

## General Information

**Patient**

Surname: \_\_\_\_\_

First name: \_\_\_\_\_

Date of birth: \_\_\_\_\_

Sex (assigned at birth):  female  male

Gender (if differs from sex assigned at birth):  
 man  non-binary  woman  self-described: \_\_\_\_\_

External ID: \_\_\_\_\_

### Declaration of consent

By signing this form, I declare that I have received comprehensive information about the genetic background related to the disease in question, as well as the possibilities and limitations of molecular genetic testing. I understand that I have the right to withdraw my consent to genetic analyses.

I have been informed, and agree, that my personal data and the data obtained in the analysis will be recorded, evaluated or stored in an pseudonymised form in scientific databases, and further, in accordance with data protection and medical confidentiality, that the request, or parts thereof, may be transmitted to a specialized cooperating laboratory.

I consent to the re-evaluation of my test results within the data storage period. If significant alterations become apparent, my doctor will be informed by e-mail.

I have been informed, and agree, that all data collected by CeGaT GmbH is electronically stored, processed, used and transmitted.

For more detailed information on data privacy as well as your rights please refer to [www.cegat.com/privacy-policy](http://www.cegat.com/privacy-policy)

### Please Note

Our panels are regularly updated to reflect current scientific research. It should therefore be recognized that there is the possibility that the list of genes on the order form may have changed slightly (genes added or removed) by the time the sample is analyzed in the laboratory. By signing this form, the physician accepts that the list of genes actually analyzed may be slightly different from what is currently listed. When NGS is utilized more than the requested genes are sequenced for each sample.

**This consent includes the permission to request tumor sample materials and reports from external sources.**

**This declaration of consent can be completely or partially withdrawn at any time. I have had sufficient time to consider giving my consent.**

I, the referring physician, confirm that I am qualified to request genetic testing for the above-mentioned patient. For minors, I declare that I have the consent of all legal guardians.

**If the patient did not sign this order form:** I, the referring physician, confirm that the patient received genetic counseling and agrees with the genetic testing. The patient's consent has been obtained in writing.

\_\_\_\_\_  
**Patient / Legal Guardian**  
 (Block letters)

\_\_\_\_\_  
**Doctor**  
 (Surname, First name)

X \_\_\_\_\_  
**Patient / Legal Guardian**  
 (Date, Signature)

X \_\_\_\_\_  
**Doctor**  
 (Date, Signature)

**Doctor's stamp / Barcode**

**Sender / Clinic**

Surname: \_\_\_\_\_

First name: \_\_\_\_\_

Institution: \_\_\_\_\_

Street: \_\_\_\_\_

Postcode/City: \_\_\_\_\_

Country: \_\_\_\_\_

Phone: \_\_\_\_\_

Email: \_\_\_\_\_

VAT: \_\_\_\_\_  
 If applicable, please include a VAT number or a copy of your business registration certificate.

**Invoice**  to sender / clinic  
 to patient / other (KVA-No.: \_\_\_\_\_)

Surname: \_\_\_\_\_

First name: \_\_\_\_\_

Street: \_\_\_\_\_

Postcode/City: \_\_\_\_\_

Country: \_\_\_\_\_

Email: \_\_\_\_\_

### If you do not check these boxes, your answer will be recorded as "No".

I consent to the storage of my genetic material for additional tests and/or quality control (for max. 10 years).  Yes  No

I consent to the storage of my test results beyond the timespan of 10 years (as required by German law).  Yes  No

I consent to the pseudonymous storage and use of surplus genetic material and/or test results for scientific research and in scientific literature.  Yes  No

**With regard to secondary findings I would like to be informed:**  Yes  No

Genetic variation may sometimes be identified, which does not fit within the scope of the requested genetic analysis (so-called secondary findings). The reporting of these variants is limited to pathogenic alterations (ACMG classes 4 and 5) within selected genes, for which a treatment or course of action exists for you or your family (according to the current guidelines of the American College of Medical Genetics and Genomics; details on genes and associated diseases can be found at [www.cegat.com/acmg-genes](http://www.cegat.com/acmg-genes)). There is no claim of a comprehensive analysis of this gene set. An absence of secondary findings cannot be used to indicate a reduced disease risk.

As part of this analysis we also examine germline changes present in leukocyte DNA. Even there is no known family history, it is possible that a clinically relevant germline variant is detected. This may be of relevance for the therapy, but possibly also for tumor follow-up, prevention or for at-risk family members. Therefore, we generally report clinically relevant germline variants (variants with therapeutic relevance or pathogenic/likely pathogenic variants only) in selected genes, unless explicitly contradicted. The results should be discussed as part of a genetic counseling.

**According to German Genetic Diagnostic Act (GenDG) we will issue the medical report to the counselling physician. Please indicate here the contact email of the counselling physician:**

Email: \_\_\_\_\_




CeGaT is accredited by  
 DAkkS according to  
 DIN EN ISO 15189:2014,  
 the College of American  
 Pathologists (CAP) and CLIA.

Indication

For targeted and effective processing, please complete the medical history form with as much detail as possible and include a copy of all existing reports.

Indication / Suspected diagnosis / Course of disease / Pedigree

 index patient

not affected

affected

known carrier

deceased

unrelated parents

consanguine parents

unborn child

abortion, stillborn child

person of unknown sex

identical twins (monozygous)

fraternal twins (dizygous)

Already initiated / carried out somatic genetic analyses

Clinical report(s) added

Laboratory report(s) of Pathology / Cytology / Cytogenetics / Flow Cytometry added

Transplants (bone marrow, tissue, stem cells)  No  Yes, (please specify) \_\_\_\_\_

Sample material: Liquid biopsy (cfDNA)

Liquid Biopsy samples are specimens that can only be withdrawn using special collection tubes that stabilize the cell-free DNA. If you are planning a diagnostic examination based on cfDNA, please use such collection tubes. We gladly provide such special collection tubes. Please contact us in time at tumor@cegat.de to order the tubes.

3 x 10ml cfDNA tubes (if cerebrospinal fluid or fluid from cysts is to be used as starting material, please reduce the amount taken accordingly if necessary)

Type of primary sample for cfDNA isolation:

Blood  Ascites  Liquor  Pancreatic cyst fluid  Other: \_\_\_\_\_

Inquiry

All relevant variants in a named exon are analysed. Exon numbers refer to coding exons (CDS) in a given transcript. Diagnostics is not necessarily limited to the example hotspot mutations listed. Exons not named and all variants within are not part of the analysis.

| Gene   | NM_Nr.      | Enriched region (incl. example hotspot (HS)-variants)                        | Gene   | NM_Nr.         | Enriched region (incl. example hotspot (HS)-variants)                                |
|--------|-------------|--|--|----------------|--|
| AKT1   | NM_005163.2 | Exon 2 (incl. HS E17)  | HRAS   | NM_005343.4    | Exons 1-3 (incl. HS G12, Q61)  |
| ALK    | NM_004304.5 | Exons 22-25 (incl. HS F1174, G1202, F1245, R1275)                            | IDH1   | NM_005896.4    | Exon 2 (incl. HS R132)   |
| AR     | NM_000044.6 | Exons 4, 5, 8  | IDH2   | NM_002168.4    | Exon 4 (incl. HS R140, R172)   |
| BRAF   | NM_004333.6 | Exons 11, 15 (incl. HS V600)   | JAK2   | NM_004972.4    | Exon 12 (incl. HS V617)  |
| CDKN2A | NM_000077.5 | Entire coding region   | KIT  | NM_000222.3    | Exons 9, 11, 13, 14, 17, (incl. HS W557_K558del, D816)                               |
| CTNNB1 | NM_001904.4 | Exons 2, 6, 7 (incl. HS S37, S45, K335, N387)                                | KRAS   | NM_004985.5    | Exons 1-3 (incl. HS G12, G13, Q61)   |
| EGFR   | NM_005228.5 | Exons 2, 3, 6, 7, 15, 18-21 (incl. HS A289, G598, E746_A750del, T790, L858)  | MET  | NM_001127500.3 | Exons 13, 15, 18 (incl. HS L982_D1028del, T1010, Y1248, Y1253), MET Exon 14 skipping |
| ERBB2  | NM_004448.4 | Exons 8, 17, 19-21 (incl. HS S310, R678, V842)                               | NRAS   | NM_002524.5    | Exons 1-3 (incl. HS G12, Q61)  |
| ERBB3  | NM_001982.4 | Exons 3, 7-9, 23 (incl. HS V104, E928)                                       | PDGFRA   | NM_006206.6    | Exons 11, 13, 17 (incl. HS D842)   |
| ESR1   | NM_000125.4 | Exons 4, 5, 7, 8 (incl. HS K303, Y537, D538, E380Q, L536H, Y537C/N/S, D538G) | PIK3CA   | NM_006218.4    | Exons 1, 4, 7, 9, 13, 20 (incl. HS R93, E542, E545, H1047)                           |
| FGFR1  | NM_023110.3 | Exons 11-13 (incl. HS N577, K687)  | PTEN   | NM_000314.8    | Entire coding region   |
| FGFR2  | NM_000141.5 | Exons 6, 8, 11-13 (incl. HS S252, N549)                                      | RET  | NM_020975.6    | Exons 10, 11, 13-16 (incl. HS C634)  |
| FGFR3  | NM_000142.5 | Exons 6, 8, 13 (incl. HS R248, S249, Y375)                                   | TERT   | NM_198253.3    | Promotor HS c.-124 (C228), c.-146 (C250)   |
| GNA11  | NM_002067.5 | Exons 4, 5 (incl. HS R183, Q209)   | TP53   | NM_000546.6    | Entire coding region   |
| GNAQ   | NM_002072.5 | Exons 2, 4, 5 (incl. HS T96, R183, Q209)                                     | <b>DNA-based detection of selected structural variations in these genes:</b> |                |  |
| GNAS   | NM_000516.7 | Exon 8 (incl. HS 201)  | ALK, RET, ROS1, FGFR2, FGFR3, NTRK1  |                |  |
| H3-3A  | NM_002107.7 | Exon 1 (incl. HS K27, G34)   |  |                |  |

Remarks:

For further information and advice please do not hesitate to contact our Diagnostic Support team.  
www.cegat.com/diagnostic-support · diagnostic-support@cegat.com  
Phone +49 7071 56544-55