

Genetic Tumor Diagnostics

*Every patient deserves to receive
personalized precision medicine.*

CancerPrecision®

CancerPrecision® is the first choice genetic diagnostics for cancer patients. The panel provides a better understanding of tumor behavior and its likelihood of responding to treatment. In this way, tumor profiling contributes to medicine tailored to the patient, often leading to a better outcome or reduced adverse effects.

There is no 'one-size-fits-all' in cancer medicine, as every patient's tumor is unique. Thus, it is crucial to understand the disease history and every single tumor as best as possible. CancerPrecision®, our most extensive cancer panel, covering more than 700 tumor-associated genes and therapy-relevant fusions in more than 30 genes, provides a valid diagnosis and guidelines for action to determine the most effective therapy to increase the chances of recovery. All the analyzed data are listed in a comprehensive report, including a graphical representation of results and detailed information on applicable drugs. Thus, by choosing CancerPrecision®, you will receive a high level of professionalism and the best support to find the most effective treatment for each patient.

Genetics in Tumor Development

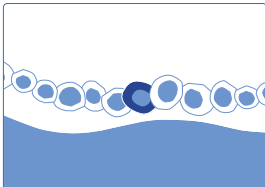
Tumors develop from cells as a consequence of mutations in genes. Mutations usually occur randomly and are typically corrected by the cell's DNA repair systems. However, exposure to carcinogens, such as tobacco smoke or UV radiation increases the number of mutations. A not correctly repaired mutation can result in altered protein function, leading to dysfunction of cellular processes and possibly the beginning of cancer. Spontaneously obtained mutations are called somatic mutations. The genetic alterations initially drive the loss of growth control, the proliferation of cell clones with reduced mortality rate, and finally the distribution of tumor cells to distant organs (metastases). The somatic mutations acquired by tumors in the course of the disease are individual and differ not only between different cancer entities but also from patient to patient – every tumor is unique. Thus, cancer is a multifactorial and heterogeneous genetic disease.

NGS-Guided Oncogenetics – A New Era of Cancer Management

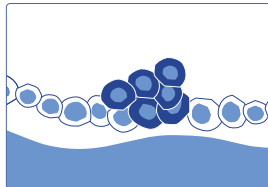
The individual set of tumor-specific mutations helps the tumor to survive and develop resistance against therapeutic agents. To choose a promising treatment strategy, a deep and accurate look into the molecular underpinnings of individual tumors is required. The use of next-generation sequencing (NGS) has initiated a new era in cancer therapy and is a driving force to change the future in personalized precision medicine. Through NGS analysis of genetic mutations, we can tailor the oncological treatments to each patient's features and each cancer genomic alterations to maximize the curative effect, minimize damage to healthy tissues, and optimize resources.¹⁻³

Tumor Progression and Increase in Genetic Diversity

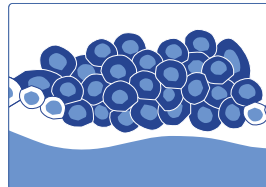
1. Initial mutation



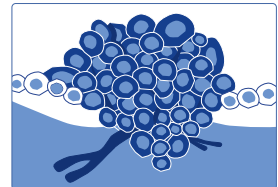
2. Growth



3. Further mutations



4. Metastases



Genetic Tumor Diagnostics

The decision-making basis for choosing the best possible analysis strategy

Genetic analysis of the tumor is essential for choosing the optimal treatment. The table below describes the variety of genetic molecular profiling tests offered. The choice of test depends on the samples available and, in particular, on the objective of the desired diagnosis.



CancerPrecision®
Full molecular analysis



CancerDetect®
Analysis of hotspot regions & monitoring



CancerNeo®
Identification of neoantigens



CancerEssential®
Analysis of specific selected genes

Sample type	Solid tumor tissue	Liquid biopsy	Liquid biopsy	Solid tumor tissue	Solid tumor tissue
Scope	> 700 genes (full coding) and selected structural variants in > 30 genes		Hotspot regions in 31 genes and fusions in 6 genes, <i>TP53</i> and <i>PTEN</i> full coding	Whole exome and transcriptome sequencing	Disease specific gene sets covering up to 64 genes and selected structural variants in 8 genes
Normal tissue comparison	✓		X	✓	X
Detailed drug options list	✓		✓	✓	✓
Detection threshold (NAF*)	5%		0.25%	5%	5%
Minimal tumor fraction	20%		1%	20%	20%
SNV and Indels	✓		✓	✓	✓
CNV	✓		X	✓	X
TMB	✓		X	✓	X
MSI	✓		X	✓	✓**
HRD	✓		X	✓	X
Fusion gene analysis / structural variants (DNA-based)	✓		✓	✓	✓
Additional option: RNA-based fusion transcript analysis (CancerFusionRx®)	✓**	X	X	✓**	✓**
HPV/EBV/MCV/CMV infection	✓		X	✓	X
HLA Typing	✓		X	✓	X
Neoantigen	X		X	✓	X
Pharmacogenetics variants (selection)	✓		X	✓	X
CHIP detection	✓		X	✓	X
Representation of biological pathways and coverage profile (Copy number variations)	✓		X	✓	X

* Novel allele frequency

** Extra order



CancerPrecision®

First choice genetic diagnostics for cancer patients

Enables Targeted Treatment for Your Patients

There is no 'one-size-fits-all' in cancer medicine, as every patient's tumor is unique. Thus, it is crucial to understand the disease history and every single tumor as best as possible. Comprehensive genomic tumor profiling helps to detect clinically relevant mutations in cancer-associated genes of solid tumors and provides valuable information for selecting the most efficient treatment for each patient.

CancerPrecision® provides an optimal molecular genetic tumor profiling using NGS and forms the basis for personalized, biomarker-based cancer therapy.

We at CeGaT have fully committed ourselves to this aim. With our long-term experience in genetic diagnostics, we have optimized our somatic tumor diagnostics to identify the somatic alterations that promote tumor growth, are responsible for drug resistance, and represent potential therapeutic targets. By using NGS technology, we analyze a panel of **more than 700 tumor-associated genes and selected therapy-relevant fusions in more than 30 genes**. Concerning immunotherapies, we determine, tumor mutational burden (TMB), microsatellite instability (MSI), and viral infection (HPV, EBV, MCV, CMV). In addition, we determine the homologous recombination deficiency (HRD) status, which provides key information, allowing for the prediction of PARP inhibitor- and platinum-based chemotherapy response caused by synthetic lethality. After a processing time of 2-3 weeks, the generated data are summarized in a comprehensive report using current scientific knowledge to support you, as the treating physician, in finding efficient treatment for each patient.

Optionally, RNA-level testing can also be included in addition to the primary order. Our portfolio includes the targeted RNA-based fusion analysis, CancerFusionRx®, which enables the detection of fusion transcripts with both *de novo* and known partners in more than 200 genes. Variations in these genes are known to significantly impact tumor pathogenesis, progression, and metastasis (more details on page 15). We also offer RNA transcriptome analysis to assess gene expression in over 200 tumor-relevant genes. The results can support the validation of DNA findings at the RNA level, provide recommendations for further analysis (such as IHC staining), and identify potential therapeutic targets.

Key Facts of CancerPrecision®

- ✗ Full sequencing and analysis of more than 700 tumor-associated genes and fusions in more than 30 genes using tumor-normal comparison
- ✗ High average sequencing of 500-1,000x coverage allows detection of therapy-relevant variants in subclones
- ✗ Sensitivity: > 97,6%*, Specificity: > 99.9%
- ✗ Analysis of tumor mutational burden (TMB), microsatellite instability (MSI), and viral infection (HPV, EBV, MCV, CMV) – essential biomarkers for immunotherapies
- ✗ Analysis of homologous recombination deficiency (HRD) – an essential biomarker for PARP inhibition
- ✗ Analysis of single nucleotide variants (SNVs), insertions and deletions (Indels), translocations, and copy number variants (CNVs)
- ✗ Besides therapy-relevant somatic (tumor-specific) mutations also disease causing and therapy-relevant germline variants are reported
- ✗ Selected pharmacogenetically relevant germline variants necessary for drug dose adjustment in your patients
- ✗ A list of all eligible drugs, with EMA and/or FDA approval, for which corresponding biomarkers could be detected in the tumor
- ✗ Detection of mosaic variants: CHIP (Clonal Hematopoiesis of Indeterminate Potential)

Optional services:

- ✗ RNA-based fusion transcript analysis from tumor RNA analyzing >200 genes (CancerFusionRx®).
- ✗ Transcriptome sequencing of tumor RNA to gain further insights on significant expression changes and their potential therapeutic relevance.



For the detailed gene directory visit:
www.cegat.com/cancerprecision

* Based on a high-quality sample with 20% tumor content for detecting a somatic heterozygous variant.

Medical Report

The medical report contains the results from the genetic testing requested by you, as the referring physician. Each single medical report is prepared and discussed by an interdisciplinary team of molecular biologists and medical doctors to guarantee the highest quality.

1 Patient details

Name, date of birth, sex of the patient, and external ID, suspected diagnosis or indication for molecular genetic testing.

2 Results – Overview

On the first page, we provide an overview of the major characteristics of the tumor depicted in boxes. The results which are important for a patient's individual therapy decision are highlighted in colour. Separate boxes present TMB, MSI, and HRD score of the analyzed tumor sample, give summary information on copy number alterations and state details on detected germline variants. Moreover, we provide evidence for possible clonal hematopoiesis of indeterminate potential (CHIP) and for an HPV, EBV, MCV or CMV infection.

3 Findings of therapeutic relevance

In this section, the details of variants/biomarkers with therapeutic relevance are listed. For each gene, the somatic change is depicted in detail as well as the effect of the variant on the protein. In addition, for each variant/biomarker, the therapeutic option(s) are listed including EMA/FDA approval.

PGX

If a pharmacogenetically relevant variant is detected, the gene, including the change and the effect on the protein, is presented. In addition, the affected therapy, including the resulting phenotype, is listed (not shown in this sample report). Additionally, a separate non-tumor treatment-specific PGX report can be requested.

CHIP

In case of evidence for possible clonal hematopoiesis of indeterminate potential, the gene, the variant, and the transcript, including the NAF in blood and tumor sample, are listed (not shown in this sample report).



CeGAT GmbH | Heubachstraße 16 | 82124 Gräfelfing | Germany
Dr. Jochen Doe
Paul-Dirnen-Straße 23
72074 Stuttgart
GERMANY

Name	Doe, Jane
Date	DD.MM.YYYY
Sex	Female
Report ID	CEG_XXXXXX

1

Report of somatic tumor variants – Doe, Jane (DD.MM.YYYY)

Initiation: Breast cancer

Tumor sample

Sample of the primary tumor
Tissue type: breast
ID: MMT177Y
Date: 12.05.2019
(bioinformatics)

Tumor matched normal

7.5 Volume

Age: 52 y.o.

All exons covered

No evidence for CNV

Score 0-14

coverage of 100.0 %

Homologous recombination events detected

No evidence for a possible HRD

Score 0-5

coverage of 100.0 %

Copy number

No evidence for copy number alterations related to DNA and RNA level

Tumor Status

classified tumor (yes)
BRCA1, BRCA2

Ancestral genome
BRCA1, BRCA2

Mitochondria

No evidence for mt-related calls
mtDNA in the tumor sample

Genotype variants

Detection of a pathogenic germline variant in gene BRCA1

Pharmacogenetics

No evidence for germline variants that may affect drug tolerance

CNV

No evidence for CNV

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Version: 1.0 | Date of last update: 12.05.2019




Notes: Sample Type: Diagnostic (Solid Tumor) and NGS-BIOPSY Page 1 of 1

COPY NUMBER ALTERATIONS:

Our sequencing data provide evidence for the presence of copy number alterations (deletions and/or amplifications) of large genomic segments. Apart from the copy number variants listed in the table below, there is no evidence for the presence of further strong amplifications or of homozygous deletions of therapeutically relevant genes.

Chromosomal region	Biological category	Method	Cov. number	Affected genes with potential therapeutic relevance
chr1:1-100M	Deletion	array	-1.5	APOL1

The identified groups of variants observed depend on the sequenced tumor content and its sequencing quality. Copy-neutral, as well as unbalanced, are indicated on the basis of the NGS data and should be assessed as tentative value. The set of candidate genes represents a tentative only and refers to lists of associations. Please be aware that copy number variants may occur at a larger number of genes. Possible interactions between these genes may give rise to prediction of single gene effects on the analyzed phenotype.

RECOMMENDATION

The obtained variant c.3847_TGGAGT>T>A at TRS3, p.Gln1282Ser in gene BRCA2 is a germline variant. It was already recommended genetic counselling.

The results of this report should be evaluated against this patient's current clinical status and should be reviewed by an interdisciplinary tumor board.

Please do not hesitate to contact us if you have any questions.

Medical report written by: xxx
Prepared by: xxx, xxx
With kind regards,

Dr. Jochen Doe | Dr. Sandra Böhm
Email: jdoe@cegat.de, sb@cegat.de
CeGAT GmbH - Genomic Center




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Tumor to Normal Tissue Comparison

The only accurate way to determine somatic variants

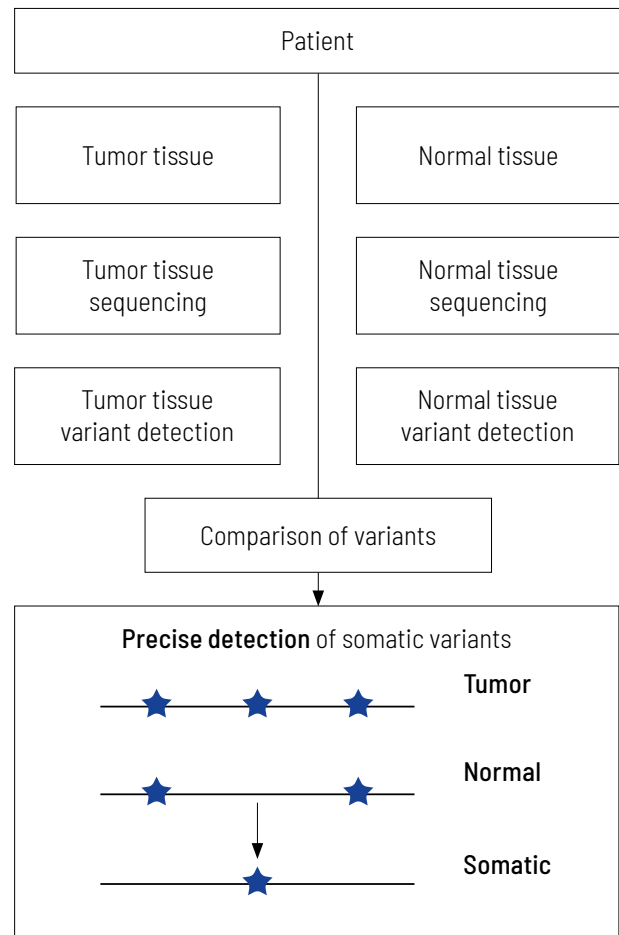
Precise information on tumor genetics is needed for correct interpretation. In tumor diagnostics, it is highly important to discriminate between variants that are restricted to the tumor (somatic variants) compared to those also present in the healthy tissue (germline variants).

The only accurate way to determine variants in the healthy tissue is to sequence the matching normal tissue together with the tumor tissue. Methods trying to replace the sequencing of normal tissue by bioinformatics approaches fail to clearly distinguish between germline and somatic variants, especially when the tumor content of the sample is high.^{4,5} Sequencing just tumor tissue can lead to an incorrect calculation of the TMB, which in the worst case may result in patients not receiving optimal treatment.⁶

Comparing tumors with matching normal tissue is mandatory for obtaining meaningful results. Diagnostic tests that do not analyze tumors and matching normal tissue usually give non-accurate results. We at CeGaT always sequence tumor tissue and matching normal tissue for our CancerPrecision® Diagnostic.

Therefore, we always sequence DNA from the tumor as well as from normal tissue (mostly blood).

The sequencing data of both tissues are compared, and thereby truly somatic variants are determined.



Comprehensive Tumor Profile at a Glance

Understanding the molecular genetic tumor profile is essential for personalizing the patient's treatment and identifying additional treatment options. The number of biomarkers we address in our CancerPrecision® report is very high. Therefore, the results are grouped into major categories and presented as boxes. The boxes with treatment-relevant findings are highlighted in color.

We present individual boxes for tumor content, TMB, MSI, and HRD scoring of the analyzed tumor sample, structural variant findings, tumor driver mutations, evidence for viral infections (HPV, EBV, MCV, CMV), germline variants (that explain the patient's disease), pharmacogenetic variants with implications on cancer treatments, and possible clonal hematopoiesis of indeterminate potential (CHIP).

Tumor Tissue & Tumor Content (TC) Primary tumor sample from MM/YYYY 75% diagnostically Diag-TC min 20%	Germline Variants No evidence for pathogenic or likely pathogenic alterations	Tumor Drivers Identified tumor drivers: <i>VEGFA, EGFR, CDKN2A, CCND2, TERT, TP53</i> Relevant genes without oncogenic alterations: <i>ATRX, BRAF</i>	Fusions, Structural Variants EGFRvIII Detection on RNA and DNA level	Pharmacogenetics Detection of a germline variant in gene <i>UGT1A1</i>
Tumor Mutational Burden (TMB) 1.4 Var/Mb High ≥ 10	Microsatellite Instability (MSI) No evidence for an infection with HPV, EBV, MCV or CMV in the tumor sample Score 0.15 Indication of MSI ≥ 0.33	Homologous Recombination Deficiency (HRD) No evidence for HRD Score 2 Indication of HRD ≥ 30	Viral Infection No evidence for an infection with HPV/EBV/CMV/MCV in the tumor sample	CHIP No evidence for CHIP

Variants with Potential Therapeutic Relevance

Guidance on potentially effective drugs

For each gene, the somatic change is depicted in detail, and the resulting therapeutic options are stated, including the EMA/FDA approval (A). These options are the basis for discussion in a molecular tumor board (MTB). At the end of the medical report, in the appendix/supplement, we provide

an extensive list of possible therapeutic strategies for each identified somatic changes (B). This list includes drug classes and names as well as their approval (FDA/EMA) and limiting conditions.

Variants with Potential Therapeutic Relevance:

A)

Gene	Functional category	Variant	NAF	Effect on protein function	Therapeutic option for discussion in the MTB	Approved by EMA/FDA	Approved for current entity
<i>BRCA2</i> (germline)	frameshift	c.3847_3848delGT; p.Val1283Lysfs*2 and loss of the wildtype-allele in tumor	het.	inactivating	PARP-Inhibitor	EMA* & FDA*	EMA* & FDA*

B)

Drug name	Tumor entity	Approval	Approval limited to biomarkers/others	Approval in combination with other drugs
Niraparib PARP-Inhibitor	fallopian tube carcinoma	EMA	advanced or relapsed cancer, prior response to platinum-based chemotherapy	
		FDA	cancer associated with homologous recombination deficiency (HRD) adult patients, advanced or recurrent cancer, prior response to platinum-based chemotherapy	
	ovarian cancer	EMA	advanced or relapsed cancer, prior response to platinum-based chemotherapy	
		FDA	cancer associated with homologous recombination deficiency (HRD) adult patients, advanced or recurrent cancer, prior response to platinum-based chemotherapy	
	primary peritoneal carcinoma	EMA	advanced or relapsed cancer, prior response to platinum-based chemotherapy	
		FDA	cancer associated with homologous recombination deficiency (HRD) adult patients, advanced or recurrent cancer, prior response to platinum-based chemotherapy	
Olaparib PARP-Inhibitor	breast cancer	EMA	germline BRCA1/2 variant, HER2-negative or HR-positive adult patients, locally advanced or metastatic breast cancer, prior endocrine or chemo therapy	
		FDA	deleterious or suspected deleterious germline BRCA mutation, HER2-negative or HR-positive adult patients, high risk or metastatic cancer, prior adjuvant or neo-adjuvant therapy	
	fallopian tube carcinoma	EMA	deleterious or suspected deleterious germline or somatic BRCA mutation adult patients, advanced (FIGO stages III and IV) cancer, prior response to platinum-based chemotherapy	
		FDA	cancer associated with homologous recombination deficiency (HRD) adult patients, advanced cancers, prior response to platinum-based chemotherapy	Bevacizumab

Sample report: Exemplary for the *BRCA2* variant detected and the resulting therapeutic options in a breast cancer patient. Top panel (A): An excerpt from Table 1 of the findings, listing variants with therapeutic relevance. Lower part (B): An excerpt of the drug listing. In addition to the drugs shown, other drugs are also described.

For more details, please see sample report:
www.cegat.com/cancerprecision



Pathway Illustration

For a detailed understanding of altered signaling

Cancer arises due to aberrant cell behavior concerning cell growth and survival. Both processes become uncontrollable in the course of tumor development. Typically, all cellular processes are strongly regulated and controlled by a complex network of signaling pathways.

Our medical report provides a comprehensive view of the network of cancer-associated signaling pathways and their molecular “key players” and all relevant genetic alterations and available drug classes to:

- ✕ understand the interactions between the different signaling pathways and
- ✕ counteract possible tumor bypass strategies.

Tumors contain mutations in genes that have key roles in these complex signaling pathways. In this context, a single genetic alteration can affect multiple pathways. Thus, it is crucial to understand the interplay of signaling pathways, which are affected by the genetic variants, next to detecting disease-associated mutations.

This approach helps to identify possible bypass strategies of a given tumor to consider all possible therapeutic options, including effective combination therapies.

Considered signaling pathways

- ✕ Signaling via receptor tyrosine kinases
- ✕ Cell cycle
- ✕ DNA damage repair
- ✕ Hormone pathways
- ✕ Wnt pathway
- ✕ Hedgehog pathway
- ✕ Hippo pathway
- ✕ Apoptosis pathway
- ✕ Epigenetic regulators

TMB Determination and MSI Prediction

The basis for therapeutic decisions on immunotherapies with checkpoint inhibitors

Tumor mutational burden (TMB) — the number of somatic mutations per megabase (Mut/Mb) — is a reliable predictive biomarker for responses to treatment with immune checkpoint inhibitors. The higher the number of genetic variations within a tumor cell, the more mutated proteins are expressed. These mutated proteins are processed into short fragments (peptides) presented on the surface of tumor cells. Such mutated peptides are called neoantigens. Neoantigens are highly immunogenic. This means they are very effectively recognized by immune cells, particularly T cells. T cells are able to eliminate tumor cells upon antigen recognition directly. Therefore, the higher the number of mutations, the higher the chance that neoantigens are presented on tumor cells, and thus the more efficient is tumor eradication by T cells.

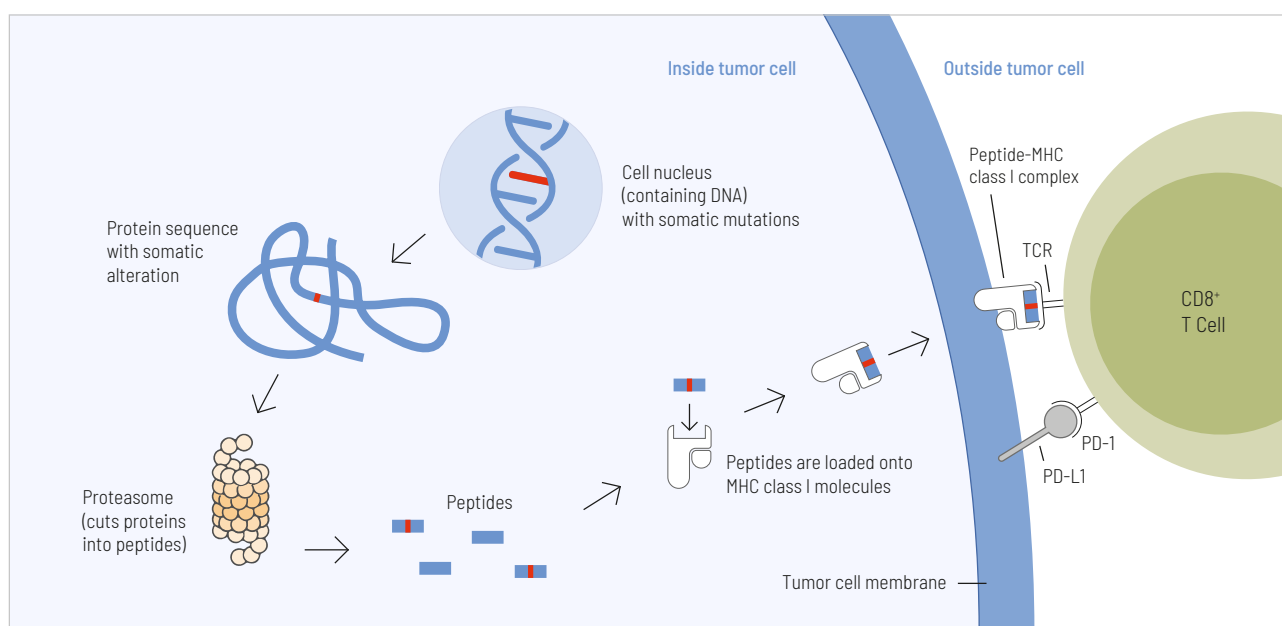
By sequencing a large gene set of both normal and tumor tissue with high sensitivity, we are able to calculate TMB precisely. This metric is used to categorize tumors into low and high mutational load. We list the classification of TMB, as well as the exact mutation rate of the tumor sample. When calculating TMB, the size of the panel is crucial for the precision of the results. With a size of 2.96 Mb, CancerPrecision® is well above the minimum requirement of 1.5 Mb and ensures a robust estimate of TMB.⁷

TMB and MSI are reliable biomarkers for predicting immune checkpoint inhibitors efficacy.⁸⁻¹⁰

MSI (microsatellite instability) is another crucial parameter for response to immune checkpoint blockade.

Microsatellites are small repetitive sequences of DNA located throughout the genome. The size of microsatellites can be altered due to failures of the DNA mismatch repair machinery.

Traditionally, MSI is detected through a comparison of satellite regions in tumor and normal tissue via PCR. However, we at CeGaT can predict the MSI status via NGS. This calculation was validated with hundreds of matched normal and tumor sample pairs across various cancer types, testing more than 2,500 target microsatellite foci.



Presentation of tumor cell-derived somatic peptides. Somatic mutations frequently arise in cancer and permanently alter the genomic information. These genetic changes can result in the expression of proteins with altered amino acid sequences. These peptides that carry a somatic change and thus display a particularly strong immunostimulatory potential can be presented on the tumor cell surface and cause an effective anti-tumor immune response.

HRD – Homologous Recombination Deficiency

Healthy cells ensure a stable and error-free genome by using different DNA repair mechanisms. Homologous recombination repair (HR) is a DNA repair pathway that acts on DNA double-strand breaks. In case of homologous recombination deficiency (HRD), this pathway is defective so that mutations, chromosomal aberrations, and other errors can accumulate in the genome. Through the resulting genomic instability, HRD facilitates tumor development and has been shown to play a role in various cancers, most prominently in breast and ovarian tumorigenesis.^{11,12} Loss-of-function genes involved in this pathway can sensitize tumors to PARP inhibitors and platinum-based chemotherapy, which target the destruction of cancer cells through synthetic lethality. To identify tumors where these medications are applicable, reliable determination of the HRD status is of utmost importance.

HR-deficient tumors are often caused by germline or somatic mutations in *BRCA1* or *BRCA2*. Therefore this pattern has formerly been referred to as *BRCAness*. Moreover, mutations in other HR genes such as *RAD51C*, *ATM*, and *PALB2* have been shown to cause HRD. It has to be mentioned that not every genetic defect in HR genes necessarily leads to HRD in the tumor. On the contrary, HRD can be caused without a detectable HR gene mutation, such as promoter methylation of *BRCAness* genes. Thus, if one tries to detect the mutations only in *BRCAness* genes, a potential HRD may remain undetected.

To ensure that HR-deficient tumors are not overlooked, we calculate the HRD score as part of every CancerPrecision® analysis independent of tumor entity.

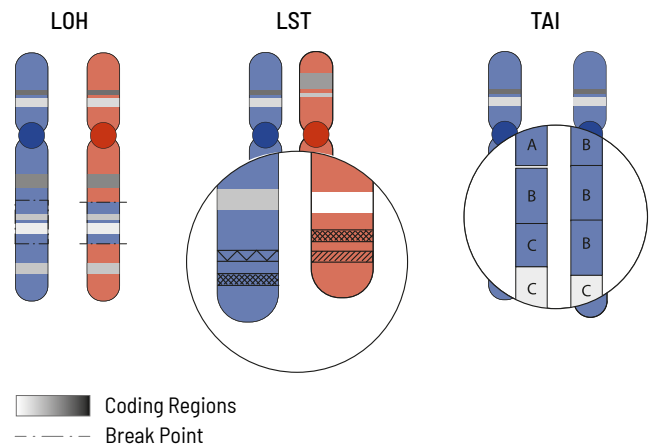
The HRD score measures overall genomic instability based on the number of Indels, substitutions and rearrangements occurring on a genome-wide level. The responsible mutations do not have to be precisely identified for this. To calculate the HRD score of the tumor sample the mutation pattern is used and calculated from three typical HRD events:

- ✗ loss of heterozygosity (LOH)
- ✗ large-scale state transition (LST)
- ✗ telomeric allelic imbalance (TAI)

LOH is the irreversible loss of a single parental allele, which is especially severe in cases where defective gene versions are retained. LOH regions are defined as larger than 15 Mb but less than the whole chromosome.

LST counts the number of transition points between abnormal chromosome regions that generate chromosomal gains or losses larger than 10 Mb.

TAI occurs when the telomeric end of a chromosome is severely shortened in one of the two parental chromosomes which causes an allelic imbalance in this region. This imbalance occurs because the repetitive DNA sequences in telomere regions are especially sensitive to HRD.



The HRD score is reported in our CancerPrecision® diagnostic report together with any identified somatic mutations and selected gene fusions as well as TMB, MSI and CNVs to provide a most comprehensive tumor analysis.

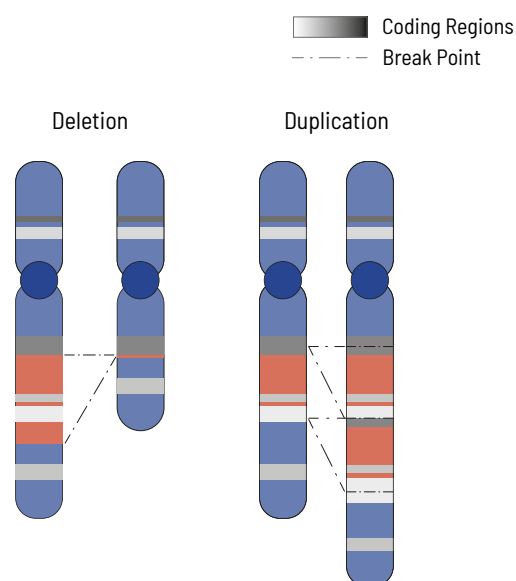
CNV Analysis

Determination of deletions/amplifications for highest therapeutic yield

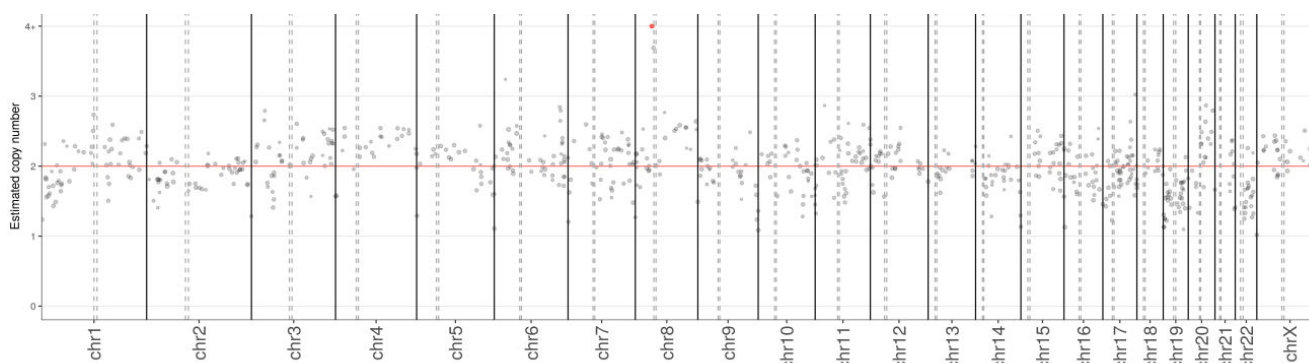
Cellular processes are tightly regulated. This regulation depends on the correct function of genes. In tumors, the copy number of genes is frequently altered, thus impairing the affected genes correct function. Increasing the copy number of a gene can increase its activity, while (partial) deletion can result in a loss of function. Therefore, chromosomal aberrations leading to copy number changes can also have therapeutic consequences.

In tumors, copy number variations (CNVs) are frequent due to the overall genomic instability. Here large chromosomal parts are often either deleted or amplified. Understanding these deletions/amplifications and knowing the genes in the affected region with therapeutic relevance is important. Therefore, deletions and amplifications are detected based on the NGS data obtained.

Deletions and amplifications are listed with the affected genes of therapeutic relevance at the beginning of the report. A complete CNV-profile of the analyzed regions is shown in the report's appendix.



CNVs often play an important role in tumor genetics. Knowing the changes in CNVs assists in choosing the optimal treatment. Therefore CNV analysis is an integral part of our somatic tumor diagnostics.



The genome of a tumor often shows many large copy number variations (CNV). The figure shows each chromosome on the X-axis. The space per chromosome corresponds to its length in base pairs. The coverage profile of the sequenced tumor sample is plotted on Y-axis. Every dot contains binned coverage data of 1 Mb of DNA. Copy numbers from zero (homozygous deletion) to 4+ copies are pictured. CNVs equal to or above 4 copies are indicated by a red colour. Please note that tumor content, as well as subclonal composition of a given tumor sample, may affect copy number estimation. Thus, the plot doesn't show copy number variation of an isolated clonal cell population but provides average measures of the CNV profile of the entire sequenced sample.

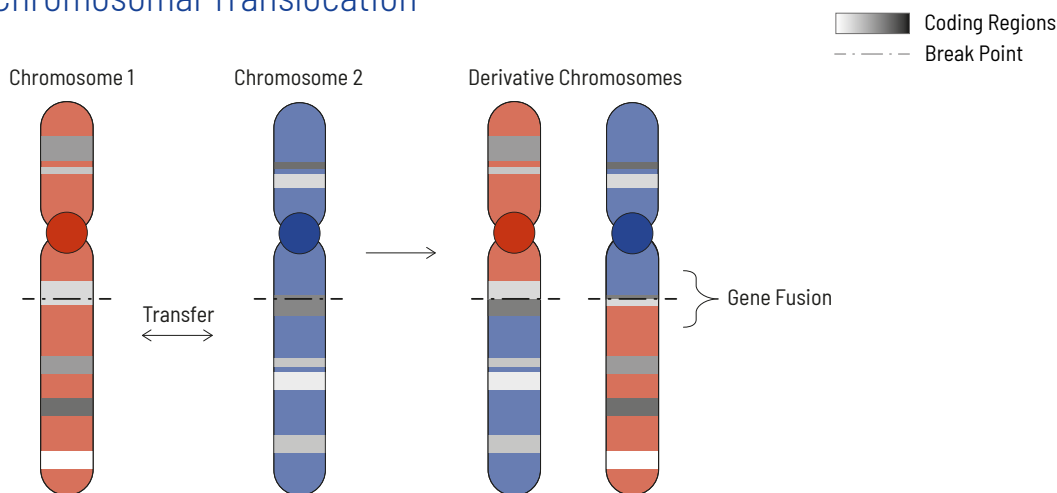
CancerFusionRx®

RNA-based identification of fusion transcripts

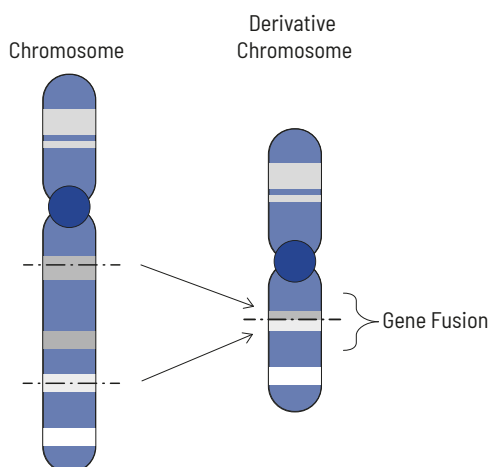
Chromosomal rearrangements frequently occur in all types of cancer. As a result, gene fusions can occur in the cancer genome. Fusions are major drivers of cancer and are therefore most relevant for treatment decisions. Conventional PCR-based methods will not detect a fusion when the other partner is not known (frequently relevant for neurotrophic tyrosine kinase, NTRK fusions). Even whole transcriptome analyses are not sensitive enough, especially when the tumor content is low.

To detect all known and previously described as well as novel gene fusions with a therapeutic option, we developed a next-generation targeted enrichment on RNA-basis. The design currently includes over 200 genes for fusion detection and over 120 exon-exon-specific enrichments with known breakpoints. This method is superior to DNA-based methods and also to whole RNA-based approaches. We strongly recommend completing the genetic tumor diagnostic by RNA enrichment for fusions for the most complete understanding of the tumor's biology.

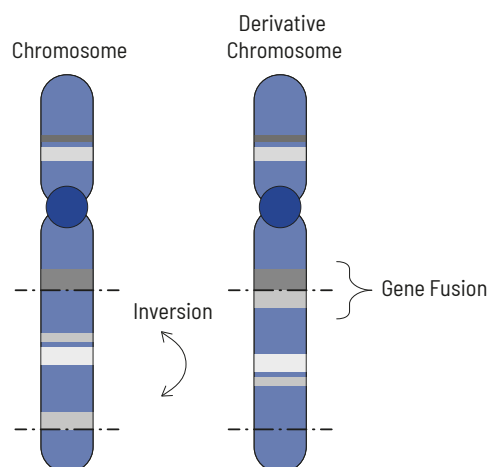
Chromosomal Translocation



Interstitial Deletion



Chromosomal Inversion



Read our Application Note for more details:
www.cegat.com/cancerfusionrx



The Power of Liquid Biopsy Testing

Access to tumor by blood analysis

Liquid biopsy analysis represents an optimal alternative testing procedure in cases where tumor tissue is unavailable, e.g., irresectable tumors or poor patient conditions. The basis of liquid biopsy (LB) analysis is cell-free DNA (cfDNA) which is increasingly released into the bloodstream by necrotic and apoptotic cells in patients with cancer and other types of diseases. Circulating cfDNA is released from both normal and tumor cells. The fraction of tumor-derived cfDNA (circulating tumor DNA/cfDNA) depends on tumor entity, tumor stage, tumor burden, and other factors and therefore is not the same in every patient. Since only a fraction of circulating cfDNA is derived from the tumor, highly sensitive methods are required to detect minimal cfDNA concentrations.

CeGaT has established and validated extensive liquid biopsy panels assessing cell-free DNA. CancerPrecision® uses liquid biopsy testing to provide a complete genetic profile of the patient's tumor, supporting the choice of the best possible therapy. A tumor content of at least 20% is required for this analysis. Since the content of cfDNA can be less than 20%, CeGaT also offers CancerDetect®, a duplex UMI*-based panel. CancerDetect® identifies sequence variants in actionable, most prevalent hotspots with a minimal allele frequency of 0.25%. This highly sensitive detection of tumor-specific biomarkers represents an excellent tool for monitoring treatment response or the occurrence of resistance mutations. In addition, the method's high sensitivity makes failure much less likely, even with a low tumor fraction in the sample.

* Unique molecular identifier

Advantages of liquid biopsy

- ✕ Non-invasive
- ✕ Rapid and precise diagnosis
- ✕ Real-time monitoring of therapies and early detection of relapse or progression

CancerDetect®

Highly sensitive detection of actionable variants from liquid biopsy samples with low tumor content

Liquid biopsy analysis detects cell-free DNA (cfDNA) released into the bloodstream by necrotic and apoptotic cells and thus offers an optimal alternative when tumor tissue is unavailable or for disease monitoring. However, only a fraction of circulating DNA originates from the tumor itself. Therefore, highly sensitive methods are required to detect these minimal cfDNA concentrations. We at CeGaT established our CancerDetect® panel using duplex UMI-based technology, which detects sequence variants in actionable, most prevalent hotspots.

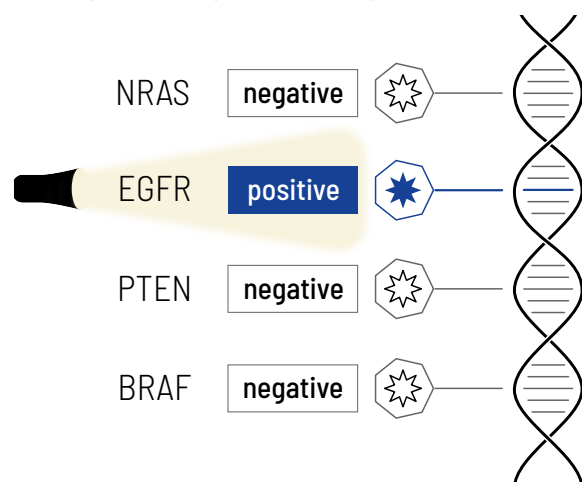
In addition, the sampling is non-invasive and easily repeatable, making CancerDetect® an excellent approach for monitoring analysis. By very sensitive detection of tumor-specific biomarkers, the analysis of cfDNA can be used as a surrogate marker for treatment response during medical follow-up.

For many liquid biopsy-based somatic analyses, it is helpful to look at changes in the results over time and interpret them in the clinical context. With the new monitoring report layout, the data from serial CancerDetect® analyses are summarized in one report and can be interpreted at a glance. The results of each additional sample are integrated into existing reports. An updated progression graph and corresponding tables clearly show a trend of the monitored changes based on the variant frequency. Conclusions can be drawn about the course of the disease, and therapy success and the occurrence of resistance mutations can be recognized in time.

Key Facts of CancerDetect®

- ✗ Liquid biopsy enables the detection of variants with potential therapeutic relevance in patients where the tumor is inaccessible, allowing to gain information about the tumor and to address treatment
- ✗ Provides a list of all eligible drugs, with EMA and/or FDA approval, for which corresponding biomarkers could be detected in the tumor
- ✗ Highly sensitive and accurate detection of actionable, most prevalent driver mutations in 31 genes and gene fusions in 6 genes with very low allele frequencies by using duplex UMI-based technology (NAF $\geq 0.25\%$)
- ✗ High coverage: 50,000–100,000x raw coverage
- ✗ Simple, non-invasive, and repeatable sampling provides the best conditions for longitudinal follow-up testing and disease monitoring
- ✗ By very sensitive detection of tumor-specific biomarkers, the analysis of cfDNA can be used to track tumor dynamics in real-time and intervene or adjust treatment if necessary (e.g., at acquired drug resistance)
- ✗ In the case of serial sampling, the results of previous analyses are automatically taken into account and the progression is depicted clearly in a figure. The focus here is on possible changes in the variant frequencies of important driver mutations over time.
- ✗ The monitoring system has a flexible structure and considers the frequency change of each somatic variant separately. Therefore, it is possible to integrate newly occurring changes into the progression report at any time.

Multiple Hotspot Testing



CancerDetect® Sample Case

Patient and Indication:

- ✗ 42 years old, female with metastatic non-small-cell lung cancer (NSCLC) with an *EGFR* L858R mutation in the primaries
- ✗ relapse after initial response to afatinib treatment
- ✗ recurrent tumor inoperable, no tumor biopsy possible

Primary finding:

The result of an analysis of cell-free DNA using a standard lung cancer panel remained negative.

CancerDetect® finding:

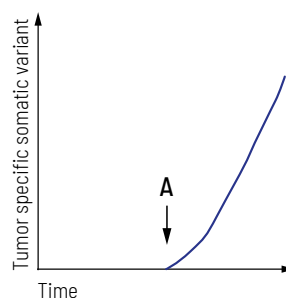
Our CancerDetect® analysis revealed a 2% tumor content in the liquid biopsy and detected the known *EGFR* L858R mutation, as well as an additional *EGFR* T790M resistance mutation. The *EGFR* T790M mutation represents one of the most common resistance mechanisms to tyrosine kinase inhibitors (TKIs) and typically occurs in NSCLC patients after first-line TKI treatment. In this patient, treatment was adjusted with the third-generation *EGFR* inhibitor osimertinib.



CancerDetect® Monitoring Applications

Application “Relapse early detection”:

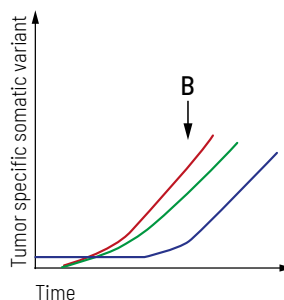
After surgery/treatment, the patient was considered tumor free. Regular LB testing revealed tumor progression showing that an increase in a tumor-specific variant accompanied the recurrence of the tumor. This biomarker's highly sensitive detection may detect the tumor's relapse earlier than conventional imaging techniques.



A = time of clinically-detectable recurrence or relapse

Application “Monitoring during treatment”:

After treatment, the patient underwent strong regression, resulting in stable disease. Longitudinal monitoring provides an up-to-date molecular profile of the tumor and detects emerging treatment resistance in time. Here, two additional subclones occur besides the primary tumor mutation, forcing the treatment to be adjusted appropriately.



B = time of clinically-detectable recurrence or relapse and acquired resistance

CancerMRD

Tissue-informed monitoring of minimal residual disease for patients with solid tumors

Minimal residual disease testing (MRD) refers to the small number of circulating tumor DNA (ctDNA) molecules in the bloodstream during or after treatment originating from the smallest amounts of residual cancer cells in the body.

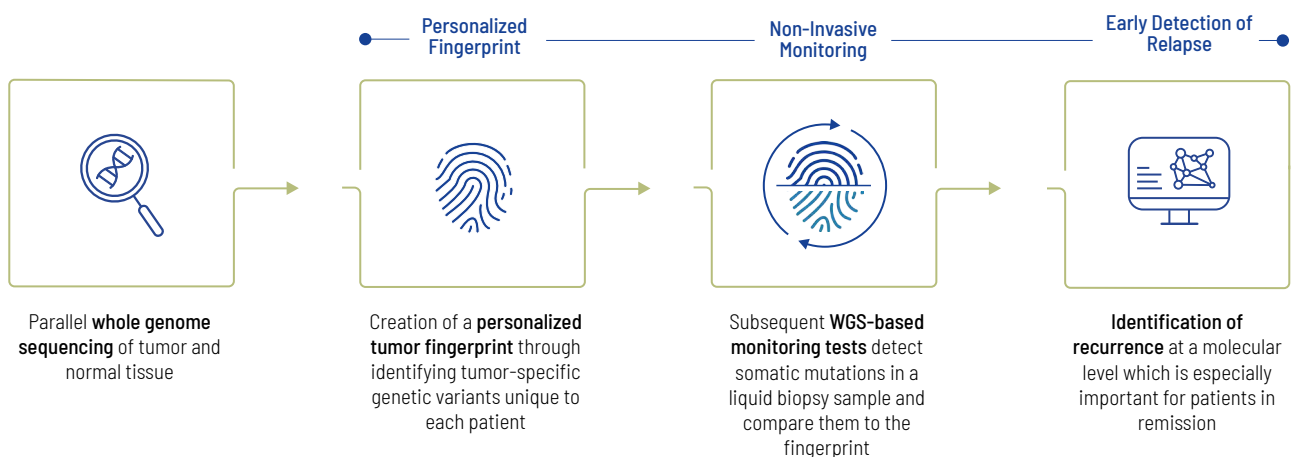
This type of monitoring is becoming a new alternative to dynamically check for treatment effectiveness and predict possible recurrence in cancer patients. Disease monitoring using liquid biopsy as a sample type allows for a repeatable and non-invasive sample collection process for the patients and the detection of a possible relapse at an earlier stage, for example, compared to imaging.

CancerMRD involves two main components: initial fingerprinting of the tumor, where the solid tumor tissue and EDTA blood are sequenced using WGS, and tumor-specific variants are detected, excluding germline variants. The next step is subsequent monitoring of the tumor-specific variants using liquid biopsy. The monitoring reports include information on detected tumor percentages and a progression graph, visually representing ctDNA detection throughout performed tests.

Key Facts of CancerMRD

- ✗ Tissue-informed approach detects tumor-specific mutations via WGS, analyzing both tumor and normal tissue. For this initial fingerprinting, a solid tumor sample and a blood sample (EDTA blood) is required.
- ✗ Subsequent MRD monitoring only requires liquid biopsy samples and uses existing fingerprint.
- ✗ Simple, non-invasive, and repeatable sampling provides the best conditions for longitudinal follow-up testing and monitoring.
- ✗ With serial sampling, previous monitoring results are incorporated into the findings and depicted in a visual graph to illustrate progression.
- ✗ Using CancerMRD, a tumor content of 0,1% and lower can be detected in a liquid biopsy sample.
- ✗ Long-term monitoring tracks disease progression, which can be used for treatment-relevant decisions (such as adjuvant treatment or de-escalating treatment given continuously negative results) and early detection of a potential relapse for patients in remission.

CancerMRD Process Overview



Identify neoantigens for personalized cancer vaccine design

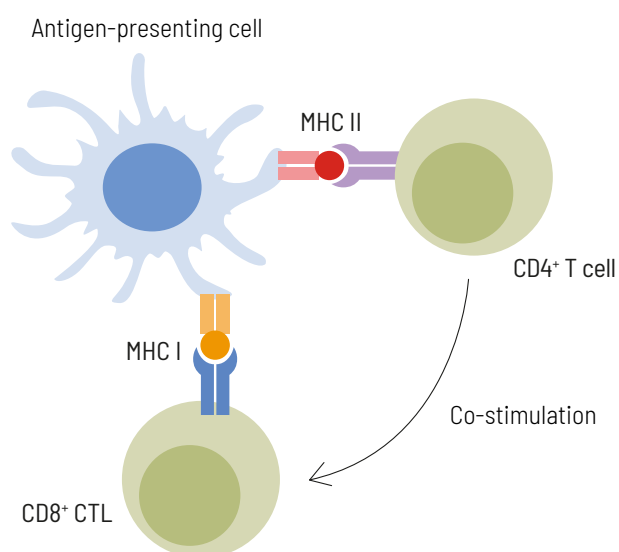
The personalization of cancer treatment is evolving rapidly. Developing a personalized cancer vaccine is a promising strategy for cancer treatment. Body cells constantly present peptides on their surface, indicating the current state of the cell. Immune cells can recognize if a cell presents normal or abnormal peptides and use this information to determine and eliminate defective cells. Abnormal peptides, so-called neoantigens, arise from DNA mutations in tumor cells and are targets for therapy using personalized vaccines.

CancerNeo® enables the analysis of a patient's tumor exome to detect tumor-specific (somatic) mutations, identifies the HLA-types, and predicts neoantigens. The expression of these neoantigens is confirmed by whole RNA sequencing (transcriptome) from the same tumor sample. Thus, our CancerNeo® provides the insights required for the design of personalized cancer vaccines – a powerful tool to boost the immune system's response to cancer cells.

Neoantigen Prediction

Neoepitopes can be recognized by CD8⁺ cytotoxic T cells (CTL) and by CD4⁺ T helper cells. Neoepitopes recognized by CD8⁺ T cells are typically 8-12 amino acids long and presented by HLA class I molecules, while neoepitopes recognized by CD4⁺ T helper cells are usually longer (13-18 amino acids in length) and presented by HLA class II molecules. For successful immunotherapy, neoantigen selection should include short and long peptides to activate both, CD4⁺ and CD8⁺ T cells. Immune responses of each individual patient can be monitored during anti-cancer vaccination by flow cytometry-based analysis of neoepitope-specific T cell activation.

Our cancer immunology experts use *in silico* algorithms based on exome sequencing and HLA typing to predict and select up to 12 eligible neoantigen epitopes individualized for each patient. The selected peptides are predicted to activate not only cytotoxic T cells but also T helper cells. Therefore, in addition to short peptides (8-12 amino acids) potentially binding to HLA class I molecules also long peptides (~17 amino acids) potentially binding to HLA class II molecules are included. To confirm the expression of the selected neoepitopes, transcriptome data by RNA sequencing of the tumor sample is done in parallel. In cases of no availability of RNA, information about neoepitope expression is retrieved from protein expression databases.



Key Facts of CancerNeo®

- ✗ Whole exome sequencing of tumor/normal tissue using CeGaT's ExomeXtra®
- ✗ Detailed assessment of somatic variants detected in more than 700 tumor-relevant genes and fusions in more than 30 genes
- ✗ Medical report with:
 - Validated list of variants with potential therapeutic relevance
 - Treatment options based on somatic variants
 - TMB determination / MSI prediction / HRD score calculation / detection of viral infections (HPV, EBV, MCV, CMV)
 - Detection of copy number variants (CNVs)
 - A List of all eligible drugs, with EMA and/or FDA approval, for which corresponding biomarkers could be detected in the tumor
 - Determination of pharmacogenetically relevant germline variants affecting the metabolism of certain tumor drugs or anesthetics
 - Assessment of the evidence for CHIP (Clonal Hematopoiesis of Indeterminate Potential)
 - Transcriptome sequencing for gene expression analysis, listing relevant findings based on aberrant gene expression by comparison case expression values with expression patterns from our large inhouse cohort
- ✗ Tumor whole RNA sequencing with rRNA depletion
- ✗ HLA typing
- ✗ Prediction of HLA class I restricted peptide epitopes (neoepitopes) spanning tumor-specific variants from sequencing data
- ✗ Selection of most relevant neoepitopes for HLA class I and HLA class II
- ✗ Second medical report with selected peptides for formulation of a vaccine

Optional services:

- ✗ RNA-based fusion transcript analysis (CancerFusionRx®) covering more than 200 genes for fusion detection and over 120 exon-exon-specific enrichments with known breakpoints
- ✗ immunohistochemical (IHC) analyses: PD-L1, CAR-T cell panel, HLA class I and class II staining (external)
- ✗ MGMT* promoter methylation analysis

* O6-Methylguanine-DNA-Methyltransferase



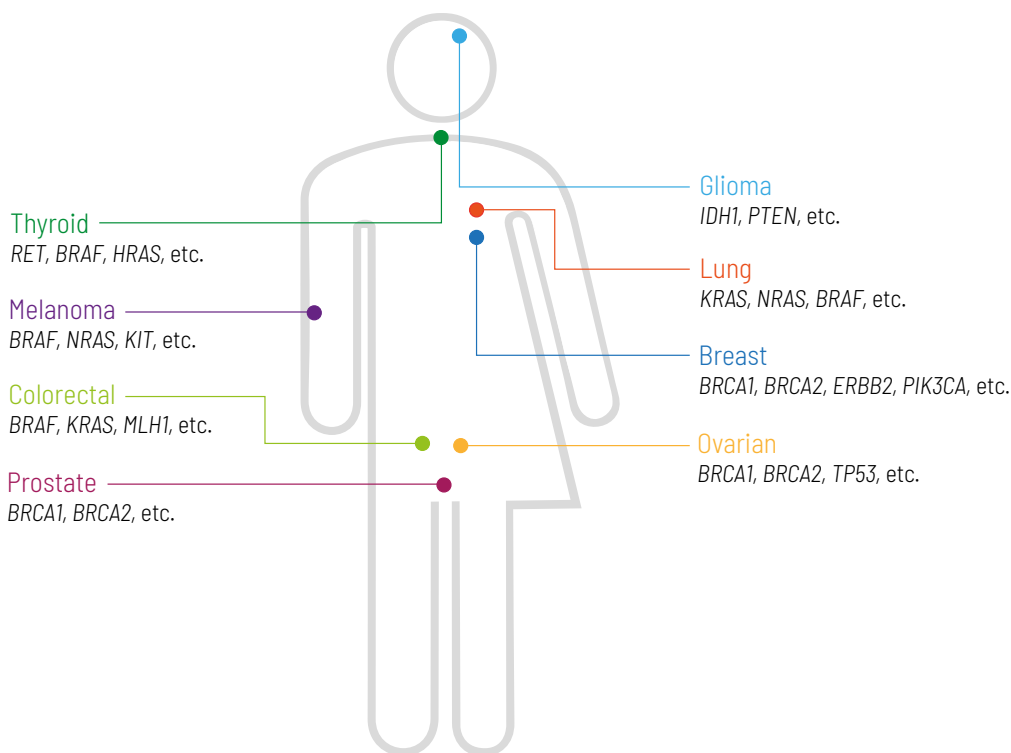
CancerEssential®

Cost-effective analysis for the identification of actionable variants in solid tumor entities

CancerEssential® has been developed in cooperation with oncologists and pathologists in order to provide a fast, cost-efficient and high-quality analysis of the most important driver mutations within the most common tumor entities. The detection of these specific mutations in tumor tissue has a clear treatment consequence with respect to approved and targeted treatment.

Key Facts of CancerEssential®

- ✕ Multigene panel testing
- ✕ Analysis of single nucleotide variants (SNVs), selected fusion genes, and microsatellite instability (MSI) status
- ✕ High average sequencing coverage: 1,000x
- ✕ Sensitivity*: > 99.8%; Specificity: > 99.9%
- ✕ A list of all eligible drugs, with EMA and/or FDA approval, for which corresponding biomarkers could be detected in the tumor



Tumor entities and most common tumor-associated genes.

* Based on a high-quality sample with 20% tumor content for detecting a somatic heterozygous variant.

Individualized detailed tumor therapy recommendation

Molecular tumor analyses have contributed significantly to a better understanding of tumor diseases. However, as they are often very complex and medical progress with drug approvals is developing rapidly, the search for therapies is very time-consuming. CancerAdvice® provides detailed information on targeted therapy recommendations for your patients, including in-label use, off-label use, and information on clinical trials. With the new service, we want to support you in the best possible way to suggest therapies for the further treatment of your patients. CancerAdvice® considers everything relevant to the patient's therapy at the given time.

The tumor profile of our extensive NGS-based diagnostics (germline and tumor) and pathological reports, such as relevant immunohistochemical results, are taken into account. Based on this information, we evaluate each case individually and list the most promising therapies based on the latest literature. For the off-label therapies indicated, we provide clinical evidence in tabular form with detailed information on study data, study conditions, biomarkers, drugs, drug dosage, and outcomes. The list of ongoing clinical trials matching targeted drug or genetic tumor alterations will be limited to five countries.

CancerAdvice® Sample Case

Treatment recommendation for a patient with Astrocytoma, WHO-Grade II, who underwent several cycles of temozolomide and/or radiotherapy. Besides the therapeutic history (not shown below), the recommendation report lists the molecular tumor profile based on CeGaT findings, and

other important biomarkers (A), followed by recommended therapies (B) and literature evidence (C). The literature evidence summarizes key facts from the corresponding clinical trial / case report including detailed information about setting and outcome.

A)

Tumor Profiling

Tumor Profiling Next Generation Sequencing

Gene	Functional category	Variant	NAF	Effect on protein function
IDH1	missense	c.395G>A; p.Arg132His	0.36	function changed
ATRX	stop_gained	c.1375A>T; p.Lys459*	0.62	inactivating
MYCN	amplification	complete gene, non focal (≥5 copies)	N/A	activating
SETD2	frameshift	c.2756_2757delAG; p.Glu919Valfs*15	0.05	inactivating
TP53	missense	c.742C>T; p.Arg248Ttp	0.71	function changed

NAF: *Novel allele frequency*, the frequency with which the mutated allele occurs in the sequencing data (1 is 100%). The observed frequencies are influenced by the tumor content as well as copy number alterations and do not directly correlate with the variant's frequency in the tumor. The somatic alterations were classified with respect to their functional effect on protein levels in the following categories: inactivating/activating/function altered, likely inactivating/activating/function altered, unknown and benign (details in the methods section of the sequencing report).

Remark: The results shown in this table are based on the patient's sequenced sample. For full details please refer to the corresponding sequencing report from CeGaT listed below in section *Additional Information*.

Tumor Profiling NGS Signatures/Scores

Biomarker	Result	Interpretation
TMB	>5 mut/mb	low
HRD	13	negative
MSI	0.17	negative

TMB: Tumor mutational load, **HRD:** Homologous recombination deficiency, **MSI:** Microsatellite instability

Remark: The results shown in this table are based on the patient's sequenced sample. For full details please refer to the corresponding sequencing report from CeGaT listed below in section *Additional Information*.

Tumor Profiling Immunohistochemistry Analysis / Other Biomarkers

Biomarker	Result	Interpretation	Comment	Analysed at (material)
p53 (IHC)	-	positive	Mutation present	xx.xx.xxxx (FFPE-ID)
IDH1 R132H (IHC)	-	positive	IDH1 mutation present	xx.xx.xxxx (FFPE-ID)
ATRX (IHC)	-	negative	ATRX loss	xx.xx.xxxx (FFPE-ID)
KI-67/Mib-1	10%	-	-	xx.xx.xxxx (FFPE-ID)
MGMT promoter methylation	31%	positive	Methylated MGMT-promoter	xx.xx.xxxx (FFPE-ID)

B)

Possible Treatment Options

Option	Biomarker	Study-ID (study name)	Drug	Phase	Localisation
1	IDH1 c.395G>A, p.R132H, NAF 36%	NCT04056910	Ivosenidib + Nivolumab	2	USA: Pennsylvania, Pittsburgh
2	IDH1 c.395G>A, p.R132H, NAF 36%	NCT05484622	Vorasidenib + Pembrolizumab	1	USA: California: LA, San Francisco; Florida: Miami; Illinois: Chicago; Massachusetts: Boston; New York; North Carolina: Durham; Texas: Huston
3	IDH1 c.395G>A, p.R132H, NAF 36% ATRX c.1375A>T; p.Lys459*, NAF: 62% ATRX (IHC) negative	NCT03212274	Olaparib	2	USA: California: Costa Mesa, Orange; Connecticut: New Haven; Florida: Coral Gables, Deerfield Beach, Miami, Plantation; Kansas: Fairway, Kansas City, Overland Park, Westwood; Maryland: Baltimore; Massachusetts: Boston; Missouri: Creve Coeur, Kansas City, Lee's Summit, North Kansas City, Saint Louis; New Hampshire: Lebanon; New York; Ohio: Columbus; Oklahoma; Pennsylvania: Pittsburgh; Tennessee: Nashville; Texas: Houston; Wisconsin: Madison
4	IDH1 c.395G>A, p.R132H, NAF 36%	NCT05345002	Retifanlimab + All-trans retinoic acid	2	USA: Pennsylvania

Perspective in Label / Off Label Therapies

Option	Biomarker	Drug Class	Drug	Availability
5	IDH1 c.395G>A, p.R132H, NAF 36%	IDH1 Inhibitor	Ivosenidib or Olutasidenib	Off Label

If several drugs of the same option are listed, this is understood to be a combination therapy.

C)

Literature Evidence 6/6

Tumor type glioma

Literature Evidence 4/6

Tumor type glioblastoma

Literature Evidence 2/6

Tumor type glioma

Appendix - Literature Evidence

Please note that the references provided may not match the patient's current situation or diagnosis. Results from clinical study data or case reports from patients with other tumor entities whose tumors have the same or similar biomarkers as your patient are also listed below. In addition, the results of clinical studies or case reports can also be listed that have not been stratified by biomarkers, but which could be a therapeutic approach for your patient according to the molecular profile of the patient's tumor. Please note that it may here have been limited to the most important sources of literature and that there is no claim to completeness.

Literature Evidence 1/6

Tumor type glioma

Study ID/Name

NCT03684811
Phase 1b/2

- cohort:

IDH1R132X-mutated glioma that relapsed or progressed on or following standard therapy and had measurable disease

- staging:

58% WHO III, WHO IV: 27%

- pretreatment:

on or following standard therapy; 42% receiving ≥3 prior regimens

- drug dosage:

olutasidenib, 150 mg orally twice daily (BID) in continuous 28-day cycles

- MRI:

88% contrast-enhancing, 12% contrast non-enhancing

- cohort size:

n=26

- endpoints:

The primary endpoints were dose-limiting toxicities (DLTs) (cycle 1) and safety in phase I and objective response rate using the Modified Response Assessment in Neuro-Oncology criteria in phase II.

Biomarker

IDH1 (function changed)

Drug Class/Name

IDH1 inhibitor: olutasidenib

Outcome

ORR: 8%

PR: 8% (2/25) (both enhancing at baseline GBM)

SD: 40% (10/25)

SD >4 months: 32% (8/25)

DCR: 48%

CBR: 48%

mPFS: 1.9 months

mPFS low grade glioma: 16.9 months (n=4)

12-month PFS rate: 20.8%

mOS: 17.2 months

12-month survival rate: 67.9%

genetic profile Patients with PR:

IDH1 R132H, TP53m, (1x ATRXm)

Publication

I de la Fuente et al., 2023, PMID: 36639513

18.2% GBM

glioma or astrocytoma

VO: AG-120) 500 mg QD, ly in Cohort 1: otoperatively, VOR.

action), with the most (rtha) before the date therapy and not be in

ally in 28-day cycles

toxicity

25

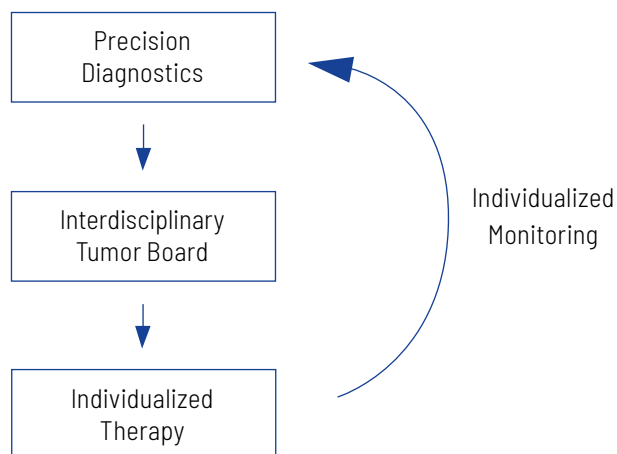
Integration of Genetic Tumor Diagnostics In Patient Management

Our somatic tumor analyses accompany you and your patients optimally - from diagnosis to monitoring.

Time is most precious in cancer patient treatment. The earlier a cancer is detected and an effective treatment is used, the better the chances for the patient.

Understanding the molecular detail of the tumor as early as possible offers the chance to use an effective treatment at an early stage. In our opinion, the best strategy is to start with a detailed diagnostic approach that includes our CancerPrecision® analysis to address the genetic changes of the tumor.

Then, the results should be discussed in a local interdisciplinary MTB. This board decides on the most promising treatment strategy based on all available information on the tumor and the patient. Finally, this individualized therapy should be applied, and the patient should be monitored for success during treatment. Depending on the individual case, this monitoring should include genetic markers, like our CancerDetect®, to address potential resistance mechanisms or detect recurrences early.



Sample Requirements and Process Overview

A tumor is altering over time. Thus, we recommend sending us the most recent tumor sample. In some cases, a collection and analysis of more than one sample can be reasonable.

Our Standard Sample Requirements Are:

Normal tissue:

- ✗ 1-2 ml EDTA blood (recommended sample type) or
- ✗ genomic DNA (1-2 µg)

Tumor tissue: (tumor content at least 20%)

- ✗ FFPE tumor block (min. tissue size 5 x 5 x 5 mm) (recommended sample type) or
- ✗ FFPE tumor tissue slides (min. 10 slices 4-10 µm, tissue size 5 x 5 mm) or
- ✗ genomic DNA (> 200 ng) or
- ✗ fresh frozen tumor tissue or
- ✗ 3 x 10 ml cfDNA tubes for liquid biopsy

Other sample material sources are possible on request.

Please note: In case of insufficient sample quality or tumor content, the analysis might fail.

Checklist of Required Materials:

- ✗ tumor tissue sample
- ✗ normal tissue sample
- ✗ completed order form
- ✗ additional medical information on patient and tumor

If you have more than one option of tumor samples, please get in touch with us (tumor@cegat.com), and we will assist you in choosing the optimal specimen for your patient.

Process of Examination



Receipt of tumor tissue, normal tissue, and order form



Sequencing of tumor and normal tissue using next-generation sequencing platforms (Illumina NovaSeq)



Detection and annotation of germline and somatic biomarkers through bioinformatic analysis of sequencing data



Analysis and interpretation of mutations by an interdisciplinary team of experts, including human geneticists and oncologists



Summary of results in a comprehensive medical report

Order possible via myCeGaT Portal

Order your genetic analyses online in the myCeGaT portal with immediate effect. To do so, scan the QR code or visit my.cegat.com

Frequently Asked Questions

Which tumor entities can be analyzed by CeGaT's CancerPrecision® tumor diagnostic?

Our comprehensive somatic tumor panel can analyze all tumor entities. CancerPrecision® covers all genes that are known to play a role in tumor development, growth, and survival and might be dysregulated in tumors in general due to mutations. Besides, the composition of CancerPrecision® is regularly updated according to the latest scientific findings to ensure that all relevant cancer-related genes are always analyzed.

When is the right time for genetic tumor diagnostics?

The sooner, the better! The longer the life span of a tumor is, and the more therapies it outlasts, the more resistance mechanisms and survival strategies are developed by the tumor and the more difficult the treatment becomes. Ideally, a comprehensive genetic tumor analysis is performed after the first diagnosis. Knowledge about cancer-specific genetic alterations is crucial for choosing the best treatment.

Which tumor tissue should be used for the analysis – the primary tumor or the latest tumor tissue/ tumor tissue of multiple metastases?

Tumors acquire changes over time and with every therapy. To ensure that the genetic analysis provides the most recent molecular profile of the tumor, we strongly recommend analyzing the latest tumor tissue, e.g., after relapse or progression during or after treatment or new metastases. Thus, the analysis and the subsequent treatment decision made by an oncologist consider possible resistance and escape mechanisms that the tumor might acquire as a result of therapy. Please note that there is always the possibility of analyzing several tumor samples (e.g., Double Best Analysis). For further questions, please contact tumor@cegat.com.

What if the latest tumor cannot be removed by surgery?

In cases where resection of newly grown tumor mass is not possible because of a hard-to-access localization in the body or because a new operation is considered too risky for the patient, we offer an analysis of liquid biopsies (e.g., blood).

In such cases, we ideally recommend the concurrent analysis of the available tumor tissue from original resection and a freshly obtained liquid biopsy sample. This approach enables robust tumor profiling based on the tumor tissue. Furthermore, that offers the chance to obtain a

comprehensive and recent picture of the tumor's genetic profile based on the analysis of the cfDNA. For liquid biopsy analysis, special blood collection tubes are required. Please get in touch with us.

Sampling of LB during treatment: The patient wants to perform LB analysis and is currently under treatment. When is the best time to take samples?

First of all, the sampling should not affect the course of therapy. Since this question is complex and cannot be answered in general, we recommend that you, as the treating physician contact us to discuss this in more detail. Please reach out to us at tumor@cegat.com.

My patient had the tumor tested and treated accordingly but got a recurrence. What should I do?

Optimal treatment of a tumor can require adapting after a certain time. For example, the tumor might be able to adapt to the treatment by finding an escape mechanism. In such a case, a recurrence can happen, and treatment needs to be adapted. Therefore, a new sample should be analyzed to identify the changes that lead to tumor growth during treatment. Then, based on the latest findings, the treatment can be adjusted.

Why do you need normal tissue?

Every human differs from other humans in tens of thousands of germline variants. Every cancer results from genetic changes in the tumor genome (somatic mutations) – cancer is considered a genetic disease. To separate somatic mutations from germline variants the individual germline variants need to be identified. When sequencing only tumor tissue this is done bioinformatically, but has been proven to result in a substantial number of mistakes. When sequencing the matched normal tissue sample (the sample from the same patient as the tumor tissue) the germline variants are directly identified, leaving no room for mistakes.

When can I expect results?

After sample and payment receipt, our current turn around time (TAT) is 2-3 weeks. We require this time for sample processing in the lab (DNA Isolation, library prep, NGS), analysis of NGS data, and for our diagnostics team to examine the data and write the medical report.

The samples sent in for analysis failed. What happened?

Our tumor diagnostic service relies on high-quality data. However, sometimes the amounts or quality of tumor DNA is insufficient. In these cases, we request alternative sample material. If no alternative sample material is available, the analysis needs to be cancelled.

Please note: for our tumor diagnostic analyses a tumor content of 20% is a prerequisite. In certain cases like analyzing liquid biopsy or fresh frozen tumor tissue, the tumor content can be just determined after NGS. Samples with tumor content below 20% cannot be used for evaluation, however, we have to invoice the analysis with the full price.

What about logistics?

CeGaT provides sample collection boxes that contain instructions and the appropriate collection equipment. Also, the boxes can be used for shipment. The sample collection boxes are free of charge and can be ordered by email, mail, or phone.

Depending on your needs, the following collection kits can be ordered from our logistics department:

- ✗ EDTA kit (contains EDTA tube)
- ✗ FFPE kit (contains Slidetrays for FFPE-slides and Bubble wrap for FFPE Block)
- ✗ LB kit (contains Streck® tubes)
- ✗ EDTA + FFPE kit (contains EDTA tube and Slidetrays for FFPE-slides and Bubble wrap for FFPE Block)
- ✗ LB + EDTA kit (contains Streck® tubes and EDTA tube)

What are the costs for the analysis?

We are happy to provide prices on request. For German customers, we can also provide information regarding reimbursement. Don't hesitate to get in touch with us at tumor@cegat.com.

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About Us

CeGaT is a global provider of genetic analyses for a wide range of medical, research, and pharmaceutical applications.

Founded in 2009 in Tübingen, Germany, the company combines state-of-the-art sequencing technology with medical expertise – with the aim of identifying the genetic causes of diseases and supporting patient care. For researchers and pharmaceutical companies, CeGaT offers a broad portfolio of sequencing services and tumor analyses. CeGaT generates the data basis for clinical studies and medical innovations and drives science forward with its own insights.

The owner-managed company stands for independence, comprehensive personal customer service, and outstanding quality. CeGaT's laboratory is accredited according to CAP/CLIA, DIN EN ISO 15189, DIN EN ISO/IEC 17025, and thus meets the highest international standards. To obtain first-class results, all processes are carried out in-house under scientific and medical supervision.



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