ITALIA
Empowering Personalized Cancer Treatment

IGH Break Apart DNA-FISH Probe

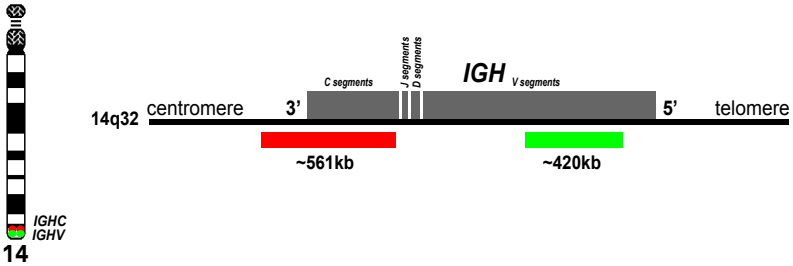
Two Color, Break Apart Probe CE

Ref: 13-014

IGH Break Apart

Intended Use

The *IGH* Break Apart DNA-FISH Probe is designed to detect the translocation involving the immunoglobulin heavy chain (*IGH*) locus on chromosome 14q32 using fluorescence *in situ* hybridization (FISH). At least 40 translocation gene partners to the *IGH* locus have been identified.[1] Rearrangements involving the *IGH* locus and specific partners are mainly found in multiple myeloma (MM)[2,3] and non-Hodgkin's lymphoma (NHL) subtypes.[1,4] The prognosis is dependent upon the translocation partner and the type of malignancy. The design of the *IGH* Break Apart DNA-FISH Probe allows the visualization of a break between the constant C domain (red) and the variable V domain (green) of the *IGH* locus and the resulting translocation.



Schematic of the *IGH* Break Apart DNA-FISH Probe:

Horizontal red and green bars indicate the region covered by the probes (approximate to scale, NCBI 36.1/HG18/2006). The directly labeled 3' *IGHC* (red) and the 5' *IGHV* (green) probes flank the most common breakpoints occuring in B-cell neoplasms.

Signal Interpretation

In normal diploid metaphase and interphase nuclei and metaphases, the *IGH* Break Apart DNA-FISH Probe generates two fusion signals (red/green or yellow) corresponding to the two normal homologous chromosomes 14 (Figure 1). In cells with chromosomal rearrangement involving the *IGH* locus, the most commonly observed pattern is one fusion, representing the normal chromosome 14, and a single red and green signal, representing the derivative chromosomes (Figure 2). Under some circumstances, faint additional green signals may be observed due to cross-hybridization with *IGH* pseudogenes on 15q11 and 16p11; this should not be confused with additional signals due to translocation. Unusual breakpoints, *IGH* deletions, additional copies of chromosome 14, unbalanced translocations, or multiple copies of derivatives may result in variant patterns and these should be confirmed by metaphase analysis whenever possible.

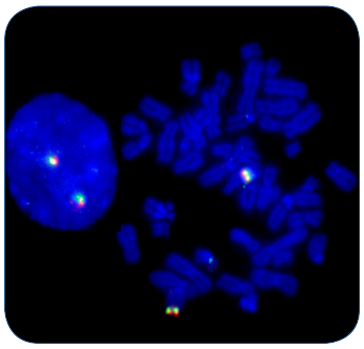


Figure 1: Normal diploid metaphase and interphase nucleus (from normal peripheral blood specimen) with 2 fusion signals (red/green or yellow).

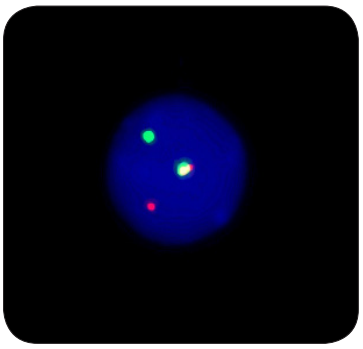


Figure 2: Interphase nuclei with 1 fusion (red/green or yellow), 1 red (3' *IGHC*), and 1 green (5' *IGHV*) signals.

References

1. Bernicot, L., et al. Cytogenet Genome Res, 2007. 118(2-4):345-52.
2. Moreau, P., et al. Blood, 2002. 100(5):1579-83.
3. Avet-Loiseau, H., et al. Blood, 2002. 99(6):2185-91.
4. Haferlach, C., et al. Leukemia, 2007. 21(12):2442-51.

Fluorescence Microscopy Filter Requirements

Fluorophore	Excitation $_{max}$	Emission $_{max}$
Green	496 nm	520 nm
Red	580 nm	603 nm
DAPI	360 nm	460 nm

Instructions for use are available at www.cancergeneticsitalia.com

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