FOUNDATIONONE®LIQUID CDx

PATIENT

TUMOR TYPE
Thyroid cancer (NOS)

REPORT DATE

COUNTRY CODE
FR

ORDERED TEST #

ABOUT THE TEST FoundationOne®Liquid CDx is a next generation sequencing (NGS) assay that identifies clinically relevant genomic alterations in circulating cell-free DNA.

PATIENT	PHYSICIAN	SPECIMEN
DISEASE Thyroid cancer (NOS)	ORDERING PHYSICIAN	SPECIMEN ID
NAME	MEDICAL FACILITY	SPECIMEN TYPE
DATE OF BIRTH	ADDITIONAL RECIPIENT	DATE OF COLLECTION
SEX	MEDICAL FACILITY ID	SPECIMEN RECEIVED
MEDICAL RECORD #	PATHOLOGIST	

Sample qualified for low depth of sequencing coverage. Sensitivity for detecting genomic alterations and signatures may be reduced and TMB may be underreported.

Genomic Signatures

Blood Tumor Mutational Burden - 4 Muts/Mb
Microsatellite status - MSI-High Not Detected
Tumor Fraction - Elevated Tumor Fraction Not Detected

Gene Alterations

For a complete list of the genes assayed, please refer to the Appendix.

BRAF V600E
IDH2 R140Q
NRAS Q61L
TERT promoter -124C>T
TP53 S215fs*32

Report Highlights

- Targeted therapies with **NCCN categories of evidence** in this tumor type: [redacted]
- Evidence-matched **clinical trial options** based on this patient's genomic findings: (p. 15)
- Variants with **prognostic implications** for this tumor type that may impact treatment decisions: ***BRAF* V600E** (p. 5), ***TERT* promoter -124C>T** (p. 7)
- Variants that may represent **clonal hematopoiesis** and may originate from non-tumor sources: ***IDH2* R140Q** (p. 6)

GENOMIC SIGNATURES	THERAPY AND CLINICAL TRIAL IMPLICATIONS
Blood Tumor Mutational Burden - 4 Muts/Mb	**No therapies or clinical trials.** See Genomic Signatures section
Microsatellite status - MSI-High Not Detected	**MSI-High not detected. No evidence of microsatellite instability in this sample (see Appendix section).**
Tumor Fraction - Elevated Tumor Fraction Not Detected	**Tumor fraction is considered elevated when ctDNA levels are high enough that aneuploidy can be detected. The fact that elevated tumor fraction was not detected in this specimen indicates the possibility of lower levels of ctDNA but does not compromise confidence in any reported alterations. However, in the setting of a negative liquid biopsy result, orthogonal testing of a tissue specimen should be considered if clinically indicated (see Genomic Signatures section).**

Electronically signed by Matthew Hiemenz, M.D. |
Roche Customer Care · www.rochefoundationmedicine.com

Sample Preparation: Foundation Medicine GmbH, Nonnenwald 2, 82377 Penzberg, Germany
Sample Analysis: Foundation Medicine GmbH, Nonnenwald 2, 82377 Penzberg, Germany

GENE ALTERATIONS		VAF %	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
BRAF -	V600E	19.7%	None	[redacted]
10 Trials see p. 15				
IDH2 -	R140Q	0.71%	None	None
1 Trial see p. 17				
NRAS -	Q61L	0.19%	None	None
10 Trials see p. 18				

VARIANTS THAT MAY REPRESENT CLONAL HEMATOPOIESIS (CH)

Genomic findings below may include nontumor somatic alterations, such as CH. The efficacy of targeting such nontumor somatic alterations is unknown. This content should be interpreted based on clinical context. Refer to appendix for additional information on CH.

IDH2 - R140Q ..... p. 6

GENE ALTERATIONS WITH NO REPORTABLE THERAPEUTIC OR CLINICAL TRIAL OPTIONS

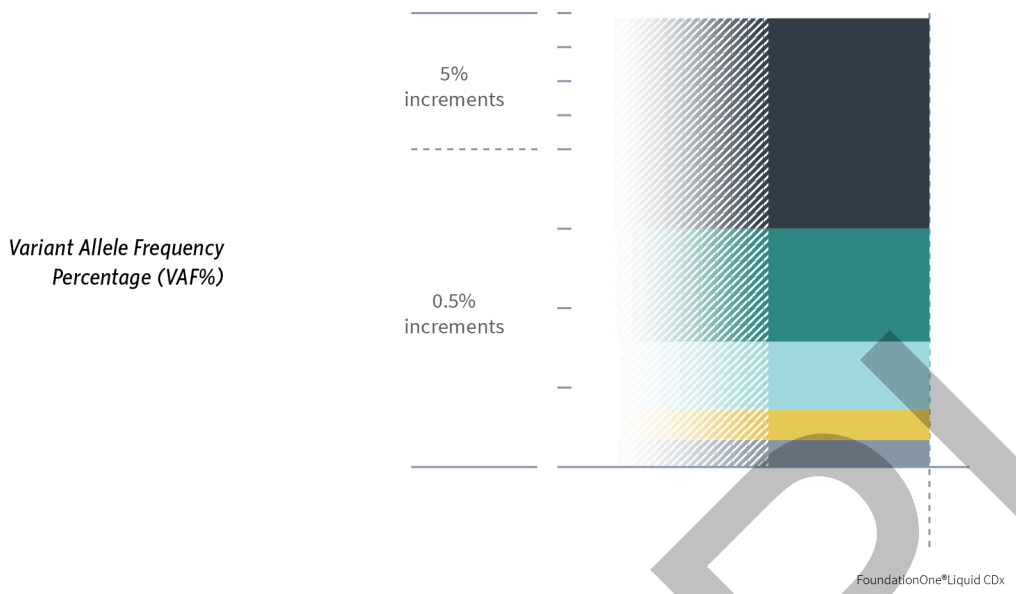
For more information regarding biological and clinical significance, including prognostic, diagnostic, germline, and potential chemosensitivity implications, see the Gene Alterations section.

TERT - promoter -124C>T ..... p. 7

TP53 - S215fs*32 ..... p. 8

NOTE Genomic alterations detected may be associated with activity of certain approved therapies; however, the therapies listed in this report may have varied clinical evidence in the patient's tumor type. Therapies and the clinical trials listed in this report may not be complete and/or exhaustive. Neither the therapies nor the trials identified are ranked in order of potential or predicted efficacy for this patient, nor are they ranked in order of level of evidence for this patient's tumor type. This report should be regarded and used as a supplementary source of information and not as the single basis for the making of a therapy decision. All treatment decisions remain the full and final responsibility of the treating physician and physicians should refer to approved prescribing information for all therapies. Therapies contained in this report may have been approved through a centralized EU procedure or a national procedure in an EU Member State. Therapies, including but not limited to the following, have been approved nationally in some EU Member States but may not be available in your Member State: Tretinoin, Anastrozole, Bicalutamide, Cyproterone, Exemestane, Flutamide, Goserelin, Letrozole, Leuprorelin, and Triptorelin. The Summary of Product Characteristics of EU-approved therapies are available at https://www.ema.europa.eu/en/medicines. The information available on EMA's website is updated in regular intervals but may not reflect the current status at any time. In the appropriate clinical context, germline testing of *APC*, *ATM*, *BAP1*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *FH*, *FLCN*, *MEN1*, *MLH1*, *MSH2*, *MSH6*, *MUTYH*, *NF1*, *NF2*, *PALB2*, *PMS2*, *POLE*, *PTEN*, *RAD51C*, *RAD51D*, *RB1*, *RET*, *SDHA*, *SDHB*, *SDHC*, *SDHD*, *SMAD4*, *STK11*, *TGFBR2*, *TP53*, *TSC1*, *TSC2*, *VHL*, and *WT1* is recommended.

Variant Allele Frequency is not applicable for copy number alterations.



HISTORIC PATIENT FINDINGS		VAF%
Blood Tumor Mutational Burden		4 Muts/Mb
Microsatellite status		MSI-High Not Detected
Tumor Fraction		Elevated Tumor Fraction Not Detected
BRAF	● V600E	19.7%
IDH2	● R140Q	0.71%
NRAS	● Q61L	0.19%
TERT	● promoter -124C>T	0.43%
TP53	● S215fs*32	0.17%

NOTE This comparison table refers only to genes and biomarkers assayed by prior FoundationOne®Liquid CDx or FoundationOne®CDx tests. Up to five previous tests may be shown.

For some genes in FoundationOne Liquid CDx, only select exons are assayed. Therefore, an alteration found by a previous test may not have been confirmed despite overlapping gene lists. Please refer to the Appendix for the complete list of genes and exons assayed. The gene and biomarker list will be updated periodically to reflect new knowledge about cancer biology.

As new scientific information becomes available, alterations that had previously been listed as Variants of Unknown Significance (VUS) may become reportable.

Tissue Tumor Mutational Burden (TMB) and blood TMB (bTMB) are estimated from the number of synonymous and non-synonymous single-nucleotide variants (SNVs) and insertions and deletions (indels) per area of coding genome sampled, after the removal of known and likely oncogenic driver events and germline SNPs. Tissue TMB is calculated based on variants with an allele frequency of ≥5%, and bTMB is calculated based on variants with an allele frequency of ≥0.5%.

Not Tested = not baited, not reported on test, or test preceded addition of biomarker or gene

Not Detected = baited but not detected on test

Detected = present (VAF% is not applicable)

VAF% = variant allele frequency percentage

Cannot Be Determined = Sample is not of sufficient data quality to confidently determine biomarker status

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