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# FAST FLUORESCENCE *IN SITU* HYBRIDIZATION PROBE KIT CATALOGUE

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## SOLID TUMORS

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# BLOOD TUMORS

# BREAST CANCER

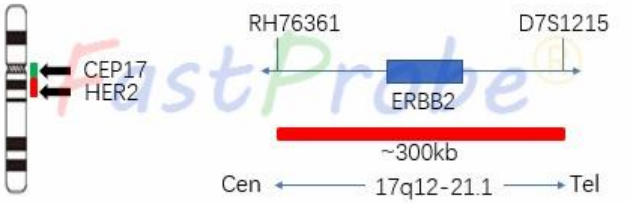
## HER2 gene amplification probe

### Background

Human epidermal growth factor receptor 2 (HER2, also known as ERBB2, Neu, ErbB-2, CD340 or p185) is a proto-oncogene HER2/neu located on the long arm 17q12 of human chromosome 17. HER2 is a member of the epidermal growth factor receptor (EGFR/ErbB) family. It has tyrosine kinase activity and is involved in signal transduction of cell growth and differentiation. The oncogenic mechanism of the HER2 oncogene includes inhibition of apoptosis, promotion of cell proliferation, increase of invasiveness of tumor cells, and promotion of tumor vascular and lymphangiogenesis. About 20% of breast cancer and 12% of gastric cancer patients show positive HER2 gene amplification.

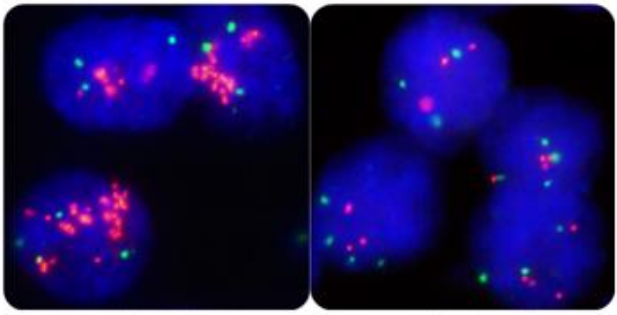
### Probe description

The HER2 gene amplification probe uses the orange-red fluorescent dye to label the HER2 gene region, and the green fluorescent dye is used to label the chromosome 17 centromere region (CEP17). The HER2 gene marker region is located at 17q12-q21.1, and the CEP17 probe binds an alpha satellite sequence, which has extremely high specificity and does not hybridize with other chromosome centromeres to produce noisy spots.




## Clinical significance

Fluorescence *in situ* hybridization (FISH) is a clinically recognized "gold standard" for HER2 detection. It can accurately and repeatedly evaluate the status of HER2 gene in cancer cells. Compared with IHC, FISH has higher consistency. The patients with positive HER2 gene amplification were effectively treated with targeted drugs such as monoclonal antibodies Herceptin and Lapatinib. The prognosis of patients with positive HER2 gene amplification was poor, and the disease-free survival and overall survival were significantly shortened.



HER2 amplification [+] HER2 amplification [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| Human HER2 gene amplification detection kit | FP-001 | HER2/CEP17 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Allison M, Nature Biotechnology 28 (2): 117-119, 2010.
Mass R, et al. Clinical Breast Cancer, Vol 6, No. 3, 240-246, 2005.
Press M, et al, Clinical Cancer Research 2005; 11(18) September 15, 2005
Sauter G, et al. J Clin Oncol 27:1323-1333, 2009.

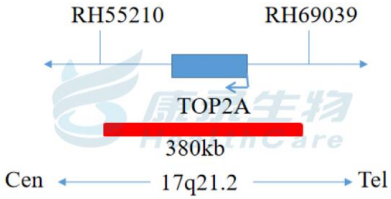
# TOP2A gene amplification probe detection kit

## Background

TOP2A gene encodes a DNA topoisomerase that participates in processes such as chromosomal concentration, chromatid separation, and release of torsional stress during DNA transcription and replication. The gene encoding this form, TOP2A, is located on chromosome 17, the beta gene located on chromosome 3, and multiple mutations in the TOP2A gene are involved in development.

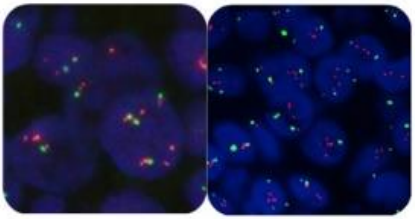
## Probe description

TOP2A gene amplification probe uses the orange-red fluorescent dye to label the TOP2A gene region, and the green fluorescent dye to label the chromosome 17 centromere region (CEP17). TOP2A gene-labeled region is located at 17q21.2, and the CEP17 probe binds an alpha satellite sequence, which has extremely high specificity and does not hybridize with other chromosome centromeres to produce noisy spots.




## Clinical significance

Patients with abnormal TOP2A gene indicates a shorter recurrence-free survival, and patients with TOP2A gene deletion have a worse prognosis. In the study of advanced breast cancer, it was found that the abnormality of TOP2A gene was significantly correlated with the protein expression and the sensitivity of tumor cells to anthracyclines. Therefore, the detection of TOP2A gene status has guiding significance for the treatment and prognosis of breast cancer.



TOP2A amplification [+] TOP2A amplification [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| TOP2A gene amplification probe detection kit | FP-008 | TOP2A/CEP17 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Brunello E, et al. (2012) Histopathology 60: 482-8.
Razis E, et al. (2011) Breast Cancer Res Treat 128: 447-56.

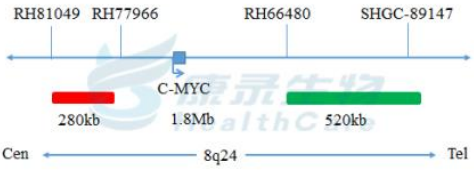
# MYC gene amplification probe detection kit

## Background

The MYC proto-oncogene is located on chromosome 8q24 and encodes a transcription factor that regulates cell growth. It is activated mainly by amplification and chromosome translocation rearrangement. MYC gene amplification is associated with the development of a variety of tumors (including breast cancer, colon cancer, lung cancer, hematopoietic tumors etc.).

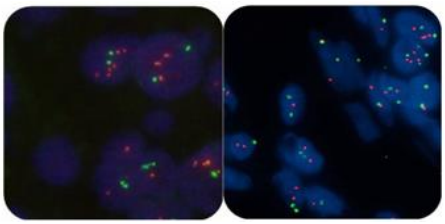
## Probe description

MYC gene amplification probe uses orange-red fluorescent dye to label MYC gene region, and green fluorescent dye to label chromosome 8 centromere region (CEP8). The MYC gene marker region is located at 8q24.21, and the CEP8 probe hybridizes with a specific alpha satellite sequence.




## Clinical significance

MYC gene amplification is a common phenomenon in tumors and can be found in a variety of malignant tumors such as breast cancer, nasopharyngeal cancer and cervical cancer. The prognosis of breast cancer patients with MYC gene amplification is poor.



MYC amplification [+] MYC amplification [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYC（8q24）gene amplification probe reagent | FP-015 | C-MYC/CEP8 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**
Fromont G, et al. (2013) Hum Pathol 44: 1617-23.
Mannuci S, et al. (2012) Adv Hematol 2012: 149780.

# LUNG CANCER

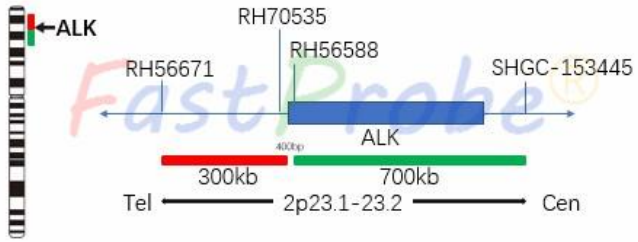
## Human ALK gene fusion detection probe

### Background

ALK gene encodes a transmembrane receptor tyrosine kinase (RTK). The ALK-NPM1 fusion protein was first discovered in anaplastic large cell lymphoma (ALCL). It has been found to mutate, amplify or rearrange in other tumors, including neuroblastoma and non-small cell lung cancer. Chromosome rearrangement is the most common cause of ALK and other genes. Fusion, including ALK/EML4, ALK/RANBP2, ALK/ATIC, ALK/TFG, ALK/NPM1, ALK/SQSTM1, ALK/KIF5B, ALK/CLTC, ALK/TPM4 and ALK/MSN.

### Probe description

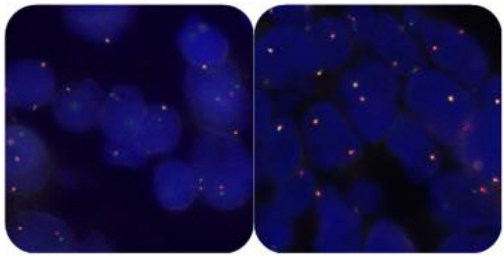
ALK gene break-apart probe uses an orange-red fluorescent dye to label the 2p23.2 region (3' end), and the green dye to label ALK gene 2p23.1-p23.2 region (5' end). ALK gene break-apart probe detects all ALK gene rearrangements and avoids missed diagnosis by a single fusion gene (such as EML4-ALK).




## Clinical significance

The positive rate of ALK gene is as high as 30-42% in NSCLC patients with adenocarcinoma, young (< 60 years old), non-smoking and no mutation in EGFR, KRAS, HER2 or P53 genes. Pathological studies suggest that the positive rate of mucinous or solid adenocarcinomas with signet ring cells is higher than that of other types of lung adenocarcinomas.

Patients with positive ALK gene fusion are sensitive to XALKORI (Crizotinib).



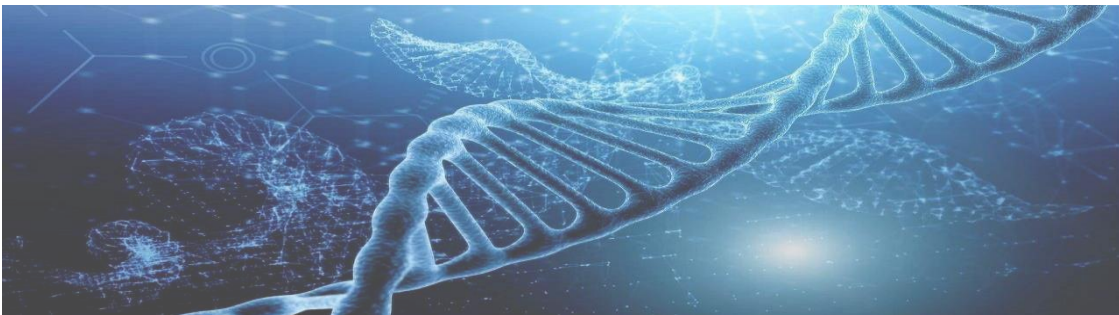
ALK fusion [+] ALK fusion [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| Human ALK gene fusion detection probe | FP-002 | ALK | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Rodig SJ, et al. (2009) Clin Cancer Res 15: 5216-23.
Sasaki T, et al. (2010) Eur J Cancer 46: 1773-80.
Von Laffert M, et al. (2013) Lung Cancer 81: 200-6.



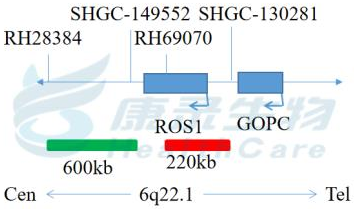
# ROS1 gene break apart probe

## Background

C-ros sarcoma ROS-receptor tyrosine kinase (ROS1) is located on chromosome 6q22 and encodes a receptor tyrosine kinase (RTK), which is involved in cell growth and proliferation, differentiation and survival. When the ROS1 gene is rearranged, the extracellular region is lost, and the transmembrane region and the intracellular tyrosine kinase region are retained. The rearrangement site mainly occurs in the 32 to 36 exons of the ROS1 gene. In non-small cell lung cancer (NSCLC), ROS1 gene is mainly fused with SLC34A2, CD74, EZR and SDC4, and continues to activate ROS1 tyrosine kinase domain and downstream signaling pathway, which leads to tumor development.

## Probe description

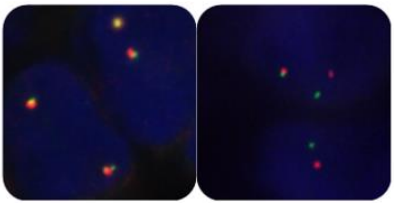
ROS1 gene break-apart probe uses orange-red fluorescent dye to label the 5' end region of the ROS1 gene, and a green fluorescent dye to label the 3' end region of the ROS1 gene. ROS1 gene break-apart is able to detect all ROS1 gene rearrangements, avoiding the missed diagnosis caused by a single gene fusion.




## Clinical significance

ROS1 gene rearrangement mainly occurs in young, non-smoking patients with lung adenocarcinoma. ROS1 gene rearrangement is different from other mutations such as EGFR, KRAS or ALK. The positive rate of ROS1 rearrangement is 1.0-3.4% in NSCLC and 5.7% in EGFR, KRAS and ALK negative population.

Patients with positive ROS1 rearrangement are sensitive to XALKORI (Crizotinib) drugs.



ROS1 break apart [-] ROS1 break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| 6q probe reagent | FP-006 | ROS1 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Brunello E, et al. (2012) Histopathology 60: 482-8.

Razis E, et al. (2011) Breast Cancer Res Treat 128: 447-56.

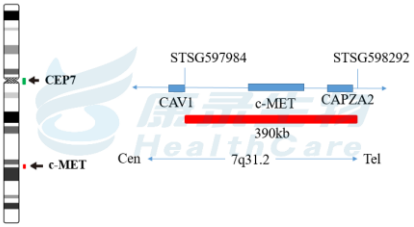
# MET gene amplification probe

## Background

MET gene is located on chromosome 7q31.2 and encodes a transmembrane tyrosine kinase receptor. The ligand of MET is hepatocyte growth factor (HGF), which is secreted by mesenchymal cells. The binding of HGF and c-MET can promote cell proliferation, migration, differentiation and morphological changes. The HGF/c-MET signaling pathway is highly regulated and plays an important role in cell proliferation, differentiation and movement.

## Probe description

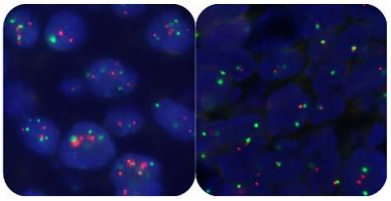
MET gene amplification probe uses orange-red fluorescent dye to label MET gene region, and green fluorescent dye to label chromosome 7 centromere region (CEP7). MET gene marker region is located at 7q31.2, and the CEP7 probe is binds a specific alpha satellite sequence.




## Clinical significance

MET gene can be amplified in a variety of tumors such as lung cancer, breast cancer, ovarian cancer, thyroid cancer, gastric cancer, colorectal cancer etc. It is an independent prognostic factor, and the prognosis of patients with MET gene amplification is poor. In NSCLC, MET gene amplification is closely related to poor prognosis and TKIs drug resistance.

MET gene amplification is one of the targets of XALKORI (Crizotinib).



MET amplification [+] MET amplification [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MET gene amplification probe reagent | FP-046 | C-MET/CEP7 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Lacroix L, et al. (2014) PLoS One 1: e84319.

Lee D, et al. (2015) Cancer Res Treat 47: 120-5.

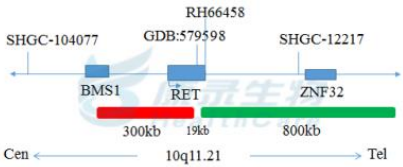
# RET gene amplification probe

## Background

RET gene is located on the long arm of chromosome 10 and encodes a receptor tyrosine kinase. It is expressed in normal neurons, sympathetic and parasympathetic ganglia, thyroid C cells, adrenal myelocytes, genitourinary tract cells, and testicular germ cells. Activation of the RET protein activates downstream signaling pathways (including RAS, MAPK, ERK, PI3K, AKT etc.), resulting in cell proliferation, migration, and differentiation. Also, it is associated with human malignancies.

## Probe description

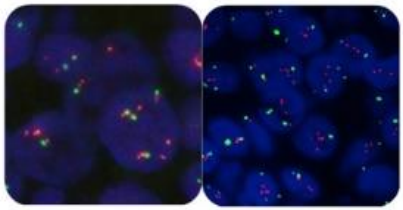
The RET gene break-apart probe uses an orange-red fluorescent dye to label 5' end of the RET gene, and a green fluorescent dye to label 3' end of the RET gene. The RET gene break-apart probe detects all RET gene rearrangements, avoiding missed diagnosis by a single gene fusion.




## Clinical significance

RET gene fusion in patients with non-small cell lung cancer (NSCLC) accounts for 1-2% frequency, and the RET gene is mutually exclusive with other genes such as EGFR, KRAS, ALK, HER2 and BRAF, i.e. the RET gene is an independent gene for driving NSCLC.

At present, there are four fusion partner genes of RET gene: KIF5B, CCDC6, TRIM33 and NCOA4, of which KIF5B is the most often fusion gene, accounting for 90%.



RET amplification [+] RET amplification [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| RET gene amplification probe reagent | FP-059 | RET | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Drilon A, et al., Ann Oncol. 2016 Jul;27(7):1286-91.
Falchook GS, et al., J Clin Oncol. 2016 May 20;34(15):e141-4.
Takashi Kohno, et al., Transl Lung Cancer Res. 2015 Apr;4(2):156-64.

# BLADDER CANCER

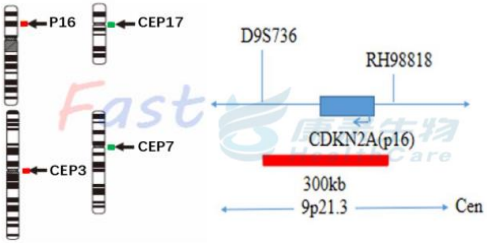
## Bladder cancer detection probe

### Background

Bladder cancer is the most common malignant tumor of the urinary system. It is more common in men. The average age of onset is 65 years. Seventy-five percent of the new cases are superficial tumors, of which 50-80% will have recurrences after treatment, and 15-25% will progress to invasive cancer. Therefore, patients with superficial bladder cancer need to pay close attention to the recurrence and deterioration of the tumor. Cystoscopy or urine exfoliative cytology is recommended for patients with hematuria over 40 years of age. However, cystoscopy can cause unnecessary pain to the patient and is not suitable for large-scale screening. Additionally, the cytological examination is insufficiently sensitive. Fluorescence *in situ* hybridization detection of urine sediment cells showed strong advantages in early diagnosis and postoperative recurrence of bladder cancer.

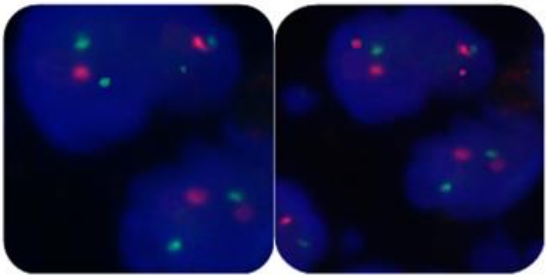
### Probe description

Bladder cancer probes consist of two groups of probes. The orange fluorescence dye is used to label the P16 gene region, the green fluorescent dye is used to label the centromere region of chromosome 17 (CEP17); the orange fluorescent dye is used to label the centromere region of chromosome 3 (CEP3), and the green fluorescent dye is used to label the centromere region of chromosome 7 (CEP7). The P16 gene marker region is located at 9p21.3, and the chromosomal centromere probes binds to a specific alpha satellite sequences.




## Clinical significance

The most common genetic alteration of urinary transitional epithelial cell carcinoma is the partial or total loss of chromosome 9 (e.g. p16 locus). In addition, the development of urinary transitional epithelial cell carcinoma is closely linked to chromosomal instability. In particular, it is closely related to the aneuploidy of chromosomes 3, 7, and 17. FISH is a non-invasive test, which can detect exfoliated cells in patient's urine. If there are two or more abnormalities in the above four indicators, or if one of the indicators has a complex abnormality, it can be determined as the urinary system transitional epithelial cell carcinoma.



P16 deletion Chromosome 7 deletion

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| Bladder Cancer Cells chromosome and gene anomaly probe detection kit | FP-009 | CEP3/CEP7 P16/CEP17 | 200µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Barocas DA, et al. (2006) BJU Int 99: 290-5.
Gallucci M, et al. (2005) J Clin Pathol 58: 367-71.

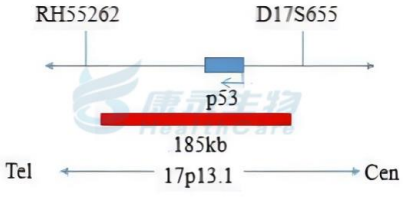
# P53 gene probe

## Background

The P53 gene highly correlates with human tumors and is an important tumor suppressor gene. The 53kD protein encoded by the P53 gene plays an important regulatory role in the cell cycle, it has a growth inhibitory effect under normal conditions, and plays an important role in DNA cell damage response, cell death and differentiation in the cell cycle.

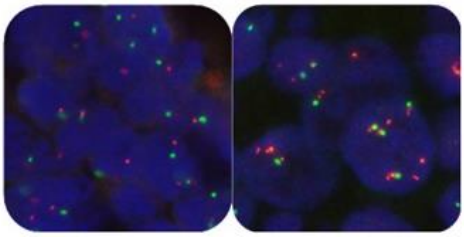
## Probe description

P53 gene amplification probe uses an orange-red fluorescent dye to label the P53 gene region, and a green fluorescent dye to label chromosome 17 centromere region (CEP17). P53 gene marker region is located at 17q13.1, and the CEP17 probe binds to a specific alpha satellite sequence.




## Clinical significance

P53 gene amplification and deletion indicate poor tumor prognosis, its insensitivity to conventional chemotherapy, and tumor inclined to metastasis.



P53 amplification [-] P53 amplification [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| CLL chromosome and gene anomaly probe detection kit | FP-014-2 | P53/CEP17 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Chang H, et al. (2010) Am J Clin Pathol 133: 70-4.
Herrera JC, et al. (2010) Biomedica 30: 390-400.

# BRAIN CANCER

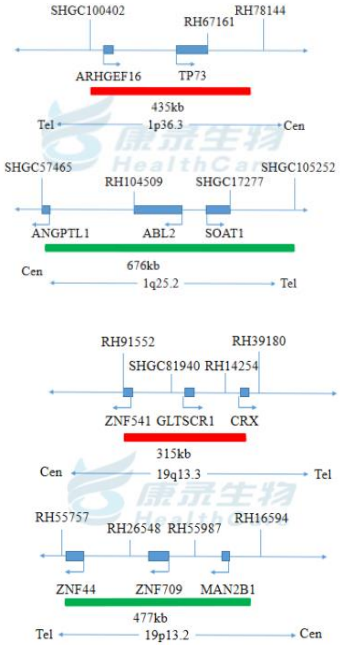
## 1p/19q gene probe

### Background

The most common genetic alteration in oligodendroglioma is the loss of heterozygosity in the long arm (19q) of chromosome 19, which occurs between 50% and 80%, and the most common deletion region is 19q13.3. The second most common is the loss of heterozygosity in the short arm (1p) of chromosome 1, which occurs between 40% and 92%.

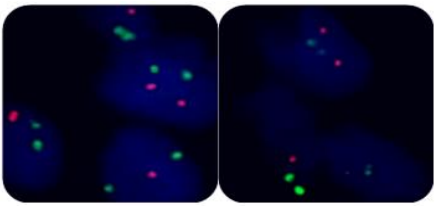
### Probe description

1p/19q deletion probe uses an orange fluorescent dye to label the short arm p36 region of chromosome 1 and a green fluorescent dye to label the long arm q13 region of chromosome 19.




### Clinical significance

The detection of 1p/19q heterozygous deletion has important implications for clinical treatment guidance and prognosis of oligodendroglioma. All patients with heterozygous deletions on chromosome 1p/19q were found sensitive to chemotherapy with PVC regimen, with an average survival of 10 years. The average survival of patients without such genetic alterations is only 2 years. The 1p/19q heterozygous deletion is an independent prognostic factor with significant prognosis, even in recurrent cases. 1p/19q heterozygous deletion is a specific molecular genetic alteration in oligodendroglioma, but it is not the only change, so detection of 1p/19q heterozygous deletion is not recommended for differential diagnosis alone. However, for patients with confirmed oligodendroglioma, detection of 1p/19q heterozygous deletions can provide valuable information to clinicians.



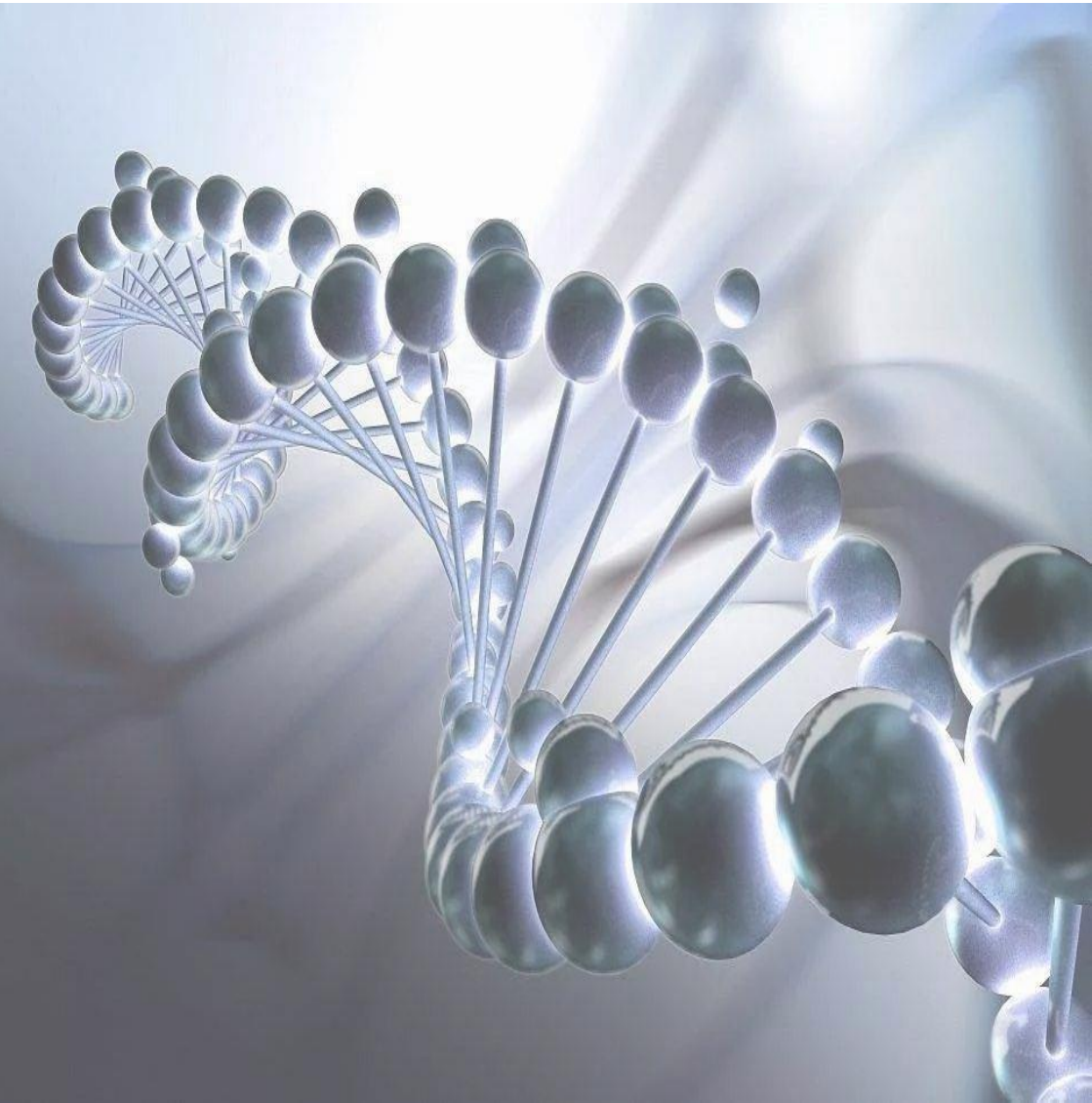
1p deletion [+] 19q deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| 1p/19q deletion probe reagent | FP-045 | 1p36/1q25<br>19q13/19p13 | 200µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Barocas DA, et al. (2006) BJU Int 99: 290-5.
Gallucci M, et al. (2005) J Clin Pathol 58: 367-71.



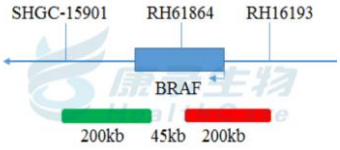
# BRAF gene break apart probe

## Background

BRAF gene is located in the q34 region of chromosome 7 and encodes a 766 aa protein. It is a silk/threonine-specific kinase and is an important transduction factor in the RAS/RAF/MEK/ERK signaling pathway which regulates cell proliferation and division. The BRAF gene can be rearranged with multiple genes such as AKAP9, FCHSD1, and BTF3L4, and plays an important role in the development of tumors. KIAA1549 gene is located in the q34 region of chromosome 7, and the KIAA1549/BRAF fusion gene can occur in 60% to 80% of hair cell astrocytoma.

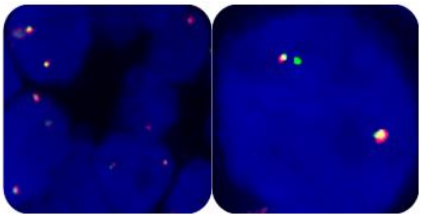
## Probe description

BRAF gene break apart probe (KIAA1549/BRAF gene fusion probe) uses an orange fluorescent dye to mark the 5'end of BRAF gene and a green fluorescent dye to mark the 3'end of BRAF gene. Because BRAF is close to KIAA1549, a conventional BRAF break aprat probe and KIAA1549/BRAF gene fusion probe cannot distinguish positive and negative samples. When BRAF rearrangement is negative, it shows a 2F signal. When BRAF gene is rearranged with other genes, it shows a typical 1R1G1F signal. When BRAF gene is fused with the KIAA1549 gene, it shows specific 1G2F signal.




## Clinical significance

Hairy cell astrocytoma is a cystic astrocytoma with a clear border and slow growth that often occurs in children and young adults. It has been found that 60%-80% of hair cell astrocytoma patients have a KIAA1549/BRAF gene fusion, and the detection of this gene fusion by FISH has a differential significance in low-grade glioma.



KIAA1549/BRAF fusion [-] KIAA1549/BRAF fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| BRAF gene break apart probe reagent | FP-016 | BRAF | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Dougherty MJ, et al. (2010) Neuro Oncol 12: 621-30.
Hutchinson KE, et al. (2013) Clin Cancer Res 19: 6696-702.

# CERVICAL CANCER

## TERC gene amplification probe

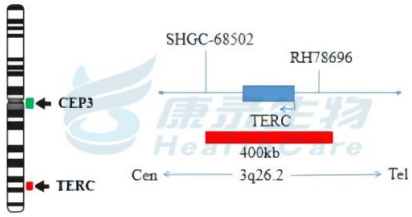
### Background

Cervical cancer is a major malignant tumor that seriously threatens women's health. Its incidence rate ranks second among female reproductive system malignancies. At present, the widespread application of cervical cytology screening and HPV testing have significantly reduced the incidence and mortality of cervical cancer, but the current screening procedures still have certain limitations. For young women, mild cytologic abnormalities are common due to HPV infection. More importantly, cervical cytology screening does not distinguish well between cervical intraepithelial neoplasia (CIN) and prediction whether it progresses. The development of CIN for cervical cancer is a long-term process, and early diagnosis and appropriate treatment may completely block it in the CIN or early stage of cancer. However, not all CIN lesions progress to high lesions, and the currently used morphological diagnosis-based methods sometimes make it difficult to accurately identify CIN and non-tumor lesions, different levels of CIN, resulting in over-treatment or under-treatment. Therefore, complementary methods are needed.

Recent studies have shown that cervical cell carcinogenesis is almost accompanied by the amplification of the long arm of chromosome 3, and the most important region involved may be the genomic locus for telomerase RNA component (TERC) which can prevent cell apoptosis. Data suggest that as the level of cervical lesions increases, the positive rate of TERC gene amplification increases. For example, the proportion of TERC gene amplification in CIN I samples is about 10%, while the proportion of TERC gene amplification in CIN II samples is as high as 60%. When the patient's pathological examination cannot determine whether the condition is CIN I or CIN II, if the TERC gene is amplified, the probability of the patient being CIN II or higher is 90%, and there is a possibility of canceration. Therefore, the detection of TERC gene amplification by FISH can contribute to the screening and early diagnosis of cervical cancer. It helps to define the pathological grade of precancerous lesions, suggesting the clinical selection of reasonable treatment methods, to avoid over-treatment or inadequate treatment.

## Probe description

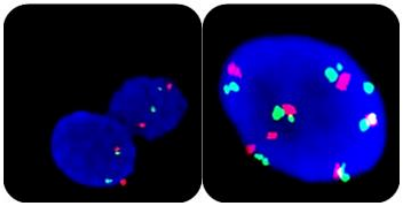
TERC gene amplification probe uses an orange-red dye to mark the TERC gene region, and a green dye to label chromosome 3 centromere region (CEP3). TERC gene marker region is located at 3q26.2, and the CEP3 probe is labeled with a specific alpha satellite sequence.




## Clinical significance

Detection of TERC gene status in patients can help to differentiate high and low cervical precancerous lesions, and improve the sensitivity and specificity of cytology and HPV detection in screening cervical lesions.

Predicting disease progression and early intervention, patients with TERC gene amplification are more than 50% likely to develop to high-level lesions.



TERC amplification [-] TERC amplification [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| TERC gene amplification probe detection kit | FP-013 | TERC/CEP3 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Dougherty MJ, et al. (2010) Neuro Oncol 12: 621-30.
Hutchinson KE, et al. (2013) Clin Cancer Res 19: 6696-702.

# NEUROBLASTOMA

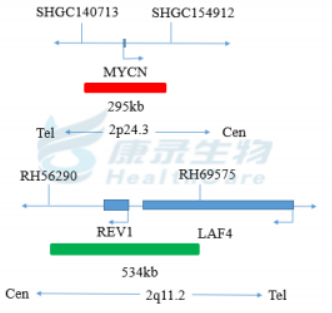
## N-MYC gene amplification probe

### Background

MYCN gene is located in the p24.3 region of chromosome 2 and encodes a 62-64 kDa transcription factor. MYCN is mainly expressed in the nervous system.

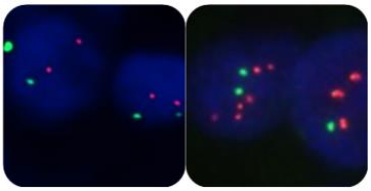
### Probe description

MYCN gene amplification probe uses an orange-red dye to mark the MYCN gene region, and a green dye to label the chromosome 2 centromere region (CEP2). The MYCN gene marker region is located at 2p24.3, and the CEP2 probe is labeled with a specific alpha satellite sequence.




### Clinical significance

MYCN gene amplification occurs in approximately 25% of patients with neuroblastoma. MYCN gene amplification is associated with infiltration, metastasis and poor prognosis of neuroblastoma. When the MYCN gene amplification factor is less than 10, the clinical treatment plan may not be treated after the complete removal of the primary tumor; when the MYCN gene amplification factor is >10, the conventional chemotherapy should be performed for 12 months after the surgical resection, and local radiotherapy is needed if necessary.



MYC amplification [-] MYC amplification [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYCN gene amplification probe reagent | FP-048 | N-MYC/LAF4 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Gessi M, et al. (2014) Neuro Oncol 16: 924-32.
Suita S, et al. (2007) J Pediatr Surg 42: 489-93.

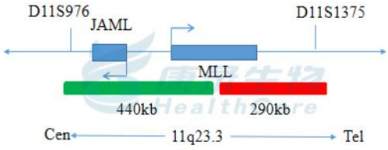
# MLL gene deletion probe

## Background

The MLL (KMT2A) gene is located in the q23.3 region of chromosome 11, which encodes a transcriptional coactivator that plays an important role in the regulation of gene expression during early development and hematopoiesis.

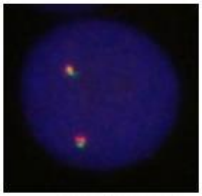
## Probe description

The MLL (KMT2A) gene detection probe uses an orange-red dye to label the MLL gene, and a green dye to label chromosome 11 centromere region (CEP11). The MLL (KMT2A) gene marker region is located at 11q23.3, and the CEP11 probe is labeled with a specific alpha satellite sequence.

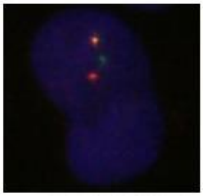



## Clinical significance

MLL (KMT2A) gene deletion is seen in primary neuroblastoma, and MLL (KMT2A) inactivation is associated with malignant progression of neuroblastoma in malignant progression of neuroblastoma without MYCN gene amplification.



MLL break apart [-]



MLL break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| KMT2A (MLL) gene break apart probe reagent | FP-026 | MLL | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Ford DJ & Dingwall AK (2015) Cancer Genet 208: 178-91.
Gindin T, et al. (2015) Hematol Oncol 33: 239-46.
Keefe JG, et al. (2010) J Mol Diagn 12: 441-52.

# MDM4 gene amplification probe

## Background

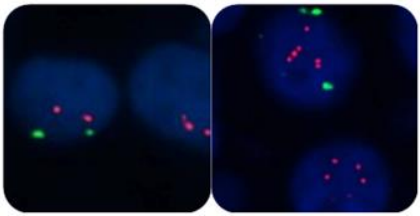
MDM4 (HDMX, MDMX) gene is located in the q32.1 region of chromosome 1, encoding a protein containing 490 amino acid residues. MDM4 is an important regulator of p53 upstream and plays a major role in apoptosis.

## Probe description

MDM4 (HDMX, MDMX) gene amplification probe uses an orange-red dye to label MDM4 gene region, and a green dye to label the chromosome 1 centromere region (CEP1). MDM4 (HDMX, MDMX) gene marker region is located at 1q32.1, and the CEP1 probe is labeled with a specific alpha satellite sequence.


## Clinical significance

MDM4 amplification is seen in 65% of primary neuroblastomas, MDM4 is a primary neuroblastoma-specific chemotherapy target, and MDM4 gene amplification patients are not sensitive to chemotherapy.



MDM4 amplification [-] MDM4 amplification [+]

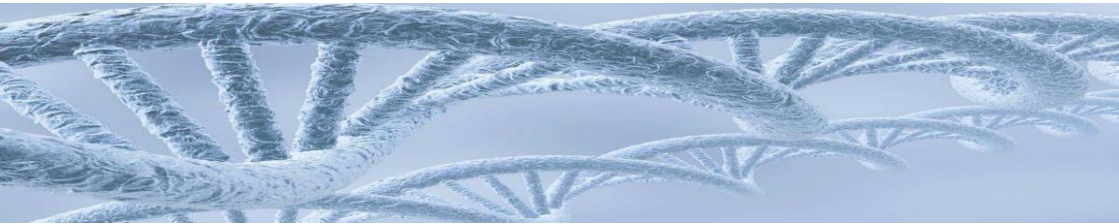
| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MDM4 gene amplification probe reagent | FP-049 | MDM4/1q21 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Duhamel LA, et al. (2012) Histopathology 60: 357-9.

Laurie NA, et al. (2006) Nature 444: 61-6.



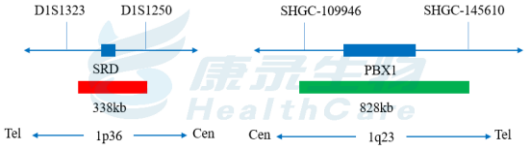
# SRD(1p36) gene deletion probe

## Background

Deletion of the 1p36 region (SRD gene) can occur in a variety of tumors, such as neuroblastoma, glioma, leukemia, lymphoma, and others.

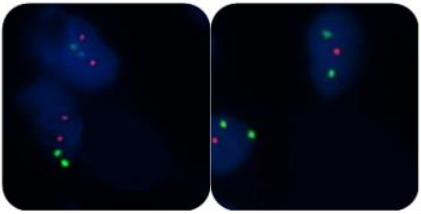
## Probe description

SRD (1p36) gene deletion probe uses an orange-red dye to label the SRD gene region, and a green dye to label chromosome 1 centromere region (CEP1). SRD gene marker region is located at 1p36, and the CEP1 probe is labeled with a specific alpha satellite sequence.




## Clinical significance

The deletion of 1p36 (SRD gene) in neuroblastoma is the most typical genetic alteration. The detection of 1p36 heterozygous deletion has a major significance in the clinical guidance and prognosis of neuroblastoma. 1p36 patients with neuroblastoma are prone to recurrence, have a poor prognosis, and are sensitive to chemotherapy.

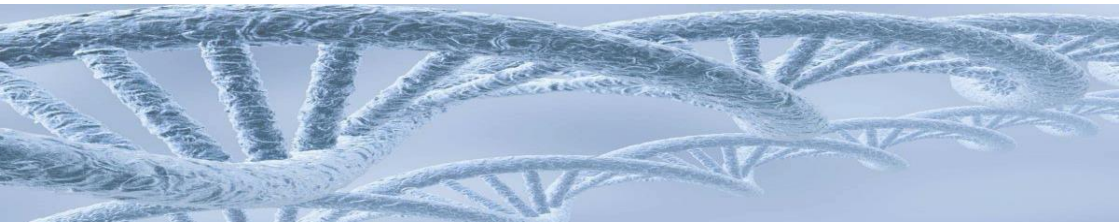


SRD gene deletion [-] SRD gene deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| SRD(1p36) gene deletion probe reagent | FP-050 | SRD(1p36) | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**
Elsir T, et al. (2011) Br J Cancer 11: 1747-54.
Hoeller S, et al. (2012) Hum Pathol 43: 405-12.



# SOFT TISSUE CANCER

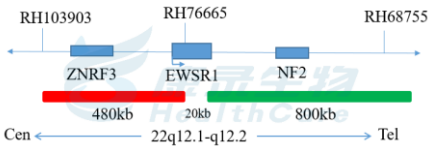
## EWSR1 gene break apart probe

### Background

The full name of the EWSR1 gene is Ewing sarcoma breakpoint region 1 gene. First discovered in Ewing's sarcoma, located at 22q12, consisting of 17 exons, encoding a nuclear protein of 656 amino acids. It is an RNA binding protein which plays an important role in mitotic cell separation, spindle formation, microtubule stability, DNA repair and cell senescence. It belongs to the cytokine TET family members, which controls cell growth.

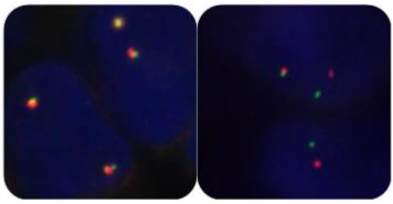
### Probe description

EWSR1 gene break apart probe uses orange dye to label the 5'end region of EWSR1 gene and green dye to label the 3'end region of EWSR1 gene. EWSR1 gene break apart probe can detect all EWSR1 gene rearrangements.




### Clinical significance

EWSR1 gene family members have TLS/FUS and TAFl5 genes, all of which are involved in gene translocation of various soft tissue sarcomas, and are fused with transcription factor genes containing the DNA binding domain to form new fusion transcription factors with obvious tumorigenic effect. Detecting whether EWSR1 gene is broken or not can be used as auxiliary diagnostic basis for Ewing's sarcoma family tumor.



EWSR1 break apart [-] EWSR1 break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| EWSR1 gene break apart probe reagent | FP-051 | EWSR1 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Rekhi B, et al. (2012) Virchows Arch 461: 687-97.

Romeo S & Dei Tos AP (2010) Virchows Arch 456: 219-34.

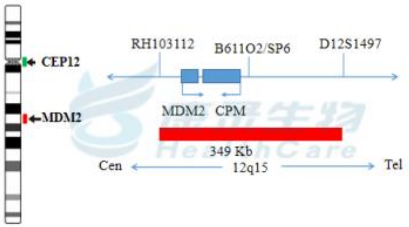
# MDM2 gene amplification probe

## Background

MDM2 gene is located in the q15 region of chromosome 12, and the encoded P90 protein can bind to P53 gene, causing P53 gene to lose its normal function, leading to tumorigenesis.

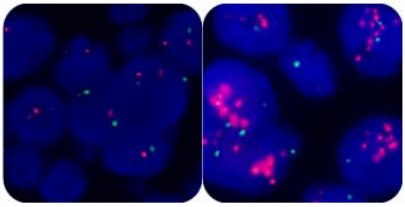
## Probe description

MDM2 gene amplification probe uses an orange-red dye to label the MDM2 gene region, and a green dye to label chromosome 12 centromere region (CEP12). MDM2 gene marker region is located at 12q15, and the CEP12 probe adopts an alpha satellite sequence, which has extremely high specificity and does not hybridize with other chromosome centromeres to produce noisy spots.




## Clinical significance

MDM2 gene amplification is the most common abnormality in fibrosarcoma and can assist in the diagnosis of fibrosarcoma; this gene amplification also occurs in osteosarcoma (16%) and esophageal cancer (13%). Used to guide the treatment of MDM2 inhibitors.



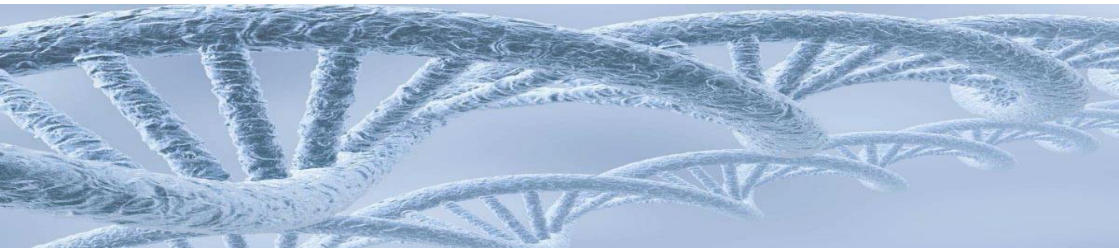
MDM2 amplification [-] MDM2 amplification [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MDM2 gene amplification probe reagent | FP-054 | MDM2/CEP12 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Larousserie F, et al. (2013) Eur J Radiol 82: 2149-53.
Lokka S, et al. (2014) BMC Clin Pathol 14: 36.



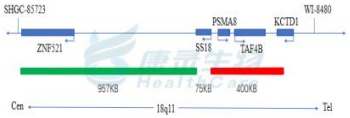
# SS18 gene break apart probe

## Background

SYT (SS18) gene is located in the q11.2 region of chromosome 18 and encodes a transcriptional co-activator. Specific SYT (SS18) gene translocation exists in 90% of synovial sarcomas.

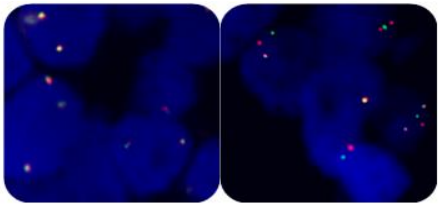
## Probe description

SYT (SS18) gene break apart probe uses an orange dye to label the 5'end region of SYT (SS18) gene and a green dye to label the 3'end region of SYT (SS18) gene. SYT (SS18) gene break apart probe can detect all SYT (SS18) gene rearrangements.




## Clinical significance

Specific chromosomal translocation t(X:18) was found in 90% of patients with synovial sarcoma (p11.2:q11.2). This translocation results in the fusion of the SYT (SS18) gene on chromosome 18 with the SSX1 or SSXE gene on the X chromosome. This is used to assist in the diagnosis of synovial sarcoma.



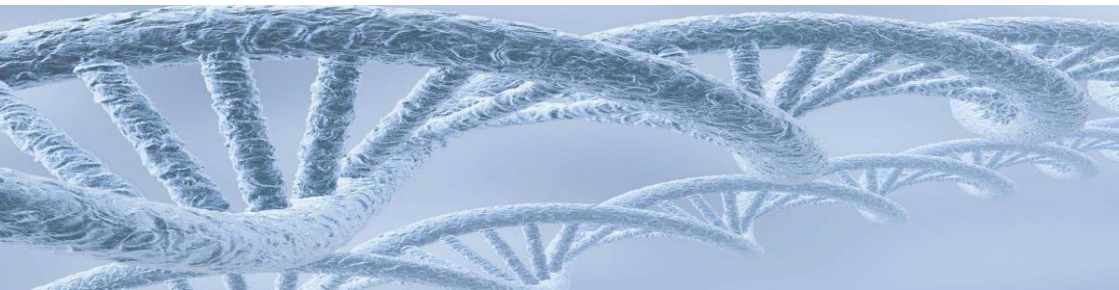
SS18 break apart [-] SS18 break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| SS18 gene break apart probe reagent | FP-055 | SS18 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Surace C, et al. (2004) Lab Invest 84: 1185-92.
Torres L, et al. (2008) Cancer Genet Cytogenet 187: 45-9.



# THYROID CANCER

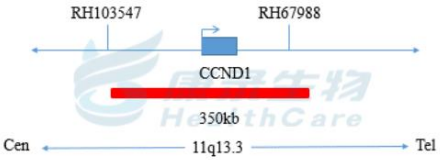
## CCND1 gene amplification probe

### Background

Human CCND1 gene is located in the q13 region of chromosome 11 and encodes cyclin D1. Its main function is to regulate the transition of the cell cycle from the early stage of DNA synthesis (G1 phase) to the DNA synthesis phase (S phase). Overexpression of CCND1 gene will affect the normal cell cycle, leading to a variety of tumor diseases. CCND1 gene amplification is present in thyroid cancer, non-small cell lung cancer, breast cancer, bladder cancer and other tumors.

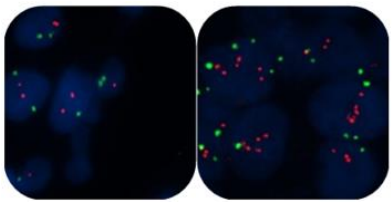
### Probe description

CCND1 gene amplification probe uses an orange-red dye to mark CCND1 gene region, and a green dye to label chromosome 11-centromere region (CEP11). CCND1 gene marker region is located at 11q13.3, and the CEP11 probe is labeled with a specific alpha satellite sequence.




### Clinical significance

CCND1 gene amplification predicts an important role in tumor development. Patients with CCND1 gene amplification have a poor prognosis and are closely related to chemotherapy resistance.



CCND1 amplification [-] CCND1 amplification [+]

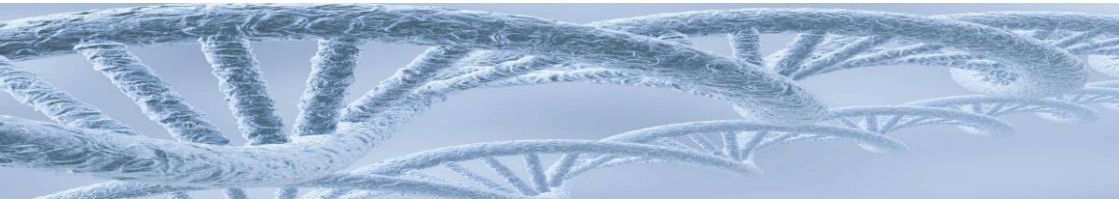
| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| CCND1 (BCL1) gene amplification probe reagent | FP-041 | CCND1/CEP11 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1240 9997

**References**

Motokura T, et al. (1991) Nature 350: 512-5.

Ormandy CJ, et al. (2003) Breast Cancer Res Treat 78: 323-35.



# ACUTE LYMPHOCYTIC LEUKEMIA

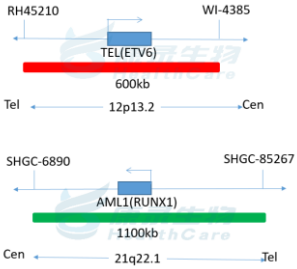
## TEL/AML1 gene fusion probe

### Background

TEL/AML1 dual-color double fusion probe aims to detect the translocation of the ETV6 (TEL) gene in chromosome 12p13.2 region and the RUNX1 (AML1) gene in the region of chromosome 21q22.12. The t(12;21)(p13.2;q22.1) translocation leads to the fusion of ETV6/RUNX1, the most common genetic recombination in patients with acute lymphoblastic leukemia (ALL) and is associated with a good prognosis. It is the highest incidence of childhood leukemia. In pediatric leukemia, acute lymphoblastic leukemia accounts for about 75%. In children with acute lymphoblastic leukemia aged 2-10, the positive rate of ETV6/RUNX1 (TEL/AML1) gene fusion accounts for about 20-25%, among which female is higher than male.

### Probe description

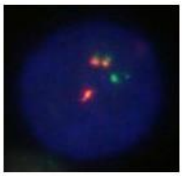
TEL probe uses an orange-red fluorescein label, and AML1 probe uses a green fluorescein label. The two probes combine to the target detection site by *in situ* hybridization. Under normal conditions (TEL/AML1 gene is not fused), it shows two orange-red signals and two green signals under a fluorescence microscope. When there is fusion, the green and orange-red signals form a yellow fusion signal due to recombination.




### Clinical significance

TEL/AML1 gene fusion has a 20-25% incidence in children with B-ALL. It has a good prognosis, but is prone to recurrence.

TEL/AML1 fusion [-]



TEL/AML1 fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| ETV6(TEL)/RUNX1(AML1) gene translocation probe reagent | FP-029 | TEL/AML1 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Morrow M, et al. (2007) Oncogene 26: 4404-14.
Peter A, et al. (2009) Eur J Haematol 83: 420-32.

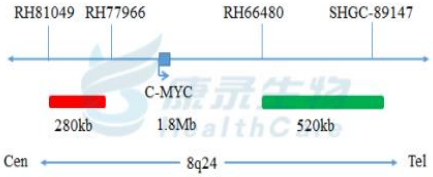
# MYC gene break apart probe

## Background

MYC proto-oncogene is located on chromosome 8q24 and encodes a transcription factor that regulates cell growth. It is mainly activated by amplification and chromosomal translocation, and its downstream target genes affect cell proliferation, DNA and protein synthesis and metabolism.

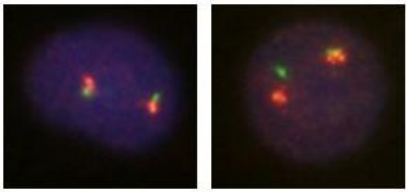
## Probe description

MYC dual-color break apart probe is a two directly labeled hybrid probe that hybridizes at the 8q24.21 region. The probe is directly labeled with an orange-red fluorescent dye that hybridizes with the proximal end of the MYC gene, and with a green fluorescent dye that hybridizes with the distal end of the MYC gene.




## Clinical significance

Abnormal MYC gene break apart occurs in 5% of B-cell acute lympocytic leukemia (B-ALL) patients and can fuse with multiple genes. Approximately, 75% of mature B-ALL patients are morphologically characterized by ALL-L3, often accompanied by a typical t(8;14)(q24;q32). Abnormal MYC gene break apart means that the prognosis is extremely poor in clinical practice.



MYC break apart [-] MYC break apart [+]

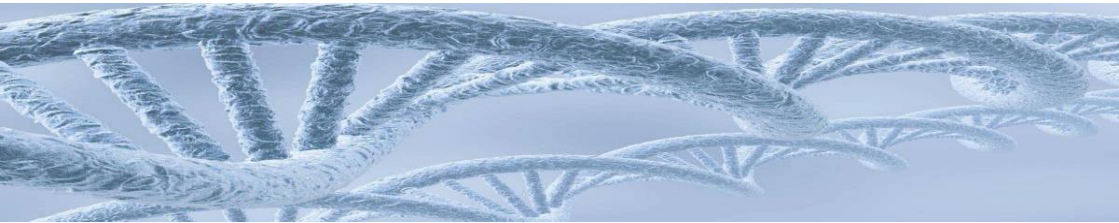
| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYC(8q24)/BCL6(3q27)/BCL2 (18q21) gene break apart probe reagent | FP-243-1 | MYC | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Boerma EG, et al. (2009) Leukemia 23: 225-34.

Haralambieva E, et al. (2004) Genes Chromosomes Cancer 40: 10-8.



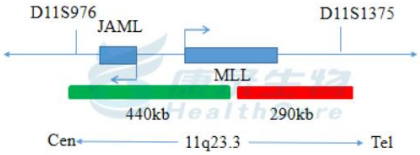
# MLL gene deletion probe

## Background

Mixed-linage leukemia or Myeloid-lymphoid leukemia (MLL) gene located at 11q23 was successfully cloned back in 1991. The MLL gene is a key gene in the regulation of hematopoietic processes, and its abnormality is closely related to the pathogenesis of leukemia.

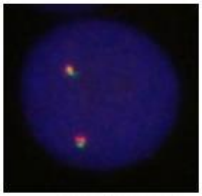
## Probe description

MLL gene 5'end region is labeled with an orange-red fluorescent dye and the 3'end is labeled with a green fluorescent dye. The translocation of 11q23 region is detected with MLL gene break probe. All MLL gene rearrangements can be detected and avoiding separate detection due to missed diagnosis caused by gene fusion.

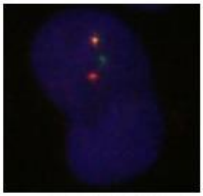



## Clinical significance

MLL gene can fuse with 51 genes after chromosomal translocation. The incidence of MLL gene changes in acute leukemia is about 5%-10%, but in infant acute lymphocytic leukemia it is up to 79%, which is a sign of poor prognosis. event-free survival in 5 years is only 26.7%.



MLL break apart [-]



MLL break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| KMT2A (MLL) gene break apart probe reagent | FP-026 | MLL | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Ford DJ & Dingwall AK (2015) Cancer Genet 208: 178-91.
Gindin T, et al. (2015) Hematol Oncol 33: 239-46.
Keefe JG, et al. (2010) J Mol Diagn 12: 441-52.

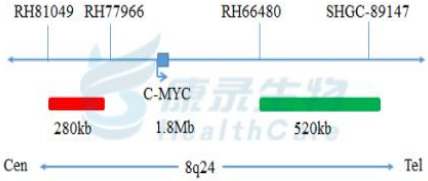
# IGH gene break apart probe

## Background

IGH separated dual-color probe aims to detect the translocation of 14q32.33 chromosome region (i.e. the IGH gene). IGH gene rearrangement is found in about 50% of non-Hodgkin's lymphoma (NHLs), and also in T-cell acute lymphocytic leukemia (T-ALL), chronic lymphocytic leukemia (CLL) and acute lymphocytic leukemia (ALL). Studies have shown that IGH gene translocation also occurs in children with T-ALL.

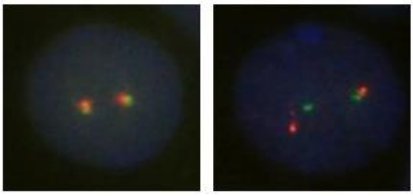
## Probe description

5'end of IGH gene region is labeled with an orange-red fluorescein, and the 3'end labeled with a green fluorescein. The translocation of 14q32 region is detected with IGH gene break probe. All IGH gene rearrangements can be detected thus avoiding separate detection due to missed diagnosis caused by gene fusion.




## Clinical significance

In ALL, the ratio of IGH to C-MYC translocation is the highest. In B-ALL and T-ALL, translocation of IGH with other genes is more common.



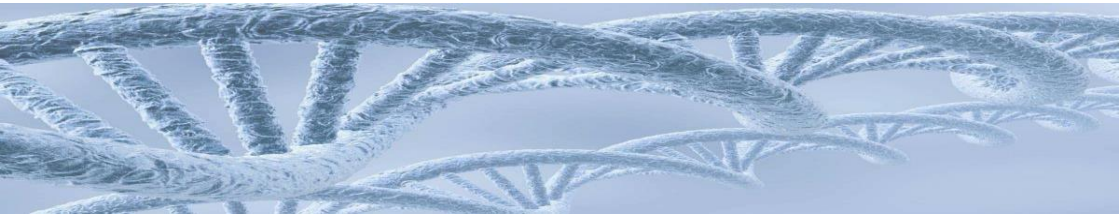
IGH break apart [-] IGH break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| BCL6/MYC/IGH/[BCL2/IGH] gene probe reagent | FP-242-3 | IGH | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Bernicot I, et al. (2007) Cytogenet Genome Res 118: 345-52.
Hehne S, et al. (2012) Pathol Res Pract 208: 510-7.
Quintero-Rivera F, et al. (2009) Cancer Genet and Cytogenet 190: 33-9.



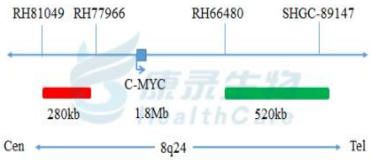
# Chromosomes 4, 10 and 17 probe

## Background

About 25% of children with acute lymphocytic leukemia (ALL) have an increased number of chromosomes, with changes in chromosomes 4, 5, 6, 10, 17 and 21 being more common, and trisomy 10 being the most common among them.

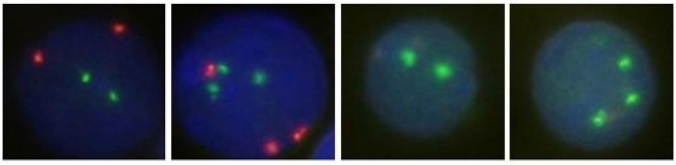
## Probe description

Chromosome 4-centromere region is labeled with an orange-red fluorescent dye and the centromere region of chromosomes 10 and 17 is labeled with a green fluorescent dye. In normal cells, two orange-red signals and two green signals are observed. When chromosome number abnormality exists, three orange-red signals or three green signals can be observed.




## Clinical significance

The 4, 10, and 17 trisomy are independent prognostic indicators, and these patients have a 7-years event-free survival greater than 90%. The method of detecting the number of CEP4/CEP10/CEP17 chromosomes provides a reference for the clinical identification, prognosis and medication of leukemia patients.



CEP4/CEP10(-) CEP4/CEP10(+) CEP17(-) CEP17(+)

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| Chromosome 4, 10 centromere probe reagent | FP-030 | 4q12/CEP10 | 100µL/Kit |
| Chromosome 17 centromere probe reagent | FP-031 | CEP17 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**
Felice et al., Leuk Lymphoma. 2011 Jul;52(7):1215-21
Savage et al., Blood. 2009 Oct 22;114(17):3533-7

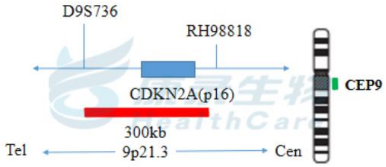
# P16 gene deletion probe

## Background

P16 gene is located on the 9p21 chromosome and is a tumor suppressor gene. P16 gene deletion is present in 10% of acute lymphocytic leukemia (ALL) patients and has a higher proportion in T-cell ALL (T-ALL). Currently, fluorescent *in situ* hybridization (FISH) technology is widely used in the diagnosis of P6 gene deletion in ALL.

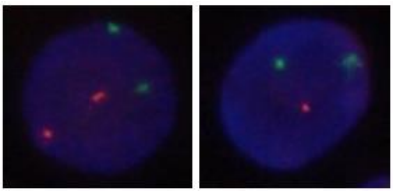
## Probe description

P16 gene deletion probe uses an orange-red fluorescent dye to label P16 gene region, and a green fluorescent dye is to label chromosome 9 centromere region (CEP9).




## Clinical significance

One of the most common abnormalities in ALL is that homozygous deletions are mostly in T-ALL, and the proportion of homozygotes and heterozygotes in B-cell ALLL (B-ALL) is comparable. The prognosis is poor.



P16 deletion [-] P16 deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| P16 gene deletion probe reagent | FP-032 | P16/CEP9 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Fry et al., Mol Cancer Ther. 2004 Nov;3(11):1427-38

# ACUTE MYELOID LEUKEMIA

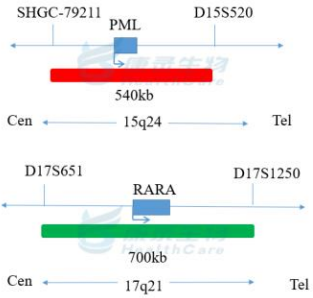
## PML/RARA gene fusion probe

### Background

Acute promyelocytic leukemia (APL) is a specific subtype of acute myeloid leukemia. In cytogenetics and molecular biology, APL has a characteristic t(15;17)(q22;21) translocation, forming a PML-RARA fusion gene. A large number of data indicate that patients carrying the PML-RARA fusion gene are predictive of sensitivity to all-trans retinoic acid (ATRA) therapy and good clinical efficacy.

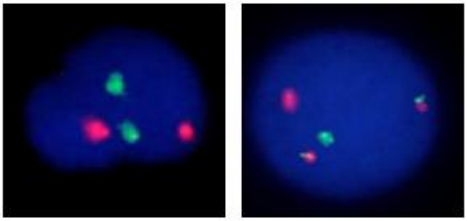
### Probe description

The two probes bind to the target detection site by *in situ* hybridization using an orange-red fluorescein-labeled PML probe and a green fluorescein-labeled RARA probe. Under normal conditions when the PML and RARA genes are not fused, results show two orange-red signals and two green signals. When a fusion gene is present, the green and orange-red signals form a yellow fusion signal due to recombination.




### Clinical significance

PML/RARA gene fusion is a hallmark of APL. PML/RARA protein fusion inhibits the differentiation and maturation of promyelocytic cells by dominant negative inhibition, thereby blocking cell differentiation leading to sustained proliferation. ATRA and arsenic trioxide can target the degradation of PML/RARA fusion protein, restore the function of wild-type PML and RARA genes, relieve their inhibition of gene transcription, induce cell differentiation and apoptosis, and effectively treat APL. The combination of ATRA and chemotherapy can achieve a complete response rate of 90% to 95%, and can achieve long-term survival of more than 70% of patients.



PML/RARA fusion [-] PML/RARA fusion[+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| RARA (17q21) probe reagent | FP-005 | PML/RARA | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Abe S, et al. (2008) Cancer Genet and Cytogenet 184: 44-7.
Sanz MA, et al. (2009) Blood 113: 1875-91.

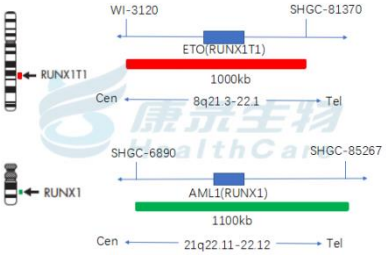
# AML1/ETO gene fusion probe

## Background

AML1/ETO gene fusion formed by chromosome 8 and chromosome 21 translocation is a common cytogenetic abnormality in patients with acute myeloid leukemia (AML), and about 12% to 20% of patients with acute myeloid leukemia have AML1/ETO gene fusion. While the positive rate of AML-M2 leukemia is 20% to 40%, and the positive rate of M2b subtype is as high as 90%, which is rare in other types of leukemia. The AML1/ETO protein fusion is a transcriptional repressor that inhibits normal AML1 protein-mediated function, alters the process of self-renewal and maturation of hematopoietic progenitor cells, and also signals the initiation of abnormal hematopoietic cell proliferation, causing the proliferation of leukemia cells.

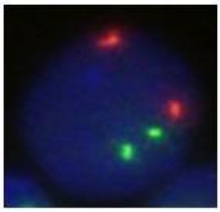
## Probe description

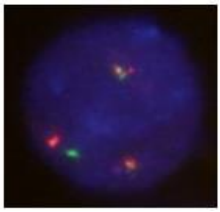
ETO probe is labeled with an orange-red fluorescent dye, and AML1 probe with a green fluorescent dye. The two probes combine to the target detection site by *in situ* hybridization. Under normal conditions when AML1 and ETO genes are not fused, the two orange-red signals and two green signals are seen. When an AML1/ETO fusion gene is present, the green and orange-red signals form a yellow fusion signal due to recombination.




## Clinical significance

AML1/ETO gene fusion can be used as AML diagnostic assistant and prognosis assessment means. Clinically, t(8;21) leukemia represents a type of acute leukemia with good prognosis. Adult patients have good response to treatment, high complete remission rate, long median survival time, but prone to recurrence. Treatment and prognosis of children are not as good as in adult patients.


AML1/ETO fusion [-]


AML1/ETO fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| AML1/ETO gene fusion detection kit | FP-004 | AML1/ETO | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1240 9997

**References**

Dayyani F, et al. (2008) Blood 111: 4338-47.
Estey E & Döhner H (2006) Lancet 368: 1894-907.
Gmidène A, et al. (2010) Med Oncol: 28 Suppl 1: 509-12.

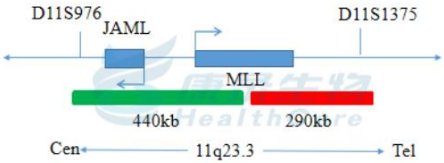
# MLL gene deletion probe

## Background

The MLL (Mixed-linage leukemia or Myeloid-lymphoid leukemia) gene is located at 11q23, and was successfully cloned back in 1991. The MLL gene is a key gene in the regulation of hematopoietic processes, and its abnormality is closely related to the pathogenesis of leukemia. According to statistics, there are at least 104 MLL gene rearrangements, and up to 64 MLL genes fusion have been identified. Most of the leukemia with MLL gene fusion are highly malignant, not sensitive to chemotherapy, and have low remission rate. Therefore, the detection of MLL gene fusion in acute leukemia is of great significance for the treatment options, residual lesion detection and prognosis.

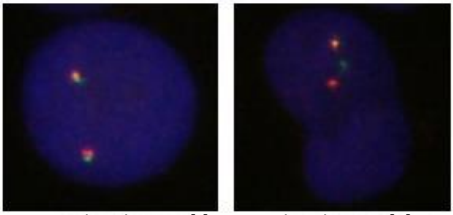
## Probe description

The MLL gene 5' end region is labeled with an orange-red fluorescent dye, and the 3' end of MLL gene labeled with a green fluorescent dye. MLL gene break apart probe is used to detect 11q23 segment translocation, and all MLL gene rearrangements could be detected, avoiding separate detection or missed diagnosis caused by gene fusion.




## Clinical significance

Common translocation forms of the MLL gene are t(4;11), t(9;11), t(11;19) and other recombinations. Eight to ten percent of acute myeloid leukemia (AML) has this abnormality. MLL recombination is present in 80% of infants with AML, suggesting a moderate risk type. Other MLL genes are recombined into high-risk types.



MLL break apart [-] MLL break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| KMT2A (MLL) gene break apart probe reagent | FP-026 | MLL | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Ford DJ & Dingwall AK (2015) Cancer Genet 208: 178-91.
Gindin T, et al. (2015) Hematol Oncol 33: 239-46.
Keefe JG, et al. (2010) J Mol Diagn 12: 441-52.

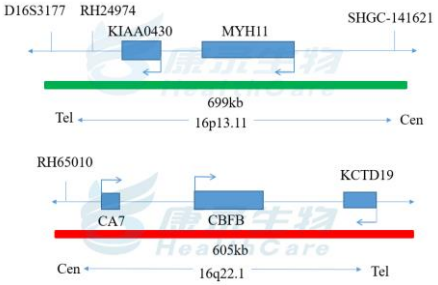
# CBFB/MYH11 gene fusion probe

## Background

Acute myeloid leukemia (AML) is a group of highly heterogeneous hematopoietic malignancies, often associated with acquired chromosomal abnormalities, the most common of which is chromosomal translocation. Chromosomal inversion of inv16 (p13q22) or translocation t(16;16) (p13; q22) found in myeloid leukemia (AML-M4) cells with eosinophilia, resulting in the MYH11 gene located at 16p13. The CBFB gene located at 16q22 is recombined to form a CBFB/MYH11 gene fusion. The detection rate of CBFB/MYH11 gene fusion in myeloid leukemia is about 7%. Since the CBFB/MYH11 gene fusion is only found in AML, according to the WHO leukemia diagnostic criteria, AML can be diagnosed by detecting the CBFB/MYH11 gene fusion.

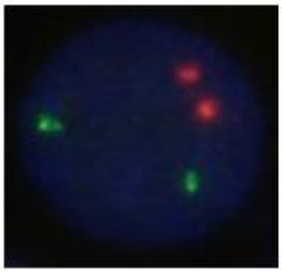
## Probe description

CBFB probe is labeled with an orange-red fluorescent dye, and MYH11 probe is labeled with a green fluorescent dye. The two probes combine to the target detection site by *in situ* hybridization. Under normal conditions the CBFB and MYH11 genes are not fused showing two orange-red signals and two green signals. When a fusion gene is present, the green and orange-red signals form a yellow fusion signal due to recombination. The method was used to detect the status of CBFB/MYH11 gene fusion providing a reference for the identification, prognosis and drug administration guidance for clinical AML leukemia patients.

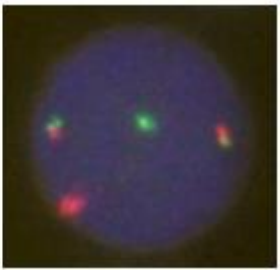



## Clinical significance

CBFB/MYH11 gene fusion can be used for the diagnosis of AML. In addition, in the case of positive CBFB/MYH11 gene fusion, the detection of CBFB/MYH11 gene fusion has become the most valuable indicator for the determination of therapeutic options and therapeutic efficacy evaluation. For example, quantitative analysis of CBFB/MYH11 gene fusion can also be used to judge the level of leukemia cells in patients, the detection of minimal residual disease and the prediction of recurrence risk. AML patients with CBFB/MYH11 gene fusion have a better prognosis, and high DFS and low recurrence rates can be achieved by HDAC regimen.



CBFB/MYH11 fusion [-]



CBFB/MYH11 fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| CBFB/MYH11 gene fusion probe reagent | FP-028 | CBFB/MYH11 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Aventín A, et al. (2002) Cancer Genet Cytogenet 134: 142-4.
Li MM, et al. (2013) Curr Genet Med Rep 1: 99-112.

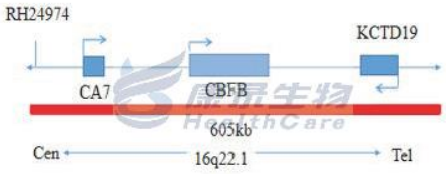
# CBFB gene break apart probe

## Background

CBFB gene break apart is a characteristic chromosomal abnormality of AML, accounting for 5-10% of total AML patients and 23% of M4 patients. It is usually found in the AML-M4E0 subtype, but less in M2, M4 and M5. It is now considered that CBFB gene break apart is a characteristic genetic alteration of M4E0.

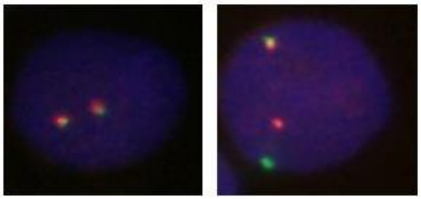
## Probe description

CBFB gene 5'end region uses an orange-red fluorescent dye, the CBFB gene 3'end uses a green fluorescent dye, and the translocation of 16q22 region is detected with MLL gene break probe. All CBFB gene rearrangements can be detected and avoiding separate detection due to missed diagnosis caused by gene fusion.




## Clinical significance

Most AML patients with CBFB gene break apart are sensitive to chemotherapy and have a good prognosis.



CBFB break apart [-] CBFB break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| CBFB gene break apart probe reagent | FP-027 | CBFB | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Krauter J, et al. (2001) Genes Chromosomes and Cancer 30: 342-8.
Li MM, et al. (2013) Curr Genet Med Rep 1: 99-112.

# CHRONIC LYMPHOCYTIC LEUKEMIA

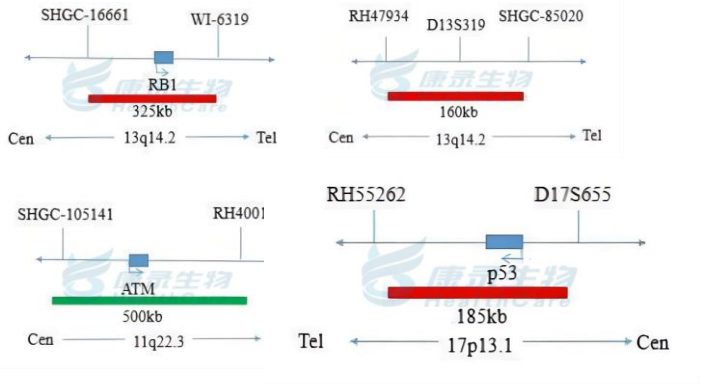
## CLL gene and chromosome detection probe

### Background

Chronic lymphocytic leukemia (CLL) is a mature B cell clonal proliferative tumor characterized by the accumulation of lymphocytes in peripheral blood, bone marrow, spleen and lymph nodes. CLL is also diagnosed in patients with persistent (3 months) peripheral blood B cell increase (≥5x$10^9$/L) accompanied by hematocytopenia or disease-related symptoms caused by bone marrow infiltration. About 80% of patients with chronic lymphocytic leukemia have chromosomal abnormalities detected by fluorescence *in situ* hybridization. The most common deletions are on chromosome 13 long arm del (13q14.1); chromosome 12 deletion or trisomy, chromosome 17 short arm deletion del(17p).

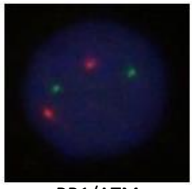
### Probe description

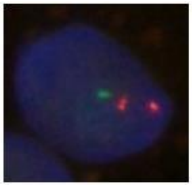
This kit consists of three sets of probes: RB1/ATM, P53/CEP17, and D13S319/CEP12. The probes of RB1, P53 and D13S319 use an orange-red fluorescent label, and ATM, CEP17 and CEP12 probes are labeled with a green fluorescence. The probes are combined with the target sites by *in situ* hybridization. Under normal conditions (no gene deletion and chromosome abnormalities), two orange-red signals and two green signals are shown under a fluorescence microscope. When there is gene deletion, there will be a lack of green or orange-red signal, and when there is a chromosomal polysomy, the centromere gene probe signal will increase. This method is used to detect gene deletion and chromosome abnormalities, and provide reference for clinical differentiation, prognosis and medication for leukemia patients.

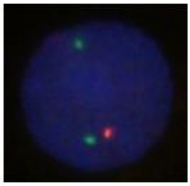


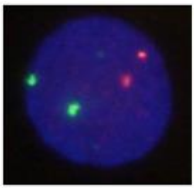
## Clinical significance

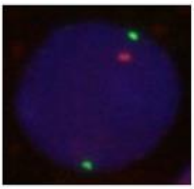
Chromosome abnormalities are found in 80% of patients with chronic lymphocytic leukemia. The most common deletion is in the long arm del 13 (13q14.1) of chromosome 13; the chromosome 12 deletion or trisomy; the short arm of chromosome 17 deletion del(17p). These abnormalities are important for the diagnosis, differential diagnosis, treatment options, and prognosis of chronic lymphocytic leukemia.


RB1/ATM deletion [-]

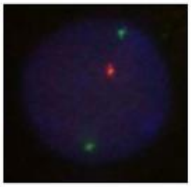

RB1/ATM deletion [+]


RB1/ATM deletion [+]


D13S319/CEP12 deletion [-]


D13S319/CEP12 deletion [+]


P53 deletion [-]


P53 deletion [+]

| Product name | Cat. No. | probe name | Specification |
|---|---|---|---|
| CLL chromosome and gene anomaly probe detection kit | FP-014-1 | RB1/ATM | 100µL/Kit |
| | FP-014-2 | P53/CEP17 | 100µL/Kit |
| | FP-014-3 | D13S319/CEP12 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Dal Bo M, , et al. (2011) Genes Chromosomes Cancer. 50(8):633-43.
Novak U, , et al. (2004) Leuk Lymphoma.45(5):887-96.
Schnaiter A et al. (2013) Hematol Oncol Clin North Am. 27(2):289-301.

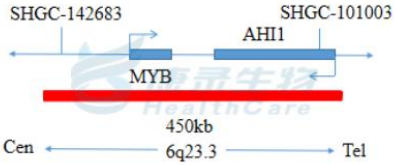
# MYB gene deletion probe

## Background

MYB/CEP6 dual-color probe aims to detect the deletion of the MYB gene at chromosome 6q23.3. The MYB gene encodes a transcript that is expressed primarily in early lymphocytes and bone marrow cells. In different types of lymphoid tumors, 6q aberration is the most common chromosomal variation, and several major deletion regions are on the long arm of chromosome 6. From 3% to 10% of chronic lymphocytic leukemia (CLL) have chromosome structural aberrations at 6q. The absence of MYB is often accompanied by a secondary change. Because traditional cytogenetic methods are not effective in detecting changes in CLL, the use of fluorescence *in situ* hybridization (FISH) molecular cytogenetic research method can diagnose and prognose CLL.

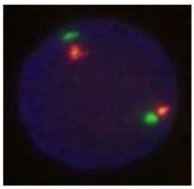
## Probe description

MYB/CEP6 is a dual-color hybrid probe in which a green fluorescent dye directly labels the CEP6 probe, which specifically acts on chromosome 6 (D6Z1), while an orange-red fluorescent dye directly labels the MYB probe, which specifically acts on the MYB gene at the chromosomal region 6q23.2-23.3.

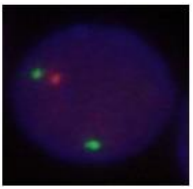



## Clinical significance

Abnormal 6q deletion is the fourth most common abnormality in B-cell CLL (B-CLL). The prognosis of 6q deletion is poor in many tumors including CLL. This probe can detect 2Mb microdeletion regions that cannot be distinguished by karyotyping analysis.



MYB deletion [-]



MYB deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYB (6q23) gene probe reagent | FP-036 | MYB/CEP6 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Urbankova H, et al. (2014) Biomed Pap Med Fac Univ Palacky Olomouc Czech Repub 158: 56-64.
Wang DM, et al. (2011) Leuk Lymphoma 52: 230-7.

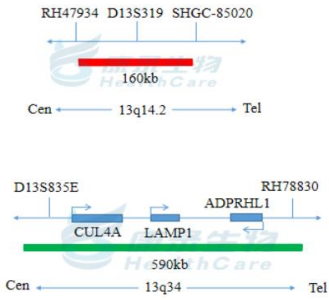
# D13S319/LAMP1 gene probe

## Background

13q14/13q34 dual-color probe is designed to detect the deletion of the long arm end of chromosome 13. The most common aberration in chronic lymphocytic leukemia (CLL) is the deletion of 13q14.2, which contains the D13S319 gene and has a good prognosis for single genetic variant. Combined with further biomarkers, morphological and clinical applications, fluorescence *in situ* hybridization (FISH) can be an important tool for predicting disease progression and overall survival in CLL patients.

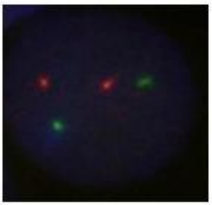
## Probe description

13q14/13q34 is a dual-color hybrid probe. The orange-red fluorescent dye directly labels the D13S319 probe and the probe specifically detects the D13S319 gene at 13q14.2. The green fluorescent dye directly labels the 13q34 probe, which specifically detects LAMP1 gene in the 13q34 region.

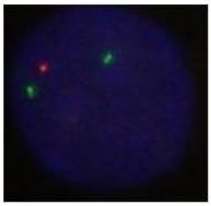



## Clinical significance

Studies have shown that the deletion of 13q has a negative impact on the survival of patients in event-free survival and overall survival. The most common aberration in CLL is the deletion of 13q14.2, which contains D13S319 gene and has a good prognosis for individual genetic variants. These abnormalities are important for the diagnosis, differential diagnosis, treatment options and prognosis in CLL.



D13S319/LAMP1 deletion [-]



D13S319/LAMP1 deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| 13 (13q14) probe reagent | FP-025 | D13S319/13q34 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Chang H, et al. (1999) Leukemia 13: 105-9.
Dal Bo M, et al. (2011) Genes Chromosomes Cancer 50: 633-43.
Liu Y, et al. (1998) Blood 86: 1911-15.

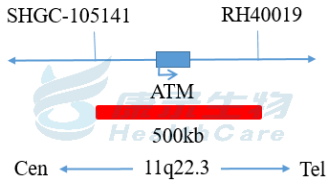
# ATM gene deletion probe

## Background

The ATM gene (ataxia telangiectasia mutated gene) is located at 11q22.3 and encodes a protein kinase involved in cell cycle regulation and activation of TP53 activity.

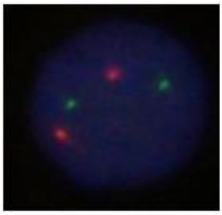
## Probe description

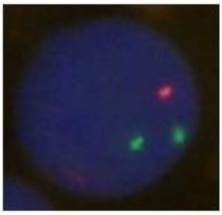
ATM gene deletion kit is a dual-color hybrid probe that directly labels ATM probe with an orange-red fluorescent dye. The probe specifically acts on the ATM gene at the chromosome 11q22.3 region, and the chromosome 11 centromere is directly labeled with a green fluorescent dye.




## Clinical significance

ATM gene deletion has a 15-20% incidence in B-cell chronic lymphocytic leukemia (B-CLL), which is associated with disease invasiveness and poor prognosis. ATM gene deletion is the most common deletion abnormality in CLL, which can guide the selection of treatment options and prognosis evaluation.


ATM deletion [-]


ATM deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| P53/[CCND1/IGH]/ATM/CSP12/ D13S25 gene probe reagent | FP-245-3 | ATM/CEP11 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Ripollés L, et al. (2006) Cancer Genet Cytogenet 171: 57-64.
Shanafelt TD, et al. (2006) Ann Intern Med 145: 435-47.
Stilgenbauer S, et al. (2002) Leukemia 16: 993-1007.

# Chromosome 12 probe

## Background

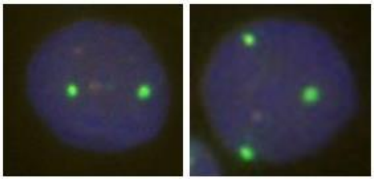
Trisomy 12 is the most common chromosome number abnormality in chronic lymphocytic leukemia (CLL), with an incidence of 10-20%. It is often characterized by unique cytogenetic abnormalities. Among other genetic disorders, patients with trisomy 12 are considered to be at low risk.

## Probe description

The centromere region of chromosome 12 is directly labeled with a green fluorescent dye.


## Clinical significance

Chromosome 12 trisomy is the most common chromosome number abnormality in B-cell CLL (B-CLL), with an abnormal proportion of more than 55%. The total survival time of trisomy 12 is low and requires early treatment.



CEP12 [-] CEP12 [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| Chromosome 12 centromere probe reagent | FP-034 | CEP12 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Puiggros et al., Biomed Res Int 2014;1-13.
Rossi et al., Blood 2013;121(8):1403-1412.
Swerdlow et al., editors, WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues, Lyon, France, IARC:2008.

# CHRONIC MYELOID LEUKEMIA

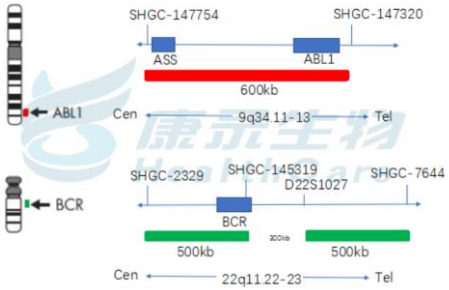
## BCR/ABL gene fusion probe

### Background

BCR/ABL is a dual-color fusion probe designed to detect specific translocations of the ABL1 gene of chromosomal region 9q34.12 and the BCR gene of 22q11.23. Random rearrangements of t(9,22) (q34.1, q11) were found in approximately 90% of patients with chronic myeloid leukemia (CML) and approximately 25% of acute lymphoblastic leukemia (ALL). Frequent translocations result in the production of the BCR/ABL gene fusion on chromosome 22. The gene product is a BCR/ABL protein with an abnormal tyrosine kinase activity. In normal cells, ABL kinase activity is well regulated by growth factors and other factors, while BCR/ABL proteins fusion result in sustained activation of downstream signaling pathways (Ras, Jak/Stat, and PI3K). Fluorescence *in situ* hybridization (FISH) allows the identification of rearrangements that could not be detected by conventional nuclear types.

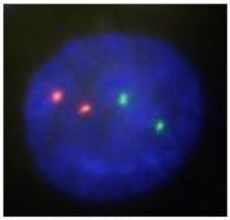
### Probe description

ABL probe uses an orange-red fluorescent label, and BCR probe uses a green fluorescent label. The two probes combine to the target detection site by *in situ* hybridization. Under normal conditions BCR and ABL genes are not fusded and the result shows two orange-red signals and two green signals. When there is fusion, the green and orange-red signals form a yellow fusion signal due to recombination.

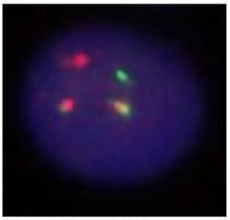



## Clinical significance

BCR/ABL gene fusion is a common cytogenetic abnormality in patients with CML and can be found in 90% of CML patients. The use of targeted therapeutic drugs depends whether a patient has a BCR/ABL gene fusion.



BCR/ABL fusion [-]



BCR/ABL fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| BCR/ABL gene fusion detection kit | FP-003 | BCR/ABL | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Hehne S, et al. (2012) Pathol Res Pract 208: 510-7.
Lim TH, et al. (2005) Ann Acad Med Singapore 34: 533-8.
Zheng X, et al. (2009) PLoS One 4: e7661.

# LYMPHOMA

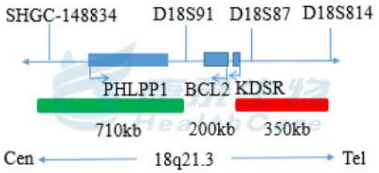
## BCL2 gene break apart probe

### Background

BCL2 is a tumor suppressor gene located in the 18q21 region. BCL2 gene encodes a mitochondrial membrane protein that regulates apoptosis and is expressed in B cells. Translocation of the BCL2 gene is usually recognized in B cell lymphoma. In particular, translocation of t(14;18)(q32.3;q21.3) is present in approximately 80% of follicular lymphoma (FL), 20%-30% of diffuse large B-cell lymphoma (DLBCL), but it rarely occurs in B-cell chronic lymphocytic leukemia (B-CLL). Therefore, the detection of BCL2 translocation by fluorescence *in situ* hybridization (FISH) may have diagnostic and prognostic significance.

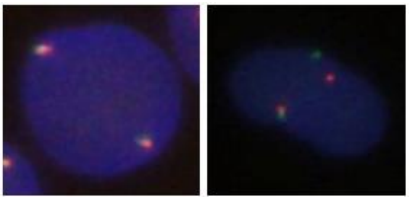
### Probe description

BCL2 is a dual-color break apart probe composed of two probes directly labeled at 18q21.33-q22.1. The green fluorescent dye labeled probe hybridizes to the proximal end of the BCL2 gene, while the orange-red fluorescent dye labeled probe hybridizes to the distal end of the BCL2 gene.




### Clinical significance

FL is a less malignant B cell tumor derived from the center of follicle development. FL is a common type of non-Hodgkin's lymphoma (NHL), accounting for 25-45% of NHL in Europe. BCL2 gene break apart can be used in the lymphoma diagnosis.



BCL2 break apart [-] BCL2 break apart [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYC(8q24)/BCL6(3q27)/BCL 2(18q21) gene break apart probe reagent | FP-243-3 | BCL2 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Da Cunha Santos G, et al. (2011) Cancer Cytopathol 119: 254-62.
Gu K, et al. (2008) Arch Pathol Lab Med 132: 1355-61.
Impera L, et al. (2008) Oncogene 27: 6187-90.
Tibiletti MG, et al. (2009) Hum Pathol 40: 645-52.
Tomita N, et al. (2009) Haematologica 94: 935-43.

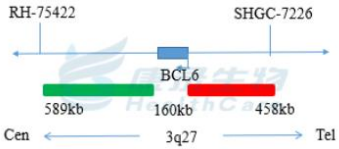
# BCL6 gene break apart probe

## Background

BCL6 gene is located at the 3q27 region, and the protein encoded by the BCL6 gene is a transcriptional repressor involved in the development and function of the lymphatic system. Chromosome recombination of the BCL6 gene region is present in different types of non-Hodgkin's lymphoma (NHL), including diffuse large B-cell lymphoma (DLBCL) and follicular lymphoma (FL). The most common translocation t(3;14)(q27;q 32.3) of BCL6 leads to fusion of the IGH-BCL6 gene. Therefore, detection of BCL6 rearrangement by fluorescence *in situ* hybridization (FISH) may be helpful in predicting clinical outcomes in patients with NHL.

## Probe description

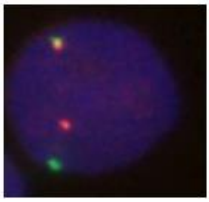
BCL6 is a dual-color break apart probe composed of two probes directly labeled to 3q27.3-q28. The green-labeled fluorescent probe directly hybridizes with the 3q27.3 proximal BCL6 gene, while the orange-red fluorescent probe directly hybridizes with the distal end of the BCL6 gene at the 3q27.3-q28.




## Clinical significance

In DLBCL, BCL6 gene can translocate with multiple genes with the incidence rate 20-40%. In FL the incidence rate is 5-15%. The diagnosis of Burkitt's lymphoma is based on typical age, morphology and immunophenotype. If any of these three features is absent or has a history of FL, it is accompanied by MYC gene breaks and BCL6 gene breaksit should be diagnosed as a grey-area lymphoma between Burkitt and DLBCL. The BCL6 gene break is an independent indicator for evaluating survival rate and recovery rate.


BCL6 break apart [-]


BCL6 break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYC(8q24)/BCL6(3q27)/BCL2 (18q21) gene break apart probe | FP-243-2 | BCL6 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Akyurek N, et al. (2012) Cancer 118: 4173-83.
Cady FM, et al. (2008) J Clin Oncol 26: 4814-9.
Ohno H (2004) Histol Histopathol 19: 637-50.
Ohno H (2006) J Clin Exp Hematop 46: 43-53.

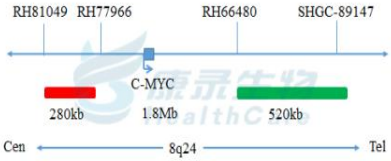
# MYC gene break apart probe

## Background

MYC proto-oncogene is located on chromosome 8q24 and encodes a transcription factor that regulates cell growth. It is mainly overactivated by amplification and chromosome translocation rearrangement, leading to activation of its downstream target genes which affect cell proliferation, DNA and protein synthesis and metabolism. In recent years, MYC gene abnormalities have become an important indicator of poor prognosis in patients with diffuse large B-cell lymphoma (DLBCL).

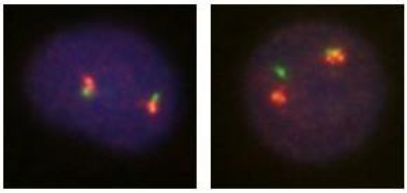
## Probe description

MYC dual color break apart probe consists of two directly labeled hybrid probes that hybridize with the 8q24.21 region. The probe labeled with the orange-red fluorescent dye hybridizes with the proximal end of the MYC gene, and the green fluorescent-labeled probe hybridizes with the distal end of the MYC gene.




## Clinical significance

MYC gene breaks in 5-10% of patients with DLBCL, and the survival time is significantly shorter than in DLBCL patients with other abnormalities. MYC gene break, BCL2 gene break or BCL6 gene break probes can be used for the diagnosis of double-hit lymphoma (DHL).



MYC break apart [-] MYC break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| MYC(8q24)/BCL6(3q27)/BCL2 (18q21) gene break apart probe | FP-243-1 | MYC | 100µL/Kit |

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**References**

Savage et al., Blood. 2009 Oct 22;114(17):3533-7.
Seo et al., Ann Lab Med. 2012 Jul;32(4):289-93.

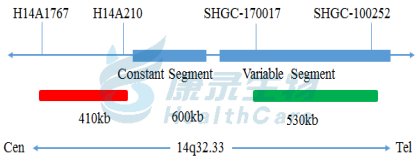
# IGH gene break apart probe

## Background

IGH separated dual-color probe is designed to detect translocation of the IGH gene at chromosome 14q32.33. IGH gene rearrangement can be used as a specific molecular marker for detecting minimal residual disease of difuse large B-cell lymphoma (DLBCL). IGH gene breaks and translocations occur in 50% of B cell Non-Hodgkin's lymphoma (NHL) and various other lymphomas, and can translocate with more than 50 genes.

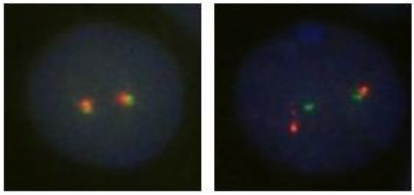
## Probe description

IGH gene break apart probe is a dual-color break apart probe, consisting of two probes directly labeled at 14q32.33. The probe labeled with orange-red fluorescence hybridizes at the proximal end of the GH gene, while the probe labeled with green fluorescence hybridizes with the distal end.




## Clinical significance

The fusion of the IGH gene with a variety of genes can be used for diagnosis, especially for B-cell and T-cell NHL, non-classical HL, and reactive hyperplasia that are not characterized by histopathology and immunohistochemistry.



IGH break apart [-] IGH break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| BCL6/MYC/IGH/[BCL2/IGH] gene probe reagent | FP-242-3 | IGH | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Bernicot I, et al. (2007) Cytogenet Genome Res 118: 345-52.
Hehne S, et al. (2012) Pathol Res Pract 208: 510-7.
Quintero-Rivera F, et al. (2009) Cancer Genet and Cytogenet 190: 33-9.

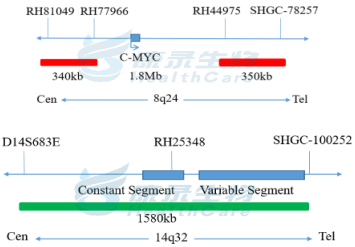
# MYC /IGH gene fusion probe

## Background

MYC proto-oncogene is located on chromosome 8q24 encoding transcription factor closely related to cell growth and proliferation, as well as tumorigenesis. Translocation of the MYC gene is considered to be a cytogenetic marker of Burkitt's lymphoma (BL), but is also present in other types of lymphoma. About 80% of BL cases have a translocation between the c-MYC gene locus and the Ig gene locus (t(8;14) (q24;q32)), thus forming a highly active genes rearrangement, initiating c-MYC transcription, enhancing c-MYC expression, promoting malignant transformation, and ultimately leading to tumorigenesis. Detection of the t(8;14) (q24;q32) helps to diagnose Burkitt's lymphoma and can guide the treatment of high-grade B-cell lymphoma.

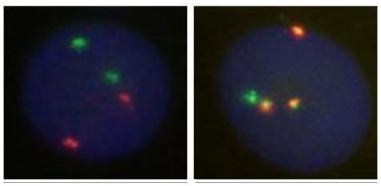
## Probe description

MYC/IGH is a dual-color, double-fusion probe consisting of a green fluorescent IGH probe across known IGH breakpoint, and an orange-red fluorescent MYC probe across known MYC breakpoint.




## Clinical significance

t(8;14) can be used to assist in the diagnosis of BL and guide the treatment of high-grade B-cell lymphoma. The prognosis of lymphoma with MYC/IGH translocation is poor.



MYC/IGH fusion [-] MYC/IGH fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| [MAFB/IGH][CCND3/IGH][MYC/IGH] gene fusion probe reagent | FP-234-3 | C-MYC/IGH | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

May P, et al. (2010) Cancer Genet Cytogenet 198: 71-5.
Perkins A, et al. (2008) Hematology Am Soc Hematol Educ Program 2008: 341-8.
Veronese ML, et al. (1995) Blood 85: 2132-8.

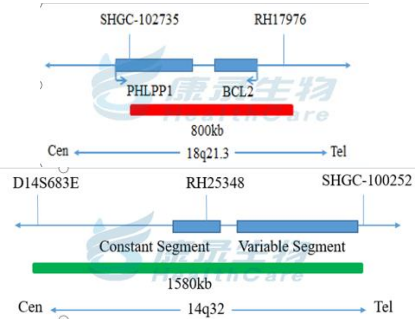
# BCL2/IGH gene fusion probe

## Background

BCL2/IGH dual-color fusion probe is designed to detect the translocation of t(14;18)(q32.3;q21.3) involving BCL2 and IGH genes. The translocation of the IGH (immunoglobulin heavy chain locus) and BCL2 (B-cell lymphoma) genes is a marker of follicular lymphoma (FL). FL is one of the most common non-Hodgkin's lymphoma (NHL). The t(14;18)(q32.3;q21.3) translocation is present in approximately 80% of patients with FL, but it is also found in 20-30% of diffuse large B-cell lymphoma (DLBCL) patients.

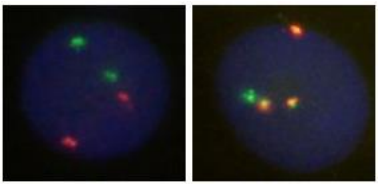
## Probe description

BCL2 probe is labeled with an orange-red fluorescent dye while IGH probe is labeled with a green fluorescent dye. Under normal conditions BCL2 gene and IGH gene are not fused and the result shows two orange-red signals and two green signals. When there is a BCL2/IGH gene fusion, the green and orange-red signals form a yellow fusion signal due to recombination.




## Clinical significance

The t(14;18) translocation occurs in 85% of FL and about 30% of diffuse lymphoma (DL) with a poor prognosis. Studies have shown that BCL2/IGH translocation rearrangement plays a role in stimulating B cell hyperproliferation.



BCL2/IGH fusion [-] BCL2/IGH fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| BCL6/MYC/IGH/[BCL2/IGH] gene probe reagent | FP-242-4 | BCL2/IGH | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Baró C, et al. (2011) Leuk Res 35: 256-9.
Da Cunha Santos G, et al. (2011) Cancer Cytopathol 119: 254-62.
Einerson RR, et al. (2005) Am J Clin Pathol 124: 421-9.
Gu K, et al. (2008) Arch Pathol Lab Med 132: 1355-61.
Nguyen-Khac F, et al. (2011) Am J Blood Res 1: 13-21.
Weinberg OK, et al. (2007) J Mol Diagn 9: 530-7.

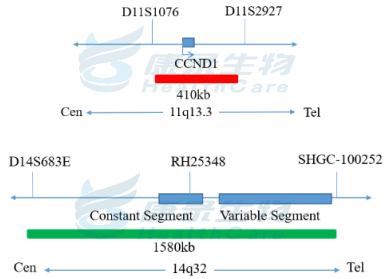
# CCND1 (BCL1)/IGH gene fusion probe

## Background

CCND1/IGH dual-color fusion probe is used to detect t(11;14) (q13.3; q32.3) translocations which has been detected in up to 95% of mantle cell lymphoma (MCL). t(11;14) is also present in other lymphoproliferative diseases, such as prolymphoblastic leukemia (PLL) and plasma cell myeloma.

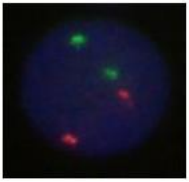
## Probe description

CCND1 probe is labeled with an orange-red fluorescent dye while IGH probe is labeled with a green fluorescent dye. Under normal conditions when CCND1 and IGH genes are not fused, the result shows two orange-red signals and two green signals. When a gene fusion is present, the green and orange signals recombine to form yellow fusion signal.




## Clinical significance

MCL is a subtype of non-Hodgkin's lymphoma (NHL) with poor prognosis. t(11;14) (q13.3;q32.3) can be used for the auxiliary diagnosis of MCL. It can also be used for the MCL and chronic lymphocytic leukemia (CLL) differentiation.



CCND1/IGH fusion [-]

CCND1/IGH fusion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| [IGH/CCND1]/[IGH/MAF]/[IGH/MAFB]/[IGH/FGFR3] gene fusion probe reagent | FP-233-1 | IGH/CCND1 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Bentz JS, et al. (2004) Cancer 102: 124-31.
Li JY, et al. (1999) Am J Pathol 154: 1449-52.

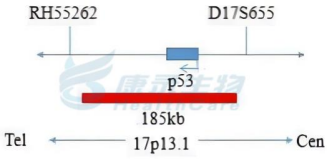
# P53 gene probe gene probe

## Background

The P53 gene highly correlates with human tumors and acts as a tumor suppressor gene. The 53kD protein encoded by the P53 gene plays an important regulatory role in the cell cycle, has a growth inhibitory effect under normal conditions, and plays an important role in DNA damage response, cell death and the cell cycle differentiation.

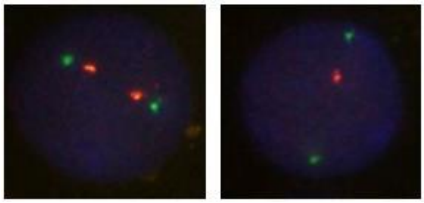
## Probe description

The P53 gene probe uses an orange-red fluorescent probe for the P53 gene region, and a green fluorescent probe for the chromosome 17-centromere region (CEP17). The P53 gene marker region is located at 17q13.1, and CEP17 probe is labeled within the alpha satellite sequence.




## Clinical significance

Deletion of the P53 gene indicates a poor response to chemo-radiotherapy and patients prone to metastasis. The detection of the P53 deletion can be used for early diagnosis and as an indicator for therapeutic efficacy and prognosis.



P53 deletion [-] P53 deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| CLL chromosome and gene anomaly probe detection kit | FP-014-2 | P53/CEP17 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Chang H, et al. (2010) Am J Clin Pathol 133: 70-4.
Herrera JC, et al. (2010) Biomedica 30: 390-400.

# MULTIPLE MYELOMA (MM)

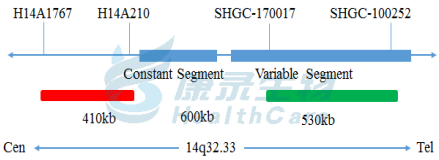
## IGH gene break apart probe

### Background

The IGH gene rearrangement has been shown to be an early event in the multiple myeloma (MM), usually occurring at the 14q32 region. The breakpoints are mainly in the D and J regions, occurring in about 50-60% of MM patients. Partner chromosomes of the IGH gene translocation mainly include 11q13 (BCL1/CCND1), 4p16.3 (FGFR3), 16q23 (MAF), 20q11 (MAFB) and 6p21 (CCND3).

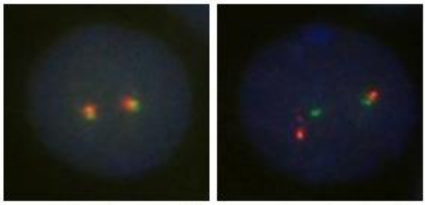
### Probe description

IGH is a dual-color break apart probe consisting of two probes hybridizing with 14q32.33. The orange-red fluorescent probe hybridizes to the proximal end of the IGH gene, while the green fluorescent probe hybridizes to the distal end of the IGH gene.




### Clinical significance

IGH gene break and translocation are complex and involve multiple genes. They are commonly found in acute lymphocytic leukemia (ALL), MM and lymphoma. The IGH gene break apart can be used as a marker for malignant cloning of myeloma cells, not affected by clinical stages and immune types. Thus, it can be used as a strong basis for MM diagnosis.



IGH break apart [-] IGH break apart [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| BCL6/MYC/IGH/[BCL2/IGH] gene probe reagent | FP-242-3 | IGH | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Bernicot I, et al. (2007) Cytogenet Genome Res 118: 345-52.
Hehne S, et al. (2012) Pathol Res Pract 208: 510-7.

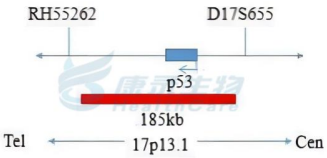
# P53 gene probe gene probe

## Background

The P53 gene highly correlates with human tumors and acts as a tumor suppressor gene. The 53kD protein encoded by the P53 gene plays an important regulatory role in the cell cycle, has a growth inhibitory effect under normal conditions, and plays an important role in DNA damage response, cell death and the cell cycle differentiation.

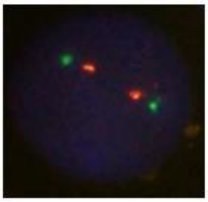
## Probe description

The P53 gene probe uses an orange-red fluorescent probe for the P53 gene region, and a green fluorescent probe for the chromosome 17-centromere region (CEP17). The P53 gene marker region is located at 17q13.1, and CEP17 probe is labeled within the alpha satellite sequence.

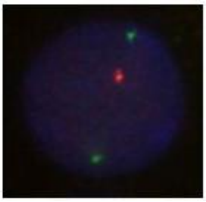



## Clinical significance

P53 deletion occurs in about 30% of newly diagnosed multiple myeloma (MM). It predicts poor prognosis for patients receiving conventional chemotherapy.



P53 deletion [-]



P53 deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| CLL chromosome and gene anomaly probe detection kit | FP-014-2 | P53/CEP17 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Chang H, et al. (2005) Blood 105: 358-60.
Chang H, et al. (2010) Am J Clin Pathol 133: 70-4.
Herrera JC, et al. (2010) Biomedica 30: 390-400.
Lozanski G, et al. (2004) Blood 103: 3278-81.
Tavor S, et al. (2011) Leuk Lymphoma 52: 642-7.

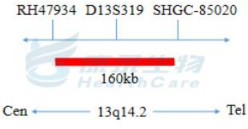
# D13S319/LAMP1 gene probe

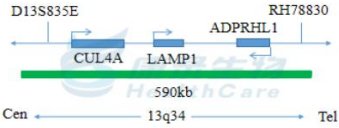
## Background

The D13S319/LAMP1 gene probe detects the human D13S319 STS marker region located on chromosome band 13q14.2 and the LAMP1 (CD107a/LAMPA/LGP120) gene, on chromosome band 13q34. Abnormalities in the two regions are commonly found in multiple myeloma (MM), but also occur in other malignacies.

## Probe description

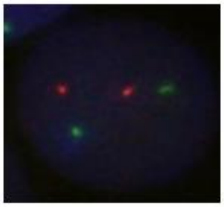
13q14/13q34 is a dual-color hybrid probe. The orange-red fluorescent dye directly labels the D13S319 probe and specifically detects the D13S319 gene at 13q14.2. The green fluorescent dye directly labels the 13q34 probe, which specifically detects LAMP1 gene at the 13q34 region.



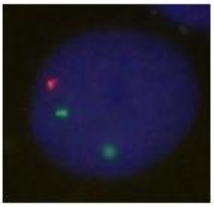




## Clinical significance

Clinical studies have found that the occurrence and development of MM is accompanied by a variety of specific changes in the number or structure of related genes at the cytogenetic level. Chromosome 13 haplotypes occur in 85% of patients with MM, and are adverse prognostic factor found.



D13S319/LAMP1 [-]



D13S319/LAMP1 [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| 13 (13q14) probe reagent | FP-025 | D13S319/13q34 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Dal Bo M, et al. (2011) Genes Chromosomes Cancer 50: 633-43.
La Starza R, et al. (2018) Molecular Cytogenetics 11: 6.
Ouillette P, et al. (2011) Clin Cancer Res 21: 6778-90.

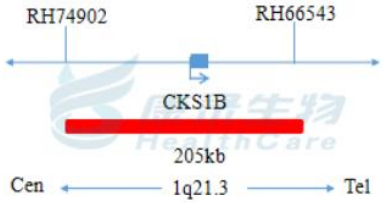
# 1q21 gene amplification probe

## Background

Chromosome 1 abnormality is one of the most common cytogenetic findings in multiple myeloma (MM). A major feature of B cell malignancies is the slow increase in malignant plasma cells grown in the bone marrow. The CKS1B gene is located at the end of chromosome 1, band 1q21. In the progression of myeloma disease, tandem repetition and skip translocations of the 1q21 band occur, whereas in patients with multiple myeloma, 1q amplification is associated with poor prognosis.

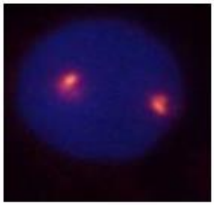
## Probe description

1q21 gene amplification detection probe uses an orange-red fluorescent label 1q21 region, and the 1q21 probe binds to the target detection site by *in situ* hybridization. This method is used to detect abnormalities of MM genes, and provide clinical reference for the differentiation, prognosis and medication for leukemia patients.

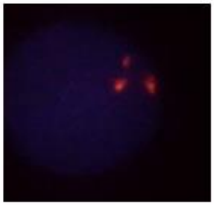



## Clinical significance

1q21 (CKS1B) is the most common genetic abnormality in MM. The expansion of CKS1B gene leads to the up-regulation of cell cycle, which causes many proliferative diseases. 1q21 amplification is often associated with MM phenotype infiltration, poor prognosis and rapid disease progress.



1q21 amplification [-]



1q21 amplification [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| 1q21 gene amplification probe reagent | FP-022 | 1q21 | 100µL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Chang H, et al. (2010) Bone Marrow Transplant 45: 117-21.
Kulkarni MS, et al. (2202) Leukemia 16:127-34.
Shaughnessy J, et al. (2005) Hematology 10: 117-26.
Walker BA, et al. (2010) Blood 116: 56-65.
Zhan F, et al. (2007) Blood 109: 4995-5001.

# RB1 gene deletion probe

## Background

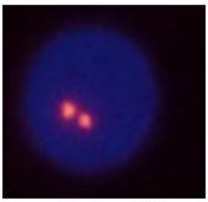
RB1 gene is located in the 13q14.2 region. Its encoded protein acts as a tumor suppressor and plays an important role in cell cycle and genomic DNA stability.

## Probe description

RB1 gene deletion detection probe uses an orange-red fluorescent label and binds to the target detection site by *in situ* hybridization.


## Clinical significance

This method is used to detect the abnormalities in multiple myeloma (MM) genes, and provide clinical reference for the differentiation, prognosis and medication for leukemia patients. Some reseachers recommend MM differential diagnosis at the cytogenetic level. These changes are closely related to the prognosis of patients. Patients with RB1 gene deletion have a moderate prognosis with a median survival of 40 months.



RB1 deletion [-]

RB1 deletion [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| RB1 gene deletion probe reagent | FP-021 | RB1 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Chang H, et al. (2010) Bone Marrow Transplant 45: 117-21.
Kulkarni MS, et al. (2202) Leukemia 16:127-34.
Shaughnessy J, et al. (2005) Hematology 10: 117-26.
Walker BA, et al. (2010) Blood 116: 56-65.
Zhan F, et al. (2007) Blood 109: 4995-5001.

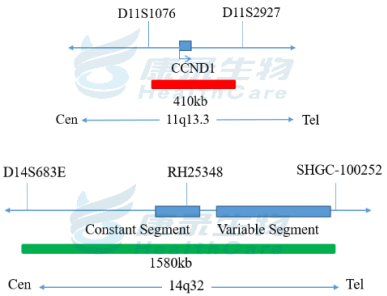
# CCND1 (BCL1)/IGH gene fusion probe

## Background

CCND1/IGH dual-color double fusion probe is used to detect the translocation of t(11;14)(q13.3;q32.3) which often occurs in multiple myeloma (MM). This translocation exists in the CCND1 gene near the IGH (immunoglobulin heavy chain) gene, which leads to overexpression of the CCDN1 gene. Detection of t(11;14) translocation has important clinical significance.

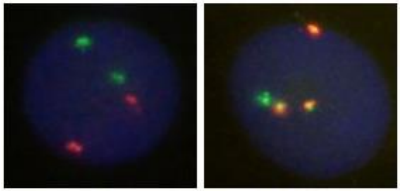
## Probe description

CCND1/IGH is a dual-color, double-fusion probe labeled with an orange-red fluorescent dye within the CCND1 probe and an IGH probe labeled with green fluorescence. Under normal conditions when CCND1 and IGH genes are not fused, the result shows two orange-red signals and two green signals. When there is gene fusion, the green and orange-red signals form a yellow fusion signal as recombination result.




## Clinical significance

t(11;14) is one of the most common abnormal translocations in MM. MM patients with t(11;14) translocation and no other genetic changes have a good prognosis, with a median survival of 50 months.



CCND1/IGH fusion [-] CCND1/IGH fusion [-]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| [IGH/CCND1]/[IGH/MAF]/[IGH/MAFB]/[IGH/FGFR3] gene fusion probe reagent | FP-233-1 | IGH/CCND1 | 100μL/Kit |

E-mail: sales@biognost.hr | Phone #: +385 1 240 9997

**References**

Bentz JS, et al. (2004) Cancer 102: 124-31.
Li JY, et al. (1999) Am J Pathol 154: 1449-52.
Siebert R, et al. (1998) Ann of Oncol 9: 519-26.
Vaandrager JW, et al. (1996) Blood 88: 1177-82.

# MYELODYSPLASTIC SYNDROME

## MDS gene and chromosome detection probe

### Background

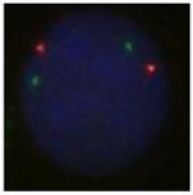
Myelodysplastic syndrome (MDS) is a group of heterogeneous diseases that are thought to originate from hematopoietic stem cells and are malignant clonal diseases characterized by bone marrow failure, blood cell dysplasia, and high conversion to acute myeloid leukemia. Studies have shown that 40% to 60% of patients with MDS have non-random chromosomal abnormalities, of which -5/5q-, -7/7q-, +8, 20q- and -Y are the most common.

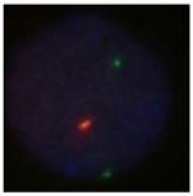
### Probe description

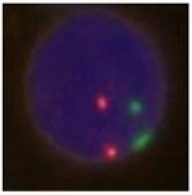
This kit uses an orange-red fluorescent dye to label CSF1R, EGR1, D7S486, D7S522, D20S108 and CEPY probes, and a green fluorescent dye to label D5S630, CEP7, CEP8, CEPX and Yq12 probes. The probes bind to the target detection site by *in situ* hybridization. Under normal conditions (no gene deletion and chromosome abnormality), two orange-red signals and two green signals are shown under a fluorescence microscope. When there is a gene deletion, there will be a lack of green or orange-red signal, and when there is a chromosomal polysomy, the centromere gene probe signal will increase. The detection of gene deletion and chromosome abnormality by FISH method is of great clinical significance for the diagnosis, treatment and prognosis of MDS.

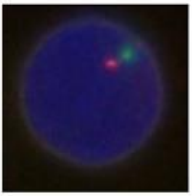
### Clinical significance

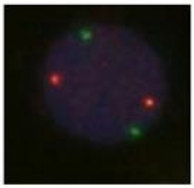
Some chromosomal abnormalities have specific diagnostic value among the common chromosome abnormalities in MDS patients. Immunosuppressive therapy is effective in some patients with simple +8, 20q- or Y- chromosomes. Karyotyping is also of great value in the classification, treatment and prognosis of MDS. For example, patients with single Y-, 5q- or 20q- chromosomes have better prognosis, while those with complex chromosome abnormalities (≥3 abnormalities) or chromosome 7 abnormalities have worse prognosis, while those with other abnormalities have moderate prognosis.

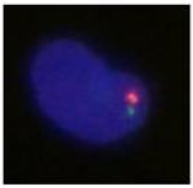

CSF1R/D5S630 [-]

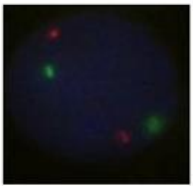

CSF1R/D5S630 [+]

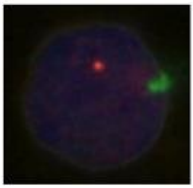

D7S486/CEP7 [-]

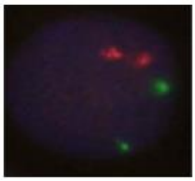

D7S486/CEP7 [+]


EGR1/D5S630 [-]


EGR1/D5S630 [+]


D7S522/CEP7 [-]


D7S522/CEP7 [+]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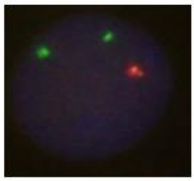
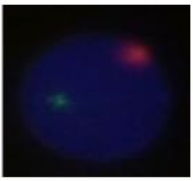
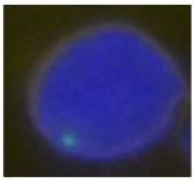

D20S108/CEP8 [+]


CEPX/CEPY [-]


CEPX/CEPY [+]

| Product name | Cat. No. | probe name | Specification |
|---|---|---|---|
| MDS chromosome and gene anomaly probe detection kit | FP-011-1 | D7S486/CEP7 | 100µL/Kit |
| | FP-011-2 | D7S522/CEP7 | 100µL/Kit |
| | FP-011-3 | CSF1R/D5S630 | 100µL/Kit |
| | FP-011-4 | EGR1/D5S630 | 100µL/Kit |
| | FP-011-5 | D20S108/CEP8 | 100µL/Kit |
| | FP-011-6 | CEPY/CEPX | 100µL/Kit |
| | FP-011-7 | Yq12/CEPX | 100µL/Kit |

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**References**

Boultwood J, et al. (2010) Blood 116: 5803-11.
Coleman JF, et al. (2011) Am J Clin Pathol 135: 915-20.
Tefferi A, et al. (2009) N Engl J Med 361: 1872-85.

# Chromosome 8 probe

## Background

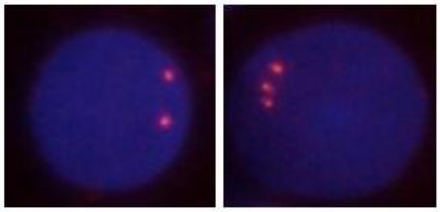
Trisomy 8 is the most common cytogenetic abnormality detected in myelodysplastic syndrome (MDS) patients with the estimated incidence 4-7%.

## Probe description

The centromere region of chromosome 8 is directly labeled with an orange-red fluorescent dye.


## Clinical significance

MDS patients with simple +8 respond well to immunosuppressive therapy and show median overall survival around 23.8 months.



CEP8 [-] CEP8 [+]

| Product name | Cat. No. | Probe name | Specification |
|---|---|---|---|
| Chromosome 8 centromere probe reagent | FP-018 | CEP8 | 100µL/Kit |

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**References**

Coleman JF, et al. (2011) Am J Clin Pathol 135: 915-20.
Kawankar N, et al. (2010) Hematology, 16:131-8.

BIOGNOST®
MEDICAL PRODUCTS

# FISH Fast Probes List

| Diagnosis | Cat. # | Description | Name | Format | Volume |
|---|---|---|---|---|---|
| Non-Small Cell Lung Cancer | FP-002 | ALK gene fusion detection probe | ALK | CE-IVD/RUO | 100µL |
| | FP-006 | 6q(ROS1) gene detection probe | ROS1 | CE-IVD/RUO | 100µL |
| | FP-046 | MET gene detection probe | C-MET/CEP7 | CE-IVD/RUO | 100µL |
| | FP-082 | MAML2(11q21) gene break apart detection probe | MAML2 | IVD/RUO | 100µL |
| | FP-231-1 | NTRK1 gene break apart detection probe | NTRK1 | CE-IVD/RUO | 100µL |
| | FP-231-2 | NTRK2(9q21) gene break apart detection probe | NTRK2 | CE-IVD/RUO | 100µL |
| | FP-231-3 | NTRK3(15q25) gene break apart detection probe | NTRK3 | CE-IVD/RUO | 100µL |
| | FP-227 | PDL1(9p24)/CSP9 gene amplification detection probe | PD-L1/CEP9 | IVD/RUO | 100µL |
| | FP-002 | ALK gene fusion detection probe | ALK | CE-IVD/RUO | 100µL |
| | FP-006 | 6q(ROS1) gene detection probe | ROS1 | CE-IVD/RUO | 100µL |
| | FP-046 | MET gene detection probe | C-MET/CEP7 | CE-IVD/RUO | 100µL |
| | FP-082 | MAML2(11q21) gene break apart detection probe | MAML2 | IVD/RUO | 100µL |
| | FP-231-1 | NTRK1 gene break apart detection probe | NTRK1 | CE-IVD/RUO | 100µL |
| | FP-231-2 | NTRK2(9q21) gene break apart detection probe | NTRK2 | CE-IVD/RUO | 100µL |
| | FP-231-3 | NTRK3(15q25) gene break apart detection probe | NTRK3 | CE-IVD/RUO | 100µL |
| | FP-227 | PDL1(9p24)/CSP9 gene amplification detection probe | PD-L1/CEP9 | IVD/RUO | 100µL |
| Breast Cancer | FP-001 | HER2 gene amplification detection probe | HER2/CEP17 | CE-IVD/RUO | 100µL |
| | FP-008 | TOP2A gene amplification detection probe | TOP2A | IVD/RUO | 100µL |
| | FP-083 | ETV6/NTRK3 gene fusion t(12;15) detection probe | ETV6/NTRK3 | IVD/RUO | 100µL |
| | FP-041 | CCND1(BCL1) gene amplification detection probe | CCND1/CEP11 | IVD/RUO | 100µL |
| | FP-203 | EPOR(19p13) gene break apart detection probe | EPOR | IVD/RUO | 100µL |
| Stomach Cancer | FP-001 | HER2 gene amplification detection probe | HER2 | CE-IVD/RUO | 100µL |
| Bladder Cancer | FP-009 | Bladder Cancer Cells chromosome and gene anomaly detection probe | CEP3/CEP7 ; P16/CEP17 | CE-IVD/RUO | 200µL |
| | FP-014-2 | CLL chromosome and gene anomaly detection probe | P53/CEP17 | CE-IVD/RUO | 100µL |
| Cervical Cancer | FP-013 | TERC gene amplification detection probe | TERC | CE-IVD/RUO | 100µL |
| Brain Cancer | FP-045 | 1p/19q deletion detection probe | 1p/19q | CE-IVD/RUO | 200µL |
| | FP-016 | BRAF gene break apart detection probe | BRAF | CE-IVD/RUO | 100µL |
| Lymphoma | FP-243-2 | MYC(8q24) ; BCL6(3q27) ; BCL2(18q21) gene break apart detection probe | BCL6 | CE-IVD/RUO | 100µL |
| | FP-243-3 | MYC(8q24) ; BCL6(3q27) ; BCL2(18q21) gene break apart detection probe | BCL2 | CE-IVD/RUO | 100µL |
| | FP-242-3 | BCL6 ; MYC ; IGH ; BCL2/IGH gene detection probe | IGH | CE-IVD/RUO | 100µL |
| | FP-234-3 | MAFB/IGH ; CCND3/IGH ; MYC/IGH gene fusion detection probe | IGH/C-MYC | CE-IVD/RUO | 100µL |
| | FP-242-4 | BCL6 ; MYC ; IGH ; BCL2/IGH gene detection probe | IGH/BCL2 | CE-IVD/RUO | 100µL |
| | FP-014-2 | CLL chromosome and gene anomaly detection probe | P53/CEP17 | CE-IVD/RUO | 100µL |
| | FP-243-1 | MYC(8q24) ; BCL6(3q27) ; BCL2(18q21) gene break apart detection probe | MYC | CE-IVD/RUO | 100µL |
| | FP-233-1 | IGH/CCND1; IGH/MAF ; IGH/MAFB ; IGH/FGFR3 gene fusion detection probe | CCND1/IGH | CE-IVD/RUO | 100µL |
| | FP-158 | MALT1 gene break apart detection probe | MALT1 | IVD/RUO | 100µL |
| | FP-159 | MALT1/IGH gene fusion t(14; 18) detection probe | MALT1/IGH | IVD/RUO | 100µL |
| | FP-160 | IRF4(6p25) gene break apart detection probe | IRF4 | IVD/RUO | 100µL |
| | FP-163 | API2/MALT1 t(11;18) gene detection probe | API2/MALT1 | IVD/RUO | 100µL |
| | FP-164 | 11q23.3/11q24.3 gene deletion detection probe | 11q23.3/CEP11 11q24.3/CEP11 | IVD/RUO | 200µL |
| | FP-227 | PDL1(9p24)/CSP9 gene amplification detection probe | PDL1/CEP9 | IVD/RUO | 100µL |
| Chronic Lymphocytic Leukemia (CLL) | FP-014-1 | CLL chromosome and gene anomaly detection probe | RB1/ATM | CE-IVD/RUO | 100µL |
| | FP-014-2 | | P53/CEP17 | CE-IVD/RUO | 100µL |
| | FP-014-3 | | D13S319/CEP12 | CE-IVD/RUO | 100µL |
| | FP-034 | Chromosome 12 centromere detection probe | CEP12 | CE-IVD/RUO | 100µL |
| | FP-245-3 | P53; CCND1/IGH ; CEP11/ATM ; CEP12/D13S25 gene detection probe | CEP11/ATM | CE-IVD/RUO | 100µL |
| | FP-025 | 13(13q14) gene detection probe | D13S319/LAMP1 | CE-IVD/RUO | 100µL |
| | FP-036 | MYB(6q23) gene detection probe | MYB/CEP6 | CE-IVD/RUO | 100µL |
| | FP-198 | D13S25(13q14) gene deletion detection probe | D13S25 | IVD/RUO | 100µL |
| | FP-200 | D13S319 gene deletion detection probe | D13S319 | IVD/RUO | 100µL |
| Acute Myeloid Leukemia/AML (Non APL) | FP-004 | AML1/ETO gene fusion detection probe | AML1/ETO | CE-IVD/RUO | 100µL |
| | FP-005 | RARA(17q21) detection probe | PML/RARA | CE-IVD/RUO | 100µL |
| | FP-027 | CBFB gene break apart detection probe | CBFB | IVD/RUO | 100µL |
| | FP-026 | KMT2A(MLL) gene break apart detection probe | MLL | CE-IVD/RUO | 100µL |
| | FP-028 | CBFBMYH11gene fusion detection probe | CBFB/MYH11 | CE-IVD/RUO | 100µL |
| | FP-043 | RARA gene break apart detection probe | RARA | IVD/RUO | 100µL |
| | FP-179 | EVI gene break apart detection probe | EVI1 | CE-IVD/RUO | 100µL |

| Diagnosis | Cat. # | Description | Name | Format | Volume |
|---|---|---|---|---|---|
| Chronic Myeloid Leukemia (CML) | FP-003 | BCRABL gene fusion detection probe | BCR/ABL | CE-IVD/RUO | 100μL |
| | FP-170 | CHIC2 gene deletion (PDGFRA break) detection probe | CHIC2(PDGFRA) | IVD/RUO | 100μL |
| | FP-174 | NUP98 gene break apart detection probe | NUP98 | IVD/RUO | 100μL |
| | FP-232-1 | FGFR1 gene break apart detection probe | FGFR1 | CE-IVD/RUO | 100μL |
| | FP-232-2 | PDGFRA ; PDGFRB gene break apart detection probe | PDGFRA | CE-IVD/RUO | 100μL |
| | FP-230-5 | ABL1 ; ABL2 ; PDGFRB ; CRLF2 ; JAK2 gene break apart detection probe | JAK2 | IVD/RUO | 100μL |
| Acute Lymphoblastic Leukemia (ALL) | FP-029 | ETV6(TEL)/RUNX1(AML1) gene translocation detection probe | TEL/AML1 | CE-IVD/RUO | 100μL |
| | FP-003 | BCRABL gene fusion detection probe | BCR/ABL | CE-IVD/RUO | 100μL |
| | FP-242-3 | BCL6 ; MYC ; IGH ; BCL2IGH gene detection probe | IGH | CE-IVD/RUO | 100μL |
| | FP-032 | P16 gene deletion detection probe | P16 | CE-IVD/RUO | 100μL |
| | FP-026 | KMT2A(MLL) gene break apart detection probe | MLL | CE-IVD/RUO | 100μL |
| | FP-030 | Chromosomes 4, 10 detection probe | CEP4/CEP10 | IVD/RUO | 100μL |
| | FP-031 | Chromosome 17 centromeric detection probe | CEP17 | IVD/RUO | 100μL |
| | FP-243-1 | MYC(8q24)/BCL6(3q27)/BCL2(18q21) gene break apart detection probe | MYC | CE-IVD/RUO | 100μL |
| | FP-062 | TCF3/PBX1 gene fusion detection probe | TCF3/PBX1 | CE-IVD/RUO | 100μL |
| | FP-230-4 | ABL1 ; ABL2 ; PDGFRB ; CRLF2 ; JAK2 gene break apart detection probe | CRLF2 | IVD/RUO | 100μL |
| | FP-183 | E2A gene break apart detection probe | E2A | CE-IVD/RUO | 100μL |
| | FP-184 | MLL gene deletion detection probe | MLL/CEP11 | IVD/RUO | 100μL |
| | FP-181 | ETV6 gene break apart detection probe | ETV6 | IVD/RUO | 100μL |
| | FP-208 | DEK/NUP214 gene fusion detection probe | DEK/NUP214 | IVD/RUO | 100μL |
| | FP-317 | TCRB (7q34) gene break apart detection probe | TCRB (7q34) | IVD/RUO | 100μL |
| Multiple Myeloma (MM) | FP-021 | RB1 gene deletion detection probe | RB1 | IVD/RUO | 100μL |
| | FP-014-2 | CLL chromosome and gene anomaly detection probe | P53/CEP17 | CE-IVD/RUO | 100μL |
| | FP-242-3 | BCL6 ; MYC ; IGH ; BCL2IGH gene detection probe | IGH | CE-IVD/RUO | 100μL |
| | FP-233-1 | IGH/CCND1 ; IGH/MAF ; IGH/MAFB ; IGH/FGFR3 gene fusion detection probe | CCND1/IGH | CE-IVD/RUO | 100μL |
| | FP-025 | 13 (13q14) gene detection probe | D13S319/LAMP1 | CE-IVD/RUO | 100μL |
| | FP-197 | 1q21 and 1p32 anomaly detection probe | 1q21 and 1p32 | CE-IVD/RUO | 100μL |
| | FP-233-2 | IGH/CCND1 ; IGH/MAF ; IGH/MAFB ; IGH/FGFR3 gene fusion detection probe | MAF/IGH | CE-IVD/RUO | 100μL |
| | FP-234-2 | MAFB/IGH ; CCND3/IGH ; MYC/IGH gene fusion detection probe | CCND3/IGH | CE-IVD/RUO | 100μL |
| | FP-233-4 | IGH/CCND1 ; IGH/MAF ; IGH/MAFB ; IGH/FGFR3] gene fusion detection probe | FGFR3/IGH | CE-IVD/RUO | 100μL |
| | FP-233-3 | IGH/CCND1 ; IGH/MAF ; IGH/MAFB ; IGH/FGFR3 gene fusion detection probe | MAFB/IGH | CE-IVD/RUO | 100μL |
| | FP-195 | 15q22 and 6q21 anomaly detection probe | 15q22/6q21 | IVD/RUO | 100μL |
| | FP-200 | D13S319 gene deletion detection probe | D13S319 | IVD/RUO | 100μL |
| Myelodysplastic Syndrome (MDS) | FP-011-1 | MDS chromosome and gene anomaly detection probe | D7S486/CEP7 | CE-IVD/RUO | 100μL |
| | FP-011-2 | | D7S522/CEP7 | CE-IVD/RUO | 100μL |
| | FP-011-3 | | CSF1R/D5S630 | CE-IVD/RUO | 100μL |
| | FP-011-4 | | EGR1/D5S630 | CE-IVD/RUO | 100μL |
| | FP-011-5 | | D20S108/CEP8 | CE-IVD/RUO | 100μL |
| | FP-011-6 | | CEPX/CEPY | CE-IVD/RUO | 100μL |
| | FP-011-7 | | Yq12/CEPX | CE-IVD/RUO | 100μL |
| | FP-018 | Chromosome 8 centromere detection probe | CEP8 | CE-IVD/RUO | 100μL |
| | FP-232-3 | PDGFRB gene break apart detection probe | PDGFRB | IVD/RUO | 100μL |
| | FP-200 | D13S319 gene deletion detection probe | D13S319 | IVD/RUO | 100μL |
| | FP-305 | 13q gene detection probe | RB1/13q34 | CE-IVD/RUO | 100μL |
| Aplastic Anemia | FP-018 | Chromosome 8 centromeric detection probe | CEP8 | CE-IVD/RUO | 100μL |
| | FP-011-1 | MDS chromosome and gene anomaly detection probe | D7S486/CEP7 | CE-IVD/RUO | 100μL |
| | FP-011-4 | MDS chromosome and gene anomaly detection probe | EGR1/D5S630 | CE-IVD/RUO | 100μL |
| | FP-020 | 20q gene deletion detection probe | 20q12/20q13.12 | CE-IVD/RUO | 100μL |
| Acute Lymphoblastic Leukemia (ALL) | FP-029 | ETV6(TEL)/RUNX1(AML1) gene translocation detection probe | TEL/AML1 | CE-IVD/RUO | 100μL |
| | FP-003 | BCRABL gene fusion detection probe | BCR/ABL | CE-IVD/RUO | 100μL |
| | FP-242-3 | BCL6 ; MYC ; IGH ; BCL2IGH gene detection probe | IGH | CE-IVD/RUO | 100μL |
| | FP-032 | P16 gene deletion detection probe | P16 | CE-IVD/RUO | 100μL |
| | FP-026 | KMT2A(MLL) gene break apart detection probe | MLL | CE-IVD/RUO | 100μL |
| | FP-030 | Chromosomes 4, 10 detection probe | CEP4/CEP10 | IVD/RUO | 100μL |
| | FP-031 | Chromosome 17 centromeric detection probe | CEP17 | IVD/RUO | 100μL |
| | FP-243-1 | MYC(8q24)/BCL6(3q27)/BCL2(18q21) gene break apart detection probe | MYC | CE-IVD/RUO | 100μL |
| Soft Tissue Cancer | FP-055 | SS18(SYT) gene break apart detection probe | SS18(SYT) | IVD/RUO | 100μL |
| | FP-054 | MDM2 gene amplification detection probe | MDM2 | CE-IVD/RUO | 100μL |
| | FP-149 | CDK4 (12q13)/SE12 detection probe | CDK4/CEP12 | IVD/RUO | 100μL |
| | FP-297 | NR4A3(9q22) gene break apart detection probe | NR4A3 | IVD/RUO | 100μL |
| Ph. Like ALL | FP-141 | CSF1R(5q32) gene break apart detection probe | CSF1R | IVD/RUO | 100μL |
| | FP-188 | ABL1(9q34) gene break apart detection probe | ABL1 | IVD/RUO | 100μL |
| | FP-189 | ABL2(1q25) gene break apart detection probe | ABL2 | IVD/RUO | 100μL |
| | FP-230-5 | ABL1 ; ABL2 ; PDGFRB ; CRLF2 ; JAK2 gene break apart detection probe | JAK2 | IVD/RUO | 100μL |
| Soft Tissue Cancer | FP-055 | SS18(SYT) gene break apart detection probe | SS18(SYT) | IVD/RUO | 100μL |
| | FP-054 | MDM2 gene amplification detection probe | MDM2 | CE-IVD/RUO | 100μL |
| | FP-149 | CDK4 (12q13)/SE12 detection probe | CDK4/CEP12 | IVD/RUO | 100μL |
| | FP-297 | NR4A3(9q22) gene break apart detection probe | NR4A3 | IVD/RUO | 100μL |

| Diagnosis | Cat. # | Description | Name | Format | Volume |
|---|---|---|---|---|---|
| Central Nervous System Tumor | FP-048 | MYCN gene amplification detection probe | N-MYC/LAF4 | IVD/RUO | 100μL |
| | FP-108 | Chromosome 7 centromeric detection probe | CEP7 (Green) | IVD/RUO | 100μL |
| Peripheral Nerve Tissue Tumor | FP-050 | SRD(1p36) gene deletion detection probe | SRD/PBX1 | IVD/RUO | 100μL |
| Prenatal Diagnosis and Postnatal Examination | FP-314 | Prenatal chromosomes detection probe | 13/21 ; 18/X/Y | CE-IVD/RUO | 200μL/10 Tests |
| Non-Hodgkin Lymphoma | FP-240 | BCL6/IGH gene fusion t(3;14) detection probe | BCL6/IGH | IVD/RUO | 100μL |
| Acute Myeloid Leukemia /AML | FP-200 | D13S319 gene deletion detection probe | D13S319 | IVD/RUO | 100μL |
| | FP-232-3 | ABL1 ; ABL2 ; PDGFRB ; CRLF2 ; JAK2 gene break apart detection probe | PDGFRB | IVD/RUO | 100μL |
| | FP-305 | 13q gene detection probe | RB1/13q34 | CE-IVD/RUO | 100μL |
| Prostate Cancer | FP-307 | TMPRSS2 gene break apart detection probe | TMPRSS2 | IVD/RUO | 100μL |
| Kidney & Vascular Tumor | FP-075 | TFE3 gene break apart detection probe | TFE3 | IVD/RUO | 100μL |
| Cartilage Tumor | FP-149 | CDK4(12q13)/SE12 detection probe | CDK4/CEP12 | IVD/RUO | 100μL |
| Myeloproliferative Disease | FP-305 | 13q gene detection probe | RB1/13q34 | CE-IVD/RUO | 100μL |
| Extraskeletal Myxoid Chondrosarcoma (EMC) | FP-297 | NR4A3(9q22) gene break apart detection probe | NR4A3 | IVD/RUO | 100μL |
| Fibroblast/Myofibroblastic Tumor | FP-181 | ETV6 gene break apart detection probe | ETV6 | IVD/RUO | 100μL |
| | FP-074 | USP6(17p13) gene break apart detection probe | USP6 | IVD/RUO | 100μL |
| | FP-053 | FUS gene break apart detection probe | FUS | IVD/RUO | 100μL |
| | FP-051 | EWSR1 gene break apart detection probe | EWSR1 | IVD/RUO | 100μL |
| Striated muscle tumor(Rhabdomyoma) | FP-056 | FKHR gene break apart detection probe | FKHR | IVD/RUO | 100μL |
| | FP-144 | PAX3(2q36) gene break apart detection probe | PAX3 | IVD/RUO | 100μL |
| Thyroid | FP-059 | RET gene break apart detection probe | RET | IVD/RUO | 100μL |
| Fibrohistiocytoma | FP-052 | DDIT3(12q13) gene break apart detection probe | DDIT3 | IVD/RUO | 100μL |
| Renal Cell Carcinoma (RCC) | FP-105 | 3p gene detection probe | 3p25/CEP3 | IVD/RUO | 100μL |
| Plasma Cell Myeloma (PCM) | FP-207 | 20q gene detection probe | D20S108 | IVD/RUO | 100μL |
| Angiosarcoma | FP-015 | MYC(8q24) gene amplification detection probe | MYC | CE-IVD/RUO | 100μL |
| Endometrial Stromal Tumor (EST)/Endometrial Cancer | FP-226 | JAZF1(7p15) gene break apart detection probe | JAZF1 | IVD/RUO | 100μL |

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