Cat Nr/REF: KBI-10729

English

For professional use only

Poseidon™ Repeat Free™ IGH (14q32) Break probe
- Optimized for Tissue Hybridization -

Introduction: Translocation involving the immunoglobulin heavy chain (IGH) locus are frequent in Multiple Myeloma and Lymphomas. Translocations involving an IgH switch region uniquely dissociate the intronic and 3' IgH enhancers, so that an oncogene might be juxtaposed to an IgH enhancer on each of the derivative chromosomes.

Intended use: The **IGH (14q32) Break** Probe is optimized to detect translocations involving the IGH gene region at 14q32 in a dual-color, split assay.

The probe is especially developed for use on paraffin sections and 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. For applications on metaphase/interphase spreads, blood smears and bone marrow cells it is advised to use KBI-10601.

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

Critical region 2 (green): The **distal IGH** 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 **IGH Break** probe is designed as a dual-color split probe to detect inversion or translocations at 14q32. 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) 14.

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	14q32 Split
Expected Signals	2F	1F1R1G

References:

Nishida K et al, 1997, Blood, 90; 526-534
Ueda Y et al, 1996, Blood, 87; 292-298

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POSEIDON™
REPEAT-FREE™ FISH PROBES

Application Manual

KBI-10729
ON IGH (14q32) Break, (tissue)

IVD
for EU only

CE

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2°C 8°C
long term storage

KREATECH DIAGNOSTICS

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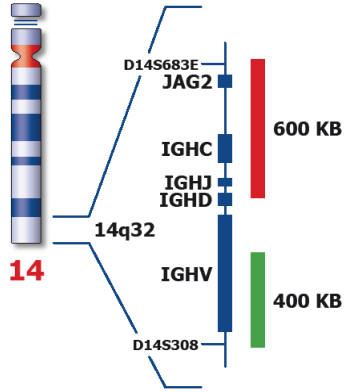
Application manual



Not to scale