Inv 16 **(p13q22)**/ **t (16; 16) (p13; q22)** GENE REARRANGEMENT, PCR QUALITATIVE

Inv 16 **(p13q22)** / **t(16;16)(p13;q22)** GENE REARRANGEMENT, PCR QUALITATIVE (Real Time PCR)

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 Inv(16) (p13q22) / t(16;16)(p13;q22) with the CBFB-MYH11 fusion gene transcript per PCR
3. This is an in-house developed assay designed as per EAC (Europe Against Cancer) protocol
4. This tests detects A, D, and E transcripts but does not distinguish between them.
5. 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. Pericentric inversion of chromosome 16, inv (16) (p13q22), is found in about 4% of cytogenetically abnormal AML cases. Inv (16) or the rarer t (16; 16) (p13; q22) creates chimeric genes encoding fusion genes that interfere with the function of CBFα and block the maturation of myeloid cells. Around 10 different CBFB-MYH11 FG transcripts have been reported. More than 85% of positive patients have the type A transcript; type D and E transcripts each represent nearly 5%, whereas all other types occur sporadically.

Uses

- For diagnostic identification of AML having morphological, imuunophenotypic or clinical features strongly suggestive of M4eo FAB subtype
- For prognostic evaluation - Presence of this translocation is associated with a favorable prognosis.