CeGaT

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

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

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

CancerMRD Fingerprint Report

Based on your samples, an “MRD fingerprint” was generated. This is a list of genetic variants that distinguishes your tumor from your normal body cells. The fingerprint can be used to detect very small amounts of tumor DNA in blood samples (“liquid biopsies”). This allows for regular monitoring to see if the tumor content changes over time.

This fingerprint contains 1501 selected variants.

The sensitivity of MRD monitoring depends on the number of variants in the fingerprint, among other factors. A larger fingerprint allows for detection of smaller amounts of tumor DNA in a blood sample.

Based on the size of this fingerprint, we expect sensitive detection of 0.1% tumor DNA in blood samples.

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

This report was generated automatically.

With kind regards,

Saskia Biskup

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

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Managing Directors: Dr. Dr. Saskia Biskup, Dr. Dirk Biskup

Additional Information

Order	**Generation of an MRD fingerprint** as basis for future MRD monitoring from blood samples
Sample material	**Tumor tissue: Tumor DNA** Sample collection MM/YYYY Tumor DNA isolation from tumor in FFPE (FFPE-ID: #) with estimated tumor content of 70% (HE staining) **Normal tissue: EDTA blood**
Sample receipt	DD.MM.YYYY (Normal-DNA: EDTA blood, ID P#) DD.MM.YYYY (Tumor-DNA, ID P#)
Methods	**DNA isolation: DNA isolation:** The isolation of tumor and normal DNA was performed at the Zentrum für Humangenetik Tübingen. Macrodissection prior to tumor and normal DNA isolation was performed, if necessary. The tumor material was assessed at BAG für Pathologie und Molekularpathologie, Prof. Dr. med. Sipos. The pathological services (confirmation of the histological diagnosis and determination of the tumor content) were carried out on our behalf by a specialist in pathology. Pathology services are not within the scope of the ISO 15189 accreditation. **Sample quality:** The suitability of a sample for molecular genetic analysis depends on the tumor content as well as on the overall material quality (e.g. impairment of quality by chemical or physical stress due to fixation, Arreaza et al., 2016 PMID: 27657050; Einaga et al., 2017, PMID: 28498833; Jones et al., 2019, PMID: 31061401). The detection of changes and the generation of the MRD fingerprint may therefore be significantly limited or not possible at all. **NGS-laboratory (WGS):** DNA from normal tissue and tumor tissue was analyzed using high-throughput sequencing on the Illumina NovaSeq 6000/NovaSeq X Plus system. For the tumor sample, a genome-wide coverage of an average of 34.43 reads was achieved, and for the normal sample, 34.77 reads were 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. Somatic sequence variants (limited to single nucleotide substitutions) were identified by comparing the tumor sample with the normal sample. These variants were then used to generate the fingerprint.

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