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CLIA #: 05D2111917 CAP #: 9441547

Hematology Profile Plus

Patient Name:		Ordering Physician:	M.D.
Date of Birth:		Physician ID:	
Gender (M/F):		Accession #:	
Client:		Specimen Type:	Tissue
		Specimen ID:	
Case #:	NGSXX-XXXXXX		
Body Site:	LYMPH NODE		

MRN:				Indication for Testing:	C84.41 Peripheral T-cell lymphoma, not elsewhere classified, lymph nodes of head, face, and neck
Collected Date:		Time:			
Received Date:		Time:			
Reported Date:		Time:			

Detected Genomic Alterations				
TERT	KMT2D	FGFR2	EPHA5	TET2
MTOR (2 mutations)	KMT2B	Autosomal chromosomal structural analysis shows low level: 6p+, +8	B cell clonality: Not detected	T cell clonality: Detected, biclonal (TRBV20-1 / TRAV16 / TRAV12-1)
t(6;7)(p25.3;q32.3) DUSP22::LINC-PINT fusion mRNA				

Results Summary

- **-Mutations in TERT, KMT2D, FGFR2, EPHA5, TET2, MTOR (2 mutations), and KMT2B genes**
  -Autosomal chromosomal structural analysis shows low level: 6p+, +8
  -t(6;7)(p25.3;q32.3) DUSP22::LINC-PINT fusion mRNA
  -B cell clonality: Not detected
  -T cell clonality: Detected, biclonal (TRBV20-1 / TRAV16 / TRAV12-1)
  -T cell markers: Increased with normal pattern
  -CD4 mRNA: Relatively increased
  -KI67 mRNA: Markedly increased
  -CD30 mRNA: Increased
  -ALK mRNA: Low level
  -EBV viral RNA: Not detected
  -HPV viral RNA: Not detected
  -TTV viral RNA: Not detected
  -HLA Genotyping:
  -HLA-A: A*01:01-A*24:02
  -HLA-B: B*15:17-B*27:05
  -HLA-C: C*07:01-C*07:02

-These findings are consistent with anaplastic large cell lymphoma (ALCL) with DUSP22 rearrangement.

Heterogeneity

There is an abnormal clone with TERT, KMT2D, FGFR2, EPHA5, TET2, MTOR (2 mutations), and KMT2B mutations.

Expression

T cell markers: Increased with normal pattern	CD4 mRNA: Relatively increased
KI67 mRNA: Markedly increased	CD30 mRNA: Increased
ALK mRNA: Low level	

Diagnostic Implications

TERT, KMT2D, FGFR2, EPHA5, TET2, MTOR (2 mutations), KMT2B	These findings are consistent with ALK-negative large T-cell lymphoma

Therapeutic Implications

FGFR2	FGFR inhibitors
EPHA5	EPHA5 inhibitors
TET2	DNA methyltransferase inhibitors
MTOR	MTOR inhibitors

Prognostic Implications

TERT	Unknown
KMT2D	Unknown
FGFR2	Poor
EPHA5	Poor
TET2	Neutral
MTOR	Poor
KMT2B	Unknown

Relevant Genes with NO Alteration

No evidence of mutation in: NOTCH, SF3B1, TP53, or MYD88

Test Description:

This is a comprehensive molecular profile which uses next generation sequencing (NGS), Sanger Sequencing and fragment length analysis testing to identify molecular abnormalities , including single nucleotide variants (SNVs), insertions/deletions (indels), copy number variants (CNVs), fusions, B- and T-cell clonality, IgVH mutation analysis and viruses (HPV, EBV, and TTV), in DNA of 284 genes and RNA in greater than 1600 genes associated with hematologic neoplasms, including leukemia, lymphoma, myeloma, myelodysplastic syndrome and myeloproliferative neoplasms. Whenever possible, clinical relevance and implications of detected abnormalities are described below.

Biological relevance of detected Alterations

- TERT. Telomerase is a ribonucleoprotein polymerase that maintains telomere ends by addition of the telomere repeat TTAGGG. The enzyme consists of a protein component with reverse transcriptase activity, encoded by this gene, and an RNA component which serves as a template for the telomere repeat. Telomerase expression plays a role in cellular senescence, as it is normally repressed in postnatal somatic cells resulting in progressive shortening of telomeres. Deregulation of telomerase expression in somatic cells may be involved in oncogenesis. Studies in mouse suggest that telomerase also participates in chromosomal repair, since de novo synthesis of telomere repeats may occur at double-stranded breaks. Alternatively spliced variants encoding different isoforms of telomerase reverse transcriptase have been identified; the full-length sequence of some variants has not been determined. Alternative splicing at this locus is thought to be one mechanism of regulation of telomerase activity. [provided by RefSeq, Jul 2008]

- KMT2D. The protein encoded by this gene is a histone methyltransferase that methylates the Lys-4 position of histone H3. The encoded proteir is part of a large protein complex called ASCOM, which has been shown to be a transcriptional regulator of the beta-globin and estrogen receptor genes. Mutations in this gene have been shown to be a cause of Kabuki syndrome. [provided by RefSeq, Oct 2010]

- FGFR2. The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein consists of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member is a high-affinity receptor for acidic, basic and/or keratinocyte growth factor, depending on the isoform. Mutations in this gene are associated with Crouzon syndrome, Pfeiffer syndrome, Craniosynostosis, Apert syndrome, Jackson-Weiss syndrome, Beare-Stevenson cutis gyrata syndrome, Saethre-Chotzen syndrome, and syndromic craniosynostosis. Multiple alternatively spliced transcript variants encoding different isoforms have been noted for this gene. [provided by RefSeq, Jan 2009]

- EPHA5. This gene belongs to the ephrin receptor subfamily of the protein-tyrosine kinase family. EPH and EPH-related receptors have been implicated in mediating developmental events, particularly in the nervous system. Receptors in the EPH subfamily typically have a single kinase domain and an extracellular region containing a Cys-rich domain and 2 fibronectin type III repeats. The ephrin receptors are divided into 2 groups based on the similarity of their extracellular domain sequences and their affinities for binding ephrin-A and ephrin-B ligands. Alternatively spliced transcript variants encoding different isoforms have been described. [provided by RefSeq, Aug 2013]

- TET2. The protein encoded by this gene is a methylcytosine dioxygenase that catalyzes the conversion of methylcytosine to 5-hydroxymethylcytosine. The encoded protein is involved in myelopoiesis, and defects in this gene have been associated with several myeloproliferative disorders. Two variants encoding different isoforms have been found for this gene. [provided by RefSeq, Mar 2011]

- MTOR. The protein encoded by this gene belongs to a family of phosphatidylinositol kinase-related kinases. These kinases mediate cellular responses to stresses such as DNA damage and nutrient deprivation. This kinase is a component of two distinct complexes, mTORC1, which controls protein synthesis, cell growth and proliferation, and mTORC2, which is a regulator of the actin cytoskeleton, and promotes cell survival and cell cycle progression. This protein acts as the target for the cell-cycle arrest and immunosuppressive effects of the FKBP12-rapamycin complex. Inhibitors of mTOR are used in organ transplants as immunosuppressants, and are being evaluated for their therapeutic potential in SARS-CoV-2 infections. Mutations in this gene are associated with Smith-Kingsmore syndrome and somatic focal cortical dysplasia type II. The ANGPTL7 gene is located in an intron of this gene. [provided by RefSeq, Aug 2020]

- KMT2B. This gene encodes a protein which contains multiple domains including a CXXC zinc finger, three PHD zinc fingers, two FY-rich domains, and a SET (suppressor of variegation, enhancer of zeste, and trithorax) domain. The SET domain is a conserved C-terminal domain that characterizes proteins of the MLL (mixed-lineage leukemia) family. This gene is ubiquitously expressed in adult tissues. It is also amplified in solid tumor cell lines, and may be involved in human cancer. Two alternatively spliced transcript variants encoding distinct isoforms have been reported for this gene, however, the full length nature of the shorter transcript is not known. [provided by RefSeq, Jul 2008]

Drug Information

Futibatinib

Futibatinib is an orally bioavailable inhibitor of the fibroblast growth factor receptor (FGFR) with potential antineoplastic activity. Futibatinib selectively and irreversibly binds to and inhibits FGFR, which may result in the nhibition of both the FGFR-mediated signal transduction pathway and tumor cell proliferation, and increased cell death in FGFR-overexpressing tumor cells.

Infigratinib

Infigratinib is an orally bioavailable pan inhibitor of human fibroblast growth factor receptors (FGFRs) with potential antiangiogenic and antineoplastic activities. Infigratinib selectively binds to and inhibits the activities of FGFRs, which may result in the inhibition of tumor angiogenesis and tumor cell proliferation, and the induction of tumor cell death. FGFRs are a family of receptor tyrosine kinases which may be upregulated in various tumor cell types and may be involved in tumor cell differentiation and proliferation, tumor angiogenesis, and tumor cell survival.

Pemigatinib

Pemigatinib is an orally bioavailable inhibitor of the fibroblast growth factor receptor (FGFR) types 1, 2, and 3 (FGFR1/2/3), with potential antineoplastic activity. Pemigatinib binds to and inhibits FGFR1/2/3, which may result in the inhibition of FGFR1/2/3-related signal transduction pathways. This inhibits proliferation in FGFR1/2/3-overexpressing tumor cells. FGFR, a family of receptor tyrosine kinases upregulated in many tumor cell types, plays a key role in cellular proliferation, migration, and survival.

Vandetanib

Vandetanib is a potent and selective inhibitor of VEGFR (vascular endothelial growth factor receptor), EGFR (epidermal growth factor receptor) and RET (REarranged during Transfection) tyrosine kinases.
VEGFR- and EGFR-dependent signalling are both clinically validated pathways in cancer, including non-small-cell lung cancer (NSCLC). RET activity is important in some types of thyroid cancer, and early data with vandetanib in medullary thyroid cancer has led to orphan-drug designation by the regulatory authorities in the USA and EU.

Vandetanib is indicated for:

-Metastatic Medullary Thyroid Cancer
-Locally advanced Medullary thyroid cancer

On April 6 2011, vandetanib was approved by the FDA to treat nonresectable, locally advanced, or metastatic medullary thyroid cancer in adult patients.

Azacitidine

Azacitidine is a pyrimidine analogue that inhibits DNA methyltransferase, impairing DNA methylation. It is also an antimetabolite of cytidine, incorporated primarily into RNA. Azacytidine has been used as an antineoplastic agent.

Azacitidine for injection is a nucleoside metabolic inhibitor indicated for the treatment of patients with the following French-American-British (FAB) myelodysplastic syndrome (MDS) subtypes: Refractory anemia (RA) or refractory anemia with ringed sideroblasts (RARS) (if accompanied by neutropenia or thrombocytopenia or requiring transfusions), refractory anemia with excess blasts (RAEB), refractory anemia with excess blasts in transformation (RAEB-T), and chronic myelomonocytic leukemia (CMMoL).

Decitabine

Decitabine is a cytidine antimetabolite analogue with potential antineoplastic activity. Decitabine incorporates into DNA and inhibits DNA methyltransferase, resulting in hypomethylation of DNA and intra-S-phase arrest of DNA replication.

Decitabine for injection is indicated for treatment of adult patients with myelodysplastic syndromes (MDS) including previously treated and untreated, de novo and secondary MDS of all French-American-British subtypes (refractory anemia, refractory anemia with ringed sideroblasts, refractory anemia with excess blasts, refractory anemia with excess blasts in transformation, and chronic myelomonocytic leukemia) and intermediate-1, intermediate-2, and high-risk International Prognostic Scoring System groups.

Decitabine also has EU approval for acute myeloid leukemia (AML).

Everolimus

Everolimus is a derivative of Rapamycin (sirolimus), and works similarly to Rapamycin as an mTOR (mammalian target of rapamycin) inhibitor. In a similar fashion to other mTOR inhibitors Everolimus' effect is solely on the mTORC1 protein and not on the mTORC2 protein.

Everolimus is a mTOR inhibitor that binds with high affinity to the FK506 binding protein-12 (FKBP-12), thereby forming a drug complex that inhibits the activation of mTOR. This inhibition reduces the activity of effectors downstream, which leads to a blockage in the progression of cells from G1 into S phase, and subsequently inducing cell growth arrest and apoptosis. Everolimus also inhibits the expression of hypoxia-inducible factor, leading to a decrease in the expression of vascular endothelial growth factor. The result of everolimus inhibition of mTOR is a reduction in cell proliferation, angiogenesis, and glucose uptake.

Everolimus is indicated for the treatment of:

Heart Transplant Rejection
Kidney Transplant Rejection
Liver Transplant Rejection
Renal angiomyolipoma, tuberous sclerosis complex
Subependymal giant cell astrocytoma, tuberous sclerosis complex
Advanced Carcinoid tumor
Locally advanced gastrointestinal origin Progressive Neuroendocrine Tumors
Locally advanced lung origin Progressive Neuroendocrine Tumors
Metastatic gastrointestinal origin Progressive Neuroendocrine Tumors
Metastatic lung origin Progressive Neuroendocrine Tumors
Pancreatic origin Progressive Neuroendocrine Tumors
Refractory Advanced Renal Cell Carcinoma
Refractory Waldenstrom's Macroglobulinaemia
Refractory, advanced Breast cancer
Unresectable gastrointestinal origin Progressive Neuroendocrine Tumors
Unresectable lung origin Progressive Neuroendocrine Tumors

Temsirolimus

Temsirolimus is an inhibitor of mTOR (mammalian target of rapamycin). Temsirolimus binds to an intracellular protein (FKBP-12), and the protein-drug complex inhibits the activity of mTOR that controls cell division. Inhibition of mTOR activity resulted in a G1 growth arrest in treated tumor cells. When mTOR was inhibited, its ability to phosphorylate p70S6k and S6 ribosomal protein, which are downstream of mTOR in the PI3 kinase/AKT pathway was blocked. In in vitro studies using renal cell carcinoma cell lines, temsirolimus inhibited the activity of mTOR and resulted in reduced levels of the hypoxia-inducible factors HIF-1 and HIF-2 alpha, and the vascular endothelial growth factor.

Temsirolimus is indicated for the treatment of renal cell carcinoma (RCC). Also investigated for use/treatment in breast cancer, lymphoma (unspecified), rheumatoid arthritis, and multiple myeloma.

Potential Clinical Trials

Trial URL	Status	Title	Disease	Drug	Sites
https://classic.clinicaltrials.gov/show/NCT04045470	Recruiting	A Pilot of a Microdevice For In Situ Candidate Drug Screening in Cutaneous Lesions of T-Cell Lymphoma	Cutaneous T Cell Lymphoma	Microdevices Standard of care therapy Standard of care systemic therapy	Dana Farber Cancer Institute, Boston, Massachusetts, United States
https://classic.clinicaltrials.gov/show/NCT03932279	Recruiting	Characterization of the Microbiome in Cutaneous T Cell Lymphoma	Cutaneous T Cell Lymphoma		Northwestern University, Chicago, Illinois, United States
https://classic.clinicaltrials.gov/show/NCT05569057	Recruiting	A Phase I Trial of SIM1811-03 in Subjects With Advanced Solid Tumors and Cutaneous T-cell Lymphoma	Cutaneous T Cell Lymphoma	SIM1811-03	Henry Ford Health, Detroit, Michigan, United States NYU Lagone Health, New York, New York, United States Icahn School of Medicine at Mount Sinai, New York, New York, United States

https://classic.clinicaltrials.gov/show/NCT05296304	Recruiting	A Study of Bexarotene Combined With Radiotherapy in People With Mycosis Fungoides	Cutaneous T-cell Lymphoma	Bexarotene Total Skin Electron Beam (TSEB)	Memorial Sloan Kettering Cancer Center (All Protocol Activities), New York, New York, United States
https://classic.clinicaltrials.gov/show/NCT05414500	Recruiting	Mogamulizumab and Brentuximab Vedotin in CTCL and Mycosis Fungoides	Cutaneous T Cell Lymphoma	Mogamulizumab Brentuximab vedotin	University of Alabama at Birmingham, Birmingham, Alabama, United States

Detailed Results

Single Nucleotide Variant (SNV) and Insertions-Deletions (INDELS)

Gene name	Hgvsp	Hgvsc	Amino acids	Codons	Consequence	Allele frequency	Read depth	Predicted effect on protein
TERT	NP_937983.2:p.Arg72Cys	NM_198253.2:c.214C>T	R/C	Cgc/Tgc	missense_variant	21.99	623	tolerated (0.2)
KMT2D	NP_003473.3:p.Gln3736Ter	NM_003482.3:c.11206C>T	Q/*	Cag/Tag	stop_gained	19.75	1023	0
FGFR2	NP_075259.4:p.Glu466Lys	NM_022970.3:c.1396G>A	E/K	Gag/Aag	missense_variant	18.49	806	deleterious (0.01)
EPHA5	NP_004430.4:p.Pro416Ser	NM_004439.5:c.1246C>T	P/S	Ccc/Tcc	missense_variant	17.3	1803	deleterious (0.01)
TET2	NP_001120680.1:p.Gln1030Ter	NM_001127208.2:c.3088C>T	Q/*	Cag/Tag	stop_gained	17.16	1037	0
MTOR	NP_004949.1:p.Met2327Ile	NM_004958.3:c.6981G>A	M/I	atG/atA	missense_variant	7.19	487	deleterious (0)
MTOR	NP_004949.1:p.Tyr1974His	NM_004958.3:c.5920T>C	Y/H	Tac/Cac	missense_variant	1.94	720	deleterious (0)
KMT2B	NP_055542.1:p.Lys553AsnfsTer52	NM_014727.1:c.1656delC	D/X	gaC/ga	frameshift_variant	1.4	570	0

Methodology and Test Background

This is a next generation sequencing (NGS) test that analyzes DNA of 284 genes and RNA of >1600 genes for abnormalities that are reported in various types of hematologic neoplasms. The assay also detects several viruses that are important in oncology, including EBV, HPV and TTV. TTV (torque teno virus) was first discovered in a patient with non-A-E hepatitis and is now regarded as a part of the human virome. In general, TTV does not cause pathology in immunocompetent individuals. TTV is considered as a marker of immune competence in patients with immunological impairment and inflammatory disorders. High TTV load is associated with increased risk of infection. In patients with organ transplant, low TTV load is associated with an increased risk of rejection.

Nucleic acid is isolated from fresh cells, peripheral blood cells, bone marrow, body fluid, or paraffin-embedded tissue. Performance of the assay may vary depending on the quantity and quality of nucleic acid, sample preparation and sample age. For optimal results, neoplastic cells should be >30% of the analyzed cells. Decalcified specimens have not been validated. For fresh bone marrow specimens with the clinical indication of myeloma, enrichment for CD138-positive cells may be performed using immunomagnetic positive selection and both the CD138-positive and CD138-negative cell fractions extracted for NGS testing and the findings integrated within the final report. Testing is performed using massive parallel sequencing of the coding DNA of the listed genes. This includes sequencing of all the exons as well as approximately 50 nucleotides at the 5' and 3' ends of each coding exon to detect splice site abnormalities. The TERT promoter region, including the hotspots at -124 and -146 bp, is also covered. Our DNA sequencing method has a sensitivity of 1% for detecting single nucleotide variants (SNVs) and small (<60 bp) insertions/ deletions (indels). Significant gene amplification and deletion (copy number variants) are also reported. In

addition, fragment length analysis is performed for CALR, FLT3, and NPM1 to enhance the detection of large indels and has a sensitivity of 2%-5% for detecting CALR, FLT3-ITD, and NPM1 indels in wildtype background. For cases with indication of acute myeloid leukemia, preliminary FLT3-ITD results based on fragment analysis will be reported. Targeted RNA NGS is performed by hybrid capture and duplicates are excluded for levels measurements. The Universal Human Reference (UHR) RNA is used as control. All detected fusion transcripts are reported. While the major focus of the RNA analysis is the detection of fusion mRNA, mutations in the expressed RNA of the analyzed genes, B- and T-cell clonality, HLA class I genotyping, and Epstein-Barr virus (EBV), human papillomavirus (HPV) and torque teno virus (TTV) viral RNA are also analyzed and reported. In cases of suspected chronic lymphocytic leukemia (CLL), IgVH mutation rate will also be reported. The sensitivity of this assay for detecting fusion mRNA is between 5% and 10%. This test specifically detects translocations that lead to the expression of fusion RNA. Translocations that lead to deregulation of expression can be addressed by this test if compared to the proper normal expression control. Since the clinical relevance of the RNA expression level of most of the genes is not well-characterized at this time, only a small subset of the genes may be described based on the suspected disease, including but not limited to MYC, BCL2, CD274, CD19, CD22, CD34, and CD138. CRLF2 mRNA levels are reported in acute lymphoblastic leukemia. CD274 (PD-L1) mRNA levels are reported when they are significantly elevated.

Based on our validation study, the following exonic regions of the genes listed below are not covered appropriately <100 X coverage and sequencing by NGS may not be reliable in these regions. The poor coverage is primarily due to the inherent difficulty in obtaining adequate sequencing coverage in regions with high GC content. No well-characterized hotspots are present in these regions. RAD51 NM_133487 chr15:40994004-40994124, BRCA1 NM_007300 chr17:41231351-41231416, FUBP1 NM_003902 chr1:78435609-78435699, CBLB NM_170662 chr3:105420938-105421303, TERT NM_198253 chr5:1295183-1295250, ARID1B NM_017519 chr6:157098715-157100605, CUX1 NM_001202543 chr7:101740644-101740781, KMT2C NM_170606 chr7:151891314-151891346 and 151935792-151935911, GALNT12 NM_024642 chr9:101569952-101570351, ATM NM_000051 chr11:108164040-108164204, CDK17 NM_001170464 chr12:96679880-96679926, RB1 NM_000321 chr13:48954189-48954220, SETBP1 NM_015559 chr18:42643044-42643692, KMT2B NM_014727 chr19:36208921-36209283, AR NM_000044 chrX:66764889-66766604, STAG2 NM_001042749 chrX:123200025-123200112.

The table below contains a partial list of the tested DNA genes. For a complete list, please go to: https://genomictestingcooperative.com/genomic-tests/gtc-hematology-profile-plus/ *(click the DNA tab)*

The table below contains a partial list of the tested RNA genes (Fusions/Expression). For a complete list, please go to: https://genomictestingcooperative.com/genomic-tests/gtc-hematology-profile-plus/ *(click the RNA tab)*

Tested genes

Genes Tested for Abnormalities in Coding Sequence												
ABL1	BCL2	CBL	CDKN2C	DICER1	FAS	IDH2	KMT2A	MEF2B	NSD1	PPM1D	SETD2	TERT
AKT1	BCL2L1	CBLB	CEBPA	DNMT3A	FBXW7	IGF1R	KMT2B	MPL	PALB2	PPP2R1A	SF3B1	TET2
AKT2	BCL6	CBLC	CHEK1	EP300	FLT3	IKZF1	KMT2C	MRE11A	PAX5	PTCH1	SMAD2	TGFBR2
AKT3	BCOR	CCND1	CHEK2	ERG	GATA1	IKZF3	KMT2D	MTOR	PBRM1	PTEN	SMAD4	TP53
ALK	BCORL1	CCND3	CIC	ETV6	GATA2	IRF4	KRAS	MUTYH	PDGFRA	PTPN11	SMARCA4	TSC1
AMER1	BCR	CD274	CREBBP	EZH2	GATA3	JAK1	MAP2K1	MYC	PDGFRB	RAD21	SMARCB1	TSC2
APC	BIRC3	CD79A	CRLF2	FAM175A	GEN1	JAK2	MAP2K2	MYD88	PHF6	RAD50	SMC1A	TSHR
ARID1A	BLM	CD79B	CSF1R	FAM46C	GNAQ	JAK3	MAP2K4	NFE2	PIK3CA	RAD51	SMO	U2AF1
ARID1B	BRAF	CDH1	CSF3R	FANCA	GNAS	KAT6A	MAP3K1	NFKBIA	PIK3R1	RB1	SOCS1	UBA1
ARID2	BRCA1	CDK12	CTNNA1	FANCC	H3F3A	KDM5C	MAP3K14	NOTCH1	PIK3R2	RHOA	SRC	WT1
ASXL1	BRCA2	CDK4	CTNNB1	FANCD2	HNF1A	KDM6A	MAPK1	NOTCH2	PIM1	RNF43	SRSF2	ZNF217
ATM	BTK	CDK6	CUX1	FANCE	HOXB13	KDR	MCL1	NOTCH3	PLCG1	RUNX1	STAG2	ZRSR2
ATRX	CALR	CDKN2A	CXCR4	FANCF	HSP90AA1	KEAP1	MDM2	NPM1	POLD1	SDHB	STAT3	-
B2M	CARD11	CDKN2B	DDR2	FANCG	IDH1	KIT	MDM4	NRAS	POLE	SETBP1	STK11	-

RNA Fusions/Expression

Fusion/Expression															
ABL1	ALK	BRAF	CREBBP	EPOR	ETV5	FGFR2	FOXO1	JAK2	MAP3K1	NOTCH1	NUP214	PCM1	PICALM	RET	RUNX1T1	TCF3
ABL2	BCL1	CBFB	CRLF2	ERG	ETV6	FGFR3	FUS	KMT2A	MECOM	NTRK1	NUP98	PDGFRA	PML	RHOA	SS18	TFG
AKT3	BCL2	CBL	CSF1R	ETV1	EWSR1	FIP1L1	GLI1	KRT18P6	MYC	NTRK2	P2RY8	PDGFRB	PTK2B	ROS2	STAT6	TYK2
ALK	BCL6	CIC	EGFR	ETV4	FGFR1	FLT3	IKZF3	LYN	MYH9	NTRK3	PBX1	PD-L1	RARA	RUNX1	TAL1	

Reference

1. T-cell Lymphoma Epidemiology: the Known and Unknown. Phan A, Veldman R, Lechowicz MJ. Phan A, et al. Curr Hematol Malig Rep. 2016 Dec;11(6):492-503. doi: 10.1007/s11899-016-0353-y. Curr Hematol Malig Rep. 2016. PMID: 27995419

2. T cell lymphoma: time to make discoveries and advance treatment. Ishitsuka K. Ishitsuka K. Int J Hematol. 2023 Apr;117(4):473-474. doi: 10.1007/s12185-023-03573-3. Epub 2023 Mar 14. Int J Hematol. 2023. PMID: 36918503

3. Emerging drugs for the treatment of cutaneous T-cell lymphoma. Cheng M, Zain J, Rosen ST, Querfeld C. Cheng M, et al. Expert Opin Emerg Drugs. 2022 Mar;27(1):45-54. doi: 10.1080/14728214.2022.2049233. Epub 2022 Mar 8. Expert Opin Emerg Drugs. 2022. PMID: 35235473

4. Targeting epigenetic regulators in the treatment of T-cell lymphoma. Ahmed N, Feldman AL. Ahmed N, et al. Expert Rev Hematol. 2020 Feb;13 (2):127-139. doi: 10.1080/17474086.2020.1711732. Epub 2020 Jan 22. Expert Rev Hematol. 2020. PMID: 31903826

Electronic Signature

Maher Albitar, M.D.

The test (sample processing, sequencing and data generation) was performed at Genomic Testing Cooperative, LCA, Genomic Testing Cooperative, LCA, 175 Technology Drive, Suite 100, Irvine, CA 92618. Medical Director Maher Albitar, M.D. Analysis of the data was performed by Genomic Testing Cooperative, LCA, 175 Technology Drive, Suite 100, Irvine, CA 92618. Medical Director: Maher Albitar, M.D.

The test was developed and its performance characteristics have been determined by Genomic Testing Cooperative, LCA. This test has not been approved by the FDA. The FDA has determined such clearance or approval is not necessary. This laboratory is CLIA certified to perform high complexity clinical testing.