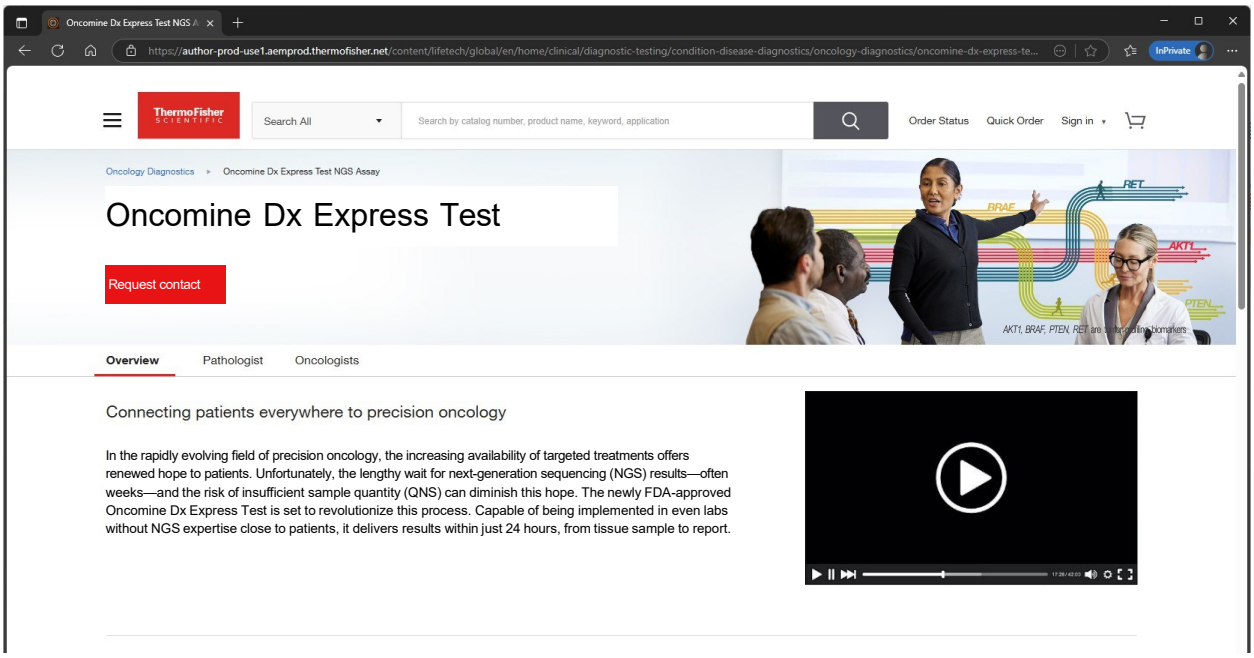


Rapid means as little as 24 hours, from patient sample to report

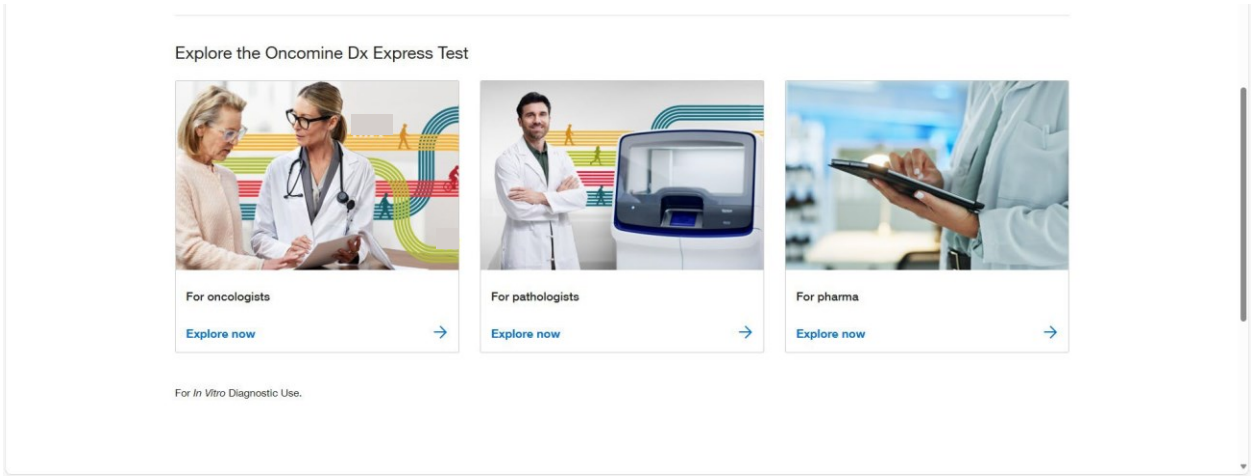
The Oncomine Dx Express Test can eliminate the lengthy wait for a complete biomarker picture. It enables pathology labs to deliver results in as little as 24 hours, facilitating faster, more informed treatment decisions so that your patients don't have to wait weeks for results.

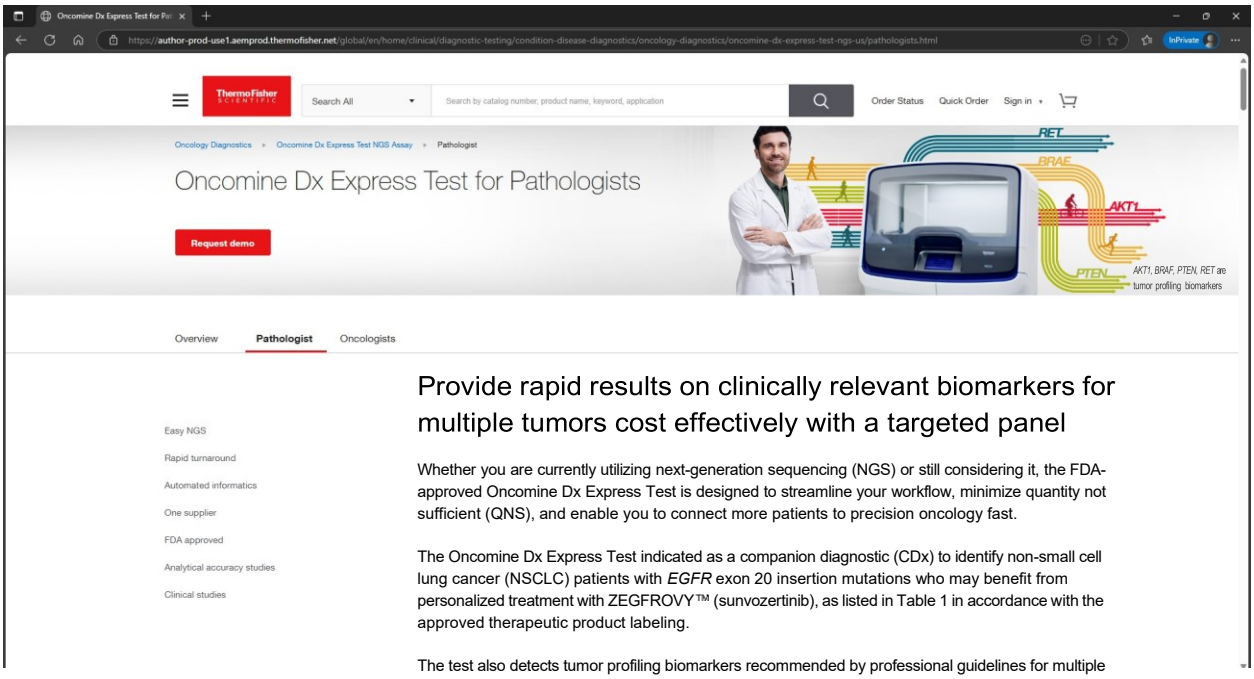
Precision oncology close to the patients

The Oncomine Dx Express Test is designed for implementation in local laboratories, enabling in-house testing. This supports timely, decentralized precision oncology by delivering NGS results close to patients.

Quantity not suficient is not an answer for the patient

The Oncomine Dx Express Test requires only 10 ng of DNA and RNA, which is significantly less sample input than other NGS technologies and therefore is more efficient even with challenging samples and small biopsies.





Provide rapid results on clinically relevant biomarkers for multiple tumors cost effectively with a targeted panel

Whether you are currently utilizing next-generation sequencing (NGS) or still considering it, the FDA-approved Oncomine Dx Express Test is designed to streamline your workflow, minimize quantity not sufficient (QNS), and enable you to connect more patients to precision oncology fast.

The Oncomine Dx Express Test indicated as a companion diagnostic (CDx) to identify non-small cell lung cancer (NSCLC) patients with *EGFR* exon 20 insertion mutations who may benefit from personalized treatment with ZEGFROVY™ (sunvozertinib), as listed in Table 1 in accordance with the approved therapeutic product labeling.

The test also detects tumor profiling biomarkers recommended by professional guidelines for multiple solid tumors (Table 2). This includes substitutions, insertions, and deletions in 42 genes, copy number variants in 10 genes, and fusions or splice variants in 18 genes relevant in NSCLC, colorectal cancer, cholangiocarcinoma, and melanoma, among others.

AKT1, BRAF, PTEN, RET are tumor profiling biomarkers

Table 1. Companion diagnostic indications

Tissue type	Gene	Variant	Targeted therapy
Non-small cell lung cancer (NSCLC)	*EGFR*	*EGFR* exon 20 insertions	ZEGFROVY™ (sunvozertinib)

Table 2. Oncomine Dx Express Test panel gene list.

DNA								**RNA**		
Substitutions, insertions, and deletions						Copy number variants		Fusions and splice variants		
AKT1	*CDK4*	*ESR1*	*HRAS*	*MAP2K2*	*PIK3CA*	*AR*	*FGFR2*	*ALK*	*FGFR2*	*NTRK3*
AKT2	*CHEK2*	*FGFR1*	*IDH1*	*MET*	*PTEN*	*EGFR*	*FGFR3*	*AR*	*FGFR3*	*NUTM1*
AKT3	*CTNNB1*	*FGFR2*	*IDH2*	*NRAS*	*RAF1*	*ERBB2*	*KRAS*	*BRAF*	*MET*	*RET*
ALK	*EGFR*	*FGFR3*	*KEAP1*	*NTRK1*	*RET*	*ERBB3*	*MET*	*EGFR*	*NRG1*	*ROS1*
AR	*ERBB2*	*FGFR4*	*KIT*	*NTRK2*	*ROS1*	*FGFR1*	*PIK3CA*	*ESR1*	*NTRK1*	*RSPO2*
ARAF	*ERBB3*	*FLT3*	*KRAS*	*NTRK3*	*STK11*			*FGFR1*	*NTRK2*	*RSPO3*
BRAF	*ERBB4*	*GNAS*	*MAP2K1*	*PDGFRA*	*TP53*					

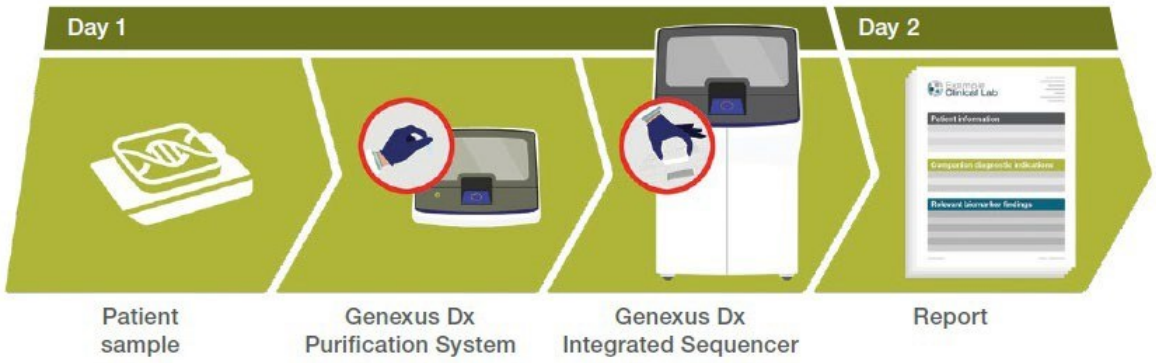
NGS made easy—2 instruments, 1 software, and as little as 20 minutes of hands-on time

The Genexus Dx System automates the NGS workflow from patient samples to reports with only two user touchpoints and as little as 20 minutes of hands-on time.

Pre-treated FFPE tissue sections are loaded onto the Genexus Dx Purification System and the instrument performs automated purification and quantification of DNA and RNA.

Library preparation, template preparation, sequencing, analysis, and reporting are performed by the Genexus Dx Integrated Sequencer. Throughout this procedure, sample and reagent information is recorded and tracked by one integrated software. This highly automated workflow helps reduce laboratory staff burden and the potential for human errors and alleviates the need for specialized bioinformatics expertise.

Explore virtual demo



Expedite critical oncology treatment choices with as little as 24 hours turnaround time

Unlike other NGS workflows, the Oncomine Dx Express Test delivers results in as little as 24 hours from pre-treated FFPE tissue sections to report*. Also, it uses a four-lane chip for flexible batching. This helps to reduce delays due to batching while maintaining operational efficiency to meet a wide range of testing demands.

* Timing varies by number of samples and type of run.

Table 3. FFPE sample-to-report turnaround times

Lane	Sample batch size	Turnaround time
1	2 samples	18 hours
2	6 samples	26 hours 50 minutes
4	12 samples	38 hours 25 minutes

Step into NGS with confidence thanks to automated informatics and reporting

The Genexus Dx Software directs the progress of the sample from creation of a run plan through automated sample preparation, library preparation, template preparation, sequencing, and analysis. The Genexus Dx Software generates the following results and reports for each sequenced sample and its associated controls.

- Quality control, key findings, and variant screens
- Run report
- Clinical test report
- Clinical laboratory report

Quality control specifications throughout the NGS workflow are automatically applied to streamline interpretation and help ensure reportable results are accurate. Positive calls are classified into 3 biomarker levels: Level 1: Companion Diagnostic (CDx) Biomarkers, Level 2: Cancer Mutations with Evidence of Clinical Significance, and Level 3: Cancer Mutations with Potential Clinical Significance.

The layout and contents of the report can be customized to facilitate a clear and concise report, providing clinicians with relevant information tailored to the patient.

One supplier for all your NGS needs

Everything from instruments, software, reagents, and consumables, as well as service and ongoing support, comes from one supplier: Thermo Fisher Scientific, which aims to make your implementation, as well as day-to-day running of this workflow, as simple as possible.

Rely on proven performance of FDA-approved test

Extensive performance studies were conducted to establish performance characteristics of the Oncomine Dx Express Test for FFPE tumor samples. A summary of selected studies is provided below. For complete studies and results, refer to the Oncomine Dx Express Test User Guide.

Limit of blank

- Per-position false positive rate: 0% across 24 blank samples representing 10 tissue types for all variant categories, except for Level 3 single nucleotide variants (SNVs). For Level 3 SNVs, the per-position false positive rate was 0.00004% after masking certain Level 3 SNVs with variant allele frequencies below 5% to prevent false positives.
- Per-sample false positive rate: 0% across the same 24 blank samples and 10 tissue types for all variant categories, except for Level 3 SNVs. For Level 3 SNVs, the per-sample false positive rate was 0.52% after masking certain Level 3 SNVs with variant allele frequencies below 5% to prevent false positives.

Limit of detection—CDx variants

- 3.24% to 4.38% allelic frequency for *EGFR* exon 20 insertion CDx variants with insertion lengths of 3, 6, 9, and 12 bp

Limit of detection—Tumor profiling variants

- 3.24% to 7.34% allelic frequency for SNVs
- 2.98% to 5.24% allelic frequency for insertions
- 3.08% to 4.67% allelic frequency for deletions
- 4.56 to 5.78 copies for CNVs
- 5.0 to 15.5 molecular counts for RNA fusion variants
- 1.5 to 4.93 imbalance scores for RNA fusions by expression imbalance

Panel reproducibility study—*EGFR* exon 20 insertions

The panel reproducibility study was conducted at three test sites to evaluate the repeatability and reproducibility of the Oncomine Dx Express Test for detection of *EGFR* exon 20 insertion variants in NSCLC starting from extracted nucleic acid.

- Reproducibility: the positive call rate was 100% for all *EGFR* exon 20 insertion variants, with no instances of no calls observed. The negative call rate was estimated using two wild-type (WT) NSCLC samples and was calculated for hotspots within the scope of the study. For WT samples, the negative call rate was 100.0%, excluding no calls.
- Repeatability: the repeatability for the detection of *EGFR* exon 20 insertion variants was estimated with respect to positive variant locations for within-run, between system, between-operator, between-site, between-lot, and total variability. When including or excluding no calls, the within-run repeatability was 100%. For WT samples, the within-run repeatability was 100%, excluding no calls.

Panel reproducibility study—tumor profiling variants

The variability across sites, operators, and instruments (reproducibility) and within-run precision performance (repeatability) was evaluated starting with the extracted nucleic acid. Three test sites, with two operators and four instruments per site, were used for the study.

Table 4. Panel reproducibility positive call rate for tumor profiling variants by variant class.

Variant type	Fold LoD level	Total calls	Observed positive calls	Observed negative calls	Observed no calls	Positive call rate (95% CIs)—no calls included	Positive call rate (95% CIs)—no calls excluded
SNV	1–1.5x	1368	1329	26	13	97.15% (96.13%, 97.91%)	98.08% (97.20%, 98.69%)
SNV	2–3x	576	575	0	1	99.83% (99.02%, 99.97%)	100% (99.34%, 100%)
Insertion	1–1.5x	504	503	0	1	99.80% (98.88%, 99.96%)	100% (99.24%, 100%)
Insertion	2–3x	144	144	0	0	100% (97.40%, 100%)	100% (97.40%, 100%)
Deletion	1–1.5x	576	561	9	6	97.40% (95.75%, 98.42%)	98.42% (97.03%, 99.17%)
Deletion	2–3x	216	216	0	0	100% (98.25%, 100%)	100% (98.25%, 100%)
CNV	1–1.5x	792	789	3	0	99.62% (98.89%, 99.87%)	99.62% (98.89%, 99.87%)
Fusion	1–1.5x	1584	1555	29	0	98.17% (97.38%, 98.72%)	98.17% (97.38%, 98.72%)
Fusion	2–3x	432	432	0	0	100% (99.12%, 100%)	100% (99.12%, 100%)
Fusion imbalance	1–1.5x	72	72	0	0	100% (94.93%, 100%)	100% (94.93%, 100%)
Splice variant	1–1.5x	288	287	1	0	99.65% (98.06%, 99.94%)	99.65% (98.06%, 99.94%)

Splice variant	2–3x	144	144	0	0	100% (97.40%, 100%)	100% (97.40%, 100%)

Table 5. Panel reproducibility negative call rate for tumor profiling variants by variant class.

Variant type	Fold LoD level	Total calls	Observed positive calls	Observed negative calls	Observed no calls	Negative call rate (95% CIs)—no calls included	Positive call rate (95% CIs)—no calls excluded
SNV	1–1.5x	2964168	1319	2945554	17295	99.37% (99.36%, 99.38%)	99.96% (99.95%, 99.96%)
SNV	2–3x	1164456	455	1160937	3064	99.70% (99.69%, 99.71%)	99.96% (99.95%, 99.96%)
Insertion	1–1.5x	593064	1	589125	3938	99.34% (99.31%, 99.36%)	100.00% (100.0%, 100%)
Insertion	2–3x	233424	0	232810	614	99.74% (99.72%, 99.76%)	100.00% (100.0%, 100%)
Deletion	1–1.5x	783648	0	746619	37029	95.27% (95.23%, 95.32%)	100.00% (100.0%, 100%)
Deletion	2–3x	307872	0	300911	6961	97.74% (97.69%, 97.79%)	100.00% (100.0%, 100%)
CNV	1–1.5x	6408	0	6408	0	100% (99.94%, 100%)	100% (99.94%, 100%)
Fusion	1–1.5x	1825056	50	1821714	3292	99.82% (99.81%, 99.82%)	100.00% (100.0%, 100%)
Fusion	2–3x	564984	88	561681	3215	99.42% (99.40%, 99.43%)	99.98% (99.98%, 99.99%)
Fusion imbalance	1–1.5x	2880	0	1414	1466	49.10% (47.27%, 50.92%)	100% (99.73%, 100%)
Splice variant	1–1.5x	7200	101	7099	0	98.60% (98.30%, 98.84%)	98.60% (98.30%, 98.84%)
Splice variant	2–3x	2160	0	2160	0	100% (99.82%, 100%)	100% (99.82%, 100%)

Repeatability—tumor profiling variants

A variance component analysis was performed for target variants tested near or above the LoD using the appropriate quantitative metric for each variant type (i.e., VAF for SNVs and indels, copy number for CNVs, and molecular counts for RNA variants). The results show a coefficient of variation (CV) of less than 10% between operators/instruments for all variants, except for one ALK, one ROS1 fusion, and one MET splice variants, which had CVs of 20.95%, 14.59%, and 11.65%, respectively. Reagent lot, within-run, and within-lab %CV varied by variant type, with the highest %CV observed for RNA variants.

Analytical accuracy—*EGFR* exon 20 insertions

The ability to identify *EGFR* exon 20 insertion variants was evaluated with FFPE NSCLC tumor specimens as compared to the reference assay. The accuracy of the Oncomine Dx Express Test for detecting EGFR exon 20 insertion in patients with NSCLC was evaluated by comparing results of the Oncomine Dx Express Test with those of a validated NGS-based orthogonal method. Positive percent agreement (PPA), negative percent agreement (NPA), and overall percent agreement (OPA) estimates, along with their respective 95% confidence intervals (CI), were calculated using the orthogonal test results as the reference and summarized in Table 6.

Table 6. Agreement between Oncomine Dx Express Test and orthogonal method for EGFR exon 20 insertion detection.

Parameter	Agreed (N)	Excluding ODxET unknowns [1]			Including ODxET unknowns [1]		
		Total (N)	Percent agreement	95% CIs	Total (N)	Percent agreement	95% CIs
PPA	84	84	100%	(95.6%, 100%)	84	100%	(95.6%, 100%)
NPA	105	110	95.5%	(89.8%, 98.0%)	111	94.6%	(88.7%, 97.5%)
OPA	189	194	97.4%	(94.1%, 98.9%)	195	96.9%	(93.5%, 98.6%)

[1] Unknowns are defined as values due to insufficient sample, or sample QC sequencing failure resulting in an invalid result or no call for the variant.

Analytical accuracy—tumor profiling variants

The accuracy of the Oncomine Dx Express Test for detecting SNVs, indels, CNVs, fusions, and RNA splice variants was evaluated by comparing its results with those obtained from validated orthogonal methods across three separate studies.

Accuracy Study I

The accuracy study I evaluated the accuracy of the Oncomine Dx Express Test in detecting various tumor profiling variants, including SNV/multi-nucleotide variants (MNVs), indels, CNVs, and RNA splice variants in FFPE clinical samples using a representative approach, comparing its results with the validated NGS orthogonal test. PPA and NPA estimates and the respective 95% confidence interval (CI) between Oncomine Dx Express Test and the orthogonal test were calculated using the orthogonal test result as reference and are summarized in Table 7.

Table 7. Agreement summary for SNVs, insertions, deletions, CNVs, and RNA tumor profiling variants.

Variant type	ODxET+, Orth+	ODxET+, Orth-	ODxET-, Orth+	ODxET-, Orth-	PPA (n/N) [95% CI]	NPA (n/N) [95% CI]
All variants	586	112	11	800035	98.2% (586/597) [96.7%, 99.0%]	100.0% (800035/800147) [100.0%, 100.0%]
All SNVs	397	47	2	387643	99.5% (397/399) [98.2%, 99.9%]	100.0% (387643/387690) [100.0%, 100.0%]
All insertions	5	1	0	61874	100.0% (5/5) [56.6%, 100.0%]	100.0% (61874/61875) [100.0%, 100.0%]
All deletions	23	2	0	78635	100.0% (23/23) [85.7%, 100.0%]	100.0% (78635/78637) [100.0%, 100.0%]
All CNV	114	32	7	4294	94.2% (114/121) [88.5%, 97.2%]	99.3% (4294/4326) [99.0%, 99.5%]
All RNA variants	47	30	2	261123	95.9% (47/49) [86.3%, 98.9%]	100.0% (261123/261153) [100.0%, 100.0%]

Abbreviations: ODxET, Oncomine Dx Express Test; Orth, orthogonal test

Accuracy Study II

The accuracy study II evaluated the accuracy of the Oncomine Dx Express Test in detecting ERBB2 CNVs, ALK fusions, and RET fusions by comparing its results with validated orthogonal assays, as summarized in Table 8.

Table 8. Agreement summary for SNVs, insertions, deletions, CNVs, and RNA tumor profiling variants.

Variant type / gene	ODxET+, Orth+	ODxET+, Orth-	ODxET-, Orth+	ODxET-, Orth-	PPA (n/N) [95% CI]	NPA (n/N) [95% CI]
All variants	72	6	0	112	100.0% (72/72) [94.9%, 100.0%]	94.9% (112/118) [89.3%, 97.6%]
Level 2 *ERBB2* CNV	29	4	0	37	100.0% (29/29) [88.3%, 100.0%]	90.2% (37/41) [77.5%, 96.1%]
All RNA variants	43	2	0	75	100.0% (43/43) [91.8%, 100.0%]	97.4% (75/77) [91.0%, 99. 3%]
Level 2 *ALK*	26	1	0	41	100.0% (26/26) [87.1%, 100.0%]	97.6% (41/42) [87.7%, 99.6%]
Level 2 *RET*	17	1	0	34	100.0% (17/17) [81.6%, 100.0%]	97.1% (34/35) [85.5%, 99.5%]

Abbreviations: ODxET, Oncomine Dx Express Test; Orth, orthogonal test

Accuracy Study III

The accuracy study III evaluated the accuracy of the Oncomine Dx Express Test in detecting EGFR T790M and EGFR L858R SNVs, and EGFR exon 19 deletions by comparing its results with an orthogonal PCR method, as summarized in Table 9.

Table 9. Agreement summary for SNVs, insertions, deletions, CNVs, and RNA tumor profiling variants.

Variant type / gene	ODxET+, Orth+	ODxET+, Orth-	ODxET-, Orth+	ODxET-, Orth-	PPA (n/N) [95% CI]	NPA (n/N) [95% CI]
All *EGFR*	23	1	0	45	100.0% (23/23) [85.7%, 100.0%]	97.8% (45/46) [88.7%, 99.6%]
Level 2 *EGFR*	23	1	0	45	100.0% (23/23) [85.7%, 100.0%]	97.8% (45/46) [88.7%, 99.6%]
SNV *EGFR*	11	1	0	45	100.0% (11/11) [74.1%, 100.0%]	97.8% (45/46) [88.7%, 99.6%]
Deletion *EGFR*	12	0	0	45	100.0% (12/12) [75.8%, 100.0%]	100.0% (45/45) [92.1%, 100.0%]

Abbreviations: ODxET, Oncomine Dx Express Test; Orth, orthogonal test

Clinical studies

Clinical study for *EGFR* exon 20 insertions

A clinical bridging study was conducted to establish reasonable assurance of safety and effectiveness of the Oncomine Dx Express Test for detection of *EGFR* exon 20 insertions in NSCLC FFPE tumor specimens to select patients for treatment with ZEGFROVY™ (sunvozertinib) in the United States. This included specimens from patients enrolled in the WU-KONG1B trial (NCT03974022) and commercially sourced biomarker-negative samples. The study evaluated the concordance between *EGFR* exon 20 insertions detected using clinical trial assays (CTAs) and the Oncomine Dx Express Test (ODxET) in the intent-to-test population and aimed to assess the clinical efficacy of the Oncomine Dx Express Test in identifying patients positive for *EGFR* exon 20 insertions who may benefit from treatment with ZEGFROVY™ (sunvozertinib).

The full analysis set consisted of 192 patients, including the primary efficacy population of 85 patients who received the 200 mg dose of sunvozertinib and 107 patients who received an unapproved dose. Overall response rates (ORRs) were evaluated by BIRC according to RECIST v1.1 for the primary efficacy population.

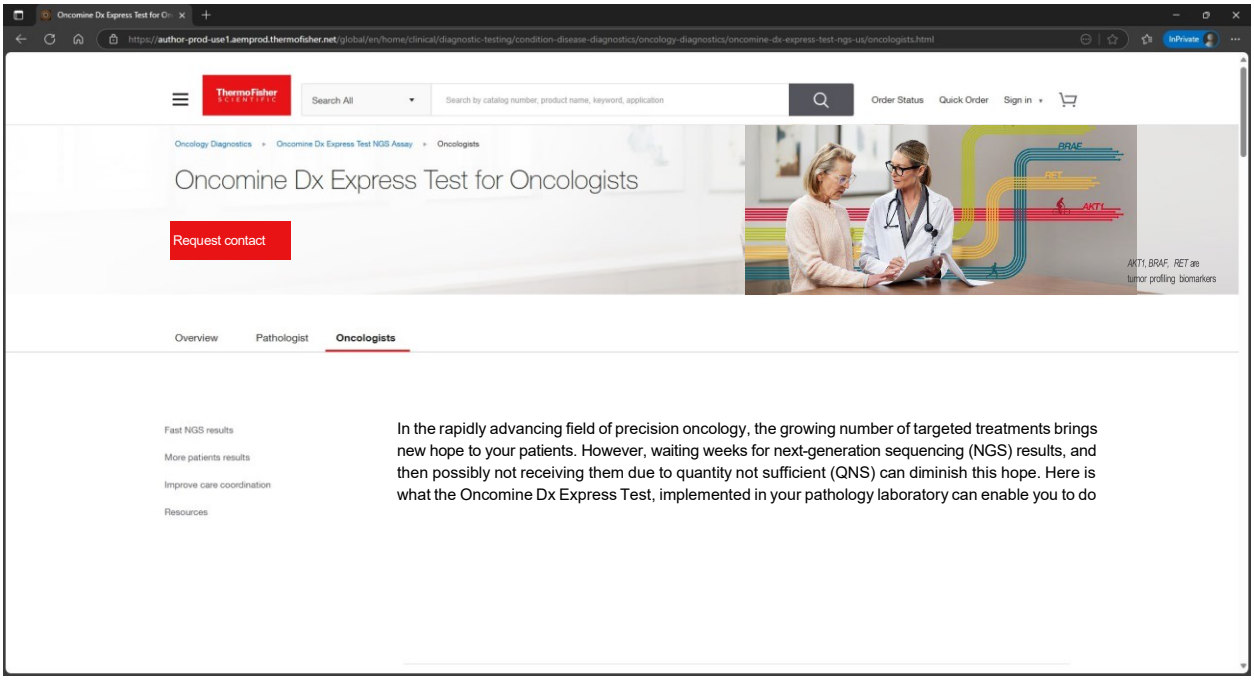
In the 200 mg cohort (N = 85), the ORR in the CTA-positive population was 46% (39/85), with 6% (5/85) of patients having a complete response (CR) and 40% (34/85) having a partial response (PR). Among these, 58 patients were both CTA-positive and tested positive for *EGFR* exon 20 insertions using the ODxET (ODxET+ | CTA+). In this subgroup (N = 58), the ORR was 41% (24/58), with 5% (3/58) patients having a CR and 36% (21/58) having a PR. These results, summarized in Table 10, demonstrate that the ORRs for the ODxET *EGFR* exon 20 insertion–positive population align with those observed in the CTA *EGFR* exon 20 insertion–positive population.

In the 200 mg cohort, the median duration of response (DoR) for the CTA-positive population was 11.1 months, with 72% of patients having a DoR ≥6 months and a median follow-up of 15.2 months. For the ODxET+ | CTA+ population, the median DoR was 9.8 months, with 63% of patients having a DoR ≥6 months and a median follow-up of 11.7 months. Additional details are provided in Table 10.

Table 10. Efficacy results of WU-KONG1B study.

Efficacy parameter	ZEGFROVY (N=85, CTA+)	ODxET+ | CTA+ (N=58)
Overall Response Rate (ORR), % (95% CI[a])	46 (35, 57)	41 (29, 55)
Complete Response, %	6	5
Partial Response, %	40	36
Duration of Response (DOR)	N=39	N=24
Median[b], months (95% CI)	11.1 (8.2, NE)	9.8 (5.6, NE)
Patients with DOR ≥6 months	72%	63%

a. 95% CI for ORR was calculated based on Clopper-Pearson exact CI method. b. Kaplan-Meier estimate using confirmed responses. NE = Not estimable.



Make treatment decisions without waiting for delayed NGS results

Oncomine Dx Express Test delivers genomic profiles in as little as 24 hours—so you can move quickly when timing matters most.

Get results for more patients

How often are you left without answers because of the technology used? Oncomine Dx Express Test is based on amplicon NGS technology, which requires significantly less sample material than other NGS technologies.

Improve care coordination

Oncomine Dx Express Test workflow can be implemented even in smaller and NGS naïve labs, so it can be implemented also in your institution. Having the pathologists and molecular pathology experts just a phone call away and available for multi-disciplinary meetings will help to improve care for your patient. In addition, the sample will stay in-house, ready for additional tests should they be needed.

Ready to speak to a Thermo Fisher Scientific representative?
We will be happy to answer your questions about bringing NGS to your laboratory.
Request contact

AKT1, BRAF, PTEN, RET are tumor profiling biomarkers

NGS biomarker reports in 24 hours

Make treatment decisions without waiting weeks for NGS results

With Oncomine™ Dx Express Test, your lab can deliver reports in 24 hours

In the rapidly advancing field of precision oncology, the growing number of targeted treatments brings new hope to your patients. However, waiting weeks for next-generation sequencing (NGS) results, and then possibly not receiving them due to quantity not sufficient (QNS) can diminish this hope. The Oncomine Dx Express Test transforms this process by delivering NGS results in just 24 hours, from tissue to report.

With this rapid turnaround time, the Oncomine Dx Express Test can help to eliminate the lengthy wait for a complete biomarker picture.

Request the Oncomine Dx Express Test from your lab to make the best-informed treatment decisions and minimize delays in patient care.

* Timing varies by number of samples and type of run.

Learn more at **thermofisher.com/oncomine-express-test**

AKT1, BRAF, PTEN, RET are tumor profiling biomarkers

Ask for rapid NGS results in mere days, not weeks. It's now achievable.

With Oncomine Dx Express Test, your local lab will be able to generate results in as little as 24 hours.

In the rapidly advancing field of precision oncology, the growing number of targeted treatments brings new hope to your patients. However, waiting weeks for next-generation sequencing (NGS) results, and then possibly not receiving them due to quantity not sufficient (QNS) can diminish this hope. The Oncomine Dx Express Test transforms this process by delivering NGS results in just 24 hours, from tissue to report.

With this rapid turnaround time, the Oncomine Dx Express Test can eliminate the lengthy wait for a complete biomarker picture. It enables your pathology lab to facilitate faster, more informed treatment decisions so that both you and your patients don't have to wait.

Request the Oncomine Dx Express Test from your lab to make the best-informed treatment decisions and minimize delays in patient care.

* Timing varies by number of samples and type of run.

Learn more at **thermofisher.com/oncomine-express-test**

ThermoFisher SCIENTIFIC

Connecting patients everywhere to precision oncology

Oncomine Dx Express Test

AKT1, *BRAF*, *PTEN*, *RET* are tumor profiling biomarkers

Connecting patients everywhere to precision oncology

A patient's tumor profile has the potential to guide precision oncology care. However, delays in obtaining results can hinder clinicians' ability to make informed decisions, potentially causing patients to miss out on targeted therapies, which can impact treatment efficacy and patient outcomes. Furthermore, a significant proportion of patients miss out on targeted therapies due to inefficiencies or lack of access to testing, highlighting the critical role of timely genomic profiling. The Ion Torrent™ Oncomine™ Dx Express Test was designed to simplify the next-generation sequencing (NGS) workflow and connect patients everywhere to precision oncology.

The Oncomine Dx Express Test offers:

Rapid results

Generate results in as little as 24 hours* to support timely therapy decisions.

Maximize genomic insights

Using only 10 ng of DNA and 10 ng of RNA from as little as two 5-micron formalin-fixed, paraffin-embedded (FFPE) slides, the Oncomine Dx Express Test enables analysis of limited tissue samples and small biopsies while reducing the risk of insufficient samples.

Tumor profiling biomarkers

The Oncomine Dx Express Test detects biomarkers recommended by professional guidelines for multiple solid tumors, including substitutions, insertions, and deletions (indels) in 42 genes, copy number variants (CNVs) in 10 genes, and fusions or splice variants in 18 genes.

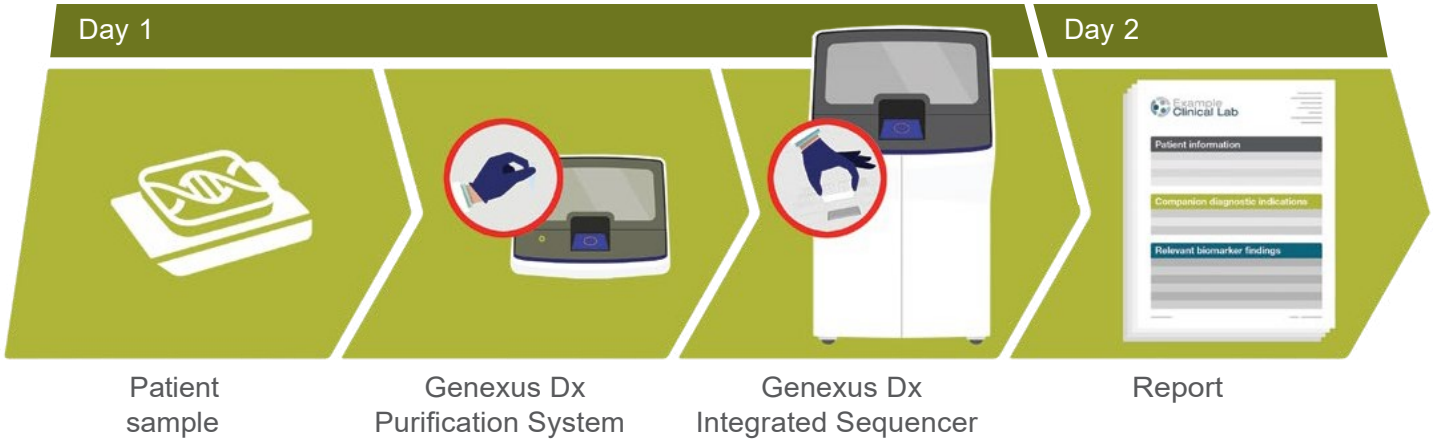
Streamline your laboratory workflow

Automated library preparation, template preparation, sequencing, analysis, and reporting, from as little as 20 minutes of hands-on time, helps reduce the risk of human errors and enhance the efficiency, accuracy, and scalability of genomic testing in your laboratory.

* Timing varies by number of samples and type of run.

A true end-to-end IVD solution from one supplier

An end-to-end IVD solution for all aspects of the NGS workflow offers seamless integration, facilitating compatibility and efficiency across the entire process. This eliminates the complexities of managing multiple vendors, streamlining procurement and support. This comprehensive approach helps simplify integration, operation, troubleshooting and maintenance, supporting consistent performance and optimal system uptime.



Rapid results for CDx and tumor profiling biomarkers

The Oncomine Dx Express Test is indicated as a companion diagnostic (CDx) on the tissue type listed in Table 1 in accordance with the approved therapeutic product labeling.

The test also detects tumor profiling biomarkers recommended by professional guidelines for multiple solid tumors (Table 2). This includes substitutions, insertions, and deletions in 42 genes, copy number variants (CNVs) in 10 genes, and fusions or splice variants in 18 genes relevant in non-small cell lung cancer, colorectal cancer, cholangiocarcinoma, and melanoma, among others.

Table 1. Companion diagnostic indications.

Tissue type	Gene	Variant	Targeted therapy
Non-small cell lung cancer (NSCLC)	*EGFR*	*EGFR* exon 20 insertions	ZEGFROVY™ (sunvozertinib)

Table 2. The Oncomine Dx Express Test panel gene list.

DNA								RNA		
Substitutions, insertions, and deletions						Copy number variants		Fusions and splice variants		
AKT1	*CDK4*	*ESR1*	*HRAS*	*MAP2K2*	*PIK3CA*	*AR*	*FGFR2*	*ALK*	*FGFR2*	*NTRK3*
AKT2	*CHEK2*	*FGFR1*	*IDH1*	*MET*	*PTEN*	*EGFR*	*FGFR3*	*AR*	*FGFR3*	*NUTM1*
AKT3	*CTNNB1*	*FGFR2*	*IDH2*	*NRAS*	*RAF1*	*ERBB2*	*KRAS*	*BRAF*	*MET*	*RET*
ALK	*EGFR*	*FGFR3*	*KEAP1*	*NTRK1*	*RET*	*ERBB3*	*MET*	*EGFR*	*NRG1*	*ROS1*
AR	*ERBB2*	*FGFR4*	*KIT*	*NTRK2*	*ROS1*	*FGFR1*	*PIK3CA*	*ESR1*	*NTRK1*	*RSPO2*
ARAF	*ERBB3*	*FLT3*	*KRAS*	*NTRK3*	*STK11*			*FGFR1*	*NTRK2*	*RSPO3*
BRAF	*ERBB4*	*GNAS*	*MAP2K1*	*PDGFRA*	*TP53*					

Experience efficiency with walkaway automation of the Genexus Dx System

Genexus Dx Purification System

The Genexus™ Dx System automates the NGS workflow from patient samples to reports with only two user touchpoints and as little as 20 minutes of hands-on time.

Pre-treated FFPE tissue sections are loaded onto the Genexus™ Dx Purification System and the instrument performs automated purification and quantification of DNA and RNA.

Genexus Dx Integrated Sequencer

Library preparation, template preparation, sequencing, analysis, and reporting is performed by the Genexus™ Dx Integrated Sequencer. Throughout this procedure, sample and reagent information is recorded and tracked by the software.

This highly automated workflow helps reduce laboratory staff burden and the potential for human errors, and alleviates the need for specialized bioinformatics expertise.

Analysis and reporting

The Genexus™ Dx Software directs the progress of the sample from creation of a run plan through automated sample preparation, library preparation, template preparation, sequencing, and analysis. The Genexus Dx Software generates the following results and reports for each sequenced sample and its associated controls.

- Quality control, key findings, and variant screens
- Run report
- Clinical test report
- Clinical laboratory report

Quality control specifications throughout the NGS workflow are automatically applied to streamline interpretation and help ensure reportable results are accurate. Positive calls are classified into three biomarker levels: Level 1: Companion Diagnostic (CDx) Biomarkers, Level 2: Cancer Mutations with Evidence of Clinical Significance, and Level 3: Cancer Mutations with Potential Clinical Significance.

The layout and contents of the report can be customized to facilitate a clear and concise report, providing clinicians with relevant and actionable information tailored to the patient.

Performance characteristics

Extensive performance studies were conducted to establish performance characteristics of the Oncomine Dx Express Test for FFPE tumor samples. A summary of selected studies is provided below. For complete studies and results, refer to the Oncomine Dx Express Test User Guide.

Limit of blank

- Per-position false positive rate: 0% across 24 blank samples representing 10 tissue types for all variant categories, except for Level 3 single nucleotide variants (SNVs). For Level 3 SNVs, the per-position false positive rate was 0.00004% after masking certain Level 3 SNVs with variant allele frequencies below 5% to prevent false positives.
- Per-sample false positive rate: 0% across the same 24 blank samples and 10 tissue types for all variant categories, except for Level 3 SNVs. For Level 3 SNVs, the per-sample false positive rate was 0.52% after masking certain Level 3 SNVs with variant allele frequencies below 5% to prevent false positives.

Limit of detection—CDx variants

- 3.24% to 4.38% allelic frequency for *EGFR* exon 20 insertion CDx variants with insertion lengths of 3, 6, 9, and 12 bp

Limit of detection—tumor profiling variants

- 3.24% to 7.34% allelic frequency for SNVs
- 2.98% to 5.24% allelic frequency for insertions
- 3.08% to 4.67% allelic frequency for deletions
- 4.56 to 5.78 copies for CNVs
- 5.0 to 15.5 molecular counts for RNA fusion variants
- 1.5 to 4.93 imbalance scores for RNA fusions by expression imbalance

Panel reproducibility study—*EGFR* exon 20 insertions

The panel reproducibility study was conducted at three test sites to evaluate the repeatability and reproducibility of the Oncomine Dx Express Test for detection of *EGFR* exon 20 insertion variants in NSCLC starting from extracted nucleic acid.

- Reproducibility: the positive call rate was 100% for all *EGFR* exon 20 insertion variants, with no instances of no calls observed. The negative call rate was estimated using two wild-type (WT) NSCLC samples and was calculated for hotspots within the scope of the study. For WT samples, the negative call rate was 100.0%, excluding no calls.
- Repeatability: the repeatability for the detection of *EGFR* exon 20 insertion variants was estimated with respect to positive variant locations for within-run, between system, between-operator, between-site, between-lot, and total variability. When including or excluding no calls, the within-run repeatability was 100%. For WT samples, the within-run repeatability was 100%, excluding no calls.

Panel reproducibility study—tumor profiling variants

The variability across sites, operators, and instruments (reproducibility) and within-run precision performance (repeatability) was evaluated starting with the extracted nucleic acid. Three test sites, with two operators and four instruments per site, were used for the study.

Table 3. Panel reproducibility positive call rate for tumor profiling variants by variant class.

Variant type	Fold LoD level	Total calls	Observed positive calls	Observed negative calls	Observed no calls	Positive call rate (95% cls)—no calls included	Positive call rate (95% cls)—no calls excluded
SNV	1–1.5x	1368	1329	26	13	97.15% (96.13%, 97.91%)	98.08% (97.20%, 98.69%)
SNV	2–3x	576	575	0	1	99.83% (99.02%, 99.97%)	100% (99.34%, 100%)
Insertion	1–1.5x	504	503	0	1	99.80% (98.88%, 99.96%)	100% (99.24%, 100%)
Insertion	2–3x	144	144	0	0	100% (97.40%, 100%)	100% (97.40%, 100%)
Deletion	1–1.5x	576	561	9	6	97.40% (95.75%, 98.42%)	98.42% (97.03%, 99.17%)
Deletion	2–3x	216	216	0	0	100% (98.25%, 100%)	100% (98.25%, 100%)
CNV	1–1.5x	792	789	3	0	99.62% (98.89%, 99.87%)	99.62% (98.89%, 99.87%)
Fusion	1–1.5x	1584	1555	29	0	98.17% (97.38%, 98.72%)	98.17% (97.38%, 98.72%)
Fusion	2–3x	432	432	0	0	100% (99.12%, 100%)	100% (99.12%, 100%)
Fusion imbalance	1–1.5x	72	72	0	0	100% (94.93%, 100%)	100% (94.93%, 100%)
Splice variant	1–1.5x	288	287	1	0	99.65% (98.06%, 99.94%)	99.65% (98.06%, 99.94%)
Splice variant	2–3x	144	144	0	0	100% (97.40%, 100%)	100% (97.40%, 100%)

Table 4. Panel reproducibility negative call rate for tumor profiling variants by variant class.

Variant type	Fold LoD level	Total calls	Observed positive calls	Observed negative calls	Observed no calls	Negative call rate (95% cls)—no calls included	Positive call rate (95% cls)—no calls excluded
SNV	1–1.5x	2964168	1319	2945554	17295	99.37% (99.36%, 99.38%)	99.96% (99.95%, 99.96%)
SNV	2–3x	1164456	455	1160937	3064	99.70% (99.69%, 99.71%)	99.96% (99.95%, 99.96%)
Insertion	1–1.5x	593064	1	589125	3938	99.34% (99.31%, 99.36%)	100.00% (100.0%, 100%)
Insertion	2–3x	233424	0	232810	614	99.74% (99.72%, 99.76%)	100.00% (100.0%, 100%)
Deletion	1–1.5x	783648	0	746619	37029	95.27% (95.23%, 95.32%)	100.00% (100.0%, 100%)
Deletion	2–3x	307872	0	300911	6961	97.74% (97.69%, 97.79%)	100.00% (100.0%, 100%)
CNV	1–1.5x	6408	0	6408	0	100% (99.94%, 100%)	100% (99.94%, 100%)
Fusion	1–1.5x	1825056	50	1821714	3292	99.82% (99.81%, 99.82%)	100.00% (100.0%, 100%)
Fusion	2–3x	564984	88	561681	3215	99.42% (99.40%, 99.43%)	99.98% (99.98%, 99.99%)
Fusion imbalance	1–1.5x	2880	0	1414	1466	49.10% (47.27%, 50.92%)	100% (99.73%, 100%)
Splice variant	1–1.5x	7200	101	7099	0	98.60% (98.30%, 98.84%)	98.60% (98.30%, 98.84%)
Splice variant	2–3x	2160	0	2160	0	100% (99.82%, 100%)	100% (99.82%, 100%)

Repeatability—tumor profiling variants

A variance component analysis was performed for target variants tested near or above the LoD using the appropriate quantitative metric for each variant type (i.e., VAF for SNVs and indels, copy number for CNVs, and molecular counts for RNA variants). The results show a coefficient of variation (CV) of less than 10% between operators/instruments for all variants, except for one *ALK,* one *ROS1* fusion, and one *MET* splice variants, which had CVs of 20.95%, 14.59%, and 11.65%, respectively. The CV for between-run variability was below 15% for all variants except for one ALK fusion and one ROS1 fusion, which had CVs of 20.95% and 17.12%, respectively. Reagent lot, within-run, and within-lab %CV varied by variant type, with the highest %CV observed for RNA variants.

Analytical accuracy—*EGFR* exon 20 insertions

The ability to identify *EGFR* exon 20 insertion variants was evaluated with FFPE NSCLC tumor specimens as compared to the reference assay. The accuracy of the Oncomine Dx Express Test for detecting *EGFR* exon 20 insertion in patients with NSCLC was evaluated by comparing results of the Oncomine Dx Express Test with those of a validated NGS-based orthogonal method. Positive percent agreement (PPA), negative percent agreement (NPA), and overall percent agreement (OPA) estimates, along with their respective 95% confidence intervals (CI), were calculated using the orthogonal test results as the reference and summarized in Table 5.

Table 5. Agreement between Oncomine Dx Express Test and orthogonal method for *EGFR* exon 20 insertion detection.

Parameter	Agreed (N)	Excluding ODxET unknowns [1]			Including ODxET unknowns [1]		
		Total (N)	Percent agreement	95% CIs	Total (N)	Percent agreement	95% CIs
PPA	84	84	100%	(95.6%, 100%)	84	100%	(95.6%, 100%)
NPA	105	110	95.5%	(89.8%, 98.0%)	111	94.6%	(88.7%, 97.5%)
OPA	189	194	97.4%	(94.1%, 98.9%)	195	96.9%	(93.5%, 98.6%)

[1] Unknowns are defined as values due to insufficient sample, or sample QC sequencing failure resulting in an invalid result or no call for the variant.

Analytical accuracy—tumor profiling variants

The accuracy of the Oncomine Dx Express Test for detecting SNVs, indels, CNVs, fusions, and RNA splice variants was evaluated by comparing its results with those obtained from validated orthogonal methods across three separate studies.

Accuracy Study I

The accuracy study I evaluated the accuracy of the Oncomine Dx Express Test in detecting various tumor profiling variants, including SNV/multi-nucleotide variants (MNVs), indels, CNVs, and RNA splice variants in FFPE clinical samples using a representative approach, comparing its results with the validated NGS orthogonal test. PPA and NPA estimates and the respective 95% confidence interval (CI) between Oncomine Dx Express Test and the orthogonal test were calculated using the orthogonal test result as reference and are summarized in Table 6.

Table 6. Agreement summary for SNVs, insertions, deletions, CNVs, and RNA tumor profiling variants.

Variant type	ODxET+, Orth+	ODxET+, Orth-	ODxET-, Orth+	ODxET-, Orth-	PPA (n/N) [95% CI]	NPA (n/N) [95% CI]
All variants	586	112	11	800035	98.2% (586/597) [96.7%, 99.0%]	100.0% (800035/800147) [100.0%, 100.0%]
All SNVs	397	47	2	387643	99.5% (397/399) [98.2%, 99.9%]	100.0% (387643/387690) [100.0%, 100.0%]
All insertions	5	1	0	61874	100.0% (5/5) [56.6%, 100.0%]	100.0% (61874/61875) [100.0%, 100.0%]
All deletions	23	2	0	78635	100.0% (23/23) [85.7%, 100.0%]	100.0% (78635/78637) [100.0%, 100.0%]
All CNV	114	32	7	4294	94.2% (114/121) [88.5%, 97.2%]	99.3% (4294/4326) [99.0%, 99.5%]
All RNA variants	47	30	2	261123	95.9% (47/49) [86.3%, 98.9%]	100.0% (261123/261153) [100.0%, 100.0%]

Abbreviations: ODxET, Oncomine Dx Express Test; Orth, orthogonal test

Accuracy Study II

The accuracy study II evaluated the accuracy of the Oncomine Dx Express Test in detecting *ERBB2* CNVs, *ALK* fusions, and *RET* fusions by comparing its results with validated orthogonal assays, as summarized in Table 7.

Table 7. Agreement summary for *ERBB2* CNV, *ALK* fusions, and *RET* fusions tumor profiling variants.

Variant type / gene	ODxET+, Orth+	ODxET+, Orth-	ODxET-, Orth+	ODxET-, Orth-	PPA (n/N) [95% CI]	NPA (n/N) [95% CI]
All variants	72	6	0	112	100.0% (72/72) [94.9%, 100.0%]	94.9% (112/118) [89.3%, 97.6%]
Level 2 *ERBB2* CNV	29	4	0	37	100.0% (29/29) [88.3%, 100.0%]	90.2% (37/41) [77.5%, 96.1%]
All RNA variants	43	2	0	75	100.0% (43/43) [91.8%, 100.0%]	97.4% (75/77) [91.0%, 99. 3%]
Level 2 *ALK*	26	1	0	41	100.0% (26/26) [87.1%, 100.0%]	97.6% (41/42) [87.7%, 99.6%]
Level 2 *RET*	17	1	0	34	100.0% (17/17) [81.6%, 100.0%]	97.1% (34/35) [85.5%, 99.5%]

Abbreviations: ODxET, Oncomine Dx Express Test; Orth, orthogonal test

Accuracy Study III

The accuracy study III evaluated the accuracy of the Oncomine Dx Express Test in detecting *EGFR* T790M and *EGFR* L858R SNVs, and *EGFR* exon 19 deletions by comparing its results with an orthogonal PCR method, as summarized in Table 8.

Table 8. Agreement summary for *EGFR* exon 19 deletions, L858R, and T790M tumor profiling variants.

Variant type / gene	ODxET+, Orth+	ODxET+, Orth-	ODxET-, Orth+	ODxET-, Orth-	PPA (n/N) [95% CI]	NPA (n/N) [95% CI]
All *EGFR*	23	1	0	45	100.0% (23/23) [85.7%, 100.0%]	97.8% (45/46) [88.7%, 99.6%]
Level 2 *EGFR*	23	1	0	45	100.0% (23/23) [85.7%, 100.0%]	97.8% (45/46) [88.7%, 99.6%]
SNV *EGFR*	11	1	0	45	100.0% (11/11) [74.1%, 100.0%]	97.8% (45/46) [88.7%, 99.6%]
Deletion *EGFR*	12	0	0	45	100.0% (12/12) [75.8%, 100.0%]	100.0% (45/45) [92.1%, 100.0%]

Abbreviations: ODxET, Oncomine Dx Express Test; Orth, orthogonal test

Clinical studies

Clinical study for *EGFR* exon 20 insertions

A clinical bridging study was conducted to establish reasonable assurance of safety and effectiveness of the Oncomine Dx Express Test for detection of *EGFR* exon 20 insertions in NSCLC FFPE tumor specimens to select patients for treatment with ZEGFROVY™ (sunvozertinib) in the United States. This included specimens from patients enrolled in the WU-KONG1B trial (NCT03974022) and commercially sourced biomarker-negative samples. The study evaluated the concordance between *EGFR* exon 20 insertions detected using clinical trial assays (CTAs) and the Oncomine Dx Express Test (ODxET) in the intent-to-test population and aimed to assess the clinical efficacy of the Oncomine Dx Express Test in identifying patients positive for *EGFR* exon 20 insertions who may benefit from treatment with ZEGFROVY™ (sunvozertinib).

The full analysis set consisted of 192 patients, including the primary efficacy population of 85 patients who received the 200 mg dose of sunvozertinib and 107 patients who received an unapproved dose. Overall response rates (ORRs) were evaluated by BIRC according to RECIST v1.1 for the primary efficacy population.

In the 200 mg cohort (N = 85), the ORR in the CTA-positive population was 46% (39/85), with 6% (5/85) of patients having a complete response (CR) and 40% (34/85) having a partial response (PR). Among these, 58 patients were both CTA-positive and tested positive for *EGFR* exon 20 insertions using the ODxET (ODxET+ | CTA+). In this subgroup (N = 58), the ORR was 41% (24/58), with 5% (3/58) patients having a CR and 36% (21/58) having a PR. These results, summarized in Table 9, demonstrate that the ORRs for the ODxET *EGFR* exon 20 insertion–positive population align with those observed in the CTA *EGFR* exon 20 insertion–positive population.

In the 200 mg cohort, the median duration of response (DoR) for the CTA-positive population was 11.1 months, with 72% of patients having a DoR ≥6 months and a median follow-up of 15.2 months. For the ODxET+ | CTA+ population, the median DoR was 9.8 months, with 63% of patients having a DoR ≥6 months and a median follow-up of 11.7 months. Additional details are provided in Table 9.

Table 9. Efficacy results of WU-KONG1B study.

Efficacy parameter	ZEGFROVY (N=85, CTA+)	ODxET+ | CTA+ (N=58)
Overall Response Rate (ORR), % (95% CI[a])	46 (35, 57)	41 (29, 55)
Complete Response, %	6	5
Partial Response, %	40	36
Duration of Response (DOR)	N=39	N=24
Median[b], months (95% CI)	11.1 (8.2, NE)	9.8 (5.6, NE)
Patients with DOR ≥6 months	72%	63%

a. 95% CI for ORR was calculated based on Clopper-Pearson exact CI method. b. Kaplan-Meier estimate using confirmed responses. NE: not estimable.

Oncomine Dx Express Test

The following reagents and supplies are available for order as needed. For detailed contents and storage information, see the Oncomine™ Dx Express Test Part II: Sequencing and Results Reports User Guide (Pub. No. MAN0024908).

Ordering information

Product	Cat. No.
Oncomine™ Dx Express Test Panel	A54103
Oncomine™ Dx Express Test FFPE DNA and RNA Control Kit	A52167
Genexus™ Dx FFPE DNA and RNA Purification	A51076
Genexus™ Dx Nucleic Acid Quantification	A51078
Genexus™ Dx Purification Supplies 2	A51081
Genexus™ Dx Library Strips 1 and 2-HD	A50430
Genexus™ Dx Templating Strips 3-GX5 and 4	A50431
Genexus™ Dx Sequencing Kit	A50432
Genexus™ Dx Barcodes 1-32 HD	A54104
Genexus™ Dx GX5™ Chip and Genexus™ Coupler	A54106
Genexus™ Dx Pipette Tips	A50426
Applied Biosystems™ MicroAmp™ EnduraPlate™ Optical 96-Well Clear GPLE Reaction Plates with Barcode	4483348
Thermo Scientific™ Adhesive PCR Plate Foils	AB0626

Learn more at thermofisher.com/oncomine-express-test

NGS biomarker reports in 24 hours

Elevate your oncology biomarker testing capabilities

Oncomine Dx Express Test: a single NGS workflow to address growing demand

Deliver genomic profiles for multiple solid tumors in as little as 24 hours*. The Ion Torrent™ Oncomine™ Dx Express Test on the Ion Torrent™ Genexus™ Dx System automates the NGS workflow, from specimen to report, with as little as 20 minutes of hands-on time. This reduces the risk of human errors and helps enhance laboratory efficiency.

With the Oncomine Dx Express Test, you'll be able to deliver results for more patients in a short time, using fewer resources in your laboratory.

Elevate your patient care with the Oncomine Dx Express Test, offering timely genomic insights using minimal sample material to personalize treatment plans.

* Timing varies by number of samples and type of run.

AKT1, BRAF, PTEN, RET are tumor profiling biomarkers

Learn more at **thermofisher.com/oncomine-express-test**

AKT1, PTEN, RET are tumor profiling biomarkers

The time to embrace NGS is now

Oncomine Dx Express Test—from extraction to report in as little as 20 minutes hands-on time

Deliver genomic profiles for multiple solid tumors in as little as 24 hours*. The Ion Torrent™ Oncomine™ Dx Express Test on the Ion Torrent™ Genexus™ Dx System automates the NGS workflow, from specimen to report, with as little as 20 minutes of hands-on time. This reduces the risk of human errors and helps enhance laboratory efficiency.

With the Oncomine Dx Express Test, you'll be able to deliver results for more patients in a short time, using fewer resources in your laboratory.

Elevate your patient care with the Oncomine Dx Express Test, offering timely genomic insights using minimal sample material to personalize treatment plans.

* Timing varies by number of samples and type of run.

Learn more at **thermofisher.com/oncomine-express-test**

AKT1, BRAF, PTEN, RET are tumor profiling biomarkers

Oncomine Dx Express Test

Connecting patients everywhere to precision oncology

A patient's tumor profile has the potential to guide precision oncology care. However, delays in obtaining results can hinder clinicians' ability to make informed decisions, potentially causing patients to miss out on targeted therapies, which may impact treatment efficacy and patient outcomes. Furthermore, a significant proportion of patients miss out on targeted therapies due to inefficiencies or lack of access to testing, highlighting the critical role of timely genomic profiling. The Ion Torrent™ Oncomine™ Dx Express Test was designed to simplify the next-generation sequencing (NGS) workflow and connect patients everywhere to precision oncology.

The Ion Torrent™ Genexus™ Dx System automates the NGS workflow, from specimen to report in as little as 24 hours* with as little as 20 minutes of hands-on time. This easy-to-use, end-to-end solution reduces manual steps while offering low sample input requirements. With the Oncomine Dx Express Test, you'll be able to deliver results for more patients in a short time, using fewer resources in your laboratory.

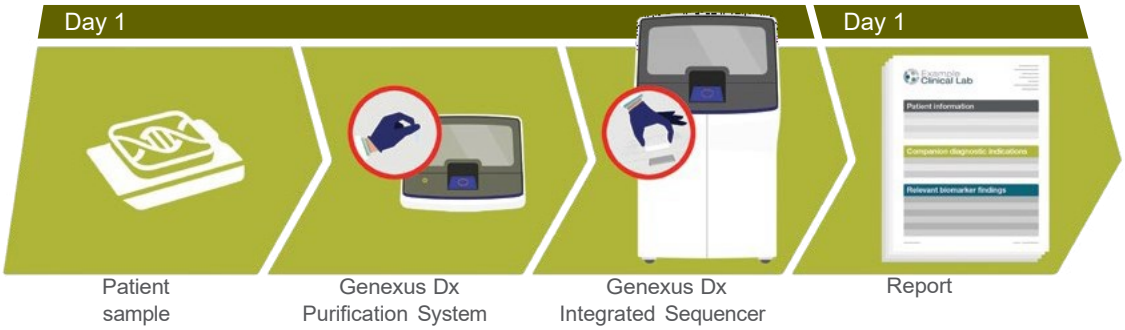
* Timing varies by number of samples and type of run.

The Oncomine Dx Express Test offers:

- **Rapid results**: Generate results in as little as 24 hours to support timely therapy decisions.
- **Companion diagnostics (CDx):** The test is indicated as a companion diagnostic (CDx) to identify non-small cell lung cancer (NSCLC) patients with *EGFR* exon 20 insertion mutations for treatment with ZEGFROVY™ (sunvozertinib) in accordance with the approved therapeutic product labeling.
- **Tumor profiling biomarkers:** The Oncomine Dx Express Test detects biomarkers recommended by professional guidelines for multiple solid tumors, including substitutions, insertions, and deletions in 42 genes, copy number variants in 10 genes, and fusions or splice variants in 18 genes.
- **Maximize genomic insights:** Using only 10 ng of DNA and 10 ng of RNA from as little as two 5-micron formalin-fixed, paraffin-embedded (FFPE) slides, the Oncomine Dx Express Test enables analysis of limited tissue samples and small biopsies while helping to reduce the risk of insufficient samples.
- **Streamline your laboratory workflow:** Automated library preparation, template preparation, sequencing, analysis, and reporting, from as little as 20 minutes of hands-on time, helps reduce the risk of human errors and enhance the efficiency, accuracy, and scalability of genomic testing in your laboratory.

A true end-to-end IVD solution from one supplier

The Genexus Dx System automates the NGS workflow from patient sample to report with only two user touchpoints. Nucleic acids (DNA and RNA) are purified and quantified by the Genexus Dx Purification System, and library preparation, template preparation, sequencing, analysis, and reporting is performed by the Genexus Dx Integrated Sequencer from as little as 20 minutes of hands-on time, which helps reduce laboratory staff burden, the potential for human errors, and alleviates the need for specialized bioinformatics expertise.



Rapid results for CDx and guideline recommendations for tumor profiling biomarkers

The Oncomine Dx Express Test is indicated as a companion diagnostic (CDx) to identify *EGFR* exon 20 insertions in patients with non-small cell lung cancer who may benefit from personalized treatment with ZEGFROVY™ (sunvozertinib), as listed in Table 1 in accordance with the approved therapeutic product labeling.

The test also detects tumor profiling biomarkers recommended by professional guidelines for multiple solid tumors (Table 2). This includes substitutions, insertions, and deletions in 42 genes, copy number variants in 10 genes, and fusions or splice variants in 18 genes relevant in NSCLC, colorectal cancer, cholangiocarcinoma, and melanoma, among others.

Table 1. Companion diagnostic indications.

Tissue type	Gene	Variant	Targeted therapy
Non-small cell lung cancer (NSCLC)	*EGFR*	*EGFR* Exon 20 insertions	ZEGFROVY™ (sunvozertinib)

Table 2. The Oncomine Dx Express Test panel gene list.

DNA								RNA		
Substitutions, insertions, and deletions						Copy number variants		Fusions and splice variants		
AKT1	*CDK4*	*ESR1*	*HRAS*	*MAP2K2*	*PIK3CA*	*AR*	*FGFR2*	*ALK*	*FGFR2*	*NTRK3*
AKT2	*CHEK2*	*FGFR1*	*IDH1*	*MET*	*PTEN*	*EGFR*	*FGFR3*	*AR*	*FGFR3*	*NUTM1*
AKT3	*CTNNB1*	*FGFR2*	*IDH2*	*NRAS*	*RAF1*	*ERBB2*	*KRAS*	*BRAF*	*MET*	*RET*
ALK	*EGFR*	*FGFR3*	*KEAP1*	*NTRK1*	*RET*	*ERBB3*	*MET*	*EGFR*	*NRG1*	*ROS1*
AR	*ERBB2*	*FGFR4*	*KIT*	*NTRK2*	*ROS1*	*FGFR1*	*PIK3CA*	*ESR1*	*NTRK1*	*RSPO2*
ARAF	*ERBB3*	*FLT3*	*KRAS*	*NTRK3*	*STK11*			*FGFR1*	*NTRK2*	*RSPO3*
BRAF	*ERBB4*	*GNAS*	*MAP2K1*	*PDGFRA*	*TP53*					

Maximize genomic insights for your patients

Compared to other NGS technologies, the Oncomine Dx Express Test helps to shorten the time to report, reduce the manual steps involved with NGS workflows, and requires less sample input (Figure 1). Faster results enable timely decision-making. Minimizing manual steps of the NGS workflow reduces the risk of human error, enabling more accurate and reliable results, and helps ensure patients everywhere have access to genomic testing.

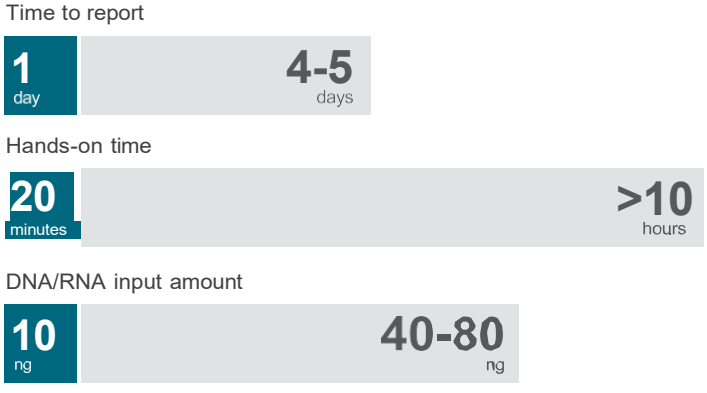


Figure 1. Comparison of NGS workflows.

Learn more at **thermofisher.com/oncomine-express-test**

Accelerate your treatment decisions with rapid NGS

Oncomine™ Dx Express Test delivers results in 24 hours —so you and your patient don't have to wait weeks

In the rapidly advancing field of precision oncology, the growing number of targeted treatments brings new hope to your patients. However, waiting weeks for next-generation sequencing (NGS) results, and then possibly not receiving them due to quantity not sufficient (QNS) can diminish this hope. The Oncomine Dx Express Test transforms this process by delivering NGS results in just 24 hours, from tissue to report.

With this rapid turnaround time, the Oncomine Dx Express Test can eliminate the lengthy wait for a complete biomarker picture.

Request the Oncomine Dx Express Test from your lab to make the best-informed treatment decisions and minimize delays in patient care.

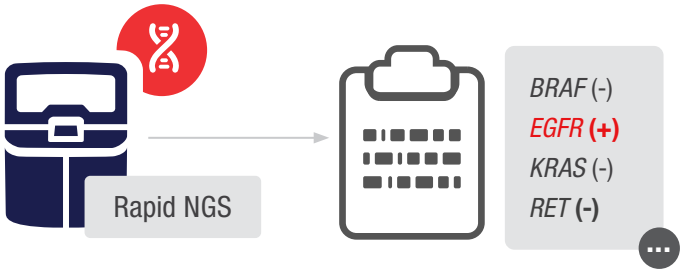
* Timing varies by number of samples and type of run.

The Oncomine Dx Express Test provides:

- **Rapid results:** Results are generated in as little as 24 hours to support timely therapy decisions.
- **Companion diagnostics (CDx):** The test is indicated as a companion diagnostic (CDx) to identify non-small cell lung cancer (NSCLC) patients with *EGFR* exon 20 insertion mutations for treatment with ZEGFROVY™ (sunvozertinib) in accordance with the approved therapeutic product labeling.
- **Tumor profiling biomarkers:** The Oncomine Dx Express Test detects biomarkers recommended by professional guidelines for multiple solid tumors, including substitutions, insertions, and deletions in 42 genes, copy number variants in 10 genes, and fusions or splice variants in 18 genes.
- **Minimized QNS:** Using DNA and RNA from as little as two formalin-fixed, paraffin-embedded (FFPE) slides, the Oncomine Dx Express Test enables analysis of limited tissue samples and small biopsies while helping to reduce the risk of insufficient samples.
- **Facilitation of MDT collaboration:** By maintaining the testing process internally, you streamline workflows, keep the specimen within the institution, enable high accuracy, and enhance collaboration among your multidisciplinary teams.

A complete report for the first visit

Results from the Oncomine Dx Express Test are generated in as little as 24 hours. This facilitates more informed treatment decisions, enabling better patient decision-making and treatment planning.



Clear insights to guide your therapy decisions

The results in a clear and concise report are classified into three biomarker levels:

- Level 1: Companion diagnostic (CDx) biomarkers noted in Table 1 of the Intended Use
- Level 2: Cancer Mutations with Evidence of Clinical Significance
- Level 3: Cancer Mutations with Potential Clinical Significance

This classification is powered by Oncomine Knowledgebase, an expertly curated proprietary database of biologically and clinically (diagnostic, prognostic, and therapeutic) relevant biomarkers.

Guideline-recommended companion diagnostic and tumor profiling biomarkers

The Oncomine Dx Express Test is indicated as a companion diagnostic (CDx) to identify *EGFR* exon 20 insertions in patients with non-small cell lung cancer who may benefit from personalized treatment with ZEGFROVY™ (sunvozertinib) as listed in Table 1 in accordance with the approved therapeutic product labeling.

The test also detects tumor profiling biomarkers recommended by professional guidelines for multiple solid tumors across the six major classes of alterations (Table 2). This includes substitutions, insertions, and deletions in 42 genes, copy number variants in 10 genes, and fusions or splice variants in 18 genes relevant in NSCLC, colorectal cancer, cholangiocarcinoma, and melanoma, among others.

Table 1. Companion diagnostic indications.

Tissue type	Gene	Variant	Targeted therapy
Non-small cell lung cancer (NSCLC)	*EGFR*	*EGFR exon 20 insertions*	ZEGFROVY™ (sunvozertinib)

Table 2. The Oncomine Dx Express Test panel gene list.

DNA								RNA		
Substitutions, insertions, and deletions						Copy number variants		Fusions and splice variants		
AKT1	*CDK4*	*ESR1*	*HRAS*	*MAP2K2*	*PIK3CA*	*AR*	*FGFR2*	*ALK*	*FGFR2*	*NTRK3*
AKT2	*CHEK2*	*FGFR1*	*IDH1*	*MET*	*PTEN*	*EGFR*	*FGFR3*	*AR*	*FGFR3*	*NUTM1*
AKT3	*CTNNB1*	*FGFR2*	*IDH2*	*NRAS*	*RAF1*	*ERBB2*	*KRAS*	*BRAF*	*MET*	*RET*
ALK	*EGFR*	*FGFR3*	*KEAP1*	*NTRK1*	*RET*	*ERBB3*	*MET*	*EGFR*	*NRG1*	*ROS1*
AR	*ERBB2*	*FGFR4*	*KIT*	*NTRK2*	*ROS1*	*FGFR1*	*PIK3CA*	*ESR1*	*NTRK1*	*RSPO2*
ARAF	*ERBB3*	*FLT3*	*KRAS*	*NTRK3*	*STK11*			*FGFR1*	*NTRK2*	*RSPO3*
BRAF	*ERBB4*	*GNAS*	*MAP2K1*	*PDGFRA*	*TP53*					

Less QNS for your patients

Compared to other NGS technologies, the Oncomine Dx Express Test requires significantly less sample input (Figure 1). The test requires as little as two 5-micron slides for tumor resections and is also compatible with core needle biopsies and fine needle aspirates. Using less sample conserves tissue and makes genomic profiling more accessible, especially for patients with limited or hard-to-obtain tissue samples.

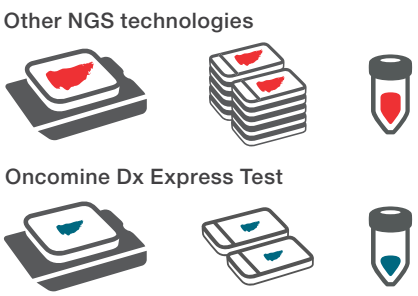


Figure 1. Comparison of specimen requirements.

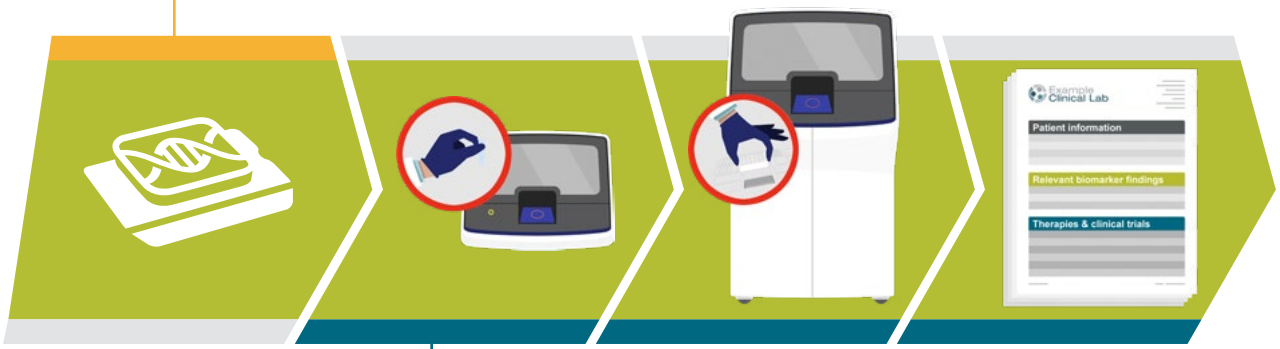
Learn more at **thermofisher.com/oncomine-express-test**

Oncomine Dx Express Test

Connecting patients everywhere to precision oncology

A patient's tumor profile has the potential to guide precision oncology care. However, delays in obtaining results can hinder clinicians' ability to make informed decisions, potentially causing patients to miss out on targeted therapies, which can impact treatment efficacy and patient outcomes. Now with the Ion Torrent™ Oncomine™ Dx Express Test on the Genexus™ Dx System, laboratories everywhere can deliver rapid genomic profiling with exceptional accuracy and ease, helping to ensure patients can benefit from the latest advancements in precision oncology.

Minimal sample input requirements mean **more samples can be profiled, including small and challenging samples, core needle biopsies, and fine needle aspirates**.



Automated nucleic acid purification, quantification, library preparation, template preparation, sequencing, analysis, and reporting **reduce manual pipetting steps and the potential for human errors, minimizing the need for specialized expertise**.

01
Vendor

One vendor for the end-to-end IVD workflow simplifies integration, operation, troubleshooting, and maintenance, **supporting consistent performance and optimal system uptime**.

46
Genes

Substitutions, insertions, and deletions in 42 genes, copy number variants in 10 genes, and fusions or splice variants in 18 genes covering **tumor profiling biomarkers recommended by professional guidelines for multiple solid tumors**.

<24
Hours

Results are generated in as little as 24 hours*, **from sample to report, to enable timely therapy decisions**.

* Timing varies by number of samples and type of run.

Learn more at **thermofisher.com/oncomine-express-test**

Oncomine Dx Express Test

Epidemiology of lung cancer

Lung cancer is the leading cause of cancer-related death in the United States. In 2025, an estimated 226,650 new cases (110,680 in men and 115,970 in women) of lung and bronchial cancer are projected to be diagnosed, and 124,730 deaths are projected (64,190 in men and 60,540 in women) [1]. Only 26.7% of all patients with lung cancer live five years or more after diagnosis [2].

Molecular diagnostic testing for therapy selection in NSCLC

Numerous gene alterations have been identified that influence therapy selection. Testing lung cancer specimens, particularly non-small cell lung cancer (NSCLC), for these alterations is crucial for identifying potentially effective targeted therapies and avoiding those unlikely to provide clinical benefit. To obtain comprehensive molecular biomarker profiling from limited biopsy tissue, multiplex technology such as next-generation sequencing (NGS) is preferred over single-gene tests, according to an expert consensus by the College of American Pathologists (CAP), the International Association for the Study of Lung Cancer (IASLC), and the Association for Molecular Pathology (AMP) guidelines [3].

For most current information regarding the essential biomarkers for lung cancer and their association with therapeutic outcomes, refer to the therapeutic labels available at Drugs@FDA.

For most current information regarding cleared or approved companion diagnostic devices, refer to List of Cleared or Approved Companion Diagnostic Devices (In Vitro and Imaging Tools).

***EGFR*: epidermal growth factor receptor.** *EGFR* encodes the epidermal growth factor receptor tyrosine kinase, a member of the ERBB/human epidermal growth factor receptor (HER) family. It is typically presented on the surface of epithelial cells and is frequently overexpressed in various human malignancies.

EGFR exon 20 insertions are less common and represent a heterogeneous group of mutations. Most *EGFR* exon 20 alterations are in-frame duplication or insertions, and generally associated with a lack of response to first-, second-, and third-generation *EGFR* TKI therapy, with some exceptions such as p.A763_Y764insFQEA and potentially p.A763_Y764insLQEA. Because some *EGFR* exon 20 insertions may be sensitive to TKIs or specific targeted therapies designed for these alterations, identifying the specific mutations is crucial. Due to their heterogeneity, NGS-based approaches are preferred, as targeted PCR-based approaches may under-detect *EGFR* exon 20 insertions.

Test intended use

The Oncomine™ Dx Express Test is a qualitative *in vitro* diagnostic test that uses targeted next-generation sequencing (NGS) technology to detect substitutions, insertions, and deletions in 42 genes, copy number variants (CNVs) in 10 genes from DNA, and fusions or splice variants in 18 genes from RNA isolated from formalin-fixed paraffin-embedded (FFPE) tumor samples using the Genexus™ Dx Integrated Sequencer.

The test is intended to be used as a companion diagnostic to identify patients who may benefit from treatment with the targeted therapy listed in Table 1 in accordance with the approved therapeutic product labeling.

Table 1. Companion diagnostic indications.

Tissue type	Gene	Variant	Targeted therapy
Non-small cell lung cancer (NSCLC)	*EGFR*	*EGFR* exon 20 insertions	ZEGFROVY™ (sunvozertinib)

Additionally, the test is intended to provide tumor mutation profiling information to be used by qualified health care professionals in accordance with professional guidelines in oncology for cancer patients with solid malignant neoplasms. Genomic findings other than those listed in Table 1 are not prescriptive or conclusive for labeled use of any specific therapeutic product.

Test performance and characteristics

The Oncomine Dx Express Test targets key regions of 46 cancer-related genes.

Substitutions, insertions, and deletions (indels) from DNA for the following 42 genes are reported for FFPE solid tumor samples: *AKT1*, *AKT2*, *AKT3*, *ALK*, *AR*, *ARAF*, *BRAF*, *CDK4*, *CHEK2*, *CTNNB1*, *EGFR*, *ERBB2*, *ERBB3*, *ERBB4*, *ESR1*, *FGFR1*, *FGFR2*, *FGFR3*, *FGFR4*, *FLT3*, *GNAS*, *HRAS*, *IDH1*, *IDH2*, *KEAP1*, *KIT*, *KRAS*, *MAP2K1*, *MAP2K2*, *MET*, *NRAS*, *NTRK1*, *NTRK2*, *NTKR3*, *PDGFRA*, *PIK3CA*, *PTEN*, *RAF1*, *RET*, *ROS1*, *STK11*, and *TP53*.

Copy number variants (CNVs) from DNA for the following 10 genes is reported for FFPE solid tumor samples: *AR*, *EGFR*, *ERBB2*, *ERBB3*, *FGFR1*, *FGFR2*, *FGFR3*, *KRAS*, *MET*, and *PIK3CA*.

Fusions and splice variants from RNA for the following 18 genes are reported for FFPE solid tumor samples: *ALK*, *AR*, *BRAF*, *EGFR*, *ESR1*, *FGFR1*, *FGFR2*, *FGFR3*, *MET*, *NRG1*, *NTRK1*, *NTRK2*, NTRK3, NUTM1, *RET*, *ROS1*, *RSPO2*, and *RSPO3*.

The performance characteristics for the Oncomine Dx Express Test were determined using DNA and RNA derived from a variety of FFPE tissue types. These FFPE tissue samples were analyzed for substitutions, insertions, deletions and copy number variants (CNVs) in DNA, as well as fusions and splice variants in RNA, including CDx and tumor profiling variants. The primary evidence supporting the Oncomine Dx Express Test's performance in detecting *EGFR* exon 20 insertion CDx variants in patients with NSCLC was obtained from data generated using intended use specimens and sample blends throughout all validation studies.

A summary of selected studies is provided below. For complete studies and results, refer to the Oncomine Dx Express Test User Guide.

Based on the data observed, the test demonstrated 0% per position false positive rates across 24 blank samples representing 10 tissue types for all variant type categories except for Level 3 SNVs. For Level 3 SNVs, the per-position false positive rate was 0.00004% after masking certain Level 3 SNVs with variant allele frequencies below 5% to prevent false positives. The per sample false positive rates across 24 blank samples representing 10 tissue types was 0% for all variant type categories except for Level 3 SNVs. For Level 3 SNVs, the per-sample false positive rate was 0.52% after masking certain Level 3 SNVs with variant allele frequencies below 5% to prevent false positives.

EGFR exon 20 insertion CDx variants demonstrated a limit of detection ranging from 3.24% to 4.38% allelic frequency with insertion lengths of 3, 6, 9, and 12 bp. Based on the data observed, the test demonstrated limits of detection for pan-cancer tumor profiling variants of between 3.24% to 7.34% allelic frequency for SNVs, 2.98% to 5.24% allelic frequency for insertions, 3.08% to 4.67% allelic frequency for deletions, 4.56 to 5.78 copies for CNVs, 5.0 to 15.5 molecular counts for RNA fusion variants, and 1.5 to 4.93 imbalance scores for RNA fusions by expression imbalance.

For *EGFR* exon 20 insertions, three test sites, with two operators and two instruments per site, were used. The positive call rate for reproducibility was 100.0% for all *EGFR* exon 20 insertion variants, with no instances of no calls observed. The negative call rate was estimated using two wild-type (WT) NSCLC samples and was calculated for hotspots within the scope of the study. For WT samples, the negative call rate was 100.0%, excluding no calls. The repeatability for the detection of *EGFR* exon 20 insertion variants was estimated with respect to positive variant locations for within-run, between system, between-operator, between-site, between-lot and total variability. When including or excluding No Calls, the within-run repeatability was 100%.

For tumor profiling variants, the variability across sites, operators, and instruments (reproducibility) and within-run precision performance (repeatability) was evaluated starting with the extracted nucleic acid. Three test sites, with two operators and four instruments per site, were used for the study. The positive call rates, excluding no calls, were between 98.08% and 100%, and negative call rates, excluding no calls, were between 98.60% and 100%. For repeatability, the results show a coefficient of variation (CV) of less than 10% between operators/instruments for all variants, except for one *ALK* fusion, one *ROS1* fusion, one *MET* splice variant, which had CVs of 20.95%, 14.59%, and 11.65%, respectively. The CV for between-run variability was below 15% for all variants, except for one *ALK* fusion and one *ROS1* fusion, which had CVs of 20.95% and 17.12%, respectively. Reagent lot, within-run and within-lab %CV varied by variant type, with the highest %CV observed for RNA variants.

The accuracy of the Oncomine Dx Express Test for detecting *EGFR* exon 20 insertion in patients with NSCLC was evaluated by comparing results of the Oncomine Dx Express Test with those of a validated NGS-based orthogonal method. Positive percent agreement (PPA), negative percent agreement (NPA), and overall percent agreement (OPA) estimates, along with their respective 95% confidence intervals (CI), were calculated using the orthogonal test results as the reference. The concordance analysis for *EGFR* exon 20 insertions showed a PPA of 100%, NPA of 95.5%, with OPA of 97.4% excluding unknowns, and PPA of 100%, NPA of 94.6%, and OPA of 96.9% when including unknowns.

The accuracy of the Oncomine Dx Express Test for detecting single nucleotide variants (SNVs), insertions and deletions (indels), copy number variants (CNVs), fusions, and RNA splice variants were evaluated by comparing its results with those obtained from validated orthogonal methods across three separate studies.

In the accuracy study I, the aggregated PPA was 98.2% across all variants (including SNVs, insertions, deletions, CNVs, fusions, and splice variants), and the aggregated NPA was 100.0% across all variants for tumor profiling variants.

In the accuracy study II, the concordance analysis for *ERBB2* CNVs, *ALK* fusions, and *RET* fusions showed an aggregated PPA of 100%, and an aggregated NPA of 94.9%.

In the accuracy study III, the concordance analysis for *EGFR* T790M and L858R variants showed an aggregated PPA of 100.0% and an aggregated NPA of 97.8%.

A clinical bridging study was conducted to establish reasonable assurance of safety and effectiveness of the Oncomine Dx Express Test for detection of *EGFR* exon 20 insertions in NSCLC FFPE tumor specimens to select patients for treatment with ZEGFROVY™ (sunvozertinib) in the United States. The point estimates of PPA, NPA, and OPA, excluding 60 samples with unknown status, were 97.9% (138/141), 100% (134/134), and 98.9% (272/275), respectively. The FAS consisted of 192 patients, including the primary efficacy population of 85 patients who received the 200 mg dose of sunvozertinib and 107 patients who received an unapproved dose. ORRs were evaluated by BIRC according to RECIST v1.1 for the primary efficacy population. In the 200 mg cohort (N = 85), the overall response rate (ORR) in the clinical trial assay (CTA)-positive population was 46% (39/85), with 6% (5/85) of patients having a complete response (CR) and 40% (34/85) having a partial response (PR). Among these, 58 patients were both CTA-positive and tested positive for *EGFR* exon 20 insertions using the ODxET (ODxET+ | CTA+). In this subgroup (N = 58), the ORR was 41% (24/58), with 5% (3/58) patients having a CR and 36% (21/58) having a PR. These results demonstrate that the ORRs for the ODxET *EGFR* exon 20 insertion–positive population align with those observed in the CTA *EGFR* exon 20 insertion–positive population. In the 200 mg cohort, the median duration of response (DoR) for the CTA-positive population was 11.1 months, with 72% of patients having a DoR ≥6 months and a median follow-up of 15.2 months. For the ODxET+ | CTA+ population, the median DoR was 9.8 months, with 63% of patients having a DoR ≥6 months and a median follow-up of 11.7 months. Additional details are provided in the user guide.

Guide to interpreting results

The test output classifies variants into the following levels according to the cancer indication:

- Level 1—Companion Diagnostics (CDx) Biomarkers noted in Table 1 of the Intended Use
- Level 2—Cancer Mutations with Evidence of Clinical Significance
- Level 3—Cancer Mutations with Potential Clinical Significance

For more information on the variants reported, see Appendix B, "Variants targeted by the Oncomine Dx Express Test" in Oncomine Dx Express Test Part I: Test Description and Performance Characteristics User Guide.

Test results should be interpreted in the context of pathological evaluation of tumors, treatment history, clinical findings, and other laboratory data.

All clinical interpretations of the variants detected should be made by a board-certified pathologist or equivalent. It is recommended that the physician ordering the test consult with a board-certified pathologist. Patients are advised to seek information from their oncologist or certified health care provider. Additional information may be obtained from NCCN Guidelines™ and IASLC/AMP NSCLC testing guidelines.

The molecular profile of a tumor can vary between primary and metastatic sites, as well as change over time in response to treatment, leading to the development of mutations that could confer resistance to therapeutic agents.

Contraindication

There are no known contraindications.

Assay warnings and limitations

1. Use of this product must be limited to personnel trained in the techniques of PCR, NGS, and the use of the Oncomine™ Dx Express Test, the Genexus™ Dx Purification System, when applicable, and the Genexus™ Dx Integrated Sequencer.
2. Users are cautioned that DNA variant-positive calls in a small number of genomic regions have been observed to generate multiple variant calls with overlapping alleles, even when only one variant is present. For details on these observed cases, see Appendix B, "Variants targeted by the Oncomine™ Dx Express Test".
3. Due to the nature of hotspot variant calling, when several variants are located in the same genomic region in close proximity to each other, the presence of a positive variant can result in a "No Call" for the neighboring variants instead of a negative call.
4. Genomic findings listed in the Oncomine Dx Express Test results report under Cancer Mutations with Evidence of Clinical Significance (Level 2) and Cancer Mutations with Potential Clinical Significance (Level 3) are not prescriptive or conclusive for labeled use of any specific therapeutic product, and clinical validation has not been performed. Confirmation of tumor mutation status using an FDA-approved CDx test is needed for therapeutic use.
5. Decisions on patient care and treatment must be based on the independent medical judgment of the treating physician, taking into consideration all applicable information concerning the patient's condition, such as patient and family history, physical examinations, information from other diagnostic tests, and patient preferences, in accordance with the standard of care in a given community.
6. The Oncomine Dx Express Test is for use with the Genexus Dx Integrated Sequencer and the Genexus Dx Purification System (for integrated workflows), or other IVD-labeled extraction chemistries.
7. The Oncomine Dx Express Test is for detecting the following somatic mutations: single-nucleotide variants (SNVs), insertions, deletions, and copy number variants (CNVs) in DNA, and fusions and splice variants in RNA.
8. The Oncomine Dx Express Test has been validated to detect and report only the variants listed in Appendix B, "Variants targeted by the Oncomine™ Dx Express Test", and has not been validated for novel variant detection.
9. The Oncomine Dx Express Test is for use with 10 ng each of DNA and RNA per sample for FFPE samples. Input levels less than or greater than this amount are not recommended.
10. Although the Genexus Dx Integrated Sequencer can perform on-board dilution of samples up to 1,024-fold, the use of samples at the upper limit of supported concentrations (512 ng/µL for FFPE DNA and RNA) has not been validated.
11. Results for samples with DNA or RNA concentration failure are reported for Nucleic Acid to Result runs. A warning message appears in the run planning screen and the run summary screen to indicate to the user that a sample does not meet the minimum concentration requirement of the assay.
12. The Oncomine Dx Express Test is for use with FFPE tumor specimens.
13. Core needle biopsy (CNB) and fine needle aspirate (FNA) cell block specimen types have not been analytically validated for the detection of tumor profiling variants targeted by Oncomine Dx Express Test.
14. The effects of potential variations in FFPE specimen fixation have not been evaluated.
15. A potential source of contamination in the procedure is nucleic acid from previous sample extraction steps. Follow good laboratory practices and all precautions and guidelines in these user guides to avoid cross-contamination between samples.
16. The Oncomine Dx Express Test is a qualitative test. The test is not for quantitative measurements of percent mutation.
17. The test is not indicated to be used for standalone diagnostic purposes, screening, monitoring, risk assessment, or prognosis.
18. For prescription use only. The test must be ordered by a qualified medical professional in accordance with clinical laboratory regulations.
19. The performance of the Oncomine Dx Express Test in samples obtained from patients that have had organ or tissue transplantation has not been evaluated.
20. A negative result does not rule out the presence of a mutation below the Limits of Detection (LoD) of the assay in the patient's tumor and should be followed by additional confirmatory testing.
21. Alterations at allele frequencies below the LoD of the assay may not be detected consistently.
22. The minimum tumor content thresholds for Oncomine Dx Express Test are ≥20% for resection and fine needle aspirate (FNA) cell block samples and ≥10% for core needle biopsy (CNB) samples, regardless of variant type.
23. For resection or surgical biopsies, macrodissect and enrich the sample for tumor content if the tumor content is less than 20% and the tumor content in the region of interest is ≥10%. For core needle biopsies and fine needle aspirates, macrodissection is not recommended due to the limiting tissue section surface areas.

24. The *ERBB2* copy number alteration call may not be accurate when tumor content is between 20-39%. Additional confirmatory testing with a clinically validated test is strongly recommended.
25. The presence of more than 70% necrotic tissue may yield unreliable sequencing results for the detection of *EGFR* exon 20 insertion mutations.
26. For fusion variants detected by expression imbalance alone (RNA exon tile fusion imbalance), confirmatory testing using a clinically validated assay is recommended.
27. The accuracy of the Oncomine Dx Express Test for detecting gene fusions in *FGFR1*, *NTRK2*, *NUTM1*, *RSPO2*, and *RSPO3* genes has not been evaluated.
28. When panel reproducibility was evaluated using extracted RNA samples, the *ALK* fusion imbalance in NSCLC demonstrated a low negative percent agreement of 28.57% (144/504).
29. When panel reproducibility was evaluated using extracted DNA samples, the *BRAF* V600E variant in colorectal cancer demonstrated a low positive percent agreement of 86.11% (62/72).

References

1. Siegel, R, et al. *Cancer statistics, 2025, CA: A Cancer Journal for Clinicians,* 75(1), 10–45.
2. Cancer Stat Facts: Lung and Bronchus Cancer, National Cancer Institute, accessed on July 29, 2024.
3. Lindeman, NI et al. Updated molecular testing guideline for the selection of lung cancer patients for treatment with targeted tyrosine kinase inhibitors: guideline from the College of American Pathologists, the International Association for the Study of Lung Cancer, and the Association for Molecular Pathology. *Archives of pathology & laboratory medicine* 142.3 (2018): 321-346.
4. Oncomine Dx Express Test User Guide

Learn more at thermofisher.com/oncomine-express-test