TRANSFERRING CODE
TO DIAGNOSIS

Order Form
Diagnostic Panel
'Somatic Tumor Panel'
General Information

CeGaT
Center for Genomics and Transcriptomics

Patient

Surname: _____

First name: _____

Date of birth: _____

Sex: ❑ male ❑ female

Material

‣ See following page 2

Invoice

❑ to patient ❑ to sender / clinic

❑ other; please specify: _____

Sender / Clinic

Surname:

First name:

Institution:

Street:

ZIP/City:

Country:

Phone:

Email:

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

VAT: _____

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 the data obtained in the analysis will be recorded, evaluated, or stored in an anonymised 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 specialised cooperating laboratory. I have been informed, and agree, that all data collected by CeGaT GmbH is electronically stored, processed, and used. I also consent to the data being transmitted electronically (e.g. by e-mail or fax).

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 anonymous storage and use of surplus genetic material and/or test results for scientific research. ❑ Yes ❑ No

Applies to TUM01 analysis only: Genetic variation may sometimes be identified, which does not fit within the scope of the requested genetic analysis (so-called incidental findings report). The reporting of these variants is limited to pathogenic alterations 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; ACMG SF V2.0; Kalia et al., 2017, PMID: 27854360). There is no claim of a comprehensive analysis of the genes included within the incidental findings report. An absence of incidental findings cannot be used to indicate a reduced disease risk.

With regard to incidental findings I would like:

❑ to be informed

❑ to NOT be informed

Applies to TUM01 analysis only: 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.

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 patient 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 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.

_____
Patient / legal representative (Block letters)

_____
Doctor (Block letters)

Doctor's stamp / Barcode

X _____
Patient / legal representative (Date, Signature)

X _____
Doctor (Date, Signature)

Contact
To discuss the diagnostic strategy
please do not hesitate to contact us.
Phone: +49 7071 565 44 55
Email: diagnostic-support@cegat.de

DAkkS Deutsche Akkreditierungsstelle D-ML-13206-01-00

CAP ACCREDITED COLLEGE of AMERICAN PATHOLOGISTS CLIA CERTIFIED ID: 99D2130225

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

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Diagnostic Panel
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Indication

CeGaT
Center for Genomics and Transcriptomics

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

Already initiated / carried out somatic genetic analyzes

❑ **Clinical report(s) added**

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

Material (tumor tissue)

❑ FFPE (Formalin-Fixed, Paraffin-Embedded)

Block number (FFPE): _____

❑ Tissue slides (minimum 10 slides)

❑ Tumor DNA (> 200 ng DNA)

❑ Frozen tissue

❑ Tumor sample in RNAlater

❑ EDTA bone marrow, proportion of neoplastic cells: _____

❑ Tumor sample from _____

Request from _____

Details of the tumor tissue

❑ Primary tumor

❑ Metastasis; Information on the primary tumor:

_____

Tissue: _____

Tumorstage/Cytogenetics. _____

Date of tumor resection: _____

Material (normal tissue)

Blood ____ ml (min. 3-5 ml EDTA-blood)

DNA ____ µg (> 2 µg DNA): _____

DNA-No: _____

❑ Saliva sample

❑ Skin biopsy

❑ Buccal mucosa

❑ Fibroblast culture

❑ others

Order Form
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Inquiry

Inquiry

❑ Tumor Immuno-Oncology (TIO01)

Sequencing of tumor and normal tissue using a comprehensive tumor panel. Automated calculation and classification of the tumor mutational burden. Microsatellite instability (MSI) is calculated based on NGS data. For additional testing of MSI by Sanger sequencing please tick the box „Analysis for Microsatellite Instability (MSI) via PCR“ (additional charges apply).

Please note: Detected variants/mutations are neither classified nor evaluated.

❑ Analysis for Microsatellite Instability (MSI) via PCR

(Marker: BAT25, BAT26, NR21, NR22, NR27)

❑ Somatic Cancer – Treatment Decision Panel (710 genes, TUM01)

ABL1, ABL2, ACD, AIP, AJUBA, AKT1, AKT2, AKT3, ALK, AMER1, ANKRD26, APC, AR, ARAF, ARHGAP35, ARID1A, ARID1B, ARID2, ARID5B, ASXL1, ASXL2, ATG2B, ATM, ATP1A1, ATR, ATRX, AURKA, AURKB, AURKC, AXIN1, AXIN2, AXL, B2M, BAP1, BARD1, BCL10, BCL11A, BCL11B, BCL2, BCL3, BCL6, BCL9, BCOR, BCORL1, BCR, BIRC2, BIRC3, BIRC5, BLM, BMPR1A, BRAF, BRCA1, BRCA2, BRD3, BRD4, BRIP1, BTK, BTNL2, BUB1B, C11ORF30, CALR, CAMK2G, CARD11, CASP8, CBFB, CBL, CBLB, CBLC, CCDC6, CCND1, CCND2, CCND3, CCNE1, CD274, CD38, CD52, CD58, CD79A, CD79B, CD82, CDC73, CDH1, CDH11, CDH2, CDK12, CDK4, CDK6, CDK8, CDKN1A, CDKN1B, CDKN1C, CDKN2A, CDKN2B, CDKN2C, CEBPA, CEP57, CHD1, CHD2, CHD4, CHEK1, CHEK2, CIC, CIITA, CKS1B, CNOT3, COL1A1, COMMD1, CREB1, CREBBP, CRKL, CRTC1, CRTC2, CSF1R, CSF2, CSF3R, CSMD1, CSNK1A1, CTCF, CTLA4, CTNNA1, CTNNB1, CUL4B, CUX1, CXCR4, CYLD, CYP2A7, DAXX, DCC, DDB2, DDR1, DDR2, DDX11, DDX3X, DDX41, DEK, DHFR, DICER1, DIS3, DIS3L2, DKC1, DNMT1, DNMT3A, DOT1L, DPYD, EBP, EGFR, EGLN1, EGR2, EGR3, ELAC2, ELANE, ELF3, EML4, EP300, EPAS1, EPCAM, EPHA2, EPHA3, EPHA4, EPHB4, EPHB6, ERBB2, ERBB3, ERBB4, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ERG, ERRFI1, ESR1, ESR2, ETNK1, ETS1, ETV1, ETV4, ETV5, ETV6, EWSR1, EXO1, EXT1, EXT2, EZH1, EZH2, FAM175A, FAM46C, FAN1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAS, FAT1, FBXW7, FES, FGF10, FGF14, FGF19, FGF2, FGF23, FGF3, FGF4, FGF5, FGF6, FGFBP1, FGFR1, FGFR2, FGFR3, FGFR4, FH, FKBP1A, FLCN, FLI1, FLT1, FLT4, FOXA1, FOXA2, FOXE1, FOXL2, FOXO1, FOXO3, FOXP1, FOXQ1, FRK, FRS2, FUBP1, FUS, FYN, G6PD, GABRA6, GALNT12, GATA1, GATA2, GATA3, GATA4, GATA6, GLDN, GLI1, GLI2, GNA11, GNA13, GNAQ, GNAS, GPC3, GPER1, GPR124, GREM1, GRIN2A, GRM3, GSK3A, H3F3A, HCK, HGF, HIF1A, HIST1H3B, HLA-A, HLA-B, HLA-C, HLA-DPA1, HLA-DPB1, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLF, HMGA2, HMGN1, HMOX2, HNF1A, HNF1B, HOXB13, HOXD8, HRAS, HSD3B1, HSP90AA1, HSP90AB1, ID3, IDH1, IDH2, IFNGR1, IFNGR2, IGF1R, IGF2, IGF2R, IKBKB, IKBKE, IKZF1, IKZF3, IL1B, IL1RN, IL2, IL21R, IL6, IL6ST, IL7R, ING4, INPP4B, INPPL1, IRF1, IRS2, ITK, JAK1, JAK2, JAK3, JUN, KAT6A, KDM5A, KDM5C, KDM6A, KDR, KEAP1, KIAA1549, KIT, KLF2, KLF4, KLHDC8B, KLHL6, KMT2A, KMT2B, KMT2C, KMT2D, KRAS, LATS1, LATS2, LCK, LIG4, LIMK2, LMO1, LRP1B, LRRK2, LTK, LYN, LZTR1, MAD2L2, MAFB, MAGEA1, MAGI1, MAGI2, MAML1, MAP2K1, MAP2K2, MAP2K3, MAP2K4, MAP2K5, MAP2K6, MAP2K7, MAP3K1, MAP3K14, MAP3K3, MAP3K4, MAP3K6, MAPK1, MAPK11, MAPK12, MAPK3, MAPK8IP1, MAX, MBD1, MC1R, MCL1, MDC1, MDM2, MDM4, MECOM, MED12, MEF2B, MEN1, MET, MGA, MGMT, MITF, MLH1, MLH3, MLLT10, MLLT3, MN1, MPL, MRE11A, MS4A1, MSH2, MSH3, MSH4, MSH5, MSH6, MSR1, MST1R, MTHFR, MTOR, MTRR, MUC1, MUC16, MUTYH, MXI1, MYB, MYC, MYCL, MYCN, MYD88, MYH11, MYH9, NBN, NCOA1, NCOA3, NCOR1, NF1, NF2, NFE2L2, NFKB1, NFKB2, NFKBIA, NFKBIE, NIN, NLRC5, NOP10, NOTCH1, NOTCH2, NOTCH3, NOTCH4, NPM1, NQO1, NR1I3, NRAS, NRG2, NSD1, NT5C2, NTHL1, NTRK1, NTRK2, NTRK3, NUMA1, NUP98, PAK3, PALB2, PALLD, PARK2, PARP1, PARP2, PARP4, PAX3, PAX5, PAX7, PBK, PBRM1, PBX1, PDCD1, PDCD1LG2, PDF, PDGFA, PDGFB, PDGFC, PDGFD, PDGFRA, PDGFRB, PDK1, PGR, PHF6, PHOX2B, PIAS4, PIGA, PIK3C2A, PIK3C2B, PIK3C2G, PIK3CA, PIK3CB, PIK3CD, PIK3CG, PIK3R1, PIK3R2, PIK3R3, PIM1, PKHD1, PLCG1, PLCG2, PML, PMS1, PMS2, POLD1, POLE, POLH, POLQ, POT1, PPM1D, PRDM1, PRDM16, PREX2, PRF1, PRKAR1A, PRKCA, PRKD1, PRKDC, PROM2, PRSS1, PRX, PSIP1, PSMB1, PSMB10, PSMB2, PSMB5, PSMB8, PSMB9, PSMC3IP, PSPH, PTCH1, PTCH2, PTEN, PTGS2, PTK2, PTK7, PTPN11, PTPRC, PTPRD, PTPRT, RAC1, RAC2, RAD21, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD54B, RAD54L, RAF1, RALGDS, RARA, RARB, RARG, RASA1, RASAL1, RB1, RBM10, RECQL4, REL, RET, RFC2, RFX5, RHBDF2, RHEB, RHOA, RICTOR, RINT1, RIPK1, RIT1, RNASEL, RNF2, RNF43, ROS1, RPL22, RPS20, RPS6KB1, RPTOR, RSF1, RUNX1, RYR1, SACS, SAMHD1, SAV1, SBDS, SCG5, SDHA, SDHAF2, SDHB, SDHC, SDHD, SEC23B, SEMA4A, SETBP1, SETD2, SETDB1, SF3B1, SGK1, SH2B1, SH2B3, SH2D1A, SHFM1, SHH, SIK2, SIN3A, SIRT1, SKP2, SLC26A3, SLIT2, SLX4, SMAD3, SMAD4, SMARCA4, SMARCB1, SMARCE1, SMC1A, SMC3, SMO, SOCS1, SOX11, SOX2, SOX9, SPEN, SPINK1, SPOP, SPRED1, SPTA1, SRC, SRD5A2, SRGAP1, SRP72, SRSF2, SSTR1, SSTR2, SSTR3, SSTR5, SSX1, STAG1, STAG2, STAT1, STAT3, STAT5A, STAT5B, STK11, SUFU, SUZ12, SYK, TAF1, TAF15, TAP1, TAP2, TBK1, TBL1XR1, TBX3, TCF3, TCF7L2, TCL1A, TEK, TERC, TERF2IP, TERT, TET1, TET2, TFE3, TGFBR2, TLR4, TLX1, TMEM127, TNF, TNFAIP3, TNFRSF11A, TNFRSF13B, TNFRSF14, TNFRSF1A, TNFRSF1B, TNFRSF25, TNFRSF8, TNFSF11, TNK2, TOP1, TOP2A, TP53, TP53BP1, TPX2, TRAF2, TRAF3, TRAF5, TRAF6, TRAF7, TRRAP, TSC1, TSC2, TSHR, TUBA4A, TUBB, TYMS, U2AF1, UBE2T, UBR5, UGT2B15, UGT2B7, UIMC1, UNG, USP34, USP9X, VEGFA, VEGFB, VHL, VKORC1, WAS, WASF3, WHSC1, WISP3, WRN, WT1, XIAP, XPA, XPC, XPO1, XRCC1, XRCC2, XRCC3, XRCC5, XRCC6, YAP1, ZFHX3, ZHX3, ZNF217, ZNRF3, ZRSR2

Additional detection of selected translocations in these genes
ALK, BCL2, BCR, BRAF, BRD4, EGFR, ERG, ETV4, ETV6, EWSR1, FGFR1, FGFR2, FGFR3, FUS, MYB, MYC, NOTCH2, NTRK1, PAX3, PDGFB, RARA, RET, ROS1, SSX1, SUZ12, TAF15, TCF3, TFE3, TMPRSS2