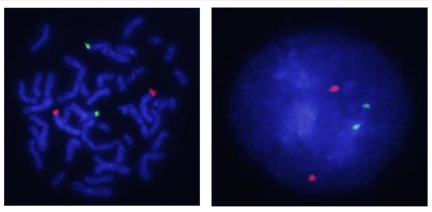
Sm Size

IGH/FGFR3 DY Translocation FISH Probe

Catalog # FT0051 Size 200 uL, 100 uL

Applications



Representative images of normal human cell (lymphocyte) stain with the dual color FISH probe. The left image is chromosomes at metaphase, and the right image is an interphase nucleus.

Hybridization position of the probes on the chromosome.

Hybridization position of the probes on the chromosome.

Specification

Probe 1	**Name:** IGH **Size:** Approximately 1800kb **Fluorophore:** FITC **Location:** 14q32
Probe 2	**Name:** FGFR3 **Size:** Approximately 1210kb **Fluorophore:** FITC **Location:** 4p16.3
Regulation Status	For research use only (RUO)
Source	Genomic DNA

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Origin	Human
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.
Self-Attestation	Abnova self-attests to comply with the U.S. Framework for Nucleic Acid Synthesis Screening
Product Description	Labeled FISH probes for identification of gene amplification using Fluorescent In Situ Hybridization T echnique. (Technology).
Reactivity	Human
Form	Liquid
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. 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.
Storage Instruction	Store at 4°C in the dark.
Note	Hybridization position of the probes on the chromosome. Hybridization position of the probes on the chromosome.

Applications

- Fluorescent *In Situ* Hybridization (Formalin/PFA-fixed paraffin-embedded sections)

  Protocol Download

- Fluorescent In Situ Hybridization (Cell)

  Protocol Download

Gene Info — FGFR3

Entrez GeneID	2261
Gene Name	FGFR3
Gene Alias	ACH, CD333, CEK2, HSFGFR3EX, JTK4
Gene Description	fibroblast growth factor receptor 3

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Omim ID	100800 109800 134934 146000 149730 162900 187600 602849 603956 610474
Gene Ontology	Hyperlink
Gene Summary	This gene encodes a member of the fibroblast growth factor receptor (FGFR) family, with its amino acid sequence being highly conserved between members and among divergent species. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. Three alternatively spliced transcript variants that encode different protein isoforms have been described. [provided by RefSeq
Other Designations	OTTHUMP00000149959|achondroplasia, thanatophoric dwarfism|hydroxyaryl-protein kinase|tyrosine kinase JTK4

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
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	-

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Pathway

- Bladder cancer
- Endocytosis
- MAPK signaling pathway
- Pathways in cancer
- Regulation of actin cytoskeleton

Disease

- Achondroplasia
- Alzheimer disease
- Carcinoma
- Cardiovascular Diseases
- Cheilitis
- Chromosome Aberrations
- Chromosome Aberrations
- Chromosome Deletion
- Cleft Lip
- Cleft Palate
- Colon cancer
- Colonic Neoplasms
- Craniosynostoses
- Diabetes Complications
- Disease Progression
- Genetic Diseases
- Genetic Predisposition to Disease

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- Intracranial Hypertension
- Kidney Neoplasms
- Lung Neoplasms
- Metabolic Syndrome X
- Musculoskeletal Abnormalities
- Neoplasm Invasiveness
- Neoplasm Recurrence
- Neoplasms
- Osteochondrodysplasias
- Osteoporosis
- Pancreatic cancer
- Pancreatic Neoplasms
- Prostate cancer
- Prostatic Neoplasms
- Recurrence
- Skin Neoplasms
- Sleep Apnea
- Syndrome
- Thanatophoric Dysplasia
- Ureteral Neoplasms
- Urinary Bladder Neoplasms

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