Genetic Analysis for acquired (somatic) Leukaemia-associated Mutations

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Patient: _____ **Date of Birth:** _____

Patient is registered in the SCNIR: ☐ Yes ☐ No

Clinical Diagnosis:

☐ Congenital Neutropenia ☐ Cyclic Neutropenia ☐ Other: _____

Somatic Panel Analysis: ☐ Primary ☐ Follow-up ☐ Analysis is urgent**(Consultation required)*

***Reason for urgen analysis:** ☐ Abnormal cytogenetics ☐ Abnormal morphology ☐ Other: _____

Previous G-CSFR analyses: ☐ Yes: ☐ positive ☐ negative ☐ No

Previous resuts of molecular genetic tests:

☐ *ELANE*	☐ *HAX 1*	☐ *G6PC3*	☐ *SBDS*	☐ other: _____
☐ positive	☐ positive	☐ positive	☐ positive	☐ positive
☐ negative	☐ negative	☐ negative	☐ negative	☐ negative
☐ not tested	☐ not tested	☐ not tested	☐ not tested	☐ not tested

Therapy: G-CSF: ☐ Yes ☐ No ☐ Other: _____

Clinical Findings: _____

Sample: ☐ 1 - 5 ml Heparinized Bone Marrow ☐ 10 - 20 ml Heparinized Peripheral Blood

Date Drawn: _____

Sender *(please print or stamp):*

Consent according to the German law for genetic testing (Gen DG)
Consent of the Patient / Legal Guardian

The storage of residual material as well as the use of residual specimen for research purpose. Data will be pseudonymized. The research includes studies on how genetic mutations may contribute to the development of leukaemia or other types of cancer. Even if no cancer is present or does not occur later in life, the material is helpful. I agree that the results will be stored for more than the legal period of ten years.

_____	_____	_____
Location, Date	Signature of the Patient / legal Guardian	Signature of Responsible Physician

Samples should be taken at the beginning of the week (Monday or Tuesday) and sent off immediately by overnight express!

Please notify the laboratory prior to sending the sample:

Phone: +49 7071 2986014 or +49 162 2052224; Fax: +49 7071 2925161

email: Labor-SCNIR@med.uni-tuebingen.de

Additional information:

List of regions/genes included in the panel:

	Gene names
Sequencing of the entire protein-coding regions (n = 29)	*ASXL1, ASXL2, BCOR, BCORL1, CBL, CEBPA, CSF3R, DDX41, DNMT3A, ETV6, EZH2, KIT, KMT2D, KRAS, NF1, NPM1, NRAS, PHF6, PTPN11, RAD21, RUNX1, SETBP1, SRSF2, STAG2, TET2, TP53, U2AF1, WT1, ZRSR2*
Sequencing of hotspot regions in leukemia-associated genes (n = 16). The DNA positions (mutated in at least 2-3 cancer patients) were selected using the whole exome and whole genome sequencing records of 9863 leukemia and MDS samples (9569 patients) in 10 studies. A detailed description of datasets is available at https://bit.ly/3XX8iKv. Genomic coordinates are available on request.	*ATM, CTCF, EP300, ETNK1, FLT3, GATA1, GATA2, IDH1, IDH2, JAK2, MPL, SF3B1, SMC1A, SMC3, SRCAP, SUZ12*