CytoCell

ogt

A Sysmex Group Company

Haematology FISH Probes for CLL



Features

- Improve confidence in result interpretation with high intensity signals and minimal background
- Enhance detection and scoring accuracy with robust, easy-to-analyse probes
- Save time and minimise mixing errors with easy-to-use, pre-mixed probes
- Optimise stock levels and minimise wastage with flexible pack sizes to meet your needs

Chronic Lymphocytic Leukaemia

Chronic Lymphocytic Leukaemia (CLL) is the most common leukaemia in adults. It affects approximately 0.6% of the worldwide population, with an annual incidence rate of 5 cases per 100,000 population[1]. However, the incidence of CLL dramatically increases with age, to more than 20 cases per 100,000 individuals aged over 70 years[1]. The course of CLL can vary from very indolent to rapidly progressive. Due to the low mitotic activity of the leukaemic cells *in vitro*, clonal chromosomal abnormalities are detected in 40-50%[2] of cases by conventional cytogenetics using B-cell mitogens. Meanwhile, FISH analysis can identify chromosomal aberrations in approximately 80% of CLLs[2], and has proven to be a powerful tool in both the diagnosis and management of CLL[2,3,4].

References

1. Swerdlow, *et al.* Editors. WHO Classification of Tumours of Haematopoietic & Lymphoid Tissues, Lyon, France, IARC:2017
2. Dohner, *et al.* N Eng J Med. 2000:343:1910-1916.
3. Rossi, *et al.* Blood. 2013;121(8):1403-1412.
4. Zent, *et al.* Blood. 2010;115(21):4154-4155.

The OGT Partnership

Behind every sample is a life that can be improved through the right care decisions.
The OGT partnership approach is key to providing the highest level of service, working closely with you to understand your unique challenges, customising our approach to meet your exact needs. Choose CytoCell® probes for your FISH analysis; our effective, accurate and simple to use products help clinical decision makers to reach the right decisions for each patient.

Alpha Satellite 12 *Plus* for CLL

Cat. No. **LPH 069-S** (5 tests) | Cat. No. **LPH 069** (10 tests)

Trisomy 12 is a recurrent abnormality in CLL, seen in 20% of cases[1] that often appears as the unique cytogenetic aberration (40-60% of cases with trisomy 12)[2]. Patients with trisomy 12 are classified as low-risk in the absence of any other genetic lesions[3].





CMP H002 v002

References

1. Swerdlow, *et al.* (eds,) WHO Classification of Tumours of Haematopoietic and Lymphoid Tissue, Lyon, France, 4th edition, IARC,2017.
2. Puiggros, *et al.* Biomed Res Int 2014;1-13.
3. Rossi, *et al.* Blood 2013;121(8):1403-1412.

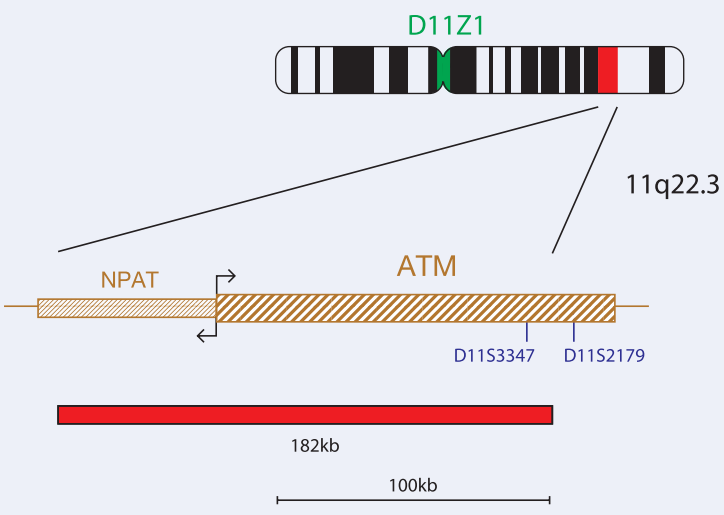
ATM Deletion

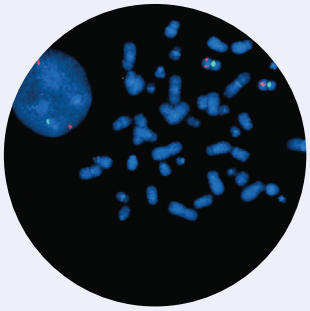
IVDR Cat. No. **CE-LPH 011-S** (5 tests) | Cat. No. **CE-LPH 011** (10 tests)

The protein kinase ATM (*ATM serine/threonine kinase*) gene at 11q22.3 is frequently deleted in cases of B-cell chronic lymphocytic leukaemia (CLL). ATM is an important checkpoint gene involved in the management of cell damage. Its function is to assess the level of DNA damage in the cell and attempt repair by phosphorylating key substrates involved in the DNA damage response pathway[1].

B-CLL is the most common leukaemia in adults; its course can vary from very indolent to rapidly progressive. Due to the low mitotic activity of the leukaemic cells *in vitro*, clonal chromosomal abnormalities are detected in 40-50%[2] of cases by conventional cytogenetics using B-cell mitogens, whereas FISH analysis identifies chromosomal aberrations in approximately 80%[2] of B-CLLs. Screening for deletions of ATM and/or TP53 is vital to allow informed therapy choices for B-CLL patients, as deletions of TP53 and ATM confer poorer prognosis in this disease[4]; therefore, the use of FISH has proven to be a powerful tool in both the diagnosis and management of patients with B-CLL[2,3,4].

Analysis of the ATM/TP53 interaction in B-CLL has shown that TP53 and ATM play an important role in the proliferation of lymphoid cancer[1]. It has been shown that ATM enhances the phosphorylation of TP53, should the damage be so great that the cell requires destruction by apoptosis (which is mediated by TP53). Deletion of ATM removes this checkpoint activity and hence activation of TP53. Thus, there is no attempt made to repair, or apoptosis of, damaged cells, despite the presence of TP53. In the absence of ATM, damaged cells are allowed to continue to proliferate[5].





CMP-H006 v004.00

References

1. Stankovic, *et al.* Blood. 2004;103(1):291-300.
2. Dohner, *et al.* N Eng J Med. 2000;343:1910-1916.
3. Zent, *et al.* Blood. 2010;115(21):4154-4155.
4. Rossi, *et al.* Blood. 2013;121(8):1403-1412.
5. Khanna, *et al.* Nature Genetics. 1998;20(4):398-400.

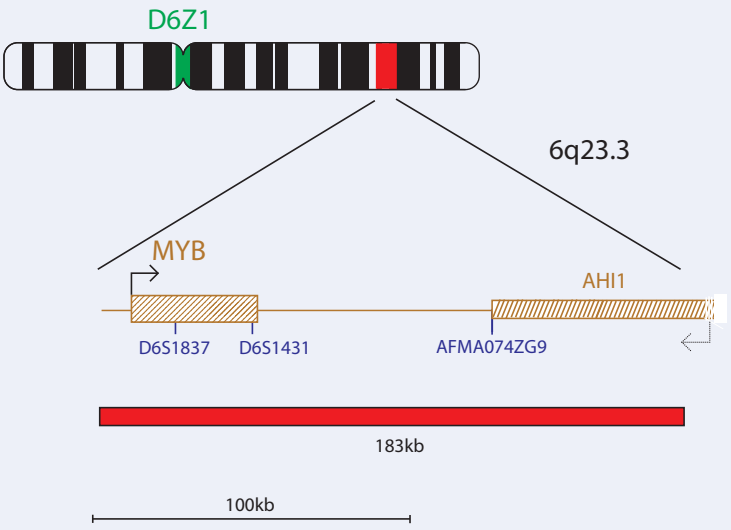
MYB Deletion

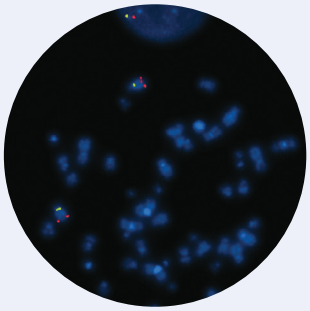
Cat. No. **LPH 016-S** (5 tests) | Cat. No. **LPH 016** (10 tests)

MYB (*MYB proto-oncogene, transcription factor*) at 6q23.3 is a transcription factor essential for haematopoiesis[1].

The long arm of chromosome 6 (6q) is frequently involved in chromosomal abnormalities in human cancer, including haematological malignancies[1]. Deletions of chromosome 6q are found in acute lymphoblastic leukaemia (ALL), chronic lymphocytic leukaemia (CLL) and high grade nodal and extranodal B-cell lymphoma, but also in breast carcinoma, melanoma, ovarian carcinoma and renal cell carcinoma[2,3].

Additionally, rearrangements involving MYB have been reported in T-cell ALL, for example the t(6;7)(q23;q34) translocation involving TRB seen in approximately 6% of patients, and focal duplications of the MYB locus, which are present in about 10% of patients[1,4].





CMP H037 v002

References

1. Clappier, *et al.* Blood. 2007;110(4):1251-1261.
2. Starostik, *et al.* Blood. 2000;95(4):1180-1187.
3. Stilgenbauer, *et al.* Leukemia.1999;13:1331-1334.
4. Van Vlierberghe, Ferrando. J of Clin Inv. 2012;122(10):3398-3406.

P53 (TP53)/ATM Probe Combination

Cat. No. **LPH 052-S** (5 tests) | Cat. No. **LPH 052** (10 tests)

The tumour suppressor TP53 (*tumor protein p53*) gene at 17p13 and the protein kinase ATM (*ATM serine/threonine kinase*) gene at 11q22.3, are frequently deleted in cases of chronic lymphocytic leukaemia (CLL).

CLL is the most common leukaemia in adults; its course can vary from very indolent to rapidly progressive. Due to the low mitotic activity of the leukaemic cells *in vitro*, clonal chromosomal abnormalities are detected in 40-50%[2] of cases by conventional cytogenetics using B-cell mitogens, whereas FISH analysis identifies chromosomal aberrations in approximately 80% of CLLs[2]. Screening for deletions of ATM and/or TP53 is vital to allow informed therapy choices for CLL patients, as deletions of TP53 and ATM confer poorer prognosis in this disease[1,2,3].

The TP53 gene is one of most important tumour suppressor genes; it acts as a potent transcription factor with fundamental role in the maintenance of genetic stability. Loss of TP53 is reported in 10% of patients with CLL, and is considered to be the poorest prognostic marker in that disease[1,4].

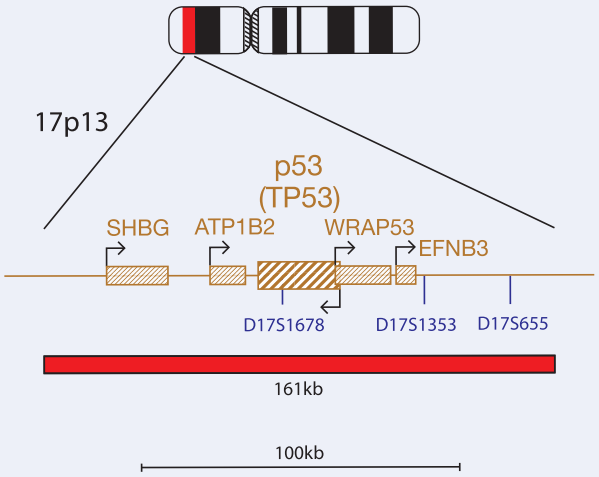
ATM is an important checkpoint gene involved in the management of cell damage; its function is to assess the level of DNA damage in the cell and attempt repair by phosphorylating key substrates involved in the DNA damage response pathway[5]. Loss of ATM is reported in 18% of patients with CLL, and is considered a poor prognostic marker in that disease[2].

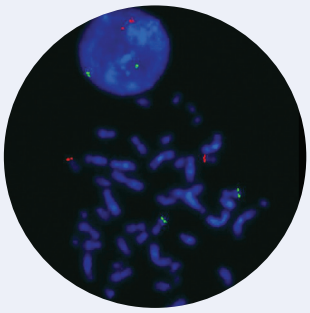
Analysis of the ATM/TP53 interaction in CLL has shown that TP53 and ATM play an important role in the proliferation of lymphoid cancer[5], it has been shown that ATM enhances the phosphorylation of TP53, should the damage be so great that the cell requires destruction by apoptosis (which is mediated by TP53). Deletion of ATM removes this checkpoint activity and hence activation of TP53. Thus, there is no attempt made to repair, or apoptosis of, damaged cells, despite the presence of TP53. In the absence of ATM, damaged cells are allowed to continue to proliferate[6].

References

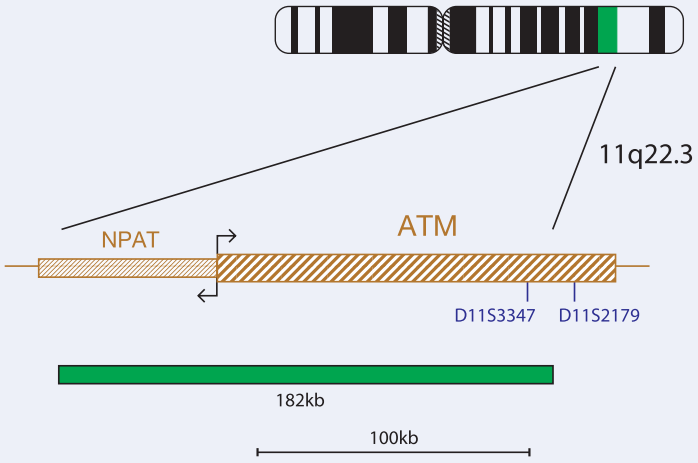
1. Rossi D, *et al*. Blood. 2013 Feb 21;121(8):1403-12.
2. Dohner, *et al*. N Eng J Med. 2000;343:1910-1916.
3. Zent, *et al*. Blood. 2010;115(21):4154-4155.
4. Baliakas P, *et al*. Leukemia. 2014;(April):1-8.
5. Stankovic, *et al*. Blood. 2004;103(1):291-300.
6. Khanna, *et al*. Nature Genetics. 1998;20(4):398-400.

P53 (TP53)/ATM Probe Combination





CMP H040 v005



CMP H041 v005

P53 (TP53) Deletion

Cat. No. **LPH 017-S** (5 tests) | Cat. No. **LPH 017** (10 tests)

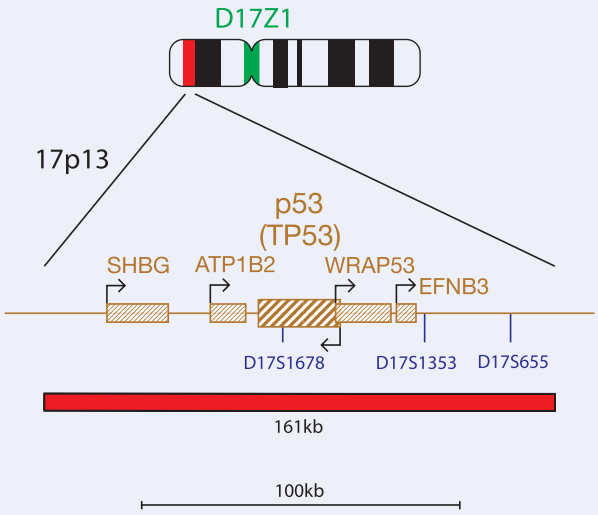
The TP53 (*tumor protein p53*) gene at 17p13 is a tumour-suppressor gene that has been shown to be deleted in a wide range of human malignancies.

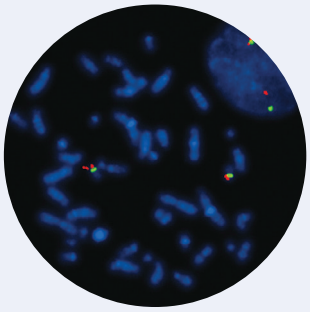
The TP53 gene is one of most important tumour suppressor genes; it acts as a potent transcription factor with fundamental role in the maintenance of genetic stability. Screening for TP53 loss is important as deletions or losses of the short arm of chromosome 17, which includes the TP53 region, are reported in many cancers and are often associated with disease progression, inferior response to treatment and/or a poor prognosis.

In particular, loss of TP53 is reported in 10% of patients with chronic lymphocytic leukaemia (CLL), and is considered to be the poorest prognostic marker in that disease[1,2]. In acute myeloid leukaemia (AML) and acute lymphoblastic leukaemia (ALL), TP53 loss is associated with a poor outcome and is often seen as a marker of disease progression or secondary disease[3-5].

TP53 loss in patients with multiple myeloma is a late event, where is seen as a marker of disease progression and is associated with a very poor prognosis[6,7].

In non-Hodgkin lymphoma, TP53 losses are reported in diffuse large B-cell lymphoma (DLBCL) often as part of 'dual-hit' lymphoma or plasmablastic phenotypes[8]. In mantle cell lymphoma (MCL), TP53 losses are associated with a poor outcome, and with a dismal outcome when seen with concurrent CDKN2A deletions[9].





CMP H039 v006

References

1. Rossi D, *et al.* Blood. 2013 Feb 21;121(8):1403-12.
2. Baliakas P, *et al.* Leukemia. 2014;(April):1-8.
3. Grimwade D, *et al.* Br J Haematol. 2010; (3):17.
4. Seifert H, *et al.* Leukemia. 2009;23(4):656-63.
5. Stengel A, *et al.* Blood. 2014;124(2):251-8.
6. Palumbo A, *et al.* J Clin Oncol. 2015 Sep 10;33(26):2863-9.
7. Fonseca R, *et al.* Leukemia. 2009 Dec;23(12):2210-21.
8. Simonitsch-Klupp I, *et al.* Leukemia. 2004 Jan;18(1):146-55.
9. Khayat AS, *et al.* BMC Gastroenterol. 2009;9:55.

13q Deletions

Rearrangements leading to the loss of all or part of the long arm of chromosome 13 are seen frequently in a wide range of haematological disorders.

Chromosome 13q aberrations occur in 16-40% of multiple myeloma cases (MM), most of them being complete monosomy 13 (85%), while the remaining 15% constitute deletion of 13q[1,2,3]. A case study of multiple myeloma patients narrowed down the critical deleted region to 13q14[4]. Historically, deletions of 13q have been associated with poor prognosis in MM, but now it is believed that its prognostic relevance may be related to its association with other concurrent genetic lesions[3,5].

Deletions affecting 13q14 are also the most frequent structural genetic aberrations in chronic lymphocytic leukaemia (CLL)[6,7,8]. This region is found to be heterozygously deleted in 30-60% and homozygously deleted in 10-20% of CLL patients[9]. The survival rate has been shown to be similar for the two groups[10]. Patients with 13q14 deletions are classified as very low risk, in the absence of any other genetic lesions[11].

Two non-coding RNA genes, DLEU1 (*deleted in lymphocytic leukemia* 1) and DLEU2 (*deleted in lymphocytic leukemia* 2), plus the genetic marker D13S319, span the pathogenic critical region of 13q14[12]. DLEU1 is considered to be the most likely CLL-associated candidate tumour suppressor gene within the 13q14 region[13]. Subsequently, D13S319, located between the RB1 gene and D13S25 and within the DLEU1 locus, was found to be deleted in 44% of CLL cases[14]. It has also been postulated that a gene telomeric to the D13S319 region, encompassing D13S25, may be important in cases with hemizygous deletions and that this gene is a putative tumour suppressor gene[15].

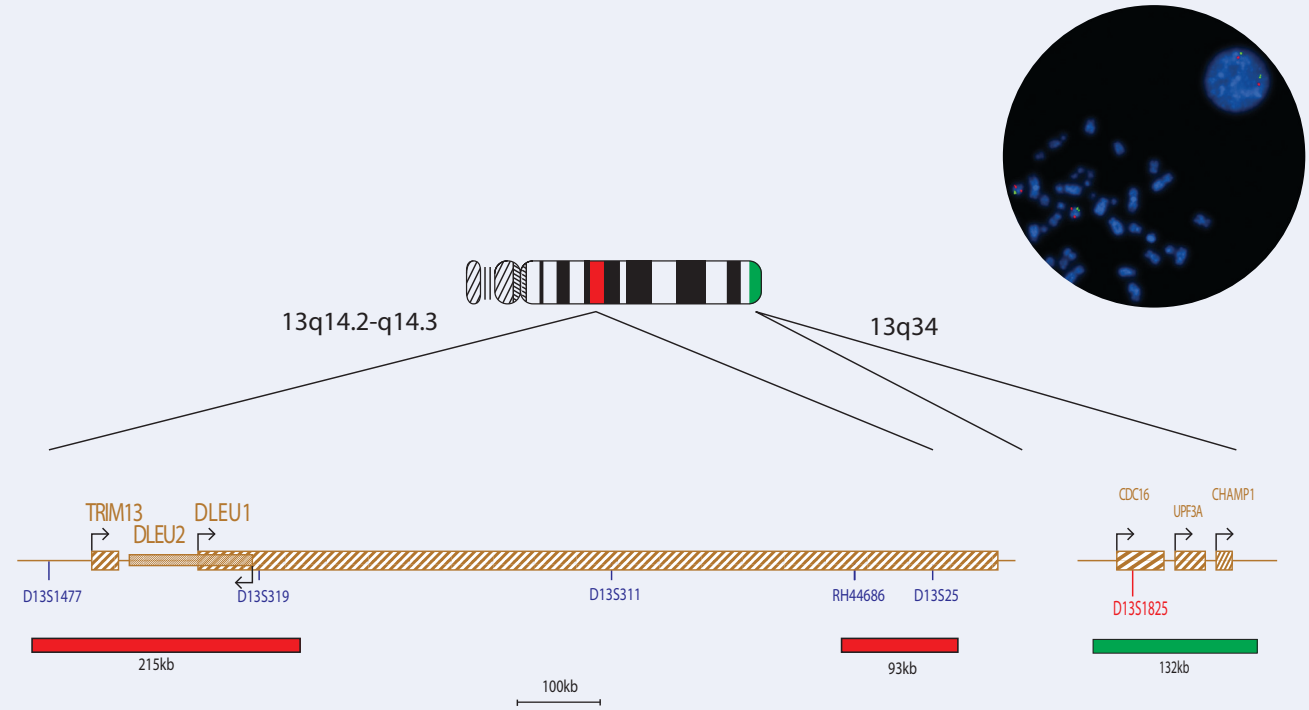
References

1. Bullrich F, *et al.* Cancer Res. 2001;61:6640-8.
2. Zojer, *et al.* Blood. 2000;95(6):1925-1930.
3. Sawyer. Cancer Genetics. 2011;204:3-12.
4. Shaughnessy J, *et al.* Blood. 2000;96:1505-11.
5. Fonseca, *et al.* Leukemia. 2009;23:2210-2221.
6. Juliusson G, *et al.* N Eng J Med. 1990;323:720-4.
7. Puiggros, *et al.* Biomed Res Int. 2014;1-13.
8. Kasar, *et al.* Nature Communications. 2015;6:1-12.
9. Hammarsund M, *et al.* FEBS Letters. 2004;556:75-80.
10. Van Dyke DL, *et al.* Br J Haematology. 2009;148:544-50.
11. Rossi, *et al.* Blood. 2013;121(8):1403-1412.
12. Liu Y, *et al.* Oncogene. 1997;15:2463-73.
13. Wolf S, *et al.* Hum Mol Genet. 2001;10:1275-85.
14. Liu Y, *et al.* Blood. 1995;86:1911-5.
15. Bullrich F, *et al.* Blood. 1996;88(8):3109-15.

13q14.3

Cat. No. **LPH 006-S** (5 tests) | Cat. No. **LPH 006** (10 tests)

The 13q14.2-q14.3 probes, labelled in red, cover the D13S319 and D13S25 markers. The 13qter subtelomere specific probe (clone 163C9), labelled in green, allows identification of chromosome 13 and acts as a control probe.



CMP-H001 v003

D13S319/13qter/12cen Deletion/Enumeration

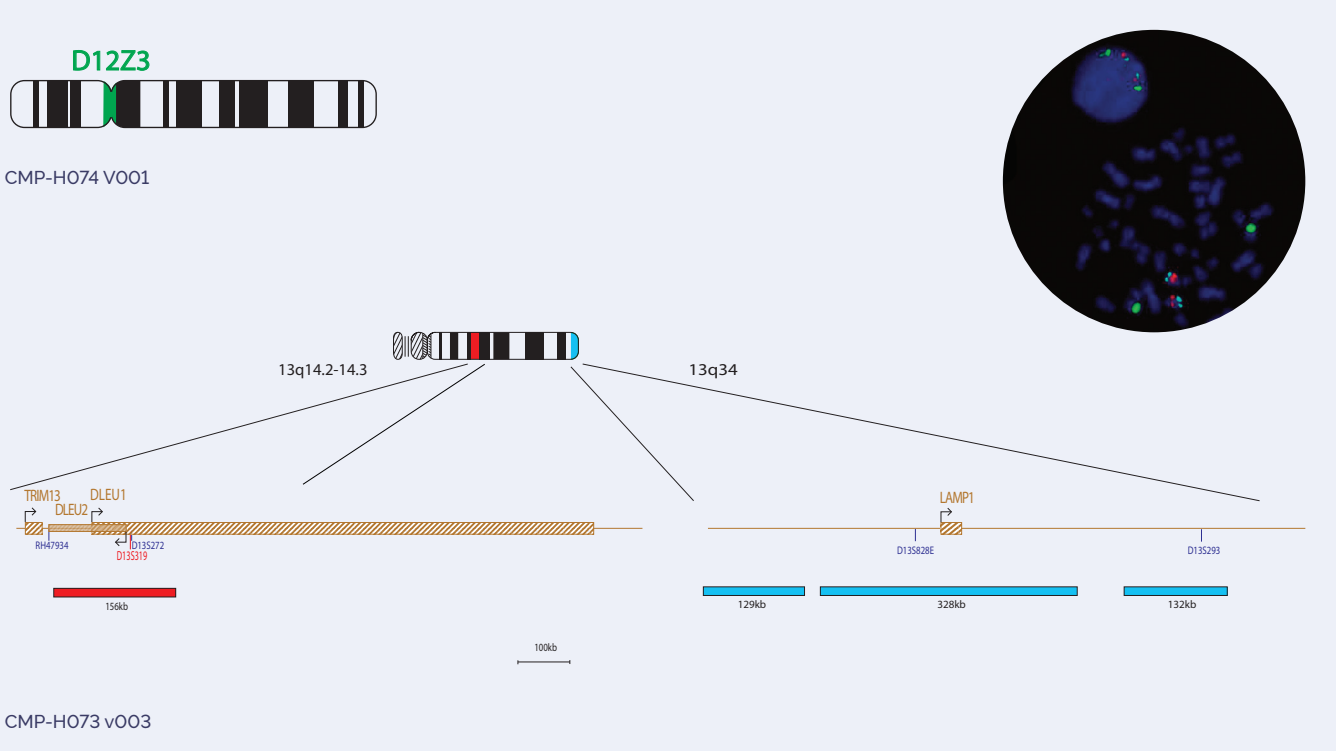
Cat. No. **LPH 066-S** (5 tests) | Cat. No. **LPH 066** (10 tests)

Deletions affecting band 13q14 and trisomy of chromosome 12 are common events in chronic lymphocytic leukaemia (CLL).

Deletions affecting 13q14 are also the most frequent structural genetic aberrations in chronic lymphocytic leukaemia (CLL)[1,2,3]. This region is found to be heterozygously deleted in 30-60% and homozygously deleted in 10-20% of CLL patients[4]. The survival rate has been shown to be similar for the two groups[5]. Patients with 13q14 deletions are classified as very low risk, in the absence of any other genetic lesions[6].

Two non-coding RNA genes, DLEU1 (*deleted in lymphocytic leukemia* 1) and DLEU2 (*deleted in lymphocytic leukemia* 2), plus the genetic marker D13S319, span the pathogenic critical region of 13q14[7]. DLEU1 is considered to be the most likely CLL-associated candidate tumour suppressor gene within the 13q14 region[8].

Trisomy 12 is a recurrent abnormality in CLL, seen in 20% of the cases[9] and often appears as the unique cytogenetic aberration (40-60% of cases with trisomy 12)[2]. Patients with trisomy 12 are classified as low-risk in the absence of any other genetic lesions[6].



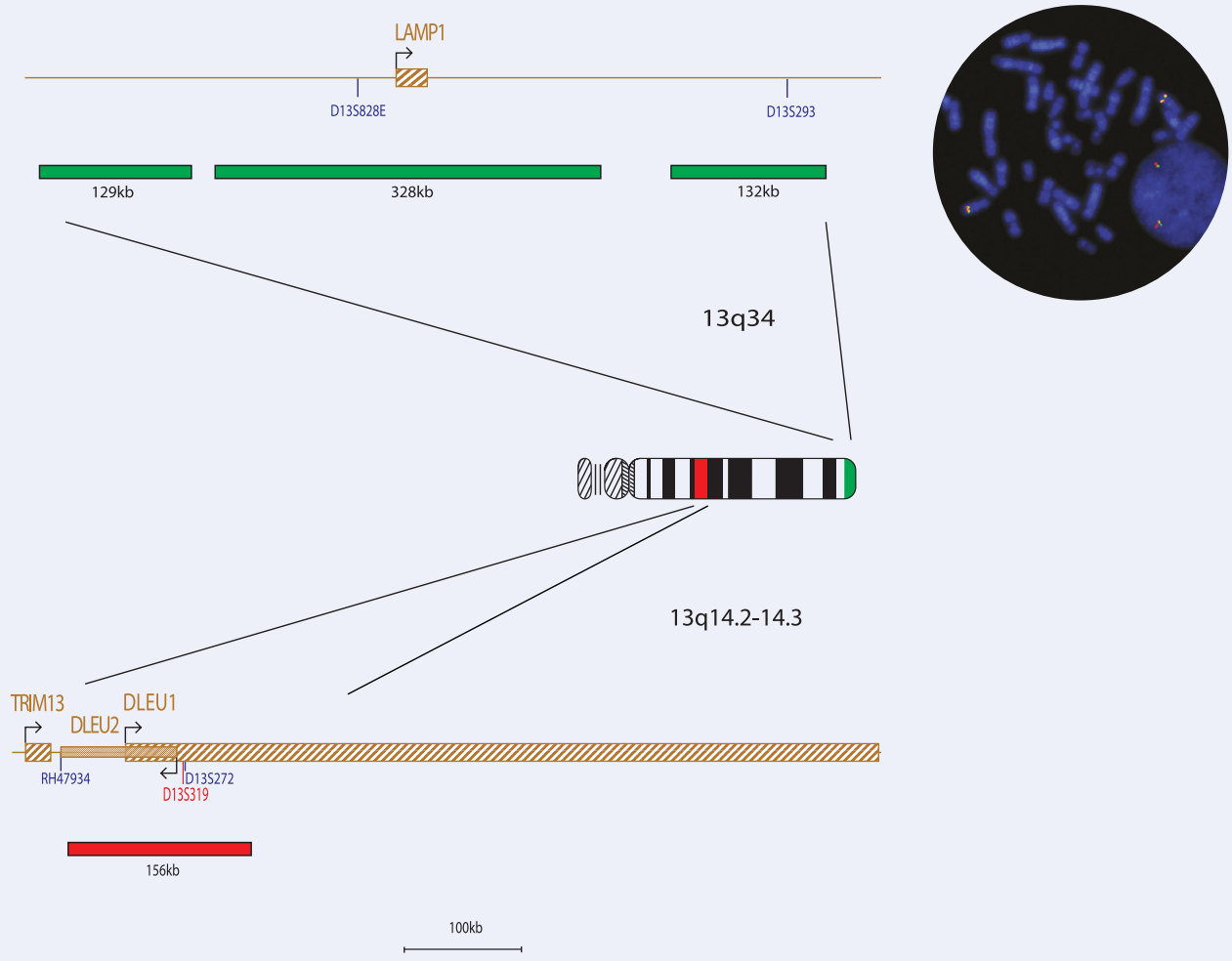
References

1. Juliusson G, *et al.* N Eng J Med 1990;323:720-4.
2. Puiggros, *et al.* Biomed Res Int 2014;1-13.
3. Kasar, *et al.* Nature Communications 2015;6:1-12.
4. Hammarsund M, *et al.* FEBS Letters 2004;556:75-80.
5. Van Dyke DL, *et al.* Br J Haematology 2009;148:544-50.
6. Rossi, *et al.* Blood 2013;121(8):1403-1412.
7. Liu Y, *et al.* Oncogene 1997;15:2463-73.
8. Wolf S, *et al.* Hum Mol Genet 2001;10:1275-85.
9. Swerdlow, *et al.* Editors. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissue, Lyon, France, 4th edition, IARC,2017.

D13S319 *Plus* Deletion

Cat. No. **LPH 068-S** (5 tests) | Cat. No. **LPH 068** (10 tests)

The D13S319 *Plus* probe, labelled in red, covers a 156kb region including the entire DLEU1 and most of the DLEU2 genes and the D13S319, D13S272 and RH47934 markers. The 13qter subtelomere specific probe, labelled in green, allows identification of chromosome 13 and acts as a control probe.

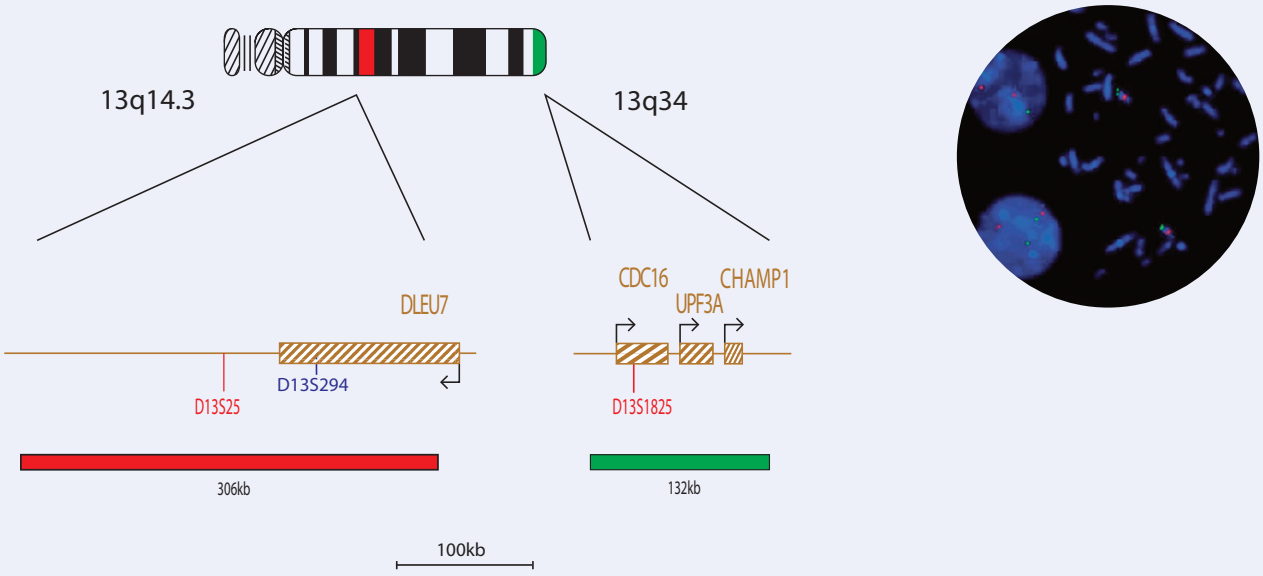


CMP-H079 v004.00

D13S25 Deletion

Cat. No. **LPH 043-S** (5 tests) | Cat. No. **LPH 043** (10 tests)

The D13S25 probe, labelled in red, covers a 306kb region including most of the DLEU7 gene and the D13S25 marker. The 13qter subtelomere specific probe (clone 163C9), labelled in green, allows identification of chromosome 13 and acts as a control probe.



CMP-H016 v004.00

IGH Breakapart and IGH *Plus* Breakapart

Recurrent rearrangements involving the IGH (*immunoglobulin heavy locus*) gene at 14q32.3 with a wide range of partner genes are seen in lymphomas and haematological malignancies[1].

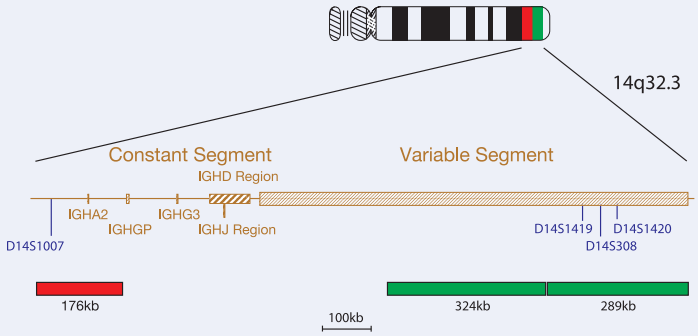
References

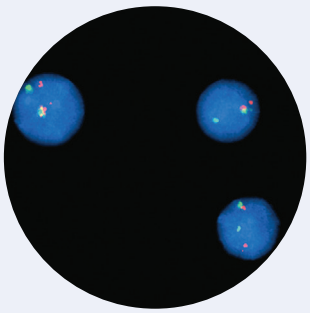
1. Gozzetti A, *et al.* Cancer Res. 2002 Oct 1;62(19):5523-7.

IGH Breakapart

Cat. No. **LPH 014-S** (5 tests) | Cat. No. **LPH 014** (10 tests)

The IGH *Plus* probe mix consists of a 176kb probe, labelled in red, covering part of the Constant region of the gene and two green probes (324kb and 289kb), covering part of the Variable segment of the gene.



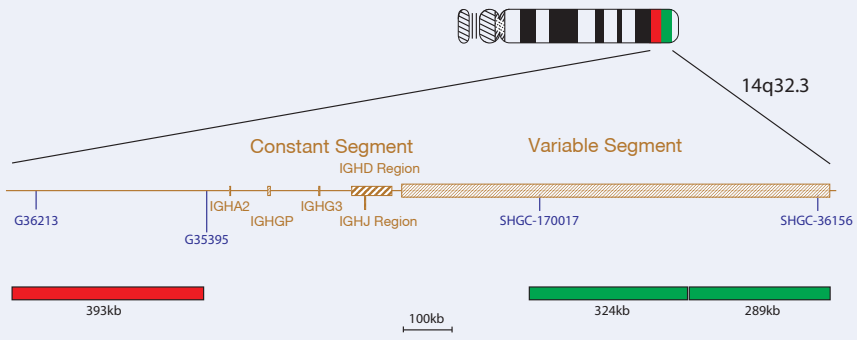


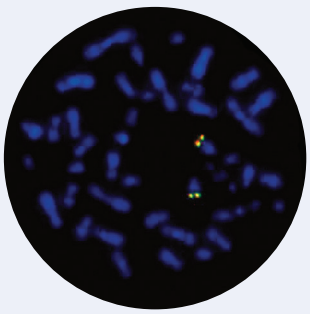
CMP H023 v003

IGH *Plus* Breakapart

IVDR Cat. No. **CE-LPH 070-S** (5 tests) | Cat. No. **CE-LPH 070** (10 tests)

The IGH *Plus* probe mix consists of a 393kb probe, labelled in red, centromeric to the Constant region of the gene and two green probes (324kb and 289kb), within the Variable segment of the gene.





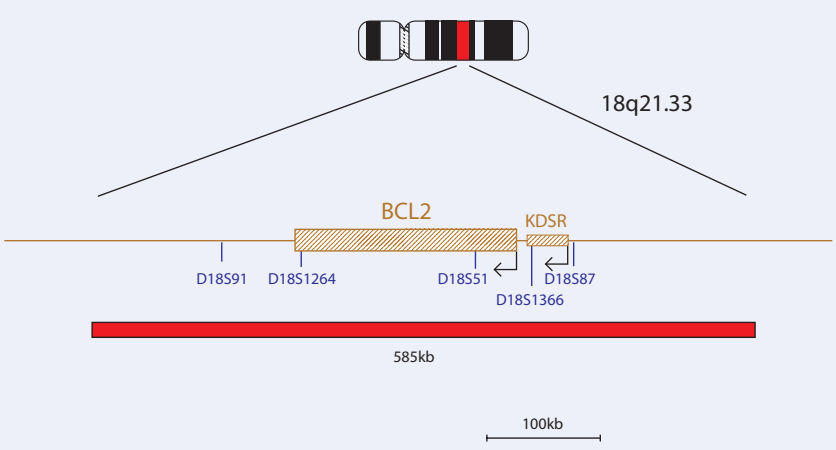
CMP-H075 v002

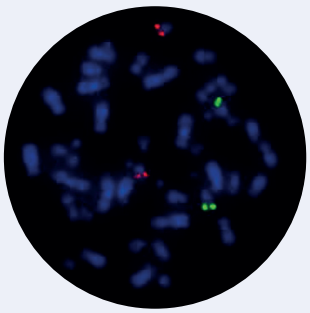
IGH/BCL2 *Plus* Translocation/Dual Fusion

Cat. No. **LPH 071-S** (5 tests) | Cat. No. **LPH 071** (10 tests)

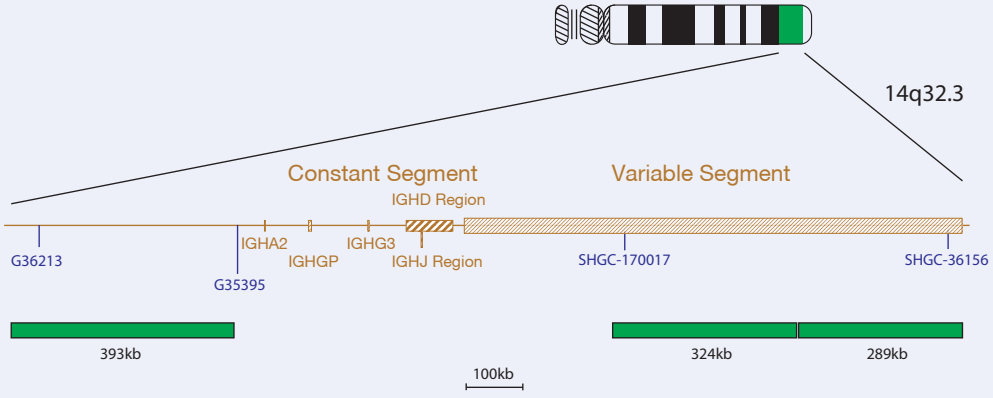
The t(14;18)(q32;q21) translocation involving the IGH (*immunoglobulin heavy locus*) gene at 14q32 and the BCL2 (*BCL2 apoptosis regulator*) gene at 18q21.33 is a recognised recurrent abnormality seen in B-cell malignancies.

IGH-BCL2 rearrangements are observed in 70-95% of follicular lymphoma (FL) cases and 20-30% of diffuse large B-cell lymphoma (DLBCL)[1]. Presence of the t(14;18) translocation in DLBCL is a predictor of outcome and has a poor prognostic effect[2]. BCL2 translocations have also been implicated in chronic B-cell lymphoproliferative disease (CLPD) and also occur occasionally in chronic lymphocytic leukaemia (CLL)[3].





CMP-H026 v002



CMP-H078 v002

References

1. Tomita N., J Clin Exp Hematop 2011;51(1):7-12.
2. Barrans *et al.* Clin Cancer Res 2003; 9; 2133.
3. Bassegio L, *et al.* Br J Haematol 2012;158(4):489-9.

CLL PROFILER Kit

Cat. No. **LPH 067-S** (2x5 tests) | Cat. No. **LPH 067** (2x10 tests)

The CLL PROFILER Kit is intended to detect deletions of TP53, ATM and D13S319, and gains of chromosome 12 centromere sequences in peripheral blood/bone marrow samples from patients with CLL.

P53 (TP53)/ATM Probe Combination

Screening for deletions of ATM and/or TP53 is vital to allow informed therapy choices for CLL patients, as deletions of TP53 and ATM confer poorer prognosis in this disease[1,2,3].

The TP53 gene is one of most important tumour suppressor genes; it acts as a potent transcription factor with fundamental role in the maintenance of genetic stability. Loss of TP53 is reported in 10% of patients with CLL, and is considered to be the poorest prognostic marker in that disease[1,4].

ATM is an important checkpoint gene involved in the management of cell damage; its function is to assess the level of DNA damage in the cell and attempt repair by phosphorylating key substrates involved in the DNA damage response pathway[5]. Loss of ATM is reported in 18% of patients with CLL, and is considered a poor prognostic marker in that disease[2].

D13S319/13qter/12cen Deletion/Enumeration

Deletions affecting band 13q14 and trisomy of chromosome 12 are common events in chronic lymphocytic leukaemia (CLL).

Deletions affecting 13q14 are also the most frequent structural genetic aberrations in chronic lymphocytic leukaemia (CLL)[6,7,8]. This region is found to be heterozygously deleted in 30-60% and homozygously deleted in 10-20% of CLL patients[9]. The survival rate has been shown to be similar for the two groups[10]. Patients with 13q14 deletions are classified as very low risk, in the absence of any other genetic lesions[1].

Trisomy 12 is a recurrent abnormality in CLL, seen in 20% of the cases[11] and often appears as the unique cytogenetic aberration (40-60% of cases)[7]. Patients with trisomy 12 are classified as low-risk in the absence of any other genetic lesions[1].

CLL PROFILER Kit Components

Probe Name	Chromosome Region	Available as Individual Probe	Page No.
P53 (TP53)/ATM Probe Combination	17p13/11q22	LPH 052	6
D13S319/13qter/12cen Deletion/Enumeration	13q14.2-14.3/12cen	LPH 066	11

References

1. Rossi D, *et al*. Blood. 2013 Feb 21;121(8):1403-12.
2. Dohner, *et al*. N Eng J Med. 2000;343:1910-1916.
3. Zent, *et al*. Blood. 2010;115(21):4154-4155.
4. Baliakas P, *et al*. Leukemia. 2014;(April):1-8.
5. Stankovic, *et al*. Blood 2004;103(1):291-300.
6. Juliusson, G *et al*. N Eng J Med 1990;323:720-4.
7. Puiggros, *et al*. Biomed Res Int 2014;1-13.
8. Kasar, *et al*. Nature Communications 2015;6:1-12.
9. Hammarsund M, *et al*. FEBS Letters 2004;556:75-80.
10. Van Dyke DL, *et al*. Br J Haematology. 2009;148:544-50.
11. Swerdlow, *et al*. Editors. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissue, Lyon, France, 4th edition, IARC,2017.

CytoCell

Haematology FISH Probes for CLL

Ordering information

UK +44 (0) 1223 294048

contact@ogt.com

ogt.com



CLL Probe Range

Probe Name	Chromosome Region	Probe Type	Control Probe	No. Tests	Cat. No.[§]
Alpha Satellite 12 *Plus* for CLL	12p11.1-q11.1	Enumeration	–	5 or 10	LPH 069
IVDR ATM Deletion	11q22.3	Deletion	D11Z1	5 or 10	CE-LPH 011
MYB Deletion	6q23.3	Deletion	D6Z1	5 or 10	LPH 016
P53 (TP53)/ATM Probe Combination	17p13/11q22	Deletion	–	5 or 10	LPH 052
P53 (TP53) Deletion	17p13	Deletion	D17Z1	5 or 10	LPH 017
13q14.3 Deletion	13q14.2-q14.3	Deletion	D13S1825	5 or 10	LPH 006
D13S319/13qter/12cen Deletion/Enumeration	13q14.2/12cen	Deletion/ Enumeration	LAMP1	5 or 10	LPH 066
D13S319 *Plus* Deletion	13q14.2	Deletion	LAMP1	5 or 10	LPH 068
D13S25 Deletion	13q14.3	Deletion	D13S1825	5 or 10	LPH 043
IGH Breakapart	14q32.3	Breakapart	–	5 or 10	LPH 014
IVDR IGH *Plus* Breakapart	14q32.3	Breakapart	–	5 or 10	CE-LPH 070
IGH/BCL2 *Plus* Translocation	14q32.3/18q21.33	Translocation	–	5 or 10	LPH 071
CLL PROFILER Kit	Various	–	–	2x5 or 2x10	LPH 067

[§]For 5 test kit add -S to catalogue number, e.g: LPH ###-S.

A Sysmex Group Company

What binds us, makes us.

Cytocell Ltd., Oxford Gene Technology, 418 Cambridge Science Park, Milton Road, Cambridge, CB4 0PZ, UK

CytoCell: This document and its contents are © Oxford Gene Technology IP Limited – 2026. All rights reserved. Trademarks: OGT™ (Oxford Gene Technology IP Ltd) CytoCell® (Cytocell Ltd). IVD: For *in vitro* diagnostic use. Product availability may vary from country to country and is subject to varying regulatory requirements. Please contact your local representatives for availability. OGT's CytoCell® IVDR-certified range of fluorescence *in situ* hybridisation (FISH) probe kits are *in vitro* diagnostic (IVD) medical devices for the detection of prenatal aneuploidies and acquired cancer-related chromosome alterations. They have been CE-marked under Regulation (EU) 2017/746 (IVDR) as Class C IVD medical devices for laboratory professional use only and are not intended for use as a standalone diagnostic or companion diagnostic. Refer to each individual FISH probe kit's Instructions for Use for their specific Intended Purpose, Indications, and Limitations.

990254 10/26 v3