diagnostics@liqomics.com
(+49) 221 69 056 597

Liqomics GmbH
Hermülheimer Str. 68
50969 Köln
Germany

Patient Name	**Max Mustermann**
Date of Birth	01/Jul/1901
Liqomics Patient ID	01_23456_78_c9
Customer ID	1234567898
Sex	male
Indication	Lymphoma
Report date	02/Oct/2024

Report of findings - Max Mustermann, *01/Jul/1901

Indication: Lymphoma

Recommendation: The results of this report should be evaluated against this patient's current clinical status and should be reviewed by an interdisciplinary tumor board. Please do not hesitate to contact us if you have any questions.

Report of minimal residual disease

Baseline ct DNA dataset: (01_23456_77_c9_01_01_ref_01_23456_77_g1_01_01)

Follow up ct DNA dataset: (01_23456_78_c9_01_01_ref_01_23456_77_g1_01_01)

Baseline ctDNA (01/Jan/2023)	Follow up ctDNA (01/Jan/2024)	MRD reduction in log-levels
8.8713 %	0.4647 %	-1.28

Report of identified variants

Gene symbol	Genetic variant	Protein variant	variant allele frequency (VAF)	Consequence
NRAS	c.181C>A	p.Q61K	10.239%	missense_variant
B2M	c.58G>C	p.A20P	0.125%	missense_variant
B2M	c.64C>T	p.Q22*	29.858%	stop_gained
SOCS1	c.179C>A	p.S60*	0.130%	stop_gained
SOCS1	c.256G>A	p.V86M	0.122%	missense_variant
SOCS1	c.591C>A	p.N197K	3.446%	missense_variant
MAP2K1	c.1052A>G	p.D351G	26.393%	missense_variant
MAP2K1	c.167A>C	p.Q56P	31.818%	missense_variant
B2M	c.199G>A	p.E67K	23.344%	missense_variant
P2RY8	c.152G>A	p.R51H	0.210%	missense_variant
MAP2K2	c.32C>T	p.A11V	0.148%	missense_variant
MAP2K2	c.567G>T	p.Q189H	0.103%	missense_variant

MAP2K2	c.682G>A	p.V228M	0.135%	missense_variant
MAP2K2	c.904G>C	p.G302R	0.128%	missense_variant
P2RY8	c.373G>A	p.V125I	48.133%	missense_variant
P2RY8	c.476C>T	p.A159V	6.862%	missense_variant
TP53	c.934A>G	p.T312A	0.140%	missense_variant
BCL2	c.181G>A	p.A61T	0.113%	missense_variant
BCL2	c.320G>A	p.R107H	0.098%	missense_variant
BCL2	c.325C>A	p.R109S	0.098%	missense_variant
BCL2	c.424G>T	p.V142L	0.103%	missense_variant
SMAD4	c.1532C>A	p.P511Q	0.137%	missense_variant
SMAD4	c.1259G>A	p.R420H	0.156%	missense_variant
SMAD4	c.755G>A	p.G252E	0.143%	missense_variant
CD79B	c.341T>C	p.F114S	0.109%	missense_variant
TP53	c.215C>G	p.P72R	90.831%	missense_variant
TP53	c.847C>A	p.R283S	0.129%	missense_variant
TP53	c.888C>G	p.H296Q	0.117%	missense_variant
TNFAIP3	c.894G>T	p.M298I	0.210%	missense_variant
TNFAIP3	c.388C>A	p.L130I	30.333%	missense_variant
NFKBIE	c.337C>T	p.L113F	0.138%	missense_variant
TNFAIP3	c.1489C>T	p.R497C	0.124%	missense_variant
BCL6	c.1756C>A	p.P586T	0.155%	missense_variant
BCL6	c.1817C>A	p.T606N	0.184%	missense_variant
BCL6	c.2013C>A	p.S671R	0.130%	missense_variant
BCL6	c.2077G>A	p.V693M	0.184%	missense_variant
BCL6	c.1535G>A	p.S512N	27.077%	missense_variant
BCL6	c.1436G>A	p.G479D	0.119%	missense_variant
BCL6	c.89T>C	p.I30T	0.142%	missense_variant
BCL6	c.587C>A	p.S196Y	0.136%	missense_variant
TNFAIP3	c.2102G>A	p.R701H	7.000%	missense_variant
NOTCH1	c.926G>A	p.G309D	0.169%	missense_variant
NOTCH1	c.665G>A	p.C222Y	0.104%	missense_variant
NOTCH1	c.5776C>A	p.R1926S	0.106%	missense_variant
NOTCH1	c.6313A>G	p.M2105V	0.107%	missense_variant
NOTCH1	c.214G>A	p.G72R	0.107%	missense_variant
NOTCH1	c.7585G>A	p.V2529I	0.107%	missense_variant
NOTCH1	c.493C>G	p.H165D	0.111%	missense_variant
NOTCH1	c.1862G>T	p.R621L	0.121%	missense_variant
NOTCH1	c.3583G>A	p.G1195R	8.700%	missense_variant
NOTCH1	c.3758G>A	p.C1253Y	9.035%	missense_variant
NOTCH1	c.3374C>T	p.A1125V	0.168%	missense_variant

NOTCH1	c.4144G>C	p.E1382Q	0.118%	missense_variant
NOTCH1	c.3289C>A	p.P1097T	0.105%	missense_variant
NOTCH1	c.2744C>T	p.P915L	11.227%	missense_variant
NOTCH1	c.2729A>G	p.D910G	0.115%	missense_variant
NOTCH1	c.5362G>A	p.G1788S	28.505%	missense_variant
NOTCH1	c.2002C>T	p.P668S	23.605%	missense_variant
STAT6	c.2024C>A	p.A675D	0.130%	missense_variant
STAT6	c.1904G>A	p.G635D	0.139%	missense_variant
STAT6	c.2182A>C	p.S728R	0.118%	missense_variant
STAT6	c.1801T>C	p.S601P	0.131%	missense_variant
STAT6	c.842A>C	p.Q281P	7.770%	missense_variant
KRAS	c.35G>A	p.G12D	5.753%	missense_variant
IKBKB	c.536G>C	p.C179S	0.126%	missense_variant
HRAS	c.319G>A	p.D107N	0.122%	missense_variant
HRAS	c.311A>G	p.K104R	0.126%	missense_variant
KRAS	c.260C>T	p.T87I	0.414%	missense_variant
KRAS	c.227A>G	p.E76G	0.226%	missense_variant
IKBKB	c.1121G>A	p.G374D	0.146%	missense_variant
KRAS	c.38G>A	p.G13D	14.129%	missense_variant
KRAS	c.255T>A	p.N85K	0.384%	missense_variant
MAP2K1	c.355C>T	p.H119Y	29.073%	missense_variant
MAP2K2	c.787G>A	p.G263R	0.112%	missense_variant

Ordered Assay
LymphoVista

Sample material
Tumor tissue: circulating / cell free tumor DNA (ctDNA)
Sample collection (gDNA): 01/Jan/2024
Sample collection (cfDNA): 01/Jan/2024
Sample received: at 14:00:00

Sender
Tumor Diagnostics Clinic
Main Street 1, 23456 Example Town, Country

Investigated regions
All investigated regions are available in Appendix 1.

DNA Isolation
Genomic (g) DNA and cell free (cf) DNA was isolated by Liqomics.

Sample quality
The material was suitable for analysis. 20 ng of cfDNA was used for analysis. Purity of cell-free (cf)DNA was estimated at 80%.

Library Preparation and NGS
A sequencing library with duplex unique molecular indices was prepared from the input cfDNA and / or the enzymatically fragmented gDNA. Libraries were sequenced on the Illumina MiSeq system by Liqomics.

Computational analysis
Trimmed reads were mapped to the human reference genome hg38 using the Burrows-Wheeler

Aligner (BWA). Subsequently, duplex-UMI filtering of the aligned sequences was conducted, followed by sequence quality control and filtering. Variants were annotated based on several internal as well as external databases. Minimal Residual Disease was assessed based on ctDNA molecule frequency using our in-house developed analysis pipeline.

Variant and MRD analysis
Only variants (SNVs/small indels) with a variant allele frequency (VAF) of ≥ 0.25% are reported. The sensitivity of variant detection is dependent on the cfDNA content of the supplied blood sample, the sample quality, and the sequencing depth. In this case, the average coverage of the targeted regions was 3158x, while the average duplex coverage of the targeted regions was 1391x. Similarly, MRD detection depends on the cfDNA content of the supplied blood sample, the sample quality, the sequencing depth and the number of variants that can be tracked for MRD detection. In this case 470 variants have been tracked for MRD with an average duplex coverage of 1244x. Please be aware that a germline origin of reported variants cannot be excluded, although germline controls have been analyzed and identified germline variants have been filtered prior to generating this report.

Additional Information
This test has been performed by Liqomics. Liqomics is a medical diagnostics lab. The test has been developed and validated as a laboratory-developed test (LDT). The limit of detection for MRD is 6.69×10^{-6}. Variants with a variant allele frequency (VAF) ≥ 0.5% are detected with a sensitivity of 94 %. The test has been performed in a controlled environment. Liqomics operates a quality management system.

Responsible for report:

Report preparation: Erika Mustermann **Approval:** Marita Musterfrau

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(Date, Signature) (Date, Signature)