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(54) **Title**: ANALYTICAL PROCESS FOR GENOTOXICITY ASSESSMENT

(57) **Abstract**: The present invention relates to an analytical process for the assessment of the genotoxic potential, also termed mutagenic or transforming activity, of an agent in respect to hematopoietic cells. The agent can be selected from natural and synthetic chemical compounds, and preferably from heterologous expression cassettes, e.g. contained in non-natural viral particles or non-natural viral nucleic acid constructs, e.g. nucleic acid constructs containing a viral element.

Analytical process for genotoxicity assessment

The present invention relates to an analytical process for the assessment of the genotoxic potential, also termed mutagenic or transforming activity, of an agent in respect to hematopoietic cells. The agent can be selected from natural and synthetic chemical compounds, and preferably from heterologous expression cassettes, e.g. contained in non-natural viral particles or non-natural viral nucleic acid constructs, e.g. nucleic acid constructs containing a viral element. The heterologous, e.g. viral element can e.g. be a promoter or enhancer region for transgene expression, a viral primer binding site, a viral 5´ region containing a U3 region, and/or a viral packaging signal.

The analytical process is suitable for assessing the genotoxic potential of viral particles for mammalian cells, e.g. for viral particles containing a nucleic acid construct intended for gene therapy. The hematopoietic cells are primary stem cells and/or stem precursor cells of the hematopoietic system, e.g. of human, murine or rat origin. The process is an in vitro process, using the primary stem cells and/or stem precursor cells of the hematopoietic system.

State of the art

Modlich et al., Blood 108 (8), 2545-2553 (2006) describe that gene transfer to primary murine lineage negative bone marrow cells by adding viral nucleic acid constructs containing a SIN (self-inactivating 3´LTR upon integration into the host genome) nucleic acid construct resulted in lower frequencies of replated cells than an LTR-driven nucleic acid construct after 28 days under cell culture conditions. Higher replating frequencies in the cell culture were detected as cell growth in a limiting dilution series and were found to be indicative of a higher transforming potential of the viral particle. A disadvantage of this method is that the increased cell growth which is determined as an indicator for transformation strongly depends on the myeloid cultivation conditions. The replating phenotype is triggered or accompanied by activation of a very limited number of proto-oncogenes (mainly Mecom). Insertional upregulation of genes of the lymphoid differentiation lineage cannot be detected. A further disadvantage is that the cultivation of cells takes a long time and that the microscopic analysis of cell growth yields no information about the underlying transforming event.

Object of the invention

It is an object of the invention to provide an alternative process for analysis of the genotoxic potential of an agent in mammalian hematopoietic cells. Preferably, the alternative process can be performed in a shorter time and/or yields a more detailed picture of the genotoxic potential.

Description of the invention

The invention achieves the object by the features of the claims, especially by providing a process for analysis of the genotoxic activity of an agent for hematopoietic cells, the process comprising the steps of adding the agent to hematopoietic stem and progenitor cells in a cell culture under cell culture conditions, cultivating these cells for a pre-determined duration to produce cultivated cells, isolating total RNA, preferably total mRNA, from the cultivated cells and determining the concentration of the RNAs encoding at least one, preferably all of the RNA sequences of Table 1, preferably using the indicated probe sequences. Generally preferred, the RNAs are mRNAs.

Table 1: RNA and preferred specific probe sequence

RNA name	probe sequence	Probe sequence SEQ ID NO:
AFAP1L1	TAGTTATCTTTGCCTTCTGATGCAATGAACGCACGTAAGCCATTCCATCCTTTCCTTGGC	1
ALS2CL	CCCTACTTTTCTGGGTGATGGCCACAATTACAGTCTACTTATTTATTCAGGATTTTTAAT	2
ARX	GTGTAATTGTTATCACTTTTCCTTGCTATCTAGTGGAGAAGTGTCACGCTCAAAATAAAA	3
BEX6	ATGCTTACTGATGCCATACCGACAATAGCCAAGATATGCAGTCAGCTTGGAGGTTCAACA	4
CCDC102A	TTTCACCTATCACACCCCTGTGAAGGGGGAGCCTGTTGGATATGTATATTGTATATATGC	5
DCTD	GCACTGTTAAATTTATCCGAGGCATAAGTAGTTCCTAGAGGAGACAGTCTATCACTCCCC	6
EHD3	GCTTATAACTGCAGTGTGTTTGTCATTAGGATTCATGTTAATACAACATATTTACCCTCG	7
GM805	ATTTTGATGATTCAAGAAAGCAGAAGGCCCAACCTTCAGTAAAACCACAGGTCTCCGGGA	8
GUCY1A3	GGAACTTTATCTAATTCAAGTCAAAAGAAGTATAGAAGCTCCATGTACGGTTCCTATAAC	9
MEX3A	GCAAAGTAAAGGTGGGAAATAAAACAGACCCATGAATTAATCAAGTCAAAGTGATGTTGC	10
MYCT1	GTCCTTTTGCTTCAAAGACAGGAGTTCACTGGGGGATTCAGAAAGCTTGCCGTTTATGTT	11
NAIP1	AATCTATGAGTTTTATGAACTCTCTAGGGGGCTTAACAACCCCTCACTGGGCAGTGTCAT	12
NOLC1	TTCGAAGTAAGCTTTTCTGACAGACATTTTGCAACAACTTGACTGTTGTATATTGACAAG	13
PA2G4	GAATGGATCCTCATTTGTAAAAATTTTTAGCCATTTTTGTTCTGAACAGTCCCTCAATCC	14
PDGFRB	CCACATTTAGACACCGGAAGTGCTATTTTATATGCTGTTAAGTTTTCCTATCTGTACTTT	15
PHLDA2	ACCATTCCGTGTTAATATTTTTTATACCATATTTTCATTCCAAATAAACAATGTCACTTT	16
SLA2	CAAAGATACACCTCCACCTGTGACTGTGCCAACATCATCACTAAATTGGAAAAAGCTGGA	17
SLC12A2	CTGCTTTGTACAGAAGTTACTGCAATAAAGGAAGTGGAGTCATCACAAGTTTAATACTTA	18
SOX14	TGGACCCTGCGCAATTTAGTTCCAGTGCCATCCAGAAGATGGGTGAAGTGCCCCACACGT	19
SOX4	AATCCTGTCCGTCACTGCCTGTCAGGTTGTTCCTATATACCTTCTGTAAATAACTTTTTT	20
SPNS2	GCTGCTGATTGTGAATCTCAAAGTCTTAAGAGAGAAGCCAAATATATATTCCTCTTGTAA	21
TBXA2R	TGAGTGCTTGGTGGACTAAGGACGGAGCTACGACATGGGGCTGACTCCTGTGAACTGCAA	22
TC1649157	TAGAGAGAGTGAAACCTTGTTCTTGCTGAGTCTTCGAGAAAGAGGACCAAGTCCCAAAGT	23

TIE1	GTGAACATGTCGCTGTTTGAGAACTTCACCTATG CGGGCATCGATGCCACAGCTGAGGAG	24
TMEM176A	GGTATTTTCTCGGAGATGATGTCTGTCAAAGAGA CTCTTCATATGGATGGTCCACCATGC	25
TMEM176B	CCTGAAGAAGTTTCTCTCCTGGCCTCAGGCCAGA ATCCACTATGGGCAGCTGTCTCTAGG	26
TOX	TCCAAGTCCTGTTATGGATAAAGCTGCCAAATGC TCACTGGCATCTTAGCTGCAGAAACA	27
ZFPM1	AGTGAGCCTGTGGGGCCGCACCACCAGGACCCT TGACACTTAATAAAGACATTCGGTGTG	28

and preferably relating the concentrations of the RNAs from cultivated cells to which the agent was added to the concentrations of RNAs determined for cells cultivated under the same cell culture conditions for the same duration in the absence of the agent.

Preferably, the concentration of at least one or all of the RNAs of Table 2 is additionally determined:

Table 2: additional RNA and preferred specific probe sequence

RNA name	probe sequence	Probe sequence SEQ ID NO:
AJUBA	GGAAGCTGGAGAGAAGAAAAATAGGTTGACTTG GTTCTAGCCGCTTGGCTGAAACTTGAA	29
BHLHA15	TCCCTGAGTACTAGTAAAATTGCCATCTGTACCT GAAAATGAAGACTTCACAGCCATTGT	30
CP	TCTGATGTCTTTGACCTTTTCCCTGGAACATACCA AACCCTAGAAATGTTTCCCCAAACA	31
ENSMUST00 000103558	TAACGACACATACATGAAGTTTAGCTGGCTTACA GTGCCTGAAAGGGCAATGGGGAAAGA	32
GLRP1	GGGGAAAAAAGCATCATTTCCATTGTTCTTTGCT CTGTGCCTTGAATCTTTTAATCAATT	33
GRTP1	AAGCAGATCACCAAAGGGGACTTTGTGACAGAG TGTCACGCATTCATGCAGAAAATCTTT	34
LCK	AATCTTATGTCTCTGTGTGTTCTGTCCTGGTGCCT AGCACACACCAGGAGCTCAATAAAA	35
NAP002592-003	TTCCCCTTCGAAAATAGGTGTTATAGTCAAGATA ATGTACTTGGGTCATAAGACAGTGTG	36
PIGA	CCAGTGTGCTAAAACATGCTCATGTCCAGTAATA AAGATGAGAACGCTGTTTTAATAGTC	37
PRMT7	TGGAGACATCACCATGGAGTTTAGGCTTGCAGAC ACCTTGAGCTGATCTCTTATTGAGAA	38
SLC35F2	CAGCCACCAGAGTGCCGCCTTCAGAAAACTTTAT GTAAATTGTTTTTGTATAAGAATAAT	39
TGM2	AAAGCGTGGAAGCCTGTGTGGGGGTCATCATCC CAAGTTAGCCCACTCCTACCTCTCTGT	40

TIMP3	ATAGTGACTTTTGGGGATAGATCTGTCTGGGAGA TAATGTGAGTCCAGGAGGCATTACTC	41
ZFP184	GGGATGGAGAGCCCATTGGGCTGTTCTGATCCAA GTATGTTATTAAAACAACATTGTGGC	42
AKAP13	TTAGTCGCACCTTCAGCTACATCAGGAATAAAAT GTCCAGCAGCAAGAAGAGCAAAGTAA	43
ASB2	CCTGGACACACTGCCGCTTCCCGGCAGGCTAATC AGATACTTGAAATATGAGAATACACA	44
ATP9A	TTCAACTTCTACTTCCTGCTTCTCGCCTGCTCGCA GTTCGTCCCAGAGATGAGGCTTGGC	45
CCR7	CAGCCACTGATACCTTTCCTCATGTTCTGCTTTTG ATTCATATATCTTTTATGAAGAAAC	46
CPLX2	GGAGGAGAAGGAGAAGGAGAAGGAGAAGGAGA AGGAGAAGGAGAAGGAGAAGGAGAAGGA	47
DUSP2	GTGGGCATCTCGCTGTAATTGGTGCTGAAAAGTT ATTTGTGTTCAACTGACATTTAACGC	48
ELOVL6	CCTAGGCCCTAAACCCATATTCAGAGGGAAAATT CACTATCAAGCCTCACAGCGAAATCA	49
EPOR	GAACGGGATTGGTGAAGCCATACTTAAAGTCAG AGCTGACCTTGGCCCTCTGAGCAGGAA	50
FGF3	GCTGTATGCTTCGGATCACTACAACGCAGAGTGT GAGTTTGTGGAACGGATCCATGAGCT	51
IGF1R	GCTAAAGCTAAGGCCACTTGAGTCTATTACTCTG CTTTTTTCTAGTAGTTAAAGCACCAC	52
ITK	ACTGCAGGTATGTCTTACCCTCTGTGGGGGCCAC AAGTCAATCATTGCTTATGGAAAAAA	53
JAKMIP1	CTGTACCAGAGCAATCTATTTATTGCCTACCGCT TGTTTTGCACTTAATAAAATAAGTTG	54
KLRB1F	GGTTTGTATTGATTGACACTCGCCAACTAGTTGA CTAATAATGGACTAATGCTGTGTTCG	55
LMO2	CTTCATTTTGAGGTGAGGCGCCCCACAGATTGTT TCTATACAAATGTAAATCTTAAAAAA	56
MEF2C	AGAGGAATAGTATGTCTCCTGGTGTAACACATAG ACCTCCAAGTGCAGGTAACACAGGTA	57
MID1	AGGTTGGATGTCACCACCACAAGGGAAAACAAA CACATGGGTTTTTCCCCAACACGATTA	58
MND1	GGCAAGAGACGGAAGAACGAGCCATGCTTGCAA AAGAACTTTCTTCATTTCGAGACCAAA	59
MYB	TGACAGTGTATCTACTGCCTTGTAGCAAAATAAA GCTATCCTCTTATTTTACATACTTCC	60
MYC	AACAGTTGAAACACAAACTCGAACAGCTTCGAA ACTCTGGTGCATAAACTGACCTAACTC	61
PIM2	CACGCTACAGGGATAGATGGACATCTGTTGACCT GGTTATACAGGTTGTTAAAAATCCAG	62
PRDM16	CTGGATACCAAATGTAATCTTTCCGATGCTACAA TGAATTTATACACGAGATTGATATGC	63
RAMP1	AGACGCTATGGTGTGACTGGGGAAAGACCATAC AGAGCTATGGGGAGCTCACTTACTGCA	64

RASGRP2	TCTGTTAGACCAAGAAGGGAACCGCAGGCACAG CAGCCTCATCGACATCGAGAGTGTGTG	65
SEMA7A	TCCCTTATCTCTTCTCAATGCACTTTAATAATGTA ACATATTACTAATAAACAAGCTATT	66
SH3KBP1	GCCAATTAAACTAAGACCAAGGTCGATTGAAGT GGAAAATGACTTCCTGCCCGTCGAAAA	67
SLC43A1	TGCACACATATATGTTACGCACATGCATATTGCA TCCTTTCCTGCAGGAGAAGGACTGAG	68
SMAD3	TATAAACGCCCTTCTAATAAACTTTTCACCGTAA AGCTCCTGAGACAGGAGCACAGTCTG	69
ST3GAL6	AATGGTGATCAACTTGACTTAAAATTGACCCTAT GGATCCAAAAGATGATGATGCTAAAC	70
TNFSF13B	CGTTGAATCTGATCCAAACCAGGAAATATAACA GACAGCCACAACCGAAGTGTGCCATGT	71
VARS	TGCTCTTGAACTAGCTCTGAGCATCACTCGAGCT GTGCGCTCCCTGCGTGCTGACTACAA	72

The step of relating the concentrations of the mRNAs determined for the cells to which the agent was added with subsequent cultivation to the concentrations of the mRNAs determined for the same type of cells which were cultivated without addition of the agent under the same cell culture conditions results in the determination of differences in the expression levels of these RNAs, which differences in expression levels are characteristic for the genotoxic effect of the agent. As the expression levels of mRNAs have been found to depend on the culture conditions, the cells are cultivated under the same culture conditions and the same duration for each comparison, preferably performed in parallel each time. The cells cultivated under the same cell culture conditions for the same duration in the absence of the agent are also referred to as a negative control or mock.

Preferably, an agent that is known to have a significant genotoxic potential is used under the same culture conditions to provide a positive control, preferably performed each time in parallel to the cells to which the agent was added, and the process comprises the step of comparing the concentrations of the mRNAs determined for the positive control to the concentrations of mRNAs determined for the cells to which the agent to be analysed was added. Generally, the process preferably comprises the comparison of expression levels of the RNAs determined for the cells to which the agent was added to the expression levels of the cellular RNAs determined for the negative control and/or of the positive control, wherein all cells were cultivated under the same cell culture conditions for the same pre-determined duration.

It has been found that the determination of the concentration of these mRNAs allows the differentiation between immortalized cells and non-immortalized cells. Therein, immortalized cells are considered to represent precancerous cells and/or tumour cells, indicating a high genotoxic activity of the agent analysed in the process. Specifically, it has been found that expression levels of the RNAs that are determined for the cells to which the agent was added, which expression levels have differences in comparison to the expression levels of the mRNAs determined for the negative control and/or no or less important differences in comparison to a positive control, are characteristic for the genotoxic activity of the agent. Using a viral particle known to have genotoxic activity as an exemplary agent and murine hematopoietic stem cells and their progenitor cells, significant differences in expression levels of the RNAs were found in comparison to the expression levels determined for the RNAs in a parallel negative control.

The step of relating the concentrations of the mRNAs determined for the hematopoietic cells to which the agent was added to the concentrations of mRNAs determined for the hematopoietic cells cultivated under the same cell culture conditions for the same duration in the absence of the agent preferably is by calculating the ratio of the specific mRNA concentrations. Generally, the concentration ratio can be replaced by the ratio of measurement values measured for the mRNA concentrations, e.g. by the ratio of fluorescence measurement values. Preferably, only the mRNAs are considered as having an expression level which significantly differs from the expression determined for the negative control. For example, a significant difference can be defined for a difference of at least a $\log_2$ of the concentration ratio bigger than +1 or smaller than -1. This exemplary cut-off for expression levels which compared to the negative control differ at least by such a factor can be used in order to limit the RNAs to those which have an important difference in expression level.

Preferably, for agents containing a nucleic acid, the copy number of this nucleic acid in relation to the genome of the cells is determined. In this manner, the influence of the copy number can be taken into account in the determination of the genotoxic risk of an agent. For agents not containing a nucleic acid, the concentration of the agent should be measured in order to take into account the concentration effect, for example by dividing the concentration of RNAs determined in the cells with agent by the concentration of the added agent.

The culture conditions comprise the composition of the cultivation medium, cultivation temperature, the composition of the gas atmosphere, and the movement of the cultivation medium, e.g. by shaking, stirring, or static incubation.

A preferred medium for the hematopoietic stem cells and their progenitor cells used in the process contains growth-promoting cytokines, especially the following cytokines: stem cell factor (SCF), preferably in addition interleukin-3 (IL-3), Flt3-ligand, interleukin-11 (IL-11), and more preferably additionally interleukin-7 (IL-7), and further optionally additionally interleukin-6 (IL-6), interleukin-15 (IL-15), thrombopoietin (TPO) and further optionally additionally at least one notch ligand (DL1 or DL4).

An advantage of the process of the invention is that it is not restricted to measure presence of cells that proliferate during a long period of cultivation as e.g. in the process of Modlich (2006), as it has been found that the RNA isolated in the process according to the invention does not necessarily contain, and preferably not contain relevant levels of the mRNA Lmo2, whereas in cells treated in the process of Modlich (2006) all cells that finally proliferated, when analysed by the process of the invention were found to express Lmo2. Therefore, the process of the invention has the advantage of identifying Lmo2, which is an indicator for precedence of adverse events in gene therapy, e.g. an indicator associated with the development of leukemia by gene therapy. As a further advantage, the process is not dependent on the expression of Lmo2 by the cells to be analysed.

Following addition of the agent to the cells in cell culture and prior to cultivating the cells, the process can comprise the step of incubating the cells in the presence of the agent and removing the agent, e.g. by exchanging the culture medium of the cells in the cell culture for fresh medium without the agent, e.g. following a prior incubation period of 1 to 3 d.

Preferably, the agent is a non-natural nucleic acid construct, optionally packaged as a viral particle. The non-natural nucleic acid construct can e.g. contain a non-natural or a natural nucleic acid sequence having the ability to integrate into genomic DNA, e.g. at least a sequence having homology to the cell, a viral primer binding site, a viral 5´ region containing a U3 region, and/or a viral packaging signal promoter sequence.

When the agent comprises a nucleic acid construct, e.g. the agent is a viral particle, the process preferably comprises the step of performing a quantitative analysis of the nucleic acid construct in total DNA obtained during the pre-determined duration from an aliquot of the cultivated cells for determination of the average copy number of the agent in the mammalian cell. Preferably, the quantitative analysis of the nucleic acid construct of the agent in total DNA obtained from the cells is made by quantitative PCR (polymerase chain reaction) using a primer pair specific for the nucleic acid construct, and preferably also a primer pair specific for a genomic DNA section of the cells, in a separate or in the same PCR. The step of collecting DNA from the cells for the quantitative analysis of the nucleic acid construct can e.g. be made at 2 to 8 d, preferably 4 to 8 d, more preferably 4 d following the addition of the agent to mammalian cells in a cell culture, in order to avoid detection of viral nucleic acids from episomes or from transiently infected cells.

The pre-determined duration of cultivating the cells following the step of adding the agent to the cells in culture can e.g. amount to 10 to 15 days, and this duration can optionally be divided into a first and a second partial duration, wherein the first partial duration of cultivating the cells is followed by a step of diluting the cells and then by cultivating the cells for the second partial duration, e.g. by re-plating the cells at lower cell number and cultivating for a second partial duration. In this embodiment, the step of diluting the cells for a second partial duration of incubation can increase the selection pressure on the cells and therefore result in more pronounced differences in the translation of mRNA species. Preferably, the first partial duration can be 2 to 10 d, preferably 6 to 8 d, and the second partial duration that follows the dilution of the cells for further cultivation can be 5 to 12 d, e.g. 5 to 7 d.

Optionally, the pre-determined duration of cultivating the cells, optionally the first partial duration can be 2 to 6 d, preferably 3 to 4 d. Such duration can have the advantage of determining concentrations of mRNAs, which preferably are mRNAs, characteristic for general toxicity of agents, whereas longer durations, especially durations of 8 to 15 d, have been found to result in specific differences in expression levels of the mRNAs regarding genotoxicity. This shows a specific advantage of the process of the invention in that it generally results in the identification of genotoxic activity of an agent at higher sensitivity and identification but also the identification of a general toxicity of an agent that prevents or reduces proliferation of the cells.

A further advantage of the process of the invention is that it does not require the replating step needed for microscopic analysis of transformed or immortalized cells and hence can use shorter pre-determined durations of cultivating cells as e.g. used in the process of Modlich et al. (2006), which uses an expansion plus limiting dilution of the murine hematopoietic stem and progenitor cells in culture for 4 weeks following transduction of cells.

The primary hematopoietic stem cells and/or stem progenitor cells obtained freshly or used after a freeze-thaw-cycle, which are used in the process of the invention, e.g. of murine origin, can be cultivated under cell culture conditions prior to adding the agent, adding nothing or an inactive compound for the negative control, and adding a known genotoxic agent as a positive control, respectively, to separate cells in culture at the same prior incubation period. This cultivation period prior to adding the agent can e.g. last for 1 to 3 d, e.g. 2 d for freshly obtained primary cells.

The step of determining the concentration of the mRNAs can be by reverse transcription followed by quantitative PCR, preferably by hybridisation of the mRNA, preferably the total RNA isolated from the cultivated cells, to nucleic acid probes which are immobilized on a substrate, e.g. arranged on a substrate as an array of probes. Arrays of nucleic acid probes immobilized on a substrate are generally known as microarrays which are suitable for quantification of hybridizing mRNAs. Optionally, concentration of mRNAs can be quantified by next generation sequencing of the reverse transcribed RNAs.

In an optional embodiment, the process contains the evaluation of the mRNAs which are considered as deregulated. Therein, the mRNAs are considered deregulated for which subsequent to normalization, preferably Quantil normalization (e.g. performed using the R-package limma – linear models for microarrays), for the concentration ratio with the negative control a $\log_2$ of bigger than +1 or smaller than -1 is found.

Preferably additionally, a normalized enrichment score (NES) is calculated for each of the mRNAs considered deregulated. The NES is calculated as described by Subramanian et al., Proc Natl Acad Sci USA (2005) Oct 25; 102(43):15545-50. In short, the NES is calculated by the steps of generating a numerical matrix of the protein encoding genes, creating a running-sum statistic with a maximum deviation from zero (Enrichment Score), determination of a nominal *P* value (Estimation of Significance Level) and adjusting the Enrichment Score for

Multiple Hypothesis Testing (Normalized Enrichment Score). Therein, an NES above 2.0 indicates a high probability that the agent has transformed the cells, an NES below 1.2 indicates a low probability that the agent has genotoxic potential, and an intermediate NES, i.e. between 1.2 and 2.0 indicates that the agent has potential genotoxic activity.

Preferably, in a subsequent step databanks are searched for the mRNAs considered deregulated, the databanks containing RNAs, which preferably are mRNAs, which have been found associated with diseases, e.g. relevant in diseases, e.g. in tumour patients, e.g. in AML, ALL or MDS patients, or in mouse models of such a disease. A hit in each databank for an RNA considered deregulated adds weight to this RNA as the overlap percentage for a hit in the databank. The result of the addition of the weight, e.g. the percentage of overlap to the at least one databank, e.g. to the $\log_2$ ratio for each mRNA, yields a numerical value reflecting the genotoxic potential.

It was found that this calculation of a value reflecting the genotoxic potential for viral particles which are currently considered as having a low genotoxic potential yields values close to zero, and that this calculation for known mutagenic viral particles yields values which are significantly bigger.

The databanks contain genes which when deregulated can have a genotoxic effect at least of viral particles. The databanks, e.g. at least one, are selected from the following ones:

1. Retroviral Tagged Cancer Gene Database (RTCGD, available from http://variation.osu.edu/rtcgd/) containing insertions detected in the vicinity of genes caused by retrovirus (RCGD-retro) or by transposons (RTCGD-transposon) in at least one murine tumour.
2. Bushman Cancer Gene List (available from www.bushmanlab.org/links/genelists) containing gene names of several cancer data bases, e.g. Atlas, CANgenes, CIS (RTCGD), human lymphoma-associated genes, a list of retrovirally induced tumours, the Sanger Cancer Development List, the Vogelstein List of chromosomal aberrations having importance in cancer development.

The invention is now described by way of examples with reference to the figure, which shows in Fig. 1 a graphic representation of exemplary NES values determined for an exemplary agent by a preferred embodiment of the process.

Example 1: Analysis of genotoxic potential by determination of mRNA concentrations in cultivated cells

Murine primary hematopoietic stem precursor cells that were isolated, cryopreserved, thawed, cultivated for 3 d in serum-free medium, preferably in StemSpan medium containing SCF, Flt3-L, IL-3, IL-11, IL-7 and expanded in IMDM medium (same cytokines) for 2 d at 37°C, 5% CO_2 atmosphere in 24-well cell culture dishes. At day 0, the agent, a positive control and medium as a negative control were added to separate dishes of the cultivated cells. The exemplary agent suspected of having a genotoxic activity was a viral particle containing a nucleic acid construct coding for the IL-2 receptor common gamma chain under an elongation factor 1 alpha short promoter, designated LVEFS. The positive control was a viral particle containing a nucleic acid construct with intact LTR regions (promoter/enhancer regions) from the spleen focus forming virus, designated RVSF.

The cells with added agent, positive control and negative control, respectively, were incubated under cell culture conditions for 4 days, then an aliquot of each cell culture was removed for extraction of genomic DNA, from which the copy number of the viral nucleic acid sequence was determined. In detail, the primers of Table 3 were used to detect the viral elements indicated.

Table 3: primers for detecting viral elements of a viral particle

viral element	function of primer or probe	primer or probe	SEQ ID NO:
WPRE	forward	GAGGAGTTGTGGCCCGTTGT	73
WPRE	reverse	TGACAGGTGGTGGCAATGCC	74
WPRE	Taqman Probe	CTGTGTTTGCTGACGCAAC	75
PTBP2	forward	TCTCCATTCCCTATGTTCATGC	76
PTBP2	reverse	GTTCCCGCAGAATGGTGAGGTG	77
PTBP2	Taqman Probe	ATGTTCCTCGGACCAACTTG	78

The cultivated cells were expanded in IMDM medium containing cytokines SCF (100 ng/ml), IL-3 (20 ng/ml), Flt-3L (100 ng/ml), IL-11 (100 ng/ml), and IL-7 (100 ng/ml) for further 4 days, then collected and re-plated at a 1:10 dilution in fresh medium of this composition and cultivated for another 7 d. Alternatively, the medium in addition contained OP9-DL1 or DL4 at a concentration of 5 µg/ml. Then total RNA was collected from the cells using RNAzol and the extraction kit from Zymo Research.

The RNA from each culture was analysed for the concentration of the following RNAs of Table 1: AFAP1L1, ALS2CL, ARX, BEX6, CCDC102A, DCTD, EHD3, GM805, GUCY1A3, MEX3A, MYCT1, NAIP1, NOLC1, PA2G4, PDGFRB, PHLDA2, SLA2, SLC12A2, SOX14, SOX4, SPNS2, TBXA2R, TC1649157, TIE1, TMEM176A, TMEM176B, TOX, ZFPM1. Additionally, the following RNAs of Table 2 were analysed: AJUBA, BHLHA15, CP, ENSMUST00000103558, GLRP1, GRTP1, LCK, NAP002592-003, PIGA, PRMT7, SLC35F2, TGM2, TIMP3, ZFP184, AKAP13, ASB2, ATP9A, CCR7, CPLX2, DUSP2, ELOVL6, EPOR, FGF3, IGF1R, ITK, JAKMIP1, KLRB1F, LMO2, MEF2C, MID1, MND1, MYB, MYC, PIM2, PRDM16, RAMP1, RASGRP2, SEMA7A, SH3KBP1, SLC43A1, SMAD3, ST3GAL6, TNFSF13B, VARS. For analysis of the RNAs, hybridisation to immobilized specific oligonucleotides contained on a chip, followed by optical detection using laser irradiation of the fluorescent dye Cyanine 3 were used.

The ratio of the mRNA concentrations were determined as the quotient of the fluorescence signal intensity determined for the cells to which the agent was added to the signal intensity determined in the negative control for each mRNA species.

The differentiation between immortalized cells and non-immortalized cells was verified by performing the conventional limiting dilution protocol of the Modlich (2006) assay in parallel. Differences between immortalized and non-immortalized cells can be assessed by the measurement of the mRNA species of Table 1. For determination of the numerical value discriminating the genotoxic potential, a normalized enrichment score (NES) was calculated for the significantly expressed mRNAs using the GSEA method. The exemplary agent LVEFS had a NES of -1.4 which was significantly different from the positive control RVSF with an NES of 2.62.

For determination of the genotoxic potential according to the database RTCGD, the significantly increased concentrations of RNA species of Table 1 and of the additional RNAs of Table 2 that were determined in the cells to which the exemplary agent LVEFS or RVSF was added, were analysed for overlaps with the database. The sample LVEFS had a mean overlap of 0 out of 44 and the RVSF 17 out of 44. This corresponds to a p-value < 0.001 and is regarded highly significant.

Fig. 1 shows the normalized enrichment scores of sample LVEFS (-1.4) and the positive control RVSF (2.62).

Claims

1. Process for analysis of the genotoxic activity of an agent for primary hematopoietic cells, the process comprising the steps of adding the agent to the primary hematopoietic cells in culture under cell culture conditions, cultivating the cells for a pre-determined duration to produce cultivated cells, characterized by the step of isolating total RNA from the cultivated cells, determining the concentration of at least one, preferably all, of the RNAs selected from the group comprising

AFAP1L1,
ALS2CL,
ARX,
BEX6,
CCDC102A,
DCTD,
EHD3,
GM805,
GUCY1A3,
MEX3A,
MYCT1,
NAIP1,
NOLC1,
PA2G4,
PDGFRB,
PHLDA2,
SLA2,
SLC12A2,
SOX14,
SOX4,
SPNS2,
TBXA2R,
TC1649157,
TIE1,
TMEM176A,
TMEM176B,
TOX, and
ZFPM1,

and relating the concentrations of the mRNAs to the concentrations of mRNAs determined for cells cultivated under the same cell culture conditions for the same duration in the absence of the agent.

2. Process according to claim 1, characterized in that the RNA is detected by hybridization to a probe having a nucleic acid sequence

Specific for RNA named	probe sequence	Probe sequence SEQ ID NO:
AFAP1L1	TAGTTATCTTTGCCTTCTGATGCAATGAACGCA CGTAAGCCATTCCATCCTTTCCTTGGC	1
ALS2CL	CCCTACTTTTCTGGGTGATGGCCACAATTACAG TCTACTTATTTATTCAGGATTTTTAAT	2
ARX	GTGTAATTGTTATCACTTTTCCTTGCTATCTAGT GGAGAAGTGTCACGCTCAAAATAAAA	3
BEX6	ATGCTTACTGATGCCATACCGACAATAGCCAAG ATATGCAGTCAGCTTGGAGGTTCAACA	4

CCDC102A	TTTCACCTATCACACCCCTGTGAAGGGGGAGCC TGTTGGATATGTATATTGTATATATGC	5
DCTD	GCACTGTTAAATTTATCCGAGGCATAAGTAGTT CCTAGAGGAGACAGTCTATCACTCCCC	6
EHD3	GCTTATAACTGCAGTGTGTTTGTCATTAGGATTC ATGTTAATACAACATATTTACCCTCG	7
GM805	ATTTTGATGATTCAAGAAAGCAGAAGGCCCAA CCTTCAGTAAAACCACAGGTCTCCGGGA	8
GUCY1A3	GGAACTTTATCTAATTCAAGTCAAAAGAAGTAT AGAAGCTCCATGTACGGTTCCTATAAC	9
MEX3A	GCAAAGTAAAGGTGGGAAATAAAACAGACCCA TGAATTAATCAAGTCAAAGTGATGTTGC	10
MYCT1	GTCCTTTTGCTTCAAAGACAGGAGTTCACTGGG GGATTCAGAAAGCTTGCCGTTTATGTT	11
NAIP1	AATCTATGAGTTTTATGAACTCTCTAGGGGGCT TAACAACCCCTCACTGGGCAGTGTCAT	12
NOLC1	TTCGAAGTAAGCTTTTCTGACAGACATTTTGCA ACAACTTGACTGTTGTATATTGACAAG	13
PA2G4	GAATGGATCCTCATTTGTAAAAATTTTTAGCCA TTTTTGTTCTGAACAGTCCCTCAATCC	14
PDGFRB	CCACATTTAGACACCGGAAGTGCTATTTTATAT GCTGTTAAGTTTTCCTATCTGTACTTT	15
PHLDA2	ACCATTCCGTGTTAATATTTTTTATACCATATTT TCATTCCAAATAAACAATGTCACTTT	16
SLA2	CAAAGATACACCTCCACCTGTGACTGTGCCAAC ATCATCACTAAATTGGAAAAAGCTGGA	17
SLC12A2	CTGCTTTGTACAGAAGTTACTGCAATAAAGGAA GTGGAGTCATCACAAGTTTAATACTTA	18
SOX14	TGGACCCTGCGCAATTTAGTTCCAGTGCCATCC AGAAGATGGGTGAAGTGCCCCACACGT	19
SOX4	AATCCTGTCCGTCACTGCCTGTCAGGTTGTTCCT ATATACCTTCTGTAAATAACTTTTTT	20
SPNS2	GCTGCTGATTGTGAATCTCAAAGTCTTAAGAGA GAAGCCAAATATATATTCCTCTTGTAA	21
TBXA2R	TGAGTGCTTGGTGGACTAAGGACGGAGCTACG ACATGGGGCTGACTCCTGTGAACTGCAA	22
TC1649157	TAGAGAGAGTGAAACCTTGTTCTTGCTGAGTCT TCGAGAAAGAGGACCAAGTCCCAAAGT	23
TIE1	GTGAACATGTCGCTGTTTGAGAACTTCACCTAT GCGGGCATCGATGCCACAGCTGAGGAG	24
TMEM176 A	GGTATTTTCTCGGAGATGATGTCTGTCAAAGAG ACTCTTCATATGGATGGTCCACCATGC	25
TMEM176 B	CCTGAAGAAGTTTCTCTCCTGGCCTCAGGCCAG AATCCACTATGGGCAGCTGTCTCTAGG	26
TOX	TCCAAGTCCTGTTATGGATAAAGCTGCCAAATG CTCACTGGCATCTTAGCTGCAGAAACA	27
ZFPM1	AGTGAGCCTGTGGGGCCGCACCACCAGGACCC TTGACACTTAATAAAGACATTCGGTGTG	28

3. Process according to one of the preceding claims, characterized in that the concentrations of all the RNAs of claim 1 are analysed.

4. Process according to one of the preceding claims, characterized by additionally determining the concentration of at least one of the RNAs selected from the group comprising

AJUBA,
BHLHA15,
CP,
ENSMUST00000103558,
GLRP1,
GRTP1,
LCK,
NAP002592-003,
PIGA,
PRMT7,
SLC35F2,
TGM2,
TIMP3,
ZFP184,
AKAP13,
ASB2,
ATP9A,
CCR7,
CPLX2,
DUSP2,
ELOVL6,
EPOR,
FGF3,
IGF1R,
ITK,
JAKMIP1,
KLRB1F,
LMO2,
MEF2C,
MID1,
MND1,
MYB,
MYC,
PIM2,
PRDM16, and
RAMP1,

and relating the concentrations of the mRNAs to the concentrations of mRNAs determined for cells cultivated under the same cell culture conditions for the same duration in the absence of the agent.

5. Process according to claim 4, characterized in that the RNA is detected by hybridization to a probe having a nucleic acid sequence

Specific for RNA named	probe sequence	Probe sequence SEQ ID NO:
AJUBA	GGAAGCTGGAGAGAAGAAAAATAGGTTGACTTG GTTCTAGCCGCTTGGCTGAAACTTGAA	29
BHLHA15	TCCCTGAGTACTAGTAAAATTGCCATCTGTACCT GAAAATGAAGACTTCACAGCCATTGT	30
CP	TCTGATGTCTTTGACCTTTTCCCTGGAACATACCA AACCCTAGAAATGTTTCCCCAAACA	31
ENSMUST00000103558	TAACGACACATACATGAAGTTTAGCTGGCTTACA GTGCCTGAAAGGGCAATGGGGAAAGA	32
GLRP1	GGGGAAAAAAGCATCATTTCCATTGTTCTTTGCT CTGTGCCTTGAATCTTTTAATCAATT	33
GRTP1	AAGCAGATCACCAAAGGGGACTTTGTGACAGAG TGTCACGCATTCATGCAGAAAATCTTT	34
LCK	AATCTTATGTCTCTGTGTGTTCTGTCCTGGTGCCT AGCACACACCAGGAGCTCAATAAAA	35
NAP002592-003	TTCCCCTTCGAAAATAGGTGTTATAGTCAAGATA ATGTACTTGGGTCATAAGACAGTGTG	36
PIGA	CCAGTGTGCTAAAACATGCTCATGTCCAGTAATA AAGATGAGAACGCTGTTTTAATAGTC	37
PRMT7	TGGAGACATCACCATGGAGTTTAGGCTTGCAGAC ACCTTGAGCTGATCTCTTATTGAGAA	38
SLC35F2	CAGCCACCAGAGTGCCGCCTTCAGAAAACTTTAT GTAAATTGTTTTTGTATAAGAATAAT	39
TGM2	AAAGCGTGGAAGCCTGTGTGGGGGTCATCATCC CAAGTTAGCCCACTCCTACCTCTCTGT	40
TIMP3	ATAGTGACTTTTGGGGATAGATCTGTCTGGGAGA TAATGTGAGTCCAGGAGGCATTACTC	41
ZFP184	GGGATGGAGAGCCCATTGGGCTGTTCTGATCCAA GTATGTTATTAAAACAACATTGTGGC	42
AKAP13	TTAGTCGCACCTTCAGCTACATCAGGAATAAAAT GTCCAGCAGCAAGAAGAGCAAAGTAA	43
ASB2	CCTGGACACACTGCCGCTTCCCGGCAGGCTAATC AGATACTTGAAATATGAGAATACACA	44
ATP9A	TTCAACTTCTACTTCCTGCTTCTCGCCTGCTCGCA GTTCGTCCCAGAGATGAGGCTTGGC	45
CCR7	CAGCCACTGATACCTTTCCTCATGTTCTGCTTTTG ATTCATATATCTTTTATGAAGAAAC	46
CPLX2	GGAGGAGAAGGAGAAGGAGAAGGAGAAGGAGA AGGAGAAGGAGAAGGAGAAGGAGAAGGA	47
DUSP2	GTGGGCATCTCGCTGTAATTGGTGCTGAAAAGTT ATTTGTGTTCAACTGACATTTAACGC	48
ELOVL6	CCTAGGCCCTAAACCCATATTCAGAGGGAAAATT CACTATCAAGCCTCACAGCGAAATCA	49
EPOR	GAACGGGATTGGTGAAGCCATACTTAAAGTCAG AGCTGACCTTGGCCCTCTGAGCAGGAA	50

FGF3	GCTGTATGCTTCGGATCACTACAACGCAGAGTGT GAGTTTGTGGAACGGATCCATGAGCT	51
IGF1R	GCTAAAGCTAAGGCCACTTGAGTCTATTACTCTG CTTTTTTCTAGTAGTTAAAGCACCAC	52
ITK	ACTGCAGGTATGTCTTACCCTCTGTGGGGGCCAC AAGTCAATCATTGCTTATGGAAAAAA	53
JAKMIP1	CTGTACCAGAGCAATCTATTTATTGCCTACCGCT TGTTTTGCACTTAATAAAATAAGTTG	54
KLRB1F	GGTTTGTATTGATTGACACTCGCCAACTAGTTGA CTAATAATGGACTAATGCTGTGTTCG	55
LMO2	CTTCATTTTGAGGTGAGGCGCCCCACAGATTGTT TCTATACAAATGTAAATCTTAAAAAA	56
MEF2C	AGAGGAATAGTATGTCTCCTGGTGTAACACATAG ACCTCCAAGTGCAGGTAACACAGGTA	57
MID1	AGGTTGGATGTCACCACCACAAGGGAAAACAAA CACATGGGTTTTTCCCCAACACGATTA	58
MND1	GGCAAGAGACGGAAGAACGAGCCATGCTTGCAA AAGAACTTTCTTCATTTCGAGACCAAA	59
MYB	TGACAGTGTATCTACTGCCTTGTAGCAAAATAAA GCTATCCTCTTATTTTACATACTTCC	60
MYC	AACAGTTGAAACACAAACTCGAACAGCTTCGAA ACTCTGGTGCATAAACTGACCTAACTC	61
PIM2	CACGCTACAGGGATAGATGGACATCTGTTGACCT GGTTATACAGGTTGTTAAAAATCCAG	62
PRDM16	CTGGATACCAAATGTAATCTTTCCGATGCTACAA TGAATTTATACACGAGATTGATATGC	63
RAMP1	AGACGCTATGGTGTGACTGGGGAAAGACCATAC AGAGCTATGGGGAGCTCACTTACTGCA	64

6. Process according to one of the preceding claims, characterized in that the agent is a virus or a viral particle containing a non-natural nucleic acid sequence, the process comprising the step of determining the copy number of the nucleic acid sequence of the viral particle in the genome of the cells.

7. Process according to one of the preceding claims, characterized in that the duration is 7 to 15 d, during which the cells are provided at least once with fresh culture medium.

8. Process according to one of the preceding claims, characterized in that under the culture conditions the medium contains cytokines consisting of the group of SCF, IL-3, Flt-3L, IL-11, IL-15, IL-6, IL-7, TPO, and Notch-ligands DL-1 and DL-4.

9. Process according to one of the preceding claims, characterized in that only those RNAs are considered deregulated for which following normalization the ratio of RNA

concentration determined for the cells to which the agent was added to the RNA concentration of cells cultivated in the absence of the agent is significantly different.

10. Process according to one of the preceding claims, characterized in that a normalized enrichment score (NES) is calculated and that an NES above 2.0 indicates a high genotoxic activity and an NES below 1.2 indicates a low genotoxic activity of the agent.

11. Process according to one of the preceding claims, characterized in that for each RNA an overlap with a databank is determined and the total number of mRNAs overlapping with a database for the cells to which the agent was added and cells cultivated in the presence of the positive control is added to a numerical value reflecting the genotoxic potential, wherein the databank is at least one selected from the databanks comprised in the group of:
    Retroviral Tagged Cancer Gene Database, and Bushman Cancer Database.

12. Process according to one of the preceding claims, characterized in that it includes separate treatment of identical primary hematopoietic cells by adding an agent of known genotoxic activity as a positive control, wherein the cells are cultivated under the same cell culture conditions and for the same duration, and determining the concentrations of the mRNAs for cells for the positive control.

13. Process according to one of the preceding claims, characterized in that the numerical value is calculated by a Fisher's exact test, where a $p\text{-value} < 0.05$ (agent vs. positive control) is regarded statistically significant, reflecting a lower genotoxic potential of the agent compared to the positive control.

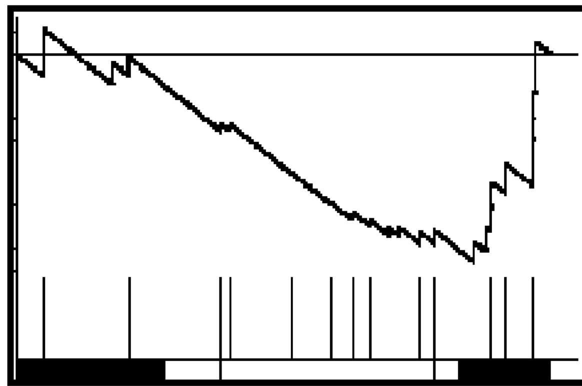
14. Process according to one of the preceding claims, characterized in that the positive control is a viral particle containing a nucleic acid construct with intact LTR regions (promoter/enhancer regions) from the spleen focus forming virus.

15. Process according to one of the preceding claims, characterized in that the concentration of the RNAs is determined as the normalized enrichment score (NES) and a NES value above 2.0 is taken as a high probability for genotoxic potential, a NES value below 1.2 is taken as a low probability for genotoxic potential, and a NES

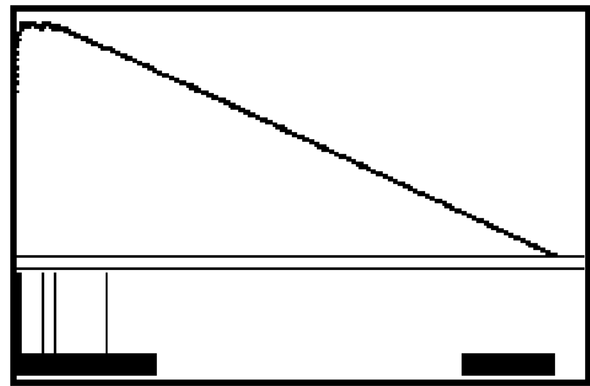
value of 1.2 to 2.0 is taken as genotoxic potential, and that the NES values of the RNAs analyzed are added and compared to the added NES values of mRNAs determined for cells cultivated under the same cell culture conditions for the same duration in the absence of the agent.

Figure

Fig. 1



LVEFS NES -1.4 p= 0.05 FDR= 0.12 Mock



RVSF NES 2.62 p< 0.001 FDR< 0.001 Mock

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2016/081351

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. [X] forming part of the international application as filed:

      [X] in the form of an Annex C/ST.25 text file.

      [ ] on paper or in the form of an image file.

   b. [ ] furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. [ ] furnished subsequent to the international filing date for the purposes of international search only:

      [ ] in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      [ ] on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. [ ] In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/081351

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MARK H. CHIN ET AL: "Induced Pluripotent Stem Cells and Embryonic Stem Cells Are Distinguished by Gene Expression Signatures", CELL STEM CELL, vol. 5, no. 1, 1 July 2009 (2009-07-01), pages 111-123, XP055013700, ISSN: 1934-5909, DOI: 10.1016/j.stem.2009.06.008 the whole document -----	1-15
X	WO 2010/070059 A1 (UNIV MAASTRICHT [NL]; ACADEMISCH ZIEKENHUIS MAASTRIC [NL]; KLEINJANS J) 24 June 2010 (2010-06-24) page 1, line 8 - line 27; claims 1-2; examples 1-10 ----- -/--	1-15

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 March 2017	06/04/2017

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1

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2014/170436 A1 (INSERM INST NAT DE LA SANTÉ ET DE LA RECH MÉDICALE [FR]; UNIVERSITÉ DE) 23 October 2014 (2014-10-23) claims 1-13; example 1 -----	1-15
X	NEWTON RONALD K ET AL: "The utility of DNA microarrays for characterizing genotoxicity", ENVIRONMENTAL HEALTH PERSPECTIVES, U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES, NATIONAL INSTITUTE OF ENVIRONMENTAL HEALTH SCIENCES, US, vol. 112, no. 4, 1 March 2004 (2004-03-01) , pages 420-422, XP002388886, ISSN: 0091-6765 the whole document -----	1-15
X	LEE MICHAEL ET AL: "cDNA microarray gene expression profiling of hydroxyurea, paclitaxel, and p-anisidine, genotoxic compounds with differing tumorigenicity results", ENVIRONMENTAL AND MOLECULAR MUTAGENESIS, WILEY-LISS, INC. CHICHESTER, GB, vol. 42, no. 2, 1 January 2003 (2003-01-01), pages 91-97, XP002388888, ISSN: 0893-6692, DOI: 10.1002/EM.10177 abstract -----	1-15
X	ALI NOWROUZI ET AL: "Retroviral Vectors: Post Entry Events and Genomic Alterations", VIRUSES, vol. 3, no. 12, 29 December 2011 (2011-12-29), pages 429-455, XP055327182, CH ISSN: 1999-4915, DOI: 10.3390/v3050429 the whole document -----	1-15
X	JULIA D SUERTH ET AL: "Alpharetroviral Self-inactivating Vectors: Long-term Transgene Expression in Murine Hematopoietic Cells and Low Genotoxicity", MOLECULAR THERAPY, vol. 20, no. 5, 14 February 2012 (2012-02-14), pages 1022-1032, XP055327184, GB ISSN: 1525-0016, DOI: 10.1038/mt.2011.309 the whole document -----	1-15
	-/--	

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INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/081351

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MODLICH U ET AL: "Cell-culture assays reveal the importance of retroviral vector design for insertional genotoxicity", BLOOD, AMERICAN SOCIETY OF HEMATOLOGY, US, vol. 108, no. 8, 6 July 2006 (2006-07-06), pages 2545-2553, XP002455802, ISSN: 0006-4971, DOI: 10.1182/BLOOD-2005-08-024976 cited in the application abstract; figure 1; table 2 -----	1-15
X	Eugenio Montini ET AL: "Genotoxicity Assay for Gene Therapy Vectors in Tumor Prone Cdkn2a-/- Mice" In: "METHODS IN ENZYMOLOGY", 1 January 2012 (2012-01-01), ACADEMIC PRESS, US, XP055326107, ISSN: 0076-6879 vol. 507, pages 171-185, DOI: 10.1016/B978-0-12-386509-0.00009-0, Sections 1 and 2.7 -----	1-15
X	SO GUN HONG ET AL: "Assessing the Risks of Genotoxicity in the Therapeutic Development of Induced Pluripotent Stem Cells", MOLECULAR THERAPY, vol. 21, no. 2, 4 December 2012 (2012-12-04), pages 272-281, XP055327237, GB ISSN: 1525-0016, DOI: 10.1038/mt.2012.255 the whole document -----	1-15

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2016/081351

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2010070059 A1	24-06-2010	EP 2199794 A1	23-06-2010
		EP 2359135 A1	24-08-2011
		US 2011250606 A1	13-10-2011
		WO 2010070059 A1	24-06-2010
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