

DNA
DIAGNOSTIC



Instruction For Use

HemaVision[®]-Screen

Screening test for 28 chromosome
translocations and more than 145
breakpoints associated with leukemia



Instruction For Use

Cat No. HV01-Screen

DNA Diagnostic A/S

www.dna-diagnostic.com

Revision 2021.04.23

IVD CE

HemaVision[®]-Screen

Multiplex RT-PCR test

Screens for 28 leukemia causing translocations

| | |
|-----------------------------------|------------------------------------|
| del1(p32) (STIL-TAL1) | t(9;12) (q34;p13) (ETV6-ABL1) |
| t(1;11) (p32;q23) (KMT2A-EPS15) | t(9;22) (q34;q11) (BCR-ABL1) |
| t(1;11) (q21;q23) (KMT2A-MLLT11) | t(10;11) (p12;q23) (KMT2A-MLLT10) |
| t(1;19) (q23;p13) (TCF3-PBX1) | t(11;17) (q23;q21) (KMT2A-MLLT6) |
| t(3;5) (q25;q34) (NPM1-MLF1) | t(11;17) (q23;q21) (ZBTB16-RARA) |
| t(3;21) (q26;q22) (RUNX1-MECOM) | t(11;19) (q23;p13.1) (KMT2A-ELL) |
| t(4;11) (q21;q23) (KMT2A-AFF1) | t(11;19) (q23;p13.3) (KMT2A-MLLT1) |
| t(5;12) (q33;p13) (ETV6-PDGFRB) | t(12;21) (p13;q22) (ETV6-RUNX1) |
| t(5;17) (q35;q21) (NPM1-RARA) | t(12;22) (p13;q11) (ETV6-MN1) |
| t(6;9) (p23;q34) (DEK-NUP214) | t(15;17) (q24;q21) (PML-RARA) |
| t(6;11) (q27;q23) (KMT2A-AFDN) | inv(16) (p13;q22) (CBFB-MYH11) |
| t(8;21) (q22;q22) (RUNX1-RUNX1T1) | t(16;21) (p11;q22) (FUS-ERG) |
| t(9;9) (q34;q34) (SET-NUP214) | t(17;19) (q22;p13) (TCF3-HLF) |
| t(9;11) (p22;q23) (KMT2A-MLLT3) | t(X;11) (q13;q23) (KMT2A-FOXO4) |

Instruction For Use for HemaVision[®]-Screen

Cat. No. HV01-Screen

25 tests per kit

Manufacturer



DNA Diagnostic A/S

Voldbjergvej 14

8240 Risskov

Denmark

Homepage: www.dna-diagnostic.com

Email: info@dna-diagnostic.com

Phone: 0045 87323050

TABLE OF CONTENTS

| | | |
|----|--|----|
| 1. | PURPOSE OF THE TEST – SCREENING FOR 28 TRANSLOCATIONS | 2 |
| 2. | PRINCIPLES OF TEST | 3 |
| 3. | KIT COMPONENTS AND STORAGE | 5 |
| 4. | EQUIPMENT AND MATERIALS REQUIRED BUT NOT PROVIDED | 6 |
| 5. | PRECAUTIONS | 7 |
| 6. | PROCEDURE | 9 |
| | Step 1 cDNA synthesis | 9 |
| | Step 2 Master PCR-I | 10 |
| | Step 3 Master PCR-II | 11 |
| | Step 4 Gel electrophoresis Master PCR-II | 12 |
| | Step 5 Interpretation of results from Master PCR-II | 12 |
| 7. | GENE ABBREVIATIONS ACCORDING TO THE HGNC | 15 |
| 8. | REFERENCES | 16 |
| 9. | REVISION HISTORY | 19 |

1. PURPOSE OF THE TEST - SCREENING FOR 28 TRANSLOCATIONS (INTENDED USE)

HemaVision®-Screen is a CE-marked *in vitro* diagnostic test for 28 leukemia causing chromosomal translocations including more than 145 breakpoints plus associated mRNA splice variants. Furthermore, it detects new breakpoints and mRNA splice variants for the 28 translocations. HemaVision®-Screen is a qualitative test intended for use on total RNA samples from human blood or bone marrow for presence of chromosomal translocations associated with leukemia. Tests should be performed and results should be analysed by professionals only. The test is intended for use as an adjunct to evaluation of Leukemia in conjunction with other clinicopathological factors (aid to diagnosis).

It is a fast one day test based on the method described by Pallisgard et al. (Ref 58). The HemaVision®-Screen test has very high sensitivity (>99%) and specificity (>99%) (Ref 59, 60).

Limit of detection is 10^{-9} µg of fusion RNA in a sample of 1 µg total RNA when the RNA quality is good.

This test provides a more detailed description of the exon organization of fusion genes originating from chromosome translocations.

HemaVision®-Screen is a qualitative test using total RNA extracted from human whole blood or bone marrow cells as starting material in the test. The test uses reverse transcription of RNA to cDNA followed by multiplex nested polymerase chain reactions (RT-PCR), agarose gel electrophoresis, and interpretation.

HemaVision®-Screen identifies chromosomes, genes and exons at the breakpoint in fusion genes. Furthermore, the test identifies mRNA splice variants from fusion genes.

The HemaVision®-Screen kit contains primers for 25 cDNA reactions and 25 (master) nested PCR tests.

The HemaVision®-Screen kit is identical to the BOX 1 of HemaVision®-28N kit (Cat No HV01-28N). Therefore, positive master reactions from HemaVision®-Screen tests must be characterized further by split-out reactions from BOX2 of the HemaVision®-28N kit.

The test is for professional use only.

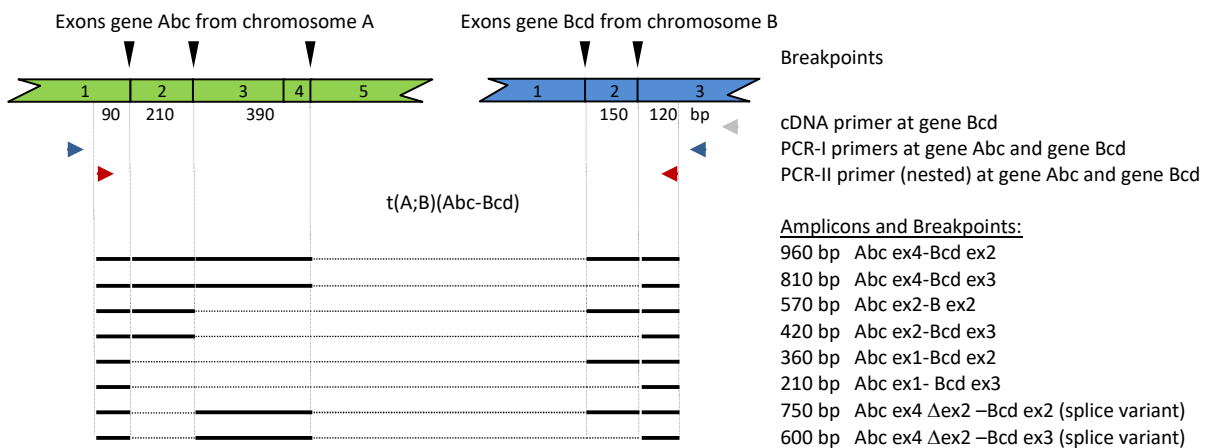


Figure 1 illustrates how HemaVision® kit HV01-Screen identifies chromosomes, fusion genes and exons at the breakpoint among 28 chromosome translocations causing leukemia. Only breakpoints for fusion genes maintaining the original translational reading frame are presented.

2. PRINCIPLES OF TEST

RNA is template for synthesis of cDNA in a reaction using Reverse Transcriptase (RT) and specific cDNA primers. The cDNA is template for PCR amplification using a hot start Taq DNA Polymerase and specific PCR primers. Many of the fusion genes have several breakpoints. Therefore, the PCR primers are designed to bind at positions enabling screening for all these breakpoints as illustrated in figure 1. The workflow of the test and an example of test results are shown in figure 2.

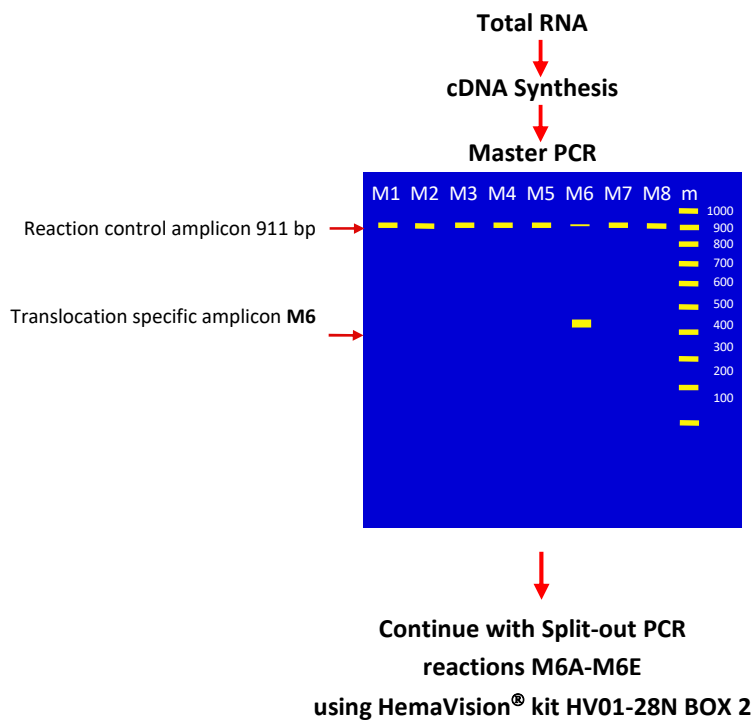


Figure 2. Workflow and results from a test with HemaVision® Cat. No. HV01-Screen.

Result: All reactions M1-M8 are positive for the reaction control amplicon of 911 bp. M6 is also positive for an amplicon approximately 400 bp.

Conclusion: Patient is positive for a translocation. Continue testing with the split-out reactions M6A-M6E from BOX 2 in HemaVision® kit HV01-28N for identification of the translocation.

RNA Preparation

Total RNA is prepared from whole blood, cell lines, or bone marrow cells with the QIAamp[®] RNA Blood Mini Kit (Qiagen Cat. No. 52304).

cDNA Synthesis

cDNA is synthesized in a reaction containing the isolated RNA using the cDNA Mix (primers) from the HemaVision[®] HV01-Screen kit and Reverse Transcriptase, 5x RT Buffer, DTT, and dNTP, DTT from the reagent module HemaVision[®] kit Cat. No. HV06-RMP.

Master PCR

The cDNA is used as a template for eight multiplex PCR amplification reactions (Master PCR-I) subsequently followed by eight nested PCR reactions (Master PCR-II). All reactions use primer mixes from the HemaVision[®] HV01-Screen kit and HemaVision DNA Polymerase, 10xbuffer, and dNTP from HemaVision[®] kit Cat. No. HV06-RMP. Each Master PCR reaction contains four, five or six pairs of translocation specific primers and one pair of reaction control primers specific for the housekeeping gene biotinidase. The Master PCR-II products are analyzed by agarose gel electrophoresis. The 911 bp reaction control band is a positive control for using intact RNA and functionality of the RT-PCR reactions. A translocation specific band show the test is positive for a translocation. The identity of this translocation is established in the split-out PCR using HemaVision[®] kit HV01-28N BOX 2.

Split-out PCR

Use HemaVision[®] kit HV01-28N BOX 2 primer mixes and HemaVision[®] kit HV06-RMP for split-out tests as described in the HemaVision[®] kit HV01-28N User Manual.

Interpretation of results

A sample is positive for a translocation when both master and split-out PCR produce bands with identical molecular size. The breakpoint is identified by the reaction number of the split-out and the molecular size of the translocation specific amplicon using Interpretation Table 11 of HemaVision[®] kit HV01-28N. More than one translocation specific band in both Master and Split-out PCR reactions shows presence of alternative spliced mRNA from the fusion gene.

Figure 2 shows workflow for testing blood or bone marrow samples with HemaVision[®] test HV01-Screen. In this example the test is positive in Master M6 showing an amplicon of approximately 400 bp. The identity of the translocation is established in a test using HemaVision[®] kit HV01-28N BOX 2 split-out primer mixes M6A-M6E.

3. KIT COMPONENTS AND STORAGE

The HemaVision® kit Cat. No. HV01-Screen contains one box with Primer Mixes (see figure 3) and a User Manual for instruction. The kit is shipped at -20°C or below and both boxes must be stored at -20°C by the customer. While performing the test always keep test components on ice (0°C). Each kit contains sufficient material for 25 Master tests.

| | | | | | | | | | |
|--|-------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | | | | | | | | | |
| | | M1 PCR-I | M2 PCR-I | M3 PCR-I | M4 PCR-I | M5 PCR-I | M6 PCR-I | M7 PCR-I | M8 PCR-I |
| | cDNA Mix | | | | | | | | |
| | | M1 PCR-II | M2 PCR-II | M3 PCR-II | M4 PCR-II | M5 PCR-II | M6 PCR-II | M7 PCR-II | M8 PCR-II |
| | | | | | | | | | |

BOX 1:

cDNA and Master PCR primer mixes:

1x 200 µL cDNA Mix (white cap)

8x 155 µL Master PCR-I (blue caps)

8x 155 µL Master PCR-II (red caps)

Figure 3 shows content of HemaVision® kit Cat. No. HV01-Screen.

NOTE: It is essential for functionality of the multiplex RT-PCR test using HemaVision® kit HV01-Screen also to obtain and use the reagents provided in HemaVision® kit **Cat. No. HV06-RMP** containing: MMLV-Reverse Transcriptase; 5x RT buffer; DTT; dNTP, HemaVision DNA Polymerase, 10x PCR buffer.

4. EQUIPMENT AND MATERIALS REQUIRED BUT NOT PROVIDED

RNA extraction:

QIAamp[®] RNA Blood Mini Kit from Qiagen Cat. No. 52304.

Reagent Module:

HemaVision[®] kit Cat. No. HV06-RMP containing: MMLV-RT; 5x RT buffer; DTT; dNTP, HemaVision DNA Polymerase, 10x PCR buffer. Use four HV06-RMP kits together with each HV01-Screen kit.

Or as an alternative use: HemaVision[®] kit Cat. No. HV04-RM containing: MMLV-RT; 5x RT buffer; DTT; dNTP and from Qiagen HotStarTaq DNA Polymerase 5 Units/ μL and 10x PCR buffer. Use four HV04-RM kits and 1000 Units HotStarTaq DNA Polymerase together with each HV01-Screen kit.

Master Mix room – No templates in this room:

Micropipettes, 0.5-10 μL , 20-200 HemaVision[®] kit Cat. No. HV06-RMP containing: MMLV-RT; 5x RT buffer; DTT; dNTP, HemaVision DNA Polymerase, 10x PCR buffer

Aerosol barrier micropipette tips, 0.5-10 μL , and 20-200 μL

Micro centrifuge

Ice bath

RNase free tubes

Disposable gloves

RNase free water

-20°C freezer for storage of kits (HV01-28N and HV06-RMP)

cDNA room:

Micropipettes, 0.5-10 μL , 20-200 μL

Aerosol barrier micropipette tips, 0.5-10 μL , and 20-200 μL

Micro centrifuge

Heating block/Water bath

Ice bath

RNase free tubes

Disposable gloves

RNase free water

-80°C freezer for storage of RNA samples

PCR room:

Micropipettes, 0.5-10 μL , 20-200 μL

Aerosol barrier micropipette tips, 0.5-10 μL , and 20-200 μL

Micro centrifuge

Thermal Cycler

Ice bath

PCR tubes (0.1 mL or 0.2 mL) and lids

Disposable gloves

Gel electrophoresis room:

Micropipettes, 0.5-10 μL

Aerosol barrier micropipette tips, 0.5-10 μL

Micro centrifuge

Equipment for agarose gel electrophoresis

Disposable gloves

Molecular size marker (e.g. 100 bp ladder)

5. PRECAUTIONS

General precautions

- The quality and concentration of the RNA sample greatly affects the results of this test. To minimize the risk of degradation by ribonucleases, we strongly recommend purification of total RNA immediately after blood or bone marrow extraction. Optionally, mononuclear cells can be purified prior to RNA extraction using Ficoll Hypaque. Do not freeze Ficoll purified cells without adding a denaturing solution [e.g. containing guanidinium isothiocyanate (GTC)] immediately after isolation and before freezing.
- Use blood from venipuncture collected into a tube containing EDTA. Alternatively, use bone marrow collected into a tube containing EDTA. Do not freeze the blood or bone marrow sample.
- Do NOT use Heparin for stabilization of blood samples.
- Always store cell samples and aqueous RNA solutions at -80°C. Even an overnight storage at -20°C may result in RNA degradation.
- When working with RNA always use gloves, as hands are a major source of ribonuclease contamination.
- The integrity and purity of RNA is important for the efficiency of the cDNA synthesis and thus detection of translocations. The quality of RNA can be checked by OD 260/280 nm measurements, agarose gel electrophoresis, or using RIN number from the Agilent Bioanalyzer.
- For more guidance on specimen collection, RNA isolation and storage please refer to “ISO 20186:2019 Molecular in vitro diagnostic examinations – Specifications for pre-examination processes for venous whole blood – Part 1: isolated cellular RNA” and CLSI guidance MM13-A “Collection, Transport, Preparation and Storage of Specimens for Molecular Methods; Approved guideline.
- RT-PCR is a very sensitive technique. Therefore, precautions must be taken to avoid false positive results caused by contamination with RNA, cDNA or PCR products from other samples.
- Dedicate four separate rooms/areas to the following activities:
 - Master mix production – no templates in here
 - cDNA synthesis
 - PCR
 - Gel electrophoresis
- A set of micropipettes, aerosol barrier pipette tips, disposable gloves and clean lab coats should be kept in each of the four rooms. The work must be organized so that mixes and reaction products only moves in the direction from 1-4. NEVER move mixes or reaction products in the opposite direction.
- Laboratory workbenches, pipettes, and lab coats must be cleaned on a regular basis.
- Use of aerosol barrier pipette tips is highly recommended during the entire procedure. It is essential to change gloves very often when handling tubes containing RNA or cDNA.
- For more general guidance on best practice in PCR testing please refer to the CLSI guidance document MM01: Molecular Methods for Clinical Genetics and Oncology Testing, 3rd Edition

Safety

- Read and understand the procedure before starting.
- Normal laboratory aseptic technique should be followed at all times.
- Treat each sample as if it is infectious.
- Wear eye protection and disposable gloves during all steps of the assay.
- The products can be discarded as normal laboratory waste
- Check the safety data sheet for the product on our website for further information or ask for a copy of it.

6. PROCEDURE

Procedural notes

- Store all test components as described in section 3: *Kit Components and Storage*.
- Do not mix reagents from different lots.
- Careful pipetting technique is essential for accurate results.
- This protocol is optimized with enzymes and buffers from HemaVision® kit Cat. No. HV06-RMP.
- This protocol is optimized for the Perkin Elmer GeneAmp 9600/9700 thermal cycler. Use of another thermal cycler may require optimization by the user.
- As a positive control for RNA quality and functionality of each RT-PCR reaction a 911 bp fragment of the housekeeping gene *beta-actin* must be present in all lanes except in reactions positive for a translocation specific amplicon where it may be weak or missing.
- As a negative control make the cDNA reaction without RNA template.

RNA preparation

- Use blood from venipuncture collected into a tube containing EDTA. Alternatively, use bone marrow collected into a tube containing EDTA. Do not freeze the blood or bone marrow sample or use samples collected in heparin tubes.
- Prepared mononuclear cells from whole blood or bone marrow by the Ficoll Hypaque method.
- Within 24 hours of collection, extract total RNA with QIAamp® RNA Blood Mini Kit (Qiagen Cat. No. 52304). Typically 5-10 µg total RNA is extracted from 1 x10⁷ mononuclear blood cells.
- Measure the RNA concentration by reading the optical density at 260 nm. An absorbance of 1 unit at 260 nm corresponds to 40 µg of RNA per mL. Adjust the concentration of RNA to 0.1 µg/µL with RNase free H₂O.
- Make 20 µL (0.1 µg/µL) RNA aliquots in RNase free tubes. Store RNA aliquots at –80°C or use RNA immediately for cDNA synthesis.

Master test

Step 1 cDNA Synthesis

1.1 In the Master Mix room prepare *cDNA Synthesis Mix* according to Table 1 using reagents from HemaVision® reagent module Cat. No. HV06-RMP.

Do not add additional volume to compensate for liquid loss during liquating. This has already been factored into the table numbers.

Table 1: *cDNA Synthesis Mix*

| Number of samples | 1 | 2 |
|------------------------|------|------|
| 5x MMLV-RT Buffer (µL) | 11.0 | 22.0 |
| 100 mM DTT (µL) | 5.5 | 11.0 |
| 10 mM dNTP Mix (µL) | 5.5 | 11.0 |
| MMLV-RT (µL) | 2.2 | 4.4 |
| Total volume (µL): | 24.2 | 48.4 |

- 1.2 In the cDNA room add 8 µL cDNA Mix (primers) from white capped tube in the HemaVision® HV01-28N kit to one tube containing 20 µL total RNA (2 µg). Mix gently and spin down for 10 seconds.
- 1.3 In a separate RNase free tube, add 8 µL of cDNA Mix to 20 µL H₂O (negative control).
- 1.4 Incubate the tubes in a heating block or water bath at 65°C for 5 minutes. Chill and hold on ice.
- 1.5 Add 22 µL of the cDNA Synthesis Mix to the tube with 28 µL RNA+cDNA Mix and the negative control tube from step 1.4. Mix gently and spin down for 10 seconds.
- 1.6 Incubate at 37°C for 45 minutes.
- 1.7 Add 50 µL H₂O to each cDNA tube.
- 1.8 Incubate at 95°C for 5 min to inactivate the MMLV-RT enzyme.
- 1.9 Chill and hold the cDNA tube on ice (0°C, do not freeze) for a maximum of three days before use in Master PCR and Split-out PCR.

Step 2 Master PCR-I

To achieve maximal sensitivity and specificity each sample is tested with both a first and a nested Master PCR reaction.

- 2.1 In the Master Mix room prepare the Master Mix PCR-I according to Table 2 using HemaVision® reagent module Cat. No. HV06-RMP. Mix and spin down for 10 seconds.
Do not add additional volume to compensate for liquid loss during liquating. This has already been factored (+10 %) into the table numbers.

Table 2: Master Mix PCR-I

| Number of samples | 1 | 2 |
|--------------------------------|----------|-----------|
| Number of PCR reactions | 8 | 16 |
| 10x PCR buffer (µL) | 22.0 | 44.0 |
| dNTP mix (µL) | 4.4 | 8.8 |
| HemaVision DNA Polymerase (µL) | 3.5 | 7.0 |
| H ₂ O (µL) | 102.1 | 204.2 |
| Total volume (µL): | 132.0 | 264.0 |

- 2.2 For each sample label the tubes in an 8-microtube strip M1 to M8.
- 2.3 Aliquot 15 µL Master Mix PCR-I to each of the PCR tubes in the 8-microtube strip(s).
- 2.4 To these tubes add 5 µL Master PCR-I primers from blue capped tubes M1-M8 to the corresponding PCR tubes. E.g. to PCR tube labeled M1 add 5 µL M1 PCR-I.
- 2.5 In the PCR room add 5 µL cDNA (from step 1.9) to each of the PCR tubes from step 2.4. Close the tubes, mix and spin for 10 seconds. Volume per tube 25 µL.
- 2.6 Transfer the tubes to a thermal cycler and start the PCR amplification using the PCR cycling parameters in Table 3.

Table 3: Master PCR-I Amplification Parameters

| Step | Time/Temperature | Cycles |
|------|---|--------|
| 1 | 15 minutes at 95°C | 1 |
| 2 | 30 seconds at 95°C 30 seconds at 58°C 1 minute 30 seconds at 72°C | 25 |
| 3 | Hold at 4°C | 1 |

Step 3 Master PCR-II (nested)

3.1 In the Master Mix room prepare the *Master Mix PCR-II* according to Table 4 using HemaVision® reagent module Cat. No. HV06-RMP. Mix and spin down for 10 seconds.

Do not add additional volume to compensate for liquid loss during liquating. This has already been factored (+10 %) into the table numbers.

Table 4: Master Mix PCR-II

| Number of samples | 1 | 2 |
|--------------------------------|-------|-------|
| Number of PCR reactions | 8 | 16 |
| 10x PCR buffer (µL) | 22.0 | 44.0 |
| dNTP mix (µL) | 4.4 | 8.8 |
| HemaVision DNA Polymerase (µL) | 3.5 | 7.0 |
| H ₂ O (µL) | 137.3 | 274.6 |
| Total volume (µL): | 167.2 | 334.4 |

3.2 For each sample label the tubes in an 8-microtube strip M1 to M8.

3.3 Aliquot 19 µL *Master Mix PCR-II* to each of the PCR tubes in the 8-microtube strip(s).

3.4 To these tubes add 5 µL Master PCR-II primers from red capped tubes M1-M8 to the corresponding PCR tubes. E.g. to PCR tube labeled M1 add 5 µL M1 PCR-II.

3.5 In the PCR room carefully open without spillage the PCR tubes containing the Master PCR-I reactions. From these tubes transfer 1 µL to the corresponding Master PCR-II tubes from step 3.3. An eight channel pipette can be used for this transfer. Close the tubes, mix and spin for 10 seconds. Volume per tube 25 µL.

3.6 Transfer the tubes to a thermal cycler and start the PCR amplification using the PCR cycling parameters in Table 5.

Table 5: Master PCR-II Amplification Parameters

| Step | Time/Temperature | Cycles |
|------|---|--------|
| 1 | 15 minutes at 95°C | 1 |
| 2 | 30 seconds at 95°C 30 seconds at 58°C 1 minute 30 seconds at 72°C | 20 |
| 3 | 10 minutes at 72°C | 1 |
| 4 | Hold at 4°C | 1 |

Step 4 Gel electrophoresis

- 4.1** Prepare a 1.5 % (w/v) agarose gel at least 10 cm long in 1X TBE buffer. Add ethidium bromide to a final concentration of 0.5 µg/mL.
- 4.2** In the Gel Electrophoresis room carefully open the PCR tubes with Master PCR-II without contaminating gloves and surroundings with drops containing high copy numbers of amplicon. Add 3 µL of 10x loading buffer into each PCR tube. Load approximately 14 µL per slot in the gel (lane 1-8). Finally load a molecular size marker to lane 9.
- 4.3** Run the gel in 1X TBE buffer until the Bromophenol blue dye has migrated approximately 3/4 of the gel.
- 4.4** Examine the gel with UV-light and document result by photography.

Step 5 Interpretation of results from Master PCR-II

- Positive for one (or more) translocation specific band(s). Continue with the corresponding Split-out reactions to identify translocation. Use HemaVision® kit HV01-28N BOX 2 and reagent module HemaVision® kit HV06-RMP.
- Positive for a translocation specific band but it is very weak or a smear. Positive for reaction control band (911 bp) in all lanes. Continue with the relevant Split-out reactions to identify translocation. Use HemaVision® kit HV01-28N BOX 2 and reagent module HemaVision® kit HV06-RMP.
- Negative for a translocation specific band and positive for reaction control band (911 bp) in all lanes M1-M8. The patient is negative for the 28 translocations shown in Table 10.
- Negative for a translocation specific band and negative for reaction control band (911 bp) in all lanes M1-M8. The test failed most likely due to 1) poor quality of RNA, or 2) use of thermal cycler with temperature profile (ramp speed) differing from ABI 9600/9700, or 3) incorrect mixing of reactions. Correct and repeat test.
- Negative for a translocation specific band and positive for reaction control band (911 bp) in some of the lanes M1-M8. The test failed most likely due to 1) use of thermal cycler with temperature profile (ramp speed) differing from ABI 9600/9700, or 2) incorrect mixing of some reactions. Correct and repeat test.
- Negative Control test is positive (band(s) present): Reaction(s) have been contaminated with DNA. Identify contamination and repeat test.

Table 10: List of translocations detected by HemaVision® kit HV01-Screen

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|---------------------|-------------------------------|-----------|
| M1 | t(X;11)(q13;q23) | KMT2A(11q23) FOXO4(Xq13.1) | 1 |
| | t(6;11)(q27;q23) | KMT2A(11q23) AFDN(6q27) | 2; 3 |
| | t(11;19)(q23;p13.1) | KMT2A(11q23) ELL(19p13.1) | 4; 5; 6 |
| | t(10;11)(p12;q23) | KMT2A(11q23) MLLT10(10p12) | 9; 10 |

Note: The interpretation table has been updated according to the HUGO Gene Nomenclature Committee (HGNC). For a list of the changes made see section “7. GENE ABBREVIATIONS ACCORDING TO THE HGNC”.

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|----------------------|--------------------------------|------------|
| M2 | t(1;11)(p32;q23) | KMT2A(11q23) EPS15 (1p32) | 7 |
| | t(11;17)(q23;q12-21) | KMT2A(11q23) MLLT6(17q21) | 8 |
| | t(11;19)(q23;p13.3) | KMT2A(11q23) MLLT1(19p13.3) | 30; 32; 34 |
| | t(10;11)(p12;q23) | KMT2A(11q23) MLLT10(10p12) | 9; 10; 12 |
| | t(9;11)(p22;q23) | KMT2A(11q23) MLLT3(9p22) | 3; 30; 35 |

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|--|------------------------------------|----------------|
| M3 | t(1;19)(q23;p13) | TCF3(19p13.3) PBX1(PRL)(1q23.3) | 13; 14; 15 |
| | t(17;19)(q22;p13) | TCF3(19p13.3) HLF(17q22) | 16; 17; 18 |
| | t(12;21)(p13;q22) | ETV6(12p13) RUNX1(21q22.3) | 19; 20; 21; 55 |
| | TAL1 ^d 40kbp deletion 1p32 | STIL(1p32) TAL1(1p32) | 22; 23 |

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|-------------------|---------------------------------|---------------|
| M4 | t(8;21)(q22;q22) | RUNX1(21q22.3) RUNX1T1(8q22) | 24; 25; 26 |
| | t(3;21)(q26;q22) | RUNX1(21q22.3) MECOM(3q26) | 25; 27; 28 |
| | t(16;21)(p11;q22) | FUS(16p11.2) ERG(21q22.3) | 29; 57 |
| | t(15;17)(q24;q21) | PML(15q24) RARA(17q21) | 50; 51; 52 |

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|---------------------|--------------------------------|----------------|
| M5 | t(4;11)(q21;q23) | KMT2A(11q23) AFF1(4q21.3) | 30; 31; 32; 33 |
| | t(10;11)(p12;q23) | KMT2A(11q23) MLLT10(10p12) | 9; 10; 11 |
| | t(11;19)(q23;p13.3) | KMT2A(11q23) MLLT1(19p13.3) | 30; 34 |
| | t(9;11)(p22;q23) | KMT2A(11q23) MLLT3(9p22) | 3; 30; 35 |
| | t(1;11)(q21;q23) | KMT2A(11q23) MLLT11(1q21) | 36 |

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|----------------------|------------------------------------|------------|
| M6 | inv(16)(p13;q22) | CBFB (16q22.1) MYH11 (16p13.11) | 47 |
| | t(9;22)(q34;q11) | BCR(22q11) ABL1(9q34.1) | 37; 38; 39 |
| | t(9;12)(q34;p13) | ETV6(12p13) ABL1(9q34.1) | 40; 41 |
| | t(5;12)(q33;p13) | ETV6(12p13) PDGFRB(5q33) | 42 |
| | t(12;22)(p13;q11-12) | ETV6(12p13) MN1(22q12.1) | 43 |

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|---|--|----------------|
| M7 | t(6;9)(p23;q34) | DEK(6p23) NUP214(9q34) | 44 |
| | t(9;9)(q34;q34) | SET(9q34) NUP214(9q34) | 45; 46 |
| | inv(16)(p13;q22) | CBFB (16q22.1) MYH11 (16p13.11) | 47 |
| | t(3;21)(q26;q22) or ----- t(1;21)(p36;q22) | RUNX1(21q22.3) RPL22P1(pseudogene) (3q26.2) ----- RUNX1(21q22.3) RPL22 (1p36.3) | 25; 27; 28; 56 |

| PCR | TRANSLOCATION | GENES | REFERENCE |
|-----------|-------------------|-------------------------------|---------------|
| M8 | t(11;17)(q23;q12) | ZBTB16(11q23) RARA(17q12) | 48; 49 |
| | t(3;21)(q26;q22) | RUNX1(21q22.3) MECOM(3q26) | 25; 27; 28 |
| | t(15;17)(q24;q21) | PML(15q24) RARA(17q21) | 50; 51; 52 |
| | t(5;17)(q35;q12) | NPM1(5q35) RARA(17q12) | 53 |
| | t(3;5)(q25.1;q35) | NPM1(5q35) MLF1(3q25.1) | 54 |
| | t(9;22)(q34;q11) | BCR(22q11) ABL1(9q34.1) | 37; 38; 39 |

7. GENE ABBREVIATIONS ACCORDING TO THE HGNC:

The HUGO Gene Nomenclature Committee (HGNC) approves a *unique* and *meaningful* name for every known human gene (read more at www.genenames.org). Table 11 contains a list of all relevant genes for the HemaVision® product series, with the old abbreviation and the corresponding HGNC abbreviation.

Table 11

| Old Abbreviation | HGNC Abbreviation | Chromosome | HGNC ID |
|------------------|-------------------|------------|------------|
| ABL | ABL1 | 9q34.1 | HGNC:76 |
| AF10 | MLLT10 | 10p12 | HGNC:16063 |
| AF17 | MLLT6 | 17q21 | HGNC:7138 |
| AF1p | EPS15 | 1p32 | HGNC:3419 |
| AF1q | MLLT11 | 1q21 | HGNC:16997 |
| AF4 | AFF1 | 4q21.3 | HGNC:7135 |
| AF6 or MLLT4 | AFDN | 6q27 | HGNC:7137 |
| AF9 | MLLT3 | 9p22 | HGNC:7136 |
| AFX1 | FOXO4 | Xq13.1 | HGNC:7139 |
| AML1 | RUNX1 | 21q22.3 | HGNC:10471 |
| BCR | BCR | 22q11 | HGNC:1014 |
| CAN | NUP214 | 9q34 | HGNC:8064 |
| CBFβ | CBFB | 16q22.1 | HGNC:1539 |
| DEK | DEK | 6p23 | HGNC:2768 |
| EAP | RPL22 | 1p36.3 | HGNC:10315 |
| E2A | TCF3 | 19p13.3 | HGNC:11633 |
| ELL | ELL | 19p13.1 | HGNC:23114 |
| ENL | MLLT1 | 19p13.3 | HGNC:7134 |
| ERG | ERG | 21q22.3 | HGNC:3446 |
| ETO | RUNX1T1 | 8q22 | HGNC:1535 |
| FUS | FUS | 16p11.2 | HGNC:4010 |
| HLF | HLF | 17q22 | HGNC:4977 |
| MDS1- EVI1 | MECOM | 3q26 | HGNC:3498 |
| MLF1 | MLF1 | 3q25 | HGNC:7125 |
| MLL | KMT2A | 11q23 | HGNC:7132 |
| MN1 | MN1 | 22q12.1 | HGNC:7180 |
| MYH11 | MYH11 | 16p13.11 | HGNC:7569 |
| NPM | NPM1 | 5q35 | HGNC:7910 |
| PBX1 | PBX1 | 1q23.3 | HGNC:8632 |
| PDGFRβ | PDGFRB | 5q31-q32 | HGNC:8804 |
| PLZF | ZBTB16 | 11q23 | HGNC:12930 |
| PML | PML | 15q24 | HGNC:9113 |
| RARα | RARA | 17q21 | HGNC:9864 |
| SET | SET | 9q34 | HGNC:10760 |
| SIL1 | STIL | 1p32 | HGNC:10879 |
| Tal1 | TAL1 | 1p32 | HGNC:11556 |
| TEL | ETV6 | 12p13 | HGNC:3495 |
| TLS | FUS | 16p11.2 | HGNC:4010 |

REFERENCES:

1. Parry P., Wei Y., Evans G.: Cloning and characterization of the t(X;11) breakpoint from a leukemic cell line identify a new member of the forkhead family. *Genes Chromosomes Cancer*. **11**: 79, 1994.
2. Prasad R., Gu Y., Alderr, H., Nakamura, T., Canaani O., Saito H., Huebner K., Gale R.P., Nowell P.C., Kuriyama K et al. Cloning of the All-1 fusion partner, The AF-6 gene, involved in acute myeloid leukemias with the t(6;11) chromosome translocation. *Cancer Res*. **53**: 5624, 1993.
3. Poirel H., Rack K., Delabesse E., Radford Weiss I., Troussard X., Debert C., Leboeuf D., bastard C., Pichard F., Veil Buzyn A., Flandrin G., Bernard O., and Macintyre E.: Incidence and characterization of MLL gene (11q23) rearrangements in acute myeloid leukemia M1 and M5. *Blood* **87**: 2496, 1996.
4. Thirman MJ., Levitan DA., Kobayashi H., Simon MC., and Rowley JD.: Cloning of ELL, a gene that fuses to MLL in a t(11;19)(q23;p13.1) in acute myeloid leukemia. *Proc. Natl. Acad. Sci., USA* **91**: 12110, 1994.
5. Mitani K., Kanda Y., Ogawa S., Tanaka T., Inazawa J., Yazaki Y., and Hirai H.: Cloning of several species of MLL/MEN chimeric cDNAs in myeloid leukemia with t(11;19)(q23;p13.1) translocation. *Blood* **85**: 2017, 1995.
6. Rubnitz JE., Behm FG., Curcio Brint AM., Pinheiro RP., Carroll AJ., Raimondi SC., Shurtleff SA., and Downing JR.: Molecular analysis of t(11;19) breakpoints in childhood acute leukemias. *Blood* **87**: 4804, 1996.
7. Bernard OA., Mauchauffe M., Mecucci C., Van den Berghe H., and Berger R.: A novel gene, AF-1p, fused to HRX in t(1;11)(p32;q23), is not related to AF-4, AF-9 nor ENL. *Oncogene* **9**: 1039, 1994.
8. Prasad R., Leshkowitz D., Gu Y., Alder H., Nakamura T., Saito H., Huebner K., Berger R., Croce CM., and Canaani E.: Leucine-zipper dimerization motif encoded by the AF17 gene fused to ALL-1 (MLL) in acute leukemia. *Proc. Natl. Acad. Sci., USA* **91**: 8107, 1994.
9. Chaplin T., Ayton P., Bernard OA., Saha V., Della Valle V., Hillion J., Gregorini A., Lillington D., Berger R., and Young BD.: A novel class of zinc finger/leucine zipper genes identified from the molecular cloning of the t(10;11) translocation in acute leukemia. *Blood* **85**: 1435, 1995.
10. Chaplin T., Bernard O., Beverloo HB., Saha V., Hagemeyer A., Berger R., and Young BD.: The t(10;11) translocation in acute myeloid leukemia (M5) consistently fuses the leucine zipper motif of AF10 onto the HRX gene. *Blood* **86**: 2073, 1995.
11. Hjorth-Sørensen B., Pallisgaard N., Grønholm M., Hokland P., Clausen N., and Jørgensen P.: A novel MLL-AF10 fusion mRNA variant in a patient with acute myeloid leukemia detected by a new asymmetric reverse transcription PCR method. *Leukemia* **11**: 1588, 1997.
12. Borkhardt A., Haas OA., Strobl W., Repp R., Mann G., Gadner H., and Lampert F.: A novel type of MLL/AF10 fusion transcript in a child with acute megakaryocytic leukemia (AML-M7). *Leukemia* **9**: 1796, 1995.
13. Kamps MP., Murre C., Sun XH., and Baltimore D.: A new homeobox gene contributes the DNA binding domain of the t(1;19) translocation protein in pre-B ALL. *Cell* **60**: 547, 1990.
14. Nourse J., Mellentin JD., Galili N., Wilkinson J., Stanbridge E., Smith SD., and Cleary ML.: Chromosomal translocation t(1;19) results in synthesis of a homeobox fusion mRNA that codes for a potential chimeric transcription factor. *Cell* **60**: 535, 1990.
15. Izraeli S., Kovar H., Gadner H., and Lion T.: Unexpected heterogeneity in E2A/PBX1 fusion messenger RNA detected by the polymerase chain reaction in pediatric patients with acute lymphoblastic leukemia. *Blood* **80**: 1413, 1992.
16. Hunger SP., Ohyashiki K., Toyama K., and Cleary ML.: Hlf, a novel hepatic bZIP protein, shows altered DNA-binding properties following fusion to E2A in t(17;19) acute lymphoblastic leukemia. *Genes Dev*. **6**: 1608, 1992.
17. Inaba T., Roberts WM., Shapiro LH., Jolly KW., Raimondi SC., Smith SD., and Look AT.: Fusion of the leucine zipper gene HLF to the E2A gene in human acute B-lineage leukemia. *Science* **257**: 531, 1992.
18. Hunger SP., Devaraj PE., Foroni L., Secker Walker LM., and Cleary ML.: Two types of genomic rearrangements create alternative E2A-HLF fusion proteins in t(17;19)-ALL. *Blood* **83**: 2970, 1994.
19. Romana SP., Poirel H., Le Coniat M., Flexor MA., Mauchauffe M., Jonveaux P., Macintyre EA., Berger R., and Bernard OA.: High frequency of t(12;21) in childhood B-lineage acute lymphoblastic leukemia. *Blood* **86**: 4263, 1995.
20. Romana SP., Mauchauffe M., Le Coniat M., Chumakov I., Le Paslier D., Berger R., and Bernard OA.: The t(12;21) of acute lymphoblastic leukemia results in a tel-AML1 gene fusion. *Blood* **85**: 3662, 1995.
21. Golub TR., Barker GF., Bohlander SK., Hiebert SW., Ward DC., Bray Ward P., Morgan E., Raimondi SC., Rowley JD., and Gilliland DG.: Fusion of the TEL gene on 12P13 to the AML1 gene on 21q22 in acute lymphoblastic leukemia. *Proc. Natl. Acad. Sci., USA* **92**: 4917, 1995.

22. Bash RO., Crist WM., Shuster JJ., Link MP., Amylon M., Pullen J., Carroll AJ., Buchanan GR., Smith RG., and Baer R.: Clinical features and outcome of T-cell acute lymphoblastic leukemia in childhood with respect to alterations at the TAL1 locus: a Pediatric Oncology Group study. *Blood* **81**: 2110, 1993.
23. Aplan PD., Lombardi DP., Ginsberg AM., Cossman J., Bertness VL., and Kirsch IR.: Disruption of the human SCL locus by "illegitimate" V-(D)-J recombinase activity. *Science* **250**: 1426, 1990.
24. Miyoshi H., Koza T., Shimizu K., Enomoto K., Maseki N., Kaneko Y., Kamada N., and Ohki M.: The t(8;21) translocation in acute myeloid leukemia results in production of an AML1-MTG8 fusion transcript. *EMBO J.* **12**: 2715, 1993.
25. Nucifora G., and Rowley JD.: AML1 and the 8;21 and 3;21 translocations in acute and chronic myeloid leukemia. *Blood* **86**: 1, 1995.
26. Downing JR., Head DR., Curcio Brint AM., Hulshof MG., Motroni TA., Raimondi SC., Carroll AJ., Drabkin HA., Willman C., and Theil KS.: An AML1/ETO fusion transcript is consistently detected by RNA-based polymerase chain reaction in acute myelogenous leukemia containing the (8;21)(q22;q22) translocation. *Blood* **81**: 2860, 1993.
27. Mitani K., Ogawa S., Tanaka T., Miyoshi H., Kurokawa M., Mano H., Yazaki Y., Ohki M., and Hirai H.: Generation of the AML1-EVI-1 fusion gene in the t(3;21)(q26;q22) causes blastic crisis in chronic myelocytic leukemia. *EMBO J.* **13**: 504, 1994.
28. Nucifora G., Begy CR., Kobayashi H., Roulston D., Claxton D., Pedersen-Bjergaard J., Parganas E., Ihle JN., and Rowley JD.: Consistent intergenic splicing and production of multiple transcripts between AML1 at 21q22 and unrelated genes at 3q26 in (3;21)(q26;q22) translocations. *Proc. Natl. Acad. Sci., USA* **91**: 4004, 1994.
29. Ichikawa H., Shimizu K., Hayashi Y., and Ohki M.: An RNA-binding protein gene, TLS/FUS, is fused to ERG in human myeloid leukemia with t(16;21) chromosomal translocation. *Cancer Res.* **54**: 2865, 1994.
30. Yamamoto K., Seto M., Iida S., Komatsu H., Kamada N., Kojima S., Koderia Y., Nakazawa S., Saito H., and Takahashi T.: A reverse transcriptase-polymerase chain reaction detects heterogenous chimeric mRNAs in leukemias with 11q23 abnormalities. *Blood* **83**: 2912, 1994.
31. Biondi A., Rambaldi A., Rossi V., Elia L., Caslini C., Basso G., Battista R., Barnui T., Mandelli F., and Masera G.: Detection of ALL-1/AF4 fusion transcript by reverse transcription-polymerase chain reaction for diagnosis and monitoring of acute leukemias with the t(4;11) translocation. *Blood* **82**: 2943, 1993.
32. Corral J., Forster A., Thompson S., Lampert F., Kaneko Y., Slater R., Kroes WG., van der Schoot CE., Ludwig WD., and Karpas A.: Acute leukemias of different lineages have similar MLL gene fusions encoding related chimeric proteins resulting from chromosomal translocation. *Proc. Natl. Acad. Sci., USA* **90**: 8538, 1993.
33. Downing JR., Head DR., Raimondi SC., Carroll AJ., Curcio Brint AM., Motroni TA., Hulshof MG., Pullen DJ., and Domer PH.: The der(11)-encoded MLL/AF-4 fusion transcript is consistently detected in t(4;11)(q21;q23)-containing acute lymphoblastic leukemia. *Blood* **83**: 330, 1994.
34. Yamamoto K., Seto M., Komatsu H., Iida S., Akao Y., Kojima S., Koderia Y., Nakazawa S., Ariyoshi Y., Takahashi T., and Ueda R.: Two distinct portions of LTG19/ENL at 19p13 are involved in t(11;19) leukemia. *Oncogene* **8**: 2617, 1993.
35. Nakamura T., Alder H., Gu Y., Prasad R., Canaani O., Kamada N., Gale R.P., Lange B., Crist W.M., and Nowell P.C.: Genes on chromosome 4, 9, and 19 involved in 11q23 abnormalities in acute leukemia share sequence homology and/or common motifs. *Proc. Natl. Acad. Sci., USA* **90**: 4631, 1993.
36. Tse W., Zhu W., Chen H.S., and Cohen A.: A novel gene, AF1q, fused to MLL in t(1;11)(q21;q23), is specifically expressed in leukemic and immature hematopoietic cells. *Blood* **85**: 650, 1995.
37. Hermans A., Heisterkamp N., von Linden M., van Baal S., Meijer D., van der Plas D., Wiedermann L.M., Groffen J., Bootsma D., and Grosveld G.: Unique fusion of bcr and c-abl genes in Philadelphia chromosome positive acute lymphoblastic leukemia. *Cell* **51**: 33, 1987.
38. Cross N.C., Melo J.V., Feng L., and Goldman J.M.: An optimized multiplex polymerase chain reaction (PCR) for detection of BCR-ABL fusion mRNAs in haematological disorders. *Leukemia* **8**: 186, 1994.
39. Hochhaus A., Reiter A., Skladny H., Melo J.V., Sick C., Berger U., Guo J.Q., Arlinghaus R.B., Hehlmann R., Goldman J.M., and Cross N.C.P.: A novel BCR-ABL fusion gene (e6a2) in a patient with Philadelphia chromosome-negative chronic myelogenous leukemia. *Blood* **88**: 2236, 1996.
40. Papadopoulos P., Ridge S.A., Boucher C.A., Stocking C., and Wiedemann L.M.: The novel activation of ABL by fusion to an ets-related gene, TEL. *Cancer Res.* **55**: 34, 1995.








41. Andreasson P., Johansson B., Carlsson M., Jarlsfelt I., Fioretos T., Mitelman F., and Höglund M.: BCR/ABL-negative chronic myeloid leukemia with ETV6/ABL fusion. *Genes, Chromosomes & Cancer* **20**: 299, 1997.
42. Golub T.R., Barker G.F., Lovett M., and Gilliland D.G.: Fusion of PDGF receptor beta to a novel ets-like gene, tel, in chronic myelomonocytic leukemia with t(5;12) chromosomal translocation. *Cell* **77**: 307, 1994.
43. Buijs A., Sherr S., van Baal S., van Bezouw S., van der Plas D., Geurts van Kessel A., Riegman P., Lekanne Deprez R., Zwarthoff E., Hagemeijer A., and Grosveld G.: Translocation (12;22)(p13;q11) in myeloproliferative disorders results in fusion of the ETS-like TEL gene on 12p13 to the MN1 gene on 22q11. *Oncogene* **10**: 1511, 1995.
44. von Lindern M., Fornerod M., van Baal S., Jaegle M., de Wit T., Buijs A., and Grosveld G.: The translocation (6;9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dec and can, and the expression of a chimeric, leukemia-specific dek-can mRNA. *Mol. Cell. Biol.* **12**: 1687, 1992.
45. von Lindern M., van Baal S., Wiegant j., Raap A., Hagemeijer A., and Grosveld G.: Can, a putative oncogene associated with myeloid leukomogenesis, may be activated by fusion of its 3'half to different genes: characterization of the set gene. *Mol. Cell. Biol.* **12**: 3346, 1992.
46. Nagata K., Kawase H., Handa H., Yano K., Yamasaki M., Ishimi Y., Okuda A., Kikuchi A., and Matsumoto K.: Replication factor encoded by a putative oncogene, set, associated with myeloid leukomogenesis. *Proc. Natl. Acad. Sci., USA* **92**: 4279, 1995.
47. Liu P.P., Hajra A., Wijmenga C., and Collins F.S.: Molecular pathogenesis of the chromosome 16 inversion in the M4Eo subtype of acute myeloid leukemia. *Blood* **85**: 2289, 1995.
48. Chen Z., Brand N.J., Chen A., Chen S.J., Tong J.H., Wang Z.Y., Waxman S., and Zelent A.: Fusion between a novel Kruppel-like zinc finger gene and the retinoic acid receptor-alpha locus due to a variant t(11;17) translocation associated with acute promyelocytic leukemia. *EMBO J.* **12**: 1161, 1993.
49. Licht J.D., Chomienne C., Goy A., Chen A., Scott A.A., Head D.R., Michaux J.L., Wu Y., DeBlasio A., Miller W.H.Jr.: Clinical and molecular characterization of a rare syndrome of acute promyelocytic leukemia associated with translocation (11;17). *Blood* **85**: 1083, 1995.
50. Pandolfi P.P., Alcalay M., Fagioli M., Zangrilli D., Mencarelli A., Diverio D., Biondi A., Lo Coco F., Rambaldi A., and Grignani F.: Genomic variability and alternative splicing generate multiple PML/RAR alpha transcripts that encode aberrant PML proteins and PML/RAR alpha isoforms in acute promyelocytic leukaemia. *EMBO J.* **11**: 1397, 1992.
51. Yoshida H., Naoe T., Fukutani H., Kiyoi H., Kubo K., and Ohno R.: Analysis of the joining sequences of the t(15;17) translocation in human acute promyelocytic leukemia: Sequence non-specific recombination between the PML and RARA genes within identical short stretches. *Genes, Chromosomes & Cancer* **12**: 37, 1995.
52. Kane J.R., Head D.R., Balazs L., Hulshof M.G., Motroni T.A., Raimondi S.C. Carroll A.J., Behm F.G., Krance R.A., Shurtleff S.A., and Downing J.R.: Molecular analysis of the PML/RARalpha chimeric gene in pediatric acute promyelocytic leukemia. *Leukemia* **10**: 1296, 1996.
53. Redner R.L., Rush E.A., Faas S., Rudert W.A. and Corey S.J.: The t(5;17) variant of acute promyelocytic leukemia expresses a nucleophosmin-retinoic acid receptor fusion. *Blood* **87**: 882, 1996.
54. Yoneda Kato N., Look A.T., Kirstein M.N., Valentine M.B., Raimondi S.C., Cohen K.J., Carroll A.J., and Morris S.W.: The t(3;5)(q25.1;q34) of myelodysplastic syndrome and acute myeloid leukemia produces a novel fusion gene, NPM-MLF1. *Oncogene* **12**: 265, 1996.
55. Satake N., Kobayashi H., Tsunematsu Y., Kawasaki H., Horikoshi Y., Koizumi S. and Kaneko Y.: Minimal residual disease with TEL-AML1 fusion transcript in childhood acute lymphoblastic leukaemia with t(12,21). *British J. of Haematology* **97**: 607, 1997.
56. Sacchi N., Nisson P.E., Watkins P.C., Faustinella F., Wijsman J. and Hagemeijer A.: AML1 fusion transcripts in t(3,21) positive leukemia: evidence of molecular heterogeneity and usage of splicing sites frequently involved in the generation of normal AML1 transcripts. *Genes, Chromosomes & Cancer* **11**: 226, 1994.
57. Kong X-T., Ida K., Ichikawa H., Shimizu K., Ohki M., Maseki N., Kaneko Y., Sako M., Kobayashi Y., Tojou A., Miura I., Kakuda H., Funabiki T., Horibe K., Hamaguchi H., Akiyama Y., Bessho F., Yanagisawa M. and Hayashi Y.: Consistent detection of TLS/FUS-ERG chimeric transcripts in acute myeloid leukemia with t(16,21)(p11,q22) and identification of a novel transcript. *Blood* **90**: 1192, 1997.
58. Pallisgaard N., Hokland P., Riishøj D.C., Pedersen B. and Jørgensen P.: Multiplex reverse transcription-polymerase chain reaction for simultaneous screening of 29 translocations and chromosomal aberrations in Acute Leukemia. *Blood* **92**: 574, 1998.

59. Kim HJ., Oh HJ., Lee JW, Jang PS., Chung NG., Kim M., Lim J., Cho B., Kim HK.: Utility of a multiplex reverse transcriptase-polymerase chain reaction assay (HemaVision) in the evaluation of genetic abnormalities in Korean children with acute leukemia: a single institution study. Korean J Pediatr. 2013 Jun;56(6):247-53.
60. Song MJ., Kim HJ., Park CH., Kim SK., Ki CS., Kim JW., Kim SH.: Diagnostic utility of a multiplex RT-PCR assay in detecting fusion transcripts from recurrent genetic abnormalities of acute leukemia by WHO 2008 classification. Diagn mol pathol. 2012 Mar;21(1):40-44.

REVISION HISTORY

| REVISION NUMBER | SECTION CHANGED | DATE |
|-----------------|--|------------|
| 9 | Updated intended use to more precisely describe. Updated 5. Precautions with more details on specimen collection and RNA extraction. Updated 6. procedure with more details on RNA extraction. | 2019.09.19 |
| 10 | Corrected mistakes in precautions where qPCR was mentioned and it should be PCR | 2020.09.15 |
| 11 | Minor editions in precautions section | 2020.10.19 |
| 12 | Changed from User Manual to Instruction For Use | 2021.04.23 |

Symbols used on tubes and boxes

| | | |
|--|---|---|
|  <p>"Conformité Européenne" ("European Conformity")</p> |  <p>In vitro Diagnostic Medical Device</p> |  <p>Consult instructions for use</p> |
| <p>REF Catalogue Number</p> |  <p>Lot number</p> | <p>CONT Contents</p> |
|  <p>Storage temperature</p> |  <p>Expiry Date</p> |  <p>Manufacturer</p> |

DNA DIAGNOSTIC

Availability / questions

Our team and distributors are always at hand to answer all your questions.
Contact us to find your nearest HemaVision® partner.

For more information, contact

DNA Diagnostic A/S
Voldbjergvej 14
DK-8240 Risskov
Denmark

Tel. +45 8732 3050
info@dna-diagnostic.com
www.dna-diagnostic.com

*DNA Diagnostic A/S was established in 1992.
DNA Diagnostic A/S is an ISO 13485 certified
developer, manufacturer, and worldwide supplier
of PCR based CE IVD marked in vitro diagnostic kits.*