MGM2450: COMPREHENSIVE MYELOID AND LYMPHOID PANEL BY NGS (SNVS, INDELS, CNVS & FUSIONS)

Report Details

Sample ID / Order ID: 10040900 / 1799134
Collection Date: 2nd June 2026
Date Received: 4th June 2026
Report Date & Time: 17th Jun 2026 10:33 AM

Specimen Information

Specimen Site: NA
Specimen Received: Bone Marrow Aspirate (BMA) in EDTA
Specimen Tested: Bone Marrow Aspirate (BMA) in EDTA
Tumor Content (%): NA

Ordering Clinician

Clinician: Dr. Veerendra Patil
Affiliation: Basavatarakam Indo American Cancer Hospital & Research Institute
Serviced By: NA
Report Status: Final

CLINICAL BACKGROUND

B-cell Acute Lymphoblastic Leukemia (B-ALL) [as per the clinical details provided in and along with the Test Requisition Form].

Test Result Summary

Result - POSITIVE

CLINICALLY RELEVANT VARIANT/S DETECTED in *BCR/ABL1* (fusion)

Gene/AMP Classification ^	Clinical relevance	Therapeutic relevance $	Interpretation
FUSION Variants			
***BCR/ABL1* (FUSION - Minor Transcript)** Total Read depth - 734x			
Tier IA (Variant of strong clinical significance & FDA approved Therapy)	Effective	Imatinib mesylate, Dasatinib	Patients with BCR-ABL1 fusion show good response to Imatinib and over 90% patients achieve complete remission (CR) after treatment.

No clinically significant SNVs, Small INDELs and CNVs have been detected in this sample

^ Refer to Glossary section for the classification criteria details.

$ Drug Approvals are based on US-FDA Guidelines. Kindly refer to local guidelines if required.

ADDITIONAL BIOMARKERS DETECTED

This section provides information about variants that do not have any therapeutic value. However, these variants may or may not have a likely oncogenic effect.

GLOSSARY

AMP Classification Criteria: Displays the classification of a biomarker according to the recommendations of the Association for Molecular Pathology (AMP) [PMID: 27993330].

Tier	Criteria
Tier IA	Variants of strong clinical significance. FDA-approved therapy or biomarkers included in professional guidelines.
Tier IB	Variants of strong clinical significance. Well-powered studies with consensus from experts in the field.

Tier	Criteria
Tier IIC	Variants of potential clinical significance. FDA-approved therapies for different cancer types or investigational therapies. Multiple small published studies with some consensus.
Tier IID	Variants of potential clinical significance. Preclinical trials or a few case reports without consensus.
Tier III	Variants of unknown clinical significance.
Tier IV	Benign or likely benign variants.

Drug approval:

The development stage of the treatment for the patient's indication as per US-FDA guidelines.

Stage	Definition
Approved	This drug is launched for the primary or a secondary patient disease
Off-Label	This drug is launched for a disease other than the primary or secondary patient diseases
Investigational	This drug is currently under clinical development in the patient disease.
Other	None of the other stages are applicable. The drug or drug class is, for example, suspended, discontinued, or withdrawn.

ACTIONABLE BIOMARKER DETAILS

BCR/ABL1 (FUSION- Minor Transcript)

Gene Fusion: *BCR*:*ABL1*	**5'Gene** *BCR*	**3'Gene:** *ABL1*
Total Read Depth: 734x	**Ensemble Gene ID:** ENST00000305877.13	**Ensemble Gene ID:** ENST00000318560.6
	Exon/Intron: E:1	**Exon/Intron:** E:2
	5'Chromosome Breakpoint (hg38): chr22:23182239:+	**3'Chromosome Breakpoint (hg38):** chr9:130854064:+

Gene Summary 1: The fusion is detected at**chr22:23182239:+** of *BCR* gene. The 5' gene is **exon 1** of ***BCR*** gene. *BCR* (Breakpoint cluster region) located at 22q11.23 with unknown normal function but known as a fusion partner to *ABL* gene in CML (Chronic Myelogenous Leukemia).

Gene Summary 2: The fusion is detected at **chr9:130854064** of *ABL1* gene. The 3' gene is **exon 2**of ***ABL1*** gene. *ABL1* (Abelson murine leukemia viral oncogene homolog 1) located at 9q34.12 is a protein which due to alternate splicing gives rise to 2 proteins of 145Kda and this is widely expressed with nuclear localization and inhibition of cell growth.

Note: Imatinib mesylate is approved to treat acute lymphoblastic leukemia in adults and children that is Philadelphia chromosome positive. Dasatinib is approved to treat acute lymphoblastic leukemia that is Philadelphia chromosome positive in adults whose disease did not respond to other drugs or who are not able to receive other drugs.

Clinical and Therapeutic Relevance: Oncogenic effect is shown to activate many pathways like the RAS, PI3K, STAT, activation of molecules of the focal adhesion complex and negative regulation of molecules which could be associated with blast crisis. This fusion has anti apoptotic activity, migratory abnormalities, induction of genetic instability and other molecular events associated with blast crisis. Ph+ ALL responds to combination chemotherapy, although complete remission is significantly less likely after standard induction regimens than in Ph ALL. A clinical study on 1521 patients demonstrated that the CR rate was 97% for the 533 Ph– patients at standard risk, and it was 90% for the 590 Ph– patients at high risk when treated with combination chemotherapy (Daunorubicin, Vincristine, L-asparaginase, Prednisone and Methotrexate in Phase I and Cyclophosphamide, Cytarabine, 6-Mercaptopurine and Methotrexate in phase II) . A clinical study on 20 Ph+ve ALL patients showed promising results when treated with Imatinib along with chemotherapy. All 15 patients (100%) treated with active disease achieved CR. The CR rates after one cycle of induction therapy were 52% for VAD, 66% for Hyper-CVAD with or without Rituximab, and 93% for Hyper-CVAD and Imatinib mesylate (*P*=.01). Another study on 24 newly diagnosed *BCR-ABL* positive patients demonstrated CR in 23 patients (96%) when treated with a combination therapy of Imatinib with chemotherapy without an increase in toxicity. A phase 2 clinical study on 36 Ph+ve ALL patients demonstrated good hematologic responses in 42% (15/36) of patients, 67% of whom remained progression-free and complete cytogenetic responses were attained by 58% (21/36) of patients when treated with Dasatinib. A clinical study on 1446 ALL patients showed poor overall survival in Ph +ve patients as compared to Ph – ve patients. Overall survival rates at 5 years were 38% for all patients, 41% for Ph– patients, and 25% for Ph+ patients. Kindly correlate clinically.

PubMed References: 16105981, 14551133, 15315963, 17496201, 31595038

DISCLAIMER

- **Decisions regarding treatment action plan should not be solely based on these test results. These findings are highly recommended to be correlated with the patient's clinical, pathological, radiological and family history for decisions on diagnosis, prognosis, or therapeutics.**
- The therapy information provided in this report is based on FDA approved drugs data, NCCN guidelines, peer-reviewed published literature, standard clinical databases, and strength of biomarker results. These therapies may or may not be suitable/beneficial to a particular patient. This clinical report summarizes potentially effective medications, potentially ineffective medications, and medications that may pose a higher risk of adverse reactions by mapping the patient's genetic alterations to the biomedical reference information. The report may also provide prognostic and diagnostic biomarkers detected or shown for the given disease context.
- The clinical trials information provided in this report is compiled from https://www.clinicaltrials.gov as per currently available data, however completeness of information provided herein cannot be guaranteed. This information should only be used as a guide and specific eligibility criteria should be reviewed thoroughly for the concerned patient. MedGenome Labs does not guarantee or promise an enrolment in any clinical trials.
- The identification of a genomic biomarker does not necessarily imply pharmacological effectiveness or ineffectiveness. The medications identified by the treating physician may or may not be suitable for use on a particular patient. Thus, the clinical report does not guarantee that any particular agent will be effective in the treatment of any particular condition. Also, the absence of a treatment option does not determine the effectiveness or predict an ineffective or safety-relevant effect of a medication selected by the treating physician.
- The classification and clinically relevant information for the reported variants is based on peer-reviewed publications, public clinical databases, medical guidelines (WHO, NCCN, ASCO, AMP) or other publicly available information and it has been ensured that the information provided is up to date at the time of report generated, however continuous updates may happen in public domains. Also, the classification of variants can change based on the updated literature evidence. Re-analysis of the results can be requested at additional cost.
- The scope of this assay limits to the detection of gene fusions in RNA transcripts.
- There is a possibility of false positives in this assay, and hence confirmation with orthogonal method is needed.
- This test has been validated at MedGenome Labs, and the fusions detected at ≥10 spanning reads are only reported.
- Possibility of false negative below the limit of detection of this assay cannot be ruled out.
- The classification of variants of unknown significance can change over time. Please contact MedGenome later for any change
- A false negative result for any variant below the LOD, i.e., 5% for SNVs and Small INDELs, cannot be ruled out.
- Non-coding RNA fusions are not reported.
- The scope of this assay includes testing for fusions in diagnostic and relapse samples while fusions in patients under remission or MRD cannot be efficiently detected by this assay, which needs to be checked at >5000x depth.

TEST DESCRIPTION

The whole genome sequencing of different subtypes of leukemia revealed new recurrent genetic and chromosomal abnormalities that could add value to the existing prognostic scoring index in different subtypes of leukemia. Several studies have been reported wherein clinical outcome was measured to correlate the significance of the mutational findings from whole genome sequencing. The scope of this COMPREHENSIVE MYELOID AND LYMPHOID PANEL BY NGS (SNVS, INDELS, CNVS & FUSIONS) testing includes a panel of genes, wherein prognostic significance of these genes and their mutations has been well studied and documented in medical literature. The panel is designed on targeted sequencing of multiple genes for the coding regions through NGS.

TEST METHODOLOGY

Sample type: Peripheral blood or bone marrow in EDTA tube

Extraction and Library Preparation: Nucleic acid extracted from blood or bone marrow was used to perform targeted gene capture by custom capture kit.

Sequencing : The QC-passed libraries were sequenced on a validated Illumina next-generation sequencing (NGS) platform, achieving a mean target

coverage depth of >250× for DNA libraries and >500× for RNA libraries.

Data Analysis: The sequences obtained were aligned to human reference genome (GRCh38.p13/) using BWA/STAR program [PMID: 20080505, 23155063,23104886] The in-house validated pipeline was designed to accurately detect all classes of genomic alterations (SNVs, INDELs, CNVs and Fusions). Only non-synonymous and splice site variants found in the coding regions were used for clinical interpretation.

Limit of Detection (LOD): The LOD for SNVs and INDELs is 5% Variant allele Frequency (VAF) and for Fusions is >10 total read support.

Variant Annotation: The mutations were annotated using our in-house annotation pipeline (VariMAT). Gene annotation of the variants was performed using VeP program [PMID: 27268795] against the Ensembl release 99 human gene Model Clinically relevant mutations were annotated using peer-reviewed publications, public clinical databases (ClinVar, HGMD, CiViC, OncoKb), medical guidelines (NCCN, ASCO, AMP). The common variants are filtered out based on the minor allele frequency (MAF) in various population databases (1000G, ExAC, gnomAD, GAsP, dbSNP, OncoCrDb (in-house curated database)) and only variants with MAF <0.01% are considered for reporting [PMID: 29155950,27535533,27535533, 26292667,27535533,31526404]

Reporting : Clinically relevant mutations were prioritized, and reports were prepared based on AMP-ASCO-CAP, WHO, ASH guidelines [PMID: 27993330,WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues; Revised 4th Edition, Volume 2] and also based on annotation metrics from OncoMD [PMID: 26928227],MedGenome's curated somatic database which includes somatic mutations from TCGA.

The transcript used for clinical reporting generally represents the canonical transcript (according to Ensembl release 99 human gene model), which is usually the longest coding transcript with strong/multiple supporting evidence. However, clinically relevant variants annotated in alternate complete coding transcripts could also be reported. Variants annotated on in-complete and nonsense mediated decay transcripts will not be reported.

CLINICAL TRIALS

The following trials are potentially best suited for your patient's indication, considering all reported treatment recommendations. See https://clinicaltrials.gov (clinical trials from NCT) or https://trialsearch.who.int (clinical trials from other registries) for more information.

Clinical trials in total : 1 **Trial countries :** IN-India, US-United States

S.No	Title	Phase and ID	Intervention	Disease	Age & Sex
1	A Study Testing the Combination of Dasatinib or Imatinib to Chemotherapy Treatment With Blinatumomab for Children, Adolescents, and Young Adults With Philadelphia Chromosome Positive (Ph+) or ABL-Class Philadelphia Chromosome-Like (Ph-Like) B-cell Acute Lymphoblastic Leukemia (B-ALL)	Phase 2: NCT06124157	Calaspargase Pegol, Cyclophosphamide, Cytarabine, Dasatinib, Daunorubicin, Doxorubicin	B Acute Lymphoblastic Leukemia	366 Days to 46 Years
	Status: Recruiting				

COVERAGE OF ANALYZED GENES

Gene	Coverage (%)	Gene	Coverage (%)	Gene	Coverage (%)
ABL1	100	*ARAF*	100	*ARID1A*	100
ASXL1	100	*ASXL2*	100	*ATM*	100
ATRX	100	*B2M*	100	*BCL2*	100
BCL6	100	*BCOR*	100	*BCORL1*	100
BIRC3	100	*BRAF*	100	*CALR*	100
CARD11	100	*CBL*	100	*CBLB*	100

Gene	Coverage (%)	Gene	Coverage (%)	Gene	Coverage (%)
CBLC	100	*CCND1*	100	*CCND3*	100
CCR4	100	*CCR7*	100	*CD28*	100
CD58	100	*CD79B*	100	*CDKN1A*	100
CDKN2A	100	*CDKN2B*	100	*CDKN2C*	100
CEBPA	100	*CREBBP*	100	*CSF3R*	100
CTNNA1	100	*CUX1*	100	*CXCR4*	100
CYLD	100	*DIS3*	100	*DNMT3A*	100
EP300	100	*EPHA7*	100	*ETNK1*	100
ETV6	100	*EZH2*	100	*FAS*	100
FBXW7	100	*FGFR3*	100	*FLT3*	100
FYN	100	*GATA1*	100	*GATA2*	100
GATA3	100	*GNA13*	100	*GNAS*	100
HNRNPA2B1	100	*HRAS*	100	*ID3*	100
IDH1	100	*IDH2*	100	*IKZF1*	100
INPP5D	100	*IRF4*	100	*ITPKB*	100
JAK1	100	*JAK2*	100	*JAK3*	100
KDM6A	100	*KIT*	100	*KLF2*	100
KLHL14	100	*KMT2A*	100	*KMT2D*	100
KRAS	100	*MAP2K1*	100	*MEF2B*	100
MFHAS1	100	*MPL*	100	*MYBBP1A*	100
MYD88	100	*NF1*	100	*NFE2*	100
NOTCH1	100	*NOTCH2*	100	*NPM1*	100
NRAS	100	*OSBPL10*	100	*PAX5*	100
PDCD1LG2	100	*PDGFRA*	100	*PDGFRB*	100
PHF6	100	*PIK3CA*	100	*PLCG1*	100
POT1	100	*PRDM1*	100	*PRKCB*	100
PRPF8	100	*PTEN*	100	*PTPN1*	100
PTPN11	100	*RAD21*	100	*RB1*	100
REL	100	*RHOA*	100	*RUNX1*	100
SETBP1	100	*SETD2*	100	*SF3B1*	100
SGK1	100	*SMARCA4*	100	*SMC1A*	100
SMC2	100	*SMC3*	100	*SOCS1*	100
SRSF2	100	*STAG2*	100	*STAT3*	100
STAT5B	100	*STAT6*	100	*SUSD2*	100
TCF3	100	*TENT5C*	100	*TET1*	100
TET2	100	*TNFAIP3*	100	*TNFRSF14*	100
TP53	100	*TRAF3*	100	*U2AF1*	100
VAV1	98.62	*WT1*	100	*XPO1*	100
ZRSR2	100				

CLINICALLY RELEVANT FUSIONS ANALYSED

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
ABL1	***BCR-ABL1*	*BCR*	*ABL1*	t(9;22)(q34.12;q11.23)	MPD, AML, ALL
ABL1	*CENPC-ABL1*	*CENPC*	*ABL1*	t(4;9)(q13.2;q34.12)	ALL
ABL1	*EML1-ABL1*	*EML1*	*ABL1*	t(9;14)(q34.12;q32.2)	ALL
ABL1	*ETV6-ABL1*	*ETV6*	*ABL1*	t(9;12)(q34.12;p13.2)	ALL, AML, MDS, MPD
ABL1	*FOXP1-ABL1*	*FOXP1*	*ABL1*	t(3;9)(p13;q34.12)	ALL, NHL
ABL1	*LSM14A-ABL1*	*LSM14A*	*ABL1*	t(9;19)(q34.12;q13.11)	ALL
ABL1	*NUP153-ABL1*	*NUP153*	*ABL1*	t(6;9)(p22.3;q34.12)	ALL
ABL1	*NUP214-ABL1*	*NUP214*	*ABL1*	t(9;9)(q34.13;q34.12)	ALL
ABL1	*RANBP2-ABL1*	*RANBP2*	*ABL1*	t(2;9)(q12.3;q34.12)	ALL
ABL1	*RCSD1-ABL1*	*RCSD1*	*ABL1*	t(1;9)(q24.2;q34.12)	ALL
ABL1	*SFPQ-ABL1*	*SFPQ*	*ABL1*	t(1;9)(p34.3;q34.12)	ALL
ABL1	*SNX1-ABL1*	*SNX1*	*ABL1*	SNX1/ABL1	ALL
ABL1	*SNX2-ABL1*	*SNX2*	*ABL1*	t(5;9)(q23.2;q34.12)	ALL
ABL1	*SPTNA1-ABL1*	*SPTNA1*	*ABL1*	SPTNA1/ABL1	ALL
ABL1	*ZMIZ1-ABL1*	*ZMIZ1*	*ABL1*	t(9;10)(q34.12;q22.3)	ALL, AML
ABL2	*ETV6-ABL2*	*ETV6*	*ABL2*	t(1;12)(q25.2;p13.2)	AML
ABL2	*PAG1-ABL2*	*PAG1*	*ABL2*	PAG1-ABL2	ALL
ABL2	*RCSD1-ABL2*	*RCSD1*	*ABL2*	t(1;1)(q24.2;q25.2)	ALL
ABL2	*ZC3HAV1-ABL2*	*ZC3HAV1*	*ABL2*	t(1;7)(q25;q34)	ALL
ALK	*ALK-CTLC*	*ALK*	*CTLC*	t(2;17)(p23;q23)	NHL
ALK	*ATIC-ALK*	*ATIC*	*ALK*	inv(2)(p23q35)	NHL
ALK	*CLTC-ALK*	*CLTC*	*ALK*	t(2;17)(p23;q23)	NHL
ALK	*DUSP22-FRA7H*	*DUSP22*	*FRA7H*	t(6;7)(p25.3;q32.3)	NHL
ALK	*MYH9-ALK*	*MYH9*	*ALK*	t(2;22)(p23;q11)	NHL
ALK	*NPM1-ALK*	*NPM1*	*ALK*	t(2;5)(p23;q35)	NHL
ALK	*RANBP2-ALK*	*RANBP2*	*ALK*	NA	MDS/MPN,JMML,CMML, AML
ALK	*RNF213-ALK*	*RNF213*	*ALK*	t(2;17)(p23;q25)	NHL
ALK	*SEC31A-ALK*	*SEC31A*	*ALK*	t(4;2)(q21.22;p23.2)	NHL
ALK	*SQSTM1-ALK*	*SQSTM1*	*ALK*	t(5;2)(q35.3;p23.2)	NHL
ALK	*TBL1XR1-TP63*	*TBL1XR1*	*TP63*	inv(3)(q26q28)	NHL
ALK	*TFG-ALK*	*TFG*	*ALK*	t(2,3)(p23;q12.2)	NHL
ALK	*TPM3-ALK*	*TPM3*	*ALK*	t(1;2)(q25;p23)	NHL
ALK	*TPM4-ALK*	*TPM4*	*ALK*	t(2;19)(p23;p13)	NHL
BCL11B	*BCL11B-TLX3*	*BCL11B*	*TLX3*	t(5;14)(q35;q32)	ALL
BCL11B	*IKZF2-BCL11B*	*IKZF2*	*BCL11B*	t(2;14)(q34;q32)	NHL
BCL2	*IGH-BCL2*	*IGH*	*BCL2*	t(14;18)(q32.33;18q21.33)	ALL, NHL
BCL3	*IGK-BCL3*	*IGK*	*BCL3*	t(2;19)(p12;q13.3)	CLL
BCL3	*IGL-BCL3*	*IGL*	*BCL3*	t(19;22)(q13.32;q11.22)	NHL
BCL6	*BCL6-MYBL1*	*BCL6*	*MYBL1*	t(3;8)(q27;q13)	NHL

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
BCL6	*IGH-BCL6*	*IGH*	*BCL6*		NHL
BIRC3	*BIRC3-MALT1*	*BIRC3*	*MALT1*	t(11;18)(q21;q21)	NHL, CLL
CBL	*KANK1-CBL*	*KANK1*	*CBL*	t(9;11)(p24.3;q23.3)	ALL
CCND1	*IGH-CCND1*	*IGH*	*CCND1*	t(11;14)(q13;q32)	NHL, CLL, MM
CCND3	*IGH-CCND3*	*IGH*	*CCND3*	t(6;14)(p21;q32)	MM, NHL
CDK6	*CDK6-KMT2A*	*CDK6*	*KMT2A*	t(7;11)(q21.2;q23.3)	ALL
CHIC2	*CHIC2-ETV6*	*CHIC2*	*ETV6*	t(4;12)(q12;p13.2)	AML, ALL
CIITA	*CIITA-CD274*	*CIITA*	*CD274*	t(9;16)(p24;p13)	NHL
CIITA	*CIITA-PDCD1LG2*	*CIITA*	*PDCD1LG2*	t(9;16)(p24;p13)	NHL
CIITA	*CIITA-RALGDS*	*CIITA*	*RALGDS*	t(9;16)(q34;p13)	NHL
CIITA	*CIITA-RMI2*	*CIITA*	*RMI2*	(16p13)	NHL
CRLF2	*IGH-CRLF2*	*IGH*	*CRLF2*	t(X;14)(p22;q32), t(Y;14)(p11;q32)	ALL
CRLF2	*P2RY8-CRLF2*	*P2RY8*	*CRLF2*	del(X)(p22p22), del(Y)(p11p11)	ALL
CSF1R	*MEF2D-CSF1R*	*MEF2D*	*CSF1R*	t(1;5)(q22;q33)	AML
CSF1R	*SSBP2-CSF1R*	*SSBP2*	*CSF1R*	t(5;5)(q14.1;q32)	ALL
CSF1R	*TBL1XR1-CSF1R*	*TBL1XR1*	*CSF1R*	t(3;5)(q26.32;q32)	ALL, NHL
CSF2RA	*CSF2RA-CRLF2*	*CSF2RA*	*CRLF2*	del(X)(p22.33p22.33)	ALL
DEK	*DEK-NUP214*	*DEK*	*NUP214*	t(6;9)(p22;q34)	AML, MDS
DEK	*NUP214-DEK*	*NUP214*	*DEK*	t(6;9)(p22;q34)	AML, MDS
DNTT	*DNTT-BLNK*	*DNTT*	*BLNK*	t(10;10)(q24;q24)	ALL
DUSP22	*DUSP22-IRF4*	*DUSP22*	*IRF4*	not specified	
EBF1	*HMGA2-EBF1*	*HMGA2*	*EBF1*	t(5;12)(q33.3;q14.3)	
EBF1	*IGH-EBF1*	*IGH*	*EBF1*	t(14;5)(q32.33;q33.3)	NHL
EGFR	*IGH-EGFR*	*IGH*	*EGFR*	t(7;14)(p11;q32)	MM
EPOR	*EPOR-CRLF2*	*EPOR*	*CRLF2*	EPOR / CRLF2	ALL
EPOR	*IGH-EPOR*	*IGH*	*EPOR*	t(14;19)(q32.33;p13.2)	ALL
EPOR	*IGK-EPOR*	*IGK*	*EPOR*	t(14;19)(q32;p13)	ALL
EPOR	*LAIR1-EPOR*	*LAIR1*	*EPOR*	t(14;19)(q32;p13)	ALL
EPOR	*THADA-EPOR*	*THADA*	*EPOR*	THADA-EPOR	ALL
ERG	*FUS-ERG*	*FUS*	*ERG*	t(16;21)(p11;q22)	AML, MDS
ETV6	*ETV6-IGH*	*ETV6*	*IGH*	t(12;14)(p13.2;q32.33)	NHL, ALL
ETV6	*MNX1-ETV6*	*MNX1*	*ETV6*	t(7;12)(q36;p13)	AML, ALL
ETV6	*PAX5-ETV6*	*PAX5*	*ETV6*	dic(9;12)(p13;p13)	ALL, NHL, CLL, MPD
FGFR1	*BCR-FGFR1*	*BCR*	*FGFR1*	t(22;8)(q11.23;p11.23)	MPD
FGFR1	*CNTRL-FGFR1*	*CNTRL*	*FGFR1*	t(8;9)(p12;q33)	MPD, NHL
FGFR1	*CPSF6-FGFR1*	*CPSF6*	*FGFR1*	t(12;8)(q15;p11.23)	MDS/MPN,JMML,CMML
FGFR1	*CUX1-FGFR1*	*CUX1*	*FGFR1*	t(7;8)(q22.1;p11.23)	ALL
FGFR1	*FGFR1OP-FGFR1*	*FGFR1OP*	*FGFR1*	t(6;8)(q27;p11.23)	MDS/MPN, JMML, CMML, MPD, ALL
FGFR1	*FGFR1OP2-FGFR1*	*FGFR1OP2*	*FGFR1*	t(12;8)(p11.23;p11.23)	MPD, NHL
FGFR1	*HERVK-FGFR1*	*HERVK*	*FGFR1*	t(8;19)(p11.2;p13.3)	AML
FGFR1	*LRRF1P1-FGFR1*	*LRRF1P1*	*FGFR1*	t(2;8)(q37.3;p11.23)	MDS

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
FGFR1	*LRRFIP1-FGFR1*	*LRRFIP1*	*FGFR1*	t(2;8)(q37.3;p11.23)	MDS
FGFR1	*MYO18A-FGFR1*	*MYO18A*	*FGFR1*	t(17;8)(q11.2;p11.23)	MPD
FGFR1	*RANBP2-FGFR1*	*RANBP2*	*FGFR1*	t(2;8)(q12.3;p11.23); t(2;8)(q13;p11 .2)	MDS/MPN, JMML, CMML
FGFR1	*TPR-FGFR1*	*TPR*	*FGFR1*	t(1;8)(q31.1;p11.23)	MPD
FGFR1	*TRIM24-FGFR1*	*TRIM24*	*FGFR1*	t(7;8)(q33;p11.23)	AML
FGFR1	*ZNF198-FGFR1*	*ZNF198*	*FGFR1*	t(8;13)(p11;q12)	MPD
FGFR1	*ZMYM2-FGFR1*	*ZMYM2*	*FGFR1*	t(8;13)(p11.23;q12.11)	MPD
FGFR3	*ETV6-FGFR3*	*ETV6*	*FGFR3*	t(4;12)(p16.3;p13.2)	ALL
FGFR3	*IGH-FGFR3*	*IGH*	*FGFR3*	t(4;14)(p16;q32)	MM
FLT3	*ZMYM2-FLT3*	*ZMYM2*	*FLT3*	t(13;13)(q12;q12)	ALL
GLIS2	*CBFA2T3-GLIS2*	*CBFA2T3*	*GLIS2*	inv(16)(p13q24)	AML
GLIS2	*GLIS2-CBFA2T3*	*GLIS2*	*CBFA2T3*	inv(16)(p13.3q24.3)	AML
HOXA11	*DPY19L1-HOXA11*	*DPY19L1*	*HOXA11*	t(7;7)(p14.2;p15.2)	ALL
HOXA11	*HOXA11-BZW2*	*HOXA11*	*BZW2*	t(7;7)(p15.2;p21.1)	AML
HOXA11	*NUP98-HOXA11*	*NUP98*	*HOXA11*	t(7;11)(p15.2;p15.4)	MDS/MPN, JMML, CMML
HOXA11	*PUM1-HOXA11*	*PUM1*	*HOXA11*	t(1;7)(p35.2;p15.2)	ALL
HOXA11	*TRB-HOXA11*	*TRB*	*HOXA11*	inv(7)(p15.2q34), t(7;7)(p15.2;q34)	AML, ALL
HOXA13	*NUP98-HOXA13*	*NUP98*	*HOXA13*	t(7;11)(p15.2;p15.4)	AML, MPD
HOXA1O	*TRB-HOXA10*	*TRB*	*HOXA10*	t(7;7)(p15.2;q34); inv(7)(p15.2q34)	ALL, NHL
HOXA9	*GATA2-HOXA9*	*GATA2*	*HOXA9*	t(3;7)(q21.3;p15.2)	AML
HOXA9	*HOXA9-ANGPT1*	*HOXA9*	*ANGPT1*	t(7;8)(p15.2;q23.1)	AML
HOXA9	*MED12-HOXA9*	*MED12*	*HOXA9*	t(X;7)(q13.1;p15.2)	ALL
HOXA9	*MSI2-HOXA9*	*MSI2*	*HOXA9*	t(7;17)(p15.2;q23)	CML
HOXA9	*NIPBL-HOXA9*	*NIPBL*	*HOXA9*	t(5;7)(p13.2;p15.2)	AML
HOXA9	*NUP98-HOXA9*	*NUP98*	*HOXA9*	t(7;11)(p15.2;p15.4)	AML, MPD
HOXA9	*TRB-HOXA9*	*TRB*	*HOXA9*	t(7;7)(p15.2;q34)	ALL
HOXC11	*NUP98-HOXC11*	*NUP98*	*HOXC11*	t(11;12)(p15.4;q13.13)	AML
HOXC13	*NUP98-HOXC13*	*NUP98*	*HOXC13*	t(11;12)(p15.4;q13.13)	AML
IKZF1	*IKZF1-BCL6*	*IKZF1*	*BCL6*	t(3;7)(q27;p12)	NHL
IL3	*IGH-IL3*	*IGH*	*IL3*	t(5;14)(q31;q32)	ALL
IQGAP2	*IQGAP2-TSLP*	*IQGAP2*	*TSLP*	IQGAP2/TSLP	ALL
JAK2	*ATF7IP-JAK2*	*ATF7IP*	*JAK2*	t(9;12)(p24.1;p13.1)	ALL
JAK2	*BCR-JAK2*	*BCR*	*JAK2*	t(9;22)(p24;q11.23)	MPD, MDS/MPN, JMML, CMML, AML, ALL, CLL
JAK2	*EBF1-JAK2*	*EBF1*	*JAK2*	t(5;9)(q33.3;p24.1)	ALL
JAK2	*ETV6-JAK2*	*ETV6*	*JAK2*	t(9;12)(p24.1;p13.2)	MPD, MDS, ALL
JAK2	*GOLGA5-JAK2*	*GOLGA5*	*JAK2*	GOLGA5-JAK2	ALL
JAK2	*HMBOX1-JAK2*	*HMBOX1*	*JAK2*	t(8;9)(p21.1;p24.1)	ALL
JAK2	*JAK2-ETV6*	*JAK2*	*ETV6*	t(9;12)(p24.1;p13.2)	ALL, MPD, MDS
JAK2	*OFD1-JAK2*	*OFD1*	*JAK2*	t(X;9)(p22.2;p24.1)	ALL

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
JAK2	*PAX5-JAK2*	*PAX5*	*JAK2*	t(9;9)(p13.2;p24.1), del(9)(p13.2;p24.1), inv(9)(p13.2;24.1)	ALL
JAK2	*PCM1-JAK2*	*PCM1*	*JAK2*	t(8;9)(p22;p24.1)	MPD, AML, ALL, NHL
JAK2	*PPFIBP1-JAK2*	*PPFIBP1*	*JAK2*	PPFIBP1-JAK2	ALL
JAK2	*RFX3-JAK2*	*RFX3*	*JAK2*	t(9;9)(p24.2;p24.1)	ALL
JAK2	*SEC31A-JAK2*	*SEC31A*	*JAK2*	t(4;9)(q21.22;p24.1)	HL
JAK2	*SMU1-JAK2*	*SMU1*	*JAK2*	t(9;9)(p21.1;p24.1)	ALL
JAK2	*SNX29-JAK2*	*SNX29*	*JAK2*	t(9;16)(p24.1;p13.13)	ALL
JAK2	*SSBP2-JAK2*	*SSBP2*	*JAK2*	t(5;9)(q14.1;p24.1)	ALL
JAK2	*STRN3-JAK2*	*STRN3*	*JAK2*	t(9;14)(p24.1;q12)	ALL
JAK2	*TERF2-JAK2*	*TERF2*	*JAK2*	TERF2-JAK2	ALL
JAK2	*TPM3-JAK2*	*TPM3*	*JAK2*	t(1;9)(q21.3;p24.1)	ALL
JAK2	*TPR-JAK2*	*TPR*	*JAK2*	TPR-JAK2	ALL
JAK2	*USP25-JAK2*	*USP25*	*JAK2*	t(9;21)(p24.1;q21.1)	ALL
JAK2	*ZBTB46-JAK2*	*ZBTB46*	*JAK2*	NA	
JAK2	*ZNF274-JAK2*	*ZNF274*	*JAK2*	t(9;19)(p24.1;q13.43)	ALL
JAK2	*ZNF340-JAK2*	*ZNF340*	*JAK2*	ZNF340-JAK2	ALL
KAT6A	*CREBBP-KAT6A*	*CREBBP*	*KAT6A*	t(16;8)(p13.3;p11.21)	AML
KAT6A	*KAT6A-CREBBP*	*KAT6A*	*CREBBP*	t(8;16)(p11;p13)	AML
KAT6A	*KAT6A-EP300*	*KAT6A*	*EP300*	t(8;22)(p11;q13)	AML
KDM5A	*NUP98-KDM5A*	*NUP98*	*KDM5A*	t(11;12)(p15.4;p13.33), t(11;12)(p15.5;p13.5)	AML
KLF2	*TPM4-KLF2*	*TPM4*	*KLF2*	TPM4-KLF2	AML
KMT2A	*KMT2A-AFF1*	*KMT2A*	*AFF1*	t(4;11)(q21.3;q23.3)	ALL
KMT2A	*KMT2A-CREBBP*	*KMT2A*	*CREBBP*	t(11;16)(q23.3;p13.3)	MDS/MPN,JMML,CMML
KMT2A	*KMT2A-ELL*	*KMT2A*	*ELL*	t(11;19)(q23;p13.1)	AML
KMT2A	*KMT2A-EP300*	*KMT2A*	*EP300*	t(11;22)(q23.3;q13.2)	AML
KMT2A	*KMT2A-EPS15*	*KMT2A*	*EPS15*	t(1;11)(p32;q23)	ALL, AML, MDS
KMT2A	*KMT2A-FOXO3*	*KMT2A*	*FOXO3*	t(11;6)(q23.3;q21)	AML
KMT2A	*KMT2A-FOXO4*	*KMT2A*	*FOXO4*	t(X;11)(q13;q23)	AML, ALL
KMT2A	*KMT2A-MLLT1*	*KMT2A*	*MLLT1*	t(11;19)(q23;p13.3)	ALL, AML
KMT2A	*KMT2A-MLLT10*	*KMT2A*	*MLLT10*	t(10;11)(p12;q23)	AML
KMT2A	*KMT2A-MLLT11*	*KMT2A*	*MLLT11*	t(1;11)(q21;q23)	AML, ALL
KMT2A	***KMT2A-MLLT3*	*KMT2A*	*MLLT3*	t(9;11)(p21;q23)	AML
KMT2A	***KMT2A-MLLT4*	*KMT2A*	*MLLT4*	t(6;11)(q27;q23)	ALL
KMT2A	*KMT2A-MLLT6*	*KMT2A*	*MLLT6*	t(11;17)(q23.3;q12)	AML
KMT2A	*KMT2A-PICALM*	*KMT2A*	*PICALM*	t(11;11)(q14;q23), inv(11)(q14q23)	AML, ALL
KMT2A	*KMT2A-SEPT6*	*KMT2A*	*SEPT6*	t(X;11)(q24;q23.3)	AML
KMT2A	*KMT2A-SEPT9*	*KMT2A*	*SEPT9*	t(11;17)(q23.3;q25.2)	MDS, AML, ALL
KMT2A	*KMT2A-TET1*	*KMT2A*	*TET1*	t(10;11)(q22;q23)	ALL

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
KMT2A	*NUP98-KMT2A*	*NUP98*	*KMT2A*	t(11;11)(inv)(p15.4;q23.3)	AML, ALL, MM, MDS, HCL
LYN	*GATAD2A-LYN*	*GATAD2A*	*LYN*	t(8;19)(q12.1;p13.11)	ALL
LYN	*NCOR1-LYN*	*NCOR1*	*LYN*	t(8;17)(q12.1;p11)	ALL
MALT1	*IGH-MALT1*	*IGH*	*MALT1*	t(14;18)(q32.33;q21.32)	NHL
MECOM	*ETV6-MECOM*	*ETV6*	*MECOM*	t(12;3)(p13.2;q26.2)	AML, MDS, MPD
MECOM	*GATA2-MECOM*	*GATA2*	*MECOM*	inv(3)(q21.3q26.2) , t(3;3)(q21.3;q26.2)	AML
MECOM	*MECOM-CDK6*	*MECOM*	*CDK6*	t(3;7)(q26.2;q21.2)	AML,MPD
MKL1	*RBM15-MKL1*	*RBM15*	*MKL1*	t(1;22)(p13.3;q13.1)	AML
MLF1	*NPM1-MLF1*	*NPM1*	*MLF1*	t(3;5)(q25;q34)	MPD
MLLT10	*PICALM-MLLT10*	*PICALM*	*MLLT10*	t(10;11)(p12;q21)	AML, ALL
MYB	*MYB-GATA1*	*MYB*	*GATA1*	t(X;6)(p11;q23)	AML
MYC	*BCL11A-MYC*	*BCL11A*	*MYC*	t(2;8)(p15;q24.21)	NHL
MYC	*BCL3-MYC*	*BCL3*	*MYC*	t(8;19)(q24.21;q13.32)	CLL
MYC	*BCL6-MYC*	*BCL6*	*MYC*	t(3;8)(q27;q24)	NHL
MYC	*BTG1-MYC*	*BTG1*	*MYC*	t(8;12)(q24.21;q22)	ALL
MYC	*IGH-MYC*	*IGH*	*MYC*	t(8;14)(q24.21;q32.33)	ALL, NHL
MYC	*IGK-MYC*	*IGK*	*MYC*	t(2;8)(p12;q24.21)	ALL, NHL
MYC	*IGL-MYC*	*IGL*	*MYC*	t(8;22)(q24.21;q11.12)	ALL, NHL
MYC	*LRMP-MYC*	*LRMP*	*MYC*	t(8;12)(q24.21;p12.1)	CLL
MYC	*MYC-SUPT3H*	*MYC*	*SUPT3H*	t(6;8)(p21.1;q24.2)	MPD
MYC	*MYC-ZBTB5*	*MYC*	*ZBTB5*	t(8;9)(q24.21;p13.2)	NHL
MYC	*MYC-ZCCHC7*	*MYC*	*ZCCHC7*	t(8;9)(q24;p13)	NHL
MYC	*RNF213-MYC*	*RNF213*	*MYC*	t(8;17)(q24.21;q25.3)	NHL
MYC	*TRA-MYC*	*TRA*	*MYC*	t(8;14)(q24.21;q11.2)	ALL
MYH11	***CBFB-MYH11*	*CBFB*	*MYH11*	inv(16)(p13q22), t(16;16)(p13;q22), del(16)(q22)	AML, MDS
MYH9	*MYH9-IL2RB*	*MYH9*	*IL2RB*	NA	ALL
NF1	*NF1-LRRC37B*	*NF1*	*LRRC37B*	(17q11)	AML
NFKB2	*IGH-NFKB2*	*IGH*	*NFKB2*	t(14;10)(q32.33;q24.32)	MM, CLL
NOTCH1	*NOTCH1-NUP214*	*NOTCH1*	*NUP214*	t(9;9)(q34.3;q34.13)	
NSD1	*NUP98-NSD1*	*NUP98*	*NSD1*	t(5;11)(q35;p15.5)	AML
NTRK3	*ETV6-NTRK3*	*ETV6*	*NTRK3*	t(12;15)(p13.2;q25.3)	AML, MPD, ALL
NUP214	*SQSTM1-NUP214*	*SQSTM1*	*NUP214*	t(5;9)(q35.3;q34.13)	ALL, AML
PAX5	*PAX5-IGH*	*PAX5*	*IGH*	t(9;14)(p13.2;q32.33)	CLL
PAX5	*PAX5-PML*	*PAX5*	*PML*	t(9;15)(p13.2;q24.1)	ALL
PBX1	*AFF1-PBX1*	*AFF1*	*PBX1*	t(1;4)(q23.3;21.3)	ALL
PBX1	***TCF3-PBX1*	*TCF3*	*PBX1*	t(1;19)(q23;p13.3)	ALL, NHL
PDGFRA	*BCR-PDGFRA*	*BCR*	*PDGFRA*	t(4;22)(q12;q11)	MPD
PDGFRA	*CDK5RAP2-PDGFRA*	*CDK5RAP2*	*PDGFRA*	t(9;4)(q33.2;q12)	MPD

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
PDGFRA	*ETV6-PDGFRA*	*ETV6*	*PDGFRA*	t(4;12)(q12;p13.2)	MPD
PDGFRA	*FIP1L1-PDGFRA*	*FIP1L1*	*PDGFRA*	del(4)(q12q12)	MPD
PDGFRA	*KIF5B-PDGFRA*	*KIF5B*	*PDGFRA*	t(10;4)(p11.22;q12)	MPD
PDGFRA	*STRN-PDGFRA*	*STRN*	*PDGFRA*	t(2;4)(p22.2;q12)	MPD
PDGFRA	*TNKS2-PDGFRA*	*TNKS2*	*PDGFRA*	TNKS2 / PDGFRA	MPD
PDGFRB	*ATF7IP-PDGFRB*	*ATF7IP*	*PDGFRB*	t(5;12)(q32;p13.1)	ALL
PDGFRB	*BIN2-PDGFRB*	*BIN2*	*PDGFRB*	t(5;12)(q32;q13.13)	MPD
PDGFRB	*CAPRIN1-PDGFRB*	*CAPRIN1*	*PDGFRB*	t(5;11)(q32;p13)	MPD
PDGFRB	*CCDC6-PDGFRB*	*CCDC6*	*PDGFRB*	t(5;10)(q32;q21.2)	MPD
PDGFRB	*CCDC88C-PDGFRB*	*CCDC88C*	*PDGFRB*	t(5;14)(q32;q32.11)	MPD
PDGFRB	*COL1A1-PDGFRB*	*COL1A1*	*PDGFRB*	t(5;17)(q32;q21.3)	MDS/MPN, JMML, CMML
PDGFRB	*DTD1-PDGFRB*	*DTD1*	*PDGFRB*	t(5;20)(q32;p11.23)	MPD
PDGFRB	*EBF1-PDGFRB*	*EBF1*	*PDGFRB*	t(5;5)(q32;q33.3); del(5)(q32q33.3)	ALL
PDGFRB	*ERC1-PDGFRB*	*ERC1*	*PDGFRB*	t(5;12)(q32;p13.33)	AML
PDGFRB	*ETV6-PDGFRB*	*ETV6*	*PDGFRB*	t(5;12)(q32;p13.2)	MDS/MPN, JMML, CMML
PDGFRB	*GIT2-PDGFRB*	*GIT2*	*PDGFRB*	t(5;12)(q32;q24.11)	MPD
PDGFRB	*GOLGA4-PDGFRB*	*GOLGA4*	*PDGFRB*	t(3;5)(p22.2;q32)	MPD
PDGFRB	*HECW1-PDGFRB*	*HECW1*	*PDGFRB*	t(5;7)(q32;p14.1)	MDS/MPN, JMML, CMML
PDGFRB	*HIP1-PDGFRB*	*HIP1*	*PDGFRB*	t(5;7)(q32;q11.23)	MDS/MPN, JMML, CMML
PDGFRB	*KANK1-PDGFRB*	*KANK1*	*PDGFRB*	t(5;9)(q32;p24.3)	MDS/MPN, JMML, CMML
PDGFRB	*MYO18A-PDGFRB*	*MYO18A*	*PDGFRB*	t(5;17)(q32;q11.2)	MPD
PDGFRB	*NDE1-PDGFRB*	*NDE1*	*PDGFRB*	t(5;16)(q32;p13.11)	MDS
PDGFRB	*NIN-PDGFRB*	*NIN*	*PDGFRB*	t(5;14)(q32;q22.1)	MPD
PDGFRB	*PDE4DIP-PDGFRB*	*PDE4DIP*	*PDGFRB*	t(1;5)(q21;q32)	MDS/MPN, JMML, CMML, MPD, ALL
PDGFRB	*PRKG2-PDGFRB*	*PRKG2*	*PDGFRB*	t(4;5)(q21;q33)	MPD
PDGFRB	*RABEP1-PDGFRB*	*RABEP1*	*PDGFRB*	t(5;17)(q32;p13.2)	MDS/MPN, JMML, CMML, MPD
PDGFRB	*SART3-PDGFRB*	*SART3*	*PDGFRB*	t(5;12)(q32;q23.3)	MDS/MPN, JMML, CMML
PDGFRB	*SNX29-PDGFRB*	*SNX29*	*PDGFRB*	SNX29/PDGFRB	ALL
PDGFRB	*SPECC1-PDGFRB*	*SPECC1*	*PDGFRB*	t(5;17)(q32;p11.2)	MDS/MPN, JMML, CMML
PDGFRB	*SPTBN1-PDGFRB*	*SPTBN1*	*PDGFRB*	t(2;5)(p16.2;q32)	MPD
PDGFRB	*SSBP2-PDGFRB*	*SSBP2*	*PDGFRB*	SSBP2-PDGFRB	ALL
PDGFRB	*TNIP1-PDGFRB*	*TNIP1*	*PDGFRB*	t(5;5)(q32;q33.1)	ALL
PDGFRB	*TP53BP1-PDGFRB*	*TP53BP1*	*PDGFRB*	t(5;15)(q32;q15.3)	MPD

Oncogenic partner	Fusion	5'Gene	3'Gene	Chromosomal Aberration	Major Disease type
PDGFRB	*TPM3-PDGFRB*	*TPM3*	*PDGFRB*	t(1;5)(q21.3;q32)	MPD
PDGFRB	*TRIP11-PDGFRB*	*TRIP11*	*PDGFRB*	t(5;14)(q32;q32.12)	AML
PDGFRB	*WDR48-PDGFRB*	*WDR48*	*PDGFRB*	t(3;5)(p22.2;q32)	MPD
PDGFRB	*ZEB2-PDGFRB*	*ZEB2*	*PDGFRB*	ZEB2/PDGFRB	ALL
PDGFRB	*ZMYND8-PDGFRB*	*ZMYND8*	*PDGFRB*	t(5;20)(q32.13;q13)	ALL
PRDM16	*ETV6-PRDM16*	*ETV6*	*PRDM16*	t(1;12)(p36.32;p13.2)	AML
PTK2B	*KDM6A-PTK2B*	*KDM6A*	*PTK2B*	KDM6A-PTK2B	ALL
RARA	*ETV6-RARA*	*ETV6*	*RARA*	t(12;17)(p13.2;q21.2)	AML
RARA	*FIP1L1-RARA*	*FIP1L1*	*RARA*	t(4;17)(q12;q21.2)	MDS/MPN, JMML, CMML, AML
RARA	*GTF2I-RARA*	*GTF2I*	*RARA*	t(7;17)(q11.23;q21.2)	AML
RARA	*NPM1-RARA*	*NPM1*	*RARA*	t(5;17)(q35.1;q21.2)	AML
RARA	*NUMA1-RARA*	*NUMA1*	*RARA*	t(11;17)(q13.4;q21.2)	AML
RARA	***PML-RARA*	*PML*	*RARA*	t(15;17)(q24;q21)	AML
RARA	*STAT5B-RARA*	*STAT5B*	*RARA*	t(17;17)(q21;q21), dup(17)(q12q21)	AML
RARA	*ZBTB16-RARA*	*ZBTB16*	*RARA*	t(11;17)(q23;q21)	AML
RUNX1 (AML1)	***ETV6-RUNX1*	*ETV6*	*RUNX1*	t(12;21)(p13;q22)	ALL
RUNX1 (AML1)	*MECOM-RUNX1*	*MECOM*	*RUNX1*	t(3;21)(q26.2;q22.1)	CML,MDS,AML
RUNX1 (AML1)	*RUNX1-CBFA2T3*	*RUNX1*	*CBFA2T3*	t(21;16)(q22.12;q24.3)	MDS,AML
RUNX1 (AML1)	*RUNX1-FGA7*	*RUNX1*	*FGA7*	t(4;21)(q28;q22)	ALL
RUNX1 (AML1)	*RUNX1-PRDM16*	*RUNX1*	*PRDM16*	t(21;1)(q22.12;p36.32)	AML,MDS
RUNX1 (AML1)	***RUNX1-RUNX1T1*	*RUNX1*	*RUNX1T1*	t(8;21)(q22;q22.1)	AML
SET	*FUS-SET*	*FUS*	*SET*	t(9;16)(q34.11;p11.2)	ALL
SET	*SET-NUP214*	*SET*	*NUP214*	t(9;9)(q34.11;q34.13)	ALL
SETD2	*SETD2-CCDC12*	*SETD2*	*CCDC12*	3p21	ALL
STIL	***TAL1-STIL*	*TAL1*	*STIL*	TAL1-STIL	ALL
TCF3	*TCF3-HLF*	*TCF3*	*HLF*	t(17;19)(q22;p13)	ALL
TCF3	*TCF3-ZNF384*	*TCF3*	*ZNF384*	t(12;19)(p13;p13)	ALL
TFE3	*NONO-TFE3*	*NONO*	*TFE3*	t(X;X)(p11;q13)	ALL
TFE3	*TFE3-NONO*	*TFE3*	*NONO*	t(X;X)(p11;q13)	ALL
TOP1	*NUP98-TOP1*	*NUP98*	*TOP1*	t(11;20)(p15.4;q12), t(11;20)(p15.4;q11)	AML
TYK2	*MYB-TYK2*	*MYB*	*TYK2*	MYB-TYK2	ALL
TYK2	*NPM1-TYK2*	*NPM1*	*TYK2*	t(5;19)(q35.1;p13.2)	NHL
TYK2	*SMARCA4-TYK2*	*SMARCA4*	*TYK2*	t(19;19)(p13.2;p13.2)	ALL
TYK2	*ZNF340-TYK2*	*ZNF340*	*TYK2*	ZNF340-TYK2	ALL

ABBREVIATIONS

aCML	*Atypical Chronic Myeloid Leukemia*
AL	*Acute Leukemia*
ALCL	*Anaplastic Large Cell Lymphoma*
ALL	*Acute Lymphoblastic Leukemia*
AML	*Acute Myeloid Leukemia*
AMKL/AM	*Acute Megakaryoblastic Leukemia*
APML/AML	*Acute Promyelocytic Leukemia*
B-ALL	*B-Cell Acute Lymphoblastic Leukemia*
B-CLL	*B-Cell Chronic Lymphoblastic Leukemia*
BL	*Burkitt Lymphoma*
BLL	*B Cell Lymphoblastic Leukemia*
CBL	*Chronic Basophilic Leukemia*
CEL	*Chronic Eosinophilic Leukemia*
CLL	*Chronic Lymphocytic Leukaemia*
CML	*Chronic Myeloid Leukemia*
CMML	*Chronic Myelomonocytic Leukemia*
DLBCL	*Diffused Large B-Cell Lymphoma*
FL	*Follicular Lymphoma*
HCL	*Hairy Cell Leukemia*
HL	*Hodgkin Lymphoma*
IMT	*Inflammatory Myofibroblastic Tumor*
JMML	*Juvenile Myelomonocytic Leukemia*
MCL	*Mantle Cell Lymphoma*
MDS	*Myelodysplastic Syndrome*
MM	*Multiple Myeloma*
MPD	*Myeloproliferative Disorder*
MPN	*Myeloproliferative Neoplasm*
MPS	*Myeloproliferative Syndrome*
NHL	*Non-Hodgkin Lymphoma*
PCL	*Plasma Cell Leukemia*
PCM	*Plasma cell Myeloma*
PCNSL	*Primary Central Nervous System Lymphoma*
PMBCL	*Primary Mediastinal B-Cell Lymphoma*
PV	*Polycythemia vera*
SLVL	*Splenic Lymphoma with Villous Lymphocytes*
SMCD	*Systemic Mast Cell Disease*
T-ALL	*T-Cell Acute Lymphoblastic Leukemia*
TLL	*T-Cell Lymphocytic Lymphoma*
TRL	*Treatment/Therapy Related Leukemia*





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END OF REPORT

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HARI IMAGING & DIAGNOSTIC CENTRE

Patient name	Ms. V. SNIGDHA	**Age/Sex**	14 Years / Female
Patient ID	20260522-125154-BE87	**Visit no**	1
Referred by	Dr. CH GIRISH GARU, MD(PEAD).	**Visit date**	22/05/2026

USG ABDOMEN AND PELVIS

Liver: Normal in size and normal in echotexture. Intrahepatic biliary radicles normal. No focal lesion.

Portal vein: 9mm, Normal.

Gall bladder: normally distended. No calculi.

CBD: 3mm, Normal.

Spleen: Enlarged in size and normal in echotexture.

Pancreas: Normal in size and normal in echotexture. MPD is normal.

Right kidney: 9.3 x 3.6 cms, normal in size and cortical echotexture normal.No calculus/ hydronephrosis.

Left kidney: 10.5 x 3.6 cms, normal in size and cortical echotexture normal.No calculus/ hydronephrosis.

Urinary bladder: Normally distended. No calculi. No mass lesion.

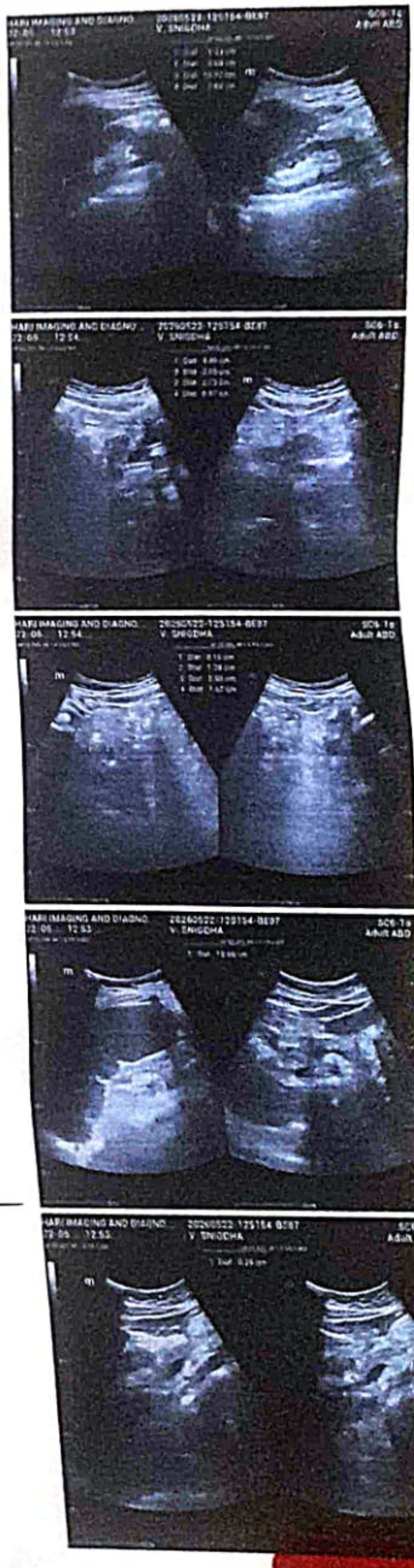
Uterus: 4.4 X 2.0 X 2.7 cms, Normal in size and normal in echotexture.

ET: 6mm.

Right Ovary:2.1 x 1.2 cms, Normal in size and echotexture.

Left Ovary: 2.5 x 1.6cms, Normal in size and echotexture.

* Few prominent thickend bowel loops in abdomen - Enteritis.
* No ascites. * No retroperitoneal nodes seen.
* No pleural effusions. * Aorta, IVC are normal.
* Right iliac fossa: Appendix is not visualized.



IMPRESSION:

*** Mild splenomegaly.**

*** Few prominent thickend bowel loops in abdomen - Enteritis.**

For clinical correlation

Dr HARISCHANDRA PRASAD. N, MBBS, DNB.
CONSULTANT RADIOLOGIST

Dr. Harischandra Prasad N.
MBBS.DNB
Consultant Radiologist
Regd. No: 51435

"Sex determination is Crime as per PC & PNDT Act. - లింగ నిర్ధారణ చట్ట ప్రకారం నేరం"

D.No.13-1-13, Old Bank Street, Kothapet, GUNTUR-522 001.

PRAGATHI DIAGNOSTICS

Old Club Road, Kothapet, GUNTUR - 522 001. Cell : 89190 78741

Patient Name: V.SNIGDHA | Age / Sex : 14 Years / Female | Date: 22/05/2026

Ref.By: Dr.CH.GIRISH.M.D,, | Lab No: 8639 | Time: 2:00PM

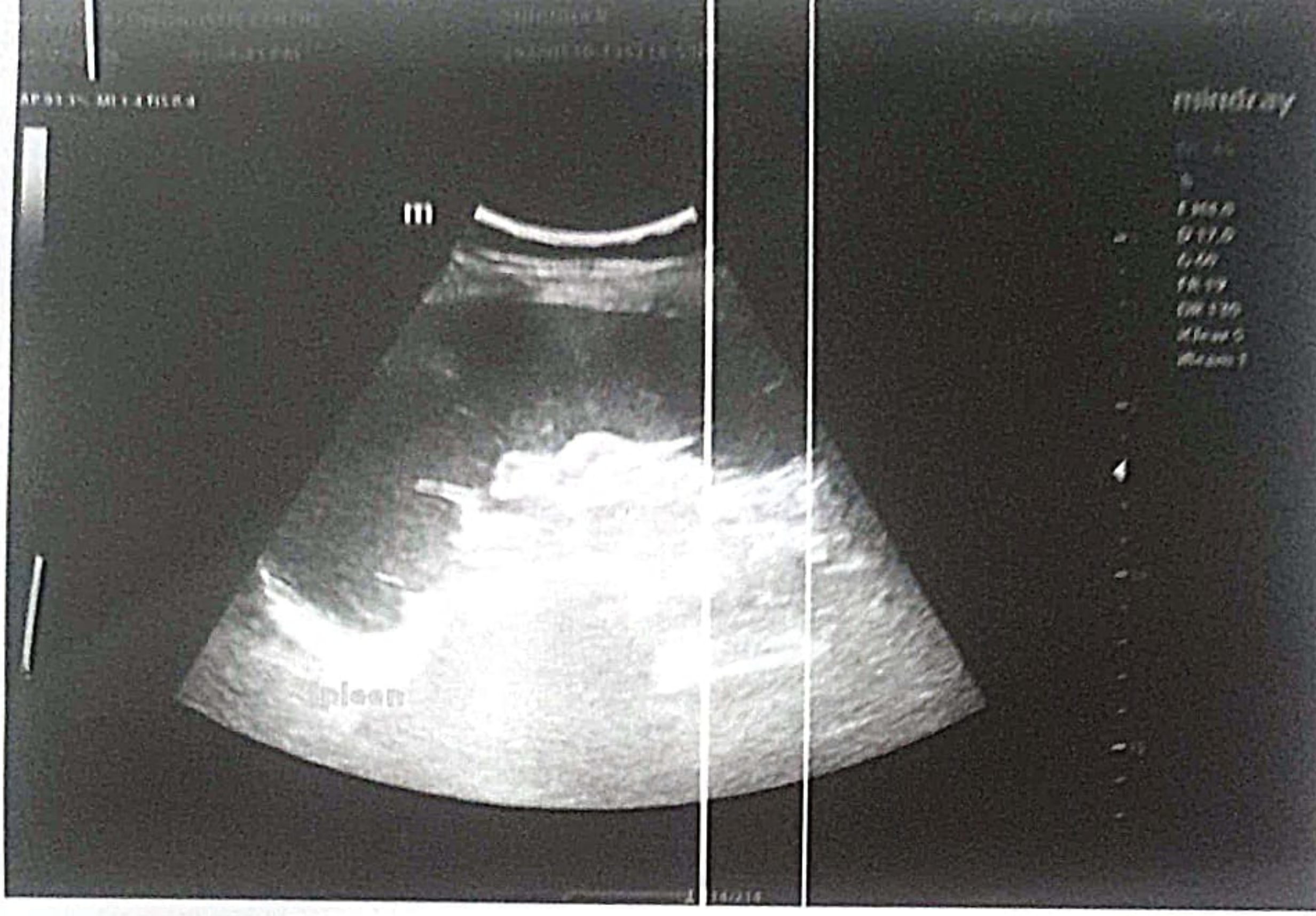
COMPLET BLOOD PITCURE

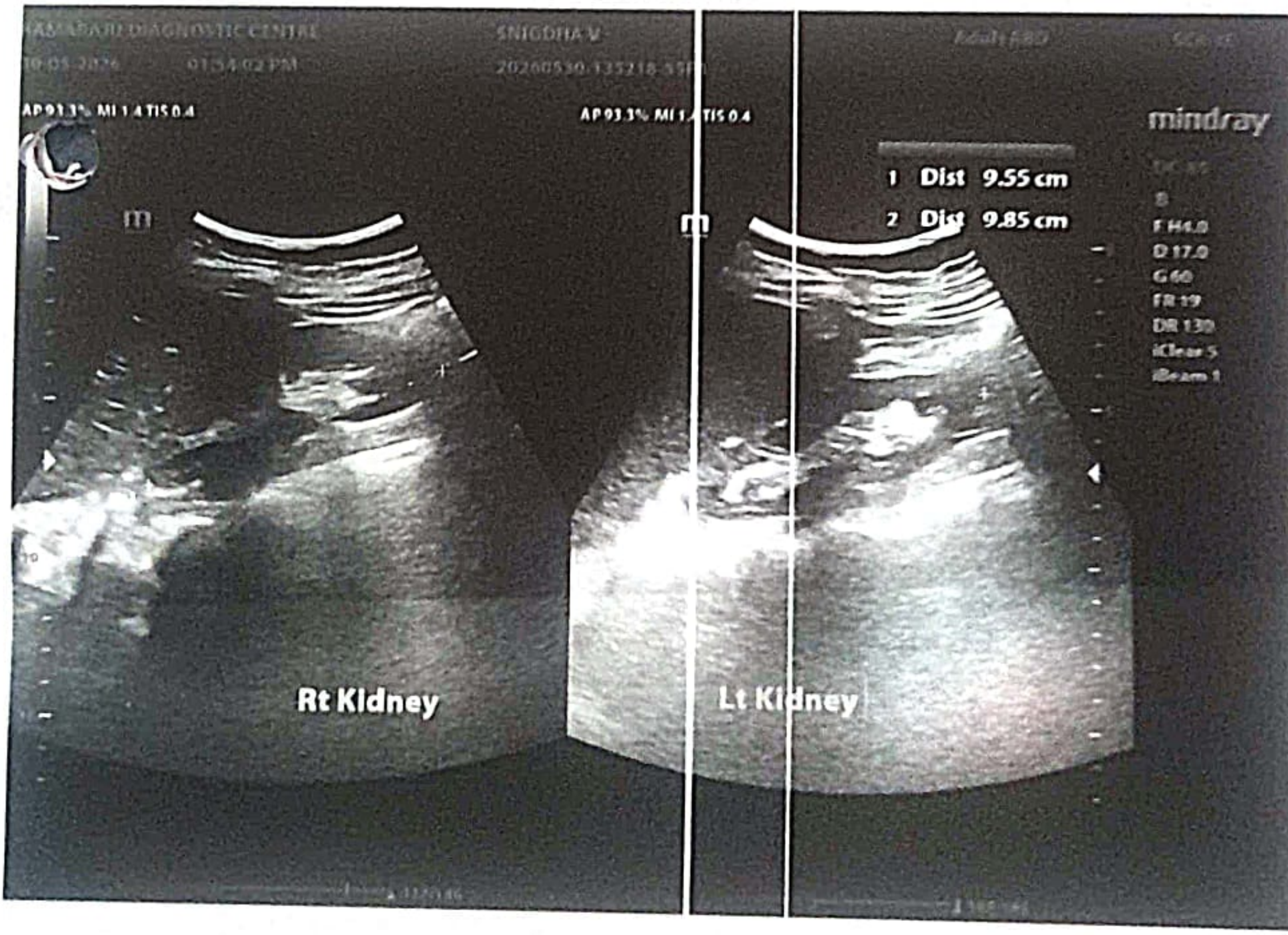
TEST	RESULT	NORMAL RANGE
TOTAL WBC COUNT	: 12.000 cells/cumm	4.000 - 11.000 cells/cumm
TOTAL RBC COUNT	: 5.18 mill/cumm	4.50 - 6.50 mill/cumm
HEMOGLOBIN	: 11.4 gms/dl	14.00 - 17.00 gms/dl
PCV	: 48.2 vol	42.00 - 52.00 vol
M[illegible]	: 93.1 Fl	76.00 - 96.00 Fl
MCH	: 22.0 Pg	27.00 - 32.00 Pg
MCHC	: 23.6 Gms/dl	32.00 - 36.00 Gms/dl
PLATELET COUNT	: 1.94.000 laks/cumm	1.50.000 - 4.50.000 laks/cumm
DIFFERENTIAL COUNT		
PLOYMORPHS	: 70 %	45.00 - 70.00 %
LYMPHOCYTES	: 20 %	20.00 - 40.00 %
MIXED CELLS	: 10 %	4.00 - 16.00 %
SEROLOGY		
C.REACTIVE PROTEIN	: 19.0 mg/l	1.00 - 6.00 mg/l

Please correlate clinically

*[illegible]dicates values out of range

Lab Incharge


Spleen


1 Dist 9.55 cm
2 Dist 9.85 cm
Rt Kidney
Lt Kidney

76026 V. SNIGDHA
14 Years Female

Rate 132 ---------- Pediatric ECG Interpretation ----------
Sinus tachycardia

PR 124
QRSD 80
QT 298
QTc 439

--AXIS--
P 47
QRS 91
T -4

12 Lead, Standard Placement

Unconfirmed Diagnosis



భారత ప్రభుత్వం

Government of India



Issue Date: 01/02/2017

వీరవల్లి స్నిగ్ధ చౌదరి

Veeravalli Snigdha Choudary

పుట్టిన తేది / DOB: 22/11/2012

స్త్రీ / Female

5250 3532 6146

నా ఆధార్, నా గుర్తింపు