

Tel. 1661-5117 www.smlab.co.kr



Report Date: 13 Jun 2025 1 of 19

Patient Name: 태양우 **Primary Tumor Site:** Gender: **Collection Date:** Sample ID: N25-37

Sample Cancer Type: Non-Small Cell Lung Cancer

Table of Contents	Page
Variant Details	2
Biomarker Descriptions	3
Alert Details	6
Relevant Therapy Summary	9

Report Highlights 3 Relevant Biomarkers 13 Therapies Available 183 Clinical Trials

2025.05.16

Relevant Non-Small Cell Lung Cancer Findings

Gene	Finding	Gene	Finding
ALK	None detected	MET	None detected
BRAF	None detected	NRG1	None detected
EGFR	EGFR p.(L858R) c.2573T>G, EGFR p.(T790M) c.2369C>T	NTRK1	None detected
ERBB2	None detected	NTRK2	None detected
FGFR1	None detected	NTRK3	None detected
FGFR2	None detected	RET	None detected
FGFR3	None detected	ROS1	None detected
KRAS	None detected		
Genomic Alt	eration Finding		
Tumor Mu	utational Burden 2.84 Mut/Mb measured		

Relevant Biomarkers

Tier	Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
IA	EGFR p.(L858R) c.2573T>G epidermal growth factor receptor Allele Frequency: 4.22% Locus: chr7:55259515 Transcript: NM_005228.5	amivantamab + lazertinib 1,2/1,II+ osimertinib 1,2/1,II+ bevacizumab† + erlotinib 2/1 erlotinib + ramucirumab 1/1 osimertinib + chemotherapy 1,2/I amivantamab + chemotherapy 1,2/II+ BAT1706 + erlotinib 2 gefitinib + chemotherapy I atezolizumab + bevacizumab + chemotherapy II+	None*	167

^{*} Public data sources included in relevant therapies: FDA1, NCCN, EMA2, ESMO

† Includes biosimilars/generics

Line of therapy: I: First-line therapy, II+: Other line of therapy
Tier Reference: Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn. 2017 Jan;19(1):4-23.

Report Date: 13 Jun 2025

Relevant Biomarkers (continued)

Tier	Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
IA	EGFR p.(T790M) c.2369C>T epidermal growth factor receptor Allele Frequency: 2.36% Locus: chr7:55249071 Transcript: NM_005228.5	osimertinib 1,2/II+ atezolizumab + bevacizumab + chemotherapy II+	None*	65
IIC	CDK4 amplification cyclin dependent kinase 4 Locus: chr12:58142242	None*	None*	6

^{*} Public data sources included in relevant therapies: FDA1, NCCN, EMA2, ESMO

Tier Reference: Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn. 2017 Jan;19(1):4-23.

Alerts informed by public data	sources: ⊘ Contraindicated, U Resistance, ✔ Breakthrough, A Fast Track
EGFR p.(L858R) c.2573T>G	
EGFR p.(T790M) c.2369C>T	

Public data sources included in alerts: FDA1, NCCN, EMA2, ESMO

Prevalent cancer biomarkers without relevant evidence based on included data sources

Microsatellite stable, UGT1A1 p.(G71R) c.211G>A, Tumor Mutational Burden

Variant Details

DNA	DNA Sequence Variants						
Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect
UGT1A1	p.(G71R)	c.211G>A	COSM4415616	chr2:234669144	99.70%	NM_000463.3	missense
EGFR	p.(T790M)	c.2369C>T	COSM6240	chr7:55249071	2.36%	NM_005228.5	missense
EGFR	p.(L858R)	c.2573T>G	COSM6224	chr7:55259515	4.22%	NM_005228.5	missense
PSMB8	p.(A18S)	c.52G>T		chr6:32811722	53.30%	NM_148919.4	missense
CSMD3	p.(D2239N)	c.6715G>A		chr8:113349898	7.24%	NM_198123.2	missense
TP53	p.(Y107_G108dup)	c.318_323dup		chr17:7579363	6.22%	NM_000546.6	nonframeshift Insertion

Copy Number Variations						
Gene	Locus	Copy Number	CNV Ratio			
CDK4	chr12:58142242	19.23	4.45			

[†] Includes biosimilars/generics

Line of therapy: I: First-line therapy, II+: Other line of therapy

Biomarker Descriptions

Microsatellite stable

Background: Microsatellites are short tandem repeats (STR) of 1 to 6 bases of DNA between 5 to 50 repeat units in length. There are approximately 0.5 million STRs that occupy 3% of the human genome¹. Microsatellite instability (MSI) is defined as a change in the length of a microsatellite in a tumor as compared to normal tissue^{2,3}. MSI is closely tied to the status of the mismatch repair (MMR) genes. In humans, the core MMR genes include MLH1, MSH2, MSH6, and PMS2⁴. Mutations and loss of expression in MMR genes, known as defective MMR (dMMR), lead to MSI. In contrast, when MMR genes lack alterations, they are referred to as MMR proficient (pMMR). Consensus criteria were first described in 1998 and defined MSI-high (MSI-H) as instability in two or more of the following five markers: BAT25, BAT26, D5S346, D2S123, and D17S250⁵. Tumors with instability in one of the five markers were defined as MSI-low (MSI-L) whereas, those with instability in zero markers were defined as MS-stable (MSS)⁵. Tumors classified as MSI-L are often phenotypically indistinguishable from MSS tumors and tend to be grouped with MSS^{6,7,8,9,10}. MSI-H is a hallmark of Lynch syndrome (LS), also known as hereditary non-polyposis colorectal cancer, which is caused by germline mutations in the MMR genes³. LS is associated with an increased risk of developing colorectal cancer, as well as other cancers, including endometrial and stomach cancer^{2,3,7,11}.

Alterations and prevalence: The MSI-H phenotype is observed in 30% of uterine corpus endothelial carcinoma, 20% of stomach adenocarcinoma, 15-20% of colon adenocarcinoma, and 5-10% of rectal adenocarcinoma^{2,3,12,13}. MSI-H is also observed in 5% of adrenal cortical carcinoma and at lower frequencies in other cancers such as esophageal, liver, and ovarian cancers^{12,13}.

Potential relevance: Anti-PD-1 immune checkpoint inhibitors including pembrolizumab¹⁴ (2014) and nivolumab¹⁵ (2015) are approved for patients with MSI-H or dMMR colorectal cancer who have progressed following chemotherapy. Pembrolizumab¹⁴ is also approved as a single agent, for the treatment of patients with advanced endometrial carcinoma that is MSI-H or dMMR with disease progression on prior therapy who are not candidates for surgery or radiation. Importantly, pembrolizumab is approved for the treatment of MSI-H or dMMR solid tumors that have progressed following treatment, with no alternative option and is the first anti-PD-1 inhibitor to be approved with a tumor agnostic indication¹⁴. Dostarlimab¹⁶ (2021) is also approved for dMMR recurrent or advanced endometrial carcinoma or solid tumors that have progressed on prior treatment and is recommended as a subsequent therapy option in dMMR/MSI-H advanced or metastatic colon or rectal cancer^{8,17}. The cytotoxic T-lymphocyte antigen 4 (CTLA-4) blocking antibody, ipilimumab¹⁸ (2011), is approved alone or in combination with nivolumab in MSI-H or dMMR colorectal cancer that has progressed following treatment with chemotherapy. MSI-H may confer a favorable prognosis in colorectal cancer although outcomes vary depending on stage and tumor location^{8,19,20}. Specifically, MSI-H is a strong prognostic indicator of better overall survival (OS) and relapse free survival (RFS) in stage II as compared to stage III colorectal cancer patients²⁰. The majority of patients with tumors classified as either MSS or pMMR do not benefit from treatment with single-agent immune checkpoint inhibitors as compared to those with MSI-H tumors^{21,22}. However, checkpoint blockade with the addition of chemotherapy or targeted therapies have demonstrated response in MSS or pMMR cancers^{21,22}.

EGFR p.(L858R) c.2573T>G, EGFR p.(T790M) c.2369C>T

epidermal growth factor receptor

Background: The EGFR gene encodes the epidermal growth factor receptor (EGFR) tyrosine kinase, a member of the ERBB/human epidermal growth factor receptor (HER) family. In addition to EGFR/ERBB1/HER1, other members of the ERBB/HER family include ERBB2/HER2, ERBB3/HER3, and ERBB4/HER4²³. EGFR ligand induced dimerization results in kinase activation and leads to stimulation of oncogenic signaling pathways including the PI3K/AKT/MTOR and RAS/RAF/MEK/ERK pathways. Activation of these pathways promote cell proliferation, differentiation, and survival^{24,25}.

Alterations and prevalence: Recurrent somatic mutations in the tyrosine kinase domain (TKD) of EGFR are observed in approximately 10-20% of lung adenocarcinoma, and at higher frequencies in never-smoker, female, and Asian populations^{26,27,28,29}. The most common mutations occur near the ATP-binding pocket of the TKD and include short in-frame deletions in exon 19 (EGFR exon 19 deletion) and the L858R amino acid substitution in exon 21³⁰. These mutations constitutively activate EGFR resulting in downstream signaling, and represent 80% of the EGFR mutations observed in lung cancer. A second group of less prevalent activating mutations include E709K, G719X, S768I, L861Q, and short in-frame insertion mutations in exon 20^{31,32,33,34}. EGFR activating mutations in lung cancer tend to be mutually exclusive to KRAS activating mutations³⁵. In contrast, a different set of recurrent activating EGFR mutations in the extracellular domain include R108K, A289V and G598V and are primarily observed in glioblastoma^{30,36}. Amplification of EGFR is observed in several cancer types including 30% of glioblastoma, 12% of esophageal cancer, 10% of head and neck cancer, 5% of bladder cancer, and 5% of lung squamous cell carcinoma^{27,28,29,36,37}. Deletion of exons 2-7, encoding the extracellular domain of EGFR (EGFRVIII), results in overexpression of a ligand-independent constitutively active protein and is observed in approximately 30% of glioblastoma^{38,39,40}.

Potential relevance: Approved first-generation EGFR tyrosine kinase inhibitors (TKIs) include erlotinib⁴¹ (2004) and gefitinib⁴² (2015), which block the activation of downstream signaling by reversible interaction with the ATP-binding site. Although initially approved for advanced lung cancer, the discovery that drug sensitivity was associated with exon 19 and exon 21 activating mutations allowed first-generation TKIs to become subsequently approved for front-line therapy in lung cancer tumors containing exon 19 or exon 21

Biomarker Descriptions (continued)

activating mutations. Second-generation TKIs afatinib⁴³ (2013) and dacomitinib⁴⁴ (2018) bind EGFR and other ERBB/HER gene family members irreversibly and were subsequently approved. First- and second-generation TKIs afatinib, dacomitinib, erlotinib, and gefitinib are recommended for the treatment NSCLC harboring EGFR exon 19 insertions, exon 19 deletions, point mutations L861Q, L858R, S768I, and codon 719 mutations, whereas most EGFR exon 20 insertions, except p.A763_Y764insFQEA, confer resistance to the same therapies^{45,46,47,48}. However, BDTX-189⁴⁹ was granted a fast track designation (2020) for the treatment of solid tumors harboring an EGFR exon 20 insertion mutations. In 2022, the FDA granted breakthrough therapy designation to the irreversible EGFR inhibitors, CLN-081 (TPC-064)⁵⁰ and sunvozertinib⁵¹, for locally advanced or metastatic non-small cell lung cancer harboring EGFR exon 20 insertion mutations. In lung cancer containing EGFR exon 19 or 21 activating mutations, treatment with TKIs is eventually associated with the emergence of drug resistance⁵². The primary resistance mutation that emerges following treatment with first-generation TKI is T790M, accounting for 50-60% of resistant cases³⁰. Third generation TKIs were developed to maintain sensitivity in the presence of T790M, Osimertinib⁵³ (2015) is an irreversible inhibitor indicated for metastatic EGFR T790M positive lung cancer and for the first-line treatment of metastatic NSCLC containing EGFR exon 19 deletions or exon 21 L858R mutations. Like first-generation TKIs, treatment with osimertinib is associated with acquired resistance. In this case, resistance is associated with the C797S mutation and occurs in 22-44% of cases⁵². The T790M and C797S mutations may be each selected following sequential treatment with a first-generation TKI followed by a third-generation TKI or vice versa⁵⁴. T790M and C797S can occur in either cis or trans allelic orientation⁵⁴. If C797S is observed following progression after treatment with a third-generation TKI in the first-line setting, sensitivity may be retained to firstgeneration TKIs⁵⁴. If C797S co-occurs in trans with T790M following sequential treatment with first- and third-generation TKIs, patients may exhibit sensitivity to combination first- and third-generation TKIs, but resistance to third-generation TKIs alone^{54,55}. However, C797S occurring in cis conformation with T790M, confers resistance to first- and third-generation TKIs54. Fourth-generation TKIs are in development to overcome acquired C797S and T790M resistance mutations after osimertinib treatment. BDTX-153556, a CNSpenetrating small molecule inhibitor, received fast track designation (2024) from the FDA for the treatment of patients with EGFR C797S positive NSCLC who have disease progression on or after a third-generation EGFR TKI. EGFR targeting antibodies including cetuximab (2004), panitumumab (2006), and necitumumab (2016) are under investigation in combination with EGFR-targeting TKIs for efficacy against EGFR mutations. The bispecific antibody, amivantamab⁵⁷, targeting EGFR and MET was approved (2021) for NSCLC tumors harboring EGFR exon 20 insertion mutations. A small molecule kinase inhibitor, lazertinib⁵⁸, was approved (2024) in combination with amivantamab as a first-line treatment for adult patients with locally advanced or metastatic NSCLC with EGFR exon 19 deletions or exon 21 L858R mutations. In 2024, a CNS penetrating small molecule, ERAS-80159 received fast track designation for the treatment of adult patients with EGFR altered glioblastoma. HLX-4260, an anti-EFGR-antibody-drug conjugate (ADC) consisting of an anti-EGFR monoclonal antibody conjugated with a novel high potency DNA topoisomerase I (topo I) inhibitor, received a fast track designation (2024) for the treatment of patients with advanced or metastatic EGFR-mutated non-small cell lung cancer whose disease has progressed on a third-generation EGFR tyrosine kinase inhibitor. CPO30161 received a fast track designation (2023) from the FDA for EGFR mutations in patients with metastatic NSCLC who are relapsed/refractory or ineligible for EGFR targeting therapy such as 3rdgeneration EGFR inhibitors including osimertinib. The Oncoprex immunogene therapy quaratusugene ozeplasmid⁶² in combination with osimertinib received a fast track designation from the FDA (2020) for NSCLC tumors harboring EGFR mutations that progressed on osimertinib alone.

CDK4 amplification

cyclin dependent kinase 4

<u>Background</u>: The CDK4 gene encodes the cyclin-dependent kinase 4 protein, a homologue of CDK6. Both proteins are serine/threonine protein kinases that are involved in the regulation of the G1/S phase transition of the mitotic cell cycle^{63,64}. CDK4 kinase is activated by complex formation with D-type cyclins (e.g., CCND1, CCND2, or CCND3), which leads to the phosphorylation of retinoblastoma protein (RB), followed by E2F activation, DNA replication, and cell-cycle progression⁶⁵. Germline mutations in CDK4 are associated with familial melanoma^{66,67,68}.

Alterations and prevalence: Recurrent somatic mutations of CDK4 codon K22 and R24 are observed in melanoma (1-2%) and lung cancer (approximately 0.1%). Codons K22 and R24 are necessary for binding and inhibition by p16/CDKN2A^{69,70,71}. CDK4 is recurrently amplified in several cancer types, most notably in sarcomas (15-20%), glioma (10-15%), adrenocortical carcinoma (5%), lung adenocarcinoma (5%), and melanoma (3%)^{27,28,29,36}.

Potential relevance: Currently, no therapies are approved for CDK4 aberrations. Amplification of region 12q14-15, which includes CDK4, is useful as an ancillary diagnostic marker of atypical lipomatous tumor/welldifferentiated liposarcoma (ALT/WDLS)⁷². Small molecule inhibitors targeting CDK4/6 including palbociclib (2015), abemaciclib (2017), and ribociclib (2017), are FDA approved in combination with an aromatase inhibitor or fulvestrant for the treatment of hormone receptor-positive, HER2-negative advanced or metastatic breast cancer.

Biomarker Descriptions (continued)

UGT1A1 p.(G71R) c.211G>A

UDP glucuronosyltransferase family 1 member A1

Background: The UGT1A1 gene encodes UDP glucuronosyltransferase family 1 member A1, a member of the UDP-glucuronosyltransferase 1A (UGT1A) subfamily of the UGT protein superfamily^{73,74}. UGTs are microsomal membrane-bound enzymes that catalyze the glucuronidation of endogenous and xenobiotic compounds and transform the lipophilic molecules into excretable, hydrophilic metabolites^{74,75}. UGTs play an important role in drug metabolism, detoxification, and metabolite homeostasis. Differential expression of UGTs can promote cancer development, disease progression, as well as drug resistance⁷⁶. Specifically, elevated expression of UGT1As are associated with resistance to many anti-cancer drugs due to drug inactivation and lower active drug concentrations. However, reduced expression and downregulation of UGT1As are implicated in bladder and hepatocellular tumorigenesis and progression due to toxin accumulation^{76,77,78,79}. Furthermore, UGT1A1 polymorphisms, such as UGT1A1*28, UGT1A1*93, and UGT1A1*6, confer an increased risk of severe toxicity to irinotecan-based chemotherapy treatment of solid tumors, due to reduced glucuronidation of the irinotecan metabolite, SN-38⁸⁰.

Alterations and prevalence: Biallelic deletion of UGT1A1 has been observed in 6% of sarcoma, 3% of brain lower grade glioma and uveal melanoma, and 2% of thymoma, cervical squamous cell carcinoma, bladder urothelial carcinoma, head and neck squamous cell carcinoma, and esophageal adenocarcinoma^{28,29}.

Potential relevance: Currently, no therapies are approved for UGT1A1 aberrations.

Report Date: 13 Jun 2025 6 of 19

Alerts Informed By Public Data Sources

Current FDA Information

Contraindicated

Not recommended



Resistance



Breakthrough



FDA information is current as of 2025-03-19. For the most up-to-date information, search www.fda.gov.

EGFR p.(L858R) c.2573T>G

patritumab deruxtecan

Cancer type: Non-Small Cell Lung Cancer

Variant class: EGFR L858R mutation or EGFRi sensitizing mutation

Supporting Statement:

The FDA has granted Breakthrough Therapy designation to a potential first-in-class HER3 directed antibody-drug conjugate, patritumab deruxtecan, for metastatic or locally advanced, EGFR-mutant non-small cell lung cancer.

https://www.cancernetwork.com/view/fda-grants-breakthrough-therapy-status-to-patritumab-deruxtecan-for-egfr-metastaticnsclc

Current NCCN Information



Contraindicated



Not recommended



Resistance



Breakthrough



A Fast Track

NCCN information is current as of 2025-03-03. To view the most recent and complete version of the guideline, go online to NCCN.org.

For NCCN International Adaptations & Translations, search www.nccn.org/global/what-we-do/international-adaptations.

Some variant specific evidence in this report may be associated with a broader set of alterations from the NCCN Guidelines. Specific variants listed in this report were sourced from approved therapies or scientific literature. These therapeutic options are appropriate for certain population segments with cancer. Refer to the NCCN Guidelines® for full recommendation.

All guidelines cited below are referenced with permission from the NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®) National Comprehensive Cancer Network, Inc. 2023. All rights reserved. NCCN makes no warranties regarding their content.

EGFR p.(T790M) c.2369C>T

afatinib

Cancer type: Non-Small Cell Lung Cancer

Variant class: EGFR T790M mutation

EGFR T790M mutation is associated with acquired resistance to first- and second-generation TKIs including erlotinib, gefitinib, dacomitinib, or afatinib.

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 3.2025]

Report Date: 13 Jun 2025 7 of 19

EGFR p.(T790M) c.2369C>T (continued)

dacomitinib

Cancer type: Non-Small Cell Lung Cancer Variant class: EGFR T790M mutation

Summary:

EGFR T790M mutation is associated with acquired resistance to first- and second-generation TKIs including erlotinib, gefitinib, dacomitinib, or afatinib.

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 3.2025]

erlotinib

Cancer type: Non-Small Cell Lung Cancer Variant class: EGFR T790M mutation

Summary:

EGFR T790M mutation is associated with acquired resistance to first- and second-generation TKIs including erlotinib, gefitinib, dacomitinib, or afatinib.

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 3.2025]

gefitinib

Cancer type: Non-Small Cell Lung Cancer Variant class: EGFR T790M mutation

Summary:

EGFR T790M mutation is associated with acquired resistance to first- and second-generation TKIs including erlotinib, gefitinib, dacomitinib, or afatinib.

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 3.2025]

Current EMA Information

EMA information is current as of 2025-03-19. For the most up-to-date information, search www.ema.europa.eu.

EGFR p.(T790M) c.2369C>T

gefitinib

Cancer type: Non-Small Cell Lung Cancer Label as of: 2023-07-17 Variant class: EGFR T790M mutation

Reference:

https://www.ema.europa.eu/en/documents/product-information/iressa-epar-product-information_en.pdf

Genes Assayed

Genes Assayed for the Detection of DNA Sequence Variants

ABL1, ABL2, ACVR1, AKT1, AKT2, AKT3, ALK, AR, ARAF, ATP1A1, AURKA, AURKB, AURKC, AXL, BCL2, BCL2L12, BCL6, BCR, BMP5, BRAF, BTK, CACNA1D, CARD11, CBL, CCND1, CCND2, CCND3, CCNE1, CD79B, CDK4, CDK6, CHD4, CSF1R, CTNNB1, CUL1, CYSLTR2, DDR2, DGCR8, DROSHA, E2F1, EGFR, EIF1AX, EPAS1, ERBB2, ERBB3, ERBB4, ESR1, EZH2, FAM135B, FGF7, FGFR1, FGFR2, FGFR3,

Genes Assayed (continued)

Genes Assayed for the Detection of DNA Sequence Variants (continued)

FGFR4, FLT3, FLT4, FOXA1, FOXL2, FOXO1, GATA2, GLI1, GNA11, GNAQ, GNAS, HIF1A, HRAS, IDH1, IDH2, IKBKB, IL6ST, IL7R, IRF4, IRS4, KCNJ5, KDR, KIT, KLF4, KLF5, KNSTRN, KRAS, MAGOH, MAP2K1, MAP2K2, MAPK1, MAX, MDM4, MECOM, MED12, MEF2B, MET, MITF, MPL, MTOR, MYC, MYCN, MYD88, MYOD1, NFE2L2, NRAS, NSD2, NT5C2, NTRK1, NTRK2, NTRK3, NUP93, PAX5, PCBP1, PDGFRA, PDGFRB, PIK3C2B, PIK3CA, PIK3CB, PIK3CD, PIK3CG, PIK3R2, PIM1, PLCG1, PPP2R1A, PPP6C, PRKACA, PTPN11, PTPRD, PXDNL, RAC1, RAF1, RARA, RET, RGS7, RHEB, RHOA, RICTOR, RIT1, ROS1, RPL10, SETBP1, SF3B1, SIX1, SIX2, SLC01B3, SMC1A, SMO, SNCAIP, SOS1, SOX2, SPOP, SRC, SRSF2, STAT3, STAT5B, STAT6, TAF1, TERT, TGFBR1, TOP1, TOP2A, TPMT, TRRAP, TSHR, U2AF1, USP8, WAS, XPO1, ZNF217, ZNF429

Genes Assayed for the Detection of Copy Number Variations

ABCB1, ABL1, ABL2, ABRAXAS1, ACVR1B, ACVR2A, ADAMTS12, ADAMTS2, AKT1, AKT2, AKT3, ALK, AMER1, APC, AR, ARAF, ARHGAP35, ARID1A, ARID1B, ARID2, ARID5B, ASXL1, ASXL2, ATM, ATR, ATRX, AURKA, AURKC, AXIN1, AXIN2, AXL, B2M, BAP1, BARD1, BCL2, BCL2L12, BCL6, BCOR, BLM, BMPR2, BRAF, BRCA1, BRCA2, BRIP1, CARD11, CASP8, CBFB, CBL, CCND1, CCND2, CCND3, CCNE1, CD274, CD276, CDC73, CDH1, CDH10, CDK12, CDK4, CDK6, CDKN1A, CDKN1B, CDKN2A, CDKN2B, CDKN2C, CHD4, CHEK1, CHEK2, CIC, CREBBP, CSMD3, CTCF, CTLA4, CTNND2, CUL3, CUL4A, CUL4B, CYLD, CYP2C9, DAXX, DDR1, DDR2, DDX3X, DICER1, DNMT3A, DOCK3, DPYD, DSC1, DSC3, EGFR, EIF1AX, ELF3, EMSY, ENO1, EP300, EPCAM, EPHA2, ERAP1, ERAP2, ERBB2, ERBB3, ERBB4, ERCC2, ERCC4, ERRFI1, ESR1, ETV6, EZH2, FAM135B, FANCA, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAT1, FBXW7, FGF19, FGF23, FGF3, FGF4, FGF9, FGFR1, FGFR2, FGFR3, FGFR4, FLT3, FLT4, FOXA1, FUBP1, FYN, GATA2, GATA3, GLI3, GNA13, GNAS, GPS2, HDAC2, HDAC9, HLA-A, HLA-B, HNF1A, IDH2, IGF1R, IKBKB, IL7R, INPP4B, JAK1, JAK2, JAK3, KDM5C, KDM6A, KDR, KEAP1, KIT, KLF5, KMT2A, KMT2B, KMT2C, KMT2D, KRAS, LARP4B, LATS1, LATS2, MAGOH, MAP2K1, MAP2K4, MAP2K7, MAP3K1, MAP3K4, MAPK1, MAPK8, MAX, MCL1, MDM2, MDM4, MECOM, MEF2B, MEN1, MET, MGA, MITF, MLH1, MLH3, MPL, MRE11, MSH2, MSH3, MSH6, MTAP, MTOR, MUTYH, MYC, MYCL, MYCN, MYD88, NBN, NCOR1, NF1, NF2, NFE2L2, NOTCH1, NOTCH2, NOTCH3, NOTCH4, NRAS, NTRK1, NTRK3, PALB2, PARP1, PARP2, PARP3, PARP4, PBRM1, PCBP1, PDCD1, PDCD1LG2, PDGFRA, PDGFRB, PDIA3, PGD, PHF6, PIK3C2B, PIK3CA, PIK3CB, PIK3R1, PIK3R2, PIM1, PLCG1, PMS1, PMS2, POLD1, POLE, POT1, PPM1D, PPP2R1A, PPP2R2A, PPP6C, PRDM1, PRDM9, PRKACA, PRKAR1A, PTCH1, PTEN, PTPN11, PTPRT, PXDNL, RAC1, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54L, RAF1, RARA, RASA1, RASA2, RB1, RBM10, RECQL4, RET, RHEB, RICTOR, RIT1, RNASEH2A, RNASEH2B, RNF43, ROS1, RPA1, RPS6KB1, RPTOR, RUNX1, SDHA, SDHB, SDHD, SETBP1, SETD2, SF3B1, SLCO1B3, SLX4, SMAD2, SMAD4, SMARCA4, SMARCB1, SMC1A, SMO, SOX9, SPEN, SPOP, SRC, STAG2, STAT3, STAT6, STK11, SUFU, TAP1, TAP2, TBX3, TCF7L2, TERT, TET2, TGFBR2, TNFAIP3, TNFRSF14, TOP1, TP53, TP63, TPMT, TPP2, TSC1, TSC2, U2AF1, USP8, USP9X, VHL, WT1, XPO1, XRCC2, XRCC3, YAP1, YES1, ZFHX3, ZMYM3, ZNF217, ZNF429, ZRSR2

Genes Assayed for the Detection of Fusions

AKT2, ALK, AR, AXL, BRAF, BRCA1, BRCA2, CDKN2A, EGFR, ERBB2, ERBB4, ERG, ESR1, ETV1, ETV4, ETV5, FGFR1, FGFR2, FGFR3, FGR, FLT3, JAK2, KRAS, MDM4, MET, MYB, MYBL1, NF1, NOTCH1, NOTCH4, NRG1, NTRK1, NTRK2, NTRK3, NUTM1, PDGFRA, PDGFRB, PIK3CA, PPARG, PRKACB, PTEN, RAD51B, RAF1, RB1, RELA, RET, ROS1, RSPO2, RSPO3, TERT

Genes Assayed with Full Exon Coverage

ABRAXAS1, ACVR1B, ACVR2A, ADAMTS12, ADAMTS2, AMER1, APC, ARHGAP35, ARID1A, ARID1B, ARID2, ARID5B, ASXL1, ASXL2, ATM, ATR, ATRX, AXIN1, AXIN2, B2M, BAP1, BARD1, BCOR, BLM, BMPR2, BRCA1, BRCA2, BRIP1, CALR, CASP8, CBFB, CD274, CD276, CDC73, CDH1, CDH10, CDK12, CDKN1A, CDKN1B, CDKN2A, CDKN2B, CDKN2C, CHEK1, CHEK2, CIC, CIITA, CREBBP, CSMD3, CTCF, CTLA4, CUL3, CUL4A, CUL4B, CYLD, CYP2C9, CYP2D6, DAXX, DDX3X, DICER1, DNMT3A, DOCK3, DPYD, DSC1, DSC3, ELF3, ENO1, EP300, EPCAM, EPHA2, ERAP1, ERAP2, ERCC2, ERCC4, ERCC5, ERRF11, ETV6, FANCA, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCH, FANCM, FAS, FAT1, FBXW7, FUBP1, GATA3, GNA13, GPS2, HDAC2, HDAC9, HLA-A, HLA-B, HNF1A, ID3, INPP4B, JAK1, JAK2, JAK3, KDM5C, KDM6A, KEAP1, KLHL13, KMT2A, KMT2B, KMT2C, KMT2D, LARP4B, LATS1, LATS2, MAP2K4, MAP2K7, MAP3K1, MAP3K4, MAPK8, MEN1, MGA, MLH1, MLH3, MRE11, MSH2, MSH3, MSH6, MTAP, MTUS2, MUTYH, NBN, NCOR1, NF1, NF2, NOTCH1, NOTCH2, NOTCH3, NOTCH4, PALB2, PARP1, PARP2, PARP3, PARP4, PBRM1, PDCD1, PDCD1LG2, PDIA3, PGD, PHF6, PIK3R1, PMS1, PMS2, POLD1, POLE, POT1, PPM1D, PPP2R2A, PRDM1, PRDM9, PRKAR1A, PSMB10, PSMB8, PSMB9, PTCH1, PTEN, PTPRT, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54L, RASA1, RASA2, RB1, RBM10, RECQL4, RNASEH2A, RNASEH2B, RNASEH2C, RNF43, RPA1, RPL22, RPL5, RUNX1, RUNX1T1, SDHA, SDHB, SDHC, SDHD, SETD2, SLX4, SMAD2, SMAD4, SMARCA4, SMARCB1, SOCS1, SOX9, SPEN, STAG2, STAT1, STK11, SUFU, TAP1, TAP2, TBX3, TCF7L2, TET2, TGFBR2, TMEM132D, TNFAIP3, TNFRSF14, TP53, TP63, TPP2, TSC1, TSC2, UGT1A1, USP9X, VHL, WT1, XRCC2, XRCC3, ZBTB20, ZFHX3, ZMYM3, ZRSR2

Relevant Therapy Summary

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
osimertinib	•	•	•	•	(IV)
amivantamab + carboplatin + pemetrexed	•	•	•	×	×
amivantamab + lazertinib	•	•	•	×	×
erlotinib + ramucirumab	•	•	×	•	×
osimertinib + chemotherapy + pemetrexed	•	×	•	×	×
bevacizumab + erlotinib	×	•	•	•	×
osimertinib + carboplatin + pemetrexed	×	•	×	×	×
osimertinib + cisplatin + pemetrexed	×	•	×	×	×
BAT1706 + erlotinib	×	×	•	×	×
bevacizumab (Allergan) + erlotinib	×	×	•	×	×
bevacizumab (Biocon) + erlotinib	×	×	•	×	×
bevacizumab (Celltrion) + erlotinib	×	×	•	×	×
bevacizumab (Mabxience) + erlotinib	×	×	•	×	×
bevacizumab (Pfizer) + erlotinib	×	×	•	×	×
bevacizumab (Samsung Bioepis) + erlotinib	×	×	•	×	×
bevacizumab (Stada) + erlotinib	×	×	•	×	×
atezolizumab + bevacizumab + carboplatin + paclitaxel	×	×	×	•	×
gefitinib + carboplatin + pemetrexed	×	×	×	•	×
befotertinib	×	×	×	×	(IV)
bevacizumab, almonertinib, chemotherapy	×	×	×	×	(IV)
EGFR tyrosine kinase inhibitor	×	×	×	×	(IV)
almonertinib, apatinib	×	×	×	×	(III)
almonertinib, chemotherapy	×	×	×	×	(III)
almonertinib, radiation therapy	×	×	×	×	(III)
almonertinib, radiation therapy, chemotherapy	×	×	×	×	(III)
befotertinib, icotinib hydrochloride	×	×	×	×	(III)
bevacizumab, osimertinib	×	×	×	×	(III)
BL-B01D1	×	×	×	×	(III)
datopotamab deruxtecan, osimertinib	×	×	×	×	(III)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Summary (continued)

In this cancer type

O In other cancer type

• In this cancer type and other cancer types

× No evidence

EGFR p.(L858R)) c.2573T>G ((continued)
----------------	---------------	-------------

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
furmonertinib	×	×	×	×	(III)
furmonertinib, osimertinib, chemotherapy	×	×	×	×	(III)
icotinib hydrochloride, catequentinib	×	×	×	×	(III)
icotinib hydrochloride, radiation therapy	×	×	×	×	(III)
JMT-101, osimertinib	×	×	×	×	(III)
osimertinib, bevacizumab	×	×	×	×	(III)
osimertinib, chemotherapy	×	×	×	×	(III)
osimertinib, datopotamab deruxtecan	×	×	×	×	(III)
sacituzumab tirumotecan	×	×	×	×	(III)
sacituzumab tirumotecan, osimertinib	×	×	×	×	(III)
savolitinib, osimertinib	×	×	×	×	(III)
SH-1028	×	×	×	×	(III)
targeted therapy	×	×	×	×	(III)
TY-9591, osimertinib	×	×	×	×	(III)
ABSK-043, furmonertinib	×	×	×	×	(II)
almonertinib	×	×	×	×	(II)
almonertinib, adebrelimab, chemotherapy	×	×	×	×	(II)
almonertinib, bevacizumab	×	×	×	×	(II)
almonertinib, chemoradiation therapy	×	×	×	×	(II)
amivantamab, bevacizumab, lazertinib	×	×	×	×	(II)
amivantamab, chemotherapy	×	×	×	×	(II)
amivantamab, lazertinib, chemotherapy	×	×	×	×	(II)
atezolizumab, bevacizumab, tiragolumab	×	×	×	×	(II)
befotertinib, bevacizumab, chemotherapy	×	×	×	×	(II)
bevacizumab, furmonertinib	×	×	×	×	(II)
BL-B01D1, osimertinib	×	×	×	×	(II)
camrelizumab, apatinib	×	×	×	×	(II)
capmatinib, osimertinib, ramucirumab	×	×	×	×	(II)
catequentinib, almonertinib	×	×	×	×	(II)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Summary (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
chemotherapy, atezolizumab, bevacizumab	×	×	×	×	(II)
EGFR tyrosine kinase inhibitor, osimertinib, chemotherapy	×	×	×	×	(II)
EGFR tyrosine kinase inhibitor, radiation therapy	×	×	×	×	(II)
furmonertinib, bevacizumab	×	×	×	×	(II)
furmonertinib, bevacizumab, chemotherapy	×	×	×	×	(II)
furmonertinib, catequentinib	×	×	×	×	(II)
furmonertinib, chemotherapy	×	×	×	×	(II)
furmonertinib, chemotherapy, bevacizumab	×	×	×	×	(II)
furmonertinib, icotinib hydrochloride	×	×	×	×	(II)
icotinib hydrochloride	×	×	×	×	(II)
icotinib hydrochloride, autologous RAK cell	×	×	×	×	(II)
icotinib hydrochloride, chemotherapy	×	×	×	×	(II)
ivonescimab, chemotherapy	×	×	×	×	(II)
lazertinib	×	×	×	×	(II)
lazertinib, bevacizumab	×	×	×	×	(II)
lazertinib, chemotherapy	×	×	×	×	(II)
lenvatinib, pembrolizumab	×	×	×	×	(II)
osimertinib, chemoradiation therapy	×	×	×	×	(II)
osimertinib, dalpiciclib	×	×	×	×	(II)
osimertinib, radiation therapy	×	×	×	×	(II)
PLB-1004, bozitinib, osimertinib	×	×	×	×	(II)
sacituzumab govitecan	×	×	×	×	(II)
sacituzumab tirumotecan, chemotherapy, osimertinib	×	×	×	×	(II)
sunvozertinib	×	×	×	×	(II)
sunvozertinib, golidocitinib	×	×	×	×	(II)
tislelizumab, chemotherapy, bevacizumab	×	×	×	×	(II)
toripalimab	×	×	×	×	(II)
toripalimab, bevacizumab, Clostridium butyricum, chemotherapy	×	×	×	×	(II)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Summary (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
toripalimab, chemotherapy	×	×	×	×	(II)
zorifertinib, pirotinib	×	×	×	×	(II)
AFM-24_I, atezolizumab	×	×	×	×	(1/11)
almonertinib, icotinib hydrochloride	×	×	×	×	(1/11)
BBT-207	×	×	×	×	(1/11)
BEBT-908, BEBT-109	×	×	×	×	(1/11)
benmelstobart, catequentinib	×	×	×	×	(I/II)
BH-30643	×	×	×	×	(1/11)
bozitinib, osimertinib	×	×	×	×	(I/II)
bozitinib, PLB-1004	×	×	×	×	(1/11)
BPI-361175	×	×	×	×	(1/11)
cetrelimab, amivantamab	×	×	×	×	(1/11)
DAJH-1050766	×	×	×	×	(1/11)
dositinib	×	×	×	×	(1/11)
EMB01	×	×	×	×	(1/11)
FWD-1509	×	×	×	×	(/)
H-002	×	×	×	×	(1/11)
ifebemtinib, furmonertinib	×	×	×	×	(1/11)
JIN-A-02	×	×	×	×	(1/11)
MRTX0902	×	×	×	×	(/)
necitumumab, osimertinib	×	×	×	×	(1/11)
quaratusugene ozeplasmid, osimertinib	×	×	×	×	(1/11)
RC-108, furmonertinib, toripalimab	×	×	×	×	(1/11)
sotiburafusp alfa, HB-0030	×	×	×	×	(1/11)
sunvozertinib, chemotherapy	×	×	×	×	(1/11)
TAS-3351	×	×	×	×	(/)
TQ-B3525, osimertinib	×	×	×	×	(I/II)
TRX-221	×	×	×	×	(I/II)
alisertib, osimertinib	×	×	×	×	(I)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Report Date: 13 Jun 2025

Relevant Therapy Summary (continued)

In this cancer type

O In other cancer type

In this cancer type and other cancer types

X No evidence

EGFR p.(L858R) c.2573T>G (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
AZD-9592	×	×	×	×	(I)
BG-60366	×	×	×	×	(I)
BPI-1178, osimertinib	×	×	×	×	(I)
cemiplimab, sarilumab	×	×	×	×	(I)
DZD-6008	×	×	×	×	(I)
genolimzumab, fruquintinib	×	×	×	×	(I)
HS-10241, almonertinib	×	×	×	×	● (I)
IBI-318, lenvatinib	×	×	×	×	(I)
KQB-198, osimertinib	×	×	×	×	(I)
LAVA-1223	×	×	×	×	(I)
MRX-2843, osimertinib	×	×	×	×	(I)
osimertinib, carotuximab	×	×	×	×	(I)
osimertinib, Minnelide	×	×	×	×	(I)
osimertinib, tegatrabetan	×	×	×	×	(I)
patritumab deruxtecan	×	×	×	×	(I)
QLH-11811	×	×	×	×	(I)
repotrectinib, osimertinib	×	×	×	×	(I)
VIC-1911, osimertinib	×	×	×	×	(I)
WJ13404	×	×	×	×	(I)
YH-013	×	×	×	×	(I)
YL-202	×	×	×	×	(I)

EGFR p.(T790M) c.2369C>T

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
osimertinib					(IV)
atezolizumab + bevacizumab + carboplatin + paclitaxel	×	×	×	•	×
bevacizumab, osimertinib	×	×	×	×	(IV)
catequentinib, osimertinib	×	×	×	×	(IV)
almonertinib, chemotherapy	×	×	×	×	(III)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Report Date: 13 Jun 2025

Relevant Therapy Summary (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
datopotamab deruxtecan, osimertinib	×	×	×	×	(III)
osimertinib, datopotamab deruxtecan	×	×	×	×	(III)
savolitinib, osimertinib	×	×	×	×	(III)
SH-1028	×	×	×	×	(III)
almonertinib	×	×	×	×	(II)
almonertinib, adebrelimab, chemotherapy	×	×	×	×	(II)
almonertinib, radiation therapy	×	×	×	×	(II)
amivantamab, bevacizumab, lazertinib	×	×	×	×	(II)
avitinib	×	×	×	×	(II)
pefotertinib	×	×	×	×	(II)
urmonertinib	×	×	×	×	(II)
urmonertinib, bevacizumab, chemotherapy	×	×	×	×	(II)
urmonertinib, radiation therapy	×	×	×	×	(II)
azertinib	×	×	×	×	(II)
envatinib, pembrolizumab	×	×	×	×	(II)
osimertinib, chemoradiation therapy	×	×	×	×	(II)
osimertinib, chemotherapy	×	×	×	×	(II)
osimertinib, radiation therapy	×	×	×	×	(II)
serplulimab, bevacizumab, chemotherapy	×	×	×	×	(II)
sulfatinib, toripalimab, chemotherapy	×	×	×	×	(II)
sunvozertinib	×	×	×	×	(II)
sunvozertinib, golidocitinib	×	×	×	×	(II)
oripalimab, bevacizumab, Clostridium butyricum, chemotherapy	×	×	×	×	(II)
AFM-24_I, atezolizumab	×	×	×	×	(1/11)
BH-30643	×	×	×	×	(/)
pozitinib, PLB-1004	×	×	×	×	(1/11)
dositinib	×	×	×	×	(/)
EMB01	×	×	×	×	(I/II)
FWD-1509	×	×	×	×	(I/II)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Summary (continued)

In this cancer type

O In other cancer type

• In this cancer type and other cancer types

X No evidence

EGFR p.(T790M) c.2369C>T (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
ifebemtinib, furmonertinib	×	×	×	×	(I/II)
JIN-A-02	×	×	×	×	(I/II)
MCLA-129	×	×	×	×	(1/11)
RC-108, furmonertinib, toripalimab	×	×	×	×	(I/II)
sunvozertinib, chemotherapy	×	×	×	×	(1/11)
YK-029A	×	×	×	×	(I/II)
alisertib, osimertinib	×	×	×	×	(I)
AZD-9592, osimertinib	×	×	×	×	(I)
BEBT-109	×	×	×	×	(I)
BG-60366	×	×	×	×	(I)
BPI-1178, osimertinib	×	×	×	×	(I)
HS-10241, almonertinib	×	×	×	×	(I)
KQB-198, osimertinib	×	×	×	×	(I)
osimertinib, Minnelide	×	×	×	×	(I)
palcitoclax, osimertinib	×	×	×	×	(I)
QLH-11811	×	×	×	×	(I)
repotrectinib, osimertinib	×	×	×	×	(I)
VIC-1911, osimertinib	×	×	×	×	(I)
YH-013	×	×	×	×	(I)
YZJ-0318	×	×	×	×	(1)

CDK4 amplification

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
abemaciclib	×	×	×	×	(II)
osimertinib, dalpiciclib	×	×	×	×	(II)
palbociclib	×	×	×	×	(II)
palbociclib, abemaciclib	×	×	×	×	(II)
PF-07220060, midazolam	×	×	×	×	(I/II)

^{*} Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Report Date: 13 Jun 2025 16 of 19

HRR Details

Gene/Genomic Alteration	Finding
LOH percentage	0.0%
Not Detected	Not Applicable

Homologous recombination repair (HRR) genes were defined from published evidence in relevant therapies, clinical guidelines, as well as clinical trials, and include - BRCA1, BRCA2, ATM, BARD1, BRIP1, CDK12, CHEK1, CHEK2, FANCL, PALB2, RAD51B, RAD51C, RAD51D, and RAD54L.

Thermo Fisher Scientific's Ion Torrent Oncomine Reporter software was used in generation of this report. Software was developed and designed internally by Thermo Fisher Scientific. The analysis was based on Oncomine Reporter (6.0.2 data version 2025.04(004)). The data presented here are from a curated knowledge base of publicly available information, but may not be exhaustive. FDA information was sourced from www.fda.gov and is current as of 2025-03-19. NCCN information was sourced from www.nccn.org and is current as of 2025-03-03. EMA information was sourced from www.ema.europa.eu and is current as of 2025-03-19. ESMO information was sourced from www.esmo.org and is current as of 2025-03-03. Clinical Trials information is current as of 2025-03-03. For the most upto-date information regarding a particular trial, search www.clinicaltrials.gov by NCT ID or search local clinical trials authority website by local identifier listed in 'Other identifiers.' Variants are reported according to HGVS nomenclature and classified following AMP/ ASCO/CAP guidelines (Li et al. 2017). Based on the data sources selected, variants, therapies, and trials listed in this report are listed in order of potential clinical significance but not for predicted efficacy of the therapies.

References

- 1. Lander et al. Initial sequencing and analysis of the human genome. Nature. 2001 Feb 15;409(6822):860-921. PMID: 11237011
- 2. Baudrin et al. Molecular and Computational Methods for the Detection of Microsatellite Instability in Cancer. Front Oncol. 2018 Dec 12:8:621. doi: 10.3389/fonc.2018.00621. eCollection 2018. PMID: 30631754
- Nojadeh et al. Microsatellite instability in colorectal cancer. EXCLI J. 2018;17:159-168. PMID: 29743854
- 4. Saeed et al. Microsatellites in Pursuit of Microbial Genome Evolution. Front Microbiol. 2016 Jan 5;6:1462. doi: 10.3389/fmicb.2015.01462. eCollection 2015. PMID: 26779133
- 5. Boland et al. A National Cancer Institute Workshop on Microsatellite Instability for cancer detection and familial predisposition: development of international criteria for the determination of microsatellite instability in colorectal cancer. Cancer Res. 1998 Nov 15;58(22):5248-57. PMID: 9823339
- 6. Halford et al. Low-level microsatellite instability occurs in most colorectal cancers and is a nonrandomly distributed quantitative trait. Cancer Res. 2002 Jan 1;62(1):53-7. PMID: 11782358
- 7. Imai et al. Carcinogenesis and microsatellite instability: the interrelationship between genetics and epigenetics. Carcinogenesis. 2008 Apr;29(4):673-80. PMID: 17942460
- 8. NCCN Guidelines® NCCN-Colon Cancer [Version 1.2025]
- 9. Pawlik et al. Colorectal carcinogenesis: MSI-H versus MSI-L. Dis. Markers. 2004;20(4-5):199-206. PMID: 15528785
- 10. Lee et al. Low-Level Microsatellite Instability as a Potential Prognostic Factor in Sporadic Colorectal Cancer. Medicine (Baltimore). 2015 Dec;94(50):e2260. PMID: 26683947
- 11. Latham et al. Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. J. Clin. Oncol. 2019 Feb 1;37(4):286-295. PMID: 30376427
- 12. Cortes-Ciriano et al. A molecular portrait of microsatellite instability across multiple cancers. Nat Commun. 2017 Jun 6;8:15180. doi: 10.1038/ncomms15180. PMID: 28585546
- 13. Bonneville et al. Landscape of Microsatellite Instability Across 39 Cancer Types. JCO Precis Oncol. 2017;2017. PMID: 29850653
- 14. https://www.accessdata.fda.gov/drugsatfda_docs/label/2025/125514s172lbl.pdf
- 15. https://www.accessdata.fda.gov/drugsatfda_docs/label/2024/125554s127lbl.pdf
- 16. https://www.accessdata.fda.gov/drugsatfda_docs/label/2024/761174s009lbl.pdf
- 17. NCCN Guidelines® NCCN-Rectal Cancer [Version 1.2025]
- 18. https://www.accessdata.fda.gov/drugsatfda_docs/label/2025/125377s132lbl.pdf
- 19. Ribic et al. Tumor microsatellite-instability status as a predictor of benefit from fluorouracil-based adjuvant chemotherapy for colon cancer. N. Engl. J. Med. 2003 Jul 17;349(3):247-57. PMID: 12867608
- 20. Klingbiel et al. Prognosis of stage II and III colon cancer treated with adjuvant 5-fluorouracil or FOLFIRI in relation to microsatellite status: results of the PETACC-3 trial. Ann. Oncol. 2015 Jan;26(1):126-32. PMID: 25361982
- 21. Hermel et al. The Emerging Role of Checkpoint Inhibition in Microsatellite Stable Colorectal Cancer. J Pers Med. 2019 Jan 16;9(1). PMID: 30654522
- 22. Ciardiello et al. Immunotherapy of colorectal cancer: Challenges for therapeutic efficacy. Cancer Treat. Rev. 2019 Jun;76:22-32. PMID: 31079031
- 23. King et al. Amplification of a novel v-erbB-related gene in a human mammary carcinoma. Science. 1985 Sep 6;229(4717):974-6. PMID: 2992089
- 24. Zhixiang. ErbB Receptors and Cancer. Methods Mol. Biol. 2017;1652:3-35. PMID: 28791631
- 25. Gutierrez et al. HER2: biology, detection, and clinical implications. Arch. Pathol. Lab. Med. 2011 Jan;135(1):55-62. PMID: 21204711
- 26. Pines et al. Oncogenic mutant forms of EGFR: lessons in signal transduction and targets for cancer therapy. FEBS Lett. 2010 Jun 18;584(12):2699-706. PMID: 20388509
- 27. Cancer Genome Atlas Research Network. Comprehensive molecular profiling of lung adenocarcinoma. Nature. 2014 Jul 31;511(7511):543-50. doi: 10.1038/nature13385. Epub 2014 Jul 9. PMID: 25079552
- 28. Weinstein et al. The Cancer Genome Atlas Pan-Cancer analysis project. Nat. Genet. 2013 Oct;45(10):1113-20. PMID: 24071849
- 29. Cerami et al. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. Cancer Discov. 2012 May;2(5):401-4. PMID: 22588877
- 30. da et al. EGFR mutations and lung cancer. Annu Rev Pathol. 2011;6:49-69. doi: 10.1146/annurev-pathol-011110-130206. PMID: 20887192

Report Date: 13 Jun 2025

References (continued)

- 31. Arcila et al. EGFR exon 20 insertion mutations in lung adenocarcinomas: prevalence, molecular heterogeneity, and clinicopathologic characteristics. Mol. Cancer Ther. 2013 Feb;12(2):220-9. PMID: 23371856
- 32. Kobayashi et al. EGFR Exon 18 Mutations in Lung Cancer: Molecular Predictors of Augmented Sensitivity to Afatinib or Neratinib as Compared with First- or Third-Generation TKIs. Clin Cancer Res. 2015 Dec 1;21(23):5305-13. doi: 10.1158/1078-0432.CCR-15-1046. Epub 2015 Jul 23. PMID: 26206867
- 33. Yasuda et al. Structural, biochemical, and clinical characterization of epidermal growth factor receptor (EGFR) exon 20 insertion mutations in lung cancer. Sci Transl Med. 2013 Dec 18;5(216):216ra177. PMID: 24353160
- 34. Chiu et al. Epidermal Growth Factor Receptor Tyrosine Kinase Inhibitor Treatment Response in Advanced Lung Adenocarcinomas with G719X/L861Q/S768I Mutations. J Thorac Oncol. 2015 May;10(5):793-9. PMID: 25668120
- 35. Karachaliou et al. KRAS mutations in lung cancer. Clin Lung Cancer. 2013 May;14(3):205-14. PMID: 23122493
- 36. Brennan et al. The somatic genomic landscape of glioblastoma. Cell. 2013 Oct 10;155(2):462-77. PMID: 24120142
- 37. Cancer Genome Atlas Network. Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature. 2015 Jan 29;517(7536):576-82. PMID: 25631445
- 38. Mitsudomi et al. Epidermal growth factor receptor in relation to tumor development: EGFR gene and cancer. FEBS J. 2010 Jan;277(2):301-8. PMID: 19922469
- 39. Gazdar. Activating and resistance mutations of EGFR in non-small-cell lung cancer: role in clinical response to EGFR tyrosine kinase inhibitors. Oncogene. 2009 Aug;28 Suppl 1:S24-31. PMID: 19680293
- 40. Gan et al. The EGFRvIII variant in glioblastoma multiforme. J Clin Neurosci. 2009 Jun;16(6):748-54. PMID: 19324552
- 41. https://www.accessdata.fda.gov/drugsatfda_docs/label/2016/021743s025lbl.pdf
- 42. https://www.accessdata.fda.gov/drugsatfda_docs/label/2021/206995s004lbl.pdf
- 43. https://www.accessdata.fda.gov/drugsatfda_docs/label/2022/201292s017lbl.pdf
- 44. https://www.accessdata.fda.gov/drugsatfda_docs/label/2020/211288s003lbl.pdf
- 45. NCCN Guidelines® NCCN-Non-Small Cell Lung Cancer [Version 3.2025]
- 46. Naidoo et al. Epidermal growth factor receptor exon 20 insertions in advanced lung adenocarcinomas: Clinical outcomes and response to erlotinib. Cancer. 2015 Sep 15;121(18):3212-3220. PMID: 26096453
- 47. Vyse et al. Targeting EGFR exon 20 insertion mutations in non-small cell lung cancer. Signal Transduct Target Ther. 2019;4:5. PMID: 30854234
- 48. Yi et al. A comparison of epidermal growth factor receptor mutation testing methods in different tissue types in non-small cell lung cancer. Int J Mol Med. 2014 Aug;34(2):464-74. PMID: 24891042
- 49. https://investors.blackdiamondtherapeutics.com/news-releases/news-release-details/black-diamond-therapeutics-granted-fast-track-designation-fda
- 50. https://investors.cullinanoncology.com/news-releases/news-release-details/fda-grants-breakthrough-therapy-designation-cullinan-oncologys
- 51. https://www.prnewswire.com/news-releases/fda-grants-breakthrough-therapy-designation-for-dizal-pharmaceuticals-dzd9008-in-patients-with-locally-advanced-or-metastatic-non-small-cell-lung-cancer-harboring-egfr-exon20-insertion-301469692.html
- 52. Madic et al. EGFR C797S, EGFR T790M and EGFR sensitizing mutations in non-small cell lung cancer revealed by six-color crystal digital PCR. Oncotarget. 2018 Dec 21;9(100):37393-37406. PMID: 30647840
- 53. https://www.accessdata.fda.gov/drugsatfda_docs/label/2024/208065s033lbl.pdf
- 54. Niederst et al. The Allelic Context of the C797S Mutation Acquired upon Treatment with Third-Generation EGFR Inhibitors Impacts Sensitivity to Subsequent Treatment Strategies. Clin. Cancer Res. 2015 Sep 1;21(17):3924-33. PMID: 25964297
- 55. Wang et al. Lung Adenocarcinoma Harboring EGFR T790M and In Trans C797S Responds to Combination Therapy of First- and Third-Generation EGFR TKIs and Shifts Allelic Configuration at Resistance. J Thorac Oncol. 2017 Nov;12(11):1723-1727. PMID: 28662863
- 56. https://investors.blackdiamondtherapeutics.com//news-releases/news-release-details/black-diamond-therapeutics-announces-corporate-update-and
- 57. https://www.accessdata.fda.gov/drugsatfda_docs/label/2025/761210s007lbl.pdf
- 58. https://www.accessdata.fda.gov/drugsatfda_docs/label/2024/219008s000lbledt.pdf
- 59. https://investors.erasca.com//news-releases/news-release-details/erasca-granted-fda-fast-track-designation-cns-penetrant-egfr
- 60. https://iis.aastocks.com/20231227/11015917-0.PDF
- 61. http://iis.aastocks.com/20230612/10770455-0.PDF

Report Date: 13 Jun 2025

References (continued)

- 62. https://www.genprex.com/news/genprex-receives-u-s-fda-fast-track-designation-for-gene-therapy-that-targets-lung-cancer/
- 63. Malumbres et al. Cell cycle, CDKs and cancer: a changing paradigm. Nat. Rev. Cancer. 2009 Mar;9(3):153-66. PMID: 19238148
- 64. Sherr et al. Targeting CDK4 and CDK6: From Discovery to Therapy. Cancer Discov. 2016 Apr;6(4):353-67. PMID: 26658964
- 65. Weinberg. The retinoblastoma protein and cell cycle control. Cell. 1995 May 5;81(3):323-30. PMID: 7736585
- 66. Rane et al. Germ line transmission of the Cdk4(R24C) mutation facilitates tumorigenesis and escape from cellular senescence. Mol. Cell. Biol. 2002 Jan;22(2):644-56. PMID: 11756559
- 67. Zuo et al. Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. Nat. Genet. 1996 Jan;12(1):97-9. PMID: 8528263
- 68. Molven et al. A large Norwegian family with inherited malignant melanoma, multiple atypical nevi, and CDK4 mutation. Genes Chromosomes Cancer. 2005 Sep;44(1):10-8. PMID: 15880589
- 69. Ceha et al. Several noncontiguous domains of CDK4 are involved in binding to the P16 tumor suppressor protein. Biochem. Biophys. Res. Commun. 1998 Aug 19;249(2):550-5. PMID: 9712735
- 70. Tsao et al. Novel mutations in the p16/CDKN2A binding region of the cyclin-dependent kinase-4 gene. Cancer Res. 1998 Jan 1;58(1):109-13. PMID: 9426066
- 71. Sotillo et al. Invasive melanoma in Cdk4-targeted mice. Proc. Natl. Acad. Sci. U.S.A. 2001 Nov 6;98(23):13312-7. PMID: 11606789
- 72. NCCN Guidelines® NCCN-Soft Tissue Sarcoma [Version 4.2024]
- 73. O'Leary et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016 Jan 4;44(D1):D733-45. PMID: 26553804
- 74. Ouzzine et al. The UDP-glucuronosyltransferases of the blood-brain barrier: their role in drug metabolism and detoxication. Front Cell Neurosci. 2014;8:349. PMID: 25389387
- 75. Nagar et al. Uridine diphosphoglucuronosyltransferase pharmacogenetics and cancer. Oncogene. 2006 Mar 13;25(11):1659-72. PMID: 16550166
- 76. Allain et al. Emerging roles for UDP-glucuronosyltransferases in drug resistance and cancer progression. Br J Cancer. 2020 Apr;122(9):1277-1287. PMID: 32047295
- 77. Izumi et al. Expression of UDP-glucuronosyltransferase 1A in bladder cancer: association with prognosis and regulation by estrogen. Mol Carcinog. 2014 Apr;53(4):314-24. PMID: 23143693
- 78. Sundararaghavan et al. Glucuronidation and UGT isozymes in bladder: new targets for the treatment of uroepithelial carcinomas?. Oncotarget. 2017 Jan 10;8(2):3640-3648. PMID: 27690298
- 79. Lu et al. Drug-Metabolizing Activity, Protein and Gene Expression of UDP-Glucuronosyltransferases Are Significantly Altered in Hepatocellular Carcinoma Patients. PLoS One. 2015;10(5):e0127524. PMID: 26010150
- 80. Karas et al. JCO Oncol Pract. 2021 Dec 3:0P2100624. PMID: 34860573