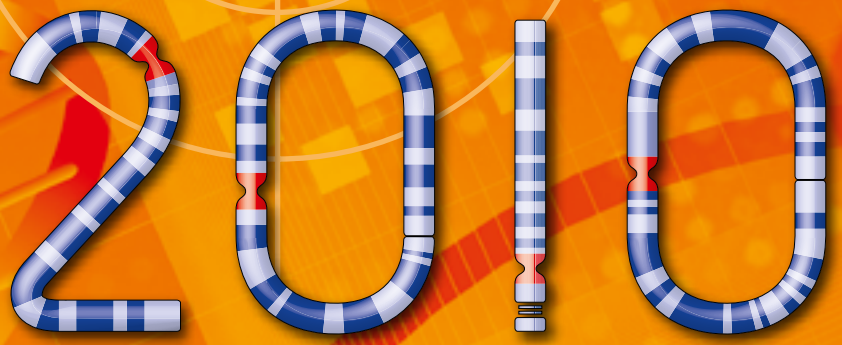
KREATECH DIAGNOSTICS PRODUCT GUIDE



KREATECH DIAGNOSTICS

INTRODUCTION

DEAR VALUED CUSTOMER

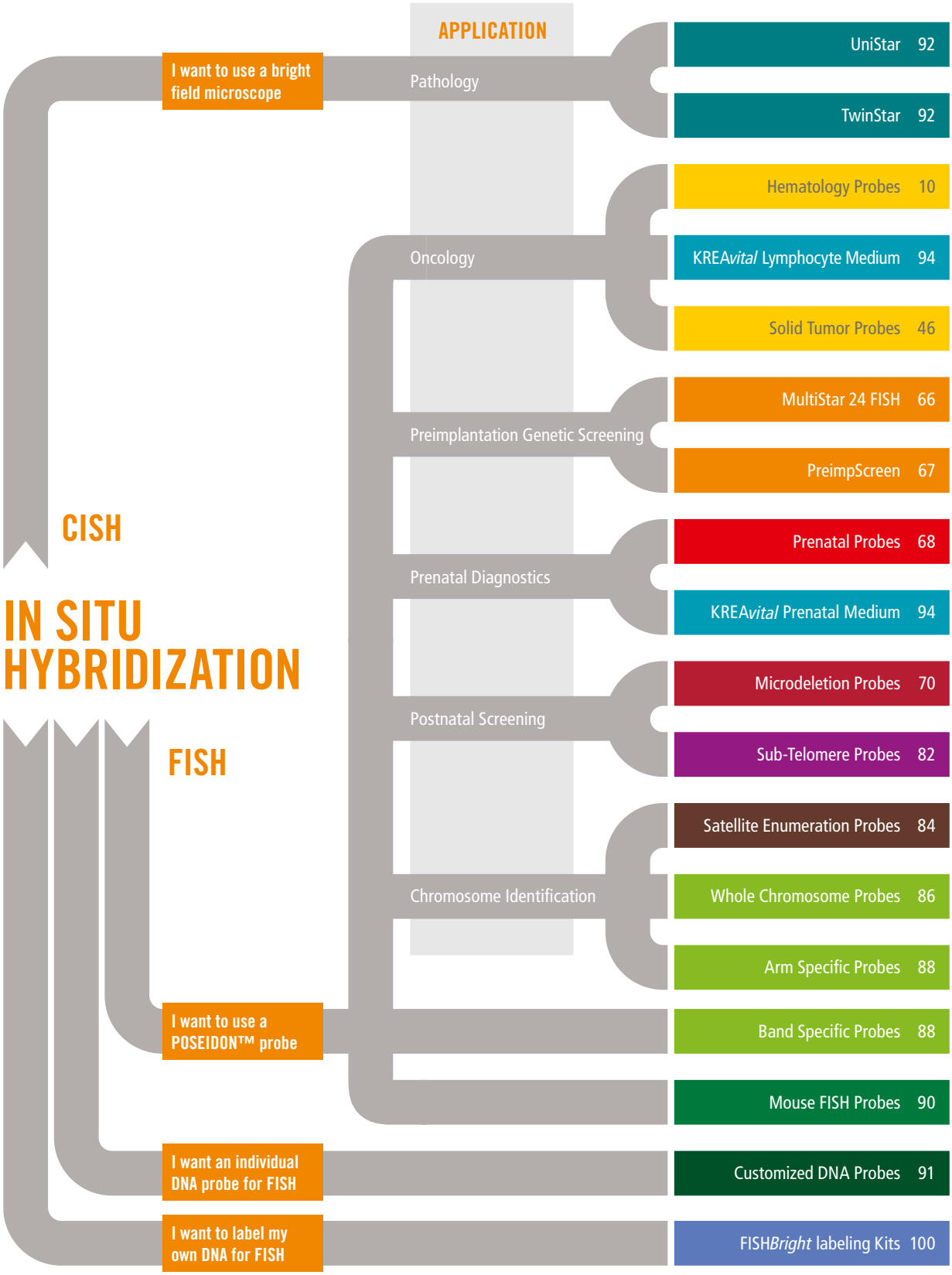
Welcome to our new Product Guide 2010 ! This catalog includes a lot of new products which we have added into our portfolio throughout last year and we would like to specifically highlight the following sections:

- Our new line of CISH products (page 92)
- New multicolor probe panels for preimplantation genetic screening (page 66)
- Our unique target labeling products based on ULS™
- And many new FISH probes, e.g. for prostate cancer (TMPRSS2-ERG), glioma and sarcoma (CDK-4), our solid tumor probes MDM4, FGFR1, and our new MYC break-apart probe for lymphoma

We hope that you will find a lot of products in this catalog suitable for your daily research. If you have any additional questions do not hesitate to contact us or visit www.kreatech.com to find the most up-to-date information about our products.

Kreatech Diagnostics

PRODUCT SELECTION GUIDE



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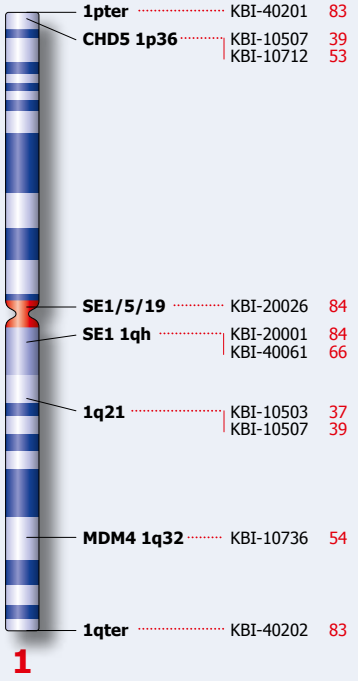
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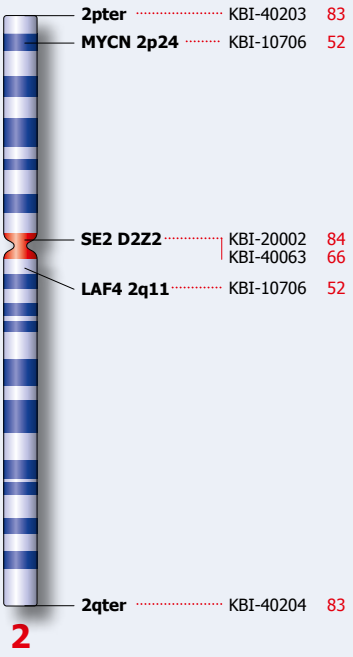
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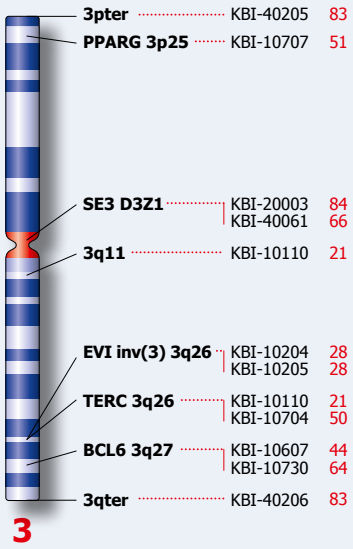
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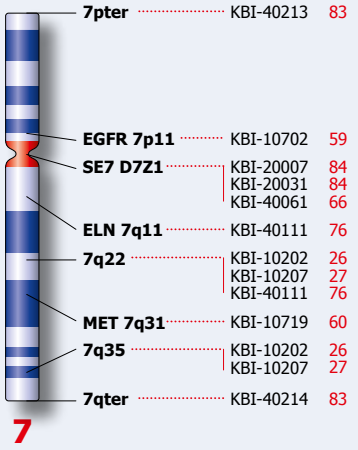
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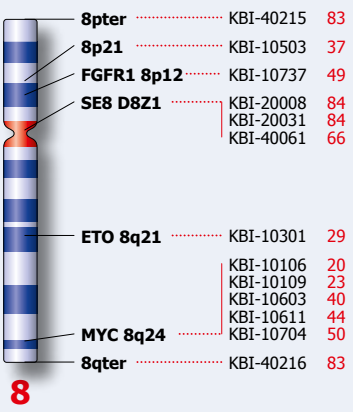
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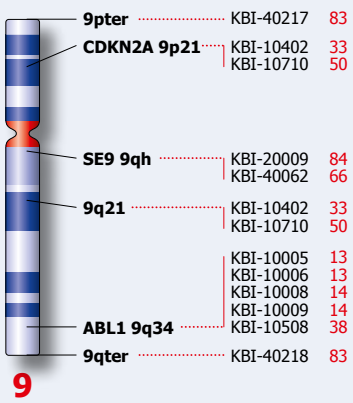
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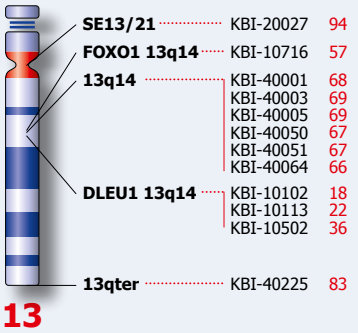
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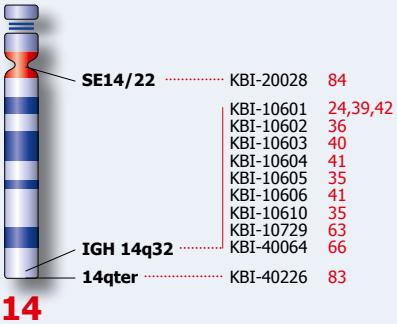
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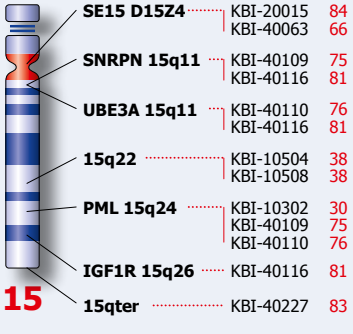
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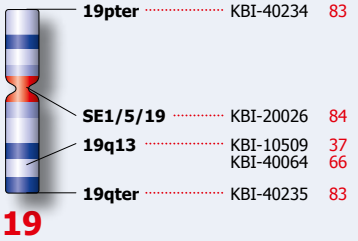
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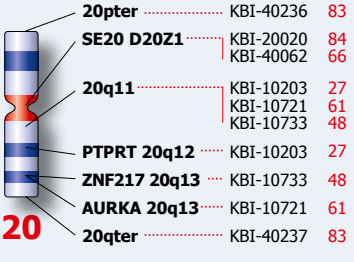
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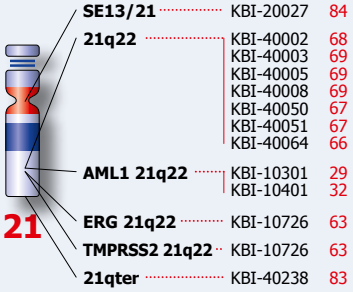
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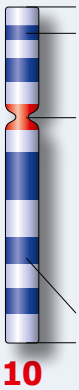

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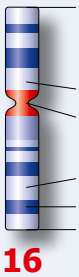

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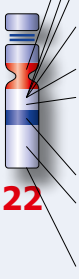

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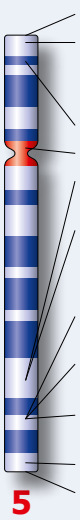

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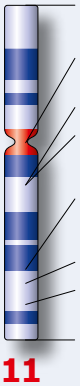

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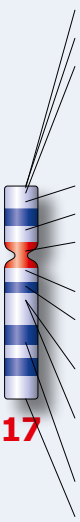

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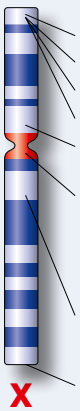

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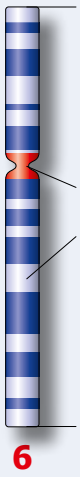

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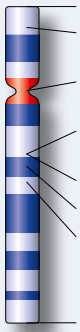

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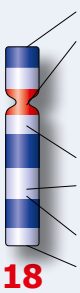

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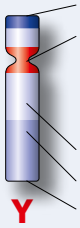

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HUGO GENE SYMBOLS

The table below gives the approved HUGO Gene Symbol and aliases used for every gene in our Poseidon FISH DNA probes according to the HUGO Gene Nomenclature Committee (HGNC).

Chromosome position	*Genes involved*	*HUGO Gene Symbols*	*Aliases*	*Cat.#*	*Page*
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1q32	MDM4	MDM4	MDMX	KBI-10736	54
1q21	S100A10	S100A10	P11, 42C, CLP11	KBI-10503 KBI-10507	37 39
2p24	MYCN	MYCN	bHLHe37, N-myc	KBI-10706	52
2q11	LAF	AFF3	MLLT2-like, LAF4	KBI-10706	52
3p25	PPARy	PPARG	PPARG1, PPARG2, NR1C3, PPARgamma	KBI-10707	51
3q26	EVI	MECOM	MDS1-EVI1, PRDM3	KBI-10204 KBI-10205	28 28
3q26	hTERC	TERC	TR, hTR, TRC3, SCARNA19	KBI-10110 KBI-10204 KBI-10205 KBI-10704	21 28 28 50
3q27	BCL6	BCL6	ZBTB27, LAZ3, BCL5, BCL6A	KBI-10607 KBI-10730	44 64
4p16	FGFR3	FGFR3	CEK2, JTK4, CD333	KBI-10602	36
4p16	WHSC1	WHSC1	MMSET, NSD2	KBI-40107	78
4q12	CHIC2	CHIC2	BTL	KBI-10003 KBI-10007	16 16
4q12	FIP1L1	FIP1L1	DKFZp586K0717	KBI-10003 KBI-10007	16 16
4q12	PDGFRA	PDGFRA	CD140a, PDGFR2	KBI-10003 KBI-10007	16 16
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5q31	EGR1		TIS8, G0S30, NGFI-A, KROX-24, ZIF-268, AT225, ZNF225	KBI-10208 KBI-10209 KBI-10210 KBI-10709	25 25 26 59
5q33	CSF1R	CSF1R	C-FMS, CSFR, CD115	KBI-10209 KBI-10210	25 26
5q33	PDGFRB	PDGFRB	JTK12, CD140b, PDGFR1	KBI-10004 KBI-40064	17 66
5q33	RPS14	RPS14	EMTB	KBI-10209 KBI-10210	25 26
5q35	NSD1	NSD1	ARA267, FLJ22263, KMT3B	KBI-40113	74
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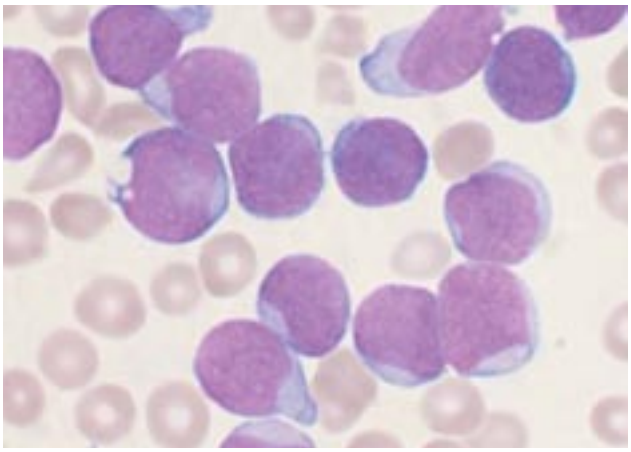
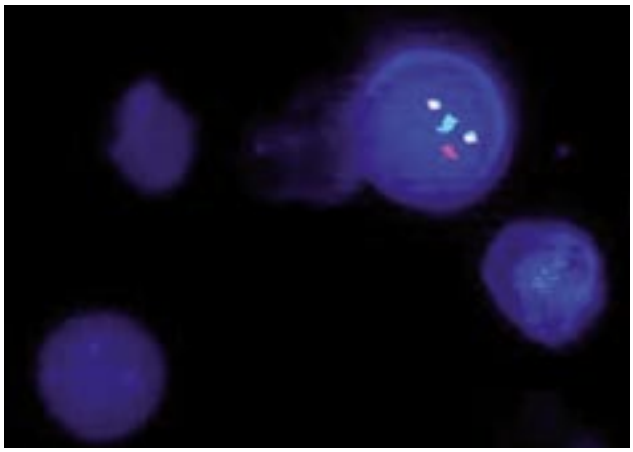
8p12	FGFR1	FGFR1	H2, H3, H4, H5, CEK, FLG, BFGFR, N-SAM, CD331	KBI-10737	49
8q21	ETO	RUNX1T	CDR, ETO, MTG8, ZMYND2	KBI-10301	29
8q24	C-MYC	MYC	c-Myc, bHLHe39	KBI-10106 KBI-10109 KBI-10603 KBI-10611 KBI-10704	20 23 40 44 50
9p21	p16	CDKN2A	CDK4I, p16, INK4a, MTS1, CMM2, ARF, p19, p14, INK4, p16INK4a, p19Arf	KBI-10402 KBI-10710	33 50
9q34	ABL	ABL1	JTK7, c-ABL, p150	KBI-10005 KBI-10006 KBI-10008 KBI-10009 KBI-10508	13 13 14 14 38
9q34	ASS	ASS1	CTLN1	KBI-10508 KBI-10006 KBI-10008 KBI-10009	38 13 14 14
10q23	PTEN	PTEN	MMAC1, TEP1, PTEN1	KBI-10718	60
11q13	BCL1	CCND1	U21B31	KBI-10604	41
11q13	CCND1	CCND1	U21B31	KBI-10604 KBI-10605 KBI-10609 KBI-10734	41 35 43 62
11q13	MYEOV	MYEOV	OCIM	KBI-10605	35
11q22	ATM	ATM	TEL1, TELO1	KBI-10103 KBI-10108 KBI-10114	19 22 23
11q23	MLL	MLL	TRX1, HRX, ALL-1, HTRX1, CXXC7, MLL1A, KMT2A	KBI-10303 KBI-10711	30 53

Chromosome position	Genes involved	HUGO Gene Symbols	Aliases	Cat.#	Page
11q23	PLZF	ZBTB16	PLZF	KBI-10502	36
12p13	TEL	ETV6		KBI-10401	32
				KBI-10403	33
12q13	CDK4	CDK4	PSK-J3	KBI-10725	58
12q13	CHOP	DDIT3	CHOP10, GADD153, CHOP	KBI-10714	56
12q13	GLI	GLI1		KBI-10104	21
				KBI-10108	22
12q15	MDM2	MDM2	HDM2, HDMX, MGC5370	KBI-10717	58
13q14	DLEU	DLEU1	LEU1, XTP6, NCRNA00021	KBI-10102	18
				KBI-10113	22
				KBI-10502	36
13q14	FKHR	FOXO1	FKH1	KBI-10716	57
14q32	IGH	IGH@	IGHDY1, IGH	KBI-10601	24,39,42
				KBI-10602	36
				KBI-10603	40
				KBI-10604	41
				KBI-10605	35
				KBI-10606	41
				KBI-10610	35
				KBI-10729	63
15q11	SNRPN	SNRPN	SMN, SM-D, HCERN3, SNRNP-N, SNURF-SNRPN, RT-LI	KBI-40109	75
15q11	UBE3A	UBE3A	AS, ANCR, E6-AP, FLJ26981	KBI-40110	76
				KBI-40116	81
15q22	SMAD6	SMAD6	HsT17432	KBI-10504	38
				KBI-10508	38
15q24	PML	PML	MYL, TRIM19, RNF71	KBI-10302	30
				KBI-40109	75
				KBI-40110	76
15q26	IGF1R	IGF1R	JTK13, CD221, IGFIR, MGC18216, IGFR	KBI-40116	81
16p11	FUS	FUS	TLS, FUS1, hnRNP-P2	KBI-10715	57
16q22	CBFB	CBFB	PEBP2B	KBI-10304	31
16q23	MAF	MAF	c-MAF	KBI-10610	35
17p13	AURKB	AURKB	Aik2, IPL1, AurB, AIM-1, ARK2, STK5	KBI-10722	61
17p13	LIS	PAFAH1B1	LIS1, PAFAH	KBI-40101	77
17p13	p53	TP53	p53, LFS1	KBI-10011	15
				KBI-10112	19
				KBI-10113	22
				KBI-10114	23
				KBI-10509	37
				KBI-10738	65
17p11	RAI1	RAI1	DKFZP434A139, SMCR, SMS, KIAA1820, MGC12824	KBI-40101	77
17q11	NF1	NF1		KBI-40114	74
17q12	ERBB2	ERBB2	NEU, HER-2, CD340, HER2	KBI-10701	47
				KBI-10735	48
17q21	RARA	RARA	RAR, NR1B1	KBI-10302	30
				KBI-10305	31
17q21	TOP2A	TOP2A		KBI-10724	47
				KBI-10735	48
17q22	MPO	MPO		KBI-10011	15
				KBI-40114	74
18q11	SYT	SS18	SYT	KBI-10713	56
18q21	BCL2	BCL2	Bcl-2	KBI-10606	41
18q21	MALT	MALT1		KBI-10608	42
				KBI-10731	64
19q13	CD37	CD37	TSPAN26	KBI-10509	37
				KBI-40064	66
20q11	MAPRE1	MAPRE1	EB1	KBI-10203	27
				KBI-10721	61
				KBI-10733	48
20q12	PTPRT	PTPRT	RPTPrho, KIAA0283	KBI-10203	27
20q13	AURKA	AURKA	BTAK, AurA, STK7, ARK1	KBI-10721	61
20q13	ZNF217	ZNF217	ZABC1	KBI-10733	48
21q22	AML	RUNX1	PEBP2A2, AMLCR1	KBI-10301	29
21q22	ERG	ERG	erg-3, p55	KBI-10726	63
21q22	TMPRSS2	TMPRSS2	PRSS10	KBI-10726	63
22q11	BCR	BCR	D22S662, CML, PHL, ALL	KBI-10005	13
				KBI-10006	13
				KBI-10008	14
				KBI-10009	14
22q11	CLH22	CLTCL1	CLTD, CLH22, CHC22	KBI-40102	71,73
22q11	DGCR2	DGCR2	KIAA0163, LAN, IDD, DGS-C, SEZ-12	KBI-40102	71,73
				KBI-40103	72,73
22q12	EWS	EWSR1	EWS	KBI-10708	55
22q13	SHANK3	SHANK3	SPANK-2, prosap2, KIAA1650, PSAP2	KBI-40102	71,73
				KBI-40103	72,73
				KBI-40104	72,73
Xp22	KAL	KAL1	KALIG-1	KBI-40115	80
Xp22	SHOX	SHOX	PHOG, GCFX, SS, SHOXY	KBI-40112	79
Xp22	STS	STS	ARCS	KBI-40115	80
Xp11	TFE3	TFE3	TFEA, bHLHe33	KBI-10741	65
				KBI-40051	67
Xq13	XIST	XIST	NCRNA00001, DXS1089, swd66	KBI-40108	79

ONCOLOGY PROBES - HEMATOLOGY PROBES





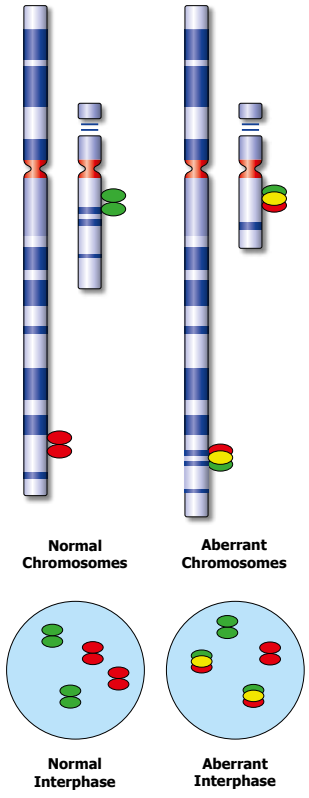
From the 25,000 genes in the human genome, approximately 350 genes have been causally linked to the development of cancer. Variant or aberrant function of these so-called cancer genes may result from changes in genome copy number (through amplification, deletion, chromosome loss, or duplication), changes in gene and chromosome structure (through chromosomal translocation, inversion, or other rearrangements that lead to chimeric transcripts or deregulated gene expression) and point mutations (including base substitutions, deletions, or insertions in coding regions and splice sites). The vast majority (90%) of cancer genes are mutated or altered through chromosomal aberrations in somatic tissue, about 10% are altered in the germ line, thereby transmitting heritable cancer susceptibility through successive generations. In addition to high resolution chromosome banding and advanced chromosomal imaging technologies, chromosome aberrations in cancer cells can be analyzed with an increasing number of large-scale, comprehensive genomic and molecular genetic technologies – including fluorescence *in situ* hybridization (FISH).

Chromosomal translocation (t) is the process by which a break in at least two different chromosomes occurs, with exchange of genetic material between the chromosomes.

Translocation, Dual-Fusion Assay

Dual-fusion, dual-color FISH assays for translocation utilizes large probes that span 2 breakpoints or flanking regions on the different chromosomes. Dual-fusion, dual-color FISH is optimal for detection of low levels of nuclei possessing a simple balanced translocation, as it greatly reduces the number of normal background nuclei with an abnormal signal pattern.

Translocation, Dual-Fusion Assay



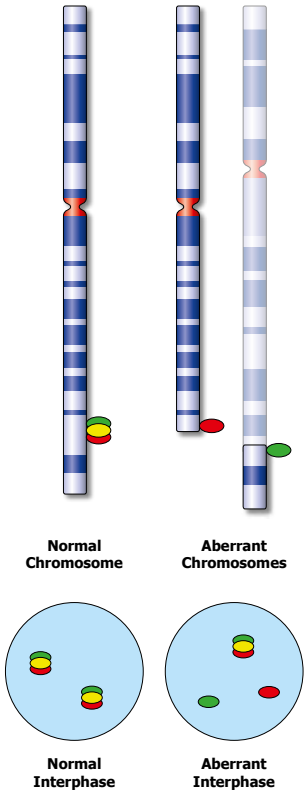
Expected signal pattern:

In normal intact cells, two separate red and two separate green individual signals will be visible, whereas a reciprocal translocation will generate two fused red/green signals (often appearing as single yellow signals), accompanied by one red and one green signal (representing the normal chromosomes).

Translocation, Break-Apart or Split Assay

FISH using dual-color, break-apart probes is very useful in the evaluation of genes known to have multiple translocation partners; the differently colored probes hybridize to targets on opposite sides of the breakpoint of the affected gene.

Translocation, Break or Split Assay



Expected signal pattern:

In normal cells two sets of red/green-fused signals (representing the two alleles) will be visible. In an abnormal diploid cell, in which one allele has been split by a translocation, a separated red and green signal will be visible in addition to the normal fused signal.

Chronic Myeloproliferative Disorders (CMPD)

Chromosomal translocations in chronic myeloproliferative diseases (CMPD) almost invariably result in expression of constitutively activated fusion tyrosine kinases. The hallmark of these diseases is CML, where the BCR/ABL activated tyrosine kinase results from the balanced reciprocal Philadelphia chromosome translocation t(9;22).

Chronic Myelogenous Leukemia (CML) - BCR/ABL t(9;22)

CML is a malignant chronic myeloproliferative disorder (MPD) of the hematopoietic stem cell. All CML have a t(9;22) causing fusion of the 3' ABL region at 9q34 with the 5' BCR region at 22q11. This chimeric BCR/ABL gene encodes a constitutively activated protein tyrosine kinase with profound effects on cell cycle, adhesion, and apoptosis. Understanding this process has led to the development of the drug imatinib mesylate (Gleevec™), the first in a new class of genetically targeted agents, this is a major advance in cancer treatment. Several different approaches are used to analyze the BCR/ABL t(9;22)(q34;q11) by FISH each providing different details about this translocation.

BCR/ABL Product Family

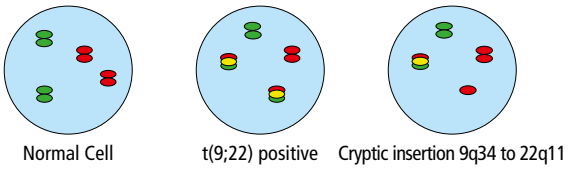
The Philadelphia chromosome is an abnormally short chromosome 22 that is one of the two chromosomes involved in a translocation with chromosome 9. This translocation t(9;22)(q34;q11) takes place in a single bone marrow cell and, through the process of clonal expansion, gives rise to the leukemia.

ABL and BCR are normal genes on chromosomes 9 and 22, respectively. The ABL gene encodes a tyrosine kinase enzyme whose activity is tightly controlled. In the formation of the Ph translocation, two fusion genes are generated: BCR-ABL on the Ph chromosome and ABL-BCR on the chromosome 9 participating in the translocation. The BCR-ABL gene encodes a protein with deregulated tyrosine kinase activity.

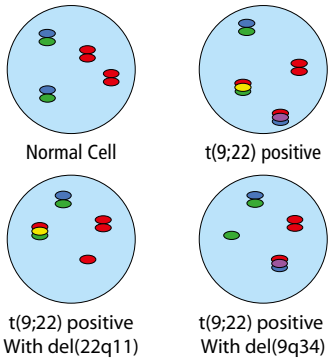
The presence of this protein in the CML cells is strong evidence of its pathogenetic role. The efficacy in CML of a drug that inhibits the BCRABL tyrosine kinase has provided the final proof that the BCR-ABL oncoprotein is the unique cause of CML. The Poseidon portfolio contains now 4 different probes for BCR/ABL to suit all needs for the detection of t(9;22) by FISH:

Interpretation guidelines for Poseidon BCR/ABL Probes

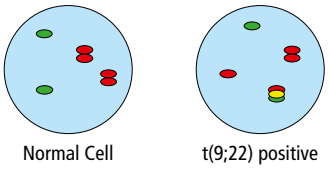
BCR/ABL t(9;22) Dual-color, Dual-Fusion Probe



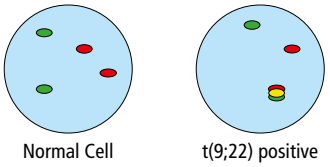
BCR/ABL t(9;22) Triple-color, Dual-Fusion Probe

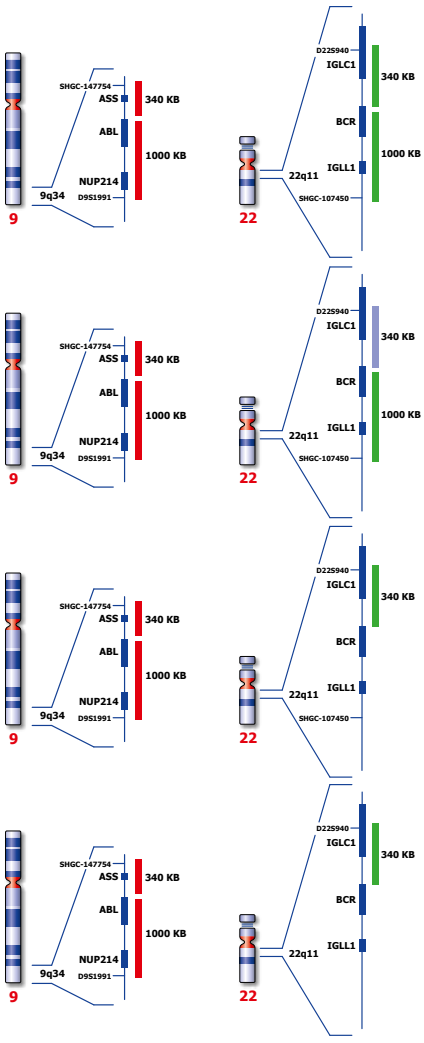


BCR/ABL t(9;22) Dual-color, Single-Fusion Extra Signal Probe



BCR/ABL t(9;22) Dual-color, Single-Fusion Probe



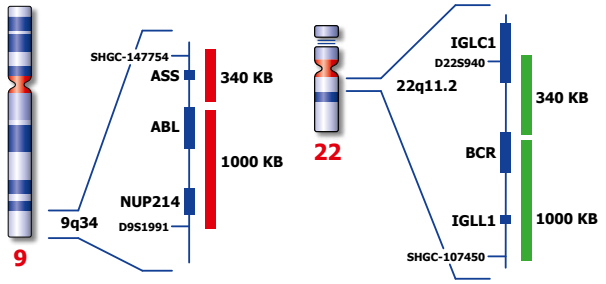


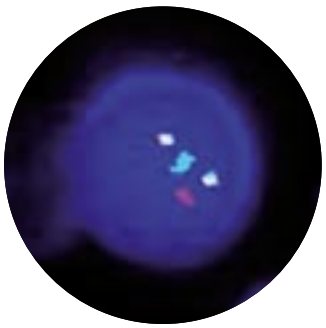
ON BCR/ABL t(9;22), Fusion

The BCR/ABL t(9;22) Fusion 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 ABL into the BCR region not detectable by karyotyping and therefore described as Ph-negative.

Cat.# KBI-10005 BCR/ABL t(9;22), Fusion





BCR/ABL 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

Literature:

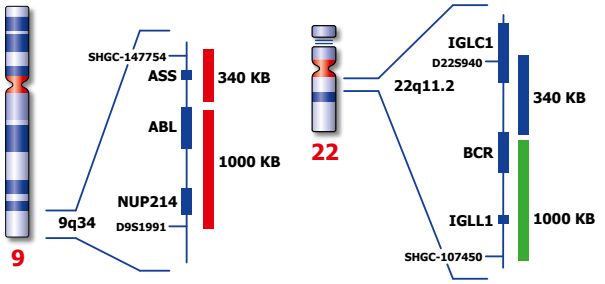
Morris et al, 1990, Blood, 76: 1812-1818.
Dewald et al, 1998, Blood, 91: 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science 250, 559-562

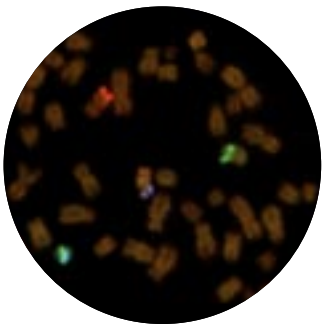
Ordering information	*Color*	*Tests*	*Cat#*
ON BCR/ABL t(9;22) Fusion	red/green	10	KBI-10005
ON BCR/ABL t(9;22) Fusion	red/green	20	KBI-12005

ON BCR/ABL t(9;22), TC, D-Fusion

The BCR/ABL t(9;22), TC, D-Fusion probe is a triple-color, dual-fusion probe build 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.

Cat.# KBI-10006 BCR/ABL t(9;22), TC, D-Fusion





BCR/ABL t(9;22), TC, D-Fusion probe hybridized on patient material showing translocation of distal BCR (1BG1RB1R1G).
Image kindly provided by Prof Siebert, Kiel

Literature:

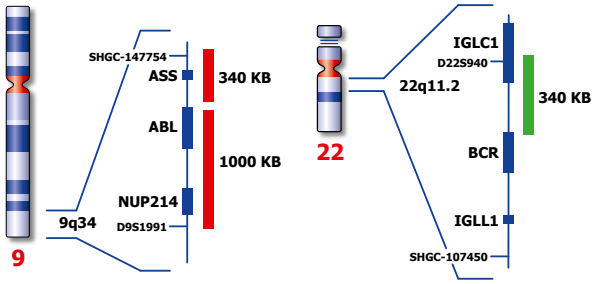
Morris et al, 1990, Blood, 76: 1812-1818.
Dewald et al, 1998, Blood, 91: 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science 250, 559-562

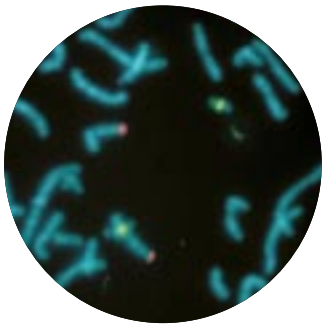
Ordering information	*Color*	*Tests*	*Cat#*
ON BCR/ABL t(9;22) TC, D-Fusion	red/green/blue	10	KBI-10006

ON BCR/ABL t(9;22), DC, S-Fusion, ES

A single-fusion assay is preferably used for the initial screening of CML and ALL patients. By adding an additional region proximal to the breakpoints on chromosome 9q34, this probe will provide an extra signal on the der(9q34) in case of a t(9;22). The Philadelphia chromosome, der(22q), is visualized by the fusion signal.

Cat.# KBI-10008 BCR/ABL t(9;22), Dual-Color, Single-Fusion, Extra Signal





BCR/ABL t(9;22), DC, S-Fusion, ES hybridized to a normal metaphase (2R2G).

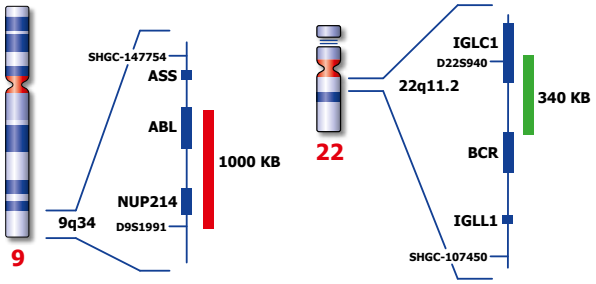
Literature:
Morris et al, 1990, Blood, 76: 1812-1818.
Dewald et al, 1998, Blood, 91: 3357-3365.
Kolomietz et al, 2001, Blood, 97; 3581-3588.
Huntly et al, 2003, Blood, 102; 1160-1168.
Tkachuk et al., 1990, Science 250, 559-562

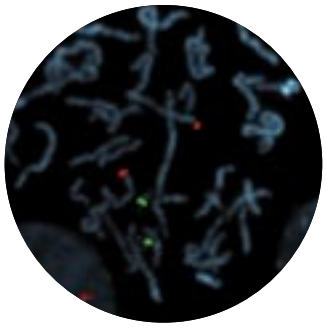
Ordering information	Color	Tests	Cat#
ON BCR/ABL t(9;22) DC, S-Fusion, ES	red/green	10	KBI-10008

ON BCR/ABL t(9;22), DC, S-Fusion

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.

Cat.# KBI-10009 BCR/ABL t(9;22) Dual-Color, Single-Fusion





BCR/ABL t(9;22), DC, S-Fusion hybridized to a normal metaphase (2R2G).

Literature:
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

Ordering information	Color	Tests	Cat#
ON BCR/ABL t(9;22) DC, S-Fusion	red/green	10	KBI-10009

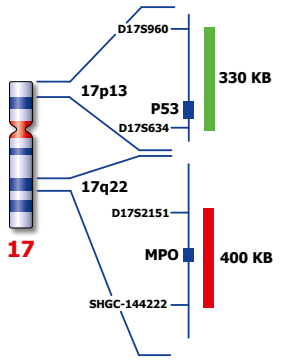
CML secondary chromosomal changes

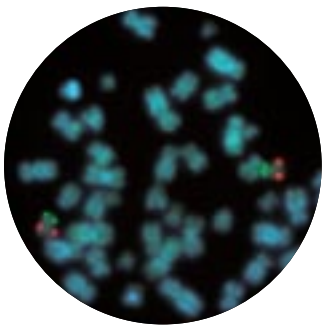
ON p53 (17p13) / MPO (17q22) "ISO 17q"

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 p53 (17p13) / MPO (17q22) "ISO 17q" probe is optimized to detect copy numbers of the p53 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 p53 at 17p13 is expected.

Cat.# KBI-10011 p53 (17p13) / MPO (17q22) "ISO 17q"





p53 (17p13) / MPO (17q22) "ISO 17q" hybridized to a normal metaphase (2R2G).

Literature:

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

Ordering information	*Color*	*Tests*	*Cat#*
ON p53 (17p13) / MPO (17q22) "ISO 17q"	green/red	10	KBI-10011

SE 8 (D8Z1)
SE 7 (D7Z1) / SE 8 (D8Z1)

Gain of chromosome 8 is the most common secondary chromosomal aberration in CML (approx. 34%).

Cat.# KBI-20008 SE 8 (D8Z1)
Cat.# KBI-20031 SE 7 (D7Z1) / SE 8 (D8Z1)

See description under Satellite Enumeration probes on page 84.

Ordering information	*Color*	*Tests*	*Cat#*
SE 8 (D8Z1)	red/green	10	KBI-20008
SE 7 (D7Z1) / SE 8 (D8Z1)	red/green	10	KBI-20031

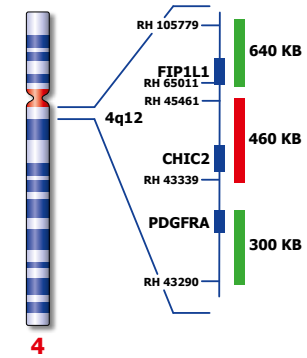
Other Myeloproliferative Diseases:

ON FIP1L1-CHIC2-PDGFRA (4q12) Del, Break

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 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.

Cat.# KBI-10003 FIP1L1-CHIC2-PDGFRA (4q12) Del, Break



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

Literature:

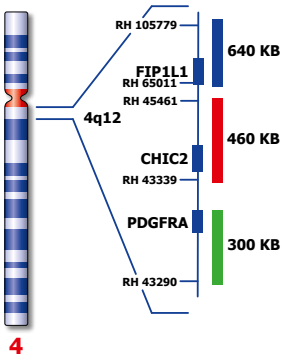
Cools et al, N Engl J Med, 2003, 348, 1201-1214.
Godlib et al, Blood, 2004, 103, 2879-2891.

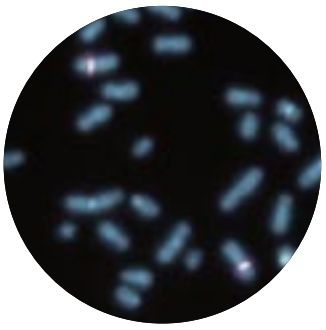
Ordering information	Color	Tests	Cat#
ON FIP1L1-CHIC2-PDGFRA (4q12) Del, Break	red/green	10	KBI-10003

ON FIP1L1-CHIC2-PDGFRA (4q12) Del, Break, TC

The FIP1L1-CHIC2-PDGFRA triple-color 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. The split of the green and blue signal will indicate a translocation at 4q12 independent of a possible chromosome 4 polyploidy.

Cat.# KBI-10007 FIP1L1-CHIC2-PDGFRA (4q12) Del, Break, Triple-Color





FIP1L1-CHIC2-PDGFRA (4q12) Del, Break, TC probe hybridized to a normal metaphase (2BRG).

Literature:

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

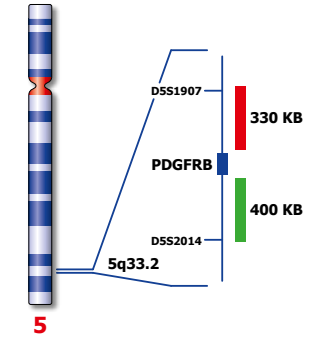
Ordering information	Color	Tests	Cat#
ON FIP1L1-CHIC2-PDGFRA (4q12) Del, Break, TC	red/green/blue	10	KBI-10007

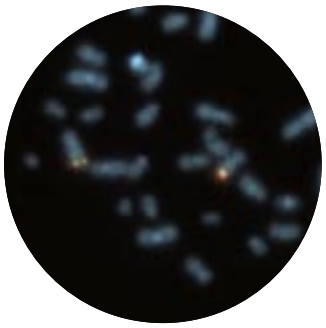
ON PDGFRB (5q33) Break

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 or TEL gene on 12p13, causing a t(5;12) translocation. Cytogenetic responses are achieved with imatinib in patients with PDGFRB fusion positive, BCR/ABL negative CMPDs.

The PDGFRB probe is optimized to detect translocations involving the PDGFRB region at 5q33 in a dual-color, split assay.

Cat.# KBI-10004 PDGFRB (5q33) Break





PDGFRB (5q33) Break probe hybridized to a normal metaphase (2RG).

Literature:

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

Ordering information	*Color*	*Tests*	*Cat#*
ON PDGFRB (5q33) Break	red/green	10	KBI-10004

ON FGFR1 (8p12) Break

FGFR1 has been implicated in the tumorigenesis of haematological malignancies, where it is frequently involved in balanced chromosomal translocations, including cases of chronic myeloid leukaemia (BCR-FGFR1 fusion) and the 8p11 myeloproliferative syndrome/stem cell leukaemia–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.

Cat.# KBI-10737 FGFR1 (8p12) Break

See description under Solid Tumors on page 49.

Ordering information	*Color*	*Tests*	*Cat#*
FGFR1 (8p12) Break	red/green	10	KBI-10737

Chronic Lymphocytic Leukemia (CLL)

CLL accounts for about 30% of all leukemias in Europe and the USA. Distinct clonal chromosomal abnormalities can be identified in up to 90% of CLL cases of the B-cell lineage. By FISH the most common chromosomal changes in CLL and their frequencies have been identified as shown in the table below.

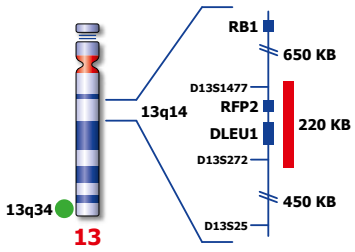
Del(13q14)	55%
Del(11q)	18%
Trisomy 12q	16%
Del(17p)	7%
Del(6q)	6%
Trisomy 8q	5%
t(14q32)	4%
Trisomy 3q	3%

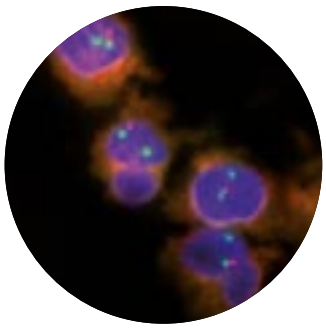
ON DLEU (13q14) / 13qter

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

Cat.# KBI-10102 DLEU (13q14) / 13qter





DLEU (13q14) / 13qter probe hybridized to patient material showing a 13q14 deletion (1R2G).
Image kindly provided by Dr. Dastugue, Toulouse

Literature:

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

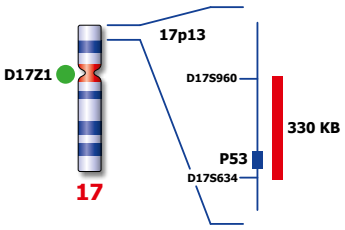
Ordering information	*Color*	*Tests*	*Cat#*
ON DLEU (13q14) / 13qter	red/green	10	KBI-10102

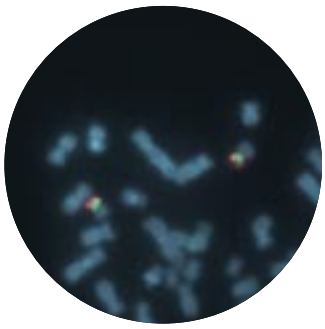
ON p53 (17p13) / SE 17

The p53 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 p53 have been reported in numerous tumor types and are associated with poor prognosis in CLL.

The p53 (17p13) specific DNA probe is optimized to detect copy numbers of the p53 gene region at 17p13. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification.

Cat.# KBI-10112 p53 (17p13) / SE 17





p53 (17p13) / SE 17 probe hybridized to a normal metaphase (2R2G).

Literature:

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

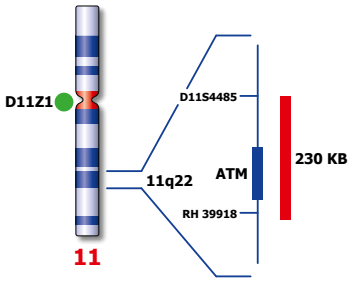
Ordering information	Color	Tests	Cat#
ON p53 (17p13) / SE 17	red/green	10	KBI-10112
ON p53 (17p13) / SE 17	red/green	20	KBI-12112

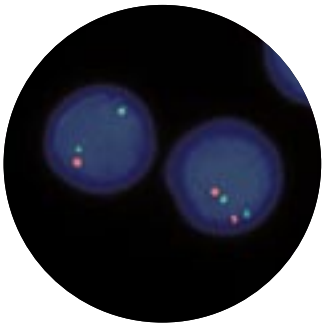
ON ATM (11q22) / SE 11

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 DNA 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 probe is included to facilitate chromosome identification.

Cat.# KBI-10103 ATM (11q22) / SE 11





ATM (11q22) / SE 11 hybridized to patient material showing a 11q22 deletion at the ATM gene region observed (1R2G).
Image kindly provided by Dr Wenzel, Basel

Literature:

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

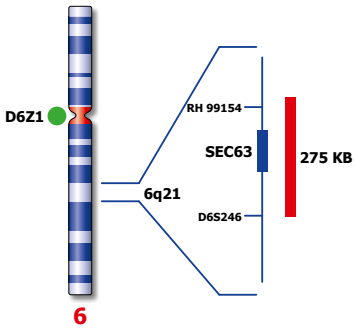
Ordering information	Color	Tests	Cat#
ON ATM (11q22) / SE 11	red/green	10	KBI-10103

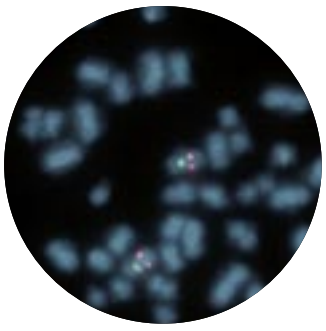
ON 6q21 / SE 6

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 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 DNA probe is optimized to detect copy numbers of 6q at region 6q21.The chromosome 6 satellite enumeration probe (SE 6) at D6Z1 is included to facilitate chromosome identification.

Cat.# KBI-10105 6q21 / SE 6





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

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

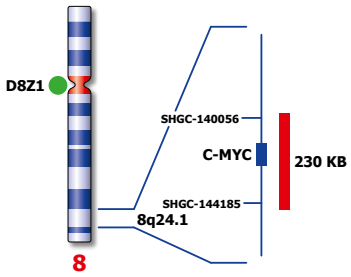
Ordering information	Color	Tests	Cat#
ON 6q21 / SE 6	red/green	10	KBI-10105

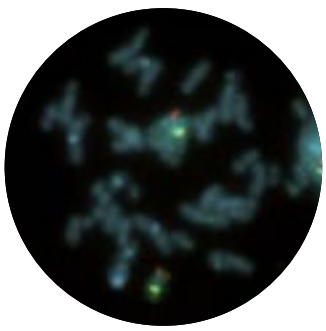
ON C-MYC (8q24) / SE 8

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

The C-MYC (8q24) specific DNA probe is optimized to detect copy numbers of the C-MYC gene region at 8q24. The chromosome 8 satellite enumeration probe (SE 8) at D8Z1 is included to facilitate chromosome identification.

Cat.# KBI-10106 C-MYC (8q24) / SE 8





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

Literature:
Greil et al, 1991, Blood, 78: 180-191.
Note:
This probe should not be used to detect translocations involving C-MYC.

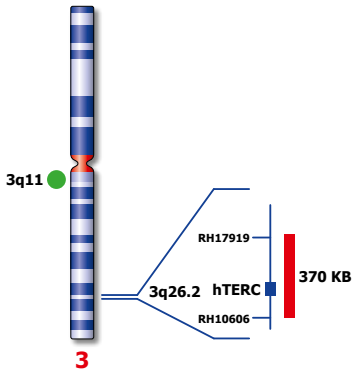
Ordering information	Color	Tests	Cat#
ON C-MYC (8q24) / SE 8	red/green	10	KBI-10106

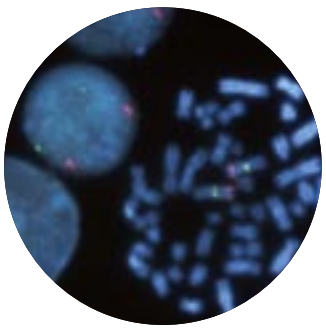
ON hTERC (3q26) / 3q11

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 within a 1- to 2-Mb genomic segment containing several potential cancer genes including hTERC, the human telomerase RNA gene.

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

Cat.# KBI-10110 hTERC (3q26) / 3q11





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

Literature:

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

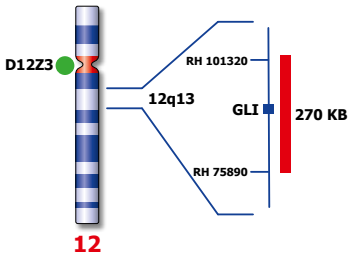
Ordering information	*Color*	*Tests*	*Cat#*
ON hTERC (3q26) / 3q11	red/green	10	KBI-10110

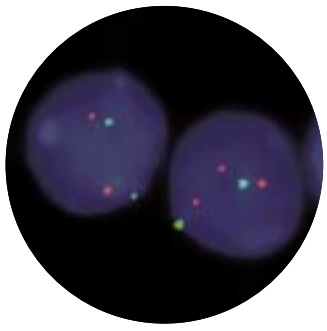
ON GLI (12q13) / SE 12

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, **GLI**, RAP1B, A2MR, and IFNG, were found to be coamplified.

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

Cat.# KBI-10104 GLI (12q13) / SE 12





GLI (12q13) / SE 12 hybridized to patient material showing GLI (12q13) amplification (3R2G).
Image kindly provided by Dr Wenzel, Basel

Literature:

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

Ordering information	*Color*	*Tests*	*Cat#*
ON GLI (12q13) / SE 12	red/green	10	KBI-10104

CLL probe combinations

Most of the CLL probes are also available as combinations covering two critical loci in one hybridization. This is of particular interest if patient material is limited. The disadvantage is that no internal control is added. The following CLL probe combinations are available:

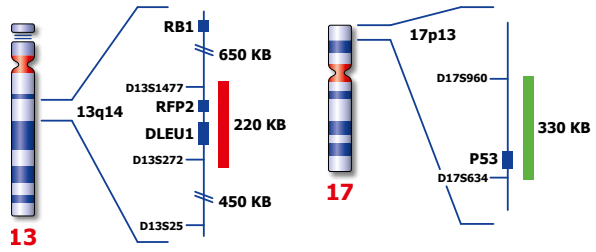
ON DLEU (13q14) / p53 (17p13)

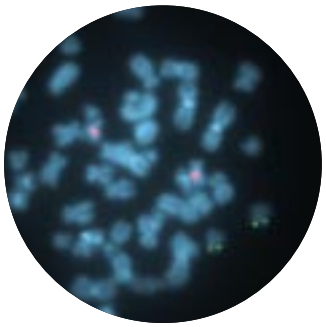
Deletion of DLEU at 13q14 indicates a rather good prognosis, deletion of p53 at 17p13 is associated with poor prognosis.

ON ATM (11q22) / GLI (12q13)

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

Cat.# KBI-10113 DLEU (13q14) / p53 (17p13)





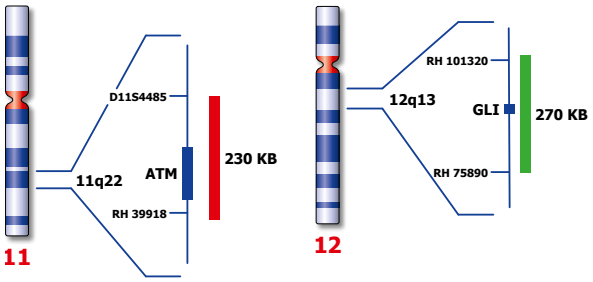
DLEU (13q14) / p53 (17p13) hybridized to a normal metaphase (2R2G).

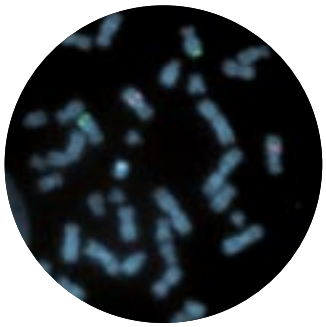
Literature:

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

Ordering information	Color	Tests	Cat#
ON DLEU (13q14) / p53 (17p13)	red/green	10	KBI-10113

Cat.# KBI-10108 ATM (11q22) / GLI (12q13)





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

Literature:

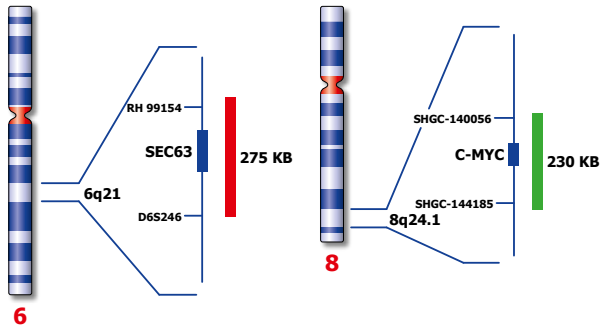
Döhner H et al, 1997, Blood, 7; 2516-2522
Boultwood J, 2001, J. Clin. Pathol., 54; 512-516
Dierlamm J et al, 1998, Genes Chromosomes Cancer, 20; 155-166
Döhner H at al, 1999, J. Molec. Med., 77; 266-281

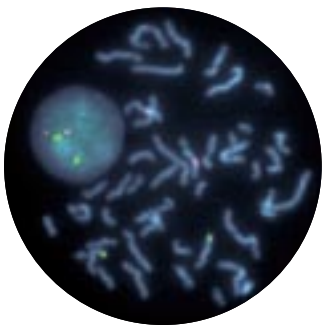
Ordering information	Color	Tests	Cat#
ON ATM (11q22) / GLI (12q13)	red/green	10	KBI-10108

ON 6q21 / MYC (8q24)

Deletion of 6q21 indicates an intermediate risk category, amplification of C-MYC at 8q24 is associated with poor prognosis.

Cat.# KBI-10109 6q21 / MYC (8q24)





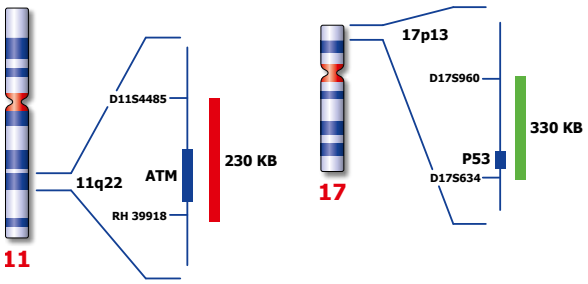
6q21 / MYC (8q24) hybridized to a normal interphase/ metaphase (2R2G).

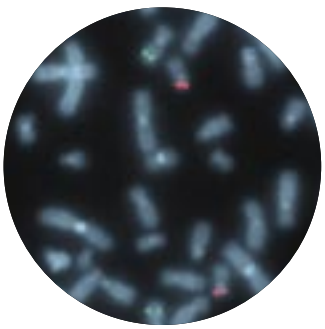
Ordering information	Color	Tests	Cat#
ON 6q21 / C-MYC (8q24)	red/green	10	KBI-10109

ON p53 (17p13) / ATM (11q22)

Deletion of p53 and ATM are both indicating poor prognosis in CLL.

Cat.# KBI-10114 p53 (17p13) / ATM (11q22)





p53 (17p13) / ATM (11q22) hybridized to a normal metaphase (2R2G).

Ordering information	Color	Tests	Cat#
ON p53 (17p13) / ATM (11q22)	red/green	10	KBI-10114

Other relevant CLL probes:

ON IGH (14q32) Break

Cat.# KBI-10601 IGH (14q32) Break
See description under Multiple Myeloma on page 39.

Ordering information	*Color*	*Tests*	*Cat#*
ON IGH (14q32) Break	red/green	10	KBI-10601

SE 12 (D12Z3)

Cat.# KBI-20012 SE 12 (D12Z3)
See description under Satellite Enumeration probes on page 85.

Ordering information	*Color*	*Tests*	*Cat#*
SE 12 (D12Z3)	red/green	10	KBI-20012

Myelodysplastic Syndromes (MDS)

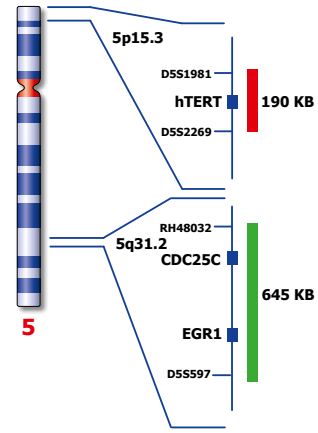
The myelodysplastic syndromes (MDS) are a heterogeneous group of hematopoietic disorders characterized in most patients by peripheral blood cytopenia with hypercellular bone marrow and dysplasia of the cellular elements. Cytogenetic studies play a major role in confirmation of diagnosis and prediction of clinical outcome in MDS, and have contributed to the understanding of its pathogenesis. Clonal chromosomal abnormalities are detected by routine karyotyping techniques in 40%–70% of cases of de novo MDS, and 95% of cases of therapy-related MDS.

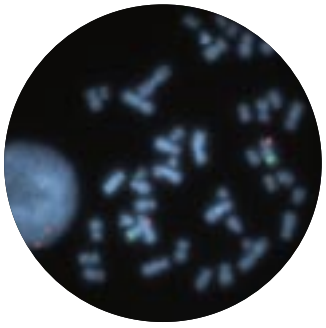
ON hTERT (5p15) / 5q31

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

The 5q- specific DNA probe is optimized to detect copy numbers at the CDC25C/EGR1 gene region at 5q31. The hTERT gene region at 5p15 is included to facilitate chromosome identification.

Cat.# KBI-10208 hTERT (5p15) / 5q31





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

Literature:

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

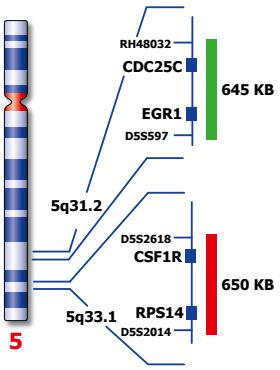
Ordering information	*Color*	*Tests*	*Cat#*
ON hTERT (5p15) / 5q31	red/green	10	KBI-10208

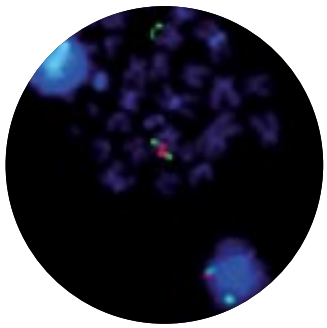
ON MDS 5q- (5q31; 5q33)

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 DNA 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.

Cat.# KBI-10209 MDS 5q- (5q31; 5q33)





MDS 5q- (5q31; 5q33) probe hybridized to patient material showing a 5q33 deletion (1R2G).
Image kindly provided by Dr Mohr, Dresden

Literature:

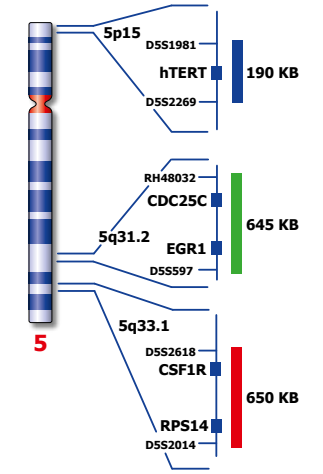
Boultwood J e.a., Blood 2002; 99: 4638-4641
Zhao N e.a., PNAS 1997; 94: 6948-6953
Wang e.a., Haematologica 2008; 93: 994-1000
Ebert BL e.a., Nature 2008: 451: 335-339
Mohamedali A and Mufti GJ, Brit J Haematol 2008; 144: 157-168

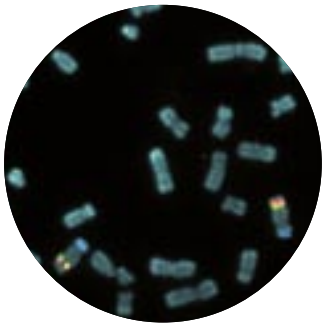
Ordering information	*Color*	*Tests*	*Cat#*
ON MDS 5q- (5q31; 5q33)	red/green	10	KBI-10209

ON MDS 5q- (5q31; 5q33) / hTERT (5p15) TC

The 5q- specific DNA 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 hTERT gene region at 5p15.

Cat.# KBI-10210 MDS 5q- (5q31; 5q33) / hTERT (5p15), Triple-Color





MDS 5q- (5q31; 5q33) / hTERT (5p15) probe hybridized to a normal metaphase (2R2G2B).

Literature:

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

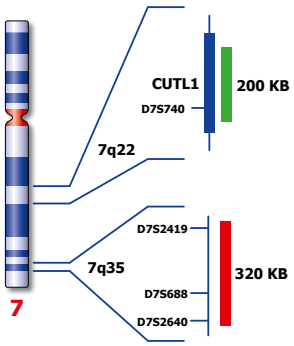
Ordering information	Color	Tests	Cat#
ON MDS 5q- (5q31; 5q33) / hTERT (5p15) TC	red/green/blue	10	KBI-10210

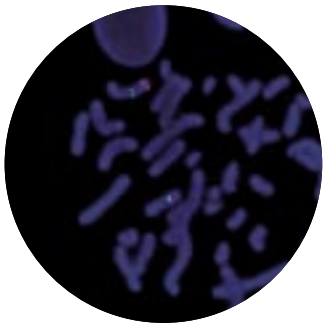
ON MDS 7q- (7q22; 7q35)

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 (CUTL1) gene region is located in the 7q22 critical region.

The 7q- specific DNA probe is optimized to detect copy number of 7q at 7q22 and at 7q35 simultaneously in a dual-color assay

Cat.# KBI-10202 MDS 7q- (7q22; 7q35)





MDS 7q- (7q22; 7q35) hybridized to patient material showing a 7q35 deletion (1R2G).
Image kindly provided by Prof Jauch, Heidelberg

Literature:

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

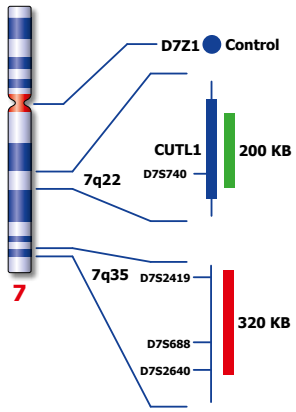
Ordering information	Color	Tests	Cat#
ON MDS 7q- (7q22; 7q35)	red/green	10	KBI-10202

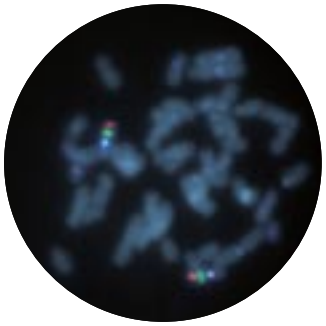
ON MDS 7q- (7q22; 7q35) / SE 7 TC

The 7q- specific DNA probe is optimized to detect copy number of 7q at 7q22 and at 7q35 simultaneously in a dual-color assay.

The chromosome 7 satellite enumeration probe (SE 7) at D7Z1 in blue is included to facilitate chromosome identification.

Cat.# KBI-10207 MDS 7q (7q22; 7q35) / SE 7, Triple-Color





MDS 7q (7q22; 7q35) / SE 7 TC probe hybridized to a normal metaphase (2R2G2B).

Literature:

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

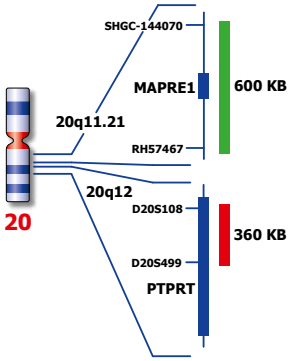
Ordering information	*Color*	*Tests*	*Cat#*
ON MDS 7q- (7q22; 7q35) / SE7 TC	red/green/blue	10	KBI-10207

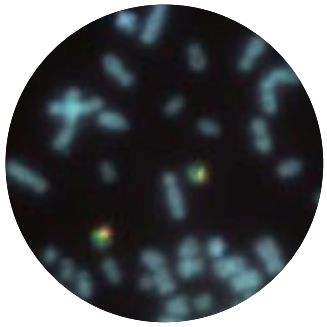
ON MDS 20q- (PTPRT 20q12) / 20q11

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 (PTPRT).

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

Cat.# KBI-10203 MDS 20q- (PTPRT 20q12) / 20q11





MDS 20q- (PTPRT 20q12) / 20q11 probe hybridized to a normal metaphase (2R2G).

Literature:

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

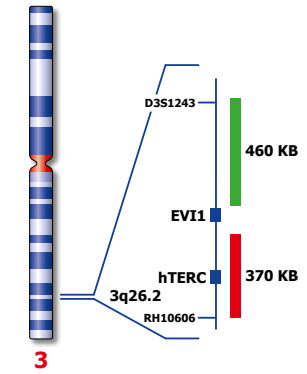
Ordering information	*Color*	*Tests*	*Cat#*
ON 20q- (PTPRT 20q12) / 20q11	red/green	10	KBI-10203

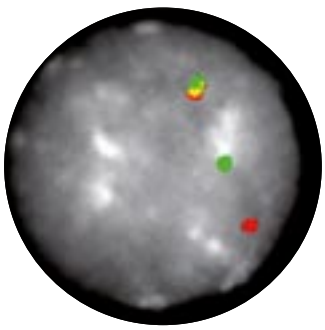
ON EVI t(3;3); inv(3) (3q26) Break

The inv(3)(q21;q26) is a recurrent cytogenetic aberration of myeloid malignancy associated with fusion of EVI1 and RPN1 and a poor disease prognosis. Genomic breakpoints in 3q26 are usually located proximal to the EVI1 locus, spanning a region of several hundred kilobases. Other recurrent and sporadic rearrangements of 3q26 also cause transcriptional activation of EVI1 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 EVI1 and neighboring gene MDS1.

The EVI t(3;3) inv(3) Break, dual-color probe is optimized to detect the inversion of chromosome 3 involving the EVI1 gene region at 3q26 in a dual-color, split assay on metaphase/ interphase spreads, blood smears and bone marrow cells.

Cat.# KBI-10204 EVI t(3;3); inv(3) (3q26) Break





EVI t(3;3);inv(3) (3q26) Break probe hybridized to patient material showing a rearrangement involving the EVI gene region at 3q26 (1RG1R1G).
Image kindly provided by Dr. Reed, London

Literature:

Levy et al, 1994, Blood, 83: 1348-1354.
Wieser et al, 2003, Haematologica, 88: 25-30.
Melo et al, 2007, Leukemia, 22, 434-437.

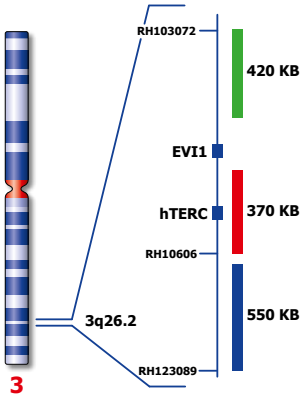
Ordering information	Color	Tests	Cat#
ON EVI t(3;3); inv(3) (3q26) Break	red/green	10	KBI-10204

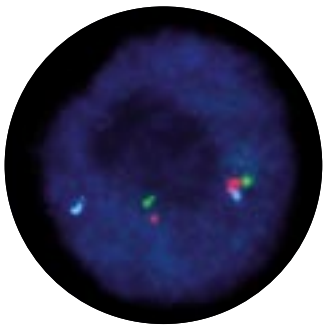
Note: In t(3;3) the breakpoint cluster can span 1.3 Mb region. The described probe set will therefore provide false negative results in cases with very distal breakpoints.

ON EVI t(3;3); inv(3), EVI (3q26) Break, TC

The EVI t(3;3) inv(3) Break, triple-color probe is optimized to detect the inversion of chromosome 3 involving the 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 now be easily discovered.

Cat.# KBI-10205 EVI t(3;3); inv(3) (3q26), Triple-Color





EVI t(3;3); inv(3) (3q26) TC probe hybridized to patient material showing a rearrangement involving the EVI gene region at 3q26 (1RGB1B1RG).
Image kindly provided by Prof Jauch, Heidelberg

Literature:

Levy et al, 1994, Blood, 83: 1348-1354.
Wieser et al, 2003, Haematologica, 88: 25-30.
Melo et al, 2007, Leukemia, 22, 434-437.

Ordering information	Color	Tests	Cat#
ON EVI t(3;3); inv(3) (3q26) Break, TC	red/green/blue	10	KBI-10205

Acute Myeloid Leukemia (AML)

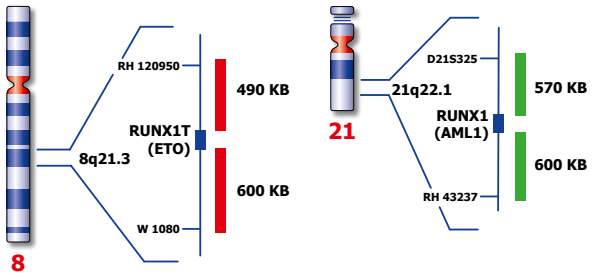
At least 80% of patients with acute myeloid leukemia (AML) have an abnormal karyotype. Cytogenetic analysis provides some of the strongest prognostic information available, predicting outcome of both remission induction and postremission therapy. Abnormalities which indicate a good prognosis include t(8;21), inv(16), and t(15;17). Patients with AML that is characterized by deletions of the long arms or monosomies of chromosomes 5 or 7; by translocations or inversions of chromosome 3, t(6;9), t(9;22); or by abnormalities of chromosome 11q23 have particularly poor prognoses with chemotherapy.

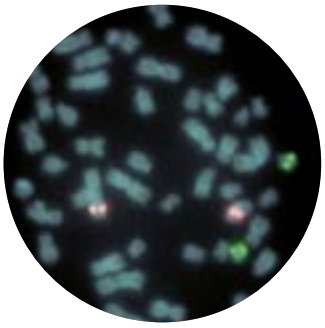
ON AML/ETO t(8;21) Fusion

t(8;21)(q22;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 AML1 (CBFA2, RUNX1) gene in the 21q22 region is fused to the ETO (MTG8 , RUNX1T) gene in the 8q22 region, resulting in one transcriptionally active gene on the 8q-derivative chromosome.

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

Cat.# KBI-10301 AML/ETO t(8;21) Fusion





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

Literature:

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

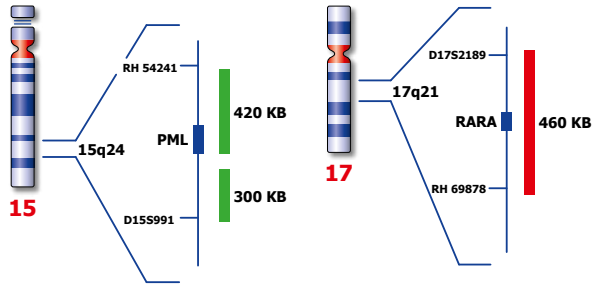
Ordering information	*Color*	*Tests*	*Cat#*
ON AML/ETO t(8;21) Fusion	red/green	10	KBI-10301

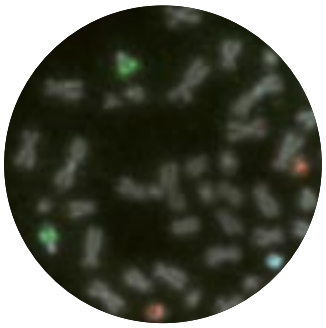
ON PML/RARA t(15;17) Fusion

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) specific DNA probe is optimized to detect the reciprocal translocation t(15;17) (q24;q21) in a dual-color, dual-fusion assay.

Cat.# KBI-10302 PML/RARA t(15,17) Fusion





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

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

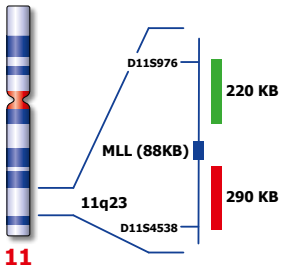
Ordering information	Color	Tests	Cat#
ON PML/RARA t(15,17) Fusion	red/green	10	KBI-10302
ON PML/RARA t(15,17) Fusion	red/green	20	KBI-12302

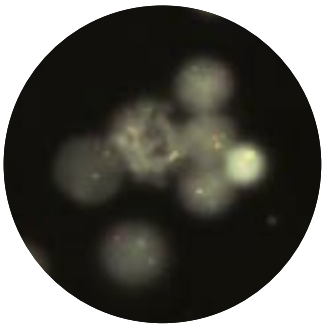
ON MLL (11q23) Break

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 MLL (Myeloid-Lymphoid Leukemia or Mixed-Lineage Leukemia) 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 MLL gene usually have a poor prognosis.

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

Cat.# KBI-10303 MLL (11q23) Break





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

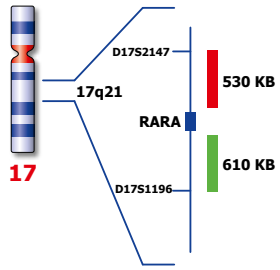
Literature:
Kobayashi et al, 1993, Blood, 81: 3027-3022
Martinez-Climent et al, 1995, Leukemia, 9: 1299-1304.

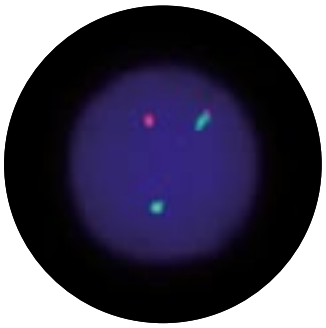
Ordering information	Color	Tests	Cat#
ON MLL (11q23) Break	red/green	10	KBI-10303

ON RARA (17q21) Break

This break apart probe can detect the numerous types of recurrent rearrangement of the RARα (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 RARα 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.

Cat.# KBI-10305 RARA (17q21) Break





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

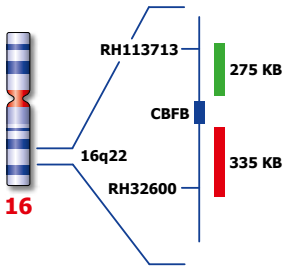
Ordering information	Color	Tests	Cat#
ON RARA (17q21) Break	red/green	10	KBI-10305

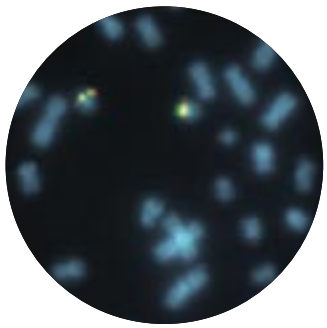
ON CBFB t(16;16); inv(16) Break

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 probe is optimized to detect the inversion of chromosome 16 involving the CBFB gene region at 16q22 in a dual-color, split assay.

Cat.# KBI-10304 CBFB t(16;16); inv(16) Break





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

Literature:

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

Ordering information	Color	Tests	Cat#
ON CBFB t(16;16); inv(16) Break	red/green	10	KBI-10304

Acute Lymphoblastic Leukemia (ALL)

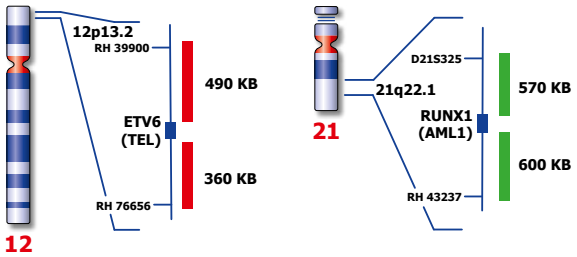
Acute lymphocytic leukemia, also called acute lymphoblastic leukemia, is a type of cancer that starts from white blood cells in the bone marrow. A number of recurring cytogenetic abnormalities are associated with distinct immunologic phenotypes of ALL and characteristic outcomes. The ETV6/AML1 fusion arising from the translocation t(12;21)(p13;q22) has been associated with a good outcome; the BCR/ABL fusion of t(9;22)(q34;q11), rearrangements of the MLL gene (11q23), and abnormalities of the short arm of chromosomes 9 involving the tumor suppressor genes p16 (INK4A) have a poor prognosis.

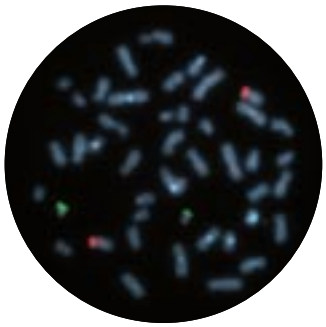
ON TEL/AML t(12;21) Fusion

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 TEL (ETV6) gene with almost the entire AML1 (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 TEL/AML t(12;21) specific DNA probe is optimized to detect the reciprocal translocation t(12;21) (p13;q22) in a dual-color, dual-fusion assay.

Cat.# KBI-10401 TEL/AML t(12;21) Fusion





TEL/AML t(12;21) Fusion probe hybridized to a normal metaphase (2R2G).

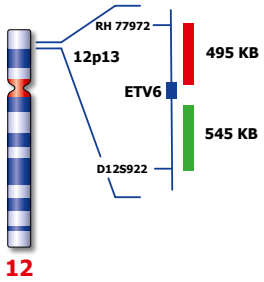
Literature:
Romana et al, 1995, Blood, 85: 3662-3670.

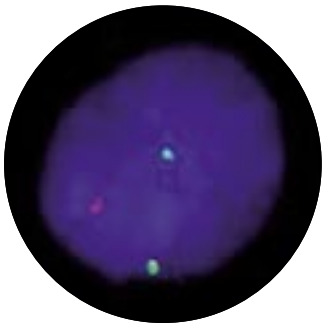
Ordering information	*Color*	*Tests*	*Cat#*
ON TEL/AML t(12;21) Fusion	red/green	10	KBI-10401

ON ETV6 (TEL) (12p13) Break

ETV6 (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-AML1 fusions can be found.

Cat.# KBI-10403 ETV6 (TEL) (12p13) Break





ETV6 (TEL) (12p13) Break probe hybridized to patient material showing a translocation involving the ETV6 region at 12p13 (1RG1R1G).
Image kindly provided by Magret Ratjen, Kiel

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

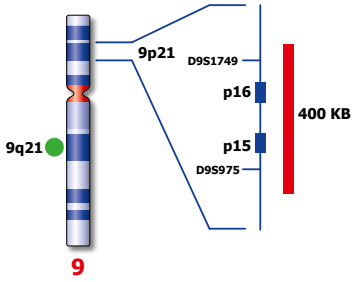
Ordering information	*Color*	*Tests*	*Cat#*
ON ETV6 (TEL) (12p13) Break	red/green	10	KBI-10403

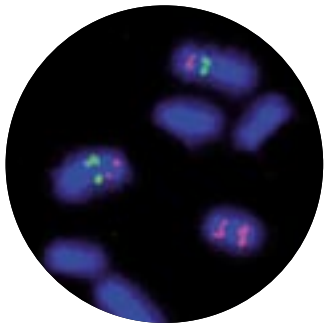
ON p16 (9p21) / 9q21

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 p16 (INK4A)/ p15 (INK4B) genes, which are cell cycle kinase inhibitors and important in leukemogenesis.

The p16 (9p21) specific DNA probe is optimized to detect copy numbers of the p16 (INK4A) gene region at region 9p21. The 9q21 region probe is included to facilitate chromosome identification.

Cat.# KBI-10402 p16 (9p21) / 9q21





p16 (9p21) / 9q21 hybridized on patient material showing an isochromosome 9.
Image kindly provided by Dr Wenzel, Basel

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

Ordering information	*Color*	*Tests*	*Cat#*
ON p16 (9p21) / 9q21	red/green	10	KBI-10402

ON MLL (11q23) Break

Cat.# KBI-10303 MLL (11q23)
See description under AML on page 30.

Ordering information	*Color*	*Tests*	*Cat#*
ON MLL (11q23) Break	red/green	10	KBI-10303

ON BCR/ABL t(9;22)

The t(9;22) BCR/ABL translocation is present in about 5% of pediatric and up to 50% of adult ALL cases, and is associated with poor prognosis.

Cat.# KBI-10005 ON BCR/ABL t(9;22) Fusion
Cat.# KBI-12005 ON BCR/ABL t(9;22) Fusion
Cat.# KBI-10006 ON BCR/ABL t(9;22) TC, D-Fusion
Cat.# KBI-10008 ON BCR/ABL t(9;22) DC, S-Fusion, ES
Cat.# KBI-10009 ON BCR/ABL t(9;22) DC, S-Fusion
See description under CML on page 13 and 14.

Ordering information	*Color*	*Tests*	*Cat#*
ON BCR/ABL t(9;22) Fusion	red/green	10	KBI-10005
ON BCR/ABL t(9;22) Fusion	red/green	20	KBI-12005
ON BCR/ABL t(9;22) TC, D-Fusion	red/green/blue	10	KBI-10006
ON BCR/ABL t(9;22) DC, S-Fusion, ES	red/green	10	KBI-10008
ON BCR/ABL t(9;22) DC, S-Fusion	red/green	10	KBI-10009

Multiple Myeloma (MM)

The cytogenetic picture in multiple myeloma (MM) is highly complex, from which non-random numerical and structural chromosomal changes have been identified. Specifically, translocations involving the immunoglobulin heavy chain gene (IGH) at 14q32 and either monosomy or deletions of chromosome 13 have been observed in a significant number of patients. More recently several additional deletions or amplifications have been identified in MM which are currently investigated in large patient studies.

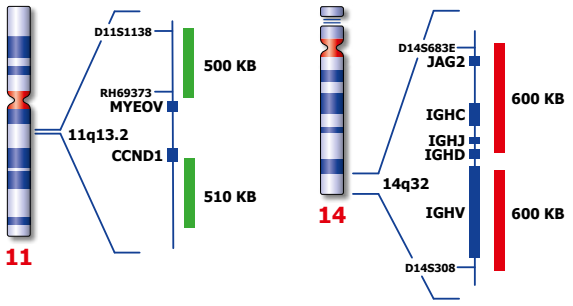
Note: Multiple Myeloma is a cancer of plasma cells. Analysis of such cells is hampered by their low frequency. Enrichment of plasma cells using CD138 is highly recommended.

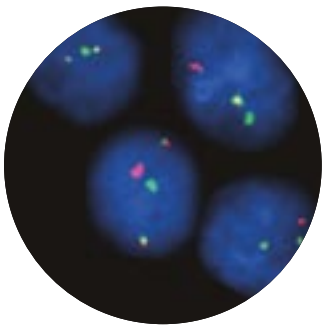
ON MYEOV/IGH t(11;14) Fusion

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) specific DNA probe is optimized to detect the reciprocal translocation t(11;14) in a dual-color, dual-fusion assay.

Cat.# KBI-10605 MYEOV/IGH t(11;14) Fusion





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

Literature:

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

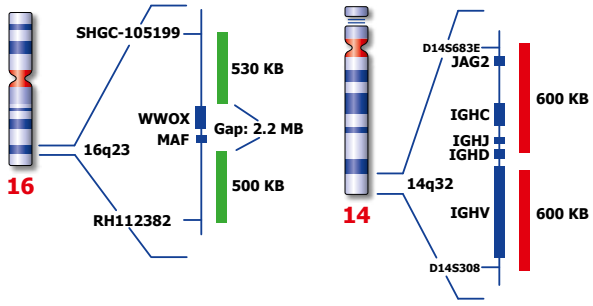
Ordering information	*Color*	*Tests*	*Cat#*
ON MYEOV/IGH t(11;14) Fusion	red/green	10	KBI-10605

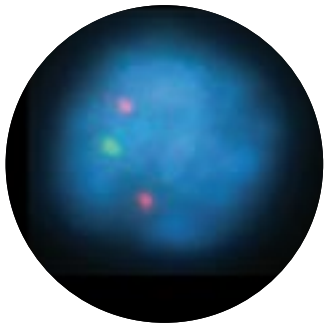
ON MAF/IGH t(14;16) Fusion

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 immunoglobulin heavy chain (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 multiple myeloma (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.

Cat.# KBI-10610 MAF/IGH t(14;16) Fusion





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

Literature:

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

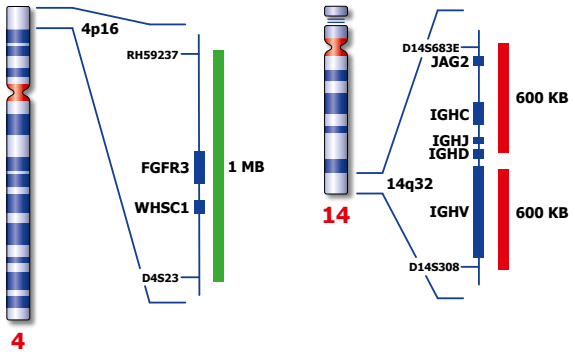
Ordering information	*Color*	*Tests*	*Cat#*
ON MAF/IGH t(14;16) Fusion	red/green	10	KBI-10610

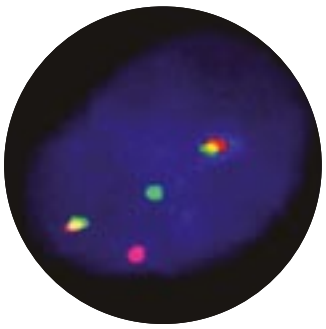
ON FGFR3/IGH t(4;14) Fusion

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 predicts for poor survival and poor response to chemotherapy.

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

Cat.# KBI-10602 FGFR3/IGH t(4;14) Fusion





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

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

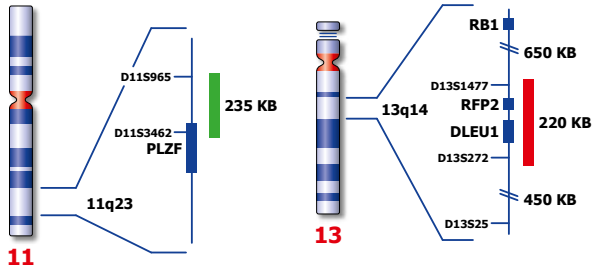
Ordering information	Color	Tests	Cat#
ON FGFR3/IGH t(4;14) Fusion	red/green	10	KBI-10602

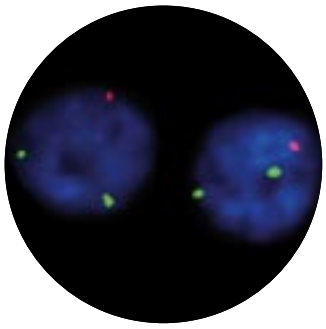
ON MM 11q23 / DLEU (13q14)

Hybridization results delineated 11q23 and 11q25 as the most frequently gained regions in 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 DNA probe is optimized to detect copy numbers at 11q23. The DLEU (13q14) specific DNA region is optimized to detect copy numbers of the DLEU gene region at 13q14.

Cat.# KBI-10502 MM 11q23 / 13q14





MM 11q23 / DLEU 13q14 probe hybridized to MM patient material showing a 13q14 deletion (1R2G).
Image kindly provided by Prof Jauch, Heidelberg

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

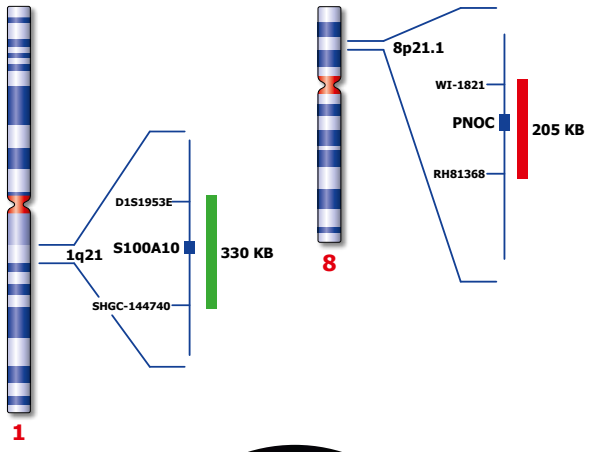
Ordering information	Color	Tests	Cat#
ON MM 11q23 / DLEU (13q14)	red/green	10	KBI-10502

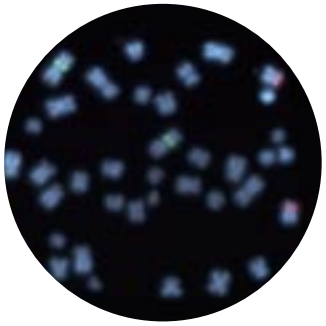
ON MM 1q21 / 8p21

Amplifications of 1q21 are concurrent with dysregulated expression of c-MAF, MMSET/FGFR3, or Del13 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 DNA probe is optimized to detect copy numbers at 1q21. The 8p21 specific DNA region is optimized to detect copy numbers at 8p21.

Cat.# KBI-10503 MM 1q21 / 8p21





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

Literature:

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

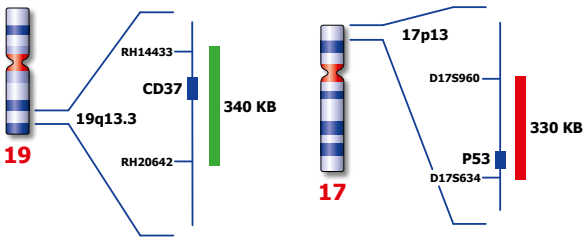
Ordering information	*Color*	*Tests*	*Cat#*
ON MM 1q21 / 8p21	red/green	10	KBI-10503

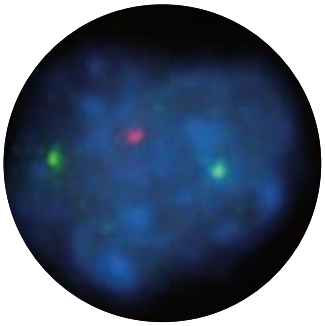
ON MM 19q13 / p53 (17p13)

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 DNA probe is optimized to detect copy numbers at 19q13. The p53 (17p13) specific DNA region is optimized to detect copy numbers of the p53 gene region at 17p13.

Cat.# KBI-10509 MM 19q13 / p53 (17p13)





MM 19q13 / p53 (17p13) hybridized to patient material showing a p53 (17p13) deletion (1R2G).
Image kindly provided by Prof Jauch, Heidelberg

Literature:

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

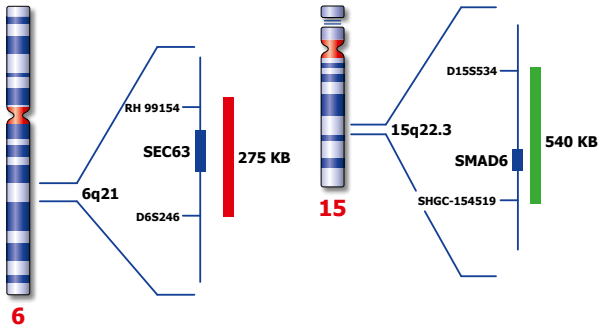
Ordering information	*Color*	*Tests*	*Cat#*
ON MM 19q13 / p53 (17p13)	red/green	10	KBI-10509

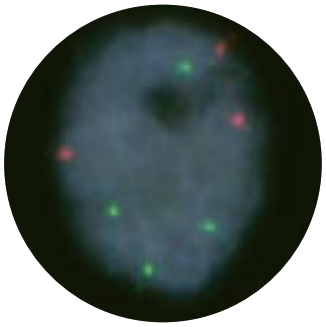
ON MM 15q22 / 6q21

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 DNA probe is optimized to detect copy numbers at 15q22. The 6q21 specific DNA region is optimized to detect copy numbers at 6q21.

Cat.# KBI-10504 MM 15q22 / 6q21





MM 15q22 / 6q21 hybridized to MM patient material with amplification of both critical regions 6q21 and 15q22.
Image kindly provided by Prof Jauch, Heidelberg

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

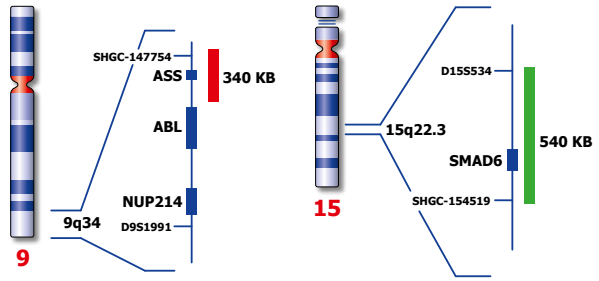
Ordering information	Color	Tests	Cat#
ON MM 15q22 / 6q21	red/green	10	KBI-10504

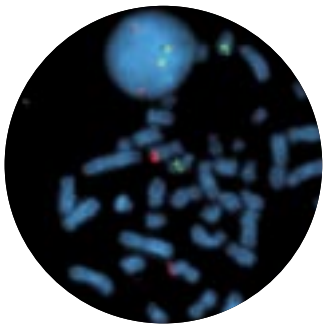
ON MM 15q22 / 9q34

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

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

Cat.# KBI-10508 MM 15q22 / 9q34





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

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

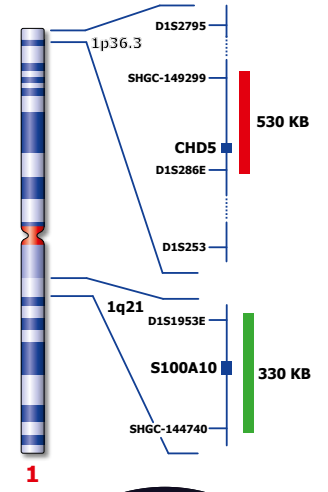
Ordering information	Color	Tests	Cat#
ON MM 15q22 / 9q34	red/green	10	KBI-10508

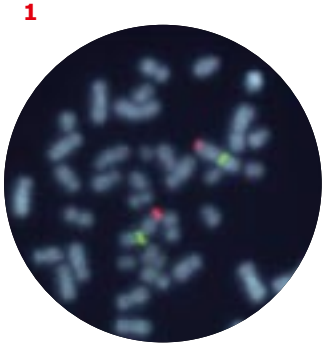
ON MM 1q21 / SRD (1p36)

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

Cat.# KBI-10507 MM 1q21 / SRD (1p36)





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

Literature:

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

Ordering information	*Color*	*Tests*	*Cat#*
ON 1q21 / SRD (1p36)	red/green	10	KBI-10507

ON IGH (14q32) Break

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.

Cat.# KBI-10601 IGH (14q32) Break

See description under Lymphoma on page 42.

Literature:

Taniwaki et al, 1994, Blood, 83: 2962-1969.
Moreau et al, 2002, Blood, 100: 1579-1583.

Ordering information	*Color*	*Tests*	*Cat#*
ON IGH (14q32) Break	red/green	10	KBI-10601

Lymphoma

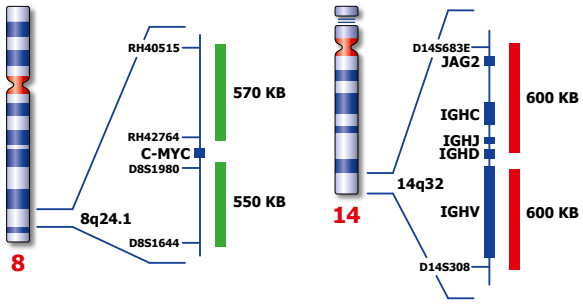
Lymphoma is a type of cancer that originates in lymphocytes. Following WHO classification there are three large groups: B cell lymphomas, T cell and natural killer cell tumors, and Hodgkin lymphoma. The IGH gene locus at chromosome band 14q32 is very frequently involved in B-cell lymphoma.

ON MYC/IGH t(8;14) Fusion

The translocation t(8;14)(q24;q32) is the characteristic chromosomal aberration of Burkitt's-type of lymphomas. This translocation fuses the C-MYC gene at 8q24 next to the IGH locus at 14q32, resulting in overexpression of the transcription factor C-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 DNA probe is optimized to detect the reciprocal translocation t(8;14) in a dual-color, dual-fusion assay.

Cat.# KBI-10603 MYC/IGH t(8;14) Fusion



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

Literature:

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

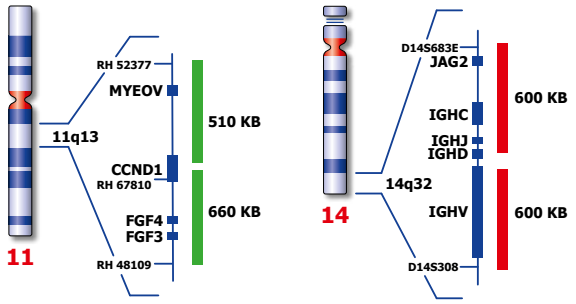
Ordering information	*Color*	*Tests*	*Cat#*
ON MYC/IGH t(8;14) Fusion	red/green	10	KBI-10603

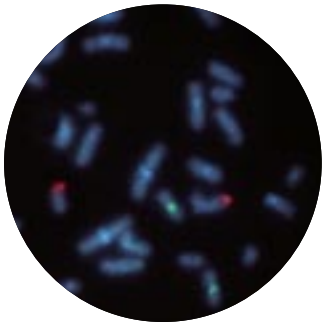
ON BCL1/IGH t(11;14) Fusion

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 BCL1 region adjacent to CCND1. 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 BCL1/IGH t(11;14)(q13;q32) specific DNA probe is optimized to detect the reciprocal translocation t(11;14) in a dual-color, dual-fusion assay.

Cat.# KBI-10604 BCL1/IGH t(11;14) Fusion





BCL1/IGH t(11;14) Fusion probe hybridized to a normal interphase/ metaphase (2R2G).

Literature:
Vaandrager et al, 1996, Blood, 88: 1177-1182.

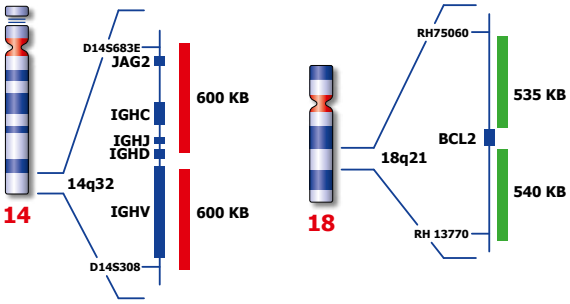
Ordering information	*Color*	*Tests*	*Cat#*
ON BCL1/IGH t(11;14) Fusion	red/green	10	KBI-10604

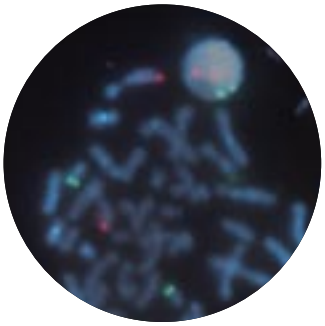
ON BCL2/IGH t(14;18) Fusion

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 regions cluster , major breakpoint region (mbr) within the 3' untranslated region of the BCL2 proto-oncogene accounts for approximately 60% of the cases and the minor cluster region (mcr) 30 kb 3' of BCL2 accounts for approximately 25% of the breakpoints.

The BCL2/IGH t(14;18)(q21;q32) specific DNA probe is optimized to detect the reciprocal translocation t(18;14) in a dual-color, dual-fusion assay.

Cat.# KBI-10606 BCL2/IGH t(14;18) Fusion





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

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

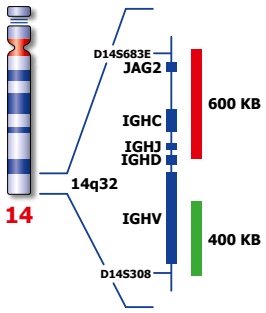
Ordering information	*Color*	*Tests*	*Cat#*
ON BCL2/IGH t(14;18) Fusion	red/green	10	KBI-10606

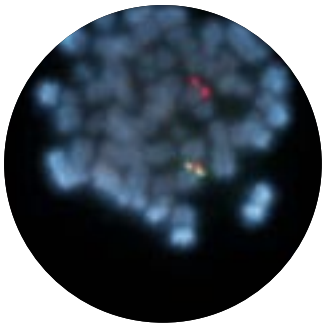
ON IGH (14q32) Break

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. Kreatech has developed this probe for the specific use on cell material (KBI-10601), or for the use on tissue (KBI-10729).

Cat.# KBI-10601 IGH (14q32) Break





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

Literature:

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

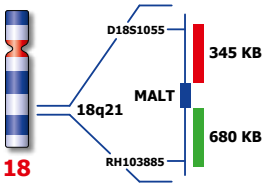
Ordering information	Color	Tests	Cat#
ON IGH (14q32) Break	red/green	10	KBI-10601

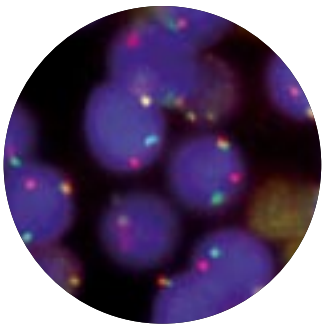
ON MALT (18q21) Break

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 MALT (18q21) is best used to analyze translocation of the MALT gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

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

Cat.# KBI-10608 MALT (18q21) Break





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

Literature:

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

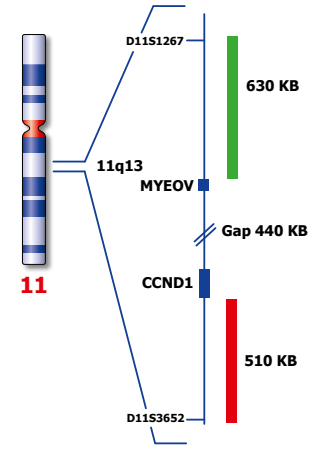
Ordering information	Color	Tests	Cat#
ON MALT (18q21) Break	red/green	10	KBI-10608

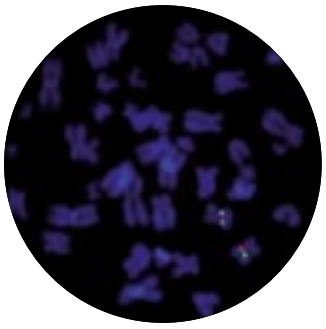
ON CCND1 (BCL1;11q13) Break

Besides the important functions in cellular growth, metabolism, and cellular differentiation, CCND1 (also 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 multiple myeloma, 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 probe KBI-10609 can be considered a very useful tool for routine diagnosis in MCL and Multiple myeloma, to be used in association to the related probes KBI-10604 and KBI-10605 probes that can detect more specifically the translocation t(11;14) in Mantle Cell Lymphoma (KBI-10604) and Multiple Myeloma (KBI-10605).

Cat.# KBI-10609 CCND1 (BCL1; 11q13) Break





CCND1 (BCL1; 11q13) Break probe hybridized to a normal metaphase (2R2G).

Literature:
Vaandrager et al, 1996, Blood, 88 (4); 1177-1182
Vaandrager et al, 1997, Blood, 89; 349-350

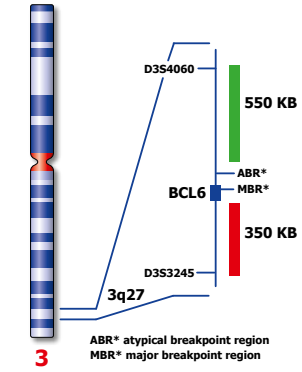
Ordering information	*Color*	*Tests*	*Cat#*
ON CCND1 (BCL1;11q13) Break	red/green	10	KBI-10609

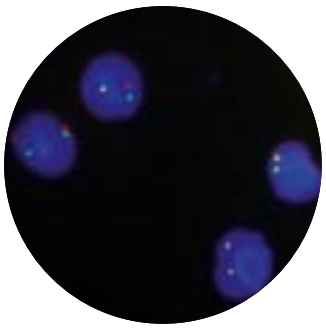
ON BCL6 (3q27) Break

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).

Note: 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 250 kb proximal to the BCL6 gene. The Poseidon BCL6 (3q27) is designed in a way to flank both possible breakpoints, thereby providing clear split signals in either case.

Cat.# KBI-10607 BCL6 (3q27)





BCL6 (3q27) Break probe hybridized to patient material (1RG1R1G).
Image kindly provided by Prof Siebert, Kiel

Literature:

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

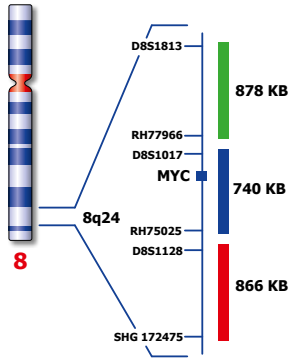
Ordering information	Color	Tests	Cat#
ON BCL6 (3q27) Break	red/green	10	KBI-10607

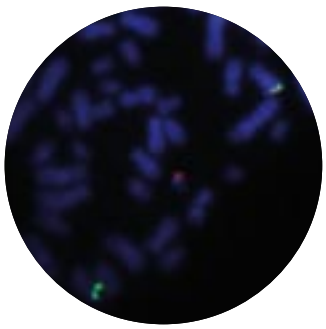
ON MYC (8q24) Break, TC

Rearrangements of the protooncogene C-myc (or 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 c-myc gene is translocated to chromosome 14 and rearranged with the immunoglobulin heavychain genes; the breakpoint occurs 5' to the c-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 mmunoglobulin light chain are translocated to chromosome 8. The rearrangement takes place 3' to the c-myc gene. At the present time the mechanism by which the oncogenic potential of the c-myc gene may be activated by these rearrangements is still controversial.

The MYC (8q24) break-apart 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.

Cat.# KBI-10611 MYC (8q24) Break, TC





MYC (8q24) Break probe hybridized to patient material showing a 8q24 proximal break (1GBR1G1BR).
Image kindly provided by Prof. Siebert, Kiel.

Literature:

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

Ordering information	Color	Tests	Cat#
ON MYC (8q24) Break, TC	red/green	10	KBI-10611

ON FGFR3/IGH t(4;14) Fusion

Cat.# KBI-10602 FGFR3/IGH t(4;14) Fusion
See description under Multiple Myeloma on page 36.

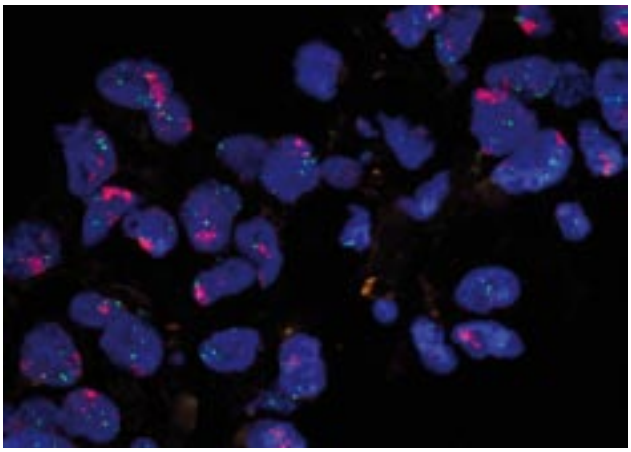
Ordering information	*Color*	*Tests*	*Cat#*
ON FGFR3/IGH t(4;14) Fusion	red/green	10	KBI-10602

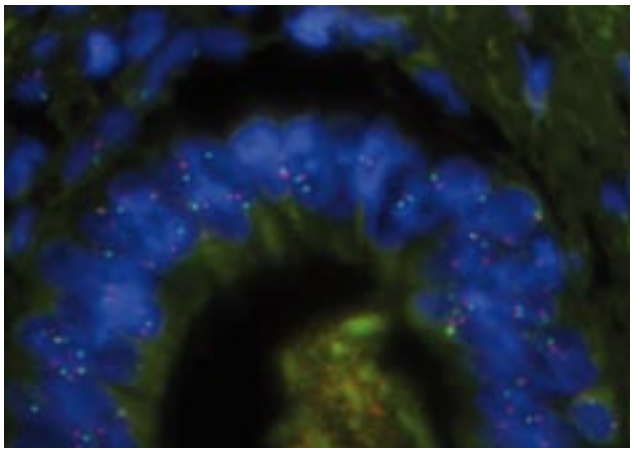
ON MYEOV/IGH t(11;14) Fusion

Cat.# KBI-10605 MYEOV/IGH t(11;14) Fusion
See description under Multiple Myeloma on page 35.

Ordering information	*Color*	*Tests*	*Cat#*
ON MYEOV/IGH t(11;14) Fusion	red/green	10	KBI-10605

ONCOLOGY PROBES - SOLID TUMORS





In solid tumors significantly high levels of chromosome abnormalities have been detected, but distinction between significant and irrelevant events has been a major challenge. Consequently, the application of cytogenetic technology as diagnostic, prognostic, or therapeutic tools for these malignancies has remained largely underappreciated. The emergence of FISH is particularly useful for solid malignancies, and the spectrum of their application is rapidly expanding to improve efficiency and sensitivity in cancer diagnosis, prognosis, and therapy selection, alone or with other diagnostic methods.

Description	*Cat#*	*Page*
ON ERBB2, Her-2/Neu (17q12) / SE 17	KBI-10701	47
ON EGFR, Her-1 (7p11) / SE 7	KBI-10702	59
ON CC hTERC (3q26) C-MYC (8q24) / SE 7 TC	KBI-10704	50
ON MYCN (2p24) / LAF (2q11)	KBI-10706	52
ON PPARγ (3p25) Break	KBI-10707	51
ON EWSR1 (22q12) Break	KBI-10708	55
ON hTERT (5p15) / 5q31 (tissue)	KBI-10709	59
ON p16 (9p21) / 9q21 (tissue)	KBI-10710	50
ON MLL (11q23) / SE 11	KBI-10711	53
ON SRD (1p36) / SE 1(1qh)	KBI-10712	53
ON SYT (18q11) Break	KBI-10713	56
ON CHOP (12q13) Break	KBI-10714	56
ON FUS (16p11) Break	KBI-10715	57
ON FKHR (13q14) Break	KBI-10716	57
ON MDM2 (12q15) / SE 12	KBI-10717	58
ON PTEN (10q23) / SE 10	KBI-10718	60

Description	*Cat#*	*Page*
ON C-MET (7q31) / SE 7	KBI-10719	60
ON AURKA (20q13) / 20q11	KBI-10721	61
ON AURKB (17p13) / SE 17	KBI-10722	61
ON TOP2A (17q21) / SE 17	KBI-10724	47
ON CDK4 (12q13) / SE 12	KBI-10725	58
ON TMPRSS2-ERG (21q22) Del, Break, TC	KBI-10726	63
ON IGH (14q32) Break (tissue)	KBI-10729	63
ON BCL6 (3q27) Break (tissue)	KBI-10730	64
ON MALT (18q21) Break (tissue)	KBI-10731	64
ON ZNF217 (20q13) / 20q11	KBI-10733	48
ON CCND1 (11q13) / SE 11	KBI-10734	62
ON TOP2A (17q21) / Her-2/neu (17q12) / SE 17 TC	KBI-10735	48
ON MDM4 (1q32) /SE 1	KBI-10736	54
ON FGFR1 (8p12) Break	KBI-10737	49
ON p53 (17p13) / SE 17 (tissue)	KBI-10738	65
ON TFE3 (Xp11) Break	KBI-10741	65

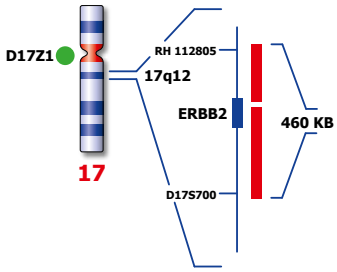
Breast Cancer

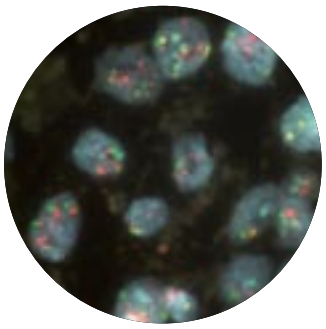
ON ERBB2, Her2/Neu (17q12) / SE 17

The Her2/Neu 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 associated with poor survival. Her2 gene amplification is a permanent genetic change that results in this continuous overexpression of Her2. A drug called trastuzumab (commonly known as Herceptin) has been developed to be effective against Her2-positive breast cancer. Her2/Neu amplification is also observed in a variety of other tumors, such as prostate, lung, colon and ovary carcinoma.

The Her2/Neu (17q12) specific DNA probe is optimized to detect copy numbers of the Her2/Neu (ERBB2) gene region at region 17q12. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification.

Cat.# KBI-10701 ERBB2, Her2/Neu (17q12) / SE 17





ERBB2, Her2/Neu (17q12) / SE 17 probe hybridized to breast tumor tissue showing amplification of Her2/Neu (ERBB2)/ SE 17.

Literature:

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

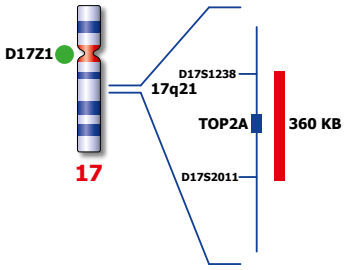
Ordering information	*Color*	*Tests*	*Cat#*
ON ERBB2, Her2/Neu (17q12) / SE 17	red/green	10	KBI-10701
ON ERBB2, Her2/Neu (17q12) / SE 17	red/green	50	KBI-14701

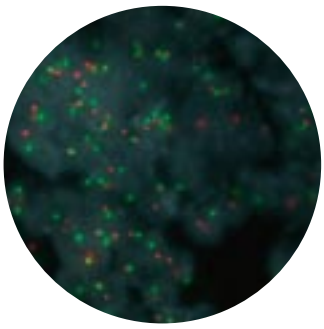
ON TOP2A (17q21) / SE 17

The Topoisomerase2A 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 dual-color 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.

Cat.# KBI-10724 TOP2A (17q21) / SE 17





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

Literature:

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

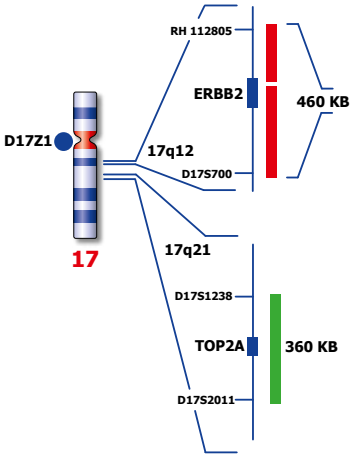
Ordering information	*Color*	*Tests*	*Cat#*
ON TOP2A (17q21) / SE 17	red/green	10	KBI-10724

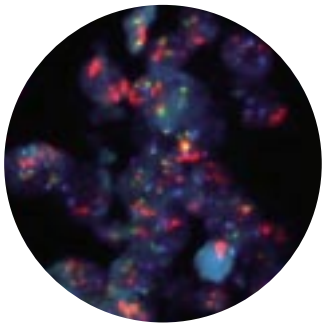
ON TOP2A (17q21) / Her2 (17q12) / SE 17 Triple-Color Probe

The presence of both TOP2A amplification and deletion in advanced cancer are associated with decreased survival, and occur frequently and concurrently with Her2 gene amplification.

The TOP2A (17q21)/ Her2 (17q12)/ SE 17 probe is designed as a triple-color 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.

Cat.# KBI-10735 TOP2A (17q21) / Her2 (17q12) / SE 17





TOP2A (17q21)/ Her2(17q12) / SE 17 TC probe hybridized to breast tumor tissue showing amplification of TOP2A/Her2.

Literature:

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

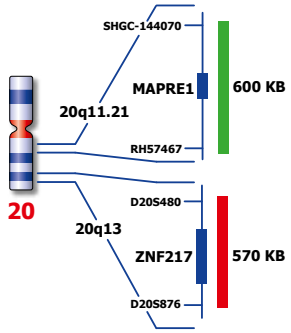
Ordering information	*Color*	*Tests*	*Cat#*
ON TOP2A (17q21) / Her 2 / SE 17	red/green	10	KBI-10735

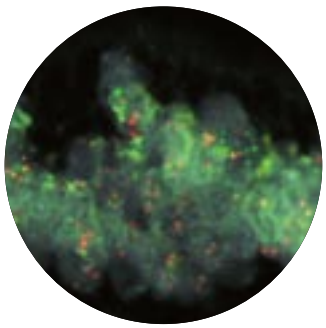
ON ZNF217 (20q13) / 20q11

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 greater 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) specific DNA probe is optimized to detect copy numbers of 20q at 20q13. The 20q11 probe is included to facilitate chromosome identification.

Cat.# KBI-10733 ZNF217 (20q13) / 20q11





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

Literature:

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

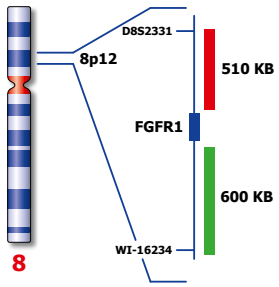
Ordering information	*Color*	*Tests*	*Cat#*
ON ZNF217 (20q13) / 20q11	red/green	10	KBI-10733

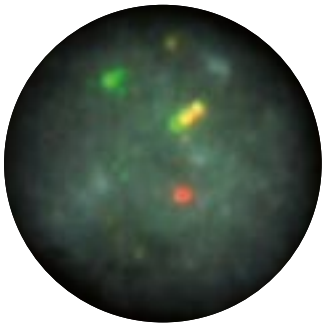
ON FGFR1 (8p12) Break

FGFR1 (fibroblast growth factor receptor 1) expression has been shown to play pivotal roles in mammary development and breast cancer tumorigenesis. It has been shown that FGFR1 amplification is found in up to 10% of breast cancers and is significantly more prevalent in patients > 50 years of age and in tumors that lack HER2 expression. Even though the prognostic impact of FGFR1 amplification in breast cancer still remains unclear, the functional data demonstrating that FGFR1 signaling is required for the survival of breast cancer cells harboring FGFR1 amplification and the relatively high prevalence of FGFR1 amplification in breast cancer support the idea that this gene may be a useful therapeutic target for a subgroup of breast cancer patients with FGFR1 gene amplification.

The FGFR1 (8p12) break-apart probe is optimized to detect translocations involving the FGFR1 gene region at 8p12 in a dual-color, split assay on metaphase/interphase spreads and paraffin embedded tissue sections.

Cat.# KBI-10737 FGFR1 (8p12) Break





FGFR1 (8p12) Break probe hybridized to patient material showing a break at 8p12 (1RG1R1G).

Literature:

Smedley et al, 1998, Hum Mol Genet. 7; 627-642.
Sohal et al, 2001, Genes Chrom. Cancer 32; 155-163.

Ordering information	*Color*	*Tests*	*Cat#*
ON FGFR1 (8p12) Break	red/green	10	KBI-10737

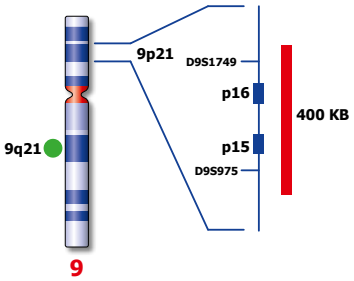
Bladder Cancer

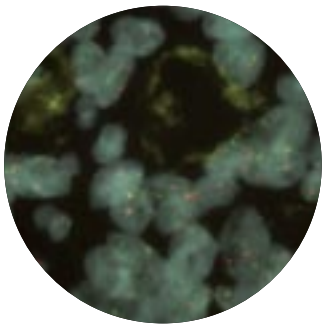
ON p16 (9p21) / 9q21 (tissue)

Homozygous and hemizygous deletions of 9p21 are the earliest and most common genetic alteration in bladder cancer. The p16 (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 p16 (9p21) specific DNA probe is optimized to detect copy numbers of the p16 gene region at region 9p21. The 9q21 region probe is included to facilitate chromosome identification.

Cat.# KBI-10710 p16 (9p21) / 9q21 (tissue)





p16 (9p21) / 9q21 (tissue) probe hybridized to tissue (2R2G).

Literature:

Stadler et al, 1994, Cancer Res, 54: 2060-2063.
Williamson et al, 1995, Hum Mol Genet, 4: 1569-1577.

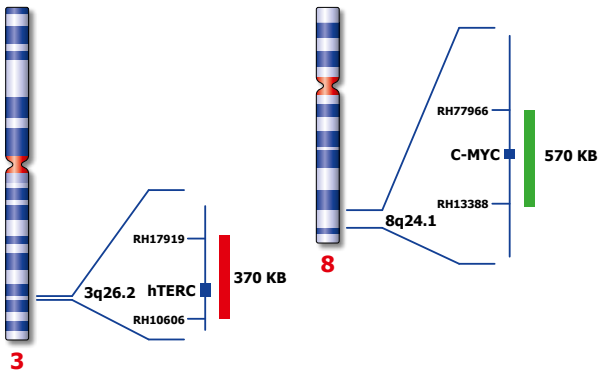
Ordering information	Color	Tests	Cat#
ON p16 (9p21) / 9q21 (tissue)	red/green	10	KBI-10710

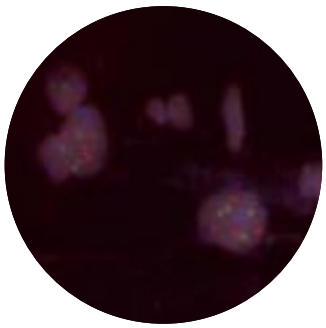
Cervical Cancer

ON CC hTERC (3q26) / C-MYC (8q24) / SE 7 TC

Cervical cancer, a potentially preventable disease, remains the second most common malignancy in women worldwide. The most consistent chromosomal gain in aneuploid tumors of cervical squamous cell carcinoma mapped to chromosome arm 3q, including the human telomerase gene locus (hTERC) at 3q26. High-level copy number increases were also mapped to chromosome 8. Integration of HPV (Human Papilloma Virus) DNA sequences into C-MYC chromosomal regions have been repeatedly observed in cases of invasive genital carcinomas and in cervical cancers. The hTERC (3q26) specific DNA Probe is optimized to detect copy numbers of the hTERC gene region at region 3q26. The C-MYC (8q24) specific DNA probe is optimized to detect copy numbers of the C-MYC gene region at 8q24. The chromosome 7 satellite enumeration probe (SE 7) at D7Z1 is included as ploidy control.

Cat.# KBI-10704 Cervical Cancer hTERC (3q26) / C-MYC (8q24) / SE 7 Triple-Color





CC hTERC (3q26) / C-MYC (8q24) / SE 7 TC 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

Literature:

Heselmeyer et al, 1996, PNAS, 93: 479-484.
Herrick et al, 2005, Cancer Res, 65: 1174-1179.

Ordering information	Color	Tests	Cat#
ON CC hTERC (3q26) / C-MYC (8q24) / SE 7 TC	red/green	10	KBI-10704

Thyroid Carcinoma

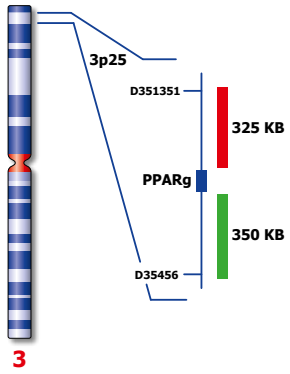
Papillary thyroid carcinoma (PTC) is the most frequent primary carcinoma of the thyroid gland. The follicular carcinomas are associated with endemic goiter and a diet with low iodine intake. PTC, conversely, are multifocal and are associated with prior radiation and high iodine intake.

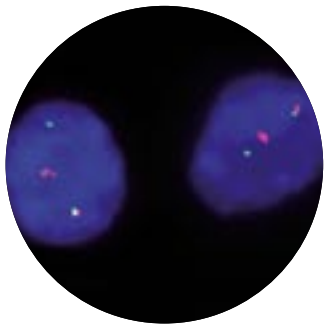
ON PPARγ (3p25), Break

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 γ (PPARγ). The close surrounding of PPAR is 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 PPARγ is best used to analyze translocation of the PPARγ (3p25) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

Cat.# KBI-10707 PPARγ (3p25) Break





PPARγ (3p25) Break probe hybridized to patient material showing a translocation at 3p25 (1RG1R1G).
Image kindly provided by Dr Valent, Paris

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

Ordering information	*Color*	*Tests*	*Cat#*
ON PPARγ (3p25), Break	red/green	10	KBI-10707

Neuroblastoma

According to the International Neuroblastoma Risk Grouping (INRG) Biology Committee MYCN remains the only genomic factor to be used currently for treatment stratification. Common data elements to be obtained by all groups include tumor cell ploidy and copy number/LOH status at chromosome bands 1p36, 11q23, and 17q23-25.

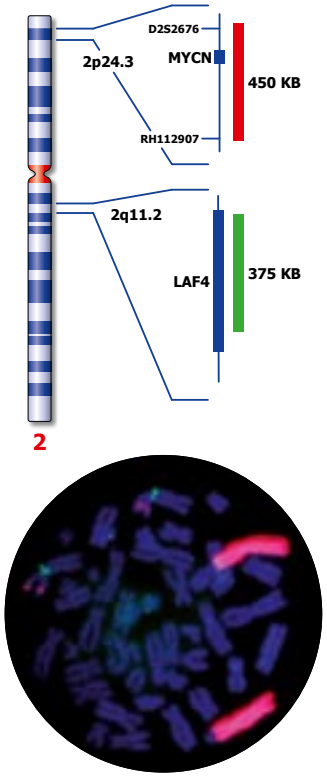
Literature:
Ambros et al, 2006, Advances in Neuroblastoma Research

ON MYCN (2p24) / LAF (2q11)

Amplification of the human N-myc protooncogene, 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) specific DNA probe is optimized to detect copy numbers of the MYCN gene region at 2p24. The LAF gene region probe at 2q11 is included to facilitate chromosome identification.

Cat.# KBI-10706 MYCN (2p24) / LAF (2q11)



MYCN (2p24) / LAF (2q11) hybridized to a cell line showing amplification of MYCN on chromosome 13 and 15.
Image kindly provided by Pasteur Workshop 2008, Paris

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

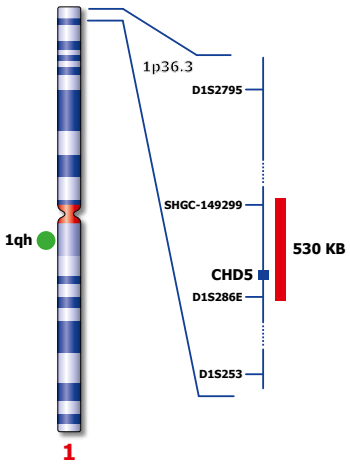
Ordering information	*Color*	*Tests*	*Cat#*
ON MYCN (2p24) / LAF (2q11)	red/green	10	KBI-10706

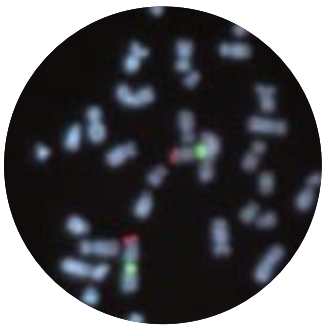
ON SRD 1p36 / SE 1(1qh)

Neuroblastomas frequently have deletions of chromosome 1p and amplification of the N-myc oncogene. These deletions tend to be large and extend to the telomere, but a common region within sub-band 1p36.3 is consistently lost. Inactivation of a tumor suppressor gene within 1p36.3 is believed to be associated with an increased risk for disease relapse. The 1p36 specific DNA probe has recently been changed to cover the recently described smallest region of consistent deletion **(SRD)** between D1S2795 and D1S253.

The SRD (1p36) specific DNA 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.

Cat.# KBI-10712 SRD (1p36) / SE 1(1qh)





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

Literature:

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

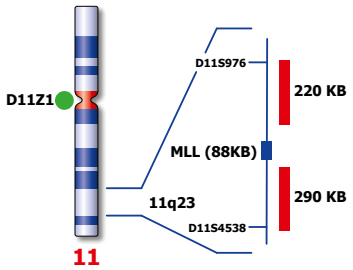
Ordering information	Color	Tests	Cat#
ON SRD (1p36) / SE1(1qh)	red/green	10	KBI-10712

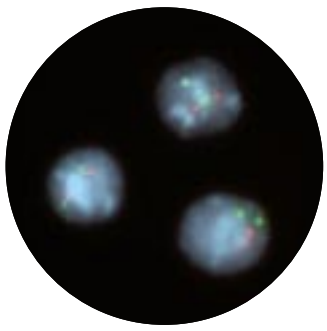
ON MLL (11q23) / SE 11

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 MLL (11q23) specific DNA probe is optimized to detect amplification or deletion involving the MLL gene region at 11q23 in a dual-color assay on metaphase/interphase spreads, blood smears and bone marrow cells. The Chromosome 11 Satellite Enumeration probe (SE 11) at D11Z1 is included to facilitate chromosome identification.

Cat.# KBI-10711 MLL (11q23) / SE 11





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

Literature:

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

Ordering information	Color	Tests	Cat#
ON MLL (11q23) / SE11	red/green	10	KBI-10711

ON p53 (17p13) / MPO (17q22) "ISO 17q"

Gain of genetic material from chromosome arm 17q (gain of segment 17q21-qter) is the most frequent cytogenetic abnormality of neuroblastoma cells. In multivariate analysis, 17q gain was more strongly associated with adverse outcome than was either stage (Stage 4 vs other combined) or 1p status.

Cat.# KBI-10011 p53 (17p13) / MPO (17q23) "ISO 17q"

See probe description under CML on page 15.

Literature:

Bown et al, 1999, N Engl J Med, 340: 1954-1961.
O'Neill, 2001, Genes Chrom Cancer, 30: 87-90.

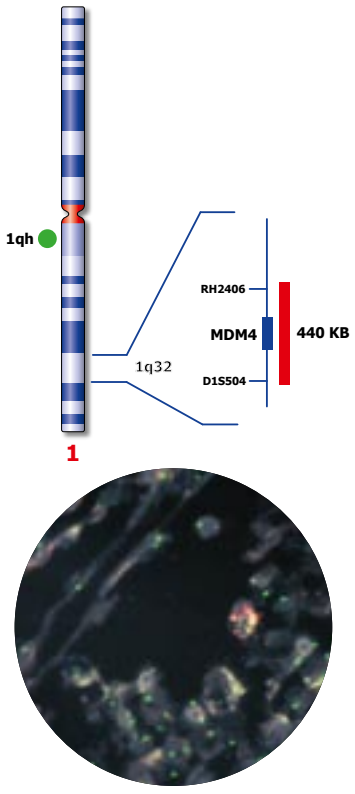
Ordering information	Color	Tests	Cat#
ON p53 (17p13) / MPO (17q22) "ISO 17q"	red/green	10	KBI-10011

ON MDM4 (1q32) / SE1

MDM4 (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 p53. MDM4, like MDM2, acts as a key negative regulator of p53 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) specific DNA 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.

Cat.# KBI-10736 MDM4 (1q32) / SE 1



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

Literature:

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

Ordering information	Color	Tests	Cat#
ON MDM4 (1q32) / SE 1	red/green	10	KBI-10736

Sarcoma

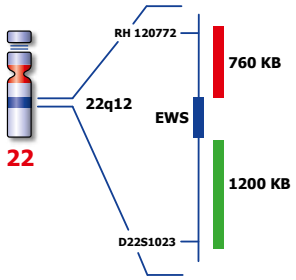
Sarcoma is a general class of less common cancers in which the cancer cells arise from or resemble normal cells in the body known as "connective tissues" (fat, muscle, blood vessels, deep skin tissues, nerves, bones, and cartilage). The benign and malignant forms have related karyotypic changes which provide an important resource for identifying the additional genetic changes that occur in the malignant compared with the benign form. In fact, the molecular biology of soft-tissue sarcomas has provided the perfect example of how cytogenetic and molecular approaches can contribute toward a clearer understanding of the development of soft-tissue sarcomas.

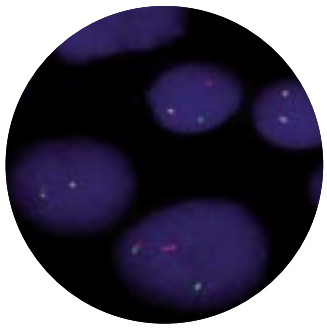
ON EWSR1 (22q12) Break

The translocation t(11;22)(q24;q12) has been independently described by several groups in the malignant cells of patients with Ewing sarcoma and can be detected in more than 90% of these tumors. The translocation involves the fusion of the human FLI1 gene on chromosome 11, with the coding sequence of the EWS gene on chromosome 22. In about 5% of the cases, however, the EWS gene is involved in variant translocations. These translocations, t(21;22)(q12;q12) and t(7;22)(p22;q12) result in the fusion of EWS with ERG and ETV1, respectively.

The Poseidon break or split probe for EWS is optimized to identify translocation involving the EWS gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

Cat.# KBI-10708 EWS (22q12) Break





EWS (22q12) Break probe hybridized to patient material showing a translocation involving the EWRS1 gene region at 22q12 (1RG1R1G).

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

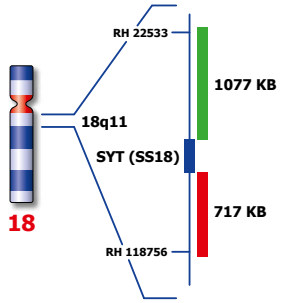
Ordering information	*Color*	*Tests*	*Cat#*
ON EWSR1 (22q12) Break	red/green	10	KBI-10708

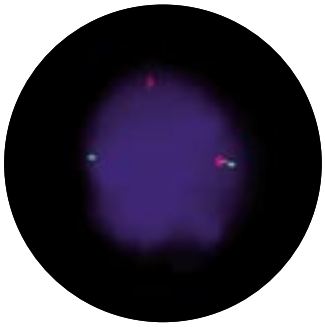
ON SYT (18q11) Break

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

A break or split probe for SYT is best used to analyze translocation of the SYT (SS18) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

Cat.# KBI-10713 SYT (18q11) Break





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

Literature:

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

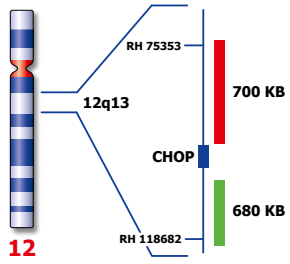
Ordering information	Color	Tests	Cat#
ON SYT (18q11) Break	red/green	10	KBI-10713

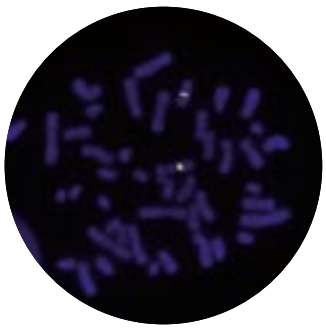
ON CHOP (12q13) Break

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)(CHOP-FUS) or t(12;22)(CHOP-EWS) translocation, both of which involve the CHOP gene at 12q13. A break or split probe for CHOP is best used to analyze translocation of the CHOP (12q13) gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

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

Cat.# KBI-10714 CHOP (12q13) Break





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

Literature:

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

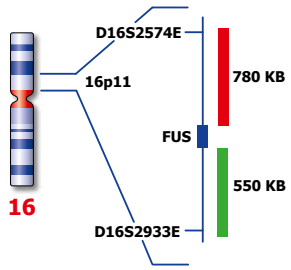
Ordering information	Color	Tests	Cat#
ON CHOP (12q13) Break	red/green	10	KBI-10714

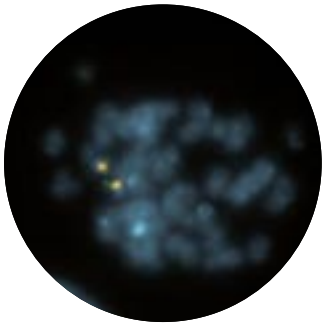
ON FUS (16p11) Break

The FUS gene was originally shown to be rearranged in myxoid liposarcomas harboring a t(12;16)(q13;p11) translocation. FUS has been shown to be involved also 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.

Cat.# KBI-10715 FUS (16p11)





FUS (16p11) Break probe hybridized to liposarcoma material (2RG).

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

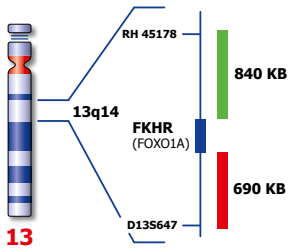
Ordering information	*Color*	*Tests*	*Cat#*
ON FUS (16p11), Break	red/green	10	KBI-10715

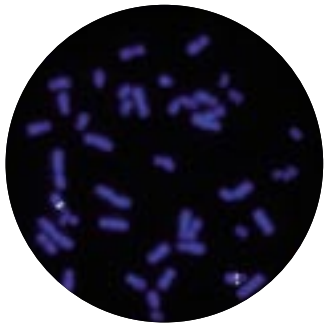
ON FKHR (13q14) Break

The t(2;13) is associated with alveolar rhabdomyosarcomas. 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 FKHR 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 FKHR gene on chromosome 13.

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

Cat.# KBI-10716 FKHR (13q14) Break





FKHR (13q14) Break probe hybridized to a normal metaphase (2RG).

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

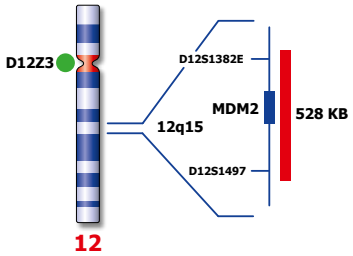
Ordering information	*Color*	*Tests*	*Cat#*
ON FKHR (13q14) Break	red/green	10	KBI-10716

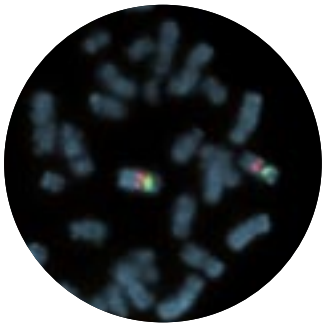
ON MDM2 (12q15) / SE 12

Fibrosarcoma is a rare soft-tissue tumor composed of fascicles of spindled fibroblast-like cells. Gains and high-level amplifications of 12q14–22 were the most common genomic imbalances, and reflected MDM2 amplification, thereby indicating the importance of this gene in the evolution of fibrosarcomas.

The MDM2 (12q15) specific DNA probe is optimized to detect copy numbers of the MDM2 gene region at region 12q15. The Chromosome 12 Satellite Enumeration probe (SE 12) at D12Z3 is included to facilitate chromosome identification.

Cat.# KBI-10717 MDM2 (12q15) / SE 12





MDM2 (12q15) / SE 12 hybridized to a normal metaphase (2R2G).

Literature:

Mitchell et al, 1995, Chrom. Res., 3; 261-262.
Reifenberger et al, 1996, Cancer Res., 15; 5141-5145.

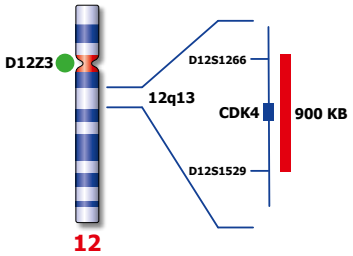
Ordering information	Color	Tests	Cat#
ON MDM2 (12q15) / SE12	red/green	10	KBI-10717

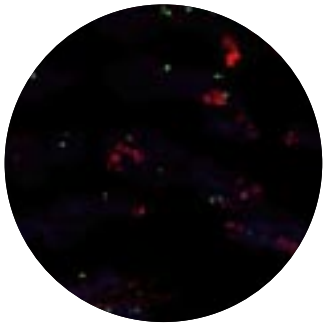
ON CDK4 (12q13) / SE 12

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) specific DNA 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.

Cat.# KBI-10725 CDK4 (12q13) / 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.

Literature:

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

Ordering information	Color	Tests	Cat#
ON CDK4 (12q13) / SE 12	red/green	10	KBI-10725

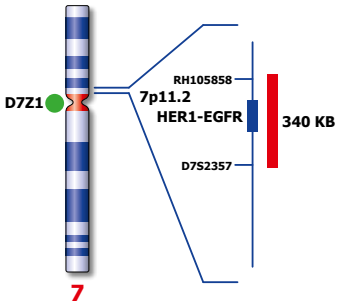
Different Cancer types

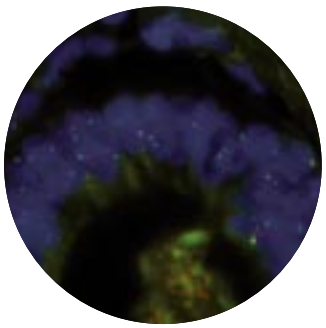
ON EGFR, Her-1 (7p11) / SE 7

Epidermal growth factor receptor (EGFR) is a cell membrane protein, providing signal transduction and cell growth. It is a member of the Her or Erb-B family of type I receptor tyrosine kinases and implicated in the development and progression of cancer of the lung, breast, intestine, and other organs. EGFR was 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) specific DNA probe is optimized to detect copy numbers of the EGFR (Her1) gene region at region 7p11. The chromosome 7 satellite enumeration probe (SE 7) at D7Z1 is included to facilitate chromosome identification.

Cat.# KBI-10702 EGFR, Her1 (7p11) / SE 7





EGFR, Her1 (7p11) / SE 7 hybridized to colon tissue (2R2G).

Literature:

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

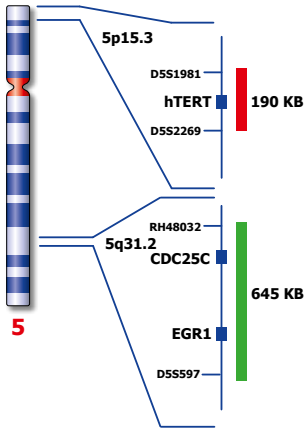
Ordering information	*Color*	*Tests*	*Cat#*
ON EGFR, Her-1 (7p11) / SE 7	red/green	10	KBI-10702

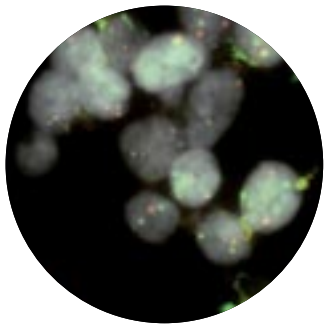
ON hTERT (5p15) / 5q31 (tissue)

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

The hTERT (5p15) 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.

Cat.# KBI-10709 hTERT (5p15) / 5q31 (tissue)





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

Literature:

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

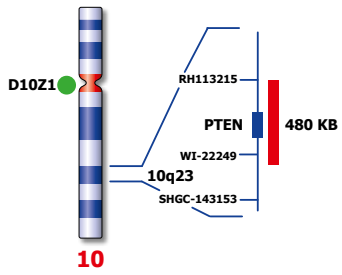
Ordering information	*Color*	*Tests*	*Cat#*
ON hTERT (5p15) / 5q31 (tissue)	red/green	10	KBI-10709

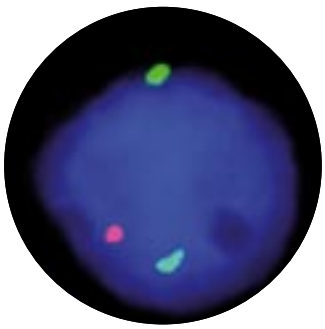
ON PTEN (10q23) / SE 10

The gene 'phosphatase and tensin homolog deleted on chromosome 10' (PTEN), is a tumor suppressor located at chromosome 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 his important role is demonstrated by the fact that it is the second most frequently mutated gene after p53. Loss of PTEN significantly correlates with the advanced forms of gliomas, but also of prostate cancer and breast tumors.

The PTEN (10q23) specific DNA 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.

Cat.# KBI-10718 PTEN (10q23) / 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

Literature:

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

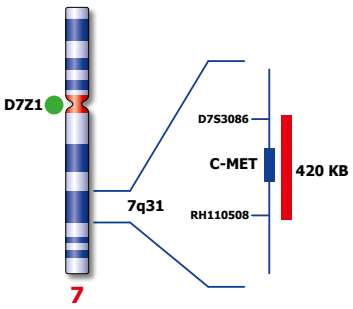
Ordering information	*Color*	*Tests*	*Cat#*
ON PTEN (10q23) / SE 10	red/green	10	KBI-10718

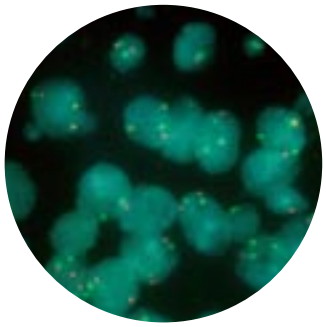
ON C-MET (7q31) / SE 7

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

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

Cat.# KBI-10719 C-MET (7q31) / SE 7





C-MET (7q31) / SE 7 probe hybridized to colon tissue (2R2G).

Literature:

Hara et al, 1998, Lab Invest 78; 1143-1153.
Tsugawa et al., 1998, Oncology 55; 475-481.

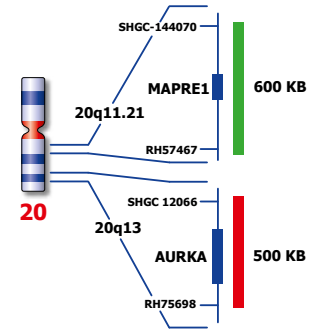
Ordering information	*Color*	*Tests*	*Cat#*
ON C-MET (7q31) / SE 7	red/green	10	KBI-10719

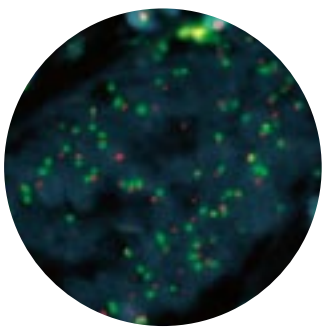
ON AURKA (20q13) / 20q11

Aurora kinase A (AURKA) covers the fundamental role of regulating proper centrosome function, important to maintain genomic stability during cell division and to ensure equal segregation of replicated chromosomes to daughter cells. Deregulated duplication and distribution of centrosomes has been implicated in mechanisms leading to mitotic spindle aberrations, aneuploidy, and genomic instability that are seen in many different tumor types. Consistent with this, AURKA amplification has been detected in approximately 12% of primary breast tumors, as well as in breast, ovarian, colon, prostate, neuroblastoma and cervical cancer cell lines. Recent investigations on new drugs developments have focused on the importance of aurora kinases for tumor suppression.

The AURKA (20q13) specific DNA 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.

Cat.# KBI-10721 AURKA (20q13) / 20q11





AURKA (20q13) / 20q11 probe hybridized to breast tumor tissue (2R2G).

Literature:

Sen et al, 2002, J of Nat Canc Inst 94; 1320-1329.
Lassmann et al, 2007, Clin Cancer Res 13; 4083-4091

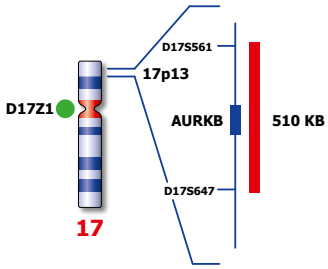
Ordering information	*Color*	*Tests*	*Cat#*
ON AURKA (20q13) / 20q11	red/green	10	KBI-10721

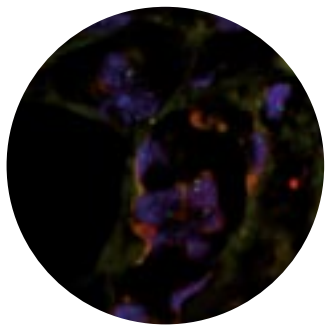
ON AURKB (17p13) / SE 17

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. Recently new drugs have been under investigation for their capacity of interfering with the aurora kinases activity related to tumor-suppressor effects.

The AURKB (17p13) specific DNA 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.

Cat.# KBI-10722 AURKB (17p13) / SE 17





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

Literature:

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

Ordering information	*Color*	*Tests*	*Cat#*
ON AURKB (17p13) / SE 17	red/green	10	KBI-10722

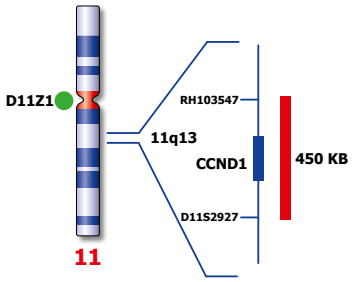
ON CCND1 (11q13) / SE 11

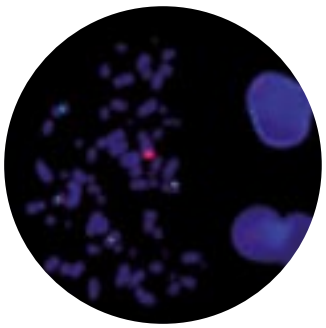
CCND1 (also named Cyclin D1 or BCL1) is a key cell cycle regulator of the G1 to S phase progression. The binding of cyclin D1 to cyclin-dependent kinase (CDKs) leads to the phosphorylation of retinoblastoma protein (pRb), subsequently triggering the release of E2F transcription factors to allow G1 to 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.

Amplification of cyclin D1 plays pivotal roles in the development of a subset of human cancers including parathyroid adenoma, breast cancer, colon cancer, lymphoma, melanoma, and prostate cancer.

The CCND1 (11q13) specific DNA 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.

Cat.# KBI-10734 CCND1 (11q13) / SE 11





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

Literature:
Okami et al, 1999, Oncogene 18; 3541-3545.
Freier et al, 2003, Cancer Res; 1179-1182

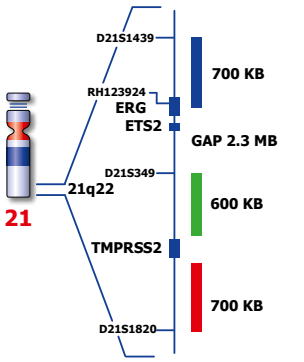
Ordering information	*Color*	*Tests*	*Cat#*
ON CCND1 (11q13) / SE 11	red/green	10	KBI-10734

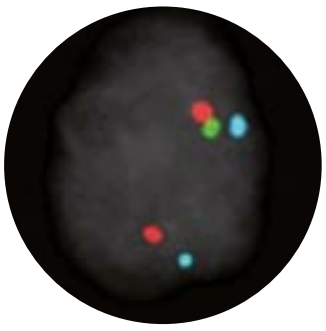
TMPRSS2-ERG (21q22) Del, Break, TC

The transmembrane protease serine 2 gene (TMPRSS2) is involved in gene fusions with ERG, ETV1 or ETV4 in prostate cancer. In recent studies it has been described 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).

Cat.# KBI-10726 TMPRSS2-ERG (21q22) Del, Break, TC





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. Texeira, Porto.

Literature:

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

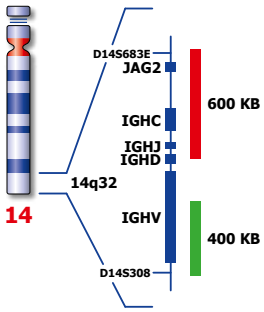
Ordering information	*Color*	*Tests*	*Cat#*
TMPRSS2-ERG (21q22) Del, Break, TC	red/green	10	KBI-10726

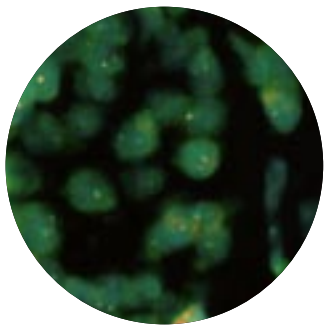
ON IGH (14q32) Break (tissue)

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. Kreatech has developed this probe for the specific use on cell material (KBI-10601), or for the use on tissue (KBI-10729).

Cat.# KBI-10729 ON IGH (14q32) Break (tissue)





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

Literature:

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

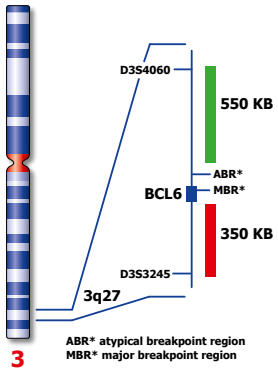
Ordering information	*Color*	*Tests*	*Cat#*
ON IGH (14q32) Break (tissue)	red/green	10	KBI-10729

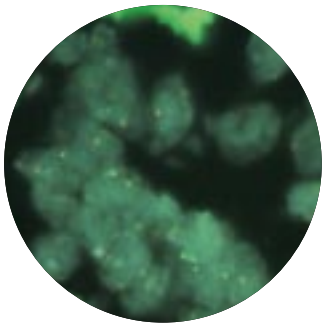
ON BCL6 (3q27) Break (tissue)

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).

Note: 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 250 kb proximal to the BCL6 gene. The Poseidon BCL6 (3q27) is designed in a way to flank both possible breakpoints, thereby providing clear split signals in either case.

Cat.# KBI-10730 ON BCL6 (3q27) 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

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

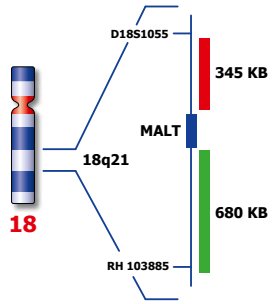
Ordering information	Color	Tests	Cat#
ON BCL6 (3q27) Break (tissue)	red/green	10	KBI-10730

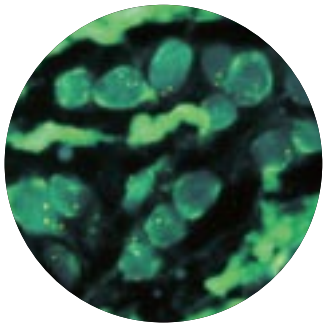
ON MALT (18q21) Break (tissue)

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 MALT (18q21) is best used to analyze translocation of the MALT gene on formalin fixed paraffin embedded tissue for routine clinical diagnosis.

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

Cat.# KBI-10731 ON MALT (18q21) Break (tissue)





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

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

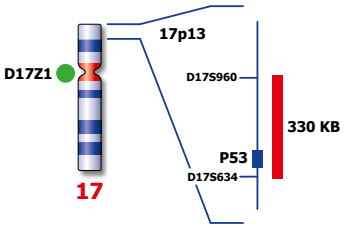
Ordering information	Color	Tests	Cat#
ON MALT (18q21) Break (tissue)	red/green	10	KBI-10731

ON p53 (17p13) / SE 17 (tissue)

The p53 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 p53 have been reported in numerous tumor types and are associated with poor prognosis in CLL.

The p53 (17p13) specific DNA probe is optimized to detect copy numbers of the p53 gene region at 17p13. The chromosome 17 satellite enumeration probe (SE 17) at D17Z1 is included to facilitate chromosome identification.

Cat.# KBI-10738 p53 (17p13) / SE 17 (tissue)



P53 (17p13) / SE 17 (tissue) probe hybridized to paraffin embedded tissue (2R2G).

Literature:

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

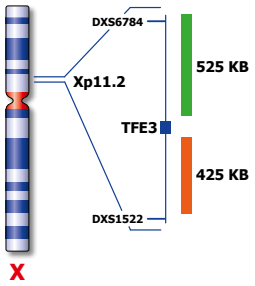
Ordering information	*Color*	*Tests*	*Cat#*
ON p53 (17p13) / SE 17 (tissue)	red/green	10	KBI-10738

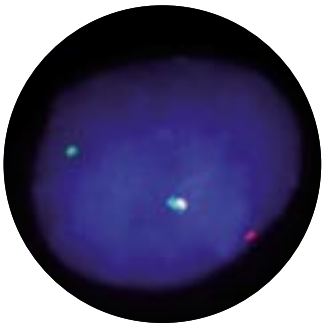
ON TFE3 (Xp11) Break

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, split assay.

Cat.# KBI-10741 TFE3 (Xp11) Break





TFE3 (Xp11) Break probe hybridized to renal cell carcinoma showing a translocation at Xp11 (1RG1R1G).
Image kindly provided by Dr. Desangles, Paris

Literature:

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

Ordering information	*Color*	*Tests*	*Cat#*
ON TFE3 (Xp11) Break	red/green	10	KBI-10741