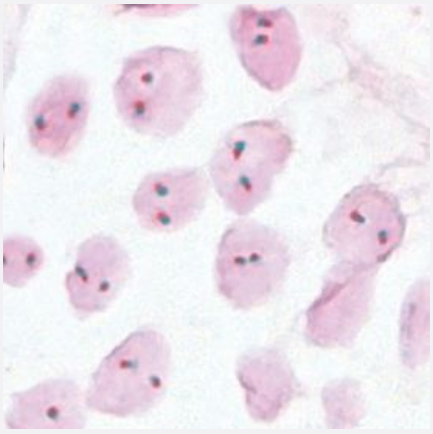
IGH Split CISH Probe

Catalog # CS0011 Size 100 uL

Applications



Chromogenic *In Situ* Hybridization (Cells)

IGH Split CISH Probe hybridized to normal interphase cells as indicated by two red/green fusion signals per nucleus.

Specification

Product Description	IGH Split CISH Probe is designed for the qualitative detection of human IGH locus at 14q32.33 in for malin-fixed, paraffin-embedded specimens by chromogenic *in situ* hybridization (CISH).
Reactivity	Human
Recommend Usage	The product is ready-to-use. No reconstitution, mixing, or dilution is required. Bring probe to room te mperature (18-25°C) and mix briefly before use.
Supplied Products	Reagent Provided: This Probe is available in one size and is composed of: Digoxigenin-labeled polynucleotides targeting sequences mapping in 14q32.33* (chr14:106,690,778-106,883,535) distal to the IGH breakpoint region Dinitrophenyl-labeled polynucleotides targeting sequences mapping in 14q32.33* (chr14:105,462,169-105,983,969) proximal to the IGH breakpoint region Formamide based hybridization buffer *according to Human Genome Assembly GRCh37/hg19
Probe Position	

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Regulatory Status	For research use only (RUO)
Storage Instruction	Store at 2-8°C in an upright position. Return to storage conditions immediately after use.
Note	The probe is intended to be used in combination with the CISH Implementation Kit 2 (Catalog #: KA5366), which provides necessary reagents for specimen pretreatment and post-hybridization processing. Hybridization signals of digoxigenin-labeled polynucleotides appear dark green distinct dotshaped (distal to the IGH breakpoint region), and dinitrophenyl-labeled polynucleotides appear bright red distinct dot-shaped (proximal to the IGH breakpoint region). Normal situation: In interphases of normal cells or cells without a translocation involving the IGH locus, two red/green fusion signals appear. Aberrant situation: One IGH locus affected by a translocation is indicated by one separate green signal and one separate red signal. Genomic aberrations due to small deletions, duplications or inversions might result in inconspicuous signal patterns. Other signal distribution may be observed in some abnormal samples which might result in a different signal pattern than described above, indicating variant rearrangements. Unexpected signal patterns should be further investigated. The digoxigenin-labeled probe and the formamide-based hybridization buffer are pre-mixed and provided in a single ready-to-use vial. Only one tube is included in the package.
Interpretation of Result	
Self-Attestation	Abnova self-attests to comply with the U.S. Framework for Nucleic Acid Synthesis Screening

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Gene Info — IGH

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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