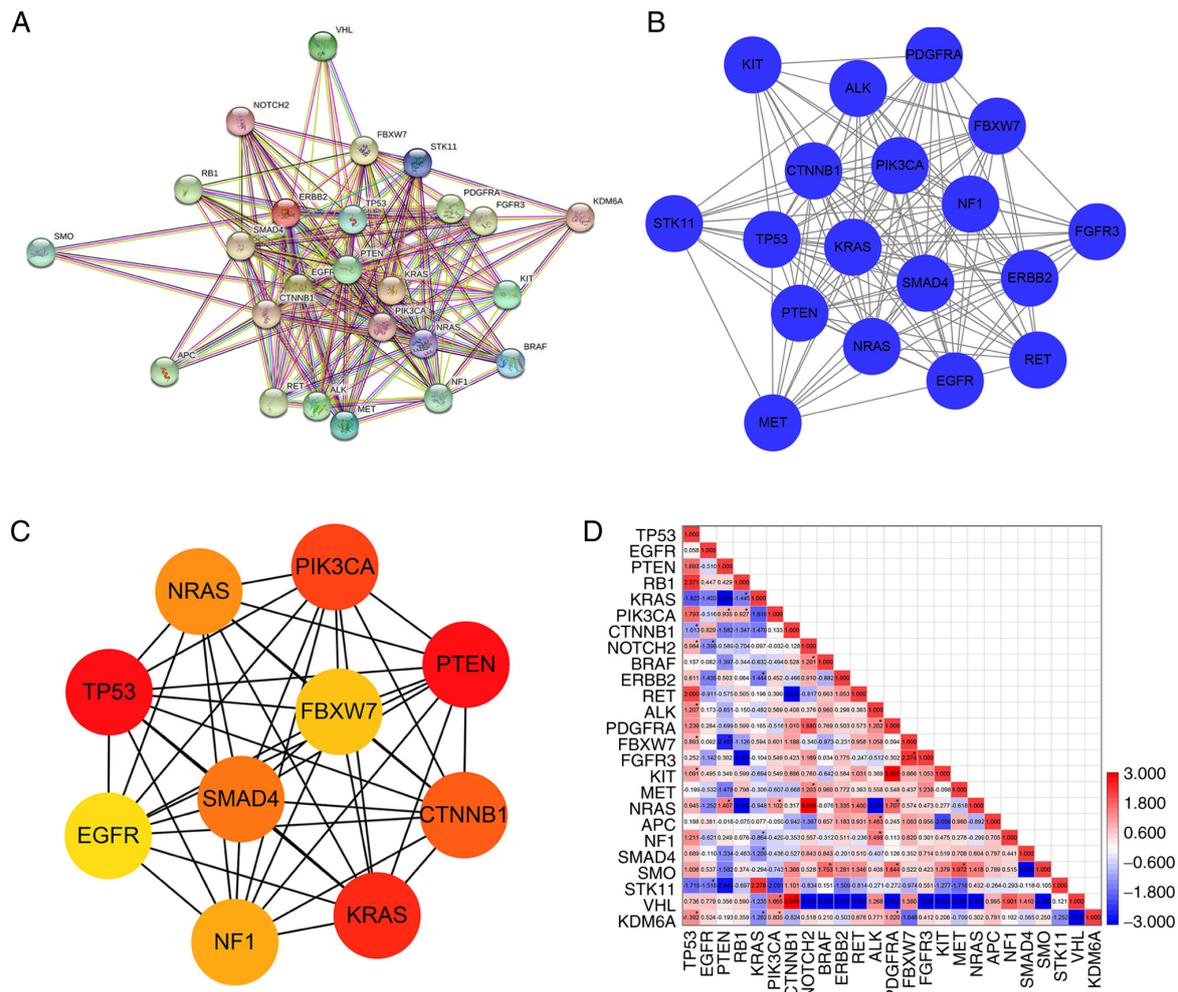


Figure 6. PPI network analysis of 25 driver genes. (A) Visual PPI network of 25 driver genes was constructed using STRING database. (B) Significant modules were extracted from the PPI network using the MCODE plug-in. (C) Top 10 hub genes were identified from the PPI network using the cytoHubba plug-in. (D) Correlations among the 25 driver genes are plotted as a heatmap using the mutual exclusivity tool in cBioPortal database. Red indicates co-occurrence, whereas blue indicates mutual exclusivity. * $P < 0.05$. PPI, protein-protein interaction.

were identified according to MCC ranking, including TP53, PTEN, KRAS, PIK3CA, CTNNB1, SMAD4, NRAS, NF1, FBXW7 and EGFR (Fig. 6C). Moreover, the mutual exclusivity tool in cBioPortal database was then used to identify potential correlations in the frequency of mutations in these 25 driver genes. Altogether, 300 gene pairs with two relationships, co-occurrence (177 gene pairs) and mutual exclusivity (123 gene pairs), were identified (Fig. 6D). Among them, 32 gene pairs were statistically significant ($P < 0.05$) in which 23 gene pairs showed co-occurrence and 9 gene pairs showed mutual exclusivity. According to the \log_2 odds ratios, the top co-occurrence and mutual exclusivity gene-pairs were PTEN-FBXW7 and CTNNB1-VHL, respectively.

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 ($P > 0.1$).

Subsequently, 13 significant driver genes and 12 clinicopathological characteristics were further evaluated by logistic regression analysis and the variables with statistical difference are shown in Table II. The effects of age and sex on these 13 gene mutations were first examined. As shown in Table II, sex was associated with EGFR ($P = 0.004$) and KRAS ($P = 0.020$) mutation in female patients was 3.428 times and 0.078 times of that in males, respectively. Moreover, the effects of mutations in the 13 driver genes on 10 clinicopathological characteristics (including histological type, clinical stage at diagnosis, T classification, N classification and M classification, as well as CEA, NSE, CYFRA21-1, SCC and CA125 levels) were also investigated. Compared with the wild type, patients with EGFR mutations were more likely to have the features of stage-IV ($P = 0.036$), metastasis ($P = 0.007$), high CEA ($P = 0.036$) and CYFRA21 ($P = 0.018$) level, and the patients with PTEN mutation had 0.066 times risk of stage III ($P = 0.032$).

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

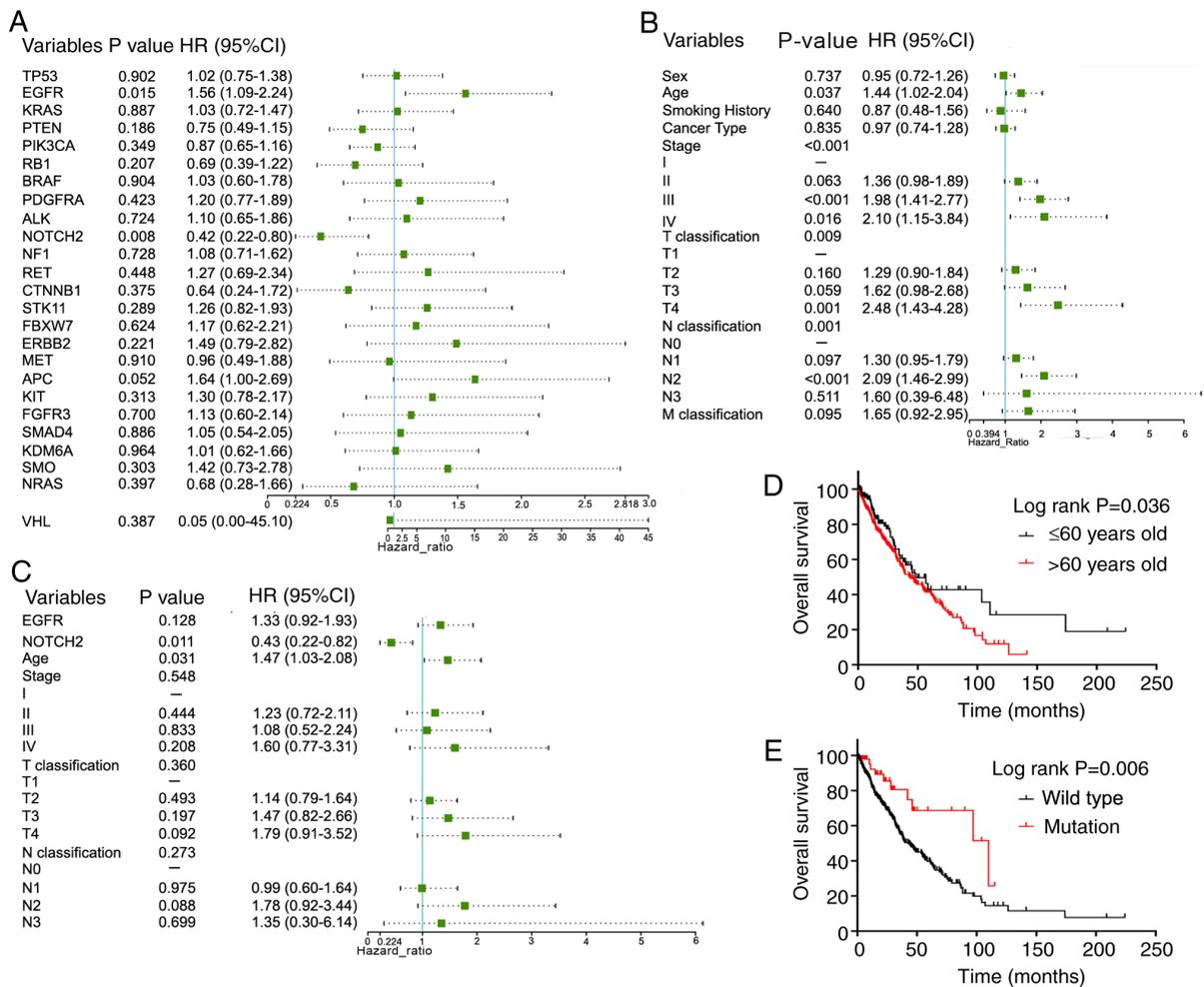


Figure 7. Survival analysis of 25 driver genes and clinical pathological characteristics in 701 patients with NSCLC from TCGA. (A) Univariate Cox regression analysis of 25 driver genes. (B) Univariate Cox regression analysis of 8 clinical pathological characteristics. (C) Multivariate Cox regression 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.

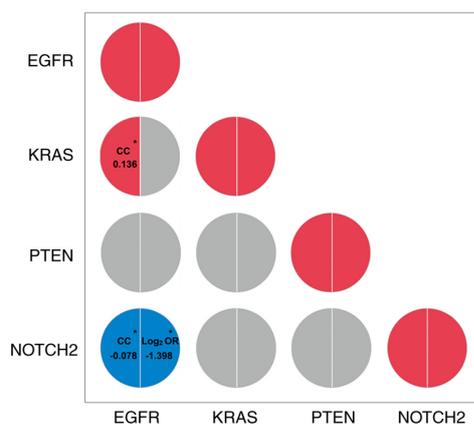


Figure 8. Correlation analysis of the genes with clinical significance. The correlations among EGFR, KRAS, PTEN and NOTCH2 mutations in 798 patients (97 patients from the clinical cohort and 701 from TCGA) are indicated on the left semi-circles, while the results from cBioPortal database were shown on 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.

References

- Bray F, Ferlay J, Soerjomataram I, Siegel RL, Torre LA and Jemal A: Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA Cancer J Clin* 68: 394-424, 2018.
- Feng RM, Zong YN, Cao SM and Xu RH: Current cancer situation in China: Good or bad news from the 2018 Global Cancer Statistics? *Cancer Commun* 39: 22, 2019.
- Wang TJ, Saad S, Qureshi YH, Jani A, Nanda T, Yaeh AM, Rozenblat T, Sisti MB, Bruce JN, McKhann GM, *et al*: Does lung cancer mutation status and targeted therapy predict for outcomes and local control in the setting of brain metastases treated with radiation? *Neuro Oncol* 17: 1022-1028, 2015.
- Zhou C, Wu YL, Chen G, Feng J, Liu XQ, Wang C, Zhang S, Wang J, Zhou S, Ren S, *et al*: Erlotinib versus chemotherapy as first-line treatment for patients with advanced EGFR mutation-positive non-small-cell lung cancer (OPTIMAL, CTONG-0802): A multicentre, open-label, randomised, phase 3 study. *Lancet Oncol* 12: 735-742, 2011.
- Lynch TJ, Bell DW, Sordella R, Gurubhagavatula S, Okimoto RA, Brannigan BW, Harris PL, Haserlat SM, Supko JG, Haluska FG, *et al*: Activating mutations in the epidermal growth factor receptor underlying responsiveness of non-small-cell lung cancer to gefitinib. *N Engl J Med* 350: 2129-2139, 2004.
- Tsang YH, Dogruluk T, Tedeschi PM, Wardwell-Ozgo J, Lu H, Espitia M, Nair N, Minelli R, Chong Z, Chen F, *et al*: Functional annotation of rare gene aberration drivers of pancreatic cancer. *Nat Commun* 7: 10500, 2016.
- Liu J, Lee W, Jiang Z, Chen Z, Jhunjhunwala S, Haverty PM, Gnad F, Guan Y, Gilbert HN, Stinson J, *et al*: Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. *Genome Res* 22: 2315-2327, 2012.
- Metzker ML: Sequencing technologies-the next generation. *Nat Rev Genet* 11: 31-46, 2010.
- Zhai H, Zhong W, Yang X and Wu YL: Neoadjuvant and adjuvant epidermal growth factor receptor tyrosine kinase inhibitor (EGFR-TKI) therapy for lung cancer. *Transl Lung Cancer Res* 4: 82-93, 2015.
- Yuan J, Zhang N, Yin L, Zhu H, Zhang L, Zhou L and Yang M: Clinical implications of the autophagy core gene variations in advanced lung adenocarcinoma treated with gefitinib. *Sci Rep* 7: 17814, 2017.
- Shaw AT, Solomon BJ, Besse B, Bauer TM, Lin CC, Soo RA, Riely GJ, Ou SI, Clancy JS, Li S, *et al*: ALK resistance mutations and efficacy of lorlatinib in advanced anaplastic lymphoma kinase-positive non-small-cell lung cancer. *J Clin Oncol* 37: 1370-1379, 2019.
- Kalemkerian GP, Narula N, Kennedy EB, Biermann WA, Donington J, Leigh NB, Lew M, Pantelas J, Ramalingam SS, Reck M, *et al*: Molecular testing guideline for the selection of patients with lung cancer for treatment with targeted tyrosine kinase inhibitors: American society of clinical oncology endorsement of the college of American pathologists/international association for the study of lung cancer/association for molecular pathology clinical practice guideline update. *J Clin Oncol* 36: 911-919, 2018.
- Wu YL, Planchard D, Lu S, Sun H, Yamamoto N, Kim DW, Tan DSW, Yang JC, Azrif M, Mitsudomi T, *et al*: Pan-Asian adapted Clinical Practice Guidelines for the management of patients with metastatic non-small-cell lung cancer: A CSCO-ESMO initiative endorsed by JSMO, KSMO, MOS, SSO and TOS. *Ann Oncol* 30: 171-210, 2019.
- Savas P, Hughes B and Solomon B: Targeted therapy in lung cancer: IPASS and beyond, keeping abreast of the explosion of targeted therapies for lung cancer. *J Thorac Dis* 5 (Suppl 5): S579-S92, 2013.
- Tian L, Chen Q, Yi X, Wang G, Chen J, Ning P, Yang K and Liu Z: Radionuclide I-131 labeled albumin-paclitaxel nanoparticles for synergistic combined chemo-radioisotope therapy of cancer. *Theranostics* 7: 614-623, 2017.
- Vogelstein B, Papadopoulos N, Velculescu VE, Zhou S, Diaz LJ and Kinzler KW: Cancer genome landscapes. *Science* 339: 1546-1558, 2013.
- Amin MB, Greene FL, Edge SB, Compton CC, Gershenwald JE, Brookland RK, Meyer L, Gress DM, Byrd DR and Winchester DP: The eighth edition AJCC Cancer Staging Manual: Continuing to build a bridge from a population-based to a more 'personalized' approach to cancer staging. *CA Cancer J Clin* 67: 93-99, 2017.
- Campbell JD, Alexandrov A, Kim J, Wala J, Berger AH, Pedamallu CS, Shukla SA, Guo G, Brooks AN, Murray BA, *et al*: Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. *Nat Genet* 48: 607-616, 2016.
- Repana D, Nulsen J, Dressler L, Bortolomeazzi M, Venkata SK, Tourna A, Yakovleva A, Palmieri T and Ciccarelli FD: The Network of Cancer Genes (NCG): A comprehensive catalogue of known and candidate cancer genes from cancer sequencing screens. *Genome Biol* 20: 1, 2019.
- Adzhubei IA, Schmidt S, Peshkin L, Ramensky VE, Gerasimova A, Bork P, Kondrashov AS and Sunyaev SR: A method and server for predicting damaging missense mutations. *Nat Methods* 7: 248-249, 2010.

21. Schwarz JM, Cooper DN, Schuelke M and Seelow D: MutationTaster2: Mutation prediction for the deep-sequencing age. *Nat Methods* 11: 361-362, 2014.
22. Guibert N, Hu Y, Feeney N, Kuang Y, Plagnol V, Jones G, Howarth K, Beeler JF, Paweletz CP and Oxnard GR: Amplicon-based next-generation sequencing of plasma cell-free DNA for detection of driver and resistance mutations in advanced non-small cell lung cancer. *Ann Oncol* 29: 1049-1055, 2018.
23. Craig DJ, Morrison T, Khuder SA, Crawford EL, Wu L, Xu J, Blomquist TM and Willey JC: Technical advance in targeted NGS analysis enables identification of lung cancer risk-associated low frequency TP53, PIK3CA, and BRAF mutations in airway epithelial cells. *BMC Cancer* 19: 1081, 2019.
24. Chen X, Liu L, Guo Z, Liang W, He J, Huang L, Deng Q, Tang H, Pan H, Guo M, *et al*: UGT1A1 polymorphisms with irinotecan-induced toxicities and treatment outcome in Asians with Lung Cancer: A meta-analysis. *Cancer Chemother Pharmacol* 79: 1109-1117, 2017.
25. Bai Y, Wu HW, Ma X, Liu Y and Zhang YH: Relationship between UGT1A1*6/*28 gene polymorphisms and the efficacy and toxicity of irinotecan-based chemotherapy. *Onco Targets Ther* 10: 3071-3081, 2017.
26. Choi YJ, Lee SH, Kim MS, Jung SH, Hur SY, Chung YJ and Lee SH: Whole-exome sequencing identified the genetic origin of a mucinous neoplasm in a mature cystic teratoma. *Pathology* 48: 372-376, 2016.
27. Tan AC, Lai GGY, Tan GS, Poon SY, Doble B, Lim TH, Aung ZW, Takano A, Tan WL, Ang MK, *et al*: Utility of incorporating next-generation sequencing (NGS) in an Asian non-small cell lung cancer (NSCLC) population: Incremental yield of actionable alterations and cost-effectiveness analysis. *Lung Cancer* 139: 207-215, 2020.
28. DiBardino DM, Rawson DW, Saqi A, Heymann JJ, Pagan CA and Bulman WA: Next-generation sequencing of non-small cell lung cancer using a customized, targeted sequencing panel: Emphasis on small biopsy and cytology. *Cytojournal* 14: 7, 2017.
29. Preusser M, Berghoff AS, Koller R, Zielinski CC, Hainfellner JA, Liebmam-Reindl S, Popitsch N, Geier CB, Streubel B and Birner P: Spectrum of gene mutations detected by next generation exome sequencing in brain metastases of lung adenocarcinoma. *Eur J Cancer* 51: 1803-1811, 2015.
30. Sonmezler O, Boga I and Bisgin A: Integration of liquid biopsies into clinical laboratory applications via NGS in cancer diagnostics. *Clin Lab*: doi: 10.7754/Clin.Lab.2019.190836.
31. Wang Y, Lai H, Fan X, Luo L, Duan F, Jiang Z, Wang Q, Leung ELH, Liu L and Yao X: Gossypol inhibits non-small cell lung cancer cells proliferation by targeting EGFR^{L858R/T790M}. *Front Pharmacol* 9: 728, 2018.
32. Centeno I, Blay P, Santamaría I, Astudillo A, Pitiot AS, Osorio FG, González-Arriaga P, Iglesias F, Menéndez P, Tardón A, *et al*: Germ-line mutations in epidermal growth factor receptor (EGFR) are rare but may contribute to oncogenesis: A novel germ-line mutation in EGFR detected in a patient with lung adenocarcinoma. *BMC Cancer* 11: 172, 2011.
33. Song P, Zhang F, Li Y, Yang G, Li W, Ying J and Gao S: Concomitant TP53 mutations with response to crizotinib treatment in patients with ALK-rearranged non-small-cell lung cancer. *Cancer Med* 8: 1551-1557, 2019.
34. Halvorsen AR, Silwal-Pandit L, Meza-Zepeda LA, Vodak D, Vu P, Sagerup C, Hovig E, Myklebost O, Børresen-Dale AL, Brustugun OT and Helland Å: TP53 mutation spectrum in smokers and never smoking lung cancer patients. *Front Genet* 7: 85, 2016.
35. Leijen S, van Geel RM, Pavlick AC, Tibes R, Rosen L, Razak AR, Lam R, Demuth T, Rose S, Lee MA, *et al*: Phase I study evaluating WEE1 inhibitor AZD1775 as monotherapy and in combination with gemcitabine, cisplatin, or carboplatin in patients with advanced solid tumors. *J Clin Oncol* 34: 4371-4380, 2016.
36. Minamimoto R, Jamali M, Gevaert O, Echegaray S, Khuong A, Hoang CD, Shrager JB, Plevritis SK, Rubin DL, Leung AN, *et al*: Prediction of EGFR and KRAS mutation in non-small cell lung cancer using quantitative ¹⁸F FDG-PET/CT metrics. *Oncotarget* 8: 52792-52801, 2017.
37. Raso MG, Behrens C, Herynk MH, Liu S, Prudkin L, Ozburn NC, Woods DM, Tang X, Mehran RJ, Moran C, *et al*: Immunohistochemical expression of estrogen and progesterone receptors identifies a subset of NSCLCs and correlates with EGFR mutation. *Clin Cancer Res* 15: 5359-5368, 2009.
38. Zhao J, Gao J, Guo L, Hu X, Liu Q, Zhao J, Liu L, Jiang J, Wang M, Liang Z, *et al*: EGFR and KRAS gene mutations in 754 patients with resectable stage I-IIIa non-small cell lung cancer and its clinical significance. *Zhongguo Fei Ai Za Zhi* 20: 617-622, 2017 (In Chinese).
39. Carey AM, Pramanik R, Nicholson LJ, Dew TK, Martin FL, Muir GH and Morris JD: Ras-MEK-ERK signaling cascade regulates androgen receptor element-inducible gene transcription and DNA synthesis in prostate cancer cells. *Int J Cancer* 121: 520-527, 2007.
40. Hsu F, De Caluwe A, Anderson D, Nichol A, Toriumi T and Ho C: EGFR mutation status on brain metastases from non-small cell lung cancer. *Lung Cancer* 96: 101-107, 2016.
41. Zhang Y, Zhu T, Liu J, Liu J, Gao D, Su T and Zhao R: FLNa negatively regulated proliferation and metastasis in lung adenocarcinoma A549 cells via suppression of EGFR. *Acta Biochim Biophys Sin* 50: 164-170, 2018.
42. Yang ZM, Ding XP, Pen L, Mei L and Liu T: Analysis of CEA expression and EGFR mutation status in non-small cell lung cancers. *Asian Pac J Cancer Prev* 15: 3451-3455, 2014.
43. Barak V, Goike H, Panaretakis KW and Einarsson R: Clinical utility of cytokeratins as tumor markers. *Clin Biochem* 37: 529-540, 2004.
44. Cho A, Hur J, Moon YW, Hong SR, Suh YJ, Kim YJ, Im DJ, Hong YJ, Lee HJ, Kim YJ, *et al*: Correlation between EGFR gene mutation, cytologic tumor markers, 18F-FDG uptake in non-small cell lung cancer. *BMC Cancer* 16: 224, 2016.
45. Molinier O, Goupil F, Debieuvre D, Auliac JB, Jeandeau S, Lacroix S, Martin F and Grivaux M: Five-year survival and prognostic factors according to histology in 6101 non-small-cell lung cancer patients. *Respir Med Res* 77: 46-54, 2020.
46. Artavanis-Tsakonas S, Rand MD and Lake RJ: Notch signaling: Cell fate control and signal integration in development. *Science* 284: 770-776, 1999.
47. Oshita F, Kasajima R and Miyagi Y: Multiplex genomic test of mutation and fusion genes in small biopsy specimen of lung cancer. *J Exp Ther Oncol* 11: 189-194, 2016.
48. Liao L, Ji X, Ge M, Zhan Q, Huang R, Liang X and Zhou X: Characterization of genetic alterations in brain metastases from non-small cell lung cancer. *FEBS Open Bio* 8: 1544-1552, 2018.
49. Chen CY, Chen YY, Hsieh MS, Ho CC, Chen KY, Shih JY and Yu CJ: Expression of notch gene and its impact on survival of patients with resectable Non-small cell lung cancer. *J Cancer* 8: 1292-1300, 2017.
50. Motooka Y, Fujino K, Sato Y, Kudoh S, Suzuki M and Ito T: Pathobiology of Notch2 in lung cancer. *Pathology* 49: 486-493, 2017.
51. Mimae T, Okada M, Hagiwara M, Miyata Y, Tsutani Y, Inoue T, Murakami Y and Ito A: Upregulation of notch2 and six1 is associated with progression of early-stage lung adenocarcinoma and a more aggressive phenotype at advanced stages. *Clin Cancer Res* 18: 945-955, 2012.
52. Baumgart A, Mazur PK, Anton M, Rudelius M, Schwamborn K, Feuchtinger A, Behnke K, Walch A, Braren R, Peschel C, *et al*: Opposing role of Notch1 and Notch2 in a Kras(G12D)-driven murine non-small cell lung cancer model. *Oncogene* 34: 578-588, 2015.
53. Ding XY, Ding J, Wu K, Wen W, Liu C, Yan HX, Chen C, Wang S, Tang H, Gao CK, *et al*: Cross-talk between endothelial cells and tumor via delta-like ligand 4/Notch/PTEN signaling inhibits lung cancer growth. *Oncogene* 31: 2899-2906, 2012.
54. Sriuranpong V, Borges MW, Ravi RK, Arnold DR, Nelkin BD, Baylin SB and Ball DW: Notch signaling induces cell cycle arrest in small cell lung cancer cells. *Cancer Res* 61: 3200-3205, 2001.
55. Baumgartner U, Berger F, Hashemi Gheinani A, Burgener SS, Monastyrskaya K and Vassella E: MiR-19b enhances proliferation and apoptosis resistance via the EGFR signaling pathway by targeting PP2A and BIM in non-small cell lung cancer. *Mol Cancer* 17: 44, 2018.
56. Karachaliou N, Cardona AF, Bracht JWP, Aldeguer E, Drozdowskyj A, Fernandez-Bruno M, Chaib I, Berenguer J, Santarpia M, Ito M, *et al*: Integrin-linked kinase (ILK) and src homology 2 domain-containing phosphatase 2 (SHP2): Novel targets in EGFR-mutation positive non-small cell lung cancer (NSCLC). *EBioMedicine* 39: 207-214, 2019.
57. Yu S, Liu D, Shen B, Shi M and Feng J: Immunotherapy strategy of EGFR mutant lung cancer. *Am J Cancer Res* 8: 2106-2115, 2018.
58. Katoh M and Katoh M: Precision medicine for human cancers with Notch signaling dysregulation (Review). *Int J Mol Med* 45: 279-297, 2020.

