Advancing Cancer Diagnostics
Improving Lives

Leica
BIOSYSTEMS

IHC & ISH Product Catalog

Novocastra Antibodies, Kreatech Probes and BOND Reagents

How To Use This Catalog

Products in this catalog are listed alphabetically in sections according to their product type. The Primary Antibodies and ISH Probes sections include products in BOND Ready-To-Use formats. This makes it easy to search for the required antibody and to identify the best available format for the intended application.

To find a product, either use the contents page to locate the appropriate section and then go directly to the product, or use the product name index at the back of the catalog.

ADDITIONAL INFORMATION

Products are listed with their product code and volume/approximate number of tests. Primary antibody listings include the clone, format, tissue utility and recommended retrieval.

Regional product availability is defined by three categories, which are detailed below:

US
United States of America.

EU
Austria, Belgium, Denmark, Finland, France, Germany, Greece, Ireland, Italy, Malta, Netherlands, Portugal, Spain, Sweden, Switzerland, United Kingdom.

ROW
All other countries not listed above.

For more specific information regarding availability in your region, please consult your Leica Biosystems sales representative.

KEY

IVD	*In vitro* diagnostic use
RUO	For Research Use Only. Not for use in diagnostic procedures
ASR	Analyte Specific Reagent. Analytical and performance characteristics are not established
GPR	General Purpose Reagent
F	Frozen
P	Paraffin
O	Other applications
W	Western blotting
P (HIER)	Paraffin sections with heat induced epitope retrieval recommended
P (ENZYME)	Paraffin sections with enzyme digestion recommended
P (ENZYME+HIER)	Parffin sections with enzyme digestion followed by heat induced epitope retrieval recommended
P (ENZYME/HIER)	Paraffin sections with enzyme digestion or heat induced epitope retrieval recommended - optimum pretreatment to be determined by end user

The first letters of the product code indicate the product type.

NCL	Concentrated primary antibody or miscellaneous products
RTU	Ready-To-Use primary antibody
RE	Manual detection or ancillary reagent
PA	BOND format primary antibody
PB	BOND format ISH probe
AR	BOND ancillary reagent
DS	BOND detection system
KBI	Kreatech IVD products
KI	Kreatech RUO products

Table Of Contents

ThermoBrite

SLIDE DENATURATION/HYBRIDIZATION SYSTEM

This programmable system automates the denaturation and hybridization steps in slide-based FISH procedures, and provides walk-away convenience for clinical and research personnel. The low cost unit accepts a wide range of sample types, is easy to use, and reduces hands-on time by more than 50% while ensuring overall precision and accuracy in FISH assays.

USER PROGRAMMABLE SETTINGS

- 40 user defined protocols and 3 operating modes
- Easy to read backlit display
- Numeric keypad allows for easy programming
- Fixed temperature setting for slide baking

EASY TO USE

- Reduces hands-on time during ISH procedures
- Does not need to be fully loaded to maintain temperature accuracy
- Slide separator keeps slides in place and allows for one hand removal

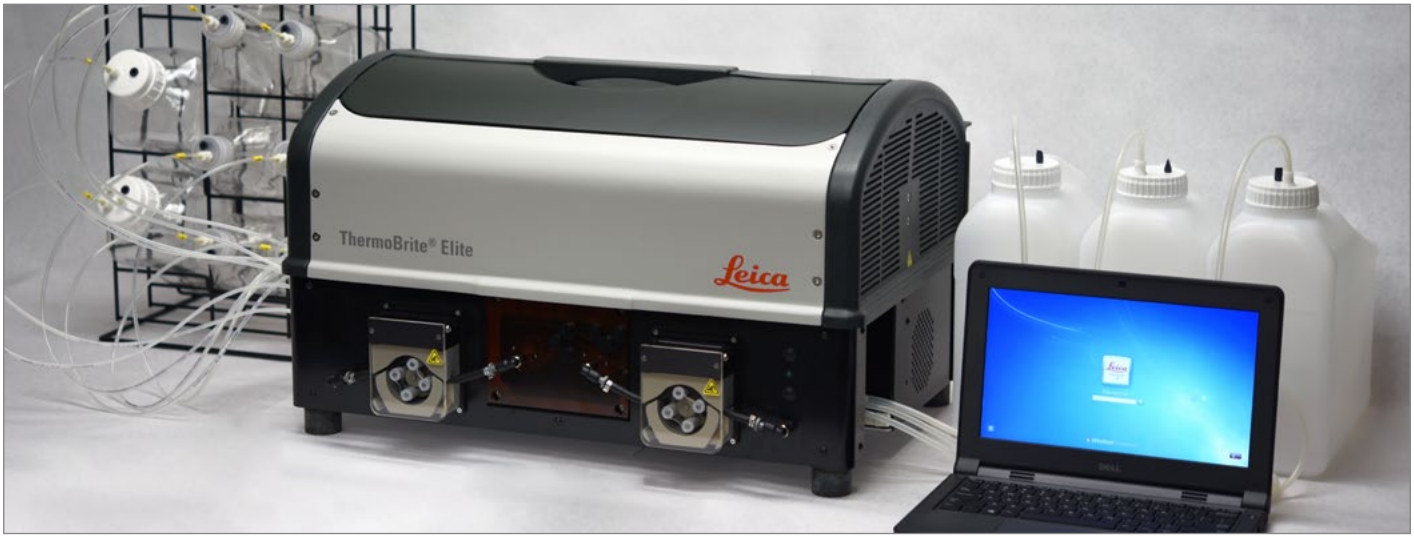
ADVANTAGES OVER MANUAL PROCESSING

- Replaces water bath and hybridization oven
- Superior temperature control compared to water bath
- No need to denature slides in toxic formamide
- No need to denature probes separately
- Eliminates many manual steps

Product Code	Product Description
ThermoBrite Slide Denaturation/Hybridization System 120V	3800-004852-001
ThermoBrite Slide Denaturation/Hybridization System 240V	3800-004852-002
Humidity Card, 10pk	3800-004970-001
ThermoBrite Temperature Verification Kit	3800-006418-001

ThermoBrite Elite

THE COMPLETE SOLUTION FOR FISH SAMPLE PREPARATION



The ThermoBrite Elite automates and standardizes the FISH slide preparation process including deparaffinization, pretreatment, denaturation/hybridization and post hybridization wash. Application of probe, counterstain and cover slipping are the only manual steps. Just load your slides and walk away. Minimal hands-on time frees up technologists for other important tasks.

The ThermoBrite Elite hybridizes with temperature controlled to +/- 1°C and can process up to twelve slides per run with the ability to adapt to smaller batches. For higher throughput, transfer slides to a standard ThermoBrite instrument to denature/hybridize and continue using your ThermoBrite Elite for new runs.

Interactive easy-to-use software

The included intuitive software enables users to run preload protocols for solid tumor/FFPE, urine, or to create up to 1,000 user defined protocols. The instrument can be programmed to work with nearly any probe or protocol, allowing the selection of up to ten input reagents and three separate waste paths.

FEATURES

- Small bench top unit
- Automated fluidic system
- Hybridization temperature precision to +/- 1°C
- Workflow based software navigation
- Open system—preloaded & custom protocols

SPEED & EFFICIENCY

- Fast protocol setup and start of run
- Hands on time reduced to 3 steps from >30 (FFPE)
- Free up technologists for other tasks
- Flexible and easy-to-use
- Increases laboratory productivity

FLEXIBILITY

- Histology (solid tumor/FFPE specimens)
- Cytology (urine and other fluids)
- Hematology (blood/bone marrow)
- Cytogenetics (metaphase/ interphase, tissue)

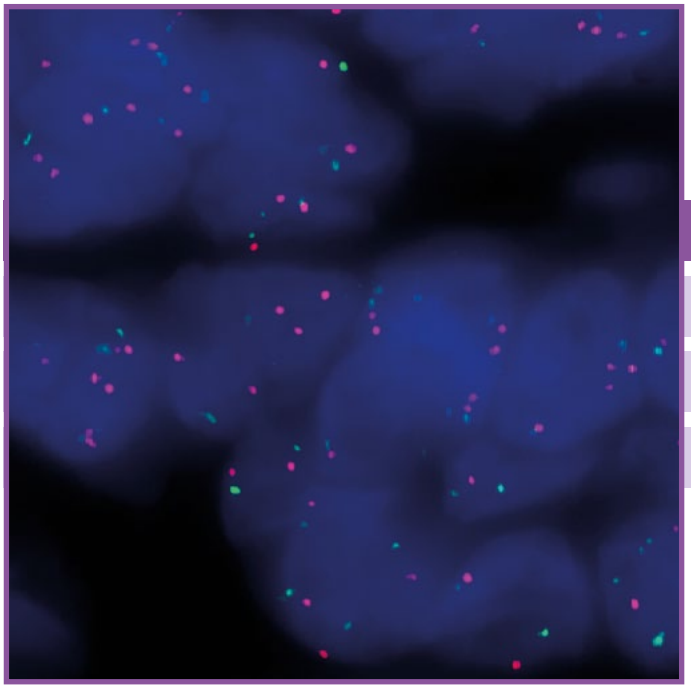
Product Code	Product Description
ThemoBrite Elite 120V	3800-007000-001
ThemoBrite Elite 240 V	3800-007000-001
Peritubes 2 tubes	3800-010022-001
Peritubes 12 tubes	3801-010021-001
Pretreatment Solution A (250 mL)	LK-110B
TBE Wash buffer (250 mL 10x)	LK-141B

Manual FISH Probes

ASR ISH Probes

ASR CISH Probes

ISH Probes



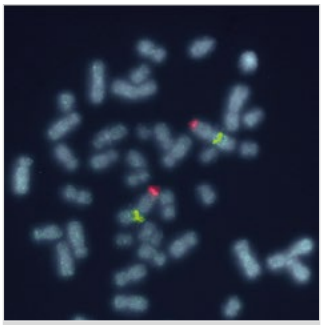
ISH PROBES

MANUAL FISH PROBES

ASR FISH PROBES

ASR CISH PROBES

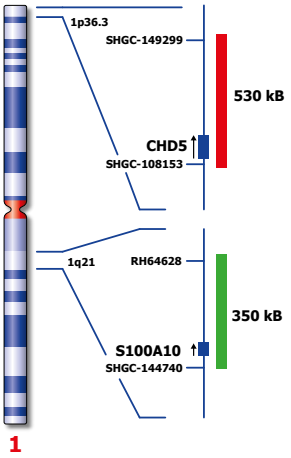
1q21 1q21 / SRD



1q21 / SRD (1p36) hybridized to a normal metaphase (2R2G).

Frequent loss of heterozygosity (LOH) on the short arm of chromosome 1 (1p) has been reported in a series of human malignancies. The combination with the potentially amplified 1q21 region allows to detect deletions at 1p36 and gain of 1q21 in a single FISH assay.

The 1q21 specific FISH probe is optimized to detect copy numbers at 1q21. The SRD 1p36 specific FISH probe is optimized to detect copy numbers of 1p at region 1p36 containing the markers D1S2795 and D1S253.

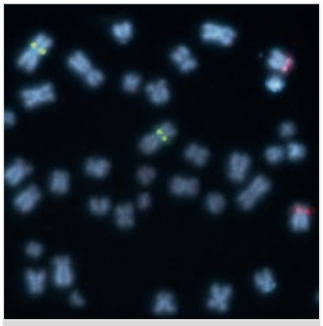


References

Cremer et al, 2005, Genes Chrom Cancer, 44; 194-203.
Shaughnessy J., 2005, Hematology, 10 suppl, 1; 117-126..

Description	Code	Color	Format	US	ROW
1q21 / SRD (1p36)	KBI-10507	Green/Red	10 Test	-	IVD
1q21 / SRD (1p36)	KI-10507	Green/Red	100 µL	RUO	-

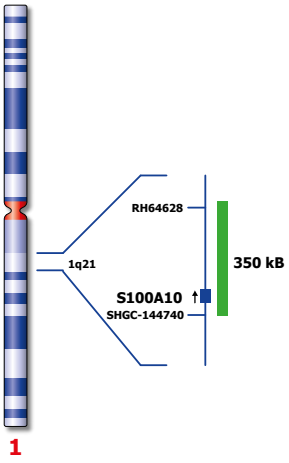
1q21 1q21 / 8p21

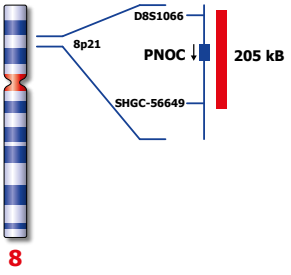


1q21 / 8p21 hybridized to a normal metaphase (2R2G).

Amplifications of 1q21 are concurrent with dysregulated expression of MAF, MMSET / FGFR3, or Deletion 13 and represent an independent unfavorable prognostic factor. Allelic losses of the chromosome 8p21-22 have been reported as a frequent event in several cancers.

The 1q21 specific FISH probe is optimized to detect copy numbers at 1q21. The 8p21 specific DNA region is optimized to detect copy numbers at 8p21.





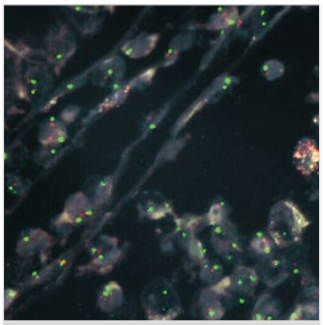
References

Shaughnessy J., 2005, Hematology, 10 suppl, 1; 117-126.
Cremer et al, 2005, Genes Chrom Cancer, 44; 194-203.

Description	Code	Color	Format	US	ROW
1q21 / 8p21	KBI-10503	Green/Red	10 Test	-	IVD
1q21 / 8p21	KI-10503	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

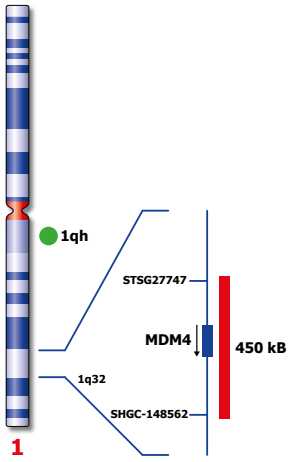
1q32 MDM4 / SE 1



MDM4 (1q32) / SE 1 probe hybridized to paraffin embedded tissue (2R2G).

MDM4 (MDM4 p53 binding protein homolog (mouse), also known as MDMX, murine double minute gene) is a relative of MDM2 that was identified on the basis of its ability to physically interact with TP53. MDM4, like MDM2, acts as a key negative suppressor of TP53 by interfering with its transcriptional activity. MDM4 amplification and/ or overexpression occurs in several diverse tumors. Studies showed an increased MDM4 copy number in 65% of human retinoblastomas compared to other tumors, qualifying MDM4 as a specific chemotherapeutic target for treatment of this tumor.

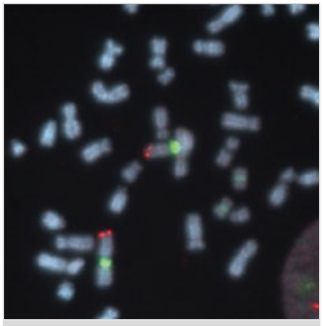
The MDM4 (1q32) FISH probe is designed as a dual-color assay to detect amplification at 1q32. The chromosome 1 Satellite Enumeration (SE 1) probe at 1qh is included to facilitate chromosome identification.



References
Riemenschneider et al, 1999, Cancer Res. 59 ; 6091-6096.
Danovi et al, 2004, Mol.Cell.Biol. 24; 5835-5843.

Description	Code	Color	Format	US	ROW
MDM4 (1q32) / SE 1	KBI-10736	Green/Red	10 Test	-	IVD
MDM4 (1q32) / SE 1	KI-10736	Green/Red	100 µL	RUO	-

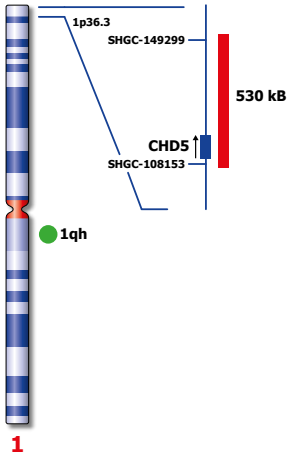
1p36 SRD / SE 1



SRD (1p36) / SE 1 probe hybridized to a normal metaphase (2R2G).

Neuroblastomas frequently have deletions of chromosome 1p and amplification of the MYCN oncogene. These deletions tend to be large and extend to the telomere, but a common region within sub-band 1p36.3 is consistently lost in these deletions. Inactivation of a tumor suppressor gene within 1p36.3 is believed to be associated with an increased risk for disease relapse.

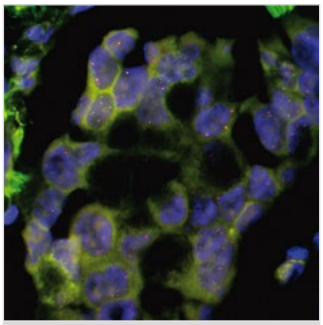
The SRD (1p36) FISH probe is optimized to detect copy numbers of the 1p36 region on chromosome 1. The chromosome 1 satellite enumeration probe (SE 1) at 1qh is included to facilitate chromosome identification.



References
Caron et al, 1993, Nat Genet, 4: 187-190.
Cheng et al, 1995, Oncogene, 10: 291-297.
White et al, 2005, Oncogene, 24: 2684-2694.

Description	Code	Color	Format	US	ROW
SRD (1p36) / SE 1 (1qh)	KBI-10712	Green/Red	10 Test	-	IVD
SRD (1p36) / SE 1 (1qh)	KI-10712	Green/Red	100 µL	RUO	-

2p23 ALK / EML4



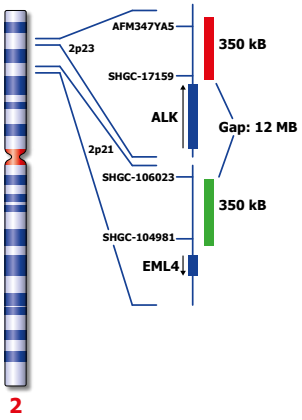
ALK/EML4 t(2;2); inv(2) Fusion probe hybridized to lung adenocarcinoma tissue showing ALK-EML4 fusion (2RG1R1G).

Image kindly provided by Prof. B. Terris, Dr. P.A. Just, Hôpital Cochin, Paris.

The inversion in 2p21 and 2p23 leading to a fusion of the kinase domain of ALK (anaplastic lymphoma kinase) and EML4 (echinoderm microtubule associated protein like 4) has been described in 5-7% of non-small cell lung cancer (NSCLC) cases. ALK and EML4 are ~12 MB apart in opposite directions; a simple inversion generates the fusion gene.

Promising results have been obtained with specific anaplastic lymphoma kinase or ALK inhibitors like crizotinib (Xalkori) in patients carrying the fusion gene ALK-EML4.

The ALK/EML4 t(2;2); inv(2) Fusion probe is designed as a dual-color assay to detect the fusion of the ALK gene with the EML4 gene by paracentric inversion with breakage and reunion occurring at bands 2p21 and 2p23.

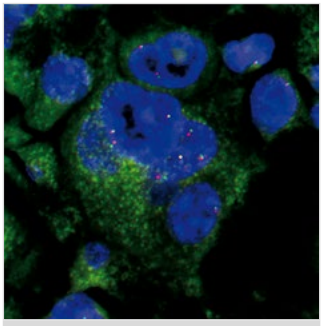


References

Soda et al, Nature, 2007, 448, 561-566.
Koivunen et al, Clin Cancer Res, 2008, 14, 4275-4283.

Description	Code	Color	Format	US	ROW
ALK (2p23) / EML4 t(2;2) inv (2) Fusion	KBI-10746	Green/Red	10 Test	-	IVD
ALK (2p23) / EML4 t(2;2) inv (2) Fusion	KI-10746	Green/Red	100 µL	RUO	-

2p23 ALK Break

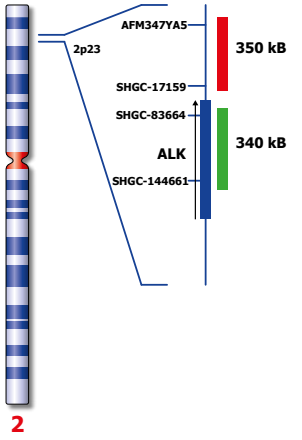


ALK (2p23) Break probe hybridized to lung adenocarcinoma tissue showing translocation involving the ALK region at 2p23 (1RG1R1G).

Image kindly provided by Prof. B. Terris, Dr. P.A. Just, Hôpital Cochin, Paris.

Translocations of the ALK (anaplastic lymphoma kinase) gene at 2p23 have originally been associated with anaplastic lymphomas, B-cell lymphomas, neuroblastomas and myofibroblastic tumors. To date at least 21 translocation partners have been described, however 80% of the translocations involves the NPM1 gene (5q35). More recently ALK rearrangements have been described in non-small cell lung cancer (NSCLC) cases. Promising results have been obtained with specific anaplastic lymphoma kinase or ALK inhibitors like crizotinib (Xalkori) in patients carrying the fusion gene ALK-EML4.

The ALK (2p23) Break probe is optimized to detect translocations involving the ALK gene region at 2p23.



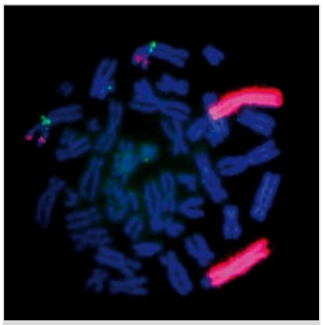
References

Soda et al, Nature, 2007, 448, 561-566.
Kwak et al, J Clin Oncol., 27(26):4247-53.
Koivunen et al, Clin Cancer Res, 2008, 14, 4275-4283.

Description	Code	Color	Format	US	ROW
ALK (2p23) Break	KBI-10747	Green/Red	10 Test	-	IVD
ALK (2p23) Break	KI-10747	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

2p24 MYCN / AFF3

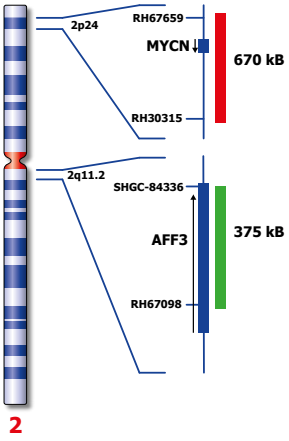


MYCN (2p24) / AFF3 (2q11) hybridized to a cell line showing amplification of MYCN on chromosome 13 and 15.

Image kindly provided by Pasteur Workshop 2008, Paris.

Amplification of the human protooncogene, v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN) is frequently seen either in extrachromosomal double minutes or in homogeneously staining regions of aggressively growing neuroblastomas. MYCN amplification has been defined by the INRG as > 4-fold MYCN signals compared to 2q reference probe signals.

The MYCN (2p24) FISH probe is optimized to detect copy numbers of the MYCN gene region at 2p24. The AFF3 gene region probe at 2q11 is included to facilitate chromosome identification.

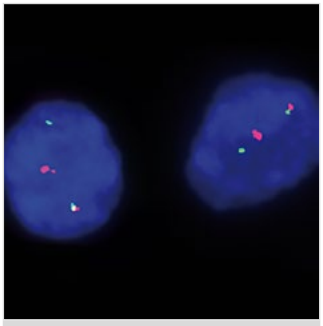


References

Shapiro et al, 1993, Am J Pathol, 142: 1339-1346.
Corvi et al, 1994, PNAS, 91: 5523-5527.

Description	Code	Color	Format	US	ROW
MYCN (2p24) / AFF3 (2q11)	KBI-10706	Green/Red	10 Test	-	IVD
MYCN (2p24) / AFF3 (2q11)	KI-10706	Green/Red	100 µL	RUO	-

3p25 PPARG Break



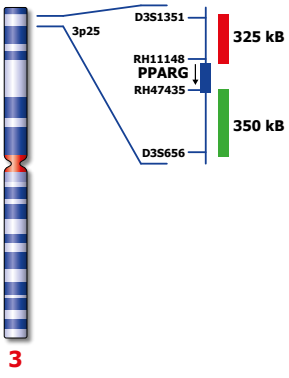
PPARG (3p25) Break probe hybridized to patient material showing a translocation at 3p25 (1RG1R1G).

Image kindly provided by Dr. Valent, Paris.

Follicular thyroid carcinoma is associated with the chromosomal translocation t(2;3)(q13;p25), fusing PAX8 (2q13) with the nuclear receptor, peroxisome proliferator-activated receptor _ (PPARG). PPARG is located in a breakpoint hot spot region, leading to recurrent alterations of this gene in thyroid tumors of follicular origin including carcinomas as well as adenomas with or without involvement of PAX8.

A break or split probe for PPARG is best used to analyze translocation of the PPARG (3p25) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

The PPARG (3p25) Break probe is optimized to detect translocations and amplification involving the PPARG gene region at 3p25 in a dual_color, split assay.

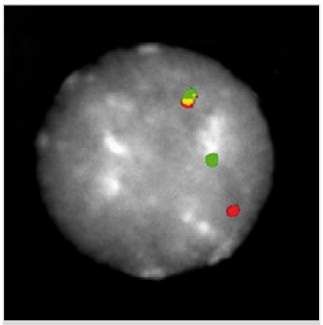


References

French et al, 2003, Am J Pathol, 162; 1053-1060.
Drieschner et al, 2006, Thyroid, 16; 1091-1096.

Description	Code	Color	Format	US	ROW
PPARG (3p25) Break	KBI-10707	Green/Red	10 Test	-	IVD
PPARG (3p25) Break	KI-10707	Green/Red	100 µL	RUO	-

3q26 MECOM Break

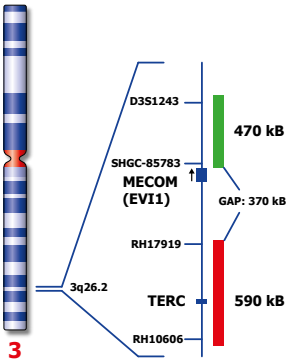


MECOM t(3;3);inv(3) (3q26) Break probe hybridized to patient material showing a rearrangement involving the MECOM gene region at 3q26 (1RG1R1G).

Image kindly provided by Dr. Reed, London.

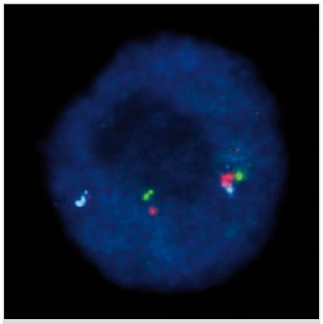
The inv(3)(q21;q26) is a recurrent cytogenetic aberration of myeloid malignancy associated with fusion of MECOM (previously known as EVI) and RPN1 and a poor disease prognosis. Genomic breakpoints in 3q26 are usually located proximal to the MECOM locus, spanning a region of several hundred kilobases. Other recurrent and sporadic rearrangements of 3q26 also cause transcriptional activation of MECOM including the translocations t(3;3)(q21;q26) and t(3;21)(q26;q22). Breakpoints in the latter rearrangements span a wider genomic region of over 1 megabase encompassing sequences distal to MECOM and neighboring gene MDS1.

The MECOM t(3;3) inv(3) Break, dual-color FISH probe is optimized to detect the inversion of chromosome 3 involving the MECOM gene region at 3q26 in a dual-color, split assay on metaphase/interphase spreads, blood smears and bone marrow cells.



Description	Code	Color	Format	US	ROW
MECOM t(3;3); inv(3) (3q26) Break	KBI-10204	Green/Red	10 Test	-	IVD
MECOM t(3;3); inv(3) (3q26) Break	KI-10204	Green/Red	100 µL	RUO	-

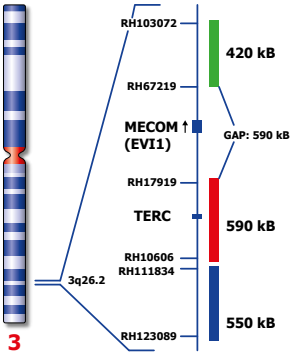
3q26 MECOM Break Triple-Color



MECOM t(3;3);inv(3) (3q26) Break probe hybridized to patient material showing a rearrangement involving the MECOM gene region at 3q26 (1RG1R1G).

Image kindly provided by Dr. Reed, London.

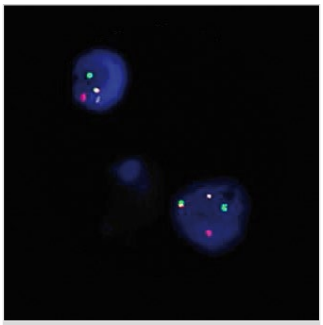
The MECOM t(3;3); inv(3)(3q26) Break Triple-Color FISH probe is optimized to detect the inversion of chromosome 3 involving the MECOM (previously known as EVI) gene region at 3q26 in a dual-color, split assay on metaphase/interphase spreads, blood smears and bone marrow cells. By using a third color breakpoint variations can also be easily observed.



Description	Code	Color	Format	US	ROW
MECOM t(3;3); inv(3) (3q26) Break, Triple-Color	KBI-10205	Green/Red/Blue	10 Test	-	IVD
MECOM t(3;3); inv(3) (3q26) Break, Triple-Color	KI-10205	Green/Red/Blue	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

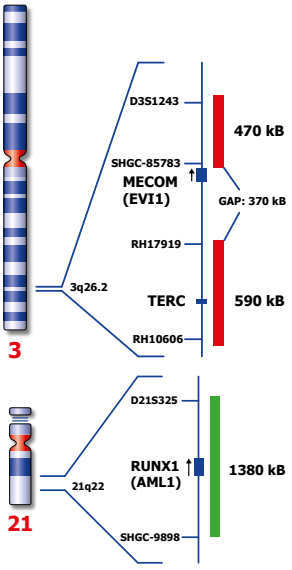
3q26 MECOM/RUNX1



MECOM / RUNX1 Fusion probe hybridized to patient material showing t(3;21) (2F1R1G)

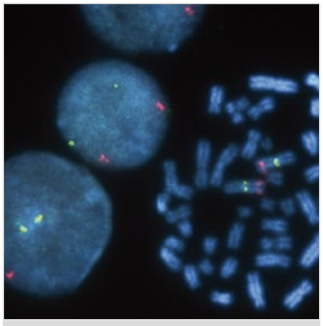
Image kindly provided by Dr. Mohr, Dresden

The chromosomal translocation t(6;9) (p22;q34) is associated with a specific subtype of acute myeloid leukemia (AML) and constitutes 0.5% to 4% of all AML cases. The translocation results in a fusion between the DEK oncogene (6p22) and the nucleoporin 214 kDa (NUP214 at 9q34; previously known as CAN). The exact mechanism by which the fusion protein DEK-NUP214 contributes to leukemia development has not been identified. Patients with t(6;9) AML have a very poor prognosis. The currently available chemotherapy does not seem to improve overall survival. However, accurate diagnosis is crucial because these patients may benefit from early allogeneic stem cell transplant. The DEK / NUP214 t(6;9) specific FISH probe has been optimized to detect the reciprocal translocation t(6;9) in a dual-color, dual-fusion assay on metaphase/interphase spreads, blood smears and bone marrow cells.



Description	Code	Color	Format	US	ROW
MECOM/RUNX1 t(3;21) Fusion	KBI-10310	Green/Red	10 Test	-	IVD
MECOM/RUNX1 t(3;21) Fusion	KI-10310	Green/Red	100 µL	RUO	-

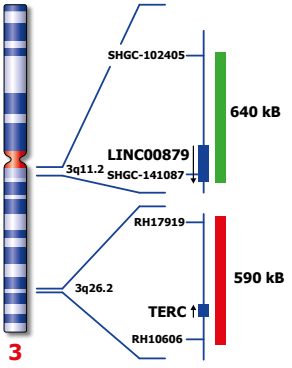
3q26 TERC / 3q11



TERC (3q26) / 3q11 probe hybridized to a normal interphase/metaphase (2R2G).

Amplification of the 3q26-q27 has a high prevalence in cervical, prostate, lung, and squamous cell carcinoma. This amplification can also be found to a lesser extent in CLL patients. The minimal region of amplification was refined to a 1- to 2-Mb genomic segment containing several potential cancer genes including TERC, the human telomerase RNA gene.

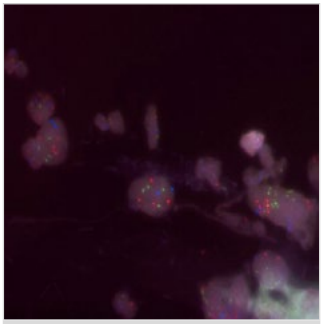
The TERC (3q26) specific FISH probe is optimized to detect copy numbers of the TERC (previously known as hTERC) gene region at region 3q26. The 3q11 region probe is included to facilitate chromosome identification.



References
Arnold et al, 1996, Genes Chrom Cancer, 16; 46-54.
Soder et al, 1997, Oncogene, 14; 1013-1021.

Description	Code	Color	Format	US	ROW
TERC (3q26) / 3q11	KBI-10110	Green/Red	10 Test	-	IVD
TERC (3q26) / 3q11	KI-10110	Green/Red	100 µL	RUO	-

3q26 TERC / MYC / SE7

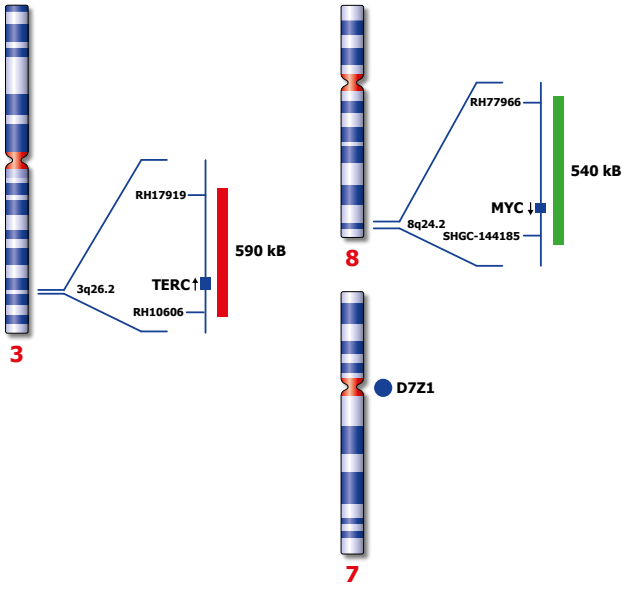


TERC (3q26) / MYC (8q24) / SE 7 Triple-Color probe hybridized to a PAP smear (destained) showing 3q26 and 8q24 amplification. The SE 7 control probe indicates a non-triploid karyotype (2B).

Image kindly provided by Dr. Weimer, Kiel.

The most consistent chromosomal gain in aneuploid tumors of cervical squamous cell carcinoma mapped to chromosome arm 3q, including the human telomerase gene locus (TERC) at 3q26. Highlevel copy number increases were also mapped to chromosome 8. Integration of HPV (Human Papilloma Virus) DNA sequences into MYC chromosomal regions have been repeatedly observed in cases of invasive genital carcinomas and in cervical cancers.

The TERC (3q26) FISH probe is optimized to detect copy numbers of the TERC gene region at region 3q26. The MYC (8q24) FISH probe is optimized to detect copy numbers of the MYC gene region at 8q24. The chromosome 7 satellite enumeration probe (SE 7) at D7Z1 is included as ploidy control.

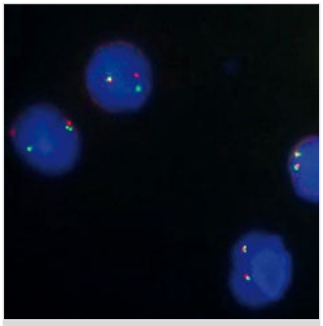


References

Xie et al, 2008, Geburtshilfe Frauenheilkunde, 68: 573.
Heselmeyer et al, 1996, PNAS, 93: 479-484.
Herrick et al, 2005, Cancer Res, 65: 1174-1179.

Description	Code	Color	Format	US	ROW
TERC (3q26) / MYC (8q24) / SE 7 Triple-Color	KBI-10704	Green/Red/Blue	10 Test	-	IVD
TERC (3q26) / MYC (8q24) / SE 7 Triple-Color	KI-10704	Green/Red/Blue	100 µL	RUO	-

3q27 BCL6 Break

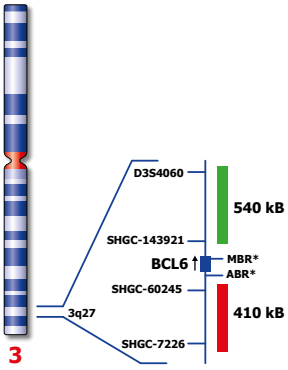


BCL6 (3q27) Break probe hybridized to patient material (1RG1R1G).

Image kindly provided by Prof. Siebert, Kiel.

Chromosomal translocations involving band 3q27 with various different partner chromosomes represent a recurrent cytogenetic abnormality in B-cell non-Hodgkin's lymphoma. A FISH strategy using two differently labeled flanking BCL6 probes provides a robust, sensitive, and reproducible method for the detection of common and uncommon abnormalities of BCL6 gene in interphase nuclei. Kreatech has developed this probe for the specific use on cell material (KBI-10607), or for the use on tissue (KBI-10730). Two different breakpoint regions have been identified; the major breakpoint region (MBR) is located within the 5' noncoding region of the BCL6 proto-oncogene, while the atypical breakpoint region (ABR) is located approximately 200 kb distal to the BCL6 gene.

The BCL6 (3q27) Break FISH probe is designed in a way to flank both possible breakpoints, thereby providing clear split signals in either case.



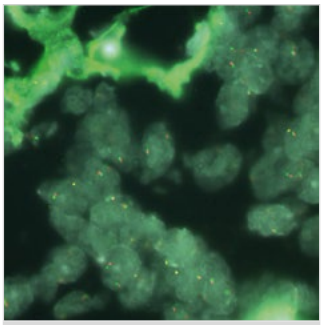
References

Butler et al, 2002, Cancer Res, 62; 4089-4094.
Sanchez-Izquierdo, 2001, Leukemia, 15; 1475-1484.

Description	Code	Color	Format	US	ROW
BCL6 (3q27) Break	KBI-10607	Green/Red	10 Test	-	IVD
BCL6 (3q27) Break	KI-10607	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

3q27 BCL6 Break (tissue)



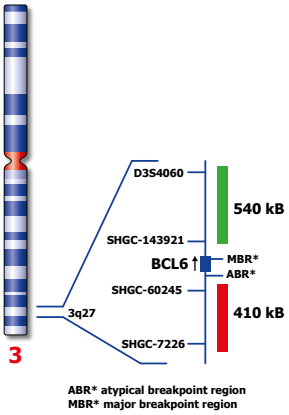
BCL6 (3q27) Break probe hybridized to patient material showing both normal (2RG) and aberrant signals (1RG1R1G).

Image kindly provided by Prof Siebert, Kiel.

Chromosomal translocations involving band 3q27 with various different partner chromosomes represent a recurrent cytogenetic abnormality in B-cell non-Hodgkin's lymphoma. A FISH strategy using two differently labeled flanking BCL6 probes provides a robust, sensitive, and reproducible method for the detection of common and uncommon abnormalities of BCL6 gene in interphase nuclei. Kreatech* has developed this probe for the specific use on cell material (KBI-10607), or for the use on tissue (KBI-10730).

Two different breakpoint regions have been identified; the major breakpoint region (MBR) is located within the 5' noncoding region of the BCL6 proto-oncogene, while the atypical breakpoint region (ABR) is located approximately 200 kb distal to the BCL6 gene. The BCL6 (3q27) Break probe is designed to flank both possible breakpoints, thereby providing clear split signals in either case.

The BCL6 (3q27) Break probe is optimized to detect translocations involving the BCL6 gene region at 3q27 in a dual_color, split assay on paraffin_embedded tissue sections.

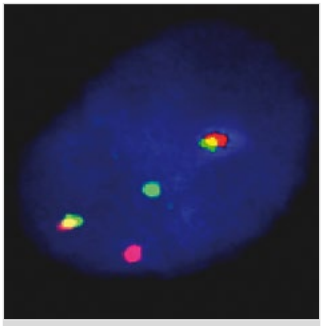


References

Butler et al, 2002, Cancer Res, 62; 4089-4094.
Sanchez-Izquierdo, 2001, Leukemia, 15; 1475-1484.

Description	Code	Color	Format	US	ROW
BCL6 (3q27) Break (tissue)	KBI-10730	Green/Red	10 Test	-	IVD
BCL6 (3q27) Break (tissue)	KI-10730	Green/Red	100 µL	RUO	-

4p16 FGFR3 / IGH

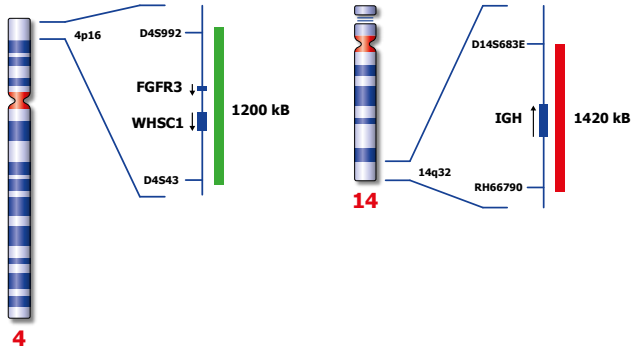


FGFR3 / IGH t(4;14) Fusion probe hybridized to MM patient material showing t(4;14) translocation (2RG1R1G).

Image kindly provided by Prof. Jauch, Heidelberg.

The t(4;14) translocation is undetectable by conventional cytogenetics. The breakpoints on chromosome 4 occur within an approximately 113-kb region located in small part of a conserved gene cluster including the transforming acidic coiled-coil protein 3 (TACC3), fibroblast growth factor receptor 3 (FGFR3), and multiple myeloma SET domain-containing protein (MMSET). The translocation is indicative for poor survival and poor response to chemotherapy.

The FGFR3 / IGH t(4;14)(p16;q32) Fusion specific FISH probe is optimized to detect the reciprocal translocation t(4;14) in a dual-color, dual-fusion assay.

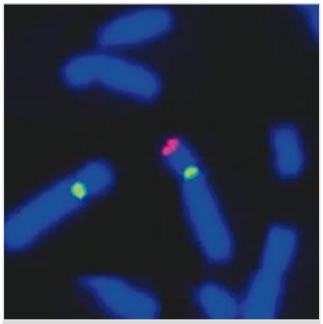


References

Chesi et al, 1997, Nat Genet, 16; 260-264.
Finelli et al, 1999, Blood, 94; 724-732.

Description	Code	Color	Format	US	ROW
FGFR3/IGH t(4;14) Fusion	KBI-10602	Green/Red	10 Test	-	IVD
FGFR3/IGH t(4;14) Fusion	KI-10602	Green/Red	100 µL	RUO	-

4p16 WHSC1 / SE 4

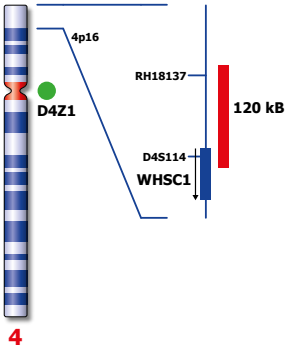


Wolf-Hirschhorn WHSC1 (4p16) / SE 4 probe hybridized to Wolf-Hirschhorn patient material showing a deletion of the WHSC1 gene region at 4p16 (1R2G).

Image kindly provided by Prof. Zollino, Rome.

Wolf-Hirschhorn syndrome (WHS) affected individuals have prenatal-onset growth deficiency followed by postnatal growth retardation and hypotonia with muscle under-development. Developmental delay/mental retardation of variable degree is present in all. FISH analysis using a WHSC1 specific FISH probe for chromosomal locus 4p16.3 detects more than 95% of deletions in WHS.

The Wolf-Hirschhorn region probe is optimized to detect copy numbers of the Wolf-Hirschhorn critical region at 4p16. The chromosome 4 Satellite Enumeration (SE 4) FISH probe at D4Z1 is included to facilitate chromosome identification.

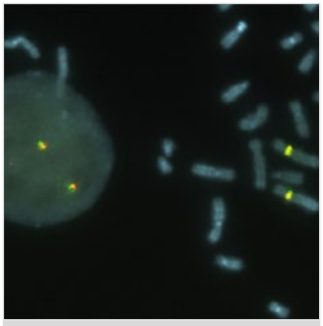


References

Gandelman et al, 1992, Am. J. Hum. Genet., 51; 571-578.
Wright et al, 1997, Hum. Mol. Genet., 6; 317-324.

Description	Code	Color	Format	US	ROW
Wolf-Hirschhorn WHSC1 (4p16) / SE 4	KBI-40107	Green/Red	10 Test	-	IVD
Wolf-Hirschhorn WHSC1 (4p16) / SE 4	KBI-45107	Green/Red	5 Test	-	IVD
WHSC1 (4p16) / SE 4	KI-40107	Green/Red	100 µL	RUO	-

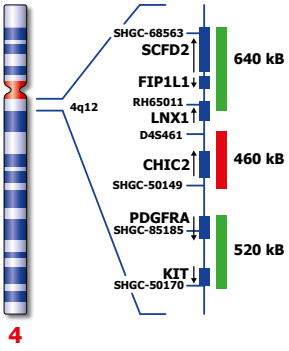
4q12 FIP1L1 / CHIC2 /PDGFRA Dual-Color



FIP1L1 / CHIC2 / PDGFRA (4q12) Deletion, Break probe hybridized to a normal interphase/metaphase (2RG).

Idiopathic hypereosinophilic syndrome (HES) and chronic eosinophilia leukemia (CEL) represent the most recent additions to the list of molecularly defined chronic myeloproliferative disorders. A novel tyrosine kinase that is generated from fusion of the Fip1-like 1 (FIP1L1) and PDGFRα (PDGFRA) genes has been identified as a therapeutic target for imatinib mesylate in hypereosinophilic syndrome (HES). This fusion results from an approximately 800-kb interstitial chromosomal deletion that includes the cysteine-rich hydrophobic domain 2 (CHIC2) locus.

The FIP1L1 / CHIC2 / PDGFRA FISH probe is optimized to detect the CHIC2 deletion at 4q12 associated with the FIP1L1 / PDGFRA fusion in a Dual-Color, split assay. It also allows the detection of translocation involving the FIP1L1 and PDGFRA region. However, chromosome 4 polyploidy may provide additional signals not associated with a translocation involving 4q12.



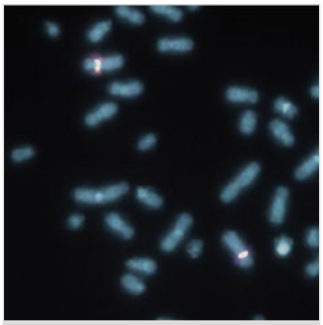
References

Cools et al, N Engl J Med, 2003, 348; 1201-1214.
Godlib et al, Blood, 2004, 103; 2879-2891.

Description	Code	Color	Format	US	ROW
FIP1L1 / CHIC2 / PDGFRA (4q12) Deletion, Break	KBI-10003	Green/Red	10 Test	-	IVD
FIP1L1 / CHIC2 / PDGFRA (4q12) Deletion, Break	KI-10003	Green/Red	100 µL	RUO	-

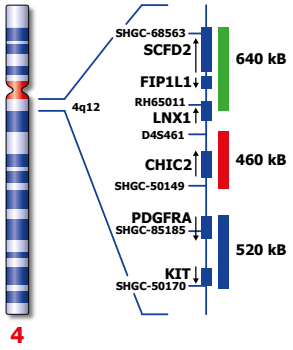
IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

4q12 FIP1L1 / CHIC2 /PDGFRA Triple-Color



FIP1L1 / CHIC2 / PDGFRA (4q12) Deletion, Break Triple-Color

The FIP1L1 / CHIC2 / PDGFRA Triple-Color FISH probe is optimized to detect the CHIC2 deletion at 4q12 associated with the FIP1L1 / PDGFRA fusion in a triple-color, split assay. It also allows the detection of translocation involving the FIP1L1 and PDGFRA region.

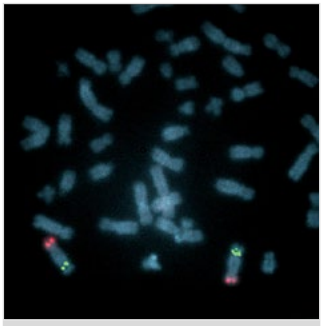


References

Cools et al, N Engl J Med, 2003, 348; 1201-1214.
Griffin et al, 2003, PNAS, 100;7830-7835.
Gotlib et al, 2004, Blood, 103;2879-2891

Description	Code	Color	Format	US	ROW
FIP1L1 / CHIC2 / PDGFRA (4q12) Deletion, Break, Triple-Color	KBI-10007	Green/Red/Blue	10 Test	-	IVD
FIP1L1 / CHIC2 / PDGFRA (4q12) Deletion, Break, Triple-Color	KI-10007	Green/Red/Blue	100 µL	RUO	-

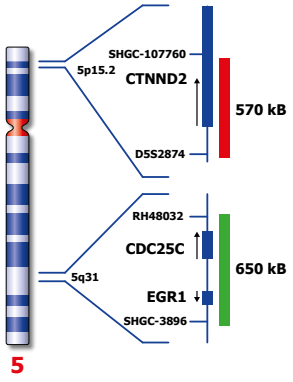
5p15 CTNND2



Cri-Du-Chat CTNND2 (5p15) / 5q31 probe hybridized to a normal metaphase 2RG).

Cri-Du-Chat syndrome is an autosomal deletion syndrome caused by a partial deletion of chromosome 5p. It is characterized by a distinctive, high-pitched, catlike cry in infancy with growth failure, microcephaly, facial abnormalities, and mental retardation throughout life. Loss of a small region in band 5p15.2 (Cri-Du-Chat critical region) correlates with all the clinical features of the syndrome with the exception of the catlike cry, which maps to band 5p15.3 (catlike cry critical region).

The Cri-Du-Chat region probe is optimized to detect copy numbers at the CTNND2 gene region in the Cri-Du-Chat critical region at 5p15.2. The 5q31 specific FISH probe is included as control probe.

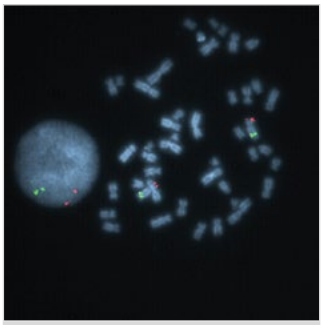


References

Overhauser et al, 1994, Hum. Mol. Genet., 3; 247-252.
Gersh et al, 1997, Cytogenet Cell Genet., 77; 246-251.

Description	Code	Color	Format	US	ROW
Cri-Du-Chat CTNND2 (5p15) / 5q31	KBI-40106	Green/Red	10 Test	-	IVD
Cri-Du-Chat CTNND2 (5p15) / 5q31	KBI-45106	Green/Red	5 Test	-	IVD
CTNND2 (5p15) / 5q31	KI-40106	Green/Red	100 µL	RUO	-

5p15 TERT / 5q31

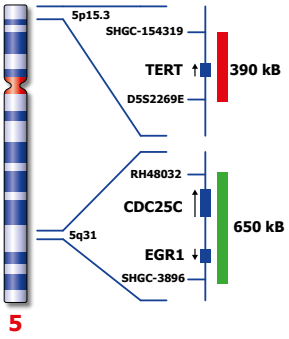


TERT (5p15) / 5q31 probe hybridized to a normal interphase/metaphase (2R2G).

Image kindly provided by Dr. Mohr, Dresden.

The TERT / 5q31 dual-color FISH probe can be used to detect deletions involving band 5q31 in MDS and RUNX1.

The 5q- specific FISH probe is optimized to detect copy numbers at the CDC25C/ EGR1 gene region at 5q31. The TERT (previously known as hTERT) gene region at 5p15 is included to facilitate chromosome identification.

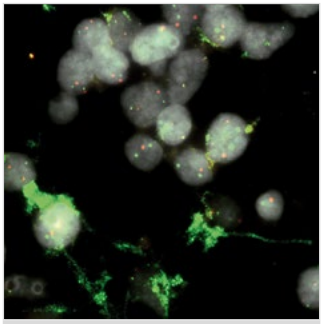


References

Zhao et al, 1997, PNAS, 94; 6948-6053.
Horrigan et al, 2000, Blood, 95; 2372-2377.

Description	Code	Color	Format	US	ROW
TERT (5p15) / 5q31	KBI-10208	Green/Red	10 Test	-	IVD
TERT (5p15) / 5q31	KI-10208	Green/Red	100 µL	RUO	-

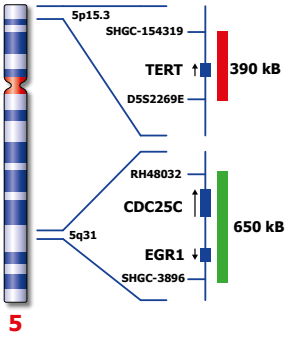
5p15 TERT / 5q31 (tissue)



TERT (5p15) / 5q31 (tissue) probe hybridized to paraffine embedded tissue (2R2G).

Amplification of the TERT gene at 5p15 has been observed in a variety of cancers, particularly lung cancer, cervical tumors, and breast carcinomas. Several studies have revealed a high frequency of TERT gene amplification in human tumors, which indicates that the TERT gene may be a target for amplification during the transformation of human malignancies and that this genetic event probably contributes to a dysregulation of TERT/ telomerase occurring in a subset of human tumors.

The TERT (5p15) FISH probe is designed as a dual-color assay to detect amplification at 5p15. The CDC25C / EGR1 (5q31) gene region probe is included as internal control.



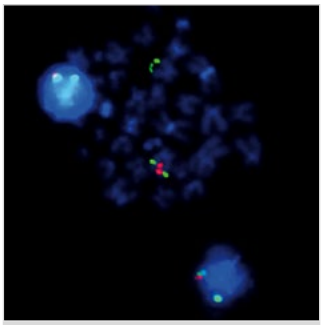
References

Bryce et al, 2000, Neoplasia, 2;197-201.
Zhang et al, 2000, Cancer Res, 60;6230-6235

Description	Code	Color	Format	US	ROW
TERT (5p15) / 5q31 (tissue)	KBI-10709	Green/Red	10 Test	-	IVD
TERT (5p15) / 5q31 (tissue)	KI-10709	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

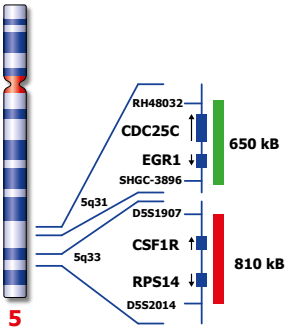
5q 5q- Dual-Color



5q- (5q31; 5q33) probe hybridized to patient material showing a 5q33 deletion (1R2G).

The presence of del(5q), either as the sole karyotypic abnormality or as part of a more complex karyotype, has distinct clinical implications for myelodysplastic syndromes (MDS) and acute myeloid leukemia. Interstitial 5q deletions are the most frequent chromosomal abnormalities in MDS and are present in 10% to 15% of MDS patients. Two different critical regions are described, one at 5q31-q33 containing the CSF1R and RPS14 gene regions, characteristic for the '5q-' syndrome, and a more proximal located region at 5q13-q31 containing the CDC25C and EGR1 gene regions.

The 5q- specific FISH probe is optimized to detect copy numbers at the CDC25C / EGR1 gene region at 5q31 and the CSF1R / RPS14 gene region at 5q33 simultaneously in a dual-color assay.

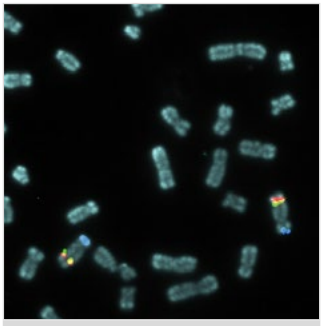


References

Boultwood J e.a., Blood 2002, 99; 4638-4641.
Zhao N e.a., PNAS 1997, 94; 6948-6953.
Wang e.a., Haematologica 2008, 93; 994-1000.
Ebert BL e.a., Nature 2008, 451; 335-339.
Mohamedali A and Mufti GJ, Brit J Haematol 2008, 144; 157-168.

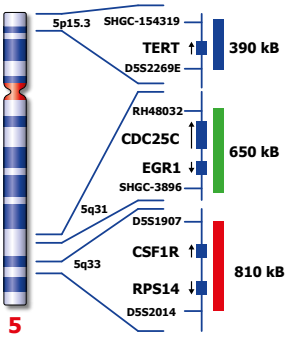
Description	Code	Color	Format	US	ROW
5q- (5q31; 5q33)	KBI-10209	Green/Red	10 Test	-	IVD
5q- (5q31; 5q33)	KI-10209	Green/Red	100 µL	RUO	-

5q 5q- Triple-Color



5q- (5q31; 5q33) / TERT (5p15)Triple-Color probe hybridized to a normal metaphase (2R2G2B).

The 5q- specific FISH probe is optimized to detect copy numbers at the CDC25C / EGR1 gene region at 5q31 and the CSF1R / RPS14 gene region at 5q33 simultaneously in a dual-color assay. The triple-color probe provides in addition to the two critical regions a control in blue targeting the TERT (previously known as hTERT) gene region at 5p15.

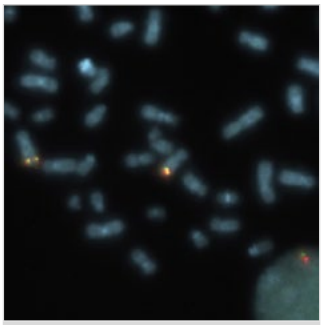


References

Boultwood J e.a., Blood 2002, 99; 4638-4641.
Zhao N e.a., PNAS 1997, 94; 6948-6953.
Wang e.a., Haematologica 2008, 93; 994-1000.
Ebert BL e.a., Nature 2008, 451; 335-339.
Mohamedali A and Mufti GJ, Brit J Haematol 2008, 144; 157-168.

Description	Code	Color	Format	US	ROW
5q- (5q31; 5q33) / TERT (5p15) Triple-Color	KBI-10210	Green/Red/Blue	10 Test	-	IVD
5q- (5q31; 5q33) / TERT (5p15) Triple-Color	KI-10210	Green/Red/Blue	100 µL	RUO	-

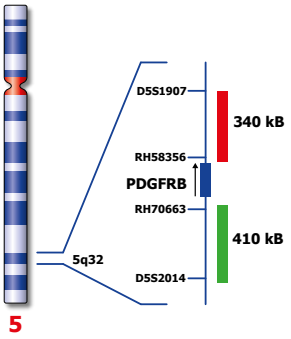
5q32 PDGFRB Break



PDGFRB (5q32) Break probe hybridized to a normal metaphase (2RG).

PDGFRB activation has been observed in patients with chronic myelomonocytic leukemia/atypical chronic myeloid leukemia and has been associated with 11 translocation partners, the best known is the ETV6 gene on 12p13, causing a t(5;12) translocation. Cytogenetic responses are achieved with imatinib in patients with PDGFRB fusion positive, BCR / ABL1 negative CMPDs.

The PDGFRB (5q32) Break FISH probe is optimized to detect translocations involving the PDGFRB region at 5q32 in a dual-color, split assay.



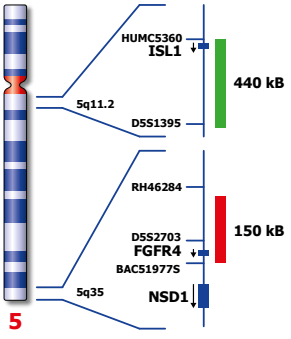
References
Wlodarska et al, 1997, Blood, 89; 1716-1722.
Wilkinson et al, 2003, Blood, 102; 4287-419.

Description	Code	Color	Format	US	ROW
PDGFRB (5q32) Break	KBI-10004	Green/Red	10 Test	-	IVD
PDGFRB (5q32) Break	KI-10004	Green/Red	100 µL	RUO	-

5q35 FGFR4 / 5q11.2

The fibroblast growth factor/fibroblast growth factor receptor (FGF / FGFR) signaling axis plays an important role in normal organ, vascular and skeletal development. It is also well documented that dysregulation of FGF-FGFR signaling via amplification, point mutation or translocations may have an important role in tumor development and progression. Alterations in FGFRs (i.e. overexpression, mutation, translocation, and truncation) are associated with a number of human cancers, including lung, myeloma, breast, gastric, colon, bladder, pancreatic, and hepatocellular carcinomas. A growing body of preclinical data demonstrates that inhibition of FGFR signaling can result in antiproliferative and/or pro-apoptic effects, thus confirming the validity of the FGFR / FGFR axis as a potential therapeutic target.

The FGFR4 (5q35) FISH probe is optimized to detect copy numbers of the FGFR4 gene region at region 5q35. The 5q11.2 probe is included to facilitate chromosome identification.

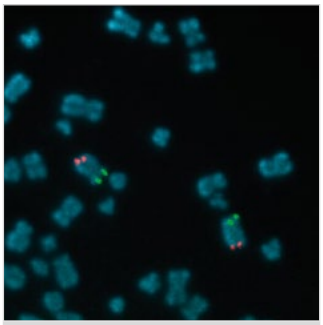


References
Brooks et al, Clin Cancer Res. 2012; 18:1855.
Dutt et al, PLoS ONE 6: e2035.1
Kunii et al, Cancer Res. 2008; 68:2340-8.
Liang et al, Clin Cancer Res. 2013;19: 2572
Liao et al, Cancer Res. 2013; 73:5195-205.
Weiss et al, Sci Transl Med. 2010; 2:62ra93.

Description	Code	Color	Format	US	ROW
FGFR4 (5q35) / 5q11.2	KBI-10756	Green/Red	10 Test	-	IVD
FGFR4 (5q35) / 5q11.2	KI-10756	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

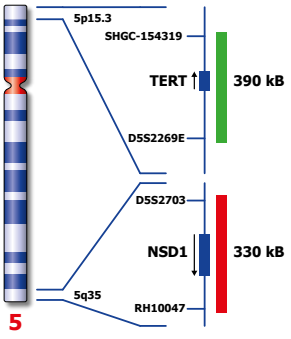
5q35 NSD1 / TERT



NSD1 (5q35) / TERT (5p15) probe hybridized to a normal metaphase (2R2G).

NSD1 microdeletions (chromosome 5q35) are the major cause of Sotos syndrome, and occur in some cases of Weaver syndrome. Sotos is a childhood overgrowth characterized by distinctive craniofacial features, advanced bone age, and mental retardation. Weaver syndrome is characterized by the same criteria but has its own specific facial characteristics. Sotos syndrome is inherited in an autosomal dominant manner. While 50% of Sotos patients in Asia are showing a chromosomal microdeletion, only 9% deletion cases are observed in the affected European population.

The NSD1 (5q35) region probe is optimized to detect copy numbers of the NSD1 gene region at 5q35.2. The TERT region specific FISH probe at 5p15 is included as control probe.

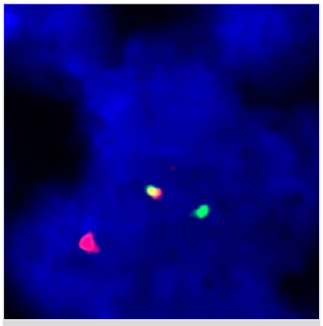


References

Douglas et al, 2003, Am. J. Hum. Genet. 72; 132-143.
Rio et al, 2003, J. Med. Genet., 40; 436-440.

Description	Code	Color	Format	US	ROW
NSD1 (5q35) / TERT (5p15)	KBI-40113	Green/Red	10 Test	-	IVD
NSD1 (5q35) / TERT (5p15)	KBI-45113	Green/Red	5 Test	-	IVD
NSD1 (5q35) / TERT (5p15)	KI-40113	Green/Red	100 µL	RUO	-

6p25 IRF4 / DUSP22 Break

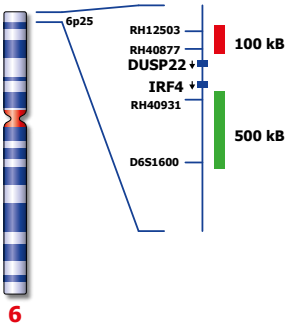


IRF4 / DUSP22 (6p25) Break.

Image kindly provided by Hopital Universitario Marqués de Valdecilla, Satander.

Rearrangements of the 6p25.3 locus define a subtype of cutaneous CD30 positive T-cell lymphomas (CTCL). Genes rearranged at the 6p25.3 locus are IRF4 (Interferon regulatory factor 4, 6p25.3) (previously known as MUM1) and the lately described DUSP22 (dual specificity phosphatase 22). FISH positivity for the IRF4 translocation showed to be highly specific (99%) for CD30 positive primary cutaneous anaplastic large cell lymphoma cases which makes FISH a useful adjunct in the differential diagnosis of CTCL. Rearrangements of the 6p25.3 locus have also been described to occur in high and low grade B-cell lymphomas, myeloma and chronic B-cell lymphoid leukemia. The IRF4 / DUSP22 (6p25) Break FISH probe detects both rearrangements involving IRF4 and DUSP22, but does not distinguish them from each other.

The IRF4 / DUSP22 (6p25) Break FISH probe is optimized to detect trans locations involving the IRF4 / DUSP22 gene region at the 6p25.3 locus in a dual-color assay on metaphase/interphase spreads, blood smears, bone marrow cells and lymph node biopsies.

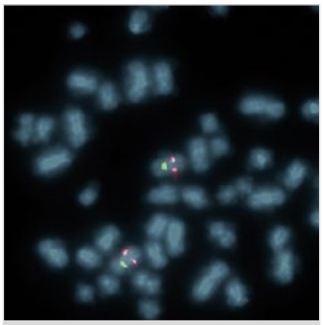


References

Bisig et al., Best Pract Res Clin Haematol, 2012, 25; 13-28.
Feldman et al., Blood, 2011, 117; 915-919.
Karai et al., Am J Surg Pathol, 2013 [Epub ahead of print].
Pham-Ledard et al., J Invest Dermatol, 2010, 130; 816-825.
Salaverria et al., Blood, 2011, 118; 139-147.
Wada et al., Mod Pathol, 2011, 24; 596-605.

Description	Code	Color	Format	US	ROW
IRF4 / DUSP22 (6p25) Break	KBI-10613	Green/Red	10 Test	-	IVD
IRF4 / DUSP22 (6p25) Break	KI-10613	Green/Red	100 µL	RUO	-

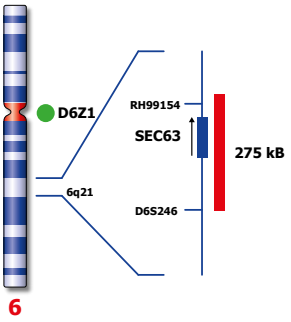
6q21 6q21 / SE 6



6q21 / SE 6 probe hybridized to a normal metaphase (2R2G).

Deletions affecting the long arm of chromosome 6 (6q) are among the most commonly observed chromosomal aberrations in lymphoid malignancies and have been identified as an adverse prognostic factor in subsets of tumors including CLL. A minimal deletion region has been identified within a 2-megabase segment of 6q21, between D6S447 and D6S246. The SEC63 gene is located within this critical region.

The 6q21 specific FISH probe is optimized to detect copy numbers of 6q at region 6q21.The chromosome 6 Satellite Enumeration FISH probe (SE 6) at D6Z1 is included to facilitate chromosome identification.



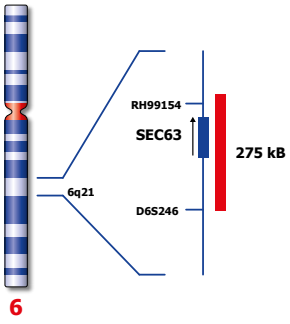
References
Sherratt et al, 1997, Chromosome Res, 5; 118-124.
Zhang et al, 2000, Genes Chrom Cancer, 27; 52-58.

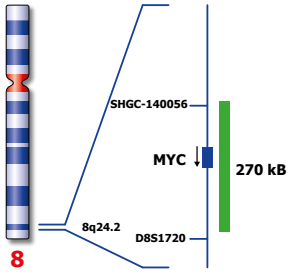
Description	Code	Color	Format	US	ROW
6q21 / SE 6	KBI-10105	Green/Red	10 Test	-	IVD
6q21 / SE 6	KI-10105	Green/Red	100 µL	RUO	-

6q21 6q21 / MYC

Deletions affecting the long arm of chromosome 6 (6q) involving band 6q21 are among the most commonly observed chromosomal aberrations in lymphoid malignancies and have been identified as adverse prognostic factor in subsets of tumors. Amplification of MYC (8q24) has been described in many types of solid tumors, such as breast, cervical and colon cancers, as well as in myeloma, non-Hodgkin's lymphoma, gastric adenocarcinomas and ovarian cancer.

The 6q21 / MYC (8q24) FISH probe is designed as a dual-color assay to detect deletions and amplifications at 6q21 and 8q24.



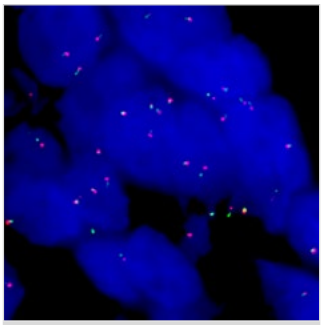


References
Zhang, Y, 2000, Genes, Chrom. And Canc. 27; 52-58
Bentz, M et al, 1995, Blood, 85; 3610-3618

Description	Code	Color	Format	US	ROW
6q21 / MYC (8q24)	KBI-10117	Green/Red	10 Test	-	IVD
6q21 / MYC (8q24)	KI-10117	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

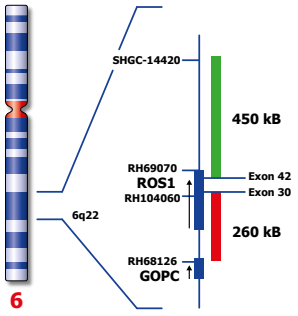
6q22 ROS1 Break



Hybridization of ROS1 (6q22) Break Probe (KBI-10752) to a tissue section harboring a ROS1 rearrangement.

Translocations involving the ROS1 (repressor of silencing 1) gene at chromosome 6q22 can increase expression of the gene by fusion with SLC34A2 (4p15), but also with other fusion partners. Elevated expression is observed in non-small cell lung cancer (NSCLC), where the success of tyrosine kinase-based therapeutics is based on inhibiting the activity of these fusion genes. The fusion of ROS1 to the GOPC (FIG; 6q22) gene, by deletion of a 240 kb DNA fragment, also results in activation of a fusion gene.

The ROS1 (6q22) Break probe is optimized to detect translocations involving the ROS1 gene region at the 6q22 locus, as well as the 240 kb deletion forming the ROS1-GOPC fusion gene, in a dual-color assay on formalin- fixed paraffin-embedded tissue samples.

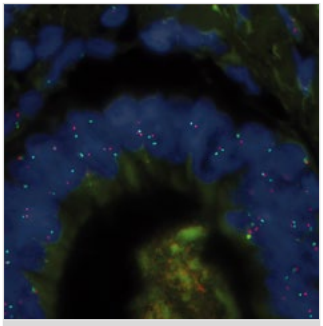


References

Charest et al, Genes Chromosomes Cancer, 2003, 37: 58-71.
Rikova et al, Cell, 2007, 131: 1190-120.
Rimkunas et al, Clin. Can. Res., 2012, 18: 4449-4457.
Takeuchi et al, Nat. Med., 2012, 18: 378-381.
Gu et al, PLoS, 2011, 6: e15640.

Description	Code	Color	Format	US	ROW
ROS1 (6q22) Break	KBI-10752	Green/Red	10 Test	-	IVD
ROS1 (6q22) Break	KI-10752	Green/Red	100 µL	RUO	-

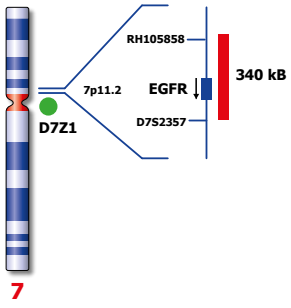
7p11 EGFR / SE 7



EGFR (7p11) / SE 7 hybridized to colon tissue (2R2G).

Epidermal growth factor receptor (EGFR) is a cell membrane protein, providing signal transduction and cell growth. It is a member of the Erb-B family of type I receptor tyrosine kinases and implicated in the development and progression of non-small cell lung carcinomas (NSCLC), breast, intestine, and other organs. EGFR has been found to act as a strong prognostic indicator in head and neck, ovarian, cervical, bladder and oesophageal cancers. In these cancers, increased EGFR expression was associated with reduced recurrence-free or overall survival.

The EGFR (7p11) FISH probe is optimized to detect copy numbers of the EGFR gene region at region 7p11. The chromosome 7 satellite enumeration (SE 7) probe at D7Z1 is included to facilitate chromosome identification.

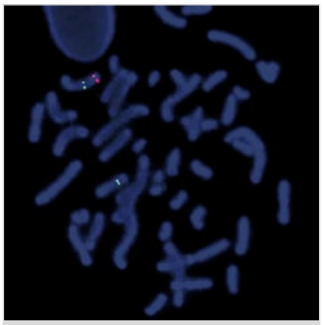


References

Wang et al, 1993, Jpn J Hum Genet, 38: 399-406.
Nicholoset al, 2001, Eur J Cancer, 37: 9-15.

Description	Code	Color	Format	US	ROW
EGFR (7p11) / SE 7	KBI-10702	Green/Red	10 Test	-	IVD
EGFR (7p11) / SE 7	KI-10702	Green/Red	100 µL	RUO	-

7q 7q-

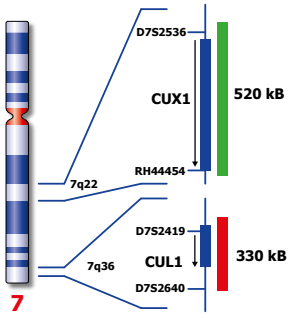


7q- (7q22; 7q36) hybridized to patient material showing a 7q36 deletion (1R2G).

Image kindly provided by Prof. Jauch, Heidelberg.

Loss of a whole chromosome 7 or a deletion of the long arm, del(7q), are recurring abnormalities in malignant myeloid diseases. Most deletions are interstitial and there are two distinct deleted segments of 7q. The majority of patients have proximal breakpoints in bands q11-22 and distal breakpoints in q31-36. The CCAAT displacement protein CUX1 gene region is located in the 7q22 critical region.

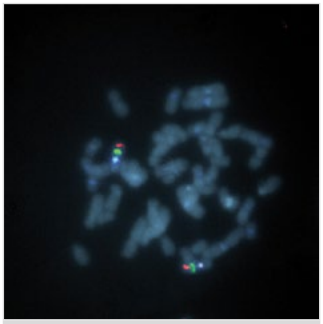
The 7q- specific FISH probe is optimized to detect copy number of 7q at 7q22 and at 7q36 simultaneously in a dual-color assay.



References
LeBeau et al., 1996, Blood, 88; 1930-1935.
Doehner et al, 1998, Blood, 92; 4031-4035.

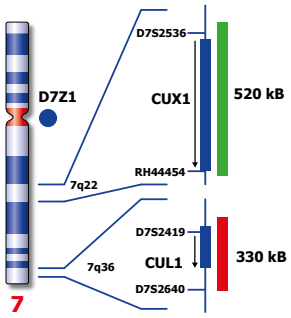
Description	Code	Color	Format	US	ROW
7q- (7q22; 7q36)	KBI-10202	Green/Red	10 Test	-	IVD
7q- (7q22; 7q36)	KI-10202	Green/Red	100 µL	RUO	-

7q 7q- Triple-Color



7q (7q22; 7q36) / SE 7 Triple-Color probe hybridized to a normal metaphase (2R2G2B).

The 7q- specific FISH probe is optimized to detect copy number of 7q at 7q22 and at 7q36 simultaneously in a dual-color assay. The chromosome 7 Satellite Enumeration FISH probe (SE 7) at D7Z1 in blue is included to facilitate chromosome identification.

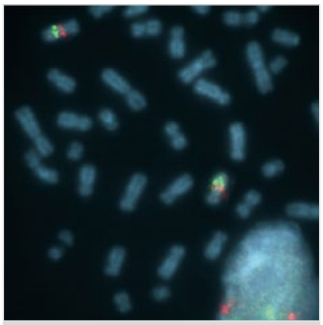


References
LeBeau et al., 1996, Blood, 88; 1930-1935.
Doehner et al, 1998, Blood, 92; 4031-4035.

Description	Code	Color	Format	US	ROW
7q- (7q22; 7q36) / SE7 Triple-Color	KBI-10207	Green/Red/Blue	10 Test	-	IVD
7q- (7q22; 7q36) / SE7 Triple-Color	KI-10207	Green/Red/Blue	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

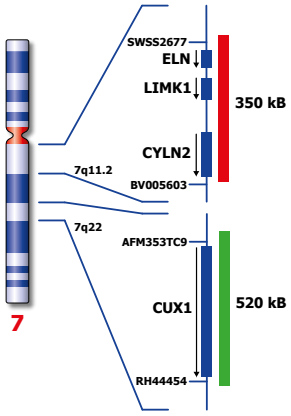
7q11 ELN / 7q22



Williams-Beuren ELN (7q11) / 7q22 probe hybridized to a normal metaphase (2RG).

Williams-Beuren syndrome (WS) is characterized by cardiovascular disease, distinctive facial features, connective tissue abnormalities, mental retardation and endocrine abnormalities. Over 99% of individuals with the clinical diagnosis of WS have this contiguous gene deletion, that encompasses the elastin (ELN) gene region including ELN, LIMK1, and the D7S613 locus.

The Williams-Beuren region probe is optimized to detect copy numbers of the ELN gene region at 7q11. The 7q22 region specific FISH probe at 7q22 is included as control probe.

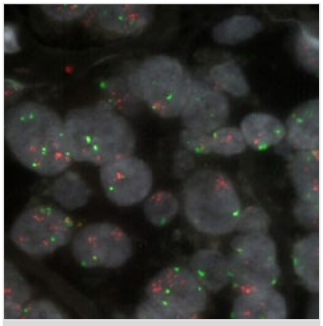


References

Ewart, et al, 1993, Nat. Genet., 5; 11-16.
Botta et al, 1999, J. Med. Genet., 36; 478-480.

Description	Code	Color	Format	US	ROW
Williams-Beuren ELN (7q11) / 7q22	KBI-40111	Green/Red	10 Test	-	IVD
Williams-Beuren ELN (7q11) / 7q22	KBI-45111	Green/Red	5 Test	-	IVD
ELN (7q11) / 7q22	KI-40111	Green/Red	100 µL	RUO	-

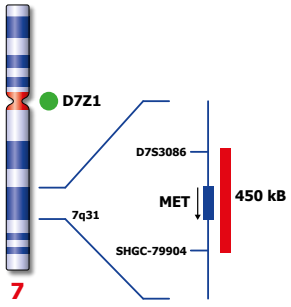
7q31 MET / SE 7



Hybridization of MET Amplification Probe (KBI-10719) to a tissue section showing MET amplification.

The MET proto-oncogene is a receptor-like tyrosine kinase that drives a physiological cellular program important for development, cell movement, cell repair and cellular growth. Aberrant execution of this program has been associated to neoplastic transformation, invasion and metastasis. Activation of MET has been reported in a significant percentage of human cancers including non-small cell lung cancer (NSCLC) and is amplified during the transition between primary tumors and metastasis.

The MET (7q31) FISH probe is optimized to detect copy numbers of the MET gene region at region 7q31. The Chromosome 7 Satellite enumeration probe (SE 7) at D7Z1 is included to facilitate chromosome identification.

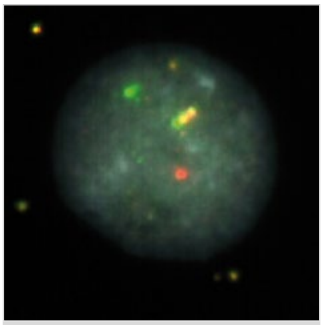


References

Go et al, 2010, J Thorac Oncol 5: 305-313.
Hara et al, 1998, Lab Invest 78; 1143-1153.
Tsugawa et al, 1998, Oncology 55; 475-481.

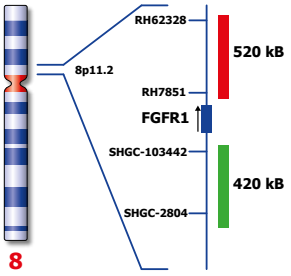
Description	Code	Color	Format	US	ROW
MET (7q31) / SE 7	KBI-10719	Green/Red	10 Test	-	IVD
MET (7q31) / SE 7	KI-10719	Green/Red	100 µL	RUO	-

8p11 FGFR1 Break



FGFR1 (8p11) Break probe hybridized to patient material showing a break at 8p11 (1RG1R1G).

FGFR1 has been implicated in the tumorigenesis of haematological malignancies, where it is frequently involved in balanced chromosomal translocations, including cases of chronic myeloid leukemia (BCR-FGFR1 fusion) and the 8p11 myeloproliferative syndrome/stem cell leukemia–lymphoma syndrome, which is characterized by myeloid hyperplasia and non-Hodgkin's lymphoma with chromosomal translocations fusing several genes, the most common being a fusion between ZNF198 and FGFR1.

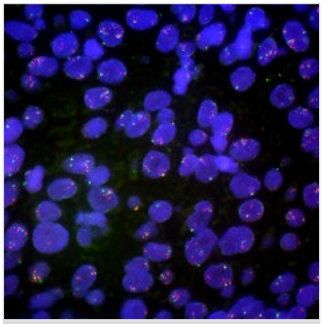


References

Smedley et al, 1998, Hum Mol Genet., 7; 627-642.
Sohal et al, 2001, Genes Chrom. Cancer, 32; 155-163.
Kwak et al, J Clin Oncol., 27(26); 4247-53.

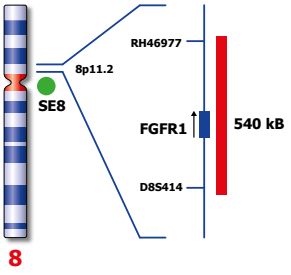
Description	Code	Color	Format	US	ROW
FGFR1 (8p11) Break	KBI-10737	Green/Red	10 Test	-	IVD
FGFR1 (8p11) Break	KI-10737	Green/Red	100 µL	RUO	-

8p11 FGFR1 / SE 8



FGFR1 gene locus amplification in FFPE tissue showing an amplification of FGFR1 gene region at 8p11.

Amplification of the fibroblast growth factor receptor type 1 gene (FGFR1) has been observed in numerous cancer types including lung cancer (especially squamous cell carcinoma) and breast cancer. With the development of new therapeutic strategies, FGFR1 amplification could act as a valuable biomarker for R&D and provide an attractive tool for clinical stratification. The FGFR1 (8p11) / SE 8 FISH probe is optimized to detect amplification involving the FGFR1 gene region at 8p11 in a dual-color assay on paraffin embedded tissue sections. The chromosome 8 satellite enumeration probe (SE 8) at D8Z1 is included to facilitate chromosome identification.



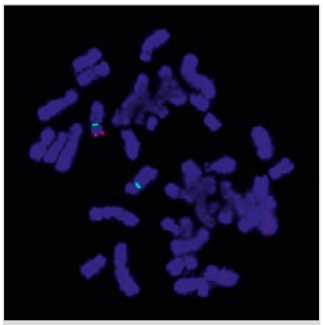
References

Weiss et al, 2010, Sci Transl. Med. 2(62); 62ra93.
Brooks et al, 2012, Clin. Cancer res. 18(7): 1855-62

Description	Code	Color	Format	US	ROW
FGFR1 (8p11) / SE 8	KBI-12754	Green/Red	20 Test	-	IVD
FGFR1 (8p11) / SE 8	KBI-14754	Green/Red	50 Test	-	IVD

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

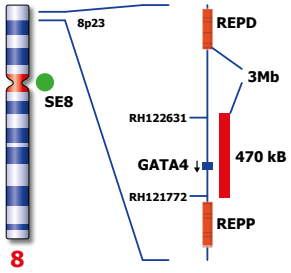
8p23 GATA4 / SE8



GATA4 (8p23) / SE 8 probe hybridized to patient material showing a deletion of the GATA4 (8p23) region (1R2G).

The deletion of GATA4 (8p23) is found in patients with congenital heart disease. Besides the deletion of the region, duplications are found of the region flanked by low copy repeats 8p-OR-REPD (distal) and –REPP (proximal). These recurrent deletions are associated with a spectrum of anomalies, including congenital diaphragmatic hernia, developmental delay and neuropsychiatric findings. GATA4 is expressed in adult heart, epithelium and gonads. During fetal development, GATA4 is expressed in yolk sac endoderm and cells involved in heart formation.

The GATA4 (8p23) / SE 8 FISH probe is optimized to detect deletions of the GATA4 gene region at 8p23 in a dual-color assay on metaphase/interphase spreads, blood smears and bone marrow cells. The Chromosome 8 Satellite Enumeration (SE) FISH probe is included to facilitate chromosome identification.

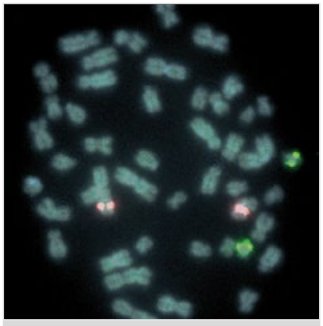


References

Bhatia et al, 1999, Prenat Diagn., 19; 863-867.
Giorda et al, 2007, Hum. Mut., 28; 459-468.
Wat et al, 2009, Am. J. Med. Genet., Part A, 149A; 1661-1677.

Description	Code	Color	Format	US	ROW
GATA4 (8p23) / SE 8	KBI-40118	Green/Red	10 Test	-	IVD
GATA4 (8p23) / SE 8	KBI-45118	Green/Red	5 Test	-	IVD
GATA4 (8p23) / SE 8	KI-40118	Green/Red	100 µL	RUO	-

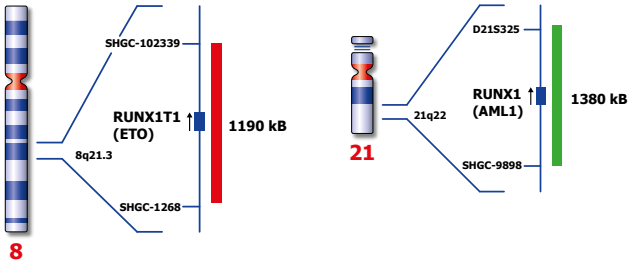
8q21 RUNX1 / RUNX1T1



RUNX1/RUNX1T1 t(8;21) Fusion probe hybridized to a normal metaphase (2R2G).

t(8;21)(q21;q22) is the most frequently observed karyotypic abnormality associated with acute myeloid leukemia (AML), especially in FAB M2. As a consequence of the translocation the RUNX1 (previously known as AML) (CBFA2) gene in the 21q22 region is fused to the RUNX1T1 (previously known as ETO) (MTG8) gene in the 8q21 region, resulting in one transcriptionally active gene on the 8q-derivative chromosome.

The RUNX1/RUNX1T1 t(8;21)(q21;q22) specific FISH probe is optimized to detect the reciprocal translocation t(8;21) in a dual-color, dual-fusion assay.

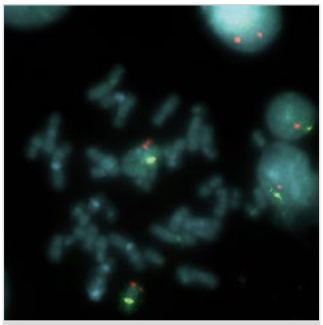


References

Sacchi et al, 1995, Genes Chrom Cancer, 79; 97-103.
Hagemeijer et al, 1998, Leukemia, 12; 96-101.

Description	Code	Color	Format	US	ROW
RUNX1/RUNX1T1 t(8;21) Fusion	KBI-10301	Green/Red	10 Test	-	IVD
RUNX1/RUNX1T1 t(8;21) Fusion	KI-10301	Green/Red	100 µL	RUO	-

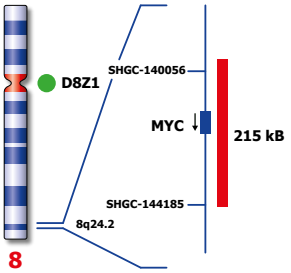
8q24 MYC / SE 8



MYC (8q24) / SE 8 hybridized to a normal metaphase (2R2G).

The MYC (previously known as C-MYC) gene produces an oncogenic transcription factor that affects diverse cellular processes involved in cell growth, cell proliferation, apoptosis and cellular metabolism. The MYC oncogene has been shown to be amplified in many types of human cancer such as bladder, breast and cervical. Amplification at 8q24 including MYC is also observed in 5% of CLL patients. MYC is also the prototype for oncogene activation by chromosomal translocation.

The MYC (8q24) specific FISH probe is optimized to detect copy numbers of the MYC gene region at 8q24. The chromosome 8 Satellite Enumeration FISH probe (SE 8) at D8Z1 is included to facilitate chromosome identification.

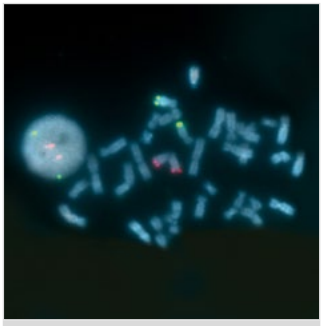


References

Greil et al, 1991, Blood, 78; 180-191.

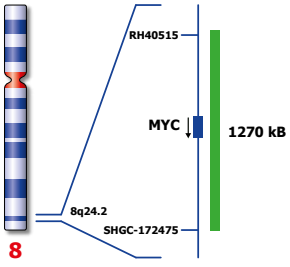
Description	Code	Color	Format	US	ROW
MYC (8q24) / SE 8	KBI-10106	Green/Red	10 Test	-	IVD
MYC (8q24) / SE 8	KI-10106	Green/Red	100 µL	RUO	-

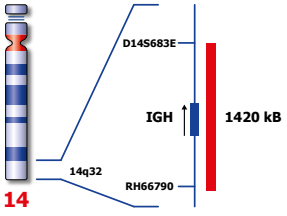
8q24 MYC/IGH t(8;14) Fusion



MYC / IGH t(8;14) Fusion probe hybridized to a normal interphase/ metaphase (2R2G).

The translocation t(8;14)(q24;q32) is the characteristic chromosomal aberration of Burkitt's-type of lymphomas. This translocation fuses the MYC gene at 8q24 next to the IGH locus at 14q32, resulting in overexpression of the transcription factor MYC. Detection of the t(8;14) is aimed to help in the diagnostic process of patients with high-grade B-cell lymphomas because treatment strategies differ between Burkitt and other high-grade lymphomas. The MYC / IGH t(8;14) (q24;q32) specific FISH probe is optimized to detect the reciprocal translocation t(8;14) in a dual-color, dual-fusion assay.





References

Veronese et al, 1995, Blood, 85;2132-2138.
Siebert et al, 1998, Blood, 91; 984-990.

Description	Code	Color	Format	US	ROW
MYC/IGH t(8;14) Fusion	KBI-10603	Green/Red	10 Test	-	IVD
MYC/IGH t(8;14) Fusion	KI-10603	Green/Red	100 µL	RUO	-

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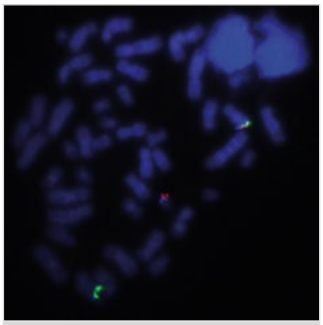
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

8q24 MYC (8q24) Break

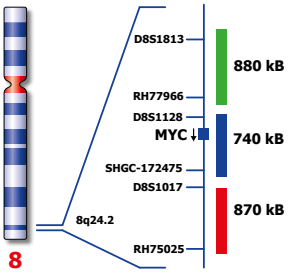


MYC (8q24) Break probe hybridized to patient material showing a 8q24 proximal break (1GBR1G1BR).

Image kindly provided by Prof. Siebert, Kiel.

Rearrangements of the protooncogene MYC (previously known as C-MYC) have been consistently found in tumor cells of patients suffering from Burkitt's lymphoma. In cases with the common t(8;14) chromosomal translocation, the MYC gene is translocated to chromosome 14 and rearranged with the immunoglobulin heavychain genes; the breakpoint occurs 5' to the MYC gene and may disrupt the gene itself separating part of the first untranslated exon from the remaining two coding exons. In Burkitt's lymphoma showing the variant t(2;8) or t(8;22) translocations, the genes coding for the k and l immunoglobulin light chain are translocated to chromosome 8. The rearrangement takes place 3' to the MYC gene.

The MYC (8q24) Break probe is optimized to detect rearrangements involving the 8q24 locus in a triple-color, split assay on metaphase/ interphase spreads, blood smears and bone marrow cells.

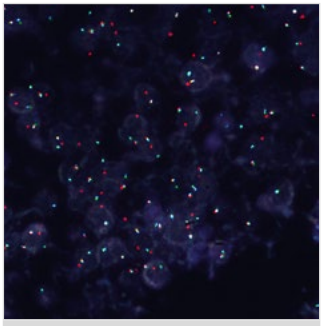


References

Fabris et al, 2003, Genes Chromosomes Cancer, 37;261-269.
Hummel et al, 2006, N Engl J Med, 354; 2419-30.

Description	Code	Color	Format	US	ROW
MYC (8q24), Triple-Color, Break	KBI-10611	Green/Red/Blue	10 Test	-	IVD
MYC (8q24), Triple-Color, Break	KI-10611	Green/Red/Blue	100 µL	RUO	-

8q24 MYC (8q24) Break (tissue)

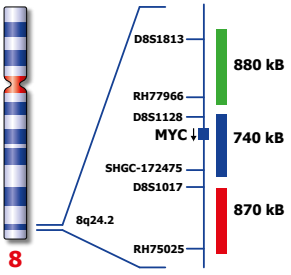


MYC (8q24) Break, TC (tissue) probe hybridized to patient material showing a 8q24 distal break (1GB1R1GBR).

Image kindly provided by N. Van Acker, Antwerp.

Rearrangements of the proto oncogene MYC (or c-myc) have been consistently found in tumor cells of patients suffering from Burkitt's lymphoma. In cases with the common t(8;14) chromosomal translocation, the MYC gene is translocated to chromosome 14 and rearranged with the immunoglobulin heavy chain genes; the breakpoint occurs 5' to the MYC gene and may disrupt the gene itself separating part of the first untranslated exon from the remaining two coding exons. In Burkitt's lymphoma showing the variant t(2;8) or t(8;22) translocations, the genes coding for the k and l immunoglobulin light chain are translocated to v-myc avian myelocytomatosis viral oncogene homolog (MYC or c-myc) chromosome 8.

The MYC (8q24) Break probe is optimized to detect rearrangements involving the 8q24 locus in a triple-color, split assay on formalin fixed paraffin embedded tissue.

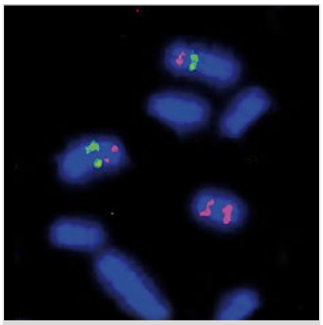


References

Fabris et al, 2003, Genes Chromosomes Cancer, 37;261-269.
Hummel et al, 2006, N Engl J Med, 354; 2419-30.

Description	Code	Color	Format	US	ROW
MYC (8q24) Triple-Color, Break (tissue)	KBI-10749	Green/Red/Blue	10 Test	-	IVD
MYC (8q24) Triple-Color, Break (tissue)	KI-10749	Green/Red/Blue	100 µL	RUO	-

9p21 CDKN2A / 9q21

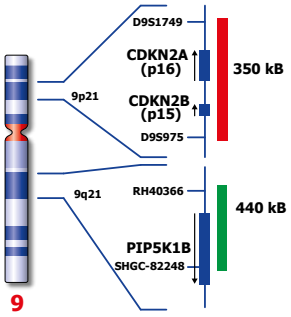


CDKN2A (9p21) / 9q21 hybridized on patient material showing an isochromosome 9.

Image kindly provided by Dr. Wenzel, Basel.

Hemizygous deletions and rearrangements of chromosome 9, band p21 are among the most frequent cytogenetic abnormalities detected in pediatric acute lymphoblastic leukemia (ALL). This deletion includes loss of the CDKN2A (previously known as p16, INK4A or MTS1) / CDKN2B (previously known as p15, INK4B or MTS2) genes, which are cell cycle kinase inhibitors and important in leukemogenesis.

The CDKN2A (9p21) specific FISH probe is optimized to detect copy numbers of the CDKN2A gene region at region 9p21. The 9q21 region probe is included to facilitate chromosome identification.

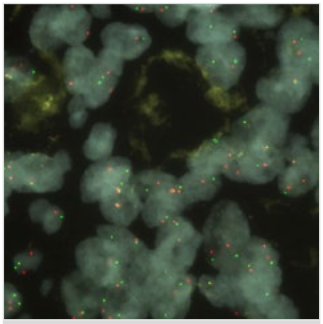


References

Dreyling et al, 1995, Blood, 86; 1931-1938.
Southgate et al, 1995, Br J Cancer, 72; 1214-1218.

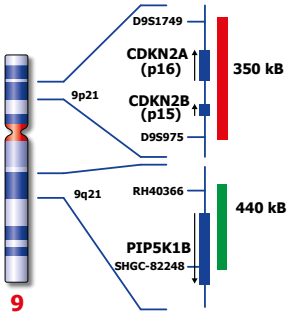
Description	Code	Color	Format	US	ROW
CDKN2A (9p21) / 9q21	KBI-10402	Green/Red	10 Test	-	IVD
CDKN2A (9p21) / 9q21	KI-10402	Green/Red	100 µL	RUO	-

9p21 CDKN2A / 9q21 (tissue)



CDKN2A (9p21) / 9q21 (tissue) probe hybridized to tissue (2R2G).

Homozygous and hemizygous deletions of 9p21 are the earliest and most common genetic alteration in bladder cancer. The CDKN2A (INK4A) gene has been identified as tumor suppressor gene in this region which is commonly deleted in bladder cancer. The loss of DNA sequences on chromosomal bands 9p21-22 has been documented also in a variety of malignancies including leukemias, gliomas, lung cancers, and melanomas. The CDKN2A (9p21) FISH probe is optimized to detect copy numbers of the CDKN2A gene region at region 9p21. The 9q21 region probe is included to facilitate chromosome identification.



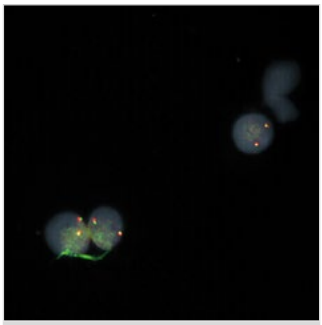
References

Stadler et al, 1994, Cancer Res, 54:2260-2063.
Williams et al, 1995, Hum Mol Genet; 4: 1569-1577.

Description	Code	Color	Format	US	ROW
CDKN2A (9p21) / 9q21 (tissue)	KBI-10710	Green/Red	10 Test	-	IVD
CDKN2A (9p21) / 9q21 (tissue)	KI-10710	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

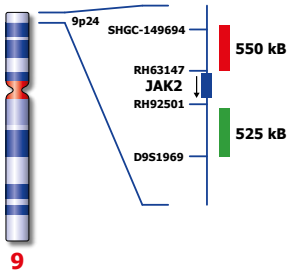
9p24 JAK2 Break



JAK2 (9p24) Break probe hybridized to bone marrow sample (2RG).

Janus Kinase 2 (JAK2) is a tyrosine kinase involved in cytokine signaling. Mutations and translocations involving the JAK2 gene region are observed in myeloproliferative neoplasms. The common JAK2617V>F point mutation and translocations results in constitutive activation of JAK2. Translocations are described with the following fusion partners: PCM1, BCR, ETV6 (TEL), SSBP2 and 3q21. Patients with the JAK2617V>F point mutation can also exhibit a numerical gain of the gene.

The JAK2 (9p24) Break FISH probe is optimized to detect translocations involving the JAK2 gene region at region 9p24 in a dual-color, split assay on metaphase/ interphase spreads. The JAK2 (9p24) Break FISH probe can not be used to detect point mutations, and it has not been optimized to detect gene amplifications.

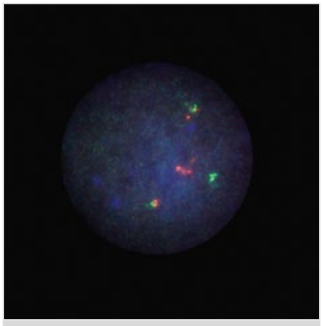


References

Najfeld V et al, 2007, Exp Hematol, 35; 1668-1676.
Smith C et al, 2008, Hum Pathol, 39; 795-810.
Poitras J et al, 2008, Genes Chromosomes Cancer, 47; 884-889.

Description	Code	Color	Format	US	ROW
JAK2 (9p24) Break	KBI-10012	Green/Red	10 Test	-	IVD
JAK2 (9p24) Break	KI-10012	Green/Red	100 µL	RUO	-

9q34 DEK / NUP214

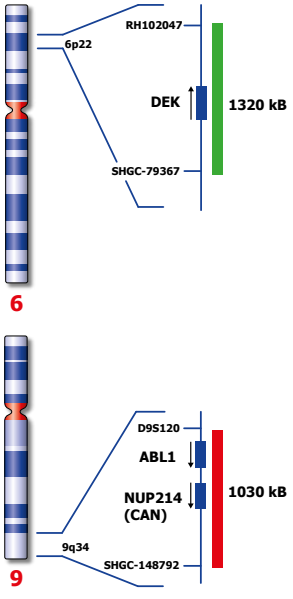


DEK / NUP214 t(6;9) Fusion probe hybridized to patient material showing a t(6;9)(p22;q34) translocation (2RG1R1G).

Image kindly provided by Dr. Stevens-Kroef, UMC St. Radboud, Nijmegen.

The chromosomal translocation t(6;9) (p22;q34) is associated with a specific subtype of acute myeloid leukemia (AML) and constitutes 0.5% to 4% of all AML cases. The translocation results in a fusion between the DEK oncogene (6p22) and the nucleoporin 214 kDa (NUP214 at 9q34; previously known as CAN). The exact mechanism by which the fusion protein DEK-NUP214 contributes to leukemia development has not been identified. Patients with t(6;9) AML have a very poor prognosis. The currently available chemotherapy does not seem to improve overall survival. However, accurate diagnosis is crucial because these patients may benefit from early allogeneic stem cell transplant.

The DEK / NUP214 t(6;9) specific FISH Probe has been optimized to detect the reciprocal translocation t(6;9) in a dual-color, dual-fusion assay on metaphase/ interphase spreads, blood smears and bone marrow cells.

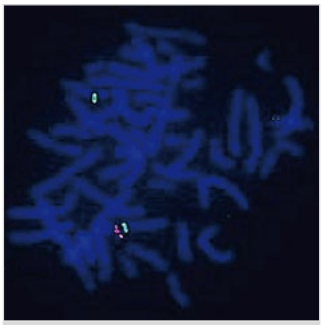


References

Von Lindern et al, 1992, Mol. Cell. Biol.,12; 1687-1697.
Ageberg et al, 2008, Gen. Chrom. Canc., 47; 276-287.
Chi et al, 2008, Arch. Pathol. Lab. Med., 132; 1835-1837.

Description	Code	Color	Format	US	ROW
DEK/NUP214 t(6;9) Fusion	KBI-10306	Green/Red	10 Test	-	IVD
DEK/NUP214 t(6;9) Fusion	KI-10306	Green/Red	100 µL	RUO	-

10p14 DiGeorge II / SE 10

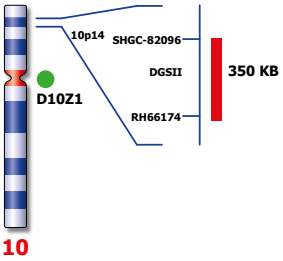


DiGeorge II(10p14) / SE 10 probe hybridized to DiGeorge II patient material showing a deletion of the DGSII region at 10p14 (1R2G).

Image kindly provided by Azzedine Aboura, Hôpital Robert Debré Paris.

DiGeorge and VCFS present many clinical problems and are frequently associated with deletions within 22q11.2, but a number of cases have no detectable molecular defect of this region. A number of single case reports with deletions of 10p suggest genetic heterogeneity of DiGeorge syndrome. FISH analysis demonstrates that these patients have overlapping deletions at the 10p13/10p14 boundary. The shortest region of deletion overlap (SRO) has been identified in a 1 cM interval including makers D10S547 and D10S585.

The DiGeorge II region probe is optimized to detect copy numbers of the DGSII at 10p14. The chromosome 10 satellite enumeration (SE 10) FISH probe at D10Z1 is included to facilitate chromosome identification.

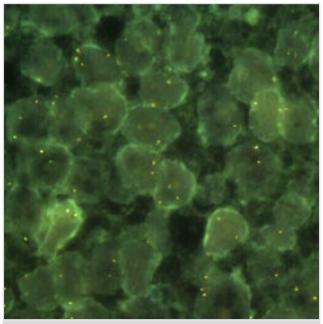


References

Monaco et al, 1991, Am. J. Med. Genet., 39; 215-216.
Schuffenhauer et al, 1998, Eur. J. Hum. Genet., 6; 213-225.

Description	Code	Color	Format	US	ROW
DiGeorge II (10p14) / SE 10	KBI-40105	Green/Red	10 Test	-	IVD
DiGeorge II (10p14) / SE 10	KBI-45105	Green/Red	5 Test	-	IVD
DiGeorge II (10p14) / SE 10	KI-40105	Green/Red	100 µL	RUO	-

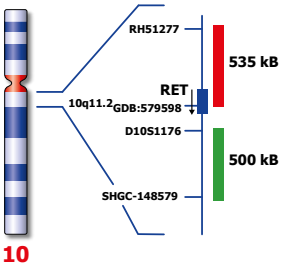
10q11 RET Break



Hybridization of RET (10q11) Break Probe (KBI-10753) to a tissue section (2RG).

Pericentric inversion of chromosome 10 involving the RET (ret proto-oncogene) gene at chromosome 10q11 is known to increase expression of the RET gene by fusion with KIF5B (10p11). Translocations with other fusion partners have also been described. Elevated expression of RET is observed in non-small cell lung cancer (NSCLC), in which the function of tyrosine kinase-based therapeutics is based on the inhibition of such fusion proteins. Translocations involving RET have also been described in thyroid carcinomas.

The RET (10q11) Break probe is optimized to detect translocations involving the RET gene region at 10q11.



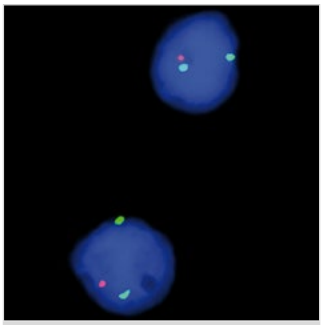
References

Chen et al, Cancer Genet Cytogenet, 2007, 178: 128-134.
Kohno et al, Nat Med, 2012, 18: 375-377.
Takeuchi et al, Nat Med, 2012, 18: 378-381.

Description	Code	Color	Format	US	ROW
RET (10q11) Break	KBI-10753	Green/Red	10 Test	-	IVD
RET (10q11) Break	KI-10753	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

10q23 PTEN / SE 10

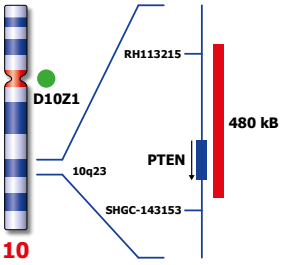


PTEN (10q23) / SE 10 probe hybridized to prostate cancer material showing deletion of PTEN gene region at 10q23 (1R2G).

Image kindly provided by Portuguese Cancer Inst., Porto.

The gene 'phosphatase and tensin homolog' (PTEN), is a tumor suppressor located at chromosome region 10q23, that plays an essential role in the maintenance of chromosomal stability, cell survival and proliferation. Loss of PTEN has been found in a wide number of tumors, and its important role is demonstrated by the fact that it is the second most frequently mutated gene after TP53. Loss of PTEN significantly correlates with the advanced forms of gliomas, but also of prostate cancer and breast tumors.

The PTEN (10q23) FISH probe is optimized to detect copy numbers of the PTEN gene region at region 10q23. The Chromosome 10 Satellite enumeration probe (SE 10) at D10Z1 is included to facilitate chromosome identification.



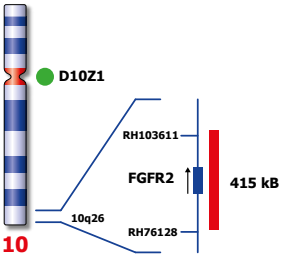
References
Cairns et al, 1997, Cancer Res, 57 ; 4997-5000.
Hermans et al, 2004, Genes Chrom Cancer, 39; 171-184.

Description	Code	Color	Format	US	ROW
PTEN (10q23) / SE 10	KBI-10718	Green/Red	10 Test	-	IVD
PTEN (10q23) / SE 10	KI-10718	Green/Red	100 µL	RUO	-

10q26 FGFR2 / SE 10

The fibroblast growth factor/fibroblast growth factor receptor (FGF / FGFR) signaling axis plays an important role in normal organ, vascular and skeletal development. It is also well documented that dysregulation of FGF-FGFR signaling via amplification, point mutation or translocations may have an important role in tumor development and progression. Alterations in FGFRs (i.e. overexpression, mutation, translocation, and truncation) are associated with a number of human cancers, including lung, myeloma, breast, gastric, colon, bladder, pancreatic, and hepatocellular carcinomas. A growing body of preclinical data demonstrates that inhibition of FGFR signaling can result in antiproliferative and/or pro-apoptic effects, thus confirming the validity of the FGFR / FGFR axis as a potential therapeutic target.

The FGFR2 (10q26) FISH probe is optimized to detect copy numbers of the FGFR2 gene region at region 10q26. The Chromosome 10 Satellite Enumeration (SE) probe is included to facilitate chromosome identification.



References
Brooks et al, Clin Cancer Res. 2012; 18:1855.
Dutt et al, PLoS ONE 6: e2035.1
Kunii et al, Cancer Res. 2008; 68:2340-8.
Liang et al, Clin Cancer Res. 2013;19: 2572
Liao et al, Cancer Res. 2013;73:5195-205.
Weiss et al, Sci Transl Med. 2010; 2:62ra93.

Description	Code	Color	Format	US	ROW
FGFR2 (10q26) / SE 10	KBI-10757	Green/Red	10 Test	-	IVD
FGFR2 (10q26) / SE 10	KI-10757	Green/Red	100 µL	RUO	-

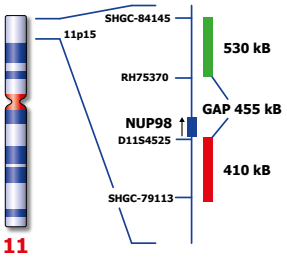
11p15 NUP98 Break

NUP98 (11p15) Break Probe hybridized to AML patient sample showing a rearrangement of 11p15 involving the NUP98 gene (1F1R1G).

Image kindly provided by Prof. Manuel R. Teixeira, Porto.

Nucleoporin 98kDa gene (NUP98) rearrangements have been identified in a wide range of hematologic malignancies, including acute myeloid leukemia (AML), acute lymphoblastic leukemia (ALL), chronic myeloid leukemia in blast crisis (CML-bc), myelodysplastic syndrome (MDS) and bilineage/ biphenotypic leukemia. The NUP98 gene is highly promiscuous with regard to its recombination spectrum, as at least 28 different partner genes have been identified for NUP98 rearrangements, all forming in-frame fusion genes. Patients with NUP98 gene rearrangements have an aggressive clinical course and the outcome of treatment is disappointing.

The NUP98 (11p15) Break FISH Probe is optimized to detect translocations involving the NUP98 gene region at 11p15 in a dual-color assay on metaphase/ interphase spreads, blood smears and bone marrow cells.

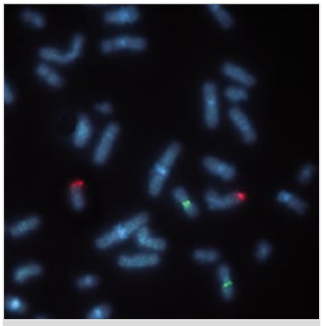


References

Gough et al, 2011, Blood, 118; 62 47-6257.
Nebral et al, 2005, Haematologica, 90; 74 6-752.
Romana et al, 2006, Leukemia, 20; 696-70 6.

Description	Code	Color	Format	US	ROW
NUP98 (11p15) Break	KBI-10311	Green/Red	10 Test	-	IVD
NUP98 (11p15) Break	KI-10311	Green/Red	100 µL	RUO	-

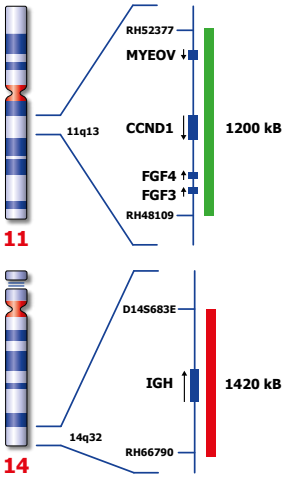
11q13 CCND1 / IGH Fusion



CCND1 / IGH t(11;14) Fusion probe hybridized to a normal interphase/ metaphase (2R2G).

Mantle cell lymphoma is a subtype of non-Hodgkin lymphoma characterized by poor prognosis. Cytogenetically t(11;14) is associated with 75% of mantle cells lymphomas. The translocation breakpoints are scattered within the 120 kb region adjacent to CCND1 (previously known as BCL1). The translocation leads to overexpression of cyclin D1 due to juxtaposition of the Ig heavy chain gene enhancer on 14q32 to the cyclin D1 gene on 11q13.

The CCND1 / IGH t(11;14)(q13;q32) specific FISH probe is optimized to detect the reciprocal translocation t(11;14) in a dual-color, dual-fusion assay.



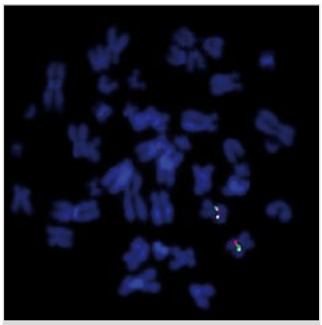
References

Vaandrager et al, 1996, Blood, 88; 1177-1182.

Description	Code	Color	Format	US	ROW
CCND1/IGH t(11;14) Fusion	KBI-10604	Green/Red	10 Test	-	IVD
CCND1/IGH t(11;14) Fusion	KI-10604	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

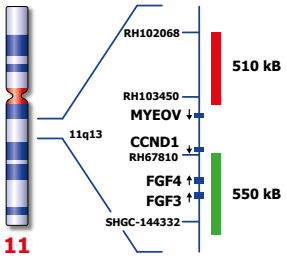
11q13 CCND1 Break



CCND1 (11q13) Break probe hybridized to a normal metaphase (2R2G).

Besides the important functions in cellular growth, metabolism, and cellular differentiation, CCND1 (previously known as Cyclin D1 or BCL1) can also function as a proto-oncogene, often dysregulated after re-arrangement by translocation. In fact, it can juxtapose into many different gene locus to drive tumorigenic effects. To date, the gene has been found to be rearranged in leukemias, in multiple myelomas (MM), and in some cases of benign parathyroid tumors. More specifically, the chromosomal translocation t(11;14)(q13:q32), involving rearrangement of the CCND1 locus, has been reported to be associated with human lymphoid neoplasia affecting mantle cell lymphomas (MCL). The rearrangement has been documented in 40-70% of cases of mantle cell lymphoma, whereas it only rarely occurs in other B cell lymphomas. In MM, the same translocation t(11;14)(q13:q32) is the most common, with a reported frequency of 15% to 20% of the cases.

For this reason, the CCND1 break apart FISH probe KBI-10609 can be considered a very useful tool for routine diagnosis in MCL and MM, to be used in association to the related FISH probes KBI-10604 and KBI-10605 that can detect more specifically the translocation t(11;14) in Mantle Cell Lymphoma (KBI-10604) and MM (KBI-10605).

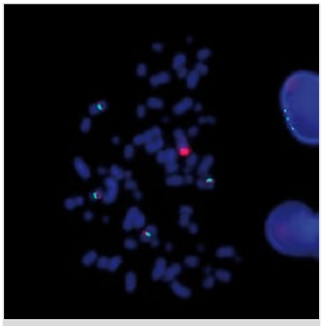


References

Vaandrager et al, 1996, Blood, 88; 1177-1182.
Vaandrager et al, Blood, 89; 349-350.

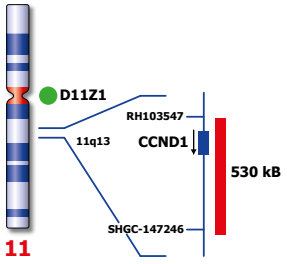
Description	Code	Color	Format	US	ROW
CCND1 (11q13) Break	KBI-10609	Green/Red	10 Test	-	IVD
CCND1 (11q13) Break	KI-10609	Green/Red	100 µL	RUO	-

11q13 CCND1 /SE 11



CCDN1 (11q13) / SE 11 probe hybridized to patient interphases / metaphase showing CCDN1 (11q13) amplification with polyploidy for chromosome 11.

CCND1 (also named Cyclin D1 or BCL1) is a key cell cycle regulator of the G1 to S phase progression. The binding of cyclin D1 to cyclin-dependent kinases (CDKs) leads to the phosphorylation of retinoblastoma protein (pRb), subsequently triggering the release of E2F transcription factors to allow G1 to S phase progression of the cell cycle. Consistent with this function, overexpression of cyclin D1 results in a more rapid progression from the G1 to S phase transition and in a reduced serum dependency in fibroblast cells, characteristics typically seen in cancer cells. The CCND1 (11q13) FISH probe is optimized to detect copy numbers of the CCND1 gene region at region 11q13. The Chromosome 11 Satellite Enumeration (SE 11) probe at D11Z1 is included to facilitate chromosome identification.

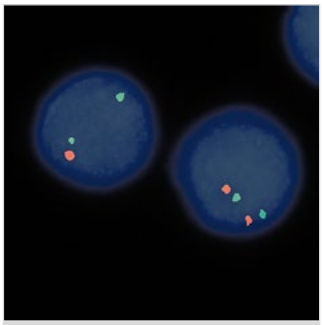


References

Okami et al, 1999, Oncogene 18; 3541-3645.
Freier et al, 2003, Cancer Res; 1179-1182.

Description	Code	Color	Format	US	ROW
CCND1 (11q13) / SE 11	KBI-10734	Green/Red	10 Test	-	IVD
CCND1 (11q13) / SE 11	KI-10734	Green/Red	100 µL	RUO	-

11q22 ATM / SE 11

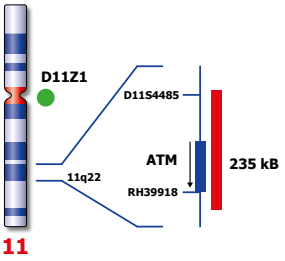


ATM (11q22) / SE 11 hybridized to patient material showing a 11q22 deletion at the ATM gene region (1R2G).

Image kindly provided by Dr. Wenzel, Basel.

Chromosome 11q22.3-23.1 deletions involving the ataxia-teleangiectasia mutated (ATM) locus are detected at diagnosis in 15-20% of cases of B-cell chronic lymphocytic leukemia (CLL) and are associated with a relatively aggressive disease. Loss of the 11q22-23 region, where the ataxia-telangiectasia mutated (ATM) gene is located, is also one of the most frequent secondary chromosomal aberrations in mantle cell lymphoma.

The ATM (11q22.3) specific FISH probe is optimized to detect copy numbers of the ATM gene region at region 11q22.3. The chromosome 11 Satellite Enumeration (SE 11) at D11Z1 FISH probe is included to facilitate chromosome identification.

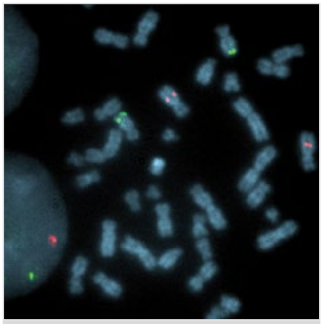


References

Doehner et al, 1997, Blood, 89; 2516-2522.
Bigoni et al, 1997, Leukemia, 11; 1933-1940.

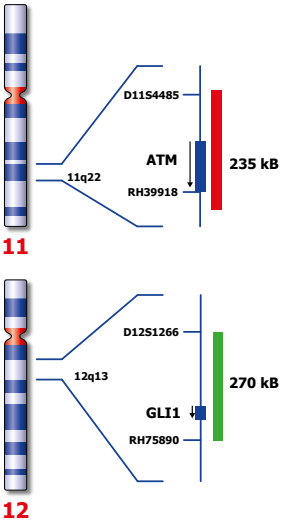
Description	Code	Color	Format	US	ROW
ATM (11q22) / SE 11	KBI-10103	Green/Red	10 Test	-	IVD
ATM (11q22) / SE 11	KI-10103	Green/Red	100 µL	RUO	-

11q22 ATM / GLI1



ATM (11q22) / GLI1 (12q13) hybridized to a normal metaphase (2R2G).

Deletion of ATM at 11q22-q23 indicates a rather poor prognosis, amplification of GLI1 (previously known as GLI) at 12q13 is associated with an intermediate prognosis.



References

Döhner H et al, 1997, Blood, 7; 2516-2522.
Boultwood J, 2001, J. Clin. Pathol., 54; 512-516.
Dierlamm J et al, 1998, Genes Chromosomes Cancer, 20; 155-166.
Döhner H at al, 1999, J. Molec. Med., 77; 266-281.

Description	Code	Color	Format	US	ROW
ATM (11q22) / GLI1 (12q13)	KBI-10108	Green/Red	10 Test	-	IVD
ATM (11q22) / GLI1 (12q13)	KI-10108	Green/Red	100 µL	RUO	-

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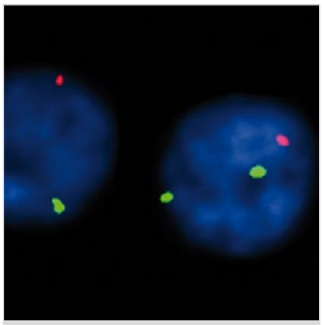
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

11q23 11q23 / DLEU1

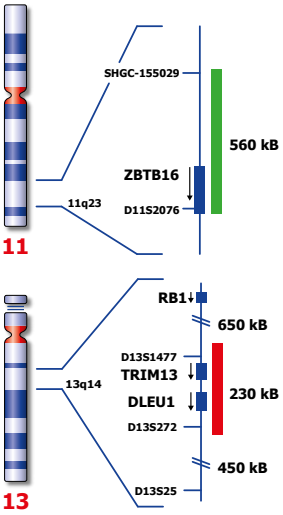


11q23 / DLEU1 13q14 probe hybridized to MM patient material showing a 13q14 deletion (1R2G).

Image kindly provided by Prof. Jauch, Heidelberg.

Hybridization results delineated 11q23 and 11q25 as the most frequently gained regions in Multiple Myeloma (MM) which supports a relevant pathogenetic role of genes in this region. Deletions of 13q14 are frequently detected by interphase FISH in patients with newly diagnosed MM, correlate with increased proliferative activity, and represent an independent adverse prognostic feature in MM.

The 11q23 specific FISH probe is optimized to detect copy numbers at 11q23. The DLEU1 (13q14) specific DNA region is optimized to detect copy numbers of the DLEU1 (previously known as DLEU) gene region at 13q14.

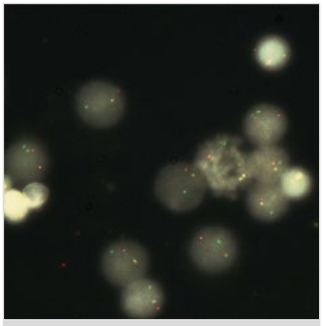


References

Gonzalez et al, 2004, Haematologica, 89; 1213-1218.
Cremer et al, 2005, Genes Chrom Cancer, 44; 194-203.

Description	Code	Color	Format	US	ROW
11q23 / DLEU1 (13q14)	KBI-10502	Green/Red	10 Test	-	IVD
11q23 / DLEU1 (13q14)	KI-10502	Green/Red	100 µL	RUO	-

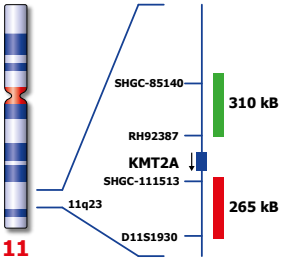
11q23 KMT2A Break



KMT2A (11q23) Break probe hybridized to patient material showing a translocation at 11q23 (1RG1R1G).

The human chromosome band 11q23 is associated with a high number of recurrent chromosomal abnormalities including translocations, insertions, and deletions. It is involved in over 20% of acute leukemias. The KMT2A (previously known as MLL) gene, named for its involvement in myeloid (usually monoblastic) and lymphoblastic leukemia, and less commonly in lymphoma, is located in the 11q23 breakpoint region. Leukemias involving the KMT2A gene usually have a poor prognosis.

The KMT2A (11q23) Break FISH probe is optimized to detect translocations involving the KMT2A gene region at 11q23 in a dual-color split assay.

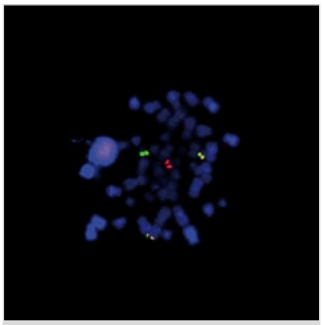


References

Kobayashi et al, 1993, Blood, 81; 3027-3022
Martinez-Climent et al, 1995, Leukemia, 9; 1299-1304.

Description	Code	Color	Format	US	ROW
KMT2A (11q23) Break	KBI-10303	Green/Red	10 Test	-	IVD
KMT2A (11q23) Break	KI-10303	Green/Red	100 µL	RUO	-

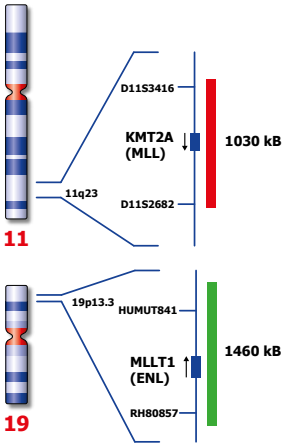
11q23 KMT2A / MLLT1



KMT2A / MLLT1 t(11;19) Fusion probe hybridized to patient material showing t(11;19) translocation (2RG1R1G).

One of the relatively frequently observed translocations (around 10 %) in human Acute Myeloid Leukemia (AML) and Acute Lymphoblastic Leukemia (ALL) involves the genes KMT2A (previously known as MLL) and MLLT1 (aka ENL) at 11q23 and 19p13. The KMT2A / MLLT1 translocation results in the generation of fusion protein that retains the MLL N-terminus, including both an A-T hook domain and a region similar to mammalian DNA methyltransferase. There are several breakpoints within the MLLT1 gene described, without clear differences in clinicohematologic features. Patients with AML and the KMT2A / MLLT1 translocation carry a poor prognosis, but noninfant children with ALL and KMT2A / MLLT1 fusion may have a favorable prognosis.

The KMT2A / MLLT1 Fusion probe is optimized to detect translocations involving the KMT2A and MLLT1 gene regions at 11q23 and 19p13 in a dual-color, fusion assay on metaphase/interphase spreads, blood smears and bone marrow cells in a dual-color, fusion assay.

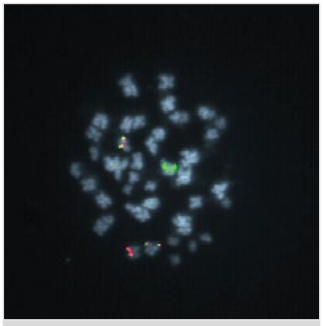


References

Mitterbauer-Hohdanner G et al, 2004, Eur J Clin Invest, 34; 12-24.
Meyer C et al, 2009, Leukemia, 23; 1490-1499.
Fu JF et al, 2007, Am J Clin Pathol, 127; 24-30.

Description	Code	Color	Format	US	ROW
KMT2A/MLLT1 t(11;19) Fusion	KBI-10307	Green/Red	10 Test	-	IVD
KMT2A/MLLT1 t(11;19) Fusion	KI-10307	Green/Red	100 µL	RUO	-

11q23 KMT2A / MLLT3

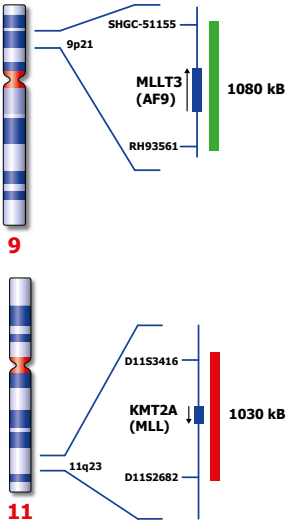


KMT2A/MLLT3 t(9;11) Fusion probe hybridized to patient material showing t(9;11) translocation (2RG1R1G).

Image kindly provided by Dr. Mohr, Dresden.

Chromosomal rearrangements involving the mixed lineage leukemia (MLL) gene at 11q23 are frequently observed in adult and childhood acute leukemia and are, in general, associated with poor prognosis. However, children with Acute Myeloid Leukemia (AML) carrying the t(9;11) KMT2A / MLLT3 (aka AF9) translocation have been described to be more sensitive to chemotherapy than patients with other 11q23 rearrangements.

The KMT2A / MLLT3 Fusion FISH probe is optimized to detect translocations involving the KMT2A (previously known as MLL) and MLLT3 gene regions at 11q23 and 9p21 in a dual-color fusion assay on metaphase/interphase spreads, blood smears and bone marrow cells.



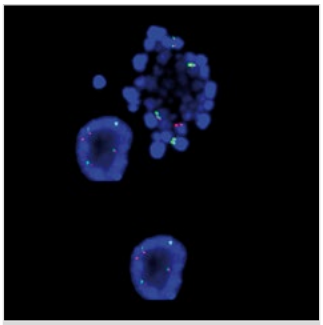
References

Von Lindern et al, 1992, Mol. Cell. Biol.,12; 1687-1697.
Ageberg et al, 2008, Gen. Chrom. Canc., 47; 276-287.
Chi et al, 2008, Arch. Pathol. Lab. Med.,132; 1835-1837.

Description	Code	Color	Format	US	ROW
KMT2A/MLLT3 t(9;11) Fusion	KBI-10308	Green/Red	10 Test	-	IVD
KMT2A/MLLT3 t(9;11) Fusion	KI-10308	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

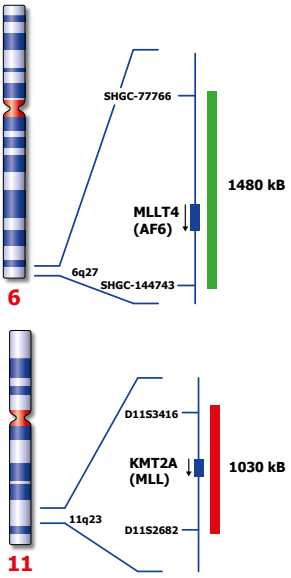
11q23 KMT2A / MLLT4



KMT2A / MLLT4 t(6;11) Fusion probe hybridized to patient material showing 47,XX,t(6;11)(q27;q23),+der(6)t(6;11)(q27;q23).

One of the relatively frequently observed translocations in human Acute Myeloid Leukemia (AML) involves the genes KMT2A and MLLT4 (previously known as AF6) at 11q23 and 6q27. The KMT2A / MLLT4 translocation results in the generation of fusion protein that retains the KMT2A N-terminus, including both an A-T hook domain and a region similar to mammalian DNA methyltransferase. The breakpoint region of the MLLT4 gene is located within intron 1 and downstream of the initiation codon. In all age groups and all phenotypes of leukemia, the KMT2A / MLLT4 translocation carries a poor prognosis.

The KMT2A / MLLT4 t(6;11) Fusion FISH probe is optimized to detect translocations involving the KMT2A (previously known as MLL) and MLLT4 gene regions at 11q23 and 6q27 in a dual-color, fusion assay on metaphase/ interphase spreads, blood smears and bone marrow cells.

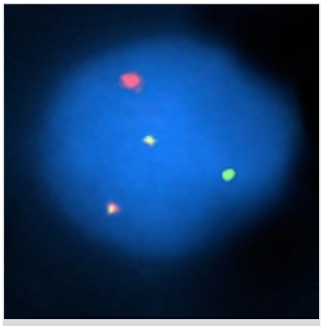


References

Mitterbauer-Hohdanner G et al, 2004, Eur J Clin Invest, 34; 12-24.
Meyer C et al, 2009, Leukemia, 23; 1490-1499.

Description	Code	Color	Format	US	ROW
KMT2A/MLLT4 t(6;11) Fusion	KBI-10309	Green/Red	10 Test	-	IVD
KMT2A/MLLT4 t(6;11) Fusion	KI-10309	Green/Red	100 µL	RUO	-

11q23 KMT2A / AFF1

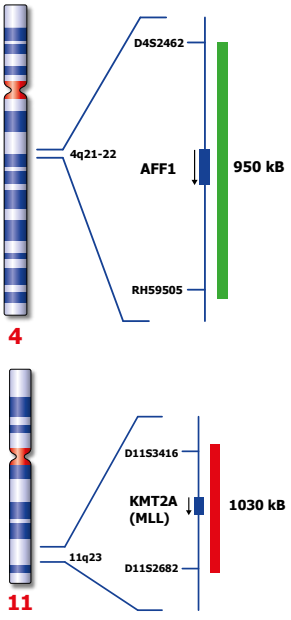


KMT2A / AFF1 t(4;11) Fusion probe. Standard t(4;11) 2 Fusion, 1 Red, 1 Green (2F1R1G).

Image kindly provided by Dr. Christine Harrison, Newcastle.

The t(4;11) KMT2A / AFF1 is the most frequently (approximately 66% according to Meyer et al.) observed translocation involving the KMT2A gene resulting in Acute Lymphoblastic Leukemia (ALL). The KMT2A / AFF1 translocation results in the generation of fusion proteins KMT2A / AFF1 and AFF1 / KMT2A; both seem to have leukemogenic properties. Furthermore, MECOM (3q26) is one of the targets of the KMT2A oncoproteins, which increased expression correlates with unfavorable prognosis in Acute Myeloid Leukemia. Patients with ALL and the KMT2A / AFF1 translocation are associated with a high risk of treatment failure.

The KMT2A / AFF1 t(4;11) Fusion FISH probe is optimized to detect translocations involving the KMT2A (previously known as MLL) and AFF1 gene regions at 4q21-22 and 11q23 in a dual-color, fusion assay on metaphase/ interphase spreads, blood smears and bone marrow cells.

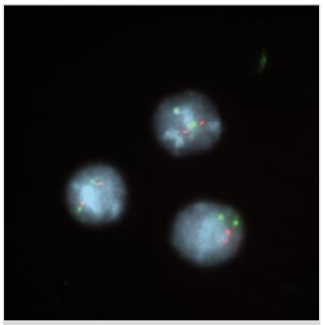


References

Harrison CJ et al, 2010, Br J Haem, 151; 132-142.
Arai S et al, 2011, Blood, 117; 6304-6314
Meyer C et al, 2009, Leukemia, 23; 1490-1499.

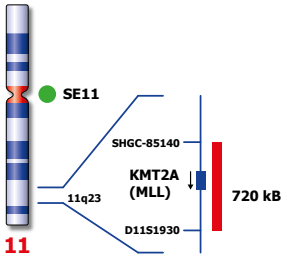
Description	Code	Color	Format	US	ROW
KMT2A/AFF1 t(4;11) Fusion	KBI-10404	Green/Red	10 Test	-	IVD
KMT2A/AFF1 t(4;11) Fusion	KI-10404	Green/Red	100 µL	RUO	-

11q23 KMT2A / SE 11



KMT2A (11q23) / SE 11 hybridized to normal interphases (2R2G).

Deletions of the long arm of chromosome 11 (11q) have been noted in primary neuroblastomas. It is assumed that a tumor suppressor gene mapping within 11q23.3 is commonly inactivated during the malignant evolution of a large subset of neuroblastomas, especially those with unamplified MYCN. The KMT2A (11q23) FISH probe is optimized to detect amplification or deletion involving the KMT2A gene region at 11q23 in a dual-color assay. The Chromosome 11 Satellite Enumeration probe (SE 11) at D11Z1 is included to facilitate chromosome identification.

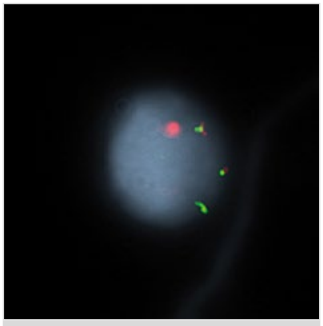


References

Guo et al, 1999, Oncogene, 18: 4948-4957.
Maris et al, 2001, Med Pediatr Oncol, 36: 24-27.

Description	Code	Color	Format	US	ROW
KMT2A (11q23) / SE 11	KBI-10711	Green/Red	10 Test	-	IVD
KMT2A (11q23) / SE 11	KI-10711	Green/Red	100 µL	RUO	-

12p13 ETV6 / RUNX1

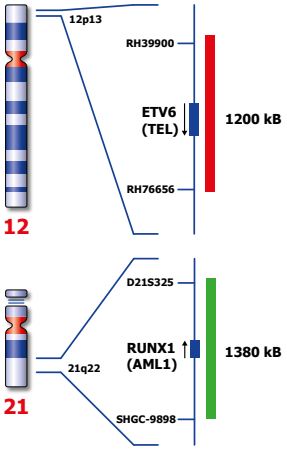


ETV6 / RUNX1 t(12;21) Fusion probe hybridized to patient material showing t(12;21)translocation (2RG1R1G).

Material kindly provided by Dr. Balogh, Budapest.

The t(12;21), a cryptic translocation rarely observed by conventional cytogenetics, was first identified by fluorescence *in situ* hybridization (FISH). In ALL blasts, this translocation fuses the 5' part of the ETV6 (previously known as TEL) gene with almost the entire RUNX1 (previously known as AML) (CBFA2) gene, producing the chimeric transcript ETV6-CBFA2. The t(12;21) (p13;q22) has also been identified as the most frequent chromosomal abnormality in childhood ALL, affecting 20% to 25% of B-lineage cases.

The ETV6 / RUNX1 t(12;21) specific FISH probe is optimized to detect the reciprocal translocation t(12;21) (p13;q22) in a dual-color, dual-fusion assay.



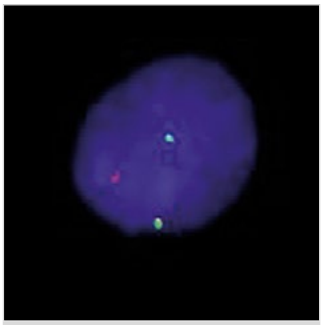
References

Romana et al, 1995, Blood, 85; 3662-3670.

Description	Code	Color	Format	US	ROW
ETV6/RUNX1 t(12;21) Fusion	KBI-10401	Green/Red	10 Test	-	IVD
ETV6/RUNX1 t(12;21) Fusion	KI-10401	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

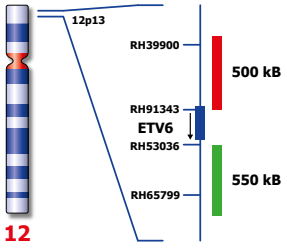
12p13 ETV6 Break



ETV6 (12p13) Break probe hybridized to patient material showing a translocation involving the ETV6 region at 12p13 (1RG1R1G).

Image kindly provided by Magret Ratjen, Kiel.

ETV6 (previously known as TEL) gene is the abbreviation for -ETS variant 6- gene. It encodes an ETS family factor which functions as a transcriptional repressor in hematopoiesis and in vascular development. The gene is located on chromosome 12p13, and is frequently rearranged in human leukemias of myeloid or lymphoid origins. Also systematic deletion of the normal ETV6 allele in patients with ETV6-RUNX1 fusions can be found.

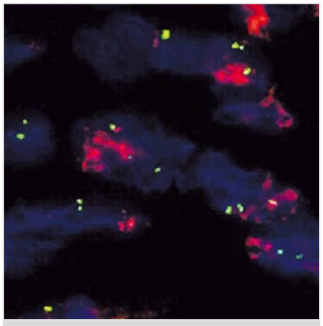


References

Golub et al, 1995, PNAS 92; 4917-4921.
Ford et al, 2001, Blood 98; 558-564.

Description	Code	Color	Format	US	ROW
ETV6 (12p13) Break	KBI-10403	Green/Red	10 Test	-	IVD
ETV6 (12p13) Break	KI-10403	Green/Red	100 µL	RUO	-

12q13 CDK4 / SE 12

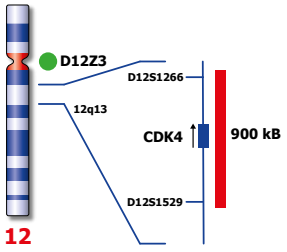


CDK4 (12q13) / SE 12 probe hybridized to liposarcoma tissue showing multiple amplification involving the CDK4 gene region at 12q13 (3+R2G).

Image kindly provided by Dr. Sapi, Hungary.

Amplification of the CDK4 gene region at 12q13-q15 has been observed in several types of cancer, especially in gliomas and sarcomas. CDK4 codes for a cyclin dependent kinase which is involved in controlling progression through the G1 phase of the cell cycle. The oncogenic potential of CDK4 activation has been related to the deregulation of the G1 phase by increasing the hyperphosphorylation of retinoblastoma tumor suppressor protein helping to cancel its growth-inhibitory effects.

The CDK4 (12q13) FISH probe is optimized to detect copy numbers of the CDK4 gene region at 12q13. The chromosome 12 satellite enumeration probe (SE 12) at D12Z3 is included to facilitate chromosome identification.

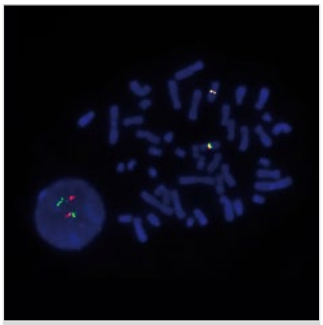


References

Kuhnen et al, 2002, Virchows Arch 441 ; 299-302.
Shimada et al, 2006, Hum Path 37(9) ; 1123-1129.

Description	Code	Color	Format	US	ROW
CDK4 (12q13) / SE 12	KBI-10725	Green/Red	10 Test	-	IVD
CDK4 (12q13) / SE 12	KI-10725	Green/Red	100 µL	RUO	-

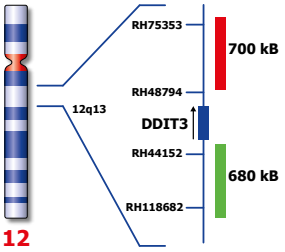
12q13 DDIT3 Break



DDIT3 (12q13) Break probe hybridized to a normal metaphase (2RG).

Liposarcoma is one of the most frequent sarcomas in adults, representing 10 to 16 percent of soft tissue sarcomas. Most patients with round cell / myxoid liposarcoma have an acquired t(12;16)(DDIT3-FUS) or t(12;22)(DDIT3-EWS) translocation, both of which involve the DDIT3 gene at 12q13. A break or split probe for DDIT3 is best used to analyze translocation of the DDIT3 (12q13) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

The DDIT3 (12q13) Break probe is optimized to detect translocations involving the DDIT3 gene region at 12q13 in a dual-color, break assay.

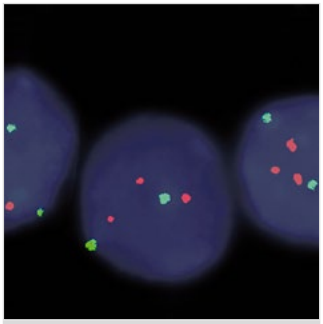


References

Panagopoulos et al, 1994, Cancer Res, 54; 6500-6503.
Schoenmakers et al, 1994, Genomics, 20; 210-222.

Description	Code	Color	Format	US	ROW
DDIT3 (12q13) Break	KBI-10714	Green/Red	10 Test	-	IVD
DDIT3 (12q13) Break	KI-10714	Green/Red	100 µL	RUO	-

12q13 GLI1 / SE 12

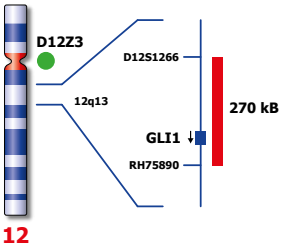


GLI1 (12q13) / SE 12 hybridized to patient material showing GLI (12q13) amplification (3R2G).

Image kindly provided by Dr. Wenzel, Basel.

Trisomy 12 is the most common numerical chromosomal aberration in patients with B-cell chronic lymphocytic leukemia (B-CLL). Partial trisomy 12 of the long arm of chromosome 12 consistently includes a smaller region at 12q13-15 and has been observed in CLL and several other tumors. A number of loci located close to either MDM2 or CDK4 / SAS, including the genes GADD153, GLI1 (previously known as GLI), RAP1B, A2MR, and IFNG, were found to be coamplified.

The GLI1 (12q13) specific FISH probe is optimized to detect copy numbers of the GLI1 gene region at region 12q13. The chromosome 12 Satellite Enumeration FISH probe (SE 12) D12Z3 is included to facilitate chromosome identification.



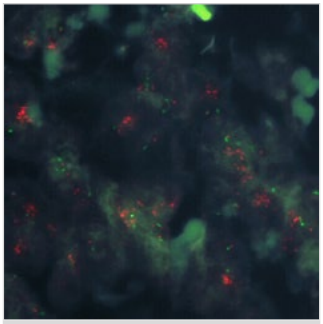
References

Merup et al, 1997, Eur J Haematol, 58; 174-180.
Dierlamm et al., 1997, Genes Chrom Cancer, 20; 155-166.

Description	Code	Color	Format	US	ROW
GLI1 (12q13) / SE 12	KBI-10104	Green/Red	10 Test	-	IVD
GLI1 (12q13) / SE 12	KI-10104	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

12q15 MDM2 / SE 12

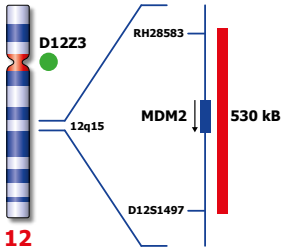


MDM2 (12q15) / SE 12 Amplification probe hybridized to patient material showing amplification of the MDM2 gene region at 12q15.

Well-differentiated liposarcoma/atypical lipomatous tumor and dedifferentiated liposarcoma are among the most common malignant soft tissue tumors presented in older adults. These tumors can be difficult to distinguish from benign lipomatous neoplasms and other high-grade sarcomas.

Amplification of the MDM2 gene has been identified in lipomatous neoplasms. The use of fluorescence *in situ* hybridization in identifying MDM2 amplification has made the MDM2 amplification probe a valuable diagnostic tool in well-differentiated liposarcomas/atypical lipomatous tumors. The MDM2 (12q15) specific DNA probe is optimized to detect copy numbers of the MDM2 region on chromosome 12. The chromosome 12 satellite enumeration probe (SE 12) at D12Z3 is included to facilitate chromosome identification.

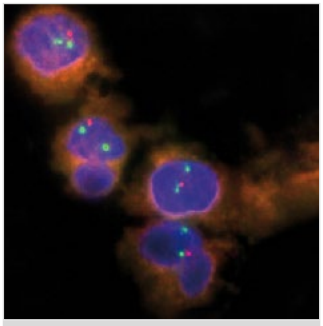
The MDM2 (12q15) FISH probe is optimized to detect copy numbers of the MDM2 gene region at region 12q15.



References
Uchida et al, 2010, Cancer Genet Cytogenet 203; 324-327.
Lucas et al, 2010, Am J Surg Pathol 34: 844-851.
Weaver et al, 2008, Mod Pathol 21: 943-949.
Mitchell et al, 1995, Chrom. Res., 3; 261-262.
Reifenberger et al, 1996, Cancer Res., 15; 5141-5145.

Description	Code	Color	Format	US	ROW
MDM2 (12q15) / SE 12	KBI-10717	Green/Red	10 Test	-	IVD
MDM2 (12q15) / SE 12	KI-10717	Green/Red	100 µL	RUO	-

13q14 DLEU1 / 13qter

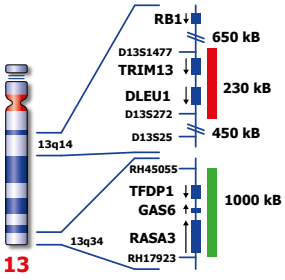


DLEU1 (13q14) / 13qter probe hybridized to patient material showing a 13q14 deletion (1R2G).

Image kindly provided by Dr. Dastugue, Toulouse.

Deletions of chromosome 13q14 have been reported not only in CLL but in a variety of human tumors, including other types of lymphoid and myeloid tumors, as well as prostate, head and neck, and non-small cell lung cancers. The deletion of 13q may be limited to a single locus (13q14), or accompanied with the loss of a larger interstitial region of the long arm of chromosome 13. A minimal critical region of 400 kb has been described containing the DLEU1, DLEU2 and RFP2 genes.

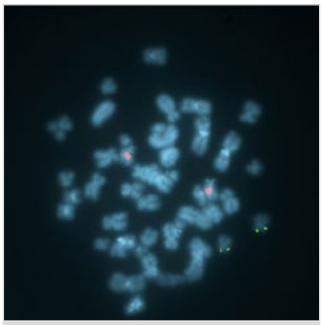
The DLEU1 (13q14) specific FISH probe is optimized to detect copy numbers of the DLEU1 (previously known as DLEU) gene region at 13q14. The 13qter (13q34) region is included to facilitate chromosome identification.



References
Wolf et al, 2001, Hum Mol Genet, 10; 1275-1285.
Corcoran et al, 1998, Blood, 91; 1382-1390.

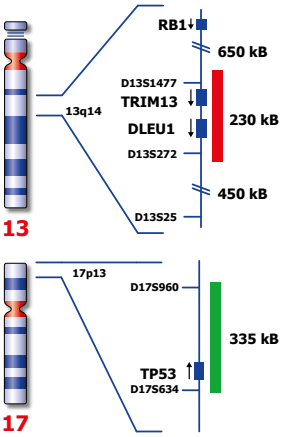
Description	Code	Color	Format	US	ROW
DLEU1 (13q14) / 13qter	KBI-10102	Green/Red	10 Test	-	IVD
DLEU1 (13q14) / 13qter	KI-10102	Green/Red	100 µL	RUO	-

13q14 DLEU1 / TP53



DLEU1 (13q14) / TP53 (17p13) hybridized to a normal metaphase (2R2G).

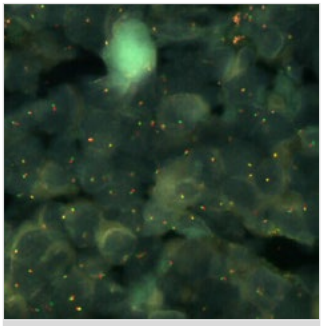
Deletion of DLEU1 (previously known as DLEU) at 13q14 indicates a rather good prognosis, deletion of TP53 (previously known as p53) at 17p13 is associated with poor prognosis.



References
Amiel A et al, 1997, Cancer Gener.Cytogenet, 97; 97-100.
Drach J et al, 1998, Blood, 92; 802-809.
Stilgenbauer S et al, 1998, Oncogene, 16; 1891 – 1897.
Wolf S et al, 2001, Hum. Molec. Genet., 10; 1275-1285.

Description	Code	Color	Format	US	ROW
DLEU1 (13q14) / TP53 (17p13)	KBI-10113	Green/Red	10 Test	-	IVD
DLEU1 (13q14) / TP53 (17p13)	KI-10113	Green/Red	100 µL	RUO	-

13q14 FOXO1 Break

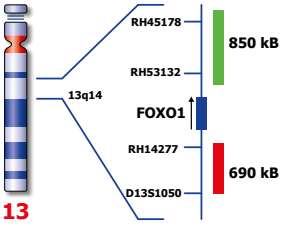


FOXO1 (13q14) Break probe hybridized to patient material (2RG).

The t(2;13) is associated with alveolar rhabdomyo-sarcomas. This translocation results in the formation of a chimeric transcript consisting of the 5' portion of PAX3, including an intact DNA-binding domain fused to the FOXO1 gene on chromosome 13. The t(1;13)(p36;q14) also seen in alveolar rhabdomyosarcomas results in the fusion of another member of the PAX family, PAX7 to the FOXO1 gene on chromosome 13.

A break or split probe for FOXO1 is best used to analyze translocation of the FOXO1 (13q14) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

The FOXO1 (13q14) Break probe is optimized to detect translocations involving the FOXO1 gene region at 13q14 in a dual-color, split assay on metaphase/ interphase spreads and paraffin embedded tissue sections.

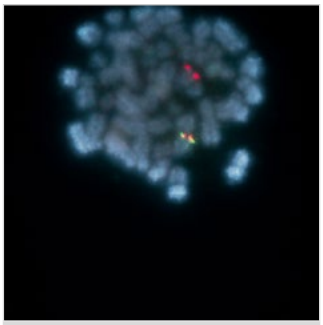


References
Barr et al, 1996, Hum. Mol. Genet., 5; 15-21.
Coignet et al, 1999, Genes Chrom. Cancer, 25; 222-229.

Description	Code	Color	Format	US	ROW
FOXO1 (13q14) Break	KBI-10716	Green/Red	10 Test	-	IVD
FOXO1 (13q14) Break	KI-10716	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

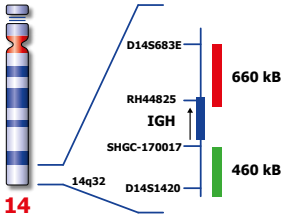
14q32 IGH Break



IGH (14q32) Break probe hybridized to patient material showing a partial deletion of 14q32 (1RG1R).

Multiple myeloma is characterized by complex rearrangements involving the IgH gene, particularly at the constant locus. The IgH rearrangement provides a useful marker of clonality in B-cell malignancies and amplification of this rearrangement is the method of choice to monitor the residual tumor cells in multiple myeloma.

The IGH (14q32) break probe is optimized to detect translocations involving the IGH gene region at 14q32 in a dual-color, split assay.

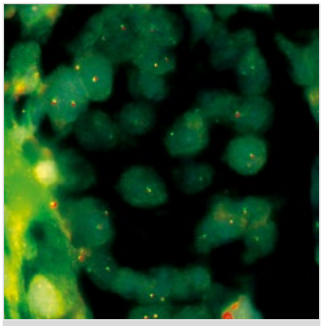


References

Taniwaki et al, 1994, Blood, 83; 2962-1969.
Gozetti et al, 2002, Cancer Research, 62; 5523-5527.

Description	Code	Color	Format	US	ROW
IGH (14q32) Break	KBI-10601	Green/Red	10 Test	-	IVD
IGH (14q32) Break	KI-10601	Green/Red	100 µL	RUO	-

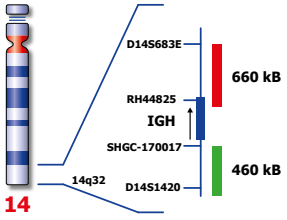
14q32 IGH Break (tissue)



IGH (14q32) Break probe hybridized to patient material showing a partial deletion of 14q32 (1RG1R).

Chromosomal rearrangements involving the immunoglobulin heavy chain gene (IGH) at 14q32 are observed in 50% of patients with B-cell non-Hodgkin's lymphoma (NHL) and many other types of Lymphomas. More than 50 translocation partners with IGH have been described. In particular t(8;14) is associated with Burkitt's lymphoma, t(11;14) is associated with Mantle cell lymphoma, t(14;18) is observed in a high proportion of follicular lymphomas and t(3;14) is associated with Diffuse Large B-Cell Lymphoma.

The IGH (14q32) Break probe is optimized to detect translocations involving the IGH gene region at 14q32 in a dual-color, split assay.

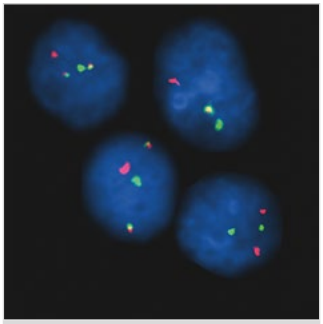


References

Taniwaki et al, 1994, Blood, 83: 2962-1969.
Gozetti et al, 2002, Cancer Research, 62: 5523-5527.

Description	Code	Color	Format	US	ROW
IGH (14q32) Break (tissue)	KBI-10729	Green/Red	10 Test	-	IVD
IGH (14q32) Break (tissue)	KI-10729	Green/Red	100 µL	RUO	-

14q32 MYEOV / IGH

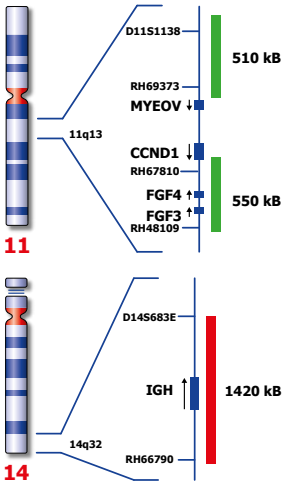


MYEOV / IGH t(11;14) Fusion probe hybridized to MM patient material showing t(11;14) translocation (2RG1R1G).

Image kindly provided by Prof. Jauch, Heidelberg.

The most common chromosomal translocation in multiple myeloma (MM) is t(11;14), resulting in up-regulation of cyclin D1. In MM the breakpoints are scattered within a 360-kb region between CCND1 and MYEOV. This breakpoint is more proximal than the t(11;14) breakpoints observed in mantle cell lymphoma or other leukemias. Patients with MM who have t(11;14)(q13;q32) seem to have an aggressive clinical course.

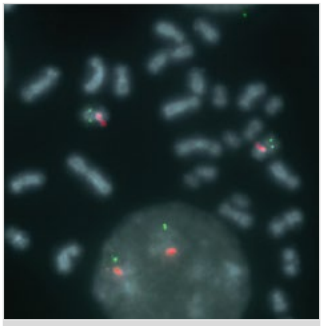
The MYEOV / IGH t(11;14)(q13;q32) Fusion specific FISH probe is optimized to detect the reciprocal translocation t(11;14) in a dual-color, dual-fusion assay.



References
Janssen et al., 2000, Blood, 95; 2691-2698.
Fonseca et al, 2002, Blood, 99; 3735-3741.

Description	Code	Color	Format	US	ROW
MYEOV/IGH t(11;14) Fusion	KBI-10605	Green/Red	10 Test	-	IVD
MYEOV/IGH t(11;14) Fusion	KI-10605	Green/Red	100 µL	RUO	-

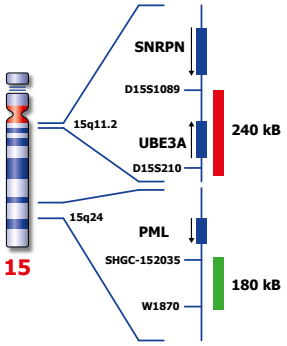
15q11 UBE3A / PML



Angelman UBE3A (15q11) / PML (15q24) probe hybridized to a normal interphase/ metaphase (2R2G).

Angelman syndrome (AS) is characterized by severe developmental delay or mental retardation, severe speech impairment, gait ataxia and/or tremulousness of the limbs, and an unique behavior with an inappropriate happy demeanor that includes frequent laughing, smiling, and excitability. In addition, microcephaly and seizures are common. AS is caused by absence of a maternal contribution to the imprinted region on chromosome 15q11-q13 including the UBE3A gene.

The AS UBE3A region probe is optimized to detect copy numbers of the UBE3A gene region at 15q11. The PML (promyelocytic leukemia) gene specific FISH probe at 15q24 is included as control probe.

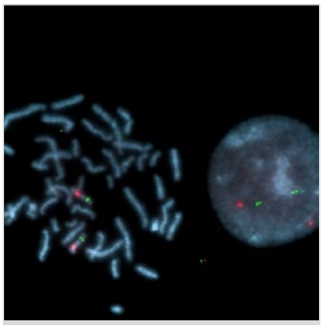


References
Matsuura et al, 1997, Nat. Genet., 15; 74-77.
Burger et al, 2002, Am. J. Med. Genet., 111; 233-237.

Description	Code	Color	Format	US	ROW
Angelman UBE3A (15q11) / PML (15q24)	KBI-40110	Green/Red	10 Test	-	IVD
Angelman UBE3A (15q11) / PML (15q24)	KBI-45110	Green/Red	5 Test	-	IVD
UBE3A (15q11) / PML (15q24)	KI-40110	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

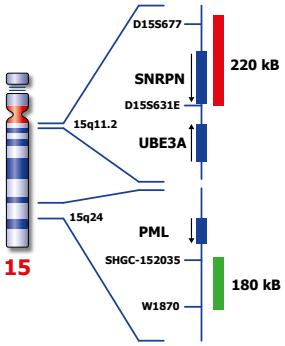
15q11 SNRPN / PML



Prader-Willi SNRPN (15q11) / PML (15q24) probe hybridized to a normal interphase/metaphase (2R2G).

Prader-Willi syndrome (PWS) is a clinically distinct disorder including diminished fetal activity, obesity, hypotonia, mental retardation, short stature, hypogonadotropic hypogonadism, strabismus, and small hands and feet.

Approximately 70% of cases of PWS arise from paternal deletion of the 15q11-q13 region including the gene SNRPN (small nuclear ribonucleoprotein polypeptide N). The PWS SNRPN region probe is optimized to detect copy numbers of the SNRPN gene region at 15q11. The PML (promyelocytic leukemia) gene specific FISH probe at 15q24 is included as control probe.

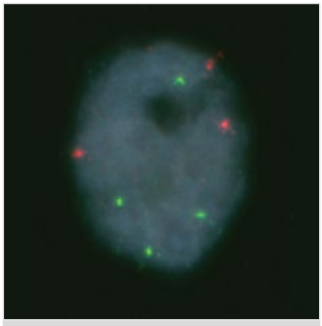


References

Knoll et al, 1989, Am. J. Med. Genet., 32; 285-290.
Ozcelik et al, 1992, Nat. Genet., 2; 265-269.

Description	Code	Color	Format	US	ROW
Prader-Willi SNRPN (15q11) / PML (15q24)	KBI-40109	Green/Red	10 Test	-	IVD
Prader-Willi SNRPN (15q11) / PML (15q24)	KBI-45109	Green/Red	5 Test	-	IVD
SNRPN (15q11) / PML (15q24)	KI-40109	Green/Red	100 µL	RUO	-

15q22 15q22 / 6q21

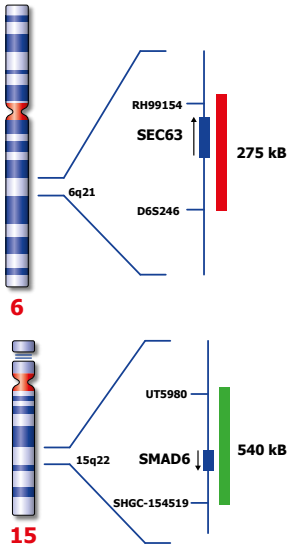


15q22 / 6q21 hybridized to MM patient material with gain of both critical regions 6q21 and 15q22.

Image kindly provided by Prof. Jauch, Heidelberg.

Chromosome 6q amplifications encompassing 6q21-22 have been observed in MM including the same region as in CLL. Amplification including band 15q22 has been reported in MM. The 15q22 specific FISH probe is optimized to detect copy numbers at 15q22.

The 6q21 specific DNA region is optimized to detect copy numbers at 6q21.

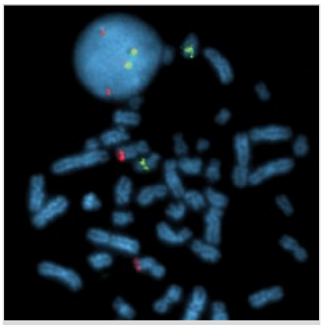


References

Cremer et al, 2005, Genes Chrom Cancer, 44; 194-203.

Description	Code	Color	Format	US	ROW
15q22 / 6q21	KBI-10504	Green/Red	10 Test	-	IVD
15q22 / 6q21	KI-10504	Green/Red	100 µL	RUO	-

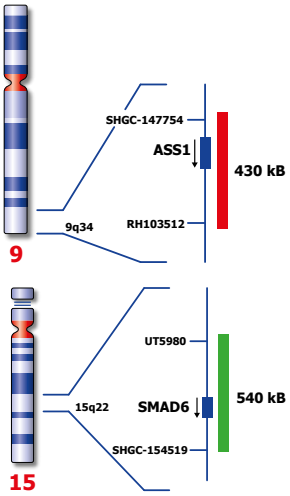
15q22 15q22 / 9q34



15q22 / 9q34 hybridized to a normal interphase/metaphase (2R2G).

The hyperdiploid subtype in MM is defined by presence of multiple trisomic chromosomes. Combination of the chromosome 9q34 and 15q22 specific regions are important regions to detect the hyperdiploid subtype in MM which is usually associated with a low frequency of IGH translocations.

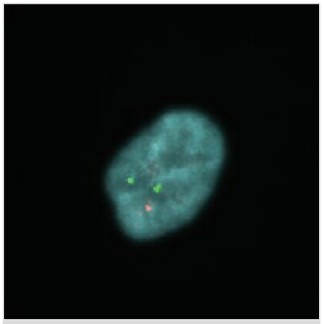
The 15q22 and 9q34 FISH probe is designed as a dual-color assay to detect amplifications at 15q22 and 9q34.



References
Cremer et al, 2005, Genes Chrom Cancer, 44; 194-203.

Description	Code	Color	Format	US	ROW
15q22 / 9q34	KBI-10508	Green/Red	10 Test	-	IVD
15q22 / 9q34	KI-10508	Green/Red	100 µL	RUO	-

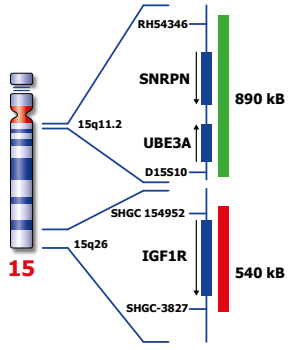
15q26 IGF1R / 15q11



IGF1R (15q26) / 15q11 probe hybridized to patient material showing a deletion of the IGF1R gene region at 15q26 (1R2G).

Congenital diaphragmatic hernia (CDH) is a severe, life-threatening, congenital anomaly characterized by variable defect in the diaphragm, pulmonary hypoplasia, and postnatal pulmonary hypertension. Deletion of the IGF1R (insulin-like growth factor 1 receptor) gene region at 15q25 is the most frequent anomaly found in CDH. The type 1 IGF receptor at 15q26 is required for normal embryonic and postnatal growth. Deletions, but also gain of an approximately 5 Mb region including the IGF1R gene has been found to have a profound effect on prenatal and early postnatal growth.

The IGF1R (15q26) specific FISH probe is optimized to detect copy numbers of the IGF1R gene region at region 15q26. The 15q11 (SNRPN / UBE3A) specific region probe is included to facilitate chromosome identification.



References
Faivre et al, 2002, Eur, J, Hum, Genet., 10; 699-706.
Okubo et al, 2003, J. Clin. Endocrinol. Metab, 88; 5981-5988.

Description	Code	Color	Format	US	ROW
IGF1R (15q26) / 15q11	KBI-40116	Green/Red	10 Test	-	IVD
IGF1R (15q26) / 15q11	KBI-45116	Green/Red	5 Test	-	IVD
IGF1R (15q26) / 15q11	KI-40116	Green/Red	100 µL	RUO	-

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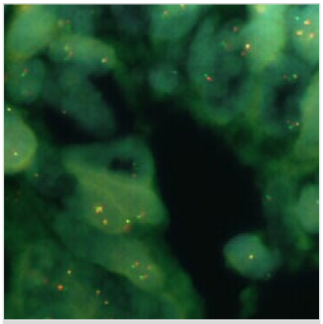
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

16p11 FUS Break

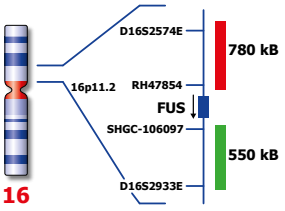


FUS (16p11) Break probe hybridized to liposarcoma material.

The fused in sarcoma (FUS) gene was originally shown to be rearranged in myxoid liposarcomas harboring a t(12;16)(q13;p11) translocation. FUS has also been shown to be involved in other recombinations: with ERG in acute myeloid leukemia carrying a t(16;21), with ATF1 in band 12q13 in angiomatoid fibrous histiocytoma, and with CREB3L2 in fibromyxoid sarcoma.

A break or split probe for FUS is best used to analyze translocation of the FUS (16p11) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

The FUS (16p11) Break probe is optimized to detect translocations involving the FUS gene region at 16p11 in a dual-color, split assay on metaphase/interphase spreads and paraffin embedded tissue sections.

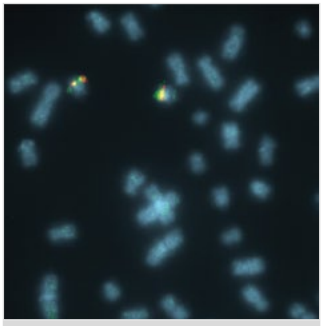


References

Shing et al, 2003, Cancer Res, 63: 4568-4576.
Storlazzi et al, 2003, Hum. Mol. Genet., 12: 2349-2358.

Description	Code	Color	Format	US	ROW
FUS (16p11) Break	KBI-10715	Green/Red	10 Test	-	IVD
FUS (16p11) Break	KI-10715	Green/Red	100 µL	RUO	-

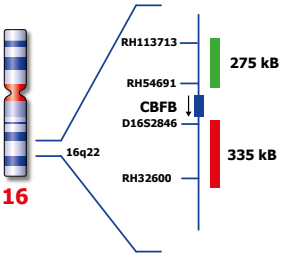
16q22 CBFB



CBFB t(16;16); inv(16) Break probe hybridized to a normal metaphase (2RG).

Inv(16)(p13;q22) and t(16;16)(p13;q22) are recurring chromosomal rearrangements in AML. In both the inversion and translocation, the critical genetic event is the fusion of the CBFB gene at 16q22 to the smooth muscle myosin heavy chain (MYH11) at 16p13. A deletion of between 150 and 350 kb centromeric to the p-arm inversion breakpoint cluster region can be observed in some patients containing the 5′ portion of the myosin heavy chain (MYH11) gene.

The CBFB t(16;16) inv(16) break FISH probe is optimized to detect the inversion of chromosome 16 involving the CBFB gene region at 16q22 in a dual-color, split assay.

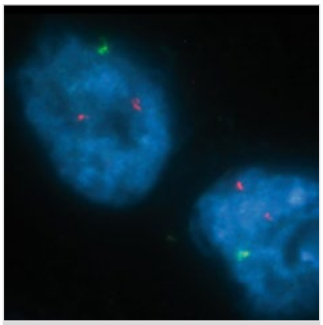


References

Dauwerse et al, 1993, Hum.Mol.Genet., 2; 1527-1534.
Marlton et al, 1995, Blood, 85; 772-779.

Description	Code	Color	Format	US	ROW
CBFB t(16;16), inv(16) Break	KBI-10304	Green/Red	10 Test	-	IVD
CBFB t(16;16), inv(16) Break	KI-10304	Green/Red	100 µL	RUO	-

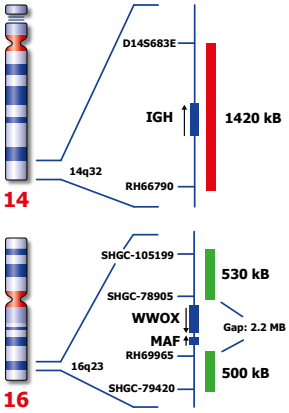
16q23 MAF/ IGH



MAF / IGH t(14;16) Fusion probe hybridized to patient material showing a deletion of the MAF gene region at 16q23 (2R1G).

Chromosome translocations involving the immunoglobulin heavy chain gene (IGH) on 14q32 are a fundamental event in the pathogenesis of many B-cell malignancies. It often is preceded by a stable pre-malignant tumor called Monoclonal Gammopathy of Undetermined Significance (MGUS), which can sporadically progress to Multiple Myeloma (MM). One of the recurrent primary rearrangements involving the IGH locus on chromosome 14q32 identified in MGUS and MM tumors is the MAF / IGH t(14;16) translocation. Following MGUS appearance, the pathogenesis of MM is thought to involve at least two pathways, which generate hyperdiploid (HRD) or nonhyperdiploid (NHRD) tumors, respectively.

The MAF / IGH is mainly present in NHRD tumors, providing important information on MM patient sub-types. Since these translocations are caused by aberrant IgH switch recombination, and possibly by aberrant somatic hypermutation in germinal center B cells, they provide information of an early and perhaps initiating event of transformation.

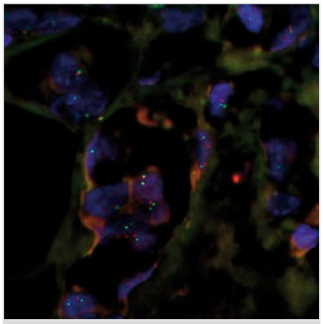


References

Chesi et at, 1998, Blood 91; 4457-4463.
Sawyer et al, 1998, Blood 92; 4269-4278.

Description	Code	Color	Format	US	ROW
MAF/IGH t(14;16) Fusion	KBI-10610	Green/Red	10 Test	-	IVD
MAF/IGH t(14;16) Fusion	KI-10610	Green/Red	100 µL	RUO	-

17p13 AURKB

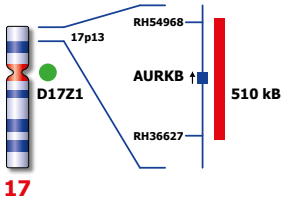


AURKB (17p13) / SE 17 probe hybridized to tumor tissue (2R2G).

Aurora kinase B (AURKB) localizes to microtubules, and is a key regulator of the mitotic cell division and chromosome segregation processes. Gain of function of AURKB correlates with cell proliferation, induction of multinuclear cells, and chromosomal instability.

The significant interest of the gene in cancer diagnostics is related to the driving function of AURKB in tumor progression, histological differentiation, and metastasis. AURKB is predictive for the aggressive recurrence of many different types of tumors, including hepatocellular carcinoma and oral squamous cell carcinoma.

The AURKB (17p13) FISH probe is optimized to detect copy numbers of the AURKB gene region at region 17p13. The Chromosome 17 Satellite Enumeration (SE 17) probe at D17Z1 is included to facilitate chromosome identification.



References

Smith et al, 2005, Br J Cancer, 93; 719-729.

Description	Code	Color	Format	US	ROW
AURKB (17p13) / SE 17	KBI-10722	Green/Red	10 Test	-	IVD
AURKB (17p13) / SE 17	KI-10722	Green/Red	100 µL	RUO	-

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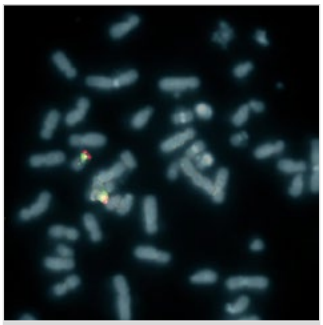
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

17p13 PAFAH1B1 / 17p11



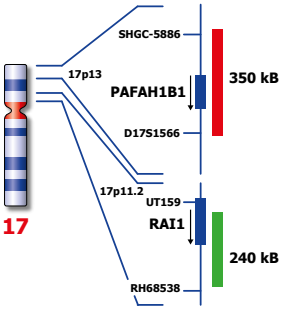
Miller-Dieker PAFAH1B1 (17p13)/ Smith-Magenis RAI1 (17p11) probe hybridized to a normal metaphase (2RG).

Miller-Dieker Syndrome (MDS) is characterized by classical lissencephaly and distinct facial features. The lissencephaly represents the severe end of the spectrum with generalized agyria or agyria with some frontal pachygyria. Submicroscopic deletions of 17p13.3 including the PAFAH1B1 (previously called LIS, platelet-activating factor acetylhydrolase) gene are found in almost 100% of patients.

The Miller-Dieker region probe is optimized to detect copy numbers of the PAFAH1B1 gene region at 17p13.3. The Smith-Magenis RAI1 region probe at 17p11.2 is serving as internal control.

Smith-Magenis Syndrome (SMS) is characterized by distinctive facial features that progress with age, developmental delay, cognitive impairment, and behavioral abnormalities. Molecular cytogenetic analysis by FISH using a DNA probe specific for the SMS critical region is recommended in cases of submicroscopic deletions and/or to resolve equivocal cases. RAI1 is the only gene known to account for a majority of features in SMS. All 17p11.2 deletions associated with SMS include a deletion of RAI1.

The Smith-Magenis region probe is optimized to detect copy numbers of the RAI1 gene region involved in Smith-Magenis syndrome at 17p11.2. The Miller-Dieker PAFAH1B1 probe at 17p13.3 is serving as internal control.

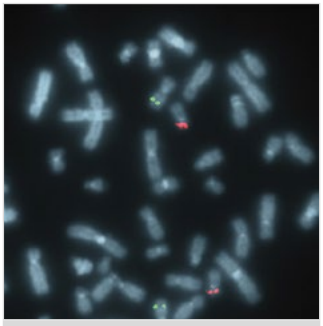


References

Kuwano et al, 1991, Am. J. Hum. Genet., 49; 707-714.
Cardoso et al, 2003, Am. J. Hum. Genet., 72; 918-930.
Smith et al, 1986, Am. J. Med. Genet., 24; 393-414.
Greenberg et al, 1991, Am. J. Med. Genet., 49; 1207-1218.
Vlangos et al, 2005, Am. J. Med. Genet., 132; 278-282.

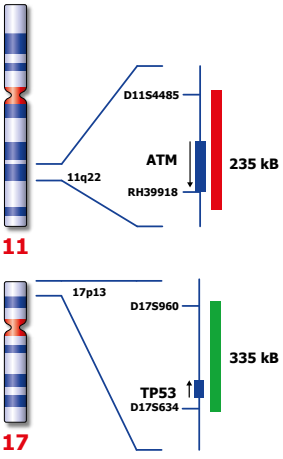
Description	Code	Color	Format	US	ROW
Miller-Dieker PAFAH1B1 (17p13) / Smith-Magenis RAI1 (17p11)	KBI-40101	Green/Red	10 Test	-	IVD
Miller-Dieker PAFAH1B1 (17p13) / Smith-Magenis RAI1 (17p11)	KBI-45101	Green/Red	5 Test	-	IVD
PAFAH1B1 (17p13) / RAI1 (17p11)	KI-40101	Green/Red	100 µL	RUO	-

17p13 TP53 / ATM



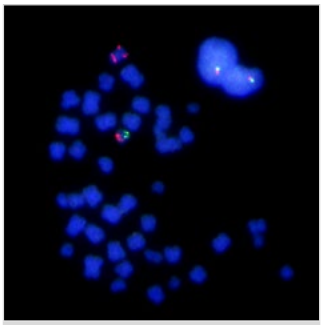
TP53 (17p13) / ATM (11q22) hybridized to a normal metaphase (2R2G).

Deletion of TP53 (previously known as p53) and ATM are both indicating poor prognosis in CLL.



Description	Code	Color	Format	US	ROW
TP53 (17p13) / ATM (11q22)	KBI-10114	Green/Red	10 Test	-	IVD
TP53 (17p13) / ATM (11q22)	KI-10114	Green/Red	100 µL	RUO	-

17p13 TP53 / MPO

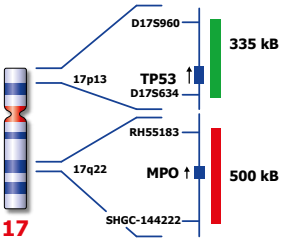


TP53 (17p13) / MPO (17q22) "ISO 17q" probe hybridized to peripheral blood of a CLL patient with an isochromosome 17 (3R1G).

Image kindly provided by Dr. Lana Harder, Kiel.

Isochromosome 17q is the most common isochromosome in cancer. It plays an important role in tumor development and progression. Hematologic malignancies such as chronic myeloid leukemia (CML) with isochromosome 17q carry a poor prognosis. Isochromosome 17q is the most common chromosome abnormality in primitive neuroectodermal tumors and medulloblastoma. Isochromosome 17q is, by convention, symbolized as i(17q).

The TP53 (17p13) / MPO (17q22) "ISO 17q" FISH probe is optimized to detect copy numbers of the TP53 gene region at 17p13 and MPO gene region at 17q22. In case of i(17q) a signal pattern of three red signals for MPO (17q22) and one signal for TP53 at 17p13 is expected.

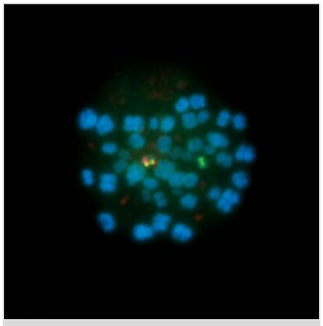


References

Becher et al, 1990, Blood, 75; 1679-1683.
Fioretos et al, 1999, Blood, 94; 225-232.

Description	Code	Color	Format	US	ROW
TP53 (17p13) / MPO (17q22) "ISO 17q"	KBI-10011	Green/Red	10 Test	-	IVD
TP53 (17p13) / MPO (17q22) "ISO 17q"	KI-10011	Green/Red	100 µL	RUO	-

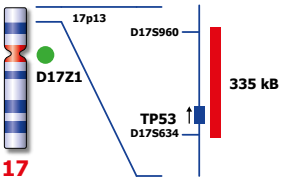
17p13 TP53 / SE 17



TP53 (17p13) / SE 17 probe hybridized to patient material showing a 17p13 deletion at the TP53 gene region (1R2G).

The TP53 tumor suppressor gene at 17p13, has been shown to be implicated in the control of normal cellular proliferation, differentiation, and apoptosis. Allelic loss, usually by deletion, and inactivation of TP53 have been reported in numerous tumor types and are associated with poor prognosis in CLL.

The TP53 (17p13) FISH probe is optimized to detect copy numbers of the TP53 gene region at 17p13. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification. Kreatech has developed this probe for the specific use on cell material (KBI-10112 / KBI-12112), or for the use on tissue (KBI-10738).



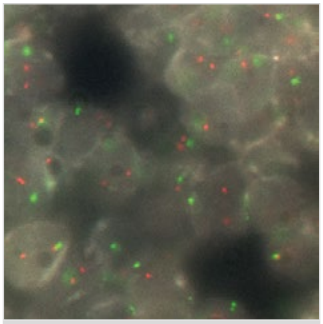
References

Amiel A et al, 1997, Cancer Gener. Cytogenet, 97; 97-100.
Drach J et al, 1998, Blood, 92; 802-809.

Description	Code	Color	Format	US	ROW
TP53 (17p13) / SE 17	KBI-10112	Green/Red	10 Test	-	IVD
TP53 (17p13) / SE 17	KBI-12112	Green/Red	20 Test	-	IVD
TP53 (17p13) / SE 17	KI-10112	Green/Red	100 µL	RUO	-
TP53 (17p13) / SE 17	KI-12112	Green/Red	200 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

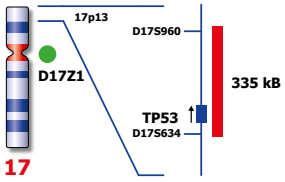
17p13 TP53 / SE 17 (tissue)



TP53 (17p13) / SE 17 (tissue) probe hybridized to paraffin embedded tissue (2R2G).

The TP53 tumor suppressor gene at 17p13, has been shown to be implicated in the control of normal cellular proliferation, differentiation, and apoptosis. Allelic loss, usually by deletion, and inactivation of TP53 have been reported in numerous tumor types and are associated with poor prognosis in CLL.

The TP53 (17p13) FISH probe is optimized to detect copy numbers of the TP53 gene region at 17p13. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification. Kreatech has developed this probe for the specific use on cell material (KBI-10112 / KBI-12112), or for the use on tissue (KBI-10738).

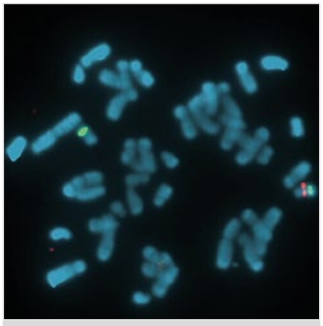


References

Amiel A et al, 1997, Cancer Gener.Cytogenet,, 97; 97-100.
Drach J et al, 1998, Blood, 92; 802-809.

Description	Code	Color	Format	US	ROW
TP53 (17p13) / SE 17 (tissue)	KBI-10738	Green/Red	10 Test	-	IVD
TP53 (17p13) / SE 17 (tissue)	KI-10738	Green/Red	100 µL	RUO	-

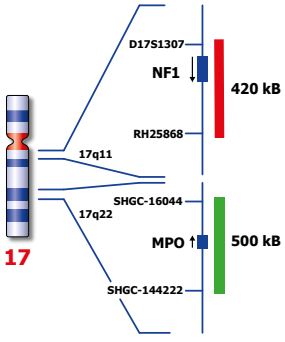
17q11 NF1 / MPO



NF1 (17q11) / MPO (17q22) probe hybridized to patient material showing a deletion of NF1 gene region at 17q11 (1R2G).

NF1, or von Recklinghausen disease, is one of the most common hereditary neurocutaneous disorders in humans and one of the most common single gene syndromes. Clinically, NF1 is characterized by café-au-lait spots, freckling, skin neurofibroma, plexiform neurofibroma, bone defects, Lisch nodules and tumors of the central nervous system. The responsible gene, NF1 (neurofibromin), was identified on chromosome 17q11. Whole NF1 gene deletions occur in 4%-5% of individuals with NF1 and can be detected by FISH analysis.

The NF1 (17q11) region probe is optimized to detect copy numbers of the NF1 gene region at 17q11.2. The MPO region specific FISH probe at 17q22 is included as control probe.

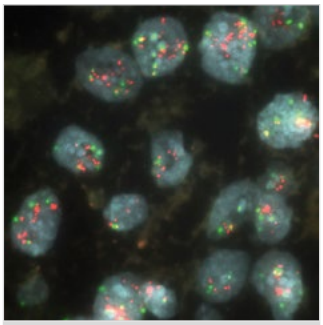


References

Riva P et al, 2000, Am. J. Hum. Genet., 66; 100-109.
Dorschner et al, 2000, Hum. Mol. Genet., 9; 35-46.

Description	Code	Color	Format	US	ROW
NF1 (17q11) / MPO (17q22)	KBI-40114	Green/Red	10 Test	-	IVD
NF1 (17q11) / MPO (17q22)	KBI-45114	Green/Red	5 Test	-	IVD
NF1 (17q11) / MPO (17q22)	KI-40114	Green/Red	100 µL	RUO	-

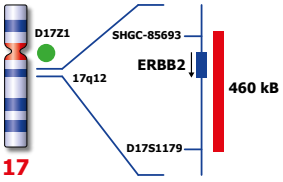
17q12 ERBB2 / SE 17



ERBB2 (17q12) / SE 17 probe hybridized to breast tumor tissue showing amplification of ERBB2 / SE 17.

The ERBB2 gene encodes a receptor tyrosine kinase involved in growth factor signaling. Overexpression of this gene is seen in about 20% of invasive breast cancers and is without proper treatment associated with poor survival. ERBB2 gene amplification is a permanent genetic change that results in this continuous overexpression of ERBB2. Trastuzumab (commonly known as Herceptin) has been developed to be effective against ERBB2-positive breast cancer. ERBB2 amplification is also observed in a variety of other tumors, such as prostate, lung, colon and ovary carcinoma.

The ERBB2 (17q12) FISH probe is optimized to detect copy numbers of the ERBB2 gene region at region 17q12. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification/enumeration.

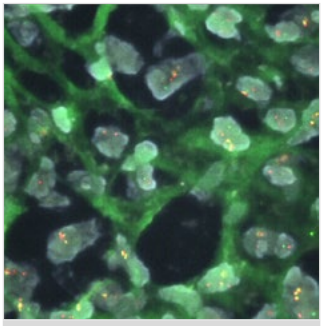


References

Pauletti et al, 1996, Oncogene, 13: 63-72.
Xing et al, 1996, Breast Cancer Res Treat, 39: 203-212.

Description	Code	Color	Format	US	ROW
ERBB2 (17q12) / SE 17	KBI-10701	Green/Red	10 Test	-	IVD
ERBB2 (17q12) / SE 17	KBI-14701	Green/Red	50 Test	-	IVD
ERBB2 (17q12) / SE 17	KI-10701	Green/Red	100 µL	RUO	-
ERBB2 (17q12) / SE 17	KI-14701	Green/Red	500 µL	RUO	-

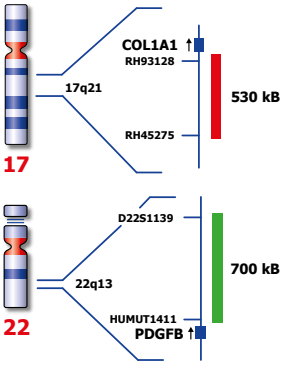
17q21 COL1A1 / PDGFB



Interphase FISH result of COL1A1/ PDGFB Fusion probe hybridized to dermatofibrosarcoma protuberans tumor tissue, showing co-localization and amplification of the fusion gene.

The diagnosis of primary soft tissue and bone tumors is often challenging as they are relatively rare. The misdiagnosis between dermatofibroma (DF) and dermatofibrosarcoma protuberans (DFSP) or giant cell fibroblastoma (GCF) might result in incorrect primary management. DFSP and GCF have in most cases diagnosed today a translocation involving the COL1A1 (collagen, type I, alpha 1) gene at 17q21 and the PDGFB (platelet-derived growth factor beta polypeptide) gene at 22q13. Also, a supernumerary ring chromosome derived from the translocation t(17;22) can be present.

The CCOL1A1/PDGFB t(17;22) Dual-Color Single-Fusion probe is optimized to detect the t(17;22)(q21;q13) involving the COL1A1 (17q21) and PDGFB (22q13) gene regions in dual-color, single-fusion assay on paraffin embedded tissue sections.



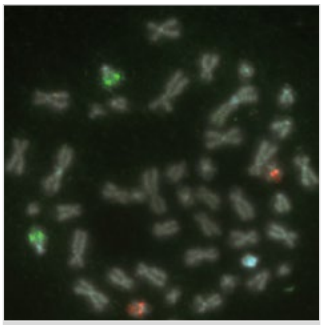
References

Maire et al, 2007, Arch Dermatol, 143; 203-210.
Labropoulos et al, 2007, Biologics, 1; 347-353.
Patel et al, 2008, Hum Path, 39; 184-193.
Sandberg, 2003, Cancer Genet Cytogenet, 140; 1-12.

Description	Code	Color	Format	US	ROW
COL1A1/PDGFB t(17;22) Dual-Color, Single-Fusion	KBI-10742	Green/Red	10 Test	-	IVD

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

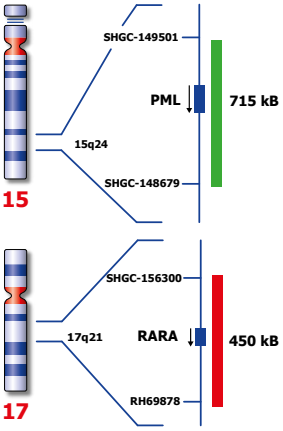
17q21 PML / RARA



PML / RARA t(15;17) Fusion probe hybridized to a normal metaphase (2R2G).

A structural rearrangement involving chromosomes 15 and 17 in acute promyelocytic leukemia (APL) was first recognized in 1977. The critical junction is located on the der(15) chromosome and consists of the 5' portion of PML fused to virtually all of the RARA gene. The PML/RARA fusion protein interacts with a complex of molecules known as nuclear co-repressors and histone deacetylase. This complex binds to the fusion protein and blocks the transcription of target genes. Other less common variant translocations fuse the RARA gene on 17q21 to the PLZF, NPM, NUMA, and STAT5b genes, respectively.

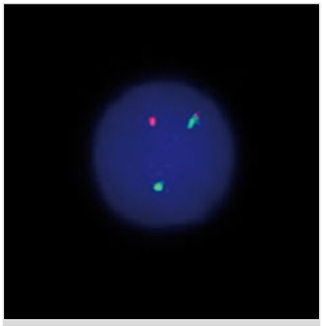
The PML/RARA t(15;17) Fusion specific FISH probe is optimized to detect the reciprocal translocation t(15;17) (q24;q21) in a dual-color, dual-fusion assay.



References
Schad et al, 1994, Mayo Clin Proc, 69; 1047-1053.
Brockman et al, 2003, Cancer Genet Cytogenet, 145; 144-151.

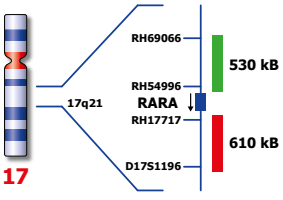
Description	Code	Color	Format	US	ROW
PML/RARA t(15;17) Fusion	KBI-10302	Green/Red	10 Test	-	IVD
PML/RARA t(15;17) Fusion	KBI-12302	Green/Red	20 Test	-	IVD
PML/RARA t(15;17) Fusion	KI-10302	Green/Red	100 µL	RUO	-
PML/RARA t(15;17) Fusion	KI-12302	Green/Red	200 µL	RUO	-

17q21 RARA Break



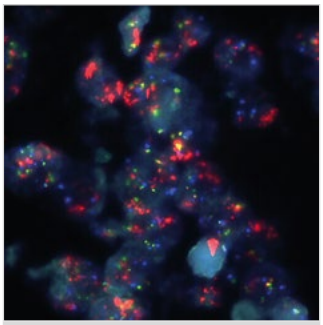
RARA (17q21) Break probe hybridized to patient material showing a translocation at 17q21 (1RG1R1G).

This break apart probe can detect the numerous types of recurrent rearrangement of the RAR_ (Retinoid acid receptor, alpha) gene with various gene partners (e.g., PML, NPM, MLL, FIP1L1, NuMA1, PLZF, amongst the others), leading to the formation of different reciprocal fusion proteins. The importance of retinoid metabolism in acute promyelocytic leukemia (APL) is highlighted by the numerous recent studies, but the different leukemogenic functions of the RAR_ fusion proteins in the neoplastic myeloid development still has to be defined, as well as the distinct clinical outcome of the patients with the variant forms of APL.



Description	Code	Color	Format	US	ROW
RARA (17q21) Break	KBI-10305	Green/Red	10 Test	-	IVD
RARA (17q21) Break	KI-10305	Green/Red	100 µL	RUO	-

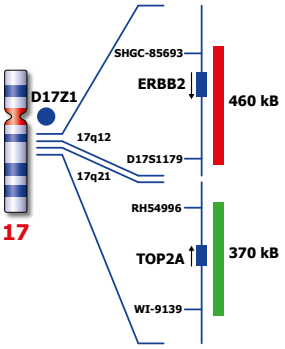
17q21 TOP2A / ERBB2 / SE 17



TOP2A (17q21) / ERBB2 (17q12) / SE 17 TC probe hybridized to breast tumor tissue showing amplification of TOP2A / ERBB2.

The presence of both TOP2A amplification and deletion in advanced cancer are associated with decreased survival, and occur frequently and concurrently with ERBB2 gene amplification.

The TOP2A (17q21) / ERBB2 (17q12) / SE 17 probe is designed as a triple-color assay to detect amplification at 17q12 as well as amplifications or deletions at 17q21. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 in blue is included to facilitate chromosome identification/enumeration.

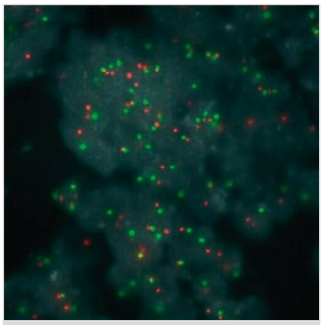


References

Järvinen et al, 1999, Genes Chromosomes Cancer 26; 142-150.
Järvinen et al, 2000, Am. J. Pathology 156; 639-647.

Description	Code	Color	Format	US	ROW
TOP2A (17q21) / ERBB2 (17q12) / SE 17, Triple-Color	KBI-10735	Green/Red/Blue	10 Test	-	IVD
TOP2A (17q21) / ERBB2 (17q12) / SE 17, Triple-Color	KI-10735	Green/Red/Blue	100 µL	RUO	-

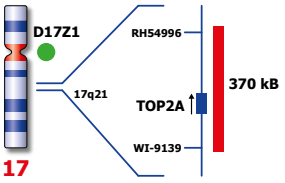
17q21 TOP2A / SE 17



TOP2A (17q21) / SE 17 probe hybridized to breast tissue (2R2G).

The Topoisomerase2A (TOP2A) enzyme, which is vital for the cell because of its role in cell replication and repair, catalyzes the relaxation of supercoiled DNA molecules to create a reversible double-strand DNA break. This enzyme is also the target of a number of cytotoxic agents, namely TOP2A inhibitors (anthracyclines, etoposide, teniposide).

The TOP2A (17q21) / SE 17 FISH probe is optimized to detect amplifications (copy numbers) or deletions of the TOP2A gene region at the 17q21. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification.



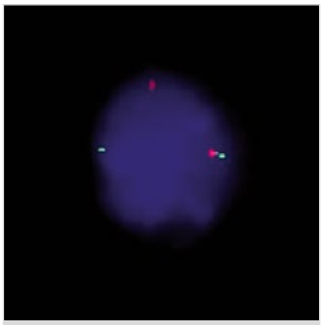
References

Järvinen et al, 1999, Genes Chromosomes Cancer 26; 142-150.
Järvinen et al, 2000, Am. J. Pathology 156; 639-647.

Description	Code	Color	Format	US	ROW
TOP2A (17q21) / SE 17	KBI-10724	Green/Red	10 Test	-	IVD
TOP2A (17q21) / SE 17	KI-10724	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

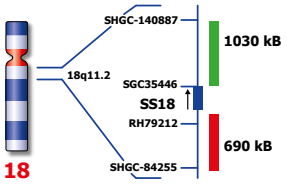
18q11 SS18 Break



SS18 (18q11) Break probe hybridized to patient material showing translocation of the SYT (SS18) gene region at 18q11 (1RG1R1G).

The characteristic chromosomal abnormality in synovial sarcoma t(X;18) (p11.2;q11.2) is present in 90% of the patients. This translocation results in the fusion of the synovial sarcoma translocation, chromosome 18 (SS18) gene to either of two distinct genes, SSX1 or SSX2, located on the X chromosome.

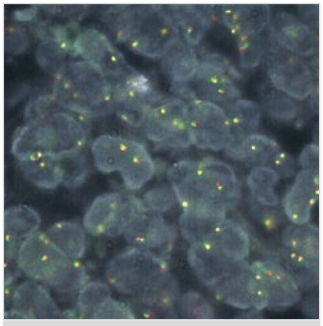
The SS18 (18q11) Break probe is optimized to detect translocations involving the SS18 gene region at 18q11 in a dual-color, split assay on paraffin embedded tissue sections.



References
Kawai et al, 1998, NEJM, 338; 153-160.
Surace et al, 2004, LabInvest., 84; 1185-1192.

Description	Code	Color	Format	US	ROW
SS18 (18q11) Break	KBI-10713	Green/Red	10 Test	-	IVD
SS18 (18q11) Break	KI-10713	Green/Red	100 µL	RUO	-

18q21 BCL2 Break (tissue)

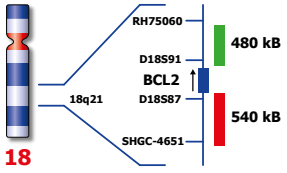


BCL2 (18q21) Break hybridized to paraffin embedded tissue (2RG).

Follicular lymphoma is a mature B-cell lymphoma characterized by the presence of the t(14;18) translocation that juxtaposes the BCL2 locus on chromosome 18q21 to the immunoglobulin H (IGH) locus on chromosome 14q32, resulting in the overexpression of the anti-apoptotic protein BCL2. Besides IGH, additional translocation partners to BCL2 have been identified (e.g. IGK at 2p11.2 and IGL at 22q11). A break or split assay is therefore best suited to detect rearrangements of the BCL2 gene region at 18q21.

The BCL2 (18q21) Break probe is optimized to detect translocations involving the BCL2 gene region at 18q21 in a dual-color, split assay on paraffin embedded tissue sections.

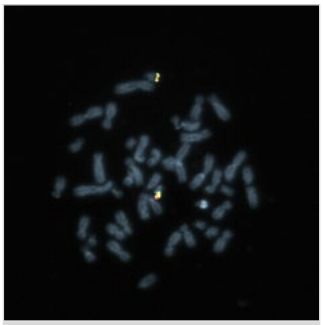
Kreatech has developed this probe for the specific use on cell material (KBI-10612), or for the use on tissue (KBI-10745).



References
Taniwaki M et al, 1995, Blood, 86; 1481-1486.
Poetsch M et al, 1996, J Clin Oncol, 14; 963- 969.
Einers R et al, 2005, Am J Clin Pathol, 124; 421-429.

Description	Code	Color	Format	US	ROW
BCL2 (18q21) Break (tissue)	KBI-10745	Green/Red	10 Test	-	IVD
BCL2 (18q21) Break (tissue)	KI-10745	Green/Red	100 µL	RUO	-

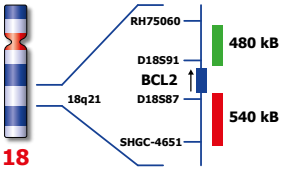
18q21 BCL2 Break



BCL2 (18q21) Break probe hybridized to a normal metaphase.

Follicular lymphoma is a mature B-cell lymphoma characterized by the presence of the t(14;18) translocation that juxtaposes the BCL2 locus on chromosome 18q21 to the immunoglobulin H (IGH) locus on chromosome 14q32, resulting in the overexpression of the anti-apoptotic protein BCL2. Next to IGH, other translocation partners to BCL2 are also known (e.g. IGK at 2p11.2 and IGL at 22q11). A break or split assay is therefore best suited to detect rearrangements of the BCL2 gene region at 18q21.

The BCL2 (18q21) Break FISH probe is optimized to detect translocations involving the BCL2 gene region at 18q21 in a dual-color, split assay on metaphase/interphase spreads, bloodsmears and bone marrow cells.

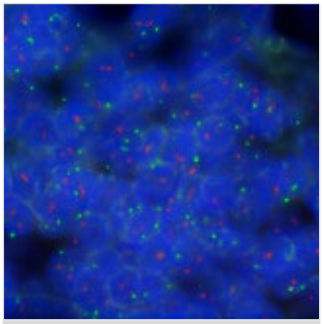


References

Taniwaki M et al, 1995, Blood, 86; 1481-1486.
Poetsch M et al, 1996, J Clin Oncol, 14; 963- 969.
Einerson R et al, 2005, Am J Clin Pathol, 124; 421-429.

Description	Code	Color	Format	US	ROW
BCL2 (18q21) Break	KBI-10612	Green/Red	10 Test	-	IVD
BCL2 (18q21) Break	KI-10612	Green/Red	100 µL	RUO	-

18q21 BCL2 / IGH (tissue)

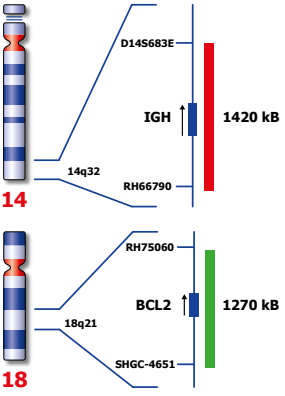


BCL2/IGH t(14;20) Fusion Probe hybridized to paraffin embedded lymph node material (2R2G).

Image kindly provided by P. May, Imperial College, Hammersmith Hospital, London

Follicular lymphoma is a mature B-Cell lymphoma, characterized by the presence of the t(14;18) translocation that juxtaposes the BCL2 locus on chromosome 18q21 to the immunoglobulin H (IGH) locus on chromosome 14q32, resulting in the overexpression of the antiapoptotic protein BCL2.

The BCL2/IGH t(14;18) Fusion probe is optimized to detect the reciprocal translocation t(14;18) in a dual-color, dual-fusion assay on formalin fixed paraffin embedded tissue samples. In addition Kreatech has developed a probe for the specific use on cell material (KBI-10606).



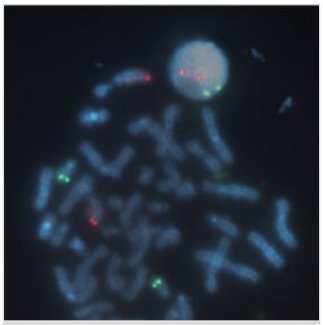
References

Taniwaki M et al, 1995, Blood, 86; 1481-1486.
Poetsch M et al, 1996, J Clin Oncol, 14; 963-969.

Description	Code	Color	Format	US	ROW
BCL2/IGH t(14;18) Fusion (tissue)	KBI-10755	Green/Red	10 Test	-	IVD
BCL2/IGH t(14;18) Fusion (tissue)	KI-10755	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

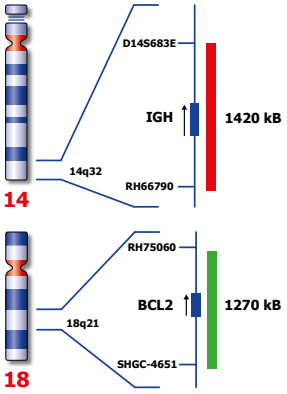
18q21 BCL2 / IGH



BCL2 / IGH t(14;18) probe hybridized to a normal interphase/metaphase (2R2G).

The t(14;18) chromosomal translocation that results in the juxtaposition of the BCL2 proto-oncogene with the heavy chain JH locus. It a common cytogenetic abnormality in human lymphoma and is observed in about 85% of follicular lymphoma (FL) and up to one-third of diffuse lymphomas (DL). Two breakpoint region clusters (brc) have been identified: a major breakpoint region (mbr) within the 3' untranslated region of the BCL2 proto-oncogene accounting for approximately 60% of the cases and a minor cluster region (mcr) 30 kb 3' of BCL2 accounting for approximately 25% of the breakpoints.

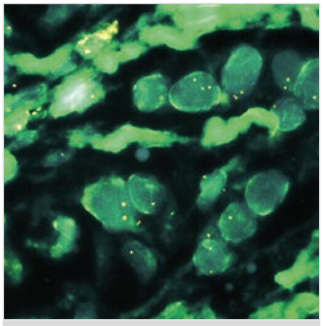
The BCL2 / IGH t(14;18)(q21;q32) specific FISH probe is optimized to detect the reciprocal translocation t(18;14), involving either of the two brc in the BCL2 gene in a dual-color, dual-fusion assay. Kreatech has optimized this FISH probe for the specific use on cell material (KBI-10606), or for the use on tissue (KBI-10755).



References
Poetsch et al, 1996, J Clin Oncol, 14; 963-969.
Vaandrager et al, 2000, Genes Chrom Cancer, 27; 85-94.

Description	Code	Color	Format	US	ROW
BCL2/IGH t(14;18) Fusion	KBI-10606	Green/Red	10 Test	-	IVD
BCL2/IGH t(14;18) Fusion	KI-10606	Green/Red	100 µL	RUO	-

18q21 MALT1 Break (tissue)

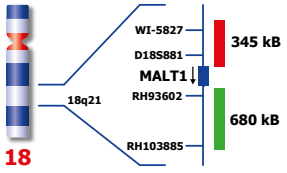


MALT1 (18q21) Break tissue probe hybridized to paraffin embedded material (2RG).

Low grade malignant lymphomas arising from mucosa associated lymphoid tissue (MALT) represent a distinct clinicopathological entity. The three major translocations seen in MALT lymphomas are t(11;18)(q21;q21) / API2-MALT1, t(14;18)(q32;q21) / IGH-MALT1 and t(1;14)(p22;q32) / IGHBCL10. A break or split probe for MALT1 (18q21) is best used to analyze translocation of the MALT1 gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

The MALT1 (18q21) Break probe is optimized to detect translocations involving the MALT1 gene region at 18q21 in a dual-color, split assay.

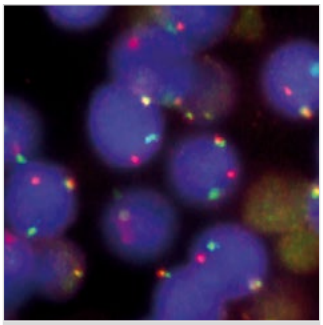
Kreatech has developed this probe for the specific use on cell material (KBI-10608), or for the use on tissue (KBI-10731).



References
Morgan et al, 1999, Cancer Res, 59; 6205-6213.
Dierlamm et al, 2000, Blood, 96; 2215-2218.

Description	Code	Color	Format	US	ROW
MALT1 (18q21) Break (tissue)	KBI-10731	Green/Red	10 Test	-	IVD
MALT1 (18q21) Break (tissue)	KI-10731	Green/Red	100 µL	RUO	-

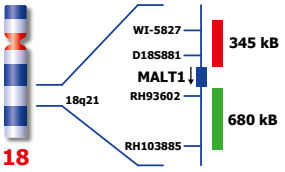
18q21 MALT1 Break



MALT1 (18q21) Break probe hybridized to patient material showing a translocation at 18q21 (1RG1RG).

Low grade malignant lymphomas arising from mucosa associated lymphoid tissue (MALT) represent a distinct clinicopathological entity. The three major translocations seen in MALT lymphomas are t(11;18)(q21;q21) / API2-MALT1, t(14;18)(q32;q21) / IGH-MALT1 and t(1;14)(p22;q32) / IGH-BCL10. A break or split probe for MALT1 (18q21) is best used to analyze translocation of the MALT1 gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

Kreatech has optimized this FISH probe for the specific use on cell material (KBI-10608), or for the use on tissue (KBI-10731).

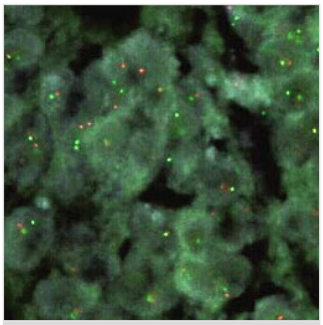


References

Morgan et al, 1999, Cancer Res, 59; 6205-6213.
Dierlamm et al, 2000, Blood, 96; 2215-2218.

Description	Code	Color	Format	US	ROW
MALT1 (18q21) Break	KBI-10608	Green/Red	10 Test	-	IVD
MALT1 (18q21) Break	KI-10608	Green/Red	100 µL	RUO	-

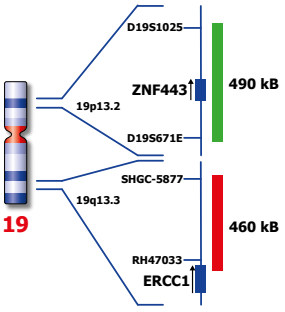
19p13 ERCC1 / ZNF443



ERCC1 (19q13) / ZNF443 (19p13) probe hybridized to paraffin embedded tissue (2R2G).

Nucleotide excision repair (NER) is the primary DNA repair mechanism that removes platinum-DNA adducts from genomic DNA. Excision repair cross-complementing rodent repair deficiency, complementation group 1 (ERCC1) is a critical gene in the NER pathway. A growing list of reports links cisplatin, carboplatin, and oxaliplatin based chemotherapy resistance to ERCC1 expression levels in several tumors. This relationship has been suggested for patients with gastric, bladder, ovarian, colorectal and non–small cell lung cancers (NSCLC). ERCC1 has been shown to be an important marker to predict responsiveness to cisplatin-based chemotherapy. Low ERCC1 gene expression correlates with prolonged survival after cisplatin-based chemotherapy.

The ERCC1 (19q13) FISH probe has been optimized to detect copy numbers of the ERCC1 gene region at 19q13. The ZNF443 (19p13) probe is included to facilitate chromosome identification.



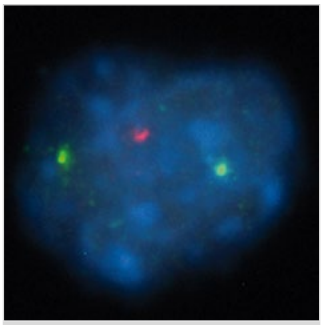
References

Olaussen et al, 2006, N. Engl. J. Med. 335; 983-991.
Ceppi et al, 2006, Ann. Oncol. 17; 1818-1825.

Description	Code	Color	Format	US	ROW
ERCC1 (19q13) / ZNF443 (19p13)	KBI-10739	Green/Red	10 Test	-	IVD
ERCC1 (19q13) / ZNF443 (19p13)	KI-10739	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

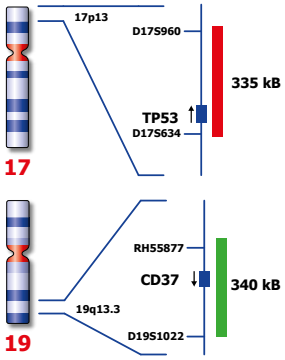
19q13 19q13 / TP53



19q13 / TP53 (17p13) hybridized to patient material showing a TP53 (17p13) deletion (1R2G).

TP53 (previously known as p53) gene deletion, which can be identified by interphase FISH in almost a third of patients with newly diagnosed MM, is a novel prognostic factor predicting for short survival of MM patients treated with conventional-dose chemotherapy. Amplification of 19q13 has been reported in a variety of cancer. The 19q13 specific FISH probe is optimized to detect copy numbers at 19q13.

The TP53 (17p13) specific DNA region is optimized to detect copy numbers of the TP53 gene region at 17p13.

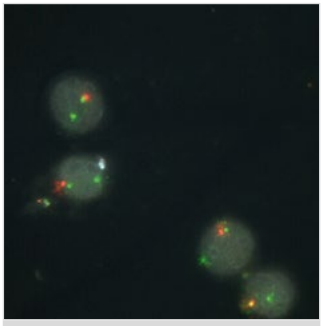


References

Drach et al, 1998, Blood, 92; 802-809.
Cremer et al, 2005, Genes Chrom Cancer, 44; 194-203.

Description	Code	Color	Format	US	ROW
19q13 / TP53 (17p13)	KBI-10509	Green/Red	10 Test	-	IVD
19q13 / TP53 (17p13)	KI-10509	Green/Red	100 µL	RUO	-

20q 20q-

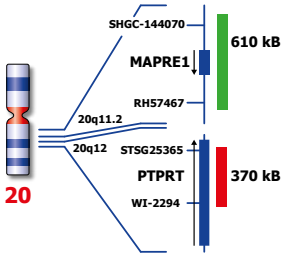


20q- (20q12) / 20q11 probe hybridized to patient material showing 20q- deletion (1R2G).

Material kindly provided by Labdia Labordiagnostik, Vienna.

Acquired deletions of the long arm of chromosome 20 are found in several hematologic conditions and particularly in the myeloproliferative disorders (MPD) and myelodysplastic syndromes and acute myeloid leukemia (MDS / AML). A minimal critical region deleted in MPD and MDS has been identified at 20q12 which includes a protein tyrosine phosphatase receptor gene.

The 20q- (20q12) specific FISH probe is optimized to detect copy numbers of 20q at region 20q12. A 20q11 region specific probe is included to facilitate chromosome identification.

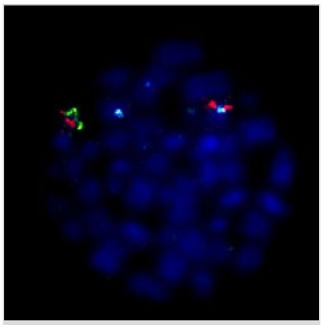


References

Bench et al, 2000, Oncogene, 19; 3902-3913.
Asimakopoulos et al, 1994, Blood, 84; 3086-3094.

Description	Code	Color	Format	US	ROW
20q- (20q12) / 20q11	KBI-10203	Green/Red	10 Test	-	IVD
20q- (20q12) / 20q11	KI-10203	Green/Red	100 µL	RUO	-

20q11.2 dic(9;20)

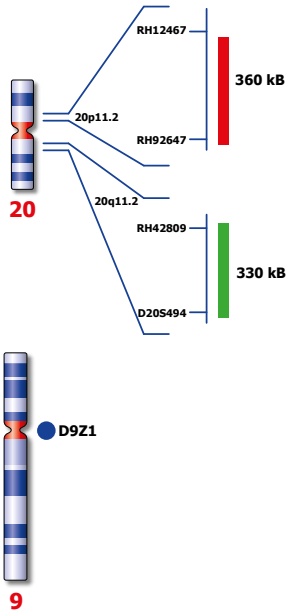


dic(9;20) Triple-Color.

Image kindly provided by Dr. Ann Nordgren, Stockholm.

The dic(9;20)(p13.2;q11.2) is a recurrent chromosomal abnormality in pediatric Bcell precursor acute lymphoblastic leukemia (BCP-ALL), which occurs in ~2% of the cases. It is associated with an intermediate outcome with relapses being relatively frequent, compared to other common cytogenetic subgroups of BCP-ALL (e.g. high hyperploidy and t(12;21)). The recent Nordic Society of Pediatric Hematology and Oncology (NOPHO) ALL treatment protocol dictates that the dic(9;20) aberration is to be excluded before assigning a patient to standard risk treatment. The dic(9;20) is an unbalanced rearrangement involving chromosomes 9 and 20, resulting in the co-localisation of the respective centromeres and concomitant loss of the chromosome arms 9p and 20q.

The dic(9;20) Triple-Color FISH probe is optimized to detect the dicentric (9;20) (p13.2;q11.2) in a triple-color assay on metaphase/interphase spreads, blood smears and bone marrow cells.

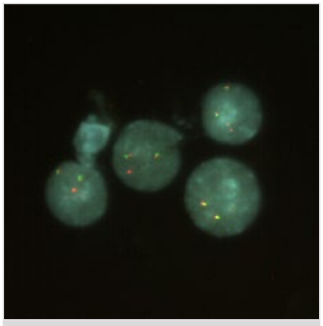


References

Forestier et al., Genes Chromosome Cancer, 2008, 47; 149-158.
Pichler H et al., Br J Haematol, 2010, 149; 93-100.
Schmiegelow K et al., Leukemia, 2010, 24; 345-54.
Zachariadis V et al., Leukemia, 2011, 25; 22-628.
Zachariadis V et al., Br J Haematol, 2012, 159; 488-491.

Description	Code	Color	Format	US	ROW
dic(9;20) Triple-Color	KBI-10405	Green/Red/Blue	10 Test	-	IVD
dic(9;20) Triple-Color	KI-10405	Green/Red/Blue	100 µL	RUO	-

20q12 MAFB /IGH

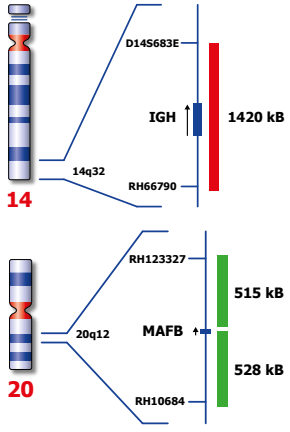


The MAFB / IGH t(14;20) Fusion FISH probe hybridized to patient material showing a complex pattern with a t(14;20) translocation.

Image kindly provided by Erasmus Medical Center, Rotterdam.

The immunoglobulin heavy chain (IGH) gene at 14q32 is an important cause of genetic deregulation in MM. Among the known fusion partners for the IGH (previously known as IGH@) gene, reciprocal translocation with the MAFB gene at 20q12 is relatively rare in MM (~2% occurrence). However, the MAFB / IGH t(14;20) translocation is associated with poor prognosis in multiple myeloma patients.

The MAFB / IGH t(14;20) Fusion FISH probe is optimized to detect the reciprocal translocation t(14;20) in a dual-color, dual-fusion assay on metaphase/ interphase spreads and bone marrow cells.

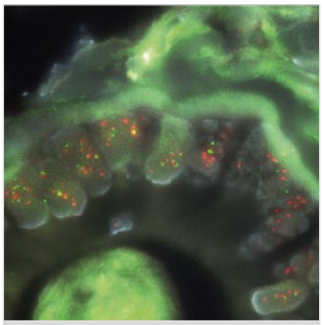


References

Boersma-Vreugdenhil GR et al, 2004, Br J Haematol, 126; 355-363.
Bergsagel PL et al, 2005, JCO, 23; 6333-6338.

Description	Code	Color	Format	US	ROW
MAFB/IGH t(14;20) Fusion	KBI-10510	Green/Red	10 Test	-	IVD
MAFB/IGH t(14;20) Fusion	KI-10510	Green/Red	100 µL	RUO	-

20q13 AURKA

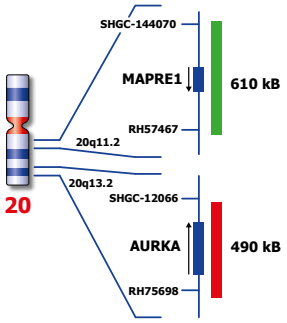


AURKA (20q13) / 20q11 probe hybridized to colorectal carcinoma material showing amplification of AURKA, gene region at 20q13.

Material kindly provided by Dr. Carvalho, Amsterdam.

Aurora kinase A (AURKA) gene amplification has been detected in approximately 12% of primary breast tumors, as well as in bladder, ovarian, colon, prostate, neuroblastoma and cervical cancer cell lines. Recent research into new drug development has focused on the importance of aurora kinases for tumor suppression. The AURKA (20q13) / 20q11 probe is designed to detect copy numbers of the AURKA gene region at region 20q13.

The AURKA (20q13) FISH probe is optimized to detect copy numbers of the AURKA gene region at region 20q13. The 20q11 specific DNA probe is included to facilitate chromosome identification.

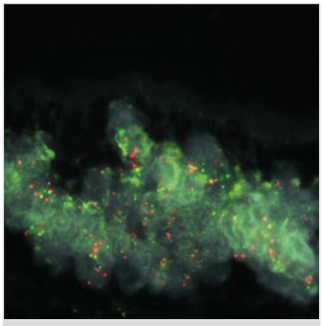


References

Uchida et al, 2010, Cancer Genet Cytogenet 203; 324-327.
Sen et al, 2002, J of Nat Canc Inst 94; 1320-1329.
Lassmann et al, 2007, Clin Cancer Res 13; 4083-4091.

Description	Code	Color	Format	US	ROW
AURKA (20q13) / 20q11	KBI-10721	Green/Red	10 Test	-	IVD
AURKA (20q13) / 20q11	KI-10721	Green/Red	100 µL	RUO	-

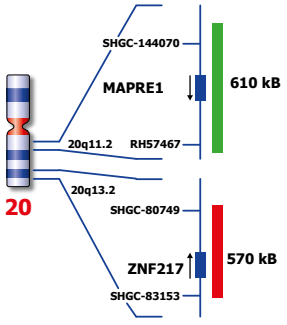
20q13 ZNF217 / 20q11



ZNF217 (20q13) / 20q11 probe hybridized to tissue (2R2G).

Zinc-finger protein 217 (ZNF217) is a Kruppel-like zinc-finger protein located at 20q13.2, within a region of recurrent maximal amplification in a variety of tumor types, and especially breast cancer cell lines and primary breast tumors. Copy number gains at 20q13 are also found in more than 25% of cancers of the ovary, colon, head and neck, brain, and pancreas, often in association with aggressive tumor behavior. ZNF217 is considered a strong candidate oncogene that may have profound effects on cancer progression, which is transcribed in multiple normal tissues, and overexpressed in almost all cell lines and tumors in which it is amplified.

The ZNF217 (20q13) FISH probe is optimized to detect copy numbers of 20q at 20q13. The 20q11 probe is included to facilitate chromosome identification.

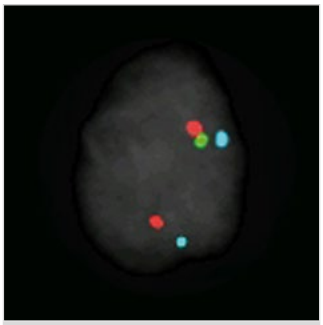


References

Tanner M et al, 2000, Clin Cancer Res, 6; 1833-1839.
Ginestier C et al, 2006, Clin Cancer Res, 12; 4533-4544.

Description	Code	Color	Format	US	ROW
ZNF217 (20q13) / 20q11	KBI-10733	Green/Red	10 Test	-	IVD
ZNF217 (20q13) / 20q11	KI-10733	Green/Red	100 µL	RUO	-

21q22 TMPRSS2-ERG



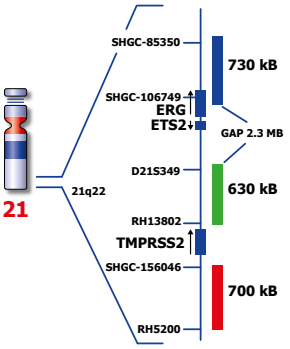
TMPRSS2-ERG (21q22) rearrangement probe hybridized to prostate carcinoma tissue showing a deletion of the TMPRSS2 (21q22) gene region associated with TMPRSS2-ERG fusion (1RGB 1RB).

Image kindly provided by Dr. Teixeira, Porto.

The transmembrane protease serine 2 gene (TMPRSS2) is involved in gene fusions with ERG, ETV1 or ETV4 in prostate cancer. It has been reported that the expression of the TMPRSS2-ERG fusion gene is a strong prognostic factor for the risk of prostate cancer recurrence in prostate cancer patients treated by surgery.

The TMPRSS2-ERG rearrangement probe is optimized to detect the deletion between TMPRSS2 and ERG at 21q22 associated with the TMPRSS2-ERG fusion in a triple-color deletion assay.

It also detects translocations involving the TMPRSS2 region such as ETV1 t(7;21), or ETV4 t(17;21).

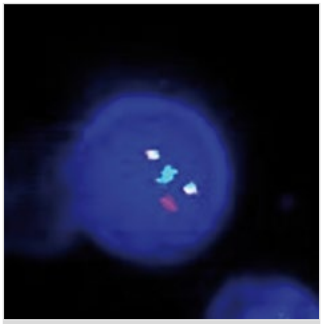


References

Perner et al, 2006 Cancer Res 66; 8337-8341.
Hermans et al, 2006, Cancer Res 66; 10658-10663.
Attard et al, 2008, Oncogene 27; 253-263.

Description	Code	Color	Format	US	ROW
TMPRSS2-ERG (21q22) Deletion, Break, Triple-Color	KBI-10726	Green/Red/Blue	10 Test	-	IVD
TMPRSS2-ERG (21q22) Deletion, Break, Triple-Color	KI-10726	Green/Red/Blue	100 µL	RUO	-

22q11 BCR / ABL1

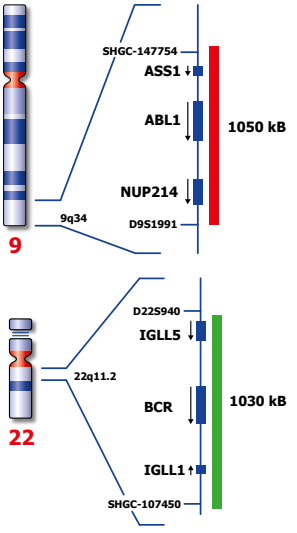


BCR / ABL1 t(9;22) Fusion probe hybridized on patient material showing t(9;22) (q34;q11) reciprocal translocation (2RG1R1G).

Image kindly provided by Monika Conchon, São Paulo.

The BCR / ABL1 t(9;22) Fusion FISH probe is optimized to detect the t(9;22) (q34;q11) reciprocal translocation in a dual-color, dual-fusion assay on metaphase/interphase spreads, blood smears and bone marrow cells.

This probe will also detect cryptic insertions of ABL1 (previously known as ABL) into the BCR region not detectable by karyotyping and therefore described as Ph-negative.



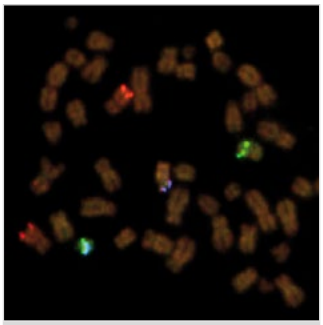
References

Morris et al, 1990, Blood, 76; 1812-1818.
Dewald et al, 1998, Blood, 91; 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science, 250; 559-562.

Description	Code	Color	Format	US	ROW
BCR/ABL1 t(9;22) Fusion	KBI-10005	Green/Red	10 Test	-	IVD
BCR/ABL1 t(9;22) Fusion	KBI-12005	Green/Red	20 Test	-	IVD
BCR/ABL1 t(9;22) Fusion	KI-10005	Green/Red	100 µL	RUO	-
BCR/ABL1 t(9;22) Fusion	KI-12005	Green/Red	200 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

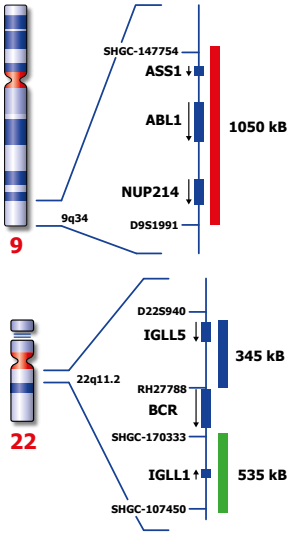
22q11 BCR / ABL1 TC



BCR / ABL1 t(9;22),Triple-Color, Dual Fusion probe hybridized on patient material showing translocation of distal BCR (1BG1RB1R1G).

Image kindly provided by Prof. Siebert, Kiel.

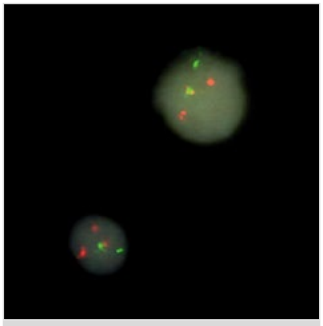
The BCR / ABL1 t(9;22) FISH probe is a triple-color, dual-fusion probe built from the same regions as the dual-color, dual-fusion probe, but the proximal BCR region is labeled in blue. Using the triple-color probe allows to distinguish between the derivative chromosome 22, the Philadelphia chromosome, which will be observed as purple (red/blue) color, while the derivative chromosome 9 will show a yellow (red/green) signal.



References
Morris et al, 1990, Blood, 76; 1812-1818.
Dewald et al, 1998, Blood, 91; 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science, 250; 559-562.

Description	Code	Color	Format	US	ROW
BCR/ABL1 t(9;22) Triple-Color, Dual-Fusion	KBI-10006	Green/Red/Blue	10 Test	-	IVD
BCR/ABL1 t(9;22) Triple-Color, Dual-Fusion	KI-10006	Green/Red/Blue	100 µL	RUO	-

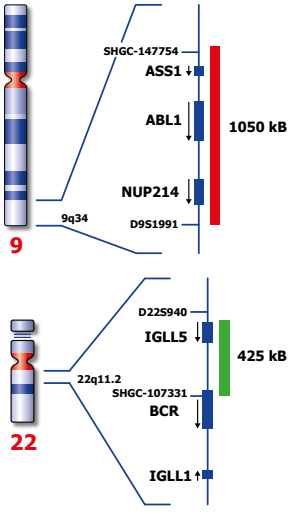
22q11 BCR / ABL1 DC



BCR / ABL1 t(9;22), Dual-Color, Single-Fusion probe hybridized to patient material showing t(9;22) translocation (1RG1R1G).

Material kindly provided by Dr. Balogh, Budapest.

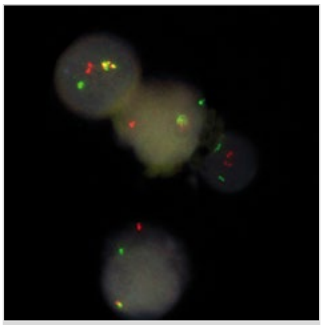
A simple dual-color, single-fusion assay is preferably used for the initial screening of CML and ALL patients. The Philadelphia chromosome, der(22q), is visualized by a fusion signal while the der(9q) shows no signal.



References
Morris et al, 1990, Blood, 76; 1812-1818.
Dewald et al, 1998, Blood, 91; 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science, 250; 559-562.

Description	Code	Color	Format	US	ROW
BCR/ABL1 t(9;22) Dual-Color, Single-Fusion, Extra Signal	KBI-10008	Green/Red	10 Test	-	IVD
BCR/ABL1 t(9;22) Dual-Color, Single-Fusion, Extra Signal	KI-10008	Green/Red	100 µL	RUO	-

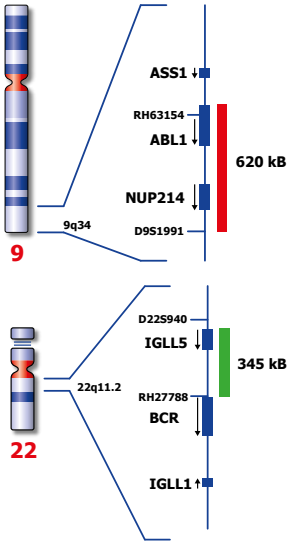
22q11 BCR / ABL1 DC



BCR / ABL1 t(9;22), Dual-Color, Single-Fusion probe hybridized to patient material showing t(9;22) translocation (1RG1R1G).

Material kindly provided by Dr. Balogh, Budapest.

A simple dual-color, single-fusion assay is preferably used for the initial screening of CML and ALL patients. The Philadelphia chromosome, der(22q), is visualized by a fusion signal while the der(9q) shows no signal.

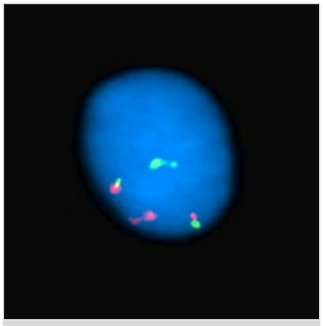


References

Morris et al, 1990, Blood, 76; 1812-1818.
Dewald et al, 1998, Blood, 91; 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science, 250; 559-562.

Description	Code	Color	Format	US	ROW
BCR/ABL1 t(9;22) Dual-Color, Single-Fusion	KBI-10009	Green/Red	10 Test	-	IVD
BCR/ABL1 t(9;22) Dual-Color, Single-Fusion	KI-10009	Green/Red	100 µL	RUO	-

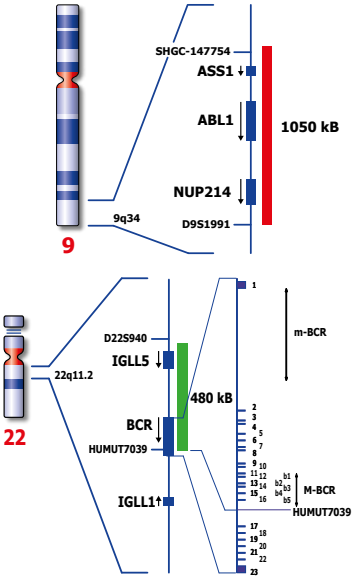
22q11 Mm-BCR / ABL1



Mm-BCR / ABL1 probe hybridized to patient material showing t(9;22) with M-BCR (1F1r1R1G).

Breakpoints in the BCR gene region can occur in different regions, predominantely in a major breakpoint cluster region (M-BCR) but can also occur in a minor breakpoint cluster region (m-BCR) or micro breakpoint cluster region (µ-BCR). Further research has indicated that CML patients with different BCR-ABL1 transcripts respond differently to treatment with Gleevec.

The Mm-BCR / ABL1 t(9;22), Dual-Color (DC), Single-Fusion (SF), Extra -Signal (ES) FISH probe is designed to differentiate between a M-BCR and m-BCR gene rearrangement by giving different signal patterns.



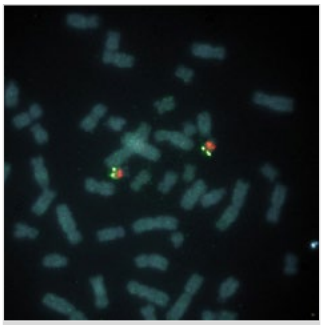
References

Dewald et al., 1998, Blood, 91; 3357-3365.
Huntly et al., 2003, Blood, 102; 1160-1168.
Sharma et al., 2010, Ann Hematol, 89; 241-7.
Tkachuk et al., 1990, Science, 250; 559-56.
Kolomietz et al., 2001. Blood, 97; 3581-3588.

Description	Code	Color	Format	US	ROW
Mm-BCR/ABL1 t(9;22) Dual-Color, Single-Fusion, Extra Signal	KBI-10013	Green/Red	10 Test	-	IVD

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

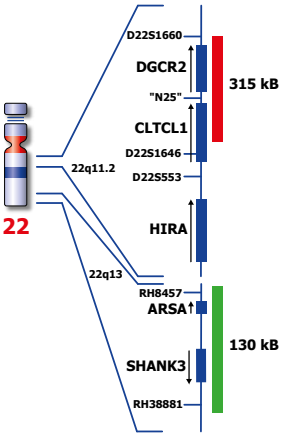
22q11 N25 / SHANK3



DiGeorge "N25" (22q11) / 22q13 (SHANK3) probe hybridized to a normal metaphase (2R2G).

The DiGeorge "N25" FISH probe was the first commercial microdeletion probe for chromosome 22q and detects the locus D22S75. This marker is located between DGCR2 and CLTCL1 (Clathrin). Both genes have been extensively investigated and their role in DiGeorge syndrome is well established.

The DiGeorge "N25" region probe covers the marker "N25" (D22S75) and adjacent region of CLTCL1 (Clathrin gene region) and DGCR2 (DiGeorge critical region gene 2). The SHANK3 FISH probe at 22q13 is serving as internal control.

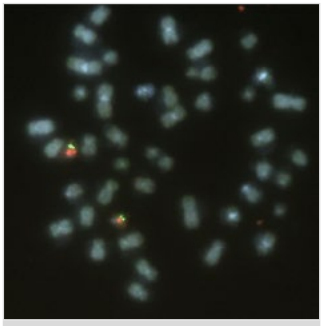


References

Sirotkin et al, 1996, Hum. Mol. Genet., 5; 617-624.
Holmes et al, 1997, Hum. Mol. Genet., 6; 357-367.
Wilson, et al, 2003, J. Med. Genet., 40; 575-584.
Luciani, et al, 2003, J. Med. Genet., 40; 690-696.

Description	Code	Color	Format	US	ROW
DiGeorge "N25" (22q11) / 22q13 (SHANK3)	KBI-40102	Green/Red	10 Test	-	IVD
DiGeorge "N25" (22q11) / 22q13 (SHANK3)	KBI-45102	Green/Red	5 Test	-	IVD
"N25" (22q11) / 22q13 (SHANK3)	KI-40102	Green/Red	100 µL	RUO	-

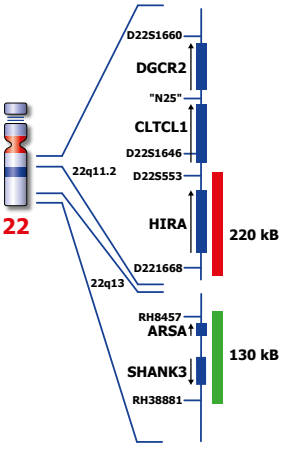
22q11 HIRA / SHANK3



DiGeorge HIRA (22q11) / 22q13 (SHANK3) probe hybridized to a normal metaphase (2R2G).

The DiGeorge HIRA (TUPLE) probe targets a putative transcriptional regulator (TUPLE1 or HIRA, HIR histone cell cycle regulation defective homolog A) which also has been identified to lie within the commonly deleted region DiGeorge syndrome. This probe is located distally to the "N25" probe.

The DiGeorge HIRA region probe is optimized to detect copy numbers of the HIRA gene region at 22q11.2. The SHANK3 probe at 22q13 is serving as internal control.

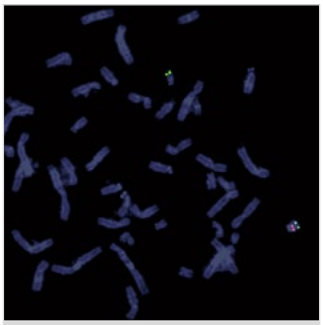


References

Lorain at al, 1996, Genome Res, 6; 43-50.

Description	Code	Color	Format	US	ROW
DiGeorge HIRA (22q11) / 22q13 (SHANK3)	KBI-40103	Green/Red	10 Test	-	IVD
DiGeorge HIRA (22q11) / 22q13 (SHANK3)	KBI-45103	Green/Red	5 Test	-	IVD
HIRA (22q11) / 22q13 (SHANK3)	KI-40103	Green/Red	100 µL	RUO	-

22q11 TBX1 / SHANK3

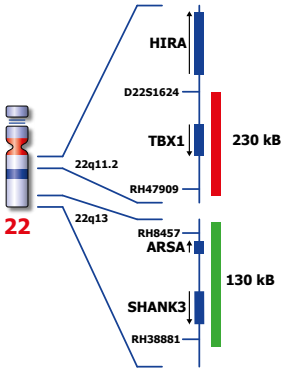


DiGeorge TBX1 (22q11) / 22q13 (SHANK3) probe hybridized to DiGeorge patient material showing a deletion of the TBX1 gene region at 22q11 (1R2G).

Image kindly provided by Dr. F. Girard- Lemaire Service de Cytogénétique (Dr. Flori), CHU Strasbourg.

The 22q11 deletion in DiGeorge syndrome/VCFS is characterized by defects in the derivatives of the pharyngeal apparatus. TBX1, a member of the T-box transcription factor family, is required for normal development of the pharyngeal arch arteries. Haploinsufficiency of TBX1 has been demonstrated to be sufficient to generate at least one important component of the DiGeorge syndrome phenotype in mice. The TBX1 is also located within the minimal critical DiGeorge region in humans.

The DiGeorge TBX1 region probe is optimized to detect copy numbers of the TBX1 gene region at 22q11.2. The subtelomeric (ST) 22qter FISH probe is included as control probe. The SHANK3 FISH probe at 22q13 is serving as internal control.

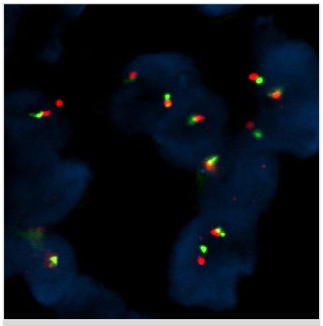


References

Lindsay et al, 2001, Nature, 410; 97-101.
Merscher et al, 2001, Cell, 104; 619-629.
Paylor et al, 2006, PNAS, 103; 7729-7734.

Description	Code	Color	Format	US	ROW
DiGeorge TBX1 (22q11) / 22q13 (SHANK3)	KBI-40104	Green/Red	10 Test	-	IVD
DiGeorge TBX1 (22q11) / 22q13 (SHANK3)	KBI-45104	Green/Red	5 Test	-	IVD
TBX1 (22q11) / 22q13 (SHANK3)	KI-40104	Green/Red	100 µL	RUO	-

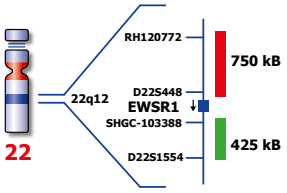
22q12 EWSR1 Break



EWSR1 (22q12) break probe hybridized to a tissue section showing co-localized and split signals.

Ewing's sarcoma is the second most frequent primary bone cancer. In most cases a translocation involving the EWSR1 gene at 22q12 and the FLI1 gene at 11q24 are observed, but several other translocation partners (ERG, ETV1, FEV, and E1A3) can also be involved.

The EWSR1 (22q12) Break probe is optimized to detect translocations involving the EWSR1 gene region at 22q12 in a dual-color, split assay on paraffin embedded tissue sections.



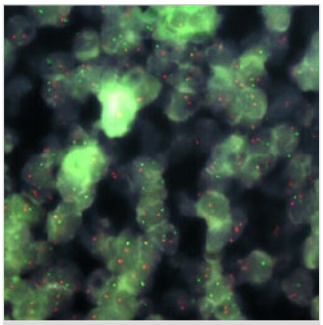
References

Zucman-Rossi, et al, 1998, PNAS, 95; 11786-11791.
Bernstein et al, 2006, Oncologist, 11; 503-519.

Description	Code	Color	Format	US	ROW
EWSR1 (22q12) Break	KBI-10750	Green/Red	10 Test	-	IVD
EWSR1 (22q12) Break	KI-10750	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

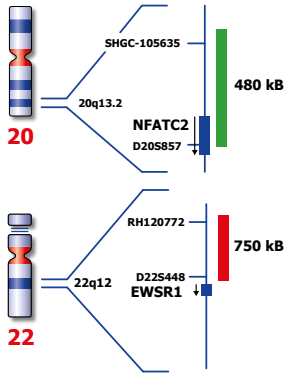
22q12 EWSR1 / NFATC



FISH result of the EWSR1/NFATC2 t(20;22) DC, S-Fusion probe.

Ewing's sarcoma is the second most frequent primary bone cancer. In most cases a translocation involving the EWSR1 gene at 22q12 and the FLI1 gene at 11q24 is observed. Several other translocation partners of the ETS gene family can also be involved. The first non-ETS family translocation partner described is the NFATC2 gene (nuclear factor of activated T-cells, cyto-plasmic, calcineurin-dependent 2) at 20q13.

The EWSR1/NFATC2 t(20;22) Dual-Color Single-Fusion probe is optimized to detect the t(20;22)(q13;q12) involving the NFATC2 (20q13) and EWSR1 (22q12) gene regions in a dual-color, single fusion assay on paraffin embedded tissue sections.

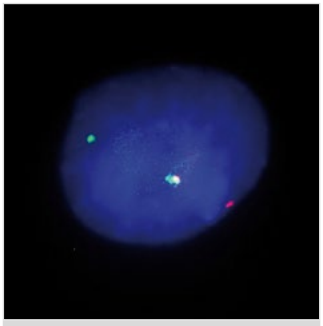


References

Szuhai et al, 2009, Clin Cancer Res, 15; 2259-2268.
Zucman-Rossi et al, 1998, PNAS, 95; 11786-11791.
Bernstein et al, 2006, Oncologist, 11; 503-519.

Description	Code	Color	Format	US	ROW
EWSR1/NFATC2 t(20;22) Dual-Color, Single-Fusion	KBI-10751	Green/Red	10 Test	-	IVD
EWSR1/NFATC2 t(20;22) Dual-Color, Single-Fusion	KI-10751	Green/Red	100 µL	RUO	-

Xp11 TFE3 Break

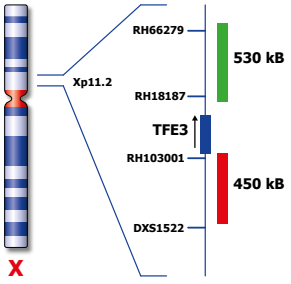


TFE3 (Xp11) Break probe hybridized to renal cell carcinoma showing a translocation at Xp11 (1RG1R1G).

Image kindly provided by Dr. Desangles, Paris.

Abnormalities of Xp11.2 region have often been observed in papillary renal cell carcinomas and are sometimes the sole cytogenetic abnormality present. The transcription factor binding to IGHM enhancer 3 (TFE3) gene, which encodes a member of the helix-loop-helix family of transcription factors, is located in this critical region and can be fused to various other chromosomal regions by translocation. Known fusion partners are NONO (Xq12), PRCC (1q21), SFPQ (1p34), CLTC (17q23) and ASPSCR1 (17q25).

The TFE3 (Xp11) Break probe is optimized to detect translocations involving the TFE3 gene region at Xp11.2 in a dual-color, break assay.



References

Sidhar et al, 1996, Hum Mol Genet, 5; 1333-1338.
Weterman et al, 1996, Proc Natl, Acad Sci, 93; 15294-15298.

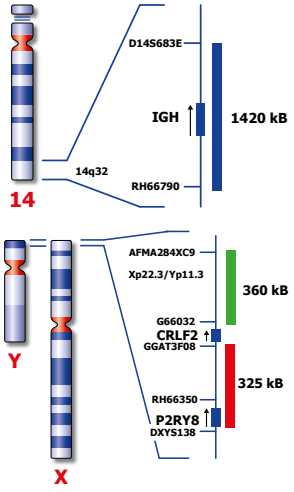
Description	Code	Color	Format	US	ROW
TFE3 (Xp11) Break	KBI-10741	Green/Red	10 Test	-	IVD
TFE3 (Xp11) Break	KI-10741	Green/Red	100 µL	RUO	-

Xp22 CRLF2 / IGH

Rearrangement of the CRLF2 (Xp22/Yp11) gene is associated with poor outcome in pediatric B-progenitor and Down syndrome-associated acute lymphoblastic leukemia (ALL).

CRLF2-IGH fusions between Xp22-14q32 or Yp11-14q32 results in a deregulated expression of the cytokine receptor gene (CRLF2). This can also be the result of the fusion with the P2RY8 promoter on Xp22 or Yp11.

Gain of chromosome X has been observed in Down syndrome-associated ALL.

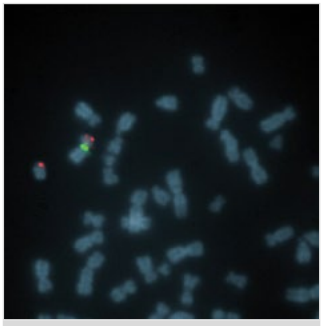


References

Mullighan et al., 2009, Nat. Genet. 41(11): 1243-1246
Russell et al., 2009, Blood, 114(13): 2688-2698

Description	Code	Color	Format	US	ROW
CRLF2 (Xp22/Yp11) Break / IGH (14q32) Fusion, Triple-Color	KBI-10406	Green/Red/Blue	10 Test	-	IVD

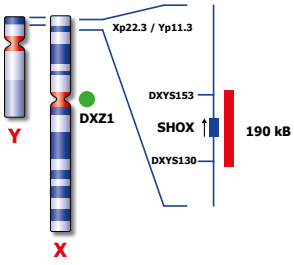
Xp22 SHOX / SE X



Short Stature SHOX (Xp22) / SE X probe hybridized to a male metaphase (2R1G).

Individuals with SHOX-related short stature have disproportionate short stature and/or wrist abnormalities consistent with those described in Madelung deformity. The SHOX genes located on the pseudoautosomal regions of the X and Y chromosomes are the only genes known to be associated with SHOX-related haploinsufficiency.

The SHOX region probe is optimized to detect copy numbers of the SHOX gene region at Xp22. The chromosome X Satellite Enumeration (SE X) FISH probe at DXZ1 is added to facilitate chromosome identification.



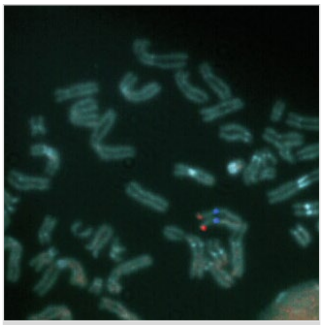
References

Rao et al, 1997, Hum. Genet., 100; 236-239.
Morizio et al, 2003, Am. J. Med. Genet., 119; 293-296.

Description	Code	Color	Format	US	ROW
Short Stature SHOX (Xp22) / SE X	KBI-40112	Green/Red	10 Test	-	IVD
Short Stature SHOX (Xp22) / SE X	KBI-45112	Green/Red	5 Test	-	IVD
SHOX (Xp22) / SE X	KI-40112	Green/Red	100 µL	RUO	-

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Xp22 STS / KAL1 / SE X

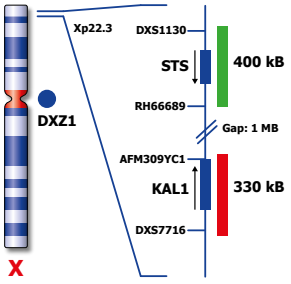


STS (Xp22) / KAL1 (Xp22) / SE X Triple-Color probe hybridized to male patient material showing a deletion of the STS gene region (1R1B).

Material kindly provided by Necker hospital, Paris.

STS (Steroid Sulfatase) disease is a chromosome X-linked disorder associated with a microdeletion of the gene within the Xp22.3 region. Deletion of the steroid sulfatase gene has been detected in individuals with recessive X-linked ichtyosis, the disease been considered one of the most frequent human enzyme deficient disorders. KAL1 (Kallmann syndrome interval gene-1) maps to the Kallmann syndrome critical region on the distal short arm of the human X chromosome. Individuals with Kallmann syndrome suffers of hypogonadotropic hypogonadism and anosmia, with clinical features of variable phenotype. It affects approximately 1 in 8000 males and 1 in 40000 females.

The STS (Xp22) region probe is optimized to detect copy numbers of the STS gene region at Xp22. The KAL1 (Xp 22) region probe is optimized to detect copy numbers of the KAL1 gene region at Xp22. The Chromosome X Satellite Enumeration (SE X) FISH probe at DXZ1 is included to facilitate chromosome identification.

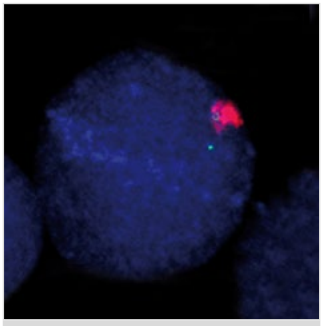


References

Alper in et al, 1997, J. Biol. Chem., 272; 20756-20763.
Meroni et al, 1996, Hum. Mol. Genet., 5; 423-431.

Description	Code	Color	Format	US	ROW
STS (Xp22) / KAL1 (Xp22) / SE X Triple-Color	KBI-40115	Green/Red/Blue	10 Test	-	IVD
STS (Xp22) / KAL1 (Xp22) / SE X Triple-Color	KBI-45115	Green/Red/Blue	5 Test	-	IVD
STS (Xp22) / KAL1 (Xp22) / SE X Triple-Color	KI-40115	Green/Red/Blue	100 µL	RUO	-

Xq12 AR / SE X

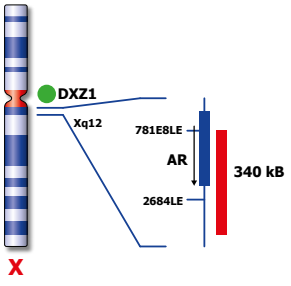


AR (Xq12) / SE X probe hybridized to VCaP prostate cancer cell showing highlevel AR gene amplification.

Image kindly provided by Prof. Trapman, Erasmus Medical Centre, Rotterdam.

The androgen receptor (AR) gene has been identified as a target gene for the Xq12 amplification found in one-third of hormone-refractory prostate cancers. The findings suggest that AR gene amplification and overexpression is involved in the emergence of prostate cancer.

The AR (Xq12) FISH probe is optimized to detect copy numbers of the AR gene region at region Xq12. The chromosome X satellite enumeration probe (SE X) at DXZ1 is included to facilitate chromosome identification.

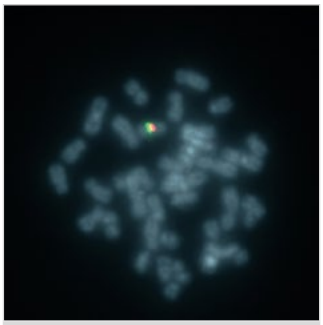


References

Visakorpi T et al, 1995, Nat. Genet. 9; 401-406.
Koivisto P et al, 1997, Cancer Res. 57 ; 314-319.

Description	Code	Color	Format	US	ROW
AR (Xq12) / SE X	KBI-10720	Green/Red	10 Test	-	IVD
AR (Xq12) / SE X	KI-10720	Green/Red	100 µL	RUO	-

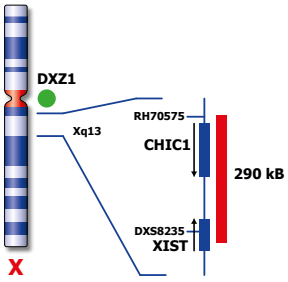
Xq13 XIST / SE X



X-Inactivation XIST (Xq13) / SE X probe hybridized to a male metaphase (1R1G).

The XIST locus is expressed only from the inactive X chromosome, resides at the putative X inactivation center, and is considered a prime player in the initiation of mammalian X dosage compensation. The severe phenotype of human females whose karyotype includes tiny ring X chromosomes has been attributed to the inability of the small ring X chromosome to inactivate. Many of the ring chromosomes lack the XIST locus, consistent with XIST being necessary for cis inactivation.

The XIST specific FISH probe is optimized to detect copy numbers of the XIST region at Xq13. The chromosome X Satellite Enumeration (SE X) FISH probe at DXZ1 is added to facilitate chromosome identification.



References
Migeon et al, 1993, PNAS, 90; 12025-12029.
Jani et al, 1995, Genomics, 27; 182-188.

Description	Code	Color	Format	US	ROW
X-Inactivation XIST (Xq13) / SE X	KBI-40108	Green/Red	10 Test	-	IVD
X-Inactivation XIST (Xq13) / SE X	KBI-45108	Green/Red	5 Test	-	IVD
XIST (Xq13) / SE X	KI-40108	Green/Red	100 µL	RUO	-

Acro-P-Arms Acro-P-Arms

Description	Code	Color	Format	US	ROW
Acro-P-Arms NOR Blue	KBI-20033B	Blue	10 Test	-	IVD
Acro-P-Arms NOR Green	KBI-20033G	Green	10 Test	-	IVD
Acro-P-Arms NOR Red	KBI-20033R	Red	10 Test	-	IVD

Human Centromere Human Centromere

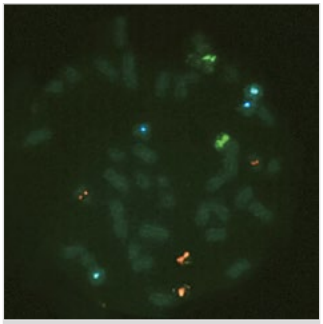
Description	Code	Color	Format	US	ROW
All Human Centromere Green	KBI-20000G	Green	10 Test	-	RUO
All Human Centromere Red	KBI-20000R	Red	10 Test	-	RUO
All Human Centromere, green	KI-20000G	Green	100 µL	RUO	-
All Human Centromere, red	KI-20000R	Red	100 µL	RUO	-

Human Telomere Human Telomere

Description	Code	Color	Format	US	ROW
All Human Telomere Green	KBI-40200G	Green	10 Test	-	RUO
All Human Telomere red	KBI-40200R	Red	10 Test	-	RUO

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Pre-imp Screen PreimpScreen PolB



Pseudo color image using PreimpScreen PolB (KBI-40050) on a metaphase spread from lymphocytes showing two signals each of chromosomes 13, 16, 18, 21, and 22, respectively.

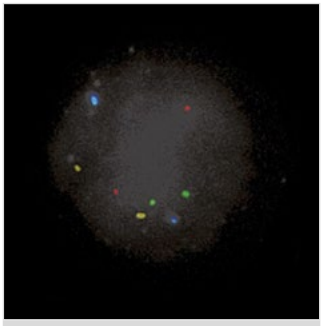
PreimpScreen PolB is designed for determining chromosome copy number in polar bodies.

The first polar body is removed from the unfertilized oocyte, and the second polar body from the zygote, shortly after fertilization. The main advantage of the use of polar bodies in preimplantation genetic screening (PGS) is that they are not necessary for successful fertilization or normal embryonic development, thus ensuring no deleterious effect for the embryo. In some countries, where the legislation bans the selection of preimplantation embryos, polar body analysis is the only possible method to perform PGS. The biopsy and analysis of the first and second polar bodies can be completed before syngamy, which is the moment from which the zygote is considered an embryo and becomes protected by the law.

References
Iaonnou D et al, 2012, Chromosome Res, 20; 447-60.
Iaonnou D et al, 2011, Mol and Cel Probes, 25;199-205.

Description	Code	Color	Format	US	ROW
PreimpScreen PolB (13 / 16 / 18 / 21 / 22)	KBI-40050	Five color	20 Test	-	IVD

Pre-imp Screen PreimpScreen Blas



Pseudo-color image on a healthy female blastomer using PreimpScreen Blas (13,18,21,X,Y) FISH panel.

Image kindly provided by Prof. D. Griffin, University of Kent, United Kingdom.

PreimpScreen Blas is designed for determination of chromosome copy number in blastomeres.

Cleavage-stage biopsy is generally performed the morning of day three post-fertilization, when normally developing embryos reach the eight-cell stage. The biopsy is usually performed on embryos with less than 50% of anucleated fragments and at an 8-cell or later stage of development. The main advantage of cleavage-stage biopsy over polar body (PB) analysis is that the genetic input of both parents can be studied, and therefore currently is the prevalent method when doing *in situ* hybridizations in preimplantation genetic screening.

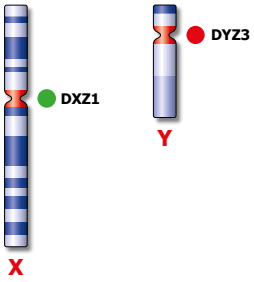
Description	Code	Color	Format	US	ROW
PreimpScreen Blas (13 / 18 / 21 / X / Y)	KBI-40051	Five color	20 Test	-	IVD

Satellite Enumeration SE X / SE Y

Sex Chromosome Abnormalities

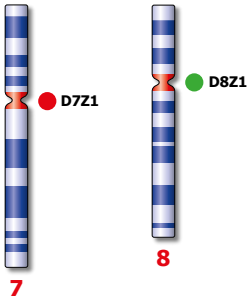
Chromosomal abnormalities involving the X and Y chromosome (sex chromosomes) are slightly less common than autosomal abnormalities and are usually much less severe in their effects. The high frequency of people with sex chromosome aberrations is partly due to the fact that they are rarely lethal conditions.

- Turner syndrome occurs when females inherit only one X chromosome – their genotype is X0.
- Metafemales or triple-X females, inherit three X chromosomes – their genotype is XXX or more rarely XXXX or XXXXX.
- Klinefelter syndrome males inherit one or more extra X chromosomes – their genotype is XXY or more rarely XXXY, XXXXY, or XY/XXY mosaic.



Description	Code	Color	Format	US	ROW
SE X (DXZ1) / SE Y (DYZ3)	KBI-20030	Green/Red	10 Test	-	IVD
SE X (DXZ1) / SE Y (DYZ3)	KI-20030	Green/Red	100 µL	RUO	-

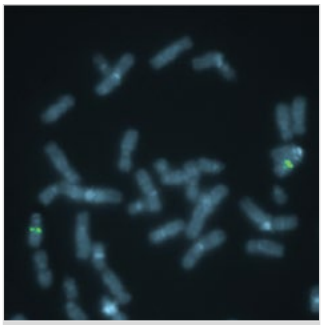
Satellite Enumeration SE 7 / SE 8



Description	Code	Color	Format	US	ROW
SE 7 (D7Z1) / SE 8 (D8Z1)	KBI-20031	Green/Red	10 Test	-	IVD
SE 7 (D7Z1) / SE 8 (D8Z1)	KI-20031	Green/Red	100 µL	RUO	-

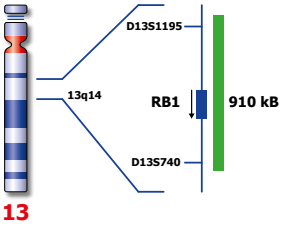
IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Prenatal RB1



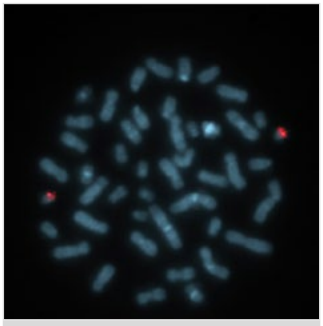
RB1 (13q14) probe hybridized to a normal metaphase (2G).

The chromosome 13 specific region probe is optimized to detect copy numbers of chromosome 13 at 13q14.2 on uncultured amniotic cells. In all PN combinations the 13q14 specific FISH probe is direct-labeled in green with PlatinumBright 495.



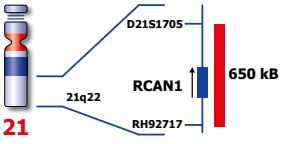
Description	Code	Color	Format	US	ROW
RB1 (13q14)	KBI-40001	Green	10 Test	-	IVD

Prenatal RCAN1



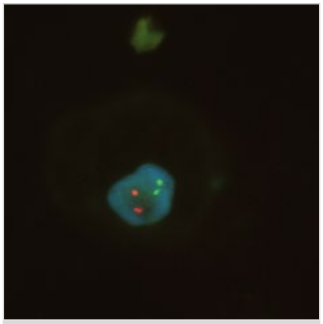
RCAN1 (21q22) probe hybridized to a normal metaphase (2R).

The chromosome 21 specific region probe is optimized to detect copy numbers of chromosome 21 at 21q22.1 on uncultured amniotic cells. In all PN combinations the 21q specific FISH probe is direct-labeled in red with PlatinumBright 550.

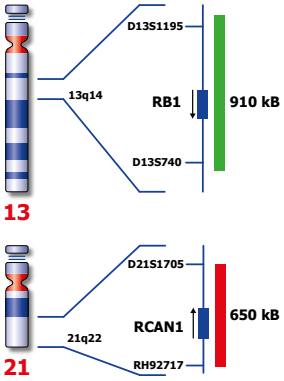


Description	Code	Color	Format	US	ROW
RCAN1 (21q22)	KBI-40002	Red	10 Test	-	IVD

Prenatal RB1 / RCAN1



RB1 (13q14)/RCAN1 (21q22) probe hybridized to a normal interphase (2R2G).



Description	Code	Color	Format	US	ROW
RB1 (13q14)/RCAN1 (21q22)	KBI-40003	Green/Red	10 Test	-	IVD
RB1 (13q14)/RCAN1 (21q22)	KI-40003	Green/Red	100 µL	RUO	-

Prenatal RCAN1 / SE X / SE Y

Sex Chromosome Abnormalities

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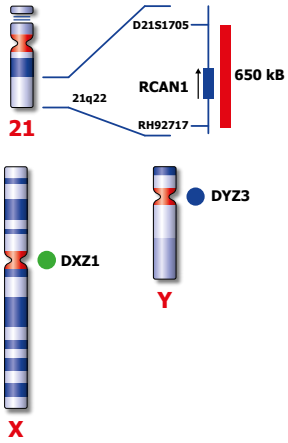
- Turner syndrome occurs when females inherit only one X chromosome – their genotype is X0.
- Metafemales or triple-X females, inherit three X chromosomes – their genotype is XXX or more rarely XXXX or XXXXX.
- Klinefelter syndrome males inherit one or more extra X chromosomes – their genotype is XXY or more rarely XXXY, XXXXY, or XY/XXY mosaic.



Description	Code	Color	Format	US	ROW
RCAN1 (21q22), SE X, SE Y	KBI-40008	Green/Red/Blue	20 Test	-	IVD
RCAN1 (21q22), SE X, SE Y	KBI-45008	Green/Red/Blue	5 Test	-	IVD
RCAN1 (21q22), SE X, Y	KI-40008	Green/Red/Blue	200 µL	RUO	-

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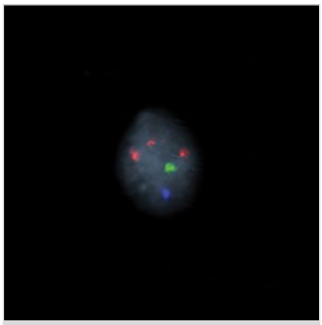
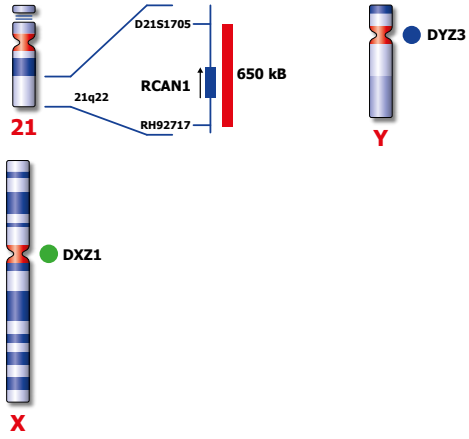
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Prenatal RB1 / RCAN1, SE X/SE Y/ SE 18



RCAN1 (21q22), SE X, Y showing trisomy 21.



Material kindly provided by Dr. Carvalho, Amsterdam.

References

Uchida et al, 2010, Cancer Genet Cytogenet, 203; 324-327.
Sen et al, 2002, J of Nat Canc Inst, 94; 1320-1329.
Lassmann et al, 2007, Clin Cancer Res, 13; 4083-4091.

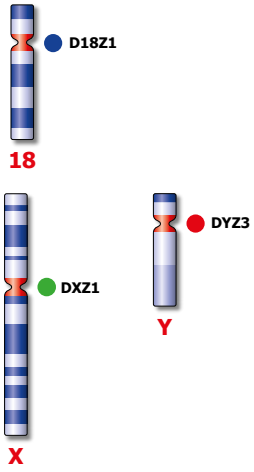
Description	Code	Color	Format	US	ROW
RB1 (13q14)/RCAN1 (21q22), SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KBI-40005	Green/Red/Blue	10 Test	-	IVD
RB1 (13q14)/RCAN1 (21q22), SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KBI-40006	Green/Red/Blue	30 Test	-	IVD
RB1 (13q14)/RCAN1 (21q22), SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KBI-40007	Green/Red/Blue	50 Test	-	IVD
RB1 (13q14)/RCAN1 (21q22), SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KI-40005	Green/Red/Blue	100 µL	RUO	-
RB1 (13q14)/RCAN1 (21q22), SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KI-40006	Green/Red/Blue	300 µL	RUO	-
RB1 (13q14)/RCAN1 (21q22), SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KI-40007	Green/Red/Blue	500 µL	RUO	-

Prenatal SE X / SE Y / SE 18

Sex Chromosome Abnormalities

Chromosomal abnormalities involving the X and Y chromosome (sex chromosomes) are slightly less common than autosomal abnormalities and are usually much less severe in their effects. The high frequency of people with sex chromosome aberrations is partly due to the fact that they are rarely lethal conditions.

- Turner syndrome occurs when females inherit only one X chromosome – their genotype is X0.
- Metafemales or triple-X females, inherit three X chromosomes – their genotype is XXX or more rarely XXXX or XXXXX.
- Klinefelter syndrome males inherit one or more extra X chromosomes – their genotype is XXY or more rarely XXXY, XXXXY, or XY/XXY mosaic.



Description	Code	Color	Format	US	ROW
SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KBI-20032	Green/Red/Blue	10 Test	-	IVD
SE X (DXZ1) / SE Y (DYZ3) / SE 18 (D18Z1)	KI-20032	Green/Red/Blue	100 µL	RUO	-

Arm Specific

Product Name	Product Code	Color	Content	CONC
Acro-P-Arms	KBI-20033B	BLUE	10 Test	5x
Acro-P-Arms	KBI-20033G	GREEN	10 Test	5x
Acro-P-Arms	KBI-20033R	RED	10 Test	5x
Arm Specific 1	KBI-30100G	GREEN	5 Test	RTU
Arm Specific 1	KBI-30100R	RED	5 Test	RTU
Arm Specific 1	KBI-30101G	GREEN	5 Test	RTU
Arm Specific 1	KBI-30101R	RED	5 Test	RTU
Arm Specific 2	KBI-30102G	GREEN	5 Test	RTU
Arm Specific 2	KBI-30102R	RED	5 Test	RTU
Arm Specific 2	KBI-30103G	GREEN	5 Test	RTU
Arm Specific 2	KBI-30103R	RED	5 Test	RTU
Arm Specific 3	KBI-30104G	GREEN	5 Test	RTU
Arm Specific 3	KBI-30104R	RED	5 Test	RTU
Arm Specific 3	KBI-30105G	GREEN	5 Test	RTU
Arm Specific 3	KBI-30105R	RED	5 Test	RTU
Arm Specific 4	KBI-30106G	GREEN	5 Test	RTU
Arm Specific 4	KBI-30106R	RED	5 Test	RTU
Arm Specific 4	KBI-30107G	GREEN	5 Test	RTU
Arm Specific 4	KBI-30107R	RED	5 Test	RTU
Arm Specific 5	KBI-30108G	GREEN	5 Test	RTU
Arm Specific 5	KBI-30108R	RED	5 Test	RTU
Arm Specific 5	KBI-30109G	GREEN	5 Test	RTU
Arm Specific 5	KBI-30109R	RED	5 Test	RTU
Arm Specific 6	KBI-30110G	GREEN	5 Test	RTU
Arm Specific 6	KBI-30110R	RED	5 Test	RTU
Arm Specific 6	KBI-30111G	GREEN	5 Test	RTU
Arm Specific 6	KBI-30111R	RED	5 Test	RTU
Arm Specific 7	KBI-30112G	GREEN	5 Test	RTU
Arm Specific 7	KBI-30112R	RED	5 Test	RTU
Arm Specific 7	KBI-30113G	GREEN	5 Test	RTU
Arm Specific 7	KBI-30113R	RED	5 Test	RTU
Arm Specific 8	KBI-30114G	GREEN	5 Test	RTU
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Arm Specific 9	KBI-30117R	RED	5 Test	RTU
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Arm Specific 10	KBI-30119R	RED	5 Test	RTU
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Arm Specific 11	KBI-30121G	GREEN	5 Test	RTU
Arm Specific 11	KBI-30121R	RED	5 Test	RTU
Arm Specific 12	KBI-30122G	GREEN	5 Test	RTU
Arm Specific 12	KBI-30122R	RED	5 Test	RTU
Arm Specific 12	KBI-30123G	GREEN	5 Test	RTU
Arm Specific 12	KBI-30123R	RED	5 Test	RTU
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Arm Specific 13	KBI-30124R	RED	5 Test	RTU
Arm Specific 14	KBI-30125G	GREEN	5 Test	RTU
Arm Specific 14	KBI-30125R	RED	5 Test	RTU
Arm Specific 15	KBI-30126G	GREEN	5 Test	RTU
Arm Specific 15	KBI-30126R	RED	5 Test	RTU
Arm Specific 16	KBI-30127G	GREEN	5 Test	RTU
Arm Specific 16	KBI-30127R	RED	5 Test	RTU
Arm Specific 16	KBI-30128G	GREEN	5 Test	RTU
Arm Specific 16	KBI-30128R	RED	5 Test	RTU
Arm Specific 17	KBI-30129G	GREEN	5 Test	RTU
Arm Specific 17	KBI-30129R	RED	5 Test	RTU
Arm Specific 17	KBI-30130G	GREEN	5 Test	RTU
Arm Specific 17	KBI-30130R	RED	5 Test	RTU
Arm Specific 18	KBI-30131G	GREEN	5 Test	RTU
Arm Specific 18	KBI-30131R	RED	5 Test	RTU
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Arm Specific 19	KBI-30134G	GREEN	5 Test	RTU
Arm Specific 19	KBI-30134R	RED	5 Test	RTU
Arm Specific 20	KBI-30135G	GREEN	5 Test	RTU
Arm Specific 20	KBI-30135R	RED	5 Test	RTU
Arm Specific 20	KBI-30136G	GREEN	5 Test	RTU
Arm Specific 20	KBI-30136R	RED	5 Test	RTU
Arm Specific 21	KBI-30137G	GREEN	5 Test	RTU
Arm Specific 21	KBI-30137R	RED	5 Test	RTU
Arm Specific 22	KBI-30138G	GREEN	5 Test	RTU
Arm Specific 22	KBI-30138R	RED	5 Test	RTU
Arm Specific X	KBI-30139G	GREEN	5 Test	RTU
Arm Specific X	KBI-30139R	RED	5 Test	RTU
Arm Specific X	KBI-30140G	GREEN	5 Test	RTU
Arm Specific X	KBI-30140R	RED	5 Test	RTU
Arm Specific Y	KBI-30141G	GREEN	5 Test	RTU
Arm Specific Y	KBI-30141R	RED	5 Test	RTU

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F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Band Specific

Product Name	Product Code	Color	Content	CONC
Band Specific 1	KBI-30200G	GREEN	20 Test	RTU
Band Specific 1	KBI-30200R	RED	20 Test	RTU
Band Specific 1	KBI-30201G	GREEN	20 Test	RTU
Band Specific 1	KBI-30201R	RED	20 Test	RTU
Band Specific 1	KBI-30202G	GREEN	20 Test	RTU
Band Specific 1	KBI-30202R	RED	20 Test	RTU
Band Specific 1	KBI-30203G	GREEN	20 Test	RTU
Band Specific 1	KBI-30203R	RED	20 Test	RTU
Band Specific 1	KBI-30204G	GREEN	20 Test	RTU
Band Specific 1	KBI-30204R	RED	20 Test	RTU
Band Specific 1	KBI-30205G	GREEN	20 Test	RTU
Band Specific 1	KBI-30205R	RED	20 Test	RTU
Band Specific 1	KBI-30206G	GREEN	20 Test	RTU
Band Specific 1	KBI-30206R	RED	20 Test	RTU
Band Specific 2	KBI-30207G	GREEN	20 Test	RTU
Band Specific 2	KBI-30207R	RED	20 Test	RTU
Band Specific 2	KBI-30208G	GREEN	20 Test	RTU
Band Specific 2	KBI-30208R	RED	20 Test	RTU
Band Specific 2	KBI-30209G	GREEN	20 Test	RTU
Band Specific 2	KBI-30209R	RED	20 Test	RTU
Band Specific 2	KBI-30210G	GREEN	20 Test	RTU
Band Specific 2	KBI-30210R	RED	20 Test	RTU
Band Specific 2	KBI-30211G	GREEN	20 Test	RTU
Band Specific 2	KBI-30211R	RED	20 Test	RTU
Band Specific 2	KBI-30212G	GREEN	20 Test	RTU
Band Specific 2	KBI-30212R	RED	20 Test	RTU
Band Specific 2	KBI-30213G	GREEN	20 Test	RTU
Band Specific 2	KBI-30213R	RED	20 Test	RTU
Band Specific 2	KBI-30214G	GREEN	20 Test	RTU
Band Specific 2	KBI-30214R	RED	20 Test	RTU
Band Specific 3	KBI-30215G	GREEN	20 Test	RTU
Band Specific 3	KBI-30215R	RED	20 Test	RTU
Band Specific 3	KBI-30216G	GREEN	20 Test	RTU
Band Specific 3	KBI-30216R	RED	20 Test	RTU
Band Specific 3	KBI-30217G	GREEN	20 Test	RTU
Band Specific 3	KBI-30217R	RED	20 Test	RTU
Band Specific 3	KBI-30218G	GREEN	20 Test	RTU
Band Specific 3	KBI-30218R	RED	20 Test	RTU
Band Specific 3	KBI-30219G	GREEN	20 Test	RTU
Band Specific 3	KBI-30219R	RED	20 Test	RTU
Band Specific 3	KBI-30220G	GREEN	20 Test	RTU
Band Specific 3	KBI-30220R	RED	20 Test	RTU
Band Specific 3	KBI-30221G	GREEN	20 Test	RTU
Band Specific 3	KBI-30221R	RED	20 Test	RTU

Product Name	Product Code	Color	Content	CONC
Band Specific 3	KBI-30222G	GREEN	20 Test	RTU
Band Specific 3	KBI-30222R	RED	20 Test	RTU
Band Specific 3	KBI-30223G	GREEN	20 Test	RTU
Band Specific 3	KBI-30223R	RED	20 Test	RTU
Band Specific 3	KBI-30224G	GREEN	20 Test	RTU
Band Specific 3	KBI-30224R	RED	20 Test	RTU
Band Specific 3	KBI-30225G	GREEN	20 Test	RTU
Band Specific 3	KBI-30225R	RED	20 Test	RTU
Band Specific 3	KBI-30226G	GREEN	20 Test	RTU
Band Specific 3	KBI-30226R	RED	20 Test	RTU
Band Specific 3	KBI-30227G	GREEN	20 Test	RTU
Band Specific 3	KBI-30227R	RED	20 Test	RTU
Band Specific 3	KBI-30228G	GREEN	20 Test	RTU
Band Specific 3	KBI-30228R	RED	20 Test	RTU
Band Specific 3	KBI-30229G	GREEN	20 Test	RTU
Band Specific 3	KBI-30229R	RED	20 Test	RTU
Band Specific 3	KBI-30230G	GREEN	20 Test	RTU
Band Specific 3	KBI-30230R	RED	20 Test	RTU
Band Specific 4	KBI-30231G	GREEN	20 Test	RTU
Band Specific 4	KBI-30231R	RED	20 Test	RTU
Band Specific 4	KBI-30232G	GREEN	20 Test	RTU
Band Specific 4	KBI-30232R	RED	20 Test	RTU
Band Specific 4	KBI-30233G	GREEN	20 Test	RTU
Band Specific 4	KBI-30233R	RED	20 Test	RTU
Band Specific 4	KBI-30234G	GREEN	20 Test	RTU
Band Specific 4	KBI-30234R	RED	20 Test	RTU
Band Specific 5	KBI-30235G	GREEN	20 Test	RTU
Band Specific 5	KBI-30235R	RED	20 Test	RTU
Band Specific 5	KBI-30236G	GREEN	20 Test	RTU
Band Specific 5	KBI-30236R	RED	20 Test	RTU
Band Specific 5	KBI-30237G	GREEN	20 Test	RTU
Band Specific 5	KBI-30237R	RED	20 Test	RTU
Band Specific 6	KBI-30238G	GREEN	20 Test	RTU
Band Specific 6	KBI-30238R	RED	20 Test	RTU
Band Specific 6	KBI-30239G	GREEN	20 Test	RTU
Band Specific 6	KBI-30239R	RED	20 Test	RTU
Band Specific 6	KBI-30240G	GREEN	20 Test	RTU
Band Specific 6	KBI-30240R	RED	20 Test	RTU
Band Specific 6	KBI-30241G	GREEN	20 Test	RTU
Band Specific 6	KBI-30241R	RED	20 Test	RTU
Band Specific 6	KBI-30242G	GREEN	20 Test	RTU
Band Specific 6	KBI-30242R	RED	20 Test	RTU
Band Specific 6	KBI-30243G	GREEN	20 Test	RTU
Band Specific 6	KBI-30243R	RED	20 Test	RTU

Band Specific (continued)

Product Name	Product Code	Color	Content	CONC
Band Specific 7	KBI-30244G	GREEN	20 Test	RTU
Band Specific 7	KBI-30244R	RED	20 Test	RTU
Band Specific 7	KBI-30245G	GREEN	20 Test	RTU
Band Specific 7	KBI-30245R	RED	20 Test	RTU
Band Specific 7	KBI-30246G	GREEN	20 Test	RTU
Band Specific 7	KBI-30246R	RED	20 Test	RTU
Band Specific 7	KBI-30247G	GREEN	20 Test	RTU
Band Specific 7	KBI-30247R	RED	20 Test	RTU
Band Specific 7	KBI-30248G	GREEN	20 Test	RTU
Band Specific 7	KBI-30248R	RED	20 Test	RTU
Band Specific 7	KBI-30249G	GREEN	20 Test	RTU
Band Specific 7	KBI-30249R	RED	20 Test	RTU
Band Specific 8	KBI-30250G	GREEN	20 Test	RTU
Band Specific 8	KBI-30250R	RED	20 Test	RTU
Band Specific 8	KBI-30251G	GREEN	20 Test	RTU
Band Specific 8	KBI-30251R	RED	20 Test	RTU
Band Specific 8	KBI-30252G	GREEN	20 Test	RTU
Band Specific 8	KBI-30252R	RED	20 Test	RTU
Band Specific 8	KBI-30253G	GREEN	20 Test	RTU
Band Specific 8	KBI-30253R	RED	20 Test	RTU
Band Specific 8	KBI-30254G	GREEN	20 Test	RTU
Band Specific 8	KBI-30254R	RED	20 Test	RTU
Band Specific 8	KBI-30255G	GREEN	20 Test	RTU
Band Specific 8	KBI-30255R	RED	20 Test	RTU
Band Specific 8	KBI-30256G	GREEN	20 Test	RTU
Band Specific 8	KBI-30256R	RED	20 Test	RTU
Band Specific 8	KBI-30257G	GREEN	20 Test	RTU
Band Specific 8	KBI-30257R	RED	20 Test	RTU
Band Specific 8	KBI-30258G	GREEN	20 Test	RTU
Band Specific 8	KBI-30258R	RED	20 Test	RTU
Band Specific 8	KBI-30259G	GREEN	20 Test	RTU
Band Specific 8	KBI-30259R	RED	20 Test	RTU
Band Specific 8	KBI-30260G	GREEN	20 Test	RTU
Band Specific 8	KBI-30260R	RED	20 Test	RTU
Band Specific 8	KBI-30261G	GREEN	20 Test	RTU
Band Specific 8	KBI-30261R	RED	20 Test	RTU
Band Specific 9	KBI-30262G	GREEN	20 Test	RTU
Band Specific 9	KBI-30262R	RED	20 Test	RTU
Band Specific 9	KBI-30263G	GREEN	20 Test	RTU
Band Specific 9	KBI-30263R	RED	20 Test	RTU
Band Specific 9	KBI-30264G	GREEN	20 Test	RTU
Band Specific 9	KBI-30264R	RED	20 Test	RTU
Band Specific 9	KBI-30265G	GREEN	20 Test	RTU
Band Specific 9	KBI-30265R	RED	20 Test	RTU

Product Name	Product Code	Color	Content	CONC
Band Specific 9	KBI-30266G	GREEN	20 Test	RTU
Band Specific 9	KBI-30266R	RED	20 Test	RTU
Band Specific 10	KBI-30267G	GREEN	20 Test	RTU
Band Specific 10	KBI-30267R	RED	20 Test	RTU
Band Specific 10	KBI-30268G	GREEN	20 Test	RTU
Band Specific 10	KBI-30268R	RED	20 Test	RTU
Band Specific 11	KBI-30269G	GREEN	20 Test	RTU
Band Specific 11	KBI-30269R	RED	20 Test	RTU
Band Specific 11	KBI-30270G	GREEN	20 Test	RTU
Band Specific 11	KBI-30270R	RED	20 Test	RTU
Band Specific 11	KBI-30271G	GREEN	20 Test	RTU
Band Specific 11	KBI-30271R	RED	20 Test	RTU
Band Specific 11	KBI-30272G	GREEN	20 Test	RTU
Band Specific 11	KBI-30272R	RED	20 Test	RTU
Band Specific 11	KBI-30273G	GREEN	20 Test	RTU
Band Specific 11	KBI-30273R	RED	20 Test	RTU
Band Specific 11	KBI-30274G	GREEN	20 Test	RTU
Band Specific 11	KBI-30274R	RED	20 Test	RTU
Band Specific 11	KBI-30275G	GREEN	20 Test	RTU
Band Specific 11	KBI-30275R	RED	20 Test	RTU
Band Specific 12	KBI-30276G	GREEN	20 Test	RTU
Band Specific 12	KBI-30276R	RED	20 Test	RTU
Band Specific 12	KBI-30277G	GREEN	20 Test	RTU
Band Specific 12	KBI-30277R	RED	20 Test	RTU
Band Specific 12	KBI-30278G	GREEN	20 Test	RTU
Band Specific 12	KBI-30278R	RED	20 Test	RTU
Band Specific 12	KBI-30279G	GREEN	20 Test	RTU
Band Specific 12	KBI-30279R	RED	20 Test	RTU
Band Specific 12	KBI-30280G	GREEN	20 Test	RTU
Band Specific 12	KBI-30280R	RED	20 Test	RTU
Band Specific 13	KBI-30281G	GREEN	20 Test	RTU
Band Specific 13	KBI-30281R	RED	20 Test	RTU
Band Specific 13	KBI-30282G	GREEN	20 Test	RTU
Band Specific 13	KBI-30282R	RED	20 Test	RTU
Band Specific 14	KBI-30283G	GREEN	20 Test	RTU
Band Specific 14	KBI-30283R	RED	20 Test	RTU
Band Specific 14	KBI-30284G	GREEN	20 Test	RTU
Band Specific 14	KBI-30284R	RED	20 Test	RTU
Band Specific 15	KBI-30285G	GREEN	20 Test	RTU
Band Specific 15	KBI-30285R	RED	20 Test	RTU
Band Specific 15	KBI-30286G	GREEN	20 Test	RTU
Band Specific 15	KBI-30286R	RED	20 Test	RTU
Band Specific 16	KBI-30287G	GREEN	20 Test	RTU
Band Specific 16	KBI-30287R	RED	20 Test	RTU

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Product Name	Product Code	Color	Content	CONC
Band Specific 18	KBI-30288G	GREEN	20 Test	RTU
Band Specific 18	KBI-30288R	RED	20 Test	RTU
Band Specific 18	KBI-30289G	GREEN	20 Test	RTU
Band Specific 18	KBI-30289R	RED	20 Test	RTU
Band Specific 18	KBI-30290G	GREEN	20 Test	RTU
Band Specific 18	KBI-30290R	RED	20 Test	RTU
Band Specific 19	KBI-30291G	GREEN	20 Test	RTU
Band Specific 19	KBI-30291R	RED	20 Test	RTU
Band Specific 19	KBI-30292G	GREEN	20 Test	RTU
Band Specific 19	KBI-30292R	RED	20 Test	RTU
Band Specific 20	KBI-30293G	GREEN	20 Test	RTU
Band Specific 20	KBI-30293R	RED	20 Test	RTU
Band Specific 21	KBI-30294G	GREEN	20 Test	RTU
Band Specific 21	KBI-30294R	RED	20 Test	RTU
Band Specific X	KBI-30295G	GREEN	20 Test	RTU
Band Specific X	KBI-30295R	RED	20 Test	RTU
Band Specific X	KBI-30296G	GREEN	20 Test	RTU
Band Specific X	KBI-30296R	RED	20 Test	RTU
Band Specific X	KBI-30297G	GREEN	20 Test	RTU
Band Specific X	KBI-30297R	RED	20 Test	RTU
Band Specific X	KBI-30298G	GREEN	20 Test	RTU
Band Specific X	KBI-30298R	RED	20 Test	RTU
Band Specific X	KBI-30299G	GREEN	20 Test	RTU
Band Specific X	KBI-30299R	RED	20 Test	RTU
Band Specific X	KBI-30300G	GREEN	20 Test	RTU
Band Specific X	KBI-30300R	RED	20 Test	RTU
Band Specific X	KBI-30301G	GREEN	20 Test	RTU
Band Specific X	KBI-30301R	RED	20 Test	RTU
Band Specific X	KBI-30302G	GREEN	20 Test	RTU
Band Specific X	KBI-30302R	RED	20 Test	RTU
Band Specific X	KBI-30303G	GREEN	20 Test	RTU
Band Specific X	KBI-30303R	RED	20 Test	RTU
Band Specific Y	KBI-30304G	GREEN	20 Test	RTU
Band Specific Y	KBI-30304R	RED	20 Test	RTU

XL Probes*

Product Name	Product Code	Color	Content	Concentration
ALK (2p23) Proximal - XL	02P008V495	GREEN	1 mL	10 x
ALK (2p23) Distal - XL	02P009V550	RED	1 mL	10 x
BCL6 (3q27) Proximal - XL	03Q009V495	GREEN	1 mL	10 x
BCL6 (3q27) Distal - XL	03Q010V550	RED	1 mL	10 x
ROS1 (6q22) Proximal - XL	06Q006V495	GREEN	1 mL	10 x
ROS1(6q22) Distal - XL	06Q007V550	RED	1 mL	10 x
SE 7 (D7Z1)-006 - XL	07C006V495	GREEN	1 mL	10 x
MET (7q31) - XL	07Q002V550	RED	1 mL	10 x
SE 8 (D8Z1)-003 - XL	08C003V495	GREEN	1 mL	10 x
FGFR1 (8p11) - XL	08P004V550	RED	1 mL	10 x
MYC (8q24) Proximal - XL	08Q007V495	GREEN	1 mL	10 x
MYC (8q24) Distal - XL	08Q008V550	RED	1 mL	10 x
RET (10q11) Proximal - XL	10Q008V550	RED	1 mL	10 x
RET (10q11) Distal - XL	10Q007V495	GREEN	1 mL	10 x
IGH (14q32) Proximal - XL	14Q004V550	RED	1 mL	10 x
IGH (14q32) Distal - XL	14Q005V495	GREEN	1 mL	10 x
SE 17 (D17Z1) - XL	17C004V495	GREEN	1 mL	10 x
TP53 (17p13) - XL	17P002V550	RED	1 mL	10 x
BCL2 (18q21) Proximal - XL	18Q003V495	GREEN	1 mL	10 x
BCL2 (18q21) Distal - XL	18Q004V550	RED	1 mL	10 x

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Manual Probes*

Product Name	Product Code	Color	Content	CONC
CKS1B (1q21)	01Q001B495	GREEN	50 µL	2 x
CKS1B (1q21)	01Q001B550	RED	50 µL	2 x
CKS1B (1q21)	01Q001I550	RED	250 µL	2 x
CKS1B (1q21)	01Q001N550	RED	50 µL	10 x
SRD (1p36)	01P001B495	GREEN	50 µL	2 x
SRD (1p36)	01P001I495	GREEN	250 µL	2 x
SRD (1p36)	01P001N495	GREEN	50 µL	10 x
ALK (2p23) Proximal	02P001B495	GREEN	50 µL	2 x
ALK (2p23) Distal	02P002B550	RED	50 µL	2 x
ALK (2p23) Proximal-HS	02P005B495	GREEN	50 µL	2 x
ALK (2p23) Distal-HS	02P006B550	RED	50 µL	2 x
SE 3 (D3Z1)	03C001C550	RED	33 µL	3 x
SE 3 (D3Z1)	03C001N415	BLUE	50 µL	10 x
3q11	03Q002B495	GREEN	50 µL	2 x
MECOM (3q26) Proximal	03Q003B495	GREEN	50 µL	2 x
MECOM (3q26) Distal-004	03Q004B550	RED	50 µL	2 x
MECOM (3q26) Distal-004	03Q004C550	RED	33 µL	3 x
MECOM (3q26) Proximal-005	03Q005C495	GREEN	33 µL	3 x
MECOM (3q26) Distal-006	03Q006C415	BLUE	33 µL	3 x
TERC (3q26)	03Q001B550	RED	50 µL	2 x
SE 4 (D4Z1)	04C001B495	GREEN	50 µL	2 x
FGFR3 (4p16)	04P001B495	GREEN	50 µL	2 x
FGFR3 (4p16)	04P001I495	GREEN	250 µL	2 x
FGFR3 (4p16) Proximal	04P002B550	RED	50 µL	2 x
FGFR3 (4p16) Distal	04P003B495	GREEN	50 µL	2 x
CHIC2 (4q12)	04Q003C550	RED	33 µL	3 x
FIP1L1 (4q12)	04Q002C495	GREEN	33 µL	3 x
PDGFRA (4q12)	04Q001B550	RED	50 µL	2 x
PDGFRA (4q12)-004	04Q004C415	BLUE	33 µL	3 x
5q11.2 (ISL1)	05Q006B495	GREEN	50 µL	2 x
PDGFRB (5q32) Distal	05Q001B495	GREEN	50 µL	2 x
PDGFRB (5q32) Proximal	05Q002B550	RED	50 µL	2 x
FGFR4 (5q35)	05Q005B550	RED	50 µL	2 x
SE 6 (D6Z1)	06C001D415	BLUE	25 µL	4 x
CCND3 (6p21)	06P003B495	GREEN	50 µL	2 x
RREB1 (6p24)	06P001D590	DARK RED	25 µL	4 x
6q21	06Q001A550	RED	100 µL	1 x
ROS1 (6q22) Distal	06Q002B495	GREEN	50 µL	2 x
ROS1 (6q22) Proximal	06Q003B495	GREEN	50 µL	2 x
ROS1 (6q22) Proximal	06Q003B550	RED	50 µL	2 x
ROS1 (6q22) Distal-SV	06Q005B550	RED	50 µL	2 x
SE 7 (D7Z1)	07C001B495	GREEN	50 µL	2 x
SE 7 (D7Z1)	07C001C495	GREEN	33 µL	3 x
SE 7 (D7Z1)-002	07C002B495	GREEN	50 µL	2 x
EGFR (7p11)	07P001B550	RED	50 µL	2 x
EGFR (7p11)	07P001C495	GREEN	33 µL	3 x
MET (7q31)	07Q001B550	RED	50 µL	2 x
SE 8 (D8Z1)	08C001B495	GREEN	50 µL	2 x
SE 8 (D8Z1)-002	08C002B495	GREEN	50 µL	2 x

Product Name	Product Code	Color	Content	CONC
FGFR1 (8p11) Proximal	08P001B495	GREEN	50 µL	2 x
FGFR1 (8p11) Distal	08P002B550	RED	50 µL	2 x
FGFR1 (8p11)	08P003B550	RED	50 µL	2 x
JAK2 (9p24) Proximal	09P003B495	GREEN	50 µL	2 x
JAK2 (9p24) Distal	09P004B550	RED	50 µL	2 x
ABL1 (9q34)	09Q001C415	BLUE	33 µL	3 x
SE 10 (D10Z1)	10C001B495	GREEN	50 µL	2 x
SE 10 (D10Z1)	10C001N495	GREEN	50 µL	10 x
RET (10q11) Distal	10Q001B495	GREEN	50 µL	2 x
RET (10q11) Proximal	10Q002B550	RED	50 µL	2 x
PTEN (10q23)	10Q006B550	RED	50 µL	2 x
FGFR2 (10q26)	10Q003B550	RED	50 µL	2 x
CCND1 (11q13)	11Q002B495	GREEN	50 µL	2 x
CCND1 (11q13)	11Q002I495	GREEN	250 µL	2 x
ATM (11q22)	11Q001B495	GREEN	50 µL	2 x
ATM (11q22)	11Q001I495	GREEN	250 µL	2 x
SE 12 (D12Z3)	12C001C495	GREEN	33 µL	3 x
SE 12 (D12Z3)	12C001J495	GREEN	167 µL	3 x
DLEU1 (13q14)	13Q001B550	RED	50 µL	2 x
DLEU1 (13q14)	13Q001C415	BLUE	33 µL	3 x
DLEU1 (13q14)	13Q001C550	RED	33 µL	3 x
DLEU1 (13q14)	13Q001I550	RED	250 µL	2 x
DLEU1 (13q14)-SV	13Q003C550	RED	33 µL	3 x
DLEU1 (13q14)-SV	13Q003J550	RED	167 µL	3 x
13q34	13Q002B495	GREEN	50 µL	2 x
13q34	13Q002C415	BLUE	33 µL	3 x
13q34	13Q002C495	GREEN	33 µL	3 x
13q34	13Q002I495	GREEN	250 µL	2 x
13q34	13Q002J415	BLUE	167 µL	3 x
IGH (14q32)	14Q001B550	RED	50 µL	2 x
IGH (14q32)	14Q001I550	RED	250 µL	2 x
IGH (14q32)-002	14Q002B550	RED	50 µL	2 x
MAF (16q23)	16Q001B495	GREEN	50 µL	2 x
MAF (16q23)	16Q001I495	GREEN	250 µL	2 x
TP53 (17p13)	17P001B550	RED	50 µL	2 x
TP53 (17p13)	17P001C550	RED	33 µL	3 x
TP53 (17p13)	17P001I550	RED	250 µL	2 x
TOP2A (17q21)	17Q003B550	RED	50 µL	2 x
MAFB (20q12)	20Q002B495	GREEN	50 µL	2 x
RCAN1 (21q22)	KI-40002	RED	100 µL	RTU
SE X (DXZ1)	23C001B495	GREEN	50 µL	2 x
SE X (DXZ1)	23C002J495	GREEN	167 µL	3 x
CRLF2 (Xp22/Yp11)	23P004C550	RED	33 µL	3 x
CRLF2 (Xp22/Yp11) Distal	23P003C495	GREEN	33 µL	3 x
CRLF2 (Xp22/Yp11) Proximal	23P002C550	RED	33 µL	3 x
SHOX (Xp22)	23P001B550	RED	50 µL	2 x
Acro-P-Arms NOR Blue	KI-20033B	BLUE	20 µL	5x
Acro-P-Arms NOR Green	KI-20033G	GREEN	20 µL	5x
Acro-P-Arms NOR Red	KI-20033R	RED	20 µL	5x

* Analyte Specific Reagents - Analytical and performance characteristics are not established.
Products in this catalog are subject to regulatory approval. Please consult your Leica Biosystems Sales Representative for availability in your region.

Manual Probes - Satellite Enumeration*

Product Name	Product Code	Color	Content	CONC
SE 1 (1qh) Blue	KI-20001B	BLUE	20 µL	5x
SE 1 (1qh) Green	KI-20001G	GREEN	20 µL	5x
SE 1 (1qh) Red	KI-20001R	RED	20 µL	5x
SE 2 (D2Z) Blue	KI-20002B	BLUE	20 µL	5x
SE 2 (D2Z) Green	KI-20002G	GREEN	20 µL	5x
SE 2 (D2Z) Red	KI-20002R	RED	20 µL	5x
SE 3 (D3Z1) Blue	KI-20003B	BLUE	20 µL	5x
SE 3 (D3Z1) Green	KI-20003G	GREEN	20 µL	5x
SE 3 (D3Z1) Red	KI-20003R	RED	20 µL	5x
SE 4 (D4Z1) Blue	KI-20004B	BLUE	20 µL	5x
SE 4 (D4Z1) Green	KI-20004G	GREEN	20 µL	5x
SE 4 (D4Z1) Red	KI-20004R	RED	20 µL	5x
SE 6 (D6Z1) Blue	KI-20006B	BLUE	20 µL	5x
SE 6 (D6Z1) Green	KI-20006G	GREEN	20 µL	5x
SE 6 (D6Z1) Red	KI-20006R	RED	20 µL	5x
SE 7 (D7Z1) Blue	KI-20007B	BLUE	20 µL	5x
SE 7 (D7Z1) Green	KI-20007G	GREEN	20 µL	5x
SE 7 (D7Z1) Red	KI-20007R	RED	20 µL	5x
SE 8 (D8Z1) Blue	KI-20008B	BLUE	20 µL	5x
SE 8 (D8Z1) Green	KI-20008G	GREEN	20 µL	5x
SE 8 (D8Z1) Red	KI-20008R	RED	20 µL	5x
SE 9 (classical) Blue	KI-20009B	BLUE	20 µL	5x
SE 9 (classical) Green	KI-20009G	GREEN	20 µL	5x
SE 9 (classical) Red	KI-20009R	RED	20 µL	5x
SE 10 (D10Z1) Blue	KI-20010B	BLUE	20 µL	5x
SE 10 (D10Z1) Green	KI-20010G	GREEN	20 µL	5x
SE 10 (D10Z1) Red	KI-20010R	RED	20 µL	5x
SE 11 (D11Z1) Blue	KI-20011B	BLUE	20 µL	5x
SE 11 (D11Z1) Green	KI-20011G	GREEN	20 µL	5x
SE 11 (D11Z1) Red	KI-20011R	RED	20 µL	5x
SE 12 (D12Z3) Blue	KI-20012B	BLUE	20 µL	5x
SE 12 (D12Z3) Green	KI-20012G	GREEN	20 µL	5x
SE 12 (D12Z3) Red	KI-20012R	RED	20 µL	5x

Product Name	Product Code	Color	Content	CONC
SE 15 (D15Z) Blue	KI-20015B	BLUE	20 µL	5x
SE 15 (D15Z) Green	KI-20015G	GREEN	20 µL	5x
SE 15 (D15Z) Red	KI-20015R	RED	20 µL	5x
SE 16 (D16Z2) Blue	KI-20016B	BLUE	20 µL	5x
SE 16 (D16Z2) Green	KI-20016G	GREEN	20 µL	5x
SE 16 (D16Z2) Red	KI-20016R	RED	20 µL	5x
SE 17 (D17Z1) Blue	KI-20017B	BLUE	20 µL	5x
SE 17 (D17Z1) Green	KI-20017G	GREEN	20 µL	5x
SE 17 (D17Z1) Red	KI-20017R	RED	20 µL	5x
SE 18 (D18Z1) Blue	KI-20018B	BLUE	20 µL	5x
SE 18 (D18Z1) Green	KI-20018G	GREEN	20 µL	5x
SE 18 (D18Z1) Red	KI-20018R	RED	20 µL	5x
SE 20 (D20Z1) Blue	KI-20020B	BLUE	20 µL	5x
SE 20 (D20Z1) Green	KI-20020G	GREEN	20 µL	5x
SE 20 (D20Z1) Red	KI-20020R	RED	20 µL	5x
SE X (DXZ1) Blue	KI-20023B	BLUE	20 µL	5x
SE X (DXZ1) Green	KI-20023G	GREEN	20 µL	5x
SE X (DXZ1) Red	KI-20023R	RED	20 µL	5x
SE Y (DYZ3) Blue	KI-20024B	BLUE	20 µL	5x
SE Y (DYZ3) Green	KI-20024G	GREEN	20 µL	5x
SE Y (DYZ3) Red	KI-20024R	RED	20 µL	5x
SE Y class. q arm Blue	KI-20025B	BLUE	20 µL	5x
SE Y class. q arm Green	KI-20025G	GREEN	20 µL	5x
SE Y class. q arm Red	KI-20025R	RED	20 µL	5x
SE 1/5/19 Blue	KI-20026B	BLUE	20 µL	5x
SE 1/5/19 Green	KI-20026G	GREEN	20 µL	5x
SE 1/5/19 Red	KI-20026R	RED	20 µL	5x
SE 13/21 Blue	KI-20027B	BLUE	20 µL	5x
SE 13/21 Green	KI-20027G	GREEN	20 µL	5x
SE 13/21 Red	KI-20027R	RED	20 µL	5x
SE 14/22 Blue	KI-20028B	BLUE	20 µL	5x
SE 14/22 Green	KI-20028G	GREEN	20 µL	5x
SE 14/22 Red	KI-20028R	RED	20 µL	5x

Manual Probes - Sub Telomeric*

Product Name	Product Code	Color	Content	CONC
Sub Telomere 1pter Blue	KI-40201B	BLUE	10 µL	5x
Sub Telomere 1pter Green	KI-40201G	GREEN	10 µL	5x
Sub Telomere 1pter Red	KI-40201R	RED	10 µL	5x
Sub Telomere 1qter Blue	KI-40202B	BLUE	10 µL	5x
Sub Telomere 1qter Green	KI-40202G	GREEN	10 µL	5x
Sub Telomere 1qter Red	KI-40202R	RED	10 µL	5x
Sub Telomere 2pter Blue	KI-40203B	BLUE	10 µL	5x
Sub Telomere 2pter Green	KI-40203G	GREEN	10 µL	5x
Sub Telomere 2pter Red	KI-40203R	RED	10 µL	5x
Sub Telomere 2qter Blue	KI-40204B	BLUE	10 µL	5x
Sub Telomere 2qter Green	KI-40204G	GREEN	10 µL	5x
Sub Telomere 2qter Red	KI-40204R	RED	10 µL	5x
Sub Telomere 3pter Blue	KI-40205B	BLUE	10 µL	5x

Product Name	Product Code	Color	Content	CONC
Sub Telomere 3pter Green	KI-40205G	GREEN	10 µL	5x
Sub Telomere 3pter Red	KI-40205R	RED	10 µL	5x
Sub Telomere 3qter Blue	KI-40206B	BLUE	10 µL	5x
Sub Telomere 3qter Green	KI-40206G	GREEN	10 µL	5x
Sub Telomere 3qter Red	KI-40206R	RED	10 µL	5x
Sub Telomere 4pter Blue	KI-40207B	BLUE	10 µL	5x
Sub Telomere 4pter Green	KI-40207G	GREEN	10 µL	5x
Sub Telomere 4pter Red	KI-40207R	RED	10 µL	5x
Sub Telomere 4qter Blue	KI-40208B	BLUE	10 µL	5x
Sub Telomere 4qter Green	KI-40208G	GREEN	10 µL	5x
Sub Telomere 4qter Red	KI-40208R	RED	10 µL	5x
Sub Telomere 5pter Blue	KI-40209B	BLUE	10 µL	5x
Sub Telomere 5pter Green	KI-40209G	GREEN	10 µL	5x

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

Manual Probes - Sub Telomeric* (continued)

Product Name	Product Code	Color	Content	CONC
Sub Telomere 5pter Red	KI-40209R	RED	10 µL	5x
Sub Telomere 5qter Blue	KI-40210B	BLUE	10 µL	5x
Sub Telomere 5qter Green	KI-40210G	GREEN	10 µL	5x
Sub Telomere 5qter Red	KI-40210R	RED	10 µL	5x
Sub Telomere 6pter Blue	KI-40211B	BLUE	10 µL	5x
Sub Telomere 6pter Green	KI-40211G	GREEN	10 µL	5x
Sub Telomere 6pter Red	KI-40211R	RED	10 µL	5x
Sub Telomere 6qter Blue	KI-40212B	BLUE	10 µL	5x
Sub Telomere 6qter Green	KI-40212G	GREEN	10 µL	5x
Sub Telomere 6qter Red	KI-40212R	RED	10 µL	5x
Sub Telomere 7pter Blue	KI-40213B	BLUE	10 µL	5x
Sub Telomere 7pter Green	KI-40213G	GREEN	10 µL	5x
Sub Telomere 7pter Red	KI-40213R	RED	10 µL	5x
Sub Telomere 7qter Blue	KI-40214B	BLUE	10 µL	5x
Sub Telomere 7qter Green	KI-40214G	GREEN	10 µL	5x
Sub Telomere 7qter Red	KI-40214R	RED	10 µL	5x
Sub Telomere 8pter Blue	KI-40215B	BLUE	10 µL	5x
Sub Telomere 8pter Green	KI-40215G	GREEN	10 µL	5x
Sub Telomere 8pter Red	KI-40215R	RED	10 µL	5x
Sub Telomere 8qter Blue	KI-40216B	BLUE	10 µL	5x
Sub Telomere 8qter Green	KI-40216G	GREEN	10 µL	5x
Sub Telomere 8qter Red	KI-40216R	RED	10 µL	5x
Sub Telomere 9pter Blue	KI-40217B	BLUE	10 µL	5x
Sub Telomere 9pter Green	KI-40217G	GREEN	10 µL	5x
Sub Telomere 9pter Red	KI-40217R	RED	10 µL	5x
Sub Telomere 9qter Blue	KI-40218B	BLUE	10 µL	5x
Sub Telomere 9qter Green	KI-40218G	GREEN	10 µL	5x
Sub Telomere 9qter Red	KI-40218R	RED	10 µL	5x
Sub Telomere 10pter Blue	KI-40219B	BLUE	10 µL	5x
Sub Telomere 10pter Green	KI-40219G	GREEN	10 µL	5x
Sub Telomere 10pter Red	KI-40219R	RED	10 µL	5x
Sub Telomere 10qter Blue	KI-40220B	BLUE	10 µL	5x
Sub Telomere 10qter Green	KI-40220G	GREEN	10 µL	5x
Sub Telomere 10qter Red	KI-40220R	RED	10 µL	5x
Sub Telomere 11pter Blue	KI-40221B	BLUE	10 µL	5x
Sub Telomere 11pter Green	KI-40221G	GREEN	10 µL	5x
Sub Telomere 11pter Red	KI-40221R	RED	10 µL	5x
Sub Telomere 11qter Blue	KI-40222B	BLUE	10 µL	5x
Sub Telomere 11qter Green	KI-40222G	GREEN	10 µL	5x
Sub Telomere 11qter Red	KI-40222R	RED	10 µL	5x
Sub Telomere 12pter Blue	KI-40223B	BLUE	10 µL	5x
Sub Telomere 12pter Green	KI-40223G	GREEN	10 µL	5x
Sub Telomere 12pter Red	KI-40223R	RED	10 µL	5x
Sub Telomere 12qter Blue	KI-40224B	BLUE	10 µL	5x
Sub Telomere 12qter Green	KI-40224G	GREEN	10 µL	5x
Sub Telomere 12qter Red	KI-40224R	RED	10 µL	5x
Sub Telomere 13qter Blue	KI-40225B	BLUE	10 µL	5x
Sub Telomere 13qter Green	KI-40225G	GREEN	10 µL	5x
Sub Telomere 13qter Red	KI-40225R	RED	10 µL	5x

Product Name	Product Code	Color	Content	CONC
Sub Telomere 14qter Blue	KI-40226B	BLUE	10 µL	5x
Sub Telomere 14qter Green	KI-40226G	GREEN	10 µL	5x
Sub Telomere 14qter Red	KI-40226R	RED	10 µL	5x
Sub Telomere 15qter Blue	KI-40227B	BLUE	10 µL	5x
Sub Telomere 15qter Green	KI-40227G	GREEN	10 µL	5x
Sub Telomere 15qter Red	KI-40227R	RED	10 µL	5x
Sub Telomere 16pter Blue	KI-40228B	BLUE	10 µL	5x
Sub Telomere 16pter Green	KI-40228G	GREEN	10 µL	5x
Sub Telomere 16pter Red	KI-40228R	RED	10 µL	5x
Sub Telomere 16qter Blue	KI-40229B	BLUE	10 µL	5x
Sub Telomere 16qter Green	KI-40229G	GREEN	10 µL	5x
Sub Telomere 16qter Red	KI-40229R	RED	10 µL	5x
Sub Telomere 17pter Blue	KI-40230B	BLUE	10 µL	5x
Sub Telomere 17pter Green	KI-40230G	GREEN	10 µL	5x
Sub Telomere 17pter Red	KI-40230R	RED	10 µL	5x
Sub Telomere 17qter Blue	KI-40231B	BLUE	10 µL	5x
Sub Telomere 17qter Green	KI-40231G	GREEN	10 µL	5x
Sub Telomere 17qter Red	KI-40231R	RED	10 µL	5x
Sub Telomere 18pter Blue	KI-40232B	BLUE	10 µL	5x
Sub Telomere 18pter Green	KI-40232G	GREEN	10 µL	5x
Sub Telomere 18pter Red	KI-40232R	RED	10 µL	5x
Sub Telomere 18qter Blue	KI-40233B	BLUE	10 µL	5x
Sub Telomere 18qter Green	KI-40233G	GREEN	10 µL	5x
Sub Telomere 18qter Red	KI-40233R	RED	10 µL	5x
Sub Telomere 19pter Blue	KI-40234B	BLUE	10 µL	5x
Sub Telomere 19pter Green	KI-40234G	GREEN	10 µL	5x
Sub Telomere 19pter Red	KI-40234R	RED	10 µL	5x
Sub Telomere 19qter Blue	KI-40235B	BLUE	10 µL	5x
Sub Telomere 19qter Green	KI-40235G	GREEN	10 µL	5x
Sub Telomere 19qter Red	KI-40235R	RED	10 µL	5x
Sub Telomere 20pter Blue	KI-40236B	BLUE	10 µL	5x
Sub Telomere 20pter Green	KI-40236G	GREEN	10 µL	5x
Sub Telomere 20pter Red	KI-40236R	RED	10 µL	5x
Sub Telomere 20qter Blue	KI-40237B	BLUE	10 µL	5x
Sub Telomere 20qter Green	KI-40237G	GREEN	10 µL	5x
Sub Telomere 20qter Red	KI-40237R	RED	10 µL	5x
Sub Telomere 21qter Blue	KI-40238B	BLUE	10 µL	5x
Sub Telomere 21qter Green	KI-40238G	GREEN	10 µL	5x
Sub Telomere 21qter Red	KI-40238R	RED	10 µL	5x
Sub Telomere 22qter Blue	KI-40239B	BLUE	10 µL	5x
Sub Telomere 22qter Green	KI-40239G	GREEN	10 µL	5x
Sub Telomere 22qter Red	KI-40239R	RED	10 µL	5x
Sub Telomere XYpter Blue	KI-40240B	BLUE	10 µL	5x
Sub Telomere XYpter Green	KI-40240G	GREEN	10 µL	5x
Sub Telomere XYpter Red	KI-40240R	RED	10 µL	5x
Sub Telomere XYqter Blue	KI-40241B	BLUE	10 µL	5x
Sub Telomere XYqter Green	KI-40241G	GREEN	10 µL	5x
Sub Telomere XYqter Red	KI-40241R	RED	10 µL	5x

* Analyte Specific Reagents - Analytical and performance characteristics are not established.
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Manual Probes - Whole Chromosome*

Product Name	Product Code	Color	Content	CONC
Whole Chromosome 1 Blue	KI-30001B	BLUE	10 µL	5x
Whole Chromosome 1 Green	KI-30001G	GREEN	10 µL	5x
Whole Chromosome 1 Red	KI-30001R	RED	10 µL	5x
Whole Chromosome 2 Blue	KI-30002B	BLUE	10 µL	5x
Whole Chromosome 2 Green	KI-30002G	GREEN	10 µL	5x
Whole Chromosome 2 Red	KI-30002R	RED	10 µL	5x
Whole Chromosome 3 Blue	KI-30003B	BLUE	10 µL	5x
Whole Chromosome 3 Green	KI-30003G	GREEN	10 µL	5x
Whole Chromosome 3 Red	KI-30003R	RED	10 µL	5x
Whole Chromosome 4 Blue	KI-30004B	BLUE	10 µL	5x
Whole Chromosome 4 Green	KI-30004G	GREEN	10 µL	5x
Whole Chromosome 4 Red	KI-30004R	RED	10 µL	5x
Whole Chromosome 5 Blue	KI-30005B	BLUE	10 µL	5x
Whole Chromosome 5 Green	KI-30005G	GREEN	10 µL	5x
Whole Chromosome 5 Red	KI-30005R	RED	10 µL	5x
Whole Chromosome 6 Blue	KI-30006B	BLUE	10 µL	5x
Whole Chromosome 6 Green	KI-30006G	GREEN	10 µL	5x
Whole Chromosome 6 Red	KI-30006R	RED	10 µL	5x
Whole Chromosome 7 Blue	KI-30007B	BLUE	10 µL	5x
Whole Chromosome 7 Green	KI-30007G	GREEN	10 µL	5x
Whole Chromosome 7 Red	KI-30007R	RED	10 µL	5x
Whole Chromosome 8 Blue	KI-30008B	BLUE	10 µL	5x
Whole Chromosome 8 Green	KI-30008G	GREEN	10 µL	5x
Whole Chromosome 8 Red	KI-30008R	RED	10 µL	5x
Whole Chromosome 9 Blue	KI-30009B	BLUE	10 µL	5x
Whole Chromosome 9 Green	KI-30009G	GREEN	10 µL	5x
Whole Chromosome 9 Red	KI-30009R	RED	10 µL	5x
Whole Chromosome 10 Blue	KI-30010B	BLUE	10 µL	5x
Whole Chromosome 10 Green	KI-30010G	GREEN	10 µL	5x
Whole Chromosome 10 Red	KI-30010R	RED	10 µL	5x
Whole Chromosome 11 Blue	KI-30011B	BLUE	10 µL	5x
Whole Chromosome 11 Green	KI-30011G	GREEN	10 µL	5x
Whole Chromosome 11 Red	KI-30011R	RED	10 µL	5x
Whole Chromosome 12 Blue	KI-30012B	BLUE	10 µL	5x
Whole Chromosome 12 Green	KI-30012G	GREEN	10 µL	5x
Whole Chromosome 12 Red	KI-30012R	RED	10 µL	5x

Product Name	Product Code	Color	Content	CONC
Whole Chromosome 13 Blue	KI-30013B	BLUE	10 µL	5x
Whole Chromosome 13 Green	KI-30013G	GREEN	10 µL	5x
Whole Chromosome 13 Red	KI-30013R	RED	10 µL	5x
Whole Chromosome 14 Blue	KI-30014B	BLUE	10 µL	5x
Whole Chromosome 14 Green	KI-30014G	GREEN	10 µL	5x
Whole Chromosome 14 Red	KI-30014R	RED	10 µL	5x
Whole Chromosome 15 Blue	KI-30015B	BLUE	10 µL	5x
Whole Chromosome 15 Green	KI-30015G	GREEN	10 µL	5x
Whole Chromosome 15 Red	KI-30015R	RED	10 µL	5x
Whole Chromosome 16 Blue	KI-30016B	BLUE	10 µL	5x
Whole Chromosome 16 Green	KI-30016G	GREEN	10 µL	5x
Whole Chromosome 16 Red	KI-30016R	RED	10 µL	5x
Whole Chromosome 17 Blue	KI-30017B	BLUE	10 µL	5x
Whole Chromosome 17 Green	KI-30017G	GREEN	10 µL	5x
Whole Chromosome 17 Red	KI-30017R	RED	10 µL	5x
Whole Chromosome 18 Blue	KI-30018B	BLUE	10 µL	5x
Whole Chromosome 18 Green	KI-30018G	GREEN	10 µL	5x
Whole Chromosome 18 Red	KI-30018R	RED	10 µL	5x
Whole Chromosome 19 Blue	KI-30019B	BLUE	10 µL	5x
Whole Chromosome 19 Green	KI-30019G	GREEN	10 µL	5x
Whole Chromosome 19 Red	KI-30019R	RED	10 µL	5x
Whole Chromosome 20 Blue	KI-30020B	BLUE	10 µL	5x
Whole Chromosome 20 Green	KI-30020G	GREEN	10 µL	5x
Whole Chromosome 20 Red	KI-30020R	RED	10 µL	5x
Whole Chromosome 21 Blue	KI-30021B	BLUE	10 µL	5x
Whole Chromosome 21 Green	KI-30021G	GREEN	10 µL	5x
Whole Chromosome 21 Red	KI-30021R	RED	10 µL	5x
Whole Chromosome 22 Blue	KI-30022B	BLUE	10 µL	5x
Whole Chromosome 22 Green	KI-30022G	GREEN	10 µL	5x
Whole Chromosome 22 Red	KI-30022R	RED	10 µL	5x
Whole Chromosome X Blue	KI-30023B	BLUE	10 µL	5x
Whole Chromosome X Green	KI-30023G	GREEN	10 µL	5x
Whole Chromosome X Red	KI-30023R	RED	10 µL	5x
Whole Chromosome Y Blue	KI-30024B	BLUE	10 µL	5x
Whole Chromosome Y Green	KI-30024G	GREEN	10 µL	5x
Whole Chromosome Y Red	KI-30024R	RED	10 µL	5x

IVD In Vitro Diagnostic Use **RUO** For Research Use Only. Not for use in diagnostic procedures **ASR** Analyte Specific Reagent **GPR** General Purpose Reagent
F Frozen **P** Paraffin **O** Other Applications **W** Western blotting

RNA Probes*

Product Name	Product Code	Content
EBER Probe	ISH5687-A	7 mL
CMV Probe	ISH5719-A	7 mL
Kappa Probe	ISH5748-A	7 mL
Lambda Probe	ISH5770-A	7 mL
RNA Positive Control Probe	ISH5894-A	7 mL
RNA Negative Control Probe	ISH5950-A	7 mL

ACD RNA Probes*

Product Name	Product Code	Content
CMV Probe	RS7750	14 mL
EBV Probe	RS7751	14 mL
Albumin Probe	RS7752	14 mL
TTF-1 Probe	RS7753	14 mL
Napsin A Probe	RS7754	14 mL
PPIB (Positive Control)	RS7755	14 mL
dapB (Negative Control)	RS7756	14 mL

DNA Probes*

Product Name	Product Code	Content	Concentration
Human Satellite DNA Probe	40V000V000	1 mL	10 x
Human Satellite DNA, Flu labeled	40V000V495	1 mL	10 x
PapV-06, Flu labeled	40V006V495	1 mL	10 x
PapV-11, Flu labeled	40V011V495	1 mL	10 x
PapV-16, Flu labeled	40V016V495	1 mL	10 x
PapV-18, Flu labeled	40V018V495	1 mL	10 x
PapV-31, Flu labeled	40V031V495	1 mL	10 x
PapV-33, Flu labeled	40V033V495	1 mL	10 x

* Analyte Specific Reagents - Analytical and performance characteristics are not established.
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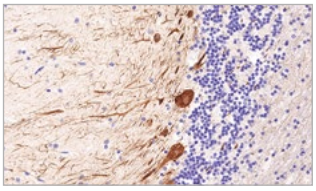

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The EP clones have been created by Epitomics Inc., using Epitomics' proprietary rabbit monoclonal antibody technology covered under Patent No.'s 5, 675, 063 and 7, 402, 409.

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