Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**< BONE MARROW REPORT>**

Case number: BM2020-001
Clinical information (diagnosis & relevant therapy): Leukemic blasts on peripheral blood
Specimen type: PB ( V )/Aspirate ( V )/Biopsy ( V )
Site: Post. iliac creast ( V )/Others ( )
Both ( )/Left ( )/Right ( V )/ NA ( )

<DIAGNOSIS>

Acute myeloid leukemia, PML-RARA, microgranular (hypogranular) variant
REC> NGS

<PERIPHERAL BLOOD FINDINGS>
Hb-WBC-PLT-Retic-RDW: 8.2g/dL-12,080/μL-34,000/μL-2.3%-15.6%
RBC: Normocytic-Normochromic-Anisocytosis(+)-Poikilocytosis(-)
WBC: Increased in number-Left shifted maturation-Blasts(70%) with bilobed nucleus-ANC(1,700/μL)
PLT: Decreased in number

<BONE MARROW DIFFERENTIAL COUNT>

| | | | |
|---|---|---|---|
| Blast | 70.8% | Pronormoblast | 1.2% |
| Promyelocyte | 2.2% | Baso. Normoblast | 2.4% |
| Myelocyte | 5.2% | Poly. Normoblast | 1.2% |
| Metamyelocyte | 4.6% | Ortho. Normoblast | 0.6% |
| Band Neutrophil | 1.2% | Lymphocyte | 6.0% |
| Seg. Neutrophil | 2.4% | Monocyte | 1.6% |
| Eosinophil | 0.4% | Plasma cell | 0.1% |
| Basophil | 0.1% | Histiocyte | |
| M:E ratio | 16.7:1 | | |

<BONE MARROW ASPIRATION FINDINGS>
Adequacy: Adequate
Erythropoiesis: Decreased in number-Dyserythropoiesis(-)
Myelopoiesis: Increased in number-Left shifted maturation-Blasts (70.8%)-Dysgranulopoiesis(-)
Megakaryopoiesis: Decreased in number-Dysplasia(-)
Lymphocytes: Decreased in number
Plasma cells: 0.1%
Abnormal cells: Negative except leukemic blasts with bilobed nuclues
Dysplasia (-)

<BIOPSY SECTION FINDINGS>
Adequacy : Adequate
Cellularity: Hypercellular (100%)
Erythropoiesis: Decreased in number
Myelopoieis: Increased in number-Left shifted maturation-Increased blasts-
Megakaryopoiesis: Decreased in number-Dysplasia(-)
Lymphocytes, Plasma cells, Abnormal cells: not remarkable

<CLOT SECTION>
: Not done

<SPECIAL STUDIES>
Cytochemistry **:** Iron stain: Storage(Grade 3-4 /Grade 6), Sideroblasts (-)-Ringed sideroblasts (-)
Peroxidase: Positive
PAS: Negative
ANAE: Negative
Immunohistochemistry: MPO+, CD3-, cCD79a-
Immunophenotyping: CD34+, CD33+, HLA-DR+, CD64+, CD13+, CD64+, cMPO+, CD117+
Cytogenetics: 46,XX,t(15;17)(q22;q12)[19]/46,XX[1], FISH,PML/RARA: Detected [88%]
Molecular genetics: *PML/RARA* gene rearrangement: Detected

<PREVIOUS BM STUDIES>
None

<COMMENTS>
None

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 1. Sample bone marrow report for a patient diagnosed with acute myeloid leukemia, *PML-RARA* according to consensus guidelines.

Medical department: MH
Requesting physician: OOO
Sample ID: 7654321
Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<Leukemia/Lymphoma Flow Cytometric Immunophenotyping Report>**

Case number: IP-001
Clinical information (diagnosis & relevant therapy): Leukemic blasts on bone marrow
Sample type (BM, PB): Bone marrow  Sample description (quality) (Viability, if tested): Moderate

<RESULT>

Consistent with B-lymphoblastic leukemia

| Antibodies used (CDs) | Fluorescence distribution | Fluorescence intensity | Antibodies used (CDs) | Fluorescence distribution | Fluorescence intensity |
|---|---|---|---|---|---|
| CD2 | negative | | CD3 | negative | |
| CD5 | negative | | CD7 | negative | |
| CD10 | positive | bright | CD19 | positive | moderate |
| CD20 | negative | | CD34 | positive | moderate |
| CD38 | positive | dim | CD13 | negative | |
| CD33 | partially expressed | dim | CD117 | negative | |
| HLA-DR | positive | bright | TdT | positive | moderate |
| cytCD3 | negative | | cytCD22 | positive | moderate |
| cytCD79a | positive | moderate | Myeloperoxidase | negative | |

A population of blasts with dim CD45 expression and low SSC is identified, which comprises approximately 80% of cells in the specimen. The blasts are positive for HLA-DR, CD10, CD38, TdT, the progenitor cell antigen, CD34, B-lineage antigens, CD19, cytCD79a and cytCD22 and myeloid antigen, CD33 (dim, partial). All the other myeloid and T-lineage antigens tested are negative. This result is consistent with B-lymphoblastic leukemia.

<PREVIOUS FLOW CYTOMETRY STUDIES>
None

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 2. Sample leukemia/lymphoma flow cytometric immunophenotyping report for a patient diagnosed with B-lymphoblastic leukemia according to consensus guidelines.


https://doi.org/10.47429/lmo.2021.11.1.1

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<Minimal residual disease (flow cytometric analysis) report>**

Case number: MRD-001
Clinical information (diagnosis & relevant therapy): Known B-ALL
Sample type (BM, PB): Bone marrow Sample description (quality) (Viability, if tested): Poor, Clot

<RESULT>

| MRD positive, abnormal immature B-cell population identified (see comment) |
|---|

<Comment>
The abnormal immature B-cells represent 0.XXX% of total nucleated cells, consistent with residual B-lymphoblastic leukemia.
Immunophenotype of Abnormal B lineage blasts:
Positive for: CD19, CD10, CD34, CD38, CD81, CD66c/CD123, CD45
Negative for CD20, CD73

<Method>
Markers performed: CD81, CD73, CD66c/CD123, CD34, CD19, CD10, CD20, CD38, CD45
Total number of events analyzed: 0,000,000
Limit of detection: 0.000%
Lower limit of quantification: 0.000%

<PREVIOUS FLOW CYTOMETRY STUDIES>
2019.12.19. IP-001 B-lymphoblastic leukemia (aberrant CD33+)

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 3. Sample minimal residual disease flow cytometric immunophenotyping report for a patient receiving follow up care for B-lymphoblastic leukemia, according to consensus guidelines.

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<Chromosome analysis report>**

Case number: CHR-001
Clinical information (diagnosis & relevant therapy): R/O Acute leukemia
Sample type (BM, PB): Bone marrow Sample description (quality) (Viability, if tested): Adequate

<RESULT>

Karyotype: 46,XY,t(15;17)(q24;q22)[16]/46,XY[4]

<INTERPRETATION>
Chromosome analysis using bone marrow aspirate revealed t(15;17) aberration in 16 cells among 20 metaphase cells analyzed. The remaining 4 metaphase cells showed a normal karyotype.
The t(15;17) chromosomal abnormality is known to be associated with PML-RARA rearrangement, which shows good prognosis in acute promyelocytic leukemia.

<RECOMMENDATION>
PML-RARA RT-PCR (qualitative/quantitative)

<LIMITATION OF TEST>
The submicroscopic or genetic aberrations can't be identified by this test. If the specimen would include cancer cells with low mitotic activity in vitro, only normal cells with a normal karyotype can be observed.

<METHOD>
Quality of specimen: Adequate Culture method: unstimulated 24 hour & 48 hour culture
Stain method: G-Banding Resolution: 400 band (not mandatory in hematologic malignancy)
Number of analyzed cells: 20 Number of karyotyped cells: 2

<PREVIOUS RESULT>
None

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 4. Sample chromosome analysis report for a patient diagnosed with acute myeloid leukemia, *PML-RARA* according to consensus guidelines.


https://doi.org/10.47429/lmo.2021.11.1.1

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<FISH report>**

Case number: FIS-001
Clinical information (diagnosis & relevant therapy): R/O Acute leukemia
Sample type (BM, PB): Bone marrow Sample description (quality) (Viability, if tested): Adequate

<RESULT>

As a result of interphase FISH using 8 probes, *KMT2A* rearrangement was found in 78% of interphase cells

<RESULT IN DETAIL>
RESULT I

| Probe | % (number) of Positive cells | Decision | Cut-off |
|---|---|---|---|
| 1) BCR-ABL1 | 0.0% ( 0/200) | Normal | 1.5% |
| 2) RUNX1-RUNX1T1 | 0.0% ( 0/200) | Normal | 1.5% |
| 3) PML-RARA | 0.0% ( 0/200) | Normal | 1.5% |
| 4) CBFB | 0.0% ( 0/200) | Normal | 1.5% |
| 5) KMT2A | 78.0% (156/200) | Abnormal | 1.5% |
| 6) EGR1/D5S721, D5S23 | 0.0% ( 0/200) | Normal | 3.8% |
| 7) D7S486/CEP7 | 0.5% ( 1/200) | Normal | 3.0% |
| 8) TP53/CEP17 | 1.0% ( 2/200) | Normal | 5.0% |

RESULT II (ISCN 2016 Nomenclature)
nuc ish(ABL1,BCR)x2[200]
nuc ish(RUNX1T1,RUNX1)x2[200]
nuc ish(PML,RARA)x2[200]
nuc ish(CBFBx2)[200]
nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)[156/200]
nuc ish(D5S721/D5S23,EGR1)x2[200]
nuc ish(D7Z1,D7S486)x2[1/200]
nuc ish(TP53,D17Z1)x2[2/200]

<INTERPRETATION>
This patient showed rearrangement of *KMT2A* genes on chromosome 11q23. The partner chromosome of *KMT2A* rearrangement cant' be identified, because FISH was performed using breakapart probe. The prognosis of *KMT2A* rearrangement except t(9;11) is known to be poor.

<RECOMMENDATION>
*KMT2A* FISH for follow up study

<LIMITATION OF TEST>
FISH results can provide informations about the target regions of probes used. It can't give informations about the rearrangement of the other non-target regions.

<METHOD>
-Specimen: uncultured bone marrow aspirates
-Analyzed number of interphase cells: 200
-FISH Probe
BCR/ABL DC, DF translocation probe
RUNX1/RUNX1T1 DC, DF translocation probe
PML/RARA DC, DF translocation probe
CBFB dual color, break apart rearrangement probe
KMT2A dual color, break apart rearrangement probe
EGR1/D5S721, D5S23 dual color, break apart rearrangement probe
D7S486/CEP7 dual color, break apart rearrangement probe
TP53 dual color probe

<PREVIOUS RESULT>
None

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 5. Sample FISH report for a patient with *KMT2A* rearrangement according to consensus guidelines.

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<Gene mutation report>**

Clinical information (diagnosis & relevant therapy): Known acute leukemia
Sample type (BM, PB): Bone marrow
Analyzed gene: *CEBPA*

<GENETIC VARIATION OBSERVED>

| Nucleotide number and base change | Codon number and amino acid change | Mutation/Polymorphism |
|---|---|---|
| c.232_233insGGAA | p.Leu78Argfs* | Mutation (known) |
| c.928_929insAGA | p.Glu309_Thr310insLys | Mutation (known) |

<INTERPRETATION>
Direct sequencing results in the coding region of *CEBPA* gene showed the presence of mutation, which is the insertion of GGAA between 232$^{th}$ and 233$^{th}$ base and this mutation induces the change in the 78$^{th}$ amino acid from Leucine to Arginine and premature truncation of translation. In addition, another mutation which is the insertion of AGA between 928$^{th}$ and 929$^{th}$ base was also found and this mutation induces the insertion of Lysine between 309$^{th}$ amino acid Glutamate and 310$^{th}$ amino acid Threonine. These two mutations are previously reported mutations.

<COMMENT>
CCAAT/enhancer binding protein α (CEBPA) plays an important role in the proliferation and differentiation of myeloid lineage cells, and the incidence of *CEBPA* mutation has been reported as 5-14% in the patients with acute myeloid leukemia (AML). *CEBPA* mutation is frequently found in the form of N-terminal frameshift mutation and C-terminal in-frame mutation, and the relationship between *CEBPA* mutation and *NPM1/FLT3-ITD* mutation is has been reported in several previous studies. *CEBPA* biallelic mutations are related with favorable prognosis in the patients with AML. This test analyzes coding and near-coding intron regions of *CEBPA* gene by direct sequencing methods. The mutation of deep intron and regulatory region of *CEBPA* gene cannot be detected by direct sequencing methods and also, deletion/duplication mutation of *CEBPA* gene cannot be also detected. The sensitivity of direct sequencing methods is r eported to be 20%, and false-negative results can be observed caused by failure to detect mutation if mutant cell exists in the small portions.

<REFERENCES>

<METHOD>
PCR and direct sequencing
Target gene: CEBPA (CCAAT/enhancer binding protein, alpha) on chromosome 19q13.1
Region of interest: CEBPA coding region
Accession number: NM_004364.3 (GRCh37/hg19)

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 6. Sample gene mutation test report for a patient with *CEBPA* mutation according to consensus guidelines.


https://doi.org/10.47429/lmo.2021.11.1.1

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<*BCR-ABL1* real-time quantitative PCR report>**

Clinical information (diagnosis & relevant therapy): Known acute leukemia
Sample type (BM, PB): Bone marrow

<RESULT>

| | |
|---|---|
| *BCR-ABL1* Quantity (Copy number) | $6.39 \times 10^4$ |
| *ABL1* Quantity (Copy number) | $1.35 \times 10^5$ |
| Major *BCR-ABL1* Quantity (IS-NCN) | 24.981600 |

Normalised copy number (NCN) = (*BCR-ABL1* copy number/*ABL* copy number) * 100
IS-NCN = NCN × IS-CAL value / NCNcal

<REFERENCE VALUE>
Negative

<METHOD>
(1) RNA extraction from specimen and Reverse transcription.
(2) Polymerase chain reaction with primers corresponding to the specific region of *BCR/ABL1* mRNA and *ABL1*
(3) Denaturation of PCR product and Hybridization with cDNA amlpified by PCR using a pair of specific primers and a specific internal double-dye probe(FAM-TAMRA) for *BCR-ABL1* mRNA and *ABL1*
This test was developed and its performance characteristics determined by Branford S et al.: Blood 2008;112:3330-3338

<PREVIOUS STUDY>

| Tested date | Specimen | Results |
|---|---|---|
| 2019-12-09 | Bone marrow | IS-NCN: 5.492483 |
| 2019-09-06 | Bone marrow | IS-NCN: 0.036618 |

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 7. Sample *BCR-ABL1* real-time quantitative PCR test report for a patient according to consensus guidelines.

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<Hemavision (Multiplex nested RT-PCR)>**

Clinical information (diagnosis & relevant therapy): Known acute leukemia
Sample type (BM, PB): Bone marrow

<RESULT>

| | |
|---|---|
| Screening PCR | Positive |
| Split-out PCR | *PML-RARA* detected |

Results shows the presence of *PML-RARA* rearrangements, which is one of known genetic abnormalities associated with leukemia

| Gene Rearrangement | Approved symbol* (Previous symbol) | Result |
|---|---|---|
| t(9;22)(q34.1;q11.2) | *BCR/ABL1* | - |
| t(15;17)(q24.1;q21.2) | *PML/RARA* | Detected |
| t(8;21)(q22;q22.1) | *RUNX1/RUNX1T1* (*AML1/ETO*) | - |
| t(12;21)(p13.2;q22.1) | *ETV6/RUNX1* (*TEL/AML1*) | - |
| inv(16)(p13.1q22) | *CBFB/MYH11* | - |
| t(1;19)(q23;p13.3) | *TCF3/PBX1* (*E2A/PBX1*) | - |
| t(6;9)(p23;q34.1) | *DEK/NUP214* | - |
| t(9;12)(q34.1;p13.2) | *ETV6/ABL1* (*TEL/ABL1*) | - |
| t(5;12)(q32;p13.2) | *ETV6/PDGFRB* (*TEL/PDGFRB*) | - |
| t(16;21)(p11.2;q22.2) | *FUS/ERG* | - |
| t(v;11q23.3) | *KMT2A* (*MLL*) rearranged** | - |
| t(12;22)(p13.2;q12.1) | *MN1/ETV6* (*MN1/TEL*) | - |
| t(3;5)(q25.3;q35.1) | *NPM1/MLF1* | - |
| t(5;17)(q35.1;q21.2) | *NPM1/RARA* | - |
| t(3;21)(q26.2;q22.1) | *RUNX1/MECOM* (*AML1/EAP/MDS/EVI1*) | - |
| t(9;9)(q34.11;q34.1) | *SET/NUP214* | - |
| TAL1 (1p32) deletion | *STIL/TAL1* (*SIL/TAL1*) | - |
| t(17;19)(q22;p13.3) | *TCF3/HLF* | - |
| t(11;17)(q23.2;q21.2) | *ZBTB16/RARA* (*PLZF/RARA*) | - |

*The official gene symbol approved by the HGNC (HUGO Gene Nomenclature Committee).

***KMT2A/AFDN, KMT2A/AFF1, KMT2A/ELL, KMT2A/MLLT1, KMT2A/MLLT3, KMT2A/EPS15, KMT2A/FOX04, KMT2A/MLLT6, KMT2A/MLLT10, KMT2A/MLLT11.*

<COMMENT>

Hemavision Leukemia multiplex PCR test allows detection of 28 known genetic abnormalities associated with leukemia by multiplex nested-PCR methods. It can detect many genetic translocations and rearrangements, in which can be missed by conventional karyotyping.

<METHOD>

(1) RNA extraction from specimen.
(2) cDNA Synthesis and Screening PCR.
(3) Second Split-out PCR.
(4) Electrophoresis.

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 8. Sample Hemavision, multiplex nested RT-PCR test report for a patient according to consensus guidelines.


https://doi.org/10.47429/lmo.2021.11.1.1

Name: OOO ID number: 1234567 Sex/Age/Date of birth: F/70/1950.01.01
Medical department: MH Requesting physician: OOO
Sample ID: 7654321 Sample date/time collected: 2020.01.03 9:00 AM
Sample date/time received: 2020.01.03 9:30 AM

**<MYELOID PANEL REPORT>**

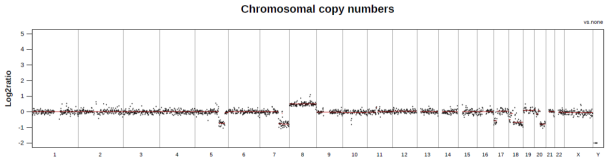
Clinical information (diagnosis & relevant therapy): Known acute leukemia
Sample type (BM, PB): Bone marrow

VARIANTS OF INTEREST

| ASCO/AMP Classification (somatic) | Gene | Accession | Nucleotide | Amino acid | VAF |
|---|---|---|---|---|---|
| Tier 1 | *TP53* | NM_000546.5 | c.742C>T | p.Arg248Trp | 76.1 |

Abbreviations: VAF (variant allele frequency).

FIGURES




INTERPRETATION AND CLINICAL SIGNIFICANCE

*TP53* mutation은 AML에서 complex karyotype, chromosome 8 gain과의 연관성이 보고되어 있으며 짧은 생존기간과 연관된 poor outcome 예측인자로 알려져 있습니다(Blood 2014 124:2379, Blood Cancer Journal (2015) 5, e331). Chromosome copy number 분석상 complex karyotype이 관찰됩니다.

METHODOLOGY

Genomic DNA extracted from this individual's sample was used for library preparation and target capture using a custom panel targeting candidate genes. Massivelly parallel sequencing was done on the NextSeq 550Dx System (Illumina). Quality control and sequence analysis was done using our custom analysis pipeline. Copy number analysis was done using our custom analysis pipeline. GRCh37 (hg19) was used as the reference sequence for mapping and variant callling. Databases used for analysis and variant annotation include Online Mendelian Inheritance in Man (OMIM), ClinVar, COSMIC, My Cancer Genome, OncoKB, c-BioPortal, dbSNP, Human Gene Mutation Database (HGMD), 1000 Genome, Exome Aggregation Consortium (ExAC), Exome Sequencing Project (ESP), and Korean Reference Genome Database (KRGDB). All variants were classified by the ACMG guidelines and benign and likely benign variants were filtered out. Variants are classified into four tiers based on their level of clinical significance in cancer diagnosis, prognosis, and/or therapeutics following the standards and guidelines established by the Association for Molecular Pathology (AMP), American Society of Clinical Oncology (ASCO), and College of American Pathologists (CAP) (Tier I, variants with strong clinical significance; Tier II, variants with potential clinical significance; Tier III, variants of unknown clinical significance; and Tier IV, variants deemed benign or likely benign).

TARGET GENES

*ABCB1, ABCB7, ABCG2, ABCG5, ABCG8, ABL1, ABL2, ACD, ACTB, ACTN1, ADA, ADAMTS13, AIRE, AK1, AK2, AKT2, ALAS2, ALDOA, AMN, ANK1, ANKRD26, AP3B1, ARID1A, ARPC1B, ASXL1, ATG2B, ATM, ATR, ATRX, AXIN1, BCL11B, BCL2, BCL6, BCOR, BCORL1, BHLHE41, BIRC3, BLM, BPGM, BRAF, BRCA1, BRCA2, BRCC3, BRINP3, BRIP1, BTG1, BTK, BTLA, C3, C4BPA, C4BPB, CALN1, CALR, CARD11, CASP10, CBL, CBLB, CBLC, CCND1, CD200, CD247, CD27, CD36, CD3D, CD3E, CD40LG, CD46, CD58, CD59, CD79B, CDAN1, CDKN1B, CDKN2A, CDKN2B, CEBPA, ... STAG2, STAT3, STAT5B, STEAP3, STX11, STXBP2, SUZ12, SYNE1, TAL1, TAL2, TAZ, TBL1XR1, TBX1, TCF3, TCIRG1, TEC, TERC, TERF1, TERF2, TERF2IP, TERT, TET1, TET2, TET3, THBD, THPO, TINF2, TLX1, TLX3, TMPRSS6, TNFAIP3, TNFRSF13B, TNFRSF14, TNFRSF1A, TOX, TP53, TPI1, TPMT, TRAF3, TRNT1, TSLP, TSR2, TUBB1, TYK2, U2AF1, U2AF2, UBE2T, UGT1A1, UGT1A7, UNC13B, UNC13D, UNC5D, USB1, USH2A, USP9X, VHL, VPS13B, VPS45, VWF, WAS, WDR1, WIPF1, WRAP53, WT1, XBP1, XIAP, XK, XRCC2, YARS2, ZAP70, ZFHX4, ZNF197, ZRSR2, MRE11A, WHSC1, STON1, OBFC1 (497 genes)*

NOTES

A list of benign and likely benign variants identified in this individual is available upon request. Variants with a population frequency greater than expected given the disease prevalence in general population were considered as benign. Silent and deep intronic variants were classified as benign or likely benign unless previously reported as clinically or biologically significant. Referring physicians and individuals being tested should understand that rare diagnostic errors may occur. Possible source of errors include PCR or sequencing errors, mapping or variant calling errors of bioinformatics algorithms, patient-specific rare polymorphisms that interfere with analysis, and mosaicisms below detection level. Although our algorithms are also designed to detect large exonic deletions/duplications, deletions/duplications of one or a few exons might be missed. Mutations in deep intron or regulatory region are usually unable to be detected by this test. We followed the AMP/ASCO/CAP guidelines for variant classification. Some of the current classification might be changed when population and disease database are updated in the future.

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5.Online Mendelian Inheritance in Man (OMIM). Johns Hopkins University; http://www.omim.org/.

Date/time of final report: 2020.01.06 3:00 PM
Test performed/reported by: OOO M.T./OOO M.D.
Address/Telephone

Supplementary Fig. 9. Sample next-generation sequencing test report for a patient according to consensus guidelines.