CeGaT GmbH | Paul-Ehrlich-Str. 23 | D-72076 Tübingen | Germany

Dr. Jane Doe
Paul-Ehrlich-Str. 23
D-72076 Tübingen

Patient	XXX, XX
ID #	Male (*DD.MM.YYYY)
Report date	xxx
Report-ID	R#

CancerMRD Monitoring Report

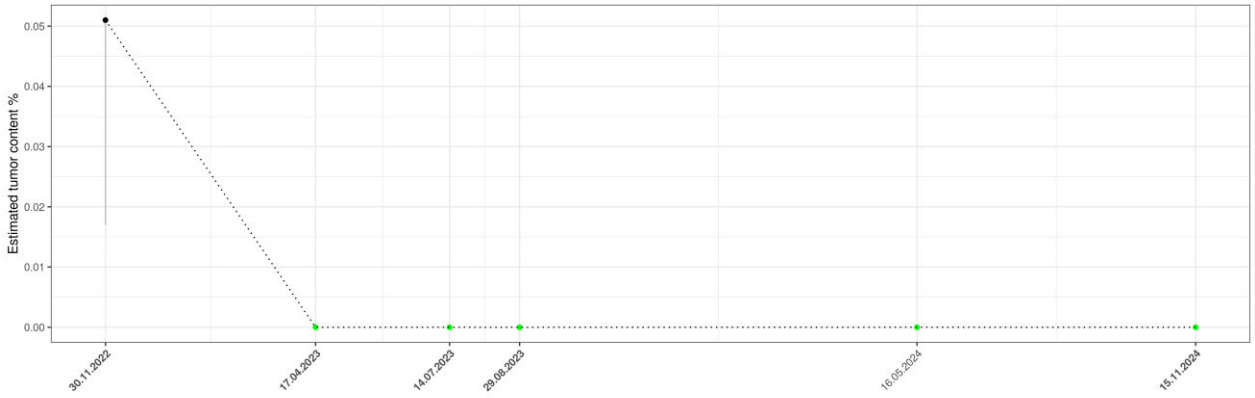
Order MRD detection from cell-free DNA of 14.07.2023 (P#_104) based on the fingerprint generated at 01/2022 (P#_21)

Result: No evidence of minimal residual disease (MRD)

- **No evidence of minimal residual disease**

Sample	Sampled At	cfDNA Amount / Concentration	Estimated Tumor content	p-value* of tumor detection	Result
P#_101	**30.11.2022**	**75.6 ng 2.7 [ng/µl]**	**0.051**	**<0.01**	**Tumor DNA detected**
P#_103	17.04.2023	42.2 ng 1.0 [ng/µl]	–	0.29	No tumor DNA found in this sample
P#_104	14.07.2023	62.4 ng 1.6 [ng/µl]	–	0.27	No tumor DNA found in this sample
P#_105	29.08.2023	56.3 ng 1.3 [ng/µl]	–	0.06	No tumor DNA found in this sample
P#_106	16.05.2024	49.4 ng 1.3 [ng/µl]	–	0.04	No tumor DNA found in this sample
P#_107	15.11.2024	51.8 ng 1.4 [ng/µl]	–	0.36	No tumor DNA found in this sample

*) The p-Value indicates whether the estimated tumor content is significantly different from random background signal. A value of 0.01 or lower means that the estimated tumor content has less than 1% probability of deriving from a tumor-free sample.



Recommendation

We recommend discussing this result together with all clinical information in an interdisciplinary tumor board.

Non-detection of MRD, falling tumor content, or no change in estimated tumor content does not necessarily prove a stable disease state or tumor regression. Rising tumor content over time is not sufficient evidence for tumor progression.

In case of questions, please do not hesitate to contact us at any time.

This report was generated automatically.

With kind regards,

Dr. med. Dr. rer. nat. Saskia Biskup
Consultant for Human Genetics

Additional Information

Order **Detection of MRD from cell-free DNA** based on the established MRD fingerprint generated at 01/2022 (P#_21)

Sampling data

Fingerprint:
04/2022 (Normal-DNA: EDTA blood, ID P#_20)
01/2022 (Tumor-DNA: Tumor DNA, ID P#_21)

MRD follow-up monitoring:
29.08.2023 (cfDNA, ID P#_105)
30.11.2022 (cfDNA, ID P#_101)
16.05.24 (cfDNA, ID P#_106)
17.04.2023 (cfDNA, ID P#_103)
15.11.2024 (cfDNA, ID P#_107)
14.07.2023 (cfDNA, ID P#_104)

CeGaT GmbH | Paul-Ehrlich-Str. 23 | D-72076 Tübingen | Germany
Tel: + 49 7071 565 44 55 | Fax: + 49 7071 565 44 56 | info@cegat.de | www.cegat.de
Court District Stuttgart - HRB 729958 | VAT No: DE265504070
Volksbank in der Region eG | IBAN: DE73 6039 1310 0543 4480 02 | SWIFT / BIC: GENODES1VBH
Managing Directors: Dr. Dr. Saskia Biskup, Dr. Dirk Biskup

Methods

DNA isolation: cell-free DNA was isolated from Streck blood at the Zentrum für Humangenetik Tübingen.

NGS-laboratory (WGS): Cell-free DNA from a blood sample was analyzed using high-throughput sequencing on the Illumina NovaSeq 6000/NovaSeq X Plus system. An average coverage of 34.9 reads per base was achieved.

Computational analysis: Sequencing data was demultiplexed using bcl2fastq2. Adapter sequences were removed using Skewer and the resulting reads were mapped to the human reference genome hg19 using Illumina DRAGEN 4.2.4. Computation of the tumor content was performed by in-house software implementing a method similar to Zviran et al. (PMID: 32483360).

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