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**PATIENT REPORT**

Patient Age/Sex: Unknown

**Specimen Collected: 11/15/2024 12:06 MST**

**X-RUNX1::RUNX1T1 (AML1::ETO) Quantitative** | **Received: 11/15/2024 12:07 MST** | **Report/Verified: 11/15/2024 12:11 MST**

| Procedure | Result | Units | Reference Interval |
|---|---|---|---|
| RUNX1::RUNX1T1 Source | Whole Blood | | |
| RUNX1::RUNX1T1 Result | Detected [f1 i1] | | |
| RUNX1::RUNX1T1/ABL1 Ratio | 1.00000 | | |

## Result Footnote

f1: RUNX1::RUNX1T1 Result

RUNX1::RUNX1T1 (AML1::ETO) fusion transcripts were detected by RT-qPCR. This indicates the presence of t(8;21) positive cells in the sample.

This result has been reviewed and approved by Margaret C. Williams, M.D.

## Test Information

i1: RUNX1::RUNX1T1 Result

INTERPRETIVE INFORMATION: RUNX1::-RUNX1T1 (AML1::-ETO) t(8;21) Quantitative

This test is designed to detect and quantify RUNX1::RUNX1T1 (AML1::ETO) fusion transcripts which result from t(8;21); RUNX1::RUNX1T1, a recurrent genetic abnormality found in a subset of patients with acute myeloid leukemia.

Methodology:
Patient RNA is isolated, reverse transcribed into cDNA, and amplified using primers specific for the RUNX1 and RUNX1T1 genes. Each PCR assay includes a standard curve for RUNX1::RUNX1T1 and the ABL1 control and a normalized copy number (NCN) is calculated (number of RUNX1::RUNX1T1 cDNA molecules/number of ABL1 cDNA molecules).

Limitations: Translocations involving other genes or gene partners will not be detected.
Limit of detection for this test is 1 in 100,000.

Results of this test must always be interpreted within the patient's clinical context and in conjunction with other relevant data. Results should not be used alone for a diagnosis of malignancy.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA-certified laboratory and is intended for clinical purposes.