

Table S1 Genes list of the 639 DNA panel

ABC1	BRD4	COL5A1	EPCAM	FGFR3	HIST3H3	KMT2B	MSI2	PCNA	PTPRT	SETD8	TEK	ZFH3
ABC9	BRIP1	CREBBP	EPHA3	FGFR4	HLA-A	KMT2C	MST1	PDCD1	QKI	SF3B1	TERT	ZNF217
ABL1	BTG1	CRKL	EPHA5	FH	HLA-B	KMT2D	MST1R	PDCD1LG2	RAB35	SGK1	TET1	ZNF703
ABL2	BTG2	CRLF2	EPHA7	FLCN	HLA-C	KNSTRN	MTAP	PDGFRA	RAC1	SH2B3	TET2	
ACE2	BTK	CSDE1	EPHB1	FLT1	HLA-DRB1	KRAS	MTHFR	PDGFRB	RAC2	SH2D1A	TGFBR1	
ACVR1	C10orf54	CSF1R	EPHB4	FLT3	HMGB1	LATS1	MTOR	PDIA3	RAD21	SHOC2	TGFBR2	
ACVR1B	C11orf30	CSF3R	EPHX1	FLT4	HMG1	LATS2	MTRR	PDK1	RAD50	SHQ1	TIPARP	
AGO2	C8orf34	CTCF	ERAP1	FOXA1	HNF1A	LGALS9	MUTYH	PDPK1	RAD51	SLC34A2	TMEM127	
AKT1	CALR	CTLA4	ERAP2	FOXL2	HOXB13	LGMN	MYB	PGR	RAD51B	SLCO1B1	TMPRSS2	
AKT2	CANX	CTNNA1	ERBB2	FOXO1	HRAS	LIG1	MYC	PHF6	RAD51C	SLIT2	TNF	
AKT3	CARD11	CTNNA1	ERBB3	FOXP1	HSD3B1	LIG3	MYCL	PHOX2B	RAD51D	SLX4	TNFAIP3	
ALK	CARM1	CTSB	ERBB4	FRS2	HSP90AA1	LMO1	MYCN	PIK3C2B	RAD52	SMAD2	TNFRSF14	
ALOX12B	CASP8	CTSL	ERCC1	FUBP1	ICOSLG	LNPEP	MYD88	PIK3C2G	RAD54L	SMAD3	TNFRSF9	
AMER1	CBFB	CTSS	ERCC2	FYN	ID3	LRP1B	MYOD1	PIK3C3	RAF1	SMAD4	TNFSF14	
ANKRD11	CBL	CUL3	ERCC3	GABRA6	IDE	LTK	NBN	PIK3CA	RANBP2	SMARCA4	TNFSF18	
APC	CBR3	CUL4A	ERCC4	GATA1	IDH1	LYN	NCOA3	PIK3CB	RARA	SMARCB1	TNFSF4	
AR	CCND1	CXCR4	ERCC5	GATA2	IDH2	LZTR1	NCOR1	PIK3CD	RASA1	SMARCD1	TNFSF9	
ARAF	CCND2	CYLD	ERF	GATA3	IFI30	MAF	NEGR1	PIK3CG	RB1	SMO	TOP1	
ARFRP1	CCND3	CYP17A1	ERG	GATA4	IFNGR1	MAGI2	NF1	PIK3R1	RBM10	SMYD3	TOP2A	
ARID1A	CCNE1	CYP19A1	ERRF1	GATA6	IGF1	MALT1	NF2	PIK3R2	RECQL	SNCAIP	TP53	
ARID1B	CD200	CYP2C19	ESR1	GID4	IGF1R	MAP2K1	NFE2L2	PIK3R3	RECQL4	SOCS1	TP53BP1	
ARID2	CD22	CYP2C8	ETV1	GLI1	IGF2	MAP2K2	NFKBIA	PIM1	REL	SOD2	TP63	
ARID5B	CD274	CYP2C9	ETV4	GNA11	IKBKE	MAP2K4	NKX2-1	PLCG2	RET	SOS1	TP73	
ASXL1	CD276	CYP2D6	ETV5	GNA13	IKZF1	MAP3K1	NKX3-1	PLK2	RFWD2	SOX10	TPMT	
ASXL2	CD40	CYP3A4	ETV6	GNAQ	IL10	MAP3K13	NOTCH1	PMAIP1	RHEB	SOX17	TPP2	
ATM	CD40LG	CYSLTR2	EWSR1	GNAS	IL7R	MAP3K14	NOTCH2	PMS1	RHOA	SOX2	TRAF2	
ATR	CD48	DAXX	EXO1	GPR124	INHA	MAPK1	NOTCH3	PMS2	RICTOR	SOX9	TRAF7	
ATRX	CD70	DCUN1D1	EZH1	GPS2	INHBA	MAPK3	NOTCH4	PNRC1	RIT1	SPEN	TSC1	
AURKA	CD74	DDR1	EZH2	GREM1	INPP4A	MAPKAP1	NPEPPS	POLB	RNF43	SPOP	TSC2	
AURKB	CD79A	DDR2	EZR	GRIN2A	INPP4B	MAX	NPM1	POLD1	ROS1	SPRED1	TSHR	
AXIN1	CD79B	DHFR	FAM175A	GRM3	INPPL1	MCL1	NQO1	POLE	RPS6KA4	SPTA1	TYMS	
AXIN2	CD80	DICER1	FAM46C	GSK3B	INSR	MDC1	NRAS	PPARG	RPS6KB2	SRC	TYRO3	
AXL	CD86	DIS3	FAM58A	GSTP1	IRF2	MDM2	NRD1	PPM1D	RPTOR	SRSF2	U2AF1	
B2M	CDA	DMD	FANCA	H3F3A	IRF4	MDM4	NSD1	PPP2R1A	RRAGC	STAG2	UGT1A1	
BABAM1	CDC42	DNAJB1	FANCC	H3F3B	IRS1	MED12	NT5C2	PPP2R2A	RRAS	STAT3	UGT1A9	
BAP1	CDC73	DNMT1	FANCD2	H3F3C	IRS2	MEF2B	NTHL1	PPP4R2	RRAS2	STAT4	UPF1	
BARD1	CDH1	DNMT3A	FANCE	HDAC1	ITGAV	MEN1	NTRK1	PPP6C	RRM1	STAT5A	VEGFA	
BBC3	CDK12	DNMT3B	FANCF	HERC1	ITGB3	MERTK	NTRK2	PRDM1	RSPO2	STAT5B	VHL	
BCL10	CDK4	DOT1L	FANCG	HGF	JAK1	MET	NTRK3	PRDM14	RTEL1	STK11	VTCN1	
BCL2	CDK6	DPYD	FANCL	HIST1H1C	JAK2	MGA	NUF2	PREX2	RUNX1	STK19	WHSC1	
BCL2L1	CDK8	DROSHA	FAS	HIST1H2BD	JAK3	MICA	NUP93	PRKAR1A	RUNX1T1	STK40	WHSC1L1	
BCL2L11	CDKN1A	DUSP4	FAT1	HIST1H3A	JUN	MICB	NUTM1	PRKCI	RXRA	SUFU	WISP3	
BCL2L2	CDKN1B	DYNC2H1	FBXW7	HIST1H3B	KAT6A	MITF	P2RY8	PRKD1	RYBP	SUZ12	WT1	
BCL6	CDKN2A	E2F3	FGF10	HIST1H3C	KDM5A	MKNK1	PAK1	PRKDC	SDC4	SYK	WWTR1	
BCOR	CDKN2B	EED	FGF12	HIST1H3D	KDM5C	MLH1	PAK3	PRSS8	SDHA	TAF1	XIAP	
BCORL1	CDKN2C	EGFL7	FGF14	HIST1H3E	KDM6A	MLH3	PAK7	PTCH1	SDHAF2	TAP1	XPC	
BCR	CEBPA	EGFR	FGF19	HIST1H3F	KDR	MPL	PALB2	PTEN	SDHB	TAP2	XPO1	
BIRC3	CENPA	EIF1AX	FGF23	HIST1H3G	KEAP1	MRE11	PARK2	PTGS2	SDHC	TAPBP	XRCC1	
BLM	CHD2	EIF4A2	FGF3	HIST1H3H	KEL	MRE11A	PARP1	PTP4A1	SDHD	TAPBPL	XRCC2	
BMP1A	CHD4	EIF4E	FGF4	HIST1H3I	KIT	MSH2	PARP2	PTPN11	SESN1	TBX3	XRCC5	
BRAF	CHEK1	ELF3	FGF6	HIST1H3J	KLF4	MSH3	PARP3	PTPRD	SESN2	TCEB1	YAP1	
BRCA1	CHEK2	EP300	FGFR1	HIST2H3C	KLHL6	MSH6	PAX5	PTPRO	SESN3	TCF3	YES1	
BRCA2	CIC	EPAS1	FGFR2	HIST2H3D	KMT2A	MSI1	PBRM1	PTPRS	SETD2	TCF7L2	ZBTB2	

The DNA panel is a hybridization capture-based NGS panel to detect single nucleotide variants (SNVs), insertion and deletion alterations (InDels), and copy number alterations (CNAs) involved in 639 cancer-associated genes in tumors. This panel is designed to provide mutation profiling of patients with solid tumors.

Table S2 Primer sequences list

Primer	Sequences (5'→3')
H-GAPDH-F	GGAGCGAGATCCCTCCAAAAT
H-GAPDH-R	GGCTGTTGTCATACTTCTCATGG
H-ETV1-F	TGGCAGTTTTTGGTAGCTCTTC
H-ETV1-R	CGGAGTGAACGGCTAAGTTTATC
H-NOTCH1-F	TGGACCAGATTGGGGAGTTC
H-NOTCH1-R	GCACACTCGTCTGTGTTGAC
H-NOTCH2-F	CCTTCCACTGTGAGTGTCTGA
H-NOTCH2-R	AGGTAGCATCATTCTGGCAGG
H-ASCL1-F	CGCGGCCAACAAAGAAGATG
H-ASCL1-R	CGACGAGTAGGATGAGACCG
H-HES1-F	CCTGTCATCCCCGTCTACAC
H-HES1-R	CACATGGAGTCCGCCGTAA
EGFR-WT-F	CTCGGATCCGCCACCATGCGACCCTCCGGGACGGC
EGFR-WT-R	CCCTCTAGACTCGAGTGCTCCAATAAATTCAGTCTT
EGFR-L858R -F	CTCGGATCCGCCACCATGCGACCCTCCGGGACGGC
EGFR-L858R -R	CCCTCTAGACTCGAGTGCTCCAATAAATTCAGTCTT
EGFR-T790M -F	CTCGGATCCGCCACCATGCGACCCTCCGGGACGGC
EGFR-T790M -R	CCCTCTAGACTCGAGTGCTCCAATAAATTCAGTCTT
ETV1-WT-F	CTCGGATCCGCCACCATGGATGGATTTTATGACCAG
ETV1-WT-R	CCCTCTAGACTCGAGATACACGTAGCCTTCGTTGTA
ETV1-E462Q-F	CTCGGATCCGCCACCATGGATGGATTTTATGACCAG
ETV1-E462Q-R	CCCTCTAGACTCGAGATACACGTAGCCTTCGTTGT
ETV1-P159S-F	CTCGGATCCGCCACCATGGATGGATTTTATGACCAG
ETV1-P159S-R	CCCTCTAGACTCGAGATACACGTAGCCTTCGTTGT

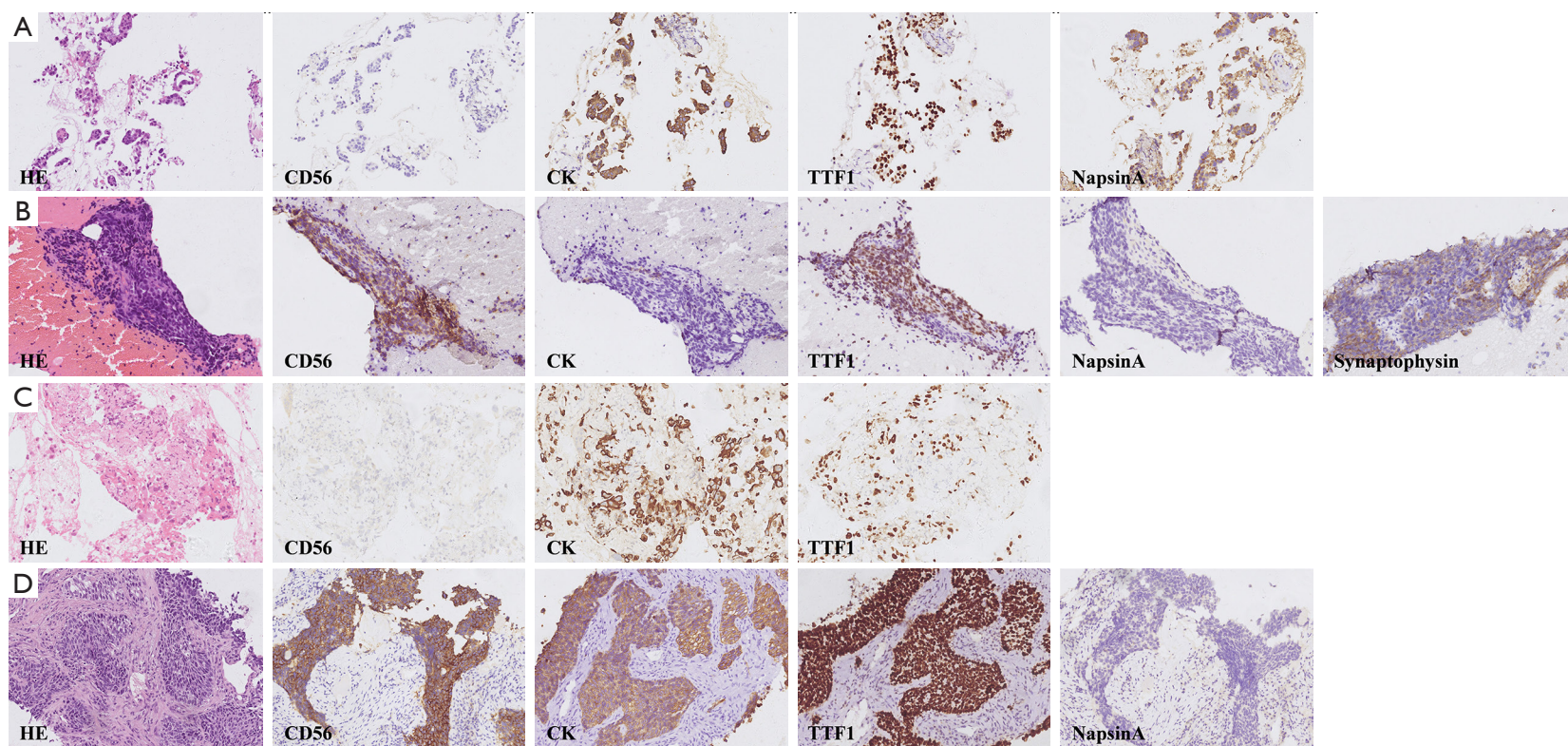


Figure S1 Pathological findings of the patients. (A) LUAD histology of case 1 before osimertinib treatment. IHC was strongly positive for CK, TTF1, and NapsinA, and negative for CD56 (200×). (B) Hematoxylin & eosin staining showed that the cells were SCLC phenotype. IHC was positive for CD56 and synaptophysin, +/- for CK, partially positive for TTF1, and negative for NapsinA (200×). (C) LUAD histology of case 2 before *EGFR*-TKI treatment. IHC was strongly positive for CK and TTF1, and negative for CD56 (200×). (D) Re-biopsy after TKI resistance showed SCLC transformation. IHC was positive for CD56, CK, TTF1, and NapsinA (200×).

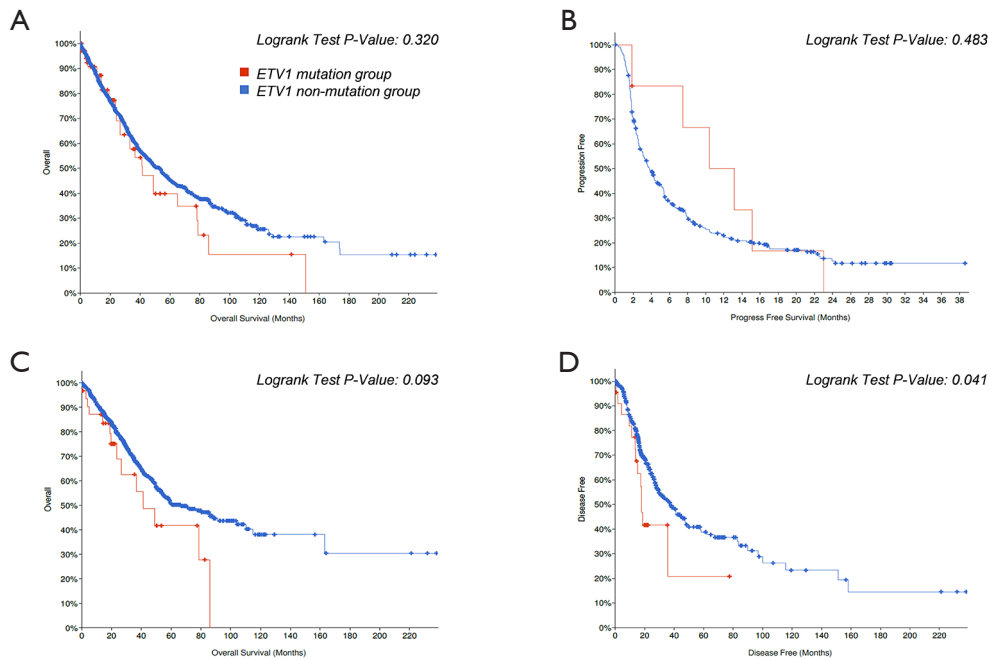


Figure S2 Survival association analysis of *ETV1* mutations. (A) Kaplan-Meier OS analysis for tumor patients with and without *ETV1* mutations in the TCGA cohorts. (B) PFS for tumor patients with and without *ETV1* mutations. (C,D) OS and DFS analysis for LUAD patients with and without *ETV1* mutations.

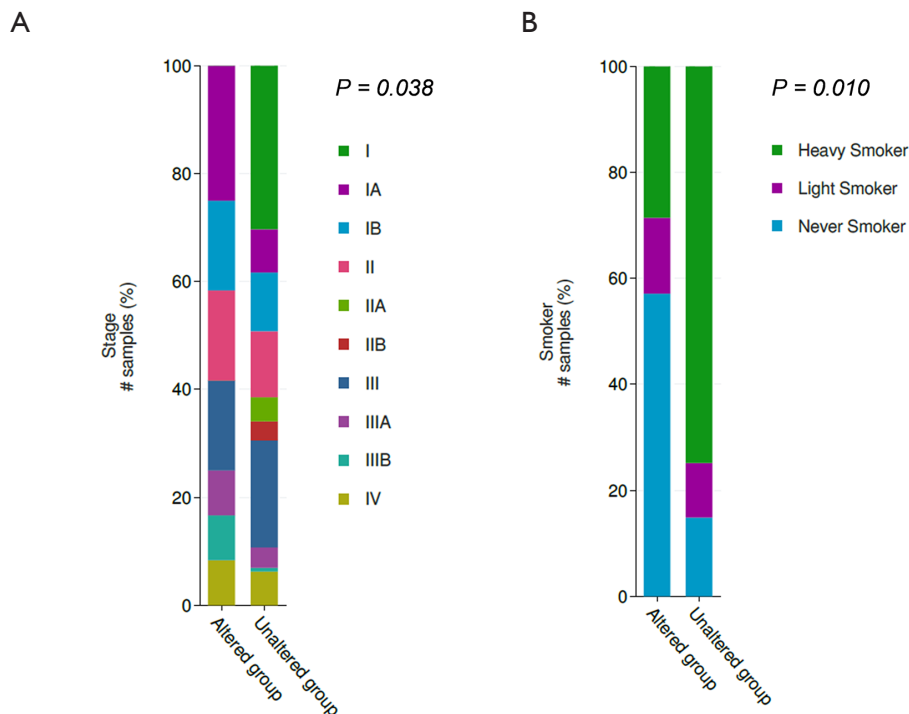


Figure S3 Clinical correlation analysis of *ETV1* mutations. (A) Comparison of tumor stage between *ETV1* mutated and non-mutated LUAD. (B) Smoking status and *ETV1* mutations.