

COMPOSITIONS AND METHODS FOR TREATING, PREVENTING OR REVERSING AGE-ASSOCIATED INFLAMMATION AND DISORDERS

FIELD OF THE INVENTION

[0001] The invention is in the field of medicinal chemistry. In particular, the invention relates to a method for treating, preventing and reversing age-associated inflammation by administering a reverse transcriptase inhibitor (RTI) to a patient in need thereof. The age-associated inflammation may be in a patient having Alzheimer's disease, amyotrophic lateral sclerosis (ALS), Parkinson's disease, Huntington's disease, vision loss, hearing loss, peripheral degenerative diseases, or cardiovascular dysfunction, frontotemporal dementia (FTD), multiple sclerosis (MS), Aicardi Goutiere's syndrome, progressive supra nuclear palsy (PSP), osteoarthritis, skin aging, atherosclerosis, chemotherapy-induced adverse effects, hematopoietic stem cell function, osteoporosis, physical function, and/or pulmonary fibrosis, or in a patient in need of wound healing or tissue regeneration.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] This invention was developed with the following funding: Glenn/AFAR Postdoctoral Fellowship, NIH P20 GM119943 COBRE pilot award; NIH F31 AG043189; NIH T32 AG041688; NIH F31 AG050365; Biotechnology and Sport Medicine Fellowships, School of Pharmacy, University of Bologna, Bologna, Italy; NIH R37 AG016667, R01 AG024353, P01 AG051449, Glenn-AFAR Breakthroughs in Gerontology Award; NIH R01 AG050582, P20 GM109035; NIH R37 AG016694, P01 AG051449.

BACKGROUND OF THE INVENTION

[0003] The number of people living to be 60 years or older is increasing worldwide. Between 2012 and 2050, the proportion of the number of people aged 60 years and over is expected to increase from 809 million to 2 billion (or 11% to 22% of the population).¹ Among the leading causes of death in the elderly are several chronic conditions including heart disease, cancer, diabetes, Alzheimer's disease, and infection. Importantly, many of these age-related diseases and aging itself are closely associated with low-level chronic inflammation.^{2,3,4} Systemic chronic inflammation can accelerate aging.⁵ Indeed, many Inflammatory markers are significant predictors of mortality in older humans.⁶

[0004] Despite this common link between aging, inflammation, and chronic diseases, limited progress has been made to understand the mechanisms that control age-related inflammation, and the causal relationship of these regulators to chronic degenerative diseases

is not completely understood. A better understanding of the role of these regulators in age-related inflammation should lead to new strategies for extending the health of the older population.

[0005] As such, there is a need in the art for better treatment and prevention of age-related inflammation and age-related disorders.

BRIEF SUMMARY OF THE INVENTION

[0006] The present invention provides a better understanding of the mechanisms underlying age-related inflammation and its role in the aging, as well as compositions and methods for preventing and reducing age-associated inflammation and disorders.

[0007] Retrotransposable elements (RTEs) are deleterious at multiple levels, and failure of host surveillance systems can thus have negative consequences. However, the contribution of RTE activity to aging and age-associated diseases was not known. The present invention is based on several empirical observations including that, during cellular senescence, LINE-1 (L1) elements become transcriptionally upregulated and activate a type-I interferon (IFN-I) response. The IFN-I response is a novel phenotype of late senescence and contributes to the maintenance of the senescence associated secretory phenotype (SASP). The IFN-I response is triggered by cytoplasmic L1 cDNA and is antagonized by reverse transcriptase inhibitors (RTIs) that inhibit the L1 reverse transcriptase (RT). Treatment of aged mice with the RTI lamivudine downregulated IFN-I activation and age-associated inflammation in several tissues. As such, RTE activation is an important component of sterile inflammation that is a hallmark of aging, and L1 RT is a relevant target for the treatment of age-associated disorders.

[0008] The present invention provides a method for treating, preventing and/or reversing age-associated inflammation in a patient in need thereof by administering a therapeutically-effective amount of at least one reverse transcriptase inhibitor (RTI) to the patient.

[0009] In a comparative assessment of several RTI drugs in a dose-response assay of the inhibition of L1 activity, two RTI drugs, censavudine and elvucitabine, displayed unexpected superior ability to inhibit mouse and human L1 activity. The present invention further provides a method for treating, preventing and/or reversing age-associated inflammation in a patient in need thereof by administering a therapeutically-effective amount of censavudine and/or elvucitabine to the patient.

[0010] The age-associated inflammation is associated with an upregulation of L1, an accumulation of cytoplasmic L1 cDNA, an activation of an IFN-I response, and/or a reinforcement of a SASP pro-inflammatory state. The RTI drug is administered in an amount

sufficient to prevent or reverse at least one of the upregulation of L1, the accumulation of cytoplasmic L1 cDNA, the activation of the IFN-I response, and/or the SASP pro-inflammatory state.

[0011] The age-associated inflammation that can be prevented, treated, or reversed with the methods of the present invention is in a patient having a disease or disorder including, but not limited to: Alzheimer's disease, amyotrophic lateral sclerosis (ALS), Parkinson's disease, Huntington's disease, vision loss, hearing loss, peripheral degenerative diseases, or cardiovascular dysfunction, frontotemporal dementia (FTD), multiple sclerosis (MS), Aicardi Goutiere's syndrome, progressive supra nuclear palsy (PSP), osteoarthritis, skin aging, atherosclerosis, chemotherapy-induced adverse effects, hematopoietic stem cell function, osteoporosis, physical function, and/or pulmonary fibrosis, or in a patient in need of wound healing or tissue regeneration. In one embodiment, the age-associated inflammation is in a patient having Alzheimer's disease. In an alternate embodiment, the age-associated inflammation is in a patient having ALS.

[0012] Also provided is a method for delaying or reversing the progression of the underlying pathology of disease disorder caused by age-associated inflammation, comprising administering to a patient in need thereof a therapeutically effective amount of at least one RTI. In some embodiments, the patient has Alzheimer's disease or ALS and experiences a decrease in one or more symptoms of Alzheimer's disease or ALS compared to before the first administration of the RTI to the patient. In some embodiments, the one or more symptoms of Alzheimer's disease comprise memory loss, misplacing items, forgetting the names of places or objects, repeating questions, being less flexible, confusion, disorientation, obsessive behavior, compulsive behavior, delusions, aphasia, disturbed sleep, mood swings, depression, anxiety, frustration, agitation, difficulty in performing spatial tasks, agnosia, difficulty with ambulation, weight loss, loss of speech, loss of short term memory or loss of long term memory.

[0013] In some embodiments, the decrease in the one or more symptoms of Alzheimer's disease is evaluated according to the DSM-5.⁷ In some embodiments, the decrease of symptoms is determined using the cognitive subscale of the Alzheimer's Disease Assessment Scale (ADAS-cog). In some embodiments, the decrease of symptoms is determined using the Clinician's Interview-Based Impression of Change (CIBIC-plus). In some embodiments, the decrease of symptoms is determined using the Activities of Daily Living (ADL) scale. In some embodiments, the decrease of symptoms is for 1-36 months.

[0014] In some embodiments, any change in the underlying pathology is identified by detection of a biomarker before and after the RTI administration. In some embodiments, the

biomarker is β -amyloid or Tau protein. In some embodiments, the biomarker is detected by PET imaging. In some embodiments, the underlying pathology is identified by measurement of β -amyloid or Tau protein in the cerebrospinal fluid. In some embodiments, the underlying pathology is identified by measurement of brain volume before and after the RTI administration. In some embodiments, the underlying pathology is reversed or delayed for at 1-36 months.

[0015] In some embodiments, the at least one RTI is a nucleoside reverse transcriptase inhibitor (NRTI). In some embodiments, the at least one NRTI is selected from: abacavir (ZIAGENTM), abacavir/lamivudine (Epzicom), abacavir/lamivudine/zidovudine (TRIZIVIRTM), adefovir, alovedine, amdoxovir, apricitabine, ATRIPLA[®], BARACLUDE[®], BIKTARVY[®], censavudine, COVIRACILTM, DAPD/DXG, D-D4FC, dexelvucitabine, didanosine (VIDEXTM), didanosine extended-release (Videx EC), dOTC, EFdA, emtricitabine (EMTRIVATM), emtricitabine/tenofovir alafenamide (DESCOVY[®]), emtricitabine/tenofovir disoproxil fumarate (TRUVADA[®]), elvucitabine, fosavudine, lamivudine/zidovudine (COMBIVIRTM), EVIPLERATM, GENVOYA[®], HIVIDTM, KIVEXATM, lamivudine (EPIVIRTM), LODENOSINETM, ODEFSEY[®], PREVEON[®], racivir, stampidine, stavudine (ZERITTM), STRIBILD[®], TENOFOVIRTM, tenofovir disoproxil fumarate (VIREADTM), TRIUMEQ[®], Trizivir, VEMLIDY[®], and/or zidovudine (RETROVIRTM). In some embodiments, the at least one NRTI is censavudine. In some embodiments, the at least one NRTI is elvucitabine.

[0016] In some embodiments, the at least one RTI is a non-nucleoside reverse transcriptase inhibitor (NNRTI). In some embodiments, the at least one NNRTI is selected from: Delavirdine (DLV), Efavirenz (EFV), Etravirine Nevirapine (NVP), and/or Rilpivirine.

[0017] In some embodiments, the patient has Alzheimer's disease and the method further comprises administering at least one second therapeutic agent useful for the treatment of the symptoms of Alzheimer's disease. In some embodiments, the at least one second therapeutic agent is selected from: donepezil, galantamine, memantine, and/or rivastigmine. In some embodiments, the at least one second therapeutic agent is an antibody that binds to β -amyloid or Tau protein. In some embodiments, the antibody binds to β -amyloid and is bapineuzumab. In some embodiments, the antibody binds to Tau protein and is ABBV-8E12. In some embodiments, the at least one second therapeutic agent is a vaccine against β -amyloid or Tau protein. In some embodiments, the at least one second therapeutic agent is an agent that reduces or alters the brain content of β -amyloid or Tau. In some embodiments, the second therapeutic agent reduces or alters the brain content of β -amyloid and is a β -secretase 1 (BACE) inhibitor. In some embodiments, the BACE inhibitor is selected from: CTS-21166,

lanabecestat (AZD3293), LY2886721, and verubecestat (MK-8931). In some embodiments, the second agent reduces or alters the brain content of Tau and is nicotinamide, or MPT0G211.

[0018] In some embodiments, the patient has ALS and the method further comprises administering at least one second therapeutic agent useful for the treatment of the symptoms of ALS. In some embodiments, the at least one second agent useful for the treatment of ALS is edaravone and/or riluzole. In other embodiments, the at least one second agent is an integrase inhibitor. In some embodiments, the integrase inhibitor is selected from: aurointricarboxylic acid, derivatives of aurointricarboxylic acid, BMS-538158, caffeic acid phenethyl ester, derivatives of caffeic acid phenethyl ester, curcumin, derivatives of curcumin, chicoric acid, derivatives of chicoric acid, 3,5-dicaffeoylquinic acid, derivatives of 3,5-dicaffeoylquinic acid, GSK364735C, L-870812, and L-25 870810, MK-0518, quercetin, derivatives of quercetin, raltegravir, S-1360, tyrphostin, derivatives of tyrphostin, and/or zintevir (AR-177).

[0019] In some embodiments, the patient is evaluated for one or more symptoms or disease pathology for 1-36 months after the first administration to the patient of the RTI.

[0020] In some embodiments, the RTI inhibits L1 reverse transcriptase activity in a cell of the patient.

[0021] Also provided is a method for preventing the onset of Alzheimer's disease in a patient suspected of having mild cognitive impairment or preclinical Alzheimer's disease, comprising administering a therapeutically effective amount of at least one RTI to a patient in need thereof.

[0022] Other implementations are also described and recited herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023] For the purpose of illustration, certain embodiments of the present invention are shown in the drawings described below. Like numerals in the drawings indicate like elements throughout. It should be understood, however, that the invention is not limited to the precise arrangements, dimensions, and instruments shown. In the drawings:

[0024] **FIG. 1** shows the activation of L1, IFN-I and SASP in senescent cells. Gene expression was assessed by RT-qPCR. Poly(A)-purified RNA was used in all L1 assays. **FIG. 1a**, Time course of L1 activation. P values were calculated relative to EP, early passage control. **FIG. 1b**, Schematic of L1 RT-PCR strategy. Blue, sense; red, antisense (AS). For primer specificity, see **FIG. 6f-h**; for primer design, see **Methods**. Primers for amplicon F were used in (a) and (e). **FIG. 1c**, Strand-specific L1 transcription was assessed using amplicons A-F. Transcription from the 5'UTR antisense promoter was also detected. SEN (L), late

senescence (16 weeks). **FIG. 1d**, Induction of *IFN- α* and *IFN- β 1* mRNA levels. **FIG. 1e**, The temporal induction of genes associated with DNA damage (*p21*, also known as *CDKN1A*), SASP (*IL-1 β* , *CCL2*, *IL-6*, *MMP3*), and the IFN-I response (*IRF7*, *IFN- α* , *IFN- β 1*, *OAS1*). Row clustering was calculated as 1-Pearson correlation. RS, replicative senescence; OIS, oncogene induced senescence (elicited by Ha-RAS infection); SIPS, stress induced premature senescence (gamma irradiation). Controls: EP, early passage; EV, empty vector infected; CTR, non-irradiated. (**a**, **c-e**), $n = 3$ independent biological samples, repeated in two independent experiments. (**a**, **c**, **d**) Data are mean $\pm$ s.d. $*P \leq 0.05$, $**P \leq 0.01$, unpaired two-sided *t*-tests.

[0025] **FIG. 2** shows the regulation of L1 activation and IFN-I induction. **FIG. 2a**, Expression and ChIP of RB1 and **FIG. 2b**, FOXA1. Expression was measured by RT-qPCR and immunoblotting (left panels). Binding to L1 elements was assessed with ChIP-qPCR (right panels). For primer specificity, see **FIG. 6b** RB1: 5'UTR, ORF1 and ORF2, primers for amplicons A, E and F, respectively. FOXA1: primers for amplicons A-E. qPCR was normalized to input chromatin. SEN (E), early senescence (8 weeks). For gel source, data see **FIG. 16**. **FIG. 2c-e**, RB1, FOXA1 or TREX1 were overexpressed (OE) or ablated with shRNAs and the effects on expression of L1, IFN- α and IFN- β 1 were determined by RT-qPCR of poly(A)-purified RNA. In all cases, lentiviral vectors were used to deliver the interventions directly into senescent cells at 12 weeks (point D, **FIG. 6a**), and cells were harvested for analysis four weeks later (point E, 16 weeks). Controls were uninfected senescent cells harvested at the same time (point E, 16 weeks). Two distinct shRNAs (a, b) were used for each gene. Primers for amplicon F were used for L1. **FIG. 2f**, RB1 was overexpressed as above and its binding to the 5'UTR was assessed by ChIP-qPCR (amplicon A). **FIG. 2g**, Activation of L1, IFN- α and IFN- β 1 expression after the triple (3X) intervention using shRB1 (a), shTREX1 (a) and FOXA1-OE in early passage cells. Lentiviral infections were performed sequentially with drug selections at each step (shRB1, puromycin $\rightarrow$ shTREX1, hygromycin $\rightarrow$ FOXA1-OE, blasticidin). **FIG. 2h**, Expression of IFN-I pathway genes was determined with the RT2 Profiler PCR array (Qiagen). Normalized mean expression is shown for all 84 genes in the array. Red symbols: significantly upregulated genes. Dashed lines demarcate the ± 2 -fold range. (**a**, **b**, **h**), $n = 3$ independent biological samples, repeated in 2 independent experiments. (**c-g**), $n = 3$ independent experiments. (**a-g**) Data are mean $\pm$ s.d. $*P \leq 0.05$, $**P \leq 0.01$, unpaired two-sided *t*-tests.

[0026] **FIG. 3** shows that the ablation of L1 relieves IFN-I activation and blunts the SASP response. **FIG. 3a**, Cells were examined by immunofluorescence (IF) microscopy using antibodies to single-stranded DNA (ssDNA) or L1 ORF1 protein. Note the bright ssDNA puncta in senescent cells that colocalized with prominent puncta of ORF1. The experiment was

independently repeated 3 times with similar results. Scale bar = 10 μ m. **FIG. 3b**, Senescent cells were treated with L1 shRNAs (using lentiviral vectors as described in **FIG. 2c, e, f**) or with 3TC (7.5 μ M) between 12 and 16 weeks of senescence. Effects on the IFN-I response were determined by RT-qPCR, ELISA or immunoblotting. For gel source data, see **FIG. 16**. **FIG. 3c**, Cells were labeled with BrdU for 2 weeks (with or without 7.5 μ M 3TC), labeled DNA was immunoprecipitated, and its L1 sequence content was quantified using a TaqMan multiplex qPCR assay¹⁶ (**FIG. 1b**, amplicon F). EP (qui), early passage quiescent cells. **FIG. 3d**, Left panel, RS cells: *IFNAR1* and *IFNAR2* genes were mutagenized using the CRISPR/Cas9 system delivered with lentivirus vectors directly into senescent cells. As with shRNA interventions, cells were infected at 12 weeks and harvested at 16 weeks of senescence (see **FIG. 1d-f**, see **Methods**). Right panel, SIPS cells: CRISPR/Cas9 intervention was performed in early passage cells and a validated clone was irradiated to induce SIPS. **FIG. 3e**, OIS and SIPS were induced as in Fig. 1d and cells were harvested 20 days (OIS) or 30 days (SIPS) later. 3TC (7.5 μ M) was present throughout. IFN-I gene expression (*IFN- α* , *IRF7*, *OAS1*) was measured by RT-qPCR. **FIG. 3f**, Cells were serially passaged into replicative senescence (RS) with 3TC (10 μ M) present throughout, and the temporal induction of SASP response genes (*IL-1 β* , *CCL2*, *IL-6*, *MMP3*) was assessed. (**b-d, f**), n = 3 independent experiments. (**e**) n = 3 independent biological samples, repeated in 2 independent experiments. (**b-f**) Data are mean $\pm$ s.d. * $P \leq 0.05$, ** $P \leq 0.01$. (**b, d-f**) unpaired two-sided *t*-tests, (**c**) 1-way ANOVA with Tukey's multiple comparisons test.

[0027] **FIG. 4** shows that L1s are activated with age in murine tissues and the IFN-I proinflammatory response is relieved by RTI treatment. **FIG. 4a**, Presence of L1 Orf1 protein in tissues was examined by IF microscopy. Quantification of ORF1 expressing cells is shown in the right panel; three animals and at least 200 cells per animal were scored for each condition. Scale bar = 4 μ m. **FIG. 4b**, Activation of L1 in senescent cells was examined by co-staining for SA- β -Gal activity and Orf1 protein by IF (male liver, 5 and 26 months). Scale bar = 4 μ m. The experiment was repeated three times independently with similar results. **FIG. 4c**, Mice were administered 3TC (2 mg/ml) in drinking water at the indicated ages for two weeks and sacrificed after treatment. Expression of p16, an IFN-I response gene (*IFN- α*), and a marker of a proinflammatory state (*IL-6*) were assessed by RT-qPCR. See **FIG. 14** for additional tissues and genes. The box plots show the range of the data (whiskers), 25th and 75 percentiles (box), means (dashed line), and medians (solid line). Each point represents one animal. 5 months, n = 8; 26 months, n = 12; 29 months, n = 6. **FIG. 4d**, Six-month-old mice were non-lethally irradiated and expression of L1, p16 and representative IFN-I response genes (*Ifn- α* , *Oas1*)

were assessed by RT-qPCR at the indicated times post-irradiation. Graphical presentation is as in (c); non-irradiated, n = 3 animals at 3 months, n = 5 animals at 6 months; irradiated, n = 4 animals at 3 months, n = 5 animals at 6 months. **FIG. 4e**, Macrophage infiltration into white adipose tissue and kidney was scored as F4/80 positive cells (% of total nuclei). n = 5 animals group (adipose); n = 8 (kidney). Skeletal muscle fiber diameter was measured (see **Methods** for details) and plotted as an aggregate box plot. n = 5 animals per group, 500 fibers total. Glomerulosclerosis was scored in periodic acid-Shiff (PAS)-stained sections (see **Methods** for details) as the sum of all glomeruli with a score of 3 or 4 divided by the total. n = 7 animals per group, 40 glomeruli per animal. Graphical presentation is as in (c). 3TC treatment was 2 weeks for white adipose and 6 months (20-26 months) for other tissues. Dashed circle demarcates a single glomerulus. Scale bar = 50 μ m. **FIG. 4f**, Breakdown of L1 surveillance mechanisms leads to chronic activation of the IFN-I response. ISD: interferon-stimulatory DNA pathway. * $P \leq 0.05$, ** $P \leq 0.01$, unpaired two-sided *t*-tests (**a**, **d**, **e**) or 1-way ANOVA with Tukey's multiple comparisons test (**c**, **e** white adipose).

[0028] **FIG. 5** is a flow chart outlining the molecular pathway of cellular senescence leading to age-associated, "sterile" inflammation.

[0029] **FIG. 6** shows the establishment of senescent cultures and analysis of L1 and IFN-I activation. **FIG. 6a**, Passaging regimen to obtain long-term replicatively senescent cells (details in **Methods**). Point A was designated as zero for time in senescence. **FIG. 6b-d**, Confirmation of the senescent status of cultures. A representative experiment is shown; other experiments were monitored in the same manner and generated data that met these benchmarks. EP, early passage control; SEN (E), early senescence (8 weeks); SEN (L), late senescence (16 weeks). **FIG. 6b**, Cells were labeled with BrdU for 6 hours. BrdU incorporation⁸ and senescence-associated β -galactosidase (SA- β -Gal) activity⁹ were determined as indicated. DNA damage foci were visualized using γ -H2AX antibodies and immunofluorescence microscopy (IF).¹⁰ **FIG. 6c**, Expression of p21 (CDKN1A) and p16 (CDKN2A) proteins was determined by immunoblotting. GAPDH was the loading control. For gel source data, see **FIG. 16**. **FIG. 6d**, Expression of genes characteristic of the SASP was determined by RT-qPCR. **FIG. 6e**, L1 activation during senescence of IMR-90 and WI-38 strains of fibroblasts was assessed by RT-qPCR using poly(A) purified RNA and primers for amplicon F (**FIG. 1b**). **FIG. 6f**, Long-range RT-PCR was performed with primers A-forward and C-reverse (amplicon G) and primers A-forward and D-reverse (amplicon H) (**FIG. 1b**, **Table 1**) and the cDNAs were cloned and sequenced. Several attempts using the same protocol on early passage proliferating cells did not yield any L1 clones. Sequences were mapped to the

unmasked reference genome demanding 100% identify. 658 clones could be thus mapped, 51 additional clones contained at least 1 mismatch and thus likely represent elements that are polymorphic in the cell line, and 58 were cloning artifacts. Among the 658 mappable clones 224 unique elements were represented (**Table 3**). Intact elements are the subset of full-length elements annotated with no ORF inactivating mutations. Size of the features corresponds to the number of times the element was represented among the 658 clones. **FIG. 6g**, Summary of long-range PCR data presented in **FIG. 6f** and **Table 3**. **FIG. 6h**, Apparent genomic copy numbers of elements detected with our amplicons (see **FIG. 1b** for locations of amplicons and **Methods** for primer design strategy). Predicted: *in silico* PCR (see **Methods** for details). Observed: qPCR was performed on 1 ng of genomic DNA and normalized to a known single copy locus. **FIG. 6i**, Activation of *IFN- α* and *IFN- β 1* genes during senescence of WI-38 and IMR-90 cells was determined by RT-qPCR. **FIG. 6j**, Confirmation of the senescent status of cells in OIS (20 days, **FIG. 6e**) and SIPS (30 days, **FIG. 6e**) by SA- β -Gal activity. EV, empty vector control; CTR, non-irradiated cells. **FIG. 6k**, Confirmation of full length L1 mRNA expression in all forms of senescence using RT-qPCR with primers for amplicons A and F on poly(A)-purified RNA. Late onset activation is shown by comparing days 9 and 20 for OIS and days 12 and 30 for SIPS. (**b-e, i-k**), $n = 3$ independent biological samples, repeated in 2 independent experiments. Data are mean $\pm$ s.d. $*P \leq 0.05$, $**P \leq 0.01$, unpaired two-sided *t*-tests.

[0030] **FIG. 7** shows the mapping of transcriptional start sites in L1 elements activated during cellular senescence. 5'RACE was performed with primers C and D (**FIG. 1a, Table 1**) on late senescent cells (16 weeks, point D in **FIG. 6a**), the products were cloned, and individual clones were Sanger sequenced (see **Methods** for details). **FIG. 7a**, A multiple sequence alignment of the 50 mappable clones against the L1HS consensus was generated with MAFFT software. The L1HS consensus is shown on top. Blue color shading of the aligned clones shows their degree of identity with the consensus. The green vertical line marks the start (position 1) of the L1HS consensus. Red vertical lines mark short gaps (1-4 nucleotides) opened in the L1HS consensus by individual clones. The consensus of the 50 clones is shown at the bottom and was generated with Jalview. The initiation of L1 transcription is known to be imprecise, with the majority of start sites occurring ± 50 bp of the consensus start site, and a subset as far down as +180 bp.¹¹ **FIG. 7b**, Summary of the mapping data and classification of clones to families of L1 elements. The relative start sites were calculated relative to the L1HS consensus start site. RepEnrich software¹² was used to assign the clones to L1 families.

[0031] **FIG. 8** shows the evolution of transcriptomic changes during progression of cellular senescence. RNA-seq was performed on early proliferating LF1 cells (EP) and cultures at 8 weeks (SEN-E) and 16 weeks (SEN-L) in senescence (points C and D, respectively, in Extended Data **FIG. 6a**). Data were analyzed using a 3-way comparison: EP versus SEN-E, EP versus SEN-L and SEN-E versus SEN-L (see **Methods** for details). **FIG. 8a**, Area-proportional generalized Venn diagrams depicting the intersections of the three comparisons for the following datasets. **i-ii**, significantly upregulated and downregulated genes (row 2x in panel b). **iii-iv**, significant KEGG pathways identified by GSEA. Note the considerable evolution the transcriptome in late senescence, exemplified by large changes (especially upregulated) in differentially expressed genes as well as pathways. **v-vi**, significantly changing genes in the IFN-I and SASP gene sets (see **Table 4** for annotation of gene sets). Note that the majority of changes in SASP genes occur early, whereas a large component of IFN-I changes is specific for late senescence. **FIG. 8b**, Summary of significantly changing genes using a fixed FDR (<0.05) and variable fold-change cutoffs (2x, 1.75x and 1.5x). **FIG. 8c**, GSEA analysis of KEGG pathways. Heatmap representation shows significantly upregulated pathways in red (also see panel e) and downregulated pathways in blue. Non-significant comparisons are shown in black; vertical annotations refer to Venn diagrams in (a, iii-iv). Note that the SASP gene set is upregulated early whereas the IFN-I gene set is upregulated late. **FIG. 8d**, Heatmaps of significantly changing genes in the IFN-I and SASP gene sets. Vertical annotations refer to Venn diagrams in (a, v-vi). **FIG. 8e**, List of significantly upregulated KEGG pathways identified using GSEA (see **Table 5** for a list of all pathways). NES, normalized enrichment scores. IFN-I and SASP gene sets are highlighted in yellow. Note the significant upregulation of IFN-I between early and late senescence. Red type identifies KEGG pathways indicative of cytosolic DNA sensing and a type I interferon response at late times. **FIG. 8f-g**, GSEA profiles of the IFN-I and SASP genesets for all comparisons; FDR is highlighted in yellow. Note that the upregulation of IFN-I is significant for EP_SEN-L and SEN-E_SEN-L but not for EP_SEN-E, and that the upregulation of SASP is significant for EP_SEN-E and EP_SEN-L but not SEN-E_SEN-L. $n = 3$ independent biological samples. Differential expression data were analyzed for significance using the GSEA GenePattern interface and the outputs were corrected for multiple comparisons by adjusting the nominal p values using the Benjamini-Hochberg method (see **Methods** for details).

[0032] **FIG. 9** shows the characterization of L1 effectors and the IFN-I response. **FIG. 9a**, Expression of TREX1 was determined by RT-qPCR and immunoblotting. For gel source data, see **FIG. 16**. **FIG. 9b**, Expression of RB family genes were compared by RT-

qPCR. Primer pairs for all genes were verified to be of equivalent efficiency. **FIG. 9c**, Enrichment of H3K9me3 and H3K27me3 on L1 elements was examined by ChIP-qPCR (PCR primers illustrated in **FIG. 1b** were used: 5'UTR, amplicon A; ORF1, amplicon E; ORF2, amplicon F). **FIG. 9d**, ChIP-seq data from ENCODE were investigated for transcription factors that bind to the L1 consensus sequence. The log₂ fold change enrichment relative to input controls is shown for the indicated cell-lines. The binding of YY1 to the L1 promoter has been documented¹³ and was used as a positive control. CEBPB was used as a negative control. A schematic illustrating L1 coordinates and relevant features is shown above. Amplicons A-E are the same as shown in **FIG. 1b**. **FIG. 9e**, Transcriptional activity of the intact L1 5'UTR or a UTR lacking the FOXA1 binding site (UTR-Δ) was determined using sense and antisense reporters cotransfected into early passage LF1 cells either with a FOXA1 expression plasmid or empty vector (EV). **FIG. 9f**, FOXA1 was knocked down in senescent cells with shFOXA1 (a) (see also **FIG. 2e** and **FIG. 10a**) and binding to the L1 5'UTR (amplicon B) was determined by ChIP-qPCR. **FIG. 9g**, Knockdown of RB1, TREX1 and ectopic expression of FOXA1 were performed in early passage cells in all single (1X), double (2X) and triple (3X) combinations and assessed by RT-qPCR using poly(A)-purified RNA for activation of L1, *IFN-α* and *IFN-β1* expression (primers for amplicon F). Three controls are shown: cells infected with irrelevant shRNA (shGFP), expression construct (LacZ), or uninfected early passage cells (EP). **FIG. 9h**, L1 5'UTR occupancy of RB1 and FOXA1 in 3X cells was determined by ChIP-qPCR performed as in **FIG. 2a, b**. Primers for amplicons A and B were used for *RB1* and *FOXA1*, respectively. For comparison, single interventions in early passage cells with shRB1 (a) or *FOXA1* cDNA expression (EP FOXA1-OE) are also shown. **FIG. 9i**, Confirmation of full length L1 mRNA expression in 3X cells using RT-qPCR with primers for amplicons A and F on poly(A)-purified RNA. CTR, cells infected with irrelevant shRNA (shGFP). **FIG. 9j**, Heat map representation showing all biological replicates for the 67 genes significantly changing expression in SEN and/or 3X cells (**FIG. 2h, Table 6**). Column clustering was calculated as 1-Pearson correlation. Rows have been grouped into functional subsets of the IFN-I response. **FIG. 9k**, Venn diagram showing the overlap between the 67 significantly changing genes. (a-f, h) n = 3 independent biological samples, repeated in two independent experiments. (g, i), n = 3 independent experiments. (a-i) Data are mean ± s.d. *P ≤ 0.05, **P ≤ 0.01, unpaired two-sided t-tests.

[0033] **FIG. 10** shows the efficacy of genetic and pharmacological interventions. **FIG. 10a**, Knockdowns with two distinct shRNAs (a, b) or **FIG. 10b**, ectopic cDNA expression were performed in senescent cells as described in **FIG. 2d, e, g** (also see **Methods**). The effectiveness of these manipulations on their targets was assessed by RT-qPCR and

immunoblotting. For gel source data see **FIG. 16**. **FIG. 10c**, RB1, TREX1 and FOXA1 mRNA and protein expression after the triple (3X) intervention (**FIG. 2f**). **FIG. 10d**, The effect of 3TC treatment on the relative abundance of L1HS sequences in senescent cells was determined by multiplex TaqMan qPCR on total DNA (primer set 6, **Table 1**). SEN entry, 0 weeks in senescence (**FIG. 1a**; point A in **FIG. 6a**). 3TC was administered continuously from SEN entry until harvest 16 weeks later. **FIG. 10e**, The dual luciferase L1 reporter system¹⁴ was used to determine the effect of 3TC dosing on retrotransposition. L1 reporters were introduced into early passage cells using lentivirus vectors (see **Methods** for details) and cells were treated with 3TC for 4 days prior to harvest and assay. JM111, a defective reporter carrying mutations in ORF1 (absence of 3TC); L1RP, a retrotransposition competent reporter. **FIG. 10f**, The effect of 3TC dosing on the IFN-I response. The experiment above (d) was processed by RT-qPCR to determine the expression of IFN- α and IFN- β 1. **FIG. 10g**, Knockdowns of L1 were performed with two distinct shRNAs (a, b) in senescent cells (as in **FIG. 2d, e, g**) or 3X cells (as in **FIG. 2g**). The effectiveness on L1 expression was assessed by RT-qPCR using poly(A)-purified RNA and primers F. **FIG. 10h**, Cells in the experiment in (g) were examined for levels of ORF1 protein by immunofluorescence (IF). Image analysis was performed with CellProfiler software (see **Methods** for details). >200 cells were examined for each condition (a.f.u., arbitrary fluorescence units). **FIG. 10i**, The L1 shRNA treatment in the experiment in (g) was substituted with 3TC treatment (10 μ M) for the same period of time. **FIG. 10j**, Five different RTIs (or combinations) were tested for effects on the IFN-I response. AZT (Zidovudine, 15 μ M), ABC (Abacavir, 15 μ M), FTC (Emtricitabine, 10 μ M), 3TC (aka Lamivudine or EpiVir, 10 μ M), TZV (Trizivir, a combination of 15 μ M AZT, 15 μ M ABC and 7.5 μ M 3TC). Cells were treated for 4 weeks between 12 and 16 weeks in senescence (**FIG. 1a**; points D and E in **FIG. 1a**). 3X cells (**FIG. 2f**) were treated with 3TC for 48 hours after the completion of the last drug selection. IFN- α expression was determined by RT-qPCR. **FIG. 10k**, A native L1 reporter (pLD143)¹⁵ was co-transfected with shRNA plasmid vectors into HeLa cells (see **Methods** for details). Retrotransposition was scored as GFP-positive cells, and shL1 knockdowns were normalized to a shLuc negative control. The absolute average retrotransposition frequency (percentage of GFP-positive cells) was 4.1, which matches the published values for the reporter used (pLD143)⁵³. **FIG. 10l**, Knockdowns of cGAS and STING were performed in senescent or 3X cells as with the other shRNAs (**FIG. 2d, e, g** and **a, g** above). **FIG. 10m**, Downregulation of interferon signaling after CRISPR-mediated inactivation of *IFNAR1* and *IFNAR2* genes was verified by the absence of IRF9 nuclear translocation and STAT2 phosphorylation in response to interferon stimulation. Cells were infected with lentivirus vectors expressing Cas9 and

gRNAs to both *IFNAR1* and *IFNAR2* (Δ IFNAR, see **Methods**). After the infection cells were re-seeded on coverslips, treated with interferon for 2 hours, and examined by IF microscopy. The experiment was repeated 3 times with similar results. (**a-i, l**) $n = 3$ independent experiments. (**k**) $n = 3$ independent biological samples, repeated in 2 independent experiments. (**a-l**) Data are mean $\pm$ s.d. $*P \leq 0.05$, $**P \leq 0.01$, unpaired two-sided t -tests.

[0034] **FIG. 11** shows the characterization of cytoplasmic DNA in senescent cells. **FIG. 11a**, Quiescent and senescent cells were treated with BrdU as in **FIG. 3a** and the cellular localization of BrdU incorporation was visualized by IF microscopy. Proliferating cells, EP(Prol), are shown as a positive control for nuclear BrdU incorporation. The signals were quantified using CellProfiler software (right panel, see **Methods**). >200 cells were examined for each condition (a.f.u., arbitrary fluorescence units). **FIG. 11b**, Senescent (and EP control) cells (neither labeled with BrdU) were fractionated into nuclear and cytoplasmic fractions, and the representation of L1 sequences in these compartments (as well as whole cells) was assessed with qPCR as in **FIG. 3a** (TaqMan multiplex qPCR assay¹⁶, amplicon F, **FIG. 1b**). Note that the Y axis units differ by 10-fold between the left and right panels. **FIG. 11c**, Cells were examined by IF microscopy for the presence of ORF1 protein, RNA-DNA hybrids, and single-stranded DNA (ssDNA). See **Methods** and **Table 2** for antibodies. The RNA-DNA signal in senescent cells largely colocalized with the ORF1 signal and was lost after RNase A treatment. The ssDNA signal also colocalized with the ORF1 signal and was exposed by RNase treatment. The experiment was repeated three times with similar results. **FIG. 11d**, The pulled-down BrdU-containing DNA (**FIG. 3c**, panel (a) above, see **Methods**) was cloned and Sanger sequenced. Of the 96 total clones examined, 37 mapped to L1. Red boxes represent the relative positions of these clones on the L1 consensus sequence. **FIG. 11e**, Senescent cells labeled with BrdU (**FIG. 3c**, panel (a) above) were immunoprecipitated with anti-BrdU antibodies, and the representation of L1 sequences in the pulled-down DNA was assessed using qPCR with primers spanning the entirety of L1 elements (**FIG. 1b, c**). **FIG. 11f**, Senescent cells were treated with L1 shRNA (using lentiviral vectors as described in **FIG. 10g**) between 12 and 16 weeks of senescence, and expression of SASP genes was determined. **FIG. 11g**, Transcription throughout murine L1 elements was assessed in a strand-specific manner using the same strategy as was applied to human L1 elements (**FIG. 1b,c**). The amplicons (designated W-Z to distinguish them from the human-specific primers) correspond to the 5'UTR (W), Orf1 (X), Orf2 (Y) and 3'UTR (Z). Also see **Methods** and **Table 1** for primer sequences (primer sets 37, 48-50). Poly(A) RNA was prepared from male white adipose tissue. A total of 12 animals were assessed (3 pools of 4 animals each) in three independent experiments. **FIG. 11h**, Expression

of the three currently active families of murine L1 elements. Primers were designed to distinguishing 5'UTR polymorphisms of the MdA, MdN and Tf families (see **Methods, Table 1** primer sets 51-53). RT-qPCR was performed as in (f) above (non-strand-specific). (**a, b, e**) $n = 3$ independent biological samples, repeated in two independent experiments. (**f**), $n = 3$ independent experiments. (**a, e-h**) Data are mean $\pm$ s.d. $*P \leq 0.05$, $**P \leq 0.01$. (**a**) 1-way ANOVA with Tukey's multiple comparisons test, (**b, e-h**) unpaired two-sided t -tests.

[0035] **FIG. 12** shows the effects of ablating L1 activation, the cytoplasmic DNA sensing pathway, or interferon signaling on expression of the IFN-I and SASP responses. **FIG. 12a**, 3X cells were treated with L1 shRNA or with 3TC for 48 hours as described in **FIG. 10g,i**. Effects on the IFN-I response were determined by RT-qPCR, ELISA or immunoblotting. For gel source data, see **FIG. 16**. **FIG. 12b**, Cells were serially passaged into replicative senescence (RS) with 3TC (10 μ M) present throughout as in **FIG. 3f**, and expression of Cdk inhibitors p21 and p16 was assessed by RT-qPCR. **FIG. 12c**, Senescent cells were treated with shRNAs against *cGAS* or *STING* between 12 and 16 weeks of senescence (as described in **FIG. 10l**), and expression of IFN-I response genes (*IFN- α* , *IRF7*, *OAS1*) was determined. **FIG. 12d**, *cGAS* and *STING* knockdowns were performed with shRNAs in 3X cells (as in panel (c) above), and expression of IFN-I genes was examined by RT-qPCR. **FIG. 12e**, *cGAS* and *STING* were knocked down in senescent cells with shRNAs (as in panel (c) above) and expression of SASP response genes (*IL-1 β* , *CCL2*, *IL-6*, *MMP3*) was assayed by RT-qPCR. **FIG. 12f, g**, The activity of K-9 was compared with 3TC in senescent and 3X cells. Senescent cultures were treated between 12 and 16 weeks (as in **FIG. 3b**) and 3X cultures for 48 hrs (as in panel (a) above). Effects on the expression of IFN-I genes (*IFN- α* , *IRF7*, *OAS1*) and SASP genes (*IL-1 β* , *IL-6*, *MMP3*) was assessed by RT-qPCR. (**a-g**), $n = 3$ independent experiments. (**a-g**) Data are mean $\pm$ s.d. $*P \leq 0.05$, $**P \leq 0.01$, unpaired two-sided t -tests.

[0036] **FIG. 13** shows the assessment of p16, L1 ORF1 and pSTAT1 expression in senescent cells and skin specimens from aged humans. **FIG. 13a**, Immunofluorescence (IF) detection of p16 and ORF1 in early passage, 3X and senescent cells. **FIG. 13b**, Representative images of combinatorial ORF1 and p16 or ORF1p and pSTAT1 staining in human dermis. The experiments shown in panels (a, b) was repeated three times independently with similar results. **FIG. 13c**, Cells were plated on cover slips, stained and quantified as described in the **Methods**. 200 cells in multiple fields were scored for each condition. a.f.u., arbitrary fluorescence units. Insets show the % of cells found in each quadrant. **FIG. 13d, e**, Abundance of ORF1 and p16 or pSTAT1 cells in human skin. Skin biopsies were cryosectioned and stained as described in the **Methods**. 200 dermal fibroblast cells in multiple fields were scored for each subject.

Aggregated data for four subjects (800 cells) are shown. **FIG. 13f**, Data in (c) and (d) were recalculated to show the relative abundance of p16+ cells among all cells, and ORF1+ cells in the p16+ pool of cells. **FIG. 13g**, Data in (e) were recalculated as in (f). **FIG. 13h**, Characteristics of the human subjects used in the analysis of dermal fibroblasts. These specimens were collected as part of the ongoing Leiden Longevity Study.¹⁶ The specimens used here were chosen randomly from left over material. The TIF assay¹⁷ relies on a two-parameter (color) visualization of telomeres (using a FISH probe) and immunofluorescent detection of DNA damage foci (using antibody to 53BP1). Because of limiting material, it was not possible to combine detection of p16 with TIFs in a three-color experiment.

[0037] **FIG. 14** shows the effects of 3TC or K-9 treatment on L1, p16, IFN-I and SASP gene expression in mouse tissues. **FIG. 14a-c**, Mice at the indicated ages were treated with 3TC continuously for two weeks (see also **FIG. 4c, e, FIG. 15d-f**, and **Methods**). For all conditions the expression of L1 mRNA, p16, three representative IFN-I response genes (*Ifn- α* , *Irf7*, *Oas1*) and three representative SASP genes (*Il-6*, *Mmp3*, *Pai1*) were assessed by RT-qPCR. In no instance was expression at 5 months + 3TC significantly different from the no drug control; therefore, these data are not shown in the figure (for all collected data, see **Table 7**). The box plots show the range of the data (whiskers), 25th and 75 percentiles (box), means (dashed line), and medians (solid line). Each point represents one animal. **FIG. 14a**, Visceral white adipose, male mice. 5 months, n=8 animals; 26 months, n=12 animals; 26 months + 3TC, n=12 animals. **FIG. 14b**, Visceral white adipose, female mice. 5 months, n=8 animals; 26 months, n=12 animals; 26 months + 3TC, n=12 animals. **FIG. 14c**, Liver, male mice. 5 months, n=8 animals; 26 months, n=10 animals; 26 months + 3TC, n=10 animals. **FIG. 14d**, Mice at the age of 26 months were treated with K-9 or 3TC in drinking water for two weeks and analyzed by RT-qPCR as above. NT, not treated. Visceral white adipose, male mice, n=7 animals for each group. Data are mean $\pm$ s.d. * $P \leq 0.05$, ** $P \leq 0.01$, 1-way ANOVA with Tukey's multiple comparisons test.

[0038] **FIG. 15** shows the combinatorial assessment of senescence, IFN-I, SASP and L1 markers and effects of 3TC on age-associated phenotypes in mouse tissues. **FIG. 15a, b**, Whole-mount IF was performed on white adipose of 5 months and 26 months old (with and without 2 weeks of 3TC treatment) male mice. In (a), loss of Lamin B1 (senescence marker) was colocalized with IL-6 (SASP marker). In (b), pStat1 (IFN-I marker) was colocalized with Orf1 (L1 marker). **FIG. 15c**, Quantification of the experiments shown in (a) and (b). Four animals and at least 200 cells per animal were scored for each condition. **FIG. 15d**, Neutral lipids were stained with BODIPY to visualize mature adipocytes in whole-mount preparations,

and macrophages were detected by IF using the F4/80 antibody. **FIG. 15e**, The effects of 2 weeks of 3TC treatment on adipogenesis were assessed by measuring mean adipocyte size (left panel), and by RT-qPCR to determine the expression of key adipogenic genes (right panels; *Acaca*, acetyl-CoA carboxylase 1; *Cebpa*, CCAAT/enhancer-binding protein alpha; *Fasn*, fatty acid synthase; *Srebp1*, sterol regulatory element-binding protein 1). The box plots show the range of the data (whiskers), 25th and 75 percentiles (box), means (dashed line), and medians (solid line). Adipocyte size (BODIPY-stained area) was calculated using CellProfiler; aggregated data for 5 animals and 500 total cells are shown. For RT-qPCR data, each point represents one animal; n = 6 animals. **FIG. 15f**, Expression of the *Ucp1* gene (thermogenin) in brown adipose tissue was determined by RT-qPCR and is represented as in (e). n = 5 animals. **FIG. 15g**, Expression of L1 mRNA was determined by RT-qPCR and is represented as in (e). 5 months, n=8 animals; 26 months, n=12 animals; 29 months, n=6 animals. **(e-g)** Data are mean $\pm$ s.d. * $P \leq 0.05$, ** $P \leq 0.01$. **(c, e left panel, f, g)** 1-way ANOVA with Tukey's multiple comparisons test, **(e right panels)** unpaired two-sided *t*-tests.

[0039] **FIG. 16** shows scans of raw immunoblots. **FIG. 16A: Panel a**, shows Blot 1 - RB1: 1. EP; 2. SEN (L); 3. OE - SEN; 4. SEN (E); **Panel b**, shows Blot 2 - TREX1: 1. EP; 2. SEN (E); 3. SEN (L); and **Panel c**, shows Blot 3 - FOXA1: 1. EP; 2. Arrest; 3. SEN (E); 4. SEN (L). **FIG. 16B: Panel d**, shows Blot 4 - RB1: 1. EP; 2. 3X; **Panel e**, shows Blot 5 - TREX1: 1. EP; 2. 3X; and **Panel f**, shows Blot 6 - FOXA1: 1. EP; 2. 3X. **FIG. 16C: Panel g**, shows Blot 7 - RB1: 1. SEN (L); 2. shRB1(b); 3. shRB1(a); 4. OE-RB1; **Panel h**, shows Blot 8 - TREX1: 1. SEN (L); 2. shTREX1 (b); 3. shTREX1 (a); 4. OE-TREX1; and **Panel i**, shows Blot 9 - FOXA1: 1. shFOXA1 (a); 2. shFOXA1 (b); 3. SEN (L); 4. OE-FOXA1. **FIG. 16D: Panel j**, shows Blot 10 - STAT2: 1. 3X; 2. shL1; 3. NRTI; 4. Δ IFNAR; 5. EP; **Panel k**, shows Blot 11 - IRF7: 1. EP; 2. shL1; 3. 3X; 4. shL1; 5. Δ IFNAR; **Panel l**, shows Blot 12 - STAT2: 1. SEN (L); 2. Δ IFNAR; 3. shL1; 4. NRTI; and **Panel m**, shows Blot 13 - IRF7: 5. SEN (L); 6. Δ IFNAR; 7. shL1; 8. NRTI. **FIG. 16E shows: Panel n**, shows Blot 14 - p16 (CDKN2A): 1. EP; 2. SEN (E); 3. SEN (L); and **Panel o**, shows Blot 15 - p21 (CDKN1A): 1. EP; 2. SEN (E); 3. SEN (L).

[0040] **FIG. 17** shows the effects of Adefovir and Lamivudine on senescence-induced increases in L1 sequence abundance, interferon gene expression, and SASP gene expression. **FIG. 17a** depicts the effects of 5 μ M Adefovir and Lamivudine on L1 sequence abundance (copy number) in three different human fibroblast cell lines: LF1, IMR90, WI38 using qPCR assays. **FIG. 17b** depicts the effects of 5 μ M Adefovir and Lamivudine on interferon gene expression of two interferon genes (*IFN- α* and *IFN- β 1*) in two cell lines (LF1 and IMR90). **FIG. 17c** depicts the effects of 5 μ M Adefovir and Lamivudine on two SASP genes (*IL-6* and *MMP3*) in the LF1 cell

line. **FIG. 17d** depicts the effects of higher doses of Adefovir and Lamivudine (10 μ M and 50 μ M) on interferon gene expression (IFN- α and IFN- β 1) in the LF1 cell line.

[0041] **FIG. 18** shows the inhibition of mouse L1 activity with eight RTI compounds: Lamivudine (3TC); Stavudine; Emtricitabine; Apricitabine; Tenofovir Disoproxil; Censavudine; Elvucitabine; and Tenofovir. A dose-response was obtained on the retrotransposition activity of active mouse LINE-1 using HeLa cells in a first experiment (**FIG. 18A**) and in a second independent experiment (**FIG. 18B**).

[0042] **FIG. 19** shows the inhibition of human L1 activity with three RTI compounds: Lamivudine (3TC); Censavudine; and Elvucitabine. A dose-response was obtained on the retrotransposition activity of active human LINE-1 using HeLa cells in a first experiment using Lamivudine (3TC); Censavudine; and Elvucitabine (**FIG. 19A**); and in a second experiment using Lamivudine (3TC) and Elvucitabine (**FIG. 19B**).

[0043] **FIG. 20** shows the cell viability of HeLa cells following treatment with 10 different RTI compounds: Lamivudine (3TC); Stavudine; Emtricitabine; Apricitabine; Tenofovir Disoproxil; Censavudine; Elvucitabine; Tenofovir; and Staurosporine.

DETAILED DESCRIPTION OF THE INVENTION

[0044] It is to be appreciated that certain aspects, modes, embodiments, variations and features of the invention are described below in various levels of detail in order to provide a substantial understanding of the present invention.

[0045] The following description of particular aspect(s) is merely exemplary in nature and is in no way intended to limit the scope of the invention, its application, or uses, which may, of course, vary. The invention is described with relation to the non-limiting definitions and terminology included herein. These definitions and terminology are not designed to function as a limitation on the scope or practice of the invention but are presented for illustrative and descriptive purposes only. While the compositions or processes are described as using specific materials or an order of individual steps, it is appreciated that materials or steps may be interchangeable such that the description of the invention may include multiple parts or steps arranged in many ways as is readily appreciated by one of skill in the art.

DEFINITIONS

[0046] The definitions of certain terms as used in this specification and the appended claims are provided below. Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0047] As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the content clearly dictates otherwise. For example, reference to "a cell" includes a combination of two or more cells, and the like.

[0048] The term "approximately" or "about" in reference to a value or parameter are generally taken to include numbers that fall within a range of 5%, 10%, 15%, or 20% in either direction (greater than or less than) of the number unless otherwise stated or otherwise evident from the context (except where such number would be less than 0% or exceed 100% of a possible value). As used herein, reference to "approximately" or "about" a value or parameter includes (and describes) embodiments that are directed to that value or parameter. For example, description referring to "about X" includes description of "X".

[0049] As used herein, the term "or" means "and/or." The term "and/or" as used in a phrase such as "A and/or B" herein is intended to include both A and B; A or B; A (alone); and B (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0050] It is understood that wherever embodiments are described herein with the language "comprising" otherwise analogous embodiments described in terms of "consisting of" and/or "consisting essentially of" are also provided. It is also understood that wherever embodiments are described herein with the language "consisting essentially of" otherwise analogous embodiments described in terms of "consisting of" are also provided.

[0051] It is to be appreciated that certain features of the invention which are, for clarity, described herein in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention that are, for brevity, described in the context of a single embodiment, may also be provided separately or in any subcombination. Further, reference to values stated in ranges include each and every value within that range.

[0052] The term "subject" refers to a mammal, including but not limited to a dog, cat, horse, cow, pig, sheep, goat, chicken, rodent, or primate. Subjects can be house pets (e.g., dogs, cats), agricultural stock animals (e.g., cows, horses, pigs, chickens, etc.), laboratory animals (e.g., mice, rats, rabbits, etc.), but are not so limited. Subjects include human subjects. The human subject may be a pediatric, adult, or a geriatric subject. The human subject may be of either sex.

[0053] The terms "effective amount" and "therapeutically-effective amount" include an amount sufficient to prevent or ameliorate a manifestation of disease or medical condition, such

as an age-associated disorder. It will be appreciated that there will be many ways known in the art to determine the effective amount for a given application. For example, the pharmacological methods for dosage determination may be used in the therapeutic context. In the context of therapeutic or prophylactic applications, the amount of a composition administered to the subject will depend on the type and severity of the disease and on the characteristics of the subject, such as general health, age, sex, body weight and tolerance to drugs. It will also depend on the degree, severity and type of disease. The skilled artisan will be able to determine appropriate dosages depending on these and other factors. The compositions can also be administered in combination with one or more additional therapeutic compounds.

[0054] As used herein, the terms "treating" or "treatment" or "to treat" or "alleviating" or "to alleviate" refer to both (1) therapeutic measures that cure, slow down, lessen symptoms of, and/or halt progression of a diagnosed disease or infection and (2) prophylactic or preventative measures that prevent or slow the development of a disease or infection.

[0055] As used herein, the term "long-term" administration means that the therapeutic agent or drug is administered for a period of at least 12 weeks. This includes that the therapeutic agent or drug is administered such that it is effective over, or for, a period of at least 12 weeks and does not necessarily imply that the administration itself takes place for 12 weeks, *e.g.*, if sustained release compositions or long acting therapeutic agent or drug is used. Thus, the subject is treated for a period of at least 12 weeks. In many cases, long-term administration is for at least 4, 5, 6, 7, 8, 9 months or more, or for at least 1, 2, 3, 5, 7 or 10 years, or more.

[0056] As used herein, the term "age-related inflammation" (or "age-associated inflammation") is an inflammation, typically a chronic, particularly a chronic systemic inflammation which occurs with increasing age. Such inflammation may be observed above the age of 30, 35 or 40 but typically is seen in subjects aged 45, 50, 55 or 60 or more. In many cases this may be a low-level inflammation.

[0057] As used herein, the term "chronic inflammation" means an inflammation (*e.g.*, an inflammatory condition) that is of persistent or prolonged duration in the body of a subject. Generally speaking, this means an inflammatory response or condition of duration of 20, 25 or 30 days or more or 1 month or more, more particular of at least 2 or 3 months or more. Chronic inflammation leads to a progressive shift in the type of cells present at the site of inflammation. Chronic inflammation may be a factor in the development of a number of diseases or disorders, including particularly degenerative diseases, or diseases or conditions associated with loss of youthful function or aging.

[0058] As used herein, the term "systemic inflammation" is inflammation which is not confined to a particular tissue or site or location in the body. The inflammation may be generalized throughout the body. Systemic inflammation typically involves the endothelium and other organ systems.

[0059] As used herein, the term "low-level inflammation" (which term is used herein as synonymous with "low-grade inflammation") is characterized by a 2- to threefold increase in the systemic concentrations of cytokines such as $\text{TNF}\alpha$, IL-6, and CRP, *e.g.*, as measured in the plasma or serum. The increase may be relative to, or as compared with, normal concentrations or reference concentrations, for example concentrations as determined in a particular reference cohort or population of subjects, *e.g.*, young subjects (*e.g.*, young adults) or healthy subjects, for example subjects who are not suffering from any disease or condition, including any inflammatory disease, or who do not have inflammation. The increase may also be relative to the level of concentration in a subject prior to development of the inflammation. Low-level inflammation may be observed in the absence of overt signs or symptoms of disease. Thus, low-level inflammation may be sub-clinical inflammation. Alternatively, a subject with low-level inflammation may not have a clinically diagnosed condition or disease but may exhibit certain signs or symptoms of an inflammatory response or inflammatory condition. In other words, there may be signs or symptoms of the effect of inflammation in the body, but this may not yet have progressed to an overt or recognized disease.

[0060] As used herein, the term "cancer inflammation" is inflammation that occurs in the context of cancer and may alternatively be defined as "cancer-associated inflammation". Inflammation has been identified as a hallmark of cancer and may be necessary for tumorigenesis and maintenance of the cancer state. Cancer symptoms are associated with inflammation. Thus, a subject with cancer may have or exhibit inflammation, which can be a low-level or peripheral inflammation as discussed above, and in particular a chronic or systemic inflammation as discussed above.

[0061] Unless otherwise defined, all terms (including technical and scientific terms) used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. It will be further understood that terms such as those defined in commonly used dictionaries, should be interpreted as having a meaning that is consistent with their meaning in the context of the relevant art and the present disclosure, and will not be interpreted in an idealized or overly formal sense unless expressly so defined herein.

PHARMACEUTICAL COMPOSITIONS

[0062] The compositions and methods of the present invention may be utilized to treat an individual in need thereof. In certain embodiments, the individual is a mammal such as a human, or a non-human mammal. When administered to an animal, such as a human, the composition or the compound is preferably administered as a pharmaceutical composition comprising, for example, a compound of the invention and a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers are well known in the art and include, for example, aqueous solutions such as water or physiologically buffered saline or other solvents or vehicles such as glycols, glycerol, oils such as olive oil, or injectable organic esters. In preferred embodiments, when such pharmaceutical compositions are for human administration, particularly for invasive routes of administration (*i.e.*, routes, such as injection or implantation, that circumvent transport or diffusion through an epithelial barrier), the aqueous solution is pyrogen-free, or substantially pyrogen-free. The excipients can be chosen, for example, to effect delayed release of an agent or to selectively target one or more cells, tissues or organs. The pharmaceutical composition can be in dosage unit form such as tablet, capsule (including sprinkle capsule and gelatin capsule), granule, lyophile for reconstitution, powder, solution, syrup, suppository, injection or the like. The composition can also be present in a transdermal delivery system, *e.g.*, a skin patch. The composition can also be present in a solution suitable for topical administration, such as a lotion, cream, or ointment.

[0063] A pharmaceutically acceptable carrier can contain physiologically acceptable agents that act, for example, to stabilize, increase solubility or to increase the absorption of a compound such as a compound of the invention. Such physiologically acceptable agents include, for example, carbohydrates, such as glucose, sucrose or dextrans, antioxidants, such as ascorbic acid or glutathione, chelating agents, low molecular weight proteins or other stabilizers or excipients. The choice of a pharmaceutically acceptable carrier, including a physiologically acceptable agent, depends, for example, on the route of administration of the composition. The preparation or pharmaceutical composition can be a self-emulsifying drug delivery system or a self-micro emulsifying drug delivery system. The pharmaceutical composition (preparation) also can be a liposome or other polymer matrix, which can have incorporated therein, for example, a compound of the invention. Liposomes, for example, which comprise phospholipids or other lipids, are nontoxic, physiologically acceptable and metabolizable carriers that are relatively simple to make and administer.

[0064] The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound

medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[0065] The phrase "pharmaceutically acceptable carrier" as used herein means a pharmaceutically acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the patient. Some examples of materials which can serve as pharmaceutically acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) phosphate buffer solutions; and (21) other non-toxic compatible substances employed in pharmaceutical formulations.

[0066] A pharmaceutical composition (preparation) can be administered to a subject by any of a number of routes of administration including, for example, orally (for example, drenches as in aqueous or non-aqueous solutions or suspensions, tablets, capsules (including sprinkle capsules and gelatin capsules), boluses, powders, granules, pastes for application to the tongue); absorption through the oral mucosa (e.g., sublingually); subcutaneously; transdermally (for example as a patch applied to the skin); and topically (for example, as a cream, ointment or spray applied to the skin). The compound may also be formulated for inhalation. In certain embodiments, a compound may be simply dissolved or suspended in sterile water. Details of appropriate routes of administration and compositions suitable for same can be found in, for example, U.S. Patent Nos. 6,110,973; 5,763,493; 5,731,000; 5,541,231; 5,427,798; 5,358,970; and 4,172,896, as well as in patents cited therein.

[0067] The formulations may conveniently be presented in unit dosage form and may be prepared by any methods well known in the art of pharmacy. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will vary depending upon the host being treated, the particular mode of administration. The amount of active ingredient that can be combined with a carrier material to produce a single dosage form

will generally be that amount of the compound which produces a therapeutic effect. Generally, out of one hundred percent, this amount will range from about 1 percent to about ninety-nine percent of active ingredient, preferably from about 5 percent to about 70 percent, most preferably from about 10 percent to about 30 percent.

[0068] Methods of preparing these formulations or compositions include the step of bringing into association an active compound, such as a compound of the invention, with the carrier and, optionally, one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association a compound of the present invention with liquid carriers, or finely divided solid carriers, or both, and then, if necessary, shaping the product.

[0069] Formulations of the invention suitable for oral administration may be in the form of capsules (including sprinkle capsules and gelatin capsules), cachets, pills, tablets, lozenges (using a flavored basis, usually sucrose and acacia or tragacanth), lyophile, powders, granules, or as a solution or a suspension in an aqueous or non-aqueous liquid, or as an oil-in-water or water-in-oil liquid emulsion, or as an elixir or syrup, or as pastilles (using an inert base, such as gelatin and glycerin, or sucrose and acacia) and/or as mouth washes and the like, each containing a predetermined amount of a compound of the present invention as an active ingredient. Compositions or compounds may also be administered as a bolus, electuary or paste.

[0070] To prepare solid dosage forms for oral administration (capsules (including sprinkle capsules and gelatin capsules), tablets, pills, dragées, powders, granules and the like), the active ingredient is mixed with one or more pharmaceutically acceptable carriers, such as sodium citrate or dicalcium phosphate, and/or any of the following: (1) fillers or extenders, such as starches, lactose, sucrose, glucose, mannitol, and/or silicic acid; (2) binders, such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinyl pyrrolidone, sucrose and/or acacia; (3) humectants, such as glycerol; (4) disintegrating agents, such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate; (5) solution retarding agents, such as paraffin; (6) absorption accelerators, such as quaternary ammonium compounds; (7) wetting agents, such as, for example, cetyl alcohol and glycerol monostearate; (8) absorbents, such as kaolin and bentonite clay; (9) lubricants, such as talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof; (10) complexing agents, such as, modified and unmodified cyclodextrins; and (11) coloring agents. In the case of capsules (including sprinkle capsules and gelatin capsules), tablets and pills, the pharmaceutical compositions may also comprise buffering agents. Solid

compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugars, as well as high molecular weight polyethylene glycols and the like.

[0071] A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared using binder (for example, gelatin or hydroxypropyl methyl cellulose), lubricant, inert diluent, preservative, disintegrant (for example, sodium starch glycolate or cross-linked sodium carboxymethyl cellulose), surface-active or dispersing agent. Molded tablets may be made by molding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent.

[0072] The tablets, and other solid dosage forms of the pharmaceutical compositions, such as dragées, capsules (including sprinkle capsules and gelatin capsules), pills and granules, may optionally be scored or prepared with coatings and shells, such as enteric coatings and other coatings well known in the pharmaceutical-formulating art. They may also be formulated so as to provide slow or controlled release of the active ingredient therein using, for example, hydroxypropyl methyl cellulose in varying proportions to provide the desired release profile, other polymer matrices, liposomes and/or microspheres. They may be sterilized by, for example, filtration through a bacteria-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions that can be dissolved in sterile water, or some other sterile injectable medium immediately before use. These compositions may also optionally contain opacifying agents and may be of a composition that they release the active ingredient(s) only, or preferentially, in a certain portion of the gastrointestinal tract, optionally, in a delayed manner. Examples of embedding compositions that can be used include polymeric substances and waxes. The active ingredient can also be in micro-encapsulated form, if appropriate, with one or more of the above-described excipients.

[0073] Liquid dosage forms useful for oral administration include pharmaceutically acceptable emulsions, lyophiles for reconstitution, micro-emulsions, solutions, suspensions, syrups and elixirs. In addition to the active ingredient, the liquid dosage forms may contain inert diluents commonly used in the art, such as, for example, water or other solvents, cyclodextrins and derivatives thereof, solubilizing agents and emulsifiers, such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor and sesame oils), glycerol, tetrahydrofuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof.

[0074] Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, coloring, perfuming and preservative agents.

[0075] Suspensions, in addition to the active compounds, may contain suspending agents as, for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth, and mixtures thereof.

[0076] Dosage forms for the topical or transdermal administration include powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and inhalants. The active compound may be mixed under sterile conditions with a pharmaceutically acceptable carrier, and with any preservatives, buffers, or propellants that may be required.

[0077] The ointments, pastes, creams and gels may contain, in addition to an active compound, excipients, such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or mixtures thereof.

[0078] Powders and sprays can contain, in addition to an active compound, excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants, such as chlorofluorohydrocarbons and volatile unsubstituted hydrocarbons, such as butane and propane.

[0079] Transdermal patches have the added advantage of providing controlled delivery of a compound of the present invention to the body. Such dosage forms can be made by dissolving or dispersing the active compound in the proper medium. Absorption enhancers can also be used to increase the flux of the compound across the skin. The rate of such flux can be controlled by either providing a rate controlling membrane or dispersing the compound in a polymer matrix or gel.

[0080] The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intraocular (such as intravitreal), intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal and intrasternal injection and infusion. Pharmaceutical compositions suitable for parenteral administration comprise one or more active compounds in combination with one or more pharmaceutically acceptable sterile isotonic aqueous or nonaqueous solutions,

dispersions, suspensions or emulsions, or sterile powders which may be reconstituted into sterile injectable solutions or dispersions just prior to use, which may contain antioxidants, buffers, bacteriostats, solutes which render the formulation isotonic with the blood of the intended recipient or suspending or thickening agents.

[0081] Examples of suitable aqueous and nonaqueous carriers that may be employed in the pharmaceutical compositions of the invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Examples of suitable aqueous and nonaqueous carriers that may be employed in the pharmaceutical compositions of the invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0082] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of the action of microorganisms may be ensured by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents that delay absorption such as aluminum monostearate and gelatin.

[0083] In some cases, in order to prolong the effect of a drug, it is desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material having poor water solubility. The rate of absorption of the drug then depends upon its rate of dissolution, which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle.

[0084] Injectable depot forms are made by forming microencapsulated matrices of the subject compounds in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of drug to polymer, and the nature of the particular polymer employed, the rate of drug release can be controlled. Examples of other biodegradable polymers include poly(orthoesters)

and poly(anhydrides). Depot injectable formulations are also prepared by entrapping the drug in liposomes or microemulsions that are compatible with body tissue.

[0085] For use in the methods of this invention, active compounds can be given *per se* or as a pharmaceutical composition containing, for example, 0.1 to 99.5% (more preferably, 0.5 to 90%) of active ingredient in combination with a pharmaceutically-acceptable carrier.

[0086] Methods of introduction may also be provided by rechargeable or biodegradable devices. Various slow release polymeric devices have been developed and tested *in vivo* in recent years for the controlled delivery of drugs, including proteinaceous biopharmaceuticals. A variety of biocompatible polymers (including hydrogels), including both biodegradable and non-degradable polymers, can be used to form an implant for the sustained release of a compound at a particular target site.

[0087] Actual dosage levels of the active ingredients in the pharmaceutical compositions may be varied so as to obtain an amount of the active ingredient that is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient.

[0088] The selected dosage level will depend upon a variety of factors including the activity of the particular compound or combination of compounds employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound(s) being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compound(s) employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0089] A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the therapeutically effective amount of the pharmaceutical composition required. For example, the physician or veterinarian could start doses of the pharmaceutical composition or compound at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved. By “therapeutically effective amount” is meant the concentration of a compound that is sufficient to elicit the desired therapeutic effect. It is generally understood that the effective amount of the compound will vary according to the weight, sex, age, and medical history of the subject. Other factors which influence the effective amount may include, but are not limited to, the severity of the patient's condition, the disorder being treated, the stability of the compound, and, if desired, another type of therapeutic agent being administered with the compound of the invention. A larger total dose

can be delivered by multiple administrations of the agent. Methods to determine efficacy and dosage are known to those skilled in the art.¹⁸

[0090] In general, a suitable daily dose of an active compound used in the compositions and methods of the invention will be that amount of the compound that is the lowest dose effective to produce a therapeutic effect. Such an effective dose will generally depend upon the factors described above.

[0091] If desired, the effective daily dose of the active compound may be administered as one, two, three, four, five, six or more sub-doses administered separately at appropriate intervals throughout the day, optionally, in unit dosage forms. In certain embodiments of the present invention, the active compound may be administered two or three times daily. In other embodiments, the active compound will be administered once daily.

[0092] The patient receiving this treatment is any animal in need, including primates, in particular humans; and other mammals such as equines bovine, porcine, sheep, feline, and canine; poultry; and pets in general.

[0093] In certain embodiments, compounds of the invention may be used alone or conjointly administered with another type of therapeutic agent.

[0094] The present disclosure includes the use of pharmaceutically acceptable salts of compounds of the invention in the compositions and methods of the present invention. In certain embodiments, contemplated salts of the invention include, but are not limited to, alkyl, dialkyl, trialkyl or tetra-alkyl ammonium salts. In certain embodiments, contemplated salts of the invention include, but are not limited to, L-arginine, benenthamine, benzathine, betaine, calcium hydroxide, choline, deanol, diethanolamine, diethylamine, 2-(diethylamino)ethanol, ethanolamine, ethylenediamine, N-methylglucamine, hydrabamine, 1H-imidazole, lithium, L-lysine, magnesium, 4-(2-hydroxyethyl)morpholine, piperazine, potassium, 1-(2-hydroxyethyl)pyrrolidine, sodium, triethanolamine, tromethamine, and zinc salts. In certain embodiments, contemplated salts of the invention include, but are not limited to, Na, Ca, K, Mg, Zn or other metal salts. In certain embodiments, contemplated salts of the invention include, but are not limited to, 1-hydroxy-2-naphthoic acid, 2,2-dichloroacetic acid, 2-hydroxyethanesulfonic acid, 2-oxoglutaric acid, 4-acetamidobenzoic acid, 4-aminosalicylic acid, acetic acid, adipic acid, l-ascorbic acid, l-aspartic acid, benzenesulfonic acid, benzoic acid, (+)-camphoric acid, (+)-camphor-10-sulfonic acid, capric acid (decanoic acid), caproic acid (hexanoic acid), caprylic acid (octanoic acid), carbonic acid, cinnamic acid, citric acid, cyclamic acid, dodecylsulfuric acid, ethane-1,2-disulfonic acid, ethanesulfonic acid, formic acid, fumaric acid, galactaric acid, gentisic acid, d-glucoheptonic acid, d-gluconic acid, d-glucuronic acid, glutamic acid, glutaric

acid, glycerophosphoric acid, glycolic acid, hippuric acid, hydrobromic acid, hydrochloric acid, isobutyric acid, lactic acid, lactobionic acid, lauric acid, maleic acid, l-malic acid, malonic acid, mandelic acid, methanesulfonic acid, naphthalene-1,5-disulfonic acid, naphthalene-2-sulfonic acid, nicotinic acid, nitric acid, oleic acid, oxalic acid, palmitic acid, pantoic acid, phosphoric acid, propionic acid, l-pyroglutamic acid, salicylic acid, sebacic acid, stearic acid, succinic acid, sulfuric acid, l-tartaric acid, thiocyanic acid, p-toluenesulfonic acid, trifluoroacetic acid, and undecylenic acid salts.

[0095] The pharmaceutically acceptable acid addition salts can also exist as various solvates, such as with water, methanol, ethanol, dimethylformamide, and the like. Mixtures of such solvates can also be prepared. The source of such solvate can be from the solvent of crystallization, inherent in the solvent of preparation or crystallization, or adventitious to such solvent.

[0096] Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the compositions.

[0097] Examples of pharmaceutically acceptable antioxidants include: (1) water-soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal-chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

ROLE OF CELLULAR SENESENCE IN AGING AND AGE-ASSOCIATED DISEASES

[0098] **FIG. 5** provides a flow chart outlining the molecular pathway of cellular senescence leading to age-associated, sterile inflammation, which are described in further detail below.

Upregulation of Retrotransposable Elements (RTEs)

[0099] RTEs have been known to be activated transcriptionally in senescent cells¹⁹ and in some mouse tissues.²⁰ Three regulators have been previously shown to be involved with regulation of L1: FOXA1, RB, TREX1. FOXA1 was reported to be upregulated in senescent cells²¹ and to bind to the L1 promoter.²² RB has been reported to represses L1 elements.²³ The complete loss of TREX1 (germline deletion) has been reported to lead to an autoimmune disease (Aicardi-Gutierrez syndrome, AGS), which is associated with L1 activation.²⁴

[0100] Although these three regulators had been reported to have a role in the regulation of L1, the data in the present disclosure provides the first demonstration that the misregulation of the **combination** of these three factors is **sufficient** to allow activation of **endogenous** L1 elements in **normal** cells. See, **Example 2**. Moreover, the present disclosure provides the first description of late senescence as a discrete temporal, and hitherto unknown, stage of senescence, and one that is characterized by the upregulation of L1 elements and triggering on an IFN-I response. See, **Example 1**.

Accumulation of Cytoplasmic L1 cDNA

[0101] The existence of cytoplasmic L1 cDNA has been known. One source has been shown to be from mitochondria.²⁵ The nuclei has been reported to "leak" chromosomal DNA into the cytoplasm in senescent cells.²⁶ These were subsequently termed "cytoplasmic chromatin fragments" (CCF)²⁷ and later described in senescent cells.²⁸ However, none of these reports mention RTEs and L1s as components of CCF.

[0102] The data in the present disclosure not only show that L1 DNA sequences are found in the cytoplasm in senescent cells, but also that they are **enriched** relative to nuclear DNA sequences. See, **Example 3**. As such, the previously-reported simple extrusion of bulk chromosomal DNA from the nucleus into the cytoplasm cannot explain the enrichment of L1 sequences observed herein.

[0103] Although it had been previously reported L1 DNA was enriched in TREX1 null cells (AGS)²⁹ and that the L1 cDNA accumulating in TREX1 knockout cells was cytoplasmic in localization,³⁰ AGS is a rare autoimmune disease that is not age-associated. In contrast, the data in the present disclosure generalizes the presence of cytoplasmic L1 DNA to cellular senescence, one of the major driver of aging and aging-associated diseases.

Induction of IFN-I and Crosstalk to Immune System, Reinforcement of SASP

[0104] Cytoplasmic DNA (and CCF in particular) has been previously reported to be recognized by the cGAS/STING sensor pathway, which consequently promotes an inflammatory state.³¹ In the context of cellular senescence, this pro-inflammatory state is known as the senescence-associated secretory phenotype (SASP). These reports showed that SASP was at least in part dependent on CCF, since knockdown of cGAS/STING pathway components reduced SASP. The IFN-I response was also reported to be a part of this pro-inflammatory cascade.³² As noted above, none of these previous reports implicated L1 elements in the promotion of SASP by CCF.

[0105] The data in the present disclosure establish that, not only does L1 DNA comprise a significant proportion of CCF that is enriched in cytoplasmic DNA relative to nuclear sequences, but it is also functionally relevant for the promotion of SASP. In particular, the data in the present disclosure show that decreasing the amount of cytoplasmic L1 DNA, either by shRNA to L1 or by blocking L1 reverse transcription with RTI drugs, reduced both the IFN-I response and SASP in senescent cells. Importantly, the data in the present disclosure represent the first evidence that RTI treatment can effectively reverse both IFN-I and the proinflammatory SASP *after* they are fully established in senescent cells. See, **Examples 3 and 4.**

[0106] All prior work relevant to therapy has been limited to interfering with the cGAS/STING sensor pathway, for example showing that shRNAs against components of the cGAS/STING pathway downregulated the IFN-I response and SASP.^{33,34} Although one could envision using small molecular inhibitors of the cGAS/STING pathway to downregulate SASP, such treatments would result in increased sensitivity to viral, bacterial and other pathogen infections.

[0107] The approach of the present invention of targeting the synthesis of L1 DNA with RTI drugs goes to the root of the problem because it targets the prime causative agent (L1 DNA itself), as opposed to downstream processing events, such as the cGAS/STING sensor pathway, or even further downstream interferon or immune signaling components. It has been appreciated in the present invention that all of these downstream components have essential cellular functions, and hence targeting them would compromise, in some aspect, normal physiological processes. On the other hand, the L1 DNA is a unique "non-self" component, whose pharmacological targeting would only be compromised by "off-target" effects.

[0108] In recent years, it has become clear that cellular senescence is one of the major drivers of organismal aging and aging-associated diseases.³⁵ Hence, there is considerable interest in "seno-therapies" to block the deleterious effects of senescent cells.³⁶ The major effort has been directed at "senolytic" drugs that selectively kill (and hence remove) senescent cells from tissues. "Senomorphics" have been classified as small molecules that suppress senescent phenotypes without cell killing. We prefer to refer to such drugs as "senostatic" drugs to emphasize that their main effect is to halt, or block the harmful effects of senescent cells, in particular the SASP.

[0109] The data of the present disclosure demonstrate that, in human cells and mouse models, RTIs are senostatic drugs that reverse the SASP of senescent cells and hence alleviate the age-associated proinflammatory state. The data of the present disclosure also describe

which specific RTIs, and which doses, are particularly effective in reversing SASP. The broad efficacy of RTIs as senostatic drugs that can treat multiple age-associated conditions has not been previously described in the art.

Promotion of Age-Associated, "Sterile" Inflammation

[0110] Sterile inflammation, also known as inflammaging, is a hallmark of aging and a contributing factor to many age-related diseases.^{37,38} The data of the present disclosure indicate that activation of L1 elements (and possibly other RTEs) promotes inflammaging, and that the L1 RT is a relevant target for the treatment of age-associated inflammation and disorders.

[0111] The data of the present disclosure provide specific examples, in aged mice, of which age-associated pathologies can be reversed, or at least downregulated, by administration of RTIs. For example, the NRTI Lamivudine (aka 3TC or Epivir) was shown to reverse or downregulate:

- Panel of IFN-I and SASP markers, measured by RT-qPCR in multiple tissues;
- Infiltration of macrophages into white adipose and kidney tissues measured by IF microscopy;
- Muscle atrophy measured by muscle fiber diameter;
- Kidney glomerulosclerosis measured by pathological evaluation of PAS-stained sections;
- Adipocyte atrophy measured microscopically by cell size and by RT-qPCR analysis of key adipogenic genes; and
- Thermogenesis measured by RT-qPCR analysis of Ucp1 expression.

[0112] Accordingly, the present invention provides that RTIs can be used as "senostatic" drugs that are able to halt, or block the harmful effects of senescent cells, in particular the SASP, and prevent or reverse age-related inflammation and disorders.

NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS (NRTIS)

[0113] NRTIs are active inhibitors of reverse transcriptase found in retroviruses such as the human immunodeficiency virus (HIV). The different nucleoside reverse transcriptase inhibitors may be activated differently but they have the same mechanism of action. NRTIs are activated generally by phosphorylation to the triphosphate form by cellular enzymes. It then competes with cellular triphosphates, which are substrates for proviral DNA by viral reverse transcriptase. NRTIs were the first type of drugs available for the treatment of human immunodeficiency virus (HIV infection) and acquired immune deficiency syndrome (AIDS).

[0114] **Table 8** provides a list of common approved NRTI drugs or NRTI combination drugs used for the treatment of HIV infection and AIDS. As described above, according to the methods of the present invention, NRTIs can be used as "senostatic" drugs that are able to halt, or block the harmful effects of senescent cells, in particular the SASP, and prevent or reverse age-related inflammation and disorders.

[0115] NRTI drugs that can be used in the methods of the present invention include, but are not limited to: Amdoxovir, Apricitabine (ATC), ATRIPLA® (efavirenz / emtricitabine / tenofovir disoproxil), BARACLUDE® (entecavir; ETV), BIKTARVY® (bictegravir / emtricitabine / tenofovir alafenamide), Censavudine (INN; BMS-986001; OBP-601; festinavir), COMBIVIR™ (zidovudine / lamivudine), COVIRACIL™ (emtricitabine; FTC), DAPD/DXG (active metabolite of DAPD - 2,6-diaminopurine dioxolane), DESCOVY® (emtricitabine / tenofovir alafenamide), D-D4FC (Dexelvucitabine; Reverset; INCB-8721; DPC 817), dOTC (2'-Deoxy-3'-Oxa-4'-Thiocytidine; BCH-10652), Elvucitabine, EMTRIVA™ (emtricitabine), EPIVIR™ (lamivudine; 3TC), EFdA (4'-Ethynyl-2-fluoro-2'-deoxyadenosine; MK-8591), EVIPLERA™ (rilpivirine / emtricitabine / tenofovir disoproxil), GENVOYA® (elvitegravir / cobicistat / emtricitabine / tenofovir alafenamide), HIVID™ (zalcitabine; ddC), KIVEXA™ (abacavir / lamivudine), LODENOSINE™ (F-ddA), ODEFSEY® (rilpivirine / tenofovir alafenamide / emtricitabine), PREVEON® (adefovir dipivoxil), Racivir (RCV; (+/-)-Emtricitabine), RETROVIR™ (zidovudine; ZDV; azidothymidine; AZT), Stampidine, STRIBILD® (Elvitegravir /cobicistat / emtricitabine / tenofovir disoproxil), TENOFOVIR™ (TDF, bis-POC PMPA), TRIUMEQ® (dolutegravir / abacavir / lamivudine), TRIZIVIR™ (abacavir / lamivudine / zidovudine), TRUVADA® (emtricitabine / tenofovir disoproxil), VEMLIDY® (tenofovir alafenamide; TAF), VIDEX™ (didanosine ddi), VIREAD™ (tenofovir disoproxil), ZIAGEN™ (abacavir; 159U89), and ZERIT™ (stavudine; d4T).

[0116] At the doses used for HIV/AIDS therapy, these drugs can cause a wide range of side effects. Common Side Effects of NRTIs include, *inter alia*, mitochondrial toxicity (associated with inhibition of mitochondrial polymerase), neuropathy, pancreatitis, hepatic steatosis and lactic acidosis, myelosuppression, symptomatic myopathy, and cardiomyopathy.³⁹ Although the NRTIs can be used at the dosage approved for HIV/AIDS treatment, lower dosages can be used for the prevention or treatment of age-related inflammation and disorders in order to avoid the side effects associated with the higher doses. In one embodiment, the dosage used for the prevention or treatment of age-related inflammation and disorders is half (50%) of the dosage approved for HIV/AIDS treatment (see **Table 9**). In an alternate embodiment, the dosage used is 75% of the dosage approved for HIV/AIDS treatment. In yet

another alternate embodiment, the dosage used is 25% of the dosage approved for HIV/AIDS treatment. In other alternate embodiments, the dosage used is 90%, 80%, 70%, 60%, 40%, 30%, 20%, or 10% of the dosage approved for HIV/AIDS treatment. In yet other alternate embodiments, the dosage used is 0.1 to 99.5%, 10 to 90%, 20 to 80%, 25 to 75%, 30 to 70%, 40 to 60% or 45 to 55% of the dosage approved for HIV/AIDS treatment.

[0117] In some embodiments, the subject undergoes long term administration of one or more RTI drugs, as defined herein. In one embodiment, the subject is treated for a period of at least 12 weeks. In many cases, long-term administration is for at least 4, 5, 6, 7, 8, 9 months or more, or for at least 1, 2, 3, 5, 7 or 10 years, or more.

AGE-ASSOCIATED DISORDERS

[0118] Given that cellular senescence is one of the major drivers of organismal aging and aging-associated diseases,⁴⁰ the methods of the present invention can be used to prevent or treat disorders or diseases that have been associated with cellular senescence, in particular in which the presence of senescent cells is likely to have a deleterious effect, by the administration of one or more senostatic RTI drugs.

[0119] Disorders or diseases that have been associated with cellular senescence include, but are not limited to, Alzheimer's disease,⁴¹ amyotrophic lateral sclerosis (ALS), atherosclerosis,⁴² Huntington's disease, vision loss, hearing loss, peripheral degenerative diseases, cardiovascular dysfunction,⁴³ atherosclerosis, frontotemporal dementia (FTD), multiple sclerosis (MS), Aicardi Goutiere's syndrome, progressive supra nuclear palsy (PSP), chemotherapy-induced adverse effects (e.g., bone marrow suppression, cardiotoxicity, cancer recurrence, blood clots, fatigue),⁴⁴ hematopoietic stem cell function,⁴⁵ osteoarthritis,⁴⁶ osteoporosis,⁴⁷ osteoporosis, Parkinson's disease,⁴⁸ physical function,⁴⁹ pulmonary fibrosis,⁵⁰ skin aging, wound healing, and/or tissue regeneration.⁵¹

METHODS OF TREATING, PREVENTING AND REVERSING AGE-ASSOCIATED INFLAMMATION WITH RTIS

[0120] Provided is a method for treating, preventing and reversing age-associated inflammation in a patient in need thereof by administering a reverse transcriptase inhibitor (RTI) to a patient in need thereof. The age-associated inflammation may be in a patient having Alzheimer's disease, amyotrophic lateral sclerosis, Parkinson's disease, Huntington's disease, vision loss, hearing loss, peripheral degenerative diseases, and cardiovascular dysfunction.

[0121] In one embodiment is provided a method for delaying or reversing the progression of the underlying pathology of an age-associated inflammatory disorder, comprising

administering to a patient in need thereof a therapeutically effective amount of at least one reverse transcriptase inhibitor (RTI). In some embodiments, the patient experiences a decrease in one or more symptoms of Alzheimer's disease compared to before the first administration of the RTI to the patient.

[0122] In another embodiment, provided is a method for preventing the onset of an age-associated inflammatory disorder in a patient suspected of having mild cognitive impairment, comprising administering at least one RTI to a patient in need thereof.

[0123] In some embodiments, the NRTI is abacavir, lamivudine, zidovudine, emtricitabine, tenofovir disoproxil fumarate, tenofovir alafenamide, didanosine, stavudine, apricitabine, alovudine, dexelvucitabine, amdoxovir, fosalvudine or elvucitabine. In other embodiments, the RTI is abacavir (Ziagen), abacavir/lamivudine (Epzicom), abacavir/lamivudine/zidovudine (Trizivir), lamivudine/zidovudine (Combivir), lamivudine (Epivir), zidovudine (Retrovir), emtricitabine/tenofovir disoproxil fumarate (Truvada), emtricitabine (Emtriva), tenofovir disoproxil fumarate (Viread), emtricitabine/tenofovir alafenamide (Descovy), didanosine (Videx), didanosine extended-release (Videx EC), or stavudine (Zerit). In another embodiment, the NRTI is censavudine.

[0124] In some embodiments, the at least one RTI is a non-nucleoside reverse transcriptase inhibitor (NNRTI). In some embodiments, the at least one NRTI is Efavirenz (EFV), Nevirapine (NVP), Delavirdine (DLV), Etravirine or Rilvipirine.

[0125] In a further embodiment, the RTI inhibits L1 reverse transcriptase activity in a cell, e.g., a brain cell, of the patient.

[0126] Where the RTI is an FDA approved drug, the RTI may be administered in therapeutically effective amounts that are approved for therapeutic use. In other embodiments, the amounts effective can be determined with no more than routine experimentation. For example, amounts effective may range from about 1 ng/kg to about 200 mg/kg, about 1 µg/kg to about 100 mg/kg, or about 1 mg/kg to about 50 mg/kg. The dosage of a composition can be at any dosage including, but not limited to, about 1 µg/kg. The dosage of a composition may be at any dosage including, but not limited to, about 1 µg/kg, about 10 µg/kg, about 25 µg/kg, about 50 µg/kg, about 75 µg/kg, about 100 µg/kg, about 125 µg/kg, about 150 µg/kg, about 175 µg/kg, about 200 µg/kg, about 225 µg/kg, about 250 µg/kg, about 275 µg/kg, about 300 µg/kg, about 325 µg/kg, about 350 µg/kg, about 375 µg/kg, about 400 µg/kg, about 425 µg/kg, about 450 µg/kg, about 475 µg/kg, about 500 µg/kg, about 525 µg/kg, about 550 µg/kg, about 575 µg/kg, about 600 µg/kg, about 625 µg/kg, about 650 µg/kg, about 675 µg/kg, about 700 µg/kg, about 725 µg/kg, about 750 µg/kg, about 775 µg/kg, about 800 µg/kg, about 825 µg/kg, about

850 µg/kg, about 875 µg/kg, about 900 µg/kg, about 925 µg/kg, about 950 µg/kg, about 975 µg/kg, about 1 mg/kg, about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, about 20 mg/kg, about 25 mg/kg, about 30 mg/kg, about 35 mg/kg, about 40 mg/kg, about 45 mg/kg, about 50 mg/kg, about 60 mg/kg, about 70 mg/kg, about 80 mg/kg, about 90 mg/kg, about 100 mg/kg, about 125 mg/kg, about 150 mg/kg, about 175 mg/kg, about 200 mg/kg, or more. In other embodiments, the dosage is 1 mg-500 mg. In some embodiments, the dosage is 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 mg. These doses may be unitary or divided and may be administered one or more times per day. The above dosages are exemplary of the average case, but there can be individual instances in which higher or lower dosages are merited, and such are within the scope of this disclosure. In practice, the physician determines therapeutically effective amounts and the actual dosing regimen that is most suitable for an individual subject, which can vary with the age, weight, and response of the particular subject.

[0127] The RTI may be administered once, twice or three times per day for 1 day to the end of life, or for 1 day to 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more years, or until the RTI causes unacceptable side effects or is no longer useful.

[0128] The patient is monitored for changes in the symptoms of the age-associated inflammatory disease. In one embodiment, there is a reduction in the symptoms. In another embodiment, the symptoms remain about the same and there is no evidence of progression. In connection with Alzheimer's disease, such symptoms include memory loss, misplacing items, forgetting the names of places or objects, repeating questions, being less flexible, confusion, disorientation, obsessive behavior, compulsive behavior, delusions, aphasia, disturbed sleep, mood swings, depression, anxiety, frustration, agitation, difficulty in performing spatial tasks, agnosia, difficulty with ambulation, weight loss, loss of speech, loss of short term memory or loss of long term memory. Methods for monitoring and quantifying any change of these symptoms can be carried out by routine methods or by routine experimentation.

[0129] In one embodiment, symptoms of mild cognitive impairment and any change in the symptoms of Alzheimer's disease is determined using the criteria set forth in DSM-5. In another embodiment, symptoms of mild cognitive impairment and the any change in the symptoms of Alzheimer's disease is determined using the Clinician's Interview-Based Impression of Change (CIBIC-plus). In another embodiment, symptoms of mild cognitive impairment and any change in symptoms is determined using the Clinician's Interview-Based Impression of Change (CIBIC-plus).

[0130] Any change in symptoms may be monitored for 1-36 months or more, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 months.

[0131] In another embodiment, the patient is monitored for a change in the underlying pathology of Alzheimer's disease. In one embodiment, there is a reduction in the underlying pathology. In another embodiment, the underlying pathology remains about the same and there is no evidence of progression.

[0132] In some embodiments, any change in the underlying pathology is identified by detection of a biomarker before and after the RTI administration. In one embodiment, the biomarker is β -amyloid or Tau protein. In another embodiment, the biomarker is detected by PET imaging. In another embodiment, the underlying pathology is identified by measurement of brain volume before and after the RTI administration.

[0133] In some embodiments, the decrease of the underlying pathology is reversed or delayed for at 1-36 months, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 months after the first administration of the RTI.

[0134] In some embodiments, the patient is also administered at least one second therapeutic agent useful for the treatment of the symptoms of an age-associated inflammatory disorder. In one embodiment, the patient is administered at least one second therapeutic agent useful for the treatment of Alzheimer's disease. In some embodiments, the at least one second therapeutic agent is donepezil, galantamine, rivastigmine, or memantine. In another embodiment, the at least one second therapeutic agent is an antibody that binds to β -amyloid or Tau protein. In another embodiment, the antibody binds to β -amyloid and is bapineuzumab. In another embodiment, the antibody binds to Tau protein and is ABBV-8E12. In another embodiment, the at least one second therapeutic agent is a vaccine against β -amyloid or Tau protein. In another embodiment, the at least one second therapeutic agent is an agent that reduces or alters the brain content of β -amyloid or Tau. In another embodiment, the second therapeutic agent reduces or alters the brain content of β -amyloid and is a β -secretase 1 (BACE) inhibitor. In another embodiment, the BACE inhibitor is CTS-21166, verubecestat (MK-8931), lanabecestat (AZD3293) or LY2886721. In another embodiment, the second agent reduces or alters the brain content of β -amyloid or Tau alters the brain content of Tau and is nicotinamide, or MPT0G211.

[0135] The at least one RTI and at least one second therapeutic agent may be administered separately or together as part of a unitary pharmaceutical composition.

[0136] When the age-associated inflammatory disorder is ALS, the patient may be administered at least one second agent useful for the treatment of the symptoms of ALS. In some embodiments, the at least one second agent is an integrase inhibitor. In some embodiments, the integrase inhibitor is raltegravir, curcumin, derivatives of curcumin, chicoric acid, derivatives of chicoric acid, 3,5-dicaffeoylquinic acid, derivatives of 3,5-dicaffeoylquinic acid, aurintricarboxylic acid, derivatives of aurintricarboxylic acid, caffeic acid phenethyl ester, derivatives of caffeic acid phenethyl ester, tyrphostin, derivatives of tyrphostin, quercetin, derivatives of quercetin, S-1360, zintevir (AR-177), L-870812, and L-25 870810, MK-0518, BMS-538158, or GSK364735C.⁵²

[0137] The patient may be monitored for improvement of the symptoms of ALS. Such symptoms include one or more of the following: difficulty walking or doing normal daily activities, tripping and falling, weakness of the legs, feet or ankles, hand weakness or clumsiness, slurred speech or trouble swallowing, muscle cramps, twitching in the arms, shoulders or tongue, inappropriate crying, cognitive changes, and behavior changes.

[0138] Any change in symptoms may be monitored for 1-36 months or more, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 months. In some embodiments, the decrease of the underlying pathology is reversed or delayed for at 1-36 months, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 months after the first administration of the RTI.

SALTS, PHARMACEUTICAL COMPOSITIONS, AND KITS

[0139] The methods of the present disclosure can be accomplished by administering an at least one RTI as the neat compound or as a pharmaceutical composition. Administration of a pharmaceutical composition, or neat compound of an RTI, can be performed before or after the clinical diagnosis of a disorder associated with age-associated inflammation. Typically, the pharmaceutical compositions are sterile, and contain no toxic, carcinogenic, or mutagenic compounds that would cause an adverse reaction when administered.

[0140] Further provided are kits comprising at least one RTI and, optionally, at least one second therapeutic agent useful for the treatment or prevention of a disorder associated with age-associated inflammation, packaged separately or together, and an insert having instructions for using these active agents. In one embodiment, the at least one RTI is packaged alone together with instructions to administered together with the at least one second therapeutic agent. The at least one RTI and the at least one second therapeutic agent can be administered

simultaneously or sequentially to achieve the desired effect. In addition, the RTI and the at least one second therapeutic agent can be administered from a single composition or two separate compositions.

[0141] Examples of the at least one second therapeutic agents useful for the treatment of Alzheimer's disease that may be in the kit include donepezil, galantamine, rivastigmine and memantine. Other optional therapeutic agents that may be in the kit include an antibody that binds to β -amyloid or Tau protein. In one embodiment, the antibody binds to β -amyloid and is bapineuzumab. In another embodiment, the antibody binds to Tau and is ABBV-8E12.

[0142] In another embodiment, the kit may contain least one second therapeutic agent that is a vaccine against β -amyloid or Tau protein.

[0143] In another embodiment, the kit may contain at least one second therapeutic agent that reduces or alters the brain content of β -amyloid or Tau protein. In some embodiments, the second therapeutic agent that alters or reduces the brain content of β -amyloid is a β -secretase 1 (BACE) inhibitor. In some embodiment, the BACE inhibitor is CTS-21166, verubecestat (MK-8931), lanabecestat (AZD3293) or LY2886721, each of which have been in clinical trials for the treatment of Alzheimer's disease.

[0144] In another embodiment, the kit may contain a second agent that reduces or alters the brain content of Tau and is nicotinamide, or MPT0G211.

[0145] In some embodiments, the patient has ALS and the kit further comprises at least one second agent useful for the treatment of ALS. In other embodiments, the RTI is packaged alone together with instructions to administer at least one second therapeutic agent for the treatment of ALS. In some embodiments, the at least one second therapeutic agent for the treatment of ALS is edaravone or riluzole.

[0146] In some embodiments, the at least one second agent is an integrase inhibitor. In some embodiments, the integrase inhibitor is raltegravir, curcumin, derivatives of curcumin, chicoric acid, derivatives of chicoric acid, 3,5-dicaffeoylquinic acid, derivatives of 3,5dicaffeoylquinic acid, aurintricarboxylic acid, derivatives of aurintricarboxylic acid, caffeic acid phenethyl ester, derivatives of caffeic acid phenethyl ester, tyrphostin, derivatives of tyrphostin, quercetin, derivatives of quercetin, S-1360, zintevir (AR-177), L-870812, and L-25 870810, MK-0518, BMS-538158, or GSK364735C.⁵³

[0147] The second therapeutic agent is administered in an amount to provide its desired therapeutic effect. The effective dosage range for each optional therapeutic agent is known in the art, and the optional therapeutic agent is administered to an individual in need thereof within such established ranges.

[0148] The present disclosure encompasses the preparation and use of salts of RTIs. As used herein, a "pharmaceutically acceptable salt" refers to salts or zwitterionic forms of the RTIs. Salts of RTIs can be prepared during the final isolation and purification of the compounds or separately by reacting the compound with a suitable acid. The pharmaceutically acceptable salts of RTIs can be acid addition salts formed with pharmaceutically acceptable acids. Examples of acids which can be employed to form pharmaceutically acceptable salts include inorganic acids such as nitric, boric, hydrochloric, hydrobromic, sulfuric, and phosphoric, and organic acids such as oxalic, maleic, succinic, and citric. Non-limiting examples of salts of RTIs include, but are not limited to, the hydrochloride, hydrobromide, hydroiodide, sulfate, bisulfate, 2-hydroxyethansulfonate, phosphate, hydrogen phosphate, acetate, adipate, alginate, aspartate, benzoate, bisulfate, butyrate, camphorate, camphorsulfonate, digluconate, glycerolphosphate, hemisulfate, heptanoate, hexanoate, formate, succinate, fumarate, maleate, ascorbate, isethionate, salicylate, methanesulfonate, mesitylenesulfonate, naphthylenesulfonate, nicotinate, 2 naphthalenesulfonate, oxalate, pamoate, pectinate, persulfate, 3 phenylpropionate, picrate, pivalate, propionate, trichloroacetate, trifluoroacetate, phosphate, glutamate, bicarbonate, para-toluenesulfonate, undecanoate, lactate, citrate, tartrate, gluconate, methanesulfonate, ethanedisulfonate, benzene sulfonate, and p toluenesulfonate salts. In addition, available amino groups present in the RTIs can be quaternized with methyl, ethyl, propyl, and butyl chlorides, bromides, and iodides; dimethyl, diethyl, dibutyl, and diamyl sulfates; decyl, lauryl, myristyl, and steryl chlorides, bromides, and iodides; and benzyl and phenethyl bromides. In light of the foregoing, any reference to RTIs appearing herein is intended to include the RTIs as well as pharmaceutically acceptable salts, hydrates, or solvates thereof.

[0149] The present disclosure encompasses the preparation and use of solvates of RTIs. Solvates typically do not significantly alter the physiological activity or toxicity of the compounds, and as such may function as pharmacological equivalents. The term "solvate" as used herein is a combination, physical association and/or solvation of a compound of the present disclosure with a solvent molecule such as, *e.g.*, a disolvate, monosolvate or hemisolvate, where the ratio of solvent molecule to compound of the present disclosure is about 2:1, about 1:1 or about 1:2, respectively. This physical association involves varying degrees of ionic and covalent bonding, including hydrogen bonding. In certain instances, the solvate can be isolated, such as when one or more solvent molecules are incorporated into the crystal lattice of a crystalline solid. Thus, "solvate" encompasses both solution-phase and isolatable solvates. RTIs can be present as solvated forms with a pharmaceutically acceptable solvent,

such as water, methanol, and ethanol, and it is intended that the disclosure includes both solvated and unsolvated forms of RTIs. One type of solvate is a hydrate. A "hydrate" relates to a particular subgroup of solvates where the solvent molecule is water. Solvates typically can function as pharmacological equivalents. Preparation of solvates is known in the art. See, e.g., Caira *et al.* (2004),⁵⁴ which describes the preparation of solvates of fluconazole with ethyl acetate and with water. Similar preparation of solvates, hemisolvates, hydrates, and the like are described by Van Tonder *et al.* (2004)⁵⁵ and Bingham *et al.* (2001).⁵⁶ A typical, non-limiting, process of preparing a solvate would involve dissolving the at least one RTI or at least one second therapeutic agent in a desired solvent (organic, water, or a mixture thereof) at temperatures above 20°C to about 25°C, then cooling the solution at a rate sufficient to form crystals, and isolating the crystals by known methods, e.g., filtration. Analytical techniques such as infrared spectroscopy can be used to confirm the presence of the solvate in a crystal of the solvate.

[0150] The at least one RTI and at least one second therapeutic agent typically are administered in admixture with a pharmaceutical carrier to give a pharmaceutical composition selected with regard to the intended route of administration and standard pharmaceutical practice. Pharmaceutical compositions for use in accordance with the present disclosure are formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and/or auxiliaries that facilitate processing of the at least one RTI and at least one second therapeutic agent.

[0151] These pharmaceutical compositions can be manufactured, for example, by conventional mixing, dissolving, granulating, dragee-making, emulsifying, encapsulating, entrapping, or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of the at least one RTI and/or at least one second therapeutic agent is administered orally, the composition typically is in the form of a tablet, capsule, powder, solution, or elixir. When administered in tablet form, the composition additionally can contain a solid carrier, such as a gelatin or an adjuvant. The tablet, capsule, and powder contain about 0.01% to about 95%, and preferably from about 1% to about 50%, of the at least one RTI and at least one second therapeutic agent. When administered in liquid form, a liquid carrier, such as water, petroleum, or oils of animal or plant origin, can be added. The liquid form of the composition can further contain physiological saline solution, dextrose or other saccharide solutions, or glycols. When administered in liquid form, the composition contains about 0.1% to about 90%, and preferably about 1% to about 50%, by weight, of the at least one RTI and at least one second therapeutic agent.

[0152] When a therapeutically effective amount of the at least one RTI and at least one second therapeutic agent is administered by intravenous, cutaneous, or subcutaneous injection, the composition is in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred composition for intravenous, cutaneous, or subcutaneous injection typically contains, an isotonic vehicle.

[0153] The at least one RTI and at least one second therapeutic agent can be readily combined with pharmaceutically acceptable carriers well-known in the art. Standard pharmaceutical carriers are described in Remington's Pharmaceutical Sciences.⁵⁷ Such carriers enable the active agents to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a subject to be treated. Pharmaceutical preparations for oral use can be obtained by adding the at least one RTI and/or the at least one second therapeutic agent to a solid excipient, optionally grinding the resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients include, for example, fillers and cellulose preparations. If desired, disintegrating agents can be added.

[0154] The at least one RTI and at least one second therapeutic agent can be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection can be presented in unit dosage form, *e.g.*, in ampules or in multidose containers, with an added preservative. The compositions can take such forms as suspensions, solutions, or emulsions in oily or aqueous vehicles, and can contain formulatory agents such as suspending, stabilizing, and/or dispersing agents.

[0155] Pharmaceutical compositions for parenteral administration include aqueous solutions of the active agent in water-soluble form. Additionally, suspensions of the at least one RTI and at least one second therapeutic agent can be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils or synthetic fatty acid esters. Aqueous injection suspensions can contain substances which increase the viscosity of the suspension. Optionally, the suspension also can contain suitable stabilizers or agents that increase the solubility of the compounds and allow for the preparation of highly concentrated solutions. Alternatively, a present composition can be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

[0156] The at least one RTI and at least one second therapeutic agent also can be formulated in rectal compositions, such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases. In addition to the formulations described previously, the at

least one RTI and at least one second therapeutic agent also can be formulated as a depot preparation. Such long-acting formulations can be administered by implantation (for example, subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the at least one RTI and at least one second therapeutic agent can be formulated with suitable polymeric or hydrophobic materials (for example, as an emulsion in an acceptable oil) or ion exchange resins.

[0157] In particular, the at least one RTI and at least one second therapeutic agent can be administered orally, buccally, or sublingually in the form of tablets containing excipients, such as starch or lactose, or in capsules or ovules, either alone or in admixture with excipients, or in the form of elixirs or suspensions containing flavoring or coloring agents. Such liquid preparations can be prepared with pharmaceutically acceptable additives, such as suspending agents. The at least one RTI and at least one second therapeutic agent also can be injected parenterally, for example, intravenously, intramuscularly, subcutaneously, or intracoronarily. For parenteral administration, the at least one RTI and at least one second therapeutic agent are typically used in the form of a sterile aqueous solution which can contain other substances, for example, salts or monosaccharides, such as mannitol or glucose, to make the solution isotonic with blood.

[0158] Some embodiments of the technology described herein can be defined according to any of the following numbered paragraphs:

1. A method for treating, preventing and/or reversing age-associated inflammation in a patient in need thereof comprising administering a therapeutically effective amount of a reverse transcriptase inhibitor (RTI) to the patient in need thereof, wherein the RTI comprises censavudine or elvucitabine.
2. The method of paragraph 1, wherein the age-associated inflammation is in a patient having Alzheimer's disease, amyotrophic lateral sclerosis (ALS), Parkinson's disease, Huntington's disease, vision loss, hearing loss, peripheral degenerative diseases, or cardiovascular dysfunction, frontotemporal dementia (FTD), multiple sclerosis (MS), Aicardi Goutiere's syndrome, progressive supra nuclear palsy (PSP), osteoarthritis, skin aging, atherosclerosis, chemotherapy-induced adverse effects, hematopoietic stem cell function, osteoporosis, physical function, and/or pulmonary fibrosis, or in a patient in need of wound healing or tissue regeneration.
3. The method of paragraph 1, wherein the age-associated inflammation is in a patient having Alzheimer's disease.

4. The method of paragraph 1, wherein the age-associated inflammation is in a patient having ALS.
5. A method for delaying or reversing the progression of the underlying pathology of a disorder caused by age-associated inflammation, comprising administering to a patient in need thereof a therapeutically effective amount of a reverse transcriptase inhibitor (RTI), wherein the RTI comprises censavudine or elvucitabine.
6. The method of paragraph 5, wherein the patient has Alzheimer's disease or ALS and experiences a decrease in one or more symptoms of Alzheimer's disease or ALS compared to before the first administration to the patient.
7. The method of paragraph 6, wherein the patient has Alzheimer's disease and the one or more symptoms comprise memory loss, misplacing items, forgetting the names of places or objects, repeating questions, being less flexible, confusion, disorientation, obsessive behavior, compulsive behavior, delusions, aphasia, disturbed sleep, mood swings, depression, anxiety, frustration, agitation, difficulty in performing spatial tasks, agnosia, difficulty with ambulation, weight loss, loss of speech, loss of short term memory or loss of long term memory.
8. The method of paragraph 6, wherein the patient has Alzheimer's disease and the decrease in the one or more symptoms are evaluated according to the DSM-5.
9. The method of paragraph 6, wherein the patient has Alzheimer's disease and the decrease of symptoms is determined using the cognitive subscale of the Alzheimer's Disease Assessment Scale (ADAS-cog).
10. The method of paragraph 6, wherein the patient has Alzheimer's disease and the decrease of symptoms is determined using the Clinician's Interview-Based Impression of Change (CIBIC-plus).
11. The method of paragraph 6, wherein the patient has Alzheimer's disease and the decrease of symptoms is determined using the Activities of Daily Living Scale (ADL).
12. The method of any one of paragraphs 6-11, wherein the decrease of symptoms is for 1-36 months.
13. The method of any one of paragraphs 6-11, wherein any change in the underlying pathology is identified by detection of a biomarker before and after the RTI administration.
14. The method of paragraph 13, wherein the biomarker is β -amyloid or Tau protein.
15. The method of paragraphs 13 or 14, wherein the biomarker is detected by PET imaging.
16. The method of paragraphs 13 or 14, wherein the biomarker is detected by measurement in the cerebrospinal fluid.
17. The method of any one of paragraphs 6-11, wherein the underlying pathology is identified by measurement of brain volume before and after the RTI administration.

18. The method of any one of paragraphs 6-17, wherein the decrease of the underlying pathology is reversed or delayed for 1-36 months.
19. A method for preventing the onset of Alzheimer's disease in a patient suspected of having mild cognitive impairment, comprising administering to a patient in need thereof a therapeutically effective amount of a reverse transcriptase inhibitor (RTI), wherein the RTI comprises censavudine or elvucitabine.
20. The method of any one of paragraphs 1-19, wherein the patient has Alzheimer's disease or mild cognitive impairment, and further comprising administering at least one second therapeutic agent useful for the treatment of the symptoms of Alzheimer's disease.
21. The method of paragraph 20, wherein the at least one second therapeutic agent is donepezil, galantamine, rivastigmine, or memantine.
22. The method of paragraph 20, wherein the at least one second therapeutic agent is an antibody that binds to β -amyloid or Tau protein.
23. The method of paragraph 22, wherein the antibody binds to β -amyloid and is bapineuzumab.
24. The method of paragraph 22, wherein the antibody binds to Tau protein and is ABBV-8E12.
25. The method of paragraph 20, wherein the at least one second therapeutic agent is a vaccine against β -amyloid or Tau protein.
26. The method of paragraph 20, wherein the at least one second therapeutic agent is an agent that reduces or alters the brain content of β -amyloid or Tau.
27. The method of paragraph 26, wherein the second therapeutic agent reduces or alters the brain content of β -amyloid and is a β -secretase 1 (BACE) inhibitor.
28. The method of paragraph 27, wherein the BACE inhibitor is CTS-21166, verubecestat (MK-8931), lanabecestat (AZD3293) or LY2886721.
29. The method of paragraph 26, wherein the second agent reduces or alters the brain content of Tau and is nicotinamide, or MPT0G211.
30. The method of any one of paragraphs 1, 2, or 4, wherein the patient has ALS, and further comprising administering at least one second agent useful for the treatment of ALS.
31. The method of paragraph 30, wherein the drug useful for the treatment of ALS is edaravone or riluzole.
32. The method of paragraph 30, wherein the at least one second agent is an integrase inhibitor.
33. The method of paragraph 32, wherein the integrase inhibitor is raltegravir, curcumin, derivatives of curcumin, chicoric acid, derivatives of chicoric acid, 3,5-dicaffeoylquinic acid, derivatives of 3,5-dicaffeoylquinic acid, aurintricarboxylic acid, derivatives of aurintricarboxylic acid, caffeic acid phenethyl ester, derivatives of caffeic acid phenethyl

ester, tyrphostin, derivatives of tyrphostin, quercetin, derivatives of quercetin, S-1360, zintevir (AR-177), L-870812, and L-25 870810, MK-0518, BMS-538158, or GSK364735C.

34. The method of any one of paragraphs 1-33, wherein the patient is evaluated for one or more symptoms or disease pathology 1-36 months after the first administration to the patient of the RTI.
35. The method of any one of paragraphs 1-34, wherein the RTI inhibits L1 reverse transcriptase activity in a cell of the patient.
36. The method of any one of paragraphs 1-35, wherein the RTI is elvucitabine.
37. The method of any one of paragraphs 1-35, wherein the RTI is censavudine.
38. The method of any one of paragraphs 1-35 further comprising administering at least one second therapeutic agent to the patient.
39. The method of paragraph 38, wherein the patient has Alzheimer's disease and the at least one second therapeutic agent is useful for the treatment of the symptoms of Alzheimer's disease.
40. The method of paragraph 38, wherein the patient has amyotrophic lateral sclerosis (ALS) and the at least one second therapeutic agent is useful for the treatment of ALS.

EXAMPLES

[0159] The invention now being generally described, it will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention.

METHODS

Cell culture

[0160] Several different strains of normal human fibroblasts were employed in this study. LF1 cells were derived from embryonic lung tissue as described.⁵⁸ These cells have been in continuous use in our laboratory since their isolation in 1996. For this study original samples frozen in 1996 and in continuous storage in our laboratory were recovered and used. IMR-90 and WI-38 cells were obtained from the ATCC. None of these cell lines are listed in the International Cell Line Authentication Committee (ICLAC) database. These normal fibroblast cell lines were cultured using physiological oxygen conditions (92.5% N₂, 5% CO₂, 2.5% O₂), in Ham's F-10 nutrient mixture (Thermo Scientific) with 15% fetal bovine serum (FBS, Hyclone). Medium was additionally supplemented with L-glutamine (2 mM), penicillin and streptomycin.⁵⁹

Cell cultures were periodically tested for mycoplasma contamination with MycoAlert® Mycoplasma Detection Kit (Lonza).

[0161] To obtain replicatively senescent (RS) cells, LF1 cultures were serially propagated until proliferation ceased. At each passage, after reaching 80% confluence cells were trypsinized and diluted 1:4. Hence each passage is equivalent to approximately two population doublings. In early passage cultures, the time between passages is constant at approximately 3 days. As cultures approached senescence the time between passages gradually increased. An interval of 2-3 weeks indicated that the culture was in its penultimate passage. At this point, after reaching 80% confluence, the cells were replated at 1:2 dilution, and this time was designated as the last passage (point A in **FIG. 2a**). Some cell growth typically does occur in the next 2-3 weeks, but the cultures do not reach 80%. Under this experimental regimen, the majority of the cells in the culture enter senescence within a 3-4 weeks window centered roughly around the time of last passage (grey bar in **FIG. 2a**). At point B (4 weeks), the cultures were trypsinized and replated as described⁶⁰ to eliminate a small fraction of persisting contact-inhibited cells. Cultures were again replated at point C (8 weeks).

[0162] Oncogene-induced senescence (OIS) was elicited by infecting proliferating LF1 cells with pLenti CMV RasV12 Neo (Addgene plasmid # 22259). Generation of lentiviral particles and the infection procedure are described below. At the end of the infection, cells were reseeded at 15-20% confluency and selected with G418 (250 µg/ml) maintained continuously until the end of the experiment. Medium was changed every 3 days until the cultures were harvested at the indicated time points. Stress-induced premature senescence (SIPS) was elicited by X-ray irradiation with 20 Gy given at a rate of 87 cGy/min in one fraction using a cesium-137 gamma source (Nordion Gammacell 40). Cells were 15-20% confluent at the time of irradiation. Medium was changed immediately after irradiation, and at 3-day intervals thereafter. 293T cells (Clontech) were used to package lentivirus vectors and were cultured at 37°C in DMEM with 10% FBS under normoxic conditions (air supplemented with 5% CO₂).

Reverse transcriptase inhibitors (RTIs)

[0163] All RTIs (lamivudine, 3TC; zidovudine, AZT; abacavir, ABC; emtricitabine, FTC) used in this study were USP grade and obtained from Aurobindo Pharma, Hyderabad, India. For Trizivir (TZV), its constituents (ABC, AZT and 3TC) were combined in the appropriate amounts.

Mouse husbandry

[0164] C57BL/6J mice of both sexes were obtained from the NIA Aged Rodent Colonies⁶¹ at 5 and 18 months of age. The 5-month old animals were sacrificed after a short

(1 week) acclimatization period, a variety of tissues were harvested, snap frozen in LN2 and stored at -80°C. The 18-month old animals were housed until they reached a desired age. Mice were housed in a specific pathogen-free AAALAC-certified barrier facility. Cages, bedding (Sani-chip hardwood bedding) and food (Purina Lab Chow 5010) were sterilized by autoclaving. Food and water (also sterilized) were provided ad libitum. A light-dark cycle of 12 hours was used (7 AM On, 7 PM Off). Temperature was maintained at 70°F, and humidity at 50%. All animals were observed daily and weighed once per week. In a pilot experiment, three cohorts of 10 animals each were treated with 3TC dissolved in drinking water (1.5 mg/ml, 2.0 mg/ml, 2.5 mg/ml) continuously from 18 months until sacrifice at 24 months. The fourth (control) cohort was provided with the same water without drug. No significant differences in behavior, weight, or survival were observed between the 4 cohorts during the entire experiment. Once during the experiment (at 20 months of age) the animals were subjected to a single tail bleed of approximately 70 μ L. The collected plasma was shipped to the University of North Carolina CFAR Clinical Pharmacology and Analytical Chemistry Core for analysis of 3TC. For the 2 mg/mL cohort the concentration of 3TC in plasma averaged 7.2 μ M. This dose of drug was chosen for further experiments to mimic the human HIV therapeutic dose (300 mg per day, 5-8 μ M in plasma).⁶² For the experiments presented in this communication animals were aged in house until they reached 26 months of age. They were then assigned randomly to two cohorts by a technician that was blinded to the appearance or other characteristics of the animals. One cohort was treated for 2 weeks with 2 mg/mL of 3TC in drinking water, and the other (control) cohort with same water without drug, administered in the same manner. At the end of the treatment period all animals were sacrificed and harvested for tissues as described above. All the animals in both cohorts were all included in all subsequent analyses. The experiment was performed on separate occasions with male and female animals. Non-lethal total body irradiation (6 Gy) was performed as described⁶³ and tissue specimens were kept on dry ice.

PCR

[0165] The ABI ViiA 7 instrument (Applied Biosystems) was used for all experiments. qPCR of DNA was performed using the TaqMan system (Applied Biosystems) as described by Coufal *et al.* (2009).⁶⁴ 100 pg of purified genomic DNA was used with the indicated primers (see **Table 1**). Reverse transcription qPCR (RT-qPCR) of RNA was performed using the SYBR Green system (Applied Biosystems). Polyadenylated RNA was used in all experiments assessing transcription of L1 elements, and total RNA was used for all other genes. Total RNA was harvested using the Trizol reagent (Invitrogen). Poly(A) RNA was isolated from total RNA

using the NEBNext Poly(A) mRNA Magnetic Isolation Module (New England Biolabs). 1 µg of total RNA, or 10 ng of poly(A) RNA, were reverse-transcribed into cDNA in 50 µL reactions using the TaqMan kit (Applied Biosystems). To assess strand-specific transcription, the random primers in the RT reaction were substituted with a strand-specific primer to the target RNA. 1 µL of each RT reaction was used in subsequent qPCR reactions. GAPDH was used as the normalization control in experiments with human cells. The arithmetic mean of Gapdh and two additional controls (Hsp90 and GusB) was used for normalization of RT-qPCR experiments with murine tissues, with the exception of liver that was normalized to Hsp90 and GusB. For measuring L1 transcription, poly(A) RNA samples were exhaustively digested with RNase-free DNase (Qiagen) prior to the synthesis of cDNA. Effectiveness of the DNase digestion was assessed using controls that omitted the RT enzyme.

Design of PCR primers

[0166] Primer sets 1 to 5 (**Table 1**, amplicons A to E in **FIG. 1b**) to human L1 were designed to preferentially amplify elements of the human-specific L1HS and evolutionarily recent primate-specific L1PA(2-6) subfamilies, as follows. First, the consensus sequences of L1HS and L1PA2 through L1PA6 elements were obtained from Repbase (Genetic Information Research Institute⁶⁵). Second, a consensus sequence of these six sequences was generated with the Clustal Omega multiple sequence alignment tool.^{66,67} Primer design was then done on the overall consensus with Primer3 and BLAST using the NCBI Primer-BLAST tool.^{68,69} L1 primer pairs were evaluated for their targets using the In-Silico PCR⁷⁰ tool against the latest genome assembly (hg38) with a minimum perfect match on 3' end of each primer equal to 15. Primers to ORF2 (primer set 6, amplicon F in **FIG. 1b**) were developed by Coufal *et al.* (2009) to preferentially target L1HS. Primers to assess transcription of active murine L1 elements (primer set 37, **Table 1**) were designed on the combined consensus sequence of the L1MdA and L1Tf families obtained from Repbase and validated as described above. L1 primer pairs, spanning the full length these elements (primer sets 48-50), were designed using the same strategy. Primer pairs specific to the three active families of murine L1 elements (primer sets 51-53) were designed exploiting polymorphisms in the 5'UTR region. RT-qPCR analysis of L1 transcription was performed on poly(A) purified RNA using the SYBR Green method. For all other (non-L1) genes, whenever possible, primers are separated by at least one intron in the genomic DNA sequence (as indicated in **Table 1**). Primers to the human IFN alpha family were designed against a consensus sequence of all the human IFN alpha gene sequences (*IFNA1*, *IFNA2*, *IFNA4*, *IFNA5*, *IFNA6*, *IFNA7*, *IFNA8*, *IFNA10*, *IFNA13*, *IFNA14*, *IFNA16*, *IFNA17*, *IFNA21*) generated with the Clustal Omega multiple sequence alignment tool. All primers against murine

targets were designed as described above and are listed in **Table 1**. Sequences of primers corresponding to a consensus of all the murine IFN alpha family genes, as well as to the *IFNB1* gene, were obtained from the publication by Gautier *et al.*⁷¹ For quantifying relative L1 genomic copy number (human cells), the TaqMan multiplex method developed by Coufal *et al.* (2009)⁷² was used. These primers are listed as set #6 and set #7 (with their corresponding VIC and 6FAM probes) in **Table 1**.

Chromatin Immunoprecipitation

[0167] All ChIP experiments were performed using the Chromatrap spin column ChIP kit (Porvair). Briefly, 2×10^6 cells were crosslinked in their culture dishes with 1% formaldehyde (10 min, room temperature), quenched with glycine, washed twice with ice-cold PBS (containing protease inhibitors), and finally scraped into a microfuge tube. Cell pellets were resuspended in 0.4 mL of hypotonic buffer and incubated for 10 min on ice. Nuclei were spun down, resuspended in 0.3 mL lysis buffer, and sonicated using a Bioruptor UCD-200 instrument (Diagenode) set to pulse on high (30 sec followed by 30 sec. rest) for a total time of 10 min. The extracts were centrifuged in a microfuge (top speed, 5 min, 4°C) to remove debris, the supernatants were transferred to new tubes, and stored at -80°C. An amount of extract containing 2 µg of DNA was combined with 4 µg of antibody and loaded on a Chromatrap solid phase Protein A matrix. Immunocomplexes were allowed to form overnight at 4°C with mild agitation, following which the samples were washed and eluted according to the manufacturer's protocol. Rabbit IgG and 1% input were used as controls. 1 µL of immunoprecipitated DNA was used in each qPCR reaction.

BrdU pull-down

[0168] To obtain quiescent cells, proliferating cells were grown to 50% confluence, serum supplementation of the medium was changed to 0.1% FBS, and incubation was continued until harvest. Quiescent and senescent cells were continuously labeled for two weeks with BrdU (BrdU Labeling Reagent, Thermo Fisher) according to the manufacturer's protocol for labeling of culture cells. Cells were harvested and counted: 5×10^5 cells were processed per condition. Genomic DNA was purified via Phenol:Chloroform extraction, RNase A treated and subsequently sheared using a Bioruptor UCD-200 instrument (pulse on Low, 30 sec on and 30 sec off, 10 min total). DNA tubes were incubated in a heat block (100°C) for exactly one minute and then flash frozen in liquid nitrogen. Tubes were let thaw at room temperature and 1 µg of purified anti-BrdU antibody (BD Pharmingen, Cat. # 555627) was added per tube together with magnetic protein A/G beads and ChIP Dilution Buffer. Immuno-slurries were incubated overnight at 4°C with constant rotation. Immuno-captured BrdU labeled

DNA was purified according to the Magna ChIP™ A/G Chromatin Immunoprecipitation Kit (Millipore Sigma). Unbound DNA was kept as input. 1 µL of immunoprecipitated DNA was used in each qPCR reaction. Alternatively, to enrich for single-stranded BrdU-labeled DNA the heat-mediated denaturation was omitted and samples were processed for BrdU pull-down as above. The DNA second strand was then generated by adding a mixture of random primers (Thermo Fisher), second strand synthesis reaction buffer, dNTPs and DNA Pol I (New England Biolabs). The reaction was incubated for 4 hrs at 16°C and subsequently purified by phenol-chloroform extraction. Following the second strand synthesis, the dsDNA was end-repaired with the End-It DNA End-Repair Kit (Epicenter, Cat. #ER0720). Blunt-ended fragments were cloned using the Zero Blunt TOPO PCR Cloning Kit (Thermo Fisher), and then used to transform One Shot TOP10 chemically competent *E. coli* (Thermo Fisher, Cat. # C404010). Individual colonies were picked and subjected to Sanger sequencing using a T7 promoter primer at Beckman Coulter Genomics.

RNA-seq

[0169] Total RNA from early passage, early and deep senescent cells (**FIG. 6a**) was extracted as described above. The total RNA was processed with the Illumina TruSeq Stranded Total RNA Ribo-Zero kit and subjected to Illumina HiSeq2500 2x125bp paired end sequencing using v4 chemistry at Beckman Coulter Genomics Inc. Over 70 million reads were obtained for each sample. The RNA-seq experiment was performed in three biological replicates.

[0170] Raw RNA-sequencing reads were aligned to the GrCh38 build of the human genome using HiSat2.⁷³ Counts mapping to the genome were determined using featureCounts.⁷⁴ Counts were then normalized using the trimmed mean of M-values (TMM) method in EdgeR.⁷⁵ EdgeR was additionally used to derive differential expression from the normalized data set. Differential expression data were then ranked by log₂ fold change and input into the GenePattern interface for GSEA Preranked, using 1000 permutations, to determine enrichment for KEGG pathways, SASP, and the interferon response.^{76,77} The outputs were then corrected for multiple comparisons by adjusting the nominal *p* value using Benjamini-Hochberg method.⁷⁸ Data were displayed using GENE-E software.⁷⁹

In silico analysis of transcription factors binding to L1

[0171] Transcription factor profiles were created using ChIP-seq data from the ENCODE project (GEO accession numbers GSE2961 and GSE32465). Transcription factor ChIP-seq and input control reads were aligned to the consensus sequence of L1HS using bowtie1.⁸⁰ The log₂ fold change enrichment was calculated per base pair of the L1HS consensus using the transcription factor ChIP-seq read coverage per million mapping reads (RPM) versus input

control RPM values and smoothed by LOESS smoothing with a parameter $\alpha=0.1$. The total number of mapping reads used in RPM normalization was determined from a separate bowtie1 alignment to the human genome (hg19).

Construction of FOXA1 reporters

[0172] L1 promoter reporter plasmids L1WT and L1 del (390-526) were obtained from Sergey Dmitriev, Institute of Bioorganic Chemistry, Moscow.^{81,82} Both contain luciferase as the reporter cloned in the sense orientation. To determine antisense transcription from the same plasmid, EYFP was inserted in the inverse orientation upstream of the L1 5' UTR as follows. The EYFP sequence was excised from pEYFP-N1 (Clontech, Cat. # 6006-1) with AgeI and NotI and blunt ended. Plasmids L1WT and L1del were digested with XbaI, blunted and treated with FastAP (Fermentas). Successful insertion of anti-sense EYFP was verified using PCR primers AAAGTTTCTTATGGCCGGGC (in EYFP) and GCTGAACTTGTGGCCGTTTA (in L1 promoter) and Sanger sequencing. Plasmid pcDNA3.1/LacZ was used as the co-transfection control. Luciferase and β -galactosidase assays were performed as described.⁸³ EYFP-N1 was used as a positive control for detecting the EYFP signal. Co-transfections were performed on early passage LF1 cells using Lipofectamine with Plus Reagent (Invitrogen) according to the manufacturer's instructions.

Lentiviral vectors

[0173] Constructs were obtained from public depositories as indicated below. Virions were produced and target cells were infected as described.⁸⁴ shRNA sequences were obtained from The RNAi Consortium (TRC),⁸⁵ cloned into third generation pLKO.1 vectors and tested for efficacy. Four selectable markers were used to allow multiple drug selections: pLKO.1 puro (2 μ g/ml) and pLKO.1 hygro (200 μ g/ml) (Addgene plasmid # 8453, 24150), pLKO.1 blast (5 μ g/ml) (Addgene plasmid # 26655), pLKO.1 neo (250 μ g/ml) (Addgene plasmid 13425). pLKO-RB1-shRNA63 and pLKO-RB1-shRNA19 (Addgene plasmids # 25641 and 25640).⁸⁶ For FOXA1 shRNAs TRCN0000014881 (a) and TRCN0000014882 (b) were used. For TREX1 shRNAs TRCN0000007902 (a) and TRCN0000011206 (b) were used. For knockdown of L1, nine shRNAs were designed and tested, of which two (shL1_11 to ORF1, AAGACACATGCACACGTATGT, and shL1_44 to ORF2 AAGACACATGCACACGTATGT) showed significant knockdown (**FIG. 10g**) and were chosen for further work. The remaining seven shRNAs produced no or minimal knockdown. For cGAS shRNAs TRCN0000128706 (a) and TRCN0000128310 (b) were used. For STING shRNAs TRCN0000161345 (a) and TRCN0000135555 (b) were used.

[0174] All ectopic expression experiments used constructs generated by the ORFeome Collaboration⁸⁷ in the lentivirus vector pLX304 (blasticidin resistant, Addgene plasmid 25890) and were obtained from the DNASU plasmid repository.⁸⁸ RB1 (ccsbBroad304_06846, HsCD00434323), TREX1 (ccsbBroad304_02667, HsCD00445909), FOXA1 (ccsbBroad304_06385, HsCD00441689).

[0175] All the interventions in senescent cells were initiated by infecting cells at 12 weeks of senescence (point D in **FIG. 6a**). Following appropriate drug selections, cells were incubated until 16 weeks of senescence (point E in **FIG. 6a**), when they were harvested for further analysis.

[0176] The 3X intervention was performed by infecting early passage LF1 cells sequentially with vectors pLKO.1 puro shRB, pLKO.1 hygro shTREX1 and pLX304 blast FOXA1 (**FIG. 10c**). After each infection, the arising drug resistant pool of cells was immediately infected with the next vector. After the third infection, the cells were harvested for further analysis 48 hours after the drug selection was complete. The infections were also performed in various combinations and in each case resulted in the activation of L1 expression, entry into senescence, and induction of an IFN-I response. The sequence above was chosen because it gave the most efficient selection of cells for further analysis. To allow an additional (fourth) intervention in 3X cells (shL1, shSTING, or shCGAS), hairpins targeting RB1 were re-cloned in pLKO.1 neo, thus freeing pLKO.1 puro for the fourth gene of interest. This allowed an efficient drug selection process and sample harvest 48 hrs after the last selection.

Retrotransposition reporters

[0177] The two-vector dual luciferase reporter system reported by Xie *et al.* (2011)⁸⁹ was adapted for lentiviral delivery. The L1RP-Fluc reporters were re-cloned from plasmids pWA355 and pWA366 into the lentiviral backbone pLX304. pWA355 contained a functional, active L1_{RP} element, whereas pWA366 contains L1RP(JM111), a mutated element carrying two missense mutations in ORF1 that is unable to retrotranspose. Early passage LF1 cells were infected with a puromycin resistant lentivirus expressing Rluc. Pooled drug resistant cells were then infected with high titer particles of pLX304-WA355 or pLX304-WA366 constructs. Immediately after infection cells were treated for four days with 3TC (at the indicated concentrations). Cells were then harvested and assayed for Rluc and Fluc luciferase activities. The native L1 retrotransposition reporter pLD143⁹⁰ was co-transfected with pLKO vectors (shLuc, shL1_11 and shL1_44) into HeLa cells using FuGene HD (Promega). Cell culture, transfection and retrotransposition assays were done as described above. Retrotransposition

activity was normalized to the activity of L1_{RP} co-transfected with shLuc. Three independent experiments were performed for each construct.

Identification of expressed L1 elements by long-range RT-PCR and 5'RACE

[0178] Total RNA was harvested from cells using the Trizol reagent (Invitrogen). The RNA was further purified using the Purelink RNA Mini kit (Invitrogen) with DNase I digestion. From the eluted total RNA, poly(A) RNA was isolated using the NEBNext Poly(A) mRNA Magnetic Isolation Module (New England Biolabs). The forward primer (MDL15UTRPRAF, primer set 1, **Table 1**) was used with either of two reverse primers (MDL15UTRPRCR, primer set 3, amplicon size 537 bp) or MDL15UTRPRDR, primer set 4, amplicon size 654 bp). A high-fidelity thermostable reverse transcriptase (PyroScript RT-PCR Master Mix Kit, Lucigen) was used with 10 ng of poly(A) mRNA per reaction and amplified for 10 cycles. No template and RNaseA-treated samples were used as negative controls. The generated amplicons were cloned into the TOPO-TA (Invitrogen) vector and the resulting plasmids were used to transform One Shot TOP10 chemically competent *E. coli*. Individual colonies were picked and subjected to Sanger sequencing using a T7 promoter sequencing primer at Beckman Coulter Genomics. 96 sequencing reactions (1 plate) were performed for each primer pair in four experiments for a total of 768 sequenced clones. Sequencing data were trimmed to remove the RT-PCR primers and BLASTed against the human genome (GRCh38) with a match/mismatch cost of +1, -4 and allowing species-specific repeats for Homo sapiens. Only perfect hits were scored and annotated for genomic coordinates. 658 clones could be mapped to the reference genome, 51 contained at least 1 mismatch and thus likely represent elements that are polymorphic in the cell line, and 58 were cloning artifacts. Whenever a clone presented multiple instances of perfect identity a fractional count was adopted, dividing the counts by the number of elements sharing the same sequence. Each mappable clone was further analyzed using L1Xplorer⁹¹ to recover the classification features of the L1 element and whether it is intact.

[0179] Alternatively, poly(A) RNA isolated as above was subjected to Rapid Amplification of cDNA Ends (RACE). Each reaction contained 10 ng of poly(A) RNA and was processed using the 5'RACE System kit (Thermo Fisher, Cat. # 18374-041). The two antisense gene-specific primers (GSP) used for 5'RACE were: for GSP1, MDL15UTRPRDR (primer set 4, **Table 1**), and for the nested GSP2, MDL15UTRPRCR (primer set 3, **Table 1**). Amplification products were cloned and sequenced as above, using a T7 promoter sequencing primer by Beckman Coulter Genomics. A total of 94 clones were sequenced; 26 contained mostly a polyG stretch generated by the tailing step in the RACE protocol and 18 could not be mapped to the human genome. The remaining 50 mappable clones contained L1 sequences and were

aligned to the L1HS consensus using a setting of >95% identity at positions 1-450.⁹² The mappable clones were also assigned to individual L1 families using RepEnrich software.⁹³ Pairwise alignments to the consensus were performed with LALIGN.⁹⁴ Multiple sequence alignments were calculated using MAFFT (Multiple Alignment using Fast Fourier Transform) with the L-INS-i algorithm (accurate for alignments of <200 sequences).⁹⁵ Alignment visualization, %-identity coloring and consensus were generated by Jalview.⁹⁶

Generation and analysis of CRISPR-Cas9 knockouts

[0180] Three distinct gRNA sequences for each chain of the IFNAR receptor (IFNAR1 and IFNAR2), listed in the GeCKO v2.0 resource (Feng Zhang Lab, MIT⁹⁷)⁹⁸, were tested and the following ones were chosen: IFNAR1 (HGLibA_29983) AACAGGAGCGATGAGTCTGTA; IFNAR2 (HGLibA_29985) GTGTATATCAGCCTCGTGTT. Cas9 and gRNAs were delivered using a single lentivirus vector (LentiCRISPR_v2, Feng Zhang Lab, MIT; Addgene plasmid #52961), carrying a puromycin resistance gene. The efficacy of the CRISPR-Cas9 mutagenesis, on the basis of which the above two gRNAs were chosen, was evaluated by treating the infected and drug-selected cells with interferon (universal type I interferon, PBL Assay Science, Cat. # 11200-1) and monitoring nuclear translocation of phospho-STAT2 and IRF9 by immunofluorescence. The absence of translocation signifies lack of IFN-I responsiveness and hence loss of IFNAR function. Experimental procedures followed the protocols provided by the Zhang lab.^{99,100} In the experiment shown in **FIG. 3h** (RS) and **FIG. 10k**, both IFNAR1 and IFNAR2 gRNAs were used to treat the same cells to further increase the efficacy of ablating the INF-I response. For early passage and senescent cells, co-infections of IFNAR1 and IFNAR2 vectors were performed followed by selection with puromycin. For senescent cells, high titer lentivirus particles were applied to senescent cells at 12 weeks in senescence (point D, **FIG. 6a**) and cells were assayed 4 weeks later (point E, **FIG. 6a**). For the experiment shown in **FIG. 3h** (SIPS), edited early passage cells were single-cell cloned. 24 single cells were isolated using the CellRaft technology (Cell Microsystems) and expanded. Genomic screening of the CRISPR cut site was performed by the CRISPR Sequencing Service (CCIB DNA Core, Massachusetts General Hospital).¹⁰¹ The successful knock out of IFNAR1 and IFNAR2 was verified in four out of the 24 expanded clonal cell lines.

Immunoblotting

[0181] Cells were harvested in Laemmli sample buffer (60 mM Tris pH 6.8, 2% SDS, 10% glycerol, 100 mM DTT) and boiled for 5 min at 100°C. Whole cell extracts (60 µg protein) were separated by SDS-PAGE and transferred onto Immobilon-FL membranes (Millipore). Nonspecific binding was blocked by incubation in 4% bovine serum albumin (BSA; Thermo

Fisher) and 0.1% Tween-20 in PBS for 1 hr at room temperature. Primary antibodies were diluted in the blocking solution and incubated overnight at 4°C. A list of all the primary antibodies is provided in **Table 2**. Secondary antibodies were diluted in blocking solution and incubated for 1 hour at room temperature. Signals were detected using the LI-COR Odyssey infrared imaging system (LI-COR Biosciences). For the quantification of signals all samples to be compared were run on the same gel. Loading standards were visualized on the same blot as the test samples using the LI-COR 2-color system. Bands were imaged and quantified using LI-COR software. All bands to be compared were quantified on the same image and were within the linear range of detection of the instrument.

Immunofluorescence microscopy performed on cells in culture

[0182] Cells were grown on glass cover slips and the samples were processed as previously described.¹⁰² Primary antibodies are listed in **Table 2**. Staining of ssDNA was performed as described by Thomas *et al.*¹⁰³ Briefly, cells seeded on coverslips were fixed on ice with 4% paraformaldehyde (PFA) for 20 min and then incubated in 100% methanol at -20°C overnight. The cells were then treated with 200 mg/mL RNase A at 37°C for 4 hrs. Cells were blocked with 3% BSA and incubated overnight at 4°C with primary antibodies diluted in 3% BSA. Images were acquired using a Zeiss LSM 710 confocal laser scanning microscope or a Nikon Ti-S inverted fluorescence microscope. All microscope settings were set to collect images below saturation and were kept constant for all images taken in one experiment, as previously described.¹⁰⁴ Image analysis was performed as described below for tissues.

PCR arrays

[0183] Total RNA was harvested from cells as indicated above (Quantitative PCR) and analyzed using the Qiagen RT² Profiler™ Human Type I Interferon Response PCR Array (Cat. # PAHS-016ZE-4). Reverse transcription reactions were performed with the Qiagen RT² First Strand Kit (Cat. # 330404) using 1 µg of total RNA as starting material. 102 µL of the completed reaction was combined with 650 µL of Qiagen RT² SYBR Green ROX qPCR Mastermix (Cat. # 330521) and 548 µL of RNase-free molecular grade water and run in the 384-well block on a ViiA 7 Applied Biosystems instrument. All procedures followed the manufacturer's protocols. All conditions were run in triplicate. The results were analyzed using the Qiagen GeneGlobe Data Analysis Center.¹⁰⁵ Briefly, C_t values were normalized to a panel of housekeeping genes (HKG). ΔC_t values were calculated between a gene of interest (GOI) and the mean HKG value. Fold changes were then calculated using 2^{-ΔΔC_t} formula. The lower limit of detection was set at C_t of 35. For any GOI to be considered significant, the following filters were set: (i) >2-fold

change in expression; and (ii) p -value >0.05 . In addition, genes with an average $C_t > 32$ in both control and test samples were also eliminated.

Enzyme Linked Immunosorbent Assay (ELISA)

[0184] Interferon β levels were quantified with the VeriKine-HS Human IFN Beta Serum ELISA Kit (PBL Assay Science, Cat. # 41415). Cell culture media were conditioned for 48 hrs before harvest. To remove particles and debris, 1 mL aliquots were spun 5 min $5,000 \times g$. All incubations were performed in a closed chamber at room temperature (22-25°C) keeping the plate away from temperature fluctuations. 50 μ L of sample buffer followed by 50 μ L of diluted antibody solution were added to each well. Finally, 50 μ L of test samples, standards or blanks were added per well. Plates were sealed and shaken at 450 rpm for 2 hrs. At the end of the incubation period the contents of the plate were removed, and the wells were washed three times with 300 μ L of diluted wash solution. 100 μ L of HRP solution was added to each well and incubated for 30 min under constant shaking. The wells were emptied and washed four times with wash solution. 100 μ L of the TMB substrate solution was added to each well. Plates were incubated in the dark for 30 min. Finally, 100 μ L of stop solution was added to each well and within 5 min absorbance at 450 nm was recorded. The values recorded for the blank controls were subtracted from the standards as well as sample values to eliminate background. Optical densities (OD) units were plotted using a 4-parameter fit for the standard curve and were used to calculate the interferon titers in the samples.

Human tissue specimens

[0185] Human skin specimens were collected as part of the Leiden Longevity Study^{106,107} and were provided by the Leiden University Medical Centre, Netherlands. Informed consent was obtained, and all protocols were approved by the ethical committee of the Leiden University Medical Centre. The samples were collected as 4 mm thickness full depth punch biopsies, embedded in optimal cutting compound (OCT), flash frozen, and stored at -80°C. The investigators were blinded to everything except the age and sex of the subjects. The OCT-embedded specimens were cryosectioned at 8 μ m thickness using a Leica CM3050S cryomicrotome. The slides were fixed with 4% PFA and 0.5% Triton X-100 in PBS (prewarmed to 37°C) for 20 min at room temperature. No further permeabilization was performed. Antibody incubation was preceded by a blocking step with 4% bovine serum albumin (BSA; fraction V, Thermo Fisher), 2% donkey serum, 2% rabbit serum and 0.1% Triton X-100 in PBS for 1 hour at room temperature. Primary antibodies were diluted in the above blocking solution (1:200) and incubated overnight at 4°C with rocking in a humidified chamber. The secondary antibodies (AlexaFluor 546 and AlexaFluor 647, Life Technologies) were also diluted in blocking solution

and incubated for 2 hrs at room temperature. Three 15 min washing steps in PBS, containing 0.2% Triton X-100, followed each antibody incubation. Nuclei were counterstained with 2 µg/mL DAPI in PBS, containing 0.2% Triton X-100, for 15 min. Stained slides were mounted with ProLong Antifade Mountant without DAPI (Life Technologies) and imaged on a Zeiss LSM 710 Confocal Laser Scanning Microscope. A z-series encompassing the full thickness of the tissue was collected for each field. All microscope settings and exposure times were set to collect images below saturation and were kept constant for all images taken in one experiment. Image analysis was performed using either CellProfiler software,¹⁰⁸ or ImageJ open source software from the NIH.¹⁰⁹ Nuclei were defined using the DAPI channel. Cell outlines were defined by radially expanding the nuclear mask using the function Propagate until an intensity threshold in the AlexaFluor 546 and AlexaFluor 647 channels was reached. The fluorescence intensity within these regions was then recorded in both channels. For each sample a total of 200 nuclei were recorded in multiple fields. Mouse tissue sections were processed and analyzed in the same way as described above.

Mouse tissue specimens

[0186] Total RNA was extracted from 50 mg of visceral adipose, small intestine, skeletal muscle, brown adipose or liver tissue by mincing followed by homogenization in Trizol (Invitrogen) using a Power Gen 125 homogenizer (Fischer Scientific). After phase separation, the RNA in the aqueous layer was purified using the Purelink RNA Mini kit (Invitrogen) with DNase I digestion. To assess gene expression by RT-qPCR 1 µg of total RNA was reverse transcribed as described above. In each individual experiment, all samples were processed in parallel and no blinding was introduced.

[0187] Imaging of whole-mount white adipose tissue followed the method described by Martinez-Santibañez *et al.* (2014).¹¹⁰ Briefly, white adipose tissue (visceral depot) were subdivided into 0.5-1 cm³ sized pieces and incubated in 10 mL of fresh fixing buffer (1% PFA in PBS pH 7.4) for 30 min at room temperature with gentle rocking. After three washing steps with PBS, the tissue blocks were cut in six equal pieces. All subsequent incubations were performed in 2 mL cylindrical microcentrifuge tubes. Primary antibody incubation was preceded by a blocking step with 5% BSA, 0.1% Saponin in PBS for 30 min at room temperature. Primary antibodies were diluted in the above blocking solution (1:200) and incubated overnight at 4°C with gentle rocking. The secondary antibodies (AlexaFluor 546, AlexaFluor 594 and AlexaFluor 647, Life Technologies) were also diluted in blocking solution and incubated for 2 hrs at room temperature. Three 10 min washing steps in PBS followed each antibody incubation. Antibody-independent staining of nuclei and lipids was performed after immuno-staining: DAPI and

BODIPY (Thermo Fisher) were diluted in PBS with 5% BSA and incubated with tissue specimens for 20 min followed by three washing steps as above. Stained samples were carefully placed on confocal-imaging optimized #1.5 borosilicate glass chamber slides. A small drop of PBS prevented drying. Acquired images were analyzed as described above.

[0188] Co-staining of SA- β -Gal activity and ORF1 protein in liver sections was performed by staining for SA- β -Gal first as described.¹¹¹ Subsequently, samples underwent heat-induced epitope retrieval by steaming for 20 min in antigen retrieval buffer (10 mM Tris, 1 mM EDTA, 0.05% Tween 20, pH 9.0). Samples were then processed for immunofluorescence staining as above (Human tissue specimens).

[0189] Kidney tissue preserved in OCT was cryosectioned, treated for 10 min with 0.5% (w/v) periodic acid, then stained with periodic acid-Schiff's (PAS) reagent (Fisher Scientific, Cat. #SS32-500) for 10 min. Stained tissue sections were mounted with Shandon Aqua Mount (Fisher Scientific, Cat. #14-390-5) and then imaged under bright field illumination. Glomerulosclerosis was scored as described.¹¹² Briefly, 40 glomeruli per animal were assessed in a blinded fashion and assigned scores of 1-4: score of 1, <25% sclerosis; 2, 25-50% sclerosis; 3, 50-75% sclerosis; 4, >75% sclerosis. The feature used to assess sclerosis was the strength and pervasiveness of PAS-positive lesions within the glomeruli. As exemplified in **FIG. 4e**, a sclerotic glomerulus is more shrunken and stains more intensely with PAS.

[0190] Quadriceps muscles were embedded in OCT, sectioned at 12 μ m thickness and mounted onto positively charged slides. Sections were stained with H&E (hematoxylin, 3 min followed by 30 eosin, sec). Mounted slides were imaged on a Zeiss Axiovert 200M microscope equipped with a Zeiss MRC5 color camera. To measure muscle fiber diameter, the shortest distance across ~100 muscle fibers per animal was measured using ImageJ software as described.¹¹³ The Kolmogorov-Smirnov test was used to assess the statistical significance of the difference between the resulting distributions.

Statistical treatments

[0191] Excel was used to perform general statistical analyses (means, s.d., *t*-tests, etc.). R software for statistical computing (64-bit version 3.3.2) was used for 1-way ANOVA and Tukey's multiple comparisons post-hoc test. For consistency of comparisons significance in all figures is denoted as follows: **P* < 0.05, ***P* < 0.01. Sample sizes were based on previously published experiments and previous experience in which differences were observed. No statistical test was used to pre-determine sample size. No samples were excluded. All attempts at replication were successful. There were no findings that were not replicated or could not be reproduced. The nature and numbers of samples analyzed (defined as *n*) in each

experiment are listed in the figure legends. The number of independent experiments is also listed in figure legends. The investigators were blinded when quantifying immunofluorescence results. Fields or sections of tissues for quantification were randomly selected and the scored, using methods as indicated for individual experiments. The investigators were also blinded when scoring glomerulosclerosis and muscle fiber diameter. For RNA-seq and PCR array experiments the statistical treatments are described under those sections (above).

EXAMPLE 1 ACTIVATION OF L1 AND INTERFERON IN CELLULAR SENESCENCE

[0192] RTE activity can promote aberrant transcription, alternative splicing, insertional mutagenesis, DNA damage and genome instability.¹¹⁴ RTE-derived sequences comprise up to two thirds of the human genome,¹¹⁵ although the great majority were active millions of years ago and are no longer intact. The only human RTE capable of autonomous retrotransposition is the long-interspersed element-1 (LINE-1, or L1). However, germline activity of L1 is a major source of human structural polymorphisms.¹¹⁶ Increasing evidence points to RTE activation in some cancers, in the adult brain, and during aging.^{117,118,119,120} Cellular defenses include heterochromatinization of the elements, small RNA pathways that target the transcripts, and anti-viral innate immunity mechanisms.¹²¹ Somatic activation of RTEs with age is conserved in yeast and *Drosophila* and reducing RTE activity has beneficial effects.¹²²

[0193] As shown in **FIG. 1a** and **FIG. 6a-e**, L1 transcription was activated exponentially during replicative senescence (RS) of human fibroblasts, increasing 4-5-fold by 16 weeks after cessation of proliferation, referred to as late senescence. Multiple RT-qPCR primers were designed to detect evolutionarily recent L1 elements (L1HS-L1PA5; **FIG. 1b**, **FIG. 6h**). Levels of L1 polyA⁺ RNA increased 4-5-fold in late senescent cells (RS) in the sense but not antisense direction throughout the entire element (**FIG. 1c**). Long-range RT-PCR amplicons (**FIG. 1b**) were Sanger sequenced to identify 224 elements dispersed throughout the genome; one third (75, 33.5%) were L1HS, of which 19 (25.3%, 8.5% of total) were intact (*i.e.*, annotated to be free of ORF-inactivating mutations; **FIG. 6f,g**). 5'RACE were also performed with the same primers and found that the majority of L1 transcripts upregulated in senescent cells initiated within or near the 5'UTR (**FIG. 7**).

[0194] L1 elements can stimulate an IFN-I response.¹²³ As shown in **FIG. 1d** and **FIG. 6i**, interferons IFN- α and IFN- β 1 were induced to high levels in late senescent cells. Cellular senescence proceeds through an early DNA damage response phase followed by the SASP response.¹²⁴ Documented here by the present data, is a third and even later phase, characterized by the upregulation of L1 and an IFN-I response (**FIG. 1e**), which has not been

previously noted, probably because most studies have focused on earlier times. Whole transcriptome RNA-seq analysis confirmed that the SASP and IFN-I responses are temporally distinct (**FIG. 8**). The late phase of L1 activation and IFN-I induction was also observed in oncogene-induced senescence (OIS) and stress-induced premature senescence (SIPS) (**FIG. 1e, FIG. 1j, k**).

EXAMPLE 2 MECHANISMS OF L1 ACTIVATION

[0195] To explore how surveillance fails during senescence, three factors were examined: TREX1, RB1 and FOXA1. TREX1 is a 3' exonuclease that degrades foreign invading DNAs and its loss has been associated with the accumulation of cytoplasmic L1 cDNA.¹²⁵ As shown in **FIG. 9a**, the expression of TREX1 was significantly decreased in senescent cells. RB1 has been shown to bind to repetitive elements, including L1s, and promote their heterochromatinization.¹²⁶ As shown in **FIG. 2a**, the expression of RB1 declined strongly in senescent cells (RS;) while that of other RB family members (RBL1, RBL2) did not change (**FIG. 9b**). RB1 enrichment in the 5'UTR of L1 elements was evident in proliferating cells, decreased in early senescence and became undetectable at later times (**FIG. 2a**). This coincided with a decrease of H3K9me3 and H3K27me3 marks in these regions (**FIG. 9c**).

[0196] To identify novel factors that interact with the L1 5'UTR, we examined the ENCODE ChIP-seq database and found that the pioneering transcription factor FOXA1 binds to this region in several cell lines (**FIG. 9d**). FOXA1 is upregulated in senescent cells.¹²⁷ As shown in **FIG. 2b**, FOXA1 bound to the central region of the L1 5'UTR. Using transcriptional reporters, we found that deletion of the FOXA1 binding site decreased both sense and antisense transcription from the L1 5' UTR¹²⁸ (**FIG. 9e**). Hence, the observed misregulation of these three factors in senescent cells could promote the activation of L1 by three additive mechanisms: loss of RB1 by relieving heterochromatin repression, gain of FOXA1 by activating the L1 promoter, and loss of TREX1 by compromising the removal of L1 cDNA.

[0197] Therefore, the effects of manipulating RB1, FOXA1 or TREX1 expression in fully senescent cells were tested using lentiviral vectors (**FIG. 10a, b**). Ectopic expression of RB1 suppressed the elevated expression of L1, IFN- α and IFN- β 1 in senescent cells, while its knockdown further enhanced their expression (**FIG. 2d**). RB1 overexpression also restored its occupancy of the L1 5'UTR (**FIG. 2c**). Conversely, knockdown of FOXA1 reduced its binding to the L1 5'UTR (**FIG. 9f**) and decreased the expression of L1, IFN- α and IFN- β 1, while overexpression of FOXA1 increased L1, IFN- α and IFN- β 1 levels (**FIG. 2e**). Congruent results

were also obtained by manipulating TREX1 (**FIG. 2g**). Hence, each of these factors had a tangible effect on regulating L1 and the IFN-I response in senescent cells.

[0198] Single or double interventions targeted at these factors elicited only modest changes in L1 and IFN-I expression in growing early passage cells. While some of these effects were statistically significant, they were dwarfed by a triple intervention (3X) of RB1 and TREX1 knockdowns combined with FOXA1 overexpression, which resulted in a massive induction of L1 and IFN-I expression (**FIG. 2f**, **FIG. 9g-i**, and **FIG. 10c**). Hence, in normal healthy cells, all three effectors have to be compromised to effectively unleash L1.

EXAMPLE 3 CONSEQUENCES OF L1 ACTIVATION

[0199] To assess IFN-I activation by L1 in more detail, we examined the expression of 84 genes in this pathway using PCR arrays. We observed a widespread response, with the majority of the genes being upregulated (**FIG. 2h**, **FIG. 9j, k**): 68% (57/84) were significantly upregulated in senescent cells, and 52% (44/84) were upregulated in 3X cells. These data verify and further extend the RNA-seq transcriptomic analysis (**FIG. 8**).

[0200] Some NRTIs developed against HIV have been found to also inhibit L1 RT activity.¹²⁹ We also developed shRNAs against L1, two of which reduced transcript levels by 40-50% and 70-90% in deeply senescent and 3X cells, respectively (**FIG. 10g**). ORF1 protein levels were correspondingly reduced in deeply senescent cells (**FIG. 5h**). Finally, the shRNAs also reduced the retrotransposition of recombinant L1 reporter constructs (**FIG. 10k**).

[0201] Cells devoid of TREX1 display cytoplasmic L1 DNA, accumulation of which can be inhibited with NRTIs.¹³⁰ While lack of BrdU incorporation is a canonical feature of senescent cells (**FIG. 6b**), longer term labeling revealed DNA that was predominantly cytoplasmic and highly enriched for L1 sequences (**FIG. 11a, b**). The synthesis of cytoplasmic L1 DNA could be almost completely blocked with the NRTI lamivudine (3TC) or shRNA to L1 (**FIG. 3a, c**). An antibody to DNA:RNA hybrids detected a cytoplasmic signal in senescent cells that largely colocalized with ORF1 protein and turned into a ssDNA signal following RNase digestion (**FIG. 11c**). Analysis of BrdU-labeled L1 sequences in senescent cells showed them to be localized throughout the L1 element (**FIG. 11d, e**). A relative increase of L1HS sequences in total cellular DNA can also be detected by a qPCR assay^{6,16,131,132} 3TC in the range of 7.5-10 μ M completely blocked this increase in senescent cells and also quenched the activity of a L1 retrotransposition reporter (**FIG. 10d, e**).

[0202] L1 knockdown with shRNA or treatment of cells with 3TC significantly reduced interferon levels, as well as reducing the IFN-I response more broadly in both late senescent

and 3X cells (**FIG. 3b, FIG. 12a**). 3TC in the range of 7.5-10 μ M optimally inhibited the IFN-I response, and was the most effective of 4 NRTIs tested (**FIG. 10f, j**). The relative efficacies of the NRTIs are consistent with their ability to inhibit human L1 RT15. 3TC also antagonized the IFN-I response in other forms of senescence, OIS and SIPS (**FIG. 3e**).

[0203] Cells were passaged in the continuous presence of 3TC from the proliferative phase into deep senescence. 3TC did not significantly affect the timing of entry into senescence, induction of p21 or p16, or the early SASP response, such as upregulation of IL- β (**FIG. 3f, FIG. 12b**). However, the magnitude of the later SASP response (such as induction of CCL2, IL-6 and MMP3) was significantly dampened. Treatment with L1 shRNA also reduced the expression levels of IL-6 and MMP3 in late senescent cells (**FIG. 11f**). Hence, while L1 activation and the ensuing IFN-I response are relatively late in onset, they contribute importantly to the mature SASP and proinflammatory phenotype of senescent cells.

[0204] 3TC did not affect L1 transcript levels (**FIG. 10i**), suggesting that the INF-I response is triggered by L1 cDNA. As this model would predict, knockdown of the cytosolic DNA sensing pathway components, cGAS or STING,¹³³ inhibited the IFN-I response in both late senescent and 3X cells (**FIG. 10l** and **FIG. 12c, d**), and also downregulated the SASP response in late senescent cells (**FIG. 12e**).

[0205] NRTIs alkyl-modified at the 5' ribose position cannot be phosphorylated and hence do not inhibit RT enzymes. However, they possess intrinsic anti-inflammatory activity by inhibiting P2X7-mediated events that activate the NLRP3 inflammasome pathway.¹³⁴ Tri-methoxy-3TC (K-9), at 10 μ M or 100 μ M, did not inhibit the IFN-I response in either late senescent or 3X cells (**FIG. 12f**). Hence, the effect of 3TC on the IFN-I pathway requires RT inhibition. At high concentrations (100 μ M), K-9 had some inhibitory activity on markers of inflammation (**FIG. 12g**).

[0206] To test the role of interferon signaling in SASP, the IFN- α/β receptors (IFNAR1 and 2) were inactivated using CRISPR/Cas9. Effective ablation of IFN-I signaling was achieved in both early passage and deep senescent cells (**FIG. 10m**). In both replicative and SIPS forms of senescence, loss of interferon signaling antagonized late (CCL2, IL-6, MMP3) but not early (IL-1 β) SASP markers (**FIG. 3d**). This further demonstrates that IFN-I signaling contributes to the establishment of a full and mature SASP response in senescent cells.

EXAMPLE 4 ACTIVATION OF L1 IN HUMAN AND MOUSE TISSUES

[0207] Activation of L1 expression in human cancers has been detected with an ORF1 antibody.¹³⁵ The same reagent showed widespread ORF1 expression in both senescent and

3X cells (**FIG. 8a, c, f**). In skin biopsies of normal aged human individuals, we found that 10.7% of dermal fibroblasts were positive for the senescence marker p16, which is in the range documented in aging primates¹³⁶ (**FIG. 13b, d, f, h**). Some of the p16 positive dermal fibroblasts were also positive for ORF1 (10.3%). Notably, we never observed ORF1 in the absence of p16 expression. We also detected, at the single cell level, the presence of phosphorylated STAT1, consistent with the presence of interferon signaling in the tissue microenvironment¹³⁷ (**FIG. 13b, e, g**). Hence, a fraction of senescent cells in normal human individuals display activation of L1, consistent with these events accumulating during the progression of senescence.

[0208] We next examined mice and found that L1 mRNA was progressively upregulated with age in several tissues (**FIG. 15g**). The detected L1 RNA sequences were predominantly sense strand, represented throughout the element, and all three active L1 families were detectable (**FIG. 11g, h**). At the protein level, the frequency of L1 Orf1 positive cells increased in tissues with age (**FIG. 4a**). Regions of Orf1 staining colocalized with senescence-associated β -galactosidase (SA- β -Gal) activity (**FIG. 4b**). Several IFN-I response genes (*Ifn- α* , *Irf7*, *Oas1*), as well as pro-inflammatory and SASP markers (*Il-6*, *Mmp3*, *Pai1*, also known as *Serpine1*), were upregulated in tissues of old mice (**FIG. 4c, FIG. 14**). An increase in L1 expression and IFN-I response genes (*Ifn- α* , *Oas1*) were also observed in an experimentally-induced model of cellular senescence (young animals subjected to sublethal irradiation; **FIG. 4d**).

[0209] Old animals (26 months) were treated for two-weeks with 3TC (administered in water at human therapeutic doses). We found a broad and significant downregulation the IFN-I response and alleviation of the SASP pro-inflammatory state (**FIG. 4c**; for the full dataset, see **FIG. 14** and **Table 7**). Expression of L1 mRNA and p16 was weakly downregulated, but in most cases, did not reach statistical significance. K-9 did not affect either the IFN-I or SASP responses. Immunofluorescence analysis of tissue sections confirmed that senescent cells expressed SASP, and Orf1-expressing cells activated IFN-I signaling (**FIG. 15a-c**). Treatment with 3TC significantly reduced both IFN-I and SASP, but not L1 expression or the presence of senescent cells. Hence, NRTIs can be categorized as "senostatic" agents, to contrast them from "senolytic" treatments that remove senescent cells from tissues.^{138,139}

[0210] Decreased adipogenesis¹⁴⁰ and thermogenesis¹⁴¹ are features of natural aging and both were increased in old animals by 2 weeks of 3TC treatment (**FIG. 15d-f**). As shown in **FIG. 4e**, longer term treatments (from 20 to 26 months of age) were effective at opposing several known phenotypes of aging: (i) macrophage infiltration of tissues, a hallmark of chronic inflammation,^{142,143} (ii) glomerulosclerosis of the kidney,¹⁴⁴ and (iii) skeletal muscle atrophy.¹⁴⁵

Macrophage infiltration of white adipose was especially responsive, returning to youthful (5 month) levels with only 2 weeks of 3TC.

[0211] The activation of endogenous L1 elements and the ensuing robust activation of an IFN-I response is a novel phenotype of senescent cells, including naturally-occurring senescent cells in tissues. This phenotype evolves progressively during the senescence response and appears to be an important, but hitherto unappreciated component of SASP. We show that the expression of three regulators, RB1, FOXA1 and TREX1 changes during senescence, and that these changes are both sufficient and necessary to allow the transcriptional activation of L1s (**FIG. 4g**). Hence, multiple surveillance mechanisms need to be defeated to unleash L1, which underscores the importance of keeping these elements repressed in somatic cells.

[0212] The activation of innate immune signaling, in response to L1 activation during cellular senescence and aging, proceeds through the interferon-stimulatory DNA (ISD) pathway. Cytoplasmic DNA can originate from several sources, such as mtDNA released from stressed mitochondria¹⁴⁶ or cytoplasmic chromatin fragments (CCF) released from damaged nuclei.^{147,148} The present results suggest that L1 cDNA is an important inducer of IFN-I in senescent cells. Remarkably, NRTI treatment effectively antagonized not only the IFN-I response but, also more broadly, reduced age-associated chronic inflammation in multiple tissues.

[0213] Sterile inflammation, also known as inflammaging, is a hallmark of aging and a contributing factor to many age-related diseases.^{149,150} The present data indicates that activation of L1 elements (and possibly other RTEs) promotes inflammaging, and that the L1 RT is a relevant target for the treatment of age-associated inflammation and disorders.

EXAMPLE 5 EFFECTS OF ADEFOVIR AND LAMIVUDINE ON SENESCENCE-INDUCED INCREASES IN L1 SEQUENCE ABUNDANCE, INTERFERON GENE EXPRESSION, AND SASP GENE EXPRESSION

[0214] The effects of Adefovir and Lamivudine on senescence-induced increases in L1 sequence abundance, interferon gene expression, and SASP gene expression were assessed in human fibroblast cell lines.

[0215] L1 sequence abundance (copy number) were assessed in three different human fibroblast cell lines: LF1, IMR90, WI38 using qPCR assays. Assays were normalized to 5S rDNA abundance. The control (CTRL) was non-treated, early passage, proliferating cells. Drugs were applied continuously, in medium, from a few passages before senescence, into senescence and then into late senescence. The "senescent" samples were harvested four months after onset of senescence. Both drugs were supplemented at 5 μ M in the medium.

Red bar in "senescent" conditions: cultures without drugs at 4 months in senescence. As shown in **FIG. 17a**, L1 copy number increased in senescence in all three cell lines, and both drugs significantly prevented this increase, with Adefovir being somewhat more effective than Lamivudine.

[0216] The effects of 5 μ M Adefovir and Lamivudine on interferon gene expression were assessed in two cell lines (LF1 and IMR90) and two interferon genes (*IFN- α* and *IFN- β 1*) as performed in **FIG. 17a**, except that the expression of the indicated genes was measured by RT-qPCR. As shown in **FIG. 17b**, the high interferon gene expression in senescent cells was significantly reduced in all cases by both drugs, and again Adefovir was somewhat more effective than Lamivudine. The red bars are cultures without drugs at 4 months in senescence.

[0217] The effects of 5 μ M Adefovir and Lamivudine on SASP gene expression were assessed in one cell line (LF1) using two SASP genes (*IL-6* and *MMP3*). CTRL was the expression in normal, pre-senescent, untreated cells. As shown in **FIG. 17c**, an increase in expression with senescence (red bars) was observed, and in both cases, SASP gene expression was significantly decreased with drug treatment, with Adefovir being somewhat more effective than Lamivudine.

[0218] Finally, the effects of high concentrations of Lamivudine and Emtricitabine (10 μ M and 50 μ M) on interferon gene expression (*IFN- α* and *IFN- β 1*) were assessed in the LF1 cell line. These were done by passaging LF1 cells into senescence, keeping them in senescence for three months, adding the drugs, keeping the cells in the presence of the drugs for 1 month, then harvesting at 4 months. Interferon gene expression was assessed by RT-qPCR. The control (CTRL) was cells treated as above but without drugs. As shown in **FIG. 17d**, at 10 μ M, Lamivudine decreased IFN-I induction, and was somewhat more effective than Emtricitabine. At 50 μ M, Lamivudine actually induced an increase in the expression of interferons, even surpassing the levels seen in untreated cell. This increase is believed to be caused by the toxicity of the drug at these high levels. In contrast, Emtricitabine at 50 μ M decreased the expression of interferons, even below the decrease observed with 10 μ M.

[0219] Accordingly, at high doses, the toxicity of RTIs can impair their ability to halt or block the harmful effects of senescent cells and their ability to prevent or reverse age-related inflammation and disorders.

EXAMPLE 6 COMPARATIVE ASSESSMENT OF SEVERAL RTIs IN A DOSE-RESPONSE ASSAY OF INHIBITION OF L1 ACTIVITY IN MOUSE AND HUMAN CELLS

[0220] Eight RTI compounds were assessed for their ability to inhibit LINE-1 (L1) activity in a mouse L1 retrotransposition assay: lamivudine (3TC); stavudine; emtricitabine; apricitabine; tenofir disoproxil; censavudine; elvucitabine; and tenofir. Three RTI compounds were assessed in a human L1 retrotransposition assay: lamivudine (3TC); censavudine; and elvucitabine.

Mouse LINE-1 Retrotransposition Assay

[0221] The dual luciferase-encoding plasmid pYX016 containing a mouse L1 element was described in Xie *et al.*, 2011.¹⁵¹ Lamivudine (3TC), stavudine (d4T), emtricitabine, apricitabine, tenofovir disoproxil and tenofovir were purchased from AK Science. Elvucitabine was obtained by custom synthesis. Censavudine was synthesized by Oncolys BioPharma. HeLa cervical cancer cells were cultivated at 37°C in a humidified 5% CO₂ incubator in Dulbecco's Modified Eagle's Medium (DMEM) - high glucose, with 4500 mg/L glucose, L-glutamine, sodium pyruvate and sodium bicarbonate (Sigma), supplemented with 10% of heat inactivated fetal bovine serum (Thermo Fisher).

[0222] Assays were performed as described in Xie *et al.*, 2011¹⁵¹ with several modifications. The reporter assay was performed in 96 well white Optical bottom plates. 6000 HeLa cells were seeded in each well 24 hours prior transfection and compound treatment. All compounds were resuspended in DMSO. Stock solution concentrations varied from 50 mM to 1.25 mM depending of the solubility of the compound. Serial dilutions (1:3) were prepared in DMSO. Ten different concentrations of each compound were tested in triplicate. Medium containing different concentrations of the compounds were prepared by adding 2 µL of the compound dilution to 1 mL of the culture medium. The final concentration of DMSO in the medium was 0.2%. FuGENE® HD transfection reagent (Promega) was used to transfect the plasmid pYX016 into the cells. The transfection mix was prepared in OpiMEM (Thermo Fisher) using a reagent to DNA ratio of 3.5:1 according to manufacturer's instructions. Culture medium was removed from the cells and discarded. The transfection mix (5 µL) was mixed with the compound containing medium (100 µL/well) and this was added onto the cells of each well. Cells were incubated for 48H at 37°C/5% CO₂.

[0223] Luciferase reporter activity was quantified with the Dual-Luciferase® Reporter Assay System (Promega) according to manufacturer's instructions for multiwell plates with the following modification: Cells were lysed directly on the multiwell plate with 30 µL of the passive

lysis buffer (PLB) for 20 min at room temperature, with gentle shaking to ensure complete cell lysis (instead of 20 μ L of PLB for 15 min). Firefly and Renilla luciferase signals were measured using a SpectraMax i3x Multi-Mode Microplate Reader. Integration times of 100 ms and 10 ms were used to measure the Firefly and Renilla signals respectively. Relative L1 activity was calculated as Firefly/Renilla *10,000. Dose response inhibition data were fit to a four-parameter logistic equation using non-linear regression (using Graphpad Prism 8), to determine IC₅₀ values for each inhibitor. The experiment was performed twice, independently.

Results

[0224] The inhibitory dose-response curves for the eight RTI compounds in the two independent experiments are provided in **FIG. 18A** and **FIG. 18B**, respectively. The IC₅₀ values are summarized in **Table 10**. Surprisingly, two RTI compounds, censavudine and elvucitabine, had much lower IC₅₀ values (about 100 nM) than the other RTI compounds, thus displaying unexpected mouse L1 inhibitory activity.

Human LINE-1 Retrotransposition Assay

[0225] Given their unexpected ability to inhibit mouse L1 activity, censavudine and elvucitabine were tested for their ability to inhibit human L1 activity. Lamivudine was also tested for comparison.

[0226] Assays for human L1 were performed in very similar manner to those for mouse. pYX017 encoding a human LINE-1 sequence¹⁵¹ was used in place of pYX016. Because the human construct yields a lower signal, compounds were incubated with cells for 72 hours instead of 48 hours, and cells were seeded at a density of 2000/well instead of 6000/well. In addition, the transfection reagent to DNA ratio was 2:1 instead of 3.5:1.

Results

[0227] The inhibitory dose-response curves for the three RTI compounds are provided in **FIG. 19A-B** and the IC₅₀ values are summarized in **Table 11**. Again, censavudine and elvucitabine displayed surprising human L1 inhibitory activity (IC₅₀ about 100 nM) when compared to lamivudine (IC₅₀ over 800 nM).

Cell Viability Assay

[0228] As described above, the toxicity of RTIs could impair their ability to halt or block the harmful effects of senescent cells and their ability to prevent or reverse age-related inflammation and disorders. The potential toxicity of lamivudine (3TC); stavudine; emtricitabine;

apricitabine; tenofir disiproxil; censavudine; elvucitabine; and tenofir was assessed in a cell viability assay at the doses used to generate the L1 inhibitory dose-response curves.

[0229] HeLa cells were treated with the different concentrations of the eight RTI compounds for 48 hours. Cell viability was measured with CellTiter-Glo® luminescent cell viability assay (Promega®) and presented as percentage of cell viability versus untreated cells. Staurosporine, known to induce cell death, was used as a control.

Results

[0230] As shown in **FIG. 20**, the eight RTI compounds did not induce any significant levels of cell death in contrast to the control, staurosporine.

[0231] In summary, censavudine and elvucitabine both displayed an unexpected ability to inhibit mouse and human L1 activity (IC₅₀ about 100 nM) without inducing toxicity in the cell viability assay at doses up to 2 µM.

[0232] Tables described in the present disclosure are provided below.

Table 1: List of primers used in PCR analysis.

Number	Designation	Sequence	Notes
Primer set 1	MDL15UTRPRAF MDL15UTRPRAR Amplicon A, Fig. 1b	GCCAAGATGGCCGAATAGGA AAATCACCCGTCTTCTGCGT	LINE-1 5'UTR, positions 12-31, sense orientation ² . LINE-1 5'UTR, positions 64-83, antisense orientation ² . Used in RT-qPCR experiments to assess expression of L1Hs RNA. Also used in ChIP experiments.
Primer set 2	MDL15UTRBF MDL15UTRBR Amplicon B, Fig. 1b	CGAGATCAAAGTCAAGGCG CCGGCCGCTTTGTTACCTA	LINE-1 5'UTR, positions 402-421, sense orientation ² . LINE-1 5'UTR, positions 454-473, antisense orientation ² . Used in RT-qPCR experiments to assess expression of L1Hs RNA. Also used in ChIP experiments.
Primer set 3	MDL15UTRCF MDL15UTRCR Amplicon C, Fig. 1b	TAAACAAAGCGGCGGGAA AGAGGTGGAGCCTACAGAGG	LINE-1 5'UTR, positions 474-492, sense orientation ² . LINE-1 5'UTR, positions 530-549, antisense orientation ² . Used in RT-qPCR experiments to assess expression of L1Hs RNA. Also used in ChIP experiments.
Primer set 4	MDL15UTRDF MDL15UTRDR Amplicon D, Fig. 1b	AGAGAGCAGTGTTCTCCCA CAGTCTGCCCGTTCTCAGAT	LINE-1 5'UTR, positions 619-638, sense orientation ² . LINE-1 5'UTR, positions 647-666, antisense orientation ² . Used in RT-qPCR experiments to assess expression of L1Hs RNA. Also used in ChIP experiments.
Primer set 5	MDL1ORF1F MDL1ORF1R Amplicon E, Fig. 1b	ACCTGAAAGTGACGGGGAGA CCTGCCTTGCTAGATTGGGG	LINE-1 ORF1, positions 1395-1414, sense orientation ² . LINE-1 ORF1, positions 1508-1527, antisense orientation ² . Used in RT-qPCR experiments to assess expression of L1Hs RNA. Also used in ChIP experiments.
Primer set 6	ORF2F ORF2R ORF2 probe Amplicon F, Fig. 1b	CAAACACCGCATATTCTCACTCA CTTCTGTGTCCATGTGATCTCA AGGTGGGAATTGAAC-VIC	LINE-1 ORF2, positions 5731-5753, sense orientation ² . LINE-1 ORF2, positions 5772-5794, antisense orientation ² . Probe for TaqMan experiments. ORF2F and ORF2R were used in SYBR Green RT-qPCR experiments to assess expression of L1Hs RNA, and in conjunction with the ORF2 probe in TaqMan qPCR experiments on genomic DNA to determine relative copy numbers of L1Hs elements. Primers were developed and validated as described ³ .
Primer set 7	5SF 5SR 5S probe	CTCGTCTGATCTCGGAAGCTAAG GCGGTCTCCCATCCAAGTAC AGGGTCGGGCCTGG-6FAM	Ribosomal 5S RNA gene, sense orientation. Ribosomal 5S RNA gene, antisense orientation. Probe for TaqMan experiments. Used for internal normalization, in conjunction with primer set 3, in TaqMan qPCR experiments on genomic DNA to determine relative copy numbers of L1Hs elements. Primers were developed and validated as described ³ .
Primer set 8	GAPDHF GAPDHRV	TTGAGGTCAATGAAGGGGTC GAAGGTGAAGGTCGGAGTCA	<i>GAPDH</i> , sense orientation. <i>GAPDH</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>GAPDH</i> gene (NM_001256799). Primers span an intron. Used as the internal normalizer in gene expression experiments.
Primer set 9	GAPDHINT4F GAPDHINT4R	CCAGGAGTGAGTGAAGACAG CTAGTTGCCATCCCAAGCA	Intron 4 of <i>GAPDH</i> , sense orientation. Intron 4 of <i>GAPDH</i> , antisense orientation. Used as a negative control in ChIP experiments.
Primer set 10	ACP1IFNAFW ACP1IFNARV1 ACP1IFNARV2	TTGATGGCAACCAAGTCCAG TCATCCCAAGCAGCAGATGA TGTTCCCAAGCAGCAGATGA	Interferon alpha consensus, sense orientation. Interferon alpha consensus, antisense orientation. Interferon alpha consensus, antisense orientation. Used in RT-qPCR experiments to assess the collective expression of human interferon alpha genes. All 3 primers were used in a single reaction.
Primer set 11	MDIFNB1FW MDIFNB1RV	ACGCCGATTGACCATCTAT GTCTCATTCCAGCCAGTGCT	<i>IFNB1</i> , sense orientation. <i>IFNB1</i> , antisense orientation.

			Used for RT-qPCR of the mRNA of the <i>IFNB1</i> gene (NM_002176).
Primer set 12	MDHSRB1AF MDHSRB1AR	ACTCTCACCTCCCATGTTGC ATCCGTGCACCTCCTGTTCTG	<i>RB1</i> , sense orientation. <i>RB1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>RB1</i> gene (NM_000321). Primers span an intron.
Primer set 13	MDHSP107AF MDHSP107AR	CCAAGAAGCGCTCTGCTGTA GCAGGGGATTCTGCATCACTA	<i>RBL1</i> , sense orientation. <i>RBL1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>RBL1</i> gene (NM_002895). Primers span an intron.
Primer set 14	MDHSP130F MDHSP130R	AGTCGCCCCACCCCTCAGAT TTCCCTCCAGCGTGTAGCTT	<i>RBL2</i> , sense orientation. <i>RBL2</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>RBL2</i> gene (NM_005611). Primers span an intron.
Primer set 15	MDTREX1CDSF MDTREX1CDSR	TCCCCTTCGGATCTTAACAC CGAAAAAGATGAGGGTCTGC	<i>TREX1</i> , sense orientation. <i>TREX1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>TREX1</i> gene (NM_007248). Primers span an intron.
Primer set 16	MDHSFOXA1F MDHSFOXA1R	GGAAGACCGGCCAGCTAGAG TGAAGGAGTAGTGGGGTCC	<i>FOXA1</i> , sense orientation. <i>FOXA1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>FOXA1</i> gene (NM_004496). Primers span an intron.
Primer set 17	JJMMP1FW JJMMP1RV	AGCCTTCCAACCTCTGGAGTAATG T CCGATGATCTCCCTGACAA	<i>MMP1</i> , sense orientation. <i>MMP1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>MMP1</i> gene (NM_001145938). Primers span an intron.
Primer set 18	JJMMP3FW JJMMP3RV	CCCACCTTACATACAGGATTGTG A CCCAGACTTTCAGAGCTTTCTCA	<i>MMP3</i> , sense orientation. <i>MMP3</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>MMP3</i> gene (NM_002422). Primers span an intron.
Primer set 19	JJIL6FW JJIL6RV	CACTGGCAGAAAACAACCTGAA ACCAGGCAAGTCTCCTCATTGA	<i>IL6</i> , sense orientation. <i>IL6</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>IL6</i> gene (NM_000600). Primers span an intron.
Primer set 20	JJIL8FW JJIL8RV	GTTTTGAAGAGGGCTGAGAATT C CCCTACAACAGACCCACACAATA C	<i>CXCL8 (IL8)</i> , sense orientation. <i>CXCL8 (IL8)</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>CXCL8</i> gene (NM_000584). Primers span an intron.
Primer set 21	JJCCL2FW JJCCL2RV	AAGACCATTGTGGCCAAGGA TTCGGAGTTTGGGTTTGCT	<i>CCL2</i> , sense orientation. <i>CCL2</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>CCL2</i> gene (NM_002982). Primers span an intron.
Primer set 22	JJCXCL2FW JJCXCL2RV	AGAATGGGCAGAAAGCTTGCT CCTTCTGGTCAGTTGGATTTGC	<i>CXCL2</i> , sense orientation. <i>CXCL2</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>CXCL2</i> gene (NM_002089). Primers span an intron.
Primer set 23	IL1BETAFW IL1BETARV	CGCCAGTGAAATGATGGCTTAT CTGGAAGGAGCACTTCATCTGT	<i>IL-1β</i> , sense orientation. <i>IL-1β</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>IL1B</i> gene (NM_000576). Primers span an intron.
Primer set 24	MDIRF9FW MDIRF9RV	CAACTGAGGCCCTTTCAA CGCCCGTTGTAGATGAAGGT	<i>IRF9</i> , sense orientation. <i>IRF9</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>IRF9</i> gene (NM_006084). Primers span an intron.
Primer set 25	MDIRF7FW	GGCTGGAAACCAACTCCG	<i>IRF7</i> , sense orientation.

	MDIRF7RV	GTTATCCCGCAGCATCACGA	<i>IRF7</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>IRF7</i> gene (NM_001572). Primers span an intron
Primer set 26	MDHSOAS1AF MDHSOAS1AR	TGGAGACCCAAAGGTTGGA AGGAAGCAGGAGGTCTCACC	<i>OAS1</i> , sense orientation. <i>OAS1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>OAS1</i> gene (NM_016816). Primers span an intron
Primer set 27	HSCGASFW HSCGASRV	ACGTGCTGTGAAAACAAAGAAG GTCCCACTGACTGTCTTGAGG	<i>cGAS</i> , sense orientation. <i>cGAS</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>MB21D1</i> gene (NM_138441). Primers span an intron
Primer set 28	HSSTING1FW HSSTING1RV	ATATCTGCGGCTGATCCTGC GGTCTGCTGGGGCAGTTTAT	<i>STING</i> , sense orientation. <i>STING</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>TMEM173</i> gene (NM_198282). Primers span an intron
Primer set 29	TICDKN1AFW TICDKN1ARV	GAGACTCTCAGGGTCGAAAACG TTCCTGTGGCGGATTAGG	<i>CDKN1A</i> , sense orientation. <i>CDKN1A</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>CDKN1A</i> gene (NM_000389). Primers span an intron
Primer set 30	TICDKN2AFW TICDKN2ARV	CGGAAGGTCCCTCAGACATC CCCTGTAGGACCTTCGGTGA	<i>CDKN2A (p16)</i> , sense orientation. <i>CDKN2A (p16)</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>CDKN2A</i> gene (NM_000077). Primers span an intron
Primer set 31	MGAPDHF MGAPDHR	CGGCCGCATCTTCTTGTTG GTGACCAGGCGCCCAATA	<i>Gapdh</i> , sense orientation. <i>Gapdh</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Gapdh</i> gene (NM_008084.3). Primers span an intron. Used as the internal normalizer in gene expression experiments.
Primer set 32	MMHSP90AB1F MMHSP90AB1R	CCACCACCCTGCTCTGTACTA CCTCTCCATGGTGCACTTCC	<i>Hsp90ab1</i> , sense orientation. <i>Hsp90ab1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Hsp90ab1</i> gene (NM_008302). Primers span an intron. Used as secondary normalizer in gene expression experiments.
Primer set 33	MMGUSBFW MMGUSBRV	CGTGACCTTTGTGAGCAACG CTGCTCCATACTCGCTCTGG	<i>Gusb</i> , sense orientation. <i>Gusb</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Gusb</i> gene (NM_010368). Primers span an intron. Used as secondary normalizer in gene expression experiments.
Primer set 34	GBCONIFNAF GBCONIFNAR	TCTGATGCAGCAGGTGGG AGGGCTCTCCAGACTTCTGCTCT G	Interferon alpha consensus, sense orientation. Interferon alpha consensus, antisense orientation. Used in RT-qPCR experiments to assess the collective expression of murine interferon alpha genes. Primers were developed and validated as described ⁴ .
Primer set 35	GBIRF7FW GBIRF7RV	CTCCTGAGCGCAGCCTTG GTTCTTACTGCTGGGGCCAT	<i>Irf7</i> , sense orientation. <i>Irf7</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Irf7</i> gene (NM_016850). Primers span an intron.
Primer set 36	MMOAS1BF MMOAS1BR	TCTGCTTTATGGGGCTTCGG TCGACTCCCATACTCCAGG	<i>Oas1</i> , sense orientation. <i>Oas1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Irf9</i> gene (NM_001083925). Primers span an intron.
Primer set 37	JKLINE1FW JKLINE1RV Amplicon W, Ext. Data Fig. 6f.	CTGCCTTGCAAGAAGAGAGC AGTGCTGCGTTCTGATGATG	Murine LINE-1 5'UTR, positions 392-412, sense orientation. Murine LINE-1 5'UTR, 596-616, antisense orientation. Used in RT-qPCR experiments to assess expression of murine L1 RNA.
Primer set 38	P16MouseF P16MouseR	CCAGGGCCGTGTGCAT TACGTGAACGTTGCCCATCA	<i>Cdkn2a</i> , sense orientation. <i>Cdkn2a</i> , antisense orientation.

			Used for RT-qPCR of the mRNA of the <i>Cdkn2a</i> gene (NM_009877). Primers span an intron.
Primer set 39	GBMMP3FW GBMMP3RV	GACTCAAGGGTGGATGCTGT CCAACTGCGAAGATCCACTG	<i>Mmp3</i> , sense orientation. <i>Mmp3</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Mmp3</i> gene (NM_0108209). Primers span an intron.
Primer set 40	GBIL6FW GBIL6RV	CGGAGAGGAGACTTCACAGAGG A TTTCCACGATTTCCAGAGAACA	<i>Il-6</i> , sense orientation. <i>Il-6</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Il6</i> gene (NM_031168). Primers span an intron.
Primer set 41	MMPAI1FW MMPAI1RV	GGAAGGGCAACATGACCAGG AGCTGCTCTTGGTCGAAAG	<i>Pai1</i> , sense orientation. <i>Pai1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Pai1</i> gene (NM_008871). Primers span an intron.
Primer set 42	APACACAF APACACAR	CTGGCTGCATCCATTATGTCA TGGTAGACTGCCCGTGTGAA	<i>Acaca</i> , sense orientation. <i>Acaca</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Acaca</i> gene (NM_133360). Primers span an intron.
Primer set 43	APFASNF APFASNR	CTGCGTGGCTATGATTATGG AGGTTGCTGTCGTCTGTAGT	<i>Fasn</i> , sense orientation. <i>Fasn</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Fasn</i> gene (NM_007988). Primers span an intron.
Primer set 44	APSREBF1F APSREBF1R	ACTTTTCCTTAACGTGGGCCT CATCTCGGCCAGTGTCTGTT	<i>Srebf1</i> , sense orientation. <i>Srebf1</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Srebf1</i> gene (NM_011480). Primers span an intron.
Primer set 45	APCEBPAF APCEBPAP	TTCGGGTCGCTGGATCTCTA TCAAGGAGAAACCACACGG	<i>C/EBPα</i> , sense orientation. <i>C/EBPα</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>C/EBPα</i> gene (NM_007678).
Primer set 46	APACACBF APACACBR	AGAAGCGAGCACTGCAAGGTTG GGAAGATGGACTCCACCTGGTT	<i>Acacb</i> , sense orientation. <i>Acacb</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Acacb</i> gene (NM_133904). Primers span an intron.
Primer set 47	APPPARGF APPPARGR	TTGCTGATGCACTGCCTAT GGAATGCGAGTGGTCTTCCA	<i>Pparg</i> , sense orientation. <i>Pparg</i> , antisense orientation. Used for RT-qPCR of the mRNA of the <i>Pparg</i> gene (NM_011146). Primers span an intron.
Primer set 48	MDMML1ORF1F MDMML1ORF1R Amplicon X, Ext. Data Fig. 6f.	ATCTGTCTCCAGGTCTGCT TCCTCCGTTTACCTTTCGCC	Murine LINE-1 ORF1, positions 1341-1360, sense orientation. Murine LINE-1 ORF1, positions 1460-1441, antisense orientation. Used in RT-qPCR experiments to assess expression of murine L1 RNA.
Primer set 49	MDMML1ORF2F MDMML1ORF2R Amplicon Y, Ext. Data Fig. 6f.	GCTTCGGTGAAGTAGCTGGA TTCGTTAGAGTACGCCGAG	Murine LINE-1 ORF2, positions 4786-4805, sense orientation. Murine LINE-1 ORF2, positions 4939-4920, antisense orientation. Used in RT-qPCR experiments to assess expression of murine L1 RNA.
Primer set 50	MDMML13UTRF MDMML13UTRR Amplicon Z, Ext. Data Fig. 6f.	AGCCAAATGGATGGACCTGG AAGGAGGGGCATAGTGCCA	Murine LINE-1 3'UTR, positions 6344-6363, sense orientation. Murine LINE-1 3'UTR, positions 6538-6519, antisense orientation. Used in RT-qPCR experiments to assess expression of murine L1 RNA.
Primer set 51	MDMML1TFF MDMML1TFR	ATCCGGACCAGAGGACAGG ATGGCGACCGCTGCTG	Murine LINE-1 5'UTR sense orientation. Murine LINE-1 5'UTR, antisense orientation. Primers amplify one of the polymorphisms of L1Tf(I-III) families.

Primer set 52	MDMML1MDNF MDMML1MDNR	AGAGAACCGGACCCAATCCA GCTTGTGCCCCCTACTCAGAC	Murine LINE-1 5'UTR sense orientation. Murine LINE-1 5'UTR, antisense orientation. Primers amplify one of the polymorphisms of L1MdN(I) families.
Primer set 53	MDMML1MDAF MDMML1MDAF	TCCCCACGGGATCCTAAGAC CTCTGCAGGCAAGCTCTCTT	Murine LINE-1 5'UTR sense orientation. Murine LINE-1 5'UTR, antisense orientation. Primers amplify one of the polymorphisms of L1MdA(IV-VII) families.

- 1 All sequences are listed in the 5'→3' orientation. Primer sets 1–30 are specific for the listed human genes; primer sets 31–53 are murine-specific.
- 2 All LINE-1 positions are relative to the L1Hs consensus sequence (Repbase, <http://www.girinst.org/repbase/>).
- 3 See Coufal, N.G. *et al.* L1 retrotransposition in human neural progenitor cells. *Nature* 460, 1127-31 (2009).
- 4 See Gautier, G. *et al.* A type I interferon autocrine-paracrine loop is involved in Toll-like receptor-induced interleukin-12p70 secretion by dendritic cells. *J. Exp. Med.* 201, 1435-46 (2005).

Table 2: List of antibodies

Antibody	Antibody species	Vendor	Catalog Number	Application
GAPDH	Rabbit	Cell Signaling	5174	Loading control for immunoblotting
GAPDH	Mouse	Sigma	G8795	Loading control for immunoblotting
p16	Mouse	Santa Cruz	sc-756	Immunoblotting
p16	Mouse	Santa Cruz	sc-56330 (JC8)	Immunofluorescence
p21	Rabbit	Santa Cruz	sc-397	Immunoblotting
RB1	Mouse	BD Biosciences	554136	Immunoblotting, ChIP
TREX1	Rabbit	Cell Signaling	12215	Immunoblotting
FOXA1	Rabbit	Abcam	ab170933	Immunoblotting
FOXA1	Goat	Abcam	ab5089	ChIP
Phospho-STAT1 (Tyr701)	Mouse	Santa Cruz	sc-8394	Immunofluorescence
Phospho-STAT2 (Tyr689)	Mouse	Millipore	07-224	Immunofluorescence
STAT2	Rabbit	Cell Signaling	4594S	Immunoblotting
IRF7	Rabbit	Abcam	ab109255	Immunoblotting
IRF9	Rabbit	Novus Bio	NBP2-16991	Immunofluorescence
BrdU	Mouse	BD Biosciences	555627	Immunofluorescence
γ -H2AX	Mouse	Millipore	05-636	Immunofluorescence
F4/80	Rat	Abcam	ab6640 (Cl:A3-1)	Immunofluorescence
ssDNA	Mouse	Enzo	MAb F7-26	Immunofluorescence
DNA-RNA hybrids	Mouse	Kerafast	ENH001 (S9.6)	Immunofluorescence
LaminB1	Goat	Santa Cruz	Sc-6216 (C-20)	Immunofluorescence
IL-6	Rabbit	Cell Signaling	12912	Immunofluorescence
Human LINE-1 ORF1	Rabbit	Gift of K.H. Burns, Johns Hopkins ¹		Immunofluorescence
Mouse LINE-1 Orf1	Rabbit	J.D. Boeke, abEA02 (RabMAb clone NYU-2-1_2		Immunofluorescence

¹ See Rodic, N. *et al.* Long interspersed element-1 protein expression is a hallmark of many human cancers. *Am. J. Pathol.* 184, 1280-6 (2014).

Table 3: List of expressed L1 elements identified by long range RT-PCR

ID	Chromosome	Coordinates (element length)	Family	Count	Intact
L1-07	chr14	63,115,693 - 63,121,722 (6,029bp)	L1HS	16	Yes
L1-09	chrX	11,934,270 - 11,940,496 (6,226bp)	L1HS	10	Yes
L1-13	chr17	66,596,080 - 66,602,096 (6,016bp)	L1HS	9	Yes
L1-20	chr14	70,546,288 - 70,552,339 (6,051bp)	L1HS	6	Yes
L1-24	chr7	49,679,257 - 49,685,289 (6,032bp)	L1HS	5	Yes
L1-25	chr4	21,158,389 - 21,164,420 (6,031bp)	L1HS	5	Yes
L1-54	chr17	9,614,984 - 9,621,024 (6,040bp)	L1HS	3	Yes
L1-55	chrX	155,515,003 - 155,521,032(6,029bp)	L1HS	2.125	Yes
L1-58	chrX	47,782,657 - 47,788,686 (6,029bp)	L1HS	2.125	Yes
L1-59	chr1	118,851,349 - 118,857,375(6,026bp)	L1HS	2.125	Yes
L1-62	chr16	9,583,477 - 9,589,517 (6,040bp)	L1HS	2.125	Yes
L1-76	chr2	166,987,450 - 166,993,486(6,036bp)	L1HS	2	Yes
L1-85	chr8	128,451,975 - 128,458,006(6,031bp)	L1HS	1.8	Yes
L1-116	chr5	104,517,585 - 104,523,614(6,029bp)	L1HS	1	Yes
L1-143	chr1	180,865,798 - 180,871,853(6,055bp)	L1HS	1	Yes
L1-171	chr10	98,781,926 - 98,787,958 (6,032bp)	L1HS	0.8	Yes
L1-172	chr6	2,416,758 - 2,422,787 (6,029bp)	L1HS	0.8	Yes
L1-180	chr3	159,094,350 - 159,100,395(6,045bp)	L1HS	1	Yes
L1-218	chr15	70,728,652 - 70,734,159 (5,507bp)	L1HS	1	Yes
Sum: L1HS intact Counts: 71.9 Individual elements: 19					
L1-06	chr7	70,193,829 - 70,199,858 (6,029bp)	L1HS	18	
L1-08	chr4	87,346,624 - 87,352,647 (6,023bp)	L1HS	11	
L1-17	chr4	78,346,978 - 78,353,011 (6,033bp)	L1HS	7	
L1-23	chr18	13,975,361 - 13,980,770 (5,409bp)	L1HS	5	
L1-31	chr9	110,787,598 - 110,793,630(6,032bp)	L1HS	4	
L1-35	chr1	196,218,871 - 196,224,903(6,032bp)	L1HS	4	
L1-37	chr3	103,555,522 - 103,561,554(6,032bp)	L1HS	4	
L1-38	chr12	3,498,696 - 3,504,729 (6,033bp)	L1HS	4	
L1-40	chr16	65,686,512 - 65,692,528 (6,016bp)	L1HS	4	
L1-41	chrX	50,018,977 - 50,025,006 (6,029bp)	L1HS	4	
L1-45	chr4	136,292,503 - 136,298,555(6,052bp)	L1HS	4	
L1-50	chr3	26,397,518 - 26,403,541 (6,023bp)	L1HS	3	
L1-56	chr20	23,422,609 - 23,428,641 (6,032bp)	L1HS	2.125	
L1-57	chr1	125,119,462 - 125,125,488(6,026bp)	L1HS	2.125	
L1-60	chr20	11,629,280 - 11,635,312 (6,032bp)	L1HS	2.125	
L1-61	chr13	76,612,324 - 76,618,354 (6,030bp)	L1HS	2.125	
L1-64	chr2	86,660,186 - 86,666,388 (6,202bp)	L1HS	2	
L1-72	chr3	132,945,507 - 132,951,535(6,028bp)	L1HS	2	
L1-80	chr5	166,966,282 - 166,972,316(6,034bp)	L1HS	2	
L1-81	chr4	19,077,399 - 19,083,430 (6,031bp)	L1HS	2	
L1-86	chr7	96,846,151 - 96,852,181 (6,030bp)	L1HS	1.8	
L1-87	chr2	230,336,570 - 230,342,014(5,444bp)	L1HS	1.8	
L1-88	chr4	135,177,641 - 135,183,248(5,607bp)	L1HS	1.8	
L1-89	chr4	52,534,972 - 52,540,999 (6,027bp)	L1HS	1.8	
L1-90	chr5	81,612,591 - 81,618,619 (6,028bp)	L1HS	2	
L1-91	chr8	128,890,989 - 128,897,136(6,147bp)	L1HS	2	
L1-96	chr11	87,339,532 - 87,345,562 (6,030bp)	L1HS	2	
L1-97	chr5	177,771,244 - 177,777,273(6,029bp)	L1HS	2	
L1-98	chr5	166,140,692 - 166,146,724(6,032bp)	L1HS	2	
L1-100	chr4	62,726,449 - 62,732,470 (6,021bp)	L1HS	1	
L1-103	chr1	80,942,648 - 80,948,701 (6,053bp)	L1HS	1	
L1-114	chr10	105,775,021 - 105,781,052(6,031bp)	L1HS	1	
L1-115	chr5	34,144,346 - 34,150,370 (6,024bp)	L1HS	1	
L1-133	chr7	113,530,583 - 113,536,613(6,030bp)	L1HS	1	
L1-135	chr1	180,330,072 - 180,336,104(6,032bp)	L1HS	1	
L1-136	chr1	118,634,254 - 118,640,283(6,029bp)	L1HS	1	

ID	Chromosome	Coordinates (element length)	Family	Count	Intact
L1-137	chrX	54,117,700 - 54,123,731 (6,031bp)	L1HS	1	
L1-138	chrX	147,650,235 - 147,656,268(6,033bp)	L1HS	1	
L1-142	chr1	187,217,153 - 187,223,183(6,030bp)	L1HS	1	
L1-144	chr12	69,772,911 - 69,778,942 (6,031bp)	L1HS	1	
L1-149	chr1	239,622,999 - 239,629,024(6,025bp)	L1HS	1	
L1-150	chr1	146,716,693 - 146,722,719(6,026bp)	L1HS	1	
L1-157	chr3	19,495,494 - 19,501,518 (6,024bp)	L1HS	1	
L1-169	chr5	58,383,173 - 58,389,205 (6,032bp)	L1HS	0.8	
L1-170	chr6	19,761,393 - 19,767,419 (6,026bp)	L1HS	0.8	
L1-173	chr2	36,112,007 - 36,118,038 (6,031bp)	L1HS	0.8	
L1-179	chr6	112,700,246 - 112,706,279(6,033bp)	L1HS	1	
L1-181	chr3	108,745,901 - 108,751,932(6,031bp)	L1HS	1	
L1-182	chr4	15,838,047 - 15,844,384 (6,337bp)	L1HS	1	
L1-184	chr8	135,872,363 - 135,878,417(6,054bp)	L1HS	1	
L1-187	chr13	58,673,408 - 58,679,295 (5,887bp)	L1HS	1	
L1-194	chr1	85,745,020 - 85,749,612 (4,592bp)	L1HS	1	
L1-196	chr15	82,882,394 - 82,888,420 (6,026bp)	L1HS	1	
L1-197	chr15	51,416,717 - 51,422,747 (6,030bp)	L1HS	1	
L1-199	chr2	4,730,230 - 4,736,261 (6,031bp)	L1HS	1	
L1-212	chr3	54,393,823 - 54,400,093 (6,270bp)	L1HS	1	

Sum: L1HS non-intact Counts: 132.1 Individual elements: 56

L1-05	chr3	141,764,155 - 141,770,160(6,005bp)	L1PA2	24	
L1-10	chr4	164,097,249 - 164,103,279(6,030bp)	L1PA2	9	
L1-12	chr17	61,106,730 - 61,112,789 (6,059bp)	L1PA2	9	
L1-18	chr22	11,955,882 - 11,962,029 (6,147bp)	L1PA2	6	
L1-22	chr12	67,896,709 - 67,902,725 (6,016bp)	L1PA2	5	
L1-27	chr3	175,781,211 - 175,786,413(5,202bp)	L1PA2	5	
L1-30	chr13	73,637,028 - 73,643,060 (6,032bp)	L1PA2	5	
L1-33	chr4	98,316,999 - 98,322,499 (5,500bp)	L1PA2	4	
L1-34	chr3	178,856,449 - 178,862,480(6,031bp)	L1PA2	4	
L1-39	chr1	169,251,062 - 169,257,094(6,032bp)	L1PA2	4	
L1-42	chr3	119,000,971 - 119,006,991(6,020bp)	L1PA2	4	
L1-53	chr5	106,424,883 - 106,430,882(5,999bp)	L1PA2	3	
L1-66	chr14	86,095,435 - 86,101,470 (6,035bp)	L1PA2	2	
L1-73	chr4	65,992,800 - 65,998,803 (6,003bp)	L1PA2	2	
L1-74	chr10	99,149,238 - 99,155,259 (6,021bp)	L1PA2	2	
L1-75	chr1	72,826,947 - 72,833,271 (6,324bp)	L1PA2	2	
L1-77	chr7	32,461,029 - 32,467,034 (6,005bp)	L1PA2	2	
L1-83	chr3	67,082,246 - 67,088,304 (6,058bp)	L1PA2	2	
L1-101	chr12	102,826,678 - 102,832,665(5,987bp)	L1PA2	1	
L1-105	chr20	25,326,450 - 25,331,184 (4,734bp)	L1PA2	1	
L1-107	chr13	50,978,555 - 50,984,571 (6,016bp)	L1PA2	1	
L1-108	chr4	102,204,431 - 102,210,459(6,028bp)	L1PA2	1	
L1-111	chrX	113,084,049 - 113,090,072(6,023bp)	L1PA2	1	
L1-118	chr21	9,333,222 - 9,339,374 (6,152bp)	L1PA2	1	
L1-123	chr2	129,037,643 - 129,043,675(6,032bp)	L1PA2	1	
L1-125	chr5	85,454,310 - 85,460,328 (6,018bp)	L1PA2	1	
L1-128	chr5	4,611,929 - 4,617,955 (6,026bp)	L1PA2	1	
L1-130	chr16	48,768,072 - 48,774,104 (6,032bp)	L1PA2	1	
L1-131	chr6	162,989,238 - 162,995,263(6,025bp)	L1PA2	1	
L1-132	chr8	68,358,979 - 68,364,479 (5,500bp)	L1PA2	1	
L1-134	chr5	65,160,518 - 65,166,549 (6,031bp)	L1PA2	1	
L1-140	chr4	119,273,614 - 119,279,671(6,057bp)	L1PA2	1	
L1-145	chr3	24,088,959 - 24,094,992 (6,033bp)	L1PA2	1	
L1-151	chr12	108,993,448 - 108,999,474(6,026bp)	L1PA2	1	
L1-164	chr17	41,200,368 - 41,206,401 (6,033bp)	L1PA2	1	
L1-167	chr3	118,910,744 - 118,916,772(6,028bp)	L1PA2	1	
L1-175	chr2	197,687,033 - 197,693,062(6,029bp)	L1PA2	1	
L1-177	chrX	154,935,536 - 154,941,561(6,025bp)	L1PA2	1	

ID	Chromosome	Coordinates (element length)	Family	Count	Intact
L1-186	chr6	83,797,243 - 83,803,271 (6,028bp)	L1PA2	1	
L1-188	chr8	87,621,331 - 87,626,401 (5,070bp)	L1PA2	1	
L1-189	chr11	100,649,611 - 100,655,672(6,061bp)	L1PA2	1	
L1-198	chr15	54,904,988 - 54,911,051 (6,063bp)	L1PA2	1	
L1-202	chr2	153,781,069 - 153,787,086(6,017bp)	L1PA2	1	
L1-209	chr1	85,923,568 - 85,927,951 (4,383bp)	L1PA2	1	
L1-211	chr2	156,251,019 - 156,257,086(6,067bp)	L1PA2	1	
L1-215	chr4	132,940,946 - 132,946,970(6,024bp)	L1PA2	1	
L1-221	chrX	50,056,644 - 50,062,676 (6,032bp)	L1PA2	1	
L1-223	chrX	113,337,323 - 113,343,354(6,031bp)	L1PA2	1	
Sum: L1PA2 Counts: 124 Individual elements: 48					
L1-03	chr19	42,768,603 - 42,774,543 (5,940bp)	L1PA3	31	
L1-04	chr8	55,046,402 - 55,052,502 (6,100bp)	L1PA3	28	
L1-11	chr12	118,657,390 - 118,663,531(6,141bp)	L1PA3	9	
L1-15	chr1	176,307,883 - 176,313,876(5,993bp)	L1PA3	7	
L1-19	chr4	175,016,241 - 175,022,252(6,011bp)	L1PA3	6	
L1-26	chr18	49,212,269 - 49,218,417 (6,148bp)	L1PA3	5	
L1-29	chr11	22,646,426 - 22,652,446 (6,020bp)	L1PA3	5	
L1-36	chr2	22,980,654 - 22,984,410 (3,756bp)	L1PA3	4	
L1-44	chr10	109,602,039 - 109,607,567(5,528bp)	L1PA3	4	
L1-46	chr7	63,728,965 - 63,735,094 (6,129bp)	L1PA3	4	
L1-48	chr14	38,631,448 - 38,637,485 (6,037bp)	L1PA3	4	
L1-49	chr19	42,743,461 - 42,749,399 (5,938bp)	L1PA3	4	
L1-52	chr4	123,632,778 - 123,638,935(6,157bp)	L1PA3	3	
L1-65	chr2	96,375,482 - 96,381,632 (6,150bp)	L1PA3	2	
L1-69	chr1	100,662,482 - 100,668,126(5,644bp)	L1PA3	2	
L1-70	chr5	25,077,154 - 25,083,186 (6,032bp)	L1PA3	2	
L1-78	chr12	78,502,931 - 78,509,088 (6,157bp)	L1PA3	2	
L1-82	chr6	80,844,240 - 80,850,277 (6,037bp)	L1PA3	2	
L1-84	chr8	69,015,505 - 69,021,651 (6,146bp)	L1PA3	2	
L1-94	chr4	88,916,060 - 88,922,204 (6,144bp)	L1PA3	2	
L1-104	chr4	142,249,845 - 142,255,868(6,023bp)	L1PA3	1	
L1-110	chr3	24,276,690 - 24,282,186 (5,496bp)	L1PA3	1	
L1-113	chr4	119,061,402 - 119,067,563(6,161bp)	L1PA3	1	
L1-117	chr12	10,343,959 - 10,349,500 (5,541bp)	L1PA3	1	
L1-121	chr3	112,658,647 - 112,664,665(6,018bp)	L1PA3	1	
L1-124	chr9	68,274,827 - 68,280,864 (6,037bp)	L1PA3	1	
L1-126	chr5	75,792,130 - 75,798,187 (6,057bp)	L1PA3	1	
L1-139	chr11	31,540,511 - 31,546,645 (6,134bp)	L1PA3	1	
L1-141	chr3	145,924,279 - 145,930,431(6,152bp)	L1PA3	1	
L1-147	chr8	91,887,863 - 91,893,862 (5,999bp)	L1PA3	1	
L1-148	chrX	94,858,876 - 94,864,901 (6,025bp)	L1PA3	1	
L1-152	chr18	55,886,913 - 55,892,940 (6,027bp)	L1PA3	1	
L1-154	chr9	125,006,549 - 125,012,715(6,166bp)	L1PA3	1	
L1-156	chr6	71,826,216 - 71,832,235 (6,019bp)	L1PA3	1	
L1-158	chr8	91,191,345 - 91,197,369 (6,024bp)	L1PA3	1	
L1-159	chr12	55,586,438 - 55,592,480 (6,042bp)	L1PA3	1	
L1-165	chr2	97,521,921 - 97,528,067 (6,146bp)	L1PA3	1	
L1-166	chr6	126,670,052 - 126,676,070(6,018bp)	L1PA3	1	
L1-174	chr12	80,143,556 - 80,149,577 (6,021bp)	L1PA3	1	
L1-176	chr12	51,562,132 - 51,568,340 (6,208bp)	L1PA3	1	
L1-178	chr9	17,536,062 - 17,542,081 (6,019bp)	L1PA3	1	
L1-183	chr12	80,074,170 - 80,080,329 (6,159bp)	L1PA3	1	
L1-185	chr6	48,733,849 - 48,740,059 (6,210bp)	L1PA3	1	
L1-190	chr4	82,171,911 - 82,177,138 (5,227bp)	L1PA3	1	
L1-191	chr15	32,045,176 - 32,051,279 (6,103bp)	L1PA3	1	
L1-192	chr17	71,351,460 - 71,357,401 (5,941bp)	L1PA3	1	
L1-193	chr5	99,339,116 - 99,345,270 (6,154bp)	L1PA3	1	
L1-195	chr5	122,509,114 - 122,515,140(6,026bp)	L1PA3	1	

ID	Chromosome	Coordinates (element length)	Family	Count	Intact
L1-200	chr10	35,855,169 - 35,861,196 (6,027bp)	L1PA3	1	
L1-201	chr12	31,159,575 - 31,165,595 (6,020bp)	L1PA3	1	
L1-203	chr14	37,766,297 - 37,772,332 (6,035bp)	L1PA3	1	
L1-206	chr14	56,013,511 - 56,019,543 (6,032bp)	L1PA3	1	
L1-210	chr2	95,866,030 - 95,872,191 (6,161bp)	L1PA3	1	
L1-214	chr4	94,835,259 - 94,841,286 (6,027bp)	L1PA3	1	
L1-217	chr7	84,049,212 - 84,055,231 (6,019bp)	L1PA3	1	
L1-219	chr16	12,069,684 - 12,075,804 (6,120bp)	L1PA3	1	
L1-222	chrX	55,680,654 - 55,686,684 (6,030bp)	L1PA3	1	
L1-224	chrX	149,432,338 - 149,438,331(5,993bp)	L1PA3	1	
Sum: L1PA3 Counts: 166 Individual elements: 58					
L1-01	chr18	9,165,216 - 9,171,138 (5,922bp)	L1PA4	46	
L1-14	chr3	29,978,961 - 29,984,962 (6,001bp)	L1PA4	7	
L1-16	chr6	83,330,453 - 83,336,586 (6,133bp)	L1PA4	7	
L1-21	chr6	139,217,130 - 139,223,263(6,133bp)	L1PA4	6	
L1-28	chr8	49,874,774 - 49,880,758 (5,984bp)	L1PA4	5	
L1-32	chr5	176,077,678 - 176,083,819(6,141bp)	L1PA4	4	
L1-43	chr5	33,095,404 - 33,101,548 (6,144bp)	L1PA4	4	
L1-47	chr4	48,864,081 - 48,870,233 (6,152bp)	L1PA4	4	
L1-51	chr5	130,779,991 - 130,786,158(6,167bp)	L1PA4	3	
L1-63	chr6	7,942,696 - 7,948,800 (6,104bp)	L1PA4	2	
L1-71	chr7	56,505,920 - 56,512,049 (6,129bp)	L1PA4	2	
L1-79	chr10	93,517,474 - 93,523,652 (6,178bp)	L1PA4	2	
L1-92	chr21	9,182,589 - 9,188,720 (6,131bp)	L1PA4	2	
L1-93	chr4	173,772,935 - 173,779,072(6,137bp)	L1PA4	2	
L1-95	chr1	125,011,752 - 125,017,885(6,133bp)	L1PA4	2	
L1-99	chr9	90,682,773 - 90,689,210 (6,437bp)	L1PA4	2	
L1-102	chr10	64,014,843 - 64,021,048 (6,205bp)	L1PA4	1	
L1-112	chr15	76,776,415 - 76,782,548 (6,133bp)	L1PA4	1	
L1-119	chr12	11,373,698 - 11,379,329 (5,631bp)	L1PA4	1	
L1-120	chr19	24,012,879 - 24,018,978 (6,099bp)	L1PA4	1	
L1-122	chr3	99,031,289 - 99,037,430 (6,141bp)	L1PA4	1	
L1-129	chr10	15,664,019 - 15,669,631 (5,612bp)	L1PA4	1	
L1-146	chr4	90,478,877 - 90,483,706 (4,829bp)	L1PA4	1	
L1-153	chrX	76,878,709 - 76,885,597 (6,888bp)	L1PA4	1	
L1-155	chr18	43,282,426 - 43,288,579 (6,153bp)	L1PA4	1	
L1-160	chr19	20,486,826 - 20,493,102 (6,276bp)	L1PA4	1	
L1-161	chr1	200,181,868 - 200,188,010(6,142bp)	L1PA4	1	
L1-162	chr11	100,034,468 - 100,040,624(6,156bp)	L1PA4	1	
L1-163	chr20	29,365,560 - 29,370,431 (4,871bp)	L1PA4	1	
L1-168	chr5	78,706,259 - 78,712,394 (6,135bp)	L1PA4	1	
L1-204	chr1	83,178,675 - 83,184,836 (6,161bp)	L1PA4	1	
L1-205	chr3	39,366,145 - 39,372,264 (6,119bp)	L1PA4	1	
L1-208	chr18	45,793,571 - 45,799,710 (6,139bp)	L1PA4	1	
L1-216	chr5	39,030,830 - 39,036,977 (6,147bp)	L1PA4	1	
Sum: L1PA4 Counts: 118 Individual elements: 34					
L1-02	chr5	80,840,410 - 80,845,999 (5,589bp)	L1PA5	36	
L1-67	chr12	370,113 - 376,219 (6,106bp)	L1PA5	2	
L1-68	chr11	95,811,406 - 95,816,742 (5,336bp)	L1PA5	2	
L1-106	chr10	109,822,318 - 109,828,350(6,032bp)	L1PA5	1	
L1-109	chrX	12,102,927 - 12,109,072 (6,145bp)	L1PA5	1	
L1-127	chr4	59,474,627 - 59,479,488 (4,861bp)	L1PA5	1	
L1-207	chr15	99,827,462 - 99,833,366 (5,904bp)	L1PA5	1	
L1-213	chr3	146,434,278 - 146,440,207(5,929bp)	L1PA5	1	
L1-220	chr18	35,720,595 - 35,726,712 (6,117bp)	L1PA5	1	
Sum: L1PA5 Counts: 46 Individual elements: 9					

Summary	Counts	%	Individual elements	%
L1HS intact	71.9	10.9	19	8.5
L1HS non-intact	132.1	20.1	56	25.0
L1PA2	124	18.8	48	21.4
L1PA3	166	25.2	58	25.9
L1 PA4	118	17.9	34	15.2
L1PA5	46	7.0	9	4.0
Sum:	658	100.0	224	100.0

Table 4: Gene list used in GSEA for IFN-I (50 genes)

Gene Symbol	Gene Name
ADAR	adenosine deaminase, RNA specific
BST2	bone marrow stromal cell antigen 2
CASP1	caspase 1
CAV1	caveolin 1
CXCL10	C-X-C motif chemokine ligand 10
DDX58	DExD/H-box helicase 58
EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2
IFI16	interferon gamma inducible protein 16
IFI27	interferon alpha inducible protein 27
IFI30	IFI30, lysosomal thiol reductase
IFI6	interferon alpha inducible protein 6
IFIH1	interferon induced with helicase C domain 1
IFIT1	interferon induced protein with tetratricopeptide repeats 1
IFIT2	interferon induced protein with tetratricopeptide repeats 2
IFIT3	interferon induced protein with tetratricopeptide repeats 3
IFITM1	interferon induced transmembrane protein 1
IFITM2	interferon induced transmembrane protein 2
IFITM3	interferon induced transmembrane protein 3
IFNA1	interferon alpha 1
IFNA2	interferon alpha 2
IFNA4	interferon alpha 4
IFNAR1	interferon alpha and beta receptor subunit 1
IFNAR2	interferon alpha and beta receptor subunit 2
IFNB1	interferon beta 1
IFNE	interferon epsilon
IFNW1	interferon omega 1
IRF1	interferon regulatory factor 1
IRF2	interferon regulatory factor 2
IRF3	interferon regulatory factor 3
IRF5	interferon regulatory factor 5
IRF7	interferon regulatory factor 7
IRF9	interferon regulatory factor 9
ISG15	ISG15 ubiquitin-like modifier
ISG20	interferon stimulated exonuclease gene 20
JAK1	Janus kinase 1
JAK2	Janus kinase 2
MAL	mal, T-cell differentiation protein
MET	MET proto-oncogene, receptor tyrosine kinase
MNDA	myeloid cell nuclear differentiation antigen
MX1	MX dynamin like GTPase 1
MX2	MX dynamin like GTPase 2
MYD88	myeloid differentiation primary response 88
NOS2	nitric oxide synthase 2
OAS1	2'-5'-oligoadenylate synthetase 1
OAS2	2'-5'-oligoadenylate synthetase 2
STAT1	signal transducer and activator of transcription 1
STAT2	signal transducer and activator of transcription 2
STAT3	signal transducer and activator of transcription 3
TMEM173	transmembrane protein 173
TNFSF10	tumor necrosis factor superfamily member 10

Table 5: GSEA analysis of KEGG pathways comparing early passage with early senescence

UPREGULATED FROM EARLY PASSAGE (EP) TO EARLY SENESENCE (SEN-E)					
PATHWAY NAME	SIZE	ES	NES	NOM p-val	FDR p-val
KEGG_ASTHMA	28	0.7237	1.7864	<1.00E-03	<1.00E-02
KEGG_GRAFT_VERSUS_HOST_DISEASE	35	0.6852	1.7654	<1.00E-03	<1.00E-02
KEGG_CELL_ADHESION_MOLECULES_CAMS	127	0.5578	1.7538	<1.00E-03	<1.00E-02
KEGG_OLFACTORY_TRANSDUCTION	367	0.4965	1.7468	<1.00E-03	<1.00E-02
KEGG_TYPE_1_DIABETES_MELLITUS	41	0.6457	1.7140	<1.00E-03	<1.00E-02
KEGG_LYSOSOME	119	0.5388	1.6878	<1.00E-03	<1.00E-02
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	67	0.5786	1.6854	<1.00E-03	<1.00E-02
KEGG_ECM_RECEPTOR_INTERACTION	84	0.5123	1.5487	<1.00E-03	<1.00E-02
KEGG_LEISHMANIA_INFECTION	68	0.5688	1.6559	1.79E-03	1.51E-02
CUSTOM_SASP	85	0.5471	1.6517	1.80E-03	1.51E-02
KEGG_PRION_DISEASES	34	0.6326	1.6397	1.84E-03	1.51E-02
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	254	0.4561	1.5705	1.62E-03	1.51E-02
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	99	0.4868	1.4920	1.73E-03	1.51E-02
KEGG_AUTOIMMUNE_THYROID_DISEASE	48	0.5605	1.5336	3.77E-03	2.66E-02
KEGG_ENDOCYTOSIS	174	0.4365	1.4427	5.21E-03	3.49E-02
KEGG_VIRAL_MYOCARDITIS	68	0.5313	1.5277	8.68E-03	5.47E-02
KEGG_RIG_1_LIKE_RECEPTOR_SIGNALING_PATHWAY	67	0.5169	1.4977	9.06E-03	5.47E-02
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	45	0.5848	1.5670	1.08E-02	6.11E-02
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	83	0.4814	1.4387	1.08E-02	6.11E-02
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	270	0.3779	1.2928	1.12E-02	6.14E-02
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	73	0.5096	1.4914	1.28E-02	6.81E-02
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	67	0.5106	1.5038	1.64E-02	8.00E-02
KEGG_STARCH_AND_SUCROSE_METABOLISM	45	0.5382	1.4727	1.68E-02	8.00E-02
KEGG_MAPK_SIGNALING_PATHWAY	263	0.3751	1.2821	1.64E-02	8.00E-02
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	21	0.6766	1.5631	2.06E-02	9.32E-02
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	60	0.5046	1.4370	2.16E-02	9.54E-02
KEGG_ABC_TRANSPORTERS	44	0.5440	1.4685	2.51E-02	1.08E-01
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	52	0.5357	1.4752	2.64E-02	1.11E-01
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	123	0.4218	1.3254	2.83E-02	1.16E-01
KEGG_OTHER_GLYCAN_DEGRADATION	16	0.6967	1.5277	3.13E-02	1.24E-01
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	32	0.5745	1.4414	3.22E-02	1.24E-01
KEGG_HEMATOPOIETIC_CELL_LINEAGE	85	0.4547	1.3563	3.42E-02	1.27E-01
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	0.6172	1.4675	3.59E-02	1.27E-01
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	0.4733	1.3664	3.54E-02	1.27E-01
KEGG_DILATED_CARDIOMYOPATHY	90	0.4453	1.3480	3.55E-02	1.27E-01
KEGG_ALLOGRAFT_REJECTION	35	0.5607	1.4452	3.92E-02	1.36E-01
KEGG_CALCIIUM_SIGNALING_PATHWAY	173	0.3956	1.2886	4.46E-02	1.52E-01
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	210	0.3708	1.2426	4.93E-02	1.62E-01
KEGG_STEROID_HORMONE_BIOSYNTHESIS	49	0.4982	1.3661	5.14E-02	1.66E-01
KEGG_LINOLEIC_ACID_METABOLISM	29	0.5664	1.3972	5.98E-02	1.90E-01
KEGG_FOCAL_ADHESION	197	0.3646	1.2184	6.69E-02	2.09E-01
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	115	0.4016	1.2474	7.64E-02	2.34E-01
KEGG_RETINOL_METABOLISM	56	0.4497	1.2695	9.09E-02	2.70E-01
KEGG_CHEMOKINE_SIGNALING_PATHWAY	183	0.3602	1.1945	9.02E-02	2.70E-01
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	112	0.3902	1.2155	9.52E-02	2.78E-01
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	53	0.4475	1.2529	1.16E-01	3.33E-01
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.5941	1.2772	1.73E-01	4.70E-01
KEGG_SPHINGOLIPID_METABOLISM	36	0.4710	1.2155	1.79E-01	4.70E-01
KEGG_REGULATION_OF_AUTOPHAGY	32	0.4748	1.2109	1.75E-01	4.70E-01
KEGG_ARACHIDONIC_ACID_METABOLISM	58	0.4212	1.1842	1.78E-01	4.70E-01
KEGG_MELANOMA	71	0.4044	1.1820	1.76E-01	4.70E-01
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	62	0.4067	1.1816	1.88E-01	4.86E-01
KEGG_AXON_GUIDANCE	127	0.3540	1.1188	2.01E-01	5.12E-01
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	0.4560	1.1899	2.08E-01	5.23E-01
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	22	0.5028	1.1791	2.20E-01	5.31E-01
KEGG_TASTE_TRANSDUCTION	50	0.4249	1.1650	2.19E-01	5.31E-01
KEGG_NITROGEN_METABOLISM	23	0.5036	1.1769	2.24E-01	5.33E-01
KEGG_PPAR_SIGNALING_PATHWAY	69	0.3797	1.1045	2.63E-01	5.77E-01
KEGG_JAK_STAT_SIGNALING_PATHWAY	148	0.3340	1.0743	2.65E-01	5.77E-01
KEGG_APOPTOSIS	86	0.3669	1.0996	2.67E-01	5.77E-01
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	44	0.4154	1.1191	2.81E-01	5.98E-01
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	63	0.3754	1.0737	2.93E-01	6.17E-01

UPREGULATED FROM EARLY PASSAGE (EP) TO EARLY SENESCENCE (SEN-E)					
PATHWAY NAME	SIZE	ES	NES	NOM p-val	FDR p-val
KEGG_INOSITOL_PHOSPHATE_METABOLISM	54	0.3887	1.0905	3.04E-01	6.32E-01
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	73	0.3662	1.0598	3.33E-01	6.77E-01
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	25	0.4434	1.0764	3.41E-01	6.86E-01
KEGG_ALZHEIMERS_DISEASE	153	0.3226	1.0359	3.57E-01	7.10E-01
CUSTOM_IFN-I	50	0.3781	1.0455	3.69E-01	7.18E-01
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	34	0.3971	1.0438	3.81E-01	7.24E-01
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	26	0.4256	1.0321	3.84E-01	7.24E-01
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	0.4687	1.0325	4.21E-01	7.67E-01
KEGG_N_GLYCAN_BIOSYNTHESIS	46	0.3798	1.0231	4.32E-01	7.67E-01
KEGG_GALACTOSE_METABOLISM	26	0.4132	1.0123	4.50E-01	7.83E-01
KEGG_GLYCEROLIPID_METABOLISM	43	0.3679	0.9942	4.71E-01	8.12E-01
KEGG_LONG_TERM_POTENTIATION	66	0.3408	0.9796	4.99E-01	8.36E-01
KEGG_RENIN_ANGIOTENSIN_SYSTEM	17	0.4406	0.9772	4.95E-01	8.36E-01
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	25	0.4094	0.9773	5.17E-01	8.41E-01
KEGG_WNT_SIGNALING_PATHWAY	149	0.3005	0.9739	5.21E-01	8.41E-01
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	92	0.3151	0.9621	5.27E-01	8.41E-01
KEGG_TGF_BETA_SIGNALING_PATHWAY	85	0.3190	0.9616	5.47E-01	8.41E-01
KEGG_BETA_ALANINE_METABOLISM	22	0.4046	0.9468	5.33E-01	8.41E-01
KEGG_ERBB_SIGNALING_PATHWAY	86	0.3133	0.9462	5.80E-01	8.41E-01
KEGG_BLADDER_CANCER	40	0.3590	0.9449	5.46E-01	8.41E-01
KEGG_TRYPTOPHAN_METABOLISM	39	0.3580	0.9438	5.65E-01	8.41E-01
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	25	0.3874	0.9353	5.43E-01	8.41E-01
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	30	0.3770	0.9349	5.68E-01	8.41E-01
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	23	0.3978	0.9310	5.80E-01	8.41E-01
KEGG_STEROID_BIOSYNTHESIS	16	0.4313	0.9285	5.80E-01	8.41E-01
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	21	0.3990	0.9236	5.81E-01	8.41E-01
KEGG_PATHWAYS_IN_CANCER	321	0.2739	0.9494	6.20E-01	8.70E-01
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	79	0.3108	0.9249	6.15E-01	8.70E-01
KEGG_CARDIAC_MUSCLE_CONTRACTION	73	0.3058	0.8963	6.30E-01	8.77E-01
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	33	0.3410	0.8707	6.63E-01	9.16E-01
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	106	0.2915	0.8919	7.09E-01	9.26E-01
KEGG_GLIOMA	62	0.3116	0.8857	6.93E-01	9.26E-01
KEGG_ADHERENS_JUNCTION	68	0.3059	0.8855	6.97E-01	9.26E-01
KEGG_FATTY_ACID_METABOLISM	42	0.3279	0.8719	6.83E-01	9.26E-01
KEGG_BASAL_CELL_CARCINOMA	55	0.3100	0.8612	7.21E-01	9.26E-01
KEGG_PENTOSE_PHOSPHATE_PATHWAY	26	0.3492	0.8408	7.11E-01	9.26E-01
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	20	0.3583	0.8338	7.01E-01	9.26E-01
KEGG_RIBOFLAVIN_METABOLISM	16	0.3816	0.8159	7.21E-01	9.26E-01
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	0.3025	0.8755	7.38E-01	9.41E-01
KEGG_GAP_JUNCTION	87	0.2863	0.8629	7.78E-01	9.58E-01
KEGG_TYPE_II_DIABETES_MELLITUS	46	0.3026	0.8226	7.91E-01	9.67E-01
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	71	0.2827	0.8316	8.21E-01	9.91E-01
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	44	0.2918	0.8032	8.31E-01	9.96E-01
KEGG_TIGHT_JUNCTION	128	0.2691	0.8537	8.45E-01	1.00E+00
KEGG_GNRH_SIGNALING_PATHWAY	98	0.2748	0.8397	8.54E-01	1.00E+00
KEGG_MELANOGENESIS	98	0.2604	0.7985	9.00E-01	1.00E+00
KEGG_THYROID_CANCER	29	0.3078	0.7626	8.66E-01	1.00E+00
KEGG_DORSO_VENTRAL_AXIS_FORMATION	24	0.3171	0.7609	8.57E-01	1.00E+00
KEGG_INSULIN_SIGNALING_PATHWAY	134	0.2351	0.7496	9.91E-01	1.00E+00
KEGG_ENDOMETRIAL_CANCER	52	0.2653	0.7338	9.37E-01	1.00E+00
KEGG_PEROXISOME	78	0.2441	0.7164	9.85E-01	1.00E+00
KEGG_RENAL_CELL_CARCINOMA	66	0.2430	0.7008	9.72E-01	1.00E+00
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	122	0.2183	0.6909	9.96E-01	1.00E+00
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	74	0.2309	0.6826	9.98E-01	1.00E+00
KEGG_NOTCH_SIGNALING_PATHWAY	47	0.2500	0.6804	9.61E-01	1.00E+00
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	44	0.2466	0.6598	9.87E-01	1.00E+00
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	0.2416	0.6441	9.89E-01	1.00E+00
KEGG_MTOR_SIGNALING_PATHWAY	51	0.2221	0.6199	9.98E-01	1.00E+00
KEGG_PROANOATE_METABOLISM	32	0.2372	0.5923	9.89E-01	1.00E+00
KEGG_HUNTINGTONS_DISEASE	170	0.1817	0.5895	1.00E+00	1.00E+00
KEGG_PYRUVATE_METABOLISM	39	0.2174	0.5683	9.96E-01	1.00E+00

DOWNREGULATED FROM EARLY PASSAGE (EP) TO EARLY SENEESCENCE (SEN-E)					
PATHWAY NAME	SIZE	ES	NES	NOM p-val	FDR p-val
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	123	-0.7308	-2.3625	<1.00E-03	<1.00E-02
KEGG_SPLICEOSOME	120	-0.6589	-2.1285	<1.00E-03	<1.00E-02
KEGG_DNA_REPLICATION	36	-0.7853	-2.0793	<1.00E-03	<1.00E-02
KEGG_CELL_CYCLE	124	-0.6132	-1.9829	<1.00E-03	<1.00E-02
KEGG_HOMOLOGOUS_RECOMBINATION	26	-0.7502	-1.8667	<1.00E-03	<1.00E-02
KEGG_RIBOSOME	87	-0.6122	-1.8588	<1.00E-03	<1.00E-02
KEGG_RNA_DEGRADATION	56	-0.6176	-1.7888	<1.00E-03	<1.00E-02
KEGG_OOCYTE_MEIOSIS	107	-0.5171	-1.6434	<1.00E-03	<1.00E-02
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	85	-0.5121	-1.6010	<1.00E-03	<1.00E-02
KEGG_BASE_EXCISION_REPAIR	33	-0.6575	-1.7074	2.19E-03	1.39E-02
KEGG_MISMATCH_REPAIR	23	-0.7278	-1.7707	2.36E-03	1.39E-02
KEGG_PROTEASOME	43	-0.5630	-1.5802	8.83E-03	5.32E-02
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.5541	-1.5345	1.53E-02	7.76E-02
KEGG_PYRIMIDINE_METABOLISM	94	-0.4476	-1.3925	2.03E-02	8.83E-02
KEGG_BASAL_TRANSCRIPTION_FACTORS	35	-0.5618	-1.4699	3.23E-02	1.21E-01
KEGG_RNA_POLYMERASE	27	-0.5679	-1.4123	4.53E-02	1.51E-01
KEGG_COLORECTAL_CANCER	62	-0.4119	-1.1964	1.75E-01	4.72E-01
KEGG_PRIMARY_IMMUNODEFICIENCY	34	-0.4517	-1.1747	2.13E-01	5.24E-01
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	16	-0.5303	-1.1852	2.27E-01	5.34E-01
KEGG_CITRATE_CYCLE_TCA_CYCLE	30	-0.4512	-1.1431	2.36E-01	5.48E-01
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.3558	-1.1053	2.44E-01	5.59E-01
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23	-0.4753	-1.1566	2.56E-01	5.74E-01
KEGG_PURINE_METABOLISM	152	-0.3191	-1.0691	2.68E-01	5.82E-01
KEGG_HISTIDINE_METABOLISM	27	-0.4347	-1.0768	3.10E-01	6.38E-01
KEGG_PHENYLALANINE_METABOLISM	18	-0.4584	-1.0618	3.65E-01	7.16E-01
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	42	-0.3858	-1.0507	3.77E-01	7.16E-01
KEGG_ETHER_LIPID_METABOLISM	30	-0.4050	-1.0352	4.00E-01	7.46E-01
KEGG_GLYCOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.4608	-1.0148	4.14E-01	7.63E-01
KEGG_PROSTATE_CANCER	89	-0.3204	-0.9982	4.27E-01	7.63E-01
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	-0.3540	-1.0074	4.30E-01	7.63E-01
KEGG_P53_SIGNALING_PATHWAY	66	-0.3441	-1.0082	4.49E-01	7.83E-01
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	-0.4277	-0.9850	4.88E-01	8.33E-01
KEGG_GLUTATHIONE_METABOLISM	48	-0.3354	-0.9456	5.51E-01	8.40E-01
KEGG_TYROSINE_METABOLISM	41	-0.3461	-0.9432	5.59E-01	8.40E-01
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	-0.4210	-0.9251	5.66E-01	8.40E-01
KEGG_NON_SMALL_CELL_LUNG_CANCER	54	-0.3267	-0.9320	5.75E-01	8.40E-01
KEGG_SELENOAMINO_ACID_METABOLISM	24	-0.3674	-0.9087	5.94E-01	8.52E-01
KEGG_VIBRIO_CHOLERAE_INFECTION	53	-0.3177	-0.9225	5.98E-01	8.52E-01
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	19	-0.3620	-0.8293	7.19E-01	9.24E-01
KEGG_LONG_TERM_DEPRESSION	70	-0.2922	-0.8691	7.45E-01	9.43E-01
KEGG_ACUTE_MYELOID_LEUKEMIA	57	-0.2957	-0.8524	7.58E-01	9.53E-01
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-0.2905	-0.8710	7.70E-01	9.60E-01
KEGG_PANCREATIC_CANCER	69	-0.2928	-0.8606	7.77E-01	9.60E-01
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	52	-0.2946	-0.8457	8.00E-01	9.72E-01
KEGG_O_GLYCAN_BIOSYNTHESIS	27	-0.2958	-0.7509	8.78E-01	1.00E+00
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	131	-0.2490	-0.8209	9.31E-01	1.00E+00
KEGG_ARGININE_AND_PROLINE_METABOLISM	48	-0.2670	-0.7389	9.36E-01	1.00E+00
KEGG_BUTANOATE_METABOLISM	34	-0.2643	-0.6990	9.55E-01	1.00E+00
KEGG_PROTEIN_EXPORT	22	-0.2643	-0.6293	9.74E-01	1.00E+00
KEGG_PARKINSONS_DISEASE	112	-0.2391	-0.7645	9.74E-01	1.00E+00
KEGG_VEGF_SIGNALING_PATHWAY	75	-0.2379	-0.7151	9.77E-01	1.00E+00
KEGG_LYSINE_DEGRADATION	39	-0.2282	-0.6218	9.89E-01	1.00E+00
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.2402	-0.6572	9.90E-01	1.00E+00
KEGG_GLYCOLYSIS_GLUONEOGENESIS	61	-0.2270	-0.6631	9.93E-01	1.00E+00
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	37	-0.2269	-0.6034	9.96E-01	1.00E+00
KEGG_OXIDATIVE_PHOSPHORYLATION	116	-0.1799	-0.5790	1.00E+00	1.00E+00

Table 6: Summary of Qiagen PCR array analysis

	<u>SEN (L) cells</u>		<u>3X cells</u>	
	Number of genes	Percent ¹	Number of genes	Percent ¹
Total genes	84	100%	84	100%
Upregulated genes	77	92%	80	95%
Downregulated genes	7	8%	4	5%
Changing genes passing filters ²	58	69%	44	52%
Passing genes upregulated	57	68%	44	52%
Passing genes downregulated	1	1%	0	0%
Changing genes failing filters	26	31%	40	48%
Genes passing filters, unique ³	23	27%	9	11%
Genes passing filters, overlap ⁴	35	42%	35	42%
Genes passing filters, total ⁵	67	80%	67	80%

¹ All percentages are calculated with respect to the total number of genes (84) found on the array. Data for all 84 genes displayed as scatter plots are shown in Fig. 2h.

² The sum of upregulated and downregulated genes that pass a set of significance filters, see Methods for definitions of filters.

³ Changing genes that pass the significance filters that are unique to either SEN (L) or 3X cells.

⁴ Changing genes that pass the significance filters that are common to (found in both) SEN (L) and 3X cells.

⁵ Changing genes that pass the significance filters that are found in SEN (L) and/or 3X cells. The heatmap representation for this set of genes (67) is shown in Extended Fig. 4j, k.

Table 7
Age group Foldchanges

	L1	pl6	IFNA	IRF7	OAS1	IL6	MMP3	PAI
05mo-WT	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
05mo-3TC	1.420	0.868	1.489	0.922	2.229	2.046	0.993	1.265
26mo-WT	6.265	2.917	13.219	1.560	1.898	8.775	3.078	6.603
26mo-3TC	3.947	2.213	6.579	1.076	1.681	2.355	1.762	2.839

T-TEST

05 VS 3TC	0.152	0.819	0.304	0.542	0.125	0.123	0.981	0.547
05 VS 26	0.001	0.001	0.000	0.001	0.207	0.001	0.022	0.110
26 VS 3TC	0.068	0.129	0.016	0.070	0.786	0.001	0.090	0.194

Individual Foldchanges

	L1	pl6	IFNA	IRF7	OAS1	IL6	MMP3	PAI
05mo-WT	1.013	0.372	0.874	1.062	0.684	0.953	0.488	0.645
	1.249	0.342	0.982	0.868	0.769	1.059	1.011	0.916
	0.884	0.412	0.394	0.835	1.441	1.003	0.663	0.695
	1.343	3.419	1.540	0.953	0.791	0.848	1.660	1.291
	1.085	1.107	1.037	1.079	0.355	0.881	0.755	2.511
	0.755	0.552	1.397	1.886	1.799	1.352	1.971	0.314
	0.979	1.408	0.557	0.679	0.977	1.112	0.913	0.596
	0.692	0.388	0.729	1.127	1.183	0.792	0.539	1.033

05mo-3TC	1.458	2.881	1.821	1.040	2.867	1.455	1.587	2.291
	1.464	0.457	2.748	1.153	1.521	0.924	0.601	0.842
	0.484	0.957	2.909	1.132	6.031	5.604	1.946	2.212
	1.829	0.270	0.645	0.684	1.317	1.622	0.711	1.683
	2.537	0.465	0.565	0.037	1.920	1.920	0.635	0.180
	0.747	0.541	0.346	0.960	1.603	0.751	0.476	0.380

26mo-WT	10.645	2.563	17.947	1.801	5.442	17.058	6.449	0.979
	3.930	1.799	1.336	1.478	0.423	3.264	1.275	1.842
	1.688	4.441	8.010	1.439	0.531	3.254	2.541	3.243
	10.959	2.315	22.657	1.891	0.516	19.464	5.831	32.301
	13.251	4.668	24.009	1.007	4.476	10.752	6.948	5.159
	2.413	4.457	17.239	2.233	0.231	4.028	1.564	0.306
	4.278	1.361	12.879	1.461	1.699	4.075	0.764	9.405
	2.796	2.689	0.531	1.971	4.666	7.083	1.161	16.692
	6.245	3.037	13.076	1.660	2.248	8.622	3.317	1.188
	4.788	1.777	10.981	1.422	0.963	3.754	1.551	1.605
	6.397	2.575	13.747	1.240	0.598	14.603	0.982	4.307
	7.793	3.327	16.220	1.120	0.986	9.347	4.554	2.206

26mo-3TC	2.819	2.290	10.115	0.540	1.658	1.116	1.044	1.034
	2.160	3.653	2.941	0.506	0.643	1.553	0.972	1.056
	2.053	1.731	4.156	0.498	0.055	2.194	1.618	2.696
	1.491	1.168	1.283	0.424	0.482	0.686	1.650	0.493
	6.524	0.844	1.601	0.954	1.094	1.395	1.033	1.562
	2.863	1.243	8.335	0.831	0.695	1.291	1.166	1.675
	7.191	3.690	19.836	0.891	7.091	8.067	4.484	2.347
	5.433	2.458	3.982	3.302	3.841	0.654	0.374	0.529
	3.817	2.135	6.531	0.993	1.945	2.119	1.543	0.747
	4.409	4.053	8.332	1.155	0.636	3.177	3.656	8.508
	5.864	1.969	5.514	0.950	0.565	1.148	1.964	6.112
	2.745	1.326	6.321	1.866	1.469	4.866	1.637	7.313

Table 8: NRTIs Approved as Anti-HIV Therapies

Trade Name	Generic Name	Formulation	Std Adult Dose
Nucleoside/nucleotide reverse transcriptase inhibitors (NRTIs)			
ZIAGEN™	Abacavir	300 mg tablet	300 mg twice a day or 600 mg once a day
EMTRIVA™	Emtricitabine	200 mg capsule	200 mg once a day
EPIVIR™	Lamivudine	150 and 300 mg tablets	150 mg twice a day or 300 mg once a day
RETROVIR™	Zidovudine	100 and 250 mg capsules	100 mg 5 times a day or 250 mg twice a day
VIREAD™	Tenofovir disoproxil	245 mg tablet	245 mg once a day
NRTI fixed-dose combinations			
KIVEXA™	Abacavir / lamivudine	Tablet comprising: 600 mg abacavir and 300 mg lamivudine	One tablet once a day
TRIZIVIR™	Abacavir / lamivudine / zidovudine	Tablet comprising: 300 mg abacavir, 150 mg lamivudine and 300 mg zidovudine	One tablet once a day
TRUVADA®	Emtricitabine / tenofovir disoproxil	Tablet comprising: 200 mg emtricitabine and 245 mg tenofovir disoproxil	One tablet once a day
DESCOVY®	Emtricitabine / tenofovir alafenamide	Tablet comprising: 200 mg emtricitabine and 10 or 25 mg tenofovir alafenamide	One tablet once a day
COMBIVIR™	Lamivudine / zidovudine	Tablet comprising: 150 mg lamivudine and 300 mg zidovudine	One tablet once a day
ATRIPLA®	Efavirenz / emtricitabine / tenofovir disoproxil	Tablet comprising: 600 mg efavirenz, 200 mg emtricitabine, and 245 mg tenofovir disoproxil	One tablet once a day
EVIPLERA™	Rilpivirine / emtricitabine / tenofovir disoproxil	Tablet comprising: 25 mg rilpivirine, 200 mg emtricitabine, and 245 mg tenofovir disoproxil	One tablet once a day
ODEFSEY®	Rilpivirine / tenofovir alafenamide / emtricitabine	Tablet comprising: 25 mg rilpivirine, 25 mg tenofovir alafenamide, and 200 mg emtricitabine	One tablet once a day
GENVOYA®	Elvitegravir / cobicistat / emtricitabine / tenofovir alafenamide	Tablet comprising: 150 mg elvitegravir, 150 mg cobicistat, 200 mg emtricitabine, 10 mg tenofovir alafenamide	One tablet once a day
STRIBILD®	Elvitegravir / cobicistat / emtricitabine / tenofovir disoproxil	Tablet comprising: 150 mg elvitegravir, 150 mg cobicistat, 200 mg emtricitabine, and 245 mg tenofovir disoproxil	One tablet once a day
TRIUMEQ®	Dolutegravir / abacavir / lamivudine	Tablet comprising: 50 mg dolutegravir, 600 mg abacavir, and 300 mg lamivudine	One tablet once a day

Table 9: Lower dosage (50%) of NRTIs

Trade Name	Generic Name	Formulation	Std Adult Dose
Nucleoside/nucleotide reverse transcriptase inhibitors (NRTIs)			
ZIAGEN™	Abacavir	150 mg tablet	150 mg twice a day or 300 mg once a day
EMTRIVA™	Emtricitabine	100 mg capsule	100 mg once a day
EPIVIR™	Lamivudine	75 and 150 mg tablets	75 mg twice a day or 150 mg once a day
RETROVIR™	Zidovudine	50 and 125 mg capsules	50 mg 5 times a day or 125 mg twice a day
VIREAD™	Tenofovir disoproxil	120 mg tablet	120 mg once a day
NRTI fixed-dose combinations			
KIVEXA™	Abacavir / lamivudine	Tablet comprising: 300 mg abacavir and 150 mg lamivudine	One tablet once a day
TRIZIVIR™	Abacavir / lamivudine / zidovudine	Tablet comprising: 150 mg abacavir, 75 mg lamivudine and 150 mg zidovudine	One tablet once a day
TRUVADA®	Emtricitabine / tenofovir disoproxil	Tablet comprising: 100 mg emtricitabine and 120 mg tenofovir disoproxil	One tablet once a day
DESCOVY®	Emtricitabine / tenofovir alafenamide	Tablet comprising: 100 mg emtricitabine and 5 or 12 mg tenofovir alafenamide	One tablet once a day
COMBIVIR™	Lamivudine / zidovudine	Tablet comprising: 75 mg lamivudine and 150 mg zidovudine	One tablet once a day
ATRIPLA®	Efavirenz / emtricitabine / tenofovir disoproxil	Tablet comprising: 300 mg efavirenz, 100 mg emtricitabine, and 120 mg tenofovir disoproxil	One tablet once a day
EVIPLERA™	Rilpivirine / emtricitabine / tenofovir disoproxil	Tablet comprising: 12 mg rilpivirine, 100 mg emtricitabine, and 120 mg tenofovir disoproxil	One tablet once a day
ODEFSEY®	Rilpivirine / tenofovir alafenamide / emtricitabine	Tablet comprising: 12 mg rilpivirine, 12 mg tenofovir alafenamide, and 100 mg emtricitabine	One tablet once a day
GENVOYA®	Elvitegravir / cobicistat / emtricitabine / tenofovir alafenamide	Tablet comprising: 75 mg elvitegravir, 75 mg cobicistat, 100 mg emtricitabine, 10 mg tenofovir alafenamide	One tablet once a day
STRIBILD®	Elvitegravir / cobicistat / emtricitabine / tenofovir disoproxil	Tablet comprising: 75 mg elvitegravir, 75 mg cobicistat, 100 mg emtricitabine, and 120 mg tenofovir disoproxil	One tablet once a day
TRIUMEQ®	Dolutegravir / abacavir / lamivudine	Tablet comprising: 25 mg dolutegravir, 300 mg abacavir, and 150 mg lamivudine	One tablet once a day

Table 10: Mouse L1 activity inhibition

Compounds	IC ₅₀ (μM), n=2		
	Exp. 1	Exp. 2	Average
Lamivudine	0.958	0.780	0.869
Stavudine	1.590	1.856	1.723
Empricitabine	0.640	0.451	0.546
Apricitabine	4.442	3.825	4.134
Tenofir Disiproxil	0.157	0.151	0.154
Tenofir	3.467	4.024	3.746
Censavudine	0.118	0.105	0.112
Elvucitabine	0.116	0.106	0.111

IC₅₀ determination for nine compounds to inhibit the retrotransposition activity of active mouse LINE-1 in HeLa cells. Retrotransposition activity was determined with the dual luciferase pYX016 reporter. Cells were treated with different concentrations of each compounds and transfected with pYX016 at the same time. Luminescence was measured at 48 H post- transfection. The experiment was performed two times independently.

Table 11: Human L1 activity inhibition

Compounds	IC ₅₀ (μM), n=2		
	Exp. 1	Exp. 2	Average
Lamivudine	0.793	0.867	0.830
Censavudine	0.053	0.092	0.072
Elvucitabine	0.094	n/a	n/a

IC₅₀ determination for three compounds to inhibit the retrotransposition activity of active human LINE-1 in HeLa cells. Retrotransposition activity was determined with the dual luciferase pYX017 reporter. Cells were treated with different concentrations of each compounds and transfected with pYX017 at the same time. Luminescence was measured at 72 H post- transfection. The experiment was performed two times independently.

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[0233] All patents, patent application, and publications cited herein are fully incorporated by reference herein.

[0234] It is to be appreciated that the Detailed Description section, and not the Summary and Abstract sections, is intended to be used to interpret the claims. The Summary and Abstract sections may set forth one or more but not all exemplary embodiments of the present invention as contemplated by the inventor(s), and thus, are not intended to limit the present invention and the appended claims in any way.

[0235] The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art, readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance.

[0236] The breadth and scope of the present invention should not be limited by any of the above-described exemplary embodiments but should be defined only in accordance with the following claims and their equivalents.

Claims

1. Use of a reverse transcriptase inhibitor (RTI) in the manufacture of a medicament for treating or preventing age-associated inflammation in a patient in need thereof, wherein the RTI is censavudine or elvucitabine, wherein the age-associated inflammation is associated with an upregulation of long-interspersed element-1 (L1), an accumulation of cytoplasmic long-interspersed element-1 (L1) cDNA, an activation of a type-I interferon (IFN-I) response, or a reinforcement of a Senescence-Associated Secretory Phenotype (SASP) pro-inflammatory state.

2. The use claim 1, wherein the RTI is to be administered in an amount sufficient to prevent or reverse the upregulation of L1.

3. The use of claim 1, wherein the RTI is to be administered in an amount sufficient to prevent or reverse the accumulation of cytoplasmic L1 cDNA.

4. The use of claim 1, wherein the RTI is to be administered in an amount sufficient to prevent or reverse the activation of the IFN-I response.

5. The use of claim 1, wherein the RTI is to be administered in an amount sufficient to prevent or reverse the SASP pro-inflammatory state.

6. The use of any one of claims 1-5, wherein the age-associated inflammation is in a patient having a disease or disorder selected from the group consisting of: Alzheimer's disease, amyotrophic lateral sclerosis (ALS), Parkinson's disease, Huntington's disease, vision loss, hearing loss, peripheral degenerative diseases, or cardiovascular dysfunction, frontotemporal dementia (FTD), multiple sclerosis (MS), Aicardi Goutiere's syndrome, progressive supra nuclear palsy (PSP), osteoarthritis, skin aging, atherosclerosis, chemotherapy-induced adverse effects, hematopoietic stem cell function, osteoporosis, physical function, and pulmonary fibrosis.

7. The use of any one of claims 1-5, wherein the age-associated inflammation is in a patient having Alzheimer's disease.

8. The use of any one of claims 1-5, wherein the age-associated inflammation is in a patient having ALS.

9. The use of claim 6, wherein the patient has Alzheimer's disease or ALS and experiences a decrease in one or more symptoms of Alzheimer's disease or ALS.

10. The use of claim 9, wherein the patient has Alzheimer's disease and the one or more symptoms comprise memory loss, misplacing items, forgetting the names of places or objects, repeating questions, being less flexible, confusion, disorientation, obsessive behavior, compulsive behavior, delusions, aphasia, disturbed sleep, mood swings, depression, anxiety, frustration, agitation, difficulty in performing spatial tasks, agnosia, difficulty with ambulation, weight loss, loss of speech, loss of short term memory or loss of long term memory.

11. The use of claim 9, wherein the patient has Alzheimer's disease and the decrease in the one or more symptoms are evaluated according to the DSM-5.

12. The use of claim 9, wherein the patient has Alzheimer's disease and the decrease of symptoms is determined using the cognitive subscale of the Alzheimer's Disease Assessment Scale (ADAS-cog).

13. The use claim 9, wherein the patient has Alzheimer's disease and the decrease of symptoms is determined using the Clinician's Interview-Based Impression of Change (CIBIC-plus).

14. The use claim 9, wherein the patient has Alzheimer's disease and the decrease of symptoms is determined using the Activities of Daily Living Scale (ADL).

15. The use of any one claims 1-14, wherein the RTI is to be administered with at least one second therapeutic agent.

16. The use of claim 15, wherein the patient has Alzheimer's disease and the at least one second therapeutic agent is useful for the treatment of the symptoms of Alzheimer's disease.

17. The use of claim 15, wherein the patient has ALS and the at least one second therapeutic agent is useful for the treatment of ALS.

18. The use of any one of claims 1-5, wherein the age-associated inflammation is in a patient having FTD.

19. The use of any one of claims 1-5, wherein the age-associated inflammation is in a patient having PSP.

20. The use of any one of claims 1-5, wherein the age-associated inflammation is in a patient having AGS.

21. The use of any one of claims 1-20, wherein the RTI is censavudine.