AML ETO (8; 21) GENE REARRANGEMENT, PCR QUALITATIVE

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Note:

1. Sensitivity of the assay is 0.01% when copies of ABL detected is 100,000
2. Limit of detection is 10 copies of 8;21 fusion gene transcripts per PCR
3. This is an in-house developed assay designed as per EAC (Europe Against Cancer) protocol
4. Test conducted on Whole blood / Bone Marrow.

Comments

Cytogenetic aberrations play a central role in the classification of AML. These aberrations are detected in 50-70% cases of AML by using standard techniques. The AML1 (CBFA2, RUNX1)-ETO (MTG8) gene fusion results from the t (8; 21) (q22; q22), which is the commonest chromosomal rearrangement associated with AML, being detected in approximately 8% of AML cases in children and young adults. Most t(8;21) positive AML's are de novo leukemias - vast majority being M2 FAB subtype. This translocation creates chimeric genes encoding fusion proteins that interfere with the function of CBFα and block the maturation of myeloid cells.

Uses

- For diagnostic identification of AML having morphological, imuunophenotypic or clinical features strongly suggestive of translocation 8; 21.
- For prognostic evaluation - Presence of this translocation is associated with a favorable prognosis.