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Patient Name: 안형준
Gender: M
Sample ID: N25-43

Primary Tumor Site: skin
Collection Date: 2025.5.26

Sample Cancer Type: Large B-Cell Lymphoma

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Report Highlights
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Relevant Biomarkers

No biomarkers associated with relevant evidence found in this sample

Prevalent cancer biomarkers without relevant evidence based on included data sources
ARID1A p.(Q1334del) c.3999_4001delGCA, MYC p.(E54D) c.162G>C

Variant Details

DNA Sequence Variants

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect
ARID1A	p.(Q1334del)	c.3999_4001delGCA	COSM298325	chr1:27100181	5.10%	NM_006015.6	nonframeshift Deletion
MYC	p.(E54D)	c.162G>C	.	chr8:128750625	40.54%	NM_002467.6	missense
TNFRSF14	p.(K17R)	c.50A>G	.	chr1:2488153	85.94%	NM_003820.3	missense
ID3	p.(T105A)	c.313A>G	.	chr1:23885498	99.80%	NM_002167.5	missense
ARID1A	p.(G864C)	c.2590G>T	.	chr1:27089634	4.26%	NM_006015.6	missense
TENT5C	p.(H67Q)	c.201C>G	.	chr1:118165691	86.32%	NM_017709.4	missense
BCL6	p.(?)	c.-66G>A	.	chr3:187463214	57.15%	NM_001706.5	unknown
TET2	p.(P29R)	c.86C>G	.	chr4:106155185	46.95%	NM_001127208.3	missense
CCND3	p.(S259A)	c.775T>G	.	chr6:41903782	90.63%	NM_001760.5	missense
NFKBIE	p.(V55A)	c.164T>C	.	chr6:44232920	99.90%	NM_004556.3	missense
NFKBIE	p.(P36L)	c.107C>T	.	chr6:44232977	99.85%	NM_004556.3	missense
TNFAIP3	p.(P714S)	c.2140C>T	.	chr6:138202223	13.83%	NM_001270507.2	missense
MYC	p.(V20F)	c.58G>T	.	chr8:128750521	38.15%	NM_002467.6	missense
MYC	p.(S21R)	c.63C>G	.	chr8:128750526	38.47%	NM_002467.6	missense
MYC	p.(Q51P)	c.152A>C	.	chr8:128750615	41.44%	NM_002467.6	missense

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect
MYC	p.(E62D)	c.186G>C	.	chr8:128750649	40.37%	NM_002467.6	missense
MYC	p.(E69D)	c.207G>C	.	chr8:128750670	40.42%	NM_002467.6	missense
MYC	p.(T73S)	c.217A>T	.	chr8:128750680	41.04%	NM_002467.6	missense
MYC	p.(G104A)	c.311G>C	.	chr8:128750774	48.90%	NM_002467.6	missense
MYC	p.(Q113H)	c.339G>C	.	chr8:128750802	39.20%	NM_002467.6	missense
MYC	p.(E119D)	c.357G>C	.	chr8:128750820	21.65%	NM_002467.6	missense
MYC	p.(G123A)	c.368G>C	.	chr8:128750831	31.88%	NM_002467.6	missense
MYC	p.(F139V)	c.415T>G	.	chr8:128750878	27.70%	NM_002467.6	missense
MYC	p.(A155_S161dup)	c.462_482dup	.	chr8:128750920	12.28%	NM_002467.6	nonframeshift Insertion
MYC	p.(K172_P177del)	c.516_533delAGACAG CGGCAGCCCGAA	.	chr8:128750976	27.18%	NM_002467.6	nonframeshift Deletion
MYC	p.(C186Y)	c.557G>A	.	chr8:128751020	26.33%	NM_002467.6	missense
MYC	p.(S249T)	c.746G>C	.	chr8:128751209	4.32%	NM_002467.6	missense
MYC	p.(S264N)	c.791G>A	.	chr8:128751254	37.31%	NM_002467.6	missense
KLLN	p.(?)	c.-1616AG>G	.	chr10:89623860	99.95%	NM_001126049.2	unknown
PTEN	p.(?)	c.-367CT>C	.	chr10:89623860	99.95%	NM_000314.8	unknown
KLLN	p.(?)	c.-1657C>G	.	chr10:89623901	100.00%	NM_001126049.2	unknown
PTEN	p.(?)	c.-326G>C	.	chr10:89623901	100.00%	NM_000314.8	unknown
ATM	p.(N1983S)	c.5948A>G	.	chr11:108183167	99.60%	NM_000051.4	missense
KMT2D	p.(L3367F)	c.10101G>C	.	chr12:49431038	37.07%	NM_003482.4	missense
KMT2D	p.(A476T)	c.1426G>A	.	chr12:49446040	3.20%	NM_003482.4	missense
DIS3	p.(N269S)	c.806A>G	.	chr13:73350079	99.70%	NM_014953.5	missense
TP53	p.(P72R)	c.215C>G	.	chr17:7579472	83.00%	NM_000546.6	missense

Biomarker Descriptions

MYC p.(E54D) c.162G>C

MYC proto-oncogene, bHLH transcription factor

Background: The MYC gene encodes the MYC proto-oncogene (c-MYC), a basic helix-loop-helix transcription factor that regulates the expression of numerous genes that control cell cycle progression, apoptosis, metabolic pathways, and cellular transformation[1,2,3,4]. MYC is part of the MYC oncogene family that includes related transcription factors MYCN and MYCL that regulate transcription in 10-15% of promoter regions[5]. MYC functions as a heterodimer in complex with the transcription factor MAX[2,6].

Alterations and prevalence: Recurrent somatic alterations are observed in both solid and hematological cancers. Recurrent somatic mutations in MYC, including codon T58, are infrequent and hypothesized to increase the stability of the MYC protein[7,8]. MYC gene amplification is particularly common in diverse solid tumors. MYC amplification is observed in 30% of serous ovarian cancer, 20% of uterine serous carcinoma, 15% of esophageal and breast cancers, and is common (1-10%) in numerous other cancer types[9,10,11]. MYC

Biomarker Descriptions (continued)

is the target of the t(8;14)(q24;32) chromosomal translocation in Burkitt's lymphoma that places MYC coding sequences adjacent to immunoglobulin region regulatory sequences, which results in increased MYC expression[12,13].

Potential relevance: B-cell lymphoma with MYC translocations that co-occur with BCL2 or BCL6 are referred to as double hit lymphoma, while co-occurrence with BCL2 and BCL6 rearrangements is referred to as triple-hit lymphoma[14,15]. MYC translocations are also indicative of high risk for multiple myeloma and is associated with poor risk in acute lymphoblastic leukemia[16,17]. Currently, no therapies are approved for MYC aberrations. Due to the high frequency of somatic MYC alterations in cancer, many approaches are being investigated in clinical trials including strategies to disrupt complex formation with MAX, including inhibition of MYC expression and synthetic lethality associated with MYC overexpression[1,18,19,20].

ARID1A p.(Q1334del) c.3999_4001delGCA

AT-rich interaction domain 1A

Background: The ARID1A gene encodes the AT-rich interaction domain 1A tumor suppressor protein[21]. ARID1A, also known as BAF250A, belongs to the ARID1 subfamily that also includes AR1D1B[21,22]. ARID1A and ARID1B are mutually exclusive subunits of the BAF variant of the SWI/SNF chromatin-remodeling complex[22,23]. The BAF complex is a multisubunit protein that consists of SMARCB1/IN1, SMARCC1/BAF155, SMARCC2/BAF170, SMARCA4/BRG1 or SMARCA2/BRM, and ARID1A or ARID1B[23]. The BAF complex remodels chromatin at promoter and enhancer elements to alter and regulate gene expression[23,24]. ARID1A binds to transcription factors and coactivator/corepressor complexes to alter transcription[22]. Recurrent inactivating mutations in BAF complex subunits, including ARID1A, lead to transcriptional dysfunction thereby, altering its tumor suppressor function[22].

Alterations and prevalence: Mutations in SWI/SNF complex subunits are the most commonly mutated chromatin modulators in cancer and have been observed in 20% of all tumors[24]. The majority of ARID1A inactivating mutations are nonsense or frameshift mutations[22]. Somatic mutations in ARID1A have been identified in 50% of ovarian clear cell carcinoma, 30% of endometrioid carcinoma, and 24-43% of uterine corpus endometrial carcinoma, bladder urothelial carcinoma, and stomach adenocarcinoma[11,23,25]. In microsatellite stable (MSS) colorectal cancer, mutations in ARID1A have been observed to correlate with increased tumor mutational burden (TMB) and expression of genes involved in the immune response[26].

Potential relevance: Currently, no therapies are approved for ARID1A aberrations. However, the FDA has granted fast track designation (2022) to HSF1 pathway inhibitor, NXP-800[27], for the treatment of platinum resistant ARID1A-mutated ovarian carcinoma. Tulmimetostat[28], dual inhibitor of EZH2 and EZH1, was also granted a fast track designation (2023) for the treatment of patients with advanced, recurrent or metastatic endometrial cancer harboring ARID1A mutations and who have progressed on at least one prior line of treatment.

Genes Assayed

Genes Assayed for the Detection of DNA Sequence Variants

BRAF, BTK, CARD11, GNA13, HIST1H1E, MTOR, SF3B1, XPO1

Genes Assayed for the Detection of Copy Number Variations

BRAF, CARD11, GNA13, HIST1H1E, MTOR, SF3B1, XPO1

Genes Assayed with Full Exon Coverage

ARID1A, ATM, B2M, BCL2, BCL6, CD79B, CDKN2A, CREBBP, EZH2, KMT2D, MYC, MYD88, PIM1, SOCS1, TNFAIP3, TNFRSF14, TP53

Thermo Fisher Scientific's Ion Torrent Oncomine Reporter software was used in generation of this report. Software was developed and designed internally by Thermo Fisher Scientific. The analysis was based on Oncomine Reporter (6.0.2 data version 2025.04(004)). The data presented here are from a curated knowledge base of publicly available information, but may not be exhaustive. FDA information was sourced from www.fda.gov and is current as of 2025-03-19. NCCN information was sourced from www.nccn.org and is current as of 2025-03-03. EMA information was sourced from www.ema.europa.eu and is current as of 2025-03-19. ESMO information was sourced from www.esmo.org and is current as of 2025-03-03. Clinical Trials information is current as of 2025-03-03. For the most up-to-date information regarding a particular trial, search www.clinicaltrials.gov by NCT ID or search local clinical trials authority website by local identifier listed in 'Other identifiers.' Variants are reported according to HGVS nomenclature and classified following AMP/ASCO/CAP guidelines (Li et al. 2017). Based on the data sources selected, variants, therapies, and trials listed in this report are listed in order of potential clinical significance but not for predicted efficacy of the therapies.

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