

Patient ID SA00148982	Patient Name TESTINGRNV, COGMF-ABNORMAL	Birth Date 2007-10-16	Gender M	Age 13
Order Number SA00148982	Client Order Number SA00148982	Ordering Physician CLIENT,CLIENT	Report Notes	
Account Information C7028846 DLMP Rochester		Collected 14 Oct 2021 06:11		

COG, AML, FISH

Result Summary

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Abnormal

Interpretation

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The result is abnormal and indicates RUNX1T1/RUNX1 fusion in 87.5% of nuclei. This result usually indicates a t(8;21).

This 8;21 translocation has been associated with both de novo and therapy-related AML and has a favorable prognosis. Molecular studies to determine KIT mutational status should be considered in core binding factor leukemias [t(8;21), inv(16)/t(16;16)] as KIT mutations confer an intermediate-risk status (Swerdlow et al., WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues. IARC Press:Lyon, 2017; page 132; NCCN Guidelines Version 3.2021, AML).

Clinical and pathologic correlation is recommended.

For monitoring response to therapy, RT-PCR for t(8;21) RUNX1T1/RUNX1 is recommended, per NCCN guidelines; Test: T821Q. Although RT-PCR testing is not available on the current specimen, this testing can be performed on blood or bone marrow collected in EDTA or ACD. Please call 800-533-1710 regarding specimen requirements for RT-PCR based tests.

Result Table

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Abnormality Name	Result	Abn%	Cutoff%
t(8;21) RUNX1T1/RUNX1 fusion	Abnormal	87.5	<4.0
11q23(MLL sep)	Normal		<10.0
t(15;17) PML/RARA fusion	Normal		<4.0
inv(16)/t(16;16) MYH11/CBFB fusion	Normal		<4.0
-5q31(D5S630x2,EGR1x1)	Normal		<12.0
-5(D5S630,EGR1)x1	Normal		<10.0
-7q31(D7Z1x2,D7S486x1)	Normal		<12.0
-7(D7Z1,D7S486)x1	Normal		<10.0
inv(3) RPN1/MECOM fusion	Normal		<4.0
t(6;9) DEK/NUP214 fusion	Normal		<4.0
12p13.2(ETV6 sep)	Normal		<10.0
t(8;16) KAT6A/CREBBP fusion	Normal		<4.0
inv(16)/t(16;16)GLIS2/CBFA2T3 fusion	Normal		<4.0
11p15.4(NUP98 sep)	Normal		<10.0
t(1;22) RBM15/MKL1 fusion	Normal		<4.0

Result

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nuc ish(RUNX1T1,RUNX1)x3(RUNX1T1 con RUNX1x2)[175/200]

Reason for Referral

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AML, COG AAML1831

Specimen

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Bone Marrow

Source

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Left posterior iliac crest

Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	William G. Morice M.D. Ph.D	24D0404292



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Method

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Locus and probes	[Strategy;#Nuclei;Class]
1p13(RBM15), 22q13(MKL1)	[DFISH;200;LDT]
3q21(RPN1), 3q26.2(MECOM)	[DFISH;200;LDT]
5p15.2(D5S630), 5q31(EGR1)	[COPY#;100;AM]
6p23(DEK), 9q34(NUP214)	[DFISH;200;LDT]
7CEN(D7Z1), 7q31(D7S486)	[COPY#;100;AM]
8p11.2(KAT6A), 16p13.3(CREBBP)	[DFISH;200;LDT]
8q22(RUNX1T1), 21q22(RUNX1)	[DFISH;200;AM]
11p15.4(3'NUP98,5'NUP98)	[BAP;100;LDT]
11q23(5'MLL[KMT2A],3'MLL[KMT2A])	[BAP;100;AM]
12p13.2(5'ETV6,3'ETV6)	[BAP;100;LDT]
15q24.1(PML), 17q21(RARA)	[DFISH;200;AM]
16p13.3(GLIS2), 16q24.3(CBFA2T3)	[DFISH;200;LDT]
16p13(MYH11), 16q22(CBFB)	[DFISH;200;LDT]

Probe strategies include:
DFISH=dual color, double fusion;
BAP=break-apart probe;

COPY#=region gain and loss.
Scoring Method: Manual

Probe vendors include:
LDT = Mayo Clinic Developed
AM = Abbott Molecular, Inc (Des Plaines, IL)

Disclaimer

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Applicable to Analyte Specific Reagent (ASR) and Laboratory Developed Tests (LDT). This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the U.S. Food and Drug Administration. This FISH test does not rule out other chromosome abnormalities.

Released By

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Jess F. Peterson, M.D.

Received: 15 Oct 2021 07:41

Reported: 25 Oct 2021 10:39

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