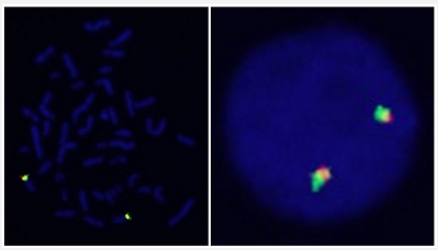
Sm Size

# IGH Split FISH Probe

Catalog # FS0069 Size 200 uL, 100 uL

## Applications



## Specification

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|---|---|
| **Product Description** | Labeled FISH probes for identification of gene split using Fluorescent In Situ Hybridization Technique. (Technology). |
| **Probe 1** | **Name:** IGH<br>**Size:** Approximately 220kb<br>**Fluorophore:** Texas Red<br>**Location:** 14q32 |
| **Probe 2** | **Name:** IGH<br>**Size:** Approximately 900kb<br>**Fluorophore:** FITC<br>**Location:** 14q32 |
| **Origin** | Human |
| **Source** | Genomic DNA |
| **Reactivity** | Human |
| **Form** | Liquid |
| **Notice** | We **strongly recommend** the customer to use FFPE FISH PreTreatment Kit 1 (Catalog #: KA2375 or KA2691) for the pretreatment of Formalin-Fixed Paraffin-Embedded (FFPE) tissue sections. |

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| **Regulation Status** | For research use only (RUO) |
| **Quality Control Testing** | Representative images of normal human cell (lymphocyte) stain with the dual color FISH probe. The l eft image is chromosomes at metaphase, and the right image is an interphase nucleus. |
| **Supplied Products** | DAPI Counterstain (1500 ng/mL ) 125 uL for each 100 uL FISH Probe |
| **Probe Position** | |
| **Storage Instruction** | Store at 4°C in the dark. |
| **Self-Attestation** | Abnova self-attests to comply with the U.S. Framework for Nucleic Acid Synthesis Screening |

## Applications

- Fluorescent In Situ Hybridization (Cell)

  Protocol Download

## Gene Info — IGH

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|---|---|
| **Entrez GeneID** | 3492 |
| **Gene Name** | IGH |
| **Gene Alias** | IGH, IGH.1@, IGHDY1, MGC72071, MGC88774 |
| **Gene Description** | immunoglobulin heavy locus |
| **Gene Ontology** | Hyperlink |

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|---|---|
| **Gene Summary** | Immunoglobulins recognize foreign antigens and initiate immune responses such as phagocytosis and the complement system. Each immunoglobulin molecule consists of two identical heavy chains and two identical light chains. This region represents the germline organization of the heavy chain locus. The locus includes V (variable), D (diversity), J (joining), and C (constant) segments. During B cell development, a recombination event at the DNA level joins a single D segment with a J segment; this partially rearranged D-J gene is then joined to a V segment. The rearranged V-D-J is then transcribed with the IGHM constant region; this transcript encodes a mu heavy chain. Later in development B cells generate V-D-J-Cmu-Cdelta pre-messenger RNA, which is alternatively spliced to encode either a mu or a delta heavy chain. Mature B cells in the lymph nodes undergo switch recombination, so that the V-D-J gene is brought in proximity to one of the IGHG, IGHA, or IGHE genes and each cell expresses either the gamma, alpha, or epsilon heavy chain. Recombination of many different V segments with several J segments provides a wide range of antigen recognition. Additional diversity is attained by junctional diversity, resulting from the random addition of nucleotides by terminal deoxynucleotidyltransferase, and by somatic hypermutation, which occurs during B cell maturation in the spleen and lymph nodes. Several V, D, J, and C segments are known to be incapable of encoding a protein and are considered pseudogenes. [provided by RefSeq |
| **Other Designations** | - |

## Disease

- Chromosome Aberrations

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