

# 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 <i>in situ</i> 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 Product	Reagent Provided:
	<ol> <li>Digoxigenin-labeled polynucleotides targeting sequences mapping in 14q32.33* (chr14:106,690, 778-106,883,535) distal to the IGH breakpoint region</li> <li>Dinitrophenyl-labeled polynucleotides targeting sequences mapping in 14q32.33* (chr14:105,462, 169-105,983,969) proximal to the IGH breakpoint region</li> <li>Formamide based hybridization buffer</li> </ol>
	*according to Human Genome Assembly GRCh37/hg19
Probe Position	

🍟 Abnova	Product Information
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 #: <u>KA5</u> <u>366</u> ), which provides necessary reagents for specimen pretreatment and post-hybridization processi ng. Hybridization signals of digoxigenin-labeled polynucleotides appear dark green distinct dotshaped ( distal to the IGH breakpoint region), and dinitrophenyl-labeled polynucleotides appear bright red disti nct 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 sign al and one separate red signal. Genomic aberrations due to small deletions, duplications or inversio ns might result in inconspicuous signal patterns. Other signal distribution may be observed in some a bnormal samples which might result in a different signal pattern than described above, indicating vari ant rearrangements. Unexpected signal patterns should be further investigated.

## Interpretation of Result

### Applications

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## Gene Info — IGH

Entrez GenelD	<u>3492</u>
Gene Name	IGH
Gene Alias	IGH, IGH.1@, IGHDY1, MGC72071, MGC88774
Gene Description	immunoglobulin heavy locus
Gene Ontology	Hyperlink



#### **Product Information**

**Gene Summary** 

Immunoglobulins recognize foreign antigens and initiate immune responses such as phagocytosi s and the complement system. Each immunoglobulin molecule consists of two identical heavy cha ins and two identical light chains. This region represents the germline organization of the heavy ch ain locus. The locus includes V (variable), D (diversity), J (joining), and C (constant) segments. Du ring 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 i s 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 s pliced to encode either a mu or a delta heavy chain. Mature B cells in the lymph nodes undergo s witch recombination, so that the V-D-J gene is brought in proximity to one of the IGHG, IGHA, or I GHE genes and each cell expresses either the gamma, alpha, or epsilon heavy chain. Recombin ation of many different V segments with several J segments provides a wide range of antigen rec ognition. Additional diversity is attained by junctional diversity, resulting from the random addition al of nucleotides by terminal deoxynucleotidyltransferase, and by somatic hypermutation, which oc curs 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 Ref Seq

#### **Other Designations**

#### Disease

<u>Chromosome Aberrations</u>