Cat Nr/REF: KBI-10304

English

For professional use only

Poseidon™ Repeat Free™ CBFB t(16;16), inv(16) Break probe

Introduction: The pericentric inversion of chromosome 16 and the t(16;16) are two recurrent aberrations in bone marrow of patients with acute myeloid leukaemia (AML). The inversion creates a novel fusion gene, CBFB (16q22) /MYH11 (16p13), which appears to be critical for leukemic transformation. In 20% of all cases the inv(16) is associated with an additional deletion of sequences proximal to the 16p-arm breakpoint.

Intended use: **The CBFB t(16;16) inv(16) Break** Probe is optimized to detect the inversion of chromosome 16 involving the CBFB gene region at 16q22 in a dual-color, split assay on metaphase/interphase spreads, blood smears and bone marrow cells.

The probe is recommended to be used in combination with a Poseidon FISH Kit providing necessary reagents to perform FISH (KBI-60002, KBI-60003 or KBI-60001) for optimal results.

Critical region 1 (red): The **distal CBFB** gene region probe is direct-labeled with Platinum*Bright*550.

Critical region 2 (green): The **proximal CBFB** gene region probe is direct-labeled with Platinum*Bright*495.

Reagent: Poseidon probes are direct-labeled DNA probes provided in a ready-to-use format. Apply 10 µl of probe to a sample area of approximately 22 x 22 mm.

Please refer to the Instructions for Use for the entire Poseidon FISH protocol.

Poseidon Repeat Free probes do not contain Cot-1 DNA. Hybridization efficiency is therefore increased and background, due to unspecific binding, is highly reduced.

Interpretation: The **CBFB Break** probe is designed as a dual-color split probe to detect inversion or translocations at 16q22. A break is defined when a red/green or yellow fusion signals (F) splits into separate red and green signals. Only red and green signals which are more than one signal diameter apart from each other are counted as a break. Co-localized red/green or yellow signals identify the normal chromosome(s) 16.

Signal patterns other than those described above may indicate variant translocations or other complex rearrangements. Investigators are advised to analyze metaphase cells for the interpretation of atypical signal patterns.

	Normal Signal Pattern	t(16;16), inv(16)
Expected Signals	2F	1F1R1G

References: Dauwerse JG et al, 1993, Hum.Mol.Genet., 2; 1527-1534
Poirel H et al, 1995, Blood, 85; 1313-1322

POSEIDON™
REPEAT-FREE™ FISH PROBES

Application Manual

KBI-10304
ON CBFB t(16;16); inv(16) Break

IVD
for EU only

CE

KREATECH Diagnostics
Vlierweg 20
1032 LG Amsterdam
The Netherlands

2°C 8°C long term storage

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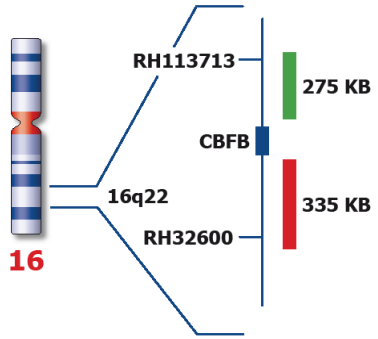

Not to scale

Application manual