Logo of the Hospital/Laboratory

Mutational analysis of the *TP53* gene

Performed by	**Requested by**
Laboratory name:	Hospital:
Laboratory address:	Referrer:
(full contact details including phone number)	Address:

Patient name/id: *	Date of sample collection:
Date of birth:	Date of sample delivery:
Gender:	Result issued:
Reason for referral:	

Type of material:
Cell separation:
Sample identification number:
Method:

Result: *TP53* MUTATION DETECTED / NOT DETECTED

Mutation No.	Variant Reference sequence: NC_000017.11 (NM_000546.6)	Variant allele frequency (VAF)	Mutation type *(optional)*	Pathogenicity
1				
2				

Optional:
Comparison with a previous sample: *We observed an increase/decrease in variant allele frequency compared to previous sample (sampling date xx.xx.xx variant allele frequency xx%).*

Conclusion:
Example: *A pathogenic variant was found within the TP53 gene. TP53 mutations are associated with adverse prognosis and poor response to chemoimmunotherapy in CLL and therefore such treatment should be avoided (PMID: 33091559 or other reference(s) of current national or international guidelines).*

Or: No pathogenic variant within the TP53 gene was detected

The result should be interpreted with respect to the proportion of tumor cells in the primary sample and the separation method used. A low proportion of tumor cells in the sample may lead to a false negative result or a decreased VAF.

Mutational analysis of the *TP53* gene

Patient name/id: *	Date of sample collection:
Date of birth:	Date of sample delivery:
Gender:	Result issued:
Reason for referral:	

Analytical method description (region sequenced, method description including bioinformatics pipeline):
Minimal coverage of the target region:
Detection limit of the method:
Variants are described according the Human Genome Variation Society (HGVS) nomenclature Version xx.xx.

Variant interpretation:
Functional impact and pathogenicity of variants was assessed based on the following tools:

The interpretation refers to the time of issuing of the report and may change in the future due to additional evidence. Validated polymorphisms and benign/likely benign variants are not included in this report and can be provided upon request.

Method limitations:
Example: *The method cannot detect large duplications and deletions, and complex rearrangements within the tested regions of TP53 gene. The procedure cannot distinguish between somatic and germline variants without testing of normal tissue from the same individual. In the case of justified suspicion of the germinal origin of a variant with VAF>50% (young age, family history), the examination needs to be repeated from non-tumor DNA.*

Analysis performed by‡: Name and function Result issued by: Name and function‡

** Unique patient identification, the date of primary sample collection and the date of the issue of the report should be on each page of the report (in a header or a footer of the document).*
‡ *Co-validation and co-signature by a second competent person is recommended (and mandatory in some countries).*